



wwPDB EM Validation Summary Report ⓘ

Mar 13, 2026 – 12:27 AM UTC

PDB ID : 7ZHJ / pdb_00007zhj
EMDB ID : EMD-14733
Title : Tail tip of siphophage T5 : tip proteins
Authors : Linares, R.; Arnaud, C.A.; Effantin, G.; Darnault, C.; Epalle, N.; Boeri Erba, E.; Schoehn, G.; Breyton, C.
Deposited on : 2022-04-06
Resolution : 3.53 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

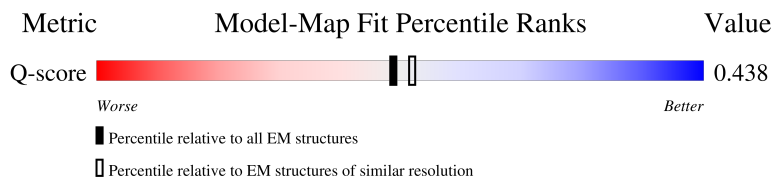
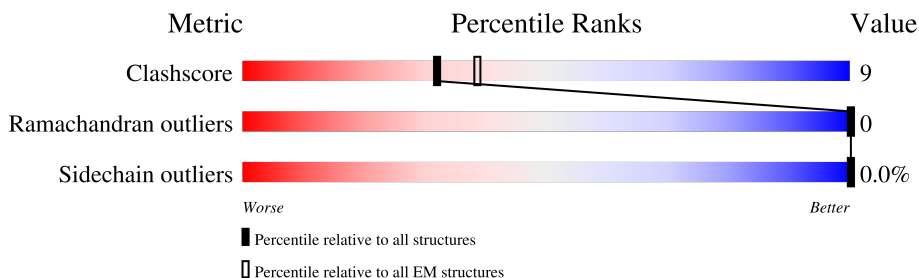
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.53 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	12947 (3.03 - 4.02)

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	J	140	39% 75% 24%
1	K	140	36% 79% 21%
1	L	140	26% 80% 20%
1	M	140	22% 73% 27%

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Mol	Chain	Length	Quality of chain
1	N	140	
1	O	140	
1	P	140	
1	Q	140	
1	R	140	
1	S	140	
1	T	140	
1	U	140	
2	G	298	
2	H	298	
2	I	298	
3	V	204	
3	W	204	
3	X	204	
3	Y	204	
3	Z	204	
3	a	204	
4	A	464	
4	B	464	
4	C	464	
4	D	464	
4	E	464	
4	F	464	
5	e	1219	
5	f	1219	

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Mol	Chain	Length	Quality of chain
5	g	1219	 97%
6	b	949	 11% 81% 18%
6	c	949	 11% 83% 17%
6	d	949	 12% 82% 18%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 74346 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 L-shaped tail fiber protein p132.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
1	Q	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
1	S	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
1	N	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
1	M	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
1	O	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
1	J	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
1	L	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
1	U	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
1	K	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
1	P	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
1	T	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		

- Molecule 2 is a protein called Minor tail protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	298	Total	C	N	O	S	0	0
			2423	1551	398	464	10		
2	H	298	Total	C	N	O	S	0	0
			2423	1551	398	464	10		
2	G	298	Total	C	N	O	S	0	0
			2423	1551	398	464	10		

- Molecule 3 is a protein called Distal tail protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
3	X	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
3	Y	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
3	W	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
3	V	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
3	Z	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		

- Molecule 4 is a protein called Tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
4	E	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
4	C	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
4	D	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
4	A	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
4	B	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		

- Molecule 5 is a protein called Pore-forming tail tip protein pb2.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	f	35	Total	C	N	O	0	0
			262	158	47	57		
5	g	35	Total	C	N	O	0	0
			262	158	47	57		
5	e	35	Total	C	N	O	0	0
			262	158	47	57		

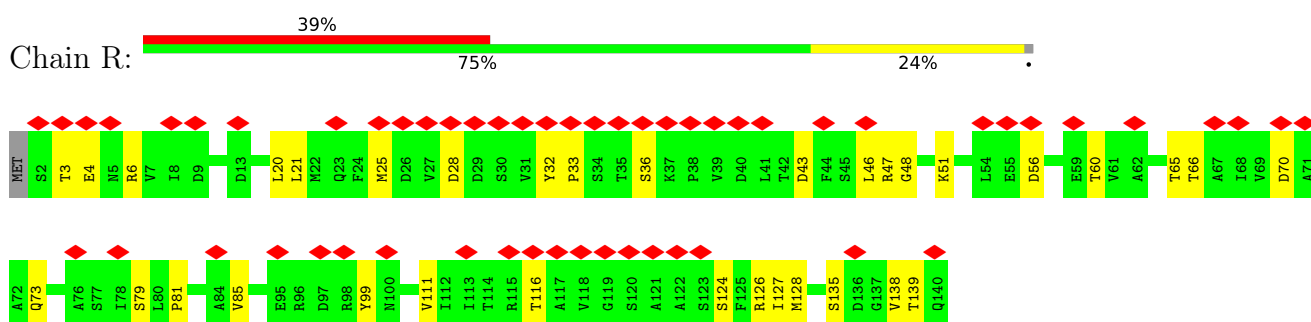
- Molecule 6 is a protein called Probable baseplate hub protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	949	Total 7577	C 4811	N 1274	O 1482	S 10	0	0
6	d	949	Total 7577	C 4811	N 1274	O 1482	S 10	0	0
6	c	949	Total 7577	C 4811	N 1274	O 1482	S 10	0	0

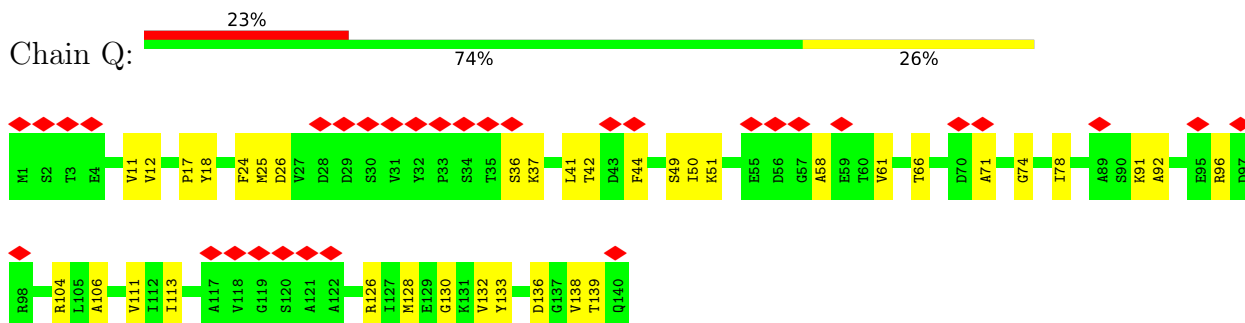
3 Residue-property plots [i](#)

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.

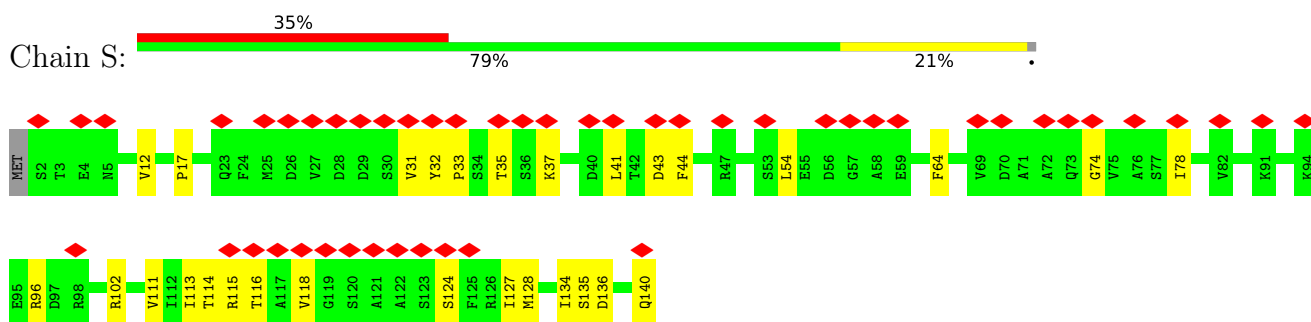
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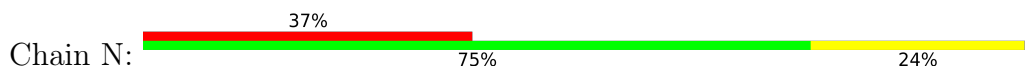
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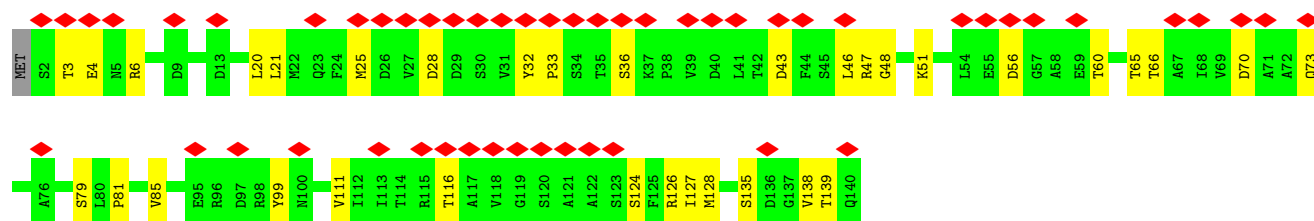


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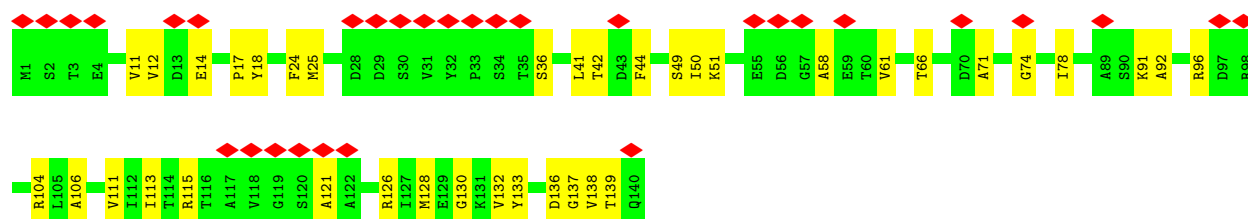
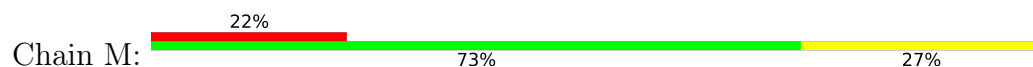


- Molecule 1: L-shaped tail fiber protein p132

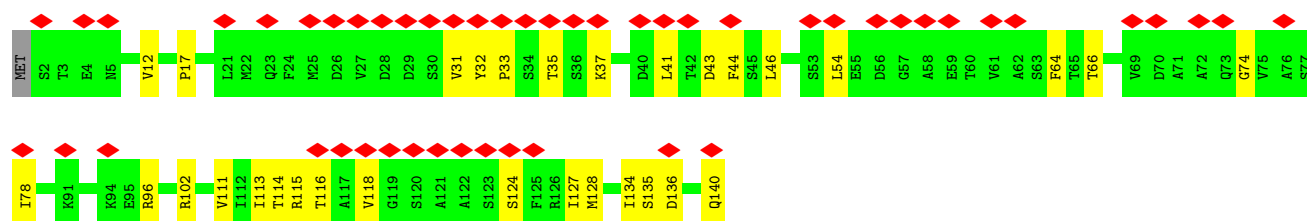
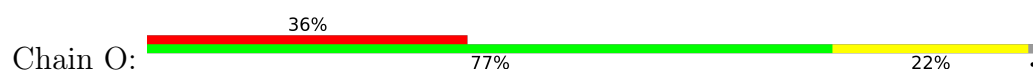




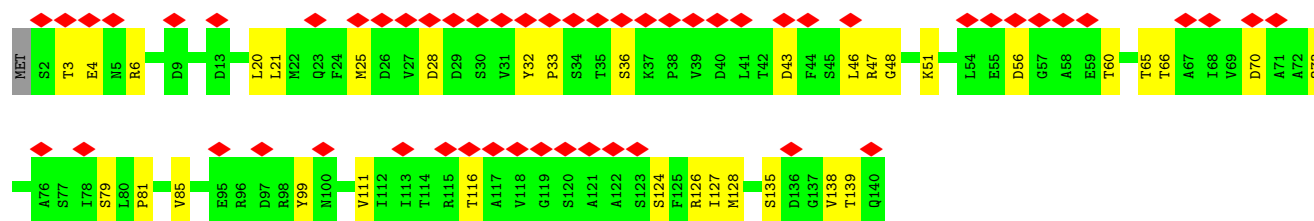
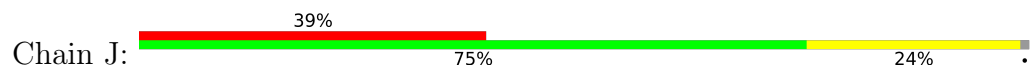
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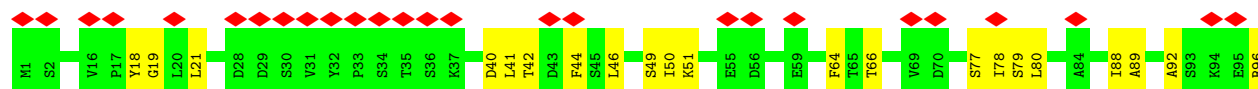
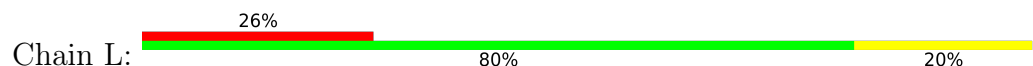
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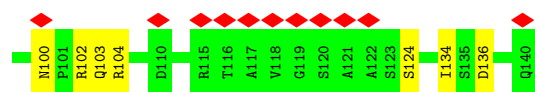


