



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 02:28 AM UTC

PDB ID : 7AEF / pdb_00007aef
EMDB ID : EMD-11745
Title : Cryo-EM structure of an extracellular contractile injection system in marine bacterium *Algoriphagus machipongonensis*, the baseplate complex in extended state applied 3-fold symmetry.
Authors : Xu, J.; Ericson, C.; Feldmueller, M.; Lien, Y.W.; Pilhofer, M.
Deposited on : 2020-09-17
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

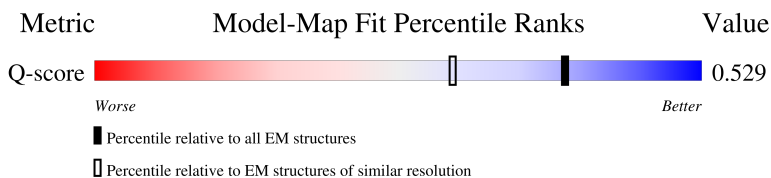
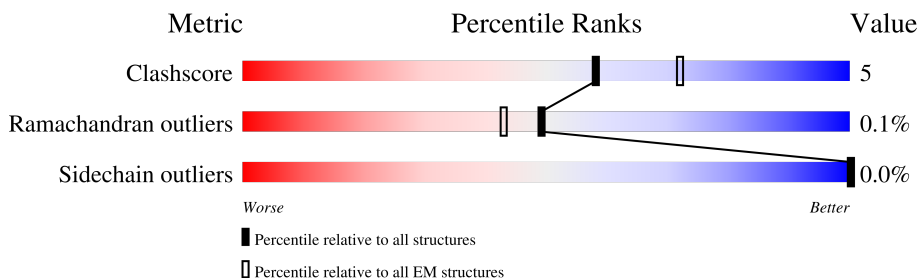
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.80 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	11806 (2.30 - 3.30)

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	933	
1	B	933	
1	C	933	
1	D	933	










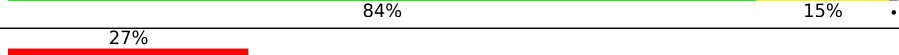

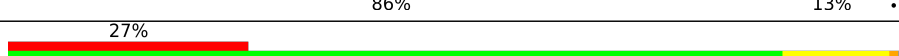

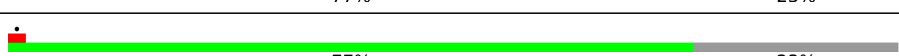
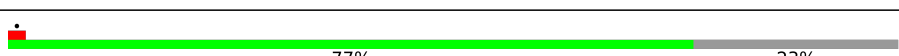
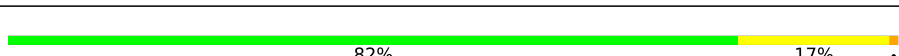



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Mol	Chain	Length	Quality of chain
1	E	933	9% 54% 41%
1	F	933	12% 53% 6% 41%
2	G	1050	12% 85% 11% . .
2	H	1050	12% 86% 9% . .
2	I	1050	15% 85% 11% . .
2	J	1050	15% 84% 11% . .
2	K	1050	14% 84% 11% . .
2	L	1050	14% 84% 11% . .
3	M	228	89% 10% .
3	N	228	90% 8% .
3	O	228	89% 10% .
3	P	228	90% 9% .
3	Q	228	89% 9% .
3	R	228	89% 10% .
4	S	137	. 88% 9% .
4	T	137	. 87% 10% .
4	U	137	. 87% 10% .
4	V	137	. 88% 9% .
4	W	137	. 86% 11% .
4	X	137	. 88% 9% .
5	Y	147	. 88% 10% .
5	Z	147	. 88% 10% .
5	a	147	. 88% 10% .
5	b	147	. 88% 11% .
5	c	147	. 88% 11% .

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Mol	Chain	Length	Quality of chain
5	d	147	 89% 10%
6	e	692	 27% 86% 8% 5%
6	f	692	 27% 86% 8% 5%
6	g	692	 26% 86% 8% 5%
6	h	692	 27% 86% 8% 5%
6	i	692	 27% 86% 8% 5%
6	j	692	 27% 86% 8% 5%
7	k	142	 26% 84% 15%
7	l	142	 27% 85% 15%
7	m	142	 27% 84% 15%
7	n	142	 27% 85% 15%
7	o	142	 27% 86% 13% 2%
7	p	142	 27% 87% 12% 2%
8	t	52	 77% 23%
8	u	52	 77% 23%
8	v	52	 77% 23%
9	q	581	 82% 17%
9	r	581	 84% 15%
9	s	581	 82% 18%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 149535 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 baseplate protein (Algo12).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	549	4447	2845	730	858	14	0	0
1	B	549	4447	2845	730	858	14	0	0
1	C	549	4447	2845	730	858	14	0	0
1	D	549	4447	2845	730	858	14	0	0
1	E	549	4447	2845	730	858	14	0	0
1	F	549	4447	2845	730	858	14	0	0

- Molecule 2 is a protein called Baseplate_J domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	G	1011	7762	4951	1284	1512	15	0	0
2	H	1011	7762	4951	1284	1512	15	0	0
2	I	1011	7762	4951	1284	1512	15	0	0
2	J	1011	7762	4951	1284	1512	15	0	0
2	K	1011	7762	4951	1284	1512	15	0	0
2	L	1011	7762	4951	1284	1512	15	0	0

- Molecule 3 is a protein called LysM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	M	225	1849	1185	304	355	5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	225	Total	C	N	O	S	0	0
			1849	1185	304	355	5		
3	O	225	Total	C	N	O	S	0	0
			1849	1185	304	355	5		
3	P	225	Total	C	N	O	S	0	0
			1849	1185	304	355	5		
3	Q	225	Total	C	N	O	S	0	0
			1849	1185	304	355	5		
3	R	225	Total	C	N	O	S	0	0
			1849	1185	304	355	5		

- Molecule 4 is a protein called Putative tail lysozyme.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	S	133	Total	C	N	O	S	0	0
			1074	690	174	207	3		
4	T	133	Total	C	N	O	S	0	0
			1074	690	174	207	3		
4	U	133	Total	C	N	O	S	0	0
			1074	690	174	207	3		
4	V	133	Total	C	N	O	S	0	0
			1074	690	174	207	3		
4	W	133	Total	C	N	O	S	0	0
			1074	690	174	207	3		
4	X	133	Total	C	N	O	S	0	0
			1074	690	174	207	3		

- Molecule 5 is a protein called Phospholipid/glycerol acyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Y	145	Total	C	N	O	S	0	0
			1192	773	190	226	3		
5	Z	145	Total	C	N	O	S	0	0
			1192	773	190	226	3		
5	a	145	Total	C	N	O	S	0	0
			1192	773	190	226	3		
5	b	145	Total	C	N	O	S	0	0
			1192	773	190	226	3		
5	c	145	Total	C	N	O	S	0	0
			1192	773	190	226	3		
5	d	145	Total	C	N	O	S	0	0
			1192	773	190	226	3		

- Molecule 6 is a protein called Putative phage tail sheath protein FI.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	e	655	Total	C	N	O	S	0	0
			5057	3204	832	1009	12		
6	f	655	Total	C	N	O	S	0	0
			5057	3204	832	1009	12		
6	g	655	Total	C	N	O	S	0	0
			5057	3204	832	1009	12		
6	h	655	Total	C	N	O	S	0	0
			5057	3204	832	1009	12		
6	i	655	Total	C	N	O	S	0	0
			5057	3204	832	1009	12		
6	j	655	Total	C	N	O	S	0	0
			5057	3204	832	1009	12		

- Molecule 7 is a protein called Phage tail protein.

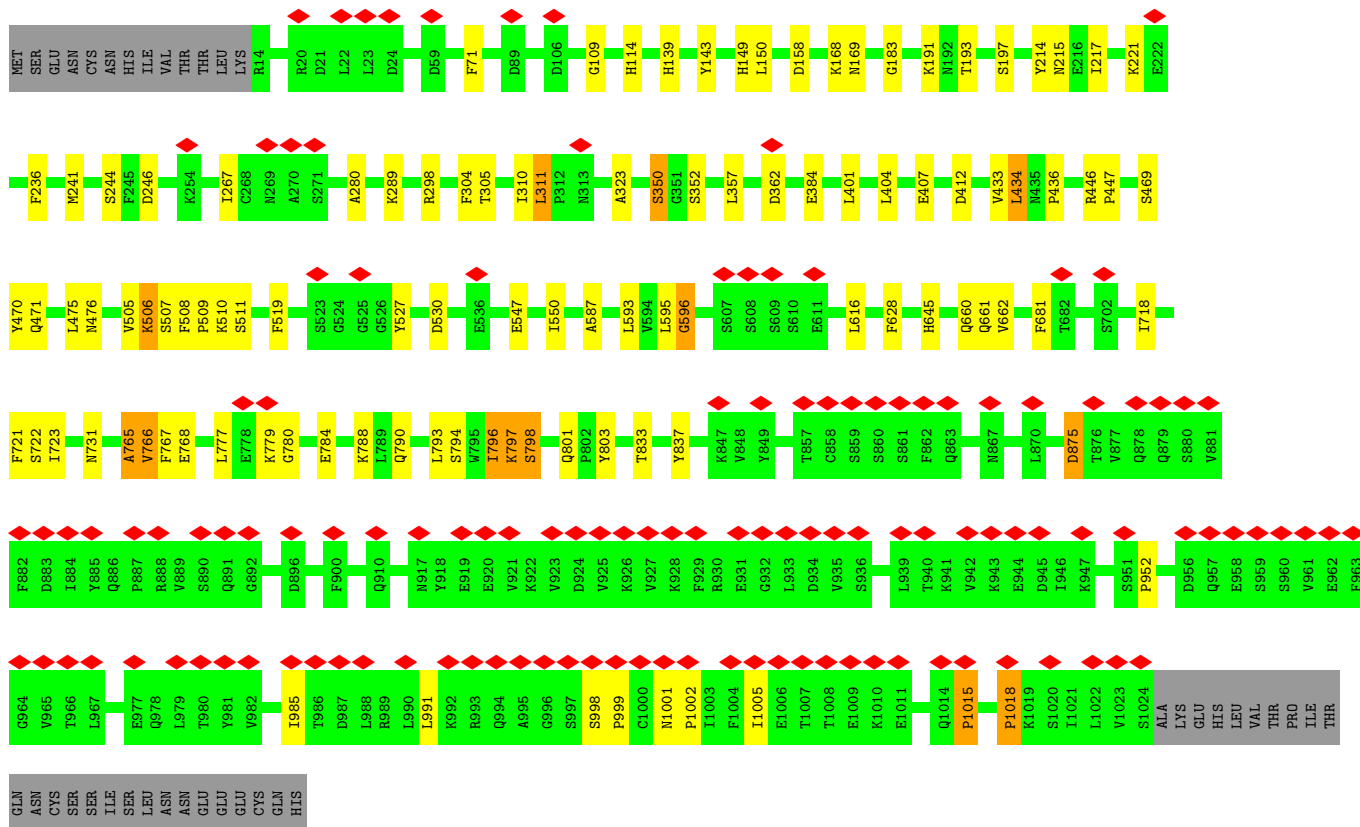
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	k	141	Total	C	N	O	S	0	0
			1145	731	190	221	3		
7	l	141	Total	C	N	O	S	0	0
			1145	731	190	221	3		
7	m	141	Total	C	N	O	S	0	0
			1145	731	190	221	3		
7	n	141	Total	C	N	O	S	0	0
			1145	731	190	221	3		
7	o	141	Total	C	N	O	S	0	0
			1145	731	190	221	3		
7	p	141	Total	C	N	O	S	0	0
			1145	731	190	221	3		

- Molecule 8 is a protein called inner protein (Algo6).

