



Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 10:54 AM JST

PDB ID : 6LT0
EMDB ID : EMD-0966
Title : cryo-EM structure of C9ORF72-SMCR8-WDR41
Authors : Tang, D.; Sheng, J.; Xu, L.; Zhan, X.; Yan, C.; Qi, S.
Deposited on : 2020-01-21
Resolution : 3.20 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

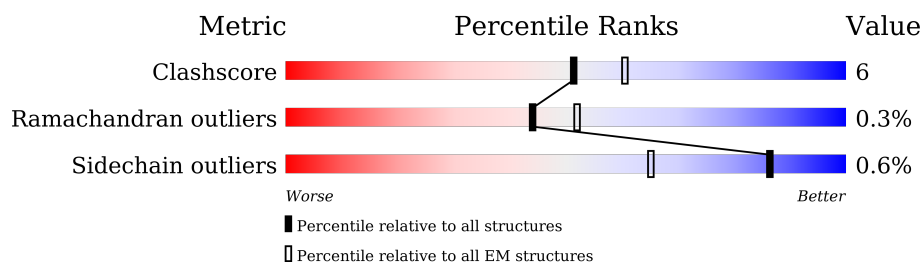
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	459	
1	D	459	
2	B	937	
2	E	937	
3	C	481	
3	F	481	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17774 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 WD repeat-containing protein 41.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	343	Total	C	N	O	S	0	0
			2693	1713	471	497	12		
1	D	343	Total	C	N	O	S	0	0
			2693	1713	471	497	12		

- Molecule 2 is a protein called Guanine nucleotide exchange protein SMCR8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3134	2026	541	551	16		
2	E	386	Total	C	N	O	S	0	0
			3134	2026	541	551	16		

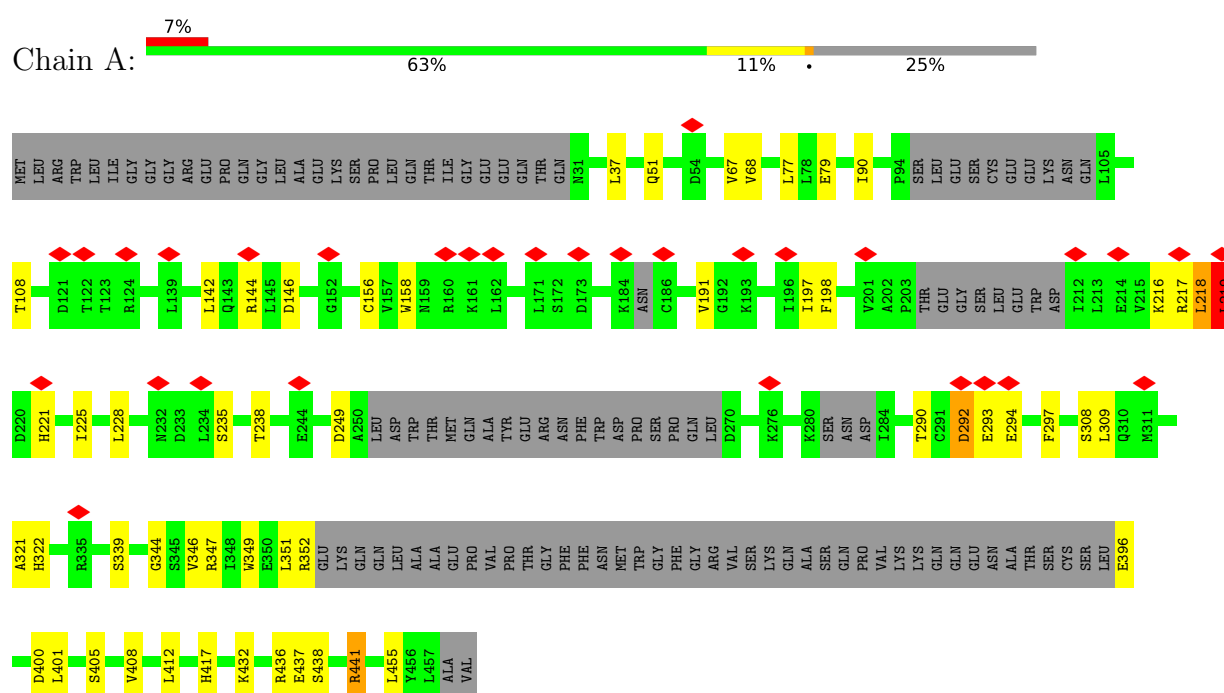
- Molecule 3 is a protein called Guanine nucleotide exchange C9orf72.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	385	Total	C	N	O	S	0	0
			3060	1980	514	550	16		
3	F	385	Total	C	N	O	S	0	0
			3060	1980	514	550	16		

3 Residue-property plots

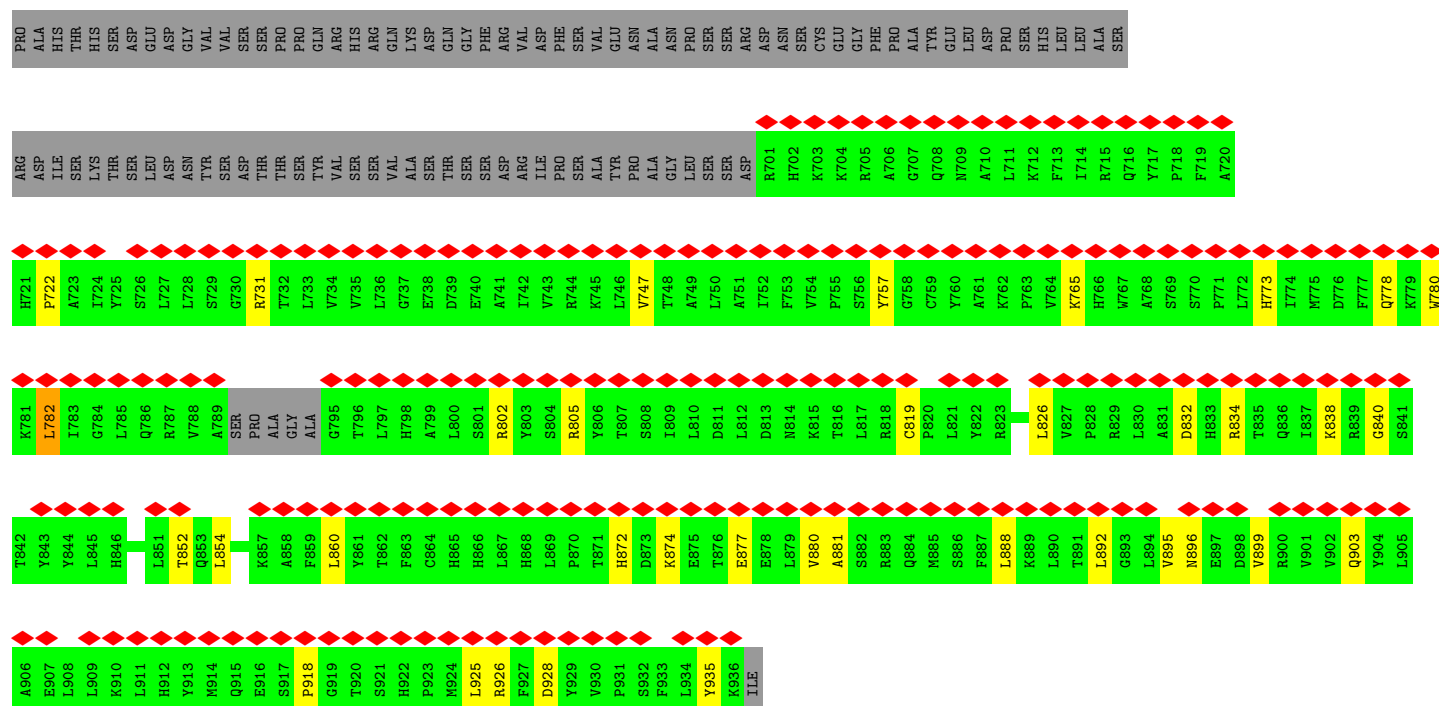
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: WD repeat-containing protein 41

