



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:50 AM UTC

PDB ID : 8JAS / pdb_00008jas
EMDB ID : EMD-36133
Title : Structure of CRL2APPBP2 bound with RxxGPAA degron (tetramer)
Authors : Zhao, S.; Zhang, K.; Xu, C.
Deposited on : 2023-05-07
Resolution : 3.54 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:

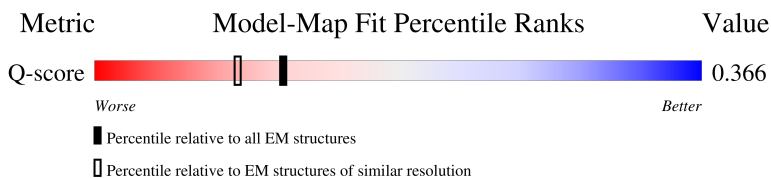
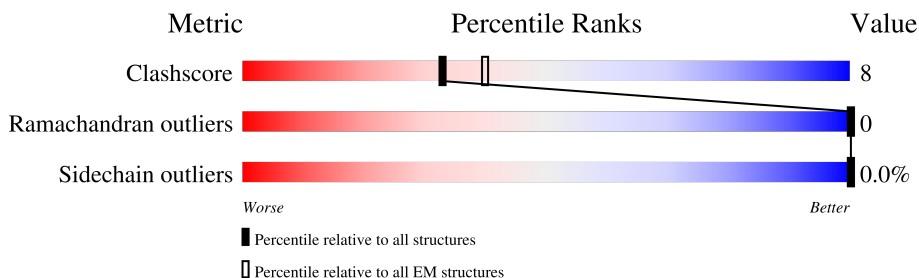
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.54 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.









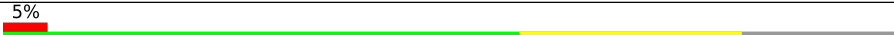
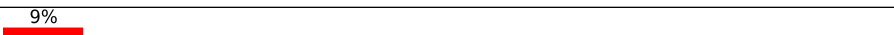
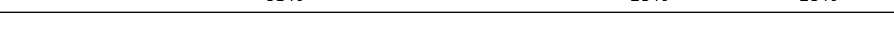
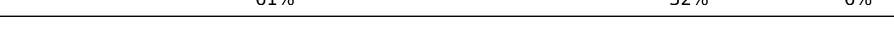
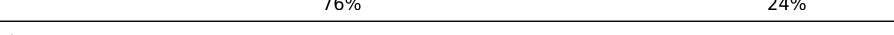






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	585	81% 17% .
1	B	585	76% 22% .
1	J	585	5% 76% 22% .
1	K	585	78% 19% .

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Mol	Chain	Length	Quality of chain
2	E	745	
2	I	745	
2	L	745	
2	U	745	
3	C	118	
3	G	118	
3	M	118	
3	Q	118	
4	D	96	
4	H	96	
4	N	96	
4	T	96	
5	F	18	
5	O	18	
5	S	18	
6	R	108	
6	V	108	

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 39287 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 Amyloid protein-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	572	Total	C	N	O	S	0	0
			4622	2951	797	853	21		
1	B	572	Total	C	N	O	S	0	0
			4622	2951	797	853	21		
1	J	572	Total	C	N	O	S	0	0
			4619	2950	797	851	21		
1	K	571	Total	C	N	O	S	0	0
			4613	2946	795	851	21		

- Molecule 2 is a protein called Cullin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	203	Total	C	N	O	S	0	0
			1726	1121	286	310	9		
2	I	636	Total	C	N	O	S	0	0
			5223	3332	878	975	38		
2	L	136	Total	C	N	O	S	0	0
			1161	751	192	210	8		
2	U	636	Total	C	N	O	S	0	0
			5223	3332	878	975	38		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1	THR	-	expression tag	UNP Q13617
I	1	THR	-	expression tag	UNP Q13617
L	1	THR	-	expression tag	UNP Q13617
U	1	THR	-	expression tag	UNP Q13617

- Molecule 3 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	97	Total	C	N	O	S	0	0
			766	487	129	146	4		
3	G	99	Total	C	N	O	S	0	0
			782	495	132	152	3		
3	M	97	Total	C	N	O	S	0	0
			766	487	129	146	4		
3	Q	96	Total	C	N	O	S	0	0
			758	479	129	147	3		

- Molecule 4 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	90	Total	C	N	O	S	0	0
			709	456	114	133	6		
4	H	96	Total	C	N	O	S	0	0
			760	487	122	145	6		
4	N	91	Total	C	N	O	S	0	0
			718	461	116	135	6		
4	T	91	Total	C	N	O	S	0	0
			722	466	116	134	6		

- Molecule 5 is a protein called SUMO-XP_211896+AA C-degron.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	S	9	Total	C	N	O	0	0
			65	39	14	12		
5	F	9	Total	C	N	O	0	0
			65	39	14	12		
5	O	6	Total	C	N	O	0	0
			32	19	6	7		

- Molecule 6 is a protein called E3 ubiquitin-protein ligase RBX1, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	81	Total	C	N	O	S	0	0
			661	417	119	116	9		
6	V	82	Total	C	N	O	S	0	0
			666	420	120	117	9		

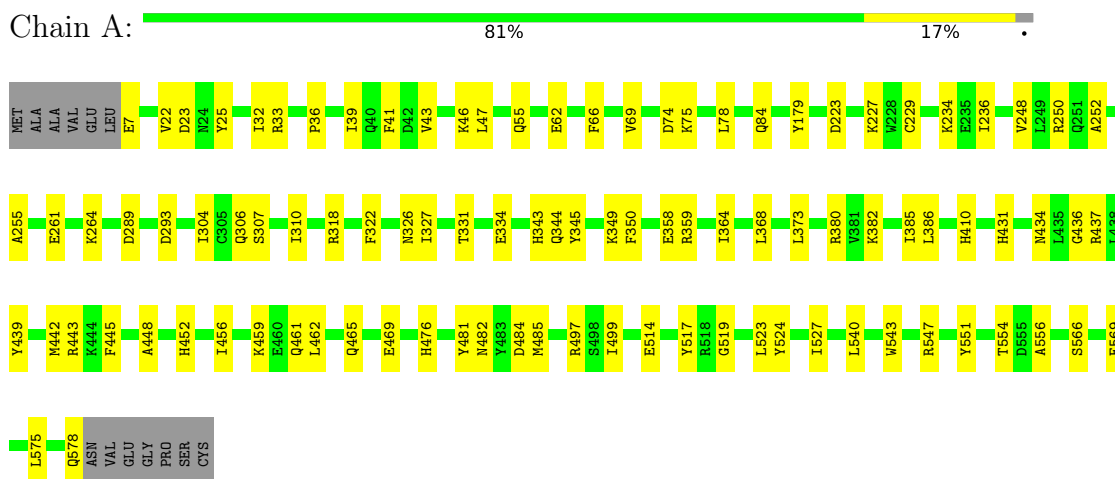
- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total 1	Zn 1	0
7	R	3	Total 3	Zn 3	0
7	K	1	Total 1	Zn 1	0
7	V	3	Total 3	Zn 3	0

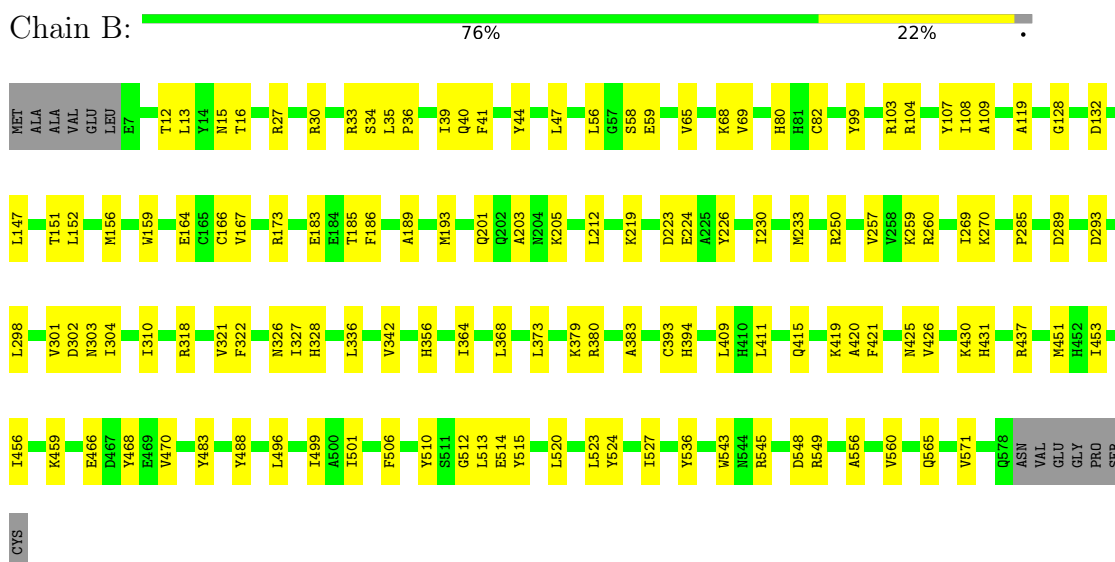
3 Residue-property plots [i](#)

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.