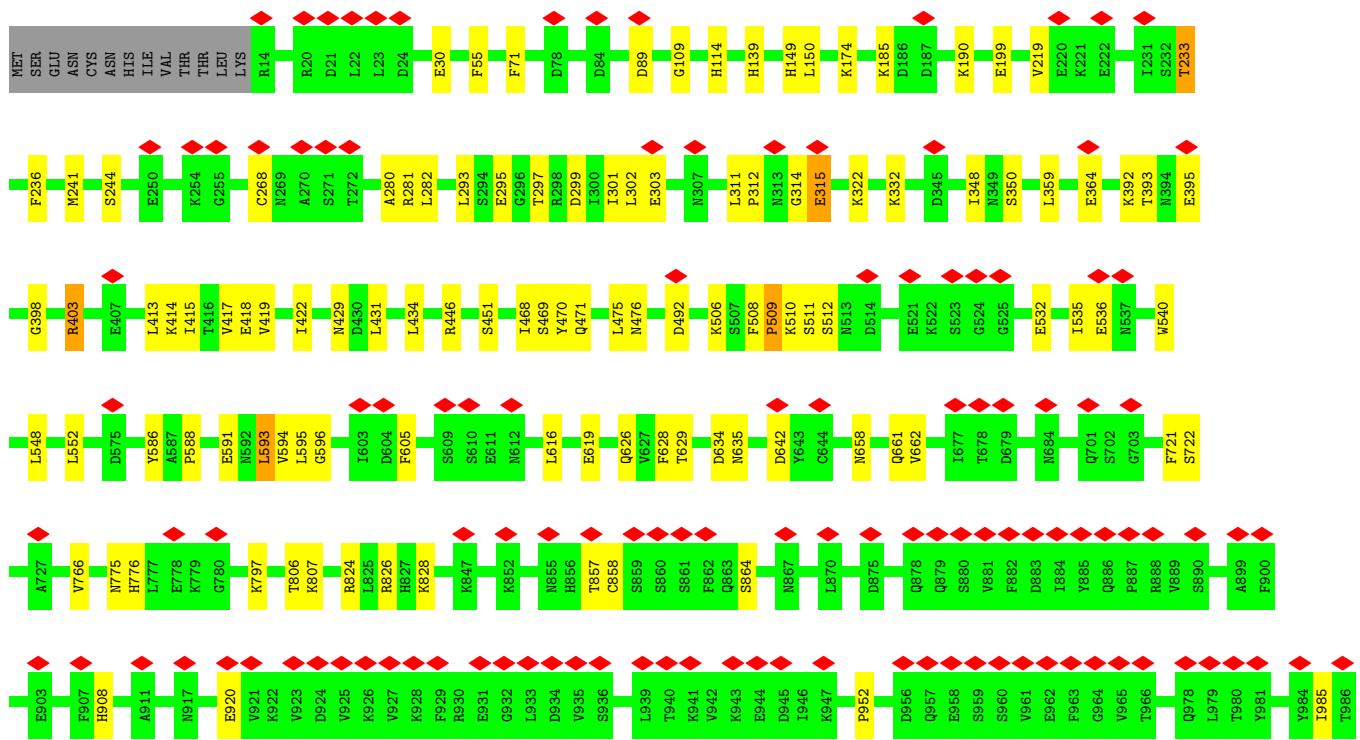
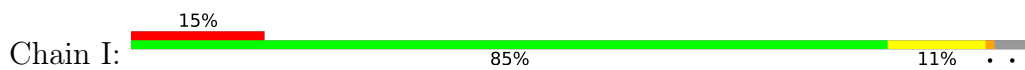
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	t	40	Total	C	N	O	S	0	0
			324	202	55	66	1		
8	u	40	Total	C	N	O	S	0	0
			324	202	55	66	1		
8	v	40	Total	C	N	O	S	0	0
			324	202	55	66	1		

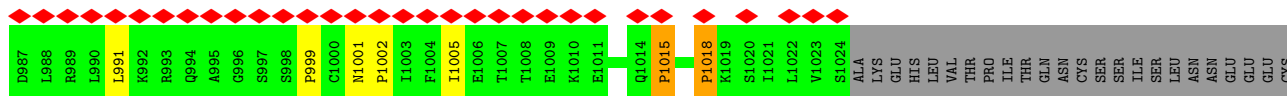
- Molecule 9 is a protein called Phosphoserine phosphatase SerB.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	q	580	4469	2771	765	920	13	0	0
9	r	580	4469	2771	765	920	13	0	0
9	s	580	4469	2771	765	920	13	0	0



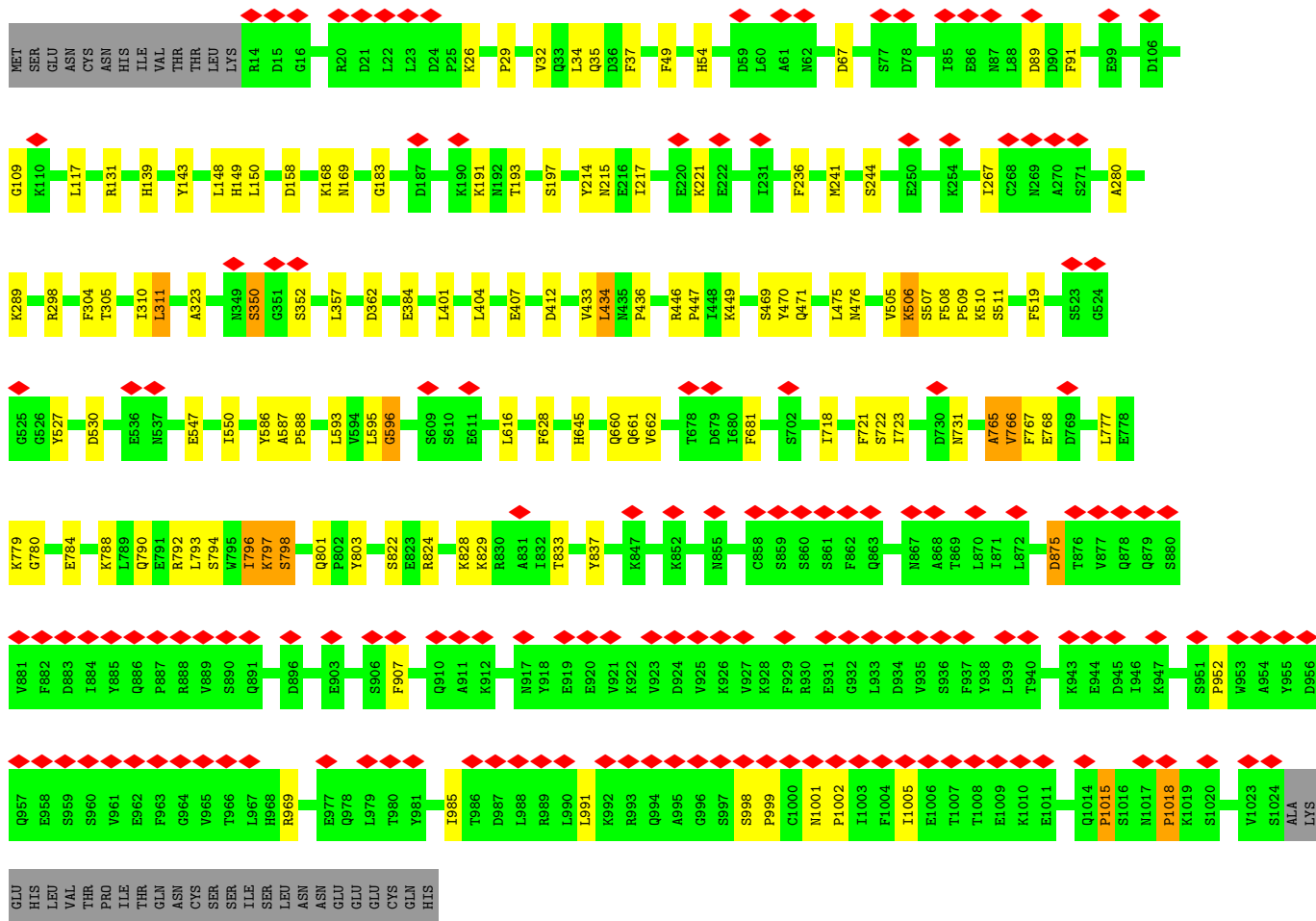
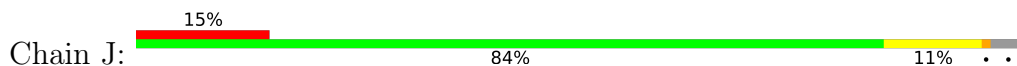
• Molecule 2: Baseplate_J domain-containing protein



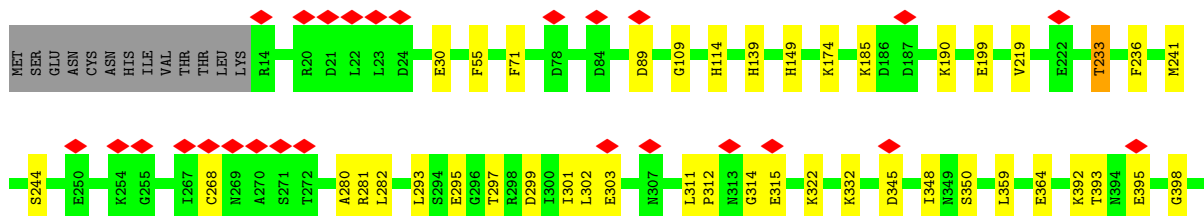
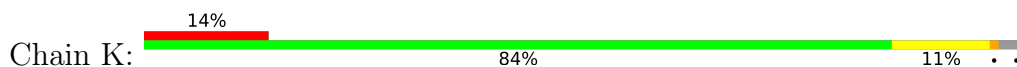


GLN
HIS

• Molecule 2: Baseplate_J domain-containing protein




• Molecule 2: Baseplate_J domain-containing protein




PRO
ILE
THR
GLN
ASN
CYS
SER
SER
ILE
LEU
ASN
ASN
GLU
GLU
GLU
CYS
GLN
HIS

- Molecule 3: LysM domain-containing protein

Chain M:  89% 10%




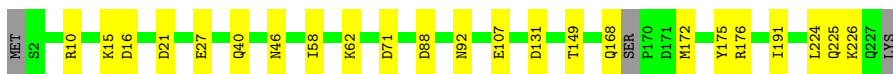
- Molecule 3: LysM domain-containing protein

Chain N:  90% 8%




- Molecule 3: LysM domain-containing protein

Chain O:  89% 10%




- Molecule 3: LysM domain-containing protein

Chain P:  90% 9%




- Molecule 3: LysM domain-containing protein

Chain Q:  89% 9%



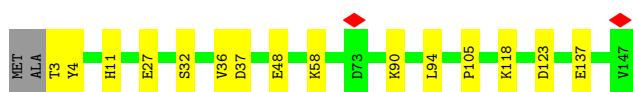
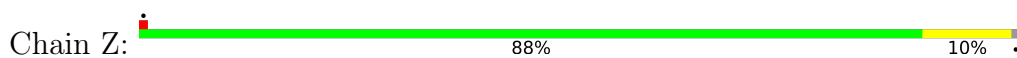
- Molecule 3: LysM domain-containing protein

Chain R:  89% 10%

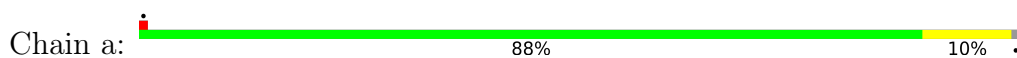


- Molecule 4: Putative tail lysozyme

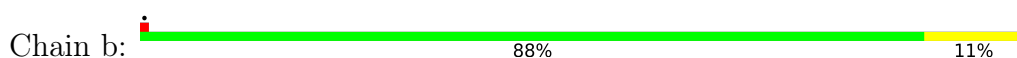
• Molecule 5: Phospholipid/glycerol acyltransferase



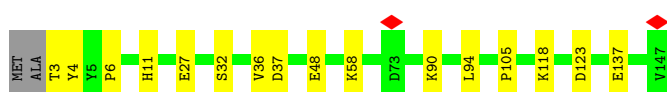
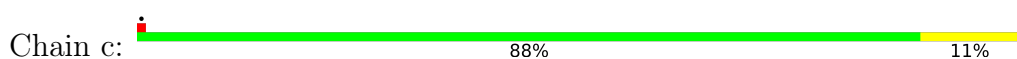
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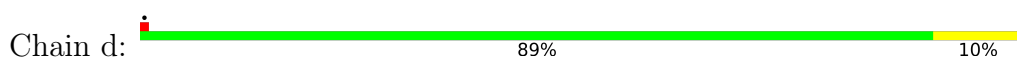
• Molecule 5: Phospholipid/glycerol acyltransferase



