



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:42 PM UTC

PDB ID : 8TQI / pdb_00008tqi
EMDB ID : EMD-41505
Title : Hemagglutinin-neuraminidase from Human parainfluenza virus type 3:
complex with rPIV3-23 and rPIV3-28 Fabs
Authors : Otrelo-Cardoso, A.R.; Jardetzky, T.S.
Deposited on : 2023-08-07
Resolution : 3.24 Å(reported)

This is a wwPDB EM Validation Summary 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:

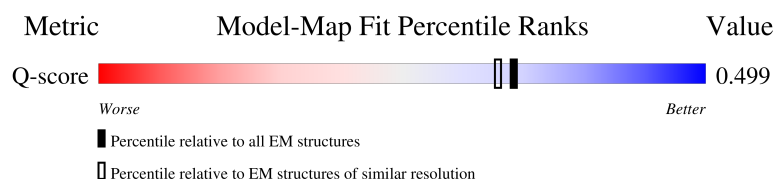
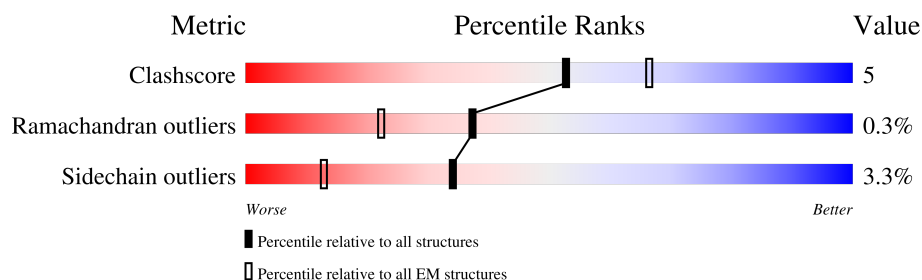
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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



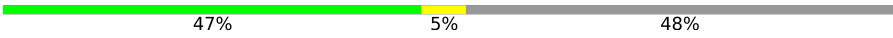
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14594 (2.74 - 3.74)

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	454	 78% 13% • 7%
1	B	454	 80% 11% • 7%
2	C	223	 41% 9% 51%
2	H	223	 48% 6% 46%

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Mol	Chain	Length	Quality of chain
3	D	214	 47% 50%
3	L	214	 47% 5% 48%
4	E	235	 39% 57%
4	I	235	 42% 53%
5	F	213	 34% 6% 60%
5	J	213	 35% 65%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 24359 atoms, of which 11831 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 Hemagglutinin-neuraminidase.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	422	Total	C	H	N	O	S	0	0
			6344	2050	3112	551	611	20		
1	B	420	Total	C	H	N	O	S	0	0
			6349	2046	3118	553	612	20		

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	573	GLY	-	expression tag	UNP P08492
A	574	SER	-	expression tag	UNP P08492
A	575	GLU	-	expression tag	UNP P08492
A	576	ASN	-	expression tag	UNP P08492
A	577	LEU	-	expression tag	UNP P08492
A	578	TYR	-	expression tag	UNP P08492
A	579	PHE	-	expression tag	UNP P08492
A	580	GLN	-	expression tag	UNP P08492
A	581	GLY	-	expression tag	UNP P08492
A	582	GLY	-	expression tag	UNP P08492
A	583	SER	-	expression tag	UNP P08492
A	584	HIS	-	expression tag	UNP P08492
A	585	HIS	-	expression tag	UNP P08492
A	586	HIS	-	expression tag	UNP P08492
A	587	HIS	-	expression tag	UNP P08492
A	588	HIS	-	expression tag	UNP P08492
A	589	HIS	-	expression tag	UNP P08492
B	573	GLY	-	expression tag	UNP P08492
B	574	SER	-	expression tag	UNP P08492
B	575	GLU	-	expression tag	UNP P08492
B	576	ASN	-	expression tag	UNP P08492
B	577	LEU	-	expression tag	UNP P08492
B	578	TYR	-	expression tag	UNP P08492
B	579	PHE	-	expression tag	UNP P08492
B	580	GLN	-	expression tag	UNP P08492
B	581	GLY	-	expression tag	UNP P08492

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Chain	Residue	Modelled	Actual	Comment	Reference
B	582	GLY	-	expression tag	UNP P08492
B	583	SER	-	expression tag	UNP P08492
B	584	HIS	-	expression tag	UNP P08492
B	585	HIS	-	expression tag	UNP P08492
B	586	HIS	-	expression tag	UNP P08492
B	587	HIS	-	expression tag	UNP P08492
B	588	HIS	-	expression tag	UNP P08492
B	589	HIS	-	expression tag	UNP P08492

- Molecule 2 is a protein called Heavy chain Fab rPIV3-28.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C	110	Total	C	H	N	O	S	0	0
			1548	504	748	130	161	5		
2	H	120	Total	C	H	N	O	S	0	0
			1687	544	820	144	174	5		

- Molecule 3 is a protein called Light chain Fab rPIV3-28.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	106	Total	C	H	N	O	S	0	0
			1543	505	745	126	164	3		
3	L	111	Total	C	H	N	O	S	0	0
			1636	533	793	133	174	3		

- Molecule 4 is a protein called Heavy chain Fab rPIV3-23.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	102	Total	C	H	N	O	S	0	0
			1444	483	688	121	147	5		
4	I	110	Total	C	H	N	O	S	0	0
			1625	531	789	135	165	5		

- Molecule 5 is a protein called Light chain Fab rPIV3-23.

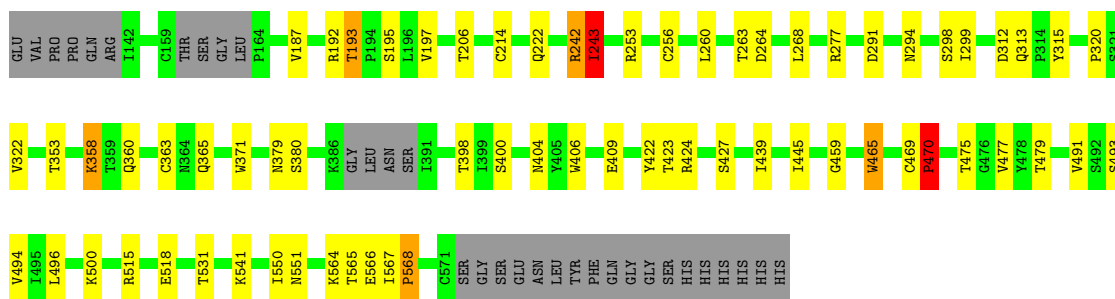
Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	85	Total	C	H	N	O	S	0	0
			1143	387	533	100	120	3		
5	J	75	Total	C	H	N	O	S	0	0
			1040	357	485	87	109	2		

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.

