



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:53 AM UTC

PDB ID : 8H37 / pdb_00008h37
EMDB ID : EMD-34453
Title : Cryo-EM Structure of the KBTBD2-CUL3-Rbx1-p85a tetrameric complex
Authors : Hu, Y.; Mao, Q.; Chen, Z.; Sun, L.
Deposited on : 2022-10-08
Resolution : 7.52 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:

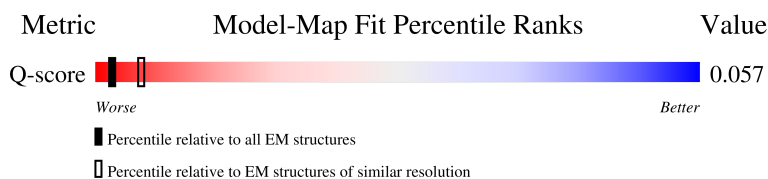
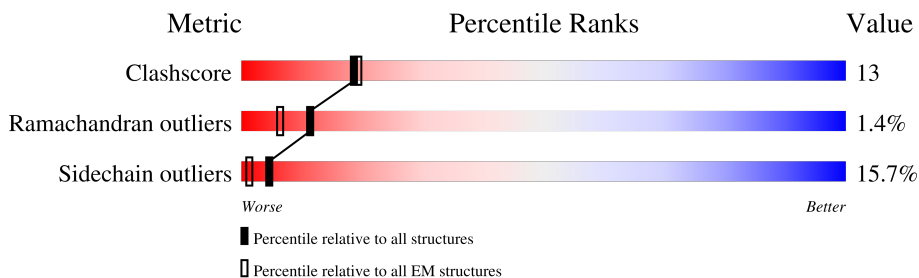
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.52 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.



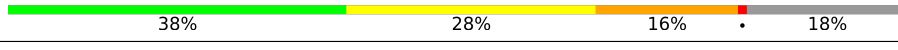
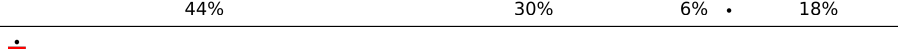
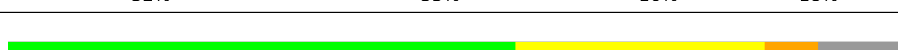
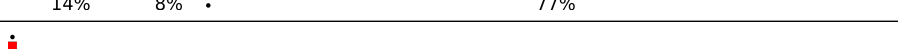
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	377 (7.02 - 8.01)

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	C	768	
1	F	768	
1	M	768	
1	O	768	

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Mol	Chain	Length	Quality of chain
2	D	108	
2	E	108	
2	Q	108	
2	R	108	
3	A	623	
3	B	623	
3	N	623	
3	P	623	
4	G	724	
4	H	724	
4	I	724	
4	J	724	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 49321 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 Cullin-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	720	Total	C	N	O	S	0	0
			5791	3633	1024	1095	39		
1	F	720	Total	C	N	O	S	0	0
			5677	3558	1010	1073	36		
1	M	720	Total	C	N	O	S	0	0
			5672	3553	1008	1074	37		
1	O	720	Total	C	N	O	S	0	0
			5767	3620	1017	1091	39		

- Molecule 2 is a protein called E3 ubiquitin-protein ligase RBX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	89	Total	C	N	O	S	0	0
			737	466	135	127	9		
2	D	89	Total	C	N	O	S	0	0
			737	466	135	127	9		
2	R	89	Total	C	N	O	S	0	0
			737	466	135	127	9		
2	Q	89	Total	C	N	O	S	0	0
			737	466	135	127	9		

- Molecule 3 is a protein called Kelch repeat and BTB domain-containing protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	567	Total	C	N	O	S	0	0
			4559	2918	750	853	38		
3	B	564	Total	C	N	O	S	0	0
			4510	2884	746	842	38		
3	N	564	Total	C	N	O	S	0	0
			4510	2880	746	846	38		
3	P	557	Total	C	N	O	S	0	0
			4423	2833	725	831	34		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	252	ASP	SER	engineered mutation	UNP Q8IY47
B	252	ASP	SER	engineered mutation	UNP Q8IY47
N	252	ASP	SER	engineered mutation	UNP Q8IY47
P	252	ASP	SER	engineered mutation	UNP Q8IY47

- Molecule 4 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	168	Total	C	N	O	S	0	0
			1424	885	256	278	5		
4	H	168	Total	C	N	O	S	0	0
			1341	828	246	263	4		
4	I	168	Total	C	N	O	S	0	0
			1360	840	250	266	4		
4	J	168	Total	C	N	O	S	0	0
			1327	816	244	263	4		

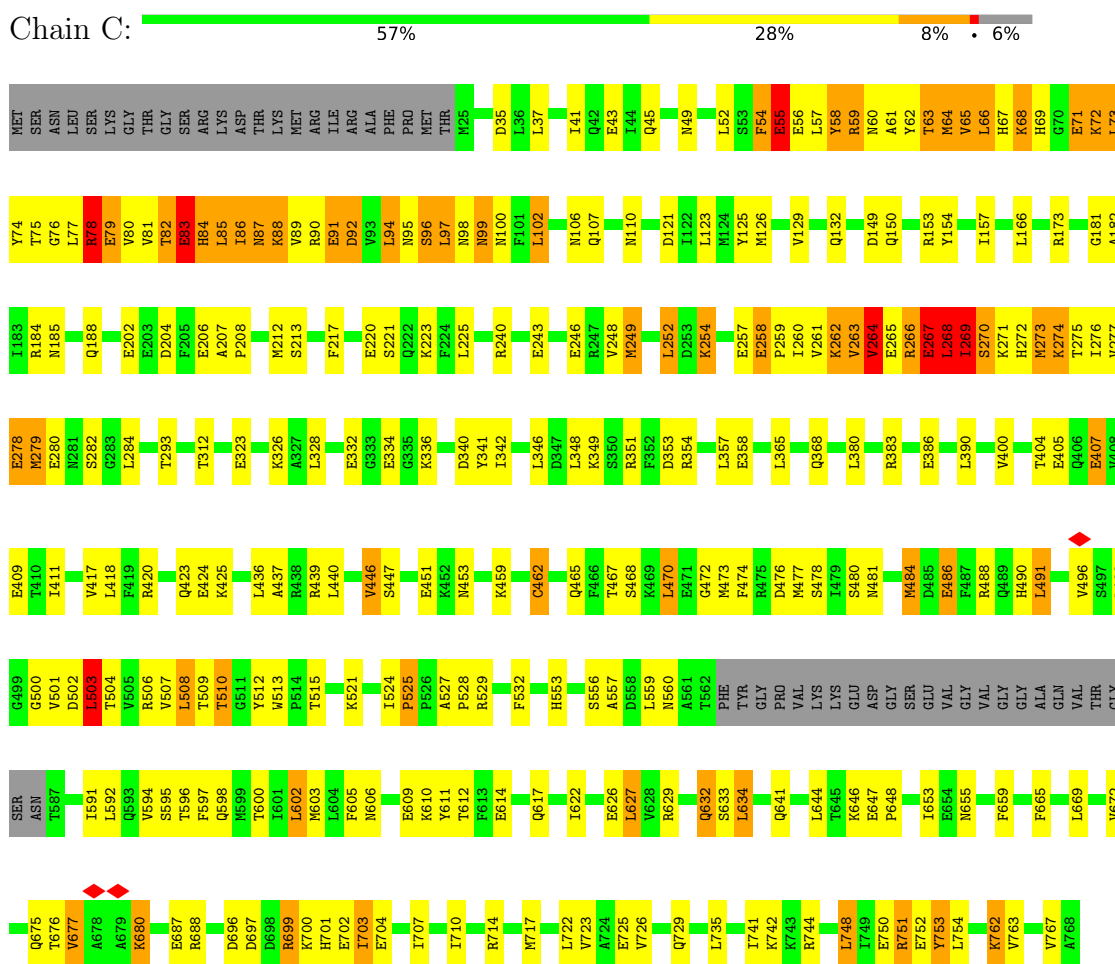
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	E	3	Total	Zn	0
			3	3	
5	D	3	Total	Zn	0
			3	3	
5	R	3	Total	Zn	0
			3	3	
5	Q	3	Total	Zn	0
			3	3	

