



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:44 AM UTC

PDB ID : 8FFJ / pdb_00008ffj
EMDB ID : EMD-29044
Title : Structure of Zanidatamab bound to HER2
Authors : Worrall, L.J.; Atkinson, C.E.; Sanches, M.; Dixit, S.; Strynadka, N.C.J.
Deposited on : 2022-12-08
Resolution : 7.50 Å(reported)

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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

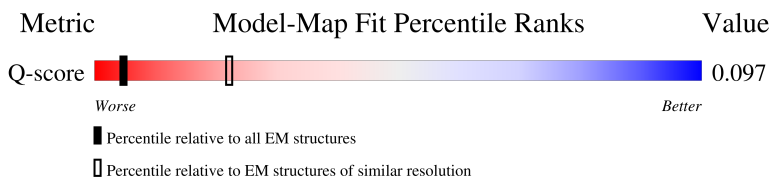
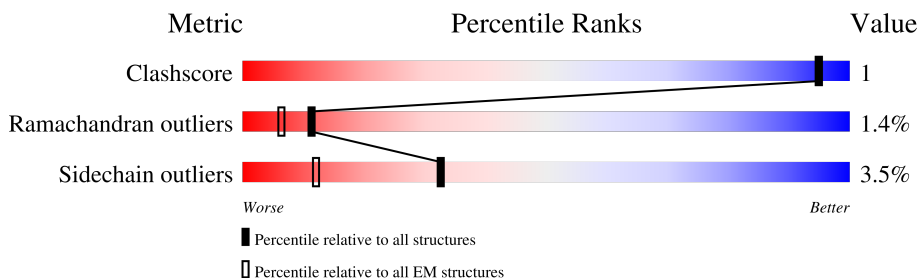
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

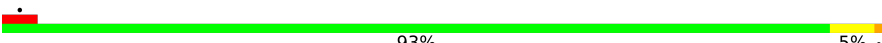
The reported resolution of this entry is 7.50 Å.

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	436 (7.00 - 8.00)

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	X	622	 93% 5% .
2	J	451	 41% 5% . 52%
3	Q	217	 5% 89% 9% .
4	I	483	 5% 22% . 75%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17582 atoms, of which 8614 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 Receptor tyrosine-protein kinase erbB-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	X	619	Total	C	H	N	O	S	0	0
			9298	2953	4542	849	898	56		

- Molecule 2 is a protein called Zanidatamab Heavy Chain A.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	J	217	Total	C	H	N	O	S	0	0
			3215	1029	1587	274	319	6		

- Molecule 3 is a protein called Zanidatamab Light Chain A.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	Q	214	Total	C	H	N	O	S	0	0
			3258	1043	1602	272	335	6		

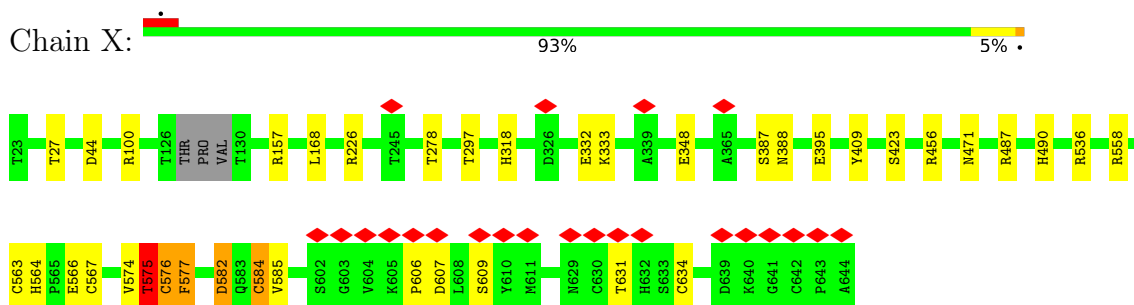
- Molecule 4 is a protein called Zanidatamab Heavy Chain B.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	I	120	Total	C	H	N	O	S	0	0
			1811	586	883	160	178	4		

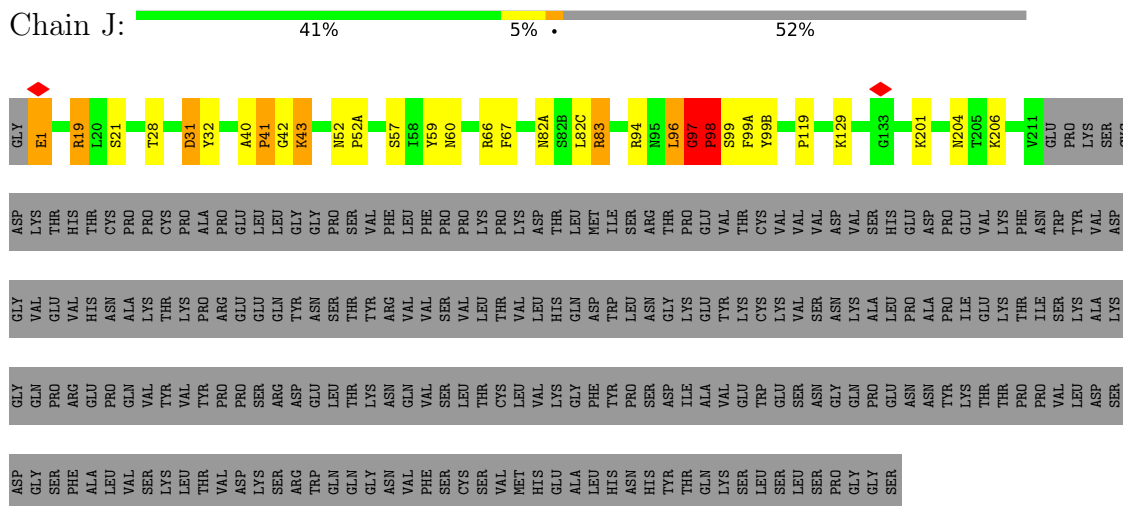
3 Residue-property plots

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.

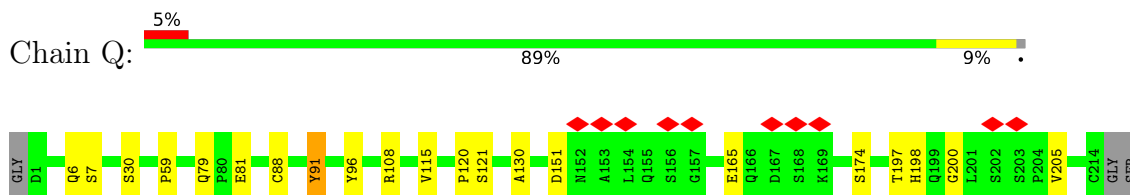
- Molecule 1: Receptor tyrosine-protein kinase erbB-2



