



Full wwPDB EM Validation Report ⓘ

Mar 15, 2026 – 01:50 AM UTC

PDB ID : 8X06 / pdb_00008x06
EMDB ID : EMD-37970
Title : Cryo-EM structure of the IR/IGF-I complex, conformation 1
Authors : Xi, Z.
Deposited on : 2023-11-03
Resolution : 3.24 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

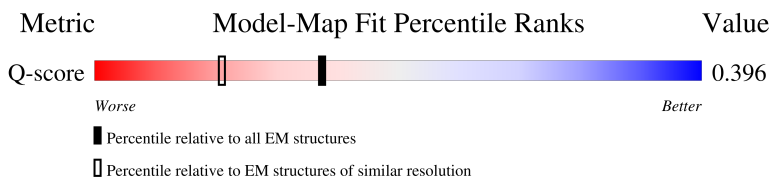
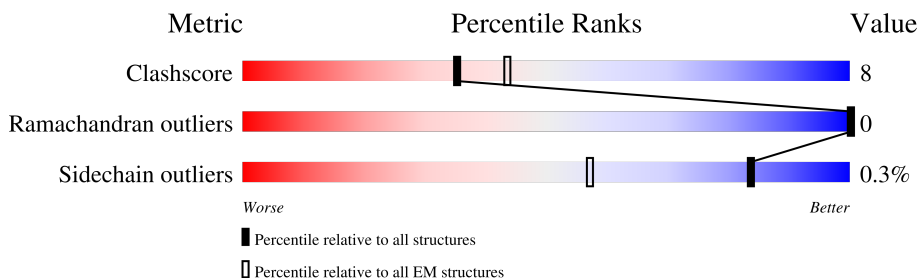
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.24 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	14594 (2.74 - 3.74)

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	1370	 32% 7% 61%
1	B	1370	 15% 81%
2	C	195	 16% 7% 76%
2	D	195	 13% 83%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7053 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 Isoform Short of Insulin receptor.

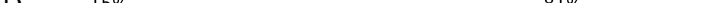
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	536	Total	C	N	O	S	0	0
			4320	2750	740	789	41		
1	B	254	Total	C	N	O	S	0	0
			2113	1372	354	381	6		

- Molecule 2 is a protein called Insulin-like growth factor I.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	46	Total	C	N	O	S	0	0
			359	225	60	67	7		
2	D	33	Total	C	N	O	S	0	0
			261	167	43	46	5		

GLY	THR	PHE	ALA	VAL	ARG
ARG	PHE	GLY	ARG	MET	GLN
ASP	LEU	VAL	ASN	GLU	PRO
GLY	GLU	VAL	CYS	ILE	ASP
SER	ILE	VAL	MET	ALA	GLY
SER	ASN	GLU	ALA	HIS	PRO
LEU	ILE	ILE	HIS	GLY	LEU
GLY	LEU	THR	ASP	ASP	GLY
PHE	LYS	SER	PHE	LEU	PRO
ARG	ASP	LEU	THR	LYS	LEU
LYS	ASP	ALA	VAL	SER	THR
SER	LEU	GLU	LYS	TYR	ALA
TYR	PRO	GLN	ILE	LEU	SER
GLU	PRO	PRO	GLY	ARG	ASN
HIS	PHE	GLY	PHE	LEU	GLY
ILE	PRO	GLY	GLY	PRO	GLU
PRO	GLU	LEU	MET	PRO	TYR
THR	GLU	SER	THR	ASN	GLY
HIS	PHE	GLU	ASP	ALA	SER
HIS	PHE	GLN	ILE	ASN	ASP
MET	PHE	VAL	TYR	ASN	VAL
ASN	HIS	LEU	GLY	PRO	VAL
GLY	SER	LEU	GLU	ARG	PHE
GLY	GLU	GLY	THR	GLY	PRO
LYS	GLY	PHE	ASP	ARG	CYS
LYS	ASN	VAL	TYR	PRO	SER
ASN	LYS	VAL	TYR	PRO	VAL
GLY	ALA	ASP	ARG	PRO	TYR
ARG	PRO	GLY	LYS	THR	VAL
ILE	GLU	GLY	GLY	LEU	PRO
LEU	SER	TYR	GLY	GLN	ASP
THR	GLU	LEU	LYS	GLU	GLU
LEU	GLU	ASP	GLY	MET	TRP
PRO	LEU	GLN	LEU	ILE	GLU
ARG	GLU	PRO	LEU	GLN	VAL
PRO	MET	ASN	PRO	MET	VAL
SER	GLY	ASP	PRO	GLY	SER
ASN	ASN	VAL	VAL	ALA	ARG
PRO	PHE	CYS	ARG	ALA	GLU
SER	GLU	PRO	TRP	GLU	LYS
	ASP	GLU	MET	ILE	ILE
	MET	ARG	ALA	ALA	THR
	GLU	VAL	PRO	ASP	LEU
	ASN	THR	GLU	GLY	LEU
	VAL	ASP	SER	MET	ARG
	PRO	LEU	LEU	ALA	GLU
	LEU	MET	LYS	TYR	LEU
	ASP	ARG	ASP	LEU	GLY
	ARG	MET	GLY	ASN	GLN
	SER	TRP	VAL	VAL	GLY
	HIS	GLN	PHE	LYS	SER
	CYS	PHE	THR	LYS	PHE
	GLN	ASN	SER	THR	GLY
	ARG	PRO	SER	HIS	VAL
	GLU	GLU	ASP	ARG	THR
	GLU	MET	MET	ASP	GLU
	ALA	ARG	TRP	LEU	ASN
	GLY	PRO	SER	ALA	GLY

- Molecule 1: Isoform Short of Insulin receptor

Chain B:  15% 81%

[illegible]

- Molecule 2: Insulin-like growth factor I

[illegible]

- Molecule 2: Insulin-like growth factor I



MET	GLY	LYS	ILE	SER	SER	LEU	PRO	THR	GLN	LEU	PHE	LYS	CYS	CYS	PHE	CYS	ASP	PHE	LEU	LYS	VAL	LYS	MET	HIS	THR	MET	SER	SER	SER	HIS	LEU	PHE	TYR	LEU	ALA	ALA	CYS	LEU	LEU	THR	PHE	THR	SER	SER	ALA	ALA	GLY	PRO	GLU	THR	L5	C6	G7	A8	V17	C18
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	148388	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.325	Depositor
Minimum map value	-0.144	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	337.92, 337.92, 337.92	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.66, 0.66, 0.66	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	A	0.12	0/4416	0.32	0/5970
1	B	0.13	0/2159	0.32	0/2909
2	C	0.12	0/364	0.35	0/488
2	D	0.15	0/264	0.47	0/351
All	All	0.12	0/7203	0.33	0/9718