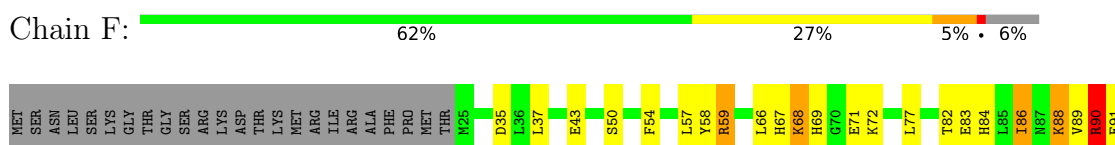
3 Residue-property plots

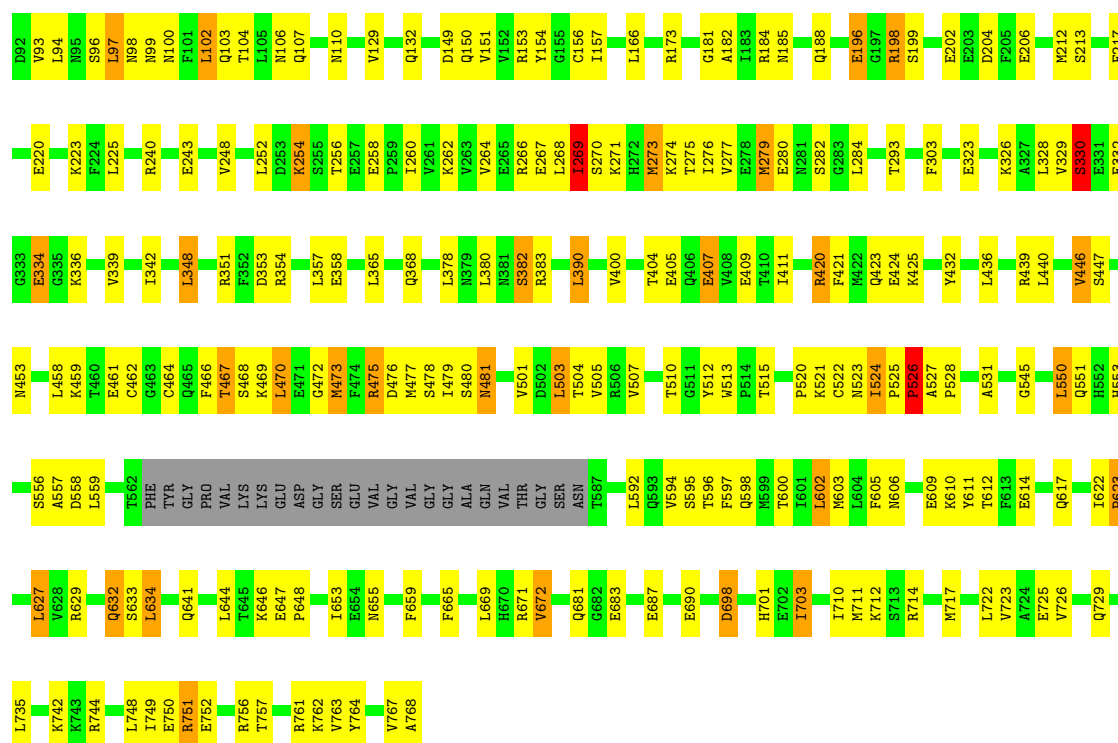
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Cullin-3

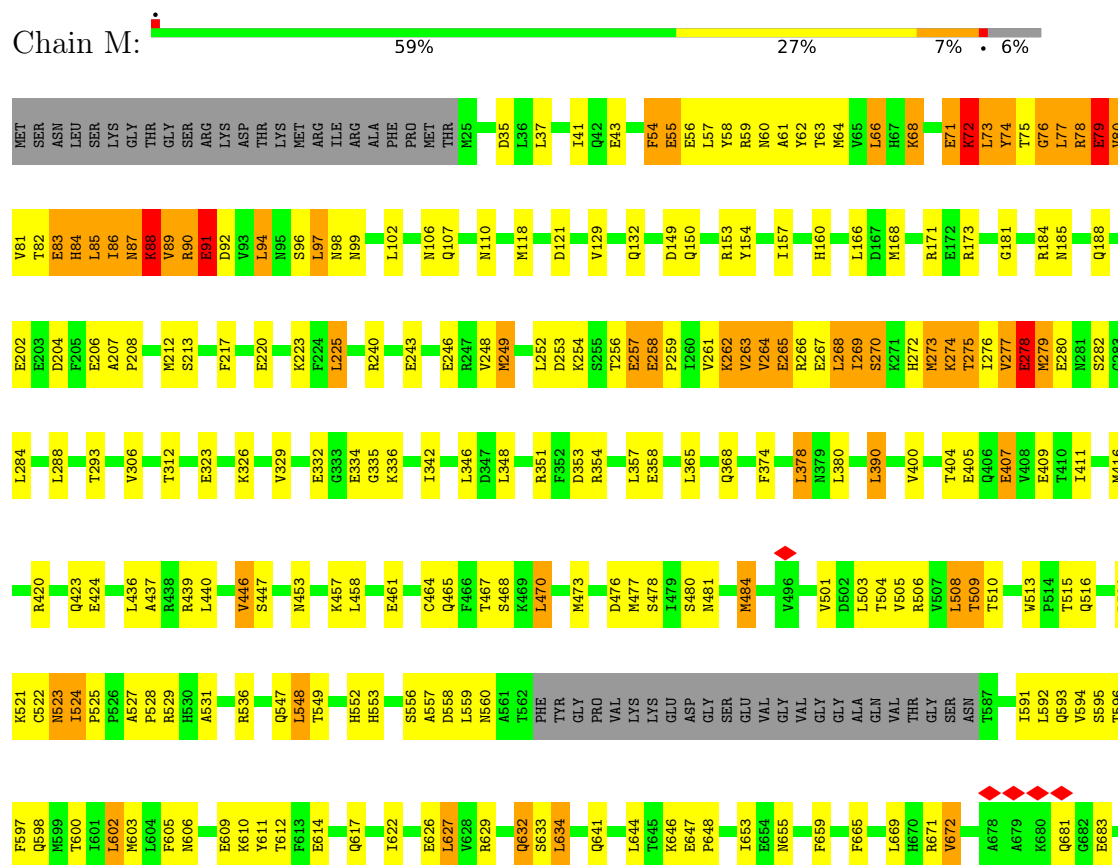


• Molecule 1: Cullin-3





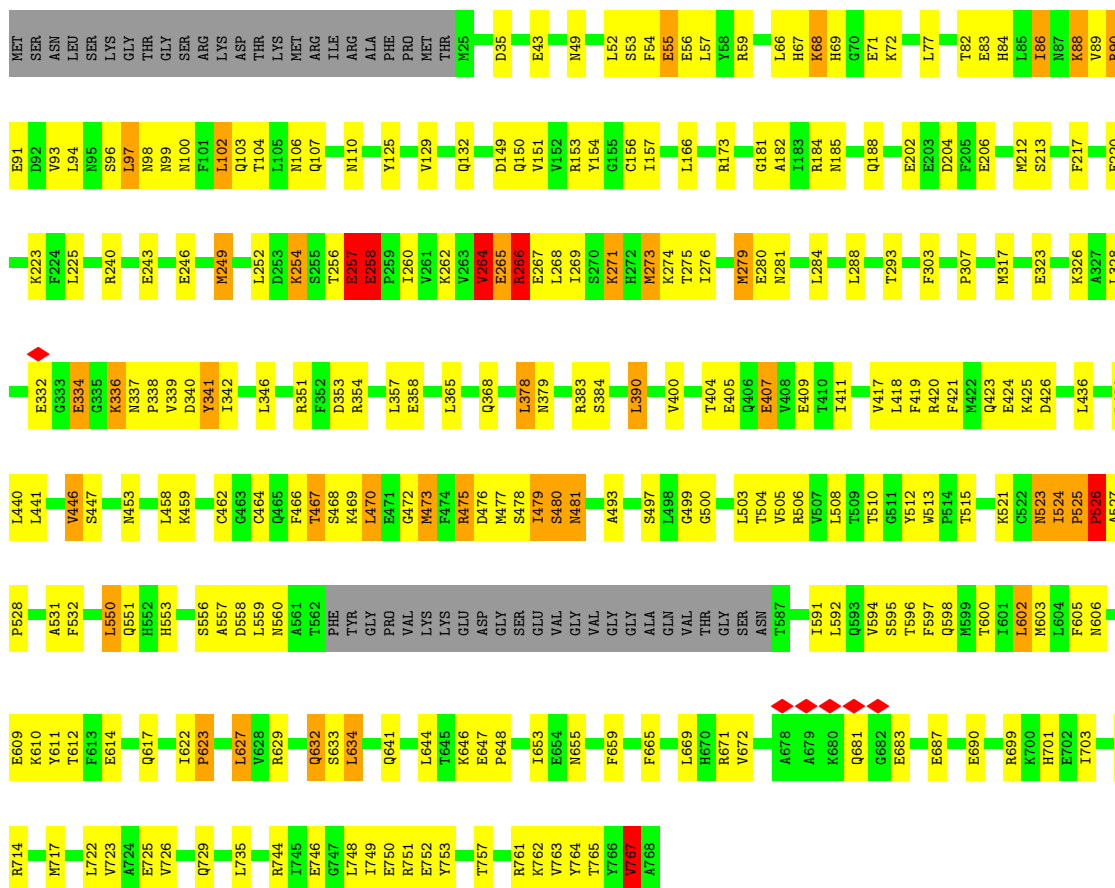
- Molecule 1: Cullin-3





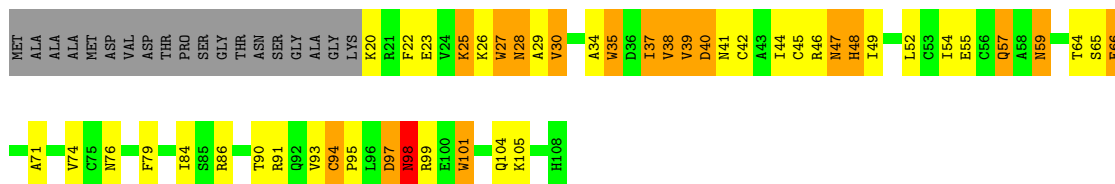
• Molecule 1: Cullin-3

Chain O: 60% 28% 5% • 6%



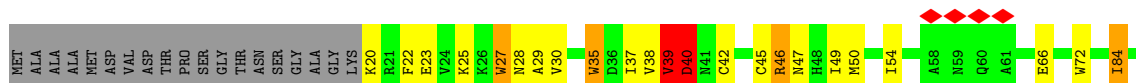
• Molecule 2: E3 ubiquitin-protein ligase RBX1