- Molecule 2: Zanidatamab Heavy Chain A



- Molecule 3: Zanidatamab Light Chain A



- Molecule 4: Zanidatamab Heavy Chain B



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

GLY	GLY	SER	GLY	GLY	GLY	SER	GLY	E1	V2	Q3	L4	W5	E6	S7	G8	G9	G10	I11	V12	Q13	P14	G15	G16	S17	L18	R19	A23	G26	F27	N28	K30	B31	T32	H35	F41	G42	K43	T54	F68	S75	K76	Y96	R98	W99	G100	G101	Y105
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Y109	Q112	L115	S119	S120	ALA	GLU	PRO	TYR	GLY	SER	ASP	LYS	THR	HIS	THR	CYS	PRO	CYS	PRO	ALA	PRO	GLU	GLU	LEU	LEU	GLY	GLY	PRO	SER	VAL	PHE	LEU	PHE	PRO	PRO	LYS	PRO	LYS	ASP	THR	LEU	ASP	THR	LEU	ASP	THR	GLU	VAL	THR	CYS	VAL	VAL	VAL	ASP
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VAL	SER	HIS	GLU	ASP	PRO	GLU	VAL	LYS	PHE	ASN	TYR	TYR	VAL	ASP	GLY	VAL	GLU	VAL	HIS	ASN	LYS	THR	LYS	PRO	ARG	GLU	GLU	GLU	TYR	ASN	THR	THR	TYR	ARG	VAL	VAL	SER	VAL	VAL	THR	LEU	GLN	ASP	TRP	ASN	GLY	LYS	GLU	TYR	LYS	CYS	LYS	VAL	VAL	ASN
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LYS	ALA	LEU	PRO	ASN	ALA	PRO	ILE	GLU	THR	PRO	ILE	SER	LYS	ALA	GLY	GLN	PRO	ARG	GLU	PRO	GLN	VAL	TYR	VAL	LEU	PRO	PRO	LYS	SER	ARG	ASP	GLU	LEU	LYS	ASN	VAL	GLN	VAL	SER	LEU	LEU	LEU	CYS	VAL	LEU	VAL	LYS	GLY	ALA	PHE	THR	ASN	PRO	SER	ASP	ILE	THR	GLN	LYS	VAL	GLU	TRP	GLU	SER	ASN	GLY
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GLN	PRO	ASN	TYR	LEU	THR	PRO	PRO	VAL	LEU	ASP	SER	ASP	GLY	SER	PHE	PHE	LEU	TYR	SER	LYS	LEU	THR	VAL	LEU	THR	VAL	ASP	ARG	TRP	GLN	GLN	THR	ASN	ASN	VAL	PHE	SER	CYS	SER	VAL	MET	HIS	GLU	ALA	LEU	HIS	ASN	HIS	TYR	THR	GLN	LYS	SER	LEU	SER	LEU	PRO
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GLY	GLY	SER
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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	27589	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 ($e^-/\text{\AA}^2$)	110	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.925	Depositor
Minimum map value	-1.082	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	358.4, 358.4, 358.4	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4, 1.4, 1.4	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	X	0.93	1/4870 (0.0%)	1.43	10/6629 (0.2%)
2	J	0.85	0/1668	1.42	10/2273 (0.4%)
3	Q	0.82	0/1694	1.40	6/2301 (0.3%)
4	I	0.85	0/951	1.34	1/1291 (0.1%)
All	All	0.89	1/9183 (0.0%)	1.42	27/12494 (0.2%)

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	X	0	14
2	J	0	8
3	Q	0	2
4	I	0	4
All	All	0	28

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	575	THR	CA-C	5.16	1.59	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	X	584	CYS	CA-CB-SG	8.62	134.22	114.40
2	J	98	PRO	CA-N-CD	-8.20	100.52	112.00
2	J	97	GLY	CA-C-O	-7.62	110.62	121.52
1	X	582	ASP	CA-CB-CG	6.81	119.41	112.60
4	I	68	PHE	CA-CB-CG	6.78	120.58	113.80
1	X	575	THR	N-CA-C	6.70	122.35	114.04
3	Q	120	PRO	CA-C-N	6.26	133.50	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	120	PRO	C-N-CA	6.26	133.50	121.54
1	X	490	HIS	CB-CG-CD2	-6.17	123.18	131.20
2	J	98	PRO	N-CD-CG	6.00	112.20	103.20
1	X	576	CYS	N-CA-C	5.82	119.41	107.37
3	Q	7	SER	N-CA-C	5.80	113.44	108.22
2	J	40	ALA	CA-C-N	5.78	127.06	119.84
2	J	40	ALA	C-N-CA	5.78	127.06	119.84
3	Q	115	VAL	N-CA-C	5.67	116.64	108.48
2	J	98	PRO	N-CA-CB	5.57	109.10	103.25
2	J	60	ASN	CA-CB-CG	5.35	117.95	112.60
2	J	67	PHE	CA-CB-CG	5.32	119.12	113.80
1	X	318	HIS	CB-CG-CD2	-5.30	124.32	131.20
2	J	31	ASP	CA-CB-CG	5.22	117.82	112.60
2	J	66	ARG	NE-CZ-NH2	5.16	123.85	119.20
1	X	584	CYS	N-CA-CB	5.16	118.19	110.19
1	X	577	PHE	CA-CB-CG	5.15	118.95	113.80
1	X	471	ASN	CA-C-N	5.02	127.32	120.54
1	X	471	ASN	C-N-CA	5.02	127.32	120.54
3	Q	59	PRO	CA-C-N	5.02	127.70	120.38
3	Q	59	PRO	C-N-CA	5.02	127.70	120.38

There are no chirality outliers.

All (28) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	I	109	TYR	Sidechain
4	I	32	THR	Peptide
4	I	95	TYR	Sidechain
4	I	98	ARG	Peptide
2	J	1	GLU	Peptide
2	J	119	PRO	Peptide
2	J	19	ARG	Sidechain
2	J	32	TYR	Sidechain
2	J	82(A)	ASN	Peptide
2	J	83	ARG	Sidechain
2	J	96	LEU	Peptide
2	J	98	PRO	Peptide
3	Q	165	GLU	Peptide
3	Q	91	TYR	Sidechain
1	X	100	ARG	Sidechain
1	X	157	ARG	Sidechain
1	X	226	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	X	332	GLU	Peptide
1	X	387	SER	Peptide
1	X	409	TYR	Sidechain
1	X	456	ARG	Sidechain
1	X	487	ARG	Sidechain
1	X	536	ARG	Sidechain
1	X	558	ARG	Sidechain
1	X	563	CYS	Peptide
1	X	564	HIS	Peptide
1	X	575	THR	Mainchain
1	X	582	ASP	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	X	4756	4542	4538	8	0
2	J	1628	1587	1588	8	0
3	Q	1656	1602	1605	4	0
4	I	928	883	885	2	0
All	All	8968	8614	8616	19	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 1.