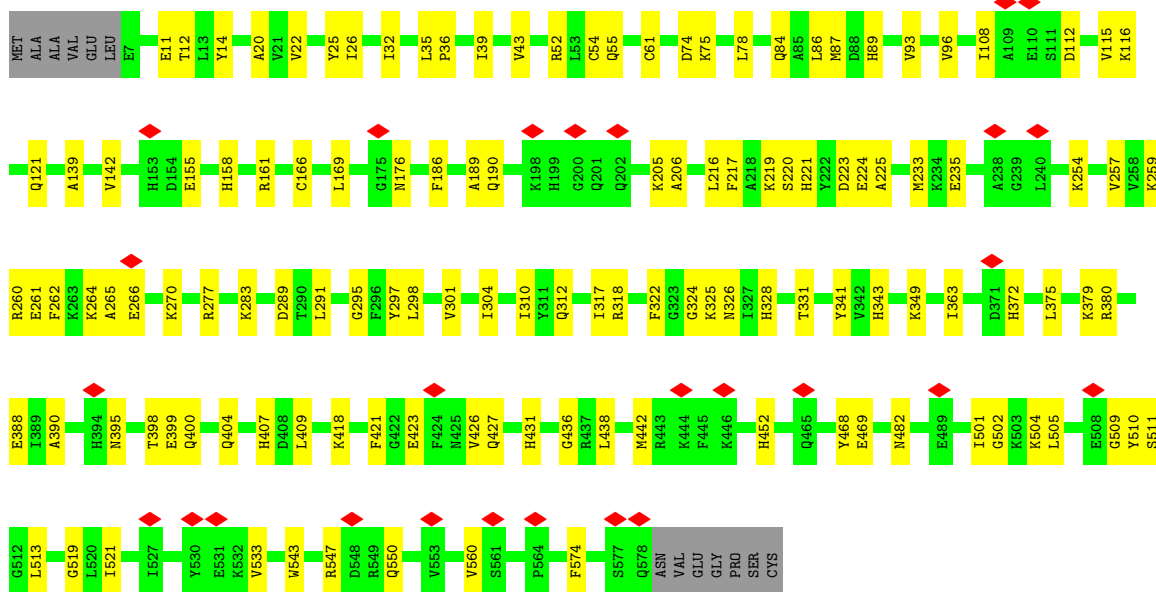
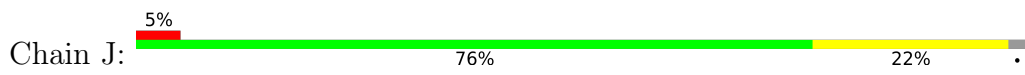
- Molecule 1: Amyloid protein-binding protein 2



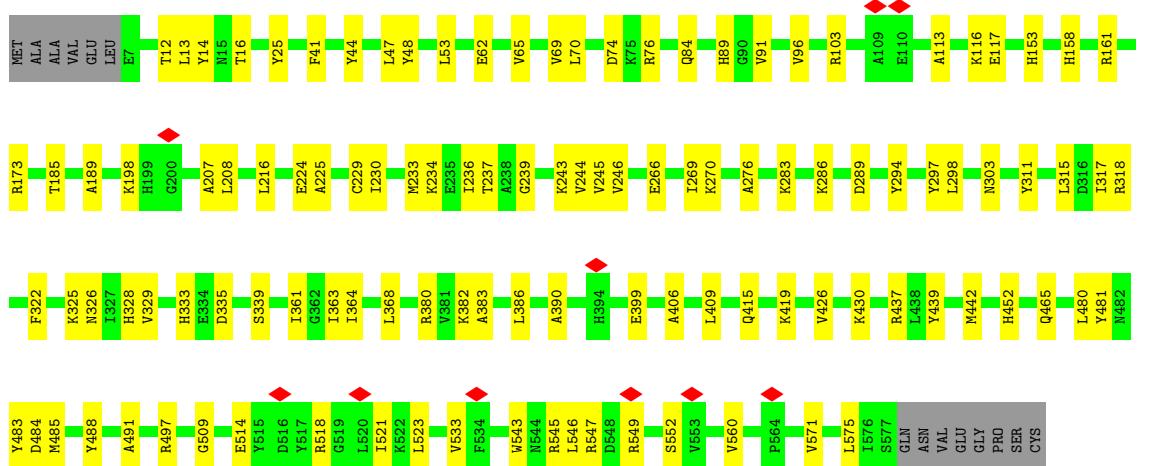
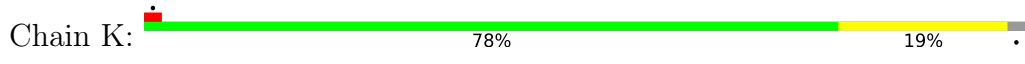
- Molecule 1: Amyloid protein-binding protein 2



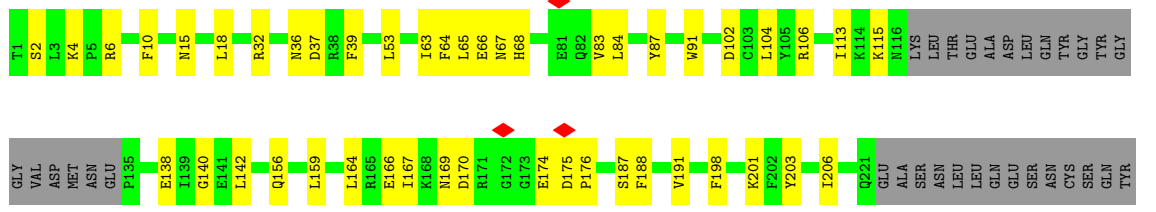
- Molecule 1: Amyloid protein-binding protein 2



• Molecule 1: Amyloid protein-binding protein 2



• Molecule 2: Cullin-2



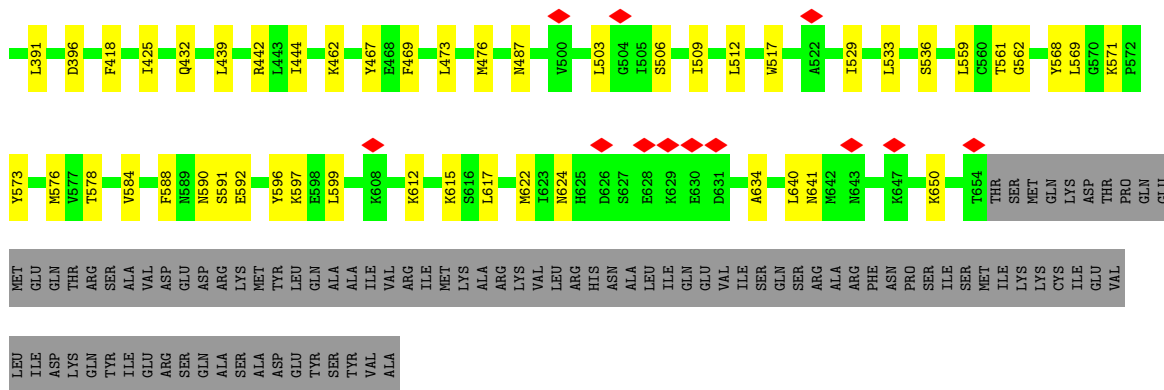


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I113	K114	K116	LYS	LEU	THR	GLU	GLY	TYR	GLY	TYR	LYS	GLY	GLY	PRO	VAL	ASP	MET	ASN	GLU	PRO	GLY	LEU	CYS	ILE	PHE	GLU	ILE	LEU	ILE	ARG	GLY	ASN	ASP	ARG	GLY	GLY	GLU	ASP	GLY	PRO	LYS	ASN	GLN	VAL	ILE	
HIS	GLY	VAL	TYR	ILE	SER	PHE	VAL	HIS	ALA	HIS	VAL	VAL	ASP	GLY	GLN	TYR	THR	LYS	ASP	PHE	GLY	VAL	GLN	GLY	TYR	ALA	GLN	ARG	GLY	ASN	ASP	ARG	GLY	GLY	GLU	ASP	GLY	PRO	LYS	ASN	GLN	VAL	ILE			
ARG	LEU	LYS	ASP	GLY	GLU	ILE	ARG	VAL	CYS	GLY	VAL	ILE	TYR	HIS	GLN	PRO	GLY	GLN	GLY	ASN	GLY	VAL	ILE	HIS	ALA	GLU	GLY	ASN	ILE	ILE	ARG	GLY	GLN	GLY	LYS	ASN	ASP	ARG	GLY	GLY	VAL	VAL	LEU	LEU		
ARG	ALA	VAL	SER	THR	GLY	LEU	PRO	HIS	HIS	ASN	HIS	GLY	VAL	ARG	ILE	ASP	VAL	THR	LYS	VAL	GLY	GLU	ALA	THR	SER	VAL	VAL	GLY	ASN	VAL	VAL	GLY	PHE	VAL	GLM	GLY	LEU	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	
GLN	HIS	PHE	MET	ASN	ALA	LEU	ASP	THR	THR	VAL	VAL	VAL	VAL	VAL	VAL	CYS	LYS	ALA	ALA	PRO	GLY	LYS	TYR	ASN	LEU	LYS	LYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
PHE	LYS	TYR	ILE	ASP	ASP	LYS	ASP	VAL	VAL	PHE	VAL	PHE	ALA	ASN	ASN	ASN	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA
VAL	SER	ALA	ASP	LEU	ASN	PHE	LYS	PHE	GLY	ASN	GLN	HIS	ASP	THR	VAL	ILE	ASP	PHE	GLN	ILE	GLY	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
LEU	PHE	TYR	GLN	HIS	PHE	SER	GLY	LYS	THR	TRP	THR	LEU	ALA	HIS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
SER	THR	GLN	MET	GLY	GLY	LYS	THR	LYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
PRO	GLN	GLY	MET	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
ILE	GLY	VAL	LEU	ILE	ASP	GLN	LYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

