



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 04:15 PM UTC

PDB ID : 9G8S / pdb_00009g8s
EMDB ID : EMD-51138
Title : C3 reconstruction of extended phiCD508 needle
Authors : Wilson, J.S.; Fagan, R.P.; Bullough, P.A.
Deposited on : 2024-07-23
Resolution : 3.96 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

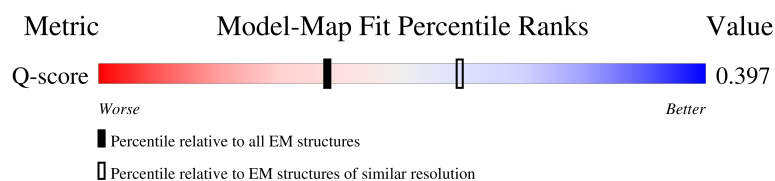
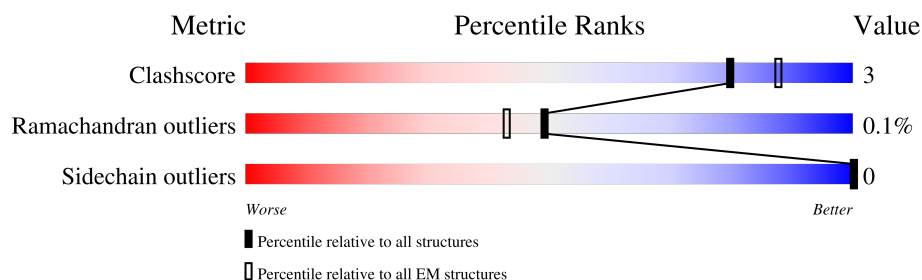
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.96 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	7646 (3.46 - 4.46)

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	378	
1	B	378	
1	C	378	
1	D	378	

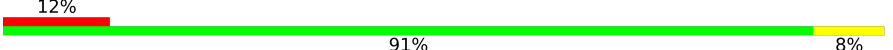
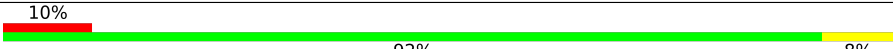
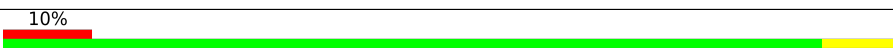
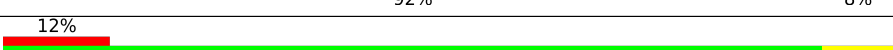
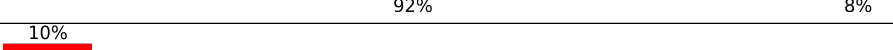
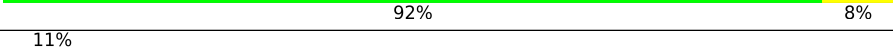
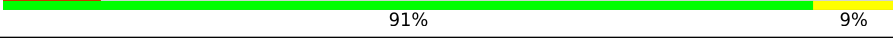
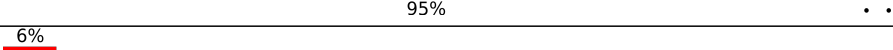
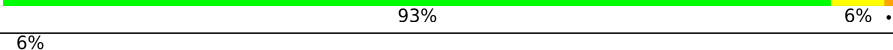
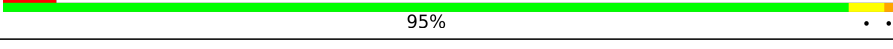
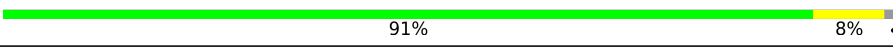
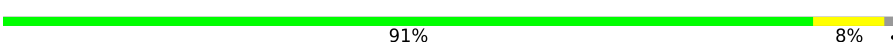
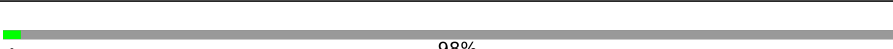
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Mol	Chain	Length	Quality of chain
1	E	378	
1	F	378	
1	G	378	
1	H	378	
1	I	378	
1	J	378	
1	K	378	
1	L	378	
2	M	157	
2	N	157	
2	O	157	
2	P	157	
2	Q	157	
2	R	157	
3	S	223	
3	T	223	
3	U	223	
3	V	223	
3	W	223	
3	X	223	
4	Y	130	
4	Z	130	
4	a	130	
4	b	130	
4	c	130	

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Mol	Chain	Length	Quality of chain
4	d	130	
5	e	460	
5	f	460	
5	g	460	
5	h	460	
5	i	460	
5	j	460	
6	k	125	
6	l	125	
6	m	125	
6	n	125	
6	o	125	
6	p	125	
7	r	112	
7	s	112	
7	v	112	
8	q	316	
8	t	316	
8	u	316	
9	w	1424	
9	x	1424	
9	y	1424	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 193849 atoms, of which 97341 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 Baseplate J family protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	C	376	Total	C	H	N	O	S	0	0
			5801	1830	2899	472	596	4		
1	G	374	Total	C	H	N	O	S	0	0
			5773	1822	2885	470	592	4		
1	A	376	Total	C	H	N	O	S	0	0
			5801	1830	2899	472	596	4		
1	H	374	Total	C	H	N	O	S	0	0
			5773	1822	2885	470	592	4		
1	B	376	Total	C	H	N	O	S	0	0
			5801	1830	2899	472	596	4		
1	I	374	Total	C	H	N	O	S	0	0
			5773	1822	2885	470	592	4		
1	D	376	Total	C	H	N	O	S	0	0
			5801	1830	2899	472	596	4		
1	J	374	Total	C	H	N	O	S	0	0
			5773	1822	2885	470	592	4		
1	E	376	Total	C	H	N	O	S	0	0
			5801	1830	2899	472	596	4		
1	K	374	Total	C	H	N	O	S	0	0
			5773	1822	2885	470	592	4		
1	F	376	Total	C	H	N	O	S	0	0
			5801	1830	2899	472	596	4		
1	L	374	Total	C	H	N	O	S	0	0
			5773	1822	2885	470	592	4		

- Molecule 2 is a protein called XkdT-related protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	N	157	Total	C	H	N	O	S	0	0
			2559	811	1295	205	241	7		
2	M	157	Total	C	H	N	O	S	0	0
			2559	811	1295	205	241	7		
2	O	157	Total	C	H	N	O	S	0	0
			2559	811	1295	205	241	7		

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Mol	Chain	Residues	Atoms						AltConf	Trace
2	P	157	Total	C	H	N	O	S	0	0
			2559	811	1295	205	241	7		
2	Q	157	Total	C	H	N	O	S	0	0
			2559	811	1295	205	241	7		
2	R	157	Total	C	H	N	O	S	0	0
			2559	811	1295	205	241	7		

- Molecule 3 is a protein called Peptidoglycan-binding LysM protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	T	197	Total	C	H	N	O	S	0	0
			3265	1030	1663	272	299	1		
3	S	197	Total	C	H	N	O	S	0	0
			3265	1030	1663	272	299	1		
3	U	197	Total	C	H	N	O	S	0	0
			3265	1030	1663	272	299	1		
3	V	197	Total	C	H	N	O	S	0	0
			3265	1030	1663	272	299	1		
3	W	197	Total	C	H	N	O	S	0	0
			3265	1030	1663	272	299	1		
3	X	197	Total	C	H	N	O	S	0	0
			3265	1030	1663	272	299	1		

- Molecule 4 is a protein called XkdM-related protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	Z	130	Total	C	H	N	O	S	0	0
			2053	651	1027	166	206	3		
4	Y	130	Total	C	H	N	O	S	0	0
			2053	651	1027	166	206	3		
4	a	130	Total	C	H	N	O	S	0	0
			2053	651	1027	166	206	3		
4	b	130	Total	C	H	N	O	S	0	0
			2053	651	1027	166	206	3		
4	c	130	Total	C	H	N	O	S	0	0
			2053	651	1027	166	206	3		
4	d	130	Total	C	H	N	O	S	0	0
			2053	651	1027	166	206	3		

- Molecule 5 is a protein called Tail sheath.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	g	460	Total	C	H	N	O	S	0	0
			7242	2299	3627	585	721	10		
5	e	460	Total	C	H	N	O	S	0	0
			7242	2299	3627	585	721	10		
5	f	460	Total	C	H	N	O	S	0	0
			7242	2299	3627	585	721	10		
5	h	460	Total	C	H	N	O	S	0	0
			7242	2299	3627	585	721	10		
5	i	460	Total	C	H	N	O	S	0	0
			7242	2299	3627	585	721	10		
5	j	460	Total	C	H	N	O	S	0	0
			7242	2299	3627	585	721	10		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	23	ALA	THR	conflict	UNP J9QE70
g	28	ALA	SER	conflict	UNP J9QE70
g	29	ALA	THR	conflict	UNP J9QE70
g	30	ALA	ASN	conflict	UNP J9QE70
e	23	ALA	THR	conflict	UNP J9QE70
e	28	ALA	SER	conflict	UNP J9QE70
e	29	ALA	THR	conflict	UNP J9QE70
e	30	ALA	ASN	conflict	UNP J9QE70
f	23	ALA	THR	conflict	UNP J9QE70
f	28	ALA	SER	conflict	UNP J9QE70
f	29	ALA	THR	conflict	UNP J9QE70
f	30	ALA	ASN	conflict	UNP J9QE70
h	23	ALA	THR	conflict	UNP J9QE70
h	28	ALA	SER	conflict	UNP J9QE70
h	29	ALA	THR	conflict	UNP J9QE70
h	30	ALA	ASN	conflict	UNP J9QE70
i	23	ALA	THR	conflict	UNP J9QE70
i	28	ALA	SER	conflict	UNP J9QE70
i	29	ALA	THR	conflict	UNP J9QE70
i	30	ALA	ASN	conflict	UNP J9QE70
j	23	ALA	THR	conflict	UNP J9QE70
j	28	ALA	SER	conflict	UNP J9QE70
j	29	ALA	THR	conflict	UNP J9QE70
j	30	ALA	ASN	conflict	UNP J9QE70

- Molecule 6 is a protein called XkdS-related protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	m	125	Total	C	H	N	O	S	0	0
			2039	658	1020	162	197	2		
6	k	125	Total	C	H	N	O	S	0	0
			2039	658	1020	162	197	2		
6	l	125	Total	C	H	N	O	S	0	0
			2039	658	1020	162	197	2		
6	n	125	Total	C	H	N	O	S	0	0
			2039	658	1020	162	197	2		
6	o	125	Total	C	H	N	O	S	0	0
			2039	658	1020	162	197	2		
6	p	125	Total	C	H	N	O	S	0	0
			2039	658	1020	162	197	2		

- Molecule 7 is a protein called Phage protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	r	112	Total	C	H	N	O	S	0	0
			1761	557	886	148	166	4		
7	v	112	Total	C	H	N	O	S	0	0
			1761	557	886	148	166	4		
7	s	112	Total	C	H	N	O	S	0	0
			1761	557	886	148	166	4		

- Molecule 8 is a protein called XkdQ-related protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	q	311	Total	C	H	N	O	S	0	0
			5014	1576	2540	422	467	9		
8	t	311	Total	C	H	N	O	S	0	0
			5014	1576	2540	422	467	9		
8	u	311	Total	C	H	N	O	S	0	0
			5014	1576	2540	422	467	9		

- Molecule 9 is a protein called Tail tape measure.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	w	24	Total	C	H	N	O	S	0	0
			377	115	189	31	41	1		
9	x	24	Total	C	H	N	O	S	0	0
			377	115	189	31	41	1		
9	y	24	Total	C	H	N	O	S	0	0
			377	115	189	31	41	1		

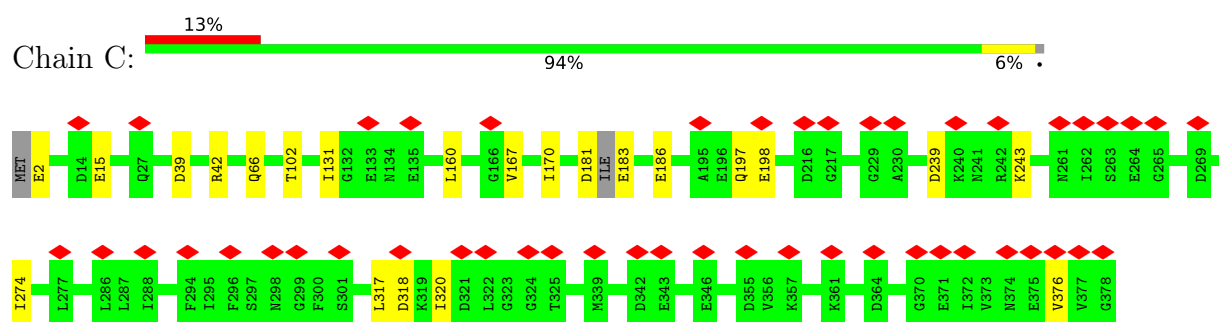
- Molecule 10 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	v	1	Total 1	Fe 1	0