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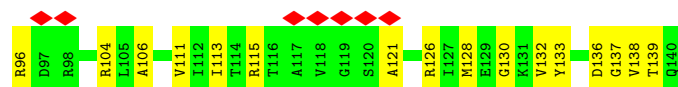
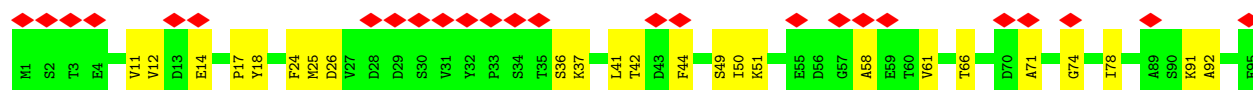


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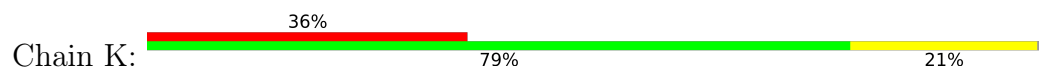




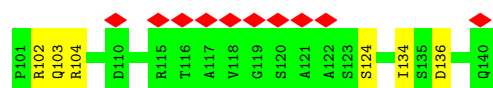
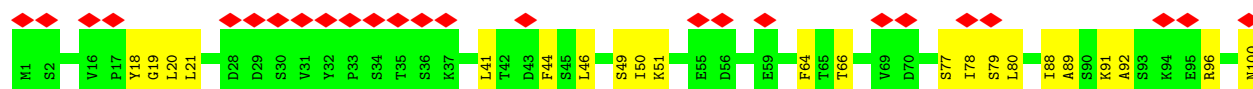
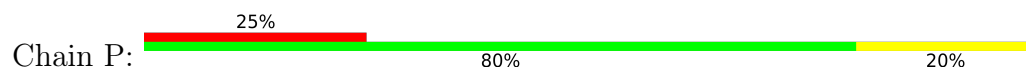
- Molecule 1: L-shaped tail fiber protein p132



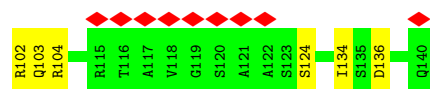
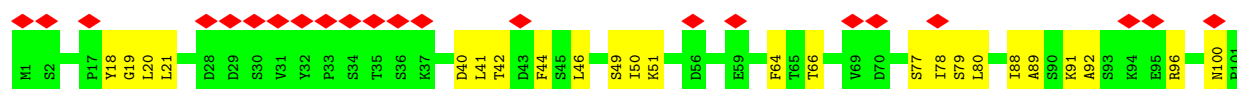
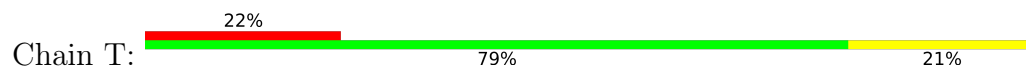
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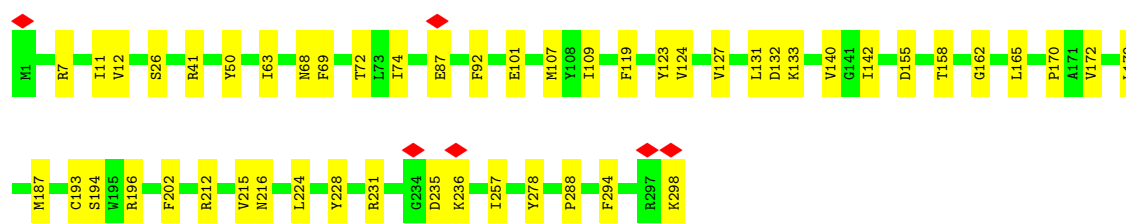
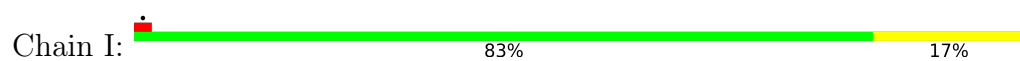
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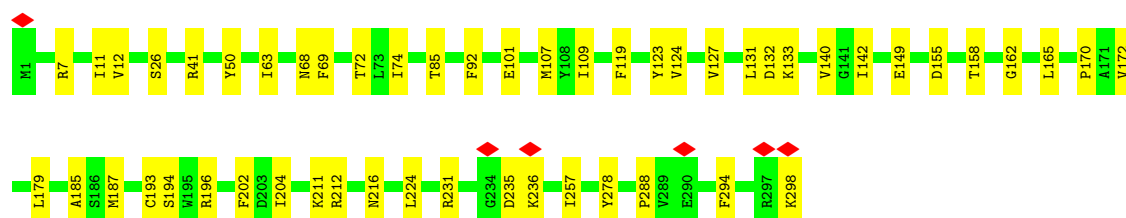
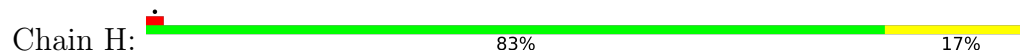
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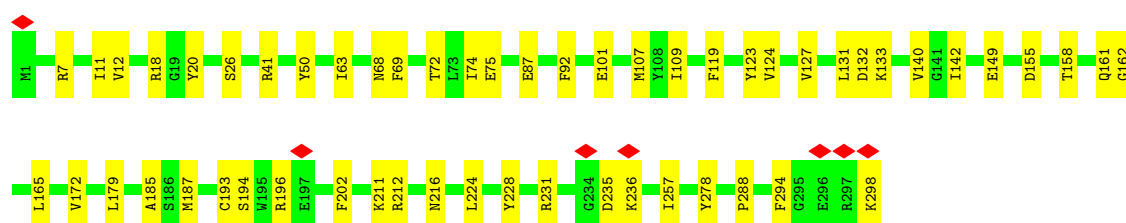
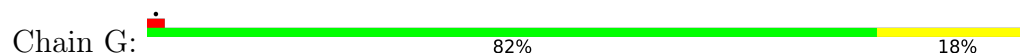
- Molecule 2: Minor tail protein



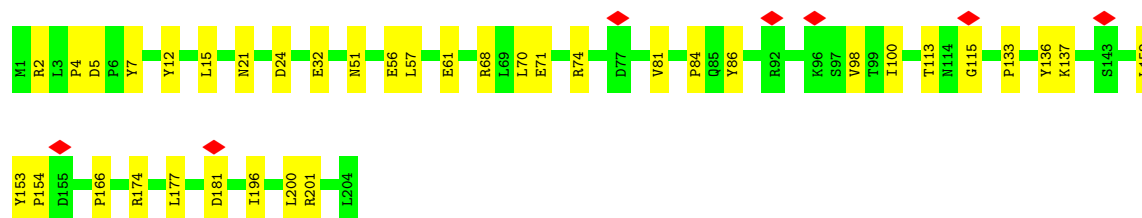
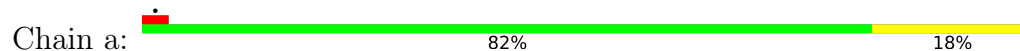
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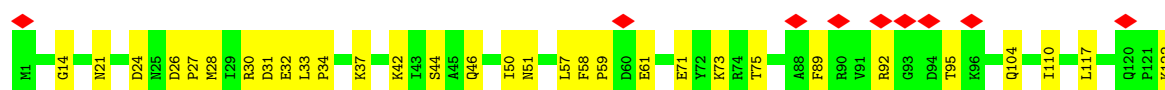
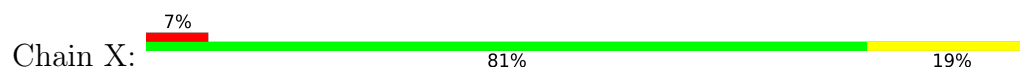
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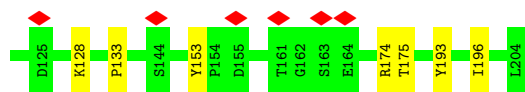


- Molecule 3: Distal tail protein

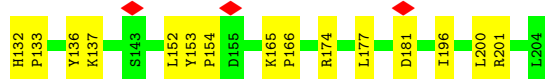
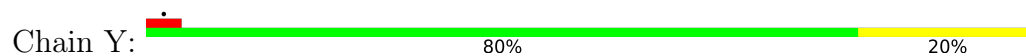


- Molecule 3: Distal tail protein

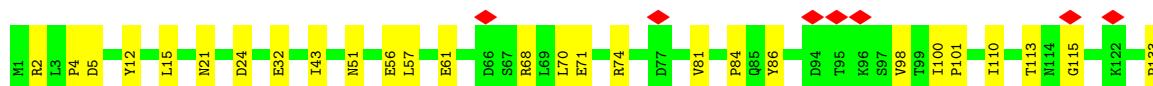
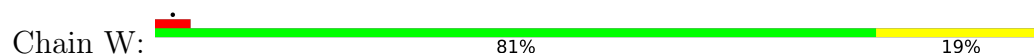




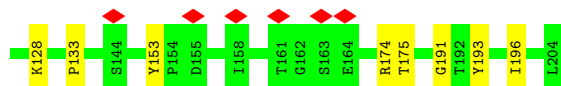
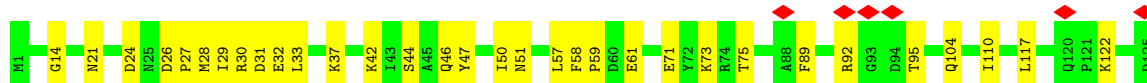
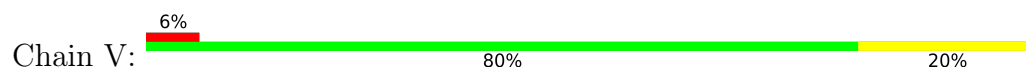
- Molecule 3: Distal tail protein



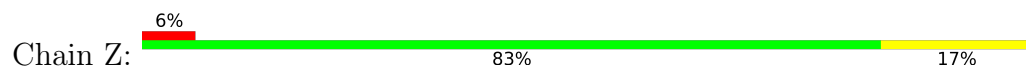
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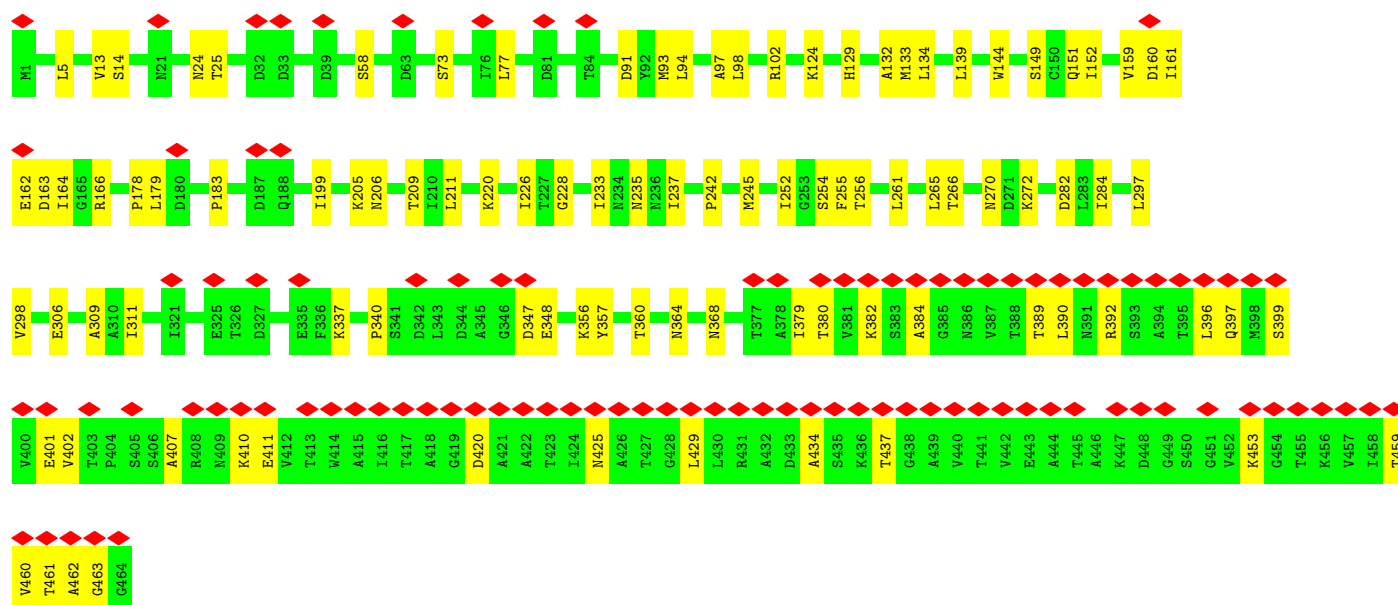
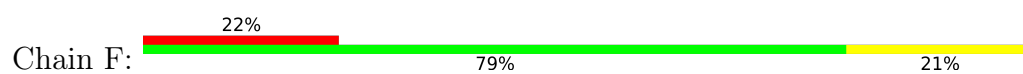
- Molecule 3: Distal tail protein



