



## wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 12:17 AM EDT

PDB ID : 7JTK  
EMDB ID : EMD-22475  
Title : Radial spoke 1 isolated from Chlamydomonas reinhardtii  
Authors : Gui, M.; Ma, M.; Sze-Tu, E.; Wang, X.; Koh, F.; Zhong, E.; Berger, B.; Davis, J.; Dutcher, S.; Zhang, R.; Brown, A.  
Deposited on : 2020-08-17  
Resolution : 3.20 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

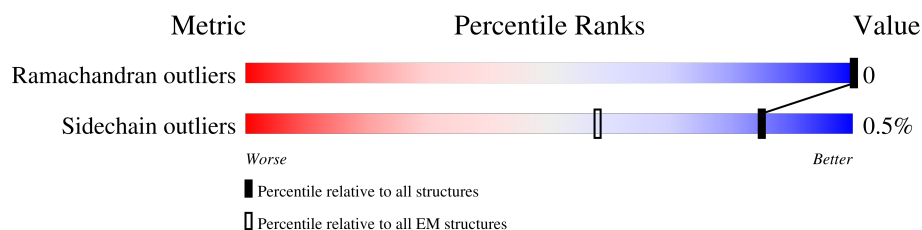
EMDB validation analysis : 0.0.1.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 1 Overall quality at a glance

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





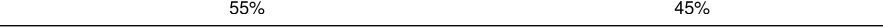
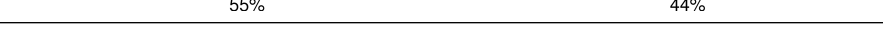
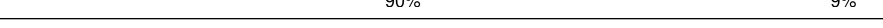

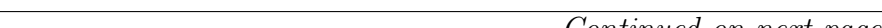
The reported resolution of this entry is 3.20 Å.

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.


















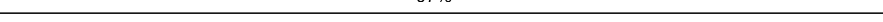









Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	814	 91% 8%
1	B	814	 92% 8%
2	C	738	 57% 42% 1%
2	D	738	 58% 42% 1%
3	E	516	 55% 45%
3	F	516	 55% 44%
4	G	465	 90% 9% 1%
4	H	465	 91% 9% 1%
5	I	521	 92% 7% 1%



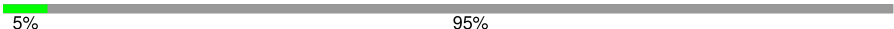


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Mol	Chain	Length	Quality of chain
5	J	521	 92% 7%
6	K	459	 93% 7%
6	L	459	 93% 7%
7	M	500	 9% 91%
7	N	500	 8% 92%
8	O	269	 93% 7%
8	P	269	 92% 7%
8	Q	269	 92% 7%
8	R	269	 93% 7%
9	S	216	 92% 8%
9	T	216	 92% 8%
10	U	204	 24% 76%
10	V	204	 89% 11%
11	W	181	 88% 10%
12	X	387	 97% ..
13	Y	346	 62% 38%
13	Z	346	 62% 38%
13	y	346	 18% 82%
13	z	346	 18% 82%
14	a	91	 92% 8%
14	b	91	 92% 8%
14	c	91	 92% 8%
14	d	91	 92% 8%
15	e	34	 100%
16	i	586	 34% 66%

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Mol	Chain	Length	Quality of chain
16	j	586	 34%66%
17	k	230	 92%7%
18	s	682	 5%95%
19	u	70	 69%29%
19	v	70	 70%29%

## 2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 72807 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 Flagellar radial spoke protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	749	Total	C	N	O	S	0	0
			5698	3611	962	1111	14		
1	B	749	Total	C	N	O	S	0	0
			5698	3611	962	1111	14		

- Molecule 2 is a protein called Flagellar radial spoke protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	427	Total	C	N	O	S	0	0
			3248	2048	577	614	9		
2	D	427	Total	C	N	O	S	0	0
			3248	2048	577	614	9		

- Molecule 3 is a protein called Flagellar radial spoke protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	284	Total	C	N	O	S	0	0
			2216	1378	398	431	9		
3	F	287	Total	C	N	O	S	0	0
			2232	1386	401	436	9		

- Molecule 4 is a protein called Flagellar radial spoke protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	421	Total	C	N	O	S	0	0
			3207	2043	535	621	8		
4	H	421	Total	C	N	O	S	0	0
			3207	2043	535	621	8		

- Molecule 5 is a protein called Flagellar radial spoke protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	483	Total	C	N	O	S	0	0
			3644	2330	623	679	12		
5	J	483	Total	C	N	O	S	0	0
			3644	2330	623	679	12		

- Molecule 6 is a protein called Flagellar radial spoke protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	428	Total	C	N	O	S	0	0
			3214	2043	544	614	13		
6	L	428	Total	C	N	O	S	0	0
			3214	2043	544	614	13		

- Molecule 7 is a protein called Flagellar radial spoke protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	47	Total	C	N	O	S	0	0
			373	243	62	67	1		
7	N	40	Total	C	N	O		0	0
			316	208	53	55			

- Molecule 8 is a protein called Flagellar radial spoke protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	249	Total	C	N	O	S	0	0
			1930	1233	327	365	5		
8	P	249	Total	C	N	O	S	0	0
			1930	1233	327	365	5		
8	Q	249	Total	C	N	O	S	0	0
			1930	1233	327	365	5		
8	R	249	Total	C	N	O	S	0	0
			1930	1233	327	365	5		

- Molecule 9 is a protein called Flagellar radial spoke protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S	199	Total	C	N	O	S	0	0
			1530	977	257	287	9		
9	T	199	Total	C	N	O	S	0	0
			1530	977	257	287	9		

- Molecule 10 is a protein called Flagellar radial spoke protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	48	Total	C	N	O	S	0	0
			382	250	64	67	1		
10	V	182	Total	C	N	O	S	0	0
			1055	649	198	206	2		

- Molecule 11 is a protein called Flagellar radial spoke protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	W	163	Total	C	N	O	S	0	0
			1241	796	210	231	4		

- Molecule 12 is a protein called Flagellar radial spoke protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	X	379	Total	C	N	O	S	0	0
			2787	1753	506	518	10		

- Molecule 13 is a protein called Flagellar radial spoke protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	213	Total	C	N	O	S	0	0
			1693	1092	296	301	4		
13	Z	213	Total	C	N	O	S	0	0
			1693	1092	296	301	4		
13	y	64	Total	C	N	O	S	0	0
			528	335	90	100	3		
13	z	64	Total	C	N	O	S	0	0
			528	335	90	100	3		

- Molecule 14 is a protein called Dynein 8 kDa light chain, flagellar outer arm.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	a	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
14	b	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
14	c	84	Total	C	N	O	S	0	0
			686	442	115	125	4		
14	d	84	Total	C	N	O	S	0	0
			686	442	115	125	4		

- Molecule 15 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	e	34	Total	C	N	O	0	0
			170	102	34	34		

- Molecule 16 is a protein called Flagellar radial spoke protein 23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	i	201	Total	C	N	O	S	0	0
			1558	1010	267	276	5		
16	j	201	Total	C	N	O	S	0	0
			1558	1010	267	276	5		

- Molecule 17 is a protein called Cytochrome b5 heme-binding domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	k	213	Total	C	N	O	S	0	0
			1756	1130	299	320	7		

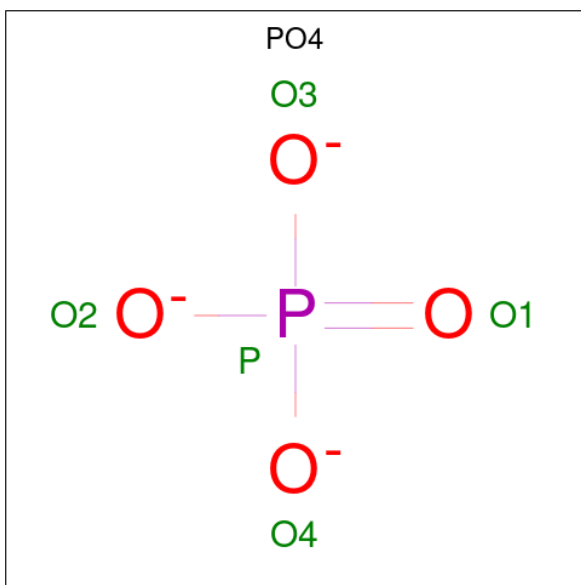
- Molecule 18 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	37	Total	C	N	O	S	0	0
			301	183	57	60	1		

- Molecule 19 is a protein called Predicted protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	u	50	Total	C	N	O	S	0	0
			427	273	73	78	3		
19	v	50	Total	C	N	O	S	0	0
			427	273	73	78	3		

- Molecule 20 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).