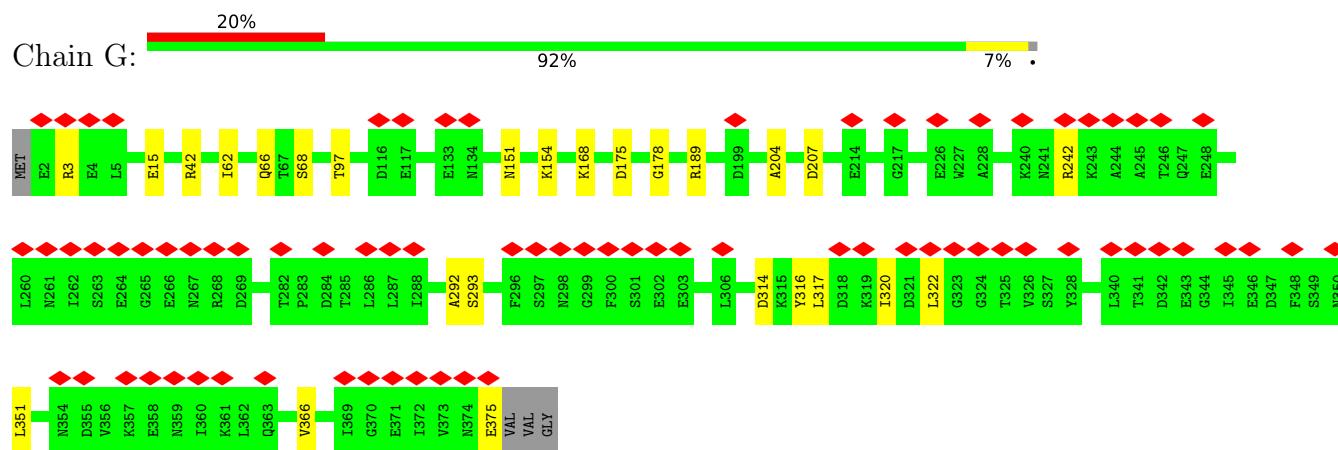
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

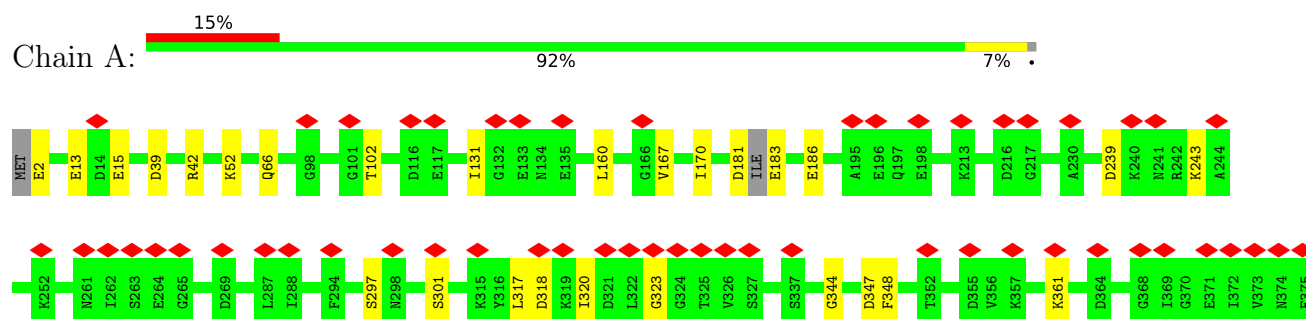
- Molecule 1: Baseplate J family protein



- Molecule 1: Baseplate J family protein



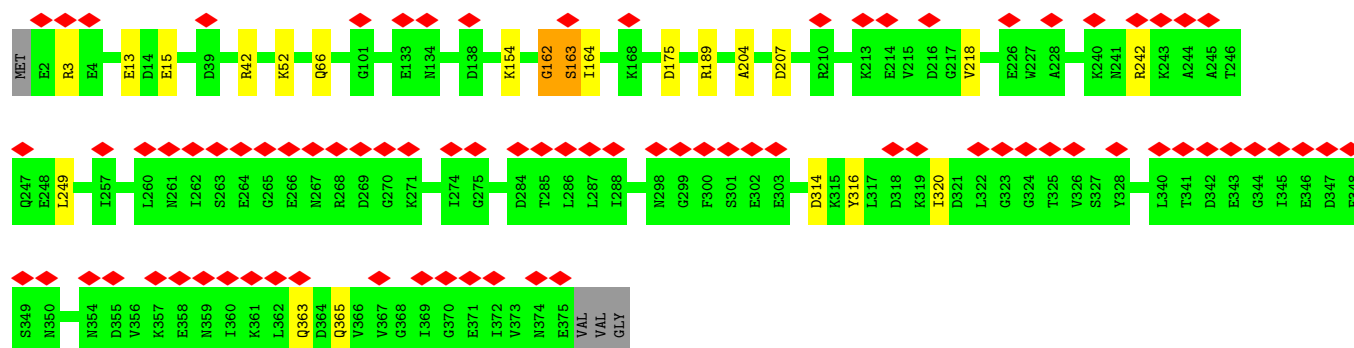
- Molecule 1: Baseplate J family protein





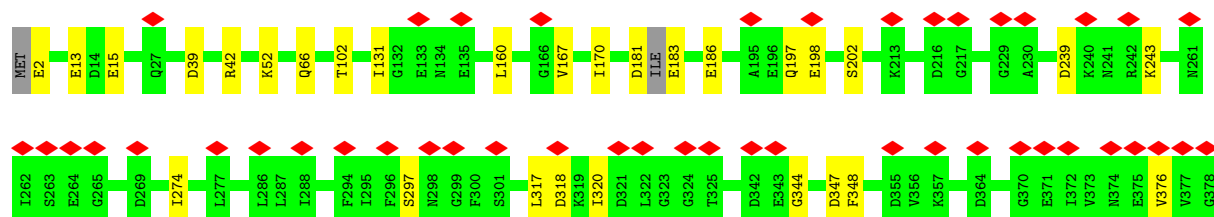
- Molecule 1: Baseplate J family protein

Chain H: 22% 93% 5% ..



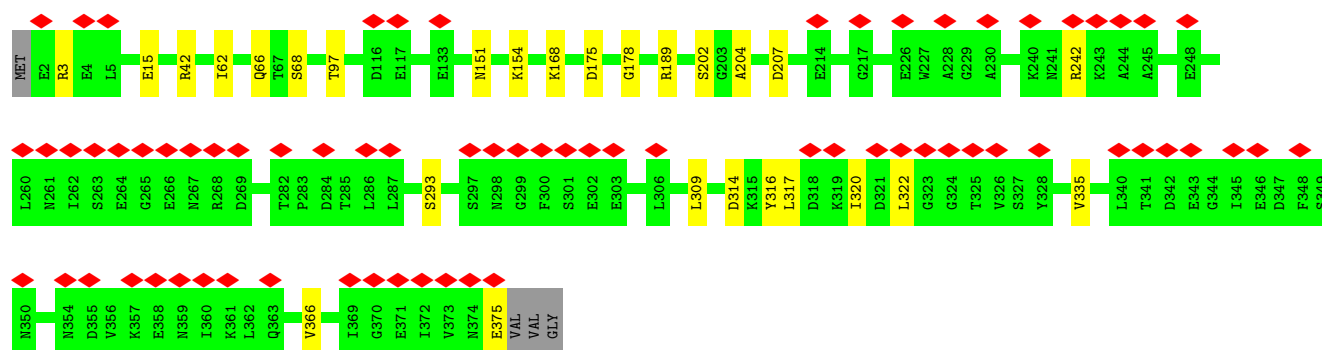
- Molecule 1: Baseplate J family protein

Chain B: 12% 92% 8% .



- Molecule 1: Baseplate J family protein

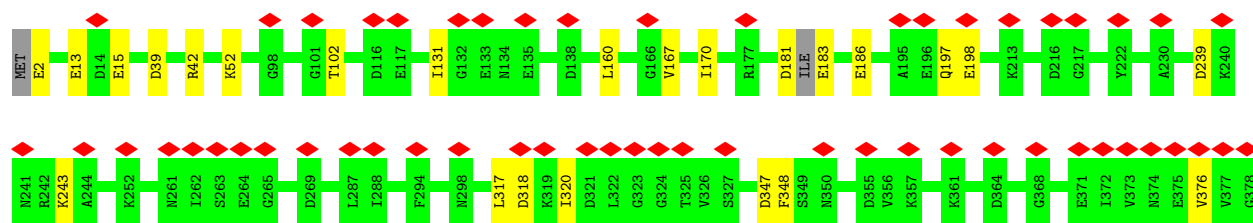
Chain I: 19% 92% 7% .



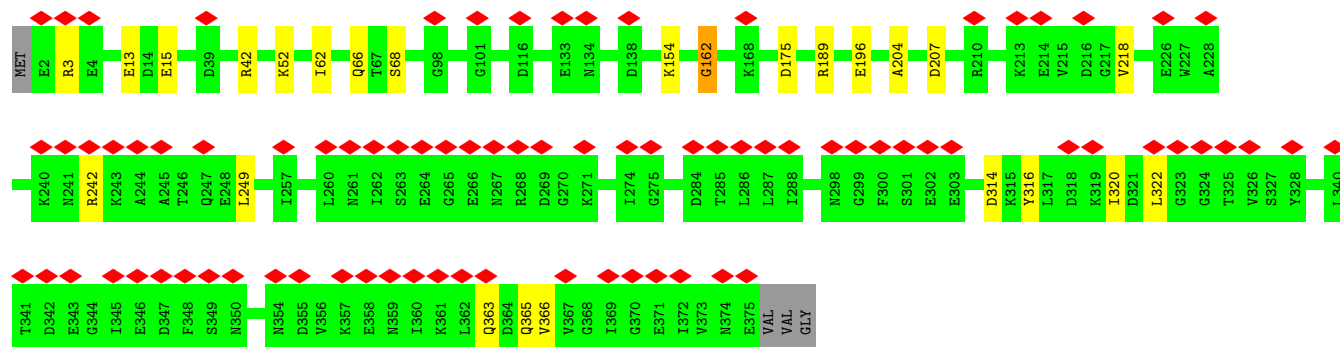
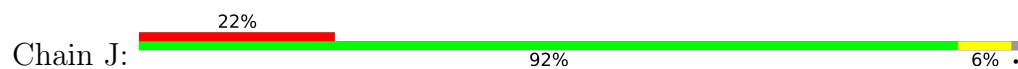
- Molecule 1: Baseplate J family protein

Chain D: 15% 93% 6% .

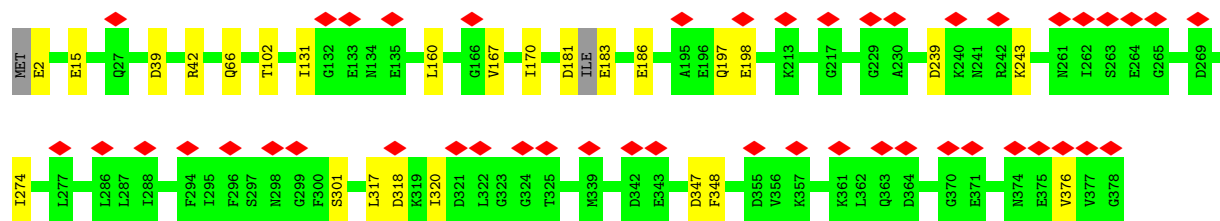
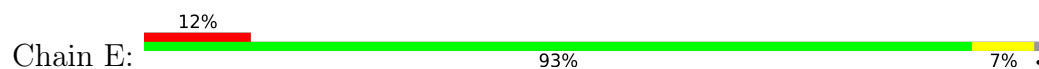




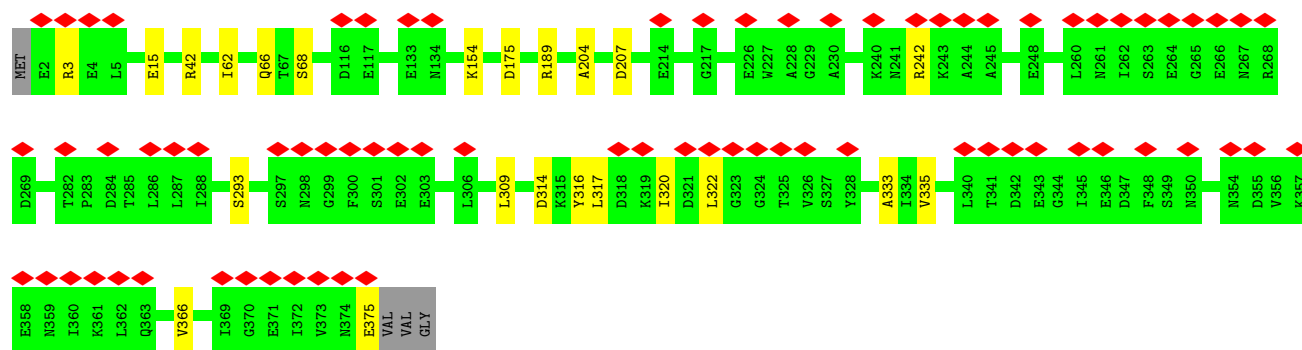
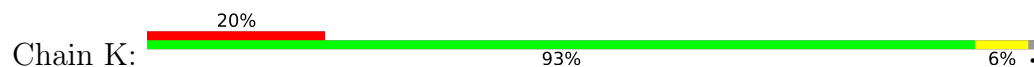
• Molecule 1: Baseplate J family protein