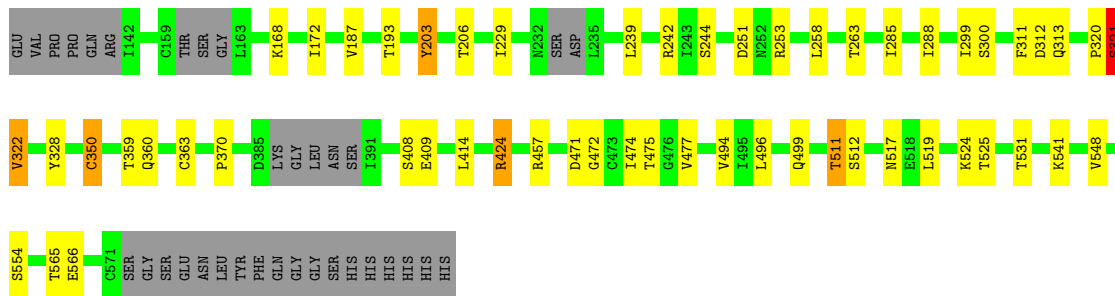
• Molecule 1: Hemagglutinin-neuraminidase

Chain A: 



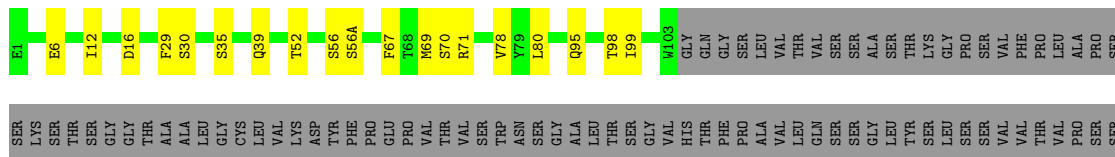
• Molecule 1: Hemagglutinin-neuraminidase

Chain B: 



• Molecule 2: Heavy chain Fab rPIV3-28

Chain C: 



SER	LEU	GLY	THR	GLN	THR	TYR	THR	ILE	CYS
SER	LEU	GLY	THR	GLN	THR	TYR	THR	ILE	CYS

● Molecule 2: Heavy chain Fab rPIV3-28



E1	V2	K3	L4	S17	W36	M69	D82A	S82B	L82C	T87	T98	I99	L100	T110	V111	S112	S113	ALA	SER	THR	THR	LYS	PRO	SER	VAL	VAL	PHE	PRO	LEU	LEU	PRO	SER	SER	SER	LEU	GLY	THR	THR	GLY	GLY	THR	THR	ALA	ALA	LEU	GLY	CYS	LEU	VAL	VAL	ASP	THR	PHE	PRO	GLU
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PRO	VAL	THR	VAL	SER	TRP	ASN	GLY	LEU	THR	SER	GLY	HIS	THR	PHE	PRO	ALA	VAL	GLN	SER	SER	GLY	LEU	SER	SER	VAL	VAL	THR	THR	VAL	PRO	SER	SER	SER	LEU	GLY	THR	THR	TYR	ILE	CYS	VAL	ASN	GLY	CYS	LEU	VAL	PRO	VAL	SER	ASN	THR	LYS	PHE	VAL	ASP
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LYS	LYS	VAL	GLU	PRO	LYS	SER	CYS
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● Molecule 3: Light chain Fab rPIV3-28



D1	Q37	G64	T69	T76	D82	V104	E105	I106	LYS	ARG	THR	VAL	ALA	ALA	PRO	SER	VAL	PHE	ILE	PHE	PHE	THR	LEU	PRO	PRO	SER	ASP	GLU	GLN	GLN	ALA	LYS	THR	GLY	THR	ALA	VAL	VAL	VAL	ASN	ASN	PHE	TYR	PRO	ARG	GLU	GLU	ALA	LYS	VAL	THR	GLN	TRP	LYS	VAL	ASP
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ASN	ALA	LEU	GLN	SER	GLY	ASN	SER	GLN	ARG	VAL	THR	LYS	ASP	SER	THR	TYR	PRO	SER	VAL	PHE	SER	THR	THR	LEU	PRO	PRO	SER	SER	LYS	ALA	ALA	ASP	TYR	GLU	LYS	HIS	LYS	VAL	TYR	ALA	CYS	GLU	VAL	THR	HIS	GLN	GLY	LEU	ARG	SER	GLU	ALA	PRO	VAL	VAL	THR	LYS	SER	PHE	ASN	ASP	ARG
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GLY	GLU	CYS
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● Molecule 3: Light chain Fab rPIV3-28



D1	L11	Q24	Q27	L33	S60	S67	G68	F71	D93	L94	A111	ALA	PRO	THR	SER	LEU	VAL	PHE	ILE	PHE	THR	LEU	PRO	PRO	THR	LEU	SER	ASP	GLU	GLN	GLN	ALA	LYS	THR	GLY	THR	ALA	VAL	VAL	VAL	LEU	LEU	ASN	HIS	ASN	PHE	THR	PRO	ARG	GLU	PRO	VAL	VAL	LYS	THR	GLN	TRP	LYS	VAL
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ASP	ASN	ALA	LEU	GLN	SER	GLY	ASN	SER	GLN	GLN	VAL	THR	GLU	GLN	ASP	SER	LYS	ASP	THR	THR	SER	LEU	SER	SER	THR	LEU	PRO	SER	SER	LYS	ASP	TYR	GLU	LYS	HIS	VAL	VAL	TYR	ALA	CYS	GLU	VAL	THR	HIS	GLN	GLY	LEU	ARG	THR	PRO	GLU	ALA	VAL	VAL	LYS	THR	LYS	PHE	ASN
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ARG	GLY	CYS
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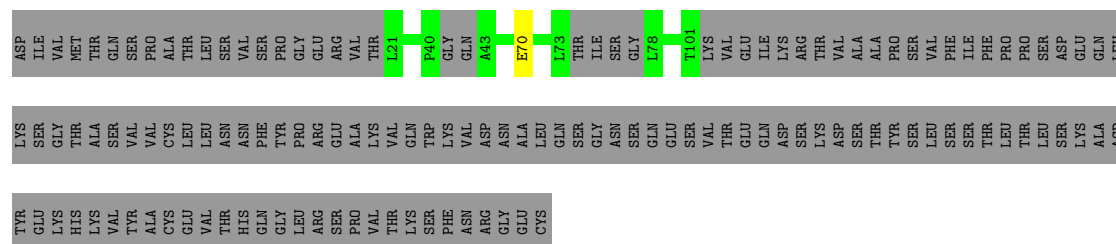
● Molecule 4: Heavy chain Fab rPIV3-23