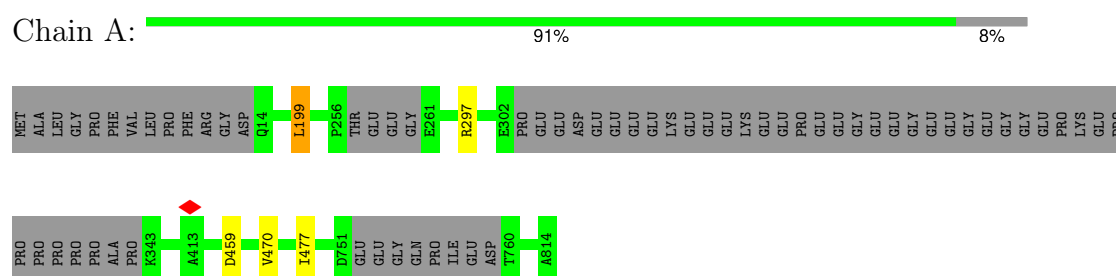


Mol	Chain	Residues	Atoms			AltConf
20	G	1	Total	O	P	0
			5	4	1	
20	H	1	Total	O	P	0
			5	4	1	
20	K	1	Total	O	P	0
			5	4	1	
20	L	1	Total	O	P	0
			5	4	1	

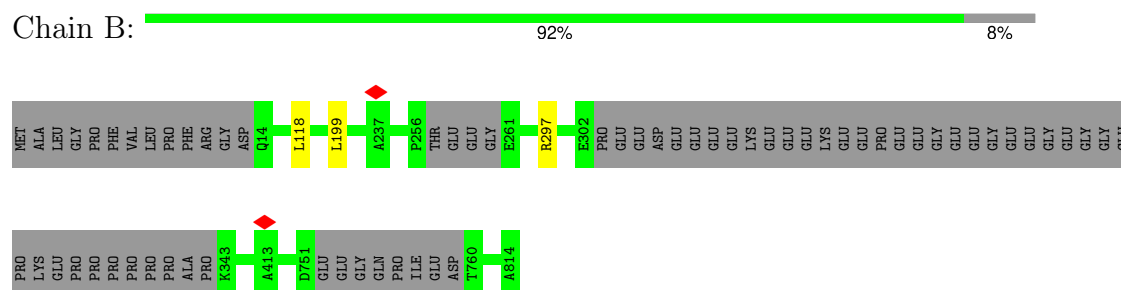
### 3 Residue-property plots [i](#)

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.

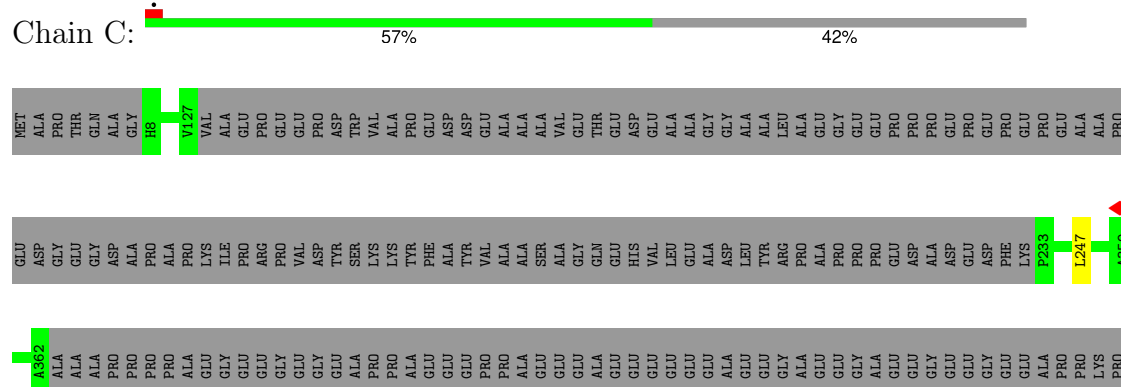
- Molecule 1: Flagellar radial spoke protein 1



- Molecule 1: Flagellar radial spoke protein 1



- Molecule 2: Flagellar radial spoke protein 2

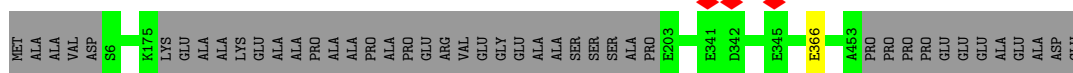




44%

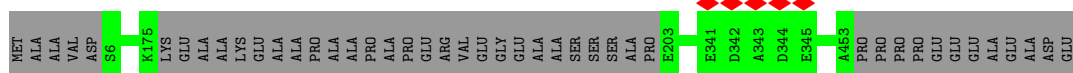
- Molecule 4: Flagellar radial spoke protein 4

9%



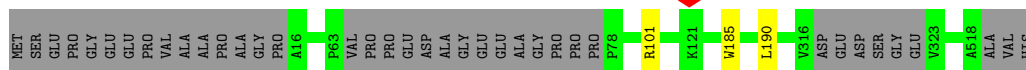
- Molecule 4: Flagellar radial spoke protein 4

9%



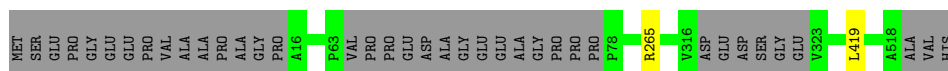
- Molecule 5: Flagellar radial spoke protein 5

7%



- Molecule 5: Flagellar radial spoke protein 5

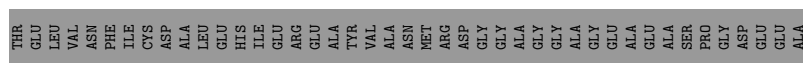
7%



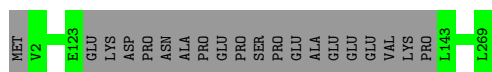
- Molecule 6: Flagellar radial spoke protein 6

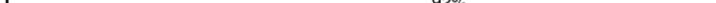
7%

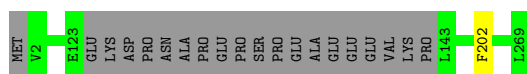


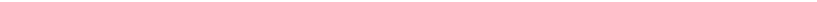


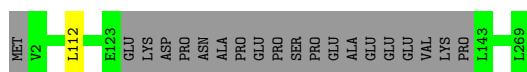
Chain 0:  93% 7%



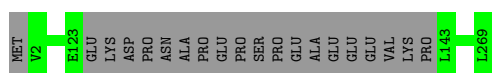
Chain P:  92% 7%



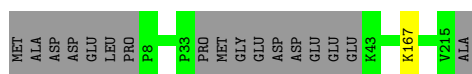
Chain Q:  92% 7%

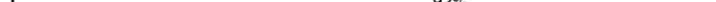


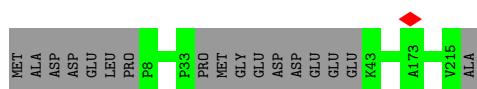
Chain R:  93% 7%



Chain S:  92% 8%

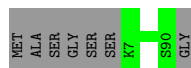


Chain T:  92% 8%





GLN	PHE	GLU	SER	MET	THR	SER	GLU	GLU	ALA	PRO	ALA	ARG	G134	R346
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------



MET  
ALA  
SER  
GLY  
SER  
SER  
K7  
S90  
GLY

- Chain c:  92% 8%

MET
ALA
SER
GLY
SER
SER
K7
H
S90
GLY

- Chain d:  92% 8%

MET
ALA
SER
GLY
SER
SER
K7
H
S90
GLY

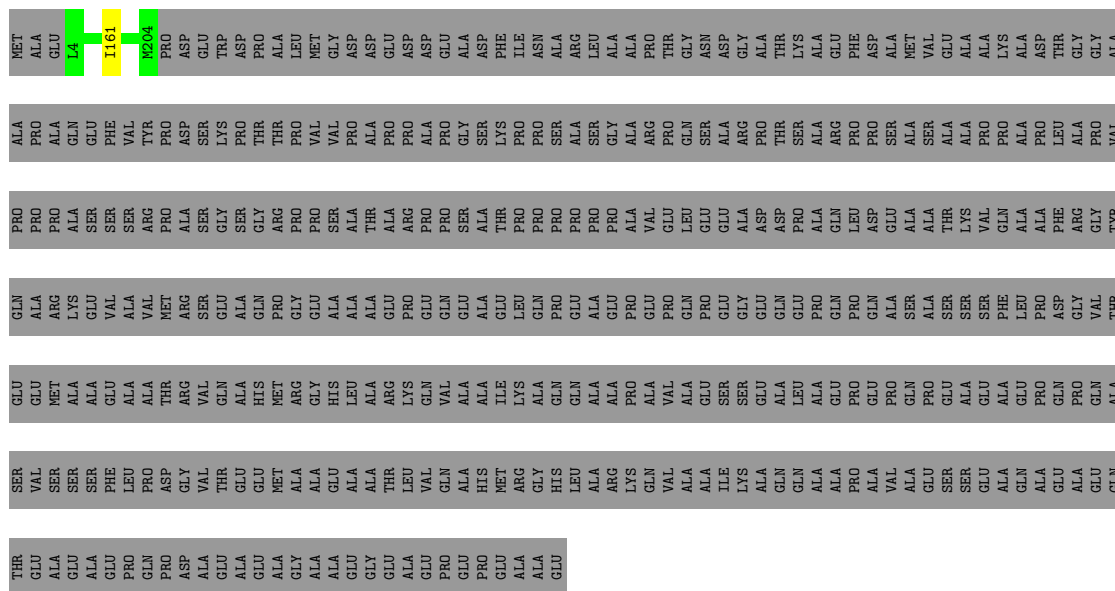
- Chain e:  100%

- Molecule 16: Flagellar radial spoke protein 23

Chain i:  34% 66%

[illegible]