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	A	4320	0	4215	64	0
1	B	2113	0	2080	32	0
2	C	359	0	331	11	0
2	D	261	0	242	6	0
All	All	7053	0	6868	110	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (110) 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:B:562:ARG:HH12	1:B:564:TYR:HB2	1.55	0.71
1:A:469:GLU:HG3	1:A:582:LYS:HB2	1.77	0.65
1:A:57:ILE:HB	1:A:82:ILE:HG12	1.79	0.64
1:B:760:VAL:HG21	1:B:769:TYR:HB2	1.80	0.64
1:B:621:ASN:HB2	1:B:624:LEU:HB2	1.81	0.62
2:C:59:MET:SD	2:C:59:MET:N	2.70	0.62
1:A:505:LEU:HD21	1:A:564:ILE:HG23	1.81	0.61
1:A:294:MET:HA	1:A:294:MET:HE2	1.84	0.59
1:A:118:ARG:NH1	1:A:120:GLU:OE1	2.36	0.59
2:C:56:ARG:O	2:C:56:ARG:NE	2.32	0.58
2:C:20:ASP:OD2	2:C:20:ASP:N	2.37	0.58
1:B:625:CYS:SG	1:B:626:LEU:N	2.78	0.57
2:D:17:VAL:HG11	2:D:57:LEU:HB3	1.87	0.56
2:D:21:ARG:NH2	2:D:58:GLU:O	2.38	0.56
1:A:300:LEU:H	1:A:300:LEU:HD12	1.71	0.55
1:B:655:GLN:N	1:B:655:GLN:OE1	2.39	0.55
1:A:508:LYS:HD3	1:A:529:TRP:H	1.71	0.55
2:D:21:ARG:HD2	2:D:63:PRO:HA	1.87	0.55
1:B:524:THR:HG23	1:B:525:VAL:HG23	1.88	0.54
1:A:405:ASN:HD22	1:A:408:LEU:HD22	1.72	0.54
2:C:17:VAL:HG21	2:C:57:LEU:HD11	1.90	0.54
1:B:604:TRP:CD1	1:B:631:LYS:HG2	2.42	0.54
1:A:81:VAL:HG21	1:A:213:LEU:HD13	1.90	0.54
1:A:41:THR:OG1	1:A:67:TYR:O	2.26	0.53
1:A:135:ARG:HH12	1:A:191:VAL:HA	1.74	0.53
1:A:199:HIS:HB3	1:A:210:SER:HA	1.91	0.52
1:A:16:ASN:OD1	1:A:19:ARG:NH2	2.41	0.52
1:B:560:ILE:HB	1:B:592:ALA:HA	1.92	0.51
1:B:572:PHE:HD2	1:B:602:TRP:HZ2	1.58	0.51
1:A:93:LEU:HB3	1:A:117:VAL:HG22	1.93	0.51
1:B:534:ILE:HG12	1:B:544:LEU:HD21	1.91	0.50
1:A:431:ASN:HB3	1:A:434:LEU:HB3	1.92	0.50
1:A:141:GLU:OE2	1:A:141:GLU:N	2.40	0.50
1:B:697:TYR:O	1:B:720:THR:OG1	2.29	0.50
1:A:13:ILE:HD12	1:A:35:ILE:HG12	1.93	0.50
1:B:774:ASP:N	1:B:774:ASP:OD1	2.44	0.50
1:A:508:LYS:HE2	1:A:529:TRP:HE3	1.77	0.49
1:A:336:ILE:O	1:A:365:SER:OG	2.31	0.49
1:A:369:LYS:HG3	1:A:401:TYR:HB3	1.95	0.49
1:A:321:ILE:HG23	1:A:326:SER:HB2	1.95	0.49
1:A:11:MET:SD	1:A:11:MET:N	2.86	0.48
1:B:695:LEU:HB3	1:B:722:VAL:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:21:ARG:HH21	2:C:63:PRO:HA	1.79	0.48
1:A:443:GLU:OE2	1:A:455:ASN:ND2	2.47	0.48
1:A:101:LEU:HD23	1:A:125:LEU:HD13	1.95	0.47
1:B:676:LEU:HB2	1:B:742:LEU:HD13	1.96	0.47
1:A:118:ARG:HG3	1:A:144:TYR:HB3	1.96	0.47
1:A:151:ASP:OD2	1:A:151:ASP:N	2.41	0.47
1:A:97:GLU:HG2	1:A:121:LYS:HD2	1.97	0.47
1:A:208:CYS:HB3	1:A:219:PRO:HA	1.95	0.47
1:A:98:MET:HE3	1:A:99:VAL:H	1.79	0.47
2:C:55:ARG:HA	2:C:55:ARG:NH1	2.30	0.47
2:D:20:ASP:OD1	2:D:20:ASP:N	2.48	0.47
1:A:480:THR:OG1	1:A:481:SER:N	2.47	0.46
2:D:21:ARG:HB2	2:D:61:CYS:HB2	1.96	0.46
1:B:781:ASP:N	1:B:781:ASP:OD1	2.48	0.46
1:A:146:VAL:HG21	1:B:892:ARG:HE	1.80	0.46
1:A:401:TYR:HA	1:A:427:PHE:HB3	1.98	0.46
2:C:11:VAL:O	2:C:14:LEU:HB2	2.16	0.46
1:A:183:TRP:CD1	1:A:189:GLN:HG2	2.51	0.45
1:A:268:ASN:OD1	1:A:268:ASN:N	2.49	0.45
1:A:202:THR:OG1	1:A:203:ALA:N	2.48	0.45
1:A:243:PRO:N	1:A:244:PRO:HD2	2.32	0.45
2:C:7:GLY:O	2:C:10:LEU:HB3	2.17	0.45
2:C:55:ARG:HH22	2:C:58:GLU:HG2	1.81	0.44
1:A:92:ALA:HB2	1:A:115:GLY:HA3	1.99	0.44
1:B:559:LYS:HG2	1:B:591:TYR:HB3	2.00	0.44
1:A:79:LEU:HD23	1:A:106:LEU:HD22	1.99	0.44
1:A:208:CYS:HA	1:A:220:ASP:H	1.82	0.44
1:A:473:LEU:HD21	1:A:492:TYR:HB2	2.00	0.44
1:A:210:SER:O	1:A:229:ARG:NH1	2.51	0.44
1:B:574:LYS:O	1:B:607:HIS:NE2	2.51	0.44
1:A:126:CYS:HB3	1:A:149:LYS:HB3	1.99	0.44
1:A:453:GLU:OE2	1:A:455:ASN:ND2	2.51	0.44
1:A:403:LEU:HD12	1:A:403:LEU:HA	1.86	0.43
1:A:353:GLU:O	1:A:357:ASN:ND2	2.51	0.43
1:B:747:LYS:O	1:B:750:THR:OG1	2.29	0.43
1:B:693:PHE:HE2	1:B:727:PRO:HD3	1.83	0.43
2:D:18:CYS:HB2	2:D:21:ARG:HG3	2.00	0.43
1:B:515:THR:OG1	1:B:516:SER:N	2.52	0.43
1:B:747:LYS:HA	1:B:747:LYS:HD3	1.78	0.43
1:A:66:VAL:HB	1:A:98:MET:HE1	2.01	0.43
1:A:318:GLU:HA	1:A:339:SER:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:584:ASP:N	1:A:584:ASP:OD1	2.50	0.43
1:B:631:LYS:O	1:B:631:LYS:HG3	2.17	0.43
1:A:56:MET:HE2	1:A:56:MET:HB2	1.95	0.42
1:A:557:LYS:O	1:A:560:THR:OG1	2.36	0.42
2:C:55:ARG:HA	2:C:55:ARG:CZ	2.49	0.42
1:A:135:ARG:NH2	1:A:192:CYS:O	2.52	0.42
1:B:604:TRP:HA	1:B:604:TRP:CE3	2.55	0.42
1:A:250:ASP:O	1:A:252:ARG:N	2.53	0.41
1:A:48:ASP:OD1	1:A:48:ASP:N	2.52	0.41
1:A:443:GLU:HB3	1:A:449:LYS:HG2	2.02	0.41
1:B:544:LEU:H	1:B:544:LEU:HD12	1.84	0.41
1:A:73:LYS:N	1:A:105:GLY:HA3	2.36	0.41
1:A:90:ASN:ND2	1:A:90:ASN:O	2.54	0.41
1:A:393:LEU:HD23	1:A:393:LEU:HA	1.88	0.41
1:A:470:ASN:O	1:A:470:ASN:ND2	2.54	0.41
1:B:555:SER:O	1:B:555:SER:OG	2.32	0.41
2:C:59:MET:HB2	1:B:907:ARG:HB2	2.02	0.41
1:A:489:TRP:HH2	1:A:534:ILE:HD13	1.86	0.41
1:B:626:LEU:HB3	1:B:630:HIS:NE2	2.36	0.41
1:A:65:ARG:NH1	1:A:97:GLU:OE1	2.54	0.41
1:A:488:ARG:HD3	1:A:550:GLY:HA3	2.03	0.41
1:A:320:THR:HA	1:A:341:ILE:HG23	2.02	0.40
1:B:632:MET:HA	1:B:632:MET:HE2	2.03	0.40
1:A:365:SER:HA	1:A:389:ARG:HB2	2.02	0.40
1:B:604:TRP:HA	1:B:604:TRP:HE3	1.87	0.40
1:A:88:PHE:HE2	1:B:902:VAL:HG11	1.86	0.40
1:B:575:LEU:HD12	1:B:575:LEU:HA	1.93	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	514/1370 (38%)	492 (96%)	22 (4%)	0	100	100
1	B	232/1370 (17%)	226 (97%)	6 (3%)	0	100	100
2	C	42/195 (22%)	42 (100%)	0	0	100	100
2	D	28/195 (14%)	25 (89%)	3 (11%)	0	100	100
All	All	816/3130 (26%)	785 (96%)	31 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	488/1215 (40%)	488 (100%)	0	100	100
1	B	231/1215 (19%)	230 (100%)	1 (0%)	84	85
2	C	39/167 (23%)	38 (97%)	1 (3%)	40	65
2	D	27/167 (16%)	27 (100%)	0	100	100
All	All	785/2764 (28%)	783 (100%)	2 (0%)	84	87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	54	LEU
1	B	675	ILE

