



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:25 PM UTC

PDB ID : 7MP6 / pdb_00007mp6
EMDB ID : EMD-23930
Title : Neurofibromin homodimer
Authors : Lupton, C.J.; Bayly-Jones, C.; Ellisdon, A.M.
Deposited on : 2021-05-04
Resolution : 6.25 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

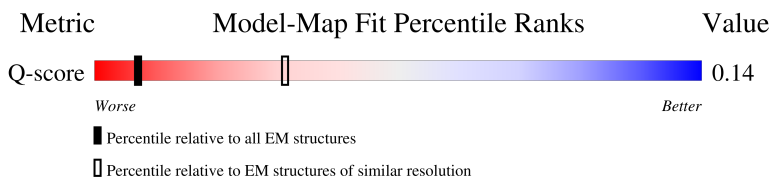
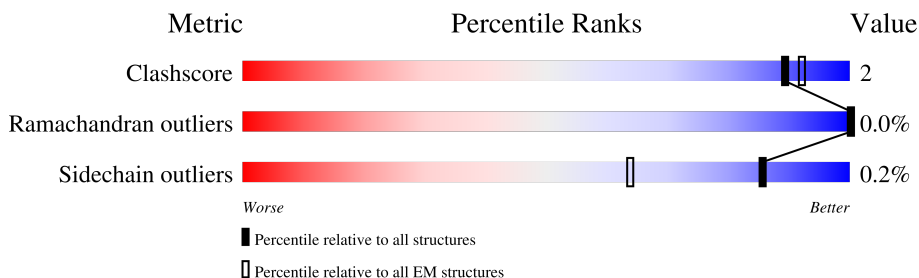
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.25 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	506 (5.75 - 6.75)

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	2826	
1	B	2826	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25464 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 I of Neurofibromin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1600	Total	C	N	O	S	0	0
			12704	8190	2127	2296	91		
1	B	1609	Total	C	N	O	S	0	0
			12760	8223	2136	2310	91		

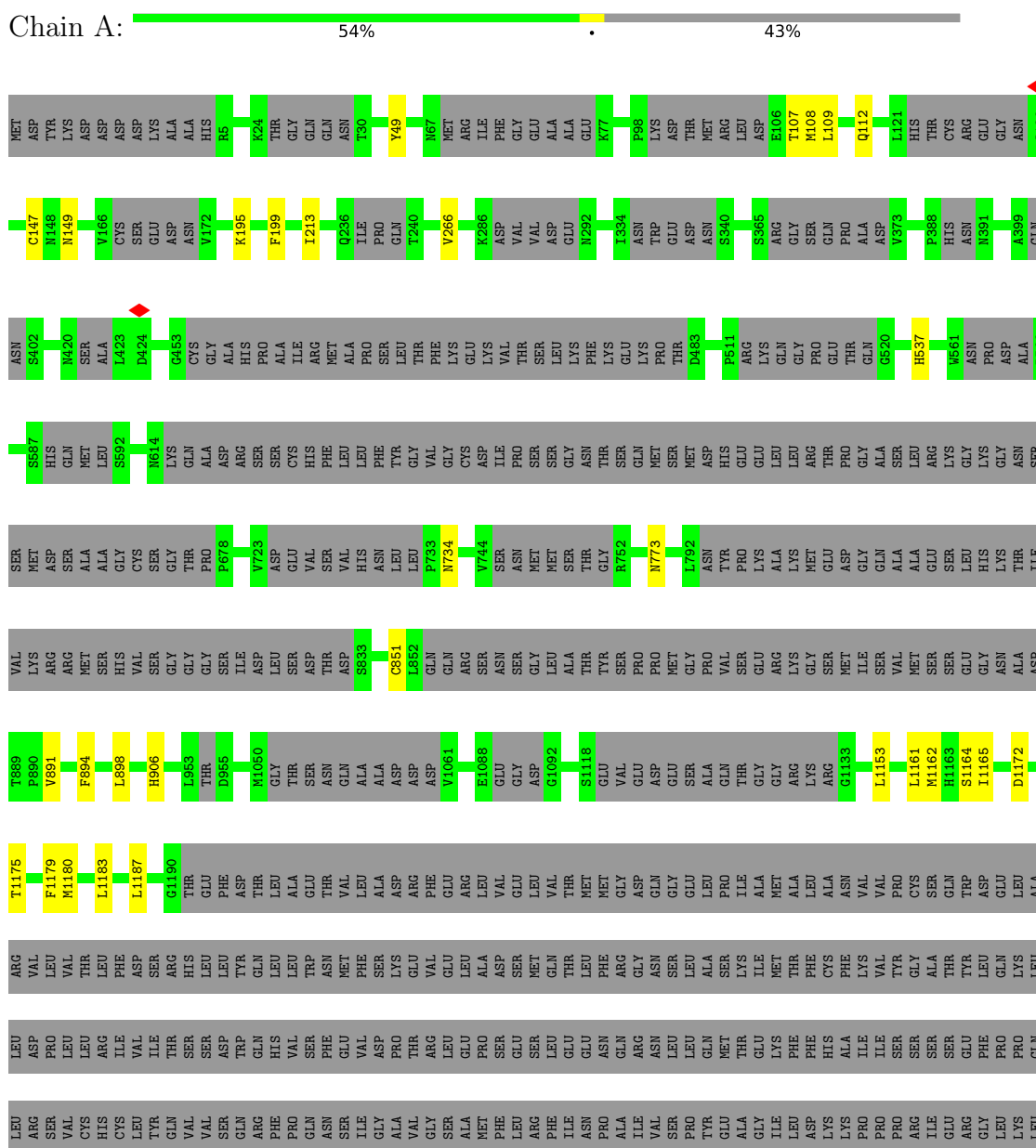
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP P21359
A	-6	ASP	-	expression tag	UNP P21359
A	-5	TYR	-	expression tag	UNP P21359
A	-4	LYS	-	expression tag	UNP P21359
A	-3	ASP	-	expression tag	UNP P21359
A	-2	ASP	-	expression tag	UNP P21359
A	-1	ASP	-	expression tag	UNP P21359
A	0	ASP	-	expression tag	UNP P21359
A	1	LYS	-	expression tag	UNP P21359
B	-7	MET	-	initiating methionine	UNP P21359
B	-6	ASP	-	expression tag	UNP P21359
B	-5	TYR	-	expression tag	UNP P21359
B	-4	LYS	-	expression tag	UNP P21359
B	-3	ASP	-	expression tag	UNP P21359
B	-2	ASP	-	expression tag	UNP P21359
B	-1	ASP	-	expression tag	UNP P21359
B	0	ASP	-	expression tag	UNP P21359
B	1	LYS	-	expression tag	UNP P21359

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: Isoform I of Neurofibromin



- Molecule 1: Isoform I of Neurofibromin

[illegible]