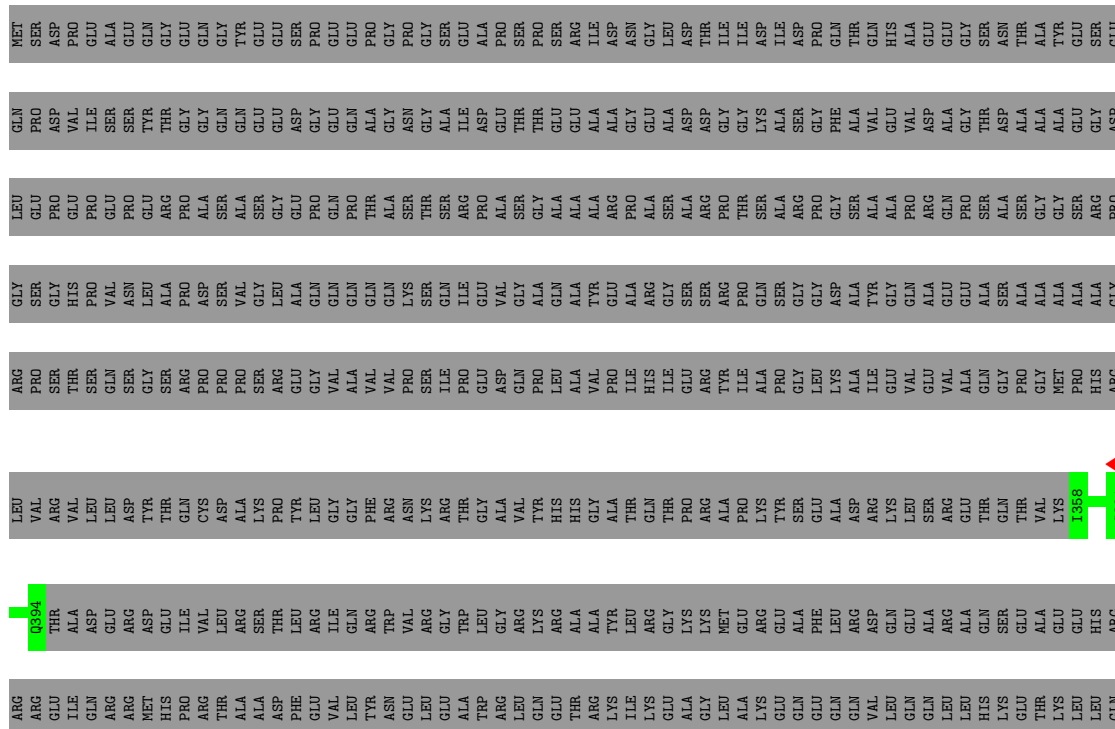
- Chain j:  34% 66%



- Molecule 17: Cytochrome b5 heme-binding domain-containing protein



- Molecule 18: Uncharacterized protein



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

Chain u:  69% . 29%

MET	SER	SER	GLN	TYR	SER	GLU	SER	ARG	PRO	LEU	HIS	GLY	SER	ALA	ALA	Q17	T18	R66	SER	GLY	THR	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain v:  70% 29%

MET	SER	SER	GLN	TYR	SER	GLU	SER	ARG	PRO	LEU	HIS	GLY	SER	ALA	ALA	Q17	Q38	R66	SER	GLY	THR	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	221836	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 ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.077	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	610.4, 610.4, 610.4	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.35	0/5844	0.52	0/7949
1	B	0.33	0/5844	0.51	0/7949
2	C	0.36	0/3301	0.48	0/4467
2	D	0.29	0/3301	0.44	0/4467
3	E	0.28	0/2239	0.44	0/3018
3	F	0.36	0/2255	0.47	0/3039
4	G	0.30	0/3289	0.47	0/4493
4	H	0.33	0/3289	0.49	0/4493
5	I	0.29	0/3733	0.44	0/5092
5	J	0.31	0/3733	0.45	0/5092
6	K	0.29	0/3305	0.44	0/4527
6	L	0.29	0/3305	0.45	0/4527
7	M	0.27	0/383	0.42	0/517
7	N	0.27	0/325	0.41	0/439
8	O	0.31	0/1971	0.46	0/2681
8	P	0.30	0/1971	0.46	0/2681
8	Q	0.30	0/1971	0.45	0/2681
8	R	0.29	0/1971	0.47	0/2681
9	S	0.31	0/1585	0.47	0/2140
9	T	0.30	0/1585	0.49	0/2140
10	U	0.27	0/390	0.41	0/530
10	V	0.26	0/1059	0.43	0/1453
11	W	0.33	0/1273	0.51	0/1737
12	X	0.31	0/2830	0.49	0/3851
13	Y	0.26	0/1736	0.43	0/2352
13	Z	0.26	0/1736	0.43	0/2352
13	y	0.26	0/539	0.39	0/726
13	z	0.29	0/539	0.42	0/726
14	a	0.31	0/702	0.50	0/945
14	b	0.32	0/702	0.53	0/945
14	c	0.32	0/702	0.56	0/945
14	d	0.27	0/702	0.52	0/945

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
16	i	0.26	0/1594	0.43	0/2157
16	j	0.31	0/1594	0.46	0/2157
17	k	0.32	0/1813	0.49	0/2482
18	s	0.25	0/305	0.47	0/411
19	u	0.35	0/437	0.46	0/589
19	v	0.32	0/437	0.46	0/589
All	All	0.31	0/74290	0.47	0/100965

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	199	LEU	Mainchain

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	741/814 (91%)	710 (96%)	31 (4%)	0	100	100
1	B	741/814 (91%)	713 (96%)	28 (4%)	0	100	100
2	C	421/738 (57%)	417 (99%)	4 (1%)	0	100	100
2	D	421/738 (57%)	411 (98%)	10 (2%)	0	100	100
3	E	278/516 (54%)	276 (99%)	2 (1%)	0	100	100
3	F	281/516 (54%)	278 (99%)	3 (1%)	0	100	100
4	G	417/465 (90%)	396 (95%)	21 (5%)	0	100	100
4	H	417/465 (90%)	400 (96%)	17 (4%)	0	100	100
5	I	477/521 (92%)	466 (98%)	11 (2%)	0	100	100
5	J	477/521 (92%)	464 (97%)	13 (3%)	0	100	100
6	K	422/459 (92%)	413 (98%)	9 (2%)	0	100	100
6	L	422/459 (92%)	415 (98%)	7 (2%)	0	100	100
7	M	45/500 (9%)	42 (93%)	3 (7%)	0	100	100
7	N	38/500 (8%)	37 (97%)	1 (3%)	0	100	100
8	O	245/269 (91%)	237 (97%)	8 (3%)	0	100	100
8	P	245/269 (91%)	238 (97%)	7 (3%)	0	100	100
8	Q	245/269 (91%)	240 (98%)	5 (2%)	0	100	100
8	R	245/269 (91%)	239 (98%)	6 (2%)	0	100	100
9	S	195/216 (90%)	190 (97%)	5 (3%)	0	100	100
9	T	195/216 (90%)	187 (96%)	8 (4%)	0	100	100
10	U	46/204 (22%)	45 (98%)	1 (2%)	0	100	100
10	V	172/204 (84%)	167 (97%)	5 (3%)	0	100	100
11	W	161/181 (89%)	150 (93%)	11 (7%)	0	100	100
12	X	377/387 (97%)	359 (95%)	18 (5%)	0	100	100
13	Y	211/346 (61%)	206 (98%)	5 (2%)	0	100	100
13	Z	211/346 (61%)	206 (98%)	5 (2%)	0	100	100
13	y	62/346 (18%)	62 (100%)	0	0	100	100
13	z	62/346 (18%)	61 (98%)	1 (2%)	0	100	100
14	a	82/91 (90%)	80 (98%)	2 (2%)	0	100	100
14	b	82/91 (90%)	75 (92%)	7 (8%)	0	100	100
14	c	82/91 (90%)	74 (90%)	8 (10%)	0	100	100
14	d	82/91 (90%)	78 (95%)	4 (5%)	0	100	100