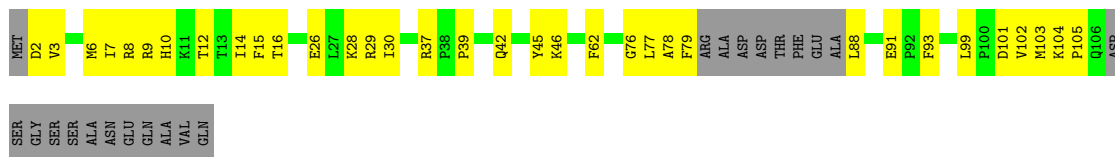
• Molecule 2: Cullin-2



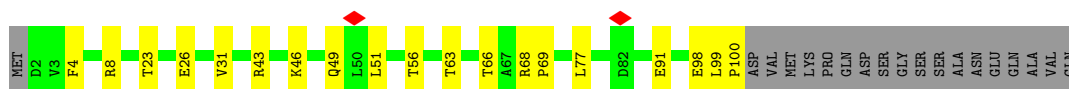
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LEU	GLN	TYR	GLY	GLY	VAL	ASP	MET	ASN	GLY	L136	I139	L142	M146	L150	I160	R161	M162	L163	D170	R171	D175	P176	M177	Q178	K179	V180	I185	F188	L200	Y203	Q204	E208	T215	Y219	E222	A223	M236	D245	E246				
E247	I248	R249	K252	Y253	L254	R255	P256	Y259	M270	L276	L278	H279	H283	I286	R287	K289	K291	R292	D293	M297	F309	H310	R311	I312	Q313	E314	L315	Q316	H317	H318	I319	L324	R325	A326	S342	I354	L358	F364	A371	V375	K382		



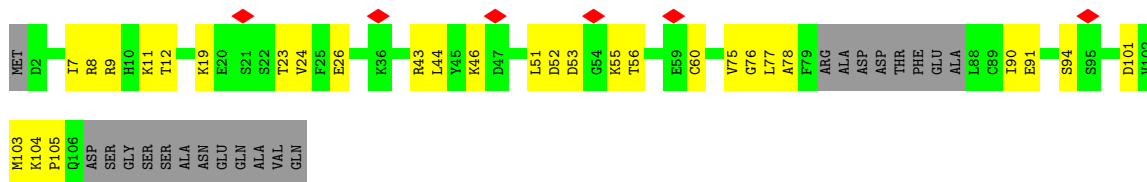
• Molecule 3: Elongin-B



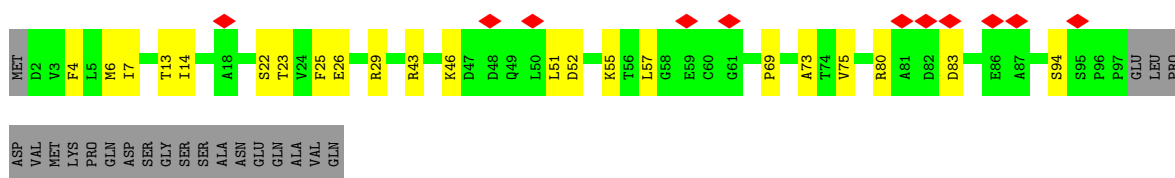
• Molecule 3: Elongin-B



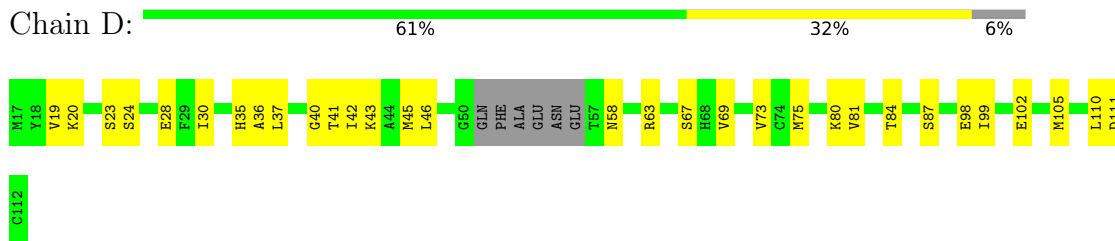
• Molecule 3: Elongin-B



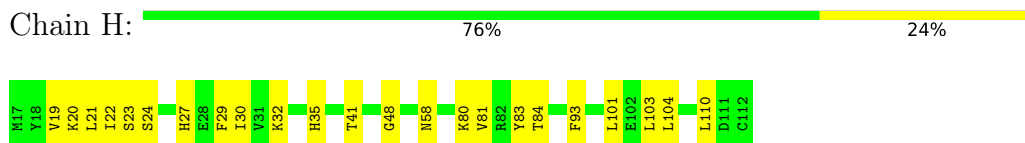
• Molecule 3: Elongin-B



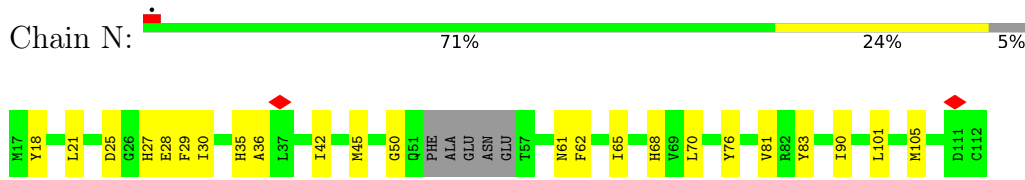
• Molecule 4: Elongin-C



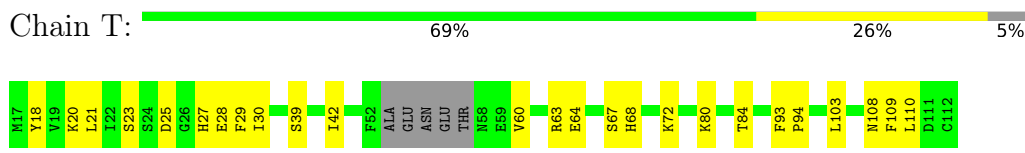
● Molecule 4: Elongin-C



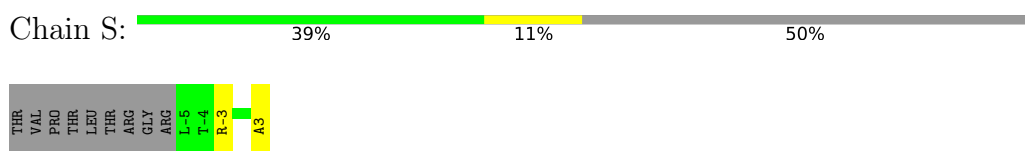
● Molecule 4: Elongin-C



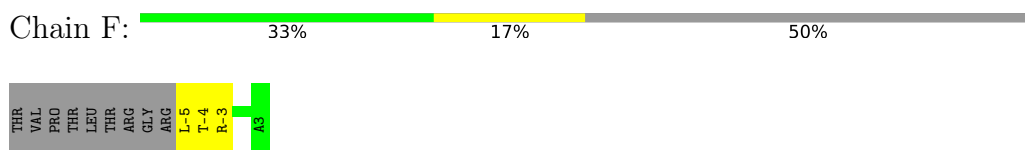
● Molecule 4: Elongin-C



● Molecule 5: SUMO-XP_211896+AA C-degron

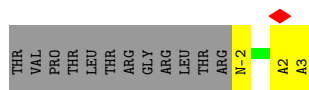


● Molecule 5: SUMO-XP_211896+AA C-degron

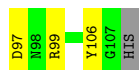


● Molecule 5: SUMO-XP_211896+AA C-degron





- Molecule 6: E3 ubiquitin-protein ligase RBX1, N-terminally processed



- Molecule 6: E3 ubiquitin-protein ligase RBX1, N-terminally processed



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	135810	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.028	Depositor
Minimum map value	-0.618	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	419.84, 419.84, 419.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

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	A	0.14	0/4721	0.32	0/6370
1	B	0.14	0/4721	0.32	0/6370
1	J	0.08	0/4718	0.23	0/6366
1	K	0.10	0/4712	0.29	0/6358
2	E	0.13	0/1769	0.36	0/2388
2	I	0.11	0/5331	0.30	0/7185
2	L	0.09	0/1189	0.25	0/1608
2	U	0.11	0/5331	0.33	0/7185
3	C	0.16	0/781	0.45	0/1055
3	G	0.12	0/798	0.33	0/1080
3	M	0.11	0/781	0.33	0/1055
3	Q	0.11	0/773	0.34	0/1045
4	D	0.14	0/724	0.33	0/977
4	H	0.15	0/777	0.33	0/1050
4	N	0.10	0/733	0.27	0/989
4	T	0.11	0/738	0.32	0/995
5	F	0.14	0/65	0.38	0/85
5	O	0.09	0/32	0.36	0/42
5	S	0.12	0/65	0.33	0/85
6	R	0.12	0/681	0.32	0/929
6	V	0.16	0/686	0.35	0/936
All	All	0.12	0/40126	0.31	0/54153