Chain E: 38% 28% 16% • 18%

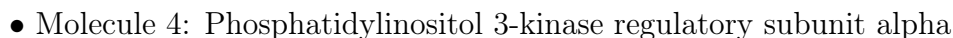


• Molecule 2: E3 ubiquitin-protein ligase RBX1

Chain D: 49% 21% 7% 5% 18%

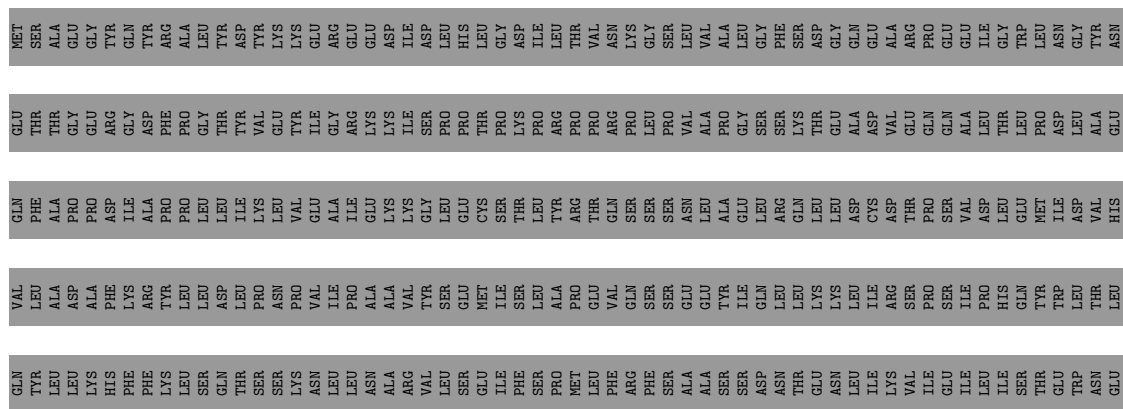
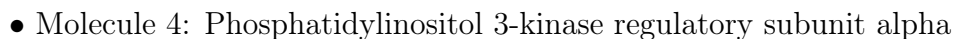


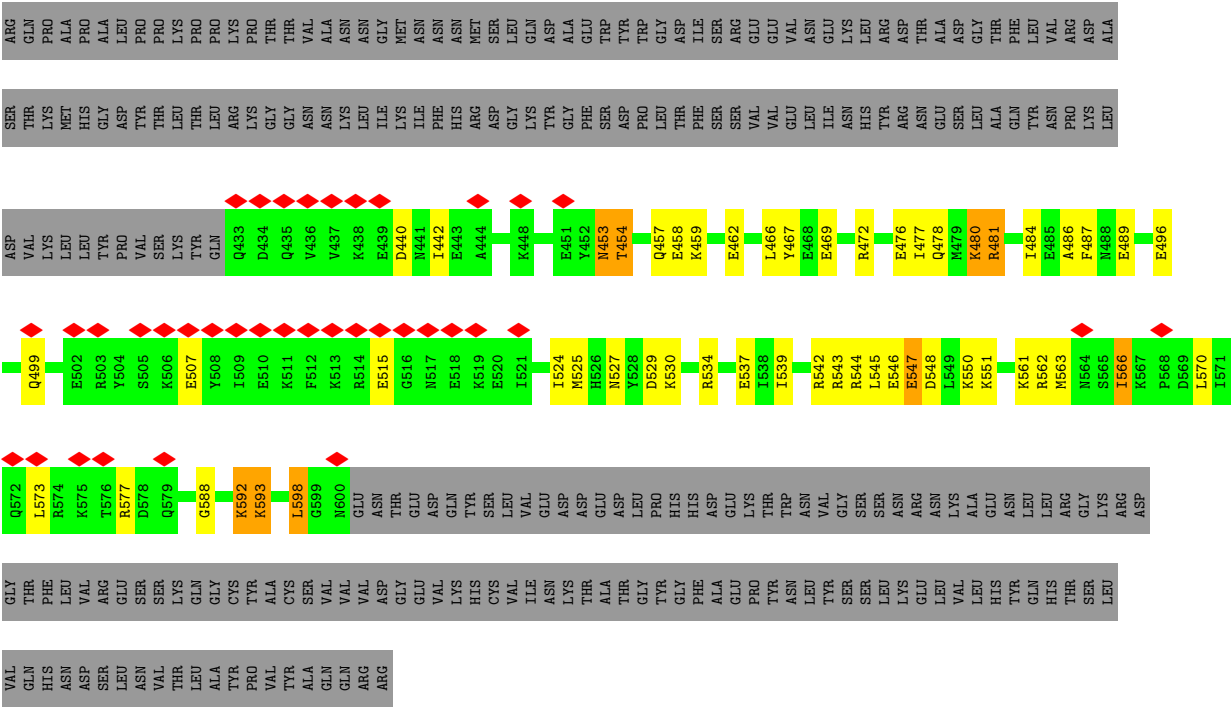




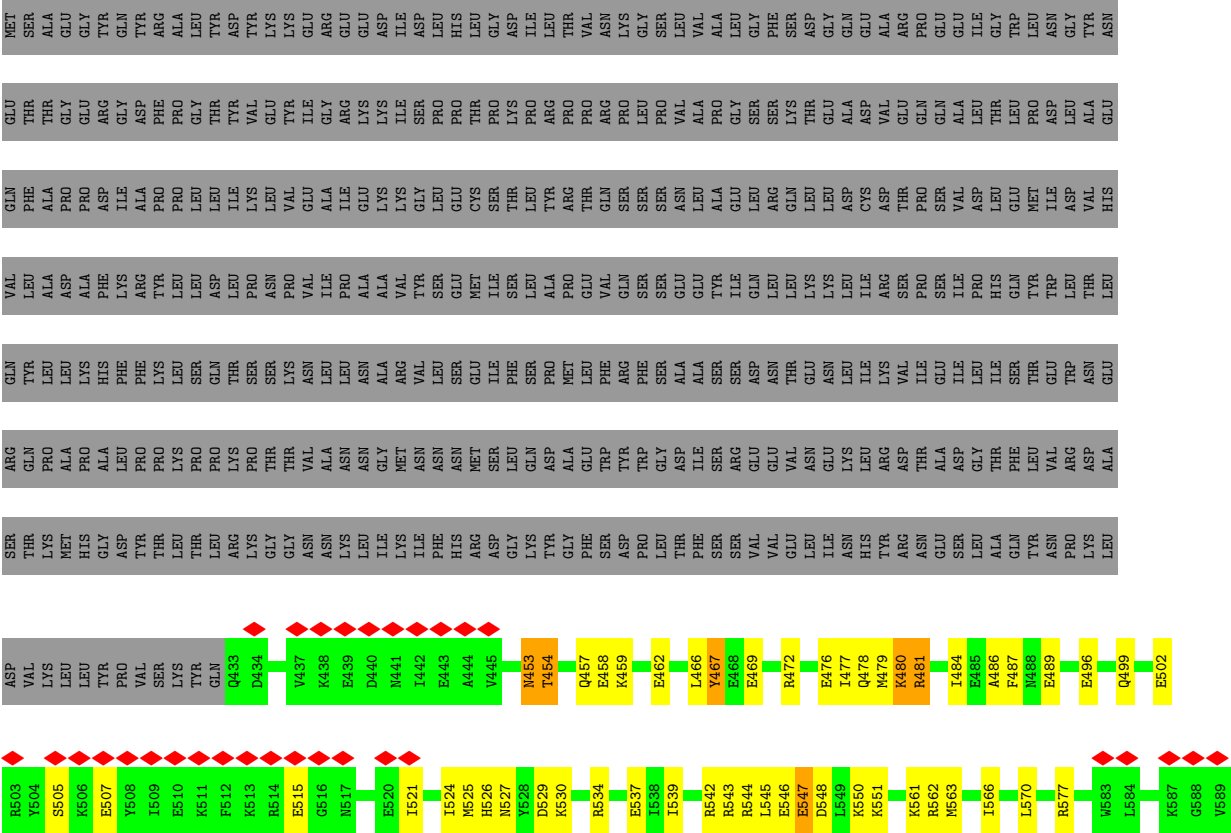
GLY	GLU	ASP	ASP	GLN	GLY	Q499	GLN	ASP	SER	ARG	GLN	VAL	GLN	VAL	GLN	VAL	GLN	GLU	MET
VAL	THR	TYR	VAL	TYR	LYS	Q502	LYS	VAL	THR	GLN	PRO	LYS	GLN	ALA	PRO	ALA	ALA	THR	SER
LYS	GLY	SER	LEU	LEU	LEU	E502	MET	LEU	MET	ALA	PRO	LEU	LEU	ASP	PRO	GLY	GLY	GLY	
CYS	VAL	VAL	S505	VAL	VAL	S505	GLY	TYR	ALA	ALA	HIS	PHE	HIS	PHE	ASP	ARG	TYR	TYR	
ILE	GLU	GLU	K506	GLU	VAL	K506	TYR	VAL	PRO	LEU	PHE	LYS	ILE	LYS	ILE	GLY	GLN	GLN	
ASN	ASP	ASP	E507	ASP	ASP	E507	THR	VAL	PRO	PRO	PHE	ALA	ALA	TYR	ASP	ASP	ASP	ASP	
LYS	GLU	GLU	K513	GLU	LYS	K513	THR	LYS	LYS	LYS	LEU	LEU	LEU	LEU	PRO	GLY	ALA	ALA	
THR	THR	ASP	R514	THR	LYS	R514	THR	LYS	PRO	PRO	PRO	PRO	PRO	LEU	LEU	GLY	ARG	ARG	
ALA	ALA	LEU	E515	LEU	GLN	E515	LEU	GLN	LEU	LYS	PRO	ASP	GLN	ASP	LEU	THR	TYR	TYR	
THR	THR	PRO	I521	HIS	Q433	I521	ARG	Q433	ARG	LYS	THR	LEU	ILE	LEU	ILE	ILE	ASP	ASP	
GLY	TYR	HIS	R522	HIS	Q434	R522	GLY	Q434	GLY	THR	SER	PRO	LYS	PRO	LYS	VAL	TYR	LYS	
TYR	TYR	ASP	I524	ASP	Q435	I524	GLY	Q435	THR	THR	SER	ASN	LEU	ASN	LEU	GLU	GLU	LYS	
PHE	PHE	GLU	M525	GLU	V436	M525	ASN	V436	THR	VAL	ASN	VAL	ASN	VAL	GLU	ILE	GLY	GLY	
ALA	ALA	LYS	H526	LYS	V437	H526	ASN	V437	ALA	ASN	LEU	ILE	ALA	ILE	ALA	ANG	ARG	ARG	
GLU	GLU	THR	N527	THR	K438	N527	LYS	K438	LYS	ASN	LEU	PRO	ILE	PRO	ANG	LYS	GLY	GLY	
PRO	PRO	TRP	Y528	TRP	E439	Y528	LEU	E439	LEU	ASN	ASN	ALA	ALA	ALA	LYS	ANG	GLU	GLU	
TYR	TYR	ASN	D529	ASN	D440	D529	ILE	D440	ILE	MET	ALA	ALA	ALA	ALA	LYS	LYS	ASP	ASP	
ASN	ASN	VAL	K530	VAL	N441	K530	LYS	N441	LYS	ARG	VAL	VAL	VAL	VAL	ILE	ILE	ILE	ILE	
GLY	GLY	GLY	R534	GLY	I442	R534	ILE	I442	ILE	ASN	VAL	TYR	TYR	TYR	GLY	SER	ASP	ASP	
TYR	TYR	SER	GLY	SER	E443	GLY	PHE	E443	PHE	ASN	LEU	SER	LEU	SER	GLY	PRO	LEU	LEU	
SER	SER	SER	ILE	SER	A444	ILE	HIS	A444	HIS	ASN	GLU	GLU	GLU	GLU	GLY	PRO	HIS	HIS	
SER	SER	ASN	I539	ASN	V445	I539	ARG	V445	ARG	MET	SER	MET	ILE	ILE	CYS	THR	LEU	LEU	
LEU	LEU	ARG	GLY	ARG	LYS	GLY	GLY	LYS	GLY	LEU	PHE	ILE	LYS	LYS	THR	LYS	GLY	GLY	
LYS	LYS	ASN	R542	ASN	L449	R542	LYS	L449	LYS	GLN	SER	LEU	SER	LEU	LEU	PRO	ILE	ILE	
GLY	GLY	LYS	R543	LYS	N453	R543	TYR	N453	TYR	ASP	ASP	ALA	ALA	PRO	TYR	ARG	THR	THR	
LEU	LEU	ALA	R544	ALA	T454	R544	PHE	T454	PHE	GLU	GLY	GLU	GLU	PRO	GLU	THR	VAL	VAL	
VAL	VAL	GLU	L545	GLU	E546	L545	GLY	E546	GLY	THR	THR	THR	THR	GLN	ARG	PRO	PRO	PRO	
LEU	LEU	ASN	E547	ASN	Q457	E547	ASP	Q457	ASP	TRP	PHE	VAL	VAL	GLN	ASN	ARG	VAL	VAL	
HIS	HIS	LEU	D548	LEU	E458	D548	SER	E458	SER	TYR	TRP	TRP	TRP	GLN	GLY	GLY	LYS	LYS	
GLN	GLN	ARG	L549	ARG	K459	L549	PRO	K459	PRO	TRP	PHE	SER	SER	SER	LEU	LEU	GLY	GLY	
HIS	HIS	GLY	K550	GLY	L551	K550	LEU	L551	LEU	GLY	SER	SER	SER	PRO	PRO	VAL	SER	SER	
THR																			