HIS	LEU	VAL	LYS	TYR	ARG
GLY	SER	SER	LEU	PRO	SER
SER	THR	VAL	LEU	ILE	SER
ALA	PRO	SER	GLY	HIS	TYR
GLN	SER	SER	ARG	HIS	ARG
VAL	PRO	ASN	LYS	GLY	ASP
GLN	TYR	VAL	LYS	ASP	SER
LYS	PRO	LEU	PHE	SER	PHE
GLN	PRO	LEU	ASP	TYR	SER
ARG	ALA	ASP	HIS	ARG	PRO
SER	LEU	GLU	LEU	THR	GLY
ALA	GLN	GLU	ILE	LEU	SER
GLY	SER	VAL	SER	LYS	+
PHE	GLN	THR	ASP	GLU	Y2171
LYS	LEU	THR	LYS	GLN	W2204
ARG	ILE	D2591	ALA	PRO	W2220
ASN	THR	V2606	PRO	TRP	+
SER	ALA	K2607	LYS	SER	W2230
ILE	ASN	Y2608	ARG	SER	+
LYS	LEU	+	GLN	PRO	K2259
LYS	ASN	S2626	GLU	LYS	GLY
LEU	LEU	+	MET	GLY	PRO
ILE	SER	F2633	GLU	SER	ASP
VAL	ASN	+	SER	GLU	THR
	SER	L2650	GLY	GLY	+
	MET	C2651	ILE	TYR	W2264
	THR	Q2652	THR	LEU	W2265
	SER	+	ALA	ALA	S2266
	LEU	E2671	PRO	THR	+
	THR	GLU	PRO	ALA	Q2281
	ALA	+	LYS	TYR	P2282
	SER	PRO	MET	PRO	+
	GLN	P2675	ARG	THR	L2246
	HIS	+	ARG	VAL	+
	SER	G2689	VAL	GLY	S2430
	PRO	+	ALA	GLN	ARG
	GLY	R2692	GLU	THR	CYS
	ILE	F2693	THR	SER	SER
	ASP	+	ASP	LEU	SER
	LYS	F2697	TYR	PRO	LYS
	GLU	SER	GLU	ARG	HIS
	ASN	LYS	MET	ALA	ARG
	VAL	GLN	GLU	LYS	LYS
	LEU	GLN	GLN	MET	SER
	SER	I2703	ARG	LEU	LEU
	PRO	+	ILE	SER	LEU
	THR	+	SER	ASP	THR
	THR	GLY	SER	MET	ASP
	GLY	ILE	SER	GLY	ILE
	HIS	ASP	GLN	GLN	MET
	CYS	GLU	GLN	PRO	GLU
	ASN	THR	HIS	SER	ASN
	SER	GLU	PRO	GLN	VAL
	GLY	THR	HIS	ALA	PRO
	ARG	GLU	LEU	ASN	MET
	THR	GLU	ARG	ASP	ASP
	ARG	SER	LYS	TYR	THR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	95564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.365	Depositor
Minimum map value	-0.873	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	515.808, 515.808, 515.808	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.388, 2.388, 2.388	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	0.72	1/12925 (0.0%)	1.28	26/17476 (0.1%)
1	B	0.73	2/12983 (0.0%)	1.28	26/17558 (0.1%)
All	All	0.73	3/25908 (0.0%)	1.28	52/35034 (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	4
1	B	0	4
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1897	ASN	C-N	15.66	1.54	1.33
1	B	1187	LEU	C-N	7.39	1.44	1.33
1	A	1187	LEU	C-N	7.34	1.44	1.33

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2074	ASP	N-CA-C	10.21	122.49	111.36
1	B	2074	ASP	N-CA-C	10.19	122.47	111.36
1	A	1893	THR	N-CA-C	-8.51	101.94	111.14
1	B	1893	THR	N-CA-C	-8.48	101.98	111.14
1	B	109	LEU	N-CA-C	-8.36	102.12	111.07
1	A	109	LEU	N-CA-C	-8.32	102.17	111.07
1	B	2693	PHE	N-CA-C	7.93	119.93	111.28
1	A	2693	PHE	N-CA-C	7.88	119.88	111.28
1	A	1891	SER	N-CA-C	7.81	120.48	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1891	SER	N-CA-C	7.79	120.46	111.11
1	A	2078	HIS	N-CA-C	7.61	121.82	112.23
1	B	2078	HIS	N-CA-C	7.61	121.82	112.23
1	A	107	THR	N-CA-C	7.17	119.77	111.02
1	B	107	THR	N-CA-C	7.15	119.74	111.02
1	A	2608	TYR	N-CA-C	6.75	119.63	111.40
1	B	2608	TYR	N-CA-C	6.73	119.62	111.40
1	A	1893	THR	N-CA-CB	6.37	119.30	110.07
1	B	1893	THR	N-CA-CB	6.32	119.23	110.07
1	A	2220	ASN	CA-CB-CG	6.23	118.83	112.60
1	B	2220	ASN	CA-CB-CG	6.20	118.80	112.60
1	B	2650	LEU	N-CA-C	6.17	118.93	111.40
1	B	2606	VAL	CA-CB-CG2	6.16	120.87	110.40
1	A	2606	VAL	CA-CB-CG2	6.14	120.84	110.40
1	A	2650	LEU	N-CA-C	6.13	118.88	111.40
1	A	2075	VAL	N-CA-C	6.02	119.48	111.17
1	B	2075	VAL	N-CA-C	5.98	119.42	111.17
1	B	2693	PHE	N-CA-CB	-5.77	101.64	110.12
1	A	2693	PHE	N-CA-CB	-5.76	101.65	110.12
1	B	773	ASN	CA-CB-CG	5.69	118.29	112.60
1	B	109	LEU	N-CA-CB	5.67	118.23	110.01
1	A	109	LEU	N-CA-CB	5.66	118.22	110.01
1	A	773	ASN	CA-CB-CG	5.65	118.25	112.60
1	A	1993	PHE	CA-CB-CG	5.61	119.41	113.80
1	A	149	ASN	N-CA-C	5.58	120.07	113.16
1	B	149	ASN	N-CA-C	5.51	119.99	113.16
1	A	2012	ASP	N-CA-CB	-5.45	102.10	110.16
1	B	1941	HIS	CA-CB-CG	-5.45	108.35	113.80
1	A	2266	SER	CA-C-N	5.16	127.15	120.44
1	A	2266	SER	C-N-CA	5.16	127.15	120.44
1	B	1941	HIS	N-CA-C	5.11	117.75	111.82
1	B	2266	SER	CA-C-N	5.11	127.09	120.44
1	B	2266	SER	C-N-CA	5.11	127.09	120.44
1	B	906	HIS	CB-CG-CD2	-5.10	124.57	131.20
1	A	906	HIS	CB-CG-CD2	-5.09	124.58	131.20
1	B	734	ASN	CB-CA-C	5.08	121.34	110.21
1	A	734	ASN	CB-CA-C	5.06	121.30	110.21
1	A	1870	GLN	N-CA-C	5.04	116.79	110.24
1	B	2346	LEU	CA-C-N	5.04	127.28	120.38
1	B	2346	LEU	C-N-CA	5.04	127.28	120.38
1	A	2346	LEU	CA-C-N	5.01	127.25	120.38
1	A	2346	LEU	C-N-CA	5.01	127.25	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2051	HIS	CB-CG-CD2	-5.00	124.70	131.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	CYS	Mainchain
1	A	1853	TYR	Sidechain
1	A	2693	PHE	Sidechain
1	A	49	TYR	Sidechain
1	B	147	CYS	Mainchain
1	B	1853	TYR	Sidechain
1	B	2693	PHE	Sidechain
1	B	49	TYR	Sidechain

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	12704	0	13032	50	0
1	B	12760	0	13087	51	0
All	All	25464	0	26119	92	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 2.

