



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 03:31 PM UTC

PDB ID : 7YFZ / pdb_00007yfh
EMDB ID : EMD-33802
Title : Cyanophage Pam3 baseplate proteins
Authors : Yang, F.; Jiang, Y.L.; Zhou, C.Z.
Deposited on : 2022-07-09
Resolution : 3.19 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

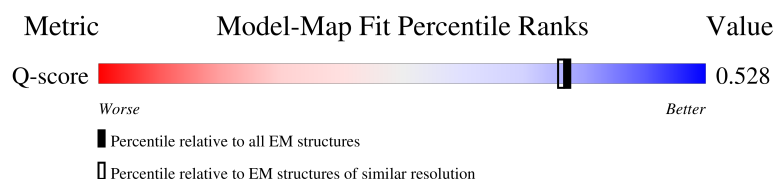
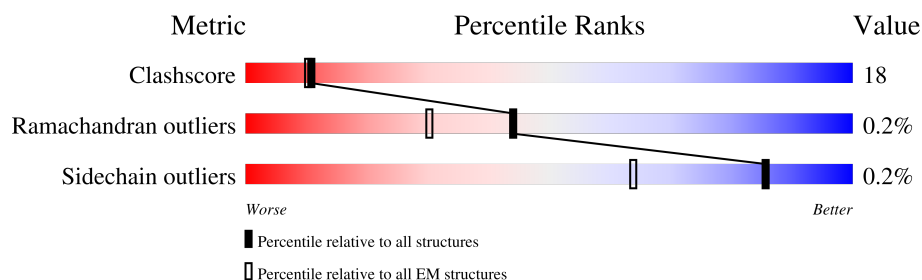
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.19 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.



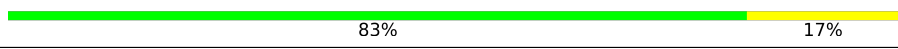
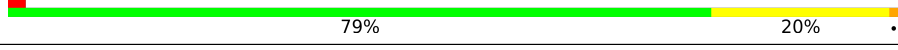
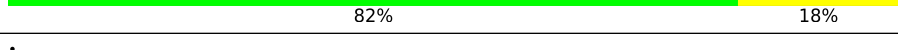
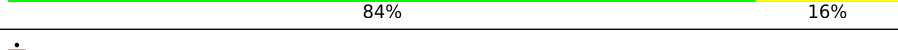
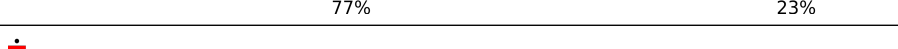
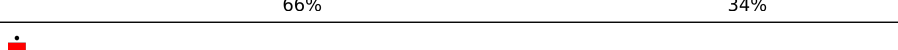
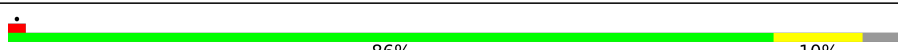
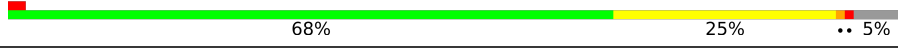
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14455 (2.69 - 3.69)

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	299	 87% 12%
1	B	299	 75% 25%
1	E	299	 76% 24%
1	F	299	 82% 18%

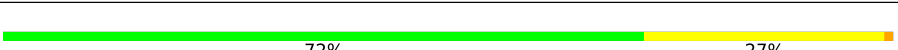
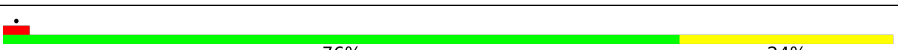
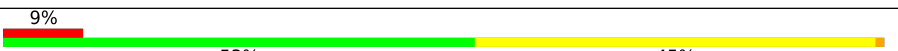
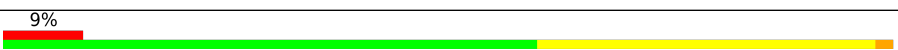
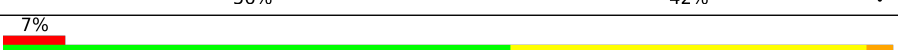
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Mol	Chain	Length	Quality of chain
1	H	299	
1	I	299	
1	K	299	
1	L	299	
1	O	299	
1	P	299	
1	Q	299	
1	R	299	
2	C	238	
2	D	238	
2	G	238	
2	J	238	
2	M	238	
2	S	238	
3	X	125	
3	n	125	
3	o	125	
3	p	125	
3	q	125	
3	r	125	
4	a	191	
4	b	191	
4	c	191	
4	d	191	
4	e	191	

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Mol	Chain	Length	Quality of chain
4	f	191	
5	h	106	
5	i	106	
5	j	106	
5	k	106	
5	l	106	
5	m	106	
6	t	229	
6	u	229	
6	v	229	
7	w	221	
7	x	221	
7	y	221	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 128850 atoms, of which 61470 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 Pam3 baseplate wedge gp22.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	299	Total	C	H	N	O	S	0	0
			4519	1439	2224	393	453	10		
1	B	299	Total	C	H	N	O	S	0	0
			4565	1439	2270	393	453	10		
1	E	299	Total	C	H	N	O	S	0	0
			4519	1439	2224	393	453	10		
1	F	299	Total	C	H	N	O	S	0	0
			4565	1439	2270	393	453	10		
1	H	299	Total	C	H	N	O	S	0	0
			4519	1439	2224	393	453	10		
1	I	299	Total	C	H	N	O	S	0	0
			4565	1439	2270	393	453	10		
1	K	299	Total	C	H	N	O	S	0	0
			4519	1439	2224	393	453	10		
1	L	299	Total	C	H	N	O	S	0	0
			4551	1439	2256	393	453	10		
1	O	299	Total	C	H	N	O	S	0	0
			4512	1439	2217	393	453	10		
1	P	299	Total	C	H	N	O	S	0	0
			4565	1439	2270	393	453	10		
1	Q	299	Total	C	H	N	O	S	0	0
			4519	1439	2224	393	453	10		
1	R	299	Total	C	H	N	O	S	0	0
			4565	1439	2270	393	453	10		

- Molecule 2 is a protein called Pam3 baseplate wedge gp23.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C	238	Total	C	H	N	O	S	0	0
			3339	1161	1507	300	353	18		
2	D	238	Total	C	H	N	O	S	0	0
			3339	1161	1507	300	353	18		
2	G	238	Total	C	H	N	O	S	0	0
			3339	1161	1507	300	353	18		

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Mol	Chain	Residues	Atoms						AltConf	Trace
2	J	238	Total	C	H	N	O	S	0	0
			3339	1161	1507	300	353	18		
2	M	238	Total	C	H	N	O	S	0	0
			3339	1161	1507	300	353	18		
2	S	238	Total	C	H	N	O	S	0	0
			3339	1161	1507	300	353	18		

- Molecule 3 is a protein called Pam3 sheath initiator gp21.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	X	120	Total	C	H	N	O	S	0	0
			1869	592	933	160	181	3		
3	n	120	Total	C	H	N	O	S	0	0
			1869	592	933	160	181	3		
3	o	120	Total	C	H	N	O	S	0	0
			1869	592	933	160	181	3		
3	p	120	Total	C	H	N	O	S	0	0
			1869	592	933	160	181	3		
3	q	120	Total	C	H	N	O	S	0	0
			1869	592	933	160	181	3		
3	r	120	Total	C	H	N	O	S	0	0
			1869	592	933	160	181	3		

- Molecule 4 is a protein called Pam3 tube initiator gp17.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	a	182	Total	C	H	N	O	S	0	0
			2119	831	777	237	270	4		
4	b	182	Total	C	H	N	O	S	0	0
			2119	831	777	237	270	4		
4	c	182	Total	C	H	N	O	S	0	0
			2119	831	777	237	270	4		
4	d	182	Total	C	H	N	O	S	0	0
			2119	831	777	237	270	4		
4	e	182	Total	C	H	N	O	S	0	0
			2119	831	777	237	270	4		
4	f	182	Total	C	H	N	O	S	0	0
			2119	831	777	237	270	4		

- Molecule 5 is a protein called Pam3 plug gp18.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	h	106	Total	C	H	N	O	S	0	0
			1660	527	833	139	160	1		
5	i	106	Total	C	H	N	O	S	0	0
			1660	527	833	139	160	1		
5	j	106	Total	C	H	N	O	S	0	0
			1660	527	833	139	160	1		
5	k	106	Total	C	H	N	O	S	0	0
			1660	527	833	139	160	1		
5	l	106	Total	C	H	N	O	S	0	0
			1660	527	833	139	160	1		
5	m	106	Total	C	H	N	O	S	0	0
			1660	527	833	139	160	1		

- Molecule 6 is a protein called Pam3 hub gp19.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	t	229	Total	C	H	N	O	S	0	0
			3538	1095	1776	313	343	11		
6	u	229	Total	C	H	N	O	S	0	0
			3538	1095	1776	313	343	11		
6	v	229	Total	C	H	N	O	S	0	0
			3538	1095	1776	313	343	11		

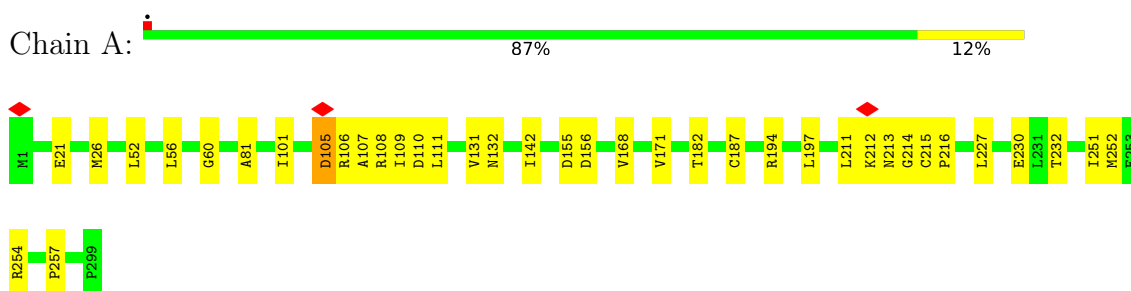
- Molecule 7 is a protein called Pam3 spike gp20.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	w	221	Total	C	H	N	O	S	0	0
			3277	1012	1633	292	329	11		
7	x	221	Total	C	H	N	O	S	0	0
			3277	1012	1633	292	329	11		
7	y	221	Total	C	H	N	O	S	0	0
			3277	1012	1633	292	329	11		

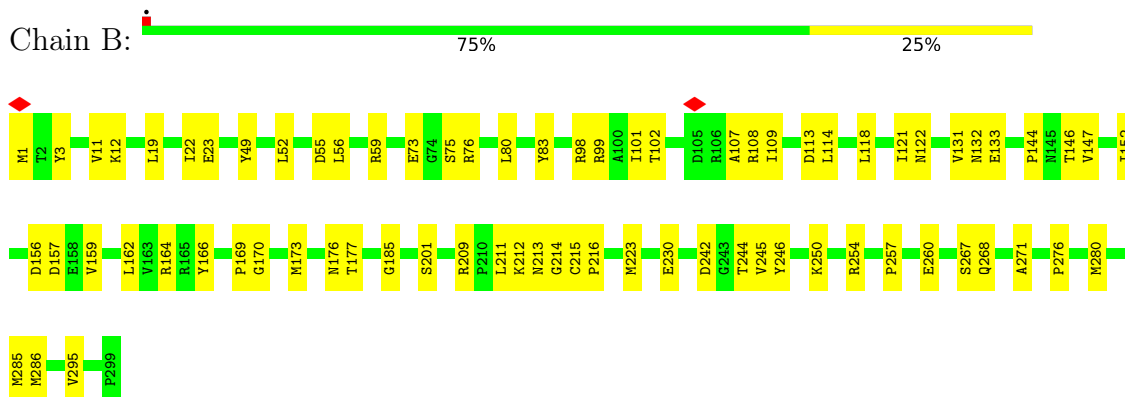
3 Residue-property plots

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.