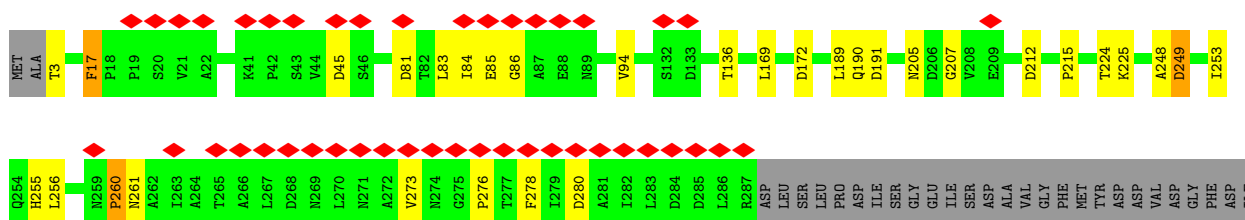
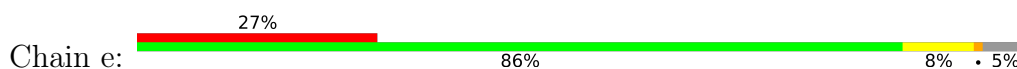
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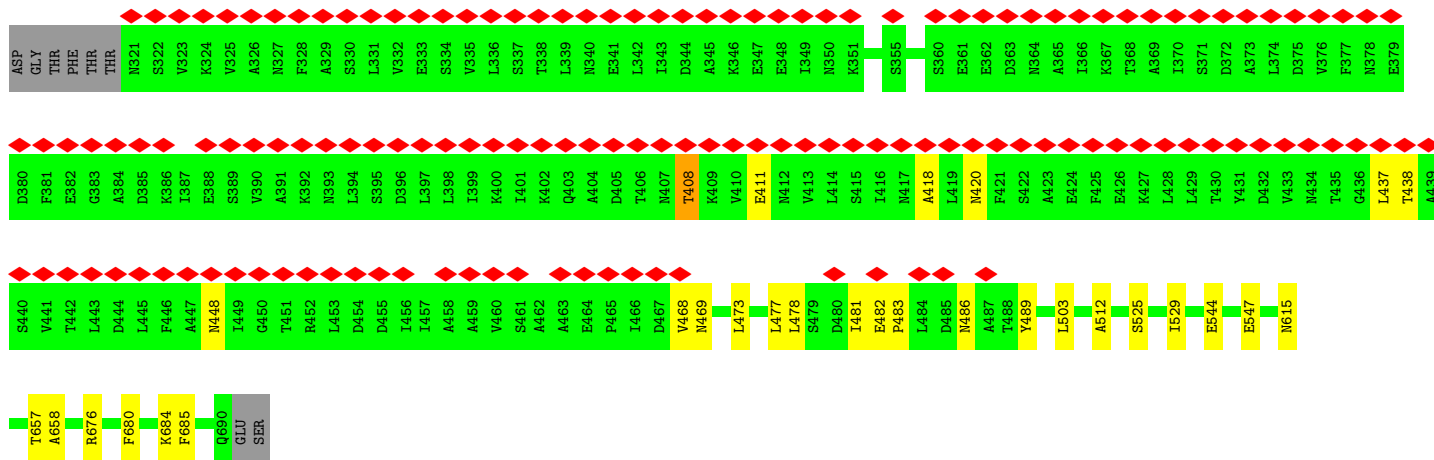


• Molecule 5: Phospholipid/glycerol acyltransferase

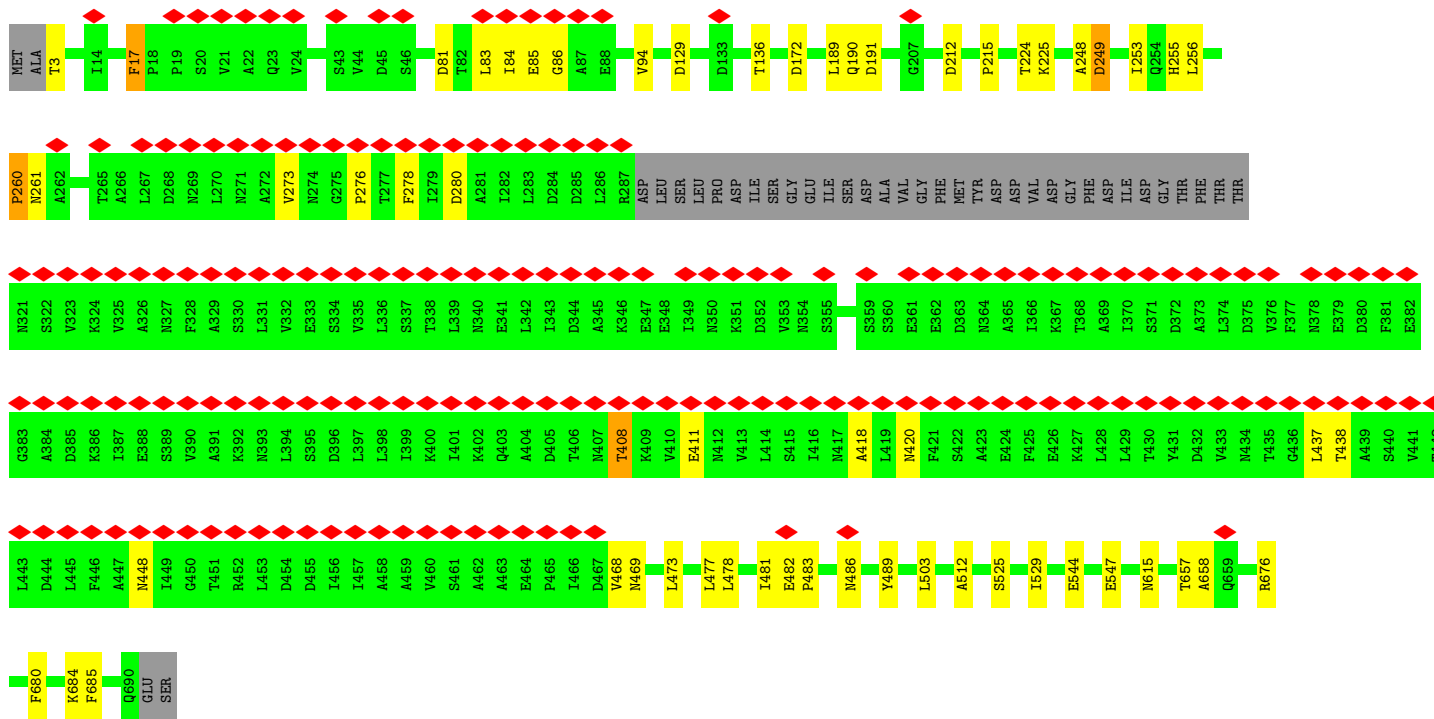
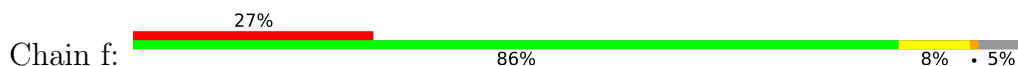


• Molecule 6: Putative phage tail sheath protein FI

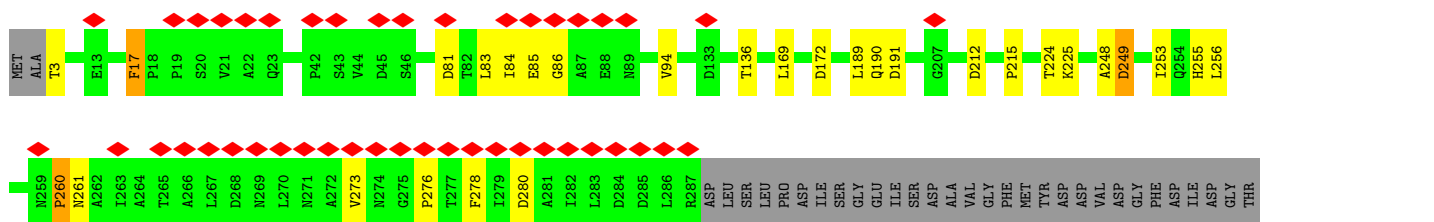
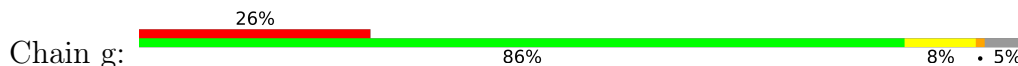


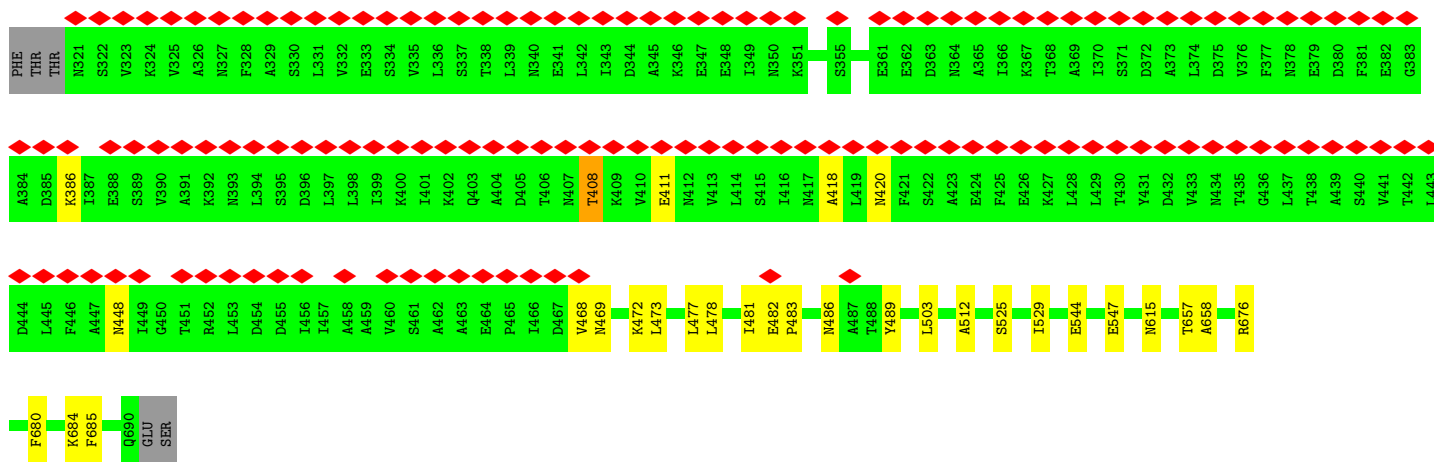


• Molecule 6: Putative phage tail sheath protein FI

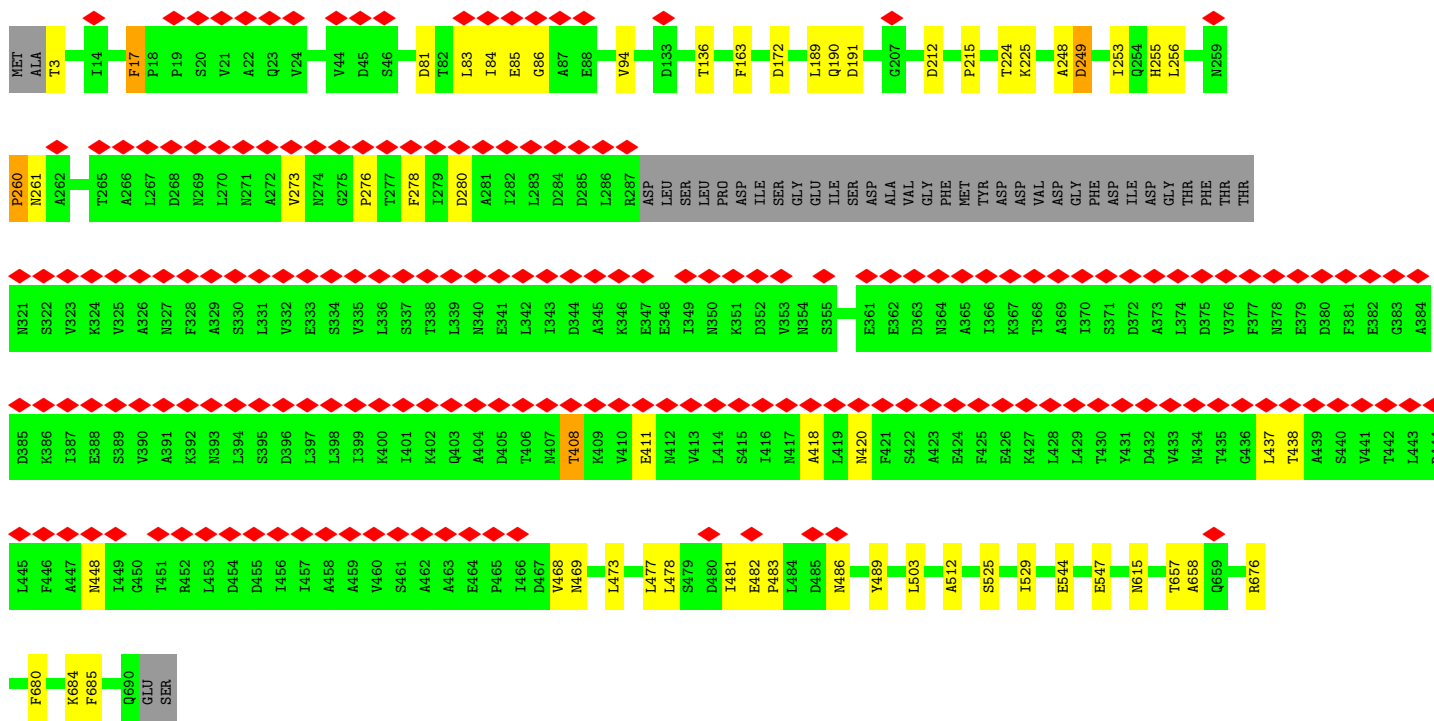
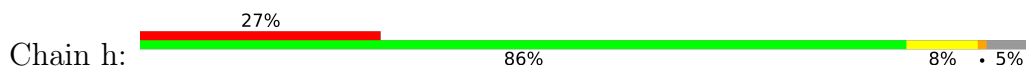