GLN	V2	S7	GLY	PRO	GLY	GLY	VAL	ARG	PRO	SER	GLN	THR	L18	I29	T30	D31	Q39	G42	GLY	L45	V48	I51	Q64	L71	D72	THR	SER	ARG	T76	K81	THR	THR	SER	VAL	THR	ALA	ALA	ALA	ASP	T87	M100N	D101	V102	T107	THR	ALA	VAL	PHE	VAL
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SER	SER	ALA	SER	THR	LYS	GLY	PRO	GLY	VAL	SER	PHE	PRO	THR	VAL	PRO	ALA	PRO	SER	SER	SER	LYS	SER	THR	SER	GLY	THR	ILE	THR	ALA	ALA	GLY	LYS	THR	PHE	PRO	GLU	ASP	LYS	VAL	THR	VAL	PRO	SER	ASN	SER	VAL	THR	GLY	ALA	LEU	THR	THR	SER	GLY	VAL	HIS	THR	PHE	PRO	ALA	VAL	VAL	LEU	GLN
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SER	SER	GLY	LEU	THR	SER	LEU	SER	VAL	VAL	PRO	SER	SER	SER	LEU	GLY	THR	GLN	THR	THR	ILE	THR	ASN	VAL	ASN	VAL	HIS	LYS	PRO	SER	ASN	THR	LYS	VAL	VAL	GLU	PRO	LYS	SER	CYS
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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	47827	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.177	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.58	Depositor
Map size (Å)	285.0, 285.0, 285.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	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	0.64	4/3311 (0.1%)	0.81	12/4526 (0.3%)
1	B	0.37	0/3308	0.64	6/4520 (0.1%)
2	C	0.15	0/816	0.34	0/1108
2	H	0.15	0/883	0.33	0/1198
3	D	0.31	0/816	0.56	2/1112 (0.2%)
3	L	0.23	0/861	0.37	0/1171
4	E	0.17	0/772	0.38	1/1053 (0.1%)
4	I	0.14	0/855	0.28	0/1165
5	F	0.52	0/624	0.77	2/849 (0.2%)
5	J	0.14	0/571	0.30	0/779
All	All	0.42	4/12817 (0.0%)	0.61	23/17481 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	470	PRO	N-CA	17.68	1.70	1.47
1	A	193	THR	C-N	16.25	1.54	1.33
1	A	568	PRO	N-CA	13.54	1.69	1.48
1	A	567	ILE	C-N	5.19	1.46	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	469	CYS	CA-C-N	14.32	137.74	119.84
1	A	469	CYS	C-N-CA	14.32	137.74	119.84
1	A	193	THR	CA-C-N	10.48	131.31	119.99
1	A	193	THR	C-N-CA	10.48	131.31	119.99
1	A	568	PRO	CA-N-CD	-8.53	100.06	112.00

There are no chirality outliers.

There are no planarity outliers.

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	3232	3112	3114	42	0
1	B	3231	3118	3122	43	0
2	C	800	748	748	7	0
2	H	867	820	822	9	0
3	D	798	745	745	2	0
3	L	843	793	800	4	0
4	E	756	688	688	18	0
4	I	836	789	792	8	0
5	F	610	533	533	7	0
5	J	555	485	485	0	0
All	All	12528	11831	11849	129	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 5.

The worst 5 of 129 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:350:CYS:SG	1:B:363:CYS:HB3	1.34	1.66
1:A:568:PRO:N	1:A:568:PRO:CA	1.69	1.46
1:A:470:PRO:N	1:A:470:PRO:CA	1.69	1.45
1:B:350:CYS:SG	1:B:363:CYS:CB	2.20	1.27
1:B:370:PRO:CB	4:E:31:ASP:OD1	1.82	1.27

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	416/454 (92%)	394 (95%)	20 (5%)	2 (0%)	24	56
1	B	412/454 (91%)	394 (96%)	17 (4%)	1 (0%)	43	72
2	C	108/223 (48%)	106 (98%)	2 (2%)	0	100	100
2	H	118/223 (53%)	110 (93%)	8 (7%)	0	100	100
3	D	104/214 (49%)	101 (97%)	3 (3%)	0	100	100
3	L	109/214 (51%)	101 (93%)	8 (7%)	0	100	100
4	E	92/235 (39%)	87 (95%)	4 (4%)	1 (1%)	11	40
4	I	102/235 (43%)	96 (94%)	5 (5%)	1 (1%)	12	42
5	F	75/213 (35%)	70 (93%)	5 (7%)	0	100	100
5	J	69/213 (32%)	63 (91%)	6 (9%)	0	100	100
All	All	1605/2678 (60%)	1522 (95%)	78 (5%)	5 (0%)	37	66

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	322	VAL
1	A	243	ILE
1	A	470	PRO
4	I	102	VAL
4	E	102	VAL

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	361/410 (88%)	346 (96%)	15 (4%)	26	56
1	B	363/410 (88%)	350 (96%)	13 (4%)	31	60
2	C	83/187 (44%)	77 (93%)	6 (7%)	13	41
2	H	91/187 (49%)	91 (100%)	0	100	100
3	D	86/188 (46%)	84 (98%)	2 (2%)	44	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	L	92/188 (49%)	89 (97%)	3 (3%)	33	62
4	E	79/204 (39%)	79 (100%)	0	100	100
4	I	93/204 (46%)	91 (98%)	2 (2%)	45	68
5	F	58/183 (32%)	55 (95%)	3 (5%)	21	51
5	J	54/183 (30%)	53 (98%)	1 (2%)	50	70
All	All	1360/2344 (58%)	1315 (97%)	45 (3%)	34	62

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	30	SER
3	D	104	VAL
2	C	39	GLN
2	C	69	MET
5	F	58	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	90	GLN
5	F	93	ASN
5	J	90	GLN
2	C	39	GLN
2	C	95	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 [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.

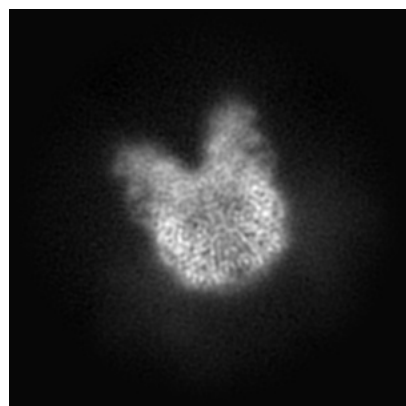
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41505. These allow visual inspection of the internal detail of the map and identification of artifacts.

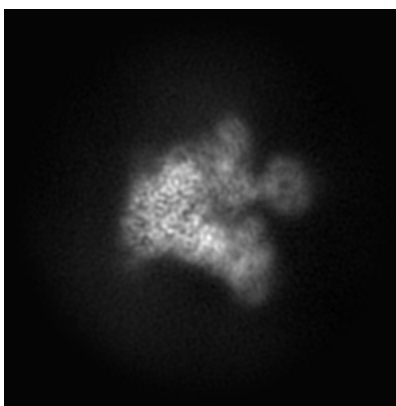
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