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	4622	0	4562	63	0
1	B	4622	0	4562	88	0
1	J	4619	0	4560	88	0
1	K	4613	0	4554	72	0
2	E	1726	0	1721	30	0
2	I	5223	0	5206	82	0
2	L	1161	0	1149	19	0
2	U	5223	0	5206	92	0
3	C	766	0	773	25	0
3	G	782	0	777	12	0
3	M	766	0	773	24	0
3	Q	758	0	753	14	0
4	D	709	0	708	27	0
4	H	760	0	749	18	0
4	N	718	0	716	18	0
4	T	722	0	718	17	0
5	F	65	0	72	4	0
5	O	32	0	26	3	0
5	S	65	0	72	3	0
6	R	661	0	603	21	0
6	V	666	0	605	19	0
7	A	1	0	0	0	0
7	K	1	0	0	0	0
7	R	3	0	0	0	0
7	V	3	0	0	0	0
All	All	39287	0	38865	659	0

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

The worst 5 of 659 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:A:22:VAL:O	1:A:25:TYR:HB2	1.66	0.94
6:R:45:CYS:HB3	6:R:83:CYS:SG	2.20	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:4:LYS:HD2	4:D:105:MET:HE1	1.66	0.76
2:E:39:PHE:HE1	2:E:104:LEU:HA	1.51	0.75
6:V:37:ILE:HD12	6:V:78:ALA:HB3	1.69	0.73

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	570/585 (97%)	555 (97%)	15 (3%)	0	100	100
1	B	570/585 (97%)	557 (98%)	13 (2%)	0	100	100
1	J	570/585 (97%)	560 (98%)	10 (2%)	0	100	100
1	K	569/585 (97%)	561 (99%)	8 (1%)	0	100	100
2	E	199/745 (27%)	196 (98%)	3 (2%)	0	100	100
2	I	632/745 (85%)	604 (96%)	28 (4%)	0	100	100
2	L	132/745 (18%)	129 (98%)	3 (2%)	0	100	100
2	U	632/745 (85%)	614 (97%)	18 (3%)	0	100	100
3	C	93/118 (79%)	84 (90%)	9 (10%)	0	100	100
3	G	97/118 (82%)	89 (92%)	8 (8%)	0	100	100
3	M	93/118 (79%)	88 (95%)	5 (5%)	0	100	100
3	Q	94/118 (80%)	86 (92%)	8 (8%)	0	100	100
4	D	86/96 (90%)	81 (94%)	5 (6%)	0	100	100
4	H	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
4	N	87/96 (91%)	87 (100%)	0	0	100	100
4	T	87/96 (91%)	83 (95%)	4 (5%)	0	100	100
5	F	7/18 (39%)	6 (86%)	1 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	O	4/18 (22%)	3 (75%)	1 (25%)	0	100	100
5	S	7/18 (39%)	7 (100%)	0	0	100	100
6	R	79/108 (73%)	76 (96%)	3 (4%)	0	100	100
6	V	80/108 (74%)	71 (89%)	9 (11%)	0	100	100
All	All	4782/6446 (74%)	4625 (97%)	157 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	492/502 (98%)	492 (100%)	0	100	100
1	B	492/502 (98%)	492 (100%)	0	100	100
1	J	491/502 (98%)	491 (100%)	0	100	100
1	K	491/502 (98%)	491 (100%)	0	100	100
2	E	189/681 (28%)	189 (100%)	0	100	100
2	I	585/681 (86%)	585 (100%)	0	100	100
2	L	127/681 (19%)	127 (100%)	0	100	100
2	U	585/681 (86%)	585 (100%)	0	100	100
3	C	87/103 (84%)	87 (100%)	0	100	100
3	G	87/103 (84%)	87 (100%)	0	100	100
3	M	87/103 (84%)	87 (100%)	0	100	100
3	Q	84/103 (82%)	84 (100%)	0	100	100
4	D	80/85 (94%)	80 (100%)	0	100	100
4	H	85/85 (100%)	85 (100%)	0	100	100
4	N	81/85 (95%)	81 (100%)	0	100	100
4	T	81/85 (95%)	81 (100%)	0	100	100
5	F	6/14 (43%)	6 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	O	1/14 (7%)	1 (100%)	0	100	100
5	S	6/14 (43%)	6 (100%)	0	100	100
6	R	70/90 (78%)	70 (100%)	0	100	100
6	V	70/90 (78%)	69 (99%)	1 (1%)	59	71
All	All	4277/5706 (75%)	4276 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	V	51	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	407	HIS
2	U	73	HIS
1	K	425	ASN
4	T	51	GLN
2	U	332	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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.

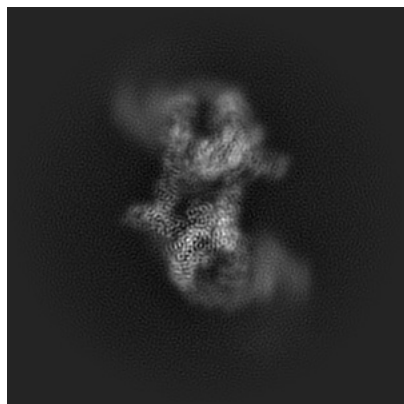
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36133. These allow visual inspection of the internal detail of the map and identification of artifacts.

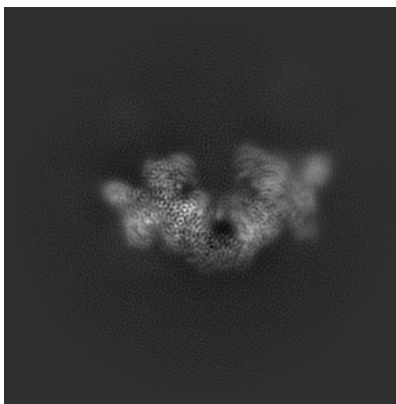
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

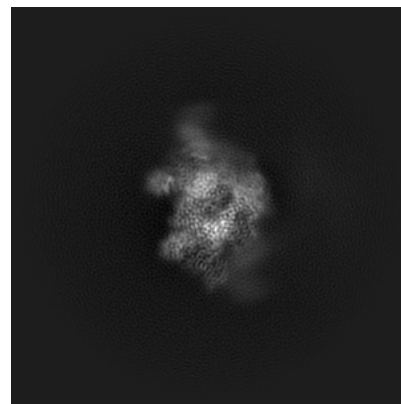
6.1.1 Primary map



X

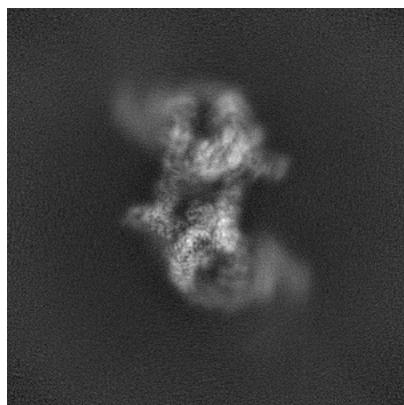


Y

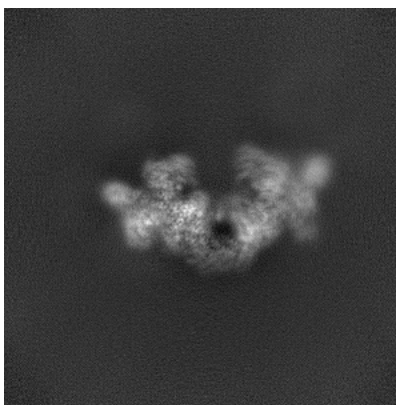


Z

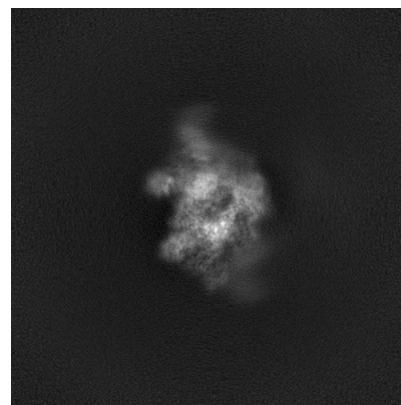
6.1.2 Raw map



X



Y

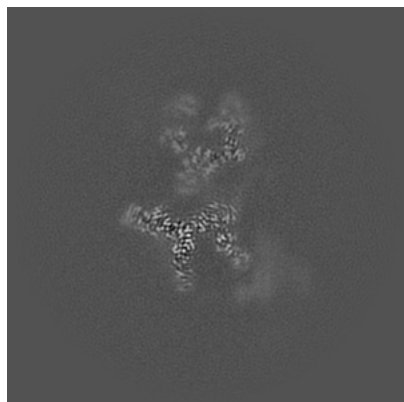


Z

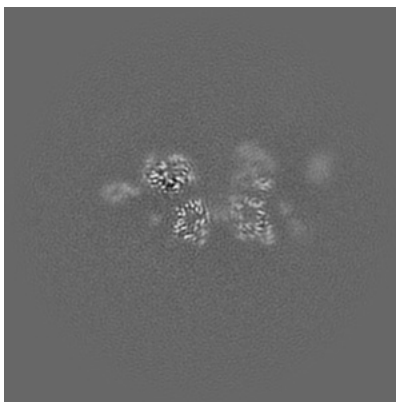
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