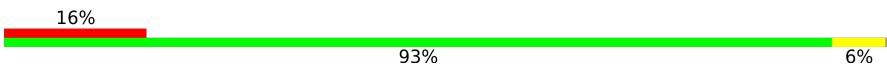
• Molecule 1: Baseplate J family protein

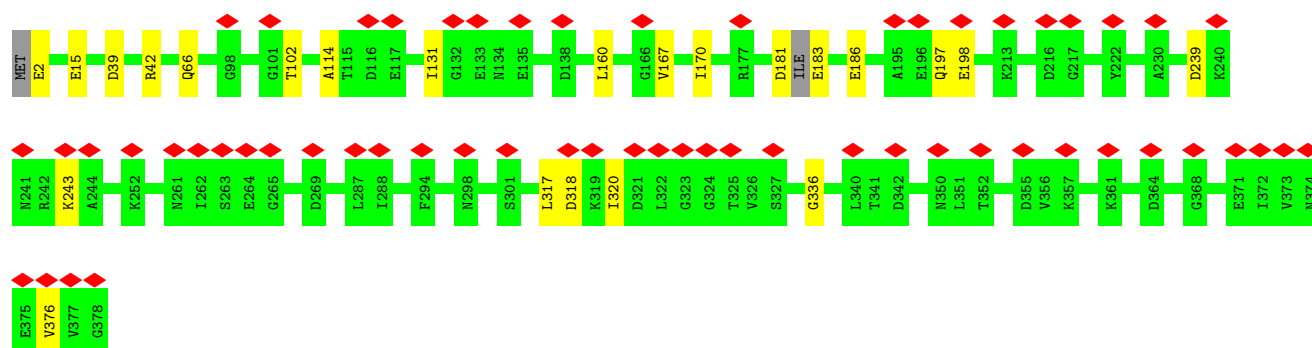


• Molecule 1: Baseplate J family protein

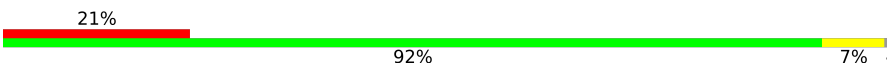


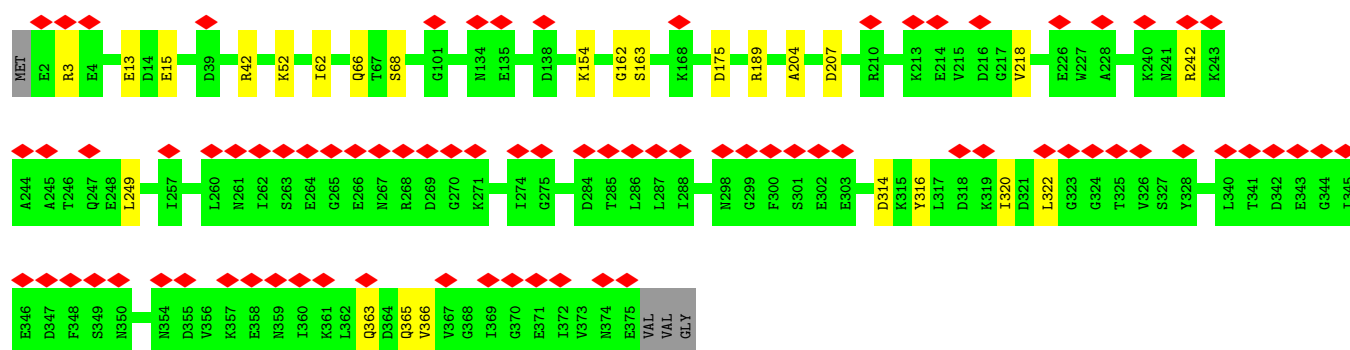
• Molecule 1: Baseplate J family protein

Chain F: 

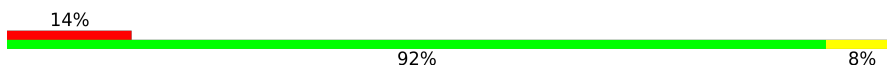


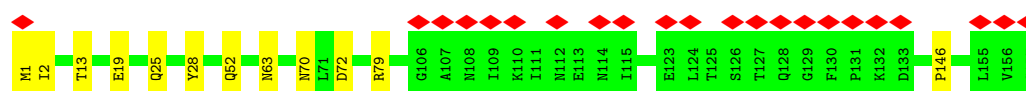
• Molecule 1: Baseplate J family protein

Chain L: 

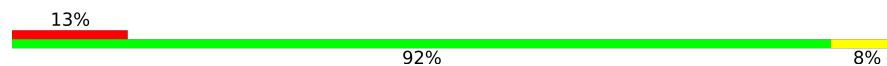


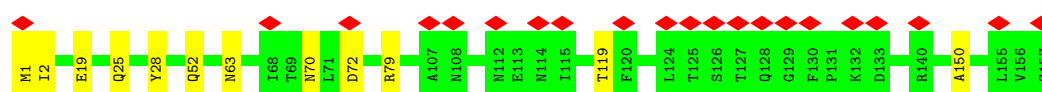
• Molecule 2: XkdT-related protein

Chain N: 

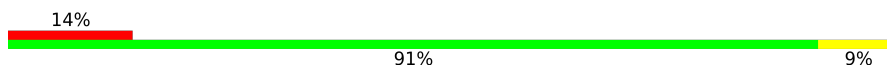


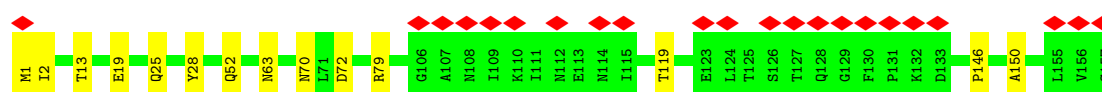
• Molecule 2: XkdT-related protein

Chain M: 

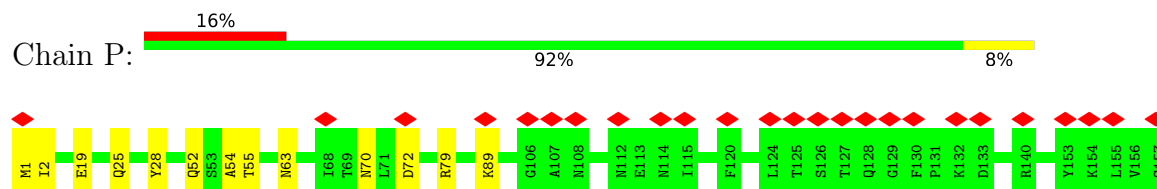


• Molecule 2: XkdT-related protein

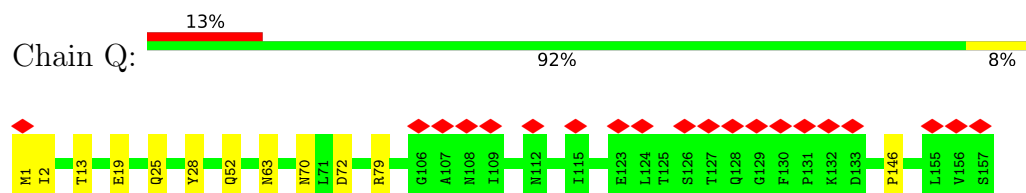
Chain O: 



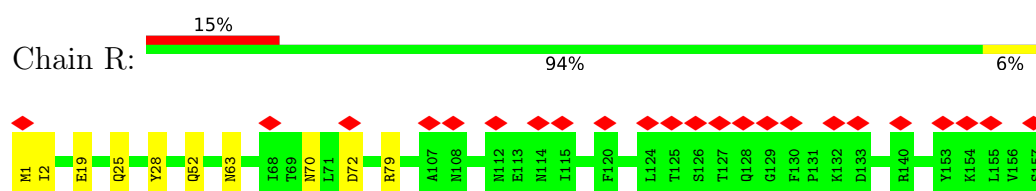
- Molecule 2: XkdT-related protein



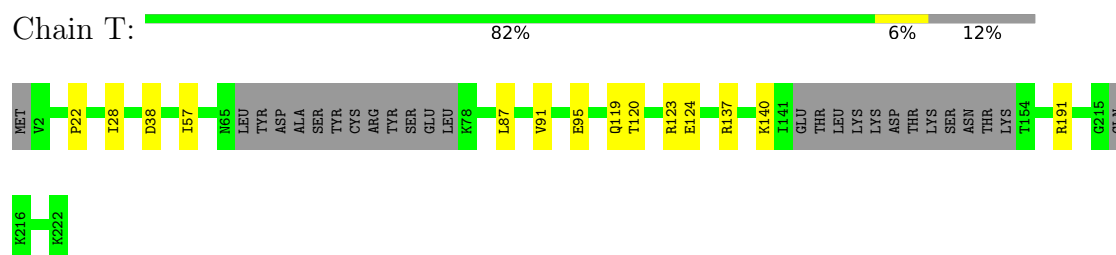
- Molecule 2: XkdT-related protein



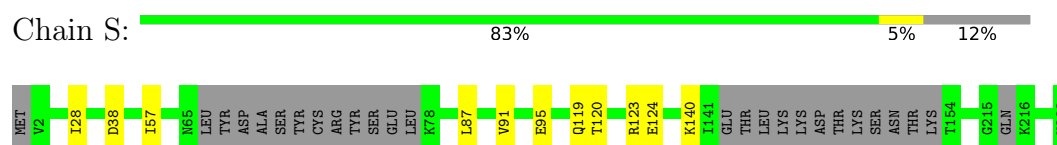
- Molecule 2: XkdT-related protein



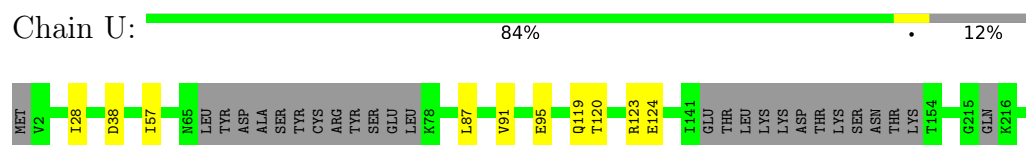
- Molecule 3: Peptidoglycan-binding LysM protein



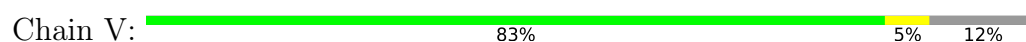
- Molecule 3: Peptidoglycan-binding LysM protein



- Molecule 3: Peptidoglycan-binding LysM protein



- Molecule 3: Peptidoglycan-binding LysM protein





- Molecule 3: Peptidoglycan-binding LysM protein

Chain W: 83% 5% 12%



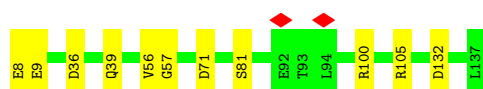
- Molecule 3: Peptidoglycan-binding LysM protein

Chain X: 83% 5% 12%



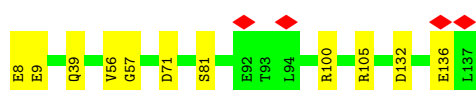
- Molecule 4: XkdM-related protein

Chain Z: 92% 8%



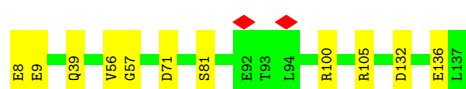
- Molecule 4: XkdM-related protein

Chain Y: 92% 8%



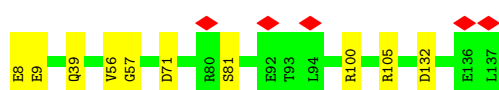
- Molecule 4: XkdM-related protein

Chain a: 92% 8%

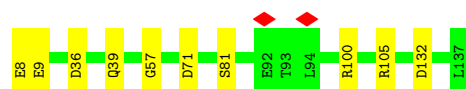
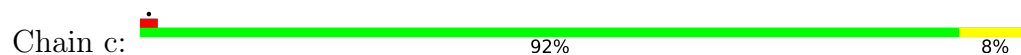


- Molecule 4: XkdM-related protein

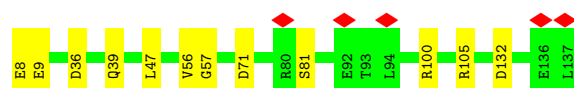
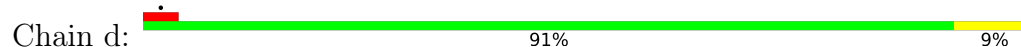
Chain b: 92% 8%