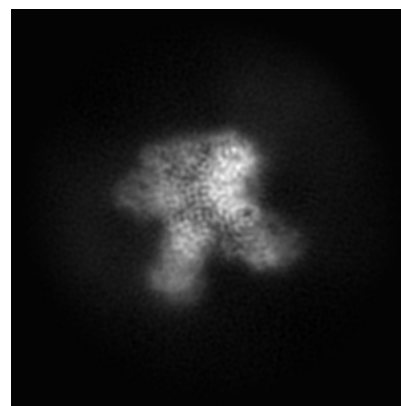
6.1.1 Primary map



X

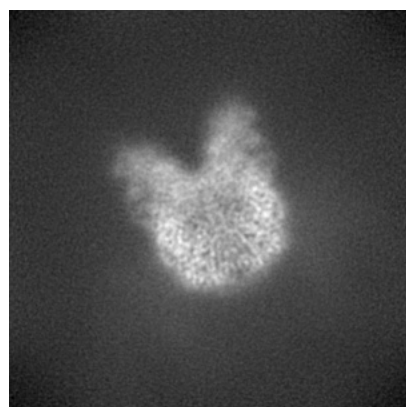


Y

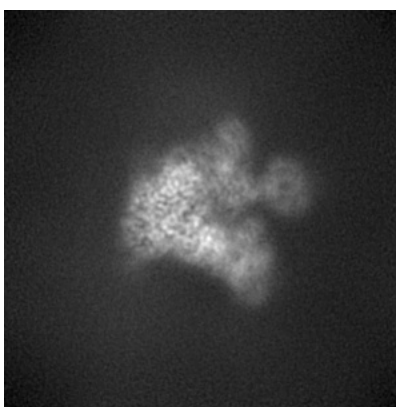


Z

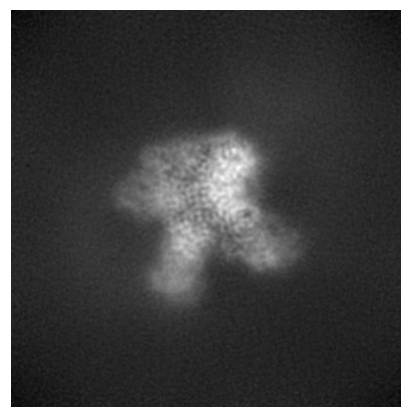
6.1.2 Raw map



X



Y

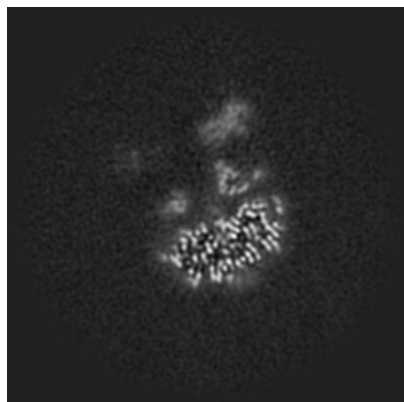


Z

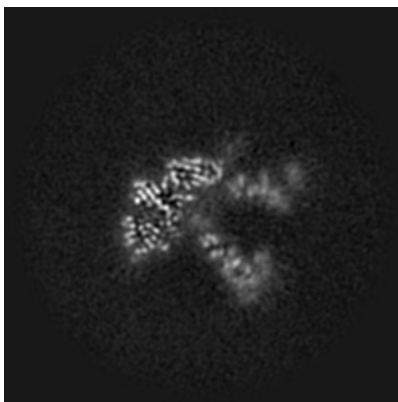
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

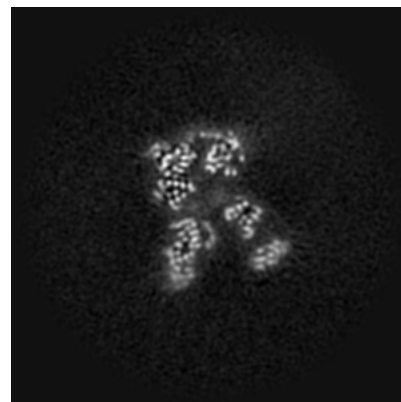
6.2.1 Primary map



X Index: 150

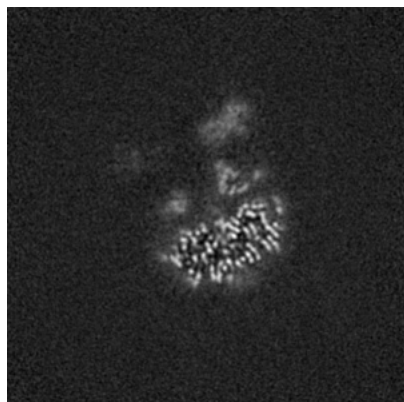


Y Index: 150

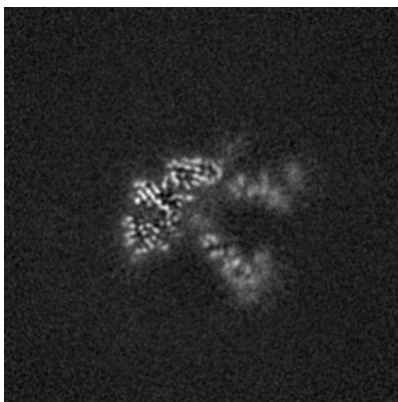


Z Index: 150

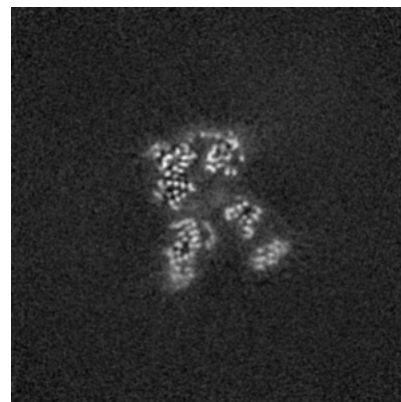
6.2.2 Raw map



X Index: 150



Y Index: 150

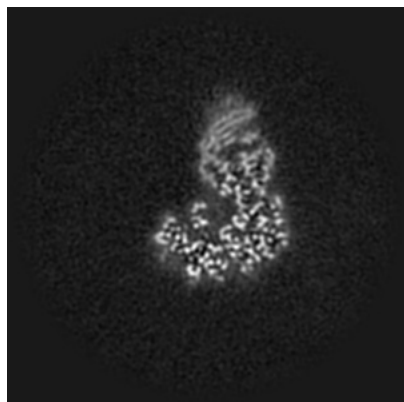


Z Index: 150

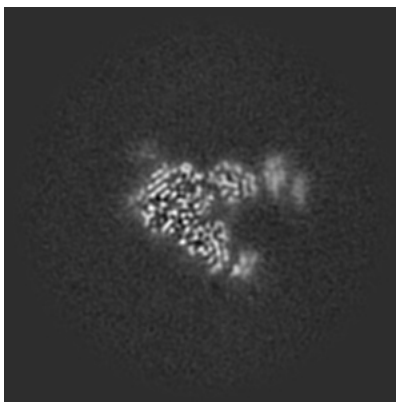
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