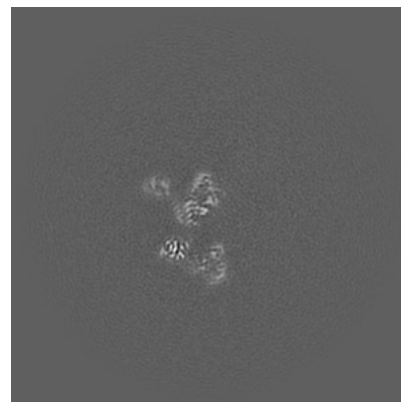
6.2.1 Primary map



X Index: 256

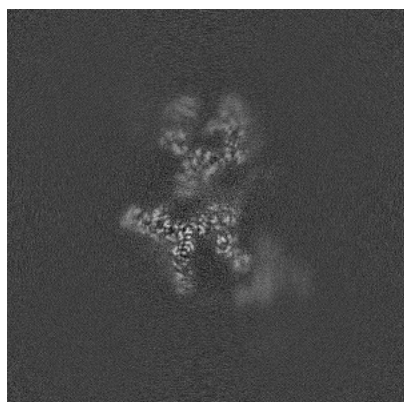


Y Index: 256

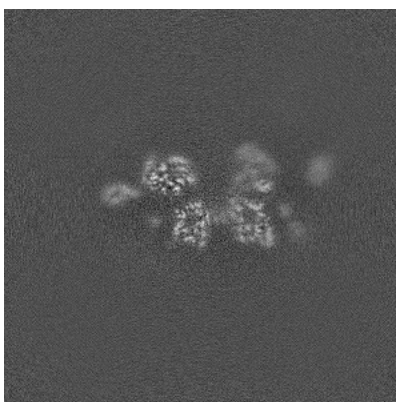


Z Index: 256

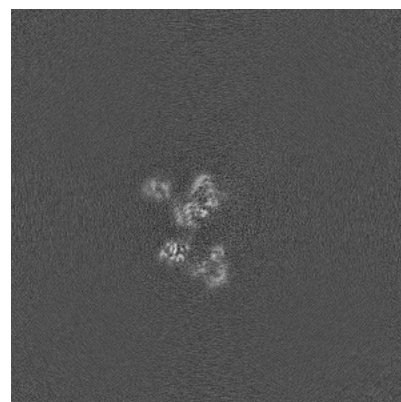
6.2.2 Raw map



X Index: 256



Y Index: 256

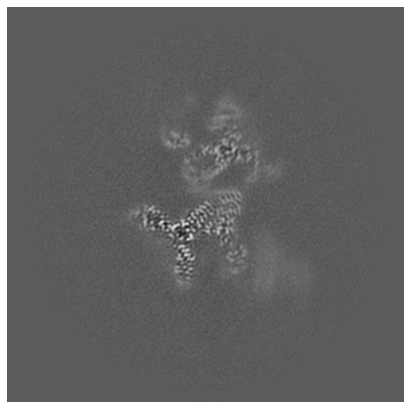


Z Index: 256

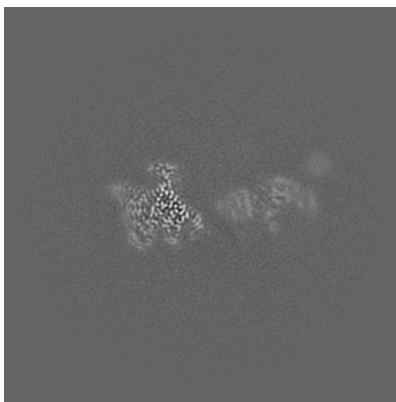
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

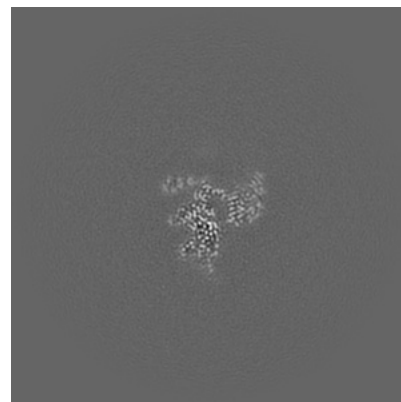
6.3.1 Primary map



X Index: 247

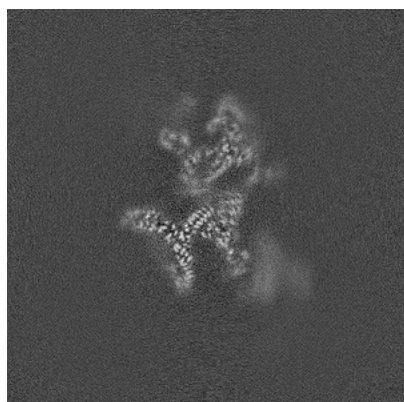


Y Index: 231

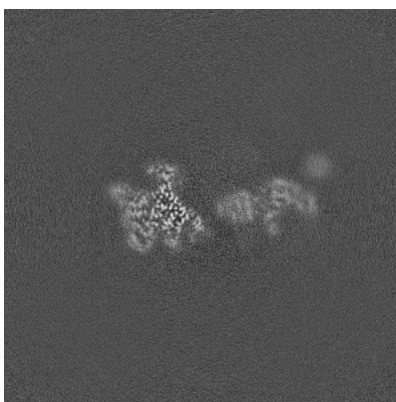


Z Index: 225

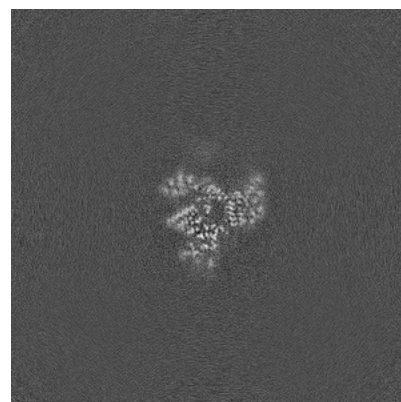
6.3.2 Raw map



X Index: 250



Y Index: 231

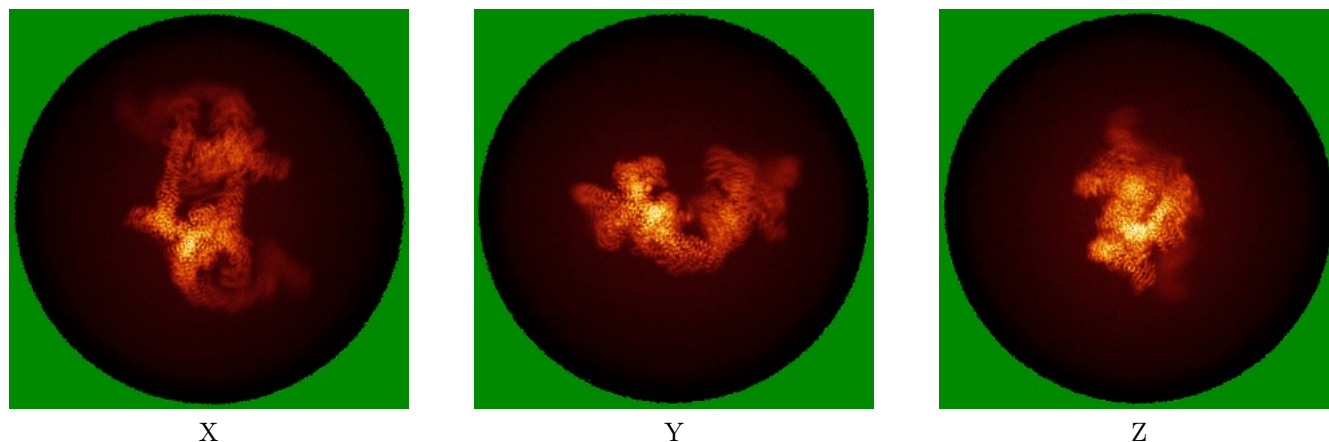


Z Index: 221

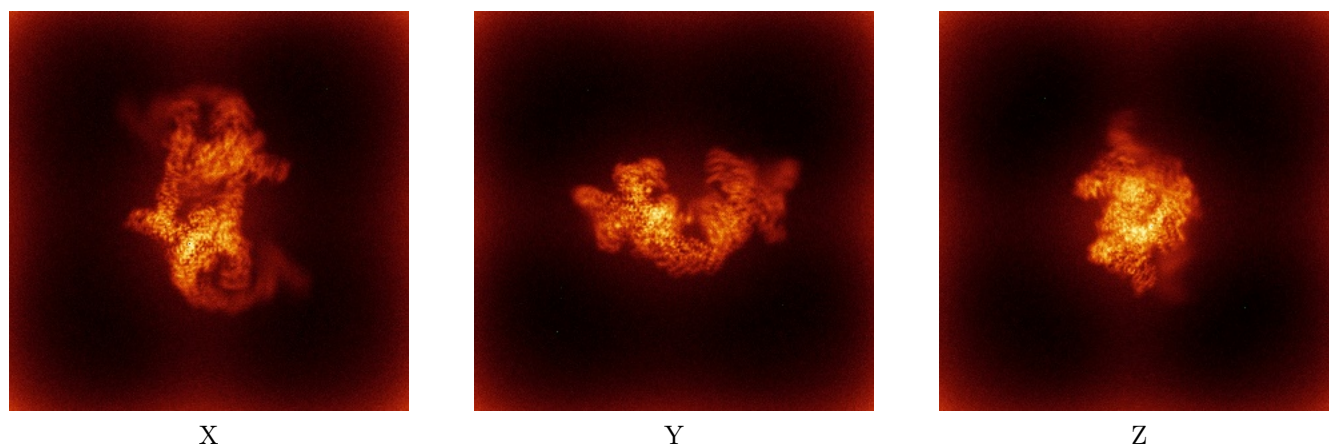
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