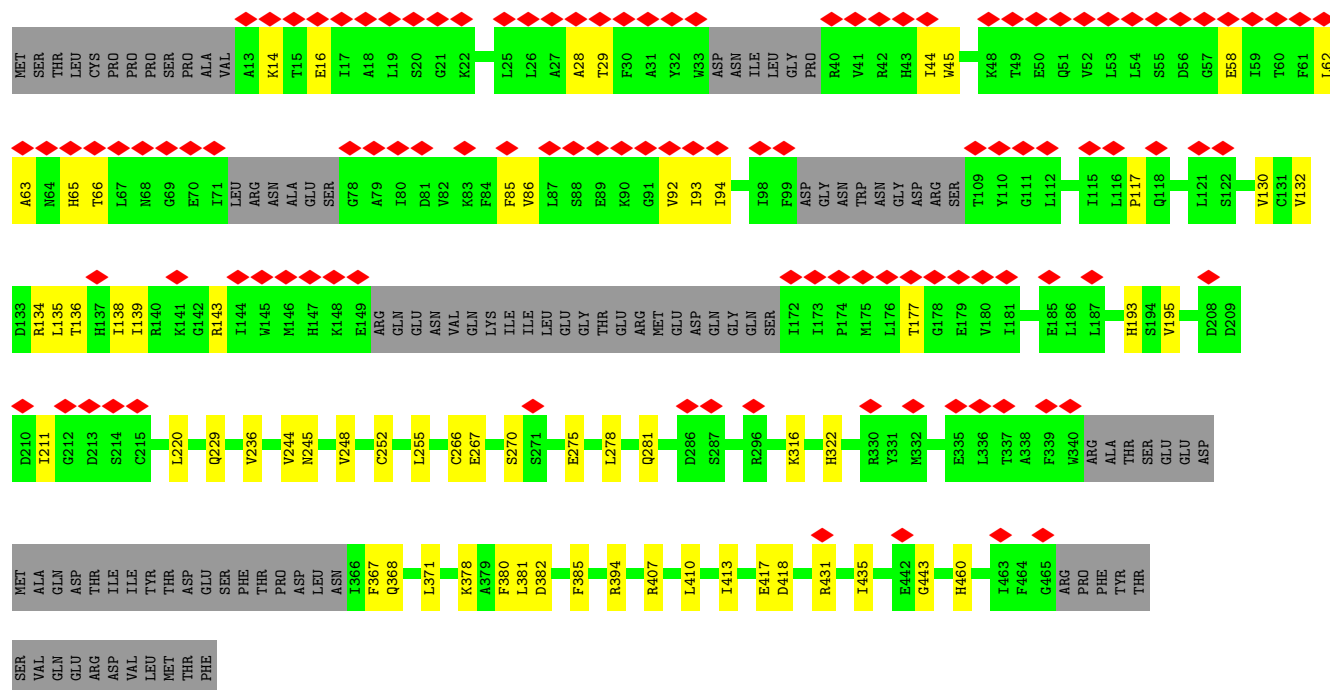


• Molecule 1: WD repeat-containing protein 41

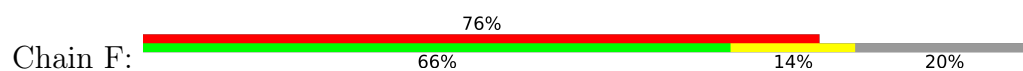




• Molecule 3: Guanine nucleotide exchange C9orf72



• Molecule 3: Guanine nucleotide exchange C9orf72



										PRO										ASP										LEU										ASN										I366										F367										Q368										D369										D309										V310										D311										T250										L251										C252										L253										F254										L255										T256										P257										A258										E259										R260										K261										S263										R264										L265										C266										E267										A268										E269										S270										S271										F272										K273										Y274										E275										S276										G277										L278										F279										V280										Q281										G282										L283										L284										K285										D286										S287										T288										G289										S290										F291										V292										L293										P294										F295										R296										Q297										V298										M299										Y300									
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	347925	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 ($e^-/\text{\AA}^2$)	5.3	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	0.145	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.026	Depositor
Map size (Å)	297.08, 297.08, 297.08	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	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	0/2735	0.67	5/3705 (0.1%)
1	D	0.31	0/2735	0.67	5/3705 (0.1%)
2	B	0.31	0/3211	0.60	1/4334 (0.0%)
2	E	0.31	0/3211	0.60	1/4334 (0.0%)
3	C	0.30	0/3122	0.59	0/4220
3	F	0.30	0/3122	0.59	1/4220 (0.0%)
All	All	0.31	0/18136	0.62	13/24518 (0.1%)

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	2
1	D	0	2
3	C	0	2
3	F	0	2
All	All	0	8

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	37	LEU	CA-CB-CG	6.36	129.93	115.30
1	A	37	LEU	CA-CB-CG	6.35	129.91	115.30
1	A	146	ASP	CB-CG-OD1	5.60	123.34	118.30
1	D	218	LEU	CA-CB-CG	5.58	128.14	115.30
1	A	218	LEU	CA-CB-CG	5.58	128.13	115.30
1	D	146	ASP	CB-CG-OD1	5.56	123.30	118.30
2	B	782	LEU	CA-CB-CG	5.40	127.72	115.30
1	D	455	LEU	CA-CB-CG	5.40	127.71	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	455	LEU	CA-CB-CG	5.38	127.69	115.30
2	E	782	LEU	CA-CB-CG	5.38	127.68	115.30
1	A	219	LEU	CA-CB-CG	5.23	127.33	115.30
1	D	219	LEU	CA-CB-CG	5.21	127.28	115.30
3	F	398	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	218	LEU	Peptide
1	A	292	ASP	Peptide
3	C	193	HIS	Peptide
3	C	195	VAL	Peptide
1	D	218	LEU	Peptide
1	D	292	ASP	Peptide
3	F	193	HIS	Peptide
3	F	195	VAL	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	2693	0	2697	28	0
1	D	2693	0	2697	27	0
2	B	3134	0	3105	47	0
2	E	3134	0	3105	34	0
3	C	3060	0	3134	46	0
3	F	3060	0	3134	59	0
All	All	17774	0	17872	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 6.