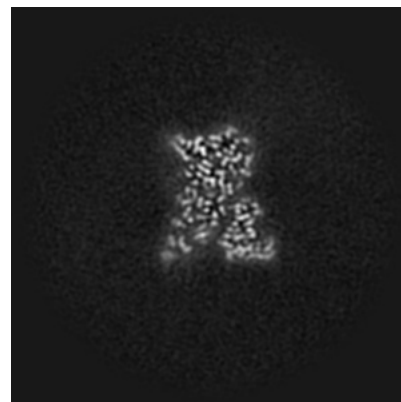
6.3.1 Primary map



X Index: 163

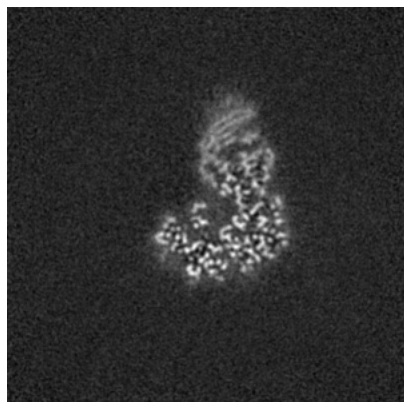


Y Index: 183

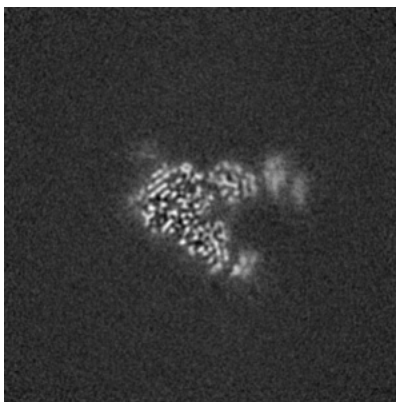


Z Index: 128

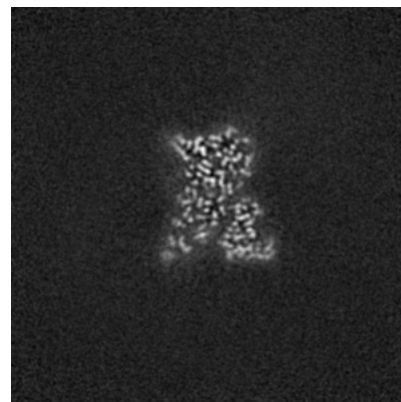
6.3.2 Raw map



X Index: 163



Y Index: 183

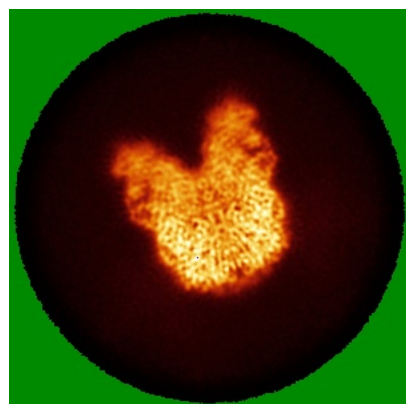


Z Index: 128

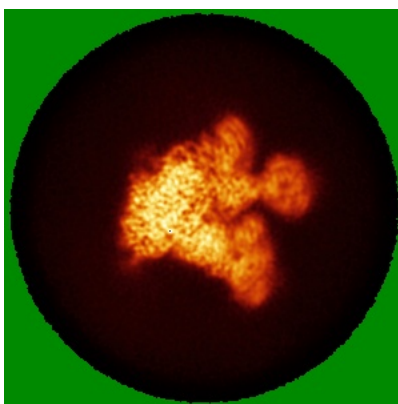
The images above show the largest variance slices of the map in three orthogonal directions.

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

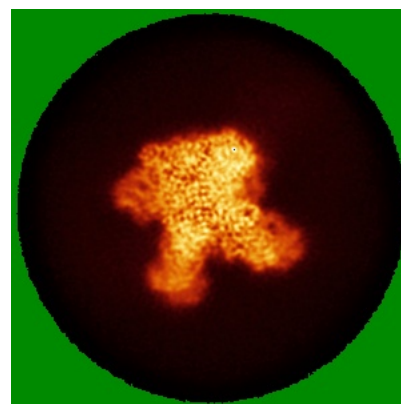
6.4.1 Primary map



X



Y

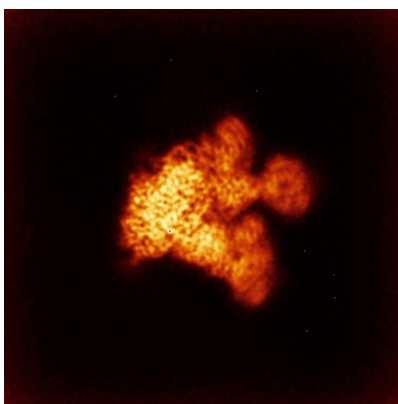


Z

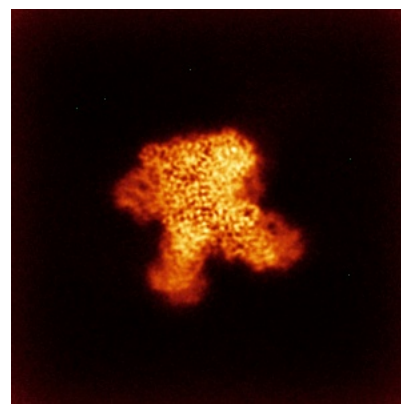
6.4.2 Raw map



X



Y

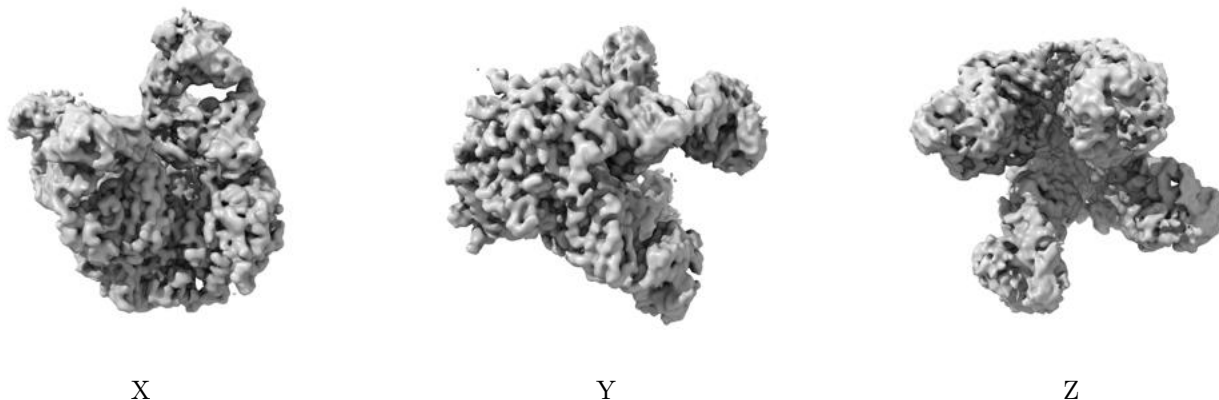


Z

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

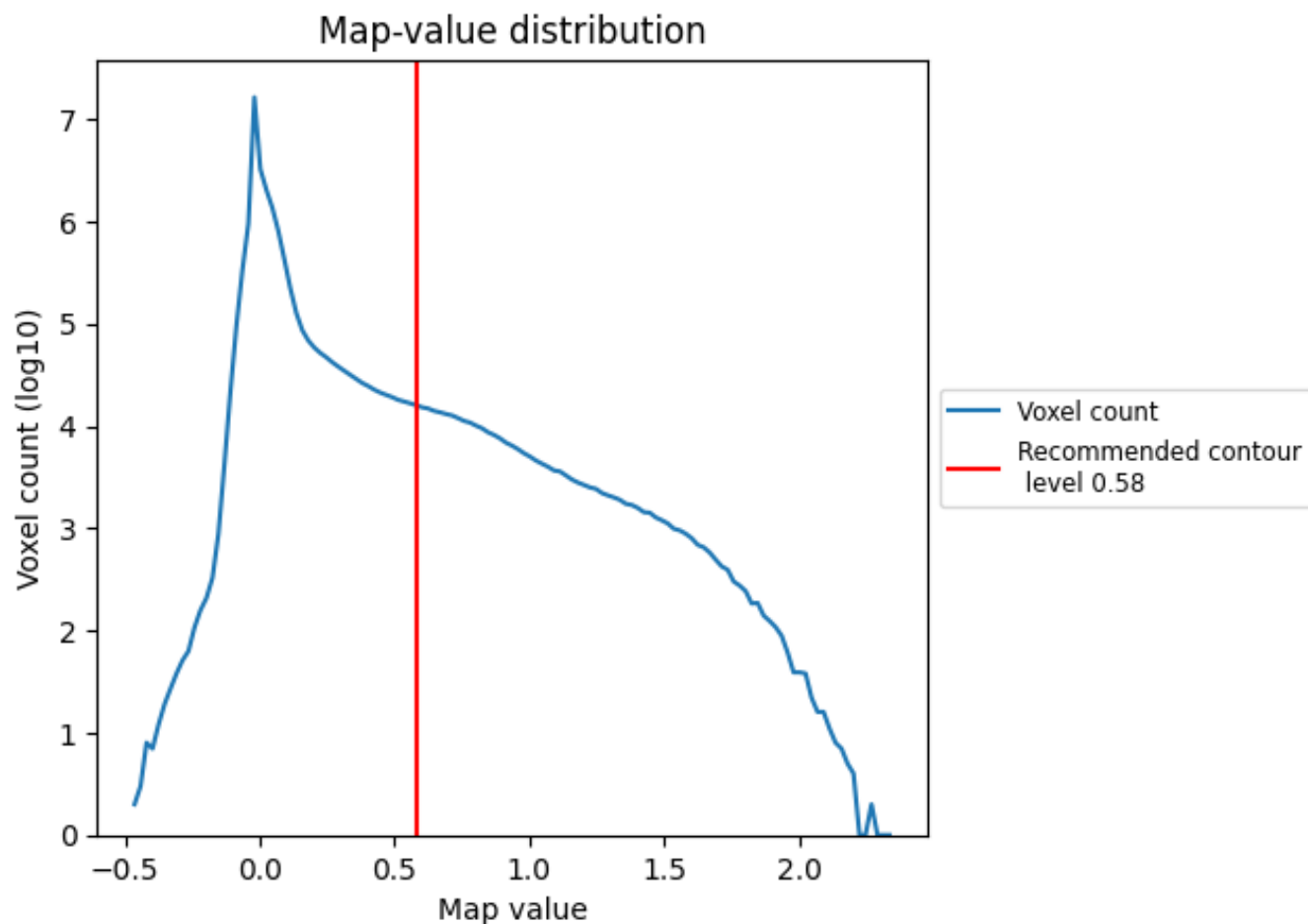
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