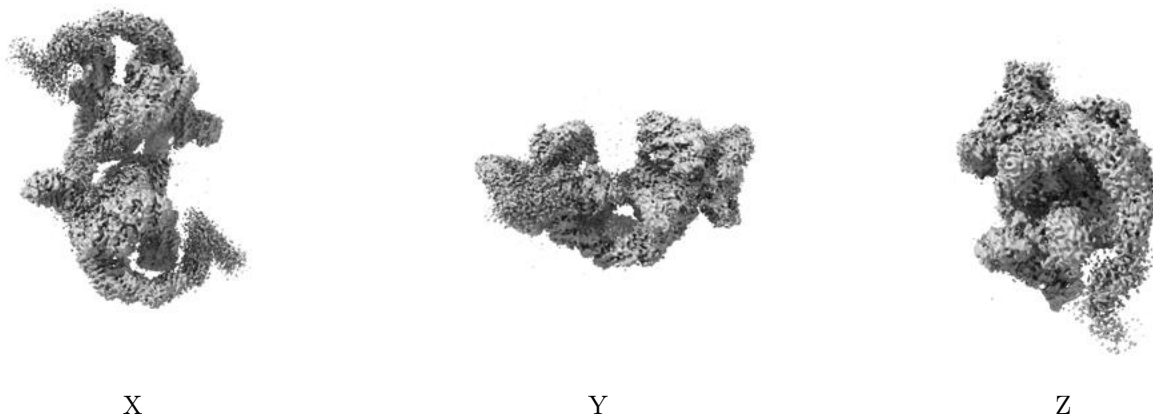
6.4.2 Raw map



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.

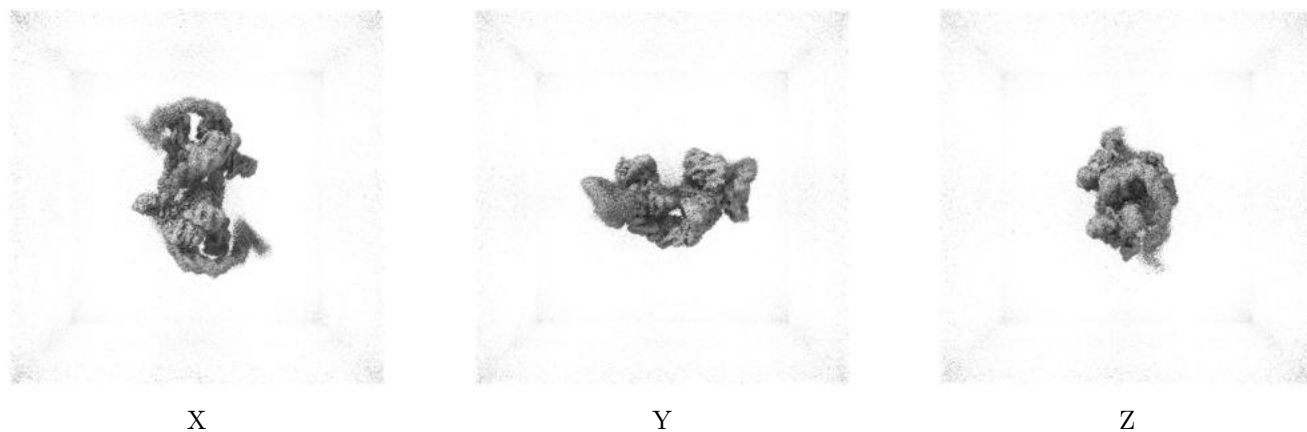
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. 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.

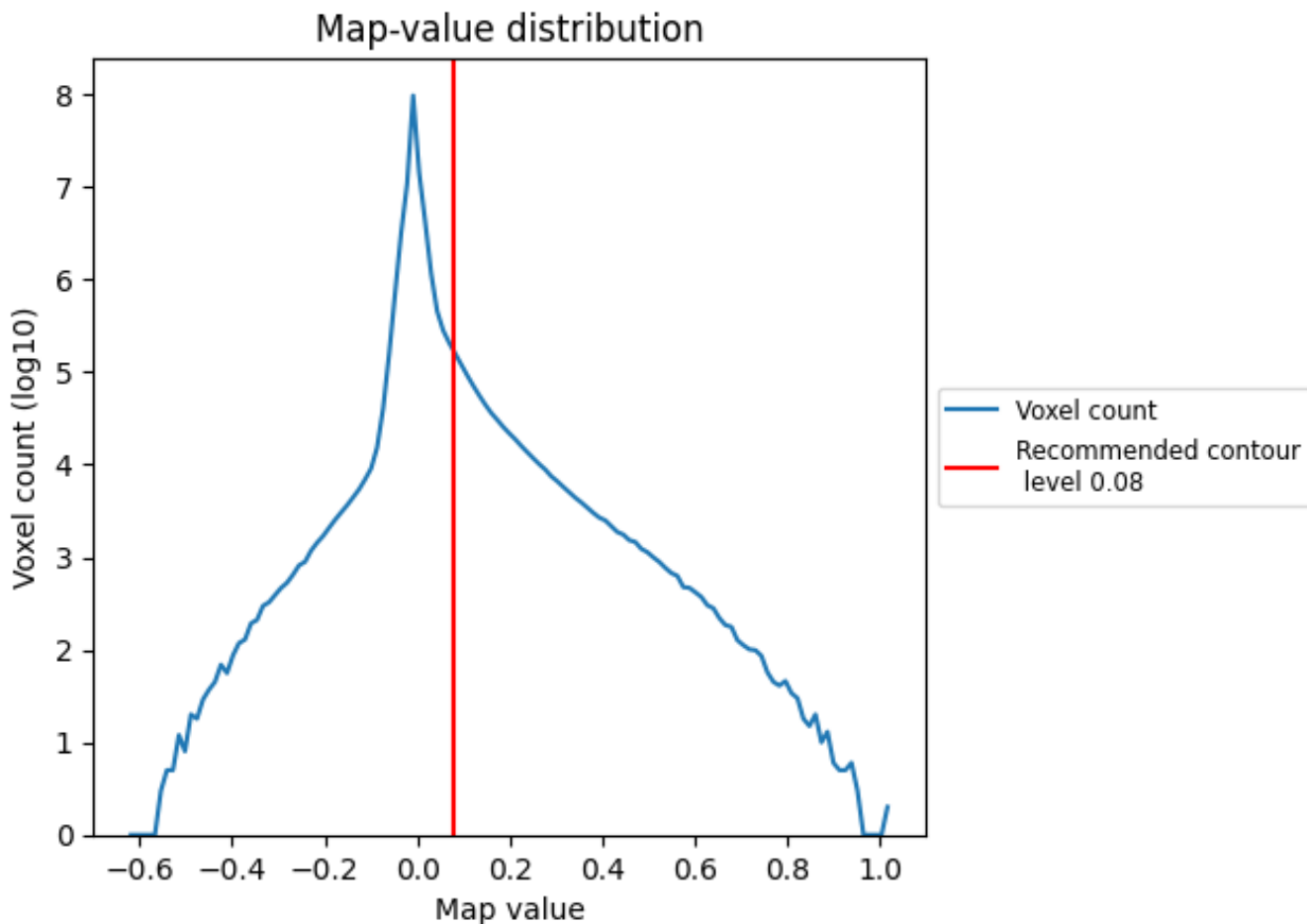
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

