



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 04:31 PM UTC

PDB ID : 6SCN / pdb_00006scn
EMDB ID : EMD-10143
Title : 33mer structure of the Salmonella flagella MS-ring protein FlhF
Authors : Johnson, S.; Fong, Y.H.; Deme, J.C.; Furlong, E.J.; Kuhlen, L.; Lea, S.M.
Deposited on : 2019-07-24
Resolution : 3.10 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:

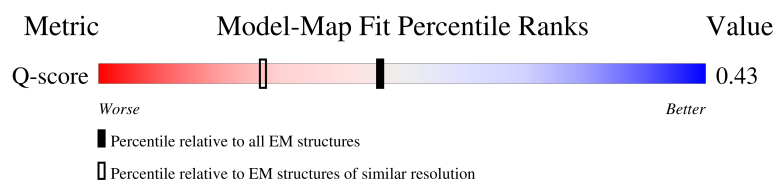
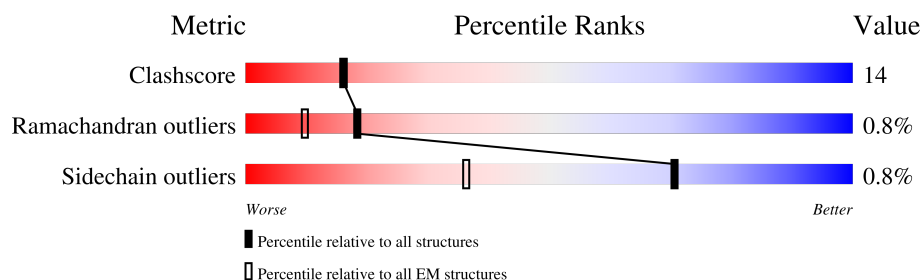
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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	14724 (2.60 - 3.60)

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	560	
1	B	560	
1	C	560	
1	D	560	

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Mol	Chain	Length	Quality of chain
1	E	560	
1	F	560	
1	G	560	
1	H	560	
1	I	560	
1	J	560	
1	K	560	
1	L	560	
1	M	560	
1	N	560	
1	O	560	
1	P	560	
1	Q	560	
1	R	560	
1	S	560	
1	T	560	
1	U	560	
1	V	560	
1	W	560	
1	X	560	
1	Y	560	
1	Z	560	
1	a	560	
1	b	560	
1	c	560	

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Mol	Chain	Length	Quality of chain
1	d	560	
1	e	560	
1	f	560	
1	g	560	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 60582 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	B	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	C	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	D	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	E	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	F	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	G	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	H	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	I	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	J	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	K	155	Total	C	N	O	S	0	0
			1224	744	230	247	3		
1	L	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	M	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	N	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	O	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	P	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	Q	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		

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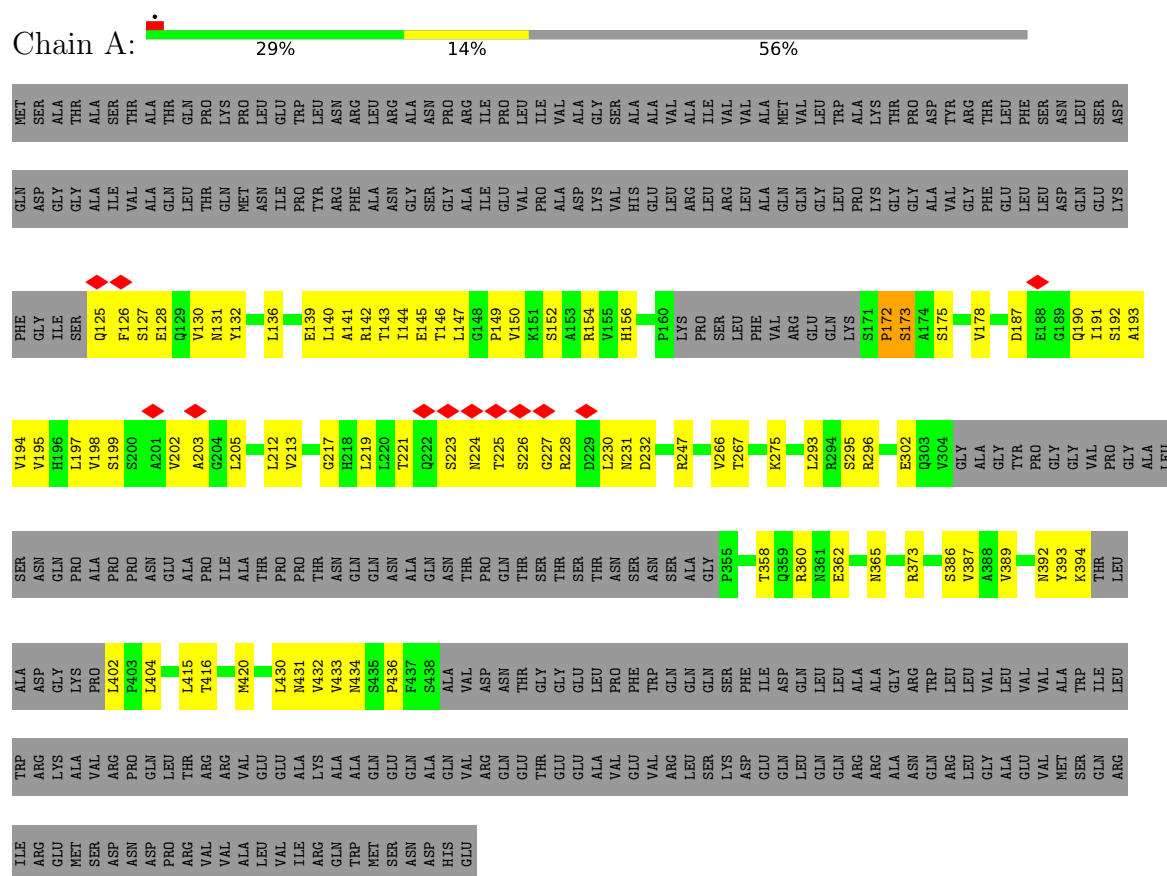
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	247	Total	C	N	O	S	0	0
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1	S	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	T	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	U	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	V	155	Total	C	N	O	S	0	0
			1224	744	230	247	3		
1	W	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	X	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	Y	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	Z	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	a	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	b	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	c	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	d	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	e	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	f	247	Total	C	N	O	S	0	0
			1897	1160	350	383	4		
1	g	155	Total	C	N	O	S	0	0
			1224	744	230	247	3		

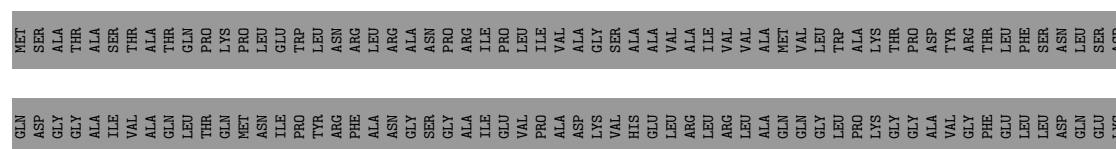
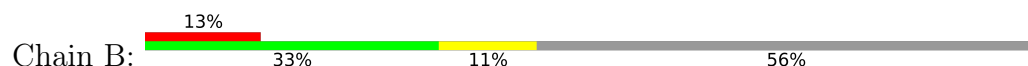
3 Residue-property plots

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

• Molecule 1: Flagellar M-ring protein

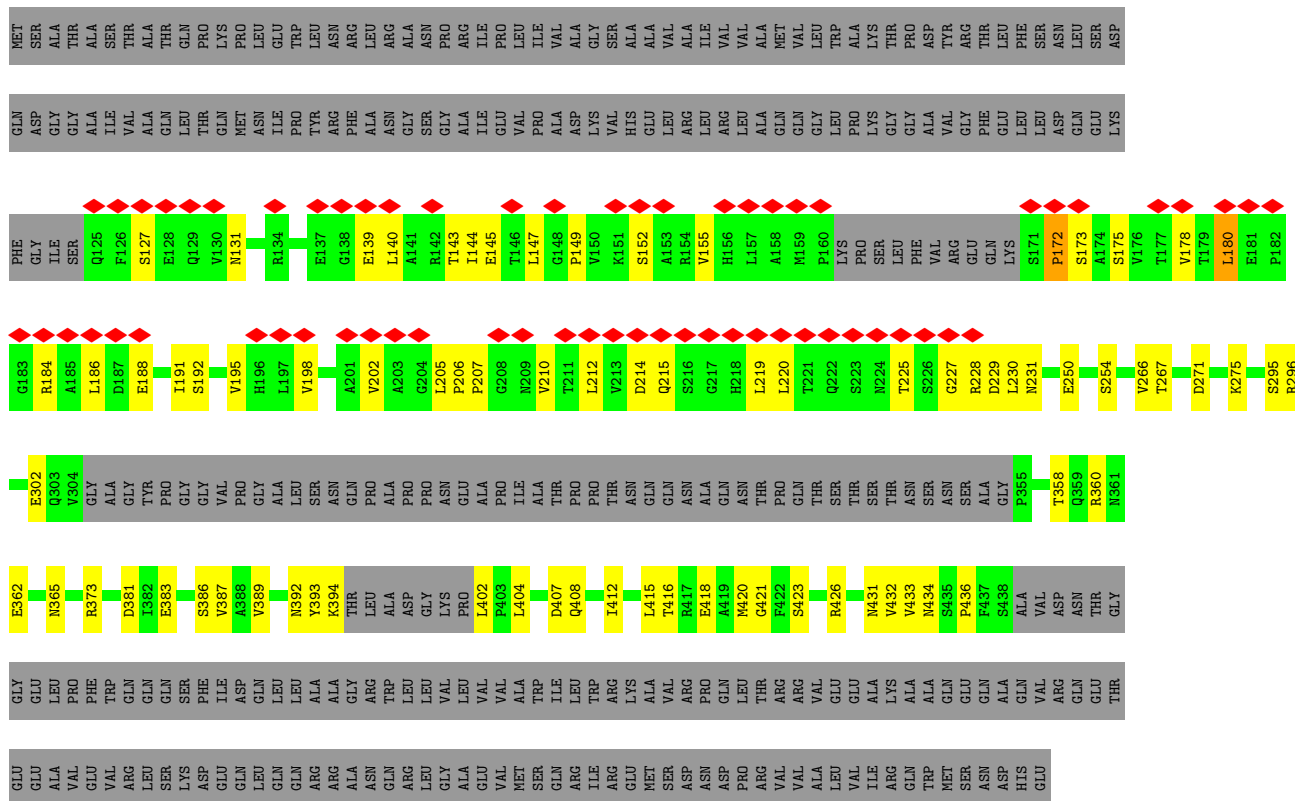
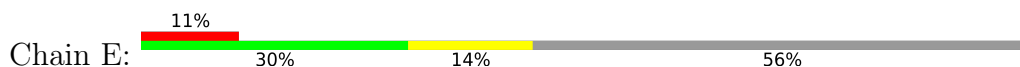