All (92) 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:1916:SER:CB	1:B:1920:LEU:HD23	1.67	1.24
1:B:1865:LEU:HA	1:B:1898:GLU:OE1	1.46	1.15
1:B:1916:SER:HB3	1:B:1920:LEU:HD23	1.14	1.09
1:A:1987:ASP:OD1	1:A:2032:ARG:NH2	1.94	0.99
1:A:1987:ASP:OD1	1:A:2032:ARG:CZ	2.18	0.92
1:A:1987:ASP:OD1	1:A:2032:ARG:NH1	2.05	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2019:SER:O	1:A:2020:GLY:O	1.90	0.88
1:B:1916:SER:HB3	1:B:1920:LEU:CD2	2.01	0.87
1:A:2015:VAL:HG11	1:B:1882:ASN:O	1.76	0.86
1:B:1920:LEU:HD12	1:B:1923:LEU:HD23	1.55	0.85
1:B:1916:SER:OG	1:B:1920:LEU:HD23	1.76	0.84
1:B:1839:LEU:HD11	1:B:1920:LEU:HD11	1.61	0.83
1:B:1916:SER:CB	1:B:1920:LEU:CD2	2.58	0.80
1:B:1839:LEU:HD13	1:B:1927:TYR:OH	1.86	0.76
1:B:2087:THR:HG23	1:B:2230:VAL:HG21	1.71	0.73
1:B:1916:SER:OG	1:B:1920:LEU:CD2	2.38	0.72
1:A:2015:VAL:HB	1:B:1882:ASN:ND2	2.04	0.72
1:A:2087:THR:HG23	1:A:2230:VAL:HG21	1.71	0.72
1:B:1889:SER:HA	1:B:1892:LYS:HE2	1.76	0.68
1:A:1889:SER:HA	1:A:1892:LYS:HE2	1.76	0.68
1:A:1179:PHE:CZ	1:A:1183:LEU:HD11	2.29	0.67
1:B:1179:PHE:CZ	1:B:1183:LEU:HD11	2.29	0.66
1:B:1834:LEU:HD22	1:B:1901:LEU:HD13	1.78	0.65
1:A:1892:LYS:HB3	1:A:1930:PRO:HG2	1.78	0.63
1:B:1839:LEU:CD1	1:B:1920:LEU:HD11	2.29	0.63
1:A:2015:VAL:HB	1:B:1882:ASN:HD22	1.61	0.63
1:A:2071:ASN:HA	1:A:2074:ASP:HB3	1.81	0.62
1:B:1165:ILE:HD11	1:B:1832:THR:HG21	1.80	0.62
1:A:1165:ILE:HD11	1:A:1832:THR:HG21	1.80	0.62
1:B:2071:ASN:HA	1:B:2074:ASP:HB3	1.81	0.62
1:A:195:LYS:HG2	1:A:199:PHE:CE2	2.35	0.61
1:B:195:LYS:HG2	1:B:199:PHE:CE2	2.35	0.61
1:A:1892:LYS:HB3	1:A:1930:PRO:CG	2.30	0.60
1:A:1987:ASP:CG	1:A:2032:ARG:HH22	2.09	0.60
1:B:1834:LEU:CD2	1:B:1901:LEU:HD13	2.32	0.60
1:A:1872:LEU:HD22	1:B:2113:CYS:HB2	1.85	0.58
1:A:2113:CYS:HB2	1:B:1872:LEU:HD22	1.85	0.58
1:B:2010:MET:HA	1:B:2010:MET:HE2	1.86	0.57
1:B:108:MET:HG2	1:B:112:GLN:NE2	2.21	0.56
1:A:108:MET:HG2	1:A:112:GLN:NE2	2.21	0.55
1:B:2087:THR:CG2	1:B:2230:VAL:HG21	2.39	0.52
1:B:1153:LEU:HD21	1:B:1164:SER:HB3	1.92	0.52
1:A:1153:LEU:HD21	1:A:1164:SER:HB3	1.92	0.51
1:A:2018:ALA:HB2	1:A:2067:LEU:HD21	1.92	0.51
1:B:1183:LEU:HD13	1:B:1833:LEU:HD22	1.92	0.51
1:A:2018:ALA:HB2	1:A:2067:LEU:CD2	2.42	0.50
1:A:1183:LEU:HD13	1:A:1833:LEU:HD22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1891:SER:OG	1:B:1931:TRP:NE1	2.23	0.50
1:A:2019:SER:C	1:A:2020:GLY:O	2.55	0.49
1:A:2087:THR:CG2	1:A:2230:VAL:HG21	2.39	0.48
1:B:1165:ILE:CD1	1:B:1832:THR:HG21	2.43	0.48
1:A:1165:ILE:CD1	1:A:1832:THR:HG21	2.43	0.48
1:A:2071:ASN:HA	1:A:2074:ASP:CB	2.44	0.47
1:B:2071:ASN:HA	1:B:2074:ASP:CB	2.44	0.47
1:A:1172:ASP:CG	1:A:1175:THR:HG23	2.40	0.46
1:B:1172:ASP:CG	1:B:1175:THR:HG23	2.40	0.46
1:A:1878:CYS:SG	1:B:2153:ALA:HB2	2.56	0.46
1:A:2153:ALA:HB2	1:B:1878:CYS:SG	2.56	0.46
1:A:1846:PRO:CG	1:B:2157:PHE:HB2	2.46	0.45
1:B:894:PHE:CE2	1:B:898:LEU:HD11	2.51	0.45
1:A:894:PHE:CE2	1:A:898:LEU:HD11	2.51	0.45
1:A:2157:PHE:HB2	1:B:1846:PRO:CG	2.46	0.45
1:A:1162:MET:HA	1:A:1165:ILE:HD12	1.99	0.45
1:B:1162:MET:HA	1:B:1165:ILE:HD12	1.99	0.45
1:B:1833:LEU:HA	1:B:1836:ILE:HG12	1.99	0.44
1:A:1833:LEU:HA	1:A:1836:ILE:HG12	1.99	0.44
1:B:213:ILE:HD13	1:B:266:VAL:HG12	2.00	0.44
1:A:2021:ASN:O	1:A:2022:VAL:C	2.60	0.44
1:A:213:ILE:HD13	1:A:266:VAL:HG12	1.99	0.44
1:A:1929:THR:HB	1:A:1930:PRO:HD3	1.99	0.44
1:B:851:CYS:HB2	1:B:891:VAL:HG21	2.00	0.43
1:B:2626:SER:HA	1:B:2633:PHE:CD1	2.53	0.43
1:A:2015:VAL:HG22	1:A:2066:MET:HB3	1.99	0.43
1:A:851:CYS:HB2	1:A:891:VAL:HG21	2.01	0.43
1:A:2626:SER:HA	1:A:2633:PHE:CD1	2.53	0.43
1:B:2079:LEU:HD23	1:B:2204:TRP:CE3	2.54	0.42
1:B:1976:TRP:CZ3	1:B:1979:LEU:HD13	2.54	0.42
1:A:2689:GLY:O	1:A:2692:ARG:HB3	2.20	0.42
1:B:2689:GLY:O	1:B:2692:ARG:HB3	2.20	0.42
1:A:2079:LEU:HD23	1:A:2204:TRP:CE3	2.54	0.42
1:B:1179:PHE:CE2	1:B:1183:LEU:HD11	2.55	0.42
1:B:1924:CYS:HA	1:B:1927:TYR:CE2	2.55	0.42
1:B:1905:PHE:CE1	1:B:1909:CYS:SG	3.13	0.41
1:A:1179:PHE:CE2	1:A:1183:LEU:HD11	2.55	0.41
1:B:2281:GLN:CG	1:B:2282:PRO:HD3	2.51	0.41
1:A:1987:ASP:CG	1:A:2032:ARG:NH2	2.70	0.41
1:A:2281:GLN:CG	1:A:2282:PRO:HD3	2.51	0.41
1:A:1180:MET:HA	1:A:1183:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2113:CYS:SG	1:A:2128:LEU:HB3	2.61	0.41
1:A:537:HIS:CD2	1:A:537:HIS:H	2.39	0.41
1:B:1103:PHE:CD1	1:B:1103:PHE:C	2.99	0.40
1:A:2213:GLN:HG3	1:A:2217:PHE:CE2	2.57	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	1532/2826 (54%)	1504 (98%)	27 (2%)	1 (0%)	48	83
1	B	1545/2826 (55%)	1518 (98%)	27 (2%)	0	100	100
All	All	3077/5652 (54%)	3022 (98%)	54 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2020	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1438/2520 (57%)	1435 (100%)	3 (0%)	87	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	1444/2520 (57%)	1441 (100%)	3 (0%)	87	87
All	All	2882/5040 (57%)	2876 (100%)	6 (0%)	85	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1161	LEU
1	A	2079	LEU
1	A	2652	GLN
1	B	1161	LEU
1	B	2079	LEU
1	B	2652	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	112	GLN
1	A	149	ASN
1	A	184	ASN
1	A	756	GLN
1	A	835	GLN
1	A	916	ASN
1	A	963	GLN
1	A	1004	ASN
1	A	1188	GLN
1	A	2021	ASN
1	A	2265	ASN
1	A	2267	GLN
1	A	2362	ASN
1	A	2393	HIS
1	A	2595	GLN
1	A	2658	ASN
1	B	39	ASN
1	B	112	GLN
1	B	149	ASN
1	B	543	GLN
1	B	736	ASN
1	B	835	GLN
1	B	916	ASN
1	B	963	GLN