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)
2:B:834:ARG:HG2	3:F:431:ARG:NH2	1.43	1.31
3:C:431:ARG:HD3	3:F:435:ILE:CD1	1.61	1.30
2:B:896:ASN:CG	3:F:368:GLN:OE1	1.91	1.08
3:C:431:ARG:CD	3:F:435:ILE:HD12	1.85	1.05
2:B:834:ARG:O	3:F:431:ARG:NH2	1.90	1.05
2:B:834:ARG:HG2	3:F:431:ARG:CZ	1.89	1.02
3:C:431:ARG:NH2	2:E:832:ASP:OD2	1.96	0.97
2:B:896:ASN:ND2	3:F:368:GLN:OE1	2.01	0.93
2:B:834:ARG:CG	3:F:431:ARG:NH2	2.30	0.93
3:C:431:ARG:HD3	3:F:435:ILE:HD12	0.88	0.87
3:C:431:ARG:CD	3:F:435:ILE:CD1	2.53	0.80
2:E:899:VAL:O	2:E:903:GLN:HB2	1.82	0.79
2:B:899:VAL:O	2:B:903:GLN:HB2	1.82	0.79
2:B:823:ARG:HH12	3:F:319:PRO:HB3	1.49	0.78
2:B:834:ARG:C	3:F:431:ARG:HH22	1.85	0.78
2:B:369:ASN:O	2:B:373:GLU:HB3	1.89	0.72
2:E:369:ASN:O	2:E:373:GLU:HB3	1.89	0.72
2:B:834:ARG:HG2	3:F:431:ARG:HH22	1.54	0.71
1:D:322:HIS:HE2	1:D:339:SER:HG	1.38	0.70
1:A:322:HIS:HE2	1:A:339:SER:HG	1.38	0.69
3:C:371:LEU:HD13	2:E:895:VAL:HG21	1.77	0.65
2:B:823:ARG:NH1	3:F:319:PRO:HB3	2.13	0.64
1:D:156:CYS:HG	1:D:158:TRP:HE1	1.45	0.63
3:C:139:ILE:O	3:C:143:ARG:HB2	1.99	0.62
3:C:368:GLN:OE1	2:E:896:ASN:ND2	2.32	0.62
1:A:156:CYS:HG	1:A:158:TRP:HE1	1.45	0.61
2:B:757:TYR:HB3	2:B:918:PRO:HG2	1.82	0.61
3:C:275:GLU:H	3:C:281:GLN:HE22	1.49	0.61
3:F:266:CYS:SG	3:F:267:GLU:N	2.74	0.61
3:F:139:ILE:O	3:F:143:ARG:HB2	1.99	0.61
2:B:354:THR:HG21	3:C:410:LEU:HD13	1.83	0.61
2:E:757:TYR:HB3	2:E:918:PRO:HG2	1.82	0.61
3:C:266:CYS:SG	3:C:267:GLU:N	2.74	0.60
3:F:275:GLU:H	3:F:281:GLN:HE22	1.49	0.60
1:A:405:SER:HG	2:B:773:HIS:HD1	1.49	0.59
2:E:354:THR:HG21	3:F:410:LEU:HD13	1.83	0.59
2:B:159:SER:HB3	2:B:165:ILE:HD11	1.85	0.59
2:E:159:SER:HB3	2:E:165:ILE:HD11	1.85	0.58
3:F:45:TRP:HE1	3:F:177:THR:HG22	1.69	0.58
2:B:823:ARG:HH12	3:F:319:PRO:CB	2.15	0.57
3:C:29:THR:HG22	3:C:44:ILE:HG12	1.87	0.57
2:B:184:LYS:HG2	2:B:188:ARG:HH21	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:29:THR:HG22	3:F:44:ILE:HG12	1.87	0.56
2:E:184:LYS:HG2	2:E:188:ARG:HH21	1.70	0.56
3:C:45:TRP:HE1	3:C:177:THR:HG22	1.69	0.56
1:A:156:CYS:SG	1:A:158:TRP:NE1	2.79	0.55
1:A:197:ILE:HG12	1:A:217:ARG:HG2	1.89	0.55
1:D:197:ILE:HG12	1:D:217:ARG:HG2	1.89	0.54
1:D:198:PHE:HB2	1:D:216:LYS:HB3	1.90	0.54
2:B:182:CYS:O	2:B:186:GLY:HA3	2.07	0.53
2:E:182:CYS:O	2:E:186:GLY:HA3	2.07	0.53
3:C:92:VAL:HA	3:C:117:PRO:HA	1.90	0.53
1:D:156:CYS:SG	1:D:158:TRP:NE1	2.79	0.53
3:C:435:ILE:HD11	3:F:431:ARG:HD3	1.91	0.53
2:B:834:ARG:CG	3:F:431:ARG:CZ	2.74	0.53
3:F:92:VAL:HA	3:F:117:PRO:HA	1.91	0.53
1:A:198:PHE:HB2	1:A:216:LYS:HB3	1.90	0.52
1:D:344:GLY:HA2	1:D:408:VAL:HG13	1.92	0.52
1:A:344:GLY:HA2	1:A:408:VAL:HG13	1.92	0.52
3:C:371:LEU:CD1	2:E:895:VAL:HG21	2.40	0.52
1:D:51:GLN:HB2	1:D:412:LEU:HD21	1.92	0.51
1:D:437:GLU:O	1:D:441:ARG:NE	2.44	0.51
2:B:852:THR:OG1	3:C:407:ARG:NH1	2.44	0.51
2:B:860:LEU:HD23	2:B:892:LEU:HD21	1.93	0.51
3:F:278:LEU:HB2	3:F:281:GLN:HE21	1.76	0.51
2:B:872:HIS:ND1	2:B:874:LYS:O	2.44	0.51
1:A:437:GLU:O	1:A:441:ARG:NE	2.44	0.50
1:A:90:ILE:HG22	1:A:108:THR:HG23	1.93	0.50
2:E:852:THR:OG1	3:F:407:ARG:NH1	2.44	0.50
1:D:290:THR:HB	1:D:297:PHE:HB2	1.93	0.50
2:E:872:HIS:ND1	2:E:874:LYS:O	2.44	0.50
3:C:278:LEU:HB2	3:C:281:GLN:HE21	1.76	0.50
2:E:860:LEU:HD23	2:E:892:LEU:HD21	1.93	0.50
3:C:229:GLN:NE2	3:C:443:GLY:O	2.43	0.50
1:A:290:THR:HB	1:A:297:PHE:HB2	1.93	0.50
1:A:346:VAL:HB	1:A:401:LEU:HB2	1.93	0.50
3:C:14:LYS:NZ	3:C:16:GLU:OE2	2.44	0.49
1:A:51:GLN:HB2	1:A:412:LEU:HD21	1.92	0.49
2:B:838:LYS:NZ	3:C:418:ASP:O	2.38	0.49
3:C:245:ASN:HA	3:C:248:VAL:HG12	1.93	0.49
1:D:417:HIS:HB2	1:D:432:LYS:HZ1	1.77	0.49
3:F:245:ASN:HA	3:F:248:VAL:HG12	1.93	0.49
1:D:90:ILE:HG22	1:D:108:THR:HG23	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:346:VAL:HB	1:D:401:LEU:HB2	1.94	0.49
1:A:351:LEU:HD23	1:A:352:ARG:HG2	1.95	0.49
2:E:888:LEU:HD22	2:E:899:VAL:HG23	1.95	0.49
3:C:58:GLU:O	3:C:62:LEU:HB2	2.13	0.49
1:D:351:LEU:HD23	1:D:352:ARG:HG2	1.95	0.49
2:B:163:HIS:O	2:B:167:GLN:CB	2.61	0.49
3:C:58:GLU:O	3:C:62:LEU:CB	2.61	0.49
3:F:58:GLU:O	3:F:62:LEU:CB	2.61	0.48
2:B:888:LEU:HD22	2:B:899:VAL:HG23	1.95	0.48
2:E:163:HIS:O	2:E:167:GLN:CB	2.61	0.48
2:B:834:ARG:CD	3:F:431:ARG:NH2	2.76	0.48
3:F:58:GLU:O	3:F:62:LEU:HB2	2.13	0.48
3:C:130:VAL:O	3:C:134:ARG:HB2	2.13	0.48
3:F:130:VAL:O	3:F:134:ARG:HB2	2.13	0.48
2:B:765:LYS:HB2	2:B:780:TRP:CD1	2.49	0.48
3:C:28:ALA:HB3	3:C:45:TRP:HB2	1.95	0.47
1:D:405:SER:OG	2:E:773:HIS:ND1	2.43	0.47
3:F:28:ALA:HB3	3:F:45:TRP:HB2	1.95	0.47
1:A:228:LEU:HD13	1:A:238:THR:HG22	1.97	0.47
2:E:765:LYS:HB2	2:E:780:TRP:CD1	2.49	0.47
3:F:14:LYS:NZ	3:F:16:GLU:OE2	2.44	0.47
1:A:417:HIS:HB2	1:A:432:LYS:HZ2	1.78	0.47
3:F:267:GLU:OE1	3:F:270:SER:N	2.47	0.47
1:A:67:VAL:HB	1:A:79:GLU:HG2	1.97	0.47