• Molecule 1: Flagellar M-ring protein





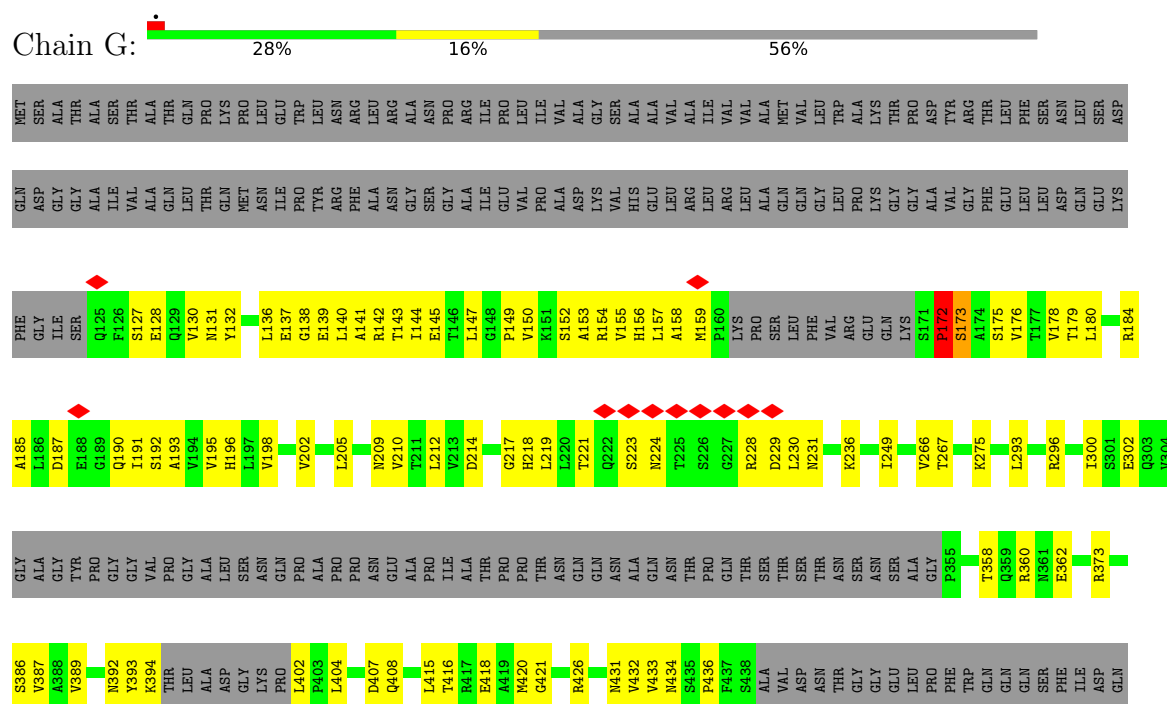
- Molecule 1: Flagellar M-ring protein



Chain F:

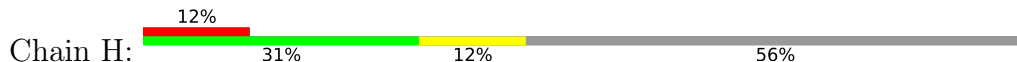


Chain G:



[illegible]

- Molecule 1: Flagellar M-ring protein



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

PHE	GLY	ILE	SER	Q125	F126	S127	E128	Q129	V130	N131	R134	L135	L136	E137	G138	E139	L140	A141	R142	T143	I144	E145	T146	L147	G148	P149	V150	K151	S152	A153	R154	V155	H156	L157	A158	M159	P160	LYS	PRO	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	S171	P172	S173	A174	S175	V176	T177	V178	T179	L180	A181
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P182	G183	R184	A185	L186	D187	E188	G189	Q190	I191	V195	H196	L197	V198	S199	A201	V202	A203	G204	L205	P206	P207	G208	N209	V210	T211	L212	V213	D214	Q215	S216	G217	H218	L219	L220	T221	Q222	S223	N224	T225	S226	G227	R228	D229	V266	T267	D271	K275	E280	S283	L293
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R296	I300	V304	GLY	ALA	GLY	THR	PRO	PRO	GLY	GLY	VAL	PRO	GLY	ALA	LEU	SER	ASN	GLN	PRO	PRO	PRO	ASN	GLU	ALA	ALA	ILE	ALA	THR	PRO	PRO	THR	ASN	GLN	ASN	GLN	ASN	ALA	GLN	ASN	THR	GLN	THR	SER	SER	THR	THR	THR	ASN	ASN	ALA	GLY	R365	R360	F362
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D369	D370	D371	D372	D373	D374	D375	D376	D377	D378	D379	D380	D381	D382	D383	D384	D385	D386	D387	D388	D389	D390	D391	D392	D393	D394	D395	D396	D397	D398	D399	D400	D401	D402	D403	D404	D405	D406	D407	D408	D409	D410	D411	D412	D413	D414	D415	D416	D417	D418	D419	D420	D421	D422	D423	D424	D425	D426	D427	D428	D429	D430	D431	D432	D433	D434	D435	D436	D437	D438	D439	D440	D441	D442	D443	D444	D445	D446	D447	D448	D449	D450	D451	D452	D453	D454	D455	D456	D457	D458	D459	D460	D461	D462	D463	D464	D465	D466	D467	D468	D469	D470	D471	D472	D473	D474	D475	D476	D477	D478	D479	D480	D481	D482	D483	D484	D485	D486	D487	D488	D489	D490	D491	D492	D493	D494	D495	D496	D497	D498	D499	D500
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GLY	GLU	LEU	PRO	PHE	TRP	GLN	GLN	SER	PHE	ILE	ASP	GLN	LEU	ALA	ALA	GLY	ARG	TRP	LEU	LEU	VAL	VAL	VAL	ALA	ALA	TRP	ILE	LEU	TRP	TRP	ARG	LYS	ALA	VAL	ARG	PRO	GLN	LEU	THR	THR	ARG	ARG	VAL	GLU	GLU	ALA	ALA	LYS	ALA	GLN	GLN	ALA	ALA	GLN	VAL	ARG	GLN	GLN	THR	GLU
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GLU GLU ALA ALA VAL VAL GLU GLU ARG ARG LEU LEU SER LYS ASP GLU GLN LEU LEU GLN GLN GLN ARG ARG ALA ALA ASN ASN MET MET SER SER GLN GLN ARG ARG ILE ILE ARG ARG GLU GLU MET MET SER SER ASP ASN ASP ASP PRO PRO ARG ARG VAL VAL VAL ALA ALA LEU VAL VAL ILE ILE ARG ARG GLN GLN TRP MET MET SER MET ASN ASN HIS GLU