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	90	ASN
1	A	152	ASN
1	A	249	GLN
1	A	313	HIS
1	A	357	ASN

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Mol	Chain	Res	Type
1	A	470	ASN
1	A	513	GLN
2	C	15	GLN
1	B	518	GLN
1	B	621	ASN
1	B	736	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.

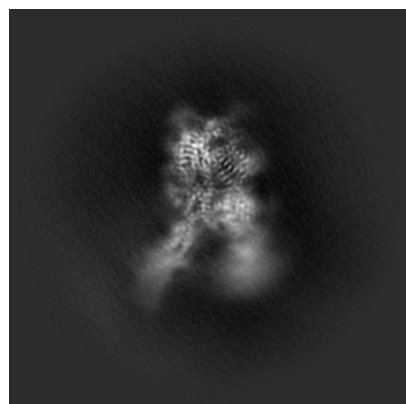
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37970. These allow visual inspection of the internal detail of the map and identification of artifacts.

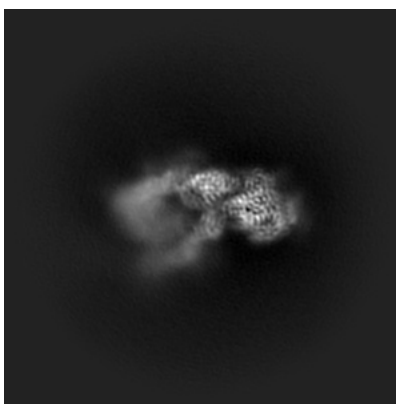
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

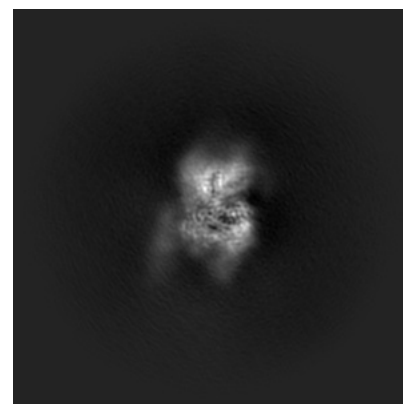
6.1.1 Primary map



X

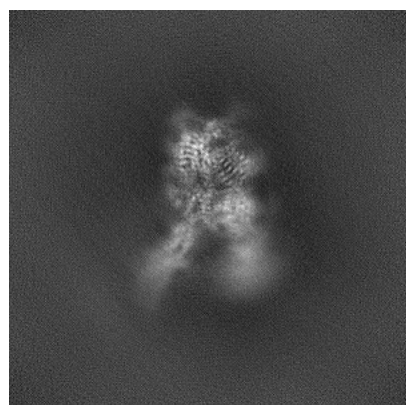


Y

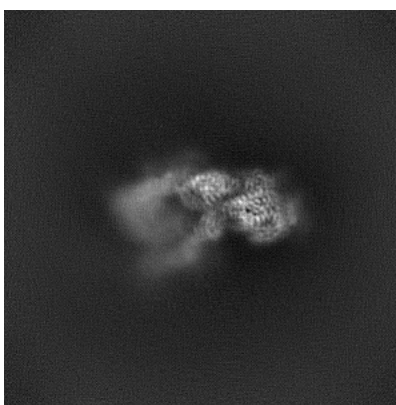


Z

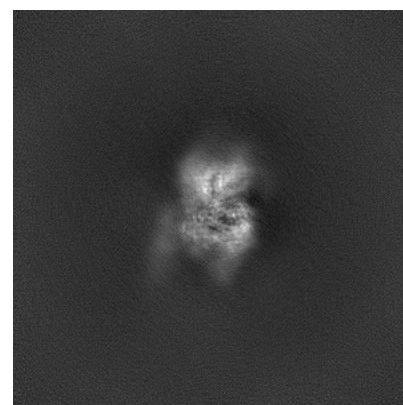
6.1.2 Raw map



X



Y

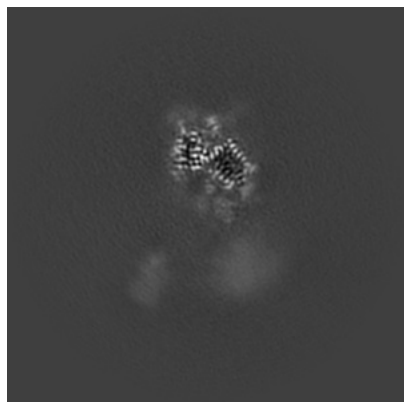


Z

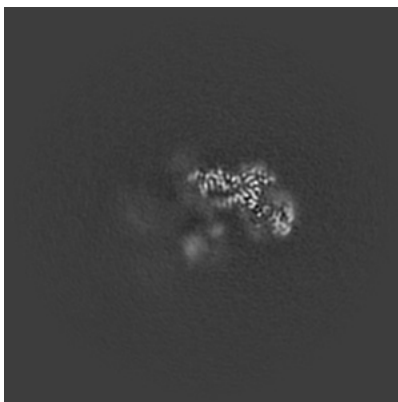
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