• Molecule 6: Putative phage tail sheath protein FI

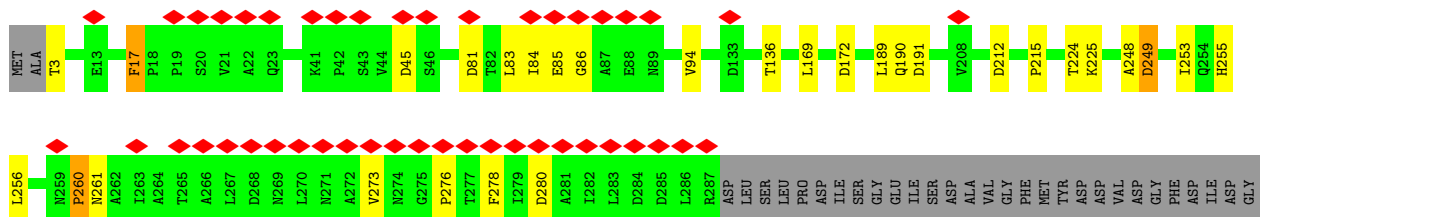
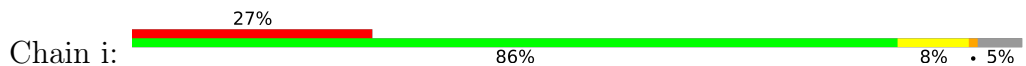


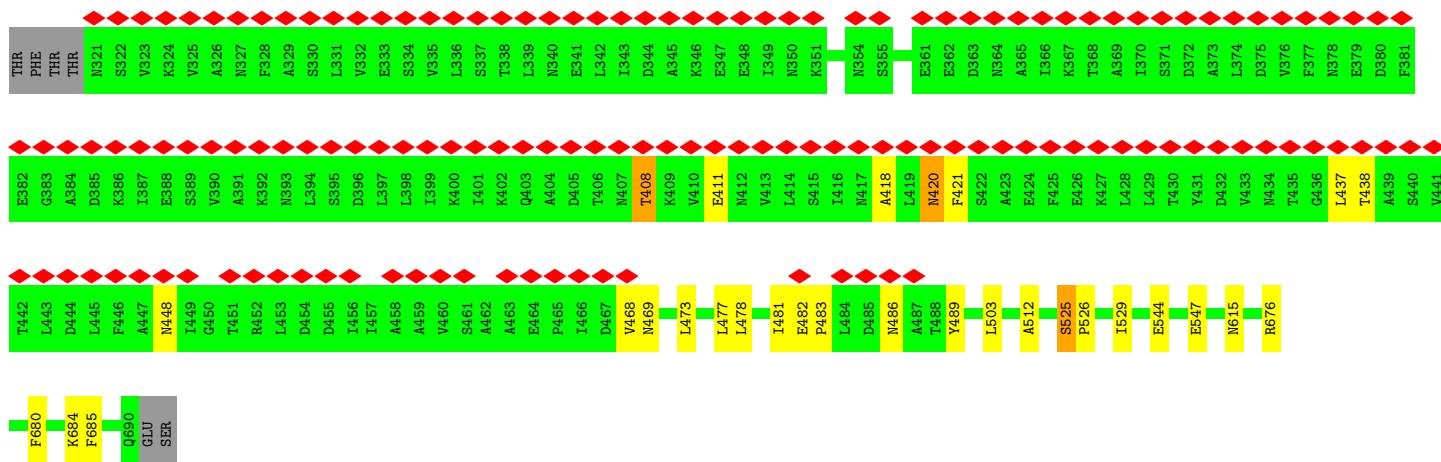


• Molecule 6: Putative phage tail sheath protein FI

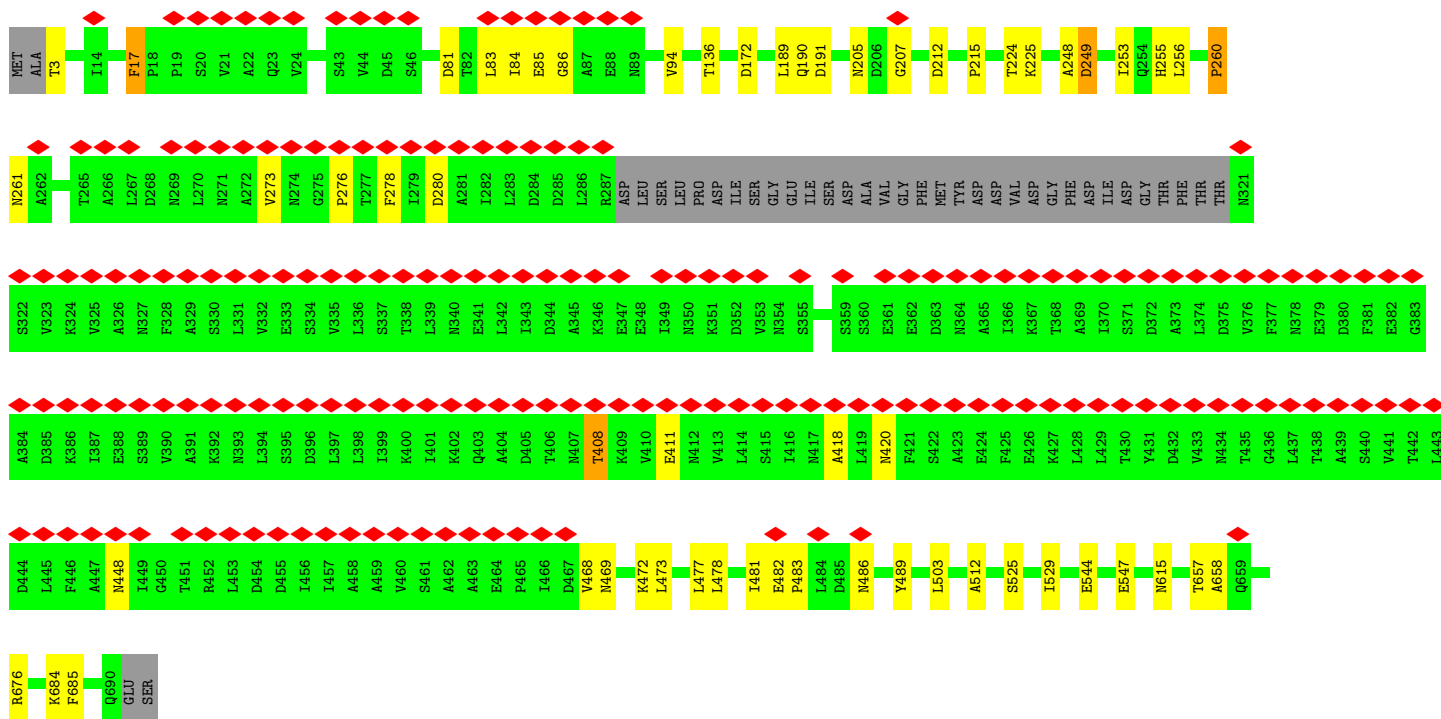
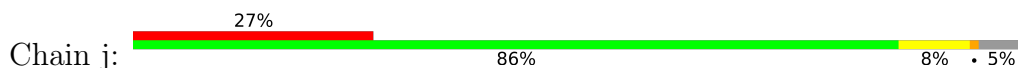


• Molecule 6: Putative phage tail sheath protein FI

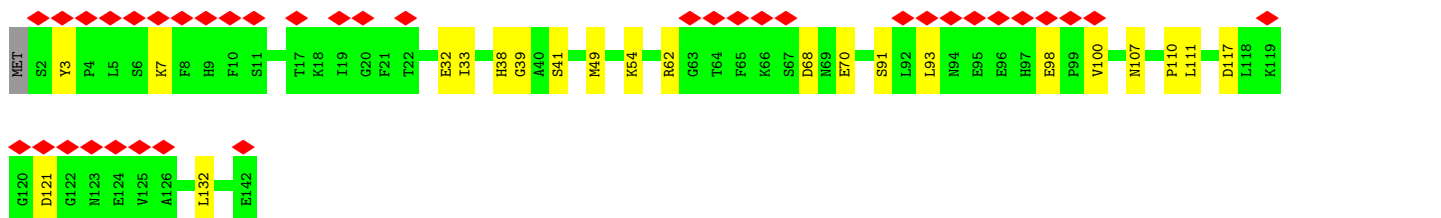
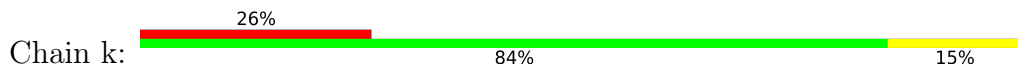




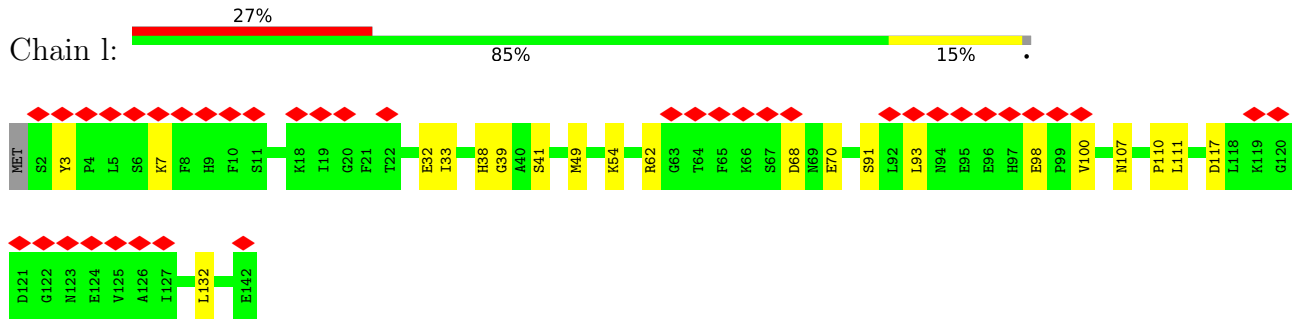
• Molecule 6: Putative phage tail sheath protein FI



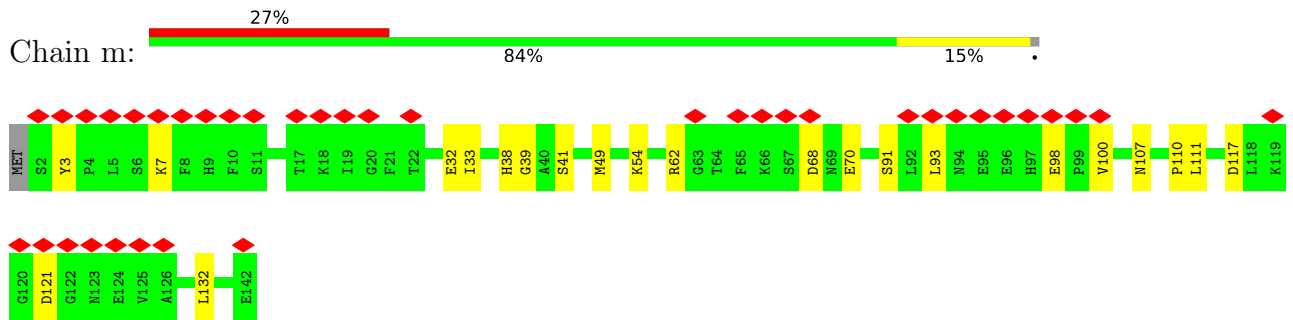
• Molecule 7: Phage tail protein



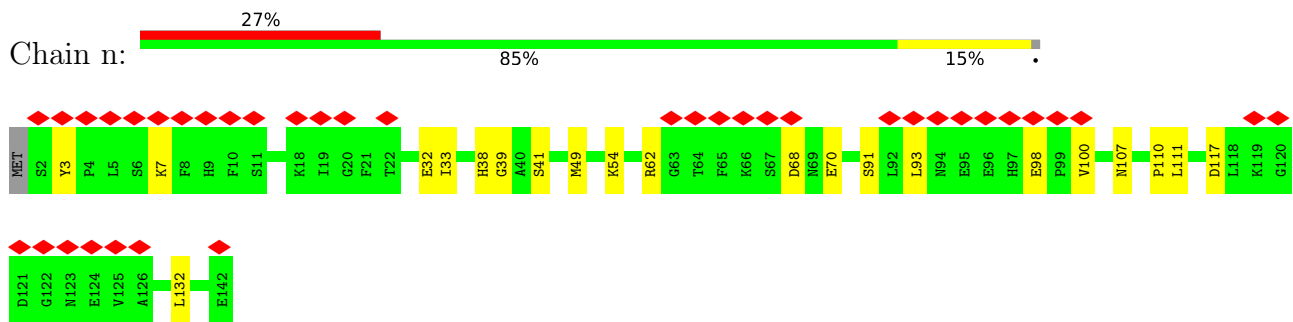
• Molecule 7: Phage tail protein



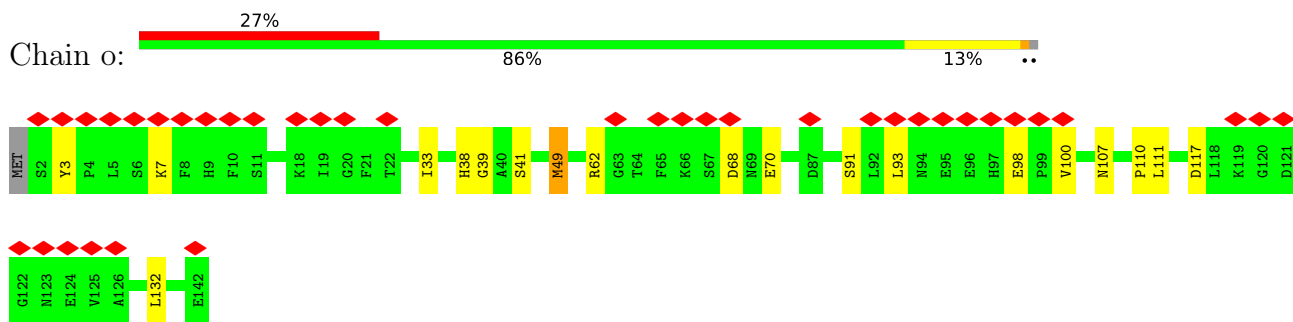
• Molecule 7: Phage tail protein



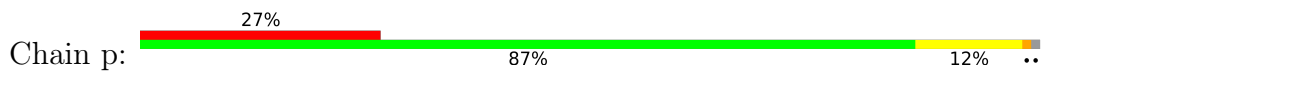
• Molecule 7: Phage tail protein

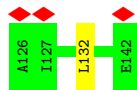
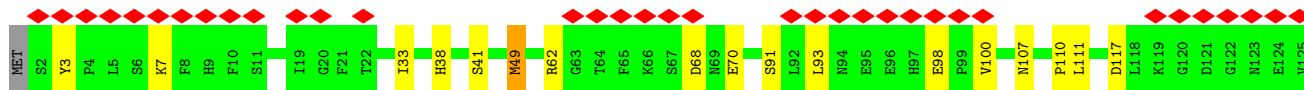