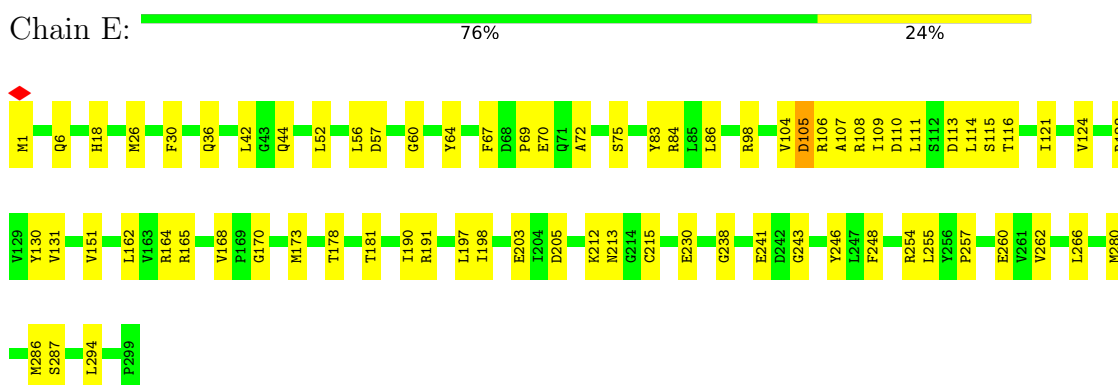
- Molecule 1: Pam3 baseplate wedge gp22



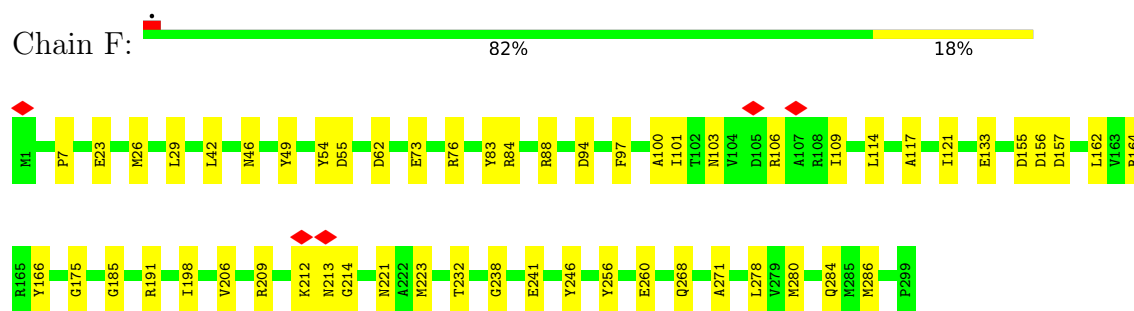
- Molecule 1: Pam3 baseplate wedge gp22



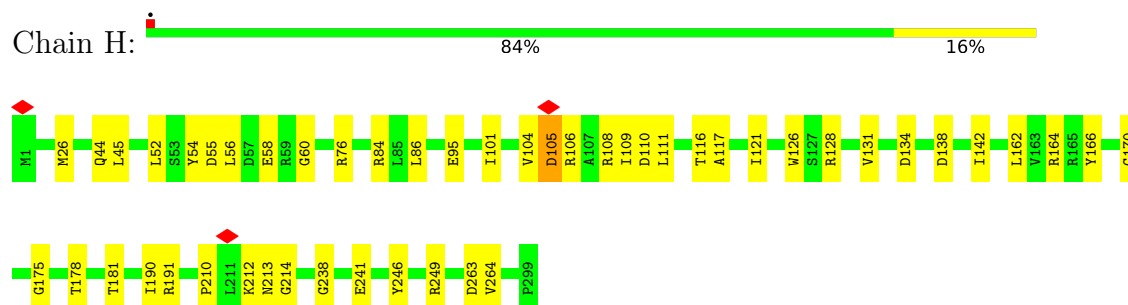
- Molecule 1: Pam3 baseplate wedge gp22



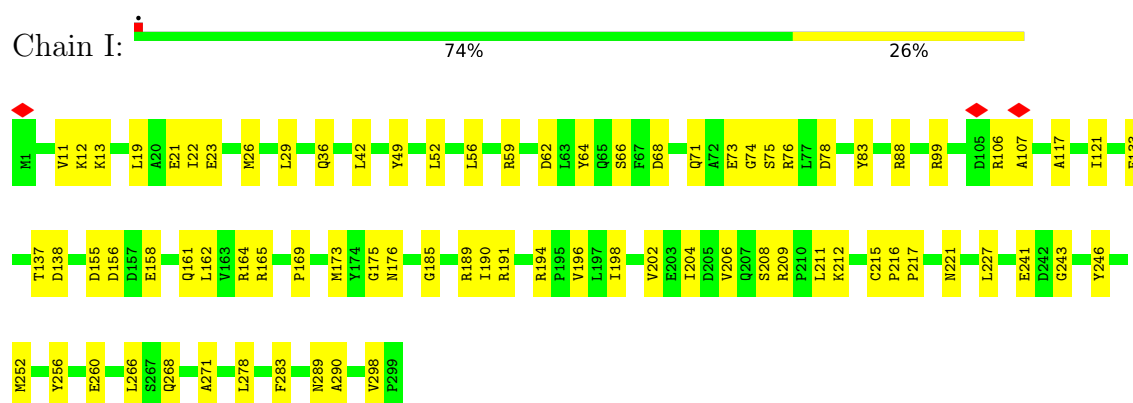
- Molecule 1: Pam3 baseplate wedge gp22



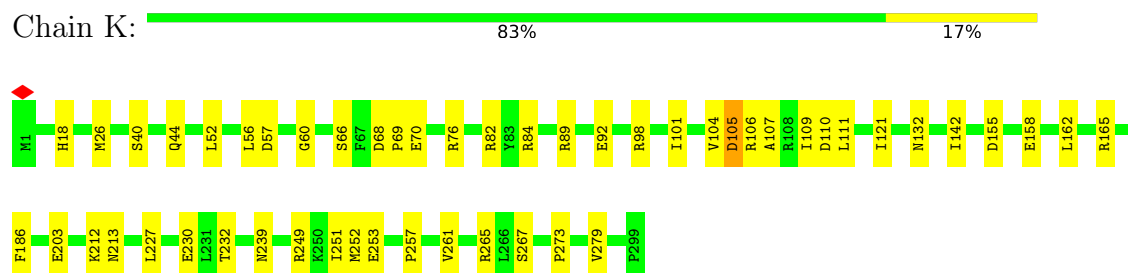
- Molecule 1: Pam3 baseplate wedge gp22



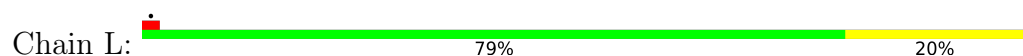
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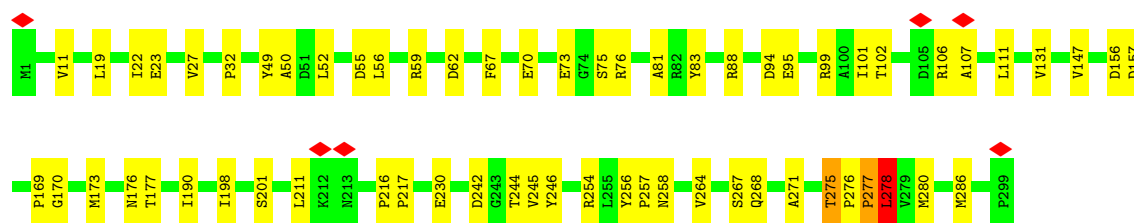


- Molecule 1: Pam3 baseplate wedge gp22



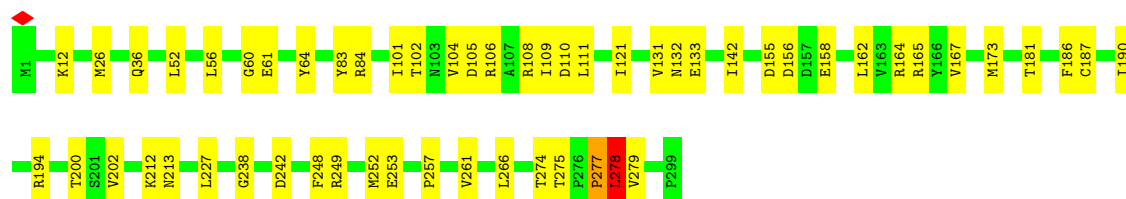
- Molecule 1: Pam3 baseplate wedge gp22





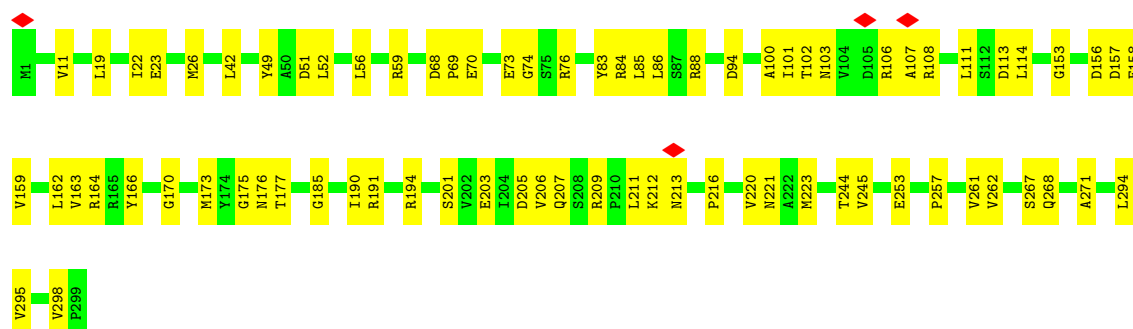
- Molecule 1: Pam3 baseplate wedge gp22

Chain O: 81% 18%



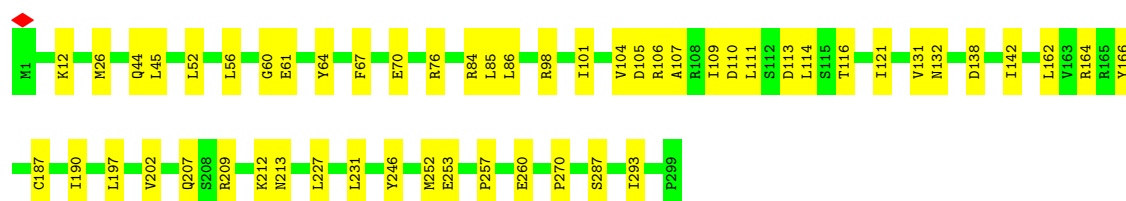
- Molecule 1: Pam3 baseplate wedge gp22

Chain P: 75% 25%



- Molecule 1: Pam3 baseplate wedge gp22

Chain Q: 82% 18%



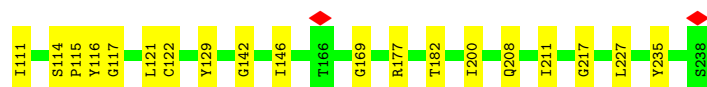
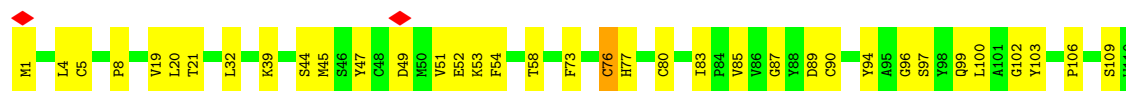
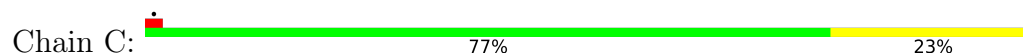
- Molecule 1: Pam3 baseplate wedge gp22