All (19) 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:X:576:CYS:HA	1:X:584:CYS:H	1.62	0.65
2:J:97:GLY:HA2	2:J:99(B):TYR:CD1	2.35	0.62
1:X:575:THR:C	1:X:584:CYS:HB2	2.27	0.60
2:J:99(B):TYR:CD1	3:Q:91:TYR:CE1	2.98	0.51
1:X:333:LYS:HD2	2:J:98:PRO:HB3	1.93	0.51
4:I:99:TRP:CZ3	4:I:105:TYR:CD2	2.99	0.51
1:X:577:PHE:H	1:X:584:CYS:N	2.09	0.49
4:I:35:HIS:HE2	4:I:99:TRP:CG	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:567:CYS:SG	1:X:576:CYS:C	2.97	0.48
2:J:99(A):PHE:CD2	3:Q:96:TYR:CE2	3.01	0.47
1:X:567:CYS:HA	1:X:575:THR:H	1.81	0.46
2:J:42:GLY:C	2:J:43:LYS:HE3	2.43	0.44
2:J:82(C):LEU:H	2:J:82(C):LEU:HD23	1.83	0.43
3:Q:6:GLN:NE2	3:Q:88:CYS:H	2.16	0.43
3:Q:198:HIS:CD2	3:Q:200:GLY:H	2.37	0.43
1:X:395:GLU:H	1:X:395:GLU:CD	2.27	0.42
1:X:566:GLU:O	1:X:575:THR:HB	2.20	0.41
2:J:97:GLY:CA	2:J:99(B):TYR:CD1	3.04	0.41
2:J:96:LEU:O	2:J:98:PRO:HD3	2.22	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	X	615/622 (99%)	533 (87%)	75 (12%)	7 (1%)	11	46
2	J	215/451 (48%)	196 (91%)	15 (7%)	4 (2%)	6	32
3	Q	212/217 (98%)	186 (88%)	22 (10%)	4 (2%)	6	32
4	I	118/483 (24%)	107 (91%)	10 (8%)	1 (1%)	16	54
All	All	1160/1773 (65%)	1022 (88%)	122 (10%)	16 (1%)	11	40

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	348	GLU
1	X	388	ASN
2	J	99	SER
3	Q	121	SER

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Mol	Chain	Res	Type
3	Q	151	ASP
1	X	585	VAL
1	X	606	PRO
1	X	607	ASP
1	X	609	SER
2	J	204	ASN
3	Q	130	ALA
4	I	101	GLY
1	X	634	CYS
2	J	41	PRO
3	Q	205	VAL
2	J	97	GLY

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	X	533/536 (99%)	525 (98%)	8 (2%)	57	72
2	J	182/396 (46%)	166 (91%)	16 (9%)	9	28
3	Q	188/189 (100%)	182 (97%)	6 (3%)	34	55
4	I	95/408 (23%)	90 (95%)	5 (5%)	20	41
All	All	998/1529 (65%)	963 (96%)	35 (4%)	32	53

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	27	THR
1	X	44	ASP
1	X	168	LEU
1	X	278	THR
1	X	297	THR
1	X	423	SER
1	X	574	VAL
1	X	631	THR
2	J	1	GLU

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Mol	Chain	Res	Type
2	J	19	ARG
2	J	21	SER
2	J	28	THR
2	J	31	ASP
2	J	41	PRO
2	J	43	LYS
2	J	52	ASN
2	J	52(A)	PRO
2	J	57	SER
2	J	59	TYR
2	J	83	ARG
2	J	94	ARG
2	J	129	LYS
2	J	201	LYS
2	J	206	LYS
3	Q	30	SER
3	Q	79	GLN
3	Q	81	GLU
3	Q	108	ARG
3	Q	174	SER
3	Q	197	THR
4	I	3	GLN
4	I	12	VAL
4	I	30	LYS
4	I	43	LYS
4	I	54	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	54	GLN
1	X	57	GLN
1	X	239	GLN
1	X	257	HIS
1	X	318	HIS
1	X	473	HIS
1	X	484	GLN
1	X	527	GLN
1	X	548	GLN
1	X	564	HIS
1	X	568	GLN
1	X	570	GLN

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Mol	Chain	Res	Type
1	X	583	GLN
1	X	624	GLN
1	X	632	HIS
3	Q	89	GLN
3	Q	160	GLN
3	Q	166	GLN
4	I	3	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

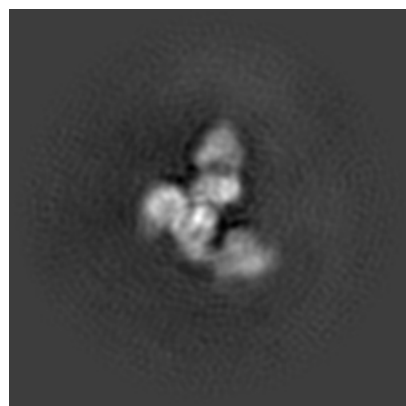
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29044. These allow visual inspection of the internal detail of the map and identification of artifacts.

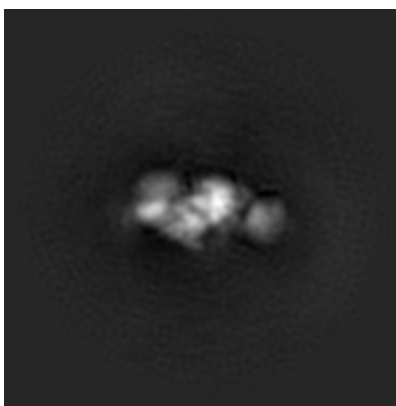
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

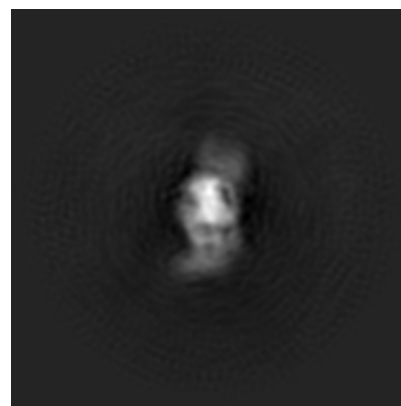
6.1.1 Primary map



X

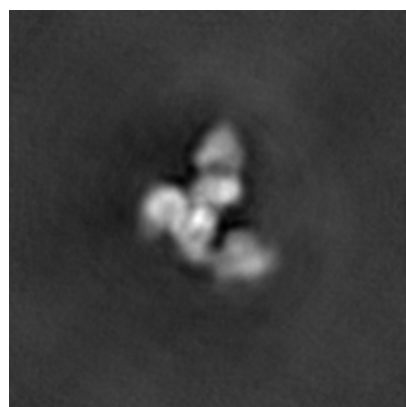


Y

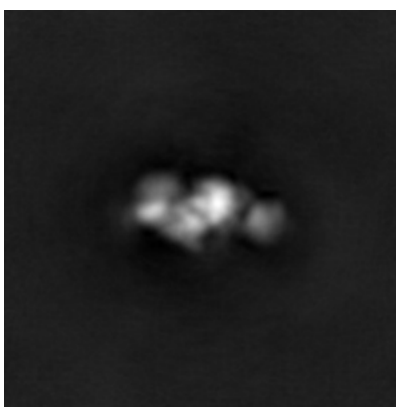


Z

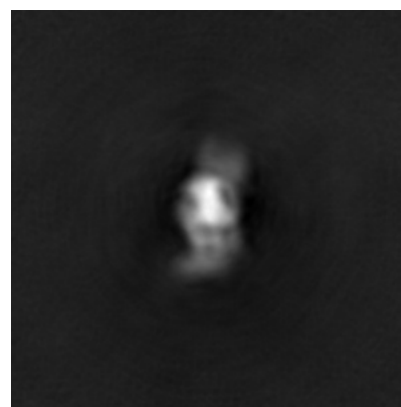
6.1.2 Raw map



X



Y

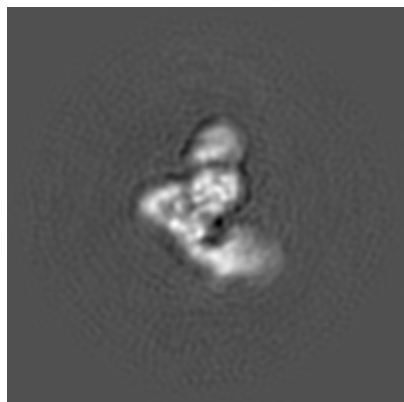


Z

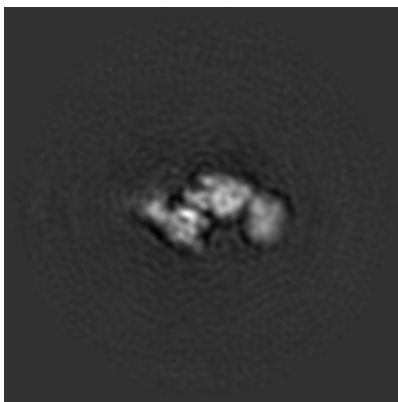
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