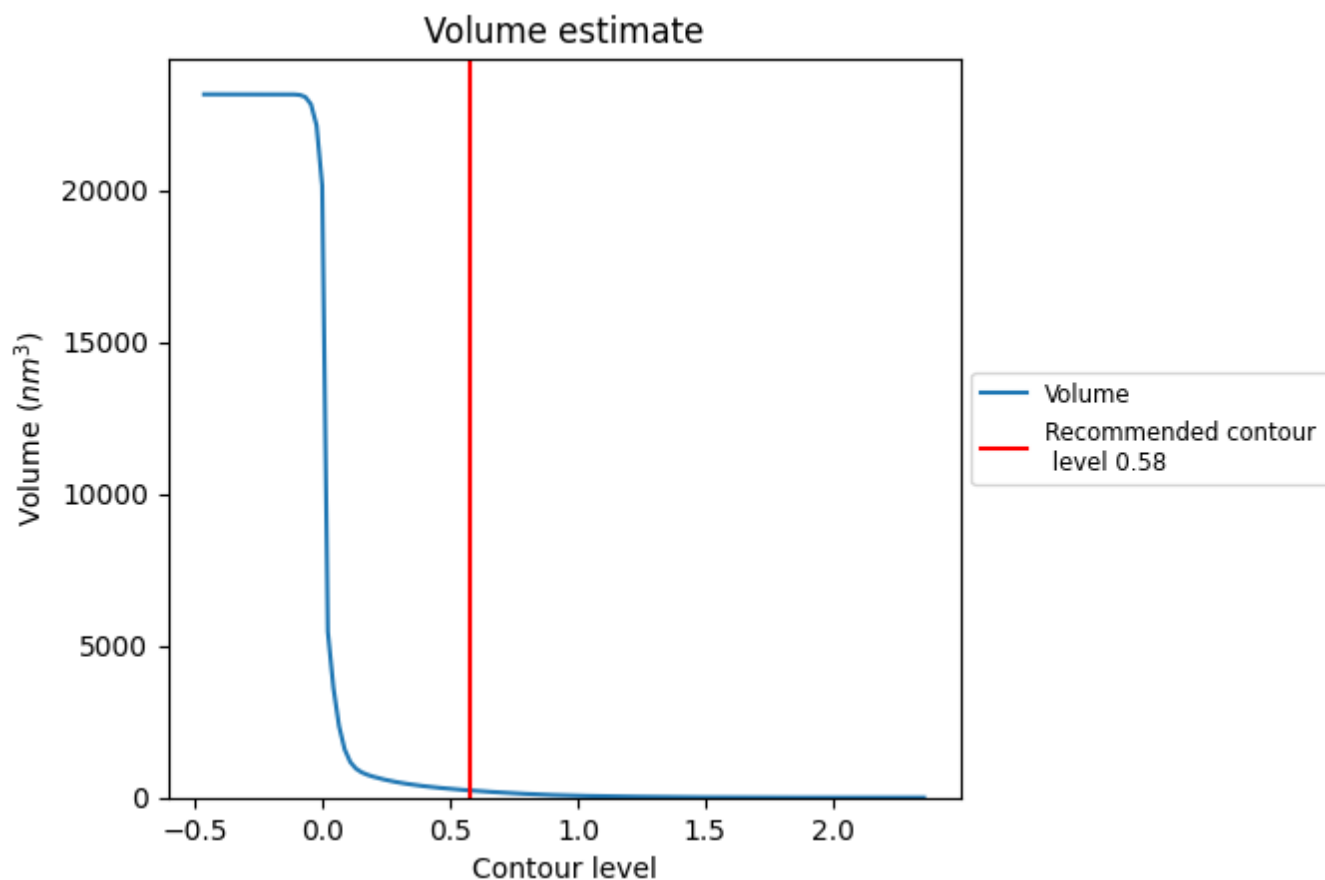
This section contains the results of statistical analysis of the map.

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.