Chain R: 84% 16%

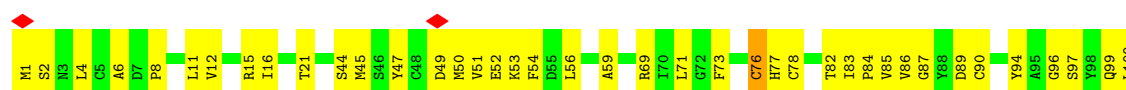




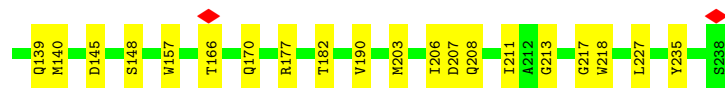
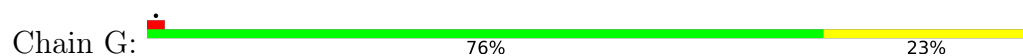
- Molecule 2: Pam3 baseplate wedge gp23



- Molecule 2: Pam3 baseplate wedge gp23



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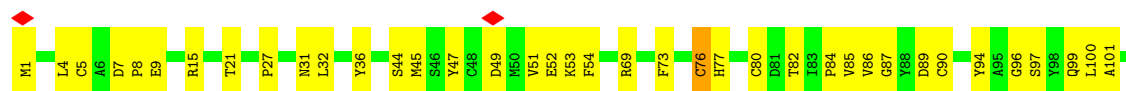


- Molecule 2: Pam3 baseplate wedge gp23

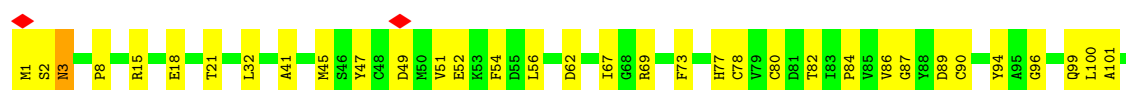




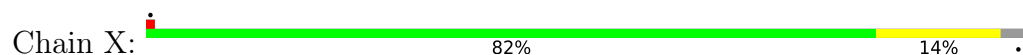
- Molecule 2: Pam3 baseplate wedge gp23



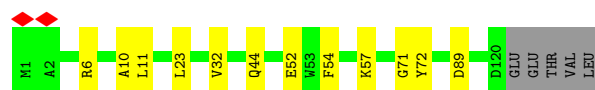
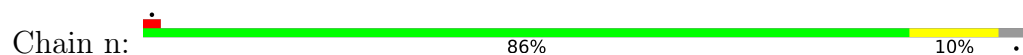
- Molecule 2: Pam3 baseplate wedge gp23



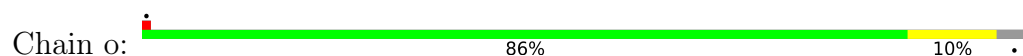
- Molecule 3: Pam3 sheath initiator gp21



- Molecule 3: Pam3 sheath initiator gp21

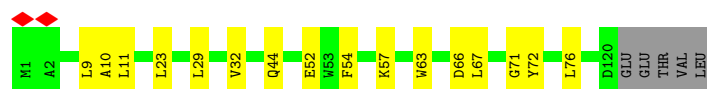


- Molecule 3: Pam3 sheath initiator gp21



- Molecule 3: Pam3 sheath initiator gp21

Chain p:  83% 13%



- Molecule 3: Pam3 sheath initiator gp21

Chain q:  78% 18%



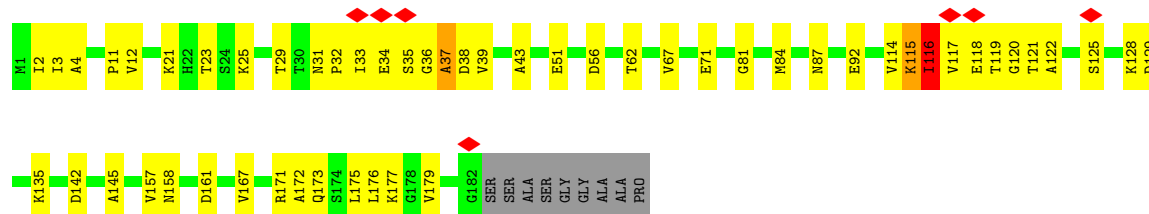
- Molecule 3: Pam3 sheath initiator gp21

Chain r:  83% 13%



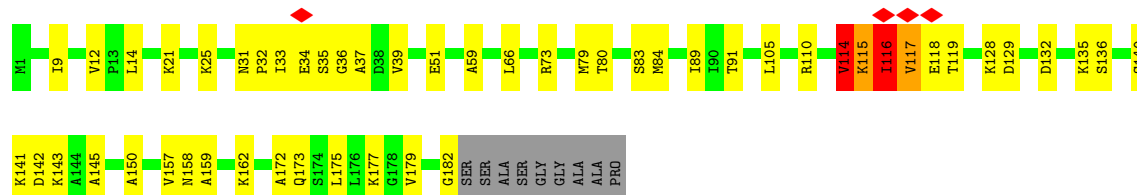
- Molecule 4: Pam3 tube initiator gp17

Chain a:  67% 27% 5%



- Molecule 4: Pam3 tube initiator gp17

Chain b:  68% 25% 5%



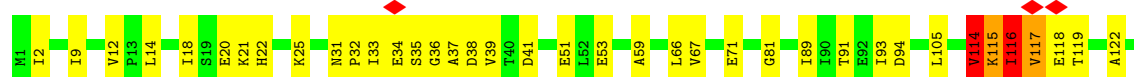
- Molecule 4: Pam3 tube initiator gp17

Chain c:  67% 26% 5%





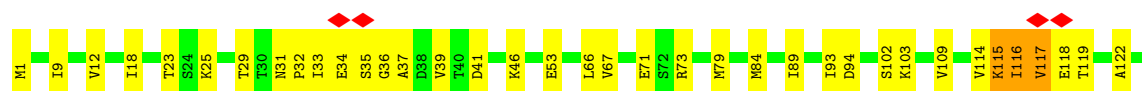
- Molecule 4: Pam3 tube initiator gp17



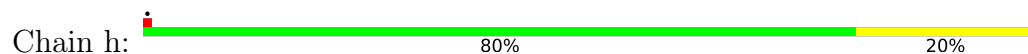
- Molecule 4: Pam3 tube initiator gp17



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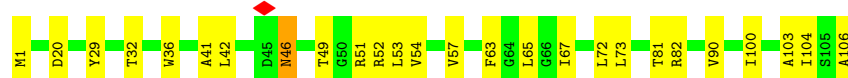
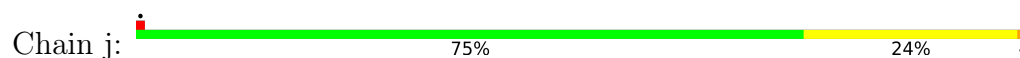
- Molecule 5: Pam3 plug gp18