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Mol	Chain	Res	Type
1	B	1004	ASN
1	B	1188	GLN
1	B	2084	HIS
1	B	2362	ASN
1	B	2366	ASN
1	B	2393	HIS
1	B	2658	ASN

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.

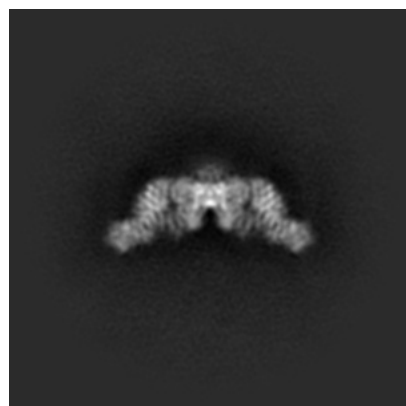
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23930. These allow visual inspection of the internal detail of the map and identification of artifacts.

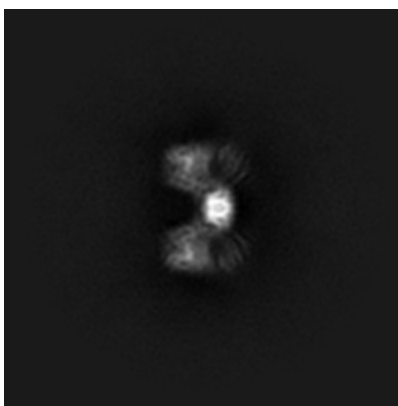
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

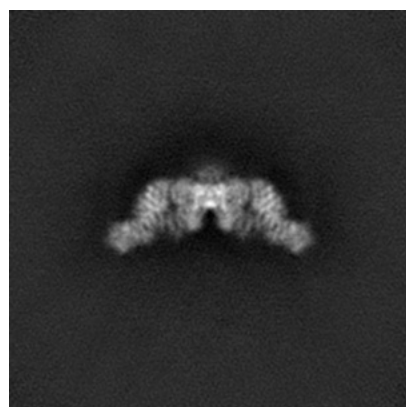


Y

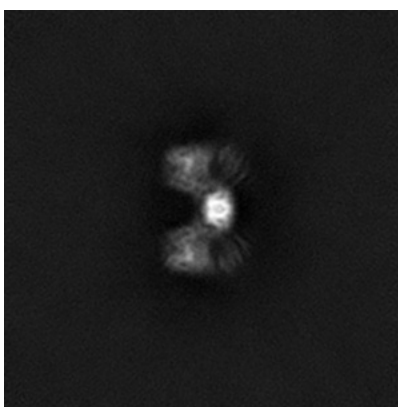


Z

6.1.2 Raw map



X



Y



Z

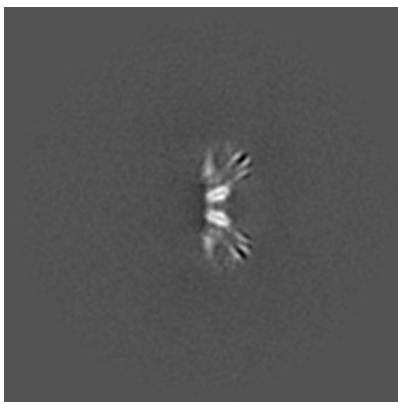
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

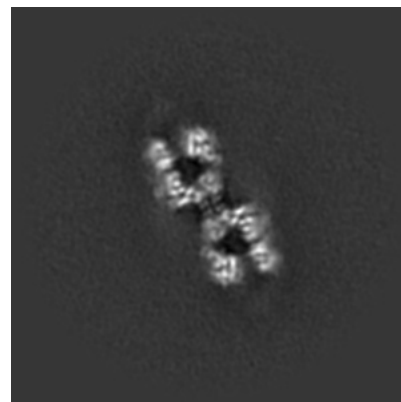
6.2.1 Primary map



X Index: 108



Y Index: 108

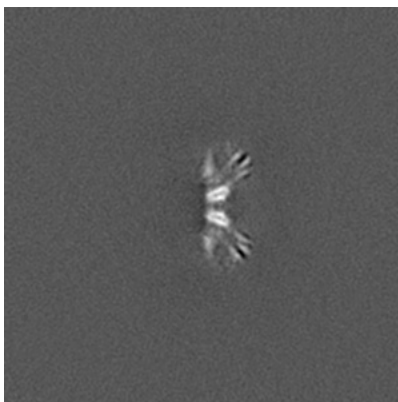


Z Index: 108

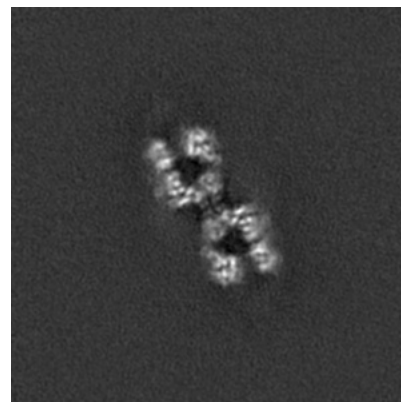
6.2.2 Raw map



X Index: 108



Y Index: 108



Z Index: 108

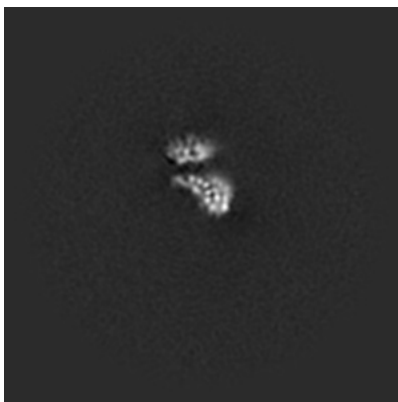
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 105