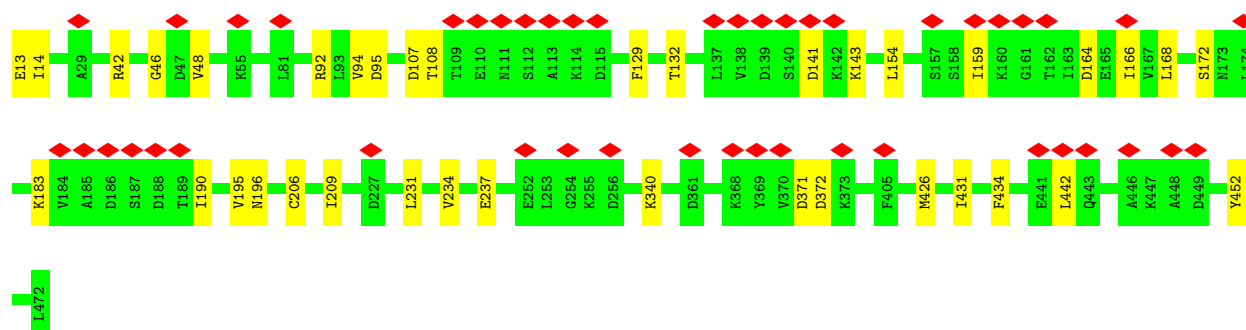
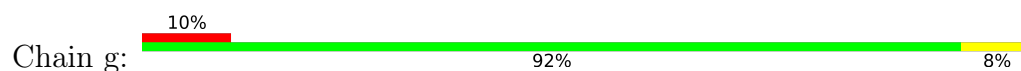
- Molecule 4: XkdM-related protein



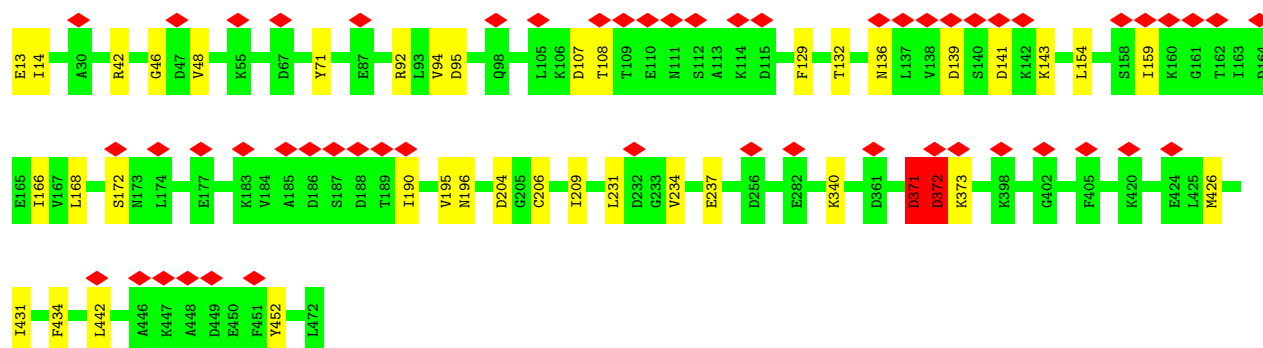
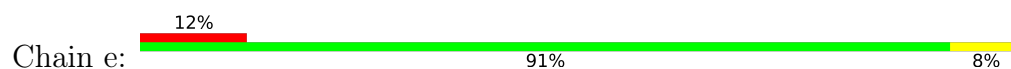
- Molecule 4: XkdM-related protein



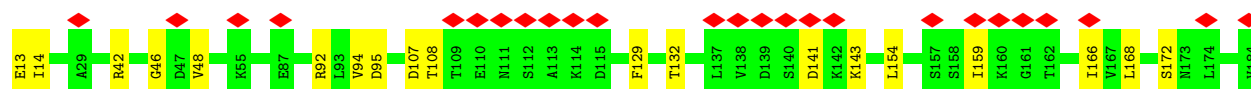
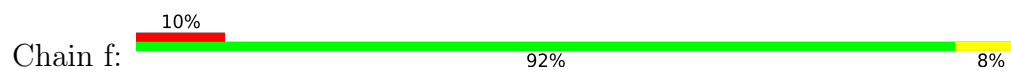
- Molecule 5: Tail sheath

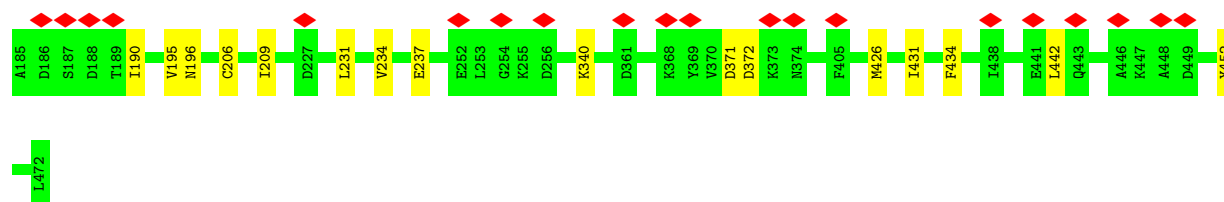


- Molecule 5: Tail sheath

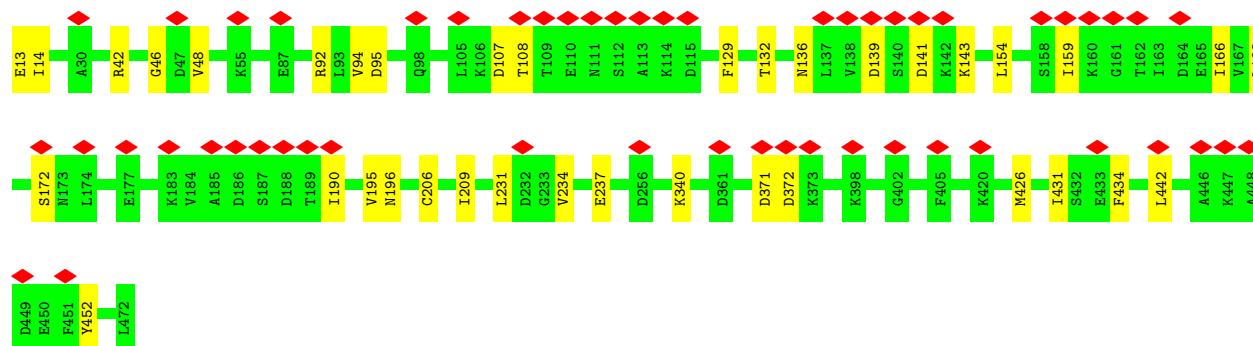


- Molecule 5: Tail sheath

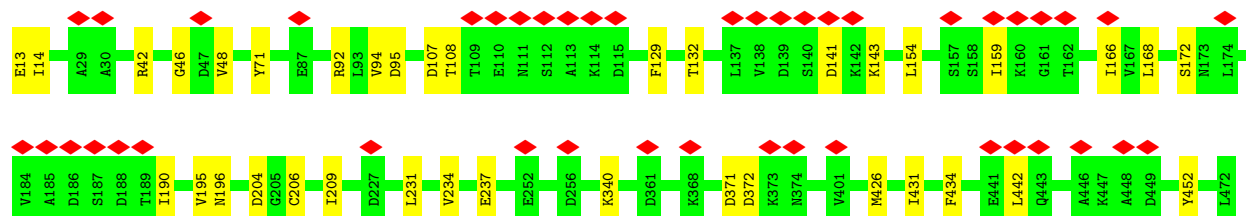




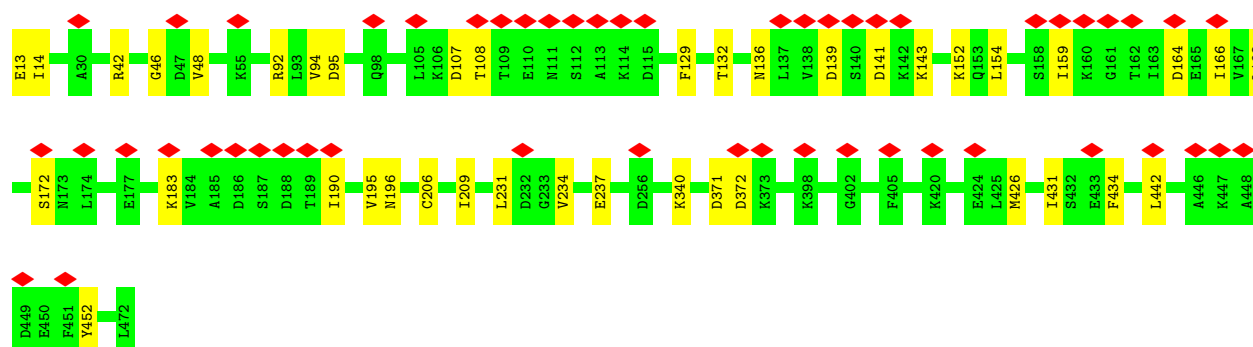
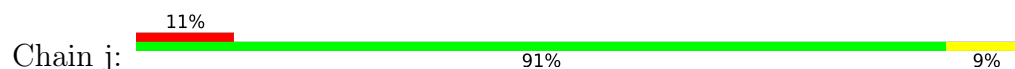
• Molecule 5: Tail sheath



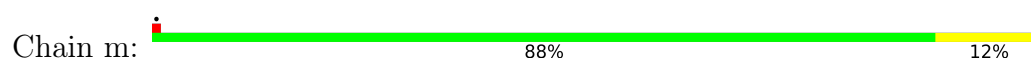
• Molecule 5: Tail sheath



• Molecule 5: Tail sheath



• Molecule 6: XkdS-related protein

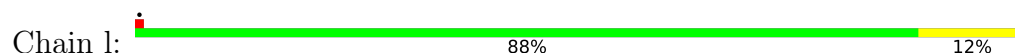




- Molecule 6: XkdS-related protein



- Molecule 6: XkdS-related protein



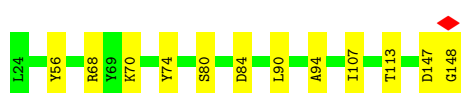
- Molecule 6: XkdS-related protein



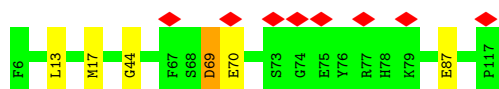
- Molecule 6: XkdS-related protein



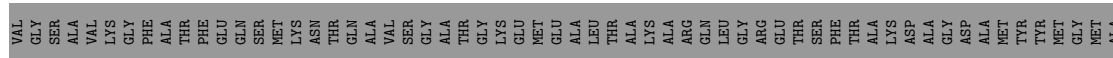
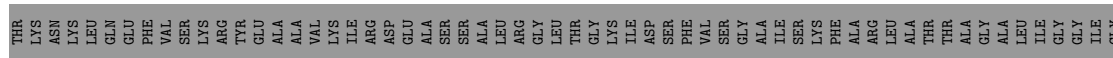
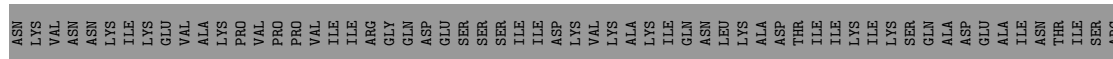
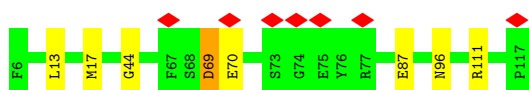
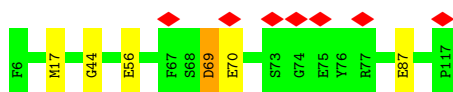
- Molecule 6: XkdS-related protein



- Molecule 7: Phage protein



- Molecule 7: Phage protein



- Molecule 9: Tail tape measure

Chain x: 

98%





SER	SER	ASN	ASN	THR	ILE	ASN	LEU	GLY	GLY	ILE	SER	ILE	ASN	VAL	GLN	ASN	SER	ASP	ASN	K1401	I1405	L1408	G1424
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	17759	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.118	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0231	Depositor
Map size (Å)	530.0, 530.0, 530.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE2

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	0.13	0/2939	0.28	0/3979
1	B	0.13	0/2939	0.28	0/3979
1	C	0.13	0/2939	0.28	0/3979
1	D	0.13	0/2939	0.28	0/3979
1	E	0.13	0/2939	0.28	0/3979
1	F	0.13	0/2939	0.28	0/3979
1	G	0.14	0/2926	0.32	0/3963
1	H	0.15	0/2926	0.36	0/3963
1	I	0.14	0/2926	0.33	0/3963
1	J	0.14	0/2926	0.32	0/3963
1	K	0.14	0/2926	0.32	0/3963
1	L	0.14	0/2926	0.32	0/3963
2	M	0.14	0/1286	0.32	0/1734
2	N	0.14	0/1286	0.32	0/1734
2	O	0.14	0/1286	0.32	0/1734
2	P	0.14	0/1286	0.32	0/1734
2	Q	0.14	0/1286	0.32	0/1734
2	R	0.14	0/1286	0.32	0/1734
3	S	0.15	0/1629	0.36	0/2191
3	T	0.16	0/1629	0.35	0/2191
3	U	0.16	0/1629	0.35	0/2191
3	V	0.15	0/1629	0.36	0/2191
3	W	0.15	0/1629	0.35	0/2191
3	X	0.15	0/1629	0.36	0/2191
4	Y	0.11	0/1038	0.29	0/1390
4	Z	0.11	0/1038	0.29	0/1390
4	a	0.11	0/1038	0.29	0/1390
4	b	0.11	0/1038	0.29	0/1390
4	c	0.11	0/1038	0.29	0/1390
4	d	0.11	0/1038	0.29	0/1390
5	e	0.20	1/3667 (0.0%)	0.38	4/4946 (0.1%)
5	f	0.15	0/3667	0.33	2/4946 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	g	0.15	0/3667	0.34	2/4946 (0.0%)
5	h	0.14	0/3667	0.33	2/4946 (0.0%)
5	i	0.14	0/3667	0.33	2/4946 (0.0%)
5	j	0.14	0/3667	0.33	2/4946 (0.0%)
6	k	0.14	0/1038	0.33	0/1399
6	l	0.14	0/1038	0.33	0/1399
6	m	0.14	0/1038	0.33	0/1399
6	n	0.14	0/1038	0.33	0/1399
6	o	0.14	0/1038	0.33	0/1399
6	p	0.14	0/1038	0.33	0/1399
7	r	0.15	0/888	0.38	0/1195
7	s	0.15	0/888	0.38	0/1195
7	v	0.15	0/888	0.38	0/1195
8	q	0.12	0/2507	0.31	0/3358
8	t	0.12	0/2507	0.31	0/3358
8	u	0.12	0/2507	0.31	0/3358
9	w	0.15	0/187	0.31	0/248
9	x	0.16	0/187	0.31	0/248
9	y	0.16	0/187	0.31	0/248
All	All	0.14	1/97884 (0.0%)	0.32	14/132015 (0.0%)