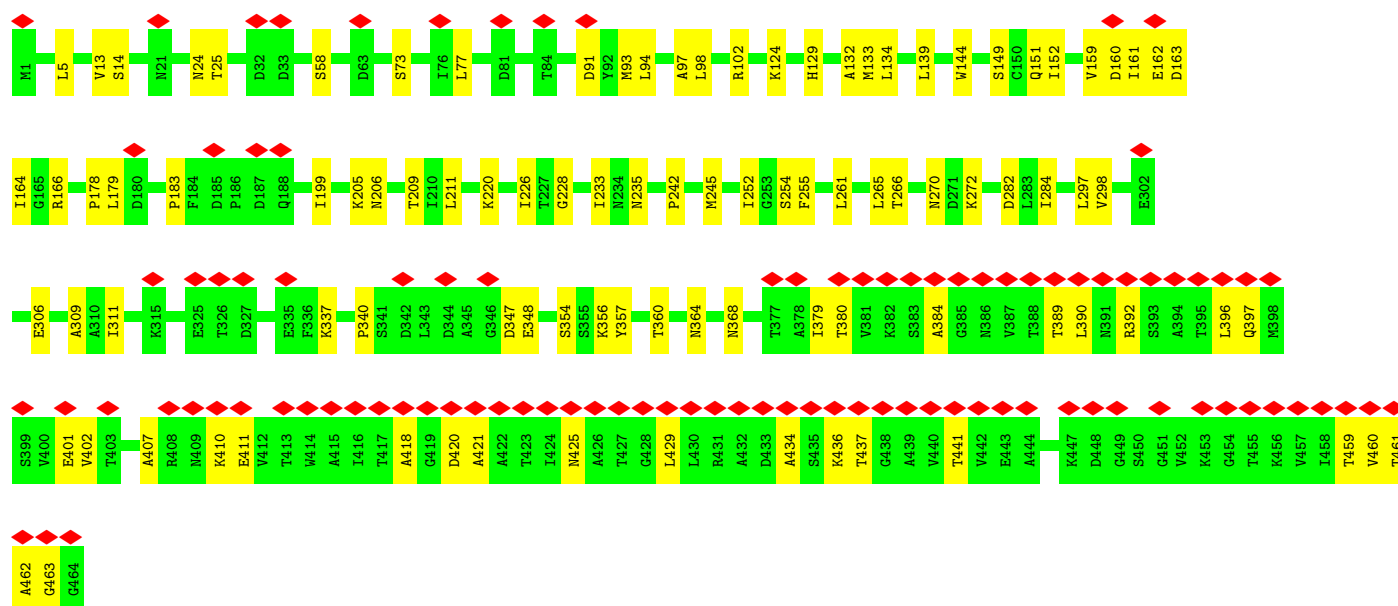
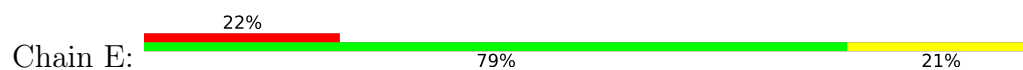
- Molecule 3: Distal tail protein



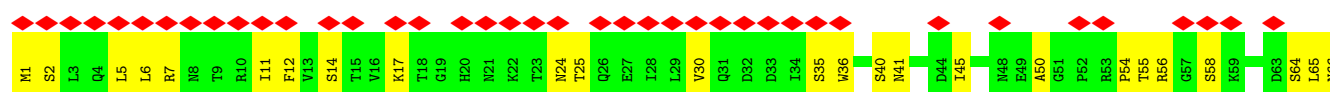
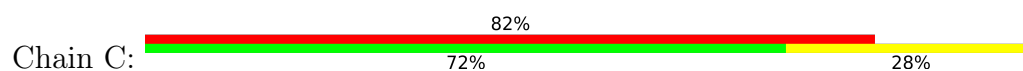
- Molecule 4: Tail tube protein

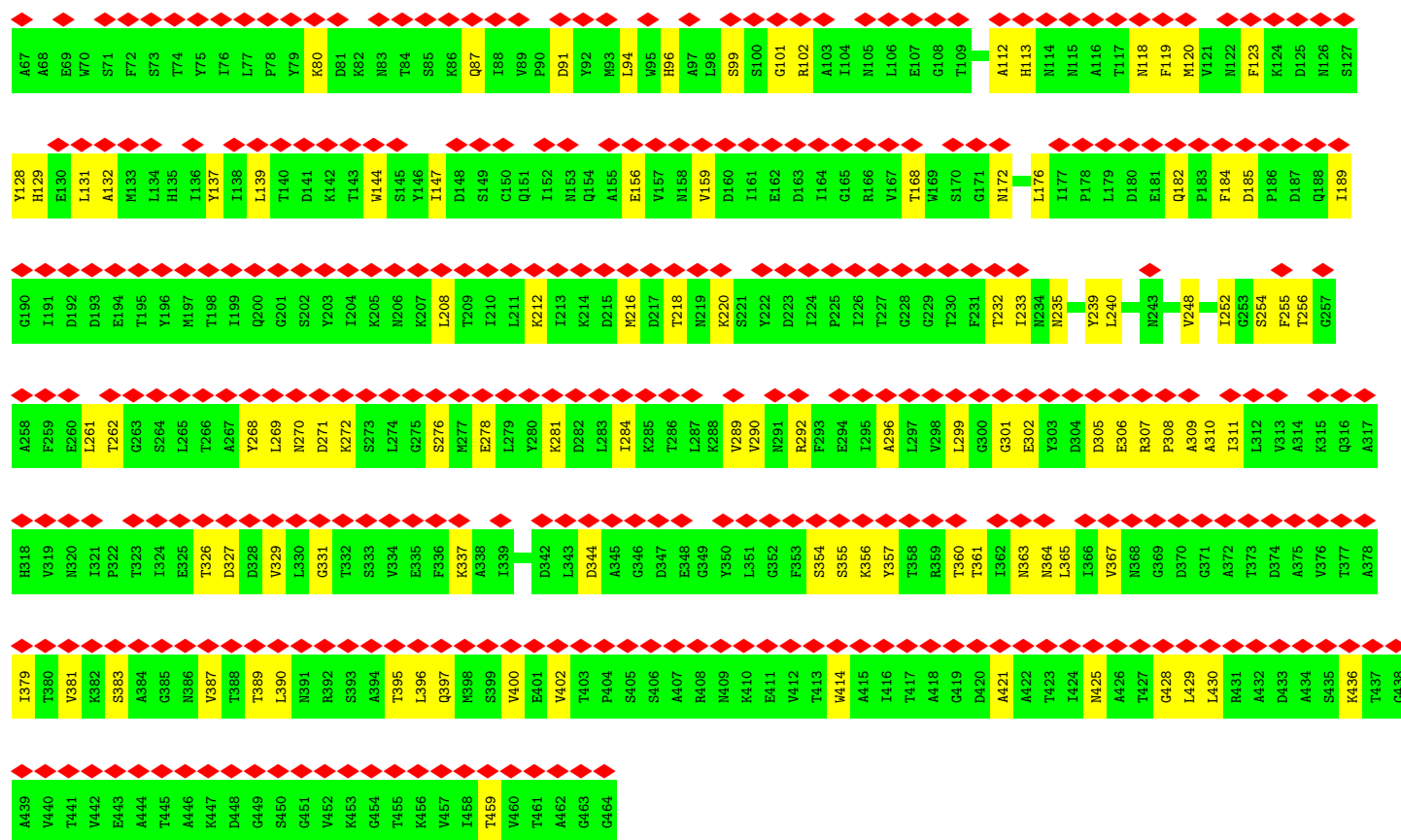


• Molecule 4: Tail tube protein

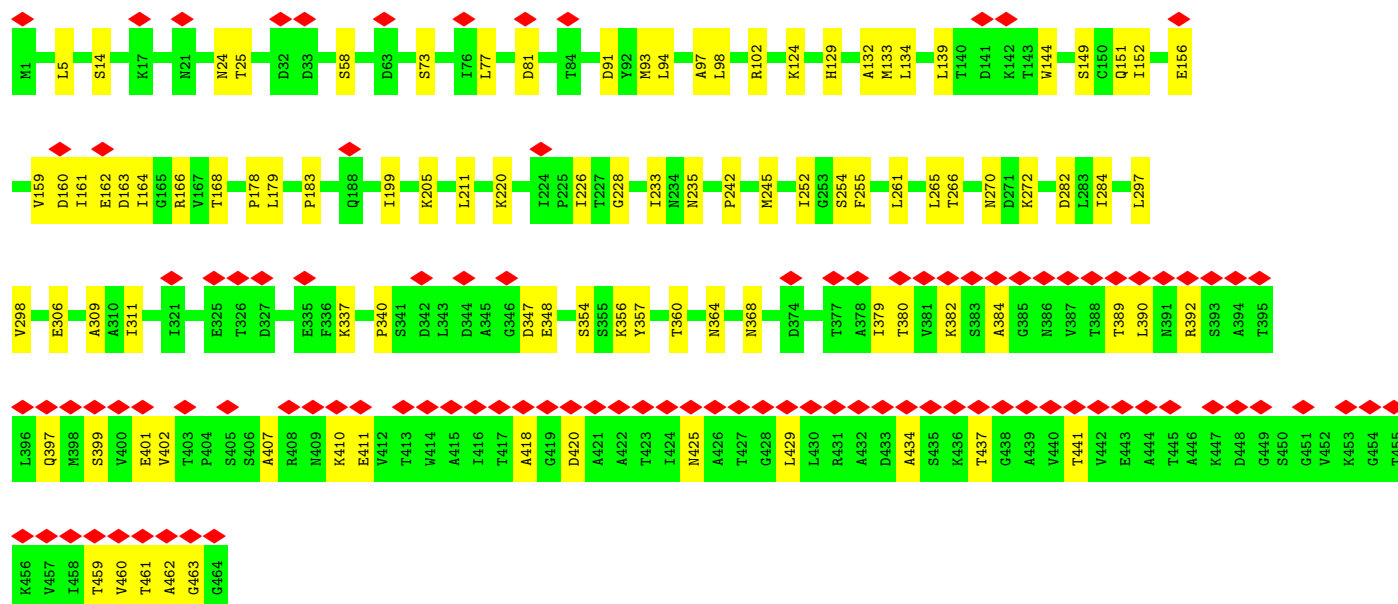
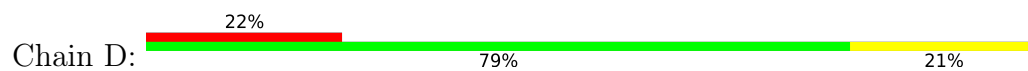