2:B:896:ASN:OD1	3:F:368:GLN:OE1	2.32	0.47
3:C:139:ILE:O	3:C:143:ARG:CB	2.63	0.47
3:C:267:GLU:OE1	3:C:270:SER:N	2.47	0.47
3:C:431:ARG:HB3	3:F:435:ILE:HD13	1.97	0.47
1:D:228:LEU:HD13	1:D:238:THR:HG22	1.97	0.47
1:D:438:SER:HA	1:D:441:ARG:HE	1.80	0.47
2:E:877:GLU:HA	2:E:880:VAL:HG12	1.97	0.47
3:F:139:ILE:O	3:F:143:ARG:CB	2.63	0.47
1:A:68:VAL:HG23	1:A:77:LEU:HB2	1.97	0.47
3:C:316:LYS:HB3	3:C:367:PHE:HB3	1.97	0.47
2:B:722:PRO:HG3	2:B:935:TYR:HE2	1.80	0.47
3:F:229:GLN:NE2	3:F:443:GLY:O	2.43	0.47
1:A:438:SER:HA	1:A:441:ARG:HE	1.80	0.46
2:B:84:THR:HG21	2:B:338:LEU:HD22	1.96	0.46
1:D:67:VAL:HB	1:D:79:GLU:HG2	1.97	0.46
1:D:400:ASP:HB2	2:E:805:ARG:HH22	1.81	0.46
2:E:84:THR:HG21	2:E:338:LEU:HD22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:VAL:HG23	1:D:77:LEU:HB2	1.97	0.46
2:E:731:ARG:NH1	2:E:928:ASP:OD1	2.49	0.46
1:A:292:ASP:O	1:A:294:GLU:N	2.49	0.46
2:E:838:LYS:NZ	3:F:418:ASP:O	2.38	0.46
2:B:731:ARG:NH1	2:B:928:ASP:OD1	2.49	0.45
2:B:877:GLU:HA	2:B:880:VAL:HG12	1.97	0.45
1:D:292:ASP:O	1:D:294:GLU:N	2.49	0.45
3:F:316:LYS:HB3	3:F:367:PHE:HB3	1.97	0.45
3:F:236:VAL:HG22	3:F:244:VAL:HG23	1.98	0.45
3:F:63:ALA:HA	3:F:66:THR:HG22	1.98	0.45
2:E:722:PRO:HG3	2:E:935:TYR:HE2	1.80	0.45
3:C:236:VAL:HG22	3:C:244:VAL:HG23	1.98	0.45
2:E:129:LYS:HE2	2:E:158:ILE:HG12	1.99	0.45
3:F:130:VAL:O	3:F:134:ARG:CB	2.65	0.45
2:B:163:HIS:O	2:B:167:GLN:HB3	2.17	0.45
2:B:362:LEU:HD23	2:B:365:GLN:HE21	1.82	0.45
1:A:219:LEU:HD23	1:A:221:HIS:H	1.83	0.44
3:C:130:VAL:O	3:C:134:ARG:CB	2.65	0.44
1:D:219:LEU:HD23	1:D:221:HIS:H	1.83	0.44
1:A:400:ASP:HB2	2:B:805:ARG:HH22	1.81	0.44
2:B:129:LYS:HE2	2:B:158:ILE:HG12	1.99	0.44
3:C:435:ILE:CD1	3:F:431:ARG:HD3	2.47	0.44
2:E:163:HIS:O	2:E:167:GLN:HB3	2.17	0.44
3:C:63:ALA:HA	3:C:66:THR:HG22	1.99	0.44
3:F:135:LEU:HA	3:F:138:ILE:HD12	1.99	0.44
3:C:135:LEU:HA	3:C:138:ILE:HD12	1.99	0.44
3:C:252:CYS:HA	3:C:255:LEU:HD13	2.00	0.44
3:F:322:HIS:HB3	3:F:460:HIS:HB3	2.00	0.44
2:B:747:VAL:HG13	2:B:782:LEU:HD11	1.99	0.44
2:B:778:GLN:HA	2:B:925:LEU:HD12	2.00	0.44
3:C:322:HIS:HB3	3:C:460:HIS:HB3	2.00	0.44
3:F:252:CYS:HA	3:F:255:LEU:HD13	2.00	0.44
3:F:380:PHE:HD2	3:F:381:LEU:HD12	1.83	0.43
2:B:826:LEU:HD11	2:B:854:LEU:HD13	2.01	0.43
2:E:362:LEU:HD23	2:E:365:GLN:HE21	1.82	0.43
2:E:826:LEU:HD11	2:E:854:LEU:HD13	2.01	0.43
1:A:235:SER:HA	1:A:249:ASP:HA	2.01	0.43
2:E:98:ASP:HA	2:E:101:ALA:HB3	2.00	0.43
1:D:235:SER:HA	1:D:249:ASP:HA	2.00	0.43
2:E:747:VAL:HG13	2:E:782:LEU:HD11	1.99	0.43
1:A:405:SER:OG	2:B:773:HIS:ND1	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:380:PHE:HD2	3:C:381:LEU:HD12	1.83	0.43
3:C:385:PHE:HA	3:C:394:ARG:HH22	1.84	0.43
1:A:321:ALA:O	1:A:347:ARG:NH1	2.52	0.43
2:B:98:ASP:HA	2:B:101:ALA:HB3	2.01	0.43
2:E:778:GLN:HA	2:E:925:LEU:HD12	2.00	0.43
3:F:378:LYS:O	3:F:382:ASP:HB2	2.19	0.42
2:E:722:PRO:HB2	2:E:819:CYS:SG	2.60	0.42
3:F:413:ILE:O	3:F:417:GLU:HB2	2.20	0.42
1:A:191:VAL:HG11	1:A:225:ILE:HB	2.01	0.42
2:B:722:PRO:HB2	2:B:819:CYS:SG	2.60	0.42
1:D:321:ALA:O	1:D:347:ARG:NH1	2.52	0.42
3:C:62:LEU:HA	3:C:65:HIS:HD2	1.85	0.42
3:C:378:LYS:O	3:C:382:ASP:HB2	2.19	0.42
3:F:385:PHE:HA	3:F:394:ARG:HH22	1.84	0.42
3:C:86:VAL:HG13	3:C:93:ILE:HG12	2.03	0.41
1:D:191:VAL:HG11	1:D:225:ILE:HB	2.01	0.41
2:E:877:GLU:O	2:E:881:ALA:HB3	2.20	0.41
3:F:62:LEU:HA	3:F:65:HIS:HD2	1.85	0.41
3:C:413:ILE:O	3:C:417:GLU:HB2	2.20	0.41
3:F:86:VAL:HG13	3:F:93:ILE:HG12	2.02	0.41
3:F:85:PHE:HB3	3:F:94:ILE:HB	2.03	0.41
3:F:211:ILE:HG13	3:F:220:LEU:HD23	2.03	0.41
3:C:211:ILE:HG13	3:C:220:LEU:HD23	2.03	0.41
3:F:132:VAL:O	3:F:136:THR:OG1	2.31	0.41
3:F:80:ILE:HG22	3:F:97:LEU:HD22	2.03	0.41
1:A:308:SER:OG	1:A:309:LEU:N	2.53	0.41
2:B:164:LYS:HA	2:B:349:LEU:HD23	2.03	0.41
2:B:877:GLU:O	2:B:881:ALA:HB3	2.20	0.41
3:C:132:VAL:O	3:C:136:THR:OG1	2.31	0.41
3:F:80:ILE:HG12	3:F:139:ILE:HG21	2.03	0.41
1:D:349:TRP:HD1	1:D:396:GLU:HG2	1.86	0.41
2:B:184:LYS:O	2:B:188:ARG:HB3	2.21	0.40
2:E:184:LYS:O	2:E:188:ARG:HB3	2.21	0.40
2:B:722:PRO:HA	2:B:725:TYR:HB3	2.03	0.40
1:D:277:LEU:HD21	1:D:307:TYR:CD1	2.57	0.40
1:A:349:TRP:HD1	1:A:396:GLU:HG2	1.86	0.40
1:A:142:LEU:HG	1:A:144:ARG:H	1.87	0.40
3:C:85:PHE:HB3	3:C:94:ILE:HB	2.03	0.40
1:D:308:SER:OG	1:D:309:LEU:N	2.53	0.40
3:F:321:CYS:HA	3:F:324:HIS:HB3	2.04	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	329/459 (72%)	277 (84%)	50 (15%)	2 (1%)	25	64
1	D	329/459 (72%)	277 (84%)	50 (15%)	2 (1%)	25	64
2	B	370/937 (40%)	315 (85%)	54 (15%)	1 (0%)	41	74
2	E	370/937 (40%)	315 (85%)	54 (15%)	1 (0%)	41	74
3	C	373/481 (78%)	334 (90%)	39 (10%)	0	100	100
3	F	373/481 (78%)	334 (90%)	39 (10%)	0	100	100
All	All	2144/3754 (57%)	1852 (86%)	286 (13%)	6 (0%)	44	74