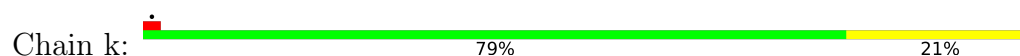
- Molecule 5: Pam3 plug gp18



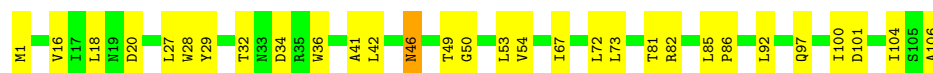
- Molecule 5: Pam3 plug gp18



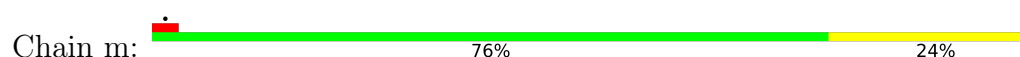
- Molecule 5: Pam3 plug gp18



- Molecule 5: Pam3 plug gp18



- Molecule 5: Pam3 plug gp18

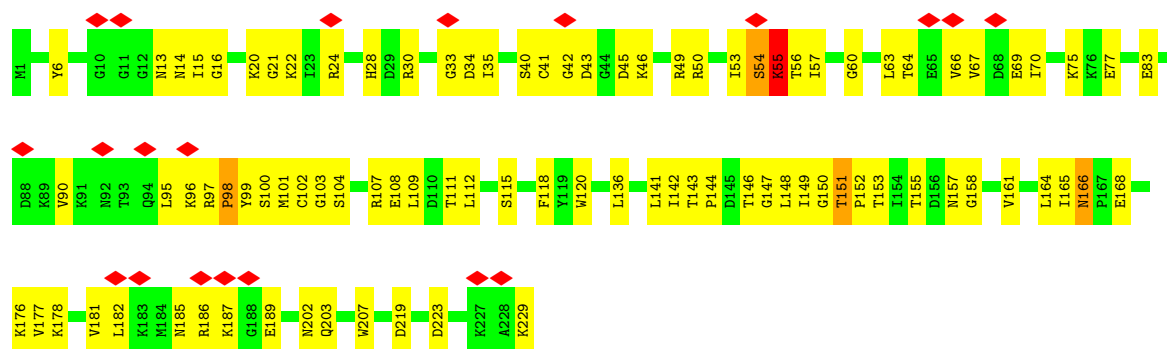


- Molecule 6: Pam3 hub gp19

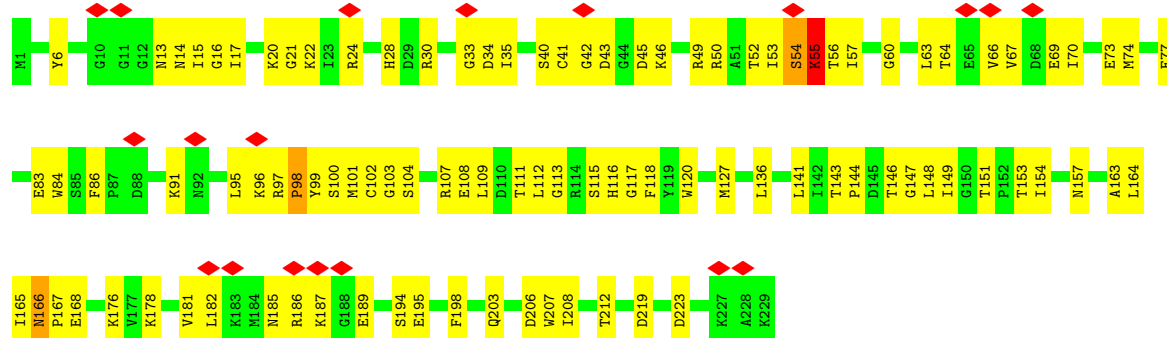


- Molecule 6: Pam3 hub gp19

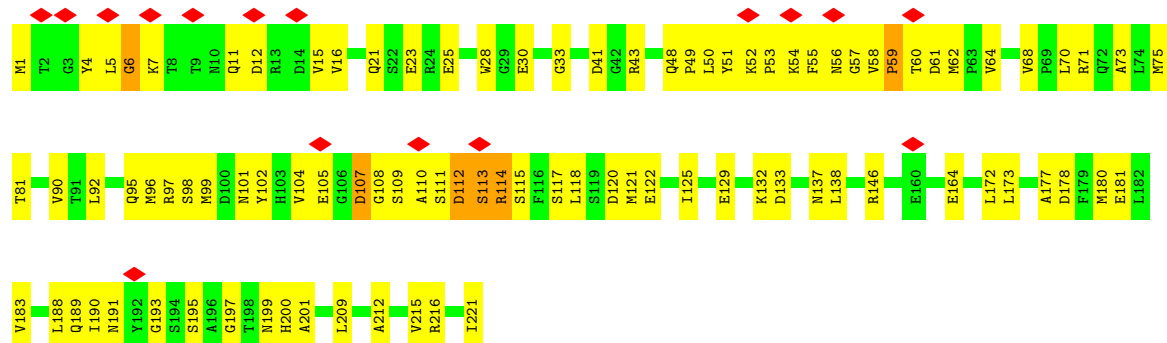




• Molecule 6: Pam3 hub gp19

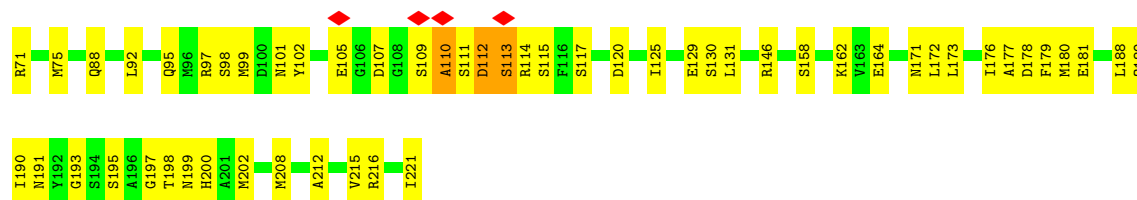


• Molecule 7: Pam3 spike gp20

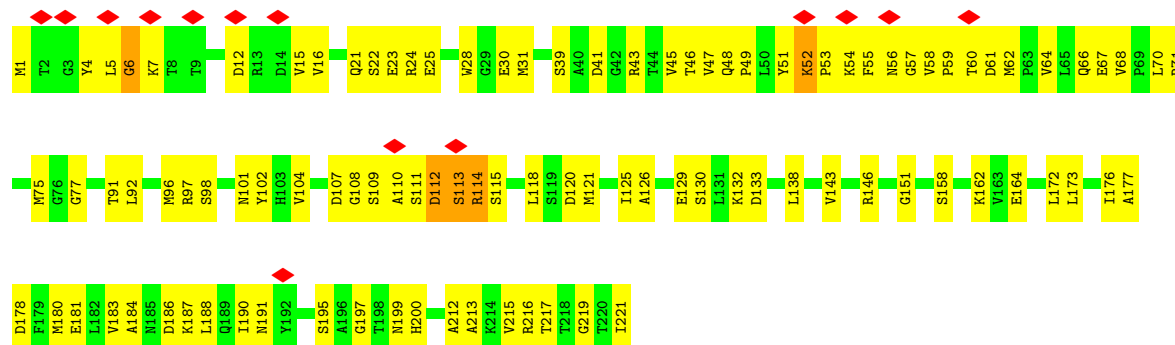


• Molecule 7: Pam3 spike gp20





• Molecule 7: Pam3 spike gp20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45155	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.008	Depositor
Map size ($\text{\AA}$)	513.60004, 513.60004, 513.60004	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.26	0/2339	0.43	0/3188
1	B	0.23	0/2339	0.41	0/3188
1	E	0.23	0/2339	0.41	0/3188
1	F	0.23	0/2339	0.40	0/3188
1	H	0.22	0/2339	0.42	0/3188
1	I	0.24	0/2339	0.41	0/3188
1	K	0.22	0/2339	0.40	0/3188
1	L	0.26	0/2339	0.45	0/3188
1	O	0.28	0/2339	0.46	1/3188 (0.0%)
1	P	0.25	0/2339	0.41	0/3188
1	Q	0.25	0/2339	0.46	2/3188 (0.1%)
1	R	0.23	0/2339	0.40	0/3188
2	C	0.27	0/1876	0.49	1/2554 (0.0%)
2	D	0.27	0/1876	0.52	1/2554 (0.0%)
2	G	0.26	0/1876	0.48	1/2554 (0.0%)
2	J	0.25	0/1876	0.44	0/2554
2	M	0.28	0/1876	0.51	1/2554 (0.0%)
2	S	0.26	0/1876	0.46	0/2554
3	X	0.24	0/951	0.42	0/1287
3	n	0.24	0/951	0.41	0/1287
3	o	0.23	0/951	0.43	0/1287
3	p	0.24	0/951	0.41	0/1287
3	q	0.24	0/951	0.42	0/1287
3	r	0.24	0/951	0.39	0/1287
4	a	0.32	0/1358	0.64	5/1835 (0.3%)
4	b	0.40	2/1358 (0.1%)	0.63	3/1835 (0.2%)
4	c	0.41	1/1358 (0.1%)	0.70	6/1835 (0.3%)
4	d	0.39	1/1358 (0.1%)	0.65	3/1835 (0.2%)
4	e	0.31	0/1358	0.62	3/1835 (0.2%)
4	f	0.29	0/1358	0.56	0/1835
5	h	0.26	0/841	0.41	0/1143
5	i	0.28	0/841	0.43	0/1143
5	j	0.27	0/841	0.41	0/1143
5	k	0.25	0/841	0.43	0/1143

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	l	0.27	0/841	0.41	0/1143
5	m	0.26	0/841	0.44	0/1143
6	t	0.34	0/1792	0.74	3/2408 (0.1%)
6	u	0.34	0/1792	0.77	4/2408 (0.2%)
6	v	0.36	0/1792	0.78	4/2408 (0.2%)
7	w	0.35	0/1669	0.76	3/2258 (0.1%)
7	x	0.36	0/1669	0.72	3/2258 (0.1%)
7	y	0.33	0/1669	0.75	6/2258 (0.3%)
All	All	0.28	4/68607 (0.0%)	0.52	50/93168 (0.1%)

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
3	X	0	1
4	b	0	1
4	c	0	1
4	d	0	1
6	t	0	3
6	u	0	3
6	v	0	2
7	w	0	3
All	All	0	15

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	c	116	ILE	N-CA	6.37	1.54	1.46
4	b	116	ILE	N-CA	6.17	1.54	1.46
4	d	116	ILE	N-CA	5.75	1.53	1.46
4	b	115	LYS	N-CA	5.43	1.52	1.45

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	b	114	VAL	O-C-N	-15.28	106.08	123.03
4	d	114	VAL	O-C-N	-14.36	107.09	123.03
4	c	114	VAL	O-C-N	-12.85	108.55	122.81
7	w	6	GLY	N-CA-C	9.83	123.84	110.58
6	t	54	SER	CA-C-N	-8.73	108.58	121.76

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	X	33	GLN	Peptide
4	b	114	VAL	Mainchain
4	c	114	VAL	Mainchain
4	d	114	VAL	Mainchain
6	t	55	LYS	Peptide

5.2 Too-close contacts [i](#)

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	2295	2224	2269	48	0
1	B	2295	2270	2269	65	0
1	E	2295	2224	2269	71	0
1	F	2295	2270	2270	56	0
1	H	2295	2224	2268	62	0
1	I	2295	2270	2269	80	0
1	K	2295	2224	2269	50	0
1	L	2295	2256	2270	68	0
1	O	2295	2217	2269	59	0
1	P	2295	2270	2269	66	0
1	Q	2295	2224	2270	56	0
1	R	2295	2270	2269	47	0
2	C	1832	1507	1766	67	0
2	D	1832	1507	1767	85	0
2	G	1832	1507	1766	63	0
2	J	1832	1507	1766	70	0
2	M	1832	1507	1766	75	0
2	S	1832	1507	1767	68	0
3	X	936	933	933	11	0
3	n	936	933	933	9	0
3	o	936	933	933	11	0
3	p	936	933	933	17	0
3	q	936	933	933	16	0
3	r	936	933	933	12	0
4	a	1342	777	1368	128	0
4	b	1342	777	1368	121	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	c	1342	777	1368	116	0
4	d	1342	777	1368	118	0
4	e	1342	777	1368	138	0
4	f	1342	777	1368	131	0
5	h	827	833	833	16	0
5	i	827	833	833	27	0
5	j	827	833	833	27	0
5	k	827	833	833	22	0
5	l	827	833	833	27	0
5	m	827	833	833	28	0
6	t	1762	1776	1776	290	0
6	u	1762	1776	1776	262	0
6	v	1762	1776	1776	293	0
7	w	1644	1633	1633	260	0
7	x	1644	1633	1633	260	0
7	y	1644	1633	1633	255	0
All	All	67380	61470	66859	2481	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 18.

The worst 5 of 2481 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:H:109:ILE:HD13	2:J:73:PHE:CE1	1.49	1.45
1:E:109:ILE:HD13	2:G:73:PHE:CE1	1.53	1.42
1:Q:109:ILE:HD13	2:S:73:PHE:CE1	1.54	1.40
1:E:109:ILE:HD13	2:G:73:PHE:CD1	1.67	1.30
1:E:109:ILE:CD1	2:G:73:PHE:CE1	2.17	1.25

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	297/299 (99%)	287 (97%)	9 (3%)	1 (0%)	36	68
1	B	297/299 (99%)	287 (97%)	10 (3%)	0	100	100
1	E	297/299 (99%)	286 (96%)	10 (3%)	1 (0%)	36	68
1	F	297/299 (99%)	284 (96%)	13 (4%)	0	100	100
1	H	297/299 (99%)	286 (96%)	10 (3%)	1 (0%)	36	68
1	I	297/299 (99%)	284 (96%)	13 (4%)	0	100	100
1	K	297/299 (99%)	285 (96%)	11 (4%)	1 (0%)	36	68
1	L	297/299 (99%)	280 (94%)	15 (5%)	2 (1%)	18	52
1	O	297/299 (99%)	283 (95%)	13 (4%)	1 (0%)	36	68
1	P	297/299 (99%)	286 (96%)	11 (4%)	0	100	100
1	Q	297/299 (99%)	287 (97%)	10 (3%)	0	100	100
1	R	297/299 (99%)	283 (95%)	14 (5%)	0	100	100
2	C	236/238 (99%)	211 (89%)	25 (11%)	0	100	100
2	D	236/238 (99%)	218 (92%)	18 (8%)	0	100	100
2	G	236/238 (99%)	217 (92%)	19 (8%)	0	100	100
2	J	236/238 (99%)	217 (92%)	19 (8%)	0	100	100
2	M	236/238 (99%)	217 (92%)	19 (8%)	0	100	100
2	S	236/238 (99%)	218 (92%)	18 (8%)	0	100	100
3	X	118/125 (94%)	113 (96%)	5 (4%)	0	100	100
3	n	118/125 (94%)	112 (95%)	6 (5%)	0	100	100
3	o	118/125 (94%)	113 (96%)	5 (4%)	0	100	100
3	p	118/125 (94%)	112 (95%)	6 (5%)	0	100	100
3	q	118/125 (94%)	113 (96%)	5 (4%)	0	100	100
3	r	118/125 (94%)	112 (95%)	6 (5%)	0	100	100
4	a	180/191 (94%)	158 (88%)	21 (12%)	1 (1%)	21	56
4	b	180/191 (94%)	164 (91%)	14 (8%)	2 (1%)	11	43
4	c	180/191 (94%)	160 (89%)	18 (10%)	2 (1%)	11	43
4	d	180/191 (94%)	165 (92%)	13 (7%)	2 (1%)	11	43
4	e	180/191 (94%)	159 (88%)	20 (11%)	1 (1%)	21	56
4	f	180/191 (94%)	166 (92%)	12 (7%)	2 (1%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	h	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
5	i	104/106 (98%)	103 (99%)	1 (1%)	0	100	100
5	j	104/106 (98%)	104 (100%)	0	0	100	100
5	k	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
5	l	104/106 (98%)	104 (100%)	0	0	100	100
5	m	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
6	t	227/229 (99%)	199 (88%)	28 (12%)	0	100	100
6	u	227/229 (99%)	204 (90%)	23 (10%)	0	100	100
6	v	227/229 (99%)	206 (91%)	21 (9%)	0	100	100
7	w	219/221 (99%)	193 (88%)	26 (12%)	0	100	100
7	x	219/221 (99%)	196 (90%)	21 (10%)	2 (1%)	14	47
7	y	219/221 (99%)	192 (88%)	27 (12%)	0	100	100
All	All	8730/8898 (98%)	8169 (94%)	542 (6%)	19 (0%)	44	73