- Molecule 1: Flagellar M-ring protein

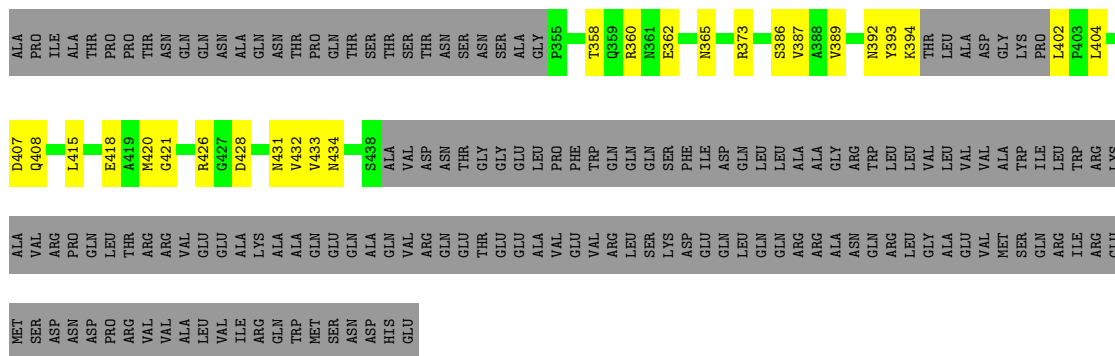


MET	SER	ALA	THR	SER	THR	ALA	GLN	PRO	PRO	LEU	GLU	TRP	LEU	ASN	ARG	ARG	LEU	ARG	ALA	ASN	PRO	ARG	ILE	LEU	ILE	VAL	ALA	GLY	SER	ALA	ALA	VAL	VAL	ALA	ALA	ILE	ILE	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ALA	ALA	LYS	THR	LYS	PRO	ASP	THR	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	LEU	SER	ASN	ASP
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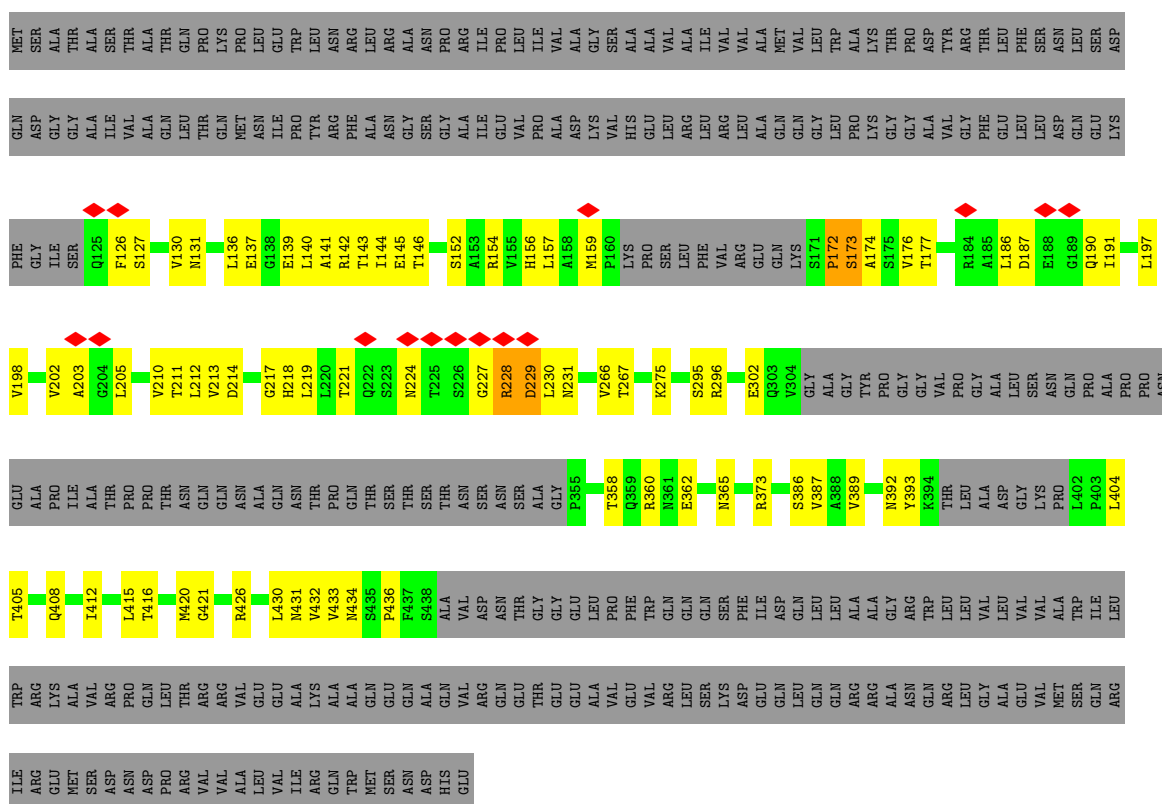
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PHE	GLY	ILE	SER	Q125	F126	S127	V130	M131	E139	L140	A141	T142	T143	I144	E145	T146	L147	G148	F149	V150	A153	R154	V155	H156	P160	LYS	PRO	SER	LEU	PHE	VAL	ARG	GLU	GLN	LYS	G171	P172	S173	V176	L180	A185	L186	D187	E188	G189	Q190	I191	S192	A193	V198
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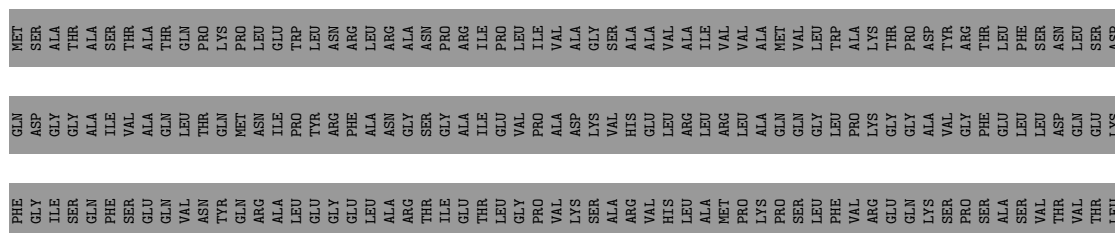
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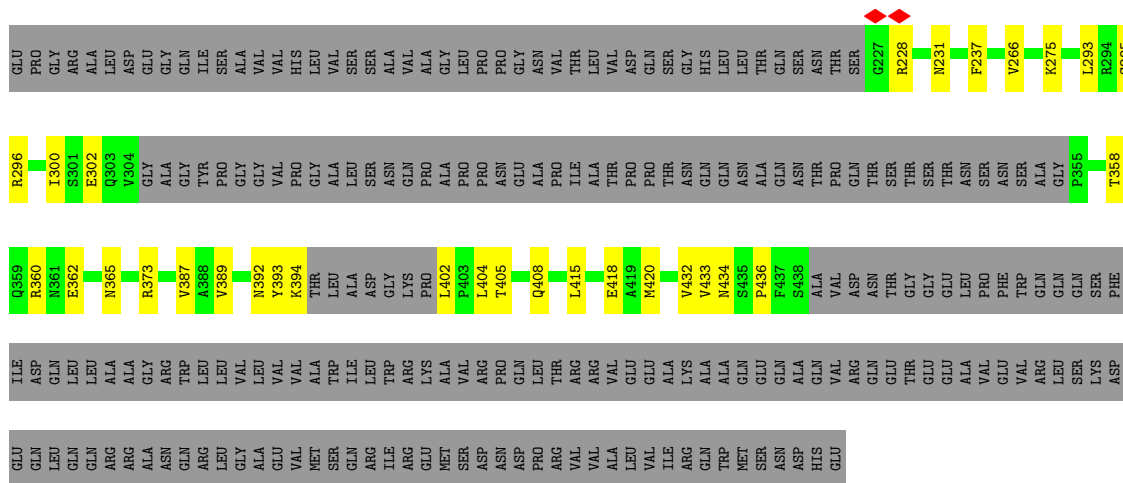


- Molecule 1: Flagellar M-ring protein

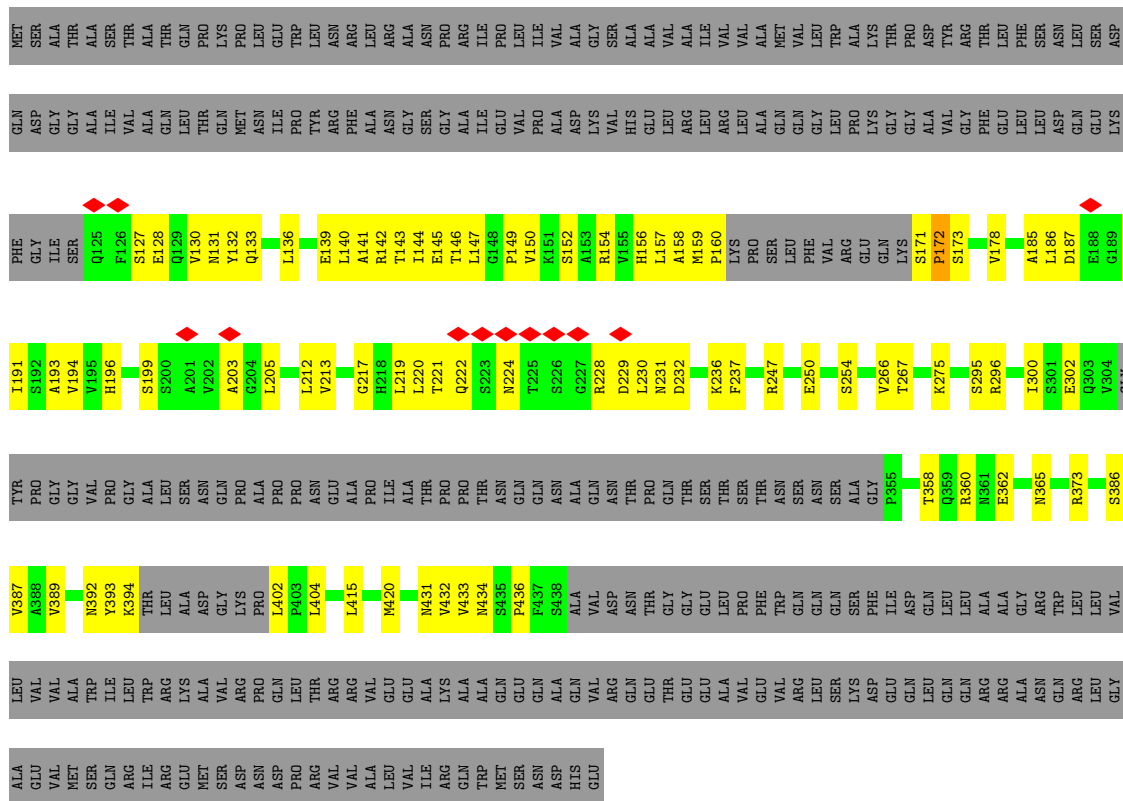


- Molecule 1: Flagellar M-ring protein

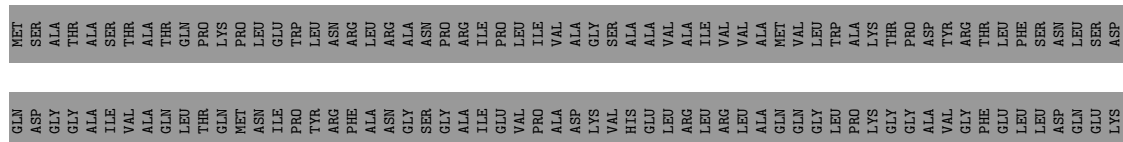
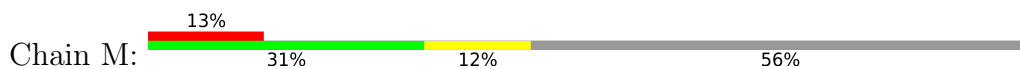




- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein



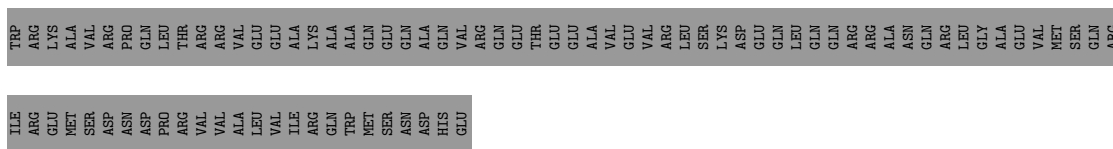


Chain Q:

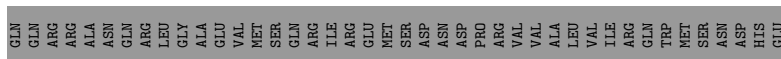
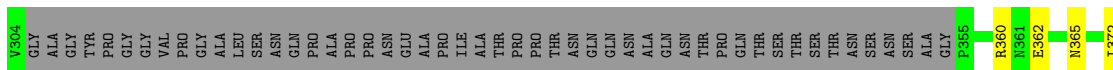
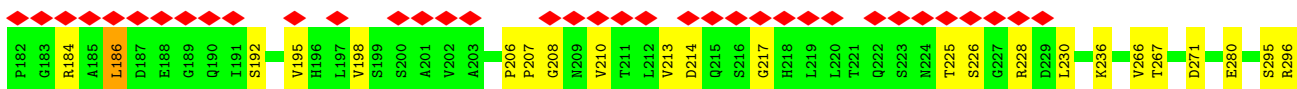
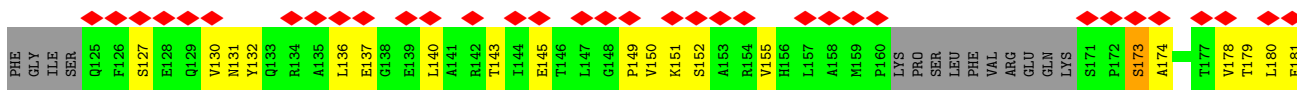
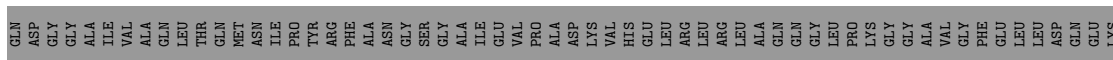
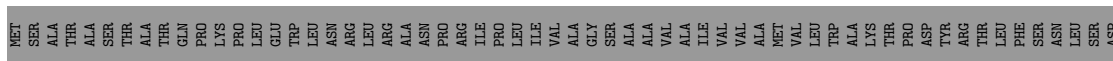
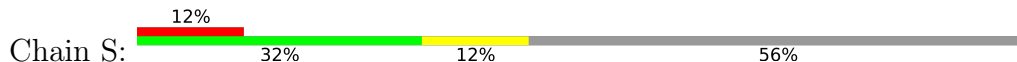


Chain R:

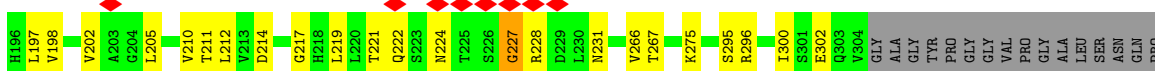
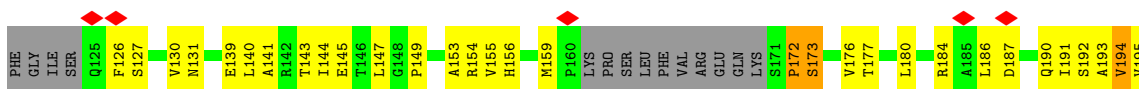
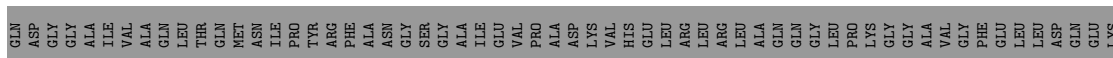
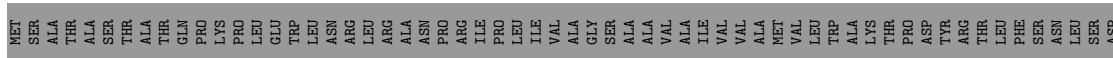


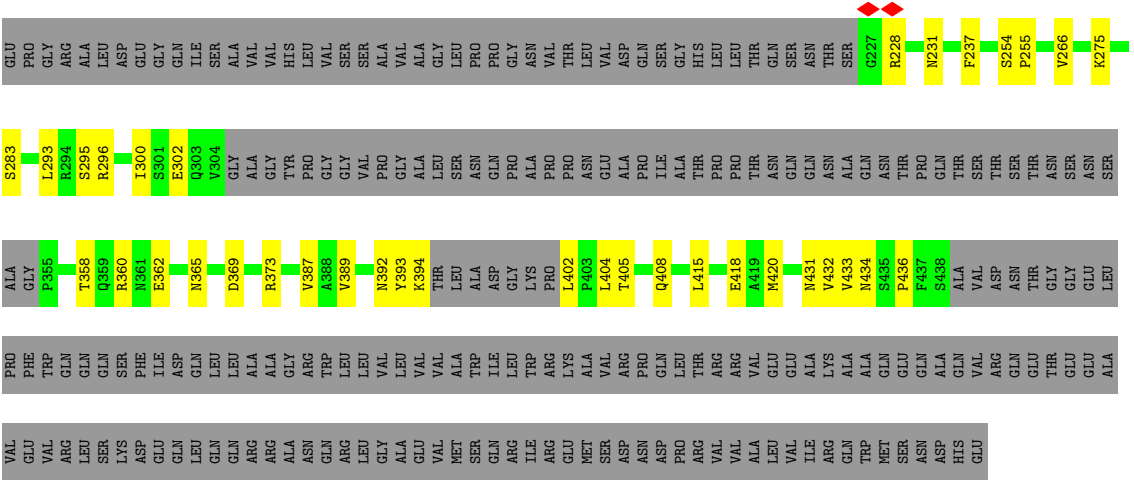


- Molecule 1: Flagellar M-ring protein

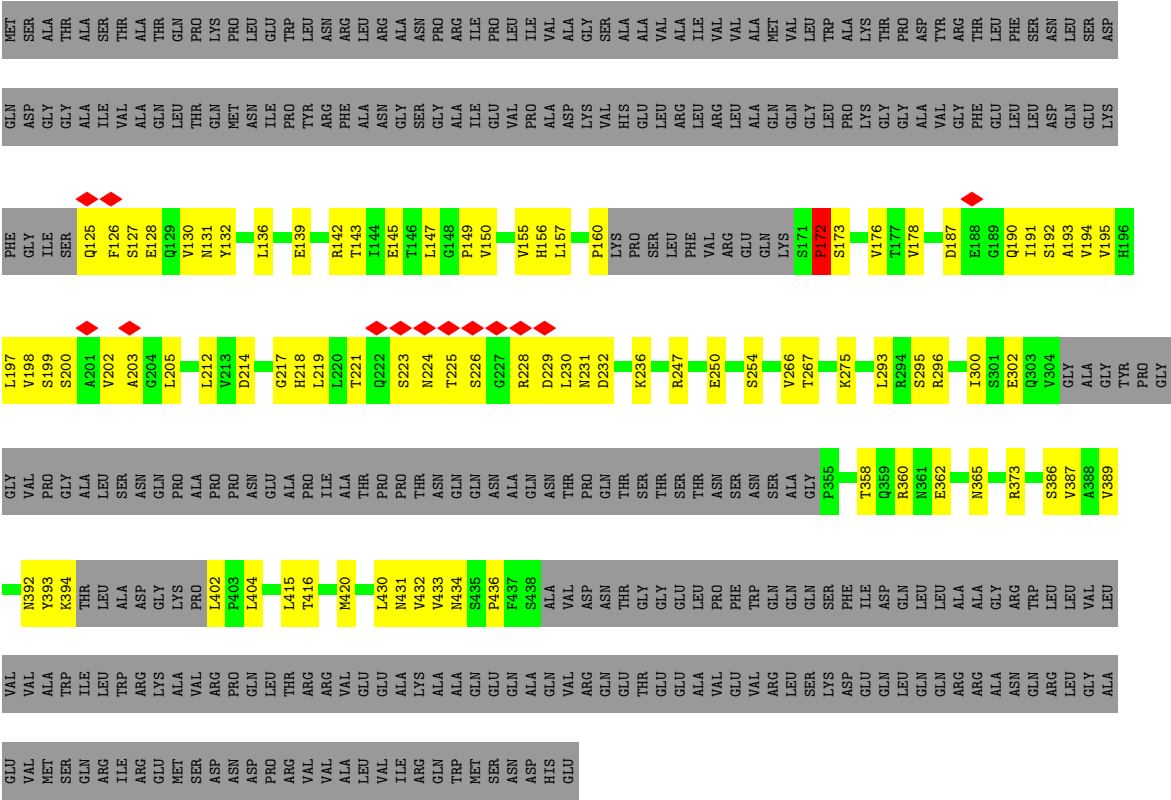


- Molecule 1: Flagellar M-ring protein

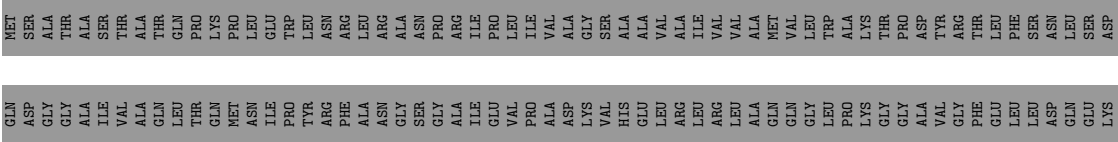
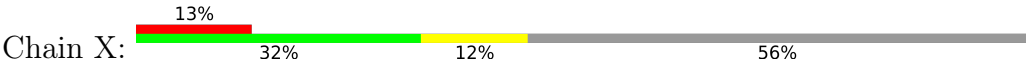