Chain H: 16% 6% 77%





● Molecule 4: Phosphatidylinositol 3-kinase regulatory subunit alpha



TYR	CYS	R590
PRO	TYR	Q591
VAL	ALA	K592
TYR	CYS	N600
ALA	SER	GLU
GLN	VAL	ASN
GLM	VAL	THR
ARG	ASP	GLU
ARG	GLY	ASP
	GLU	GLN
	VAL	TYR
	LYS	SER
	HIS	LEU
	CYS	VAL
	VAL	GLU
	ILE	ASP
	ASN	ASP
	LYS	GLU
	THR	LEU
	ALA	PRO
	THR	HIS
	GLY	ASP
	GLY	GLU
	PHE	THR
	ALA	TRP
	GLU	ASN
	PRO	VAL
	TYR	GLY
	ASN	SER
	LEU	SER
	TYR	SER
	SER	ASN
	LEU	ARG
	LYS	ASN
	GLU	LYS
	LEU	ALA
	VAL	GLU
	LEU	ASN
	HIS	LEU
	TYR	LEU
	GLN	ARG
	THR	GLY
	SER	LYS
	LEU	ARG
	VAL	ASP
	GLN	GLY
	HIS	THR
	ASN	LEU
	ASP	VAL
	SER	VAL
	LEU	ARG
	SER	GLU
	ASN	SER
	VAL	SER
	THR	LYS
	LEU	GLN
	ALA	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	239068	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.603	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.001	Depositor
Map size (Å)	511.488, 511.488, 511.488	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.664, 2.664, 2.664	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	C	0.63	12/5879 (0.2%)	0.78	15/7905 (0.2%)
1	F	0.56	1/5760 (0.0%)	0.75	8/7752 (0.1%)
1	M	0.81	30/5753 (0.5%)	0.78	13/7743 (0.2%)
1	O	0.56	2/5854 (0.0%)	0.76	11/7873 (0.1%)
2	D	0.81	1/759 (0.1%)	1.02	2/1029 (0.2%)
2	E	0.85	1/759 (0.1%)	1.06	1/1029 (0.1%)
2	Q	0.89	1/759 (0.1%)	1.04	1/1029 (0.1%)
2	R	0.83	1/759 (0.1%)	1.05	1/1029 (0.1%)
3	A	0.76	0/4667	0.86	1/6335 (0.0%)
3	B	0.42	0/4616	0.56	2/6268 (0.0%)
3	N	0.39	0/4616	0.53	2/6266 (0.0%)
3	P	0.43	0/4527	0.58	2/6151 (0.0%)
4	G	0.51	0/1443	0.69	0/1926
4	H	0.56	0/1356	0.75	0/1813
4	I	0.56	0/1376	0.77	0/1839
4	J	0.52	0/1342	0.70	0/1797
All	All	0.61	49/50225 (0.1%)	0.74	59/67784 (0.1%)

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	84	HIS	CA-C	-8.46	1.42	1.52
1	M	78	ARG	CA-C	-8.24	1.42	1.52
1	M	62	TYR	CA-C	-7.80	1.42	1.52
1	M	58	TYR	CA-C	-7.78	1.42	1.52
1	C	62	TYR	CA-C	-7.76	1.42	1.52

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	525	PRO	O-C-N	-14.29	114.74	121.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	67	HIS	N-CA-C	-11.57	100.70	112.97
1	F	67	HIS	N-CA-C	-11.54	100.74	112.97
1	M	55	GLU	N-CA-C	-10.55	99.86	111.36
1	C	55	GLU	N-CA-C	-10.54	99.88	111.36

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	C	5791	0	5773	215	0
1	F	5677	0	5575	138	0
1	M	5672	0	5583	158	0
1	O	5767	0	5730	150	0
2	D	737	0	686	23	0
2	E	737	0	686	45	0
2	Q	737	0	686	16	0
2	R	737	0	686	59	0
3	A	4559	0	4441	108	0
3	B	4510	0	4385	124	0
3	N	4510	0	4373	136	0
3	P	4423	0	4245	110	0
4	G	1424	0	1387	35	0
4	H	1341	0	1243	23	0
4	I	1360	0	1276	29	0
4	J	1327	0	1203	25	0
5	D	3	0	0	0	0
5	E	3	0	0	0	0
5	Q	3	0	0	0	0
5	R	3	0	0	0	0
All	All	49321	0	47958	1265	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 13.

The worst 5 of 1265 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)
3:B:154:ARG:HD3	3:B:357:GLN:NE2	1.43	1.33
3:N:154:ARG:HD3	3:N:357:GLN:NE2	1.43	1.30
1:M:531:ALA:HB3	2:R:27:TRP:CZ3	1.76	1.20
3:N:298:LEU:HD23	3:N:591:LEU:HD21	1.26	1.18
3:N:14:ALA:HB2	3:P:18:LEU:HD22	1.21	1.15

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	C	716/768 (93%)	628 (88%)	80 (11%)	8 (1%)	11	46
1	F	716/768 (93%)	633 (88%)	72 (10%)	11 (2%)	8	40
1	M	716/768 (93%)	648 (90%)	62 (9%)	6 (1%)	16	54
1	O	716/768 (93%)	646 (90%)	64 (9%)	6 (1%)	16	54
2	D	87/108 (81%)	60 (69%)	17 (20%)	10 (12%)	0	5
2	E	87/108 (81%)	57 (66%)	18 (21%)	12 (14%)	0	3
2	Q	87/108 (81%)	62 (71%)	19 (22%)	6 (7%)	1	11
2	R	87/108 (81%)	57 (66%)	20 (23%)	10 (12%)	0	5
3	A	561/623 (90%)	480 (86%)	76 (14%)	5 (1%)	14	51
3	B	558/623 (90%)	510 (91%)	44 (8%)	4 (1%)	18	56
3	N	558/623 (90%)	512 (92%)	42 (8%)	4 (1%)	18	56
3	P	547/623 (88%)	505 (92%)	40 (7%)	2 (0%)	30	67
4	G	166/724 (23%)	156 (94%)	10 (6%)	0	100	100
4	H	166/724 (23%)	156 (94%)	10 (6%)	0	100	100
4	I	166/724 (23%)	156 (94%)	8 (5%)	2 (1%)	10	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	J	166/724 (23%)	155 (93%)	11 (7%)	0	100	100
All	All	6100/8892 (69%)	5421 (89%)	593 (10%)	86 (1%)	11	40