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	105	ASP
4	a	116	ILE
4	b	116	ILE
4	e	116	ILE
1	A	105	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	A	253/253 (100%)	253 (100%)	0	100	100
1	B	253/253 (100%)	253 (100%)	0	100	100
1	E	253/253 (100%)	253 (100%)	0	100	100
1	F	253/253 (100%)	253 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	253/253 (100%)	253 (100%)	0	100	100
1	I	253/253 (100%)	253 (100%)	0	100	100
1	K	253/253 (100%)	253 (100%)	0	100	100
1	L	253/253 (100%)	251 (99%)	2 (1%)	73	82
1	O	253/253 (100%)	252 (100%)	1 (0%)	84	86
1	P	253/253 (100%)	253 (100%)	0	100	100
1	Q	253/253 (100%)	253 (100%)	0	100	100
1	R	253/253 (100%)	253 (100%)	0	100	100
2	C	197/197 (100%)	197 (100%)	0	100	100
2	D	197/197 (100%)	197 (100%)	0	100	100
2	G	197/197 (100%)	197 (100%)	0	100	100
2	J	197/197 (100%)	197 (100%)	0	100	100
2	M	197/197 (100%)	197 (100%)	0	100	100
2	S	197/197 (100%)	196 (100%)	1 (0%)	81	85
3	X	98/103 (95%)	98 (100%)	0	100	100
3	n	98/103 (95%)	98 (100%)	0	100	100
3	o	98/103 (95%)	98 (100%)	0	100	100
3	p	98/103 (95%)	98 (100%)	0	100	100
3	q	98/103 (95%)	98 (100%)	0	100	100
3	r	98/103 (95%)	98 (100%)	0	100	100
4	a	144/148 (97%)	142 (99%)	2 (1%)	59	77
4	b	144/148 (97%)	143 (99%)	1 (1%)	76	83
4	c	144/148 (97%)	142 (99%)	2 (1%)	59	77
4	d	144/148 (97%)	143 (99%)	1 (1%)	76	83
4	e	144/148 (97%)	142 (99%)	2 (1%)	59	77
4	f	144/148 (97%)	143 (99%)	1 (1%)	76	83
5	h	90/90 (100%)	90 (100%)	0	100	100
5	i	90/90 (100%)	90 (100%)	0	100	100
5	j	90/90 (100%)	89 (99%)	1 (1%)	65	79
5	k	90/90 (100%)	90 (100%)	0	100	100
5	l	90/90 (100%)	89 (99%)	1 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	m	90/90 (100%)	90 (100%)	0	100	100
6	t	192/192 (100%)	192 (100%)	0	100	100
6	u	192/192 (100%)	192 (100%)	0	100	100
6	v	192/192 (100%)	192 (100%)	0	100	100
7	w	180/180 (100%)	180 (100%)	0	100	100
7	x	180/180 (100%)	180 (100%)	0	100	100
7	y	180/180 (100%)	180 (100%)	0	100	100
All	All	7326/7380 (99%)	7311 (100%)	15 (0%)	85	89

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	c	115	LYS
5	j	46	ASN
4	c	116	ILE
5	l	46	ASN
4	e	116	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
3	X	16	GLN
7	y	171	ASN
4	e	173	GLN
7	y	95	GLN
7	w	144	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

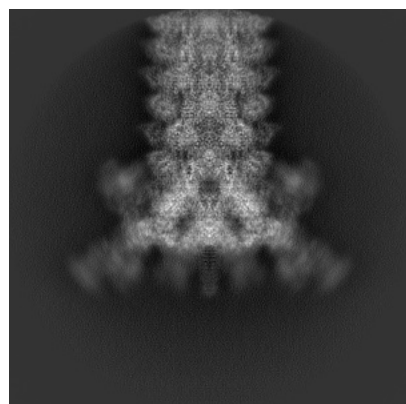
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33802. These allow visual inspection of the internal detail of the map and identification of artifacts.

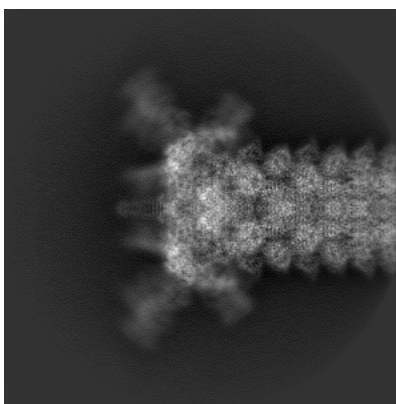
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

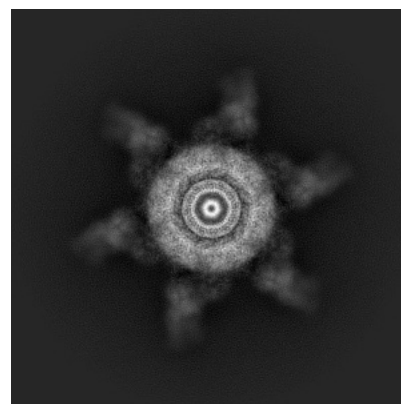
6.1.1 Primary map



X

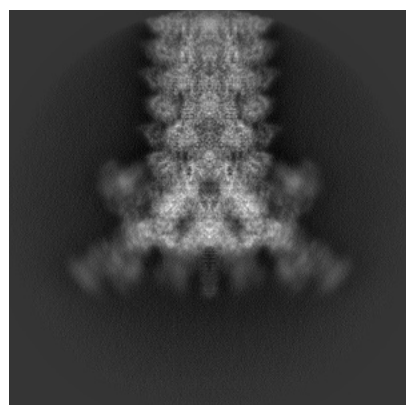


Y

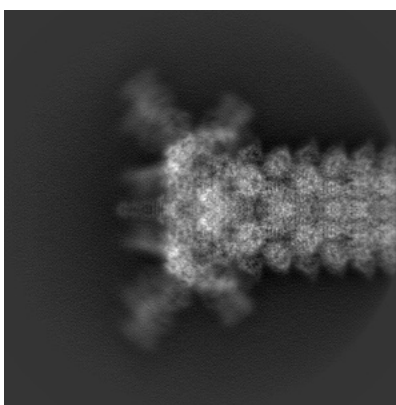


Z

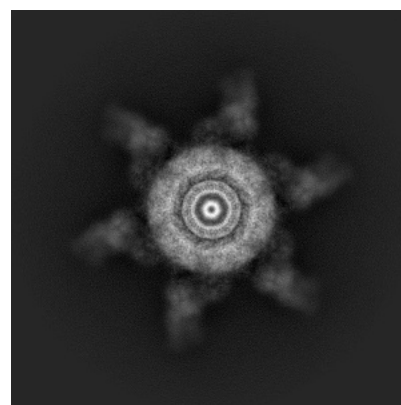
6.1.2 Raw map



X



Y

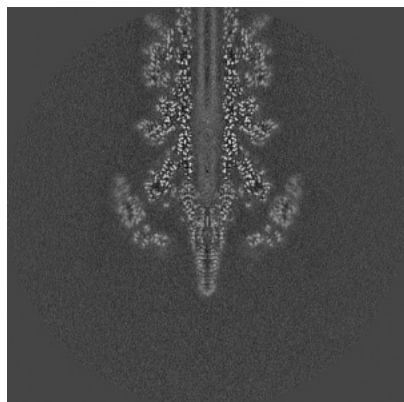


Z

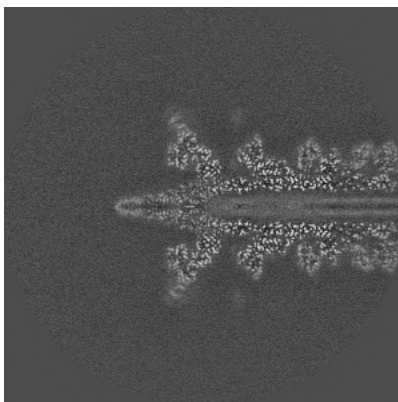
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

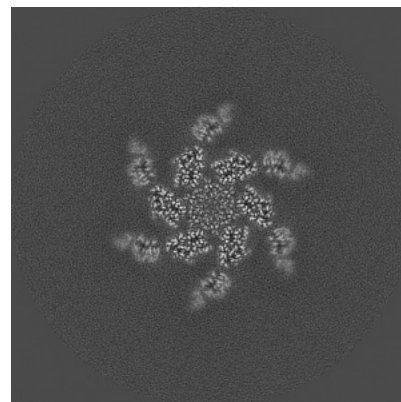
6.2.1 Primary map



X Index: 240

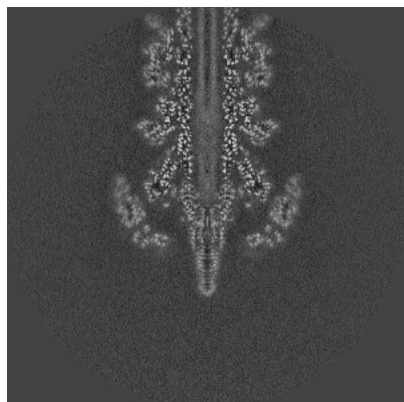


Y Index: 240

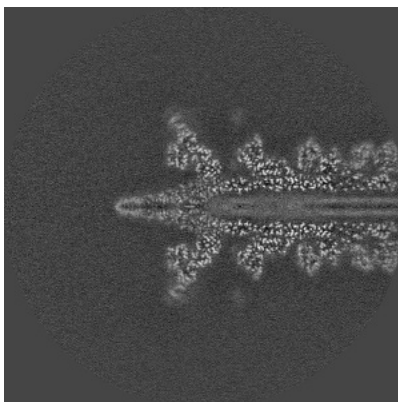


Z Index: 240

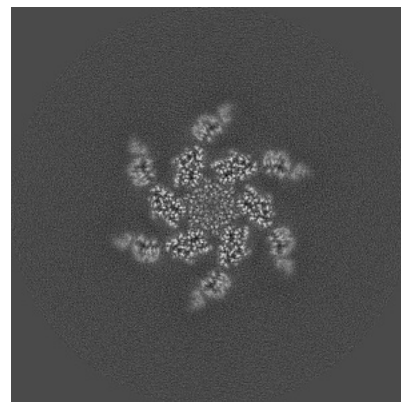
6.2.2 Raw map



X Index: 240



Y Index: 240

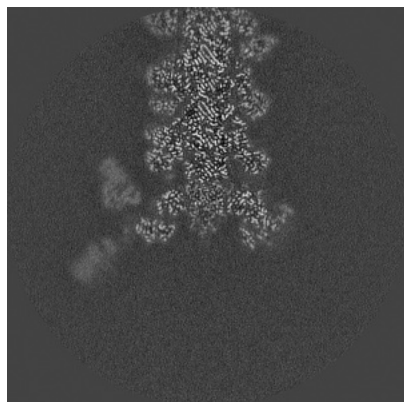


Z Index: 240

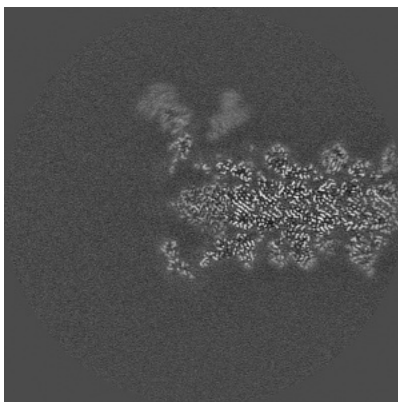
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