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	GLU
1	D	293	GLU
2	B	840	GLY
2	E	840	GLY
1	A	219	LEU
1	D	219	LEU

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	298/405 (74%)	296 (99%)	2 (1%)	84	94
1	D	298/405 (74%)	296 (99%)	2 (1%)	84	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	339/837 (40%)	335 (99%)	4 (1%)	71	88
2	E	339/837 (40%)	335 (99%)	4 (1%)	71	88
3	C	344/431 (80%)	344 (100%)	0	100	100
3	F	344/431 (80%)	344 (100%)	0	100	100
All	All	1962/3346 (59%)	1950 (99%)	12 (1%)	86	94

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	436	ARG
1	A	441	ARG
2	B	95	MET
2	B	802	ARG
2	B	834	ARG
2	B	926	ARG
1	D	436	ARG
1	D	441	ARG
2	E	95	MET
2	E	802	ARG
2	E	834	ARG
2	E	926	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	HIS
2	B	106	HIS
2	B	137	HIS
2	B	814	ASN
2	B	896	ASN
3	C	281	GLN
1	D	83	HIS
2	E	106	HIS
2	E	137	HIS
2	E	814	ASN
3	F	281	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 monosaccharides 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.

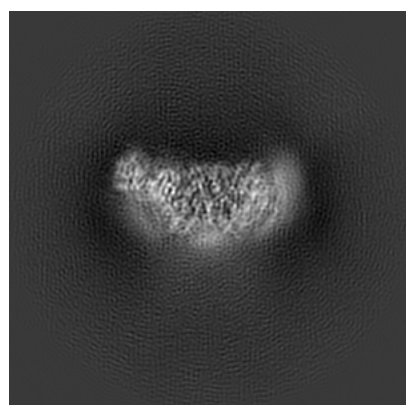
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0966. These allow visual inspection of the internal detail of the map and identification of artifacts.

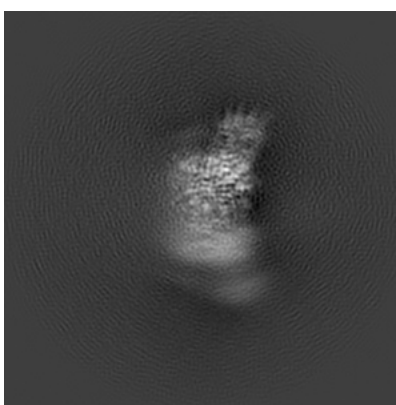
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

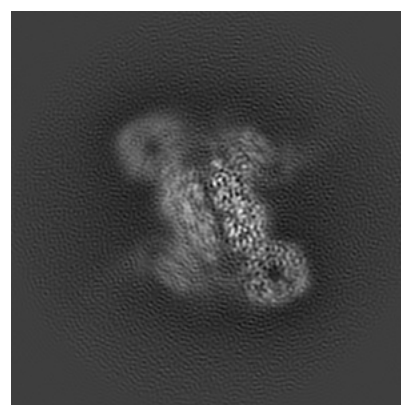
6.1.1 Primary map



X



Y

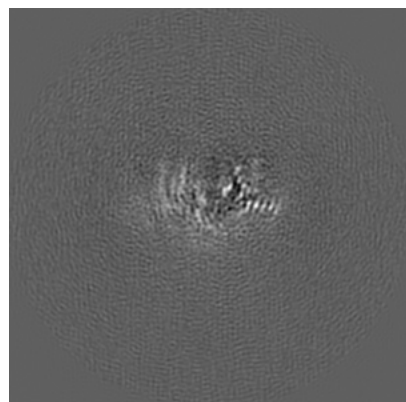


Z

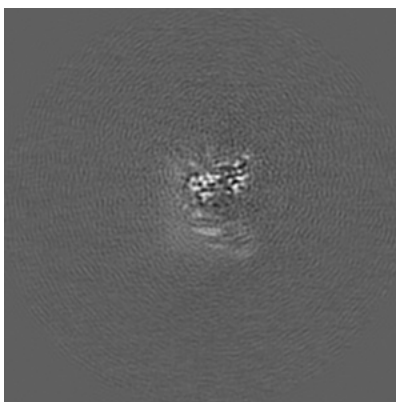
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

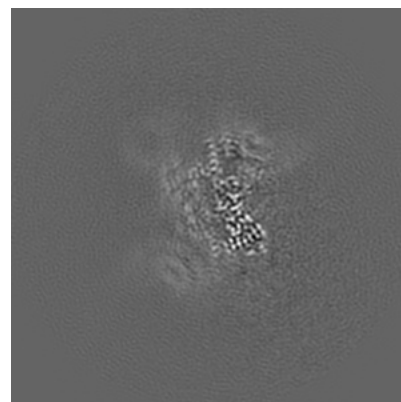
6.2.1 Primary map



X Index: 140



Y Index: 140

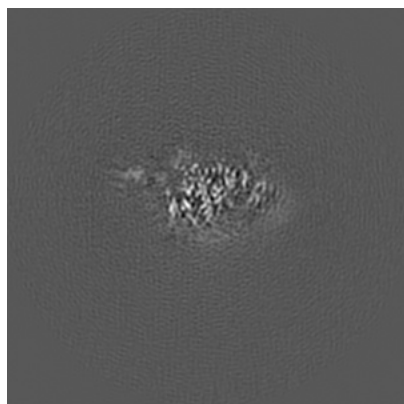


Z Index: 140

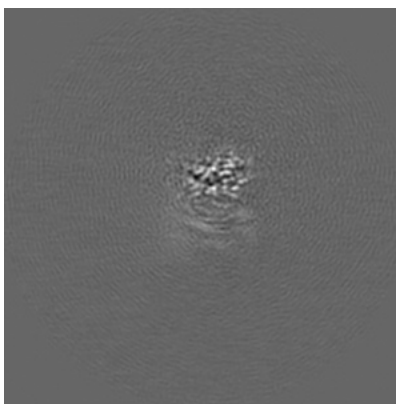
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