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	H	0	2
1	J	0	1
1	L	0	1
3	T	0	1
5	e	0	2
7	r	0	1
7	s	0	1
7	v	0	1
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	e	372	ASP	CA-CB	6.66	1.64	1.53

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	e	372	ASP	N-CA-CB	7.27	122.77	110.49
5	e	372	ASP	CA-CB-CG	6.77	119.37	112.60
5	e	372	ASP	N-CA-C	-6.47	97.02	110.80
5	g	371	ASP	CA-C-N	6.22	133.43	121.54
5	g	371	ASP	C-N-CA	6.22	133.43	121.54

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	162	GLY	Mainchain
1	H	163	SER	Peptide
3	T	140	LYS	Mainchain
5	e	371	ASP	Mainchain
5	e	372	ASP	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	2902	2899	2897	19	0
1	B	2902	2899	2897	21	0
1	C	2902	2899	2897	17	0
1	D	2902	2899	2897	16	0
1	E	2902	2899	2897	19	0
1	F	2902	2899	2897	17	0
1	G	2888	2885	2884	15	0
1	H	2888	2885	2884	12	0
1	I	2888	2885	2884	16	0
1	J	2888	2885	2884	14	0
1	K	2888	2885	2884	13	0
1	L	2888	2885	2884	13	0
2	M	1264	1295	1295	7	0
2	N	1264	1295	1295	11	0
2	O	1264	1295	1295	11	0
2	P	1264	1295	1295	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Q	1264	1295	1295	10	0
2	R	1264	1295	1295	6	0
3	S	1602	1663	1656	9	0
3	T	1602	1663	1656	11	0
3	U	1602	1663	1656	8	0
3	V	1602	1663	1656	9	0
3	W	1602	1663	1656	9	0
3	X	1602	1663	1656	9	0
4	Y	1026	1027	1026	7	0
4	Z	1026	1027	1026	7	0
4	a	1026	1027	1026	7	0
4	b	1026	1027	1026	6	0
4	c	1026	1027	1026	6	0
4	d	1026	1027	1026	8	0
5	e	3615	3627	3624	24	0
5	f	3615	3627	3624	21	0
5	g	3615	3627	3624	22	0
5	h	3615	3627	3624	22	0
5	i	3615	3627	3624	23	0
5	j	3615	3627	3624	25	0
6	k	1019	1020	1017	7	0
6	l	1019	1020	1017	10	0
6	m	1019	1020	1017	10	0
6	n	1019	1020	1017	8	0
6	o	1019	1020	1017	9	0
6	p	1019	1020	1017	8	0
7	r	875	886	885	8	0
7	s	875	886	885	10	0
7	v	875	886	885	8	0
8	q	2474	2540	2536	16	0
8	t	2474	2540	2536	16	0
8	u	2474	2540	2536	17	0
9	w	188	189	188	3	0
9	x	188	189	188	4	0
9	y	188	189	188	3	0
10	v	1	0	0	0	0
All	All	96508	97341	97221	522	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 3.

The worst 5 of 522 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:D:15:GLU:OE2	1:D:42:ARG:NH1	2.21	0.74
1:E:15:GLU:OE2	1:E:42:ARG:NH1	2.21	0.74
1:B:15:GLU:OE2	1:B:42:ARG:NH1	2.21	0.74
1:C:15:GLU:OE2	1:C:42:ARG:NH1	2.21	0.73
1:A:15:GLU:OE2	1:A:42:ARG:NH1	2.21	0.73

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	372/378 (98%)	359 (96%)	13 (4%)	0	100	100
1	B	372/378 (98%)	359 (96%)	13 (4%)	0	100	100
1	C	372/378 (98%)	359 (96%)	13 (4%)	0	100	100
1	D	372/378 (98%)	359 (96%)	13 (4%)	0	100	100
1	E	372/378 (98%)	359 (96%)	13 (4%)	0	100	100
1	F	372/378 (98%)	359 (96%)	13 (4%)	0	100	100
1	G	372/378 (98%)	363 (98%)	9 (2%)	0	100	100
1	H	372/378 (98%)	363 (98%)	8 (2%)	1 (0%)	36	69
1	I	372/378 (98%)	362 (97%)	10 (3%)	0	100	100
1	J	372/378 (98%)	364 (98%)	8 (2%)	0	100	100
1	K	372/378 (98%)	364 (98%)	8 (2%)	0	100	100
1	L	372/378 (98%)	364 (98%)	8 (2%)	0	100	100
2	M	155/157 (99%)	152 (98%)	3 (2%)	0	100	100
2	N	155/157 (99%)	152 (98%)	3 (2%)	0	100	100
2	O	155/157 (99%)	152 (98%)	3 (2%)	0	100	100
2	P	155/157 (99%)	152 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Q	155/157 (99%)	152 (98%)	3 (2%)	0	100	100
2	R	155/157 (99%)	152 (98%)	3 (2%)	0	100	100
3	S	191/223 (86%)	186 (97%)	5 (3%)	0	100	100
3	T	191/223 (86%)	186 (97%)	5 (3%)	0	100	100
3	U	191/223 (86%)	186 (97%)	5 (3%)	0	100	100
3	V	191/223 (86%)	186 (97%)	5 (3%)	0	100	100
3	W	191/223 (86%)	186 (97%)	5 (3%)	0	100	100
3	X	191/223 (86%)	186 (97%)	5 (3%)	0	100	100
4	Y	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
4	Z	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
4	a	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
4	b	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
4	c	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
4	d	128/130 (98%)	124 (97%)	4 (3%)	0	100	100
5	e	458/460 (100%)	437 (95%)	20 (4%)	1 (0%)	43	75
5	f	458/460 (100%)	438 (96%)	19 (4%)	1 (0%)	43	75
5	g	458/460 (100%)	438 (96%)	19 (4%)	1 (0%)	43	75
5	h	458/460 (100%)	438 (96%)	19 (4%)	1 (0%)	43	75
5	i	458/460 (100%)	438 (96%)	19 (4%)	1 (0%)	43	75
5	j	458/460 (100%)	438 (96%)	19 (4%)	1 (0%)	43	75
6	k	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
6	l	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
6	m	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
6	n	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
6	o	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
6	p	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
7	r	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
7	s	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
7	v	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
8	q	307/316 (97%)	288 (94%)	19 (6%)	0	100	100
8	t	307/316 (97%)	288 (94%)	19 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	u	307/316 (97%)	288 (94%)	19 (6%)	0	100	100
9	w	22/1424 (2%)	22 (100%)	0	0	100	100
9	x	22/1424 (2%)	22 (100%)	0	0	100	100
9	y	22/1424 (2%)	22 (100%)	0	0	100	100
All	All	12111/16662 (73%)	11686 (96%)	418 (4%)	7 (0%)	49	81

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	g	372	ASP
1	H	163	SER
5	f	372	ASP
5	h	372	ASP
5	i	372	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	323/325 (99%)	323 (100%)	0	100	100
1	B	323/325 (99%)	323 (100%)	0	100	100
1	C	323/325 (99%)	323 (100%)	0	100	100
1	D	323/325 (99%)	323 (100%)	0	100	100
1	E	323/325 (99%)	323 (100%)	0	100	100
1	F	323/325 (99%)	323 (100%)	0	100	100
1	G	321/325 (99%)	321 (100%)	0	100	100
1	H	321/325 (99%)	321 (100%)	0	100	100
1	I	321/325 (99%)	321 (100%)	0	100	100
1	J	321/325 (99%)	321 (100%)	0	100	100
1	K	321/325 (99%)	321 (100%)	0	100	100
1	L	321/325 (99%)	321 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	M	143/143 (100%)	143 (100%)	0	100	100
2	N	143/143 (100%)	143 (100%)	0	100	100
2	O	143/143 (100%)	143 (100%)	0	100	100
2	P	143/143 (100%)	143 (100%)	0	100	100
2	Q	143/143 (100%)	143 (100%)	0	100	100
2	R	143/143 (100%)	143 (100%)	0	100	100
3	S	180/207 (87%)	180 (100%)	0	100	100
3	T	180/207 (87%)	180 (100%)	0	100	100
3	U	180/207 (87%)	180 (100%)	0	100	100
3	V	180/207 (87%)	180 (100%)	0	100	100
3	W	180/207 (87%)	180 (100%)	0	100	100
3	X	180/207 (87%)	180 (100%)	0	100	100
4	Y	114/115 (99%)	114 (100%)	0	100	100
4	Z	114/115 (99%)	114 (100%)	0	100	100
4	a	114/115 (99%)	114 (100%)	0	100	100
4	b	114/115 (99%)	114 (100%)	0	100	100
4	c	114/115 (99%)	114 (100%)	0	100	100
4	d	114/115 (99%)	114 (100%)	0	100	100
5	e	399/399 (100%)	399 (100%)	0	100	100
5	f	399/399 (100%)	399 (100%)	0	100	100
5	g	399/399 (100%)	399 (100%)	0	100	100
5	h	399/399 (100%)	399 (100%)	0	100	100
5	i	399/399 (100%)	399 (100%)	0	100	100
5	j	399/399 (100%)	399 (100%)	0	100	100
6	k	112/112 (100%)	112 (100%)	0	100	100
6	l	112/112 (100%)	112 (100%)	0	100	100
6	m	112/112 (100%)	112 (100%)	0	100	100
6	n	112/112 (100%)	112 (100%)	0	100	100
6	o	112/112 (100%)	112 (100%)	0	100	100
6	p	112/112 (100%)	112 (100%)	0	100	100
7	r	94/94 (100%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	s	94/94 (100%)	94 (100%)	0	100	100
7	v	94/94 (100%)	94 (100%)	0	100	100
8	q	266/281 (95%)	266 (100%)	0	100	100
8	t	266/281 (95%)	266 (100%)	0	100	100
8	u	266/281 (95%)	266 (100%)	0	100	100
9	w	21/1141 (2%)	21 (100%)	0	100	100
9	x	21/1141 (2%)	21 (100%)	0	100	100
9	y	21/1141 (2%)	21 (100%)	0	100	100
All	All	10695/14304 (75%)	10695 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
8	q	139	HIS
7	s	78	HIS
2	P	112	ASN
4	a	14	ASN
8	t	139	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

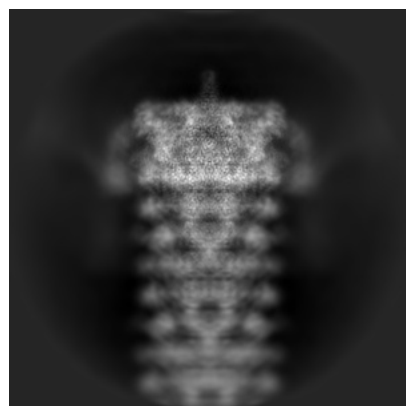
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51138. These allow visual inspection of the internal detail of the map and identification of artifacts.