• Molecule 7: Phage tail protein

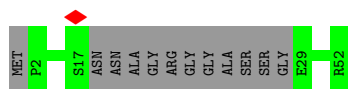
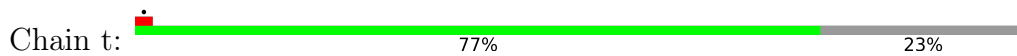


• Molecule 7: Phage tail protein

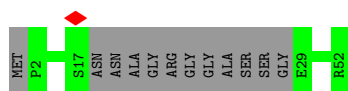
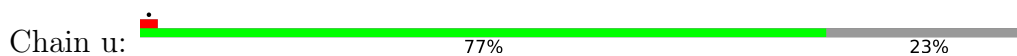




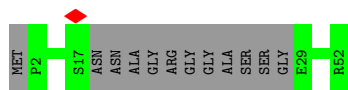
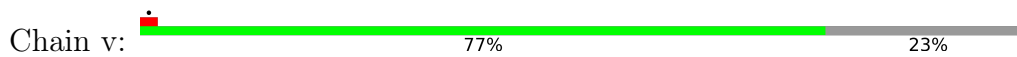
• Molecule 8: inner protein (Algo6)



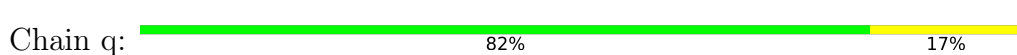
• Molecule 8: inner protein (Algo6)



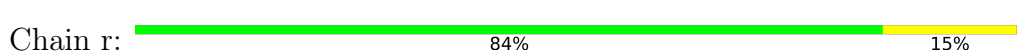
• Molecule 8: inner protein (Algo6)

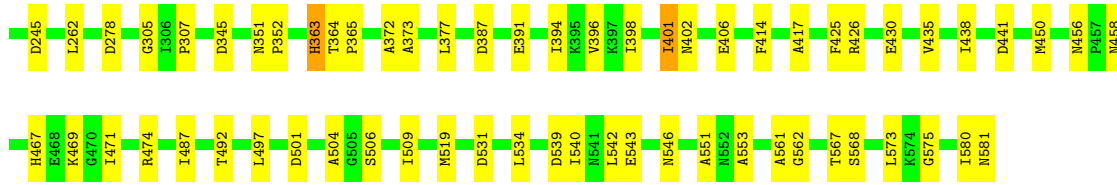


• Molecule 9: Phosphoserine phosphatase SerB

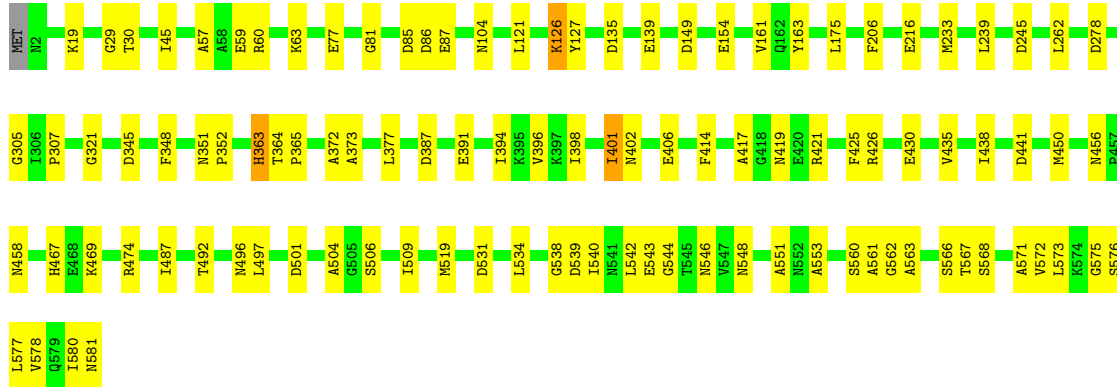
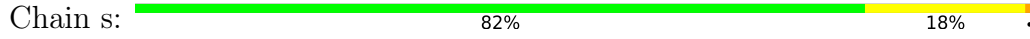


• Molecule 9: Phosphoserine phosphatase SerB





• Molecule 9: Phosphoserine phosphatase SerB



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	82969	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.219	Depositor
Minimum map value	-0.155	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	A	0.69	0/4531	1.00	7/6117 (0.1%)
1	B	0.69	0/4531	1.01	7/6117 (0.1%)
1	C	0.69	0/4531	1.00	7/6117 (0.1%)
1	D	0.69	0/4531	1.01	7/6117 (0.1%)
1	E	0.69	0/4531	1.00	7/6117 (0.1%)
1	F	0.69	0/4531	1.01	7/6117 (0.1%)
2	G	0.73	7/7935 (0.1%)	1.08	28/10781 (0.3%)
2	H	0.94	16/7935 (0.2%)	1.18	56/10781 (0.5%)
2	I	0.73	7/7935 (0.1%)	1.08	27/10781 (0.3%)
2	J	0.94	17/7935 (0.2%)	1.18	56/10781 (0.5%)
2	K	0.73	7/7935 (0.1%)	1.08	27/10781 (0.3%)
2	L	0.94	17/7935 (0.2%)	1.18	56/10781 (0.5%)
3	M	0.41	0/1889	0.64	2/2544 (0.1%)
3	N	0.45	0/1889	0.60	0/2544
3	O	0.41	0/1889	0.64	2/2544 (0.1%)
3	P	0.45	0/1889	0.60	0/2544
3	Q	0.41	0/1889	0.64	2/2544 (0.1%)
3	R	0.45	0/1889	0.60	0/2544
4	S	0.64	0/1096	1.03	2/1483 (0.1%)
4	T	0.66	0/1096	1.03	4/1483 (0.3%)
4	U	0.64	0/1096	1.03	2/1483 (0.1%)
4	V	0.66	0/1096	1.03	4/1483 (0.3%)
4	W	0.64	0/1096	1.03	4/1483 (0.3%)
4	X	0.66	0/1096	1.03	4/1483 (0.3%)
5	Y	0.69	0/1226	1.05	3/1664 (0.2%)
5	Z	0.69	0/1226	1.05	3/1664 (0.2%)
5	a	0.69	0/1226	1.05	3/1664 (0.2%)
5	b	0.69	0/1226	1.05	3/1664 (0.2%)
5	c	0.69	0/1226	1.05	3/1664 (0.2%)
5	d	0.69	0/1226	1.05	3/1664 (0.2%)
6	e	0.74	1/5155 (0.0%)	1.09	24/7021 (0.3%)
6	f	0.74	1/5155 (0.0%)	1.09	22/7021 (0.3%)
6	g	0.74	1/5155 (0.0%)	1.09	25/7021 (0.4%)
6	h	0.74	1/5155 (0.0%)	1.09	24/7021 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	i	0.74	1/5155 (0.0%)	1.09	24/7021 (0.3%)
6	j	0.74	1/5155 (0.0%)	1.09	22/7021 (0.3%)
7	k	0.90	0/1172	1.28	15/1584 (0.9%)
7	l	0.90	0/1172	1.28	15/1584 (0.9%)
7	m	0.90	0/1172	1.28	15/1584 (0.9%)
7	n	0.90	0/1172	1.28	15/1584 (0.9%)
7	o	0.90	0/1172	1.28	15/1584 (0.9%)
7	p	0.90	0/1172	1.28	15/1584 (0.9%)
8	t	0.35	0/324	0.48	0/432
8	u	0.35	0/324	0.48	0/432
8	v	0.35	0/324	0.48	0/432
9	q	0.94	1/4536 (0.0%)	1.28	46/6145 (0.7%)
9	r	0.94	2/4536 (0.0%)	1.28	48/6145 (0.8%)
9	s	0.94	1/4536 (0.0%)	1.28	47/6145 (0.8%)
All	All	0.77	81/152604 (0.1%)	1.08	708/206895 (0.3%)

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
2	G	0	5
2	H	0	2
2	I	0	4
2	J	0	2
2	K	0	4
2	L	0	2
All	All	0	19

The worst 5 of 81 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	509	PRO	C-N	26.38	1.70	1.33
2	I	509	PRO	C-N	26.38	1.70	1.33
2	G	509	PRO	C-N	26.36	1.70	1.33
2	L	506	LYS	C-N	20.74	1.67	1.33
2	H	506	LYS	C-N	20.67	1.67	1.33

The worst 5 of 708 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	446	ARG	CA-C-N	19.97	141.31	120.14
2	J	446	ARG	C-N-CA	19.97	141.31	120.14
2	H	446	ARG	CA-C-N	19.92	141.25	120.14
2	H	446	ARG	C-N-CA	19.92	141.25	120.14
2	L	446	ARG	CA-C-N	19.91	141.24	120.14

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	364	GLU	Sidechain
2	G	48	ASN	Sidechain
2	G	492	ASP	Sidechain
2	G	635	ASN	Sidechain
2	G	642	ASP	Sidechain

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	4447	0	4459	56	0
1	B	4447	0	4459	45	0
1	C	4447	0	4459	53	0
1	D	4447	0	4459	96	0
1	E	4447	0	4459	57	0
1	F	4447	0	4459	100	0
2	G	7762	0	7320	70	0
2	H	7762	0	7321	58	0
2	I	7762	0	7320	77	0
2	J	7762	0	7321	111	0
2	K	7762	0	7320	79	0
2	L	7762	0	7321	105	0
3	M	1849	0	1819	19	0
3	N	1849	0	1819	17	0
3	O	1849	0	1819	20	0
3	P	1849	0	1819	20	0
3	Q	1849	0	1819	20	0
3	R	1849	0	1819	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	S	1074	0	1076	17	0
4	T	1074	0	1076	15	0
4	U	1074	0	1076	18	0
4	V	1074	0	1076	16	0
4	W	1074	0	1076	18	0
4	X	1074	0	1076	13	0
5	Y	1192	0	1147	11	0
5	Z	1192	0	1147	12	0
5	a	1192	0	1147	12	0
5	b	1192	0	1147	13	0
5	c	1192	0	1147	13	0
5	d	1192	0	1147	11	0
6	e	5057	0	4910	62	0
6	f	5057	0	4910	63	0
6	g	5057	0	4910	61	0
6	h	5057	0	4910	60	0
6	i	5057	0	4910	62	0
6	j	5057	0	4910	59	0
7	k	1145	0	1118	12	0
7	l	1145	0	1118	10	0
7	m	1145	0	1118	12	0
7	n	1145	0	1118	13	0
7	o	1145	0	1118	12	0
7	p	1145	0	1118	11	0
8	t	324	0	337	0	0
8	u	324	0	337	0	0
8	v	324	0	337	0	0
9	q	4469	0	4361	107	0
9	r	4469	0	4361	91	0
9	s	4469	0	4361	113	0
All	All	149535	0	145191	1387	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 5.