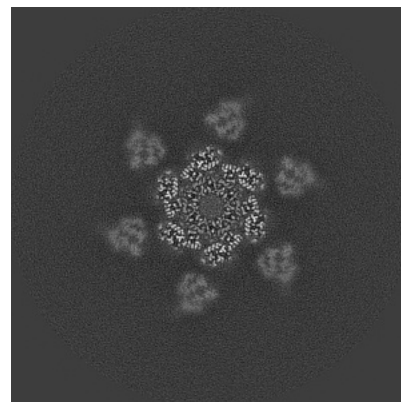
6.3.1 Primary map



X Index: 218

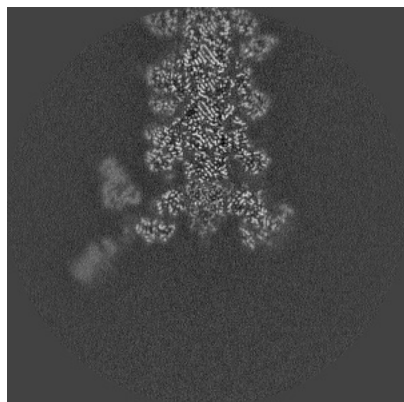


Y Index: 261

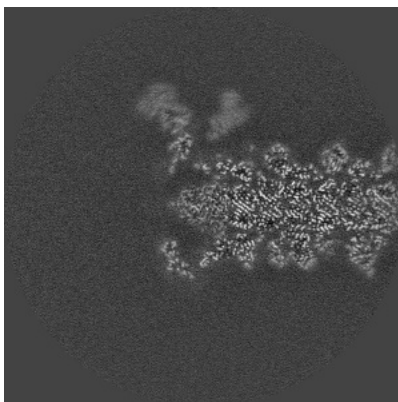


Z Index: 256

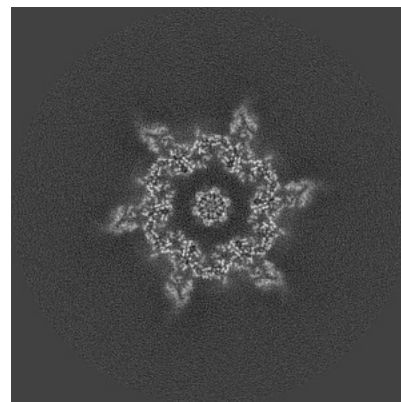
6.3.2 Raw map



X Index: 218



Y Index: 261

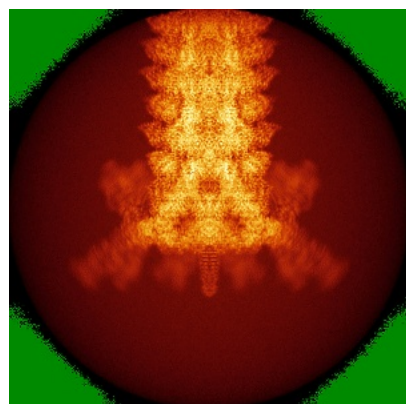


Z Index: 208

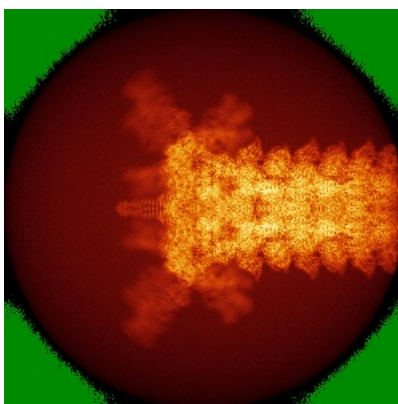
The images above show the largest variance slices of the map in three orthogonal directions.

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

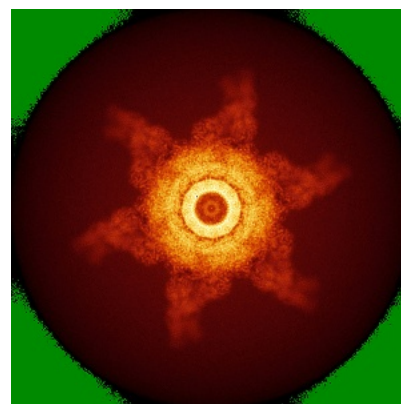
6.4.1 Primary map



X

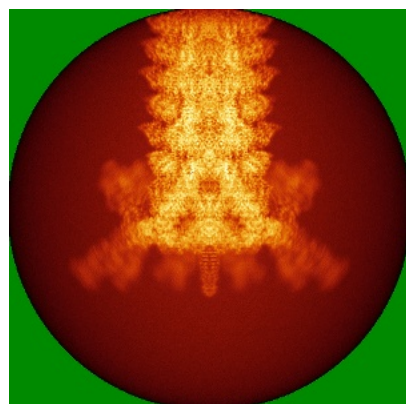


Y

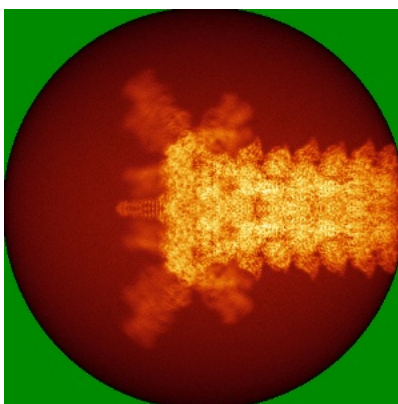


Z

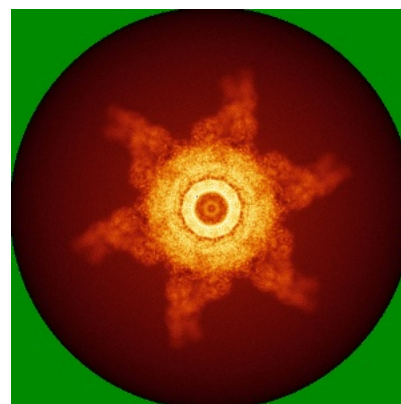
6.4.2 Raw map



X



Y

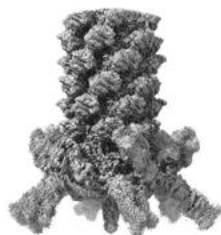


Z

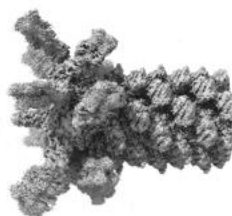
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

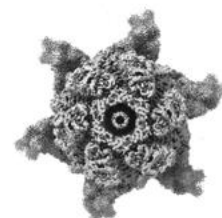
6.5.1 Primary map



X



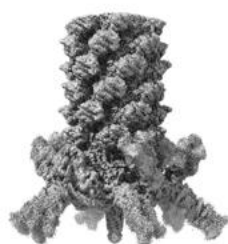
Y



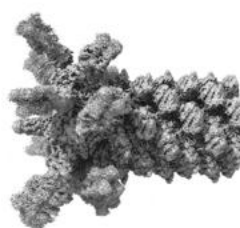
Z

The images above show the 3D surface view of the map at the recommended contour level 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

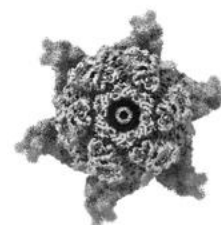
6.5.2 Raw map



X



Y



Z

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.

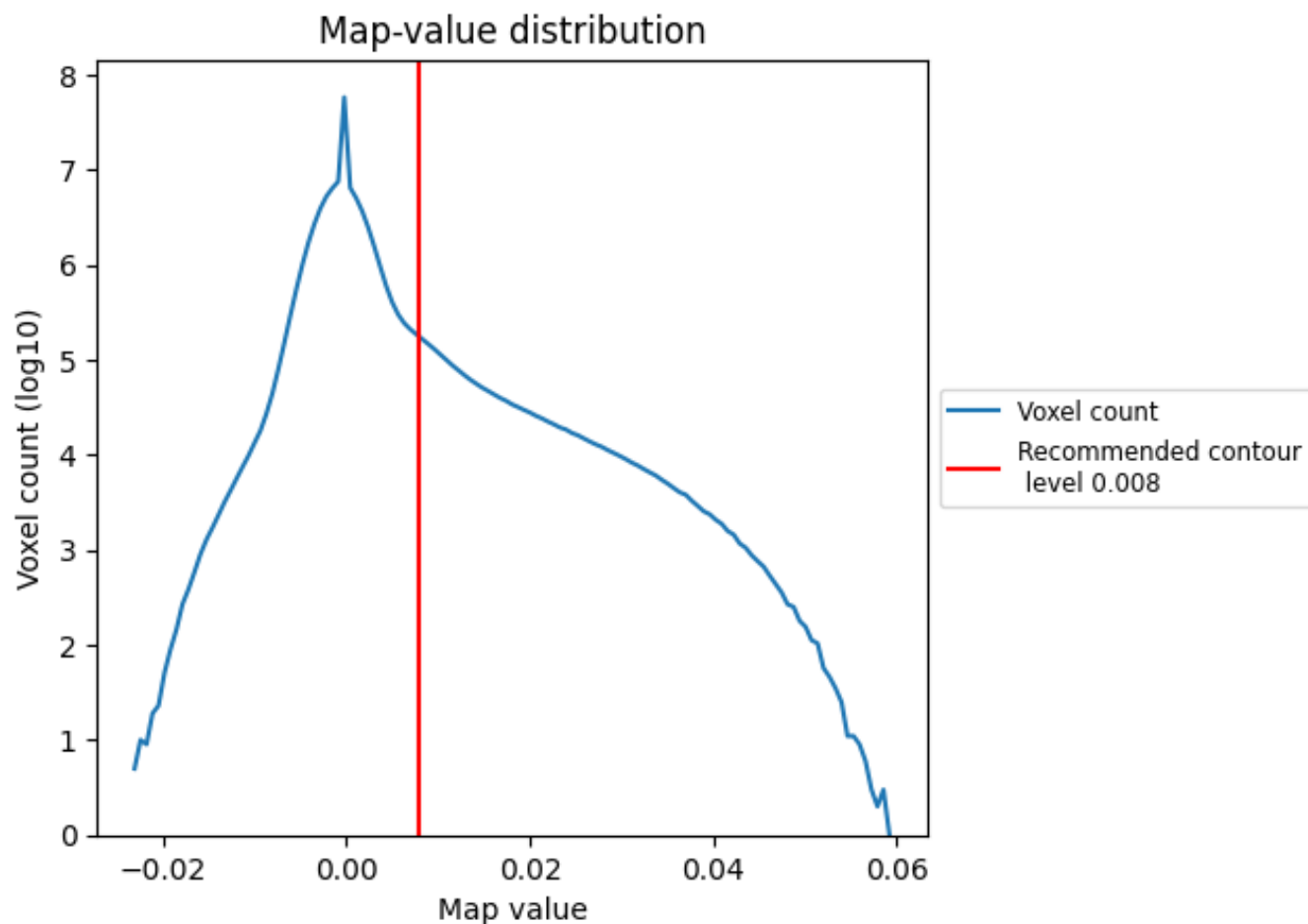
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