• Molecule 4: Tail tube protein

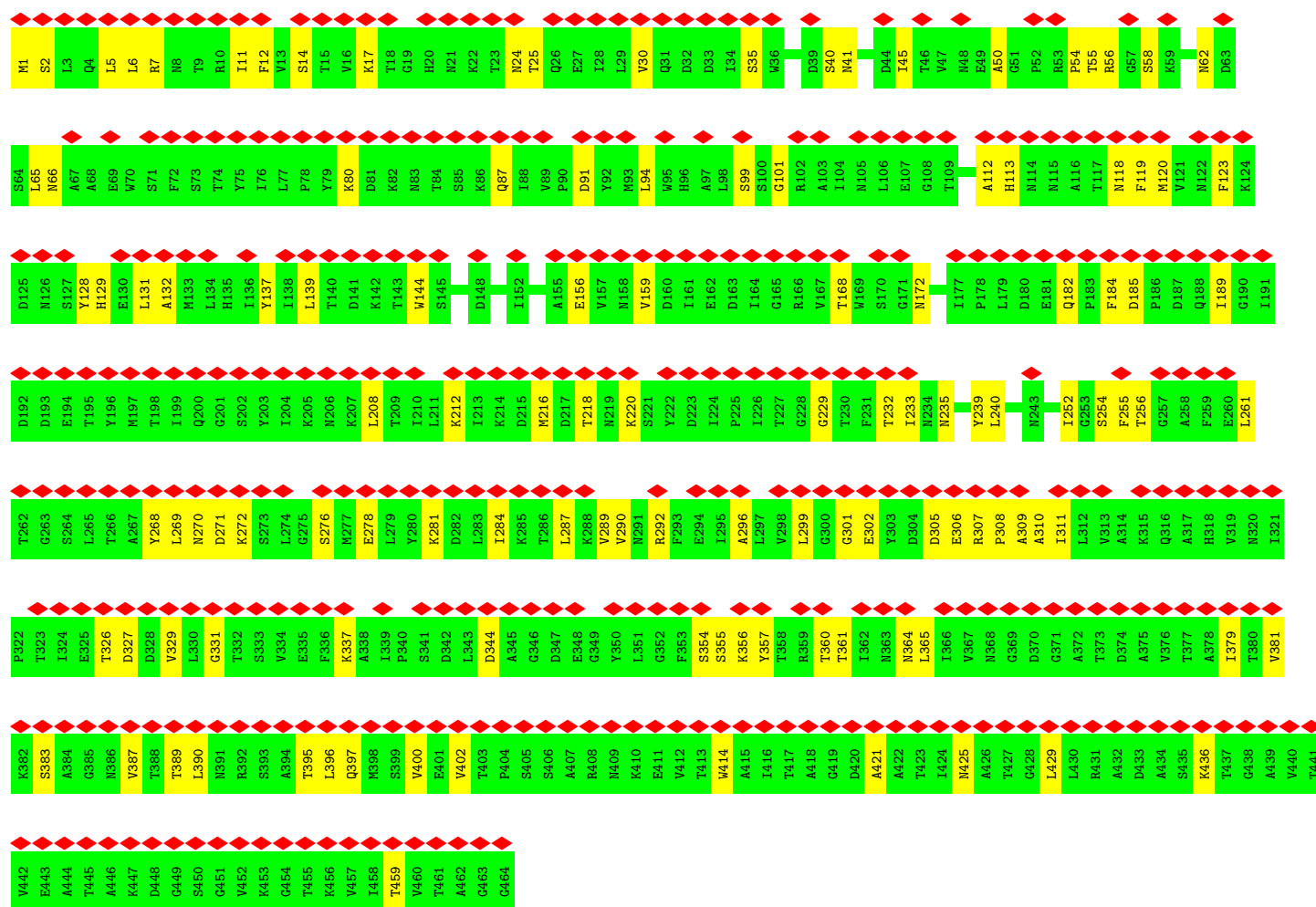
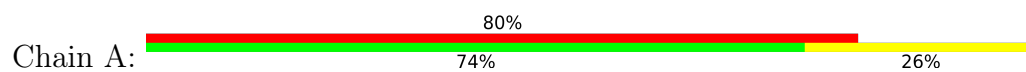




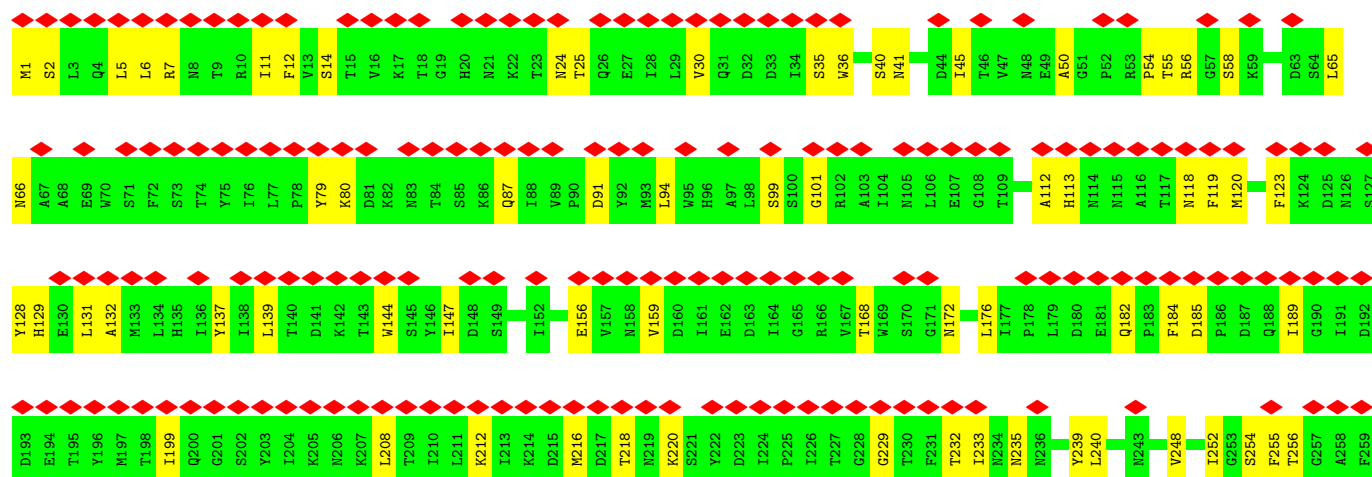
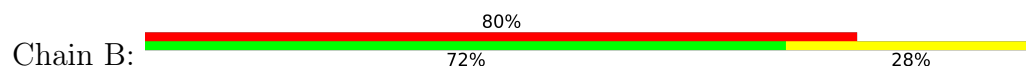
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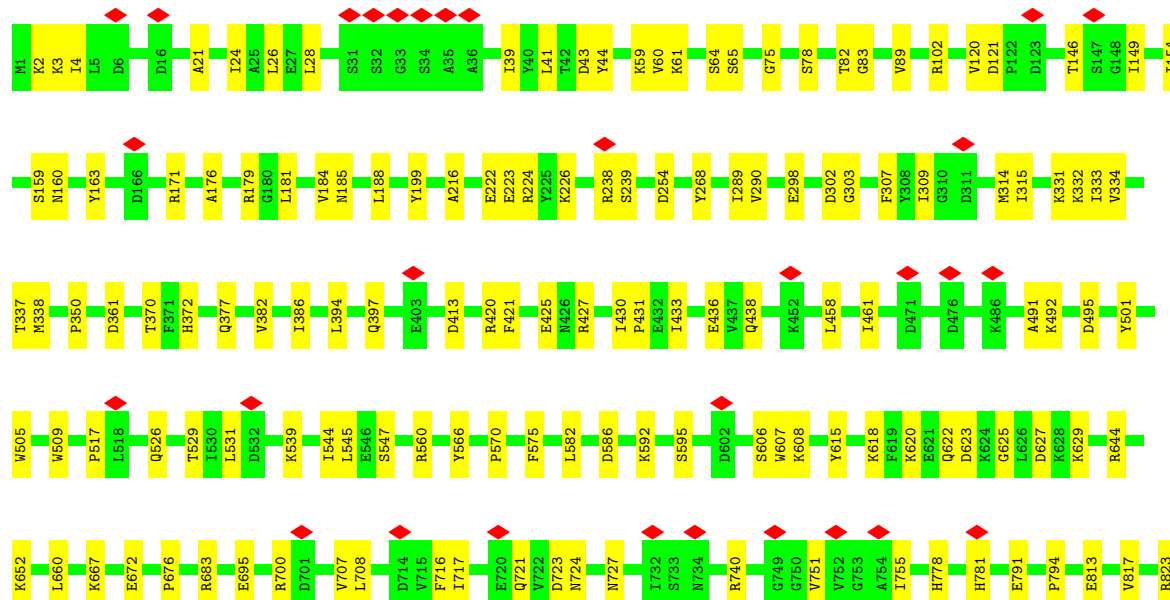


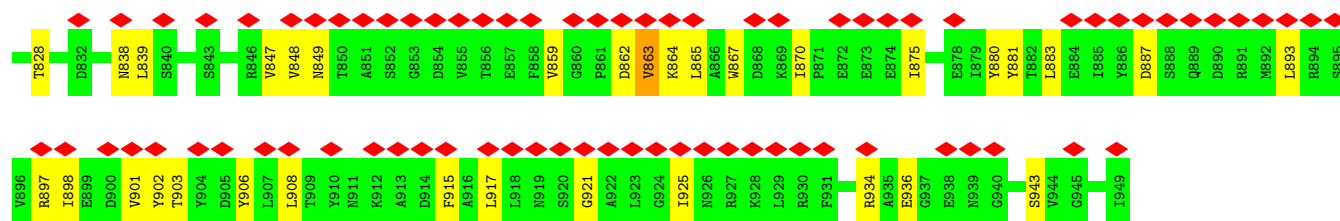
[illegible]

- Molecule 5: Pore-forming tail tip protein pb2

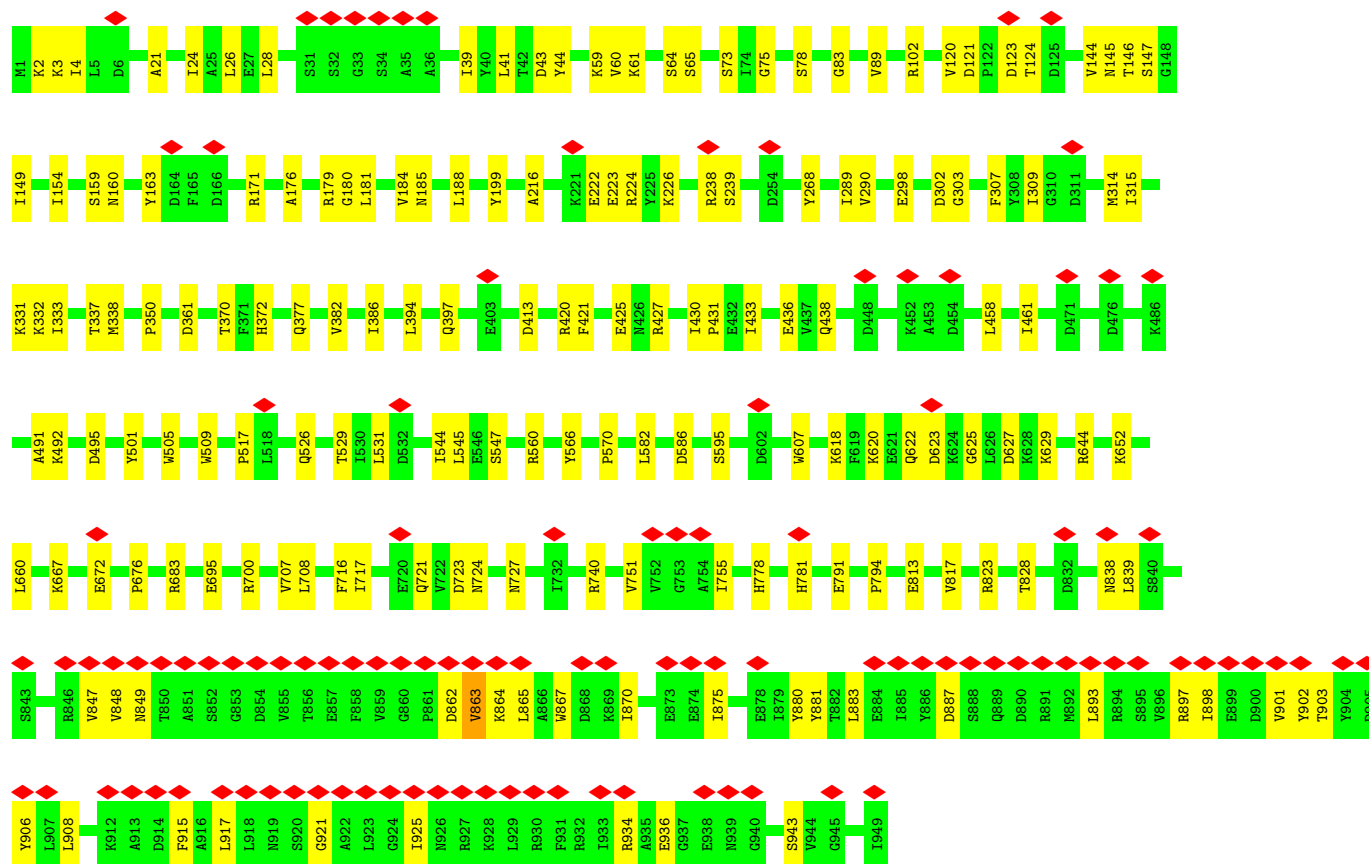
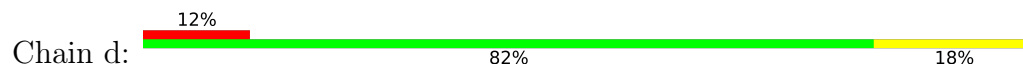
Chain g:

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

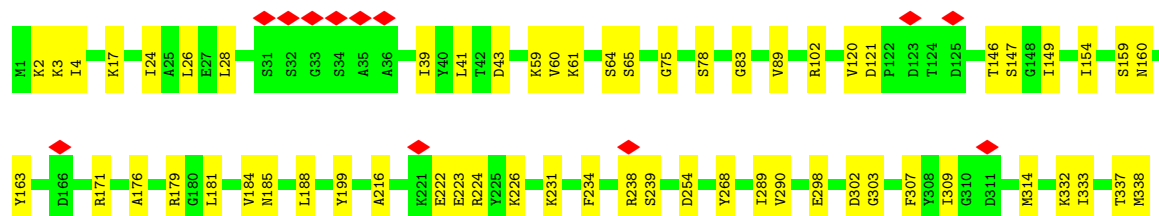
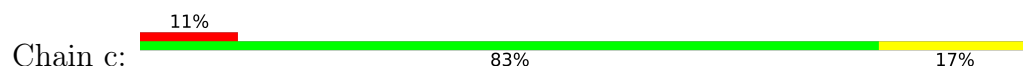