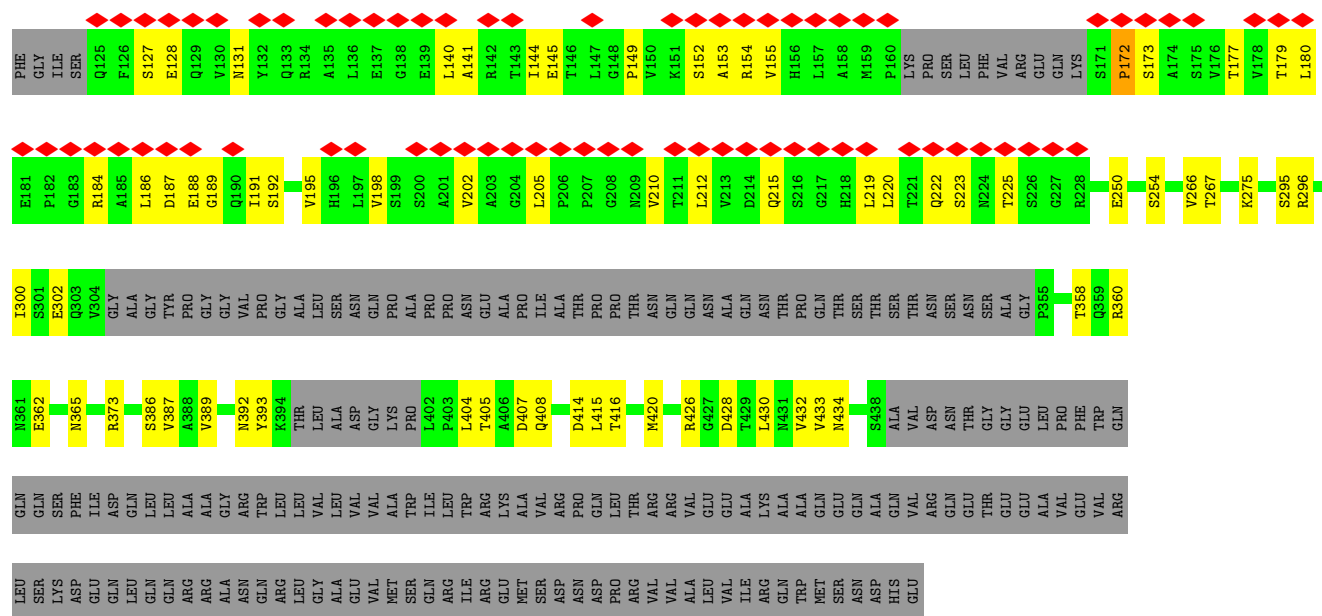


● Molecule 1: Flagellar M-ring protein

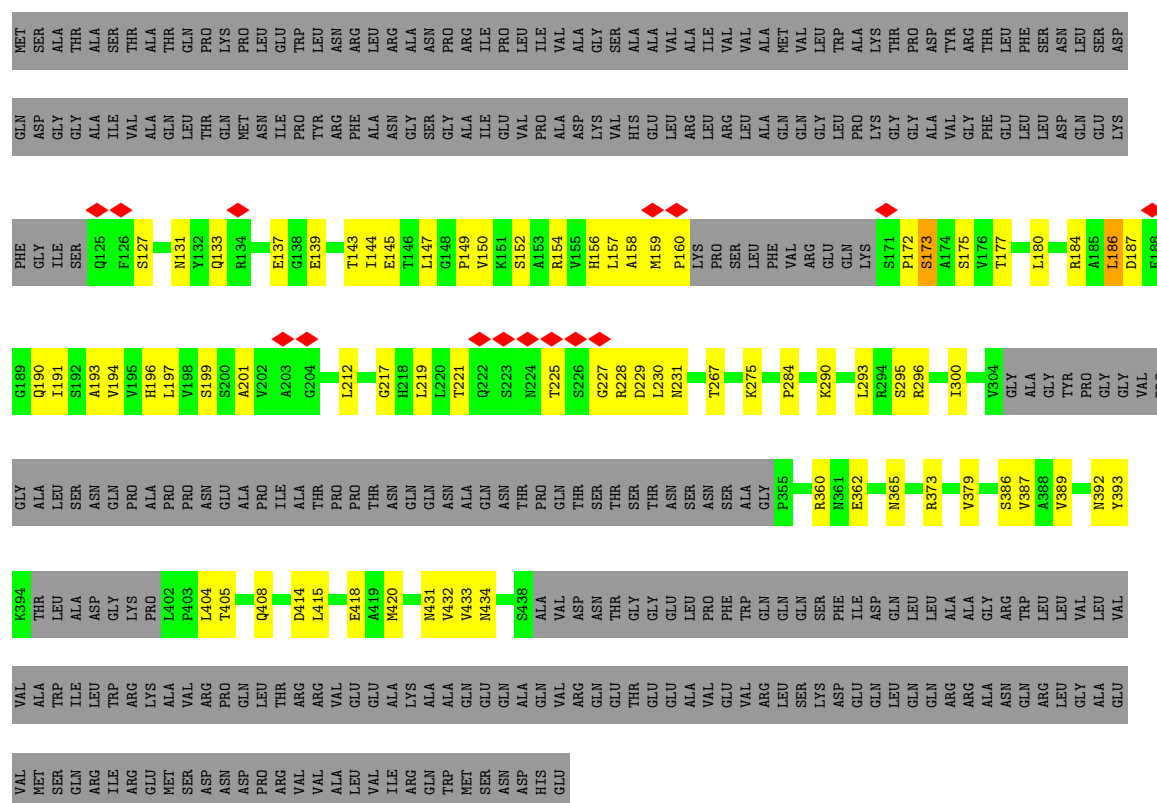
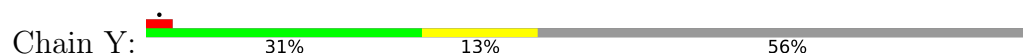


● Molecule 1: Flagellar M-ring protein





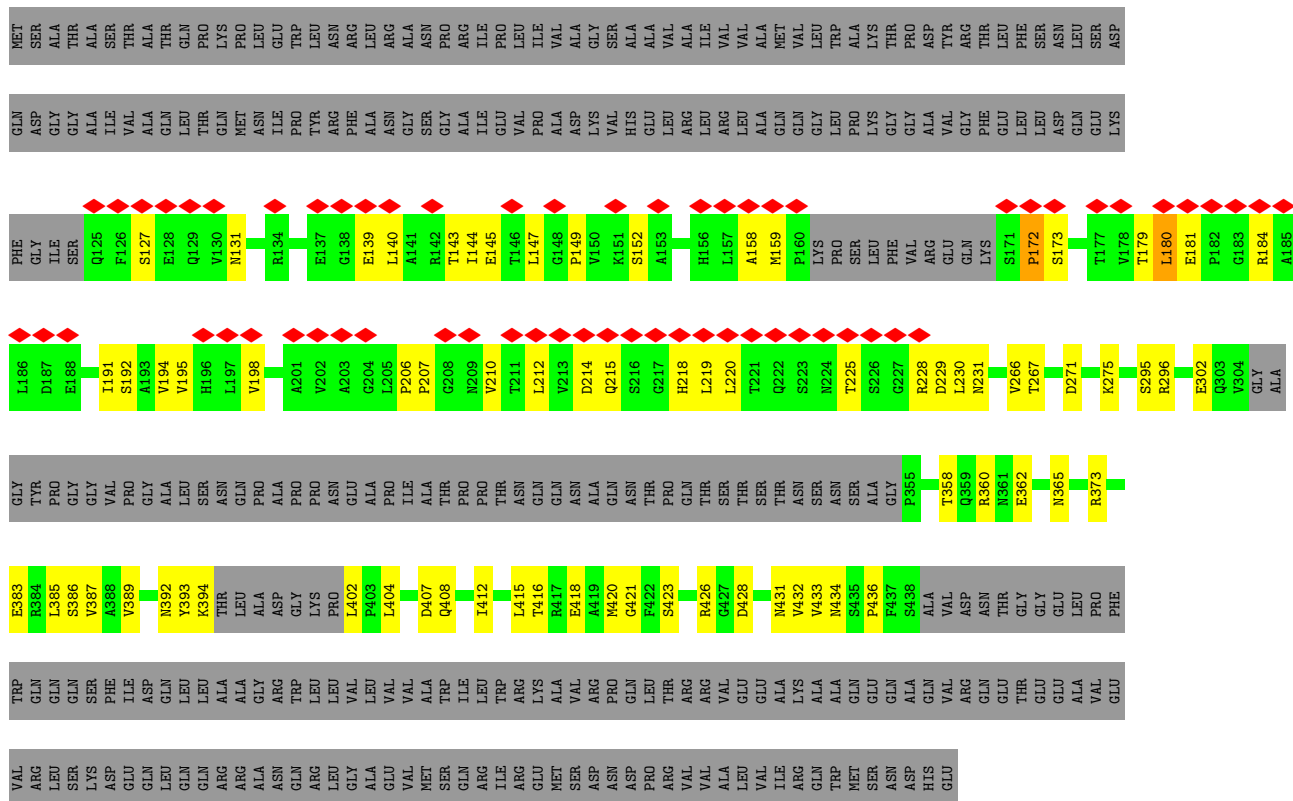
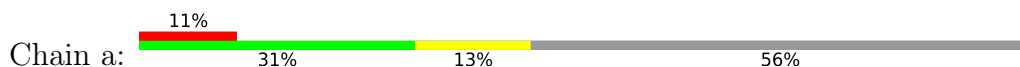
• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein



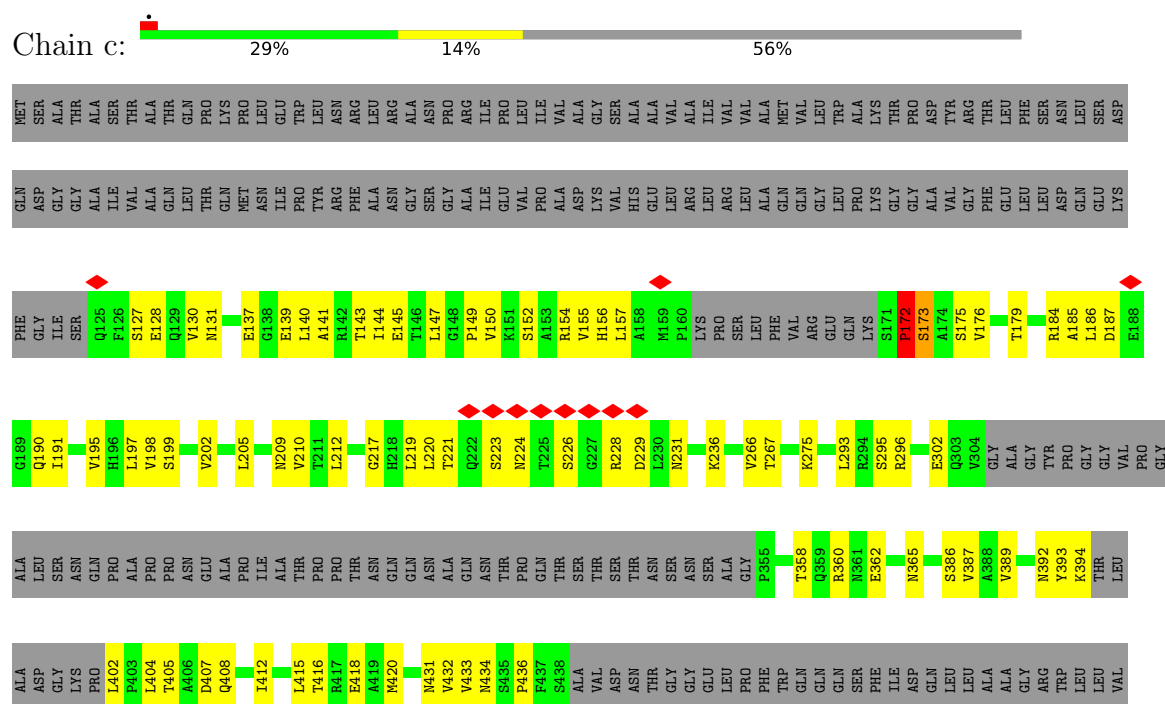
- Molecule 1: Flagellar M-ring protein



Chain b:



Chain c:





GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLN	ILE	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	ALA	GLY	LEU	PRO	PRO	GLY	ASN	VAL	THR	LEU	VAL	ASP	GLN	SER	ILE	GLY	HIS	LEU	THR	THR	GLN	SER	ASN	THR	SER	G227	R228	N231	F237	E250	S254	V266	T267			
K275	L293	R294	S295	R296	I300	S301	E302	Q303	V304	GLY	ALA	GLY	TYR	PRO	GLY	GLY	GLY	VAL	PRO	GLY	ALA	ALA	LEU	SER	ASN	GLN	PRO	ALA	ASN	PRO	GLY	ILE	ALA	THR	PRO	THR	THR	ASN	GLN	ASN	ALA	GLN	ASN	THR	PRO	GLN	THR	THR	THR	SER	THR	ASN	SER	ASN	SER	
ALA	GLY	P355	T358	Q359	R360	R361	E362	N365	R373	S386	V387	A388	V389	N392	Y393	K394	THR	LEU	ALA	ASP	GLY	LYS	PRO	L402	P403	L404	T405	Q408	L415	E418	A419	M420	V432	V433	N434	S435	P436	F437	S438	ALA	VAL	ASP	ASN	THR	THR	GLY	GLY	GLU	LEU	PRO	PHE					
TRP	GLN	GLN	SER	LYS	PHE	ILE	ASP	GLN	LEU	GLN	ALA	ALA	GLY	ARG	TRP	LEU	VAL	VAL	VAL	TRP	ILE	LEU	ARG	LYS	ALA	VAL	ARG	VAL	ARG	VAL	VAL	GLU	GLU	ILE	ALA	LYS	ALA	ALA	GLN	GLU	GLN	GLN	ALA	GLN	VAL	ARG	GLN	GLU	THR	THR	GLY	GLU	GLU	ALA	VAL	GLU
VAL	ARG	LEU	SER	LYS	ASP	GLU	GLN	LEU	GLN	GLN	ARG	ARG	ALA	ALA	ASN	GLN	ARG	LEU	GLY	ALA	GLU	VAL	VAL	MET	SER	GLN	ILE	ARG	ILE	ILE	ALA	VAL	VAL	ILE	ALA	ARG	GLN	ALA	TRP	MET	SER	ASN	ASP	HIS	GLU											