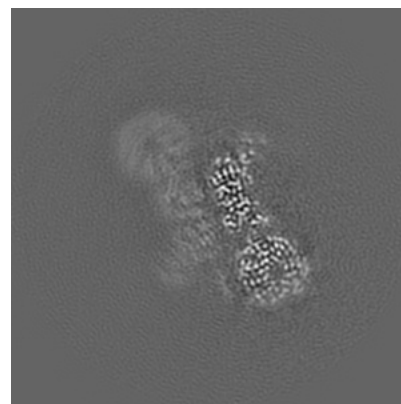
6.3.1 Primary map



X Index: 159



Y Index: 130



Z Index: 159

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

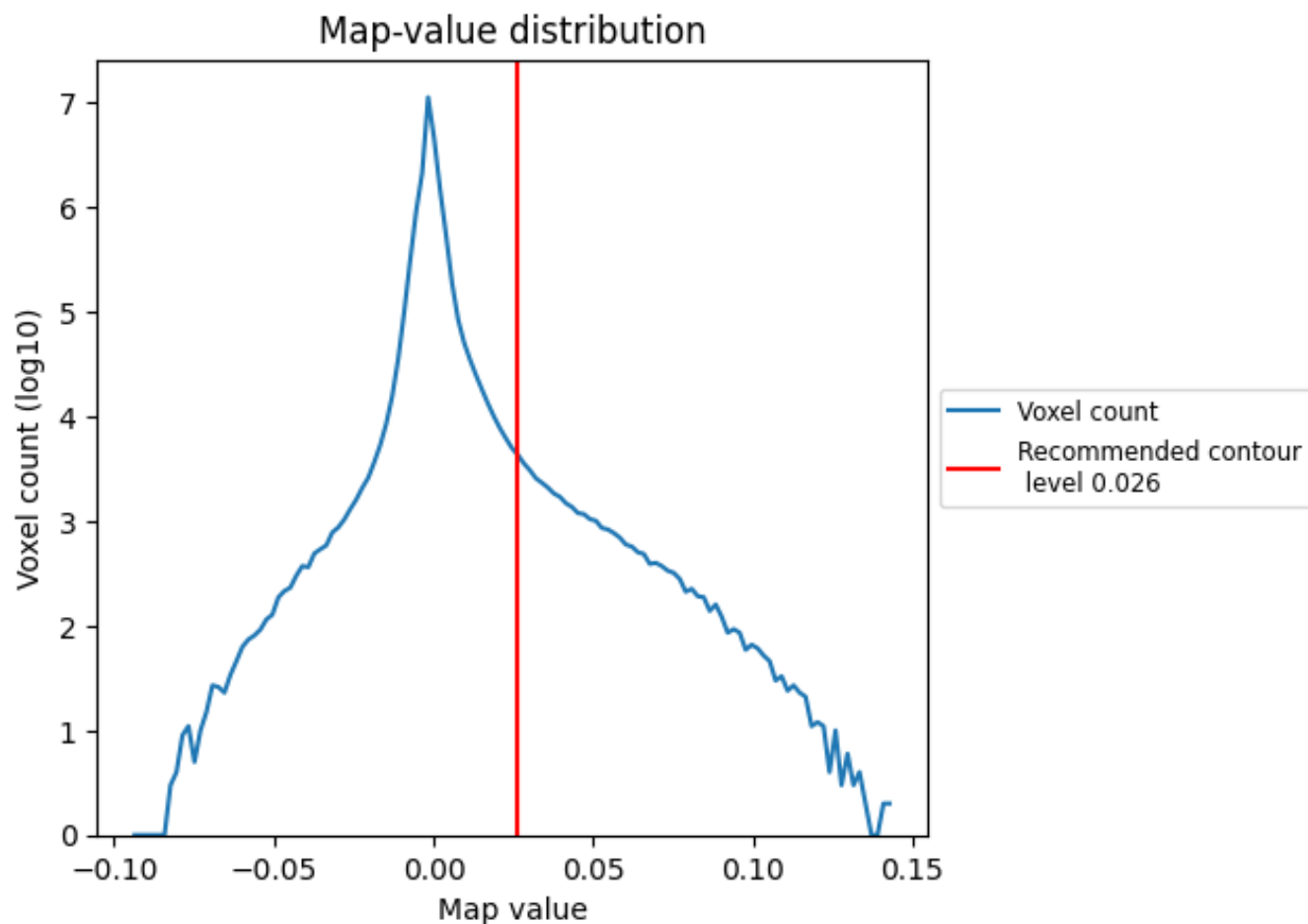
6.5 Mask visualisation

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

7 Map analysis [i](#)

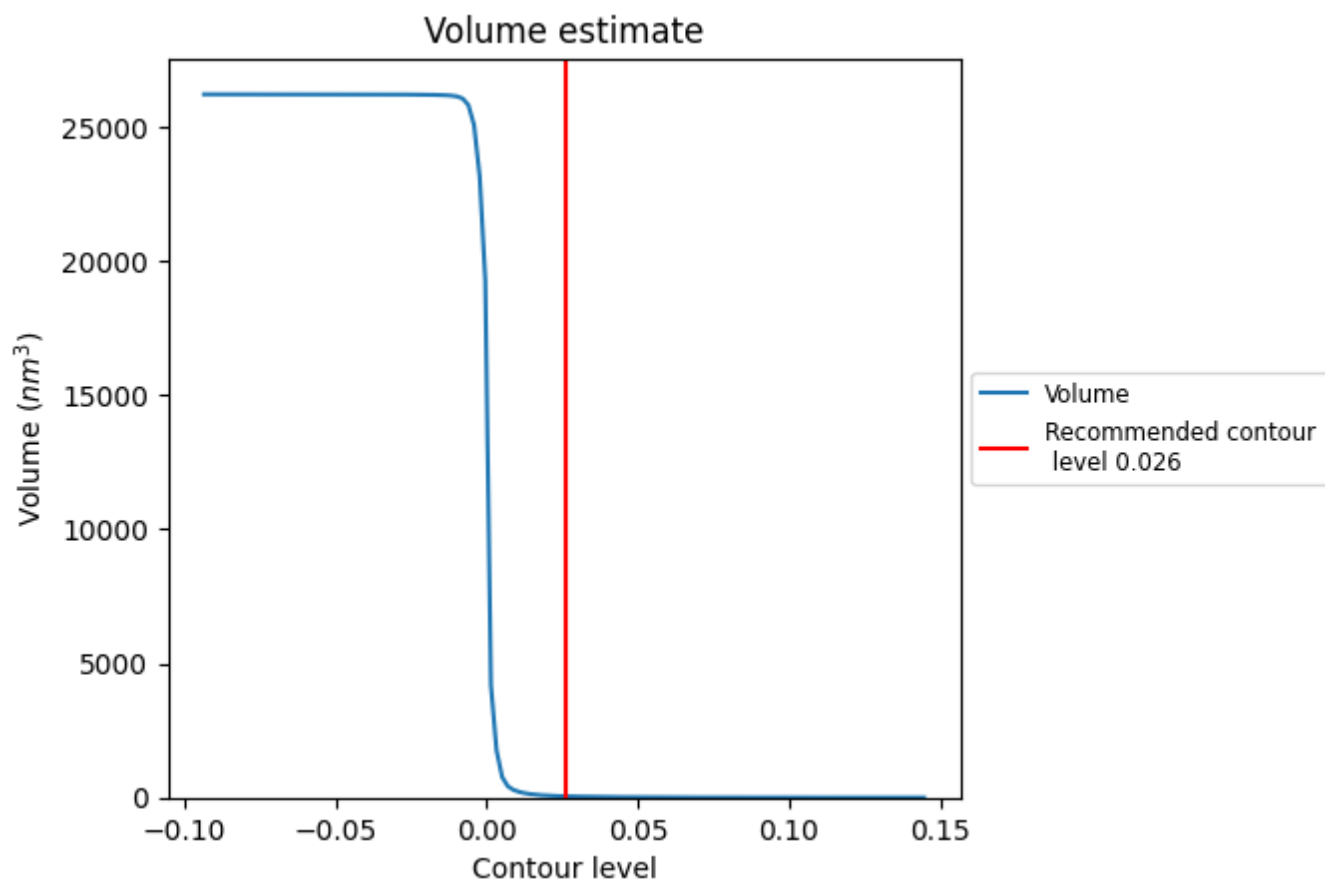
This section contains the results of statistical analysis of the map.