The worst 5 of 1387 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)
2:L:506:LYS:C	2:L:507:SER:N	1.67	1.50
2:G:509:PRO:C	2:G:510:LYS:N	1.70	1.49
2:H:506:LYS:C	2:H:507:SER:N	1.67	1.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:506:LYS:C	2:J:507:SER:N	1.67	1.47
2:I:509:PRO:C	2:I:510:LYS:N	1.70	1.47

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	547/933 (59%)	533 (97%)	14 (3%)	0	100	100
1	B	547/933 (59%)	533 (97%)	14 (3%)	0	100	100
1	C	547/933 (59%)	533 (97%)	14 (3%)	0	100	100
1	D	547/933 (59%)	533 (97%)	14 (3%)	0	100	100
1	E	547/933 (59%)	533 (97%)	14 (3%)	0	100	100
1	F	547/933 (59%)	533 (97%)	14 (3%)	0	100	100
2	G	1009/1050 (96%)	971 (96%)	35 (4%)	3 (0%)	36	66
2	H	1009/1050 (96%)	971 (96%)	35 (4%)	3 (0%)	36	66
2	I	1009/1050 (96%)	971 (96%)	35 (4%)	3 (0%)	36	66
2	J	1009/1050 (96%)	971 (96%)	35 (4%)	3 (0%)	36	66
2	K	1009/1050 (96%)	971 (96%)	35 (4%)	3 (0%)	36	66
2	L	1009/1050 (96%)	971 (96%)	35 (4%)	3 (0%)	36	66
3	M	221/228 (97%)	218 (99%)	3 (1%)	0	100	100
3	N	221/228 (97%)	217 (98%)	4 (2%)	0	100	100
3	O	221/228 (97%)	218 (99%)	3 (1%)	0	100	100
3	P	221/228 (97%)	217 (98%)	4 (2%)	0	100	100
3	Q	221/228 (97%)	219 (99%)	2 (1%)	0	100	100
3	R	221/228 (97%)	217 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	S	131/137 (96%)	130 (99%)	1 (1%)	0	100	100
4	T	131/137 (96%)	130 (99%)	1 (1%)	0	100	100
4	U	131/137 (96%)	130 (99%)	1 (1%)	0	100	100
4	V	131/137 (96%)	130 (99%)	1 (1%)	0	100	100
4	W	131/137 (96%)	130 (99%)	1 (1%)	0	100	100
4	X	131/137 (96%)	130 (99%)	1 (1%)	0	100	100
5	Y	143/147 (97%)	142 (99%)	1 (1%)	0	100	100
5	Z	143/147 (97%)	142 (99%)	1 (1%)	0	100	100
5	a	143/147 (97%)	142 (99%)	1 (1%)	0	100	100
5	b	143/147 (97%)	142 (99%)	1 (1%)	0	100	100
5	c	143/147 (97%)	142 (99%)	1 (1%)	0	100	100
5	d	143/147 (97%)	142 (99%)	1 (1%)	0	100	100
6	e	651/692 (94%)	635 (98%)	16 (2%)	0	100	100
6	f	651/692 (94%)	635 (98%)	16 (2%)	0	100	100
6	g	651/692 (94%)	635 (98%)	16 (2%)	0	100	100
6	h	651/692 (94%)	635 (98%)	16 (2%)	0	100	100
6	i	651/692 (94%)	635 (98%)	16 (2%)	0	100	100
6	j	651/692 (94%)	635 (98%)	16 (2%)	0	100	100
7	k	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
7	l	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
7	m	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
7	n	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
7	o	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
7	p	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
8	t	36/52 (69%)	36 (100%)	0	0	100	100
8	u	36/52 (69%)	36 (100%)	0	0	100	100
8	v	36/52 (69%)	36 (100%)	0	0	100	100
9	q	578/581 (100%)	565 (98%)	13 (2%)	0	100	100
9	r	578/581 (100%)	565 (98%)	13 (2%)	0	100	100
9	s	578/581 (100%)	565 (98%)	13 (2%)	0	100	100
All	All	18888/21873 (86%)	18397 (97%)	473 (2%)	18 (0%)	49	77

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	1001	ASN
2	G	1015	PRO
2	G	1018	PRO
2	H	1001	ASN
2	H	1015	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	497/842 (59%)	497 (100%)	0	100	100
1	B	497/842 (59%)	497 (100%)	0	100	100
1	C	497/842 (59%)	497 (100%)	0	100	100
1	D	497/842 (59%)	497 (100%)	0	100	100
1	E	497/842 (59%)	497 (100%)	0	100	100
1	F	497/842 (59%)	497 (100%)	0	100	100
2	G	814/955 (85%)	813 (100%)	1 (0%)	88	97
2	H	814/955 (85%)	814 (100%)	0	100	100
2	I	814/955 (85%)	813 (100%)	1 (0%)	88	97
2	J	814/955 (85%)	814 (100%)	0	100	100
2	K	814/955 (85%)	813 (100%)	1 (0%)	88	97
2	L	814/955 (85%)	814 (100%)	0	100	100
3	M	201/204 (98%)	201 (100%)	0	100	100
3	N	201/204 (98%)	201 (100%)	0	100	100
3	O	201/204 (98%)	201 (100%)	0	100	100
3	P	201/204 (98%)	201 (100%)	0	100	100
3	Q	201/204 (98%)	201 (100%)	0	100	100
3	R	201/204 (98%)	201 (100%)	0	100	100
4	S	121/125 (97%)	121 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	T	121/125 (97%)	121 (100%)	0	100	100
4	U	121/125 (97%)	121 (100%)	0	100	100
4	V	121/125 (97%)	121 (100%)	0	100	100
4	W	121/125 (97%)	121 (100%)	0	100	100
4	X	121/125 (97%)	121 (100%)	0	100	100
5	Y	134/135 (99%)	134 (100%)	0	100	100
5	Z	134/135 (99%)	134 (100%)	0	100	100
5	a	134/135 (99%)	134 (100%)	0	100	100
5	b	134/135 (99%)	134 (100%)	0	100	100
5	c	134/135 (99%)	134 (100%)	0	100	100
5	d	134/135 (99%)	134 (100%)	0	100	100
6	e	547/593 (92%)	547 (100%)	0	100	100
6	f	547/593 (92%)	547 (100%)	0	100	100
6	g	547/593 (92%)	547 (100%)	0	100	100
6	h	547/593 (92%)	547 (100%)	0	100	100
6	i	547/593 (92%)	547 (100%)	0	100	100
6	j	547/593 (92%)	547 (100%)	0	100	100
7	k	127/128 (99%)	127 (100%)	0	100	100
7	l	127/128 (99%)	127 (100%)	0	100	100
7	m	127/128 (99%)	127 (100%)	0	100	100
7	n	127/128 (99%)	127 (100%)	0	100	100
7	o	127/128 (99%)	127 (100%)	0	100	100
7	p	127/128 (99%)	127 (100%)	0	100	100
8	t	39/45 (87%)	39 (100%)	0	100	100
8	u	39/45 (87%)	39 (100%)	0	100	100
8	v	39/45 (87%)	39 (100%)	0	100	100
9	q	499/500 (100%)	499 (100%)	0	100	100
9	r	499/500 (100%)	499 (100%)	0	100	100
9	s	499/500 (100%)	499 (100%)	0	100	100
All	All	16260/19527 (83%)	16257 (100%)	3 (0%)	100	100

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

Mol	Chain	Res	Type
2	G	359	LEU
2	I	359	LEU
2	K	359	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
9	r	105	GLN
9	r	314	ASN
9	s	467	HIS
2	K	139	HIS
2	K	114	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	3
2	J	3
2	L	3
2	G	1
2	I	1
2	K	1

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	509:PRO	C	510:LYS	N	1.70
1	I	509:PRO	C	510:LYS	N	1.70
1	K	509:PRO	C	510:LYS	N	1.70
1	H	506:LYS	C	507:SER	N	1.67
1	J	506:LYS	C	507:SER	N	1.67

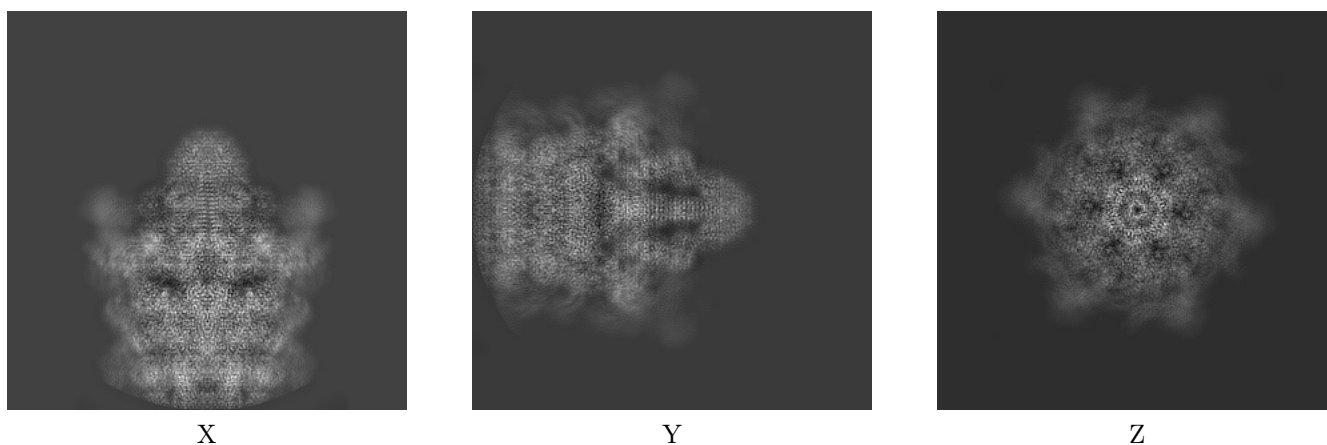
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11745. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

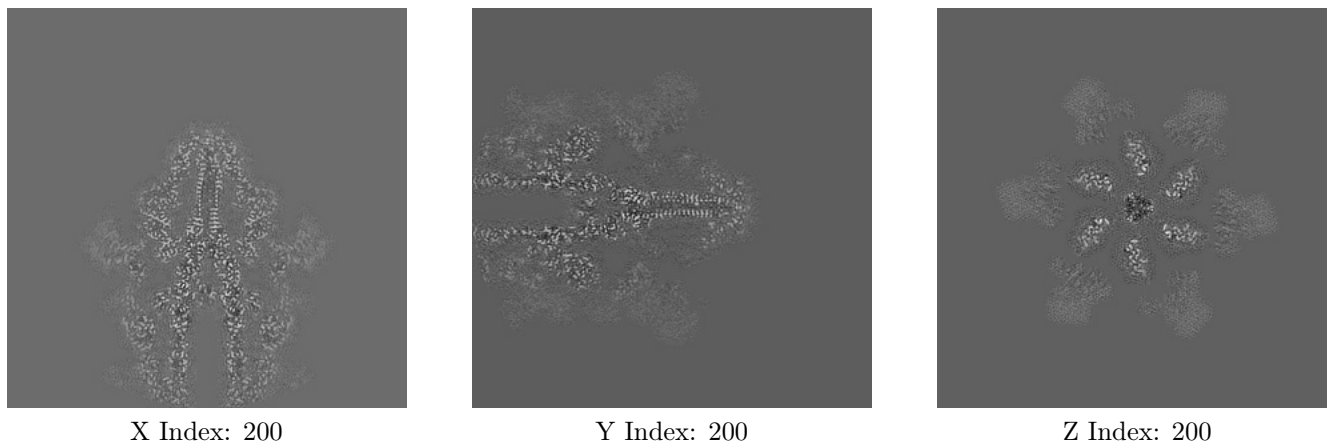
6.1.1 Primary map



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

6.2 Central slices [i](#)

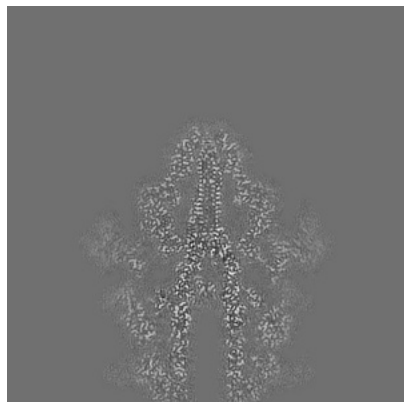
6.2.1 Primary map



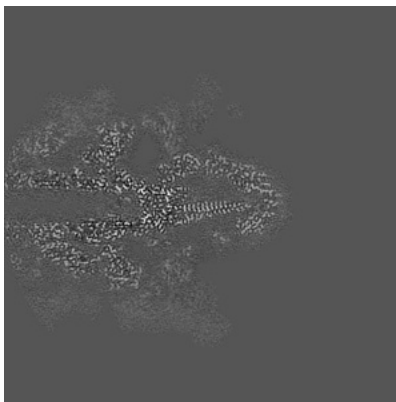
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

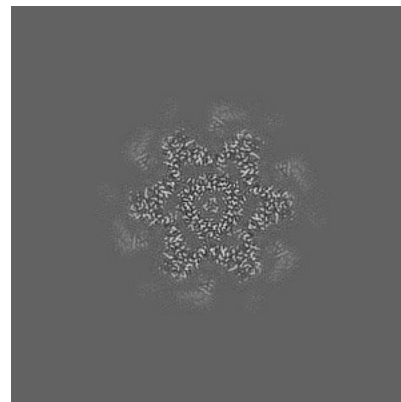
6.3.1 Primary map



X Index: 198



Y Index: 210

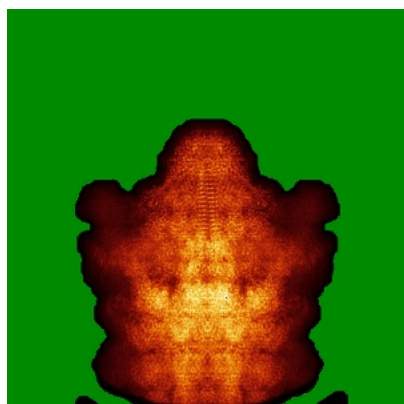


Z Index: 110

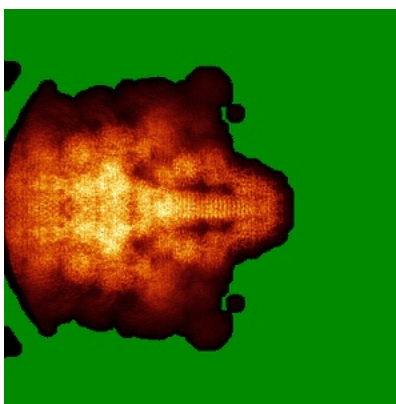
The images above show the largest variance slices of the map in three orthogonal directions.