• Molecule 6: Probable baseplate hub protein



• Molecule 6: Probable baseplate hub protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	9290	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.218	Depositor
Minimum map value	-0.096	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0418	Depositor
Map size (Å)	459.34, 459.34, 459.34	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.351, 1.351, 1.351	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	J	0.13	0/1062	0.32	0/1443
1	K	0.13	0/1062	0.32	0/1443
1	L	0.27	0/1070	0.42	0/1453
1	M	0.13	0/1070	0.30	0/1453
1	N	0.13	0/1062	0.32	0/1443
1	O	0.13	0/1062	0.31	0/1443
1	P	0.27	0/1070	0.42	0/1453
1	Q	0.13	0/1070	0.30	0/1453
1	R	0.13	0/1062	0.32	0/1443
1	S	0.13	0/1062	0.31	0/1443
1	T	0.27	0/1070	0.43	0/1453
1	U	0.13	0/1070	0.30	0/1453
2	G	0.14	0/2483	0.27	0/3370
2	H	0.14	0/2483	0.27	0/3370
2	I	0.14	0/2483	0.27	0/3370
3	V	0.21	0/1649	0.31	0/2239
3	W	0.14	0/1649	0.27	0/2239
3	X	0.21	0/1649	0.31	0/2239
3	Y	0.14	0/1649	0.26	0/2239
3	Z	0.21	0/1649	0.31	0/2239
3	a	0.13	0/1649	0.26	0/2239
4	A	0.18	0/3604	0.35	0/4904
4	B	0.18	0/3604	0.35	0/4904
4	C	0.18	0/3604	0.35	0/4904
4	D	0.14	0/3604	0.30	0/4904
4	E	0.14	0/3604	0.30	0/4904
4	F	0.13	0/3604	0.30	0/4904
5	e	0.30	0/264	0.30	0/354
5	f	0.29	0/264	0.30	0/354
5	g	0.29	0/264	0.30	0/354
6	b	0.21	0/7741	0.36	0/10502
6	c	0.21	0/7741	0.36	0/10502
6	d	0.21	0/7741	0.36	0/10502
All	All	0.18	0/75774	0.33	0/102912

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	J	1048	0	1041	23	0
1	K	1048	0	1041	21	0
1	L	1056	0	1053	25	0
1	M	1056	0	1053	26	0
1	N	1048	0	1041	23	0
1	O	1048	0	1041	22	0
1	P	1056	0	1053	26	0
1	Q	1056	0	1053	25	0
1	R	1048	0	1041	23	0
1	S	1048	0	1041	21	0
1	T	1056	0	1053	27	0
1	U	1056	0	1053	27	0
2	G	2423	0	2349	39	0
2	H	2423	0	2349	36	0
2	I	2423	0	2349	37	0
3	V	1610	0	1590	32	0
3	W	1610	0	1590	25	0
3	X	1610	0	1590	28	0
3	Y	1610	0	1590	29	0
3	Z	1610	0	1590	26	0
3	a	1610	0	1590	24	0
4	A	3546	0	3509	101	0
4	B	3546	0	3509	106	0
4	C	3546	0	3509	107	0
4	D	3546	0	3509	63	0
4	E	3546	0	3509	64	0
4	F	3546	0	3509	64	0
5	e	262	0	245	4	0
5	f	262	0	245	3	0
5	g	262	0	245	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	b	7577	0	7410	121	0
6	c	7577	0	7410	115	0
6	d	7577	0	7410	120	0
All	All	74346	0	73170	1261	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 9.

The worst 5 of 1261 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Z:31:ASP:OD1	6:c:61:LYS:HE3	1.50	1.10
3:V:31:ASP:OD1	6:d:61:LYS:HE3	1.63	0.97
3:Z:31:ASP:OD1	6:c:61:LYS:CE	2.15	0.94
3:X:31:ASP:OD1	6:b:61:LYS:HE3	1.70	0.91
1:L:100:ASN:HB3	2:G:231:ARG:HH22	1.40	0.87

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
1	K	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
1	L	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
1	M	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
1	N	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
1	O	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
1	P	138/140 (99%)	133 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
1	R	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
1	S	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
1	T	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
1	U	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
2	G	296/298 (99%)	286 (97%)	10 (3%)	0	100	100
2	H	296/298 (99%)	286 (97%)	10 (3%)	0	100	100
2	I	296/298 (99%)	286 (97%)	10 (3%)	0	100	100
3	V	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
3	W	202/204 (99%)	197 (98%)	5 (2%)	0	100	100
3	X	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
3	Y	202/204 (99%)	196 (97%)	6 (3%)	0	100	100
3	Z	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
3	a	202/204 (99%)	197 (98%)	5 (2%)	0	100	100
4	A	462/464 (100%)	445 (96%)	17 (4%)	0	100	100
4	B	462/464 (100%)	444 (96%)	18 (4%)	0	100	100
4	C	462/464 (100%)	445 (96%)	17 (4%)	0	100	100
4	D	462/464 (100%)	446 (96%)	16 (4%)	0	100	100
4	E	462/464 (100%)	446 (96%)	16 (4%)	0	100	100
4	F	462/464 (100%)	446 (96%)	16 (4%)	0	100	100
5	e	33/1219 (3%)	32 (97%)	1 (3%)	0	100	100
5	f	33/1219 (3%)	32 (97%)	1 (3%)	0	100	100
5	g	33/1219 (3%)	32 (97%)	1 (3%)	0	100	100
6	b	947/949 (100%)	907 (96%)	40 (4%)	0	100	100
6	c	947/949 (100%)	907 (96%)	40 (4%)	0	100	100
6	d	947/949 (100%)	907 (96%)	40 (4%)	0	100	100
All	All	9462/13086 (72%)	9122 (96%)	340 (4%)	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	J	118/119 (99%)	118 (100%)	0	100	100
1	K	118/119 (99%)	118 (100%)	0	100	100
1	L	119/119 (100%)	119 (100%)	0	100	100
1	M	119/119 (100%)	119 (100%)	0	100	100
1	N	118/119 (99%)	118 (100%)	0	100	100
1	O	118/119 (99%)	118 (100%)	0	100	100
1	P	119/119 (100%)	119 (100%)	0	100	100
1	Q	119/119 (100%)	119 (100%)	0	100	100
1	R	118/119 (99%)	118 (100%)	0	100	100
1	S	118/119 (99%)	118 (100%)	0	100	100
1	T	119/119 (100%)	119 (100%)	0	100	100
1	U	119/119 (100%)	119 (100%)	0	100	100
2	G	273/273 (100%)	273 (100%)	0	100	100
2	H	273/273 (100%)	273 (100%)	0	100	100
2	I	273/273 (100%)	273 (100%)	0	100	100
3	V	181/181 (100%)	181 (100%)	0	100	100
3	W	181/181 (100%)	181 (100%)	0	100	100
3	X	181/181 (100%)	181 (100%)	0	100	100
3	Y	181/181 (100%)	181 (100%)	0	100	100
3	Z	181/181 (100%)	181 (100%)	0	100	100
3	a	181/181 (100%)	181 (100%)	0	100	100
4	A	394/394 (100%)	394 (100%)	0	100	100
4	B	394/394 (100%)	394 (100%)	0	100	100
4	C	394/394 (100%)	394 (100%)	0	100	100
4	D	394/394 (100%)	394 (100%)	0	100	100
4	E	394/394 (100%)	394 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	F	394/394 (100%)	394 (100%)	0	100	100
5	e	28/980 (3%)	28 (100%)	0	100	100
5	f	28/980 (3%)	28 (100%)	0	100	100
5	g	28/980 (3%)	28 (100%)	0	100	100
6	b	834/834 (100%)	833 (100%)	1 (0%)	88	87
6	c	834/834 (100%)	833 (100%)	1 (0%)	88	87
6	d	834/834 (100%)	833 (100%)	1 (0%)	88	87
All	All	8277/11139 (74%)	8274 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	b	863	VAL
6	d	863	VAL
6	c	863	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
6	d	721	GLN
6	d	788	GLN
6	c	426	ASN
4	A	151	GLN
4	A	87	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14733. These allow visual inspection of the internal detail of the map and identification of artifacts.

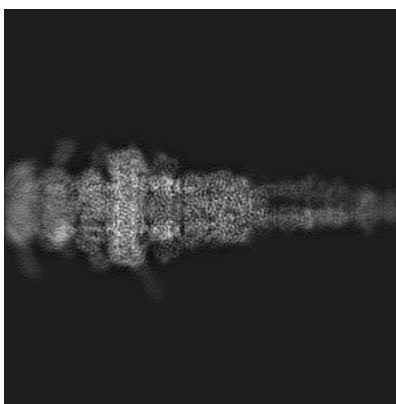
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

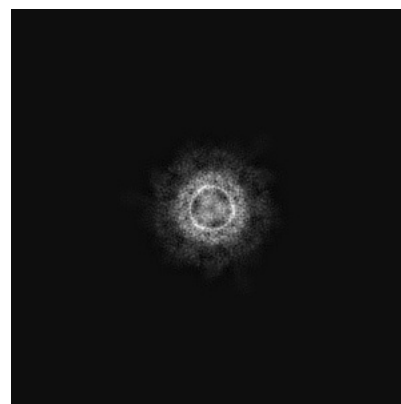
6.1.1 Primary map



X

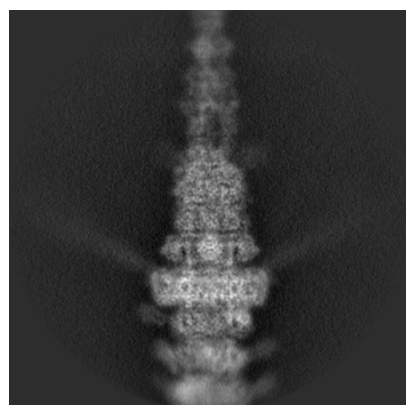


Y

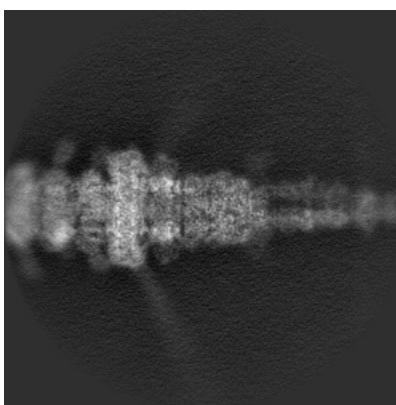


Z

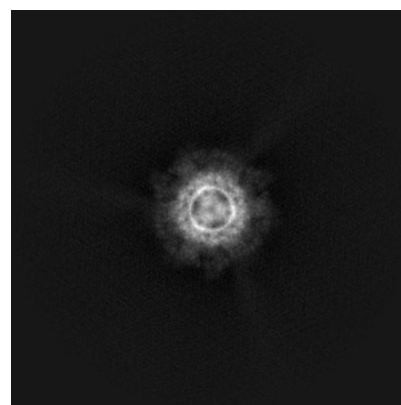
6.1.2 Raw map



X



Y

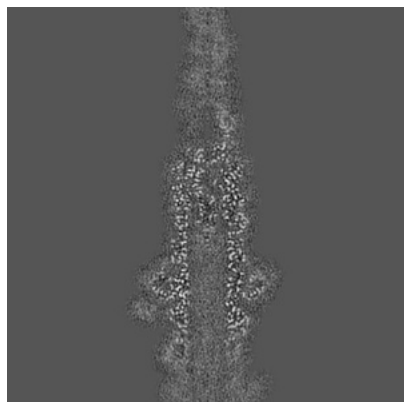


Z

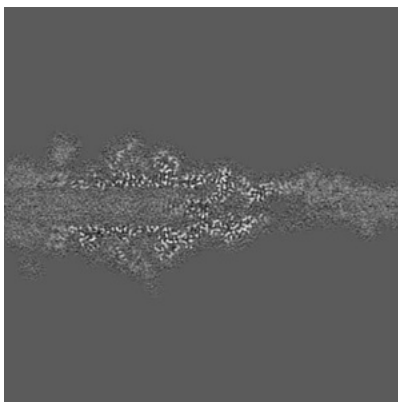
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