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.

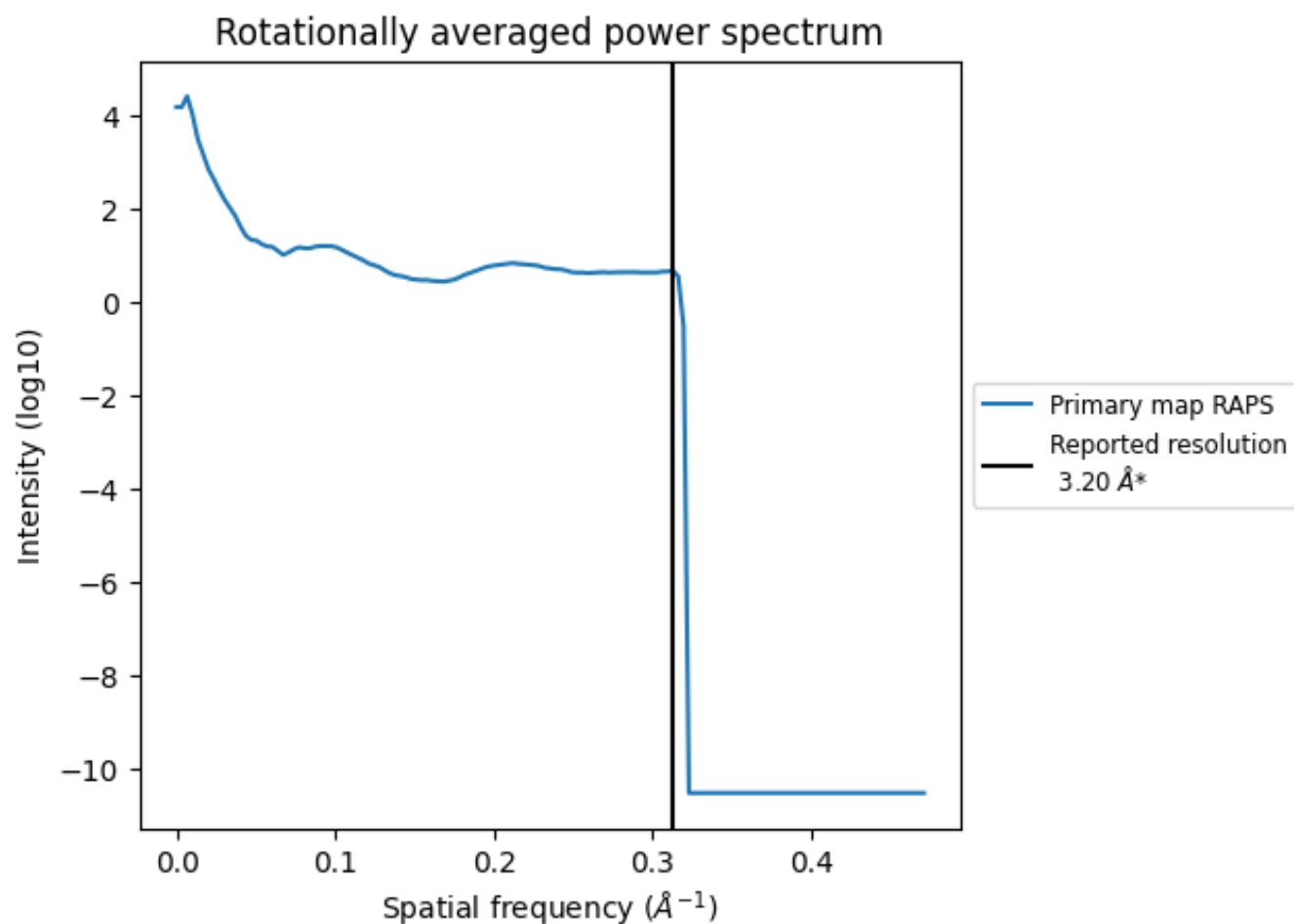
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 47 nm³; this corresponds to an approximate mass of 43 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 0.312 Å⁻¹

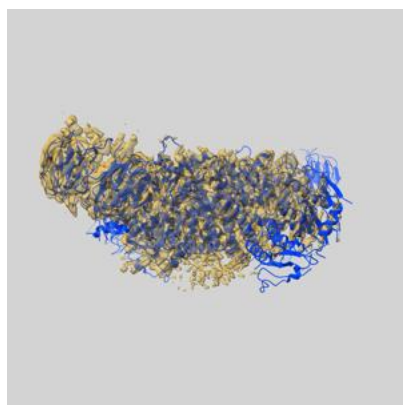
8 Fourier-Shell correlation

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

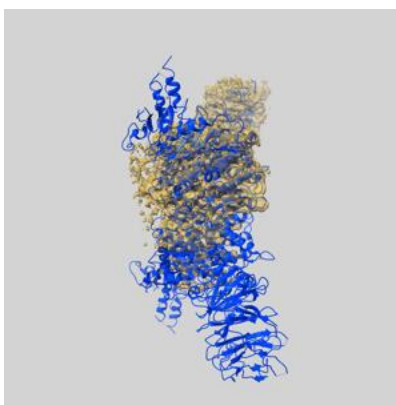
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0966 and PDB model 6LT0. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

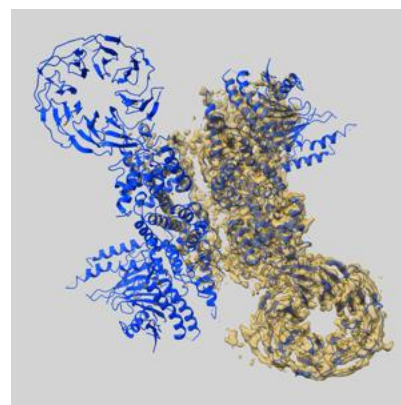
9.1 Map-model overlay [i](#)