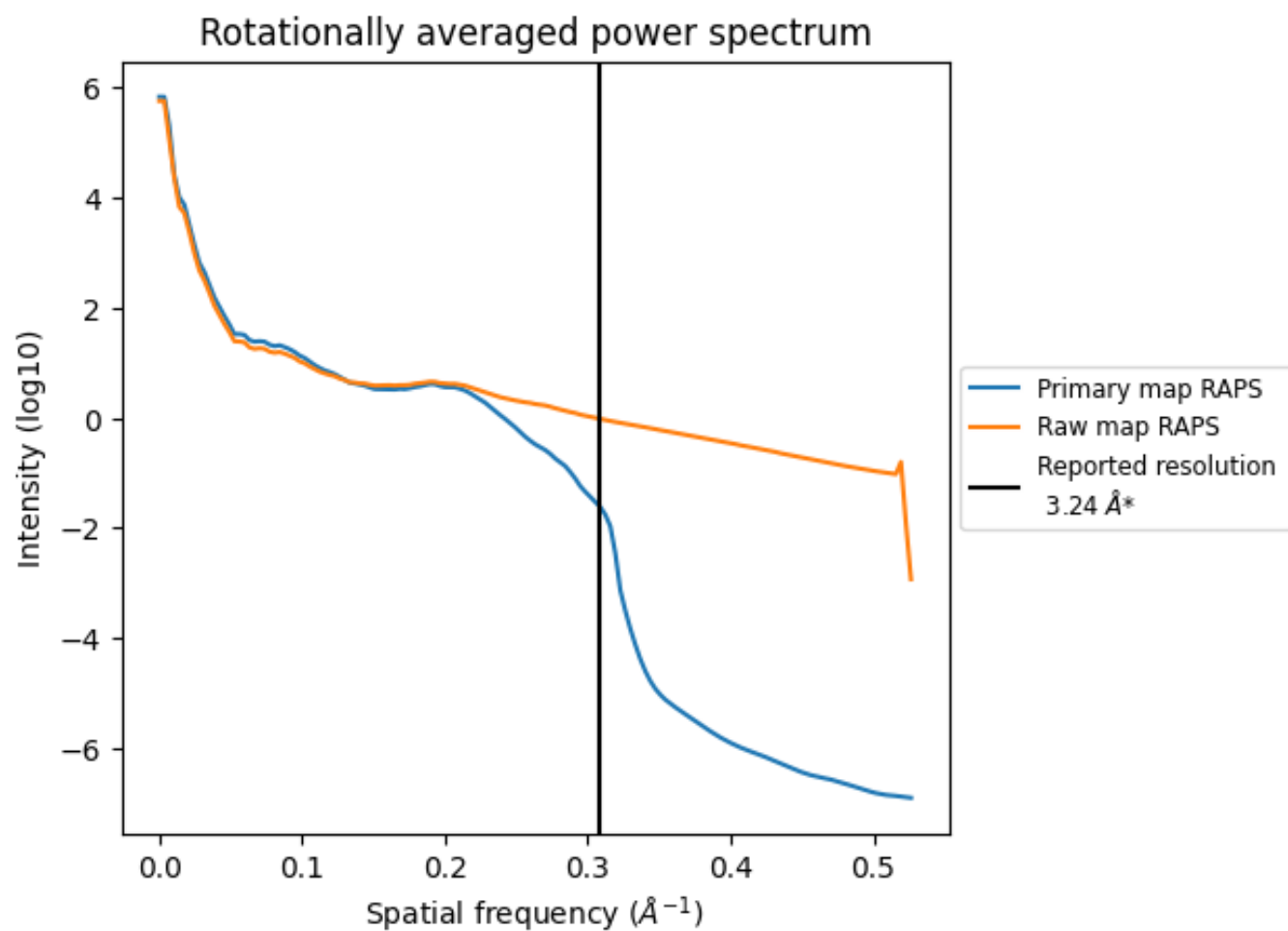
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 234 nm³; this corresponds to an approximate mass of 211 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 ⓘ

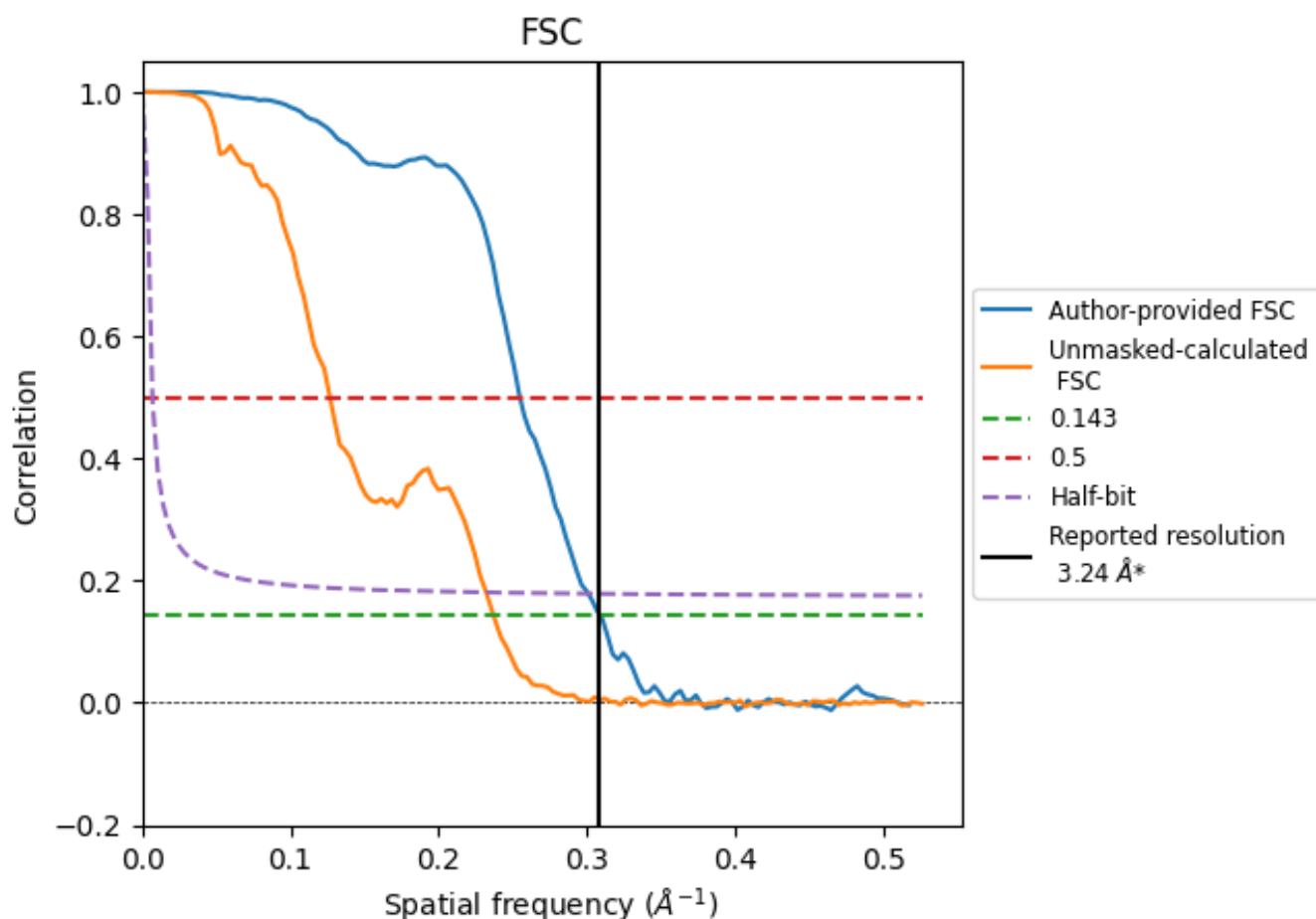


*Reported resolution corresponds to spatial frequency of $0.309 \text{ \AA}^{-1}$