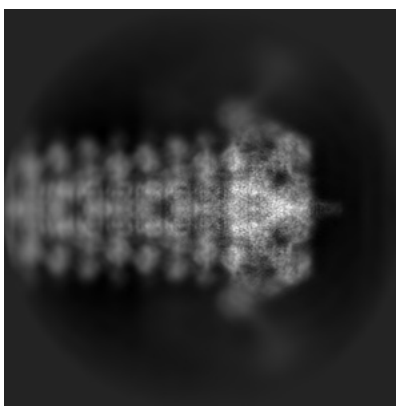
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

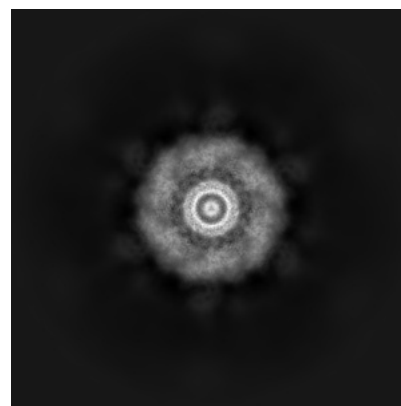
6.1.1 Primary map



X

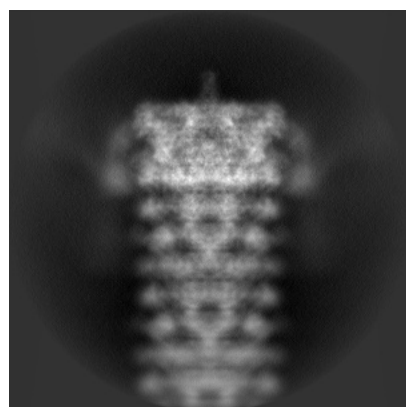


Y

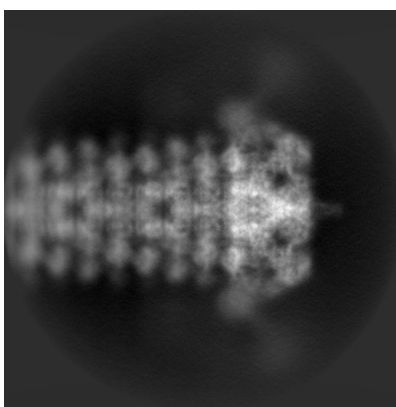


Z

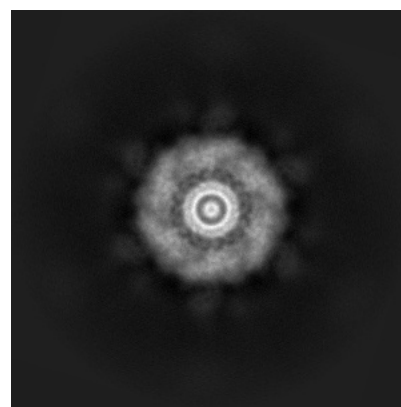
6.1.2 Raw map



X



Y



Z

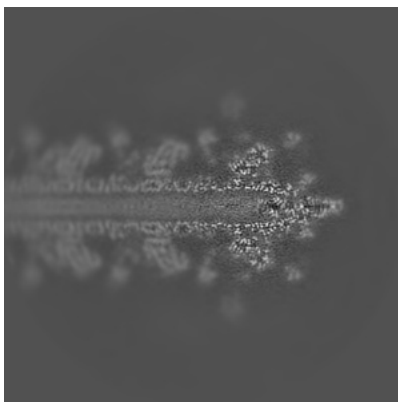
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

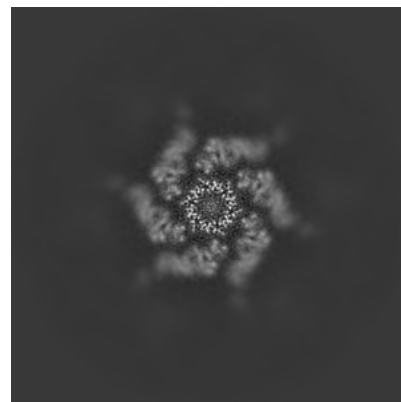
6.2.1 Primary map



X Index: 250

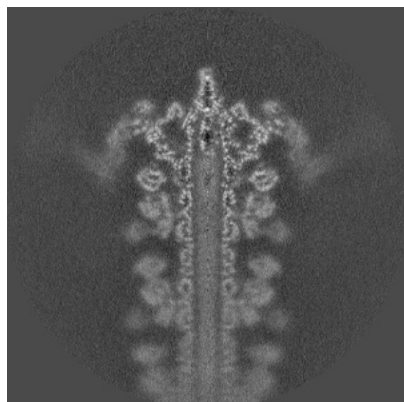


Y Index: 250

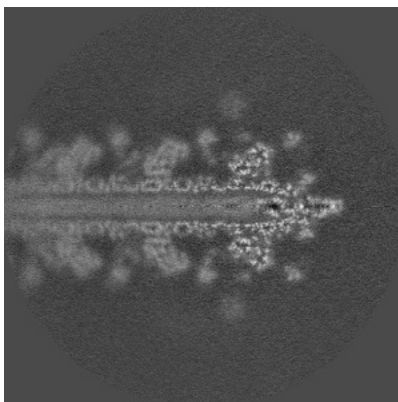


Z Index: 250

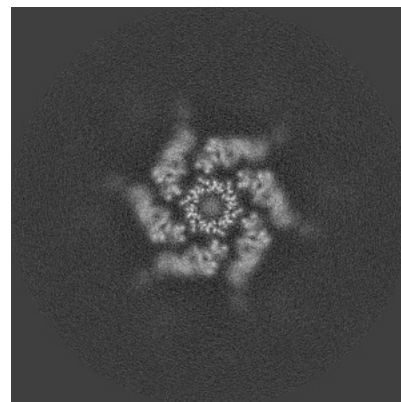
6.2.2 Raw map



X Index: 250



Y Index: 250

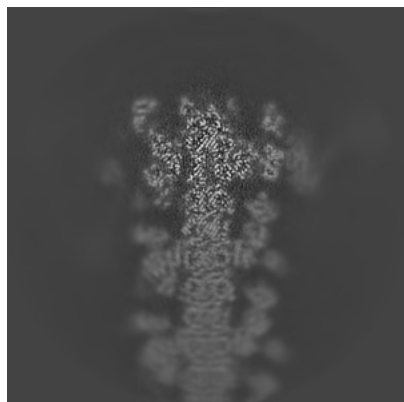


Z Index: 250

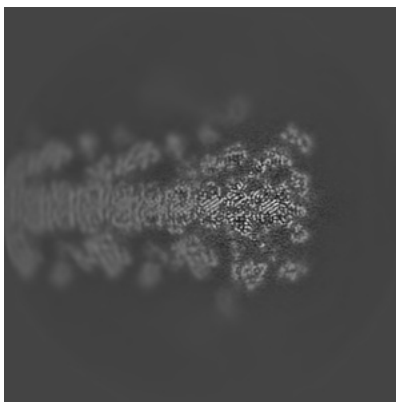
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

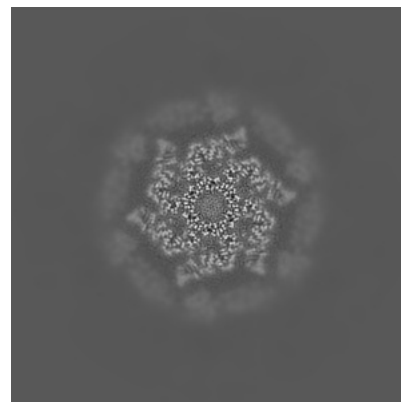
6.3.1 Primary map



X Index: 270

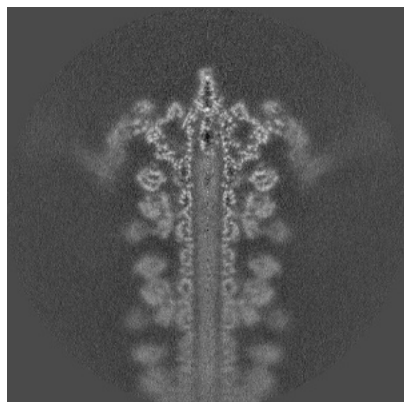


Y Index: 229

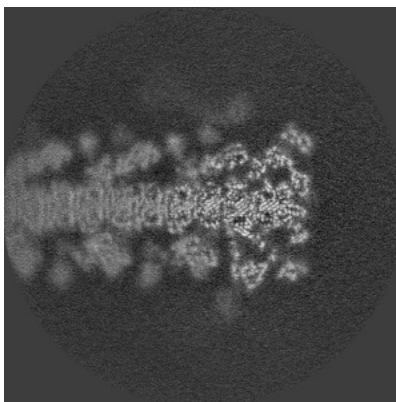


Z Index: 292

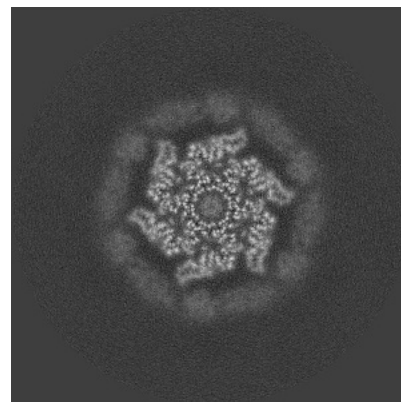
6.3.2 Raw map



X Index: 250



Y Index: 228

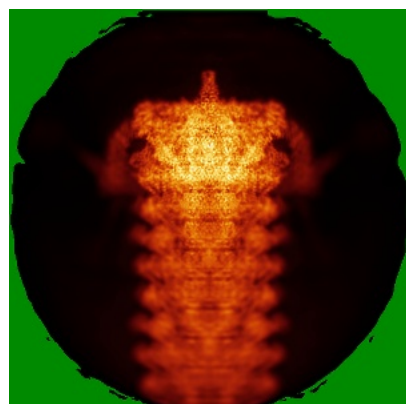


Z Index: 290

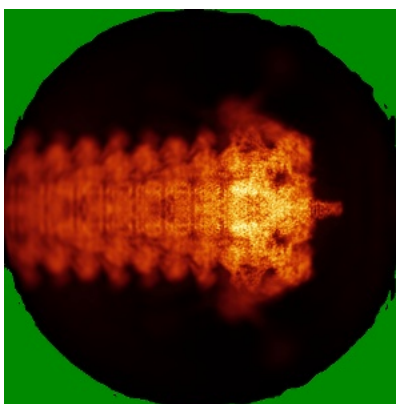
The images above show the largest variance slices of the map in three orthogonal directions.

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

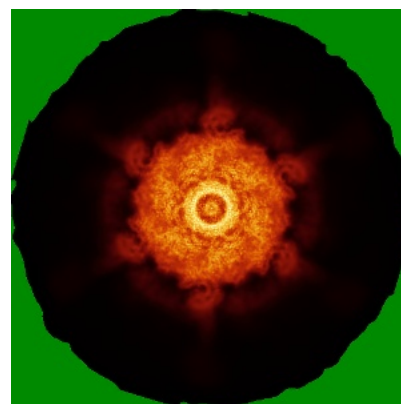
6.4.1 Primary map



X

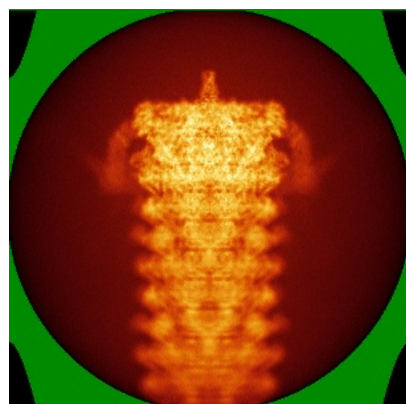


Y

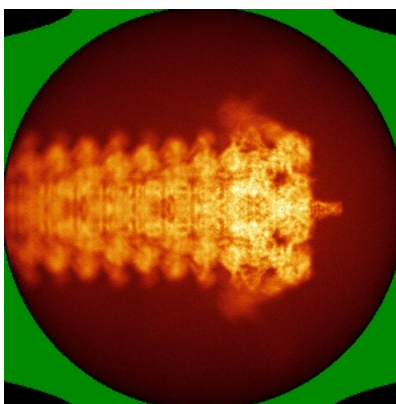


Z

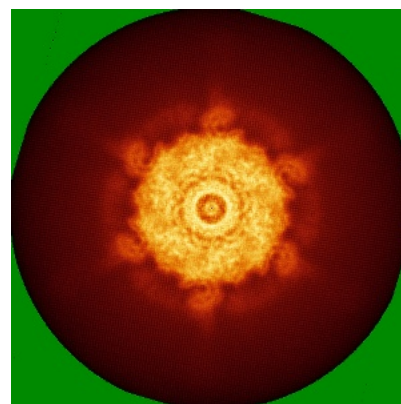
6.4.2 Raw map



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.