X



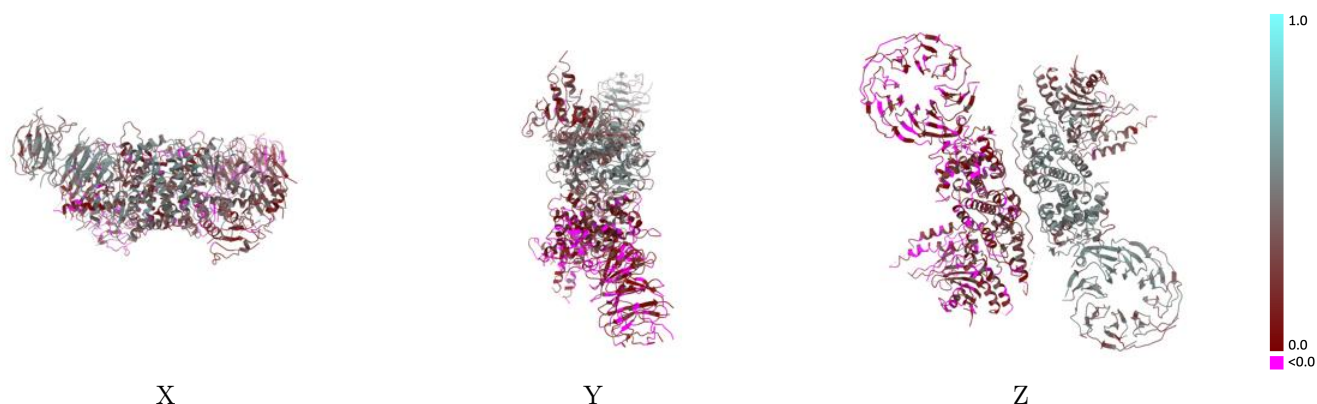
Y



Z

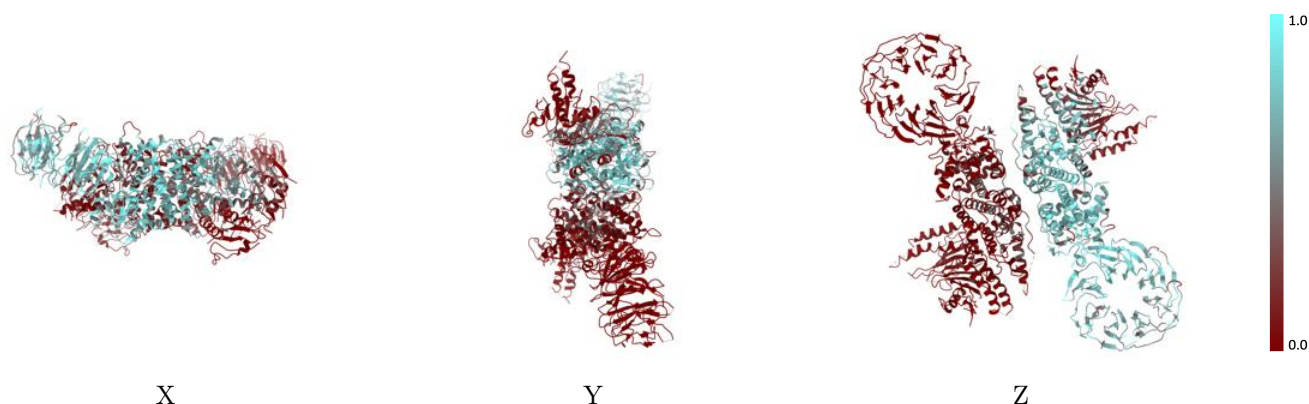
The images above show the 3D surface view of the map at the recommended contour level 0.026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



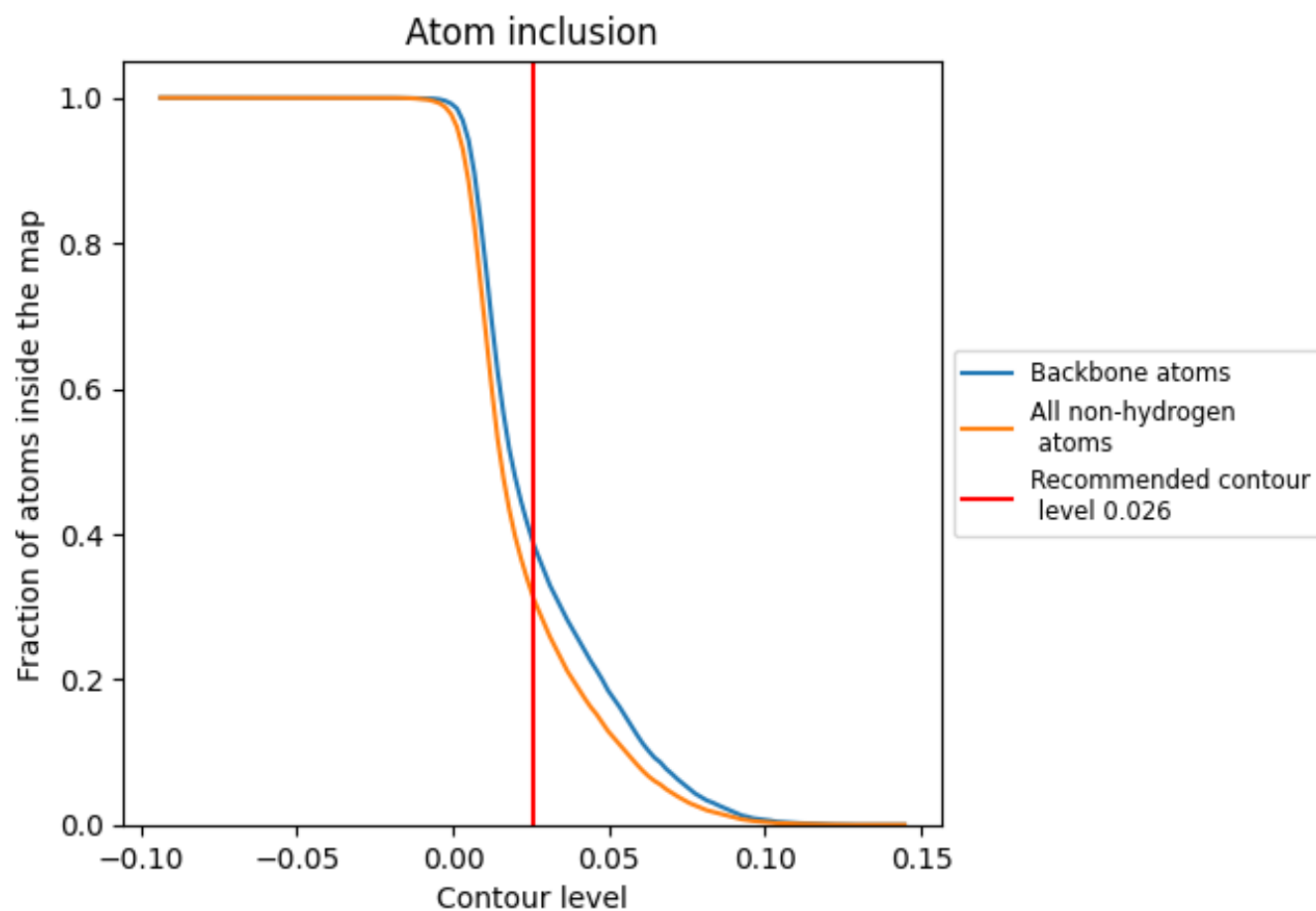
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 38% of all backbone atoms, 31% 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 (0.026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.3096	<div></div> 0.2600
A	<div></div> 0.6849	<div></div> 0.4600
B	<div></div> 0.5129	<div></div> 0.4030
C	<div></div> 0.5476	<div></div> 0.4170
D	<div></div> 0.0004	<div></div> 0.0590
E	<div></div> 0.0525	<div></div> 0.0690
F	<div></div> 0.0684	<div></div> 0.1540

1.0

0.0

<0.0