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	88	LYS
1	C	268	LEU
1	F	526	PRO
2	D	40	ASP
2	Q	40	ASP

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	C	635/693 (92%)	522 (82%)	113 (18%)	2	9
1	F	603/693 (87%)	498 (83%)	105 (17%)	2	9
1	M	604/693 (87%)	501 (83%)	103 (17%)	2	10
1	O	628/693 (91%)	520 (83%)	108 (17%)	2	9
2	D	78/90 (87%)	54 (69%)	24 (31%)	0	2
2	E	78/90 (87%)	60 (77%)	18 (23%)	1	5
2	Q	78/90 (87%)	49 (63%)	29 (37%)	0	1
2	R	78/90 (87%)	61 (78%)	17 (22%)	1	6
3	A	504/560 (90%)	377 (75%)	127 (25%)	0	4
3	B	495/560 (88%)	460 (93%)	35 (7%)	13	35
3	N	496/560 (89%)	462 (93%)	34 (7%)	14	36
3	P	477/560 (85%)	446 (94%)	31 (6%)	15	37
4	G	151/654 (23%)	123 (82%)	28 (18%)	1	8
4	H	129/654 (20%)	110 (85%)	19 (15%)	3	13
4	I	134/654 (20%)	115 (86%)	19 (14%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	J	125/654 (19%)	105 (84%)	20 (16%)	2	11
All	All	5293/7988 (66%)	4463 (84%)	830 (16%)	4	12

5 of 830 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	93	VAL
3	A	394	LEU
3	P	8	GLN
2	R	47	ASN
2	D	92	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 157 such sidechains are listed below:

Mol	Chain	Res	Type
4	G	572	GLN
4	J	453	ASN
3	B	166	GLN
4	I	572	GLN
3	P	185	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](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

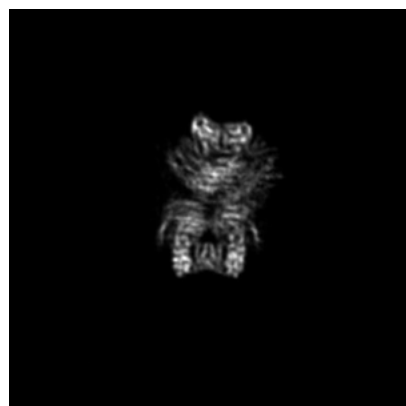
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34453. 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](#)

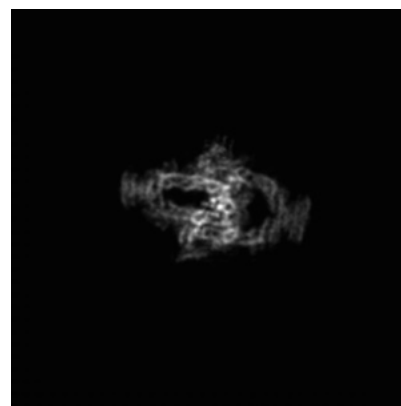
6.1.1 Primary map



X

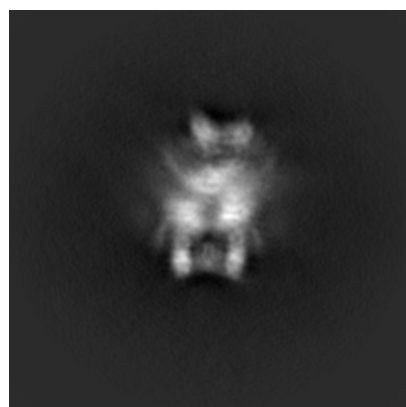


Y

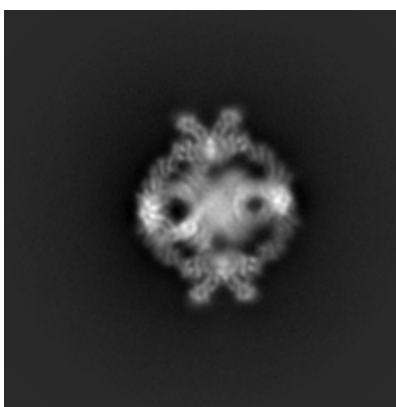


Z

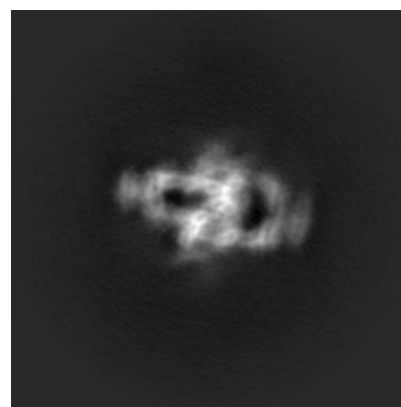
6.1.2 Raw map



X



Y



Z

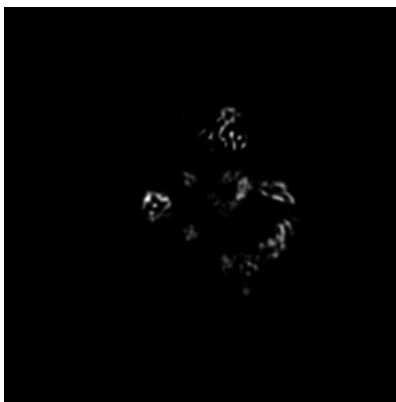
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 96