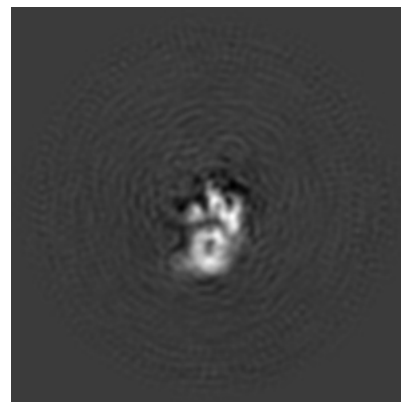
6.2.1 Primary map



X Index: 128

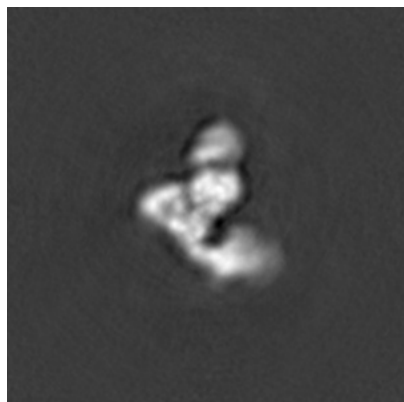


Y Index: 128

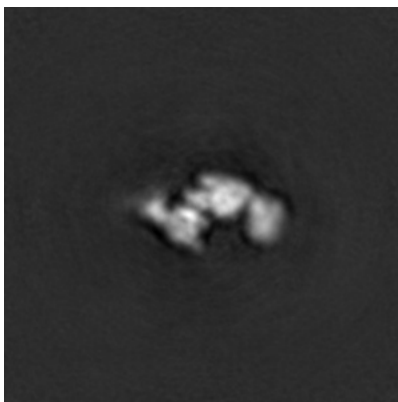


Z Index: 128

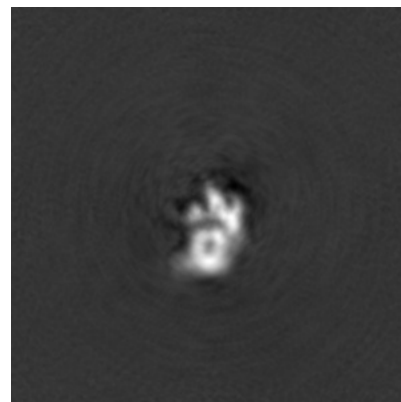
6.2.2 Raw map



X Index: 128



Y Index: 128

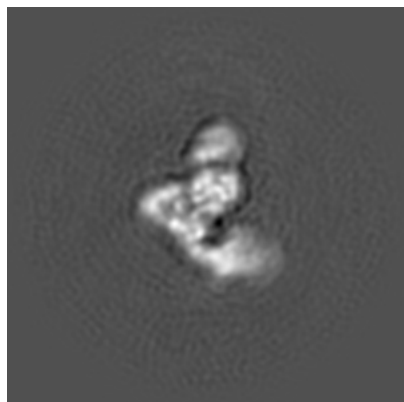


Z Index: 128

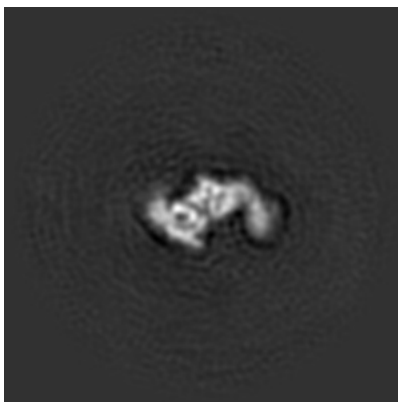
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

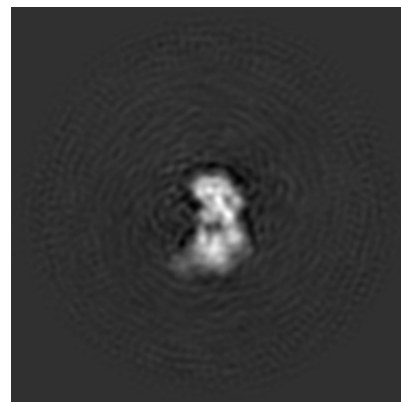
6.3.1 Primary map



X Index: 128

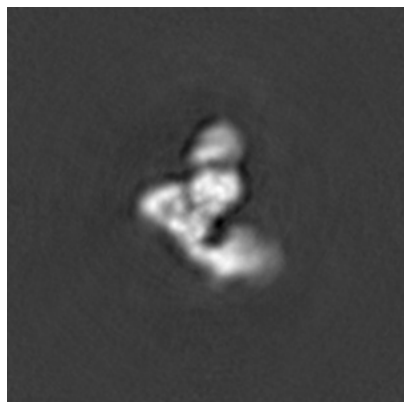


Y Index: 123

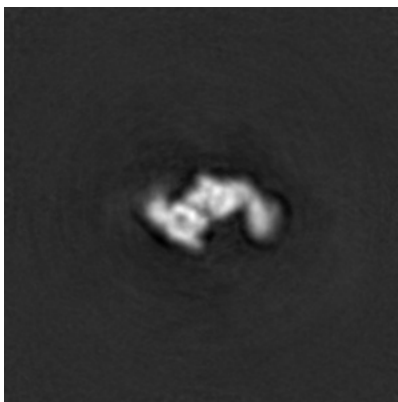


Z Index: 135

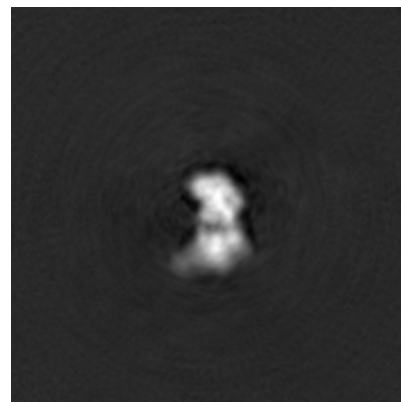
6.3.2 Raw map



X Index: 128



Y Index: 124



Z Index: 136

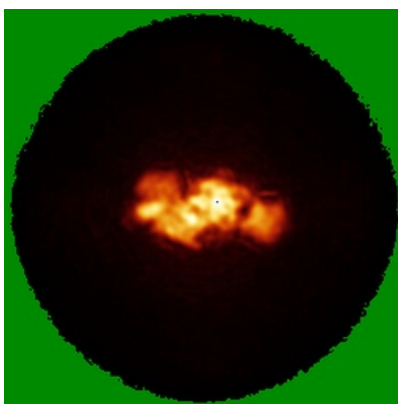
The images above show the largest variance slices of the map in three orthogonal directions.