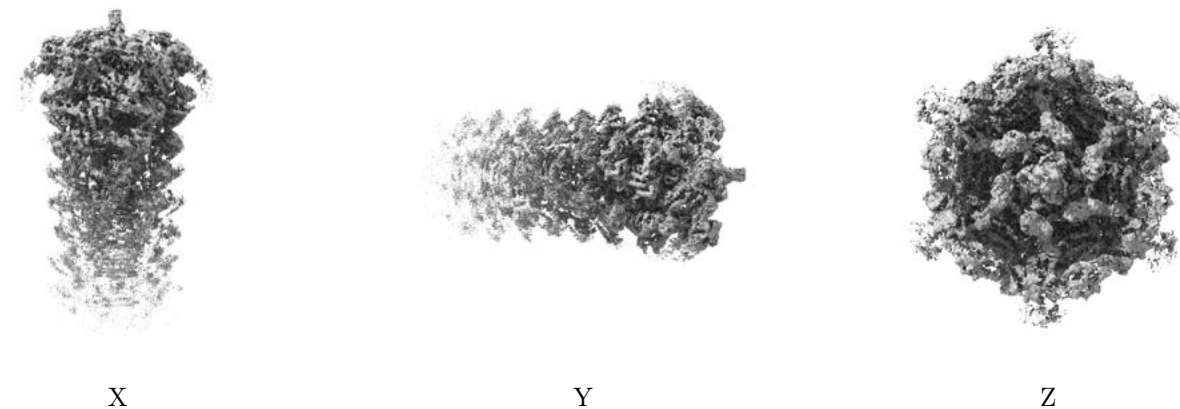
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0231. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

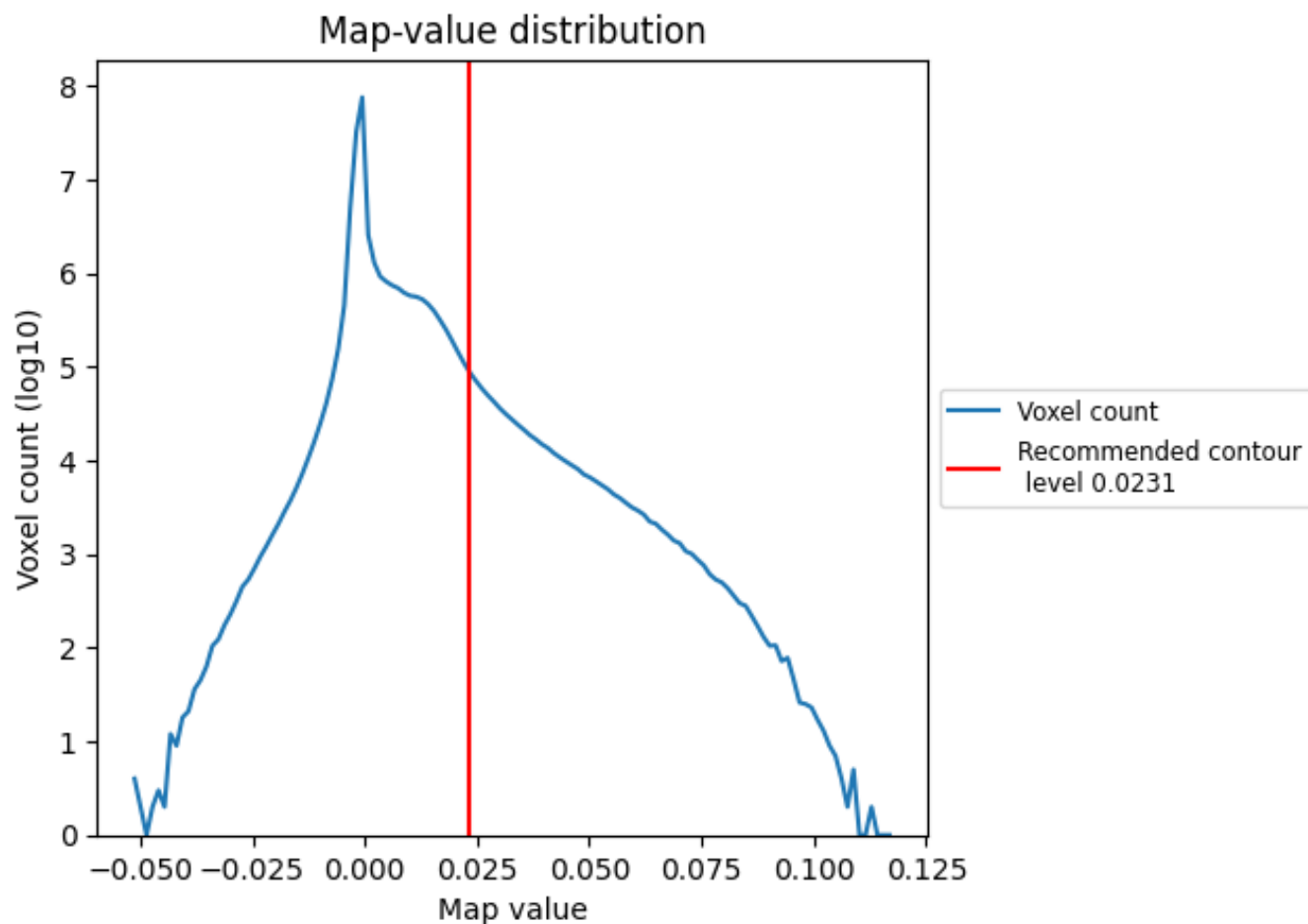
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

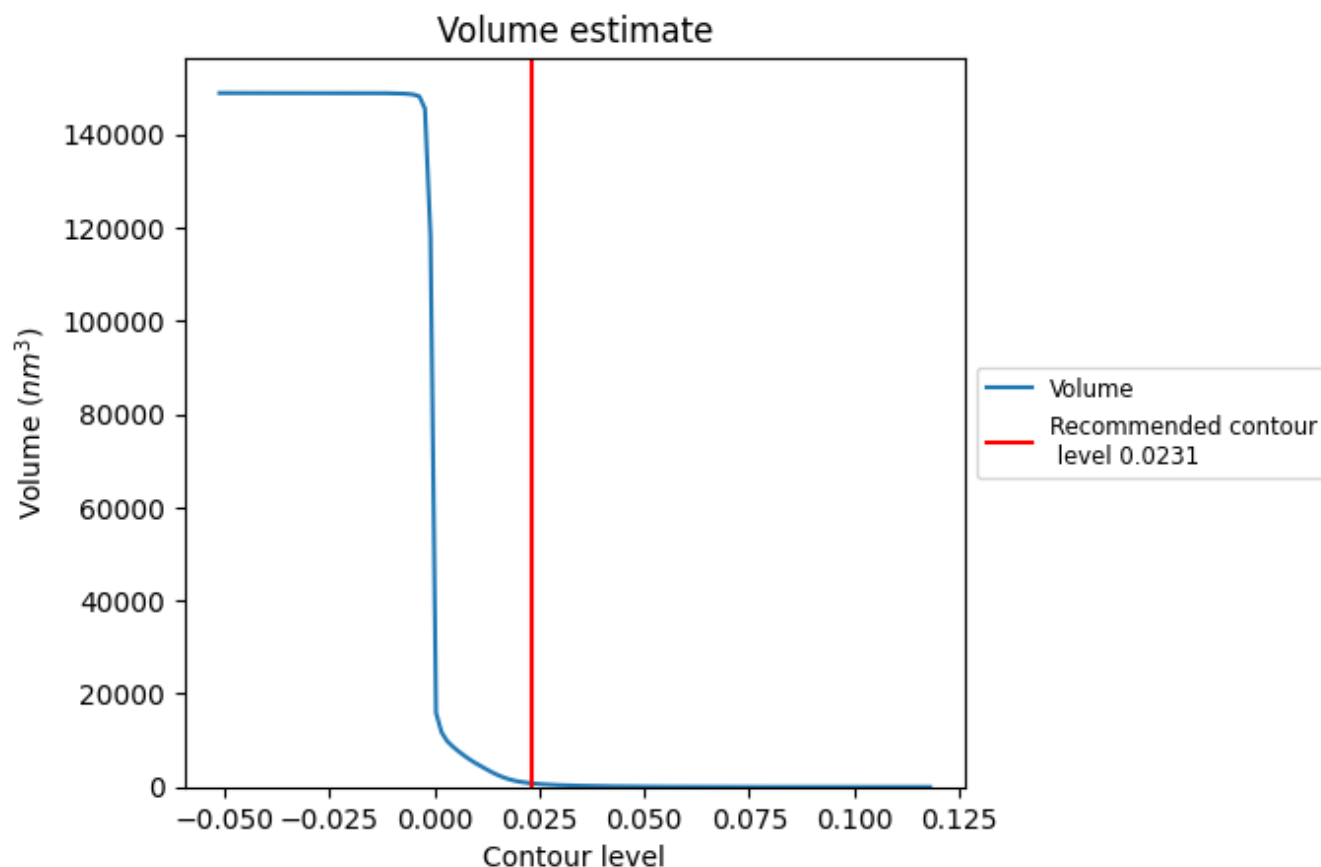
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

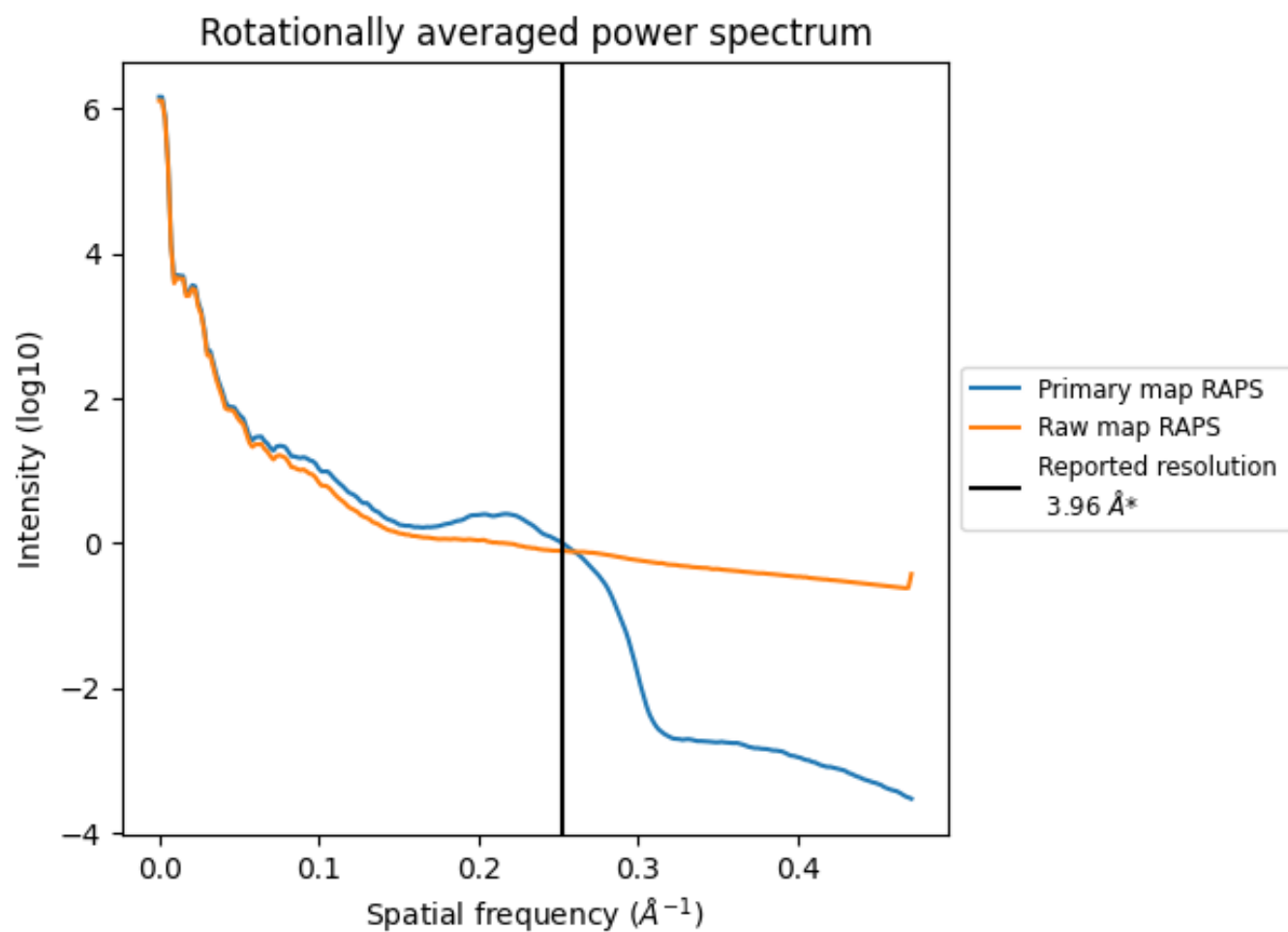
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 781 nm³; this corresponds to an approximate mass of 705 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 ⓘ