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	175233	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.036	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	355.104, 355.104, 355.104	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.822, 0.822, 0.822	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	0.31	0/1919	0.51	0/2598
1	B	0.30	0/1919	0.47	0/2598
1	C	0.31	0/1919	0.51	0/2598
1	D	0.31	0/1919	0.49	0/2598
1	E	0.30	0/1919	0.47	0/2598
1	F	0.31	0/1919	0.51	0/2598
1	G	0.31	0/1919	0.51	1/2598 (0.0%)
1	H	0.30	0/1919	0.48	0/2598
1	I	0.31	0/1919	0.50	0/2598
1	J	0.30	0/1919	0.48	0/2598
1	K	0.34	0/1236	0.44	0/1665
1	L	0.31	0/1919	0.52	0/2598
1	M	0.31	0/1919	0.50	0/2598
1	N	0.31	0/1919	0.52	1/2598 (0.0%)
1	O	0.32	0/1919	0.50	0/2598
1	P	0.30	0/1919	0.47	0/2598
1	Q	0.31	0/1919	0.50	0/2598
1	R	0.31	0/1919	0.48	0/2598
1	S	0.30	0/1919	0.48	0/2598
1	T	0.31	0/1919	0.49	0/2598
1	U	0.30	0/1919	0.48	0/2598
1	V	0.35	0/1236	0.43	0/1665
1	W	0.31	0/1919	0.53	0/2598
1	X	0.30	0/1919	0.50	0/2598
1	Y	0.31	0/1919	0.49	0/2598
1	Z	0.31	0/1919	0.52	1/2598 (0.0%)
1	a	0.30	0/1919	0.47	0/2598
1	b	0.31	0/1919	0.50	0/2598
1	c	0.31	0/1919	0.50	0/2598
1	d	0.30	0/1919	0.48	0/2598
1	e	0.31	0/1919	0.48	0/2598
1	f	0.30	0/1919	0.48	0/2598
1	g	0.34	0/1236	0.44	0/1665
All	All	0.31	0/61278	0.49	3/82935 (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	I	0	1
1	T	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Z	230	LEU	N-CA-C	-9.18	102.91	114.56
1	G	230	LEU	N-CA-C	-5.52	107.55	114.56
1	N	147	LEU	CA-CB-CG	5.44	135.36	116.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	227	GLY	Peptide
1	T	227	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1897	0	1880	75	0
1	B	1897	0	1880	43	0
1	C	1897	0	1880	60	0
1	D	1897	0	1880	70	0
1	E	1897	0	1880	61	0
1	F	1897	0	1880	71	0
1	G	1897	0	1880	83	0
1	H	1897	0	1880	53	0
1	I	1897	0	1880	59	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	1897	0	1880	67	0
1	K	1224	0	1204	24	0
1	L	1897	0	1880	67	0
1	M	1897	0	1880	55	0
1	N	1897	0	1880	71	0
1	O	1897	0	1880	76	0
1	P	1897	0	1880	58	0
1	Q	1897	0	1880	58	0
1	R	1897	0	1880	68	0
1	S	1897	0	1880	49	0
1	T	1897	0	1880	68	0
1	U	1897	0	1880	67	0
1	V	1224	0	1204	27	0
1	W	1897	0	1880	68	0
1	X	1897	0	1880	53	0
1	Y	1897	0	1880	60	0
1	Z	1897	0	1880	77	0
1	a	1897	0	1880	57	0
1	b	1897	0	1880	63	0
1	c	1897	0	1880	76	0
1	d	1897	0	1880	53	0
1	e	1897	0	1880	67	0
1	f	1897	0	1880	72	0
1	g	1224	0	1204	25	0
All	All	60582	0	60012	1721	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 14.

The worst 5 of 1721 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:G:137:GLU:HG2	1:G:157:LEU:HD13	1.51	0.92
1:R:137:GLU:HG2	1:R:157:LEU:HD13	1.52	0.91
1:H:140:LEU:HD11	1:H:155:VAL:HG21	1.53	0.90
1:N:225:THR:HG22	1:N:227:GLY:H	1.42	0.85
1:c:190:GLN:HG3	1:e:217:GLY:HA3	1.56	0.85

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	239/560 (43%)	222 (93%)	15 (6%)	2 (1%)	16	47
1	B	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	C	239/560 (43%)	227 (95%)	11 (5%)	1 (0%)	30	61
1	D	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	E	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	F	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	G	239/560 (43%)	223 (93%)	14 (6%)	2 (1%)	16	47
1	H	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	I	239/560 (43%)	226 (95%)	12 (5%)	1 (0%)	30	61
1	J	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	K	149/560 (27%)	148 (99%)	1 (1%)	0	100	100
1	L	239/560 (43%)	222 (93%)	15 (6%)	2 (1%)	16	47
1	M	239/560 (43%)	226 (95%)	11 (5%)	2 (1%)	16	47
1	N	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	O	239/560 (43%)	223 (93%)	14 (6%)	2 (1%)	16	47
1	P	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	Q	239/560 (43%)	226 (95%)	11 (5%)	2 (1%)	16	47
1	R	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	S	239/560 (43%)	224 (94%)	14 (6%)	1 (0%)	30	61
1	T	239/560 (43%)	226 (95%)	12 (5%)	1 (0%)	30	61
1	U	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	V	149/560 (27%)	148 (99%)	1 (1%)	0	100	100
1	W	239/560 (43%)	221 (92%)	15 (6%)	3 (1%)	9	35
1	X	239/560 (43%)	227 (95%)	10 (4%)	2 (1%)	16	47
1	Y	239/560 (43%)	227 (95%)	11 (5%)	1 (0%)	30	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Z	239/560 (43%)	226 (95%)	10 (4%)	3 (1%)	9	35
1	a	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	b	239/560 (43%)	226 (95%)	11 (5%)	2 (1%)	16	47
1	c	239/560 (43%)	225 (94%)	12 (5%)	2 (1%)	16	47
1	d	239/560 (43%)	224 (94%)	13 (5%)	2 (1%)	16	47
1	e	239/560 (43%)	227 (95%)	11 (5%)	1 (0%)	30	61
1	f	239/560 (43%)	224 (94%)	12 (5%)	3 (1%)	9	35
1	g	149/560 (27%)	148 (99%)	1 (1%)	0	100	100
All	All	7617/18480 (41%)	7185 (94%)	372 (5%)	60 (1%)	18	47

5 of 60 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	PRO
1	B	172	PRO
1	D	172	PRO
1	E	172	PRO
1	F	172	PRO

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	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	B	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	C	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	D	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	E	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	F	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	G	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	H	213/467 (46%)	211 (99%)	2 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	J	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	K	137/467 (29%)	137 (100%)	0	100	100
1	L	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	M	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	N	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	O	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	P	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	Q	213/467 (46%)	210 (99%)	3 (1%)	59	76
1	R	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	S	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	T	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	U	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	V	137/467 (29%)	137 (100%)	0	100	100
1	W	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	X	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	Y	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	Z	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	a	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	b	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	c	213/467 (46%)	212 (100%)	1 (0%)	81	85
1	d	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	e	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	f	213/467 (46%)	211 (99%)	2 (1%)	70	80
1	g	137/467 (29%)	137 (100%)	0	100	100
All	All	6801/15411 (44%)	6745 (99%)	56 (1%)	70	81

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	186	LEU
1	f	186	LEU
1	T	194	VAL

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Mol	Chain	Res	Type
1	f	172	PRO
1	c	172	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 274 such sidechains are listed below:

Mol	Chain	Res	Type
1	c	125	GLN
1	c	361	ASN
1	f	131	ASN
1	L	133	GLN
1	K	431	ASN

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](#)

There are no chain breaks in this entry.

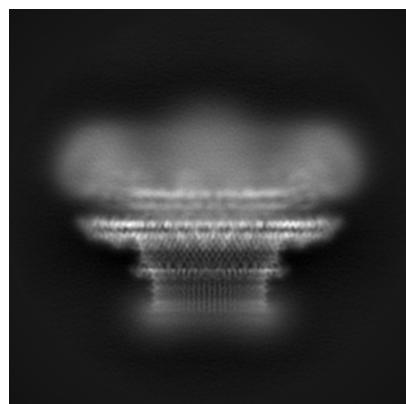
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10143. These allow visual inspection of the internal detail of the map and identification of artifacts.

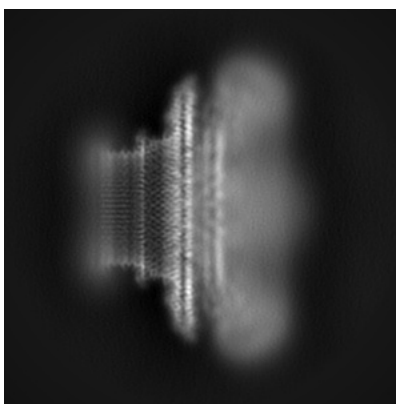
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

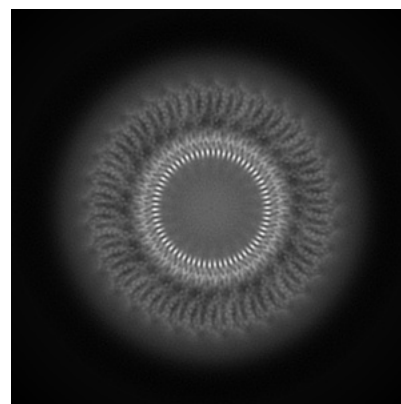
6.1.1 Primary map



X

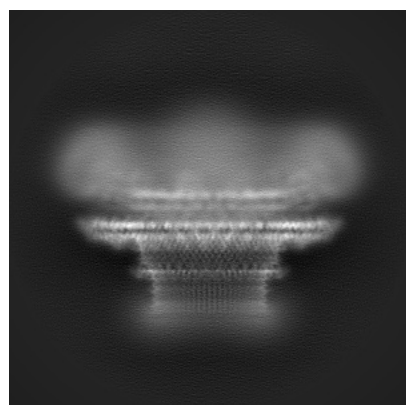


Y

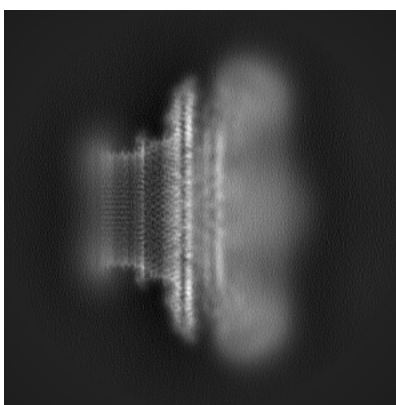


Z

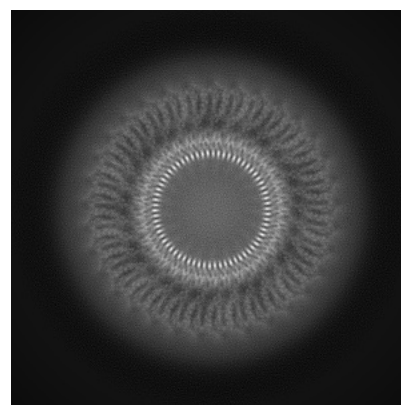
6.1.2 Raw map



X



Y

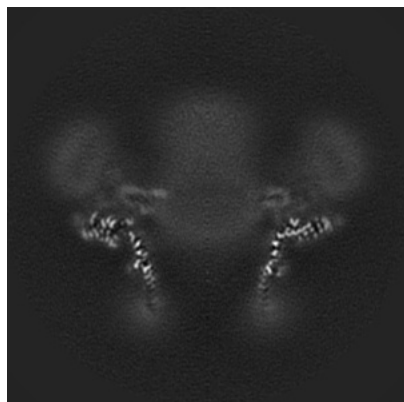


Z

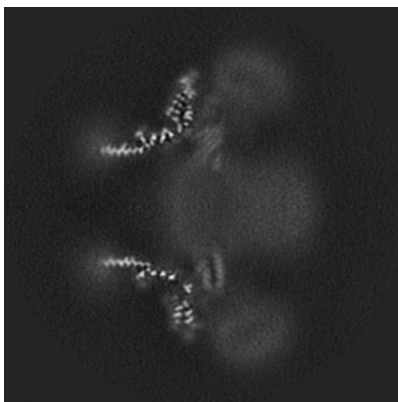
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