Y Index: 76



Z Index: 112

6.3.2 Raw map



X Index: 105



Y Index: 76

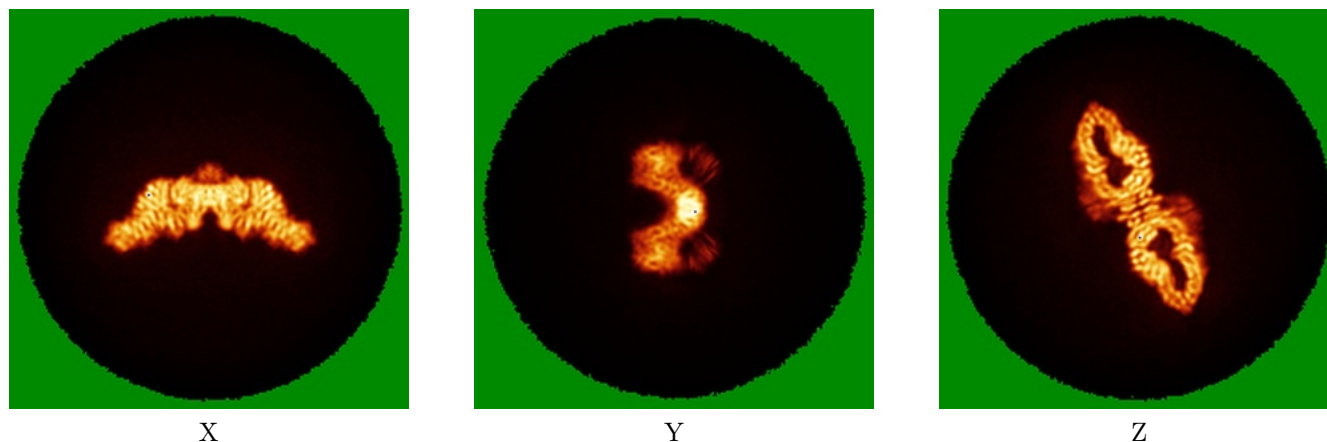


Z Index: 112

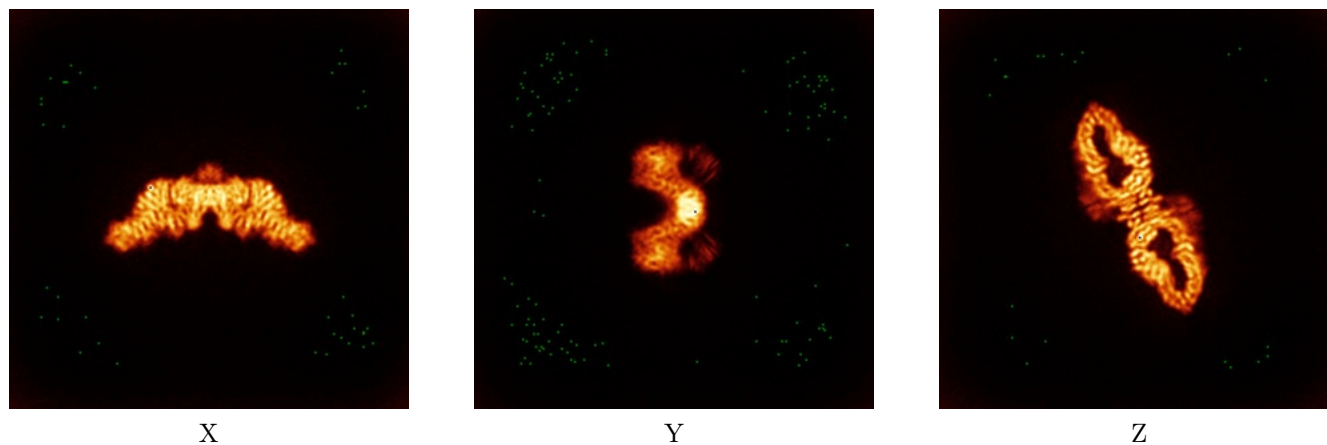
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

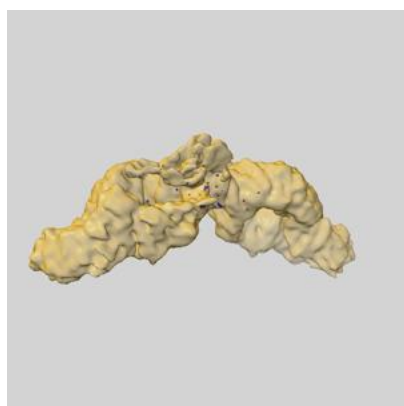
6.6 Mask visualisation [i](#)

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

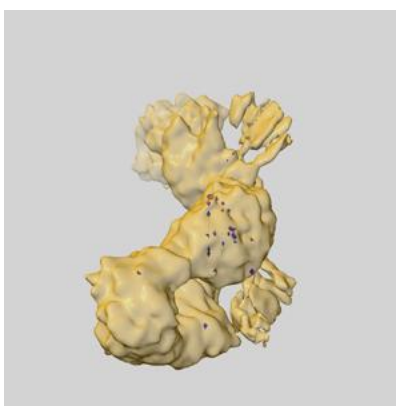
A mask typically either:

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

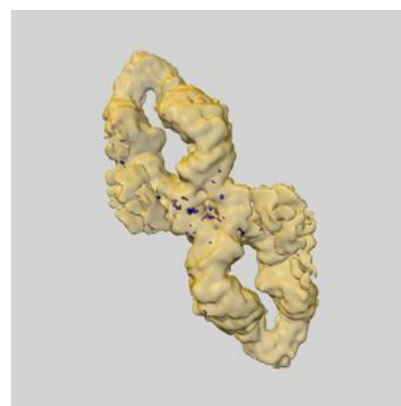
6.6.1 emd_23930_msk_1.map [i](#)