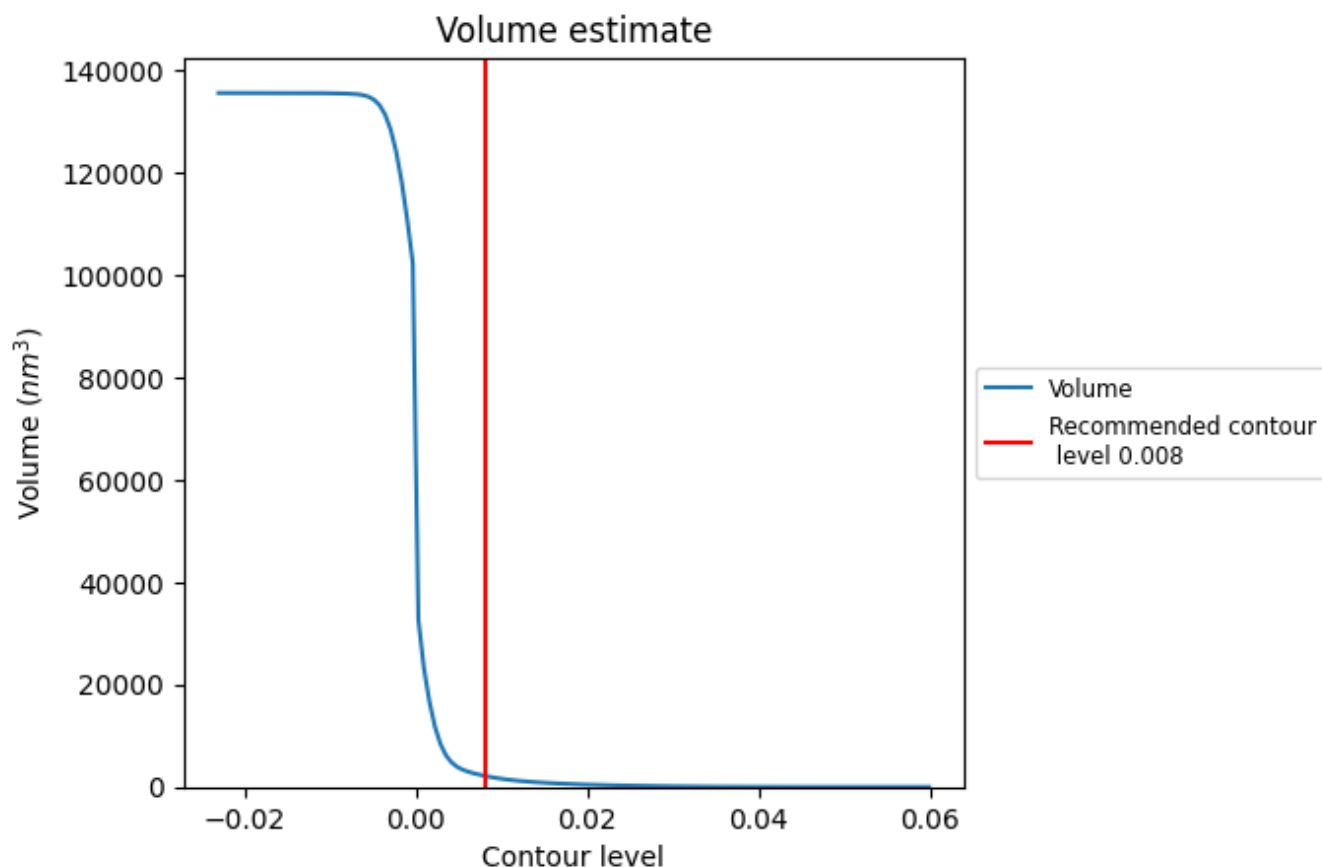
This section contains the results of statistical analysis of the map.

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.

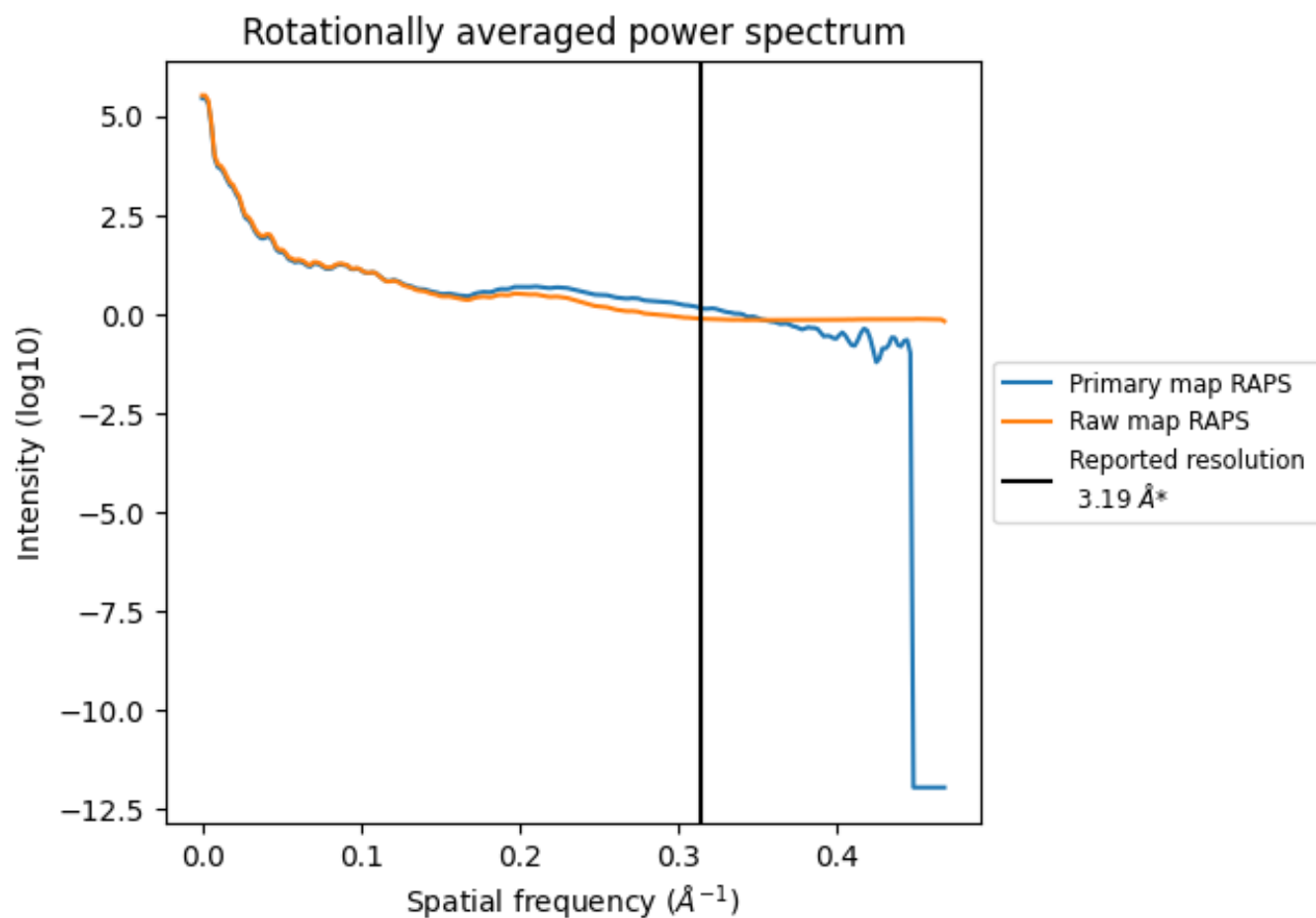
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2164 nm^3 ; this corresponds to an approximate mass of 1955 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 ⓘ