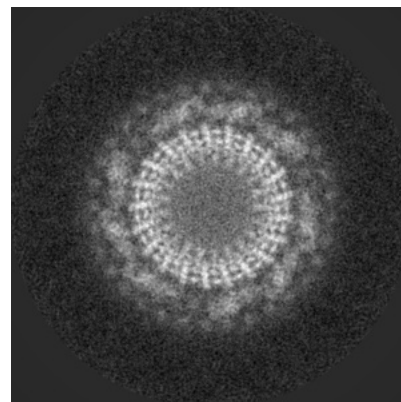
6.2.1 Primary map



X Index: 216

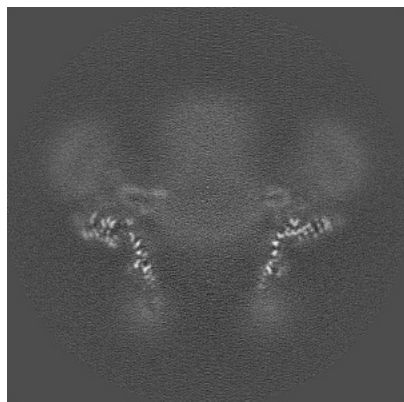


Y Index: 216

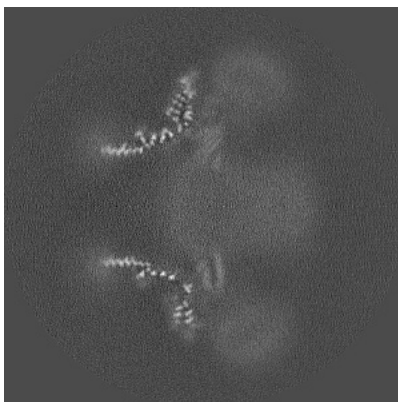


Z Index: 216

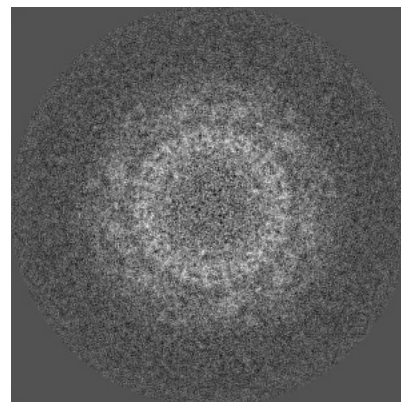
6.2.2 Raw map



X Index: 216



Y Index: 216

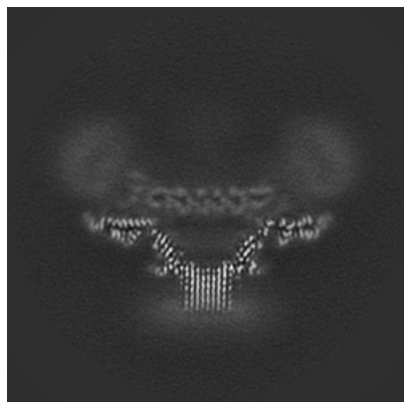


Z Index: 216

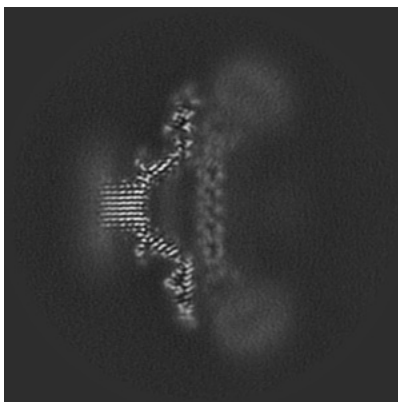
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

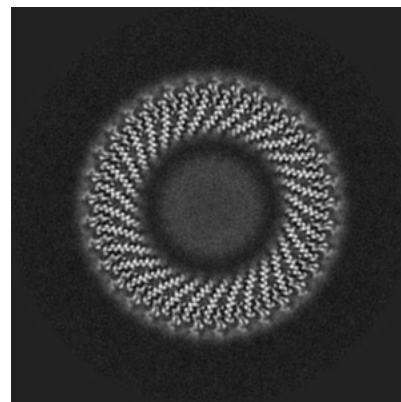
6.3.1 Primary map



X Index: 275

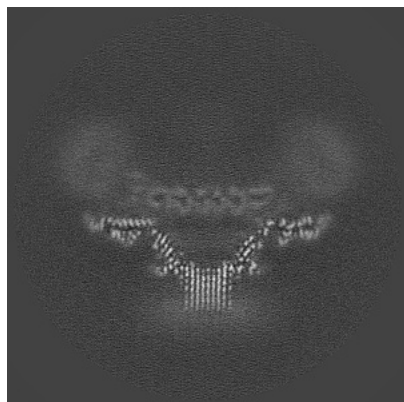


Y Index: 156

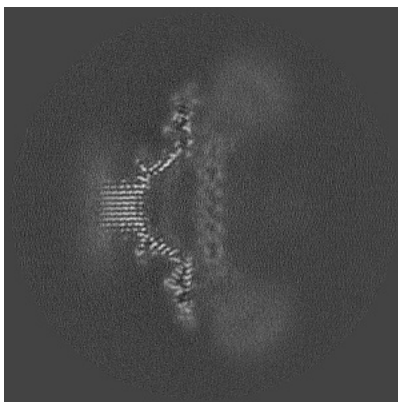


Z Index: 199

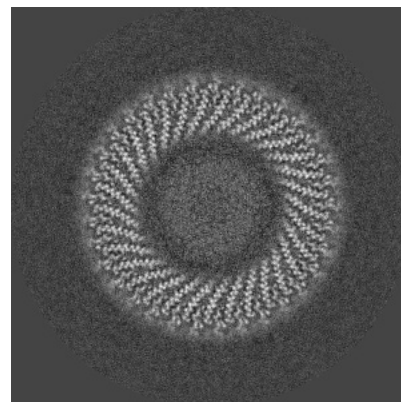
6.3.2 Raw map



X Index: 275



Y Index: 157

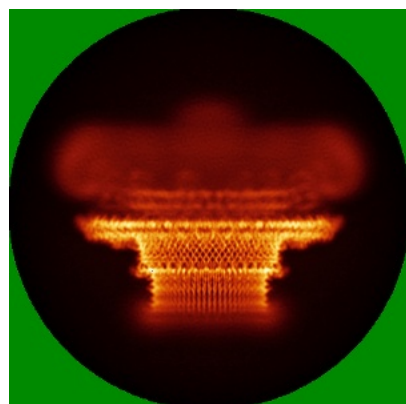


Z Index: 199

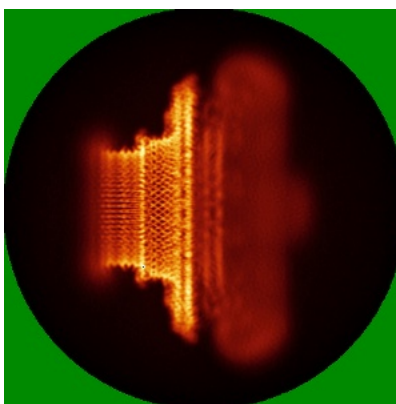
The images above show the largest variance slices of the map in three orthogonal directions.