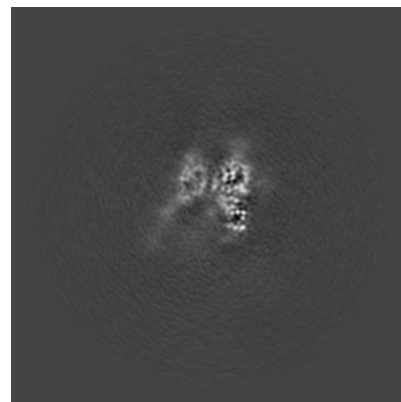
6.2.1 Primary map



X Index: 256

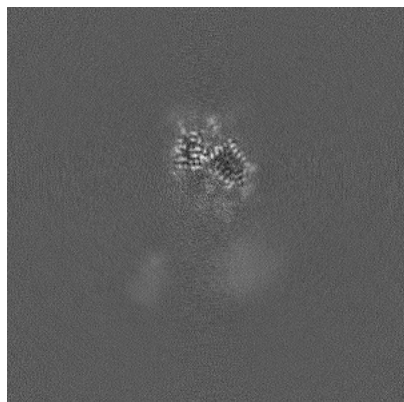


Y Index: 256

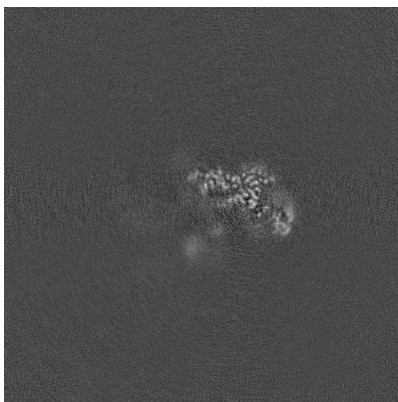


Z Index: 256

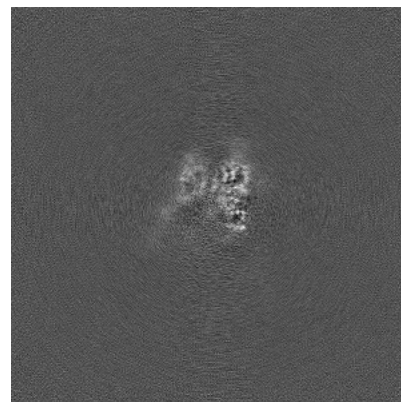
6.2.2 Raw map



X Index: 256



Y Index: 256

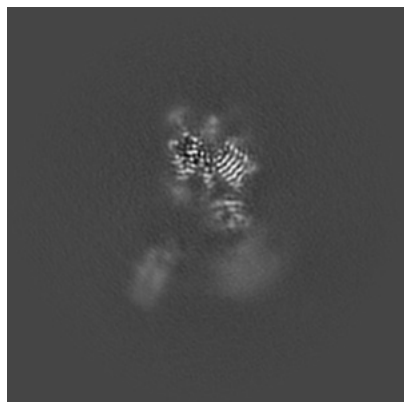


Z Index: 256

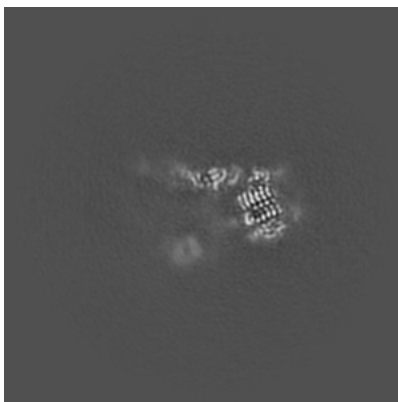
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

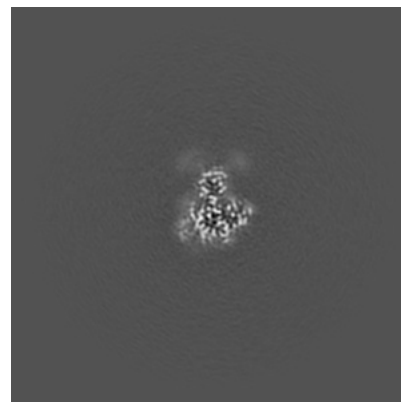
6.3.1 Primary map



X Index: 265



Y Index: 236

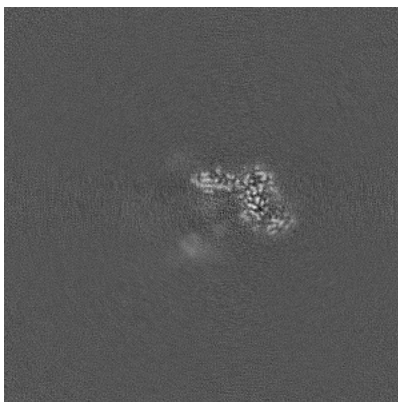


Z Index: 324

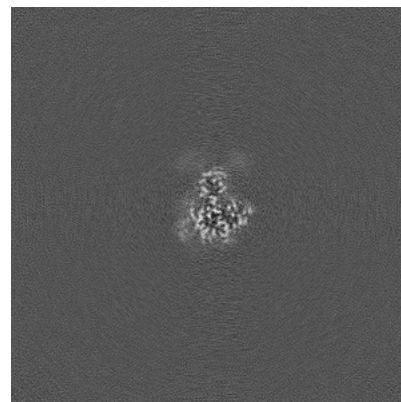
6.3.2 Raw map



X Index: 266



Y Index: 249

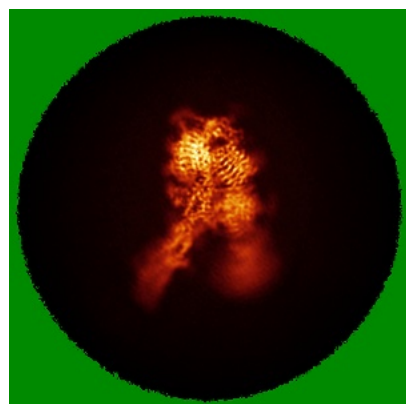


Z Index: 324

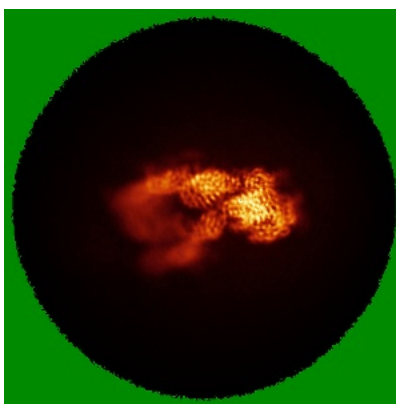
The images above show the largest variance slices of the map in three orthogonal directions.