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

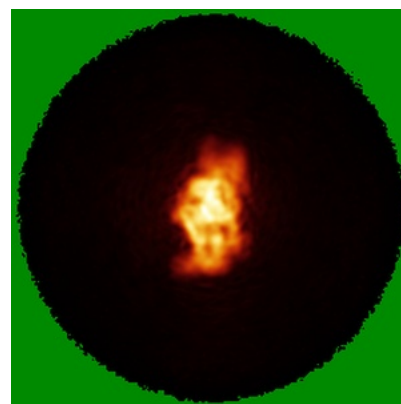
6.4.1 Primary map



X

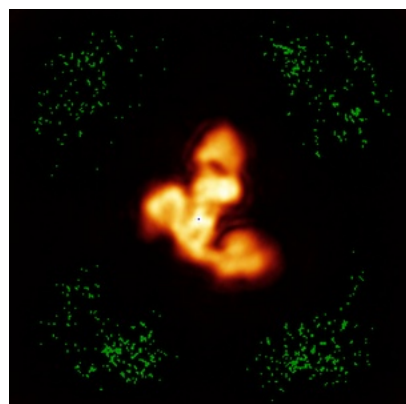


Y

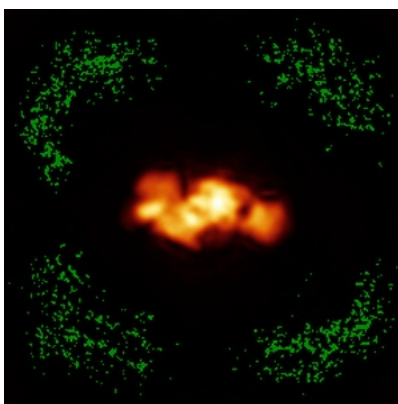


Z

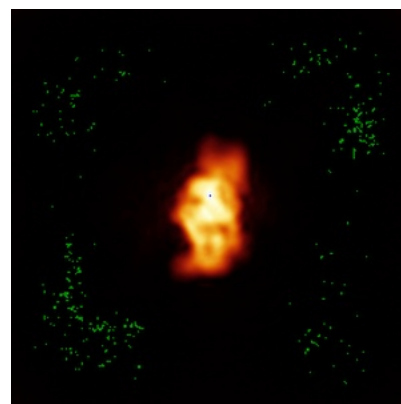
6.4.2 Raw map



X



Y

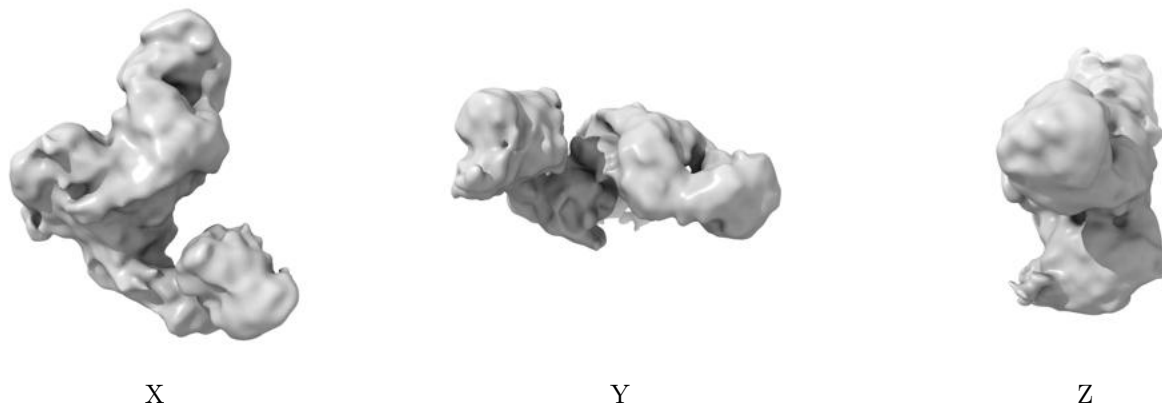


Z

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 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

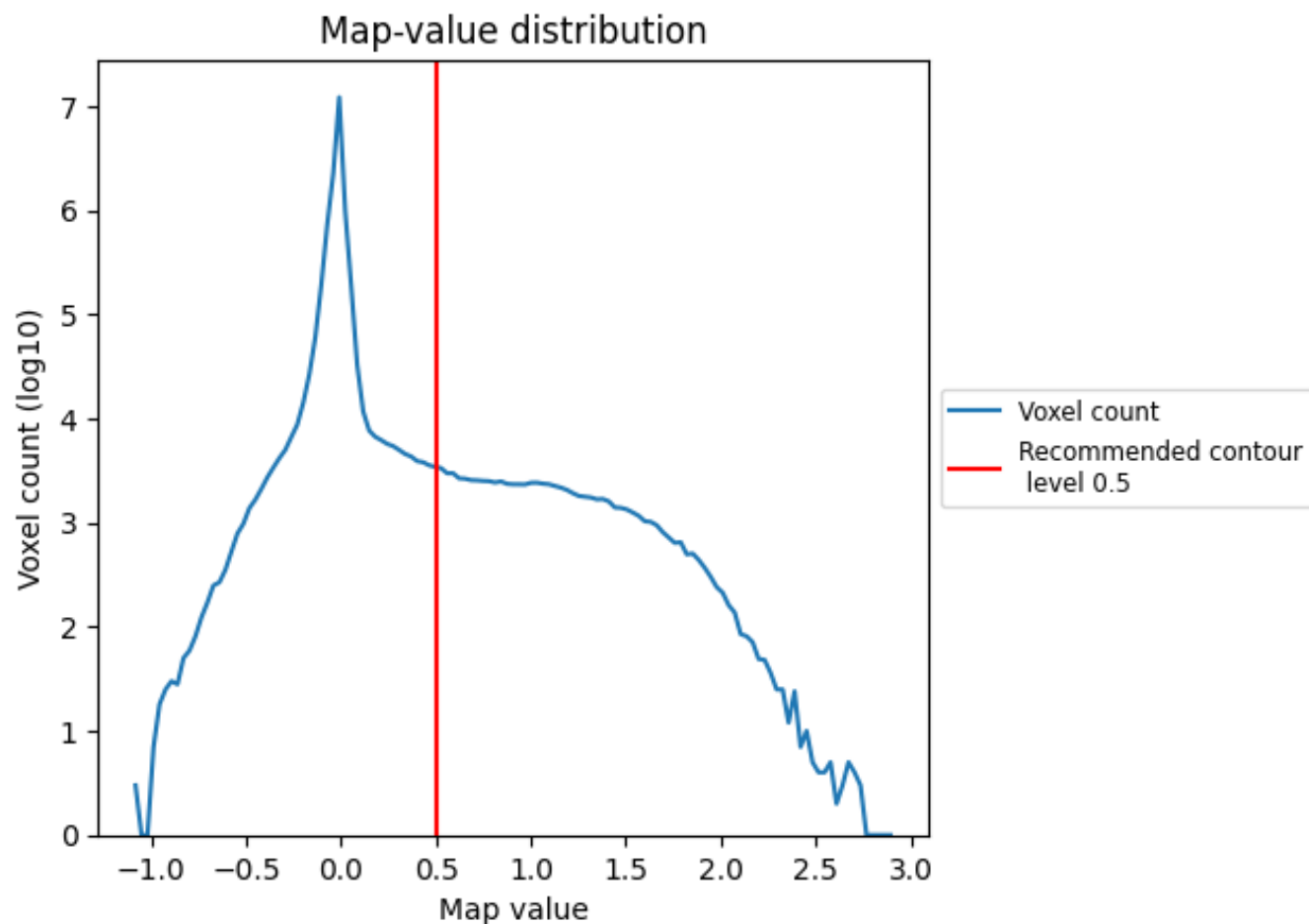
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