X



Y

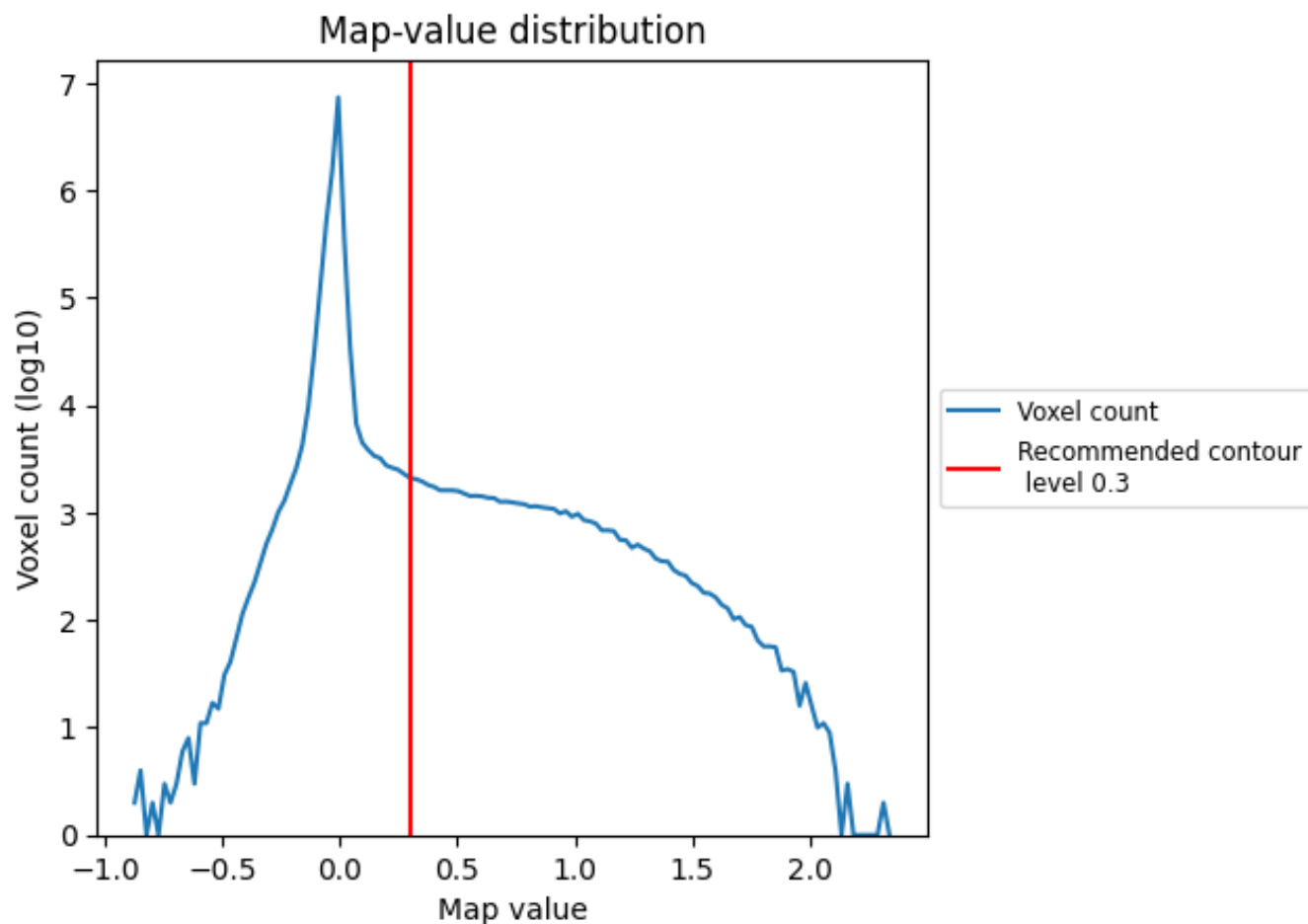


Z

7 Map analysis [i](#)

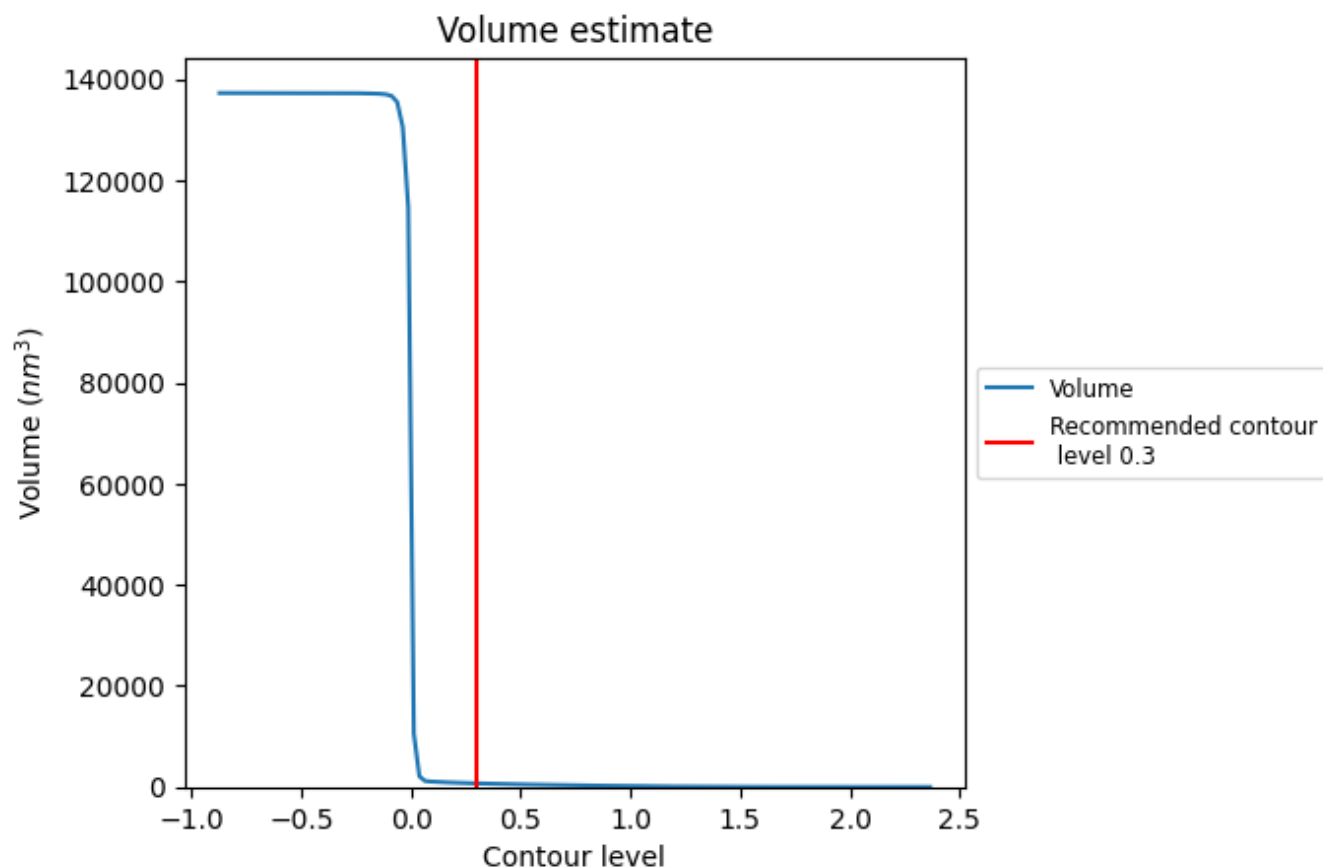
This section contains the results of statistical analysis of the map.

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.

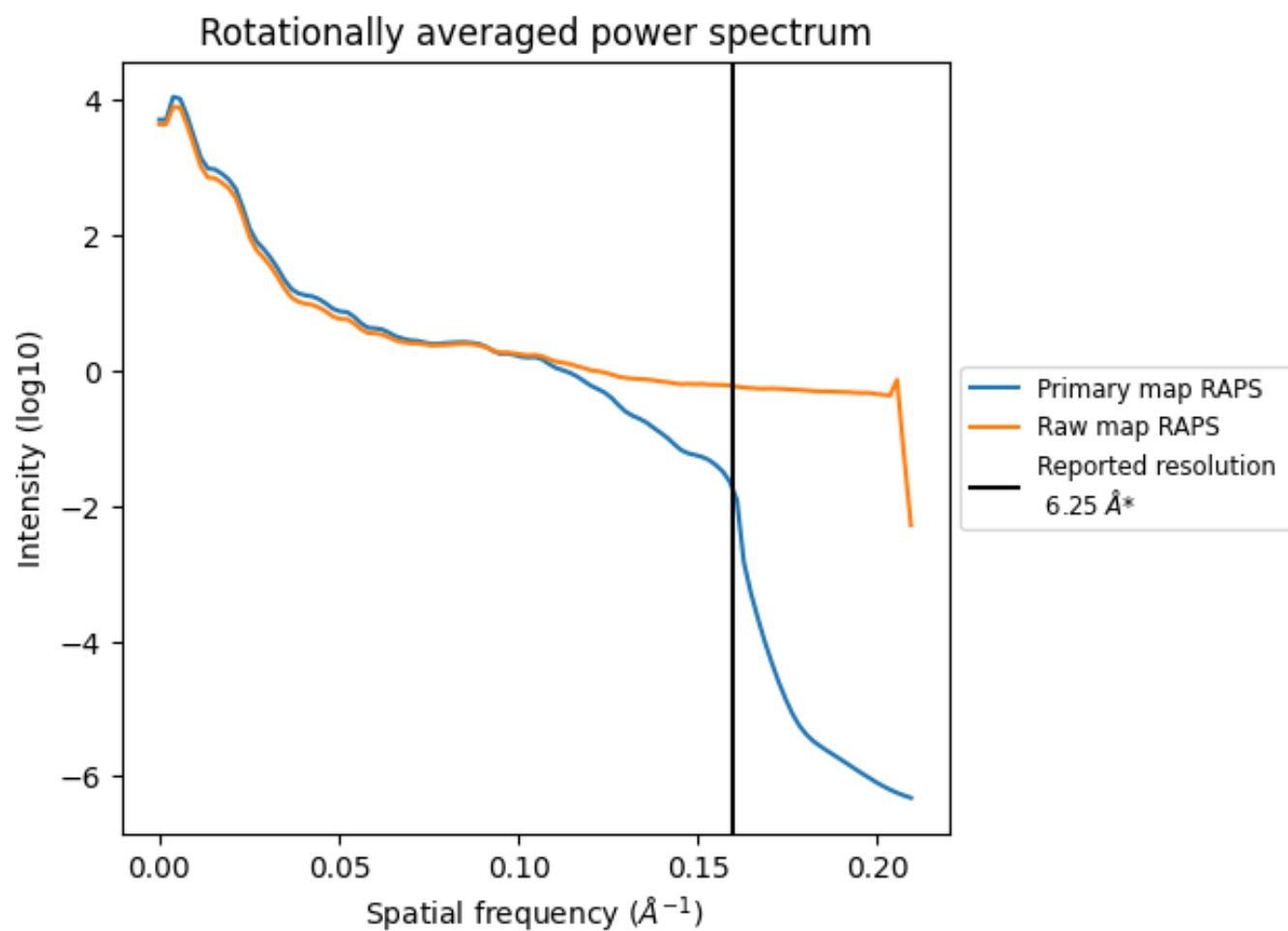
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 706 nm³; this corresponds to an approximate mass of 638 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 ⓘ