*Continued on next page...*

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	i	199/586 (34%)	190 (96%)	9 (4%)	0	100	100
16	j	199/586 (34%)	186 (94%)	13 (6%)	0	100	100
17	k	209/230 (91%)	202 (97%)	7 (3%)	0	100	100
18	s	35/682 (5%)	33 (94%)	2 (6%)	0	100	100
19	u	48/70 (69%)	46 (96%)	2 (4%)	0	100	100
19	v	48/70 (69%)	46 (96%)	2 (4%)	0	100	100
All	All	9336/14482 (64%)	9035 (97%)	301 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	586/640 (92%)	581 (99%)	5 (1%)	75	89
1	B	586/640 (92%)	583 (100%)	3 (0%)	86	93
2	C	320/517 (62%)	317 (99%)	3 (1%)	75	89
2	D	320/517 (62%)	320 (100%)	0	100	100
3	E	223/406 (55%)	222 (100%)	1 (0%)	89	94
3	F	225/406 (55%)	224 (100%)	1 (0%)	89	94
4	G	342/371 (92%)	341 (100%)	1 (0%)	91	96
4	H	342/371 (92%)	342 (100%)	0	100	100
5	I	376/403 (93%)	373 (99%)	3 (1%)	79	90
5	J	376/403 (93%)	374 (100%)	2 (0%)	86	93
6	K	334/357 (94%)	334 (100%)	0	100	100
6	L	334/357 (94%)	334 (100%)	0	100	100
7	M	39/406 (10%)	39 (100%)	0	100	100
7	N	32/406 (8%)	32 (100%)	0	100	100
8	O	203/221 (92%)	203 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	P	203/221 (92%)	202 (100%)	1 (0%)	86	93
8	Q	203/221 (92%)	202 (100%)	1 (0%)	86	93
8	R	203/221 (92%)	203 (100%)	0	100	100
9	S	150/164 (92%)	149 (99%)	1 (1%)	81	92
9	T	150/164 (92%)	150 (100%)	0	100	100
10	U	41/162 (25%)	41 (100%)	0	100	100
10	V	46/162 (28%)	46 (100%)	0	100	100
11	W	136/152 (90%)	132 (97%)	4 (3%)	37	67
12	X	281/288 (98%)	278 (99%)	3 (1%)	70	86
13	Y	189/297 (64%)	189 (100%)	0	100	100
13	Z	189/297 (64%)	189 (100%)	0	100	100
13	y	54/297 (18%)	54 (100%)	0	100	100
13	z	54/297 (18%)	54 (100%)	0	100	100
14	a	72/76 (95%)	72 (100%)	0	100	100
14	b	72/76 (95%)	72 (100%)	0	100	100
14	c	72/76 (95%)	72 (100%)	0	100	100
14	d	72/76 (95%)	72 (100%)	0	100	100
16	i	158/433 (36%)	157 (99%)	1 (1%)	84	92
16	j	158/433 (36%)	157 (99%)	1 (1%)	84	92
17	k	191/204 (94%)	189 (99%)	2 (1%)	73	87
18	s	33/553 (6%)	33 (100%)	0	100	100
19	u	47/62 (76%)	45 (96%)	2 (4%)	25	57
19	v	47/62 (76%)	46 (98%)	1 (2%)	48	74
All	All	7459/11415 (65%)	7423 (100%)	36 (0%)	85	93

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	X	370	PHE
19	v	38	GLN
16	i	56	LYS
17	k	92	ILE
3	F	278	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
8	R	183	ASN
11	W	178	ASN
17	k	45	GLN
11	W	113	GLN
12	X	233	HIS

### 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](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
20	PO4	K	501	-	4,4,4	1.00	0	6,6,6	0.46	0
20	PO4	L	501	-	4,4,4	1.01	0	6,6,6	0.47	0
20	PO4	H	501	-	4,4,4	1.00	0	6,6,6	0.44	0
20	PO4	G	501	-	4,4,4	1.01	0	6,6,6	0.47	0

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.

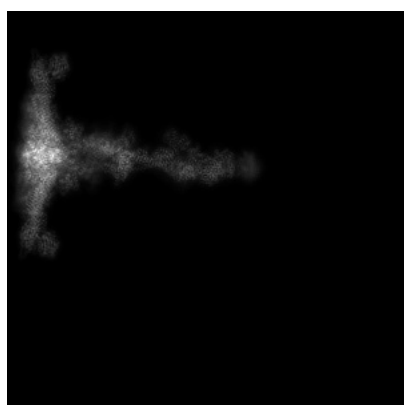
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22475. These allow visual inspection of the internal detail of the map and identification of artifacts.

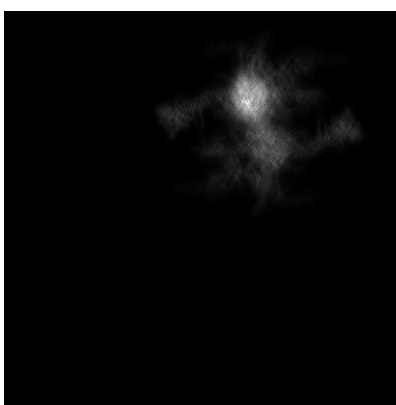
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

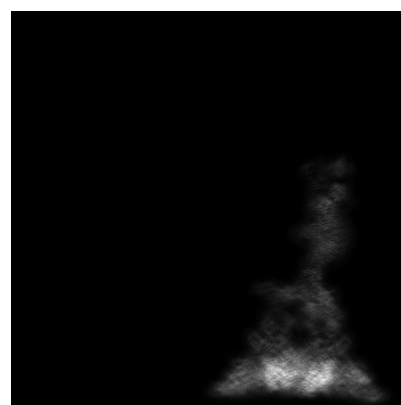
#### 6.1.1 Primary map



X



Y

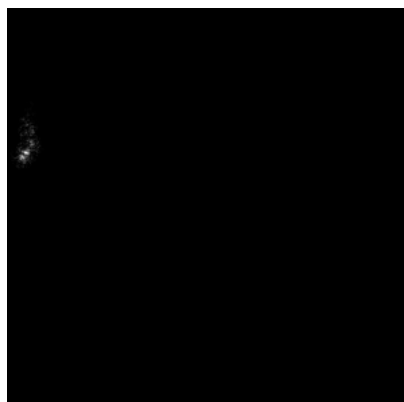


Z

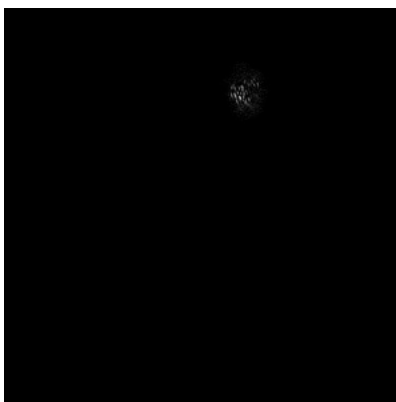
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 280



Y Index: 280

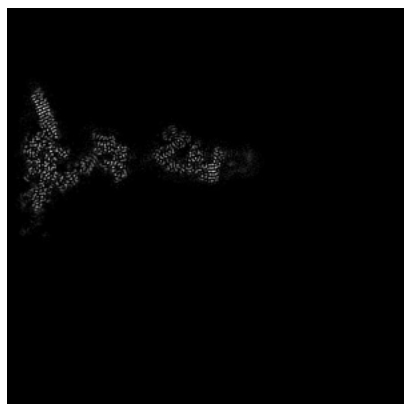


Z Index: 280

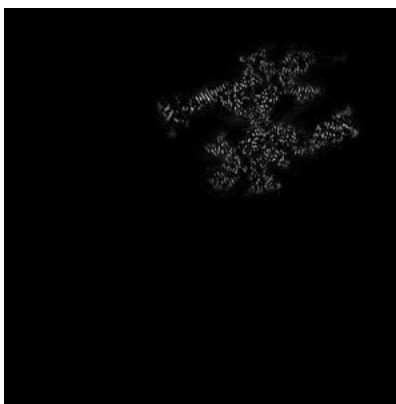
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 443



Y Index: 48

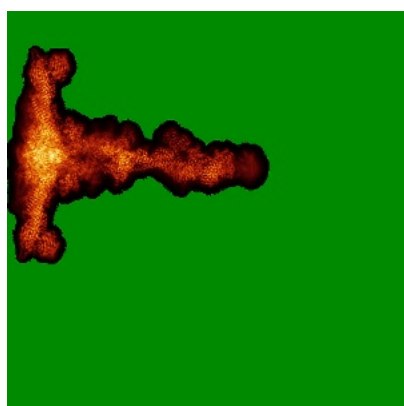


Z Index: 355

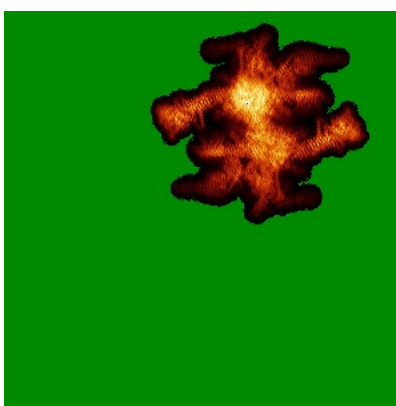
The images above show the largest variance slices of the map in three orthogonal directions.

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

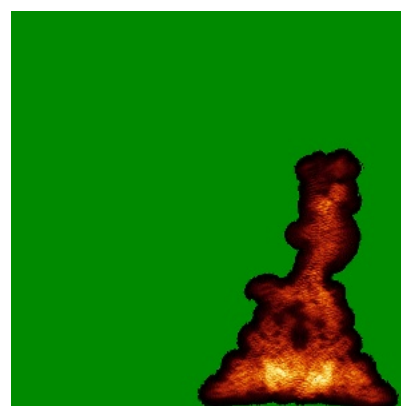
### 6.4.1 Primary map



X



Y

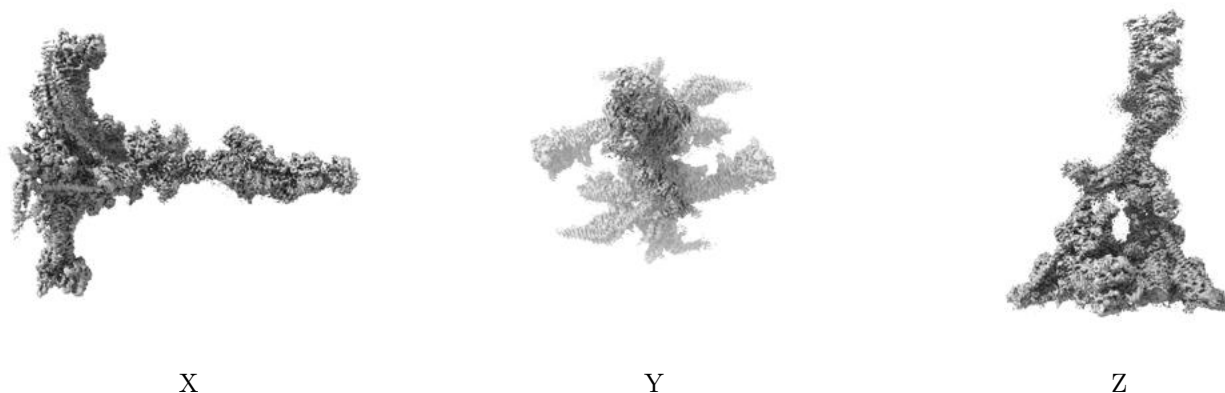


Z

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

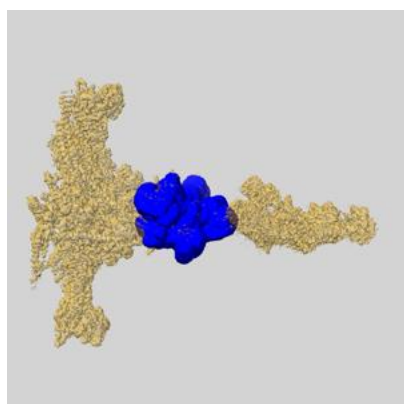
## 6.6 Mask visualisation [i](#)