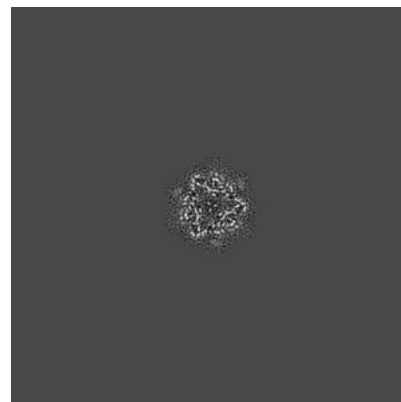
6.2.1 Primary map



X Index: 170

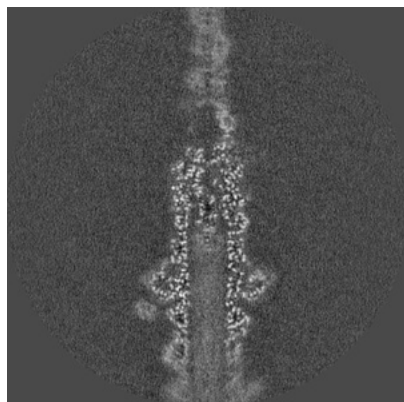


Y Index: 170

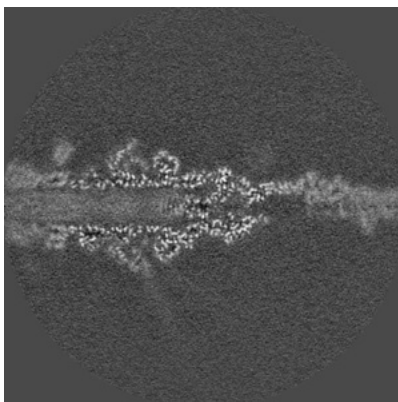


Z Index: 170

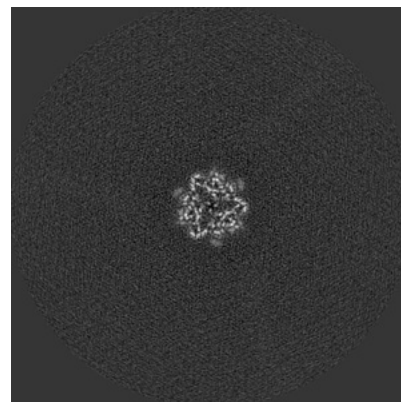
6.2.2 Raw map



X Index: 170



Y Index: 170



Z Index: 170

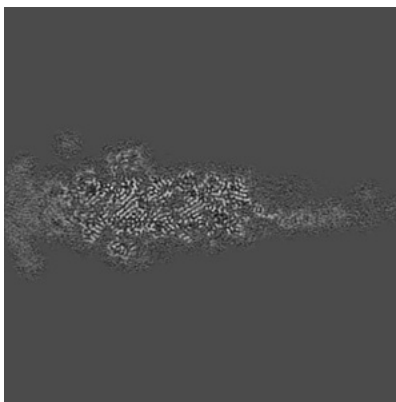
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

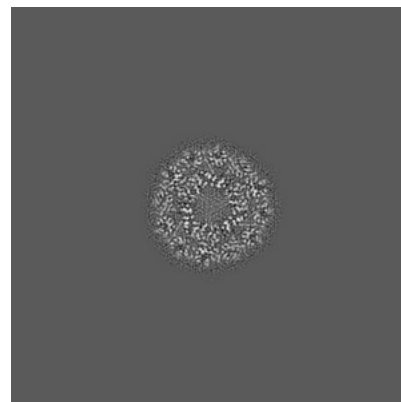
6.3.1 Primary map



X Index: 186

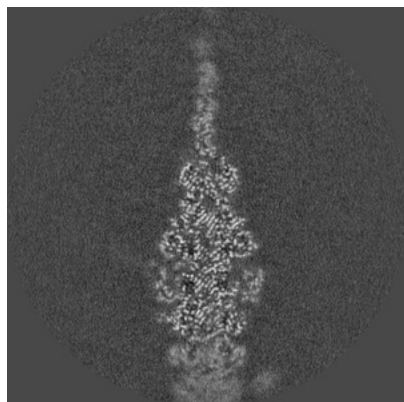


Y Index: 153

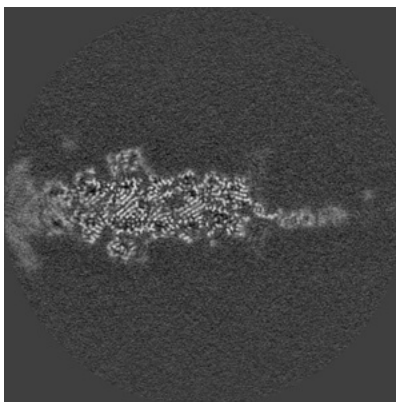


Z Index: 97

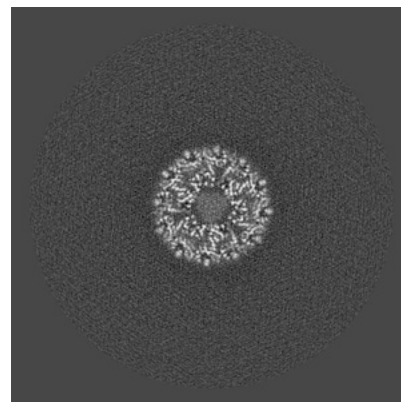
6.3.2 Raw map



X Index: 187



Y Index: 153

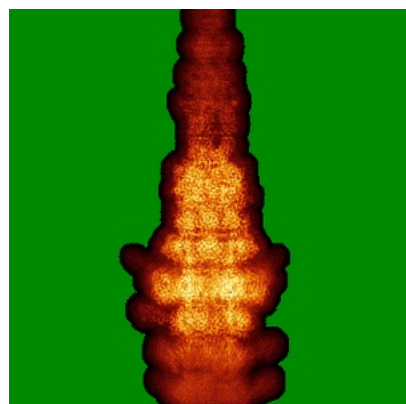


Z Index: 96

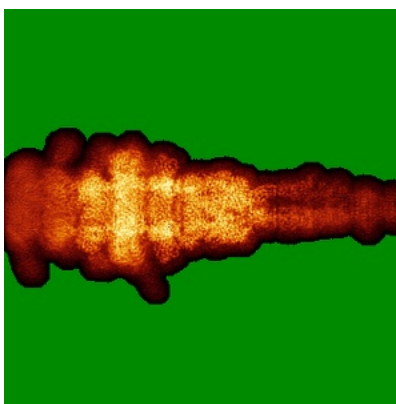
The images above show the largest variance slices of the map in three orthogonal directions.

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

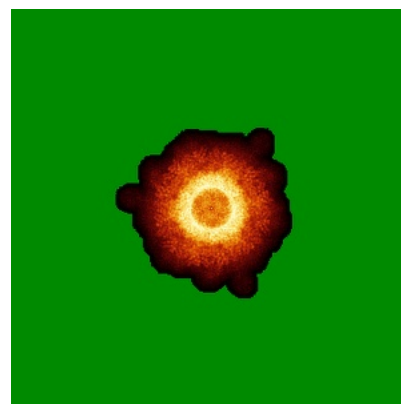
6.4.1 Primary map



X

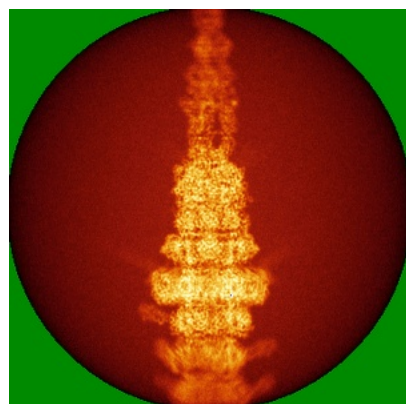


Y

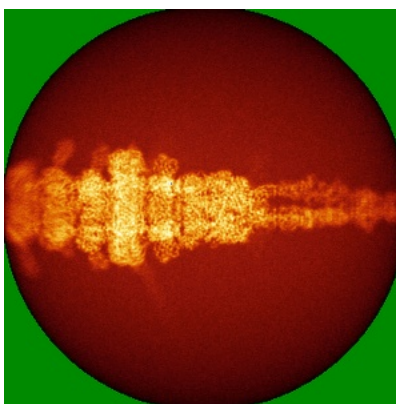


Z

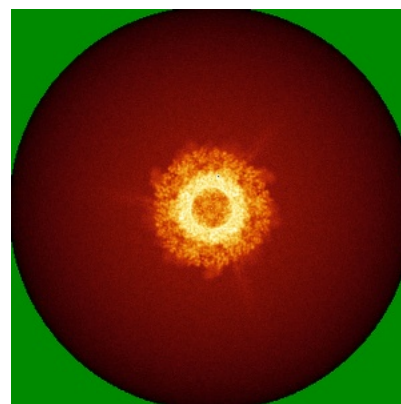
6.4.2 Raw map



X



Y

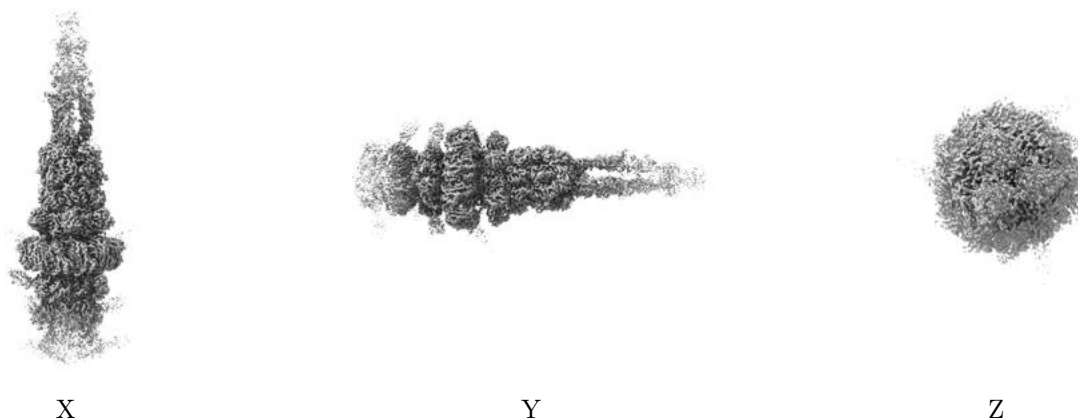


Z

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

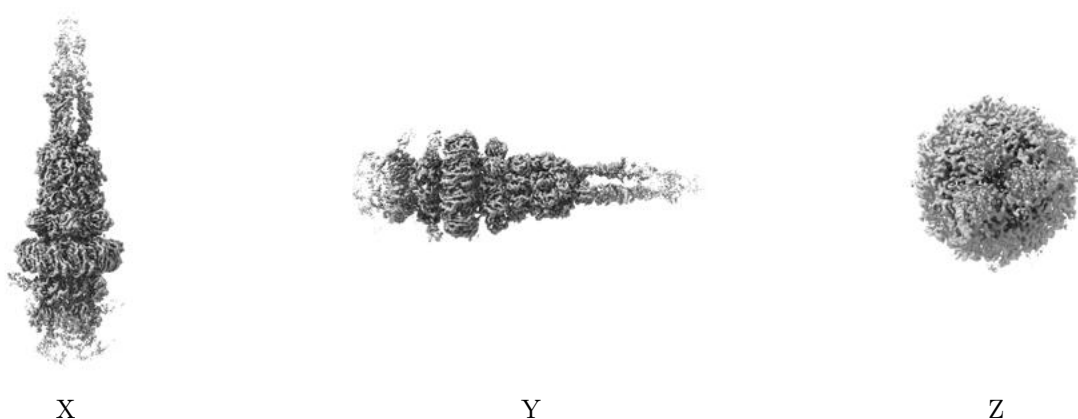
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0418. 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.