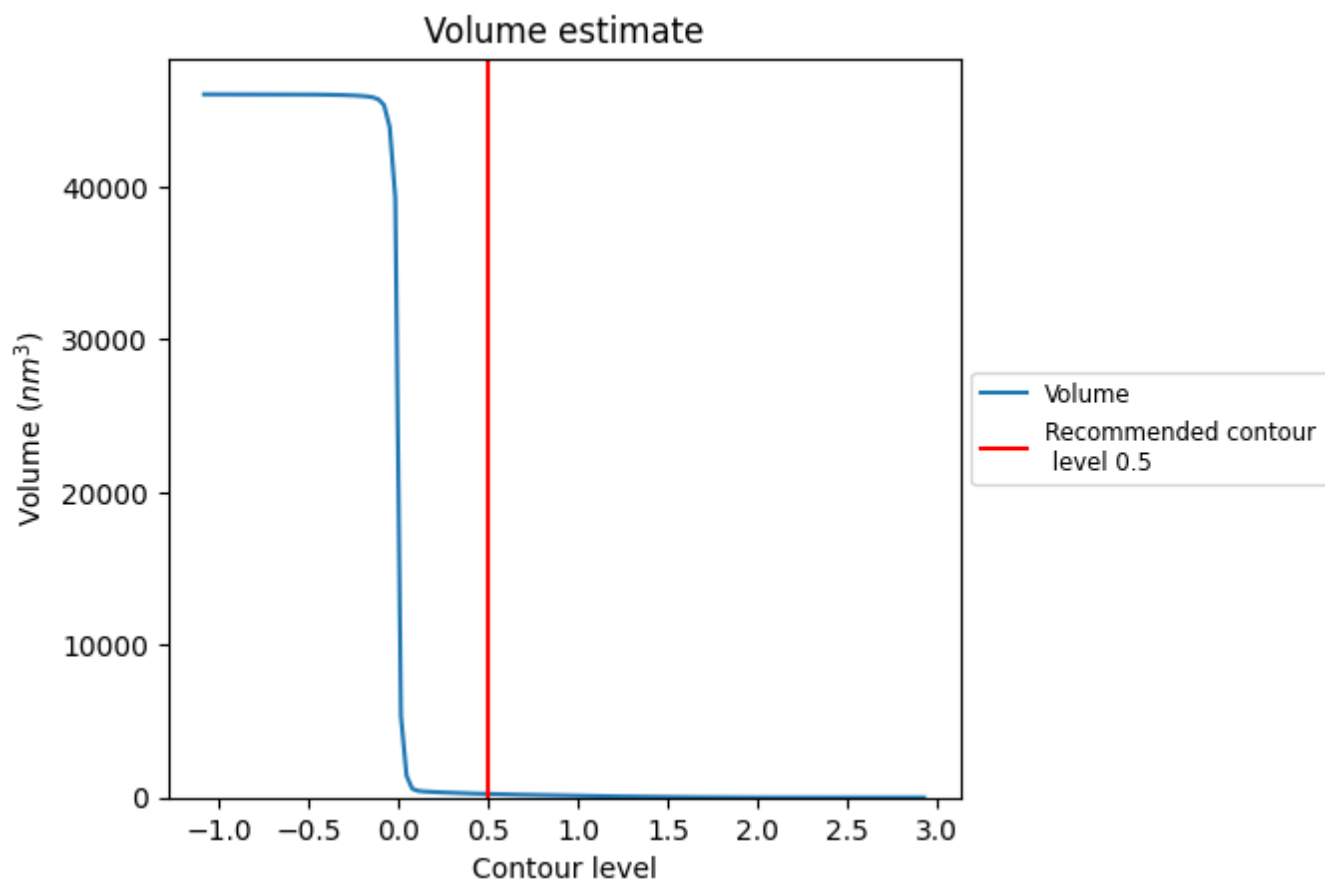
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

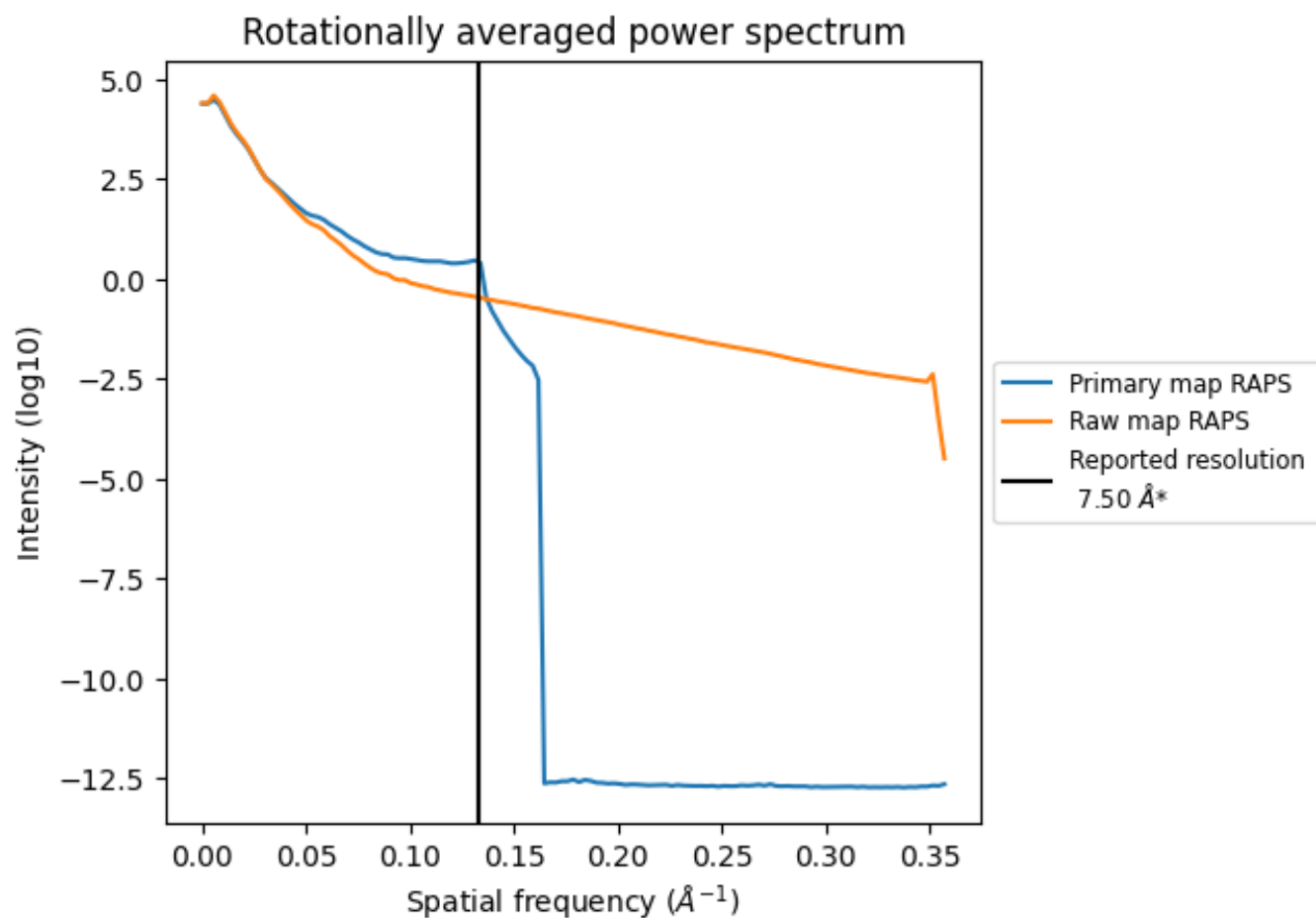
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 235 nm^3 ; this corresponds to an approximate mass of 213 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 ⓘ