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

8.2 Resolution estimates [i](#)

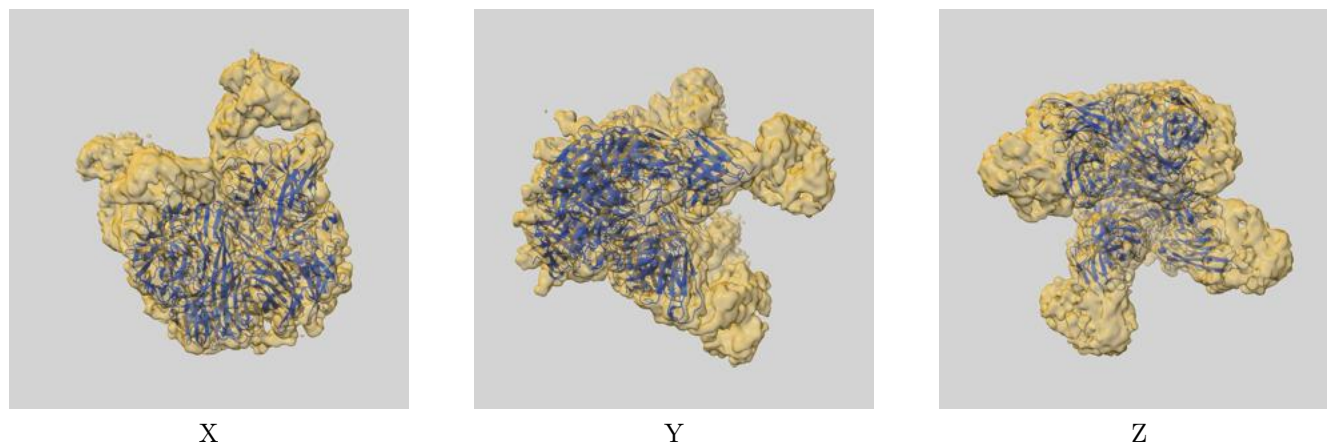
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.24	-	-
Author-provided FSC curve	3.24	3.92	3.32
Unmasked-calculated*	4.22	7.89	4.31

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

9 Map-model fit [i](#)

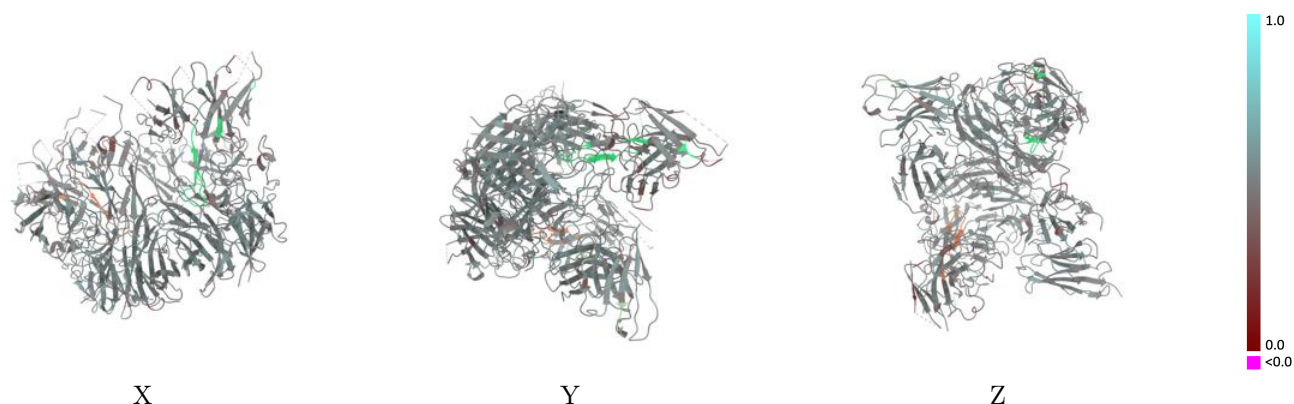
This section contains information regarding the fit between EMDB map EMD-41505 and PDB model 8TQI. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.58 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](#)

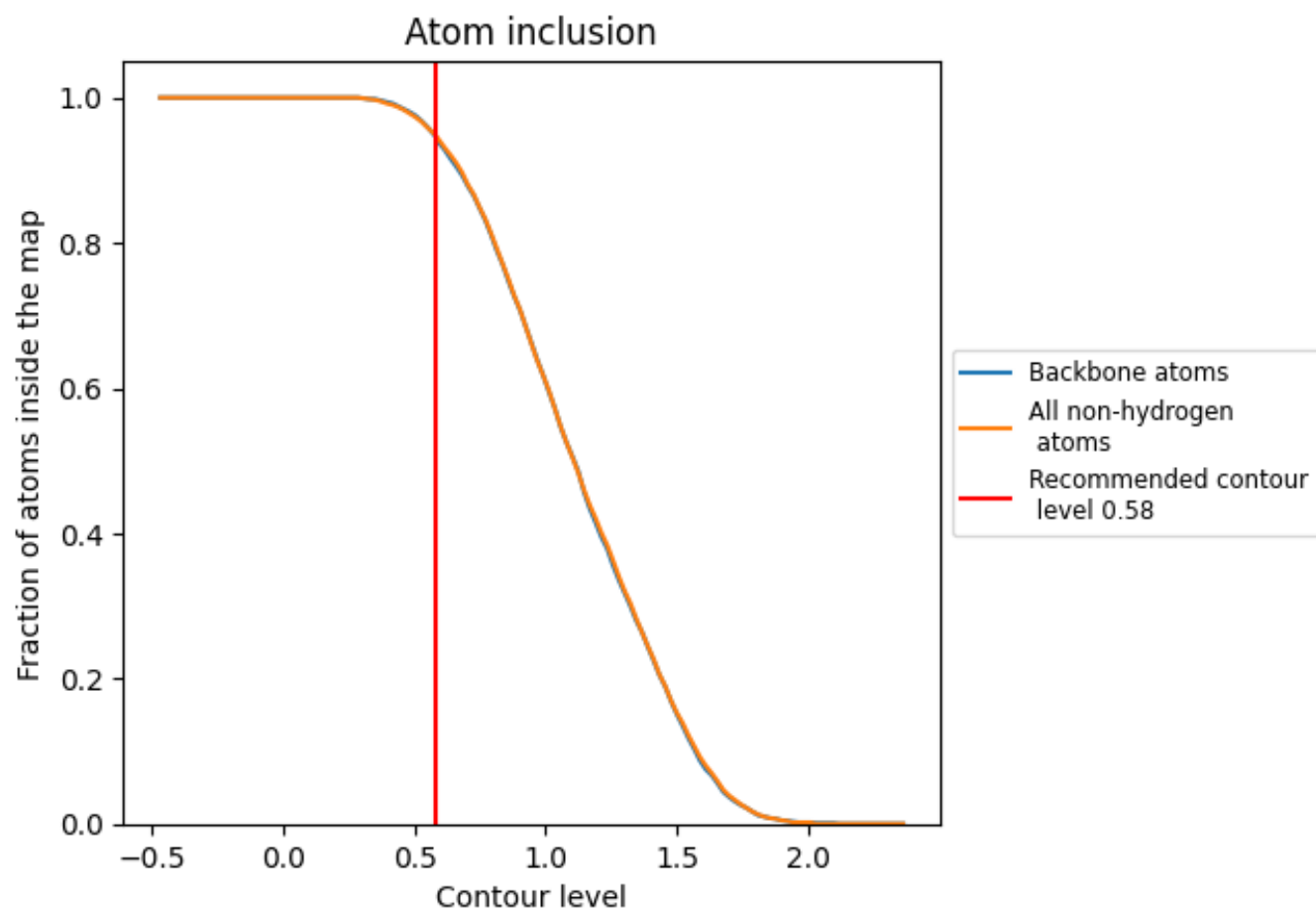


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.58) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9490	0.4990
A	0.9580	0.5120
B	0.9650	0.5070
C	0.9560	0.5090
D	0.9390	0.5050
E	0.9380	0.4700
F	0.9300	0.4650
H	0.9590	0.5080
I	0.9350	0.4760
J	0.9250	0.4610
L	0.9450	0.4990

1.0

0.0

<0.0