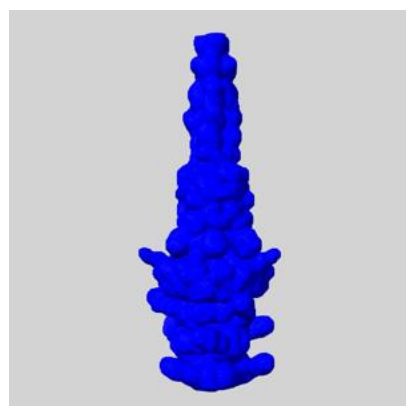
6.6 Mask visualisation [i](#)

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

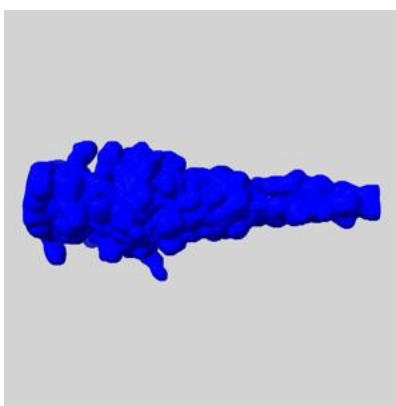
A mask typically either:

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

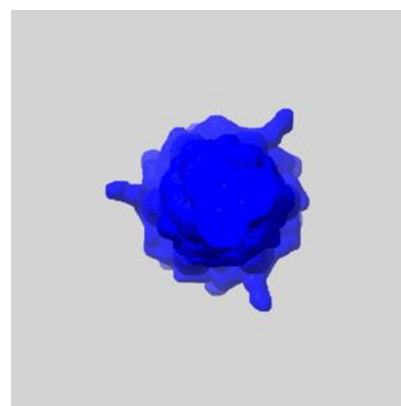
6.6.1 emd_14733_msk_1.map [i](#)



X



Y

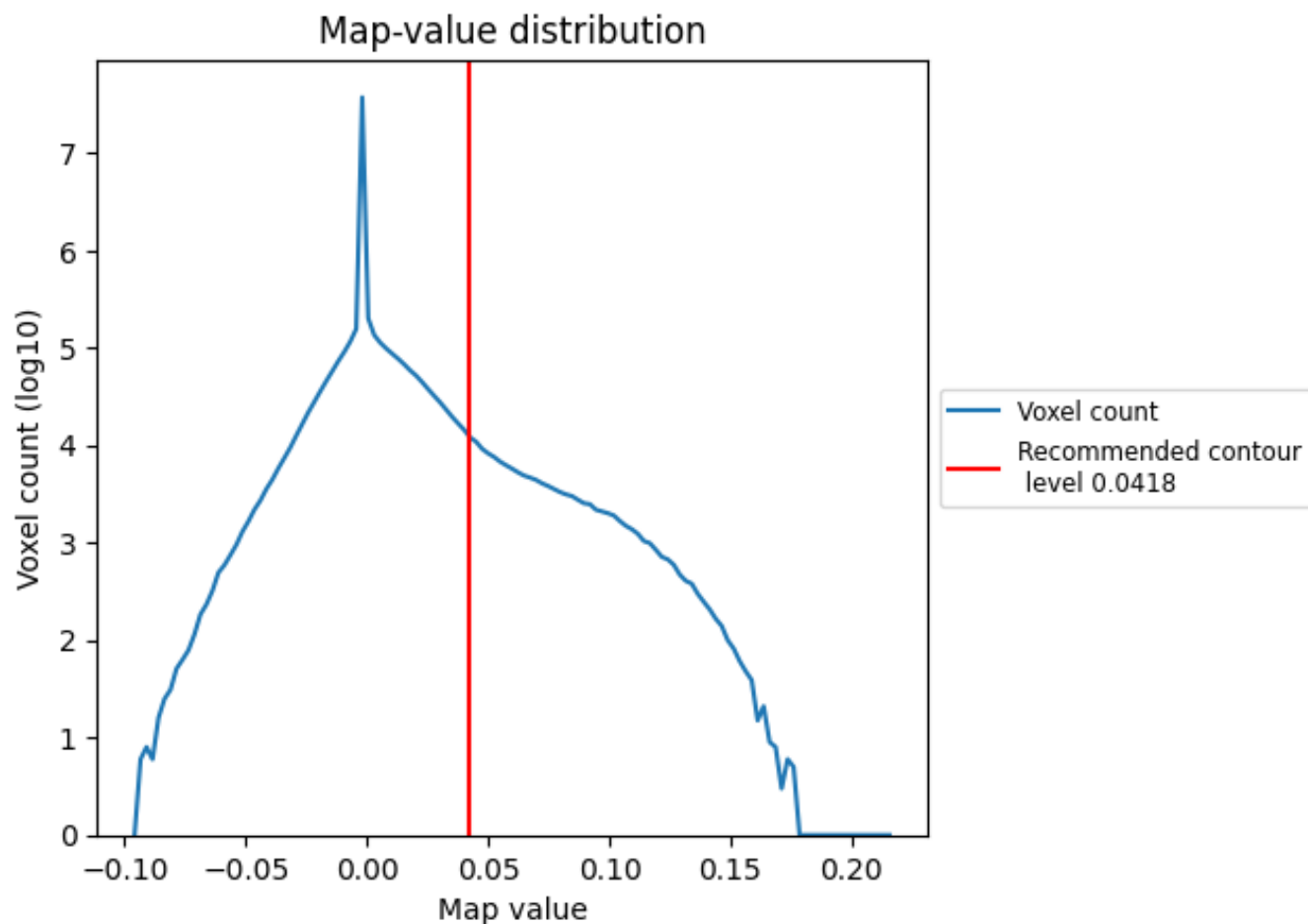


Z

7 Map analysis [i](#)

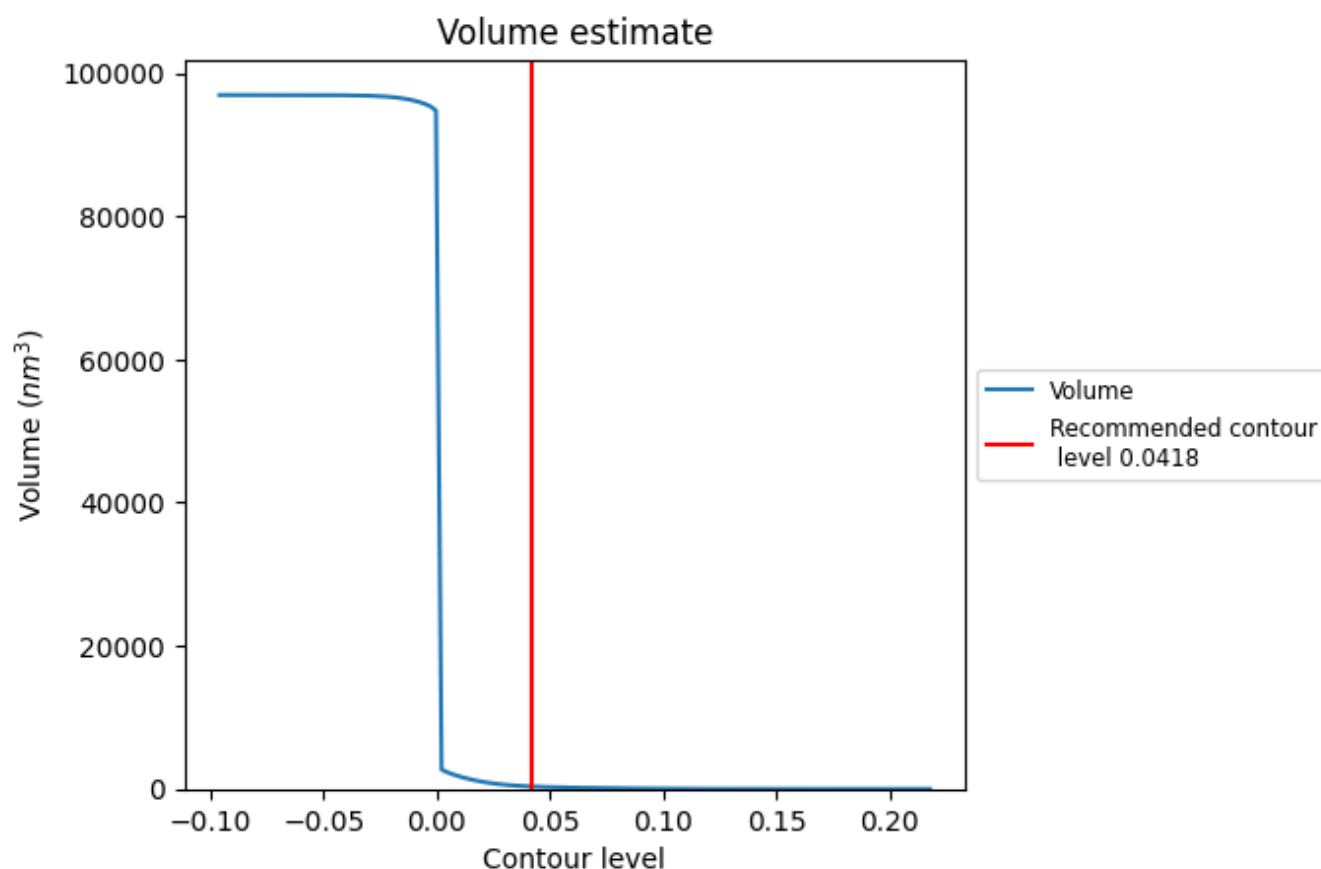
This section contains the results of statistical analysis of the map.

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.

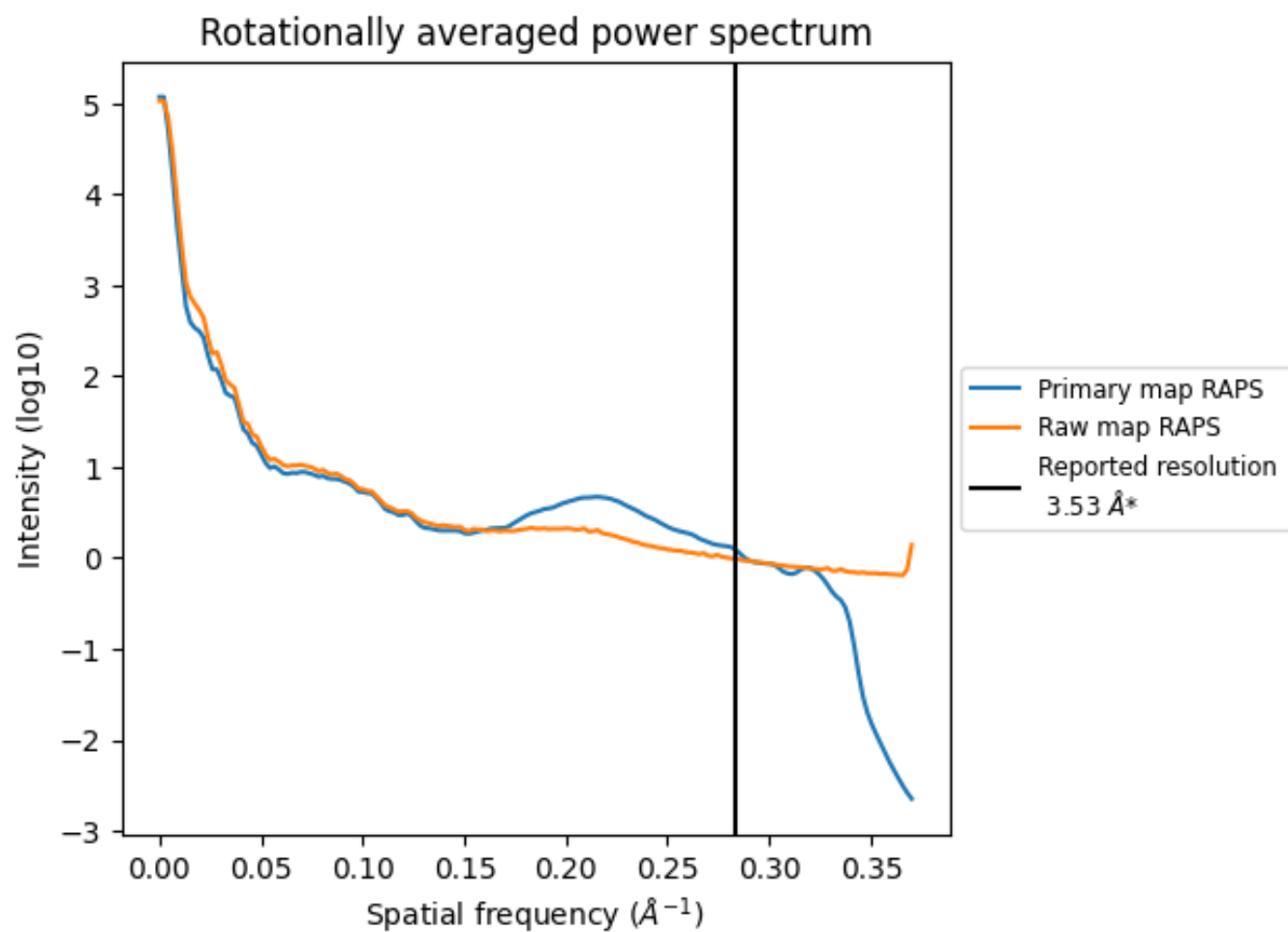
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 346 nm^3 ; this corresponds to an approximate mass of 313 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 ⓘ