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

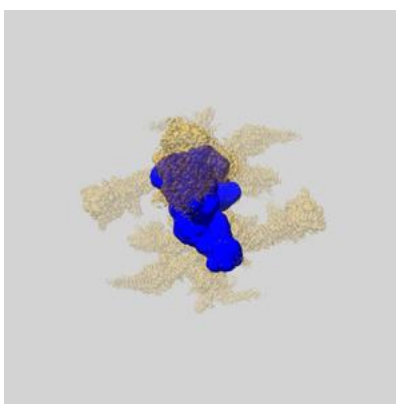
A mask typically either:

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

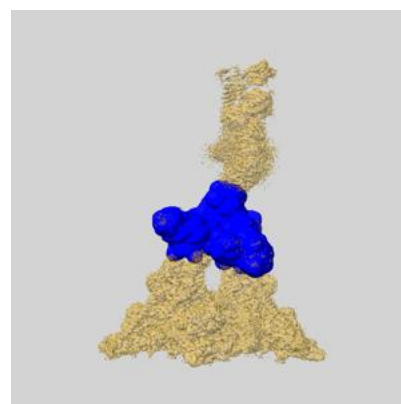
### 6.6.1 emd\_22475\_msk\_3.map [i](#)



X

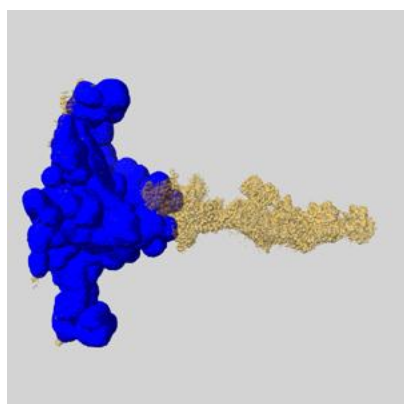


Y

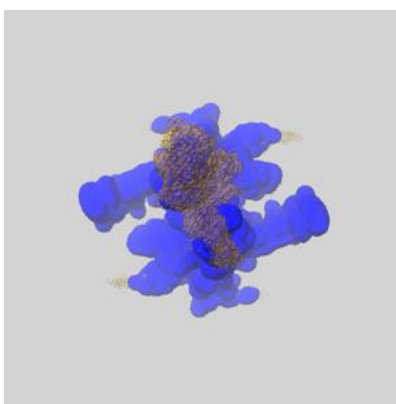


Z

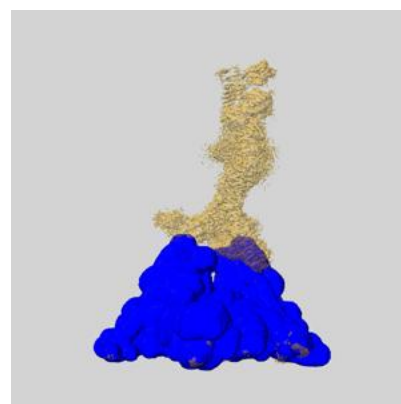
### 6.6.2 emd\_22475\_msk\_2.map [i](#)



X

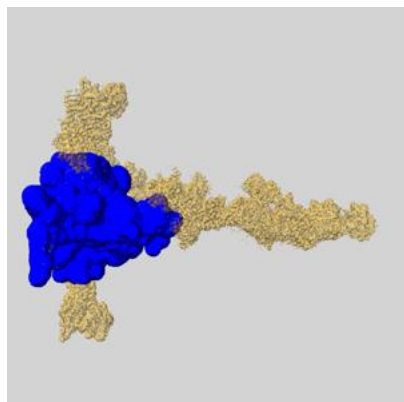


Y

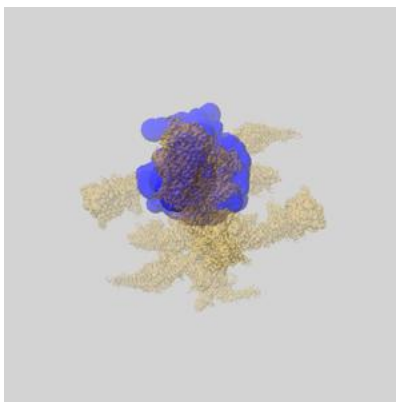


Z

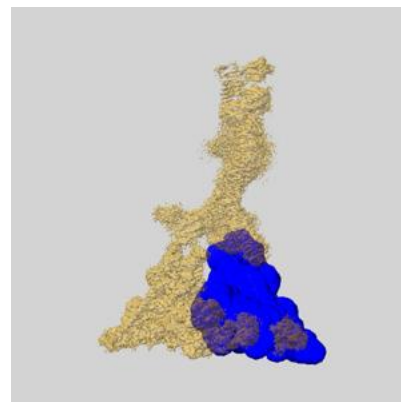
### 6.6.3 emd\_22475\_msk\_5.map [i](#)



X

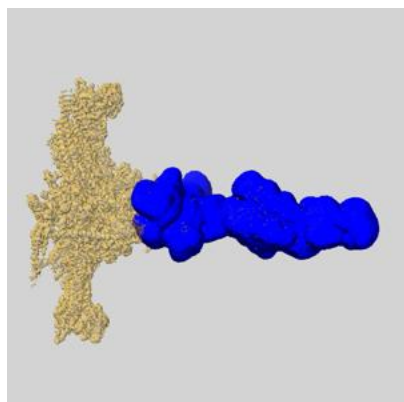


Y

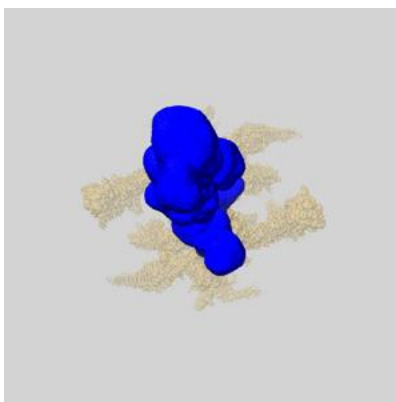


Z

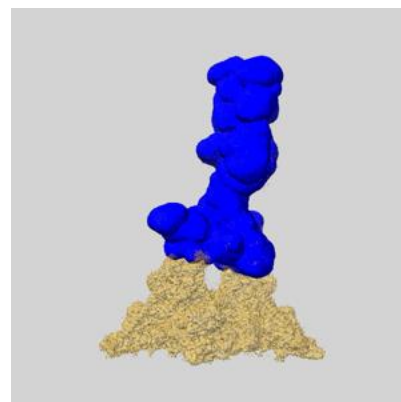
### 6.6.4 emd\_22475\_msk\_4.map [i](#)



X

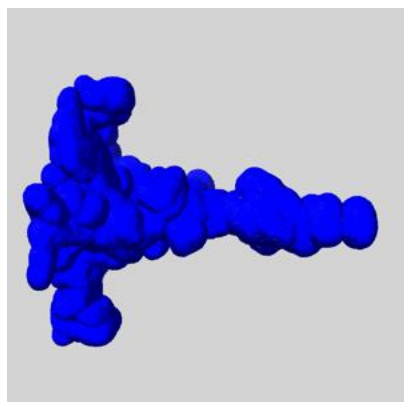


Y

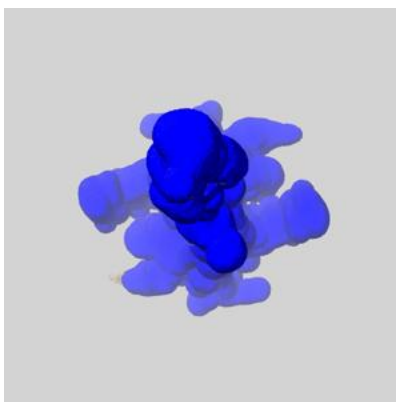


Z

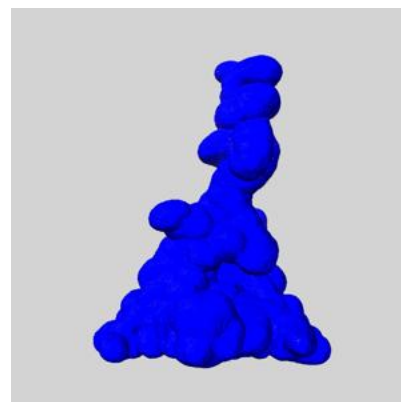
### 6.6.5 emd\_22475\_msk\_1.map [i](#)