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

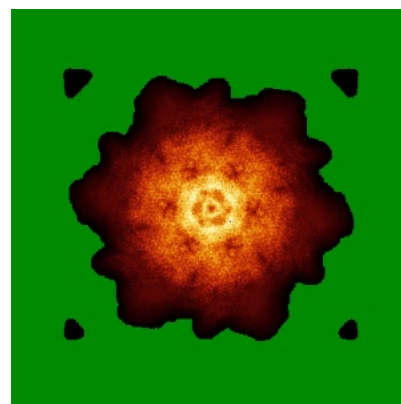
6.4.1 Primary map



X



Y

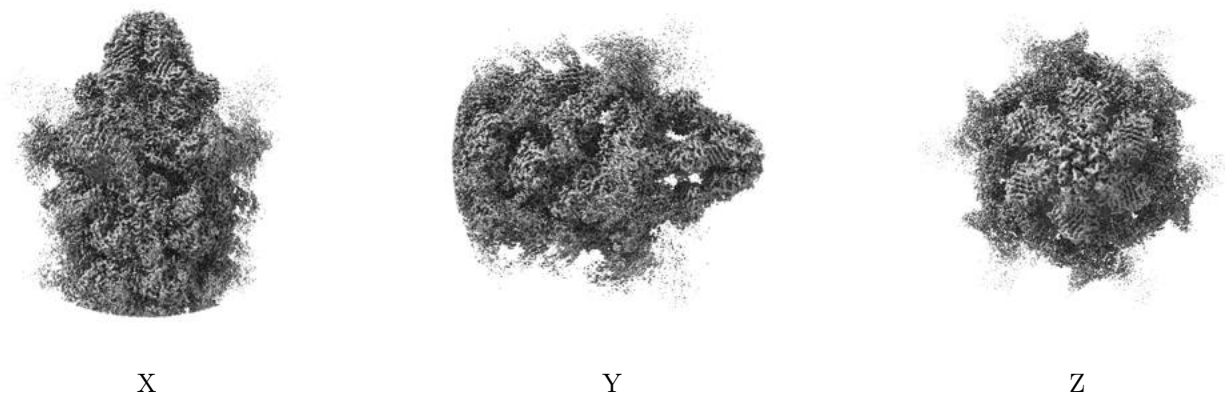


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

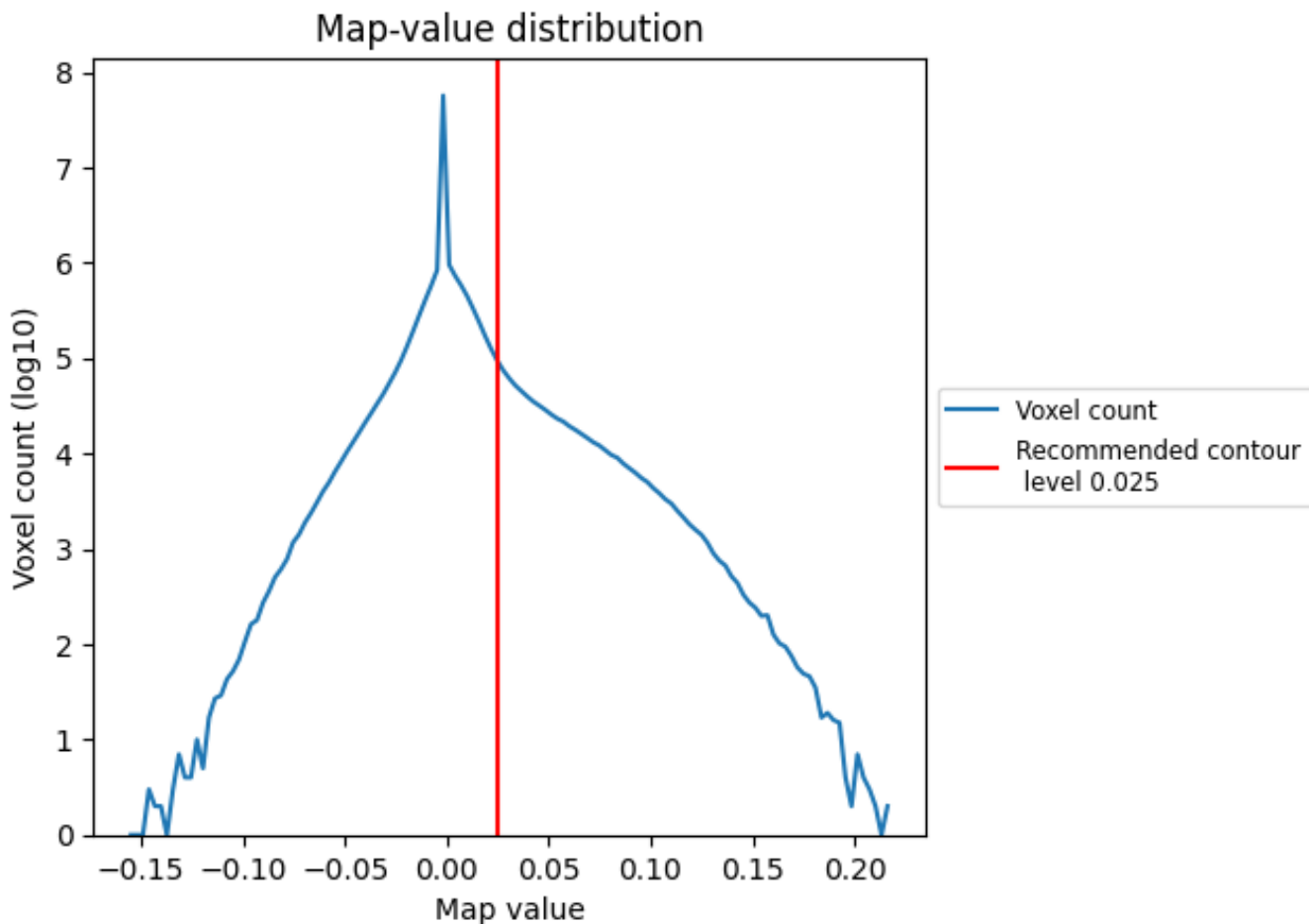
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

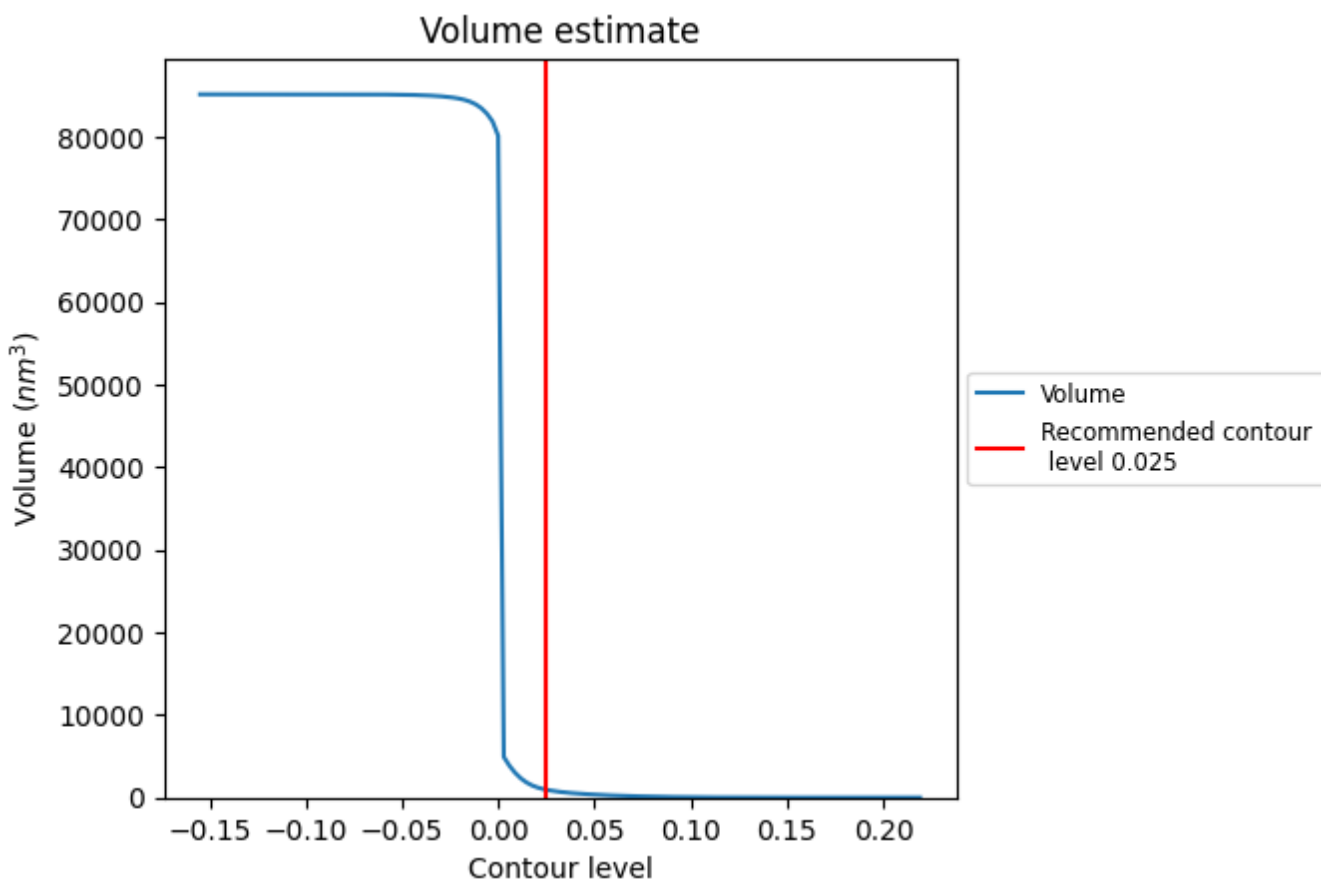
This section contains the results of statistical analysis of the map.

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.