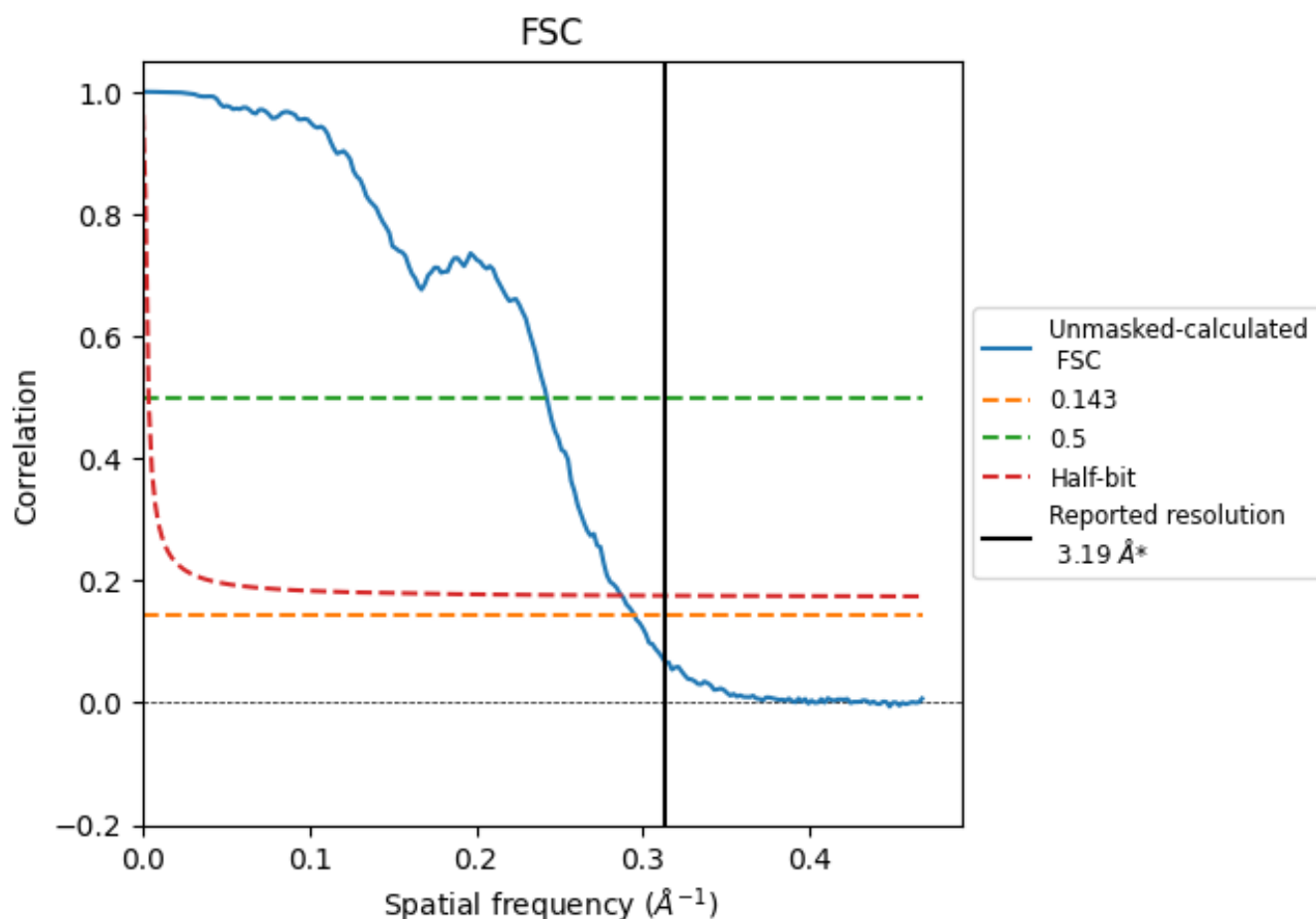


*Reported resolution corresponds to spatial frequency of 0.313 Å⁻¹

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 0.313 Å⁻¹

8.2 Resolution estimates [i](#)

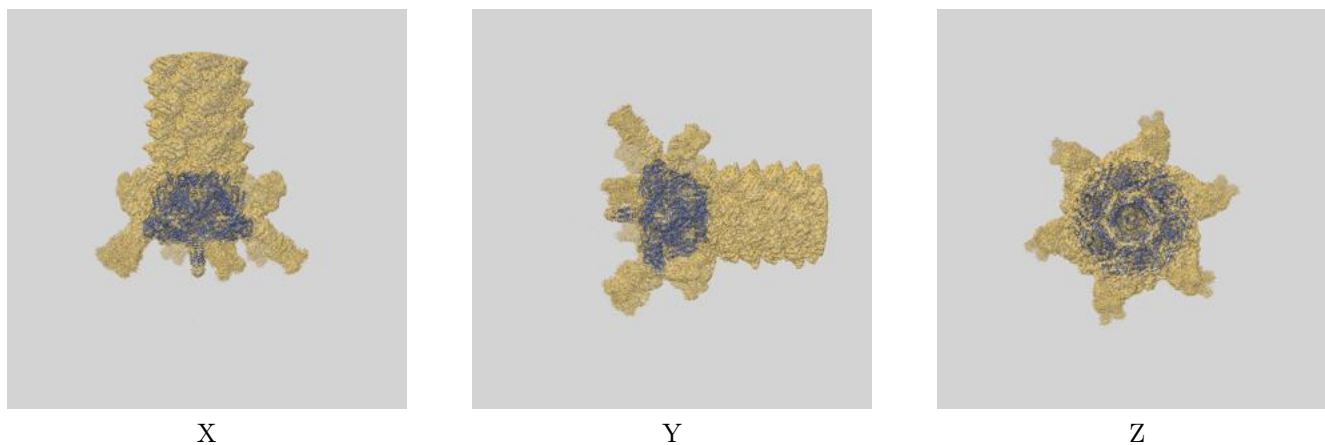
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.19	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.39	4.13	3.48

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

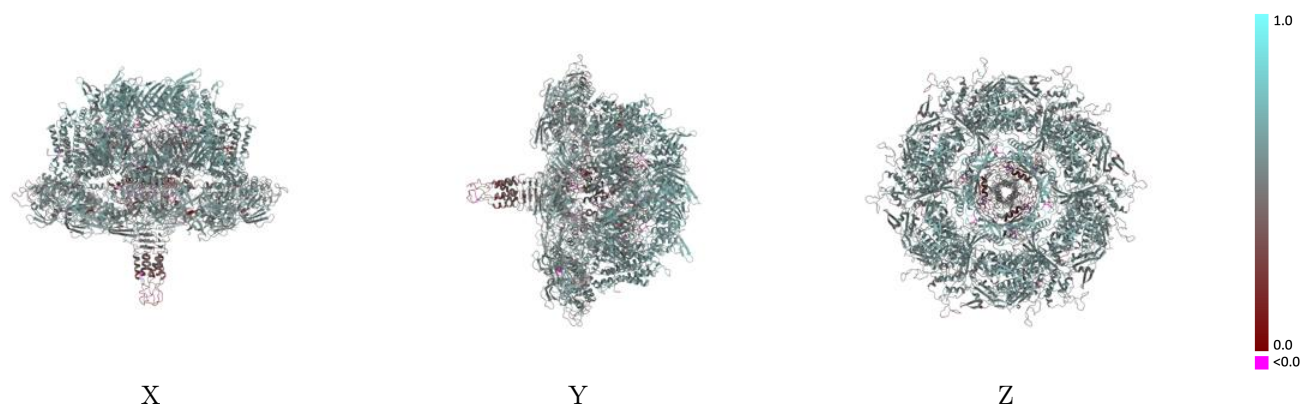
This section contains information regarding the fit between EMDB map EMD-33802 and PDB model 7YFZ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



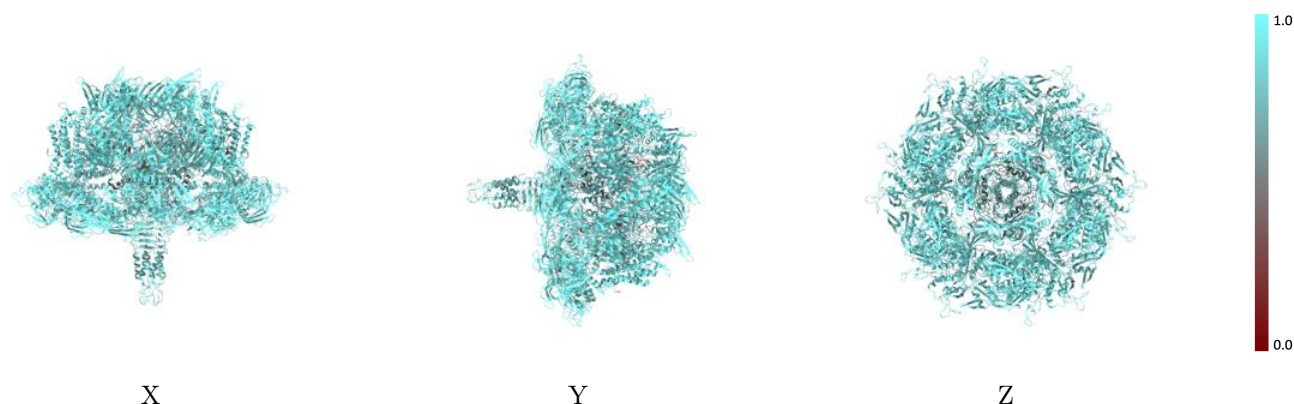
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



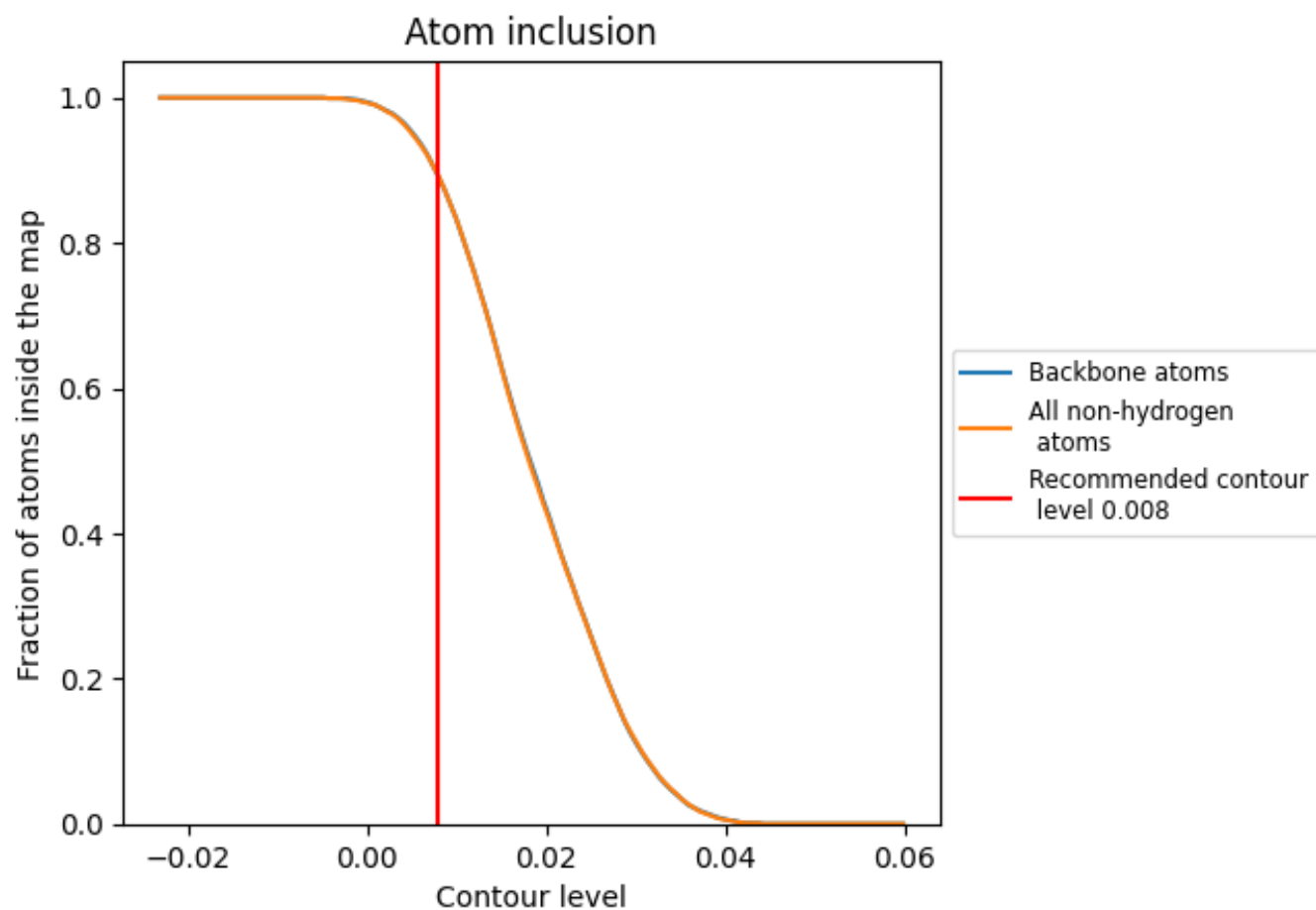
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8920	 0.5280
A	 0.9200	 0.5440
B	 0.9260	 0.5460
C	 0.9170	 0.5330
D	 0.9230	 0.5270
E	 0.9240	 0.5430
F	 0.9180	 0.5400
G	 0.9120	 0.5300
H	 0.9240	 0.5430
I	 0.9290	 0.5460
J	 0.9120	 0.5270
K	 0.9210	 0.5480
L	 0.9140	 0.5410
M	 0.9150	 0.5260
O	 0.9180	 0.5450
P	 0.9220	 0.5460
Q	 0.9210	 0.5400
R	 0.9280	 0.5470
S	 0.9110	 0.5260
X	 0.9240	 0.5850
a	 0.8820	 0.5400
b	 0.8890	 0.5470
c	 0.8800	 0.5420
d	 0.8870	 0.5420
e	 0.8810	 0.5400
f	 0.8890	 0.5470
h	 0.9200	 0.5850
i	 0.9090	 0.5670
j	 0.9030	 0.5650
k	 0.8990	 0.5710
l	 0.9100	 0.5650
m	 0.9000	 0.5730
n	 0.9240	 0.5910
o	 0.9280	 0.5830
p	 0.9270	 0.5880



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Chain	Atom inclusion	Q-score
q	 0.9310	 0.5840
r	 0.9220	 0.5880
t	 0.7650	 0.4360
u	 0.7670	 0.4400
v	 0.7640	 0.4440
w	 0.7960	 0.3940
x	 0.7920	 0.3920
y	 0.7950	 0.3930