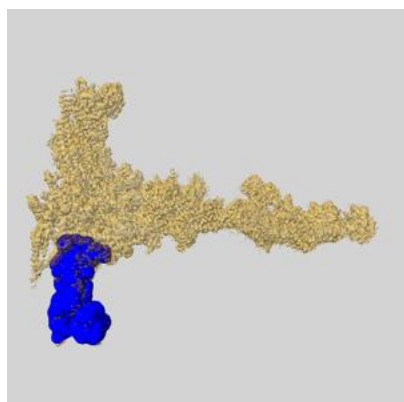
X



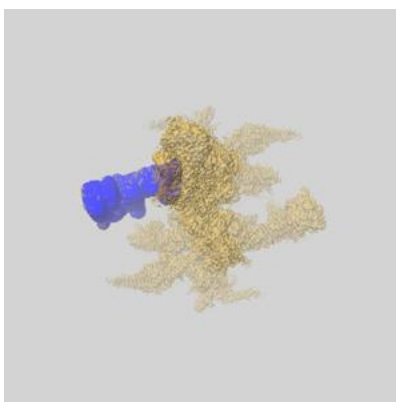
Y



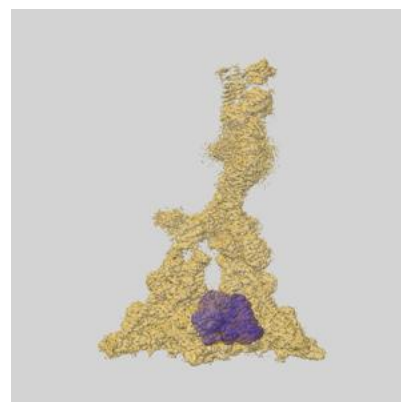
Z

6.6.6 emd\_22475\_msk\_7.map [i](#)

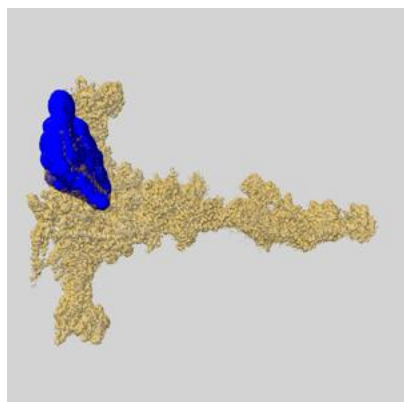
X



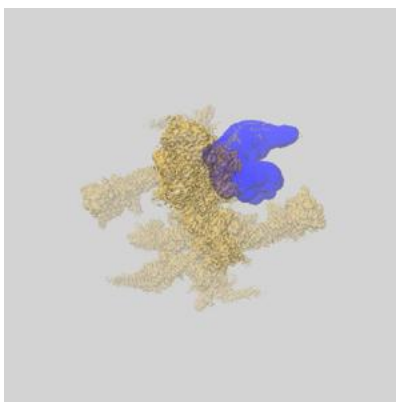
Y



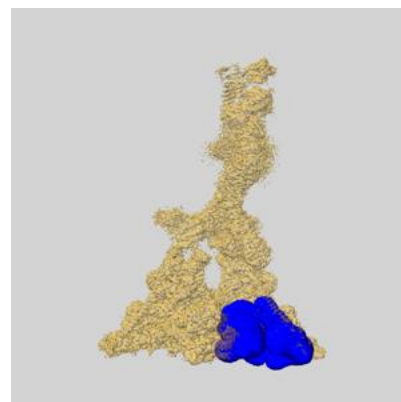
Z

6.6.7 emd\_22475\_msk\_6.map [i](#)

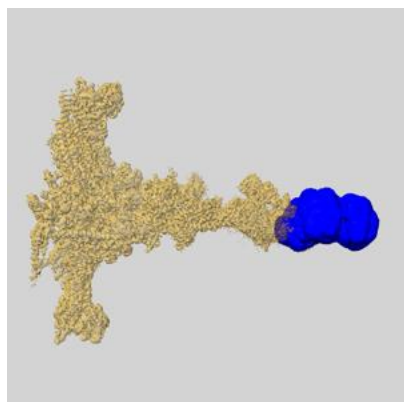
X



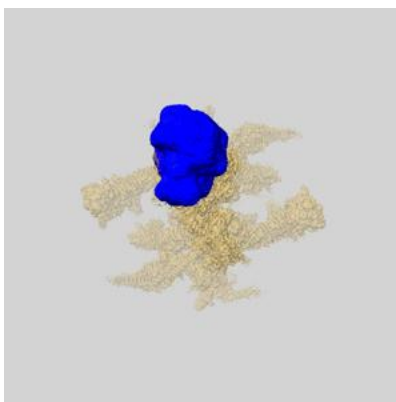
Y



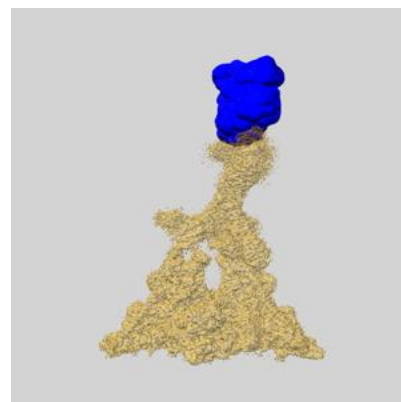
Z

6.6.8 emd\_22475\_msk\_8.map [i](#)