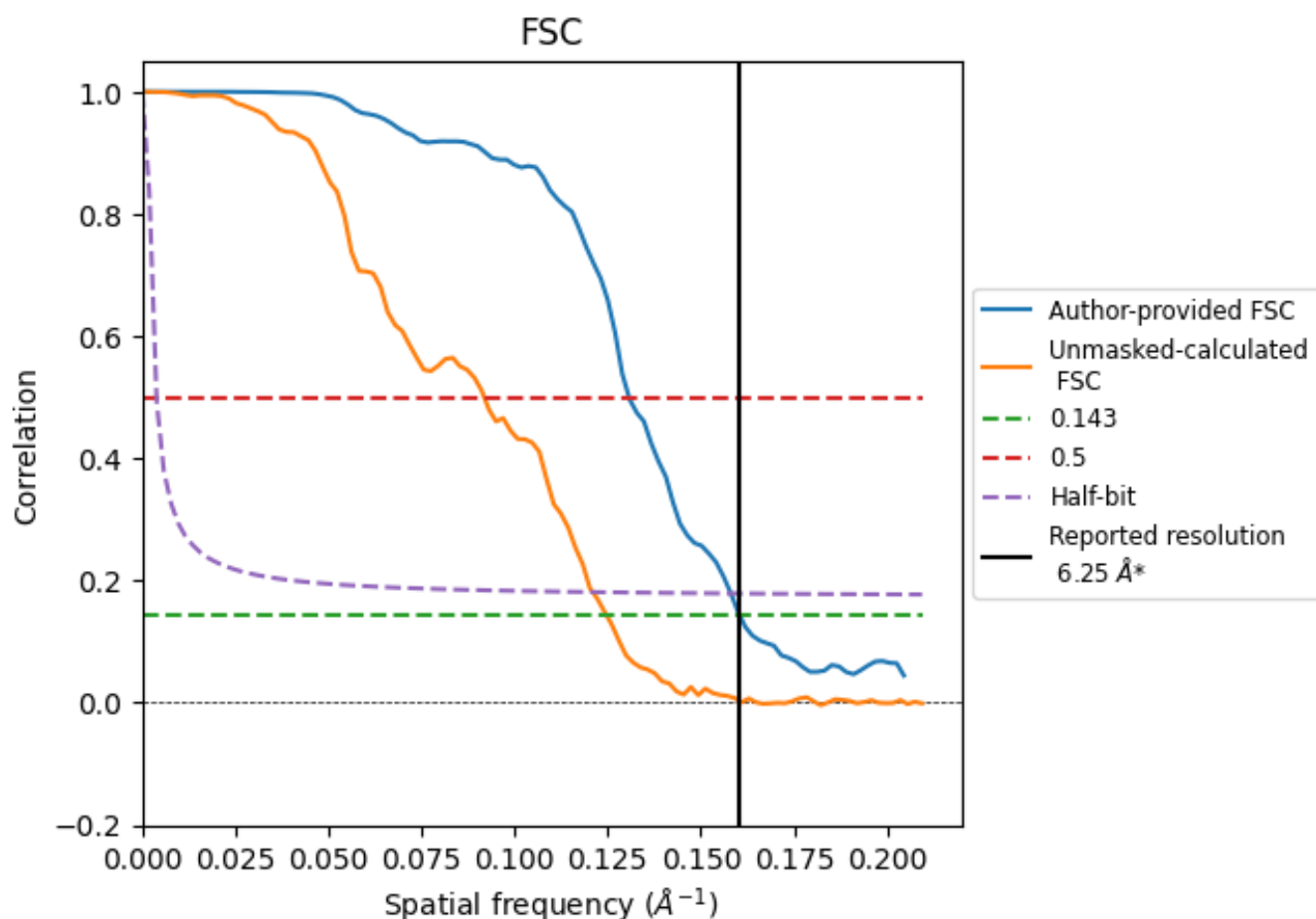


*Reported resolution corresponds to spatial frequency of $0.160 \text{ \AA}^{-1}$

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 0.160 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

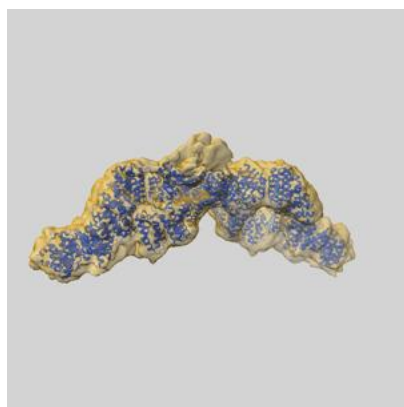
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.25	-	-
Author-provided FSC curve	6.23	7.65	6.33
Unmasked-calculated*	8.03	10.89	8.26

*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 8.03 differs from the reported value 6.25 by more than 10 %

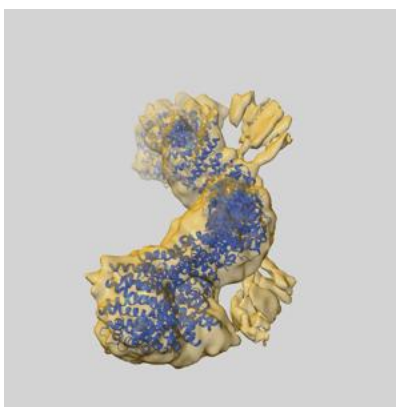
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23930 and PDB model 7MP6. Per-residue inclusion information can be found in section [3](#) on page [4](#).