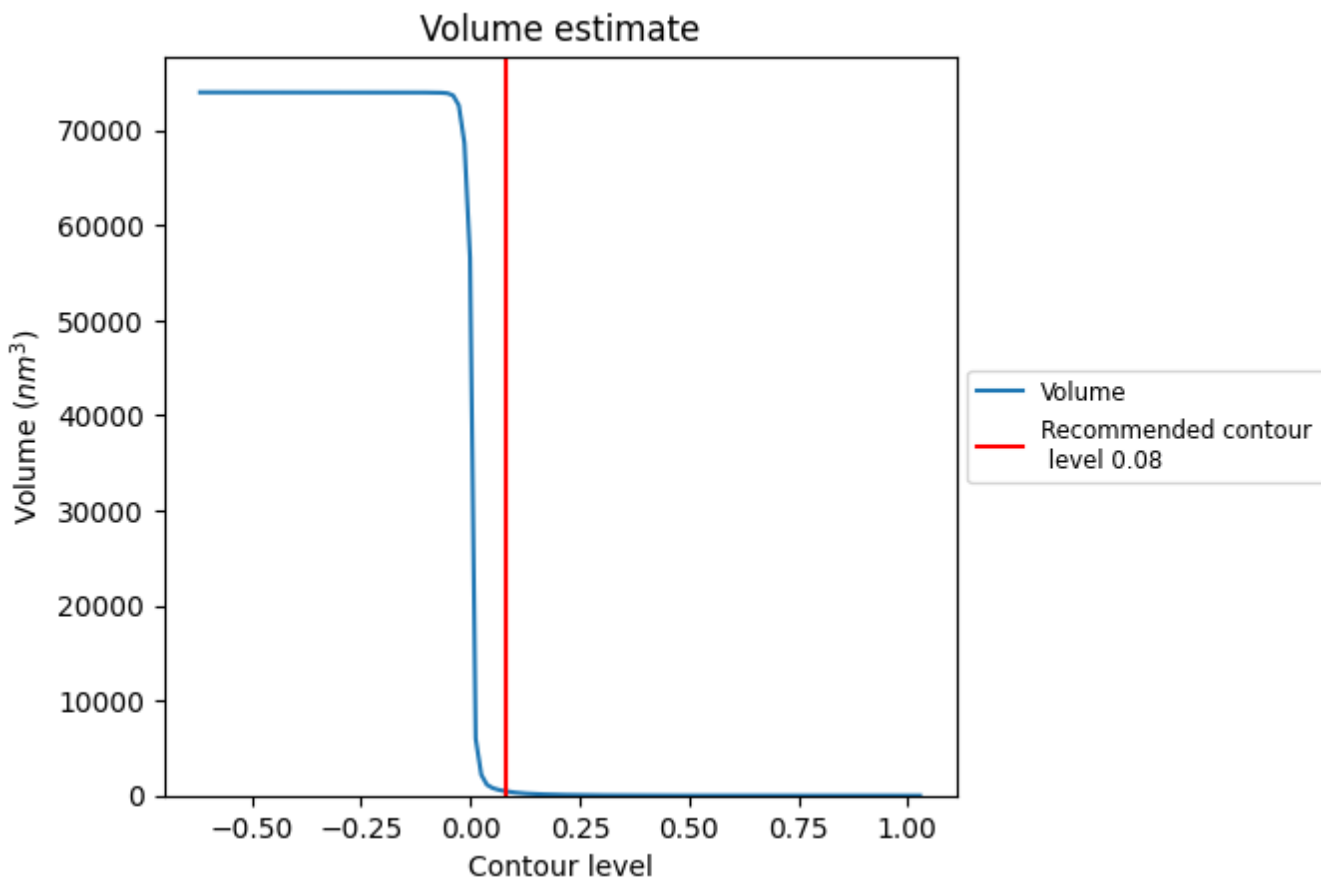
This section contains the results of statistical analysis of the map.

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.

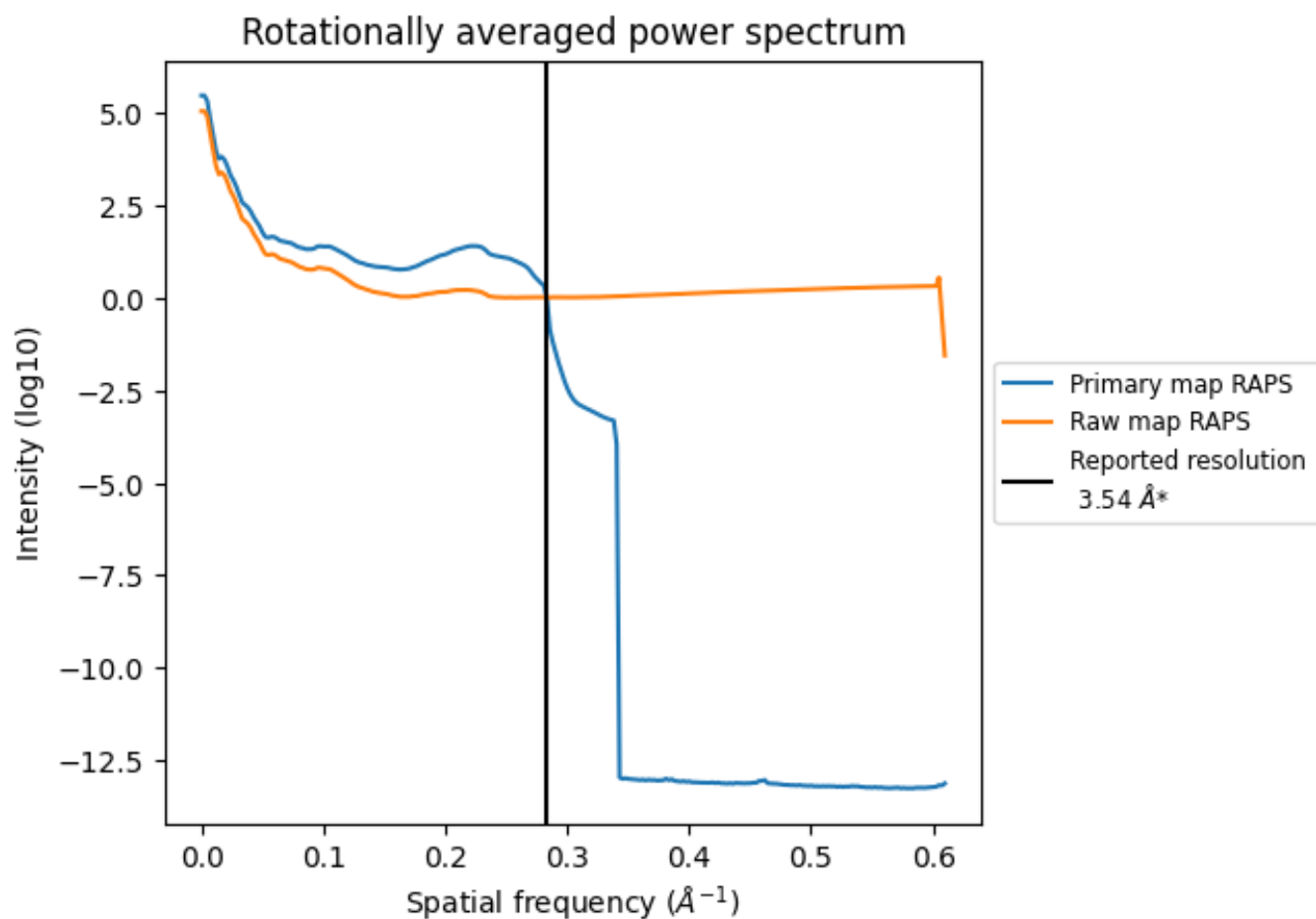
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 460 nm^3 ; this corresponds to an approximate mass of 416 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 [\(i\)](#)

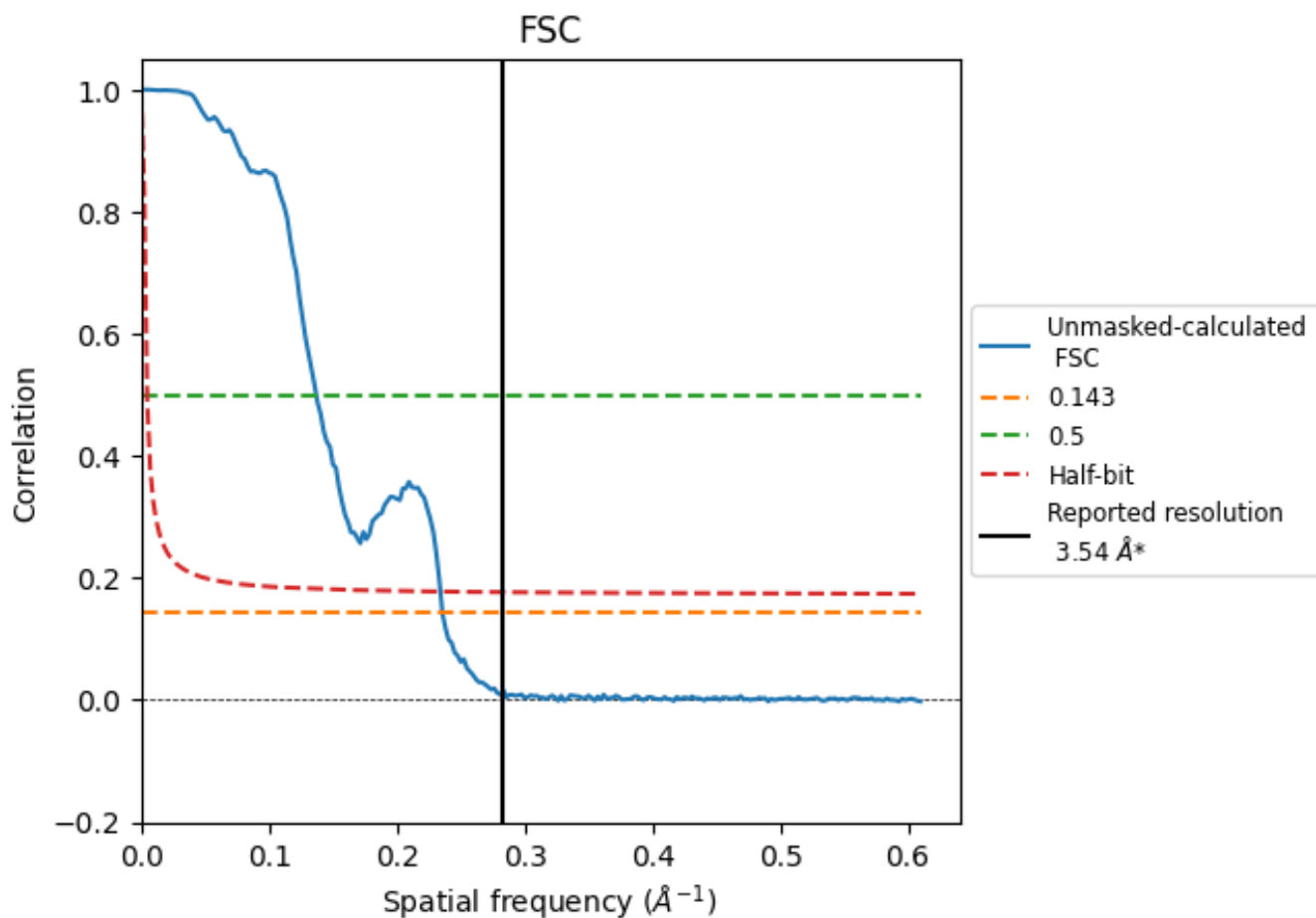


*Reported resolution corresponds to spatial frequency of 0.282 Å⁻¹

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 0.282 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.24	7.30	4.27