X



Y

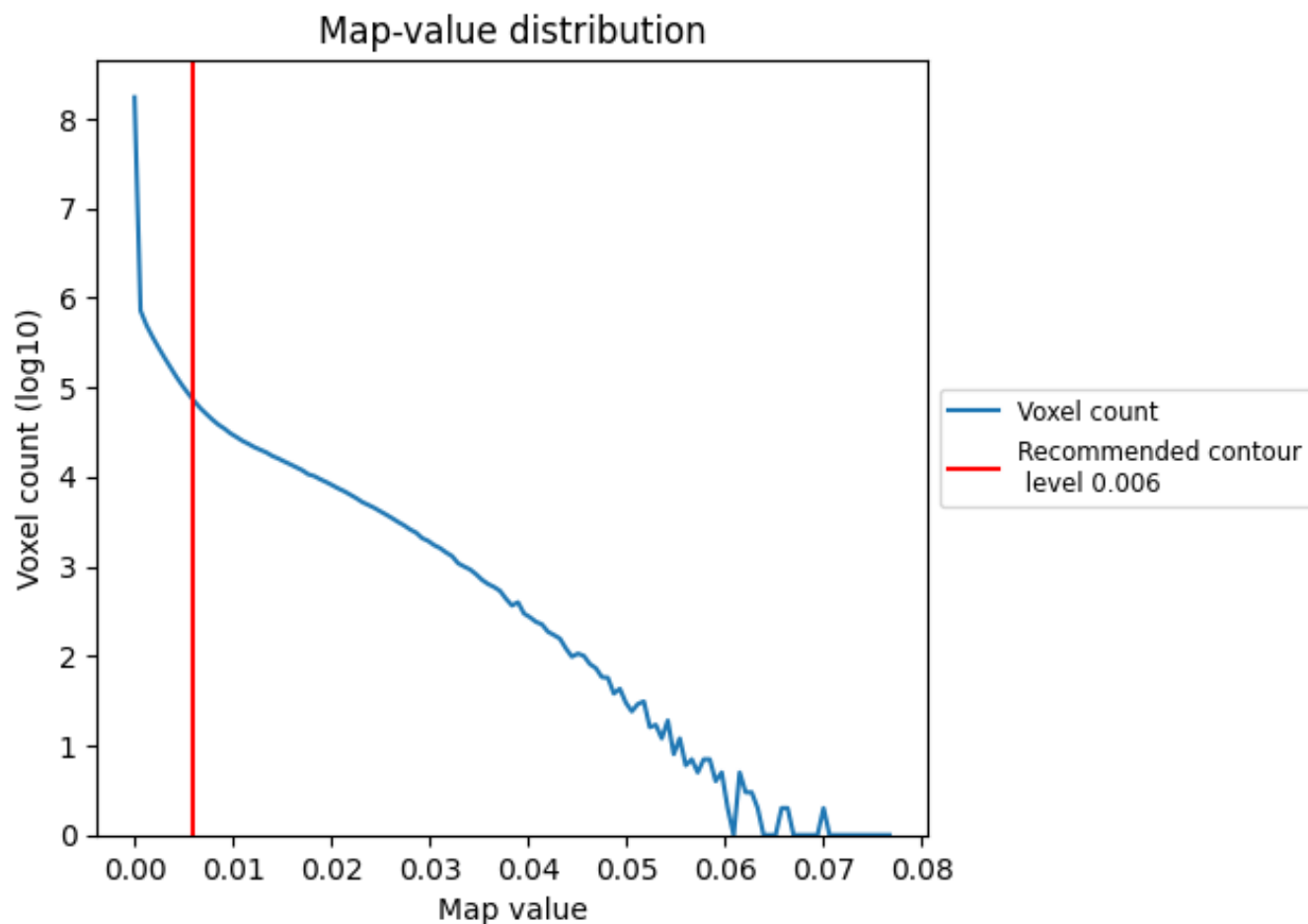


Z

## 7 Map analysis [i](#)

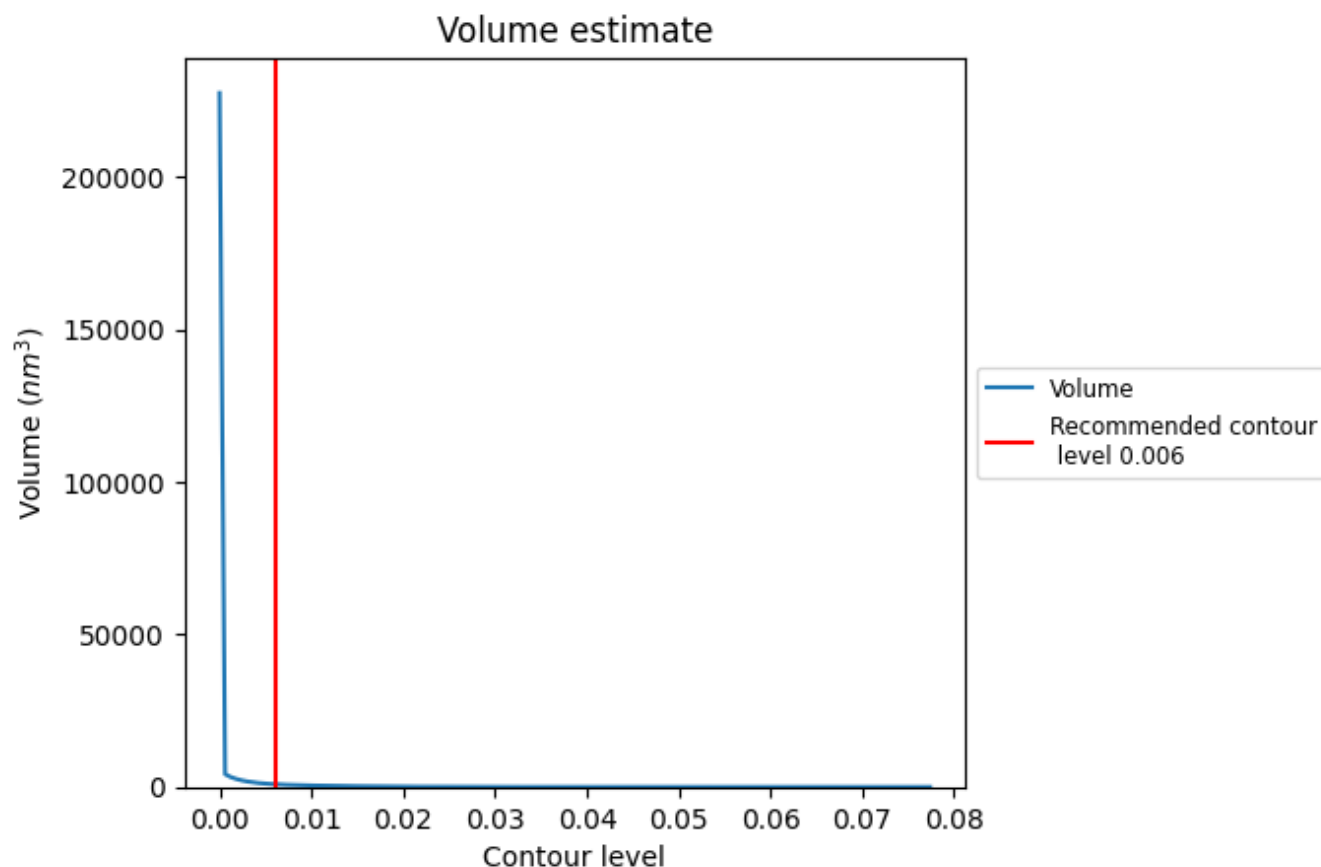
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

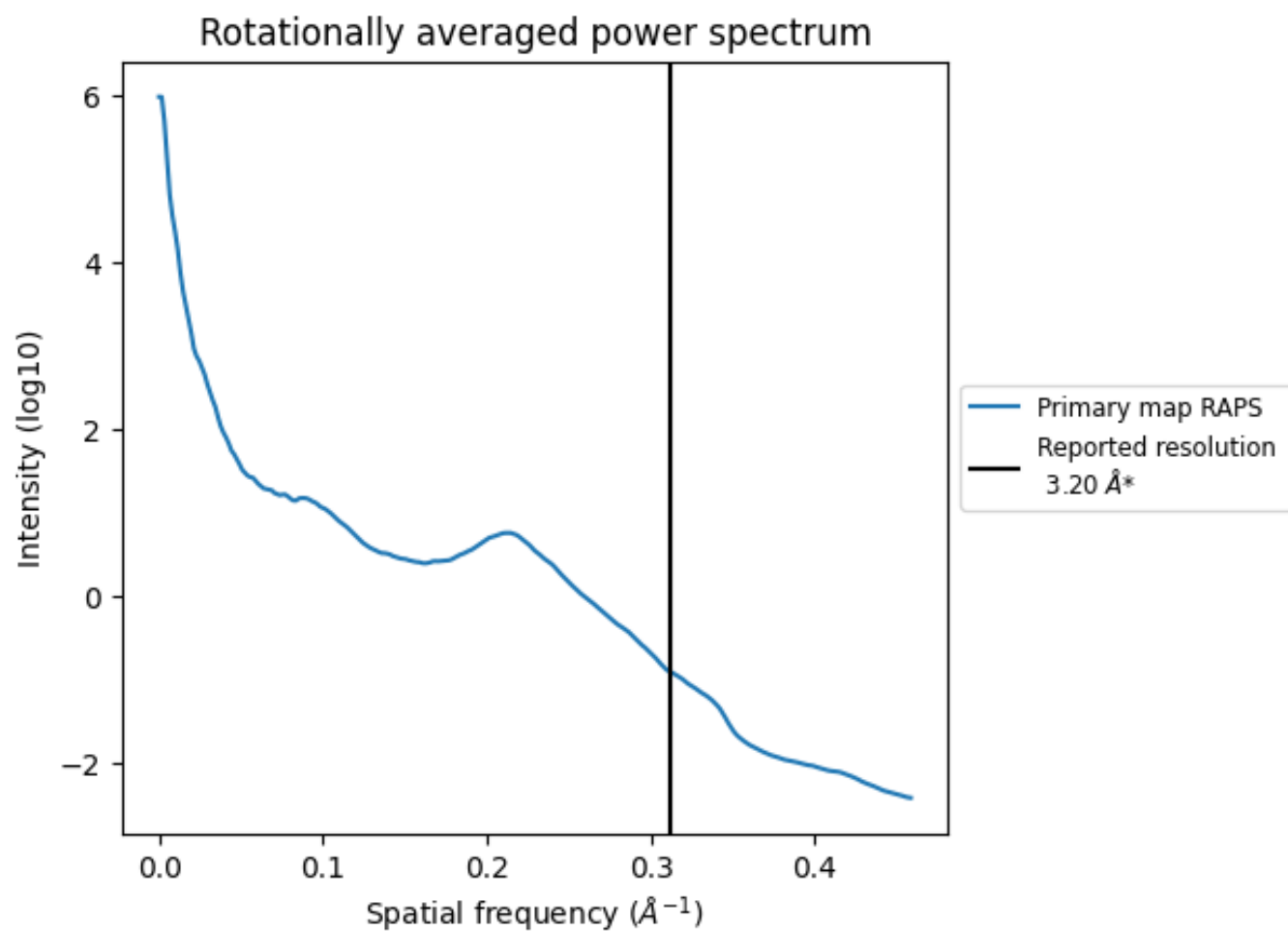
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 893  $\text{nm}^3$ ; this corresponds to an approximate mass of 806 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 0.312 Å<sup>-1</sup>

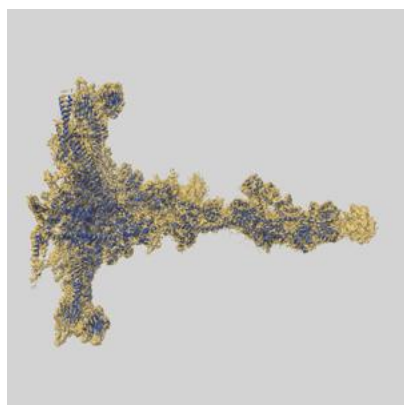
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

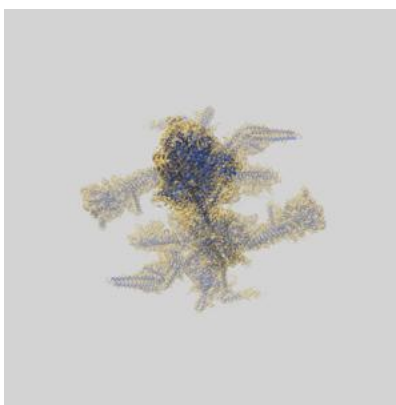
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22475 and PDB model 7JTK. Per-residue inclusion information can be found in section [3](#) on page [10](#).