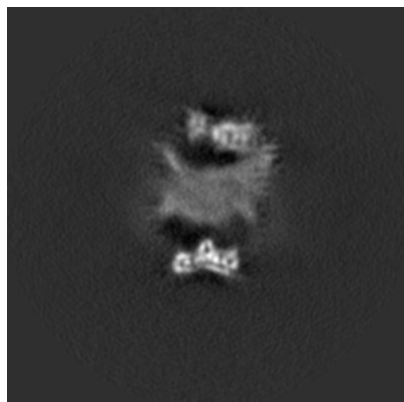


Y Index: 96

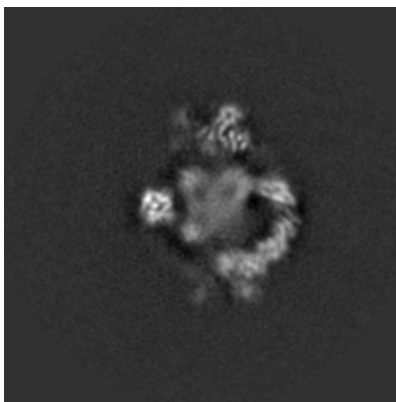


Z Index: 96

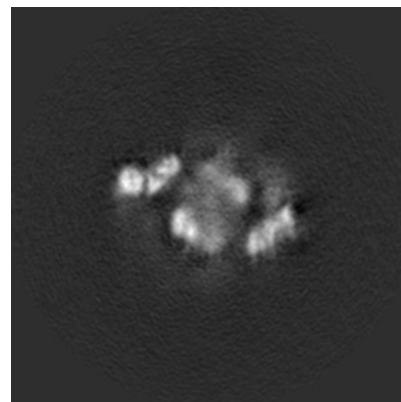
6.2.2 Raw map



X Index: 96



Y Index: 96



Z Index: 96

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

6.3 Largest variance slices [i](#)

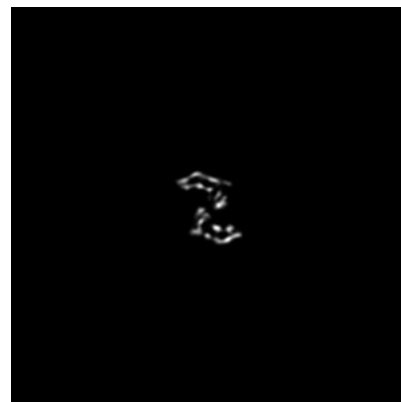
6.3.1 Primary map



X Index: 102

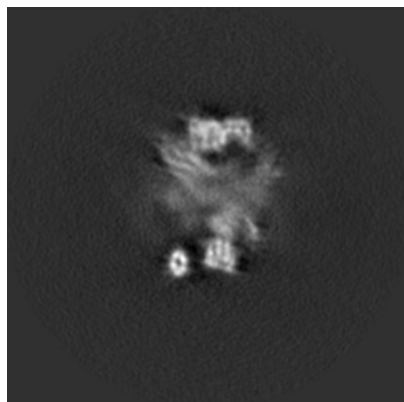


Y Index: 106

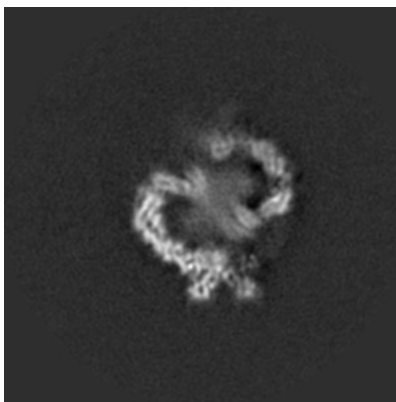


Z Index: 68

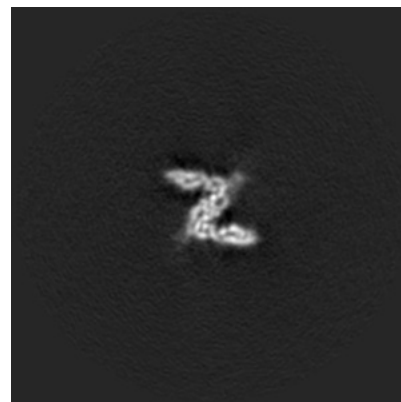
6.3.2 Raw map



X Index: 102



Y Index: 108

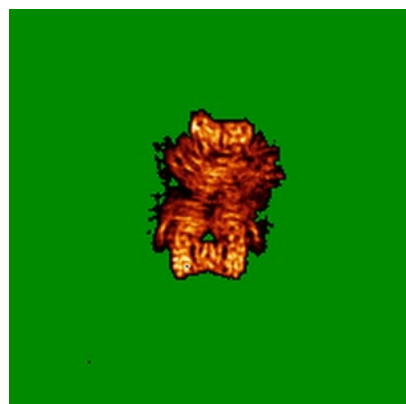


Z Index: 71

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

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

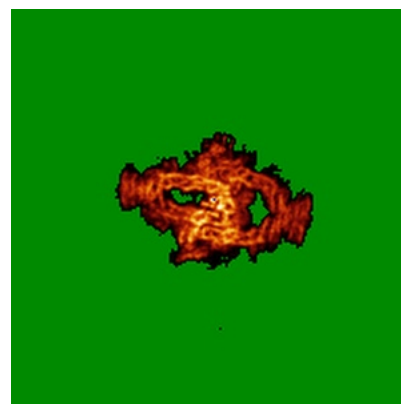
6.4.1 Primary map



X



Y

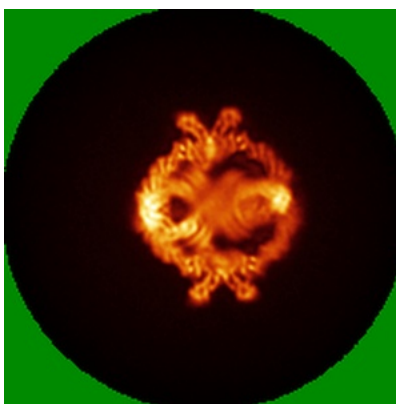


Z

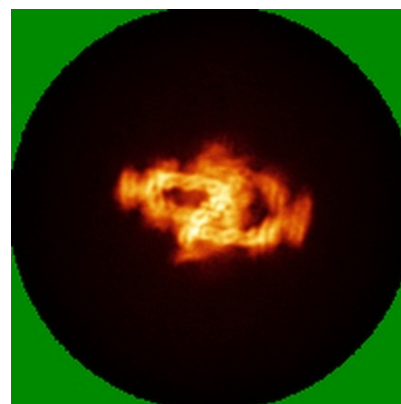
6.4.2 Raw map



X



Y

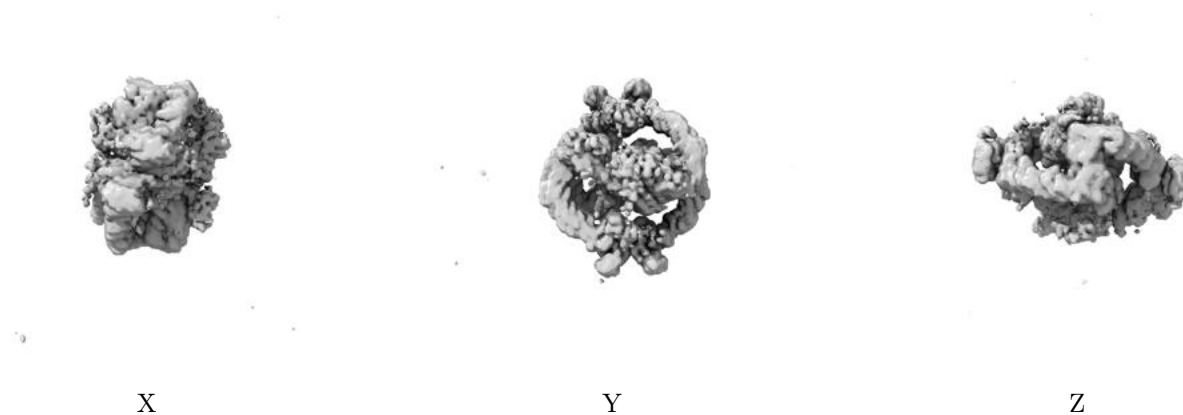


Z

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 0.001. 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.

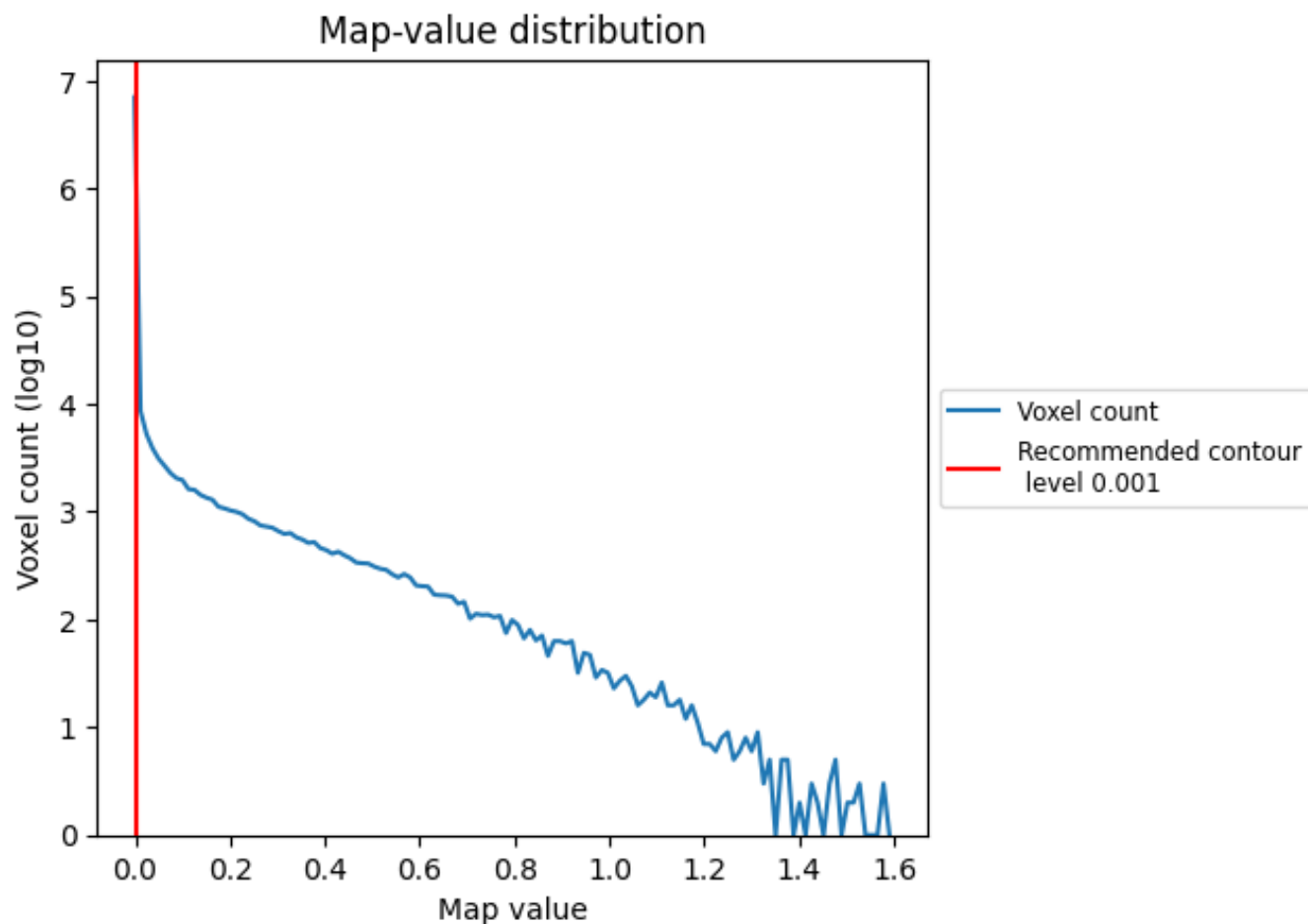
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

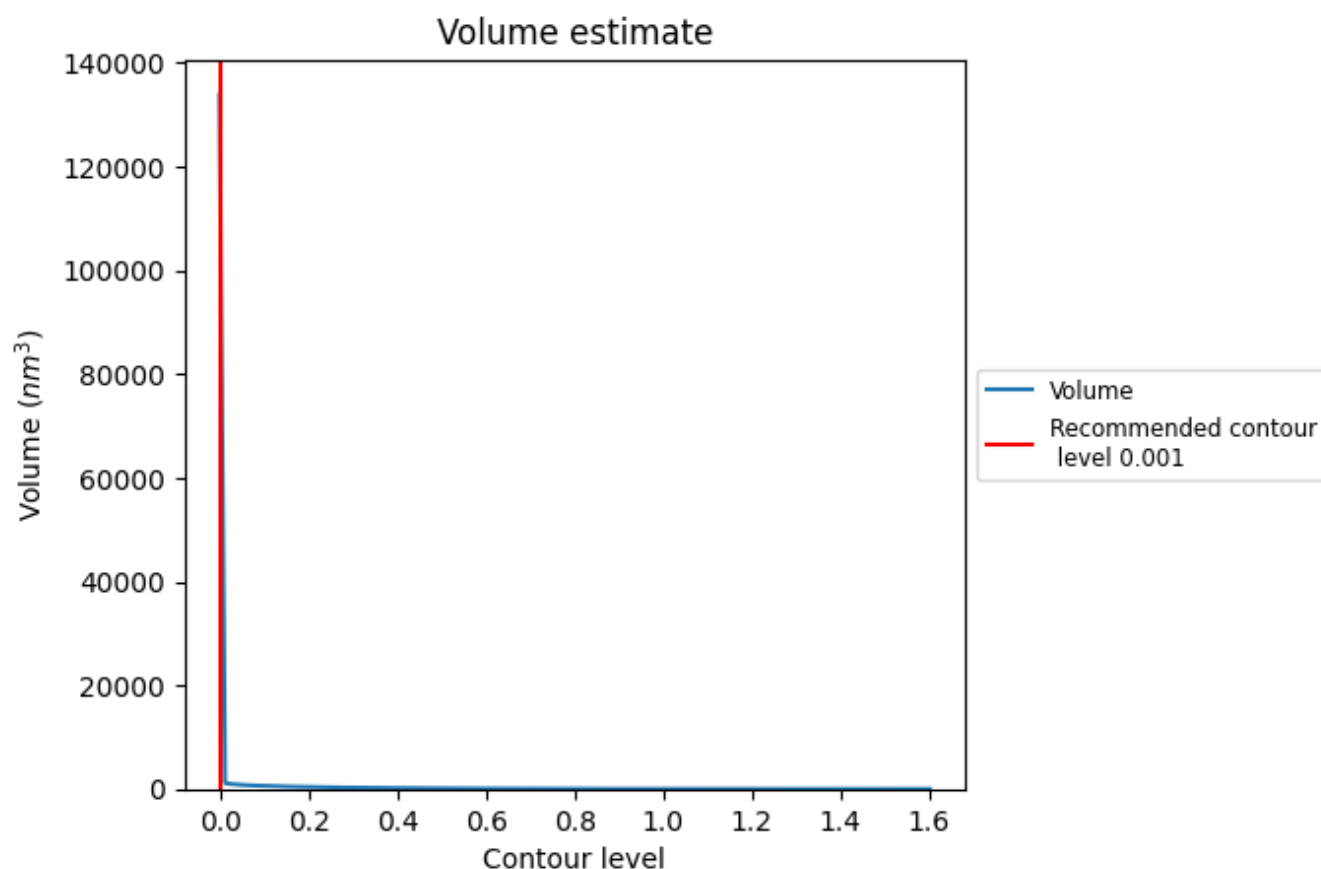
This section contains the results of statistical analysis of the map.