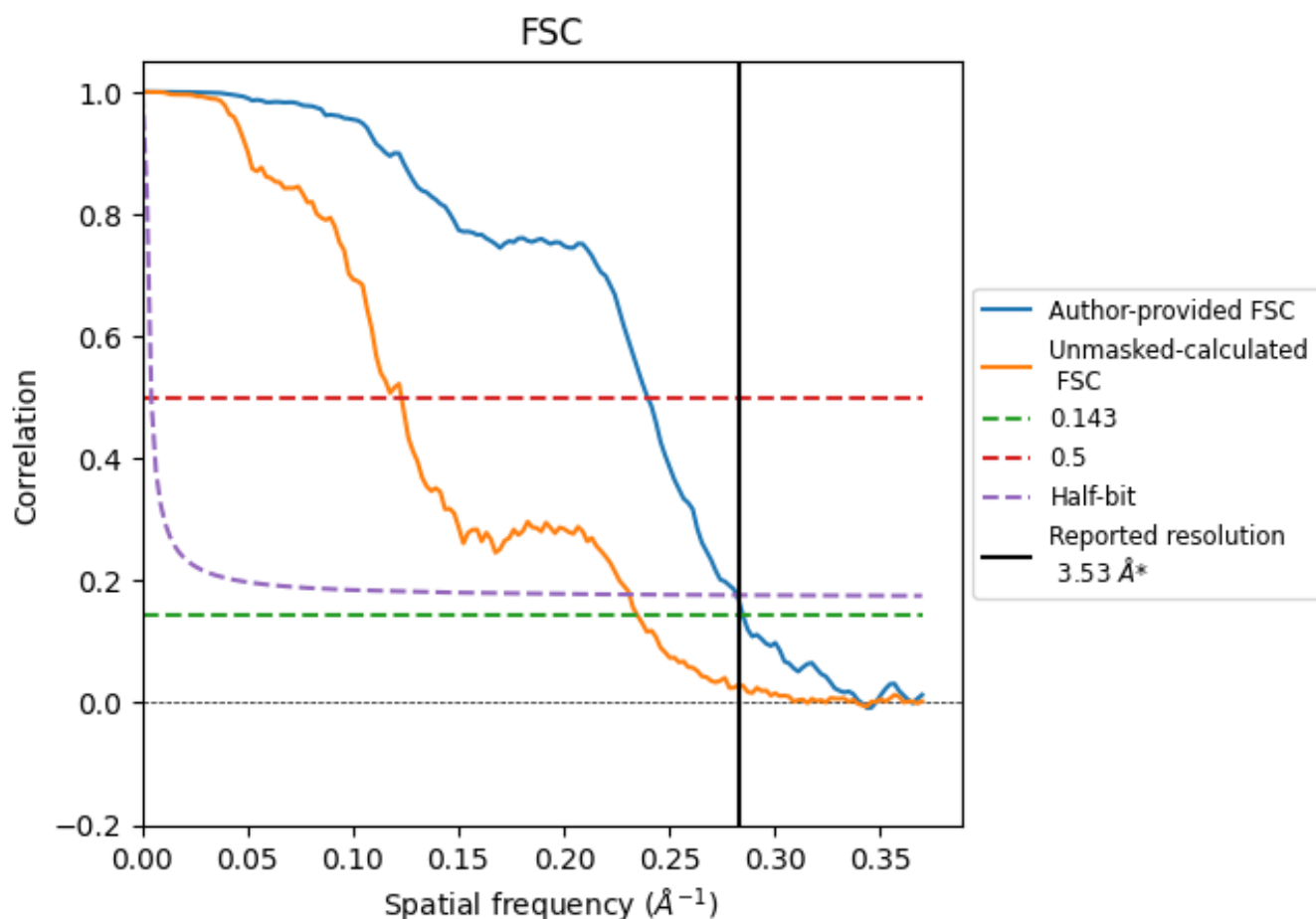


*Reported resolution corresponds to spatial frequency of 0.283 Å⁻¹

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 $0.283 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

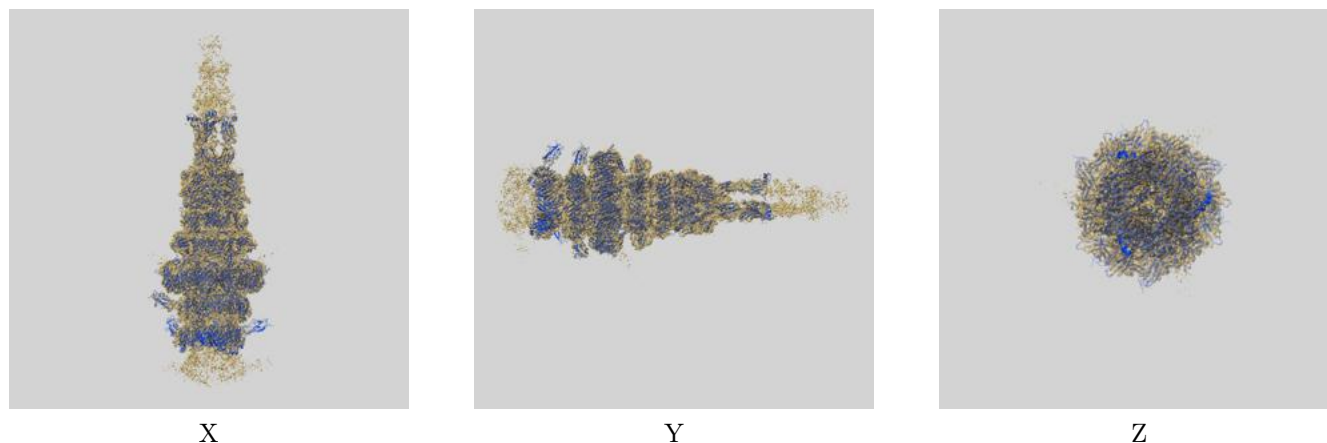
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.53	-	-
Author-provided FSC curve	3.51	4.17	3.54
Unmasked-calculated*	4.26	8.13	4.33

*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 4.26 differs from the reported value 3.53 by more than 10 %

9 Map-model fit [i](#)

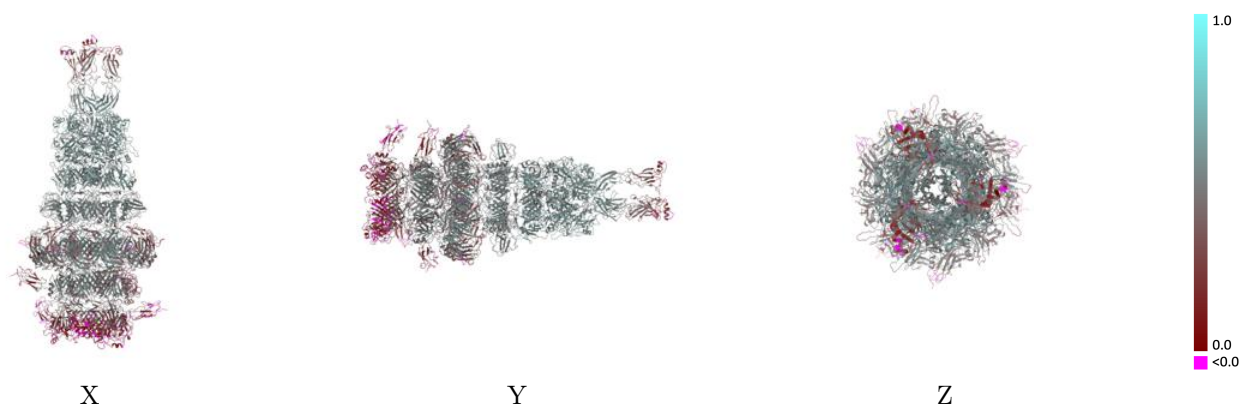
This section contains information regarding the fit between EMDB map EMD-14733 and PDB model 7ZHJ. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



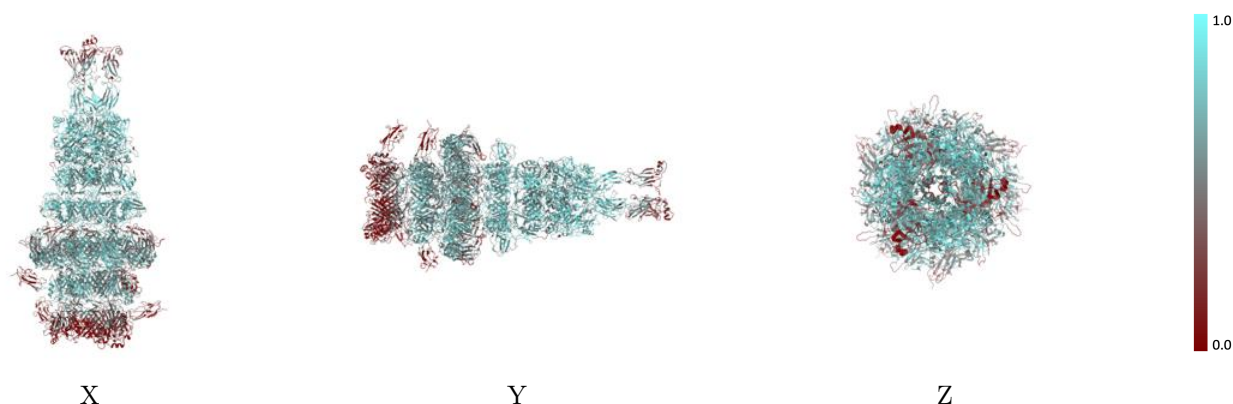
The images above show the 3D surface view of the map at the recommended contour level 0.0418 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



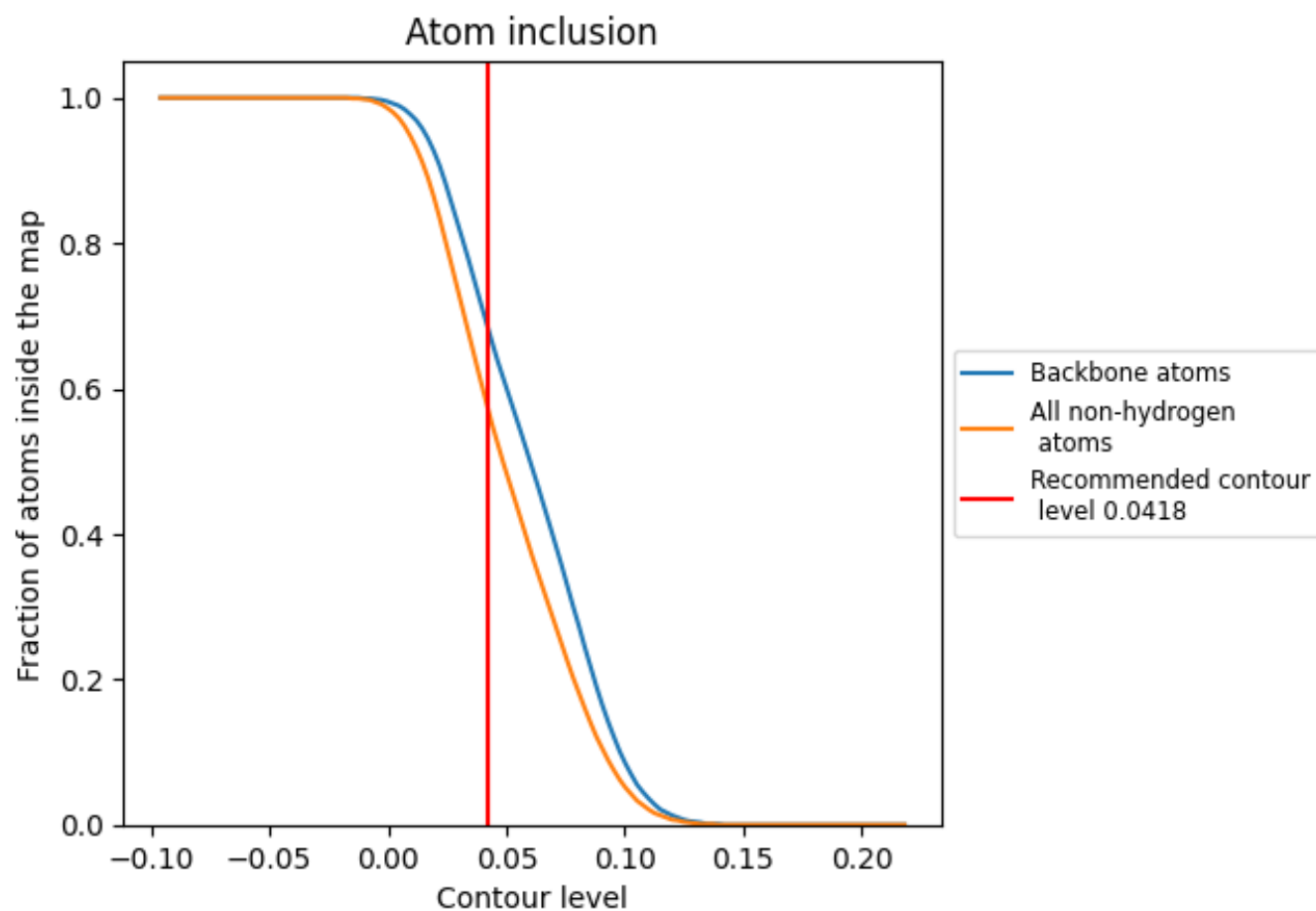
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0418).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 58% 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 (0.0418) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5780	 0.4380
A	 0.2110	 0.2100
B	 0.2090	 0.2060
C	 0.2040	 0.2020
D	 0.5810	 0.4330
E	 0.5820	 0.4350
F	 0.5830	 0.4290
G	 0.7250	 0.5260
H	 0.7280	 0.5280
I	 0.7290	 0.5250
J	 0.4770	 0.3850
K	 0.4860	 0.3920
L	 0.4990	 0.3920
M	 0.5800	 0.4360
N	 0.4740	 0.3830
O	 0.4890	 0.3910
P	 0.5120	 0.3940
Q	 0.5680	 0.4290
R	 0.4660	 0.3800
S	 0.4820	 0.3850
T	 0.5120	 0.3840
U	 0.5630	 0.4250
V	 0.7060	 0.4990
W	 0.7120	 0.5030
X	 0.7070	 0.5000
Y	 0.7180	 0.4990
Z	 0.7070	 0.5010
a	 0.7170	 0.5010
b	 0.6830	 0.5170
c	 0.6790	 0.5130
d	 0.6800	 0.5180
e	 0.6390	 0.5000
f	 0.6550	 0.4940
g	 0.6630	 0.5000