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

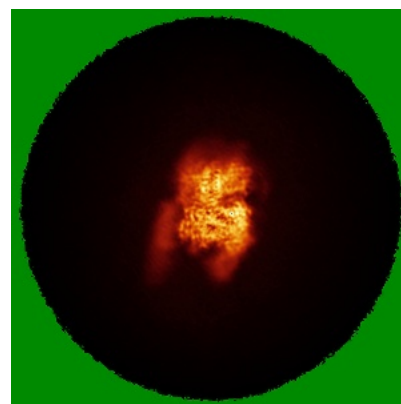
6.4.1 Primary map



X

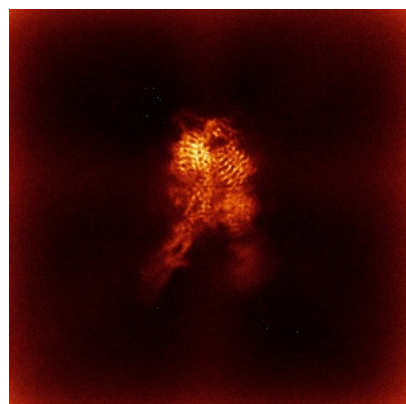


Y

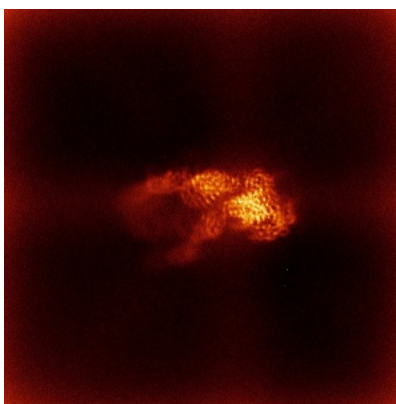


Z

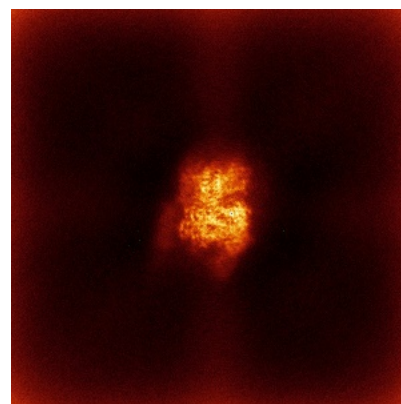
6.4.2 Raw map



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.

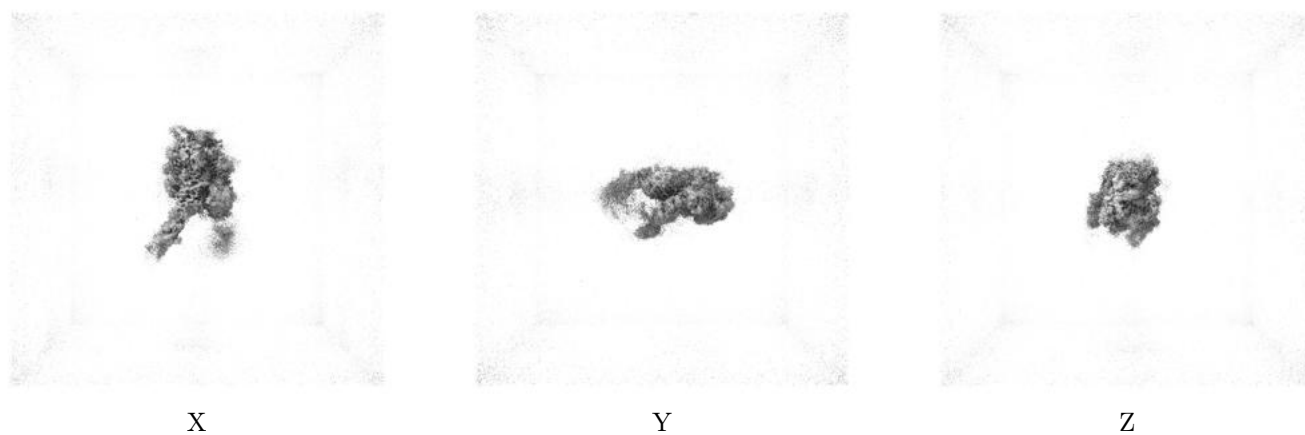
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

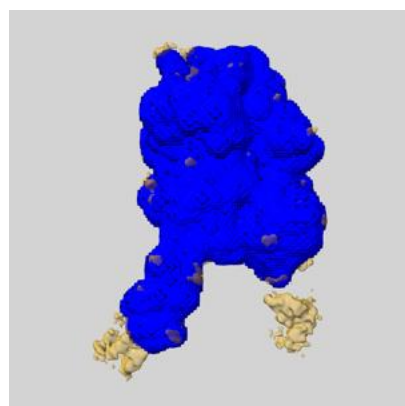
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

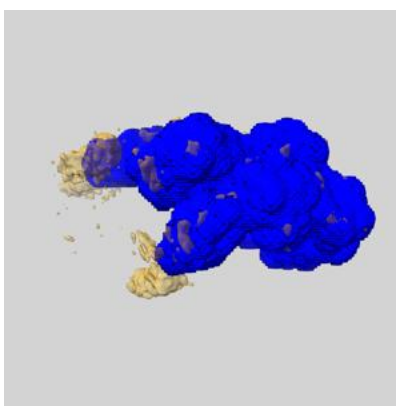
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

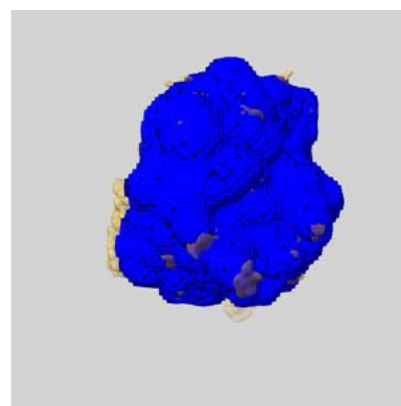
6.6.1 emd_37970_msk_1.map [i](#)