*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 4.24 differs from the reported value 3.54 by more than 10 %

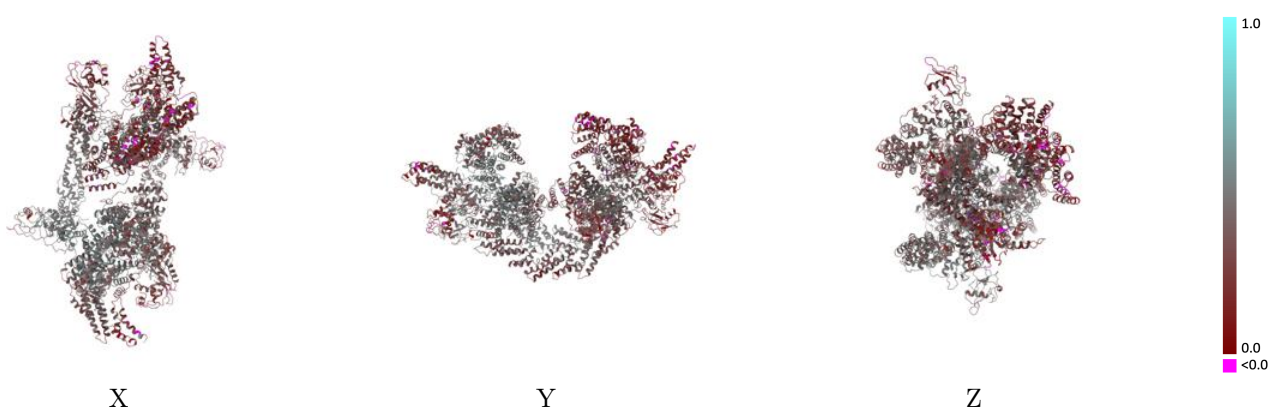
9 Map-model fit [\(i\)](#)

This section contains information regarding the fit between EMDB map EMD-36133 and PDB model 8JAS. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [\(i\)](#)

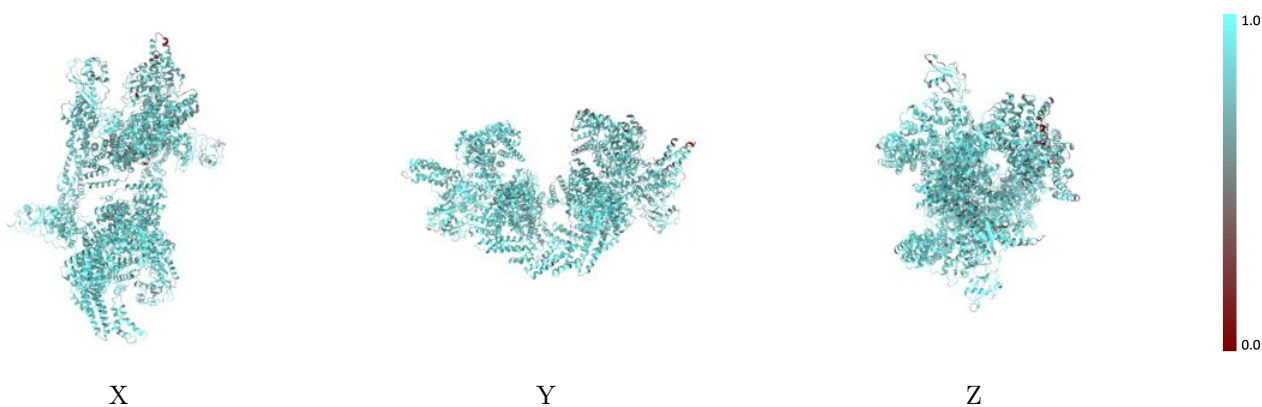
This section was not generated.

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



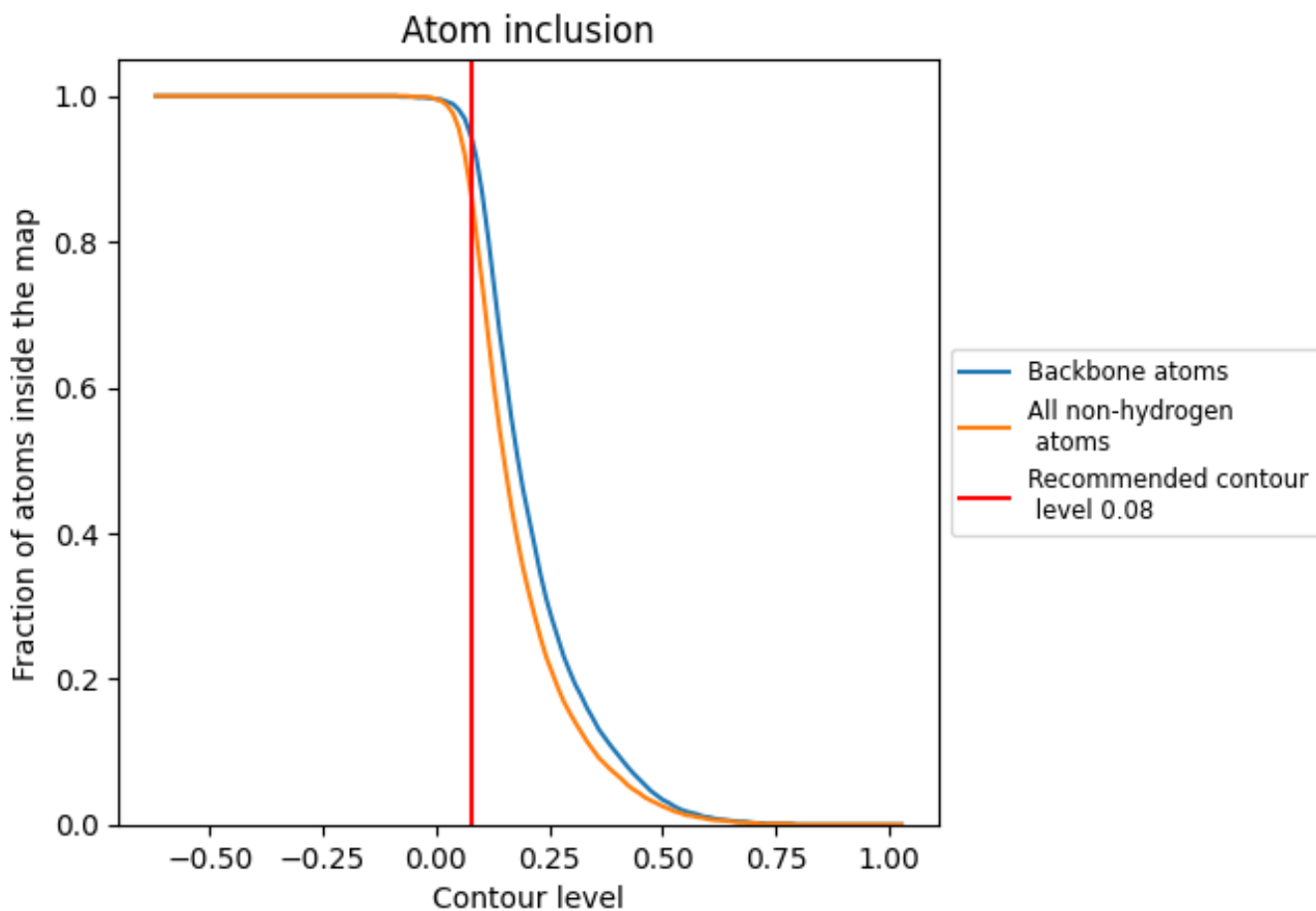
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 86% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8570	 0.3660
A	 0.8910	 0.4320
B	 0.9010	 0.4500
C	 0.8900	 0.3930
D	 0.9270	 0.4540
E	 0.8780	 0.3340
F	 0.8570	 0.4270
G	 0.9030	 0.3900
H	 0.9150	 0.4650
I	 0.8610	 0.3780
J	 0.7910	 0.2760
K	 0.8600	 0.3650
L	 0.7240	 0.1960
M	 0.7530	 0.2380
N	 0.8380	 0.2940
O	 0.7500	 0.3040
Q	 0.7520	 0.2210
R	 0.8710	 0.3900
S	 0.8730	 0.4350
T	 0.8810	 0.3420
U	 0.8510	 0.3500
V	 0.9110	 0.4710