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.

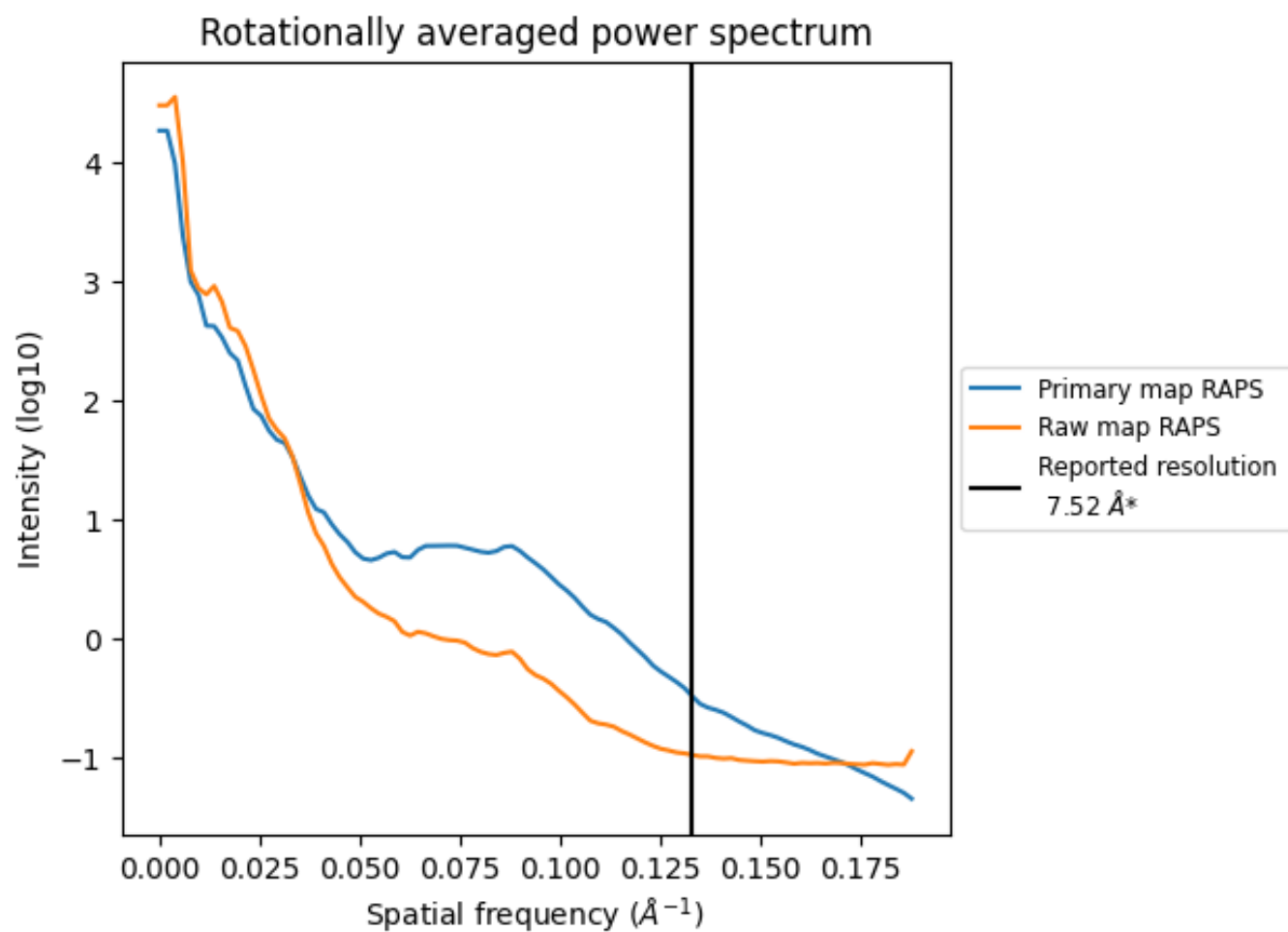
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 108428 nm^3 ; this corresponds to an approximate mass of 97946 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 ⓘ