X



Y

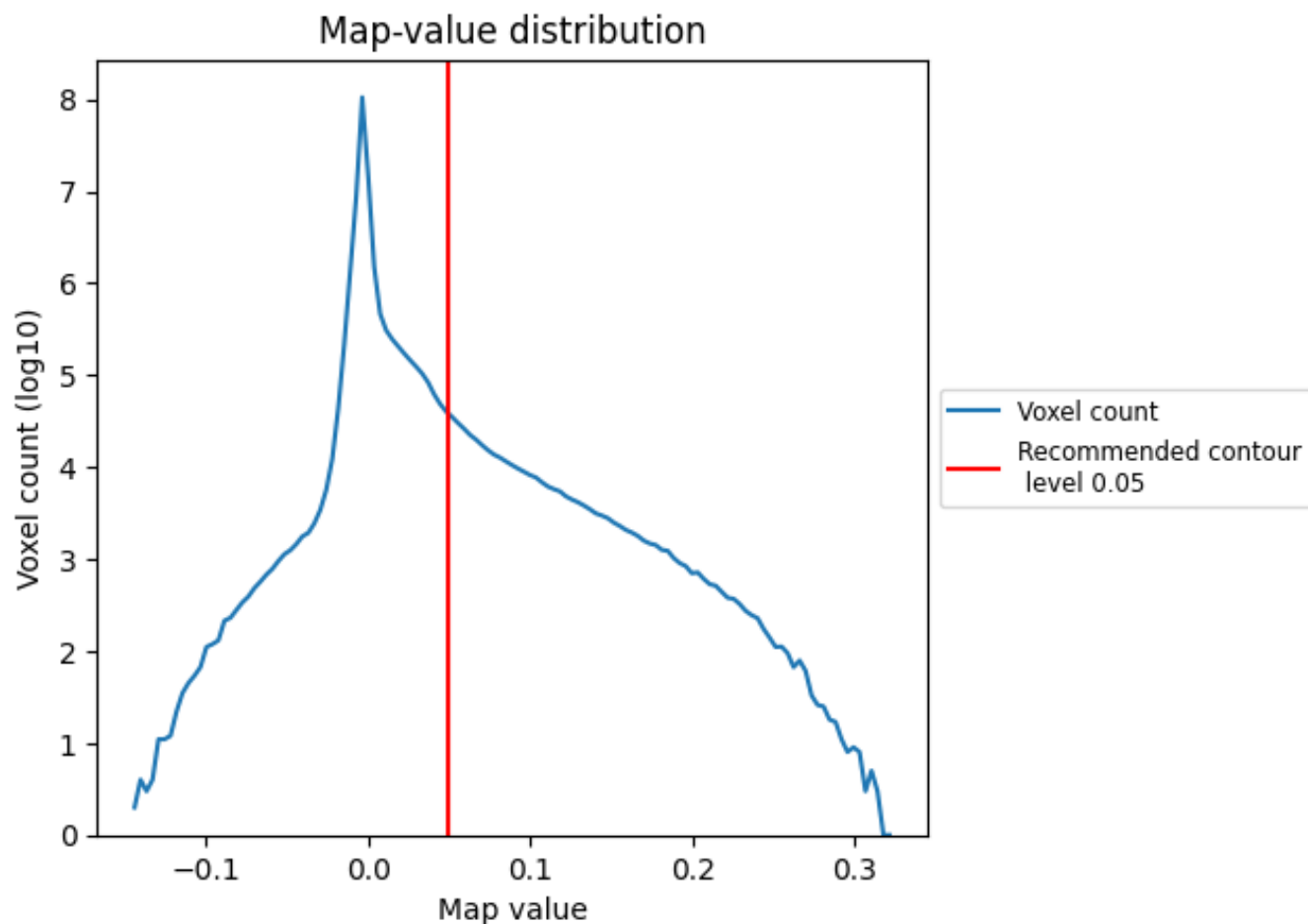


Z

7 Map analysis [i](#)

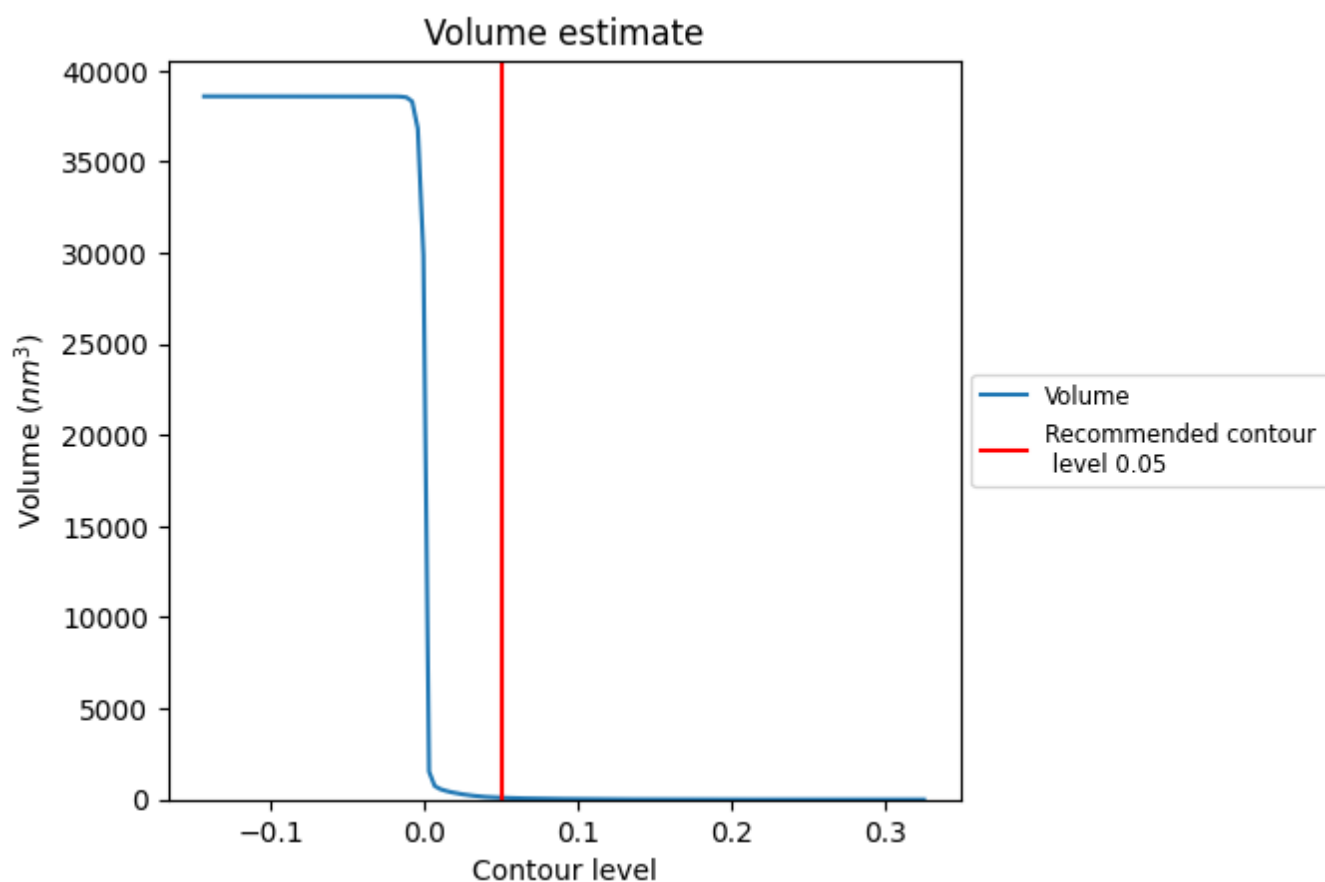
This section contains the results of statistical analysis of the map.

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.

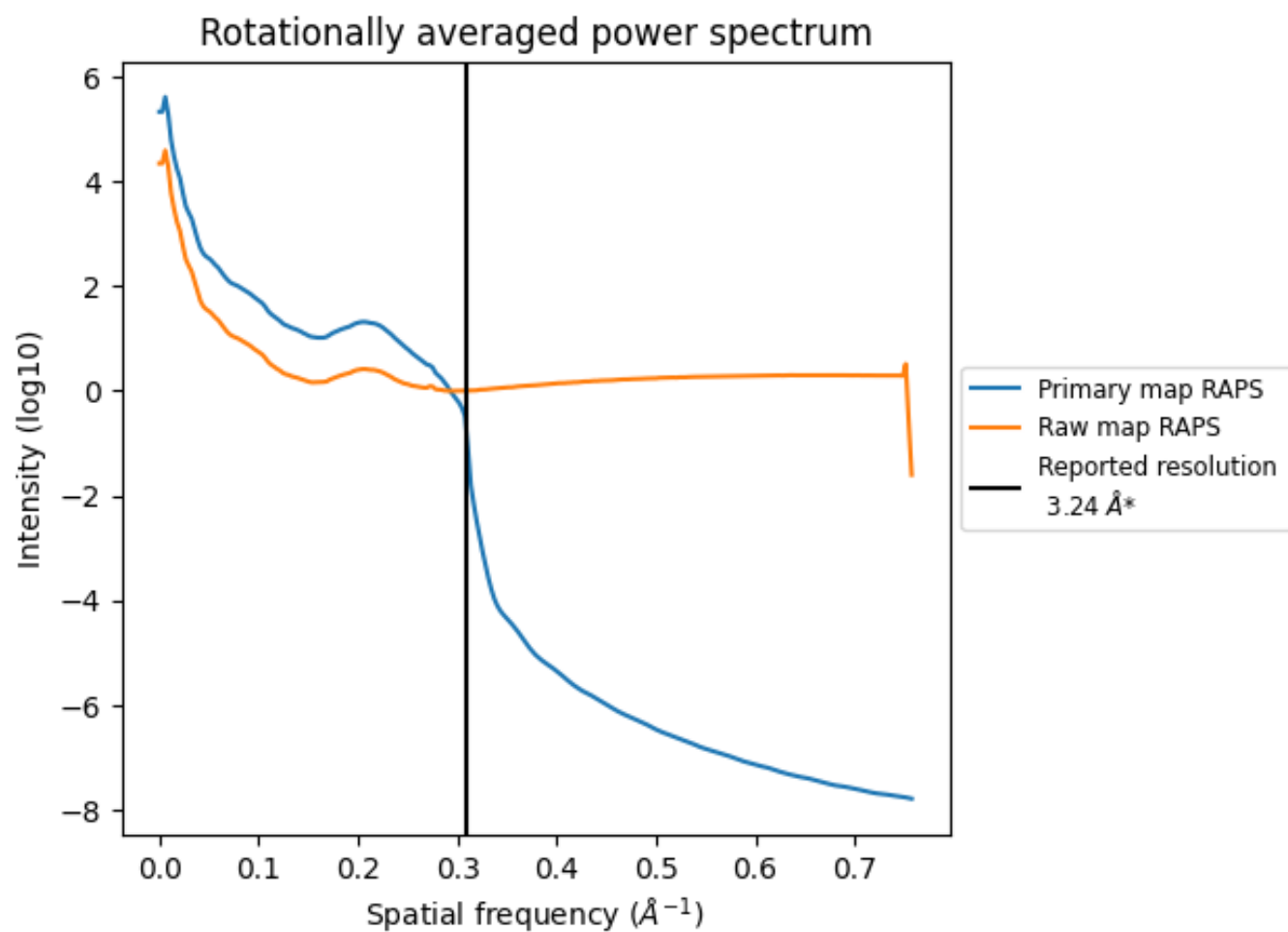
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 101 nm^3 ; this corresponds to an approximate mass of 91 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 ⓘ