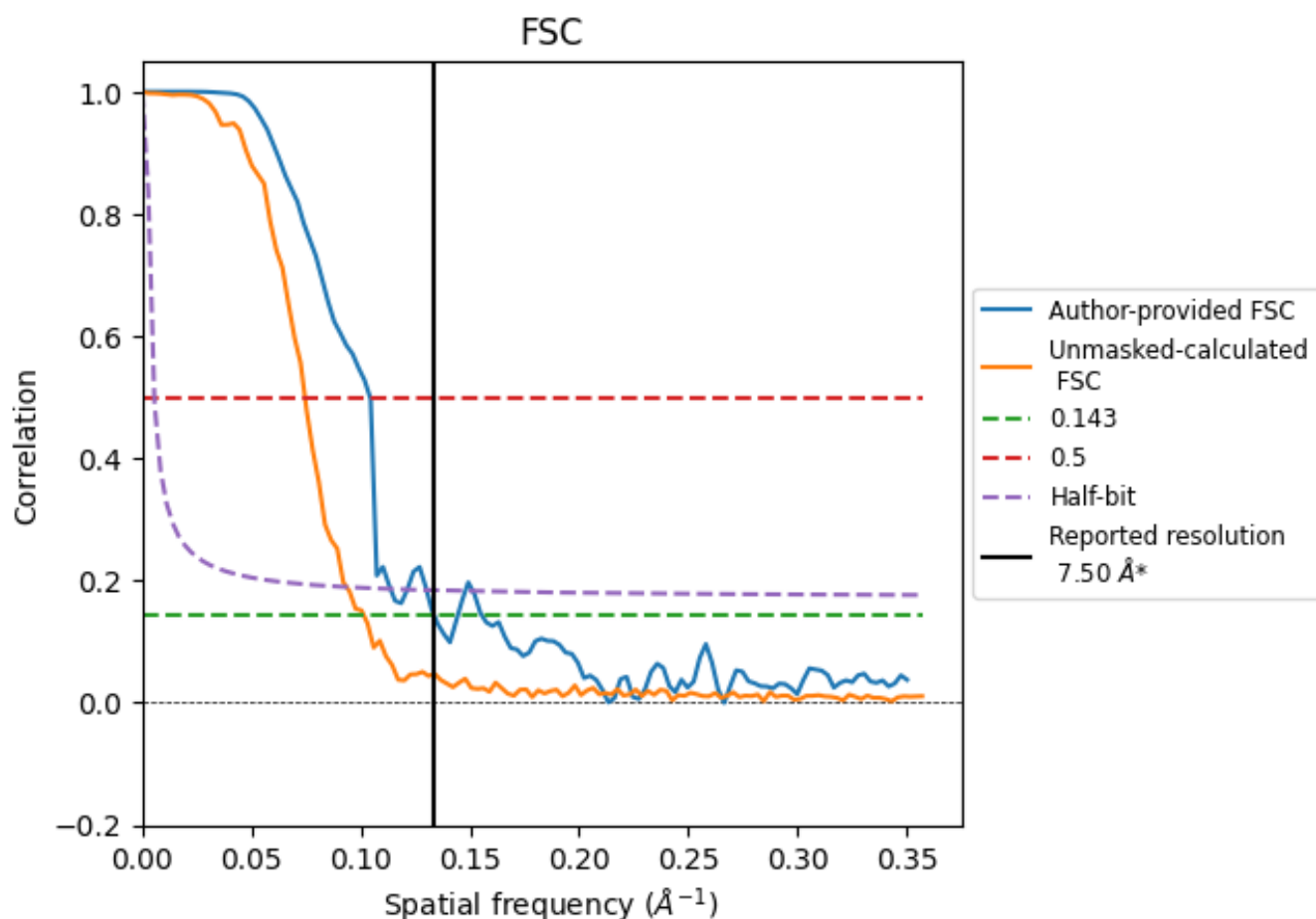


*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

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 0.133 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

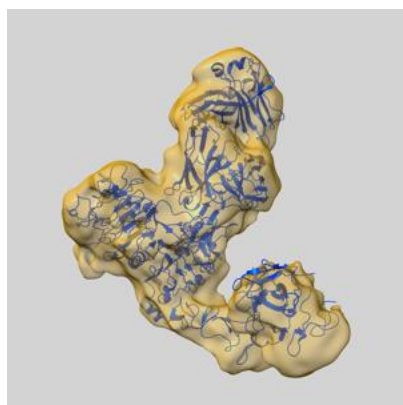
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.50	-	-
Author-provided FSC curve	7.48	9.59	8.80
Unmasked-calculated*	9.85	13.42	10.70

*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 9.85 differs from the reported value 7.5 by more than 10 %

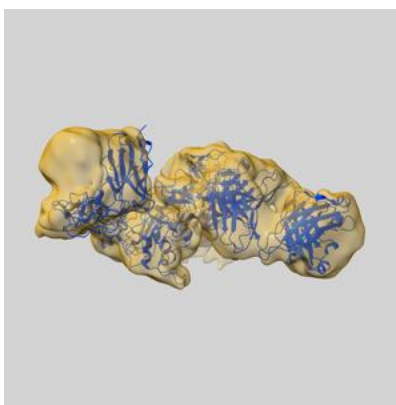
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29044 and PDB model 8FFJ. Per-residue inclusion information can be found in section [3](#) on page [4](#).