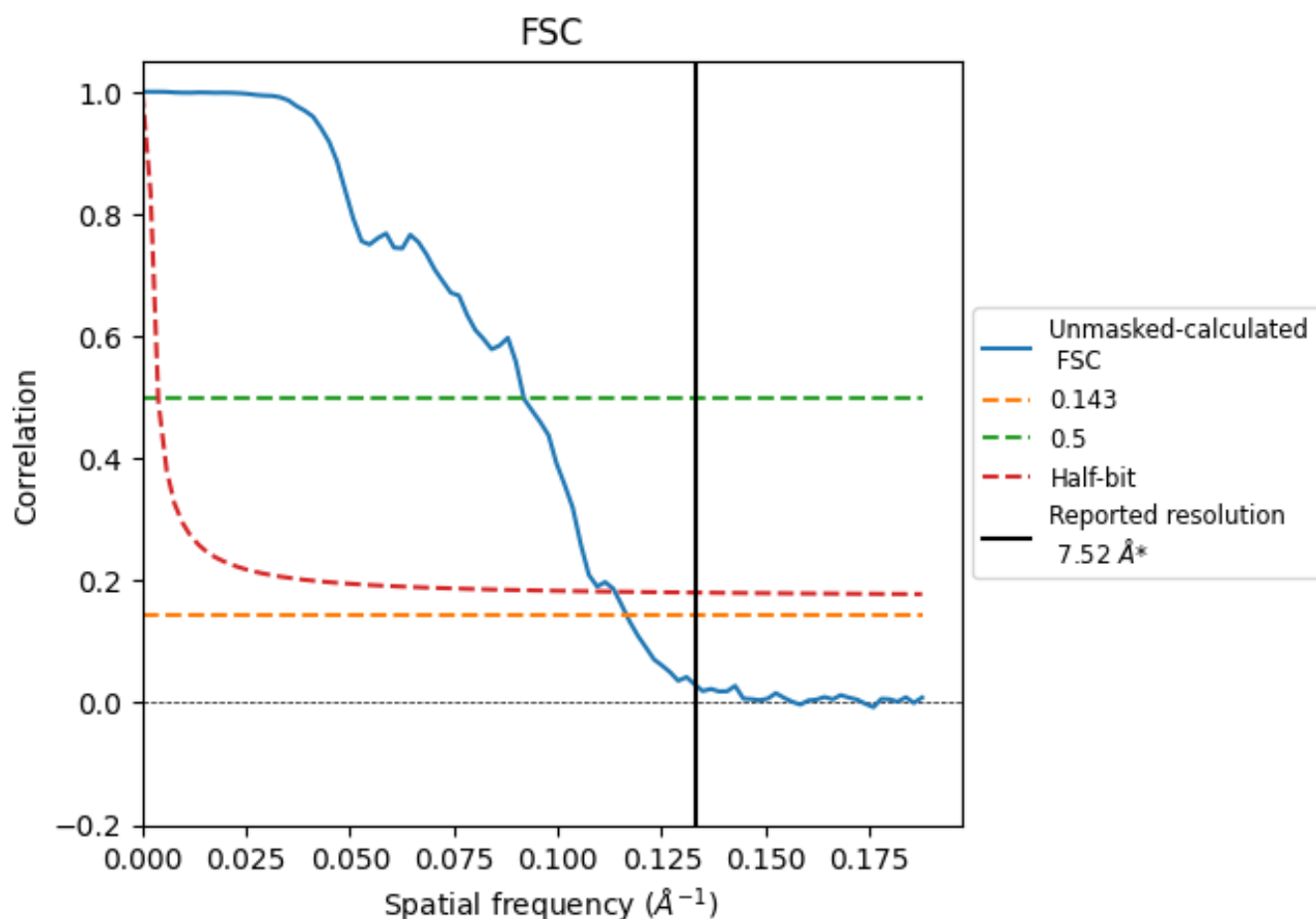


*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

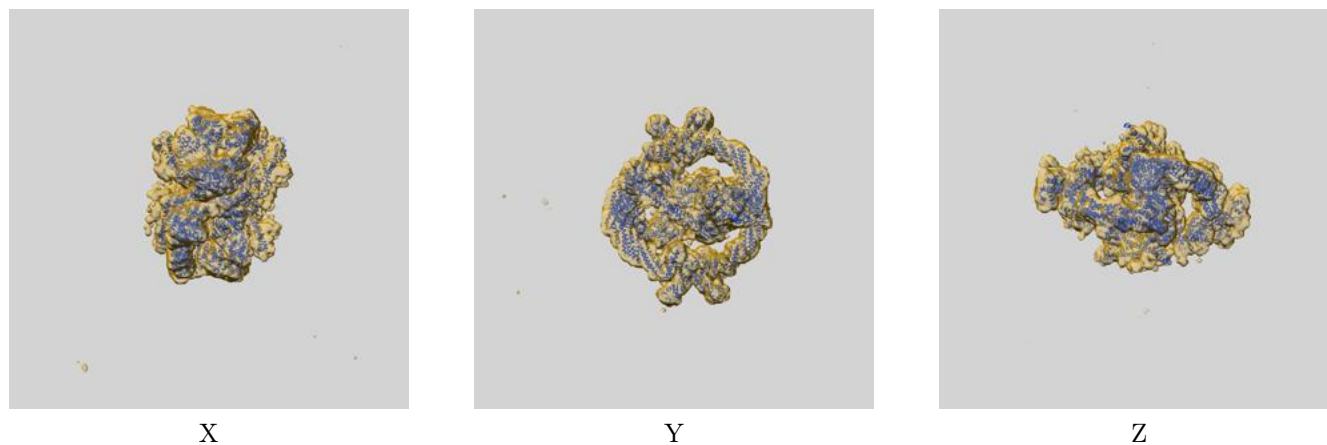
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.52	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.58	10.89	8.79

*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 8.58 differs from the reported value 7.52 by more than 10 %

9 Map-model fit [i](#)

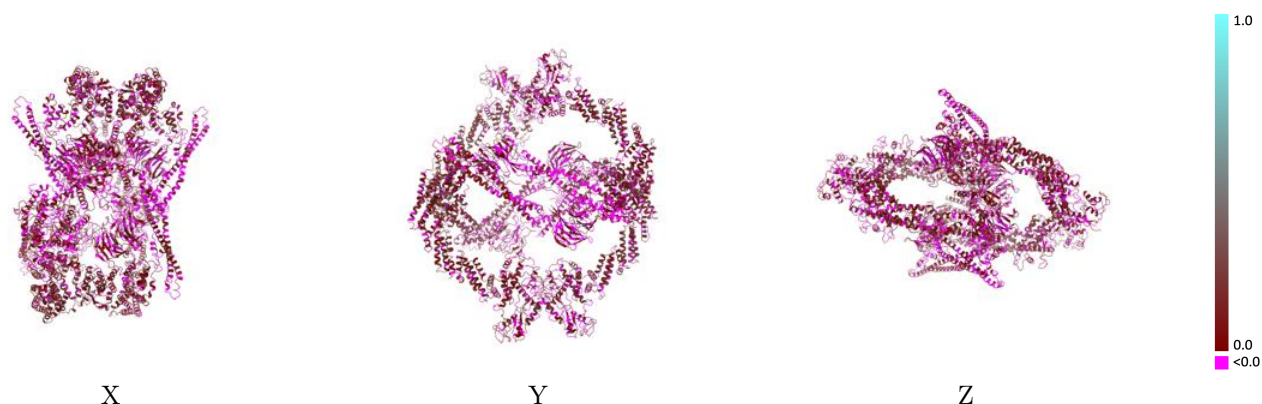
This section contains information regarding the fit between EMDB map EMD-34453 and PDB model 8H37. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



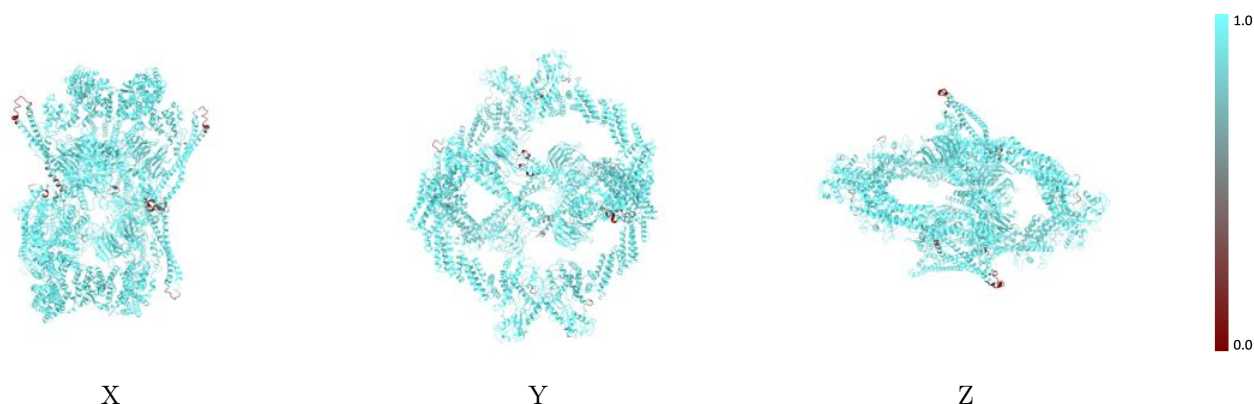
The images above show the 3D surface view of the map at the recommended contour level 0.001 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



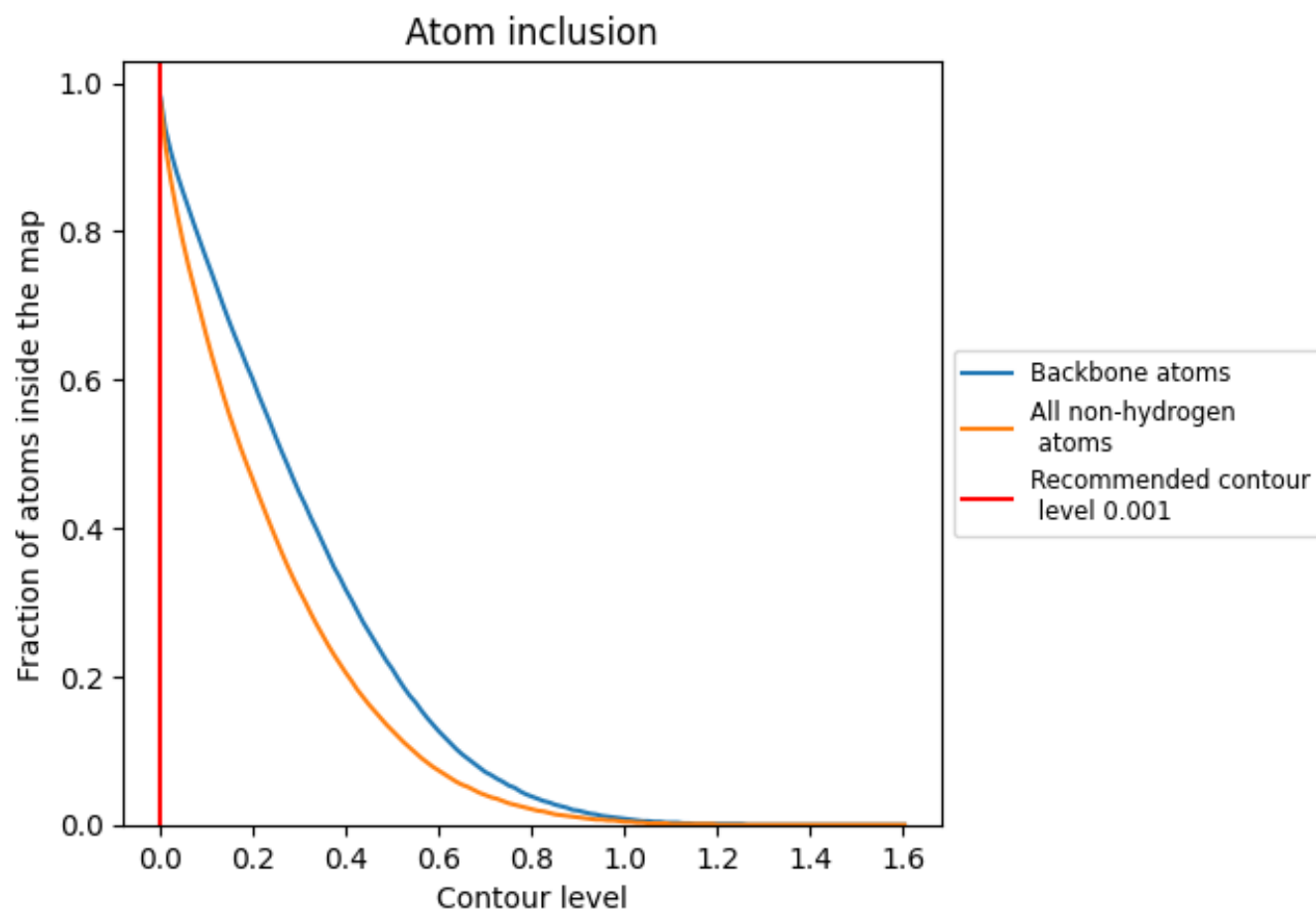
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.001).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% 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 (0.001) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9740	 0.0570
A	 0.9950	 0.0600
B	 0.9880	 0.0440
C	 0.9930	 0.1050
D	 0.9200	 0.0200
E	 0.9710	 0.0270
F	 0.9950	 0.0940
G	 0.9610	 0.0420
H	 0.9320	 0.0330
I	 0.7700	 -0.0150
J	 0.8140	 -0.0430
M	 0.9860	 0.0840
N	 0.9800	 0.0250
O	 0.9870	 0.0720
P	 0.9890	 0.0280
Q	 0.9810	 0.0150
R	 0.9490	 -0.0020