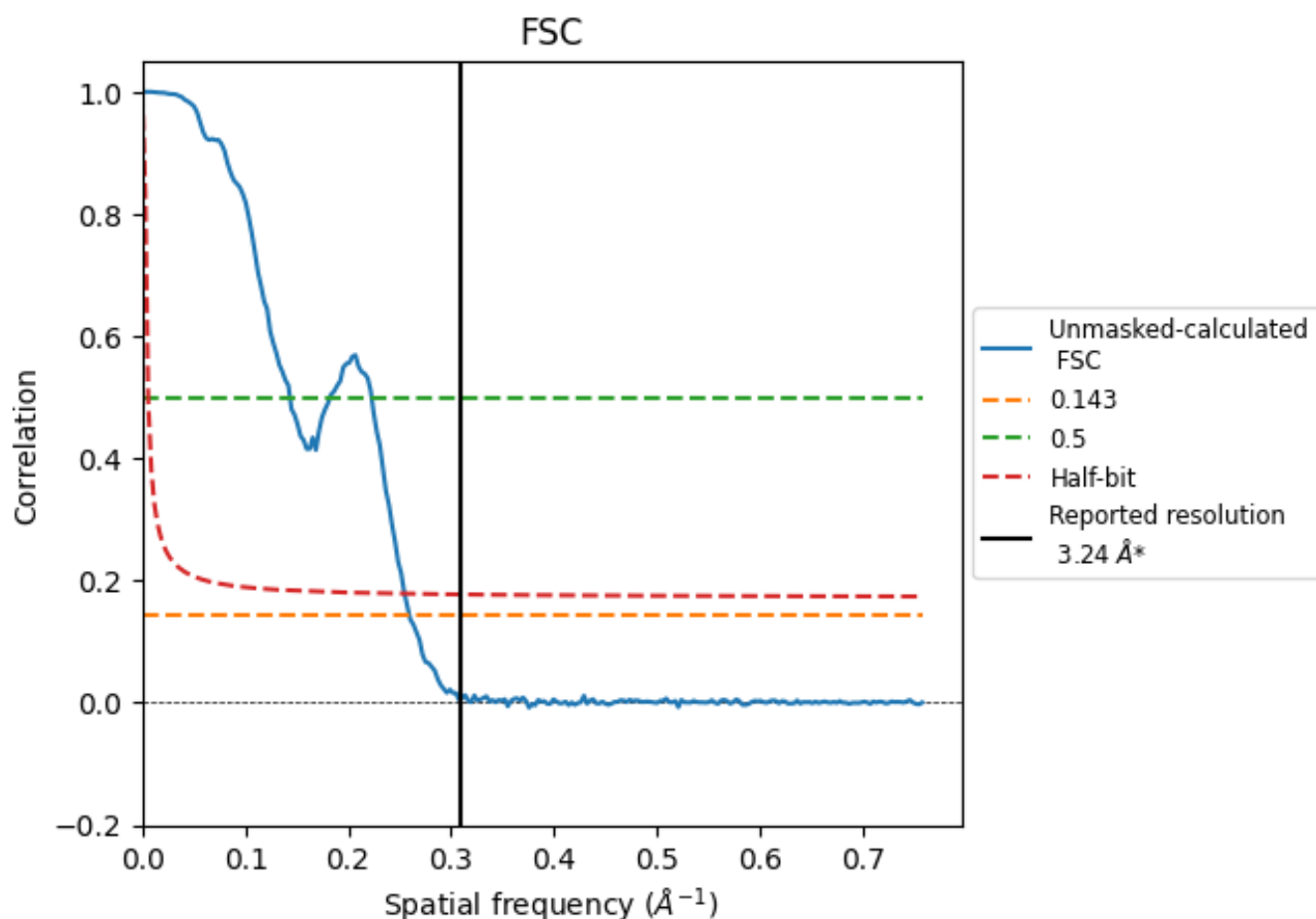


*Reported resolution corresponds to spatial frequency of 0.309 Å⁻¹

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 0.309 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

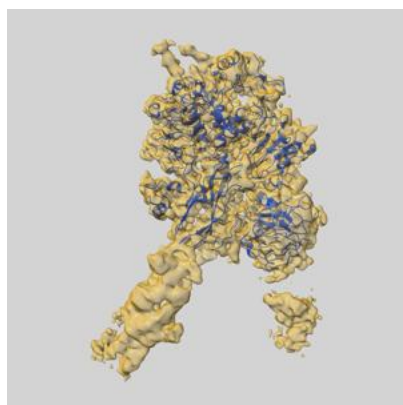
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.85	6.97	3.92

*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 3.85 differs from the reported value 3.24 by more than 10 %

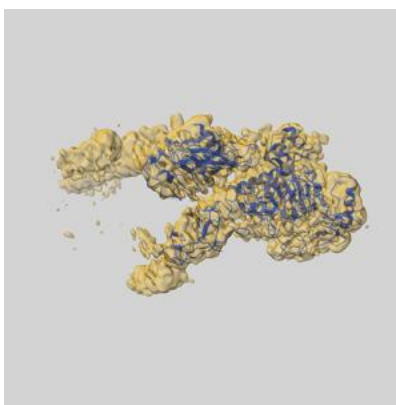
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37970 and PDB model 8X06. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

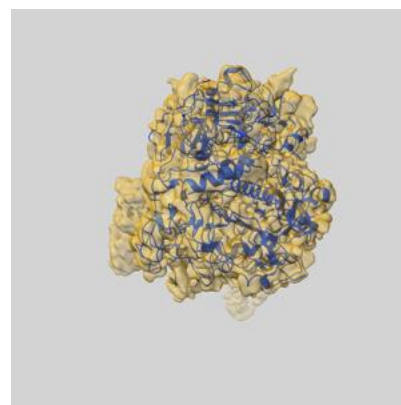
9.1 Map-model overlay [i](#)