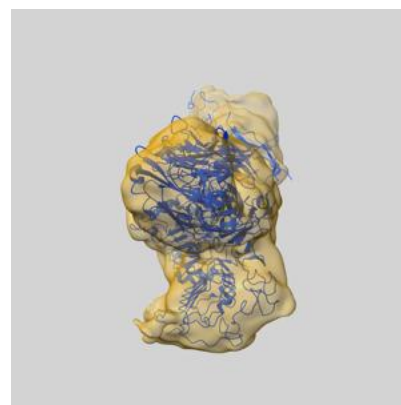
9.1 Map-model overlay [i](#)



X



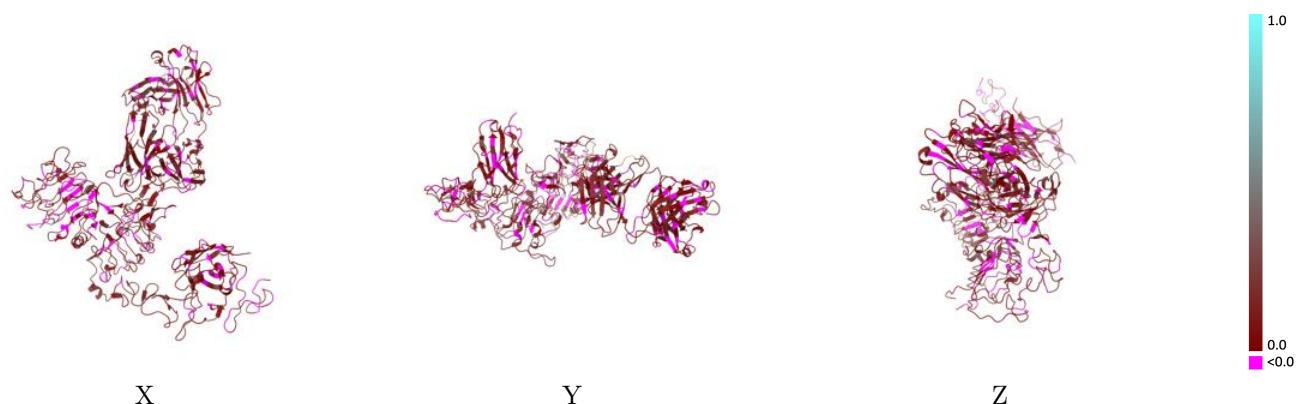
Y



Z

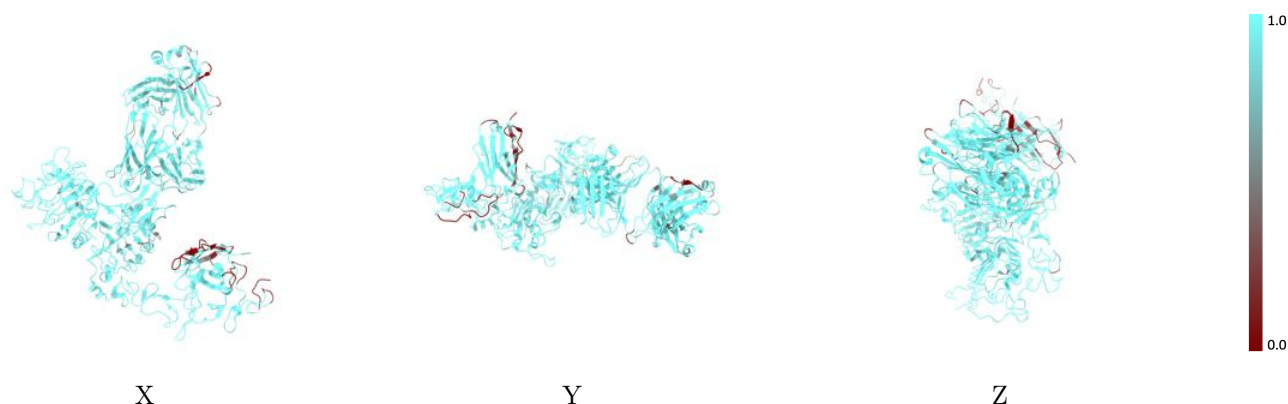
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



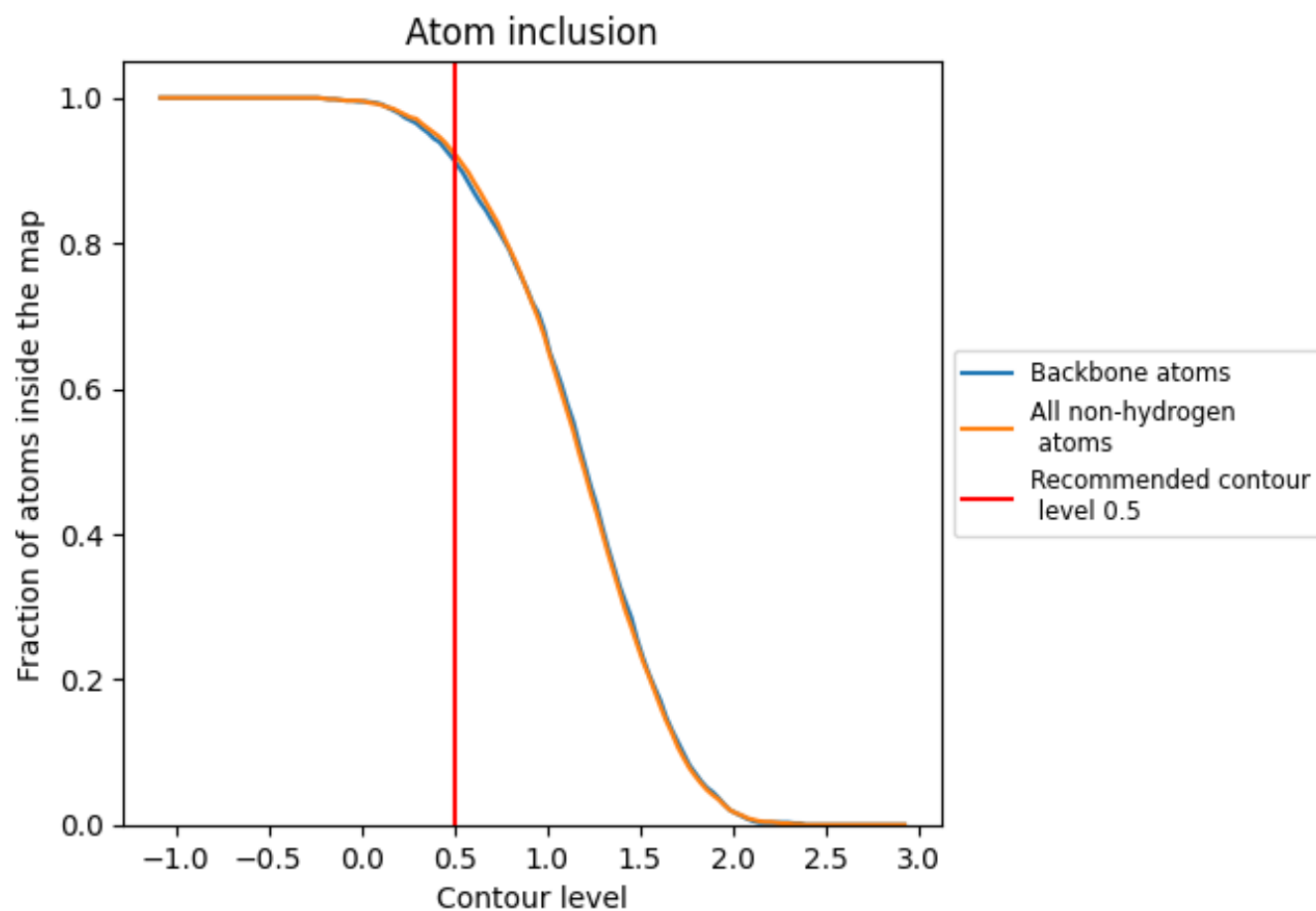
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9230	0.0970
I	0.7720	0.0830
J	0.9710	0.1030
Q	0.9270	0.0930
X	0.9420	0.0990