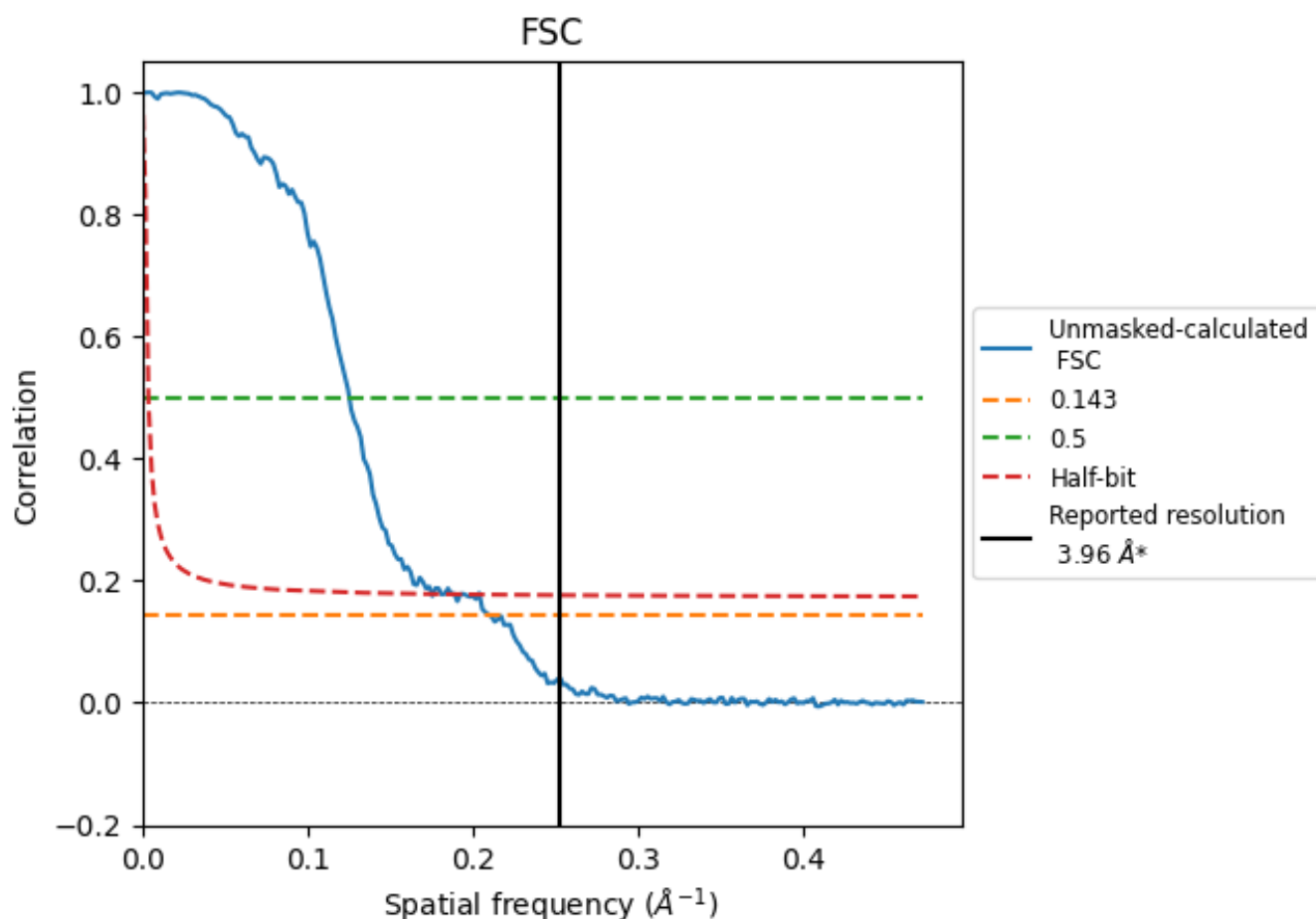


*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

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 0.253 Å⁻¹

8.2 Resolution estimates [i](#)

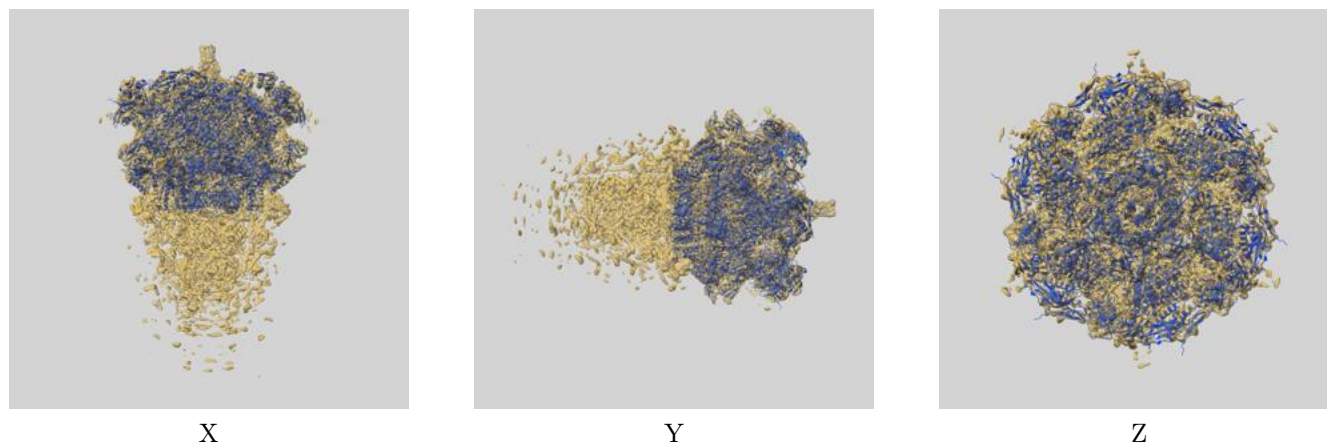
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.96	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.76	7.99	5.71

*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 4.76 differs from the reported value 3.96 by more than 10 %

9 Map-model fit [i](#)

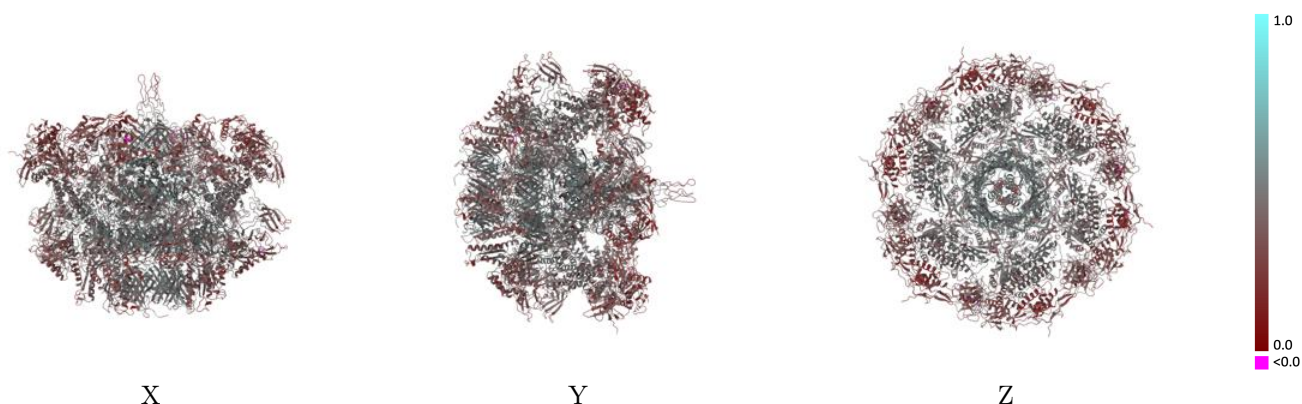
This section contains information regarding the fit between EMDB map EMD-51138 and PDB model 9G8S. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



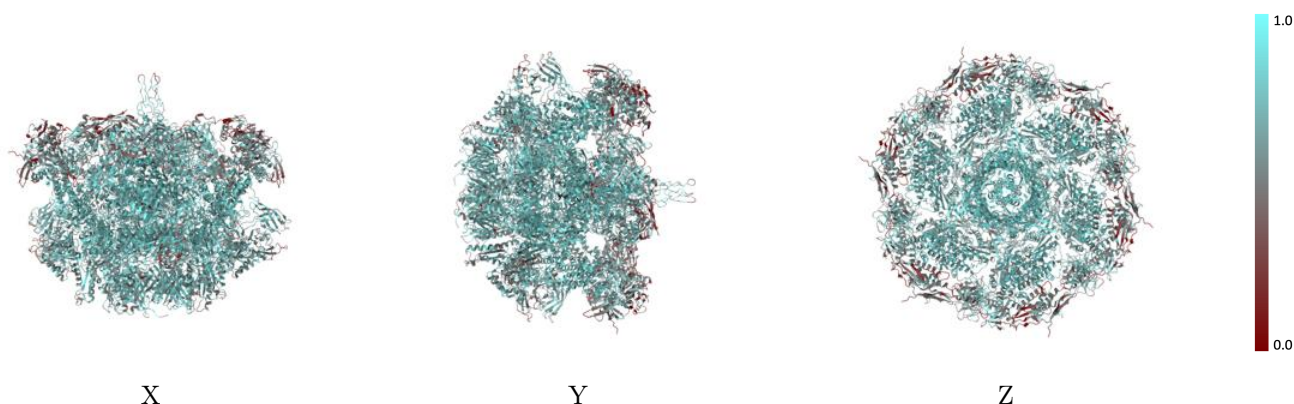
The images above show the 3D surface view of the map at the recommended contour level 0.0231 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



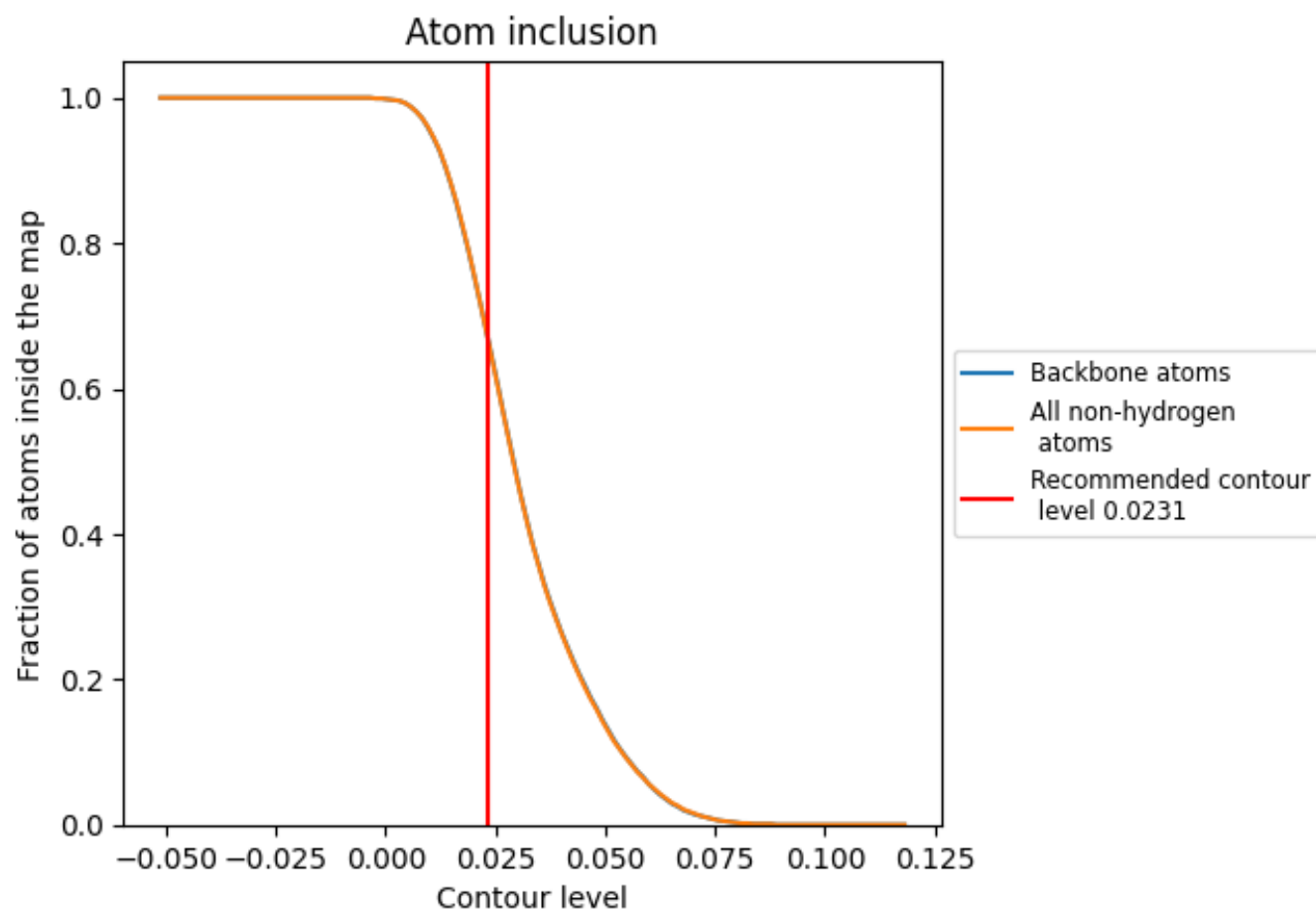
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0231).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 67% 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 (0.0231) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6740	 0.3970
A	 0.6150	 0.3560
B	 0.6250	 0.3530
C	 0.6190	 0.3510
D	 0.6130	 0.3570
E	 0.6200	 0.3510
F	 0.6120	 0.3580
G	 0.5940	 0.3440
H	 0.5760	 0.3340
I	 0.5960	 0.3460
J	 0.5740	 0.3340
K	 0.5920	 0.3440
L	 0.5740	 0.3370
M	 0.6580	 0.3740
N	 0.6510	 0.3650
O	 0.6560	 0.3620
P	 0.6490	 0.3730
Q	 0.6520	 0.3660
R	 0.6520	 0.3740
S	 0.8250	 0.5020
T	 0.7990	 0.4770
U	 0.8020	 0.4790
V	 0.8180	 0.4960
W	 0.8000	 0.4780
X	 0.8200	 0.4970
Y	 0.7390	 0.4650
Z	 0.7300	 0.4550
a	 0.7230	 0.4550
b	 0.7360	 0.4640
c	 0.7230	 0.4560
d	 0.7470	 0.4650
e	 0.6340	 0.3640
f	 0.6530	 0.3620
g	 0.6480	 0.3610
h	 0.6350	 0.3640



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Chain	Atom inclusion	Q-score
i	 0.6510	 0.3600
j	 0.6380	 0.3630
k	 0.7890	 0.4690
l	 0.7880	 0.4650
m	 0.7870	 0.4630
n	 0.7910	 0.4640
o	 0.7740	 0.4620
p	 0.7840	 0.4710
q	 0.8280	 0.5110
r	 0.7450	 0.4410
s	 0.7540	 0.4510
t	 0.8320	 0.5100
u	 0.8290	 0.5100
v	 0.7490	 0.4440
w	 0.7580	 0.4660
x	 0.7420	 0.4710
y	 0.7530	 0.4670