X



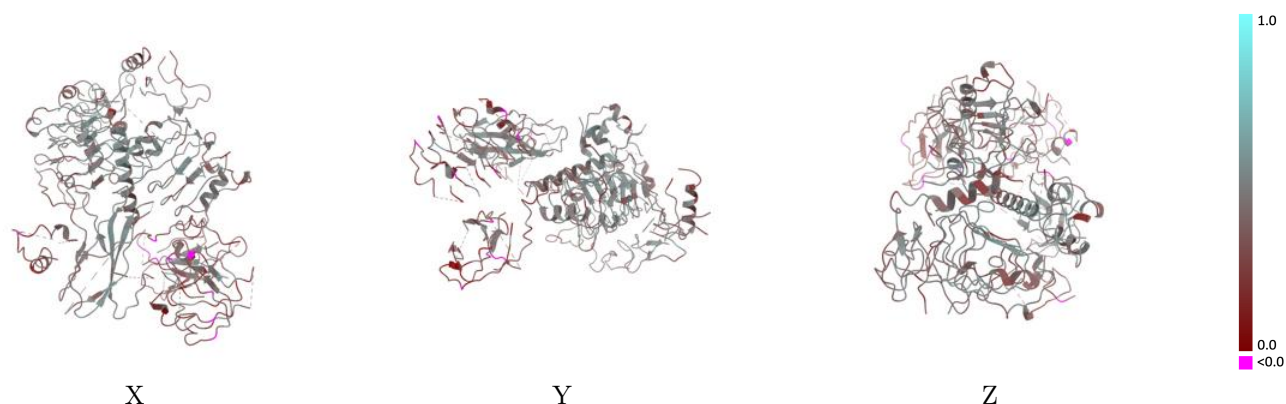
Y



Z

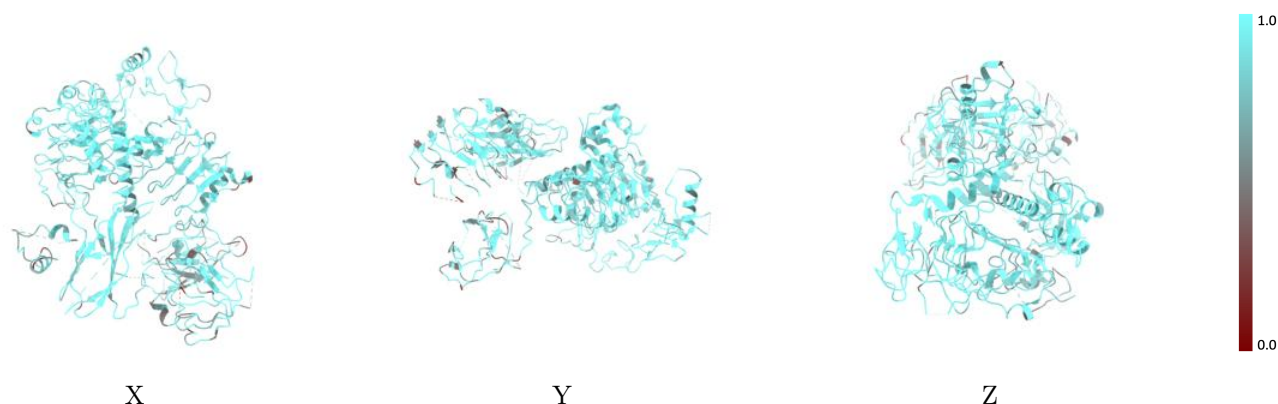
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



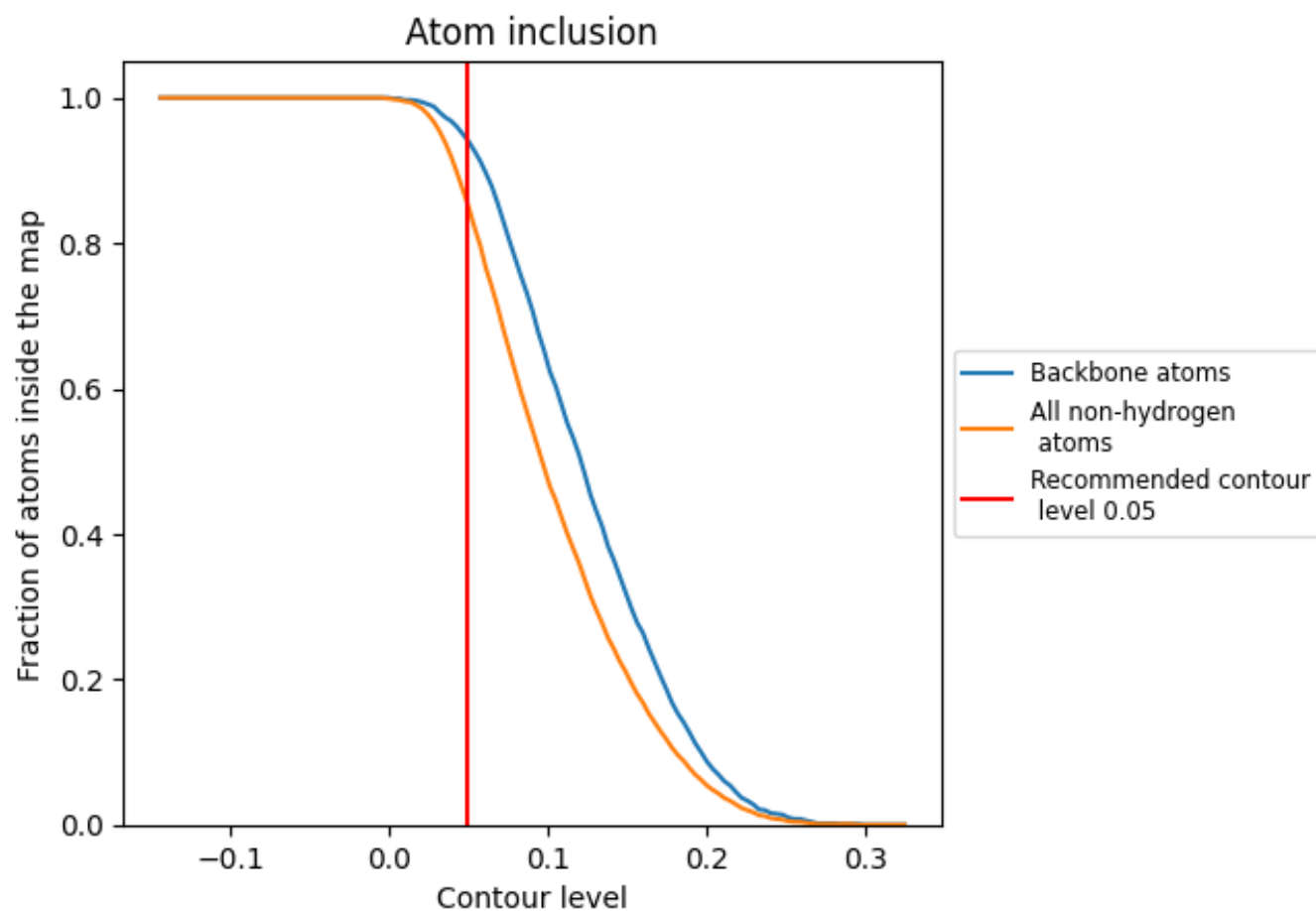
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 85% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8530	0.3960
A	0.8650	0.4040
B	0.8430	0.3850
C	0.9230	0.4590
D	0.6480	0.2660