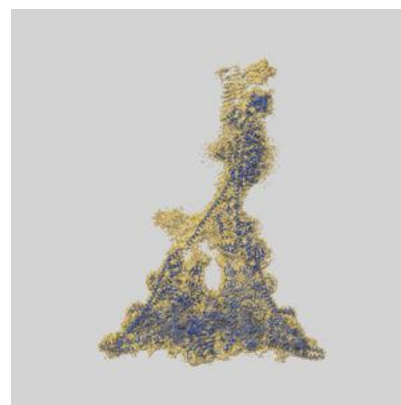
### 9.1 Map-model overlay [i](#)



X



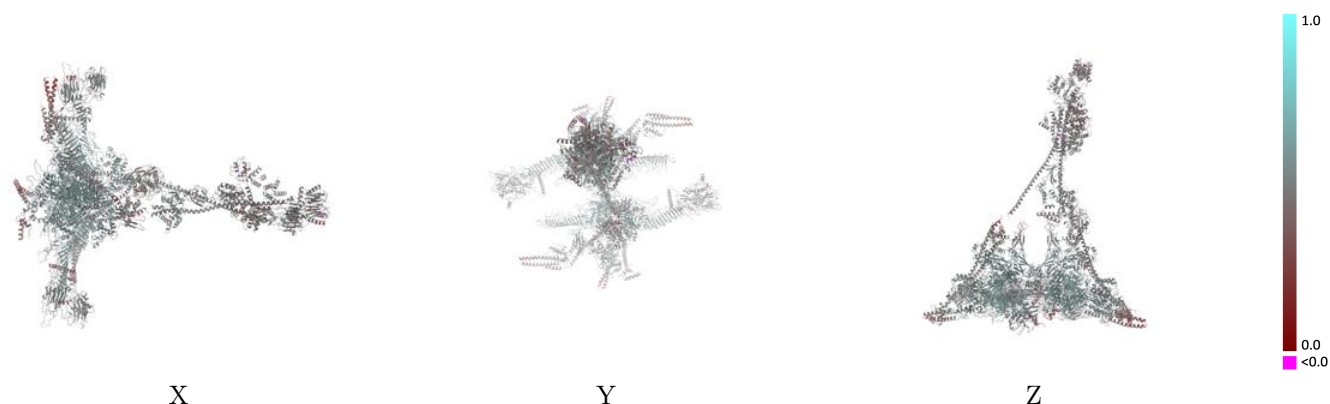
Y



Z

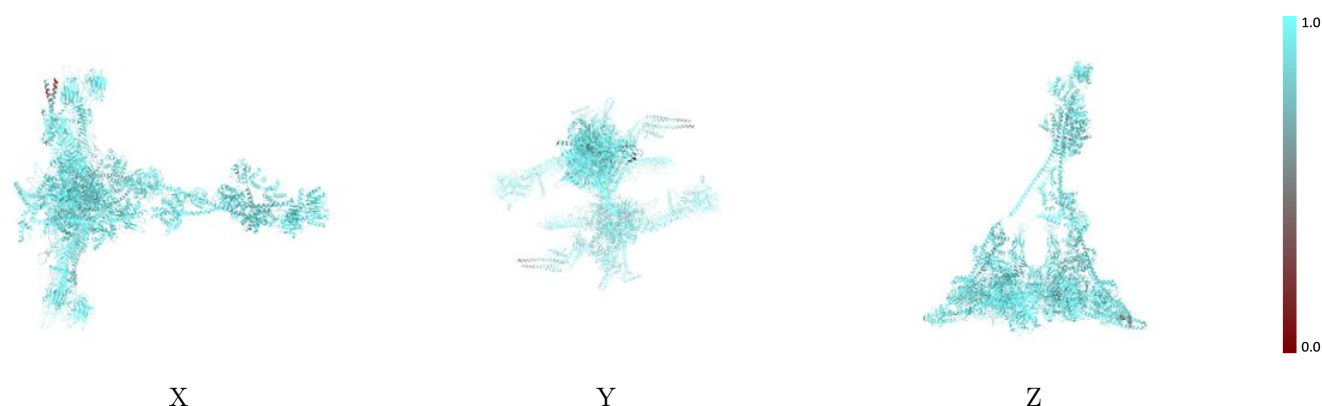
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



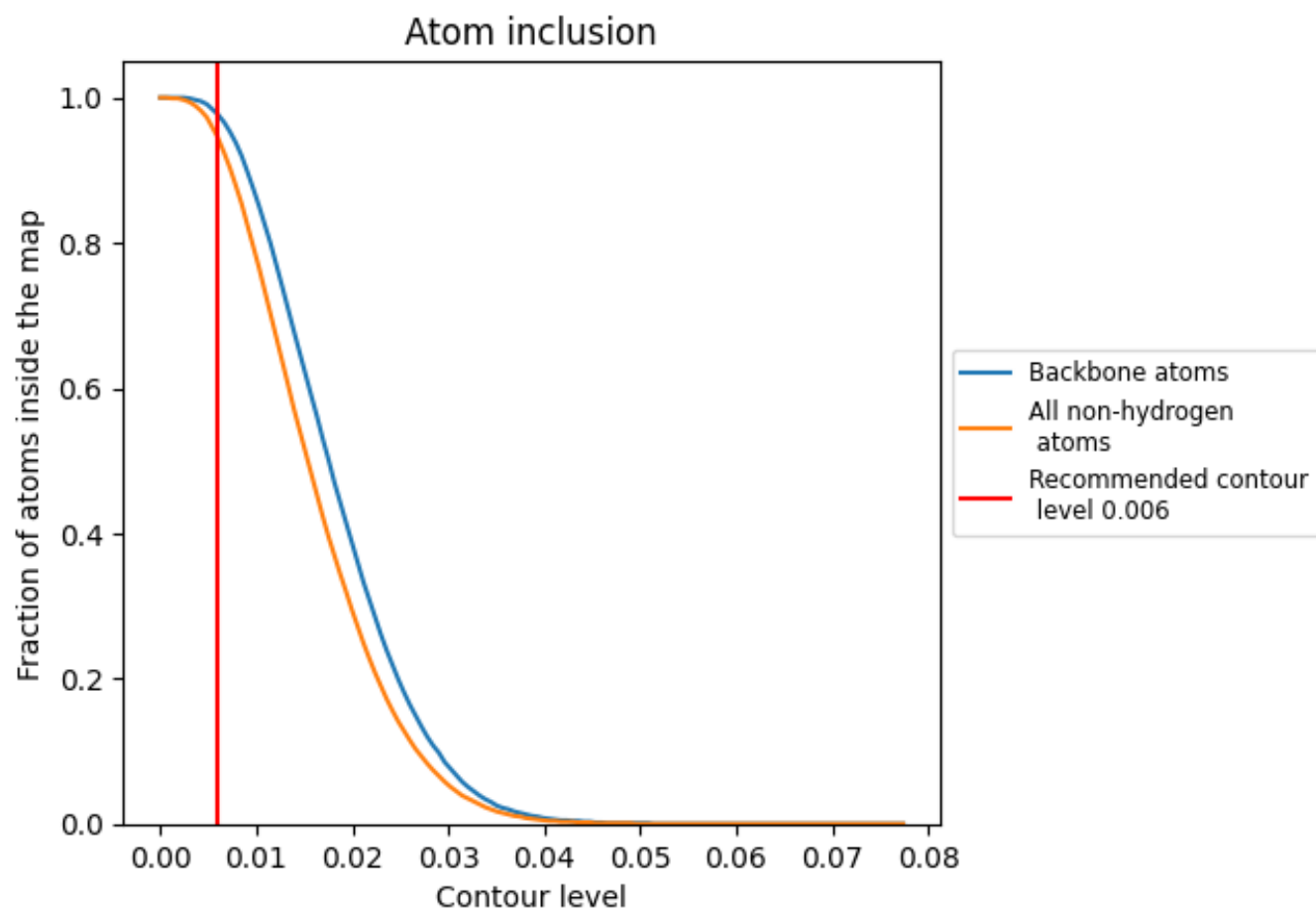
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.006).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 94% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9450	 0.5010
A	 0.9440	 0.4840
B	 0.9460	 0.4830
C	 0.8800	 0.4600
D	 0.8820	 0.4630
E	 0.9280	 0.4510
F	 0.9140	 0.4550
G	 0.9470	 0.5350
H	 0.9510	 0.5350
I	 0.9570	 0.5080
J	 0.9600	 0.5090
K	 0.9600	 0.5420
L	 0.9600	 0.5440
M	 0.9230	 0.4580
N	 0.9420	 0.5000
O	 0.9790	 0.5580
P	 0.9790	 0.5580
Q	 0.9820	 0.5600
R	 0.9820	 0.5540
S	 0.9770	 0.5350
T	 0.9740	 0.5280
U	 0.9390	 0.4470
V	 0.8760	 0.4490
W	 0.9270	 0.4640
X	 0.9180	 0.4620
Y	 0.9700	 0.5220
Z	 0.9740	 0.5230
a	 0.9700	 0.4600
b	 0.9360	 0.4650
c	 0.9270	 0.4480
d	 0.8900	 0.4240
e	 0.9000	 0.4650
i	 0.9430	 0.5030
j	 0.9580	 0.5100
k	 0.9700	 0.5060



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Chain	Atom inclusion	Q-score
s	 0.9080	 0.4380
u	 0.9470	 0.4800
v	 0.9400	 0.4560
y	 0.9690	 0.4370
z	 0.9760	 0.5030