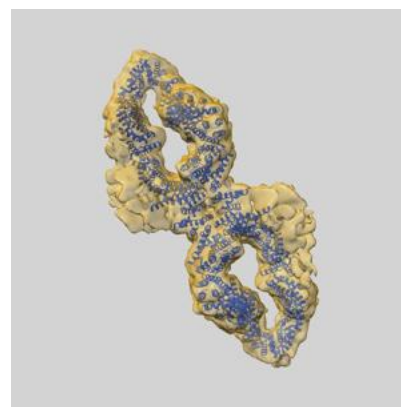
9.1 Map-model overlay [i](#)



X



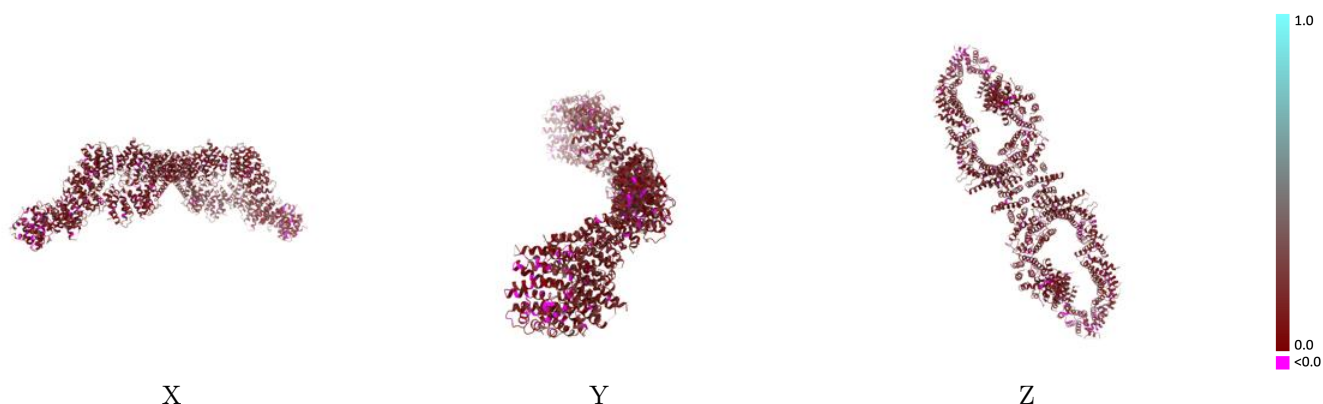
Y



Z

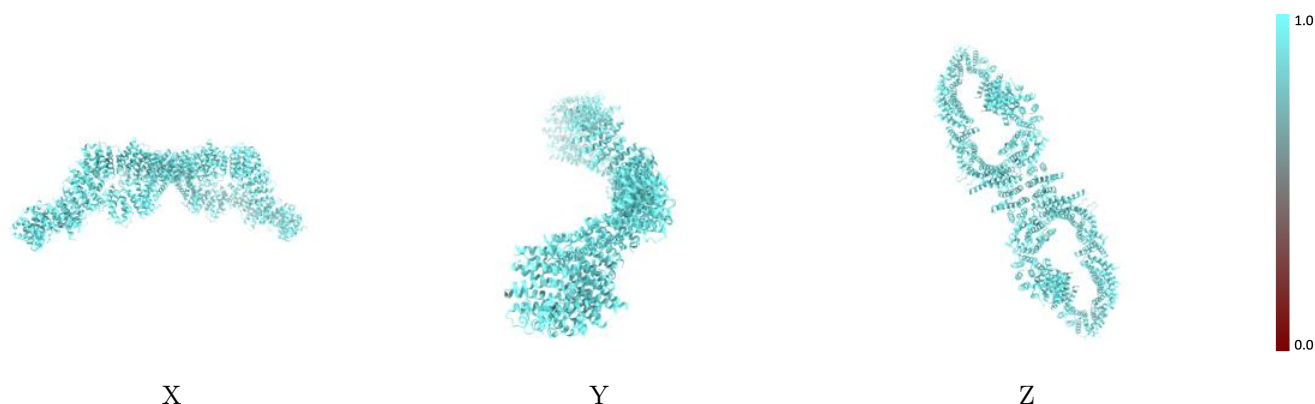
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



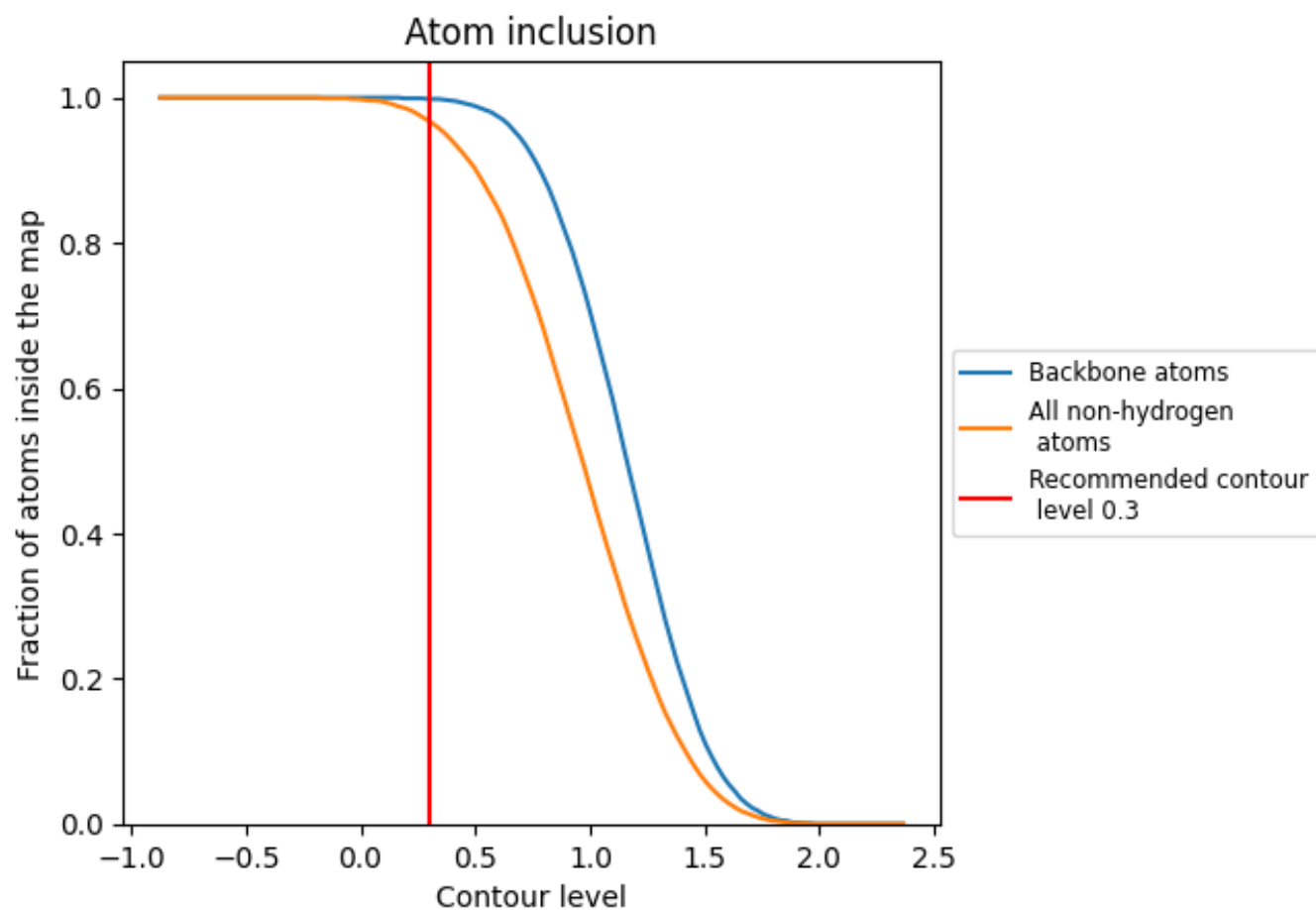
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 97% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9670	0.1400
A	0.9690	0.1400
B	0.9660	0.1390