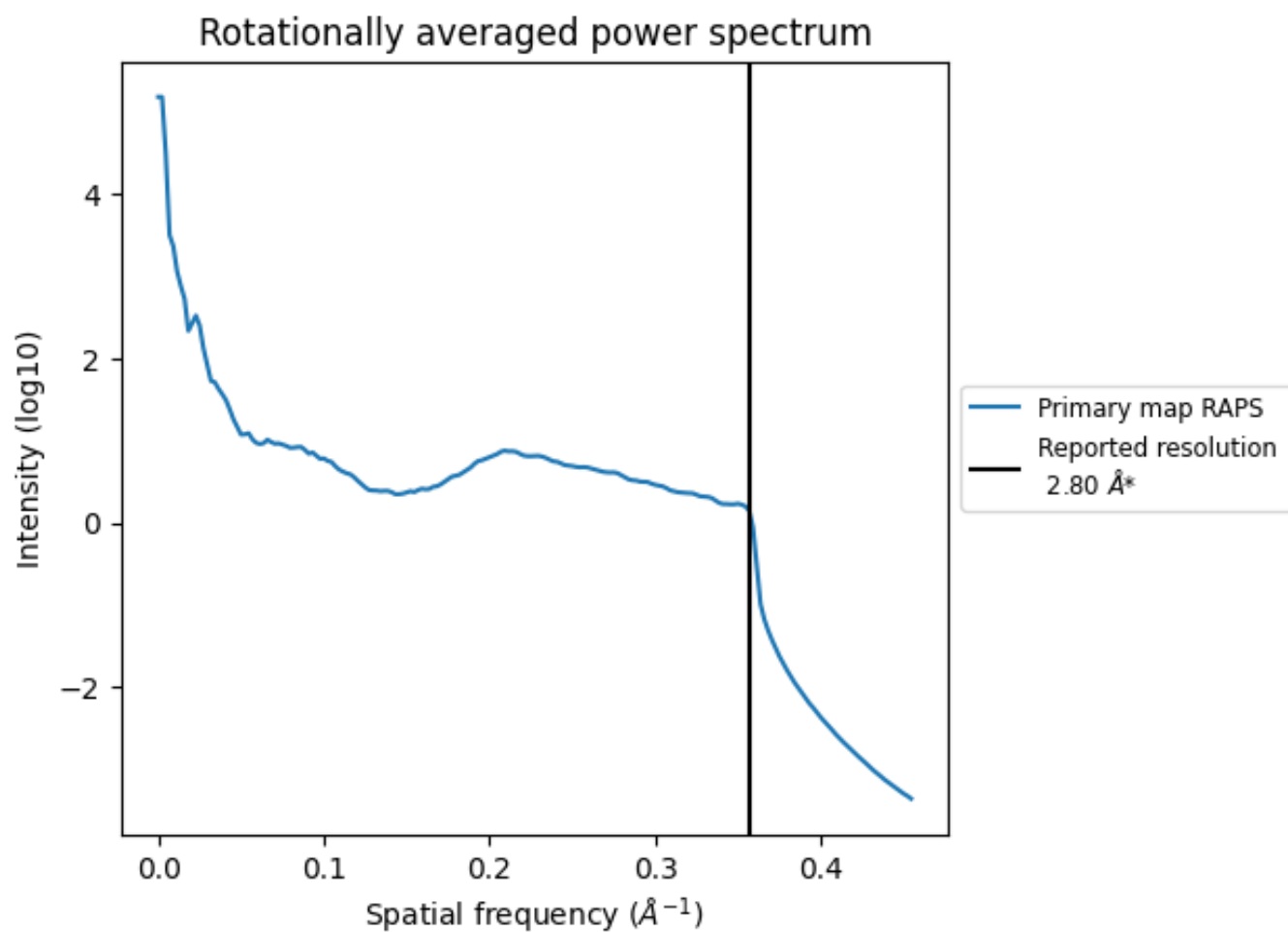
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 948 nm^3 ; this corresponds to an approximate mass of 856 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

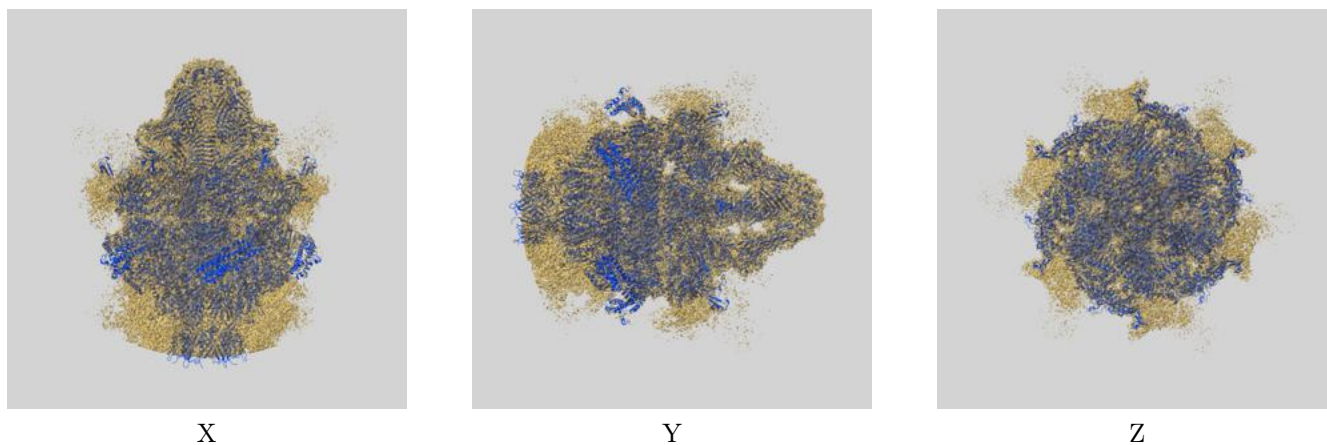
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

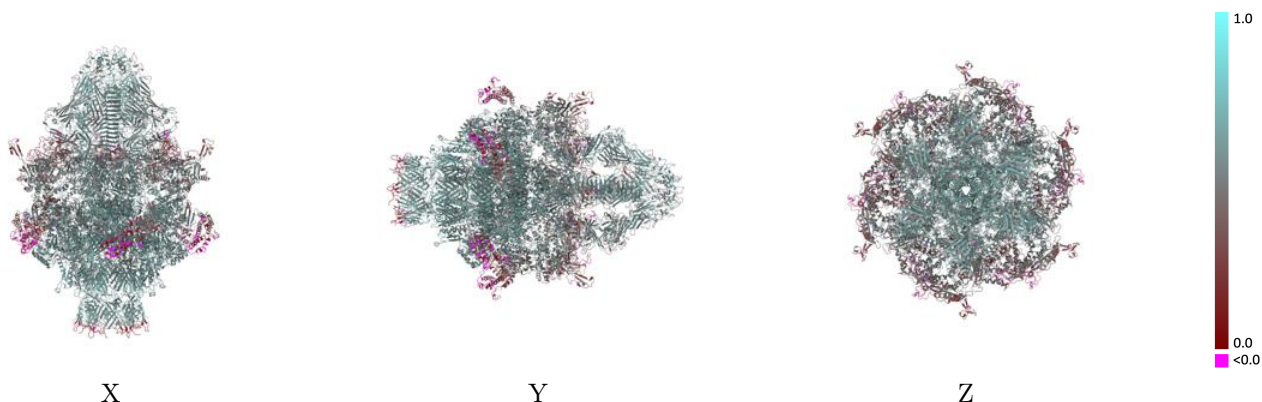
This section contains information regarding the fit between EMDB map EMD-11745 and PDB model 7AEF. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



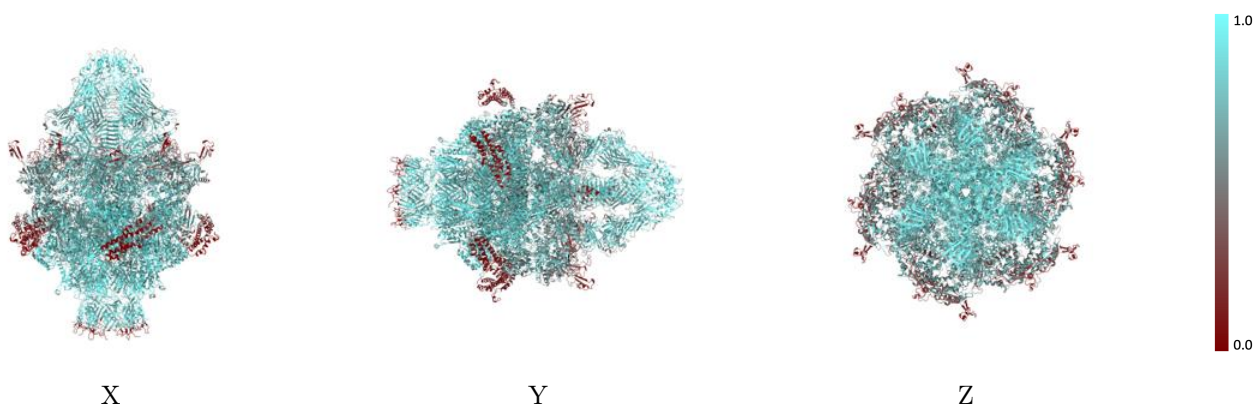
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



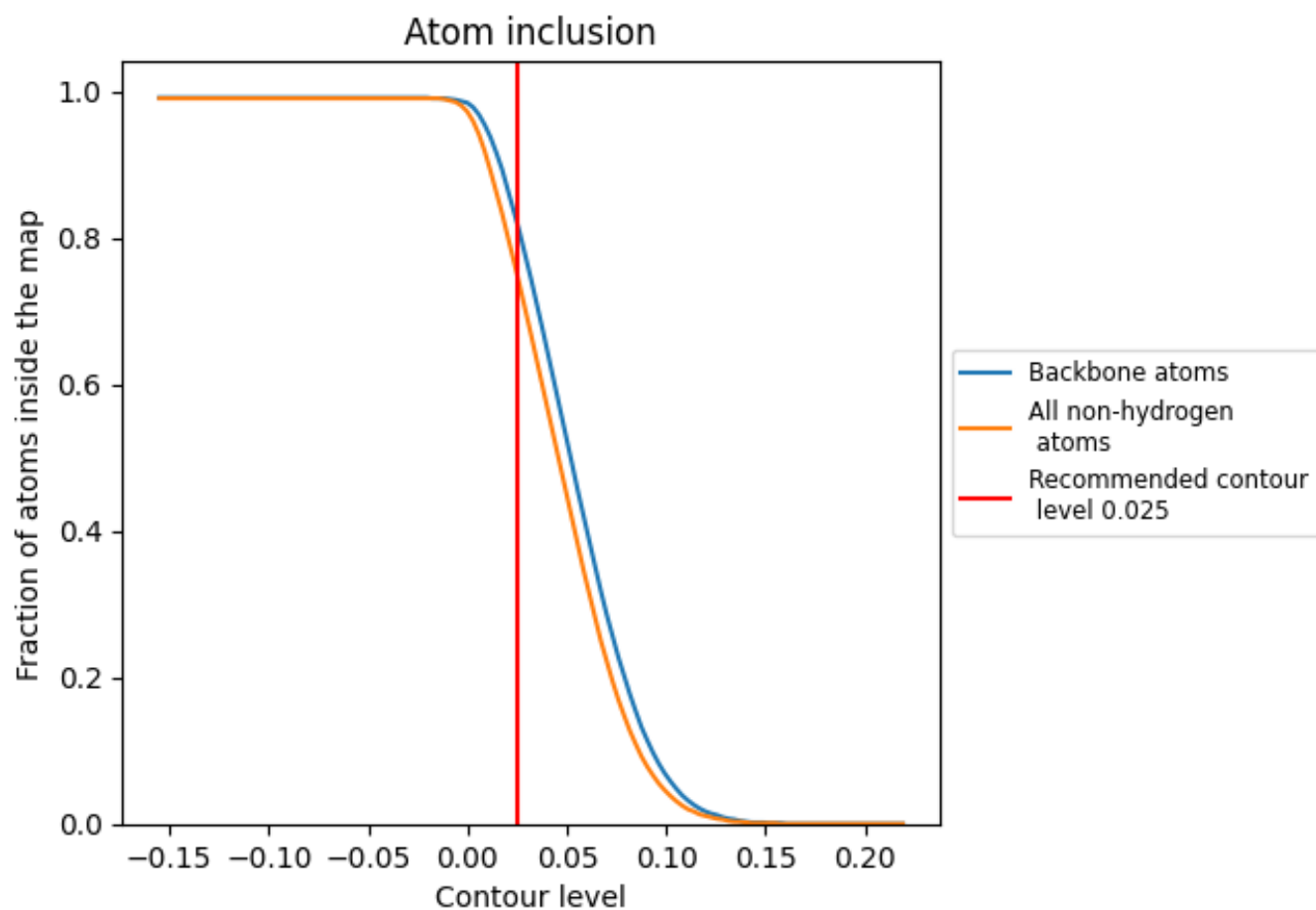
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 75% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7500	 0.5290
A	 0.6790	 0.5040
B	 0.6610	 0.5020
C	 0.6770	 0.5040
D	 0.6670	 0.5010
E	 0.6840	 0.5050
F	 0.6670	 0.5000
G	 0.7750	 0.5410
H	 0.7820	 0.5400
I	 0.7500	 0.5140
J	 0.7230	 0.4740
K	 0.7520	 0.5180
L	 0.7210	 0.4740
M	 0.9230	 0.6340
N	 0.9170	 0.6300
O	 0.9230	 0.6320
P	 0.9160	 0.6340
Q	 0.9180	 0.6330
R	 0.9140	 0.6300
S	 0.8740	 0.5930
T	 0.8520	 0.5840
U	 0.8720	 0.5890
V	 0.8540	 0.5850
W	 0.8750	 0.5910
X	 0.8510	 0.5850
Y	 0.8970	 0.6160
Z	 0.9010	 0.6190
a	 0.8900	 0.6150
b	 0.8960	 0.6190
c	 0.8950	 0.6160
d	 0.9000	 0.6210
e	 0.6400	 0.4800
f	 0.6480	 0.4780
g	 0.6440	 0.4810
h	 0.6450	 0.4790



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Chain	Atom inclusion	Q-score
i	 0.6380	 0.4800
j	 0.6430	 0.4780
k	 0.6480	 0.4770
l	 0.6460	 0.4760
m	 0.6430	 0.4710
n	 0.6520	 0.4690
o	 0.6460	 0.4710
p	 0.6460	 0.4780
q	 0.9240	 0.6240
r	 0.9230	 0.6200
s	 0.9230	 0.6240
t	 0.8110	 0.6230
u	 0.8140	 0.6180
v	 0.8070	 0.6160