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

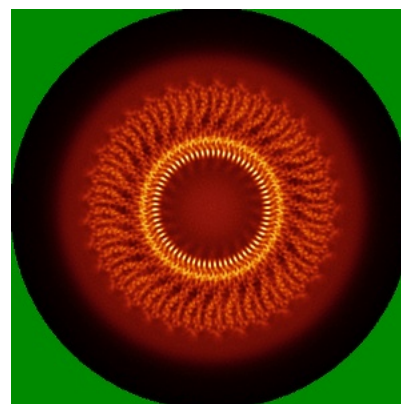
6.4.1 Primary map



X

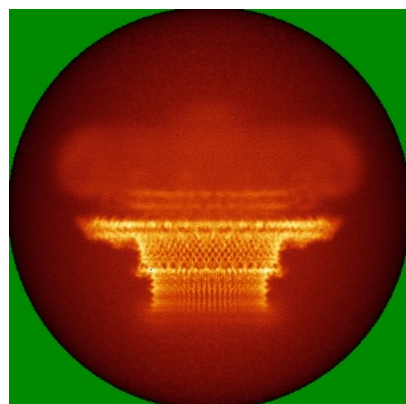


Y

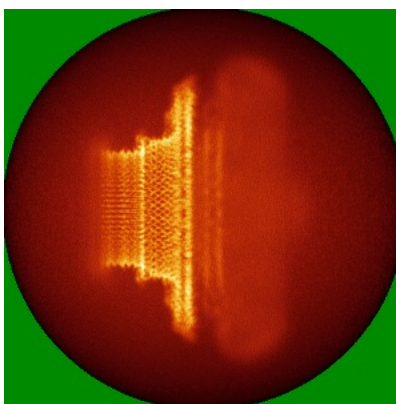


Z

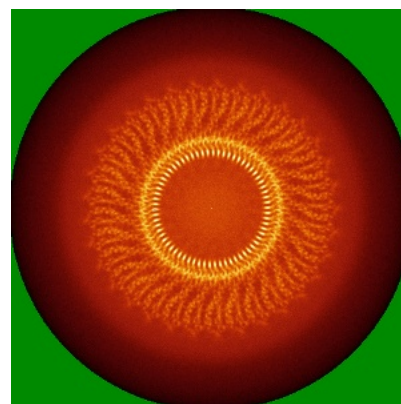
6.4.2 Raw map



X



Y

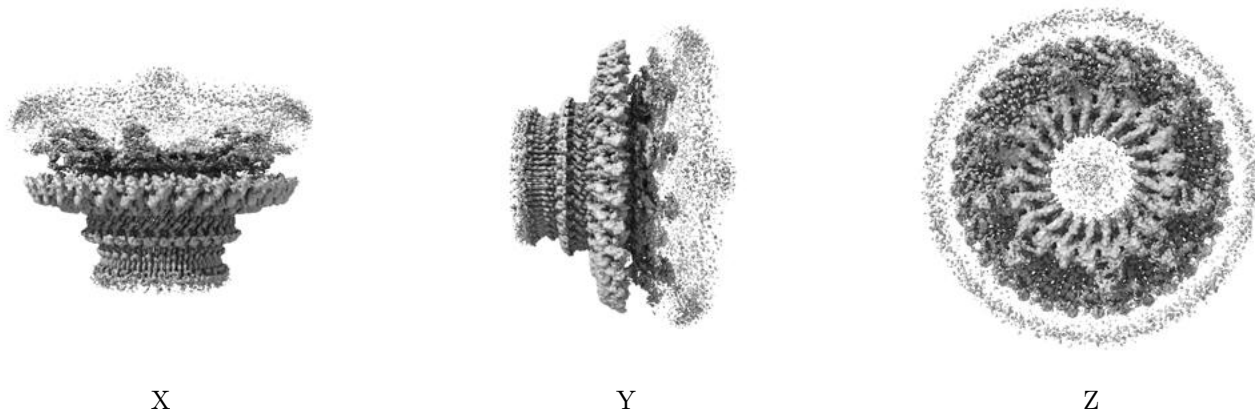


Z

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.

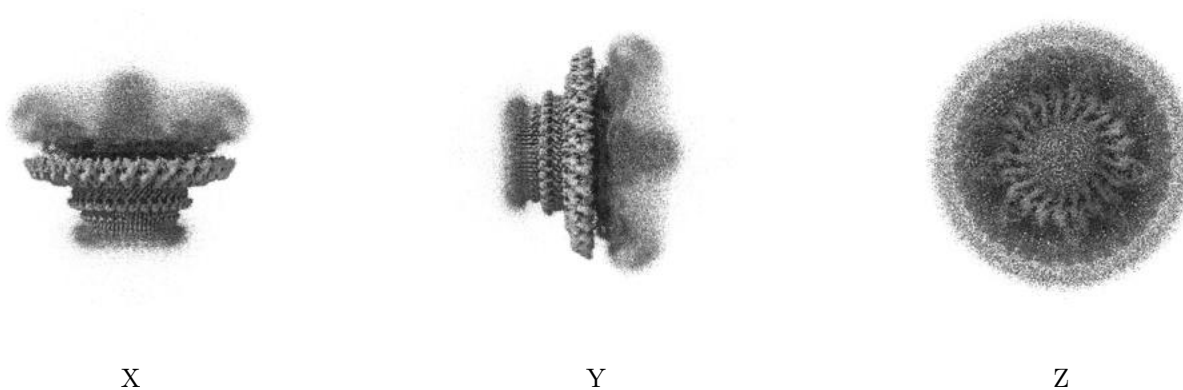
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

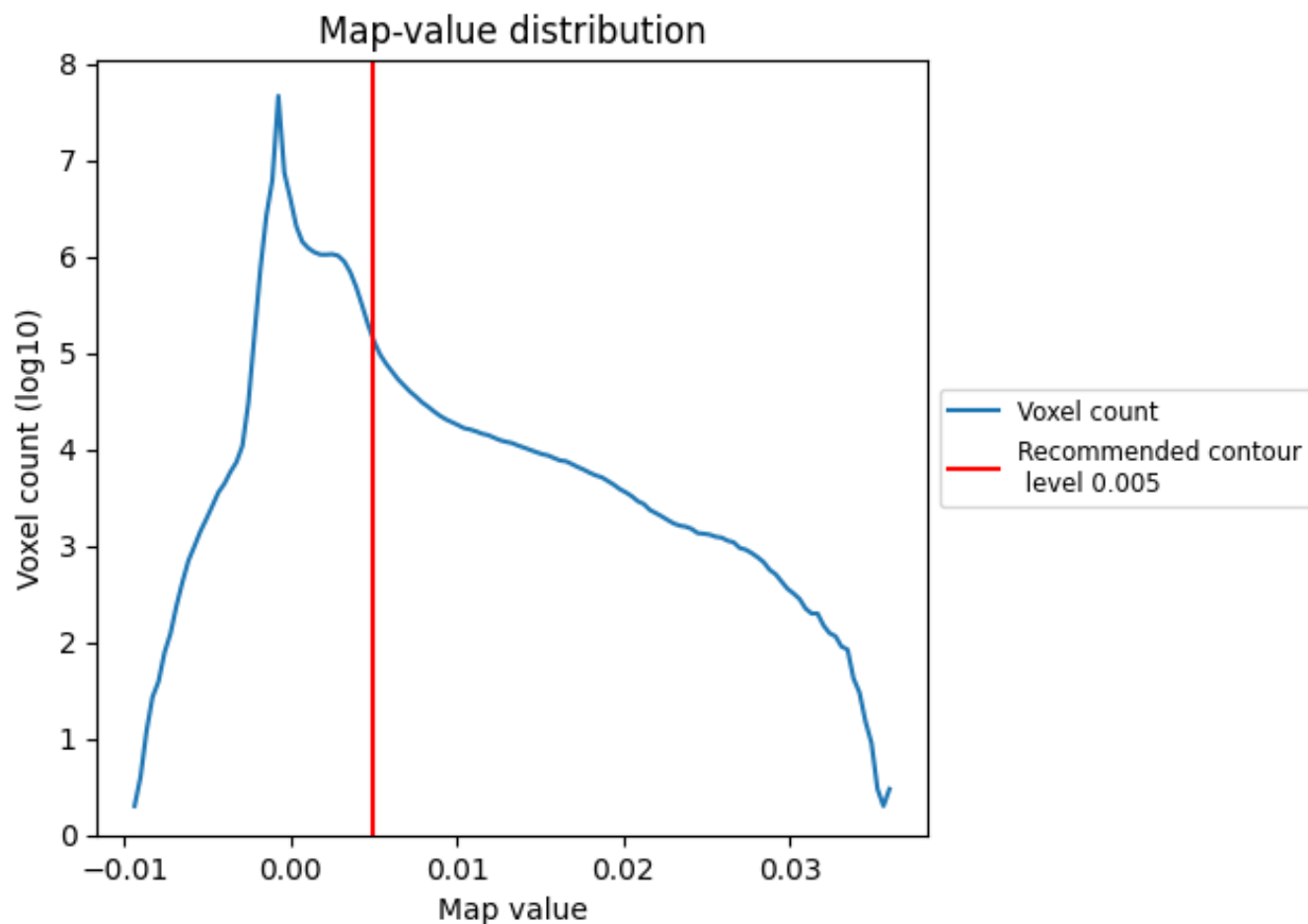
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

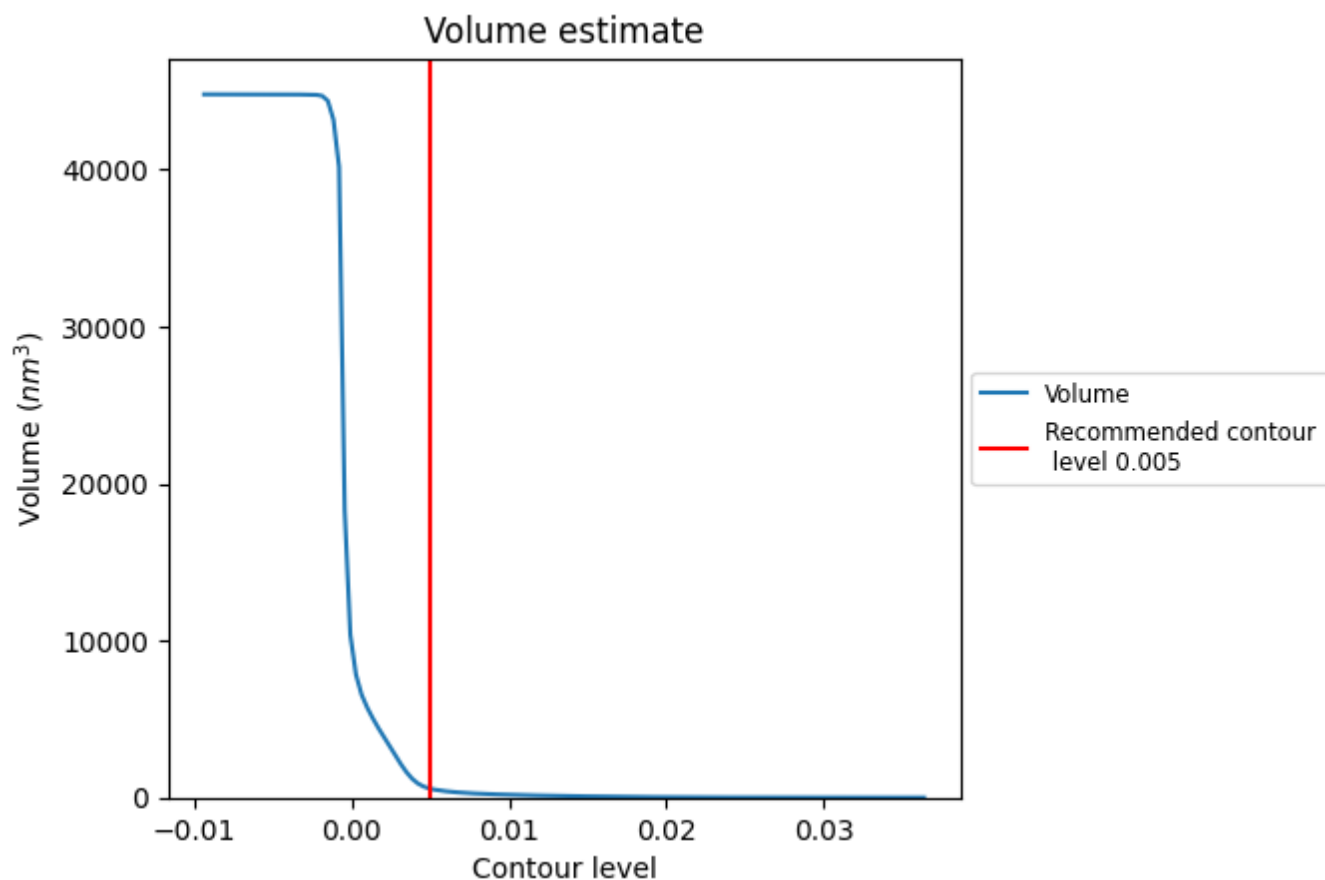
This section contains the results of statistical analysis of the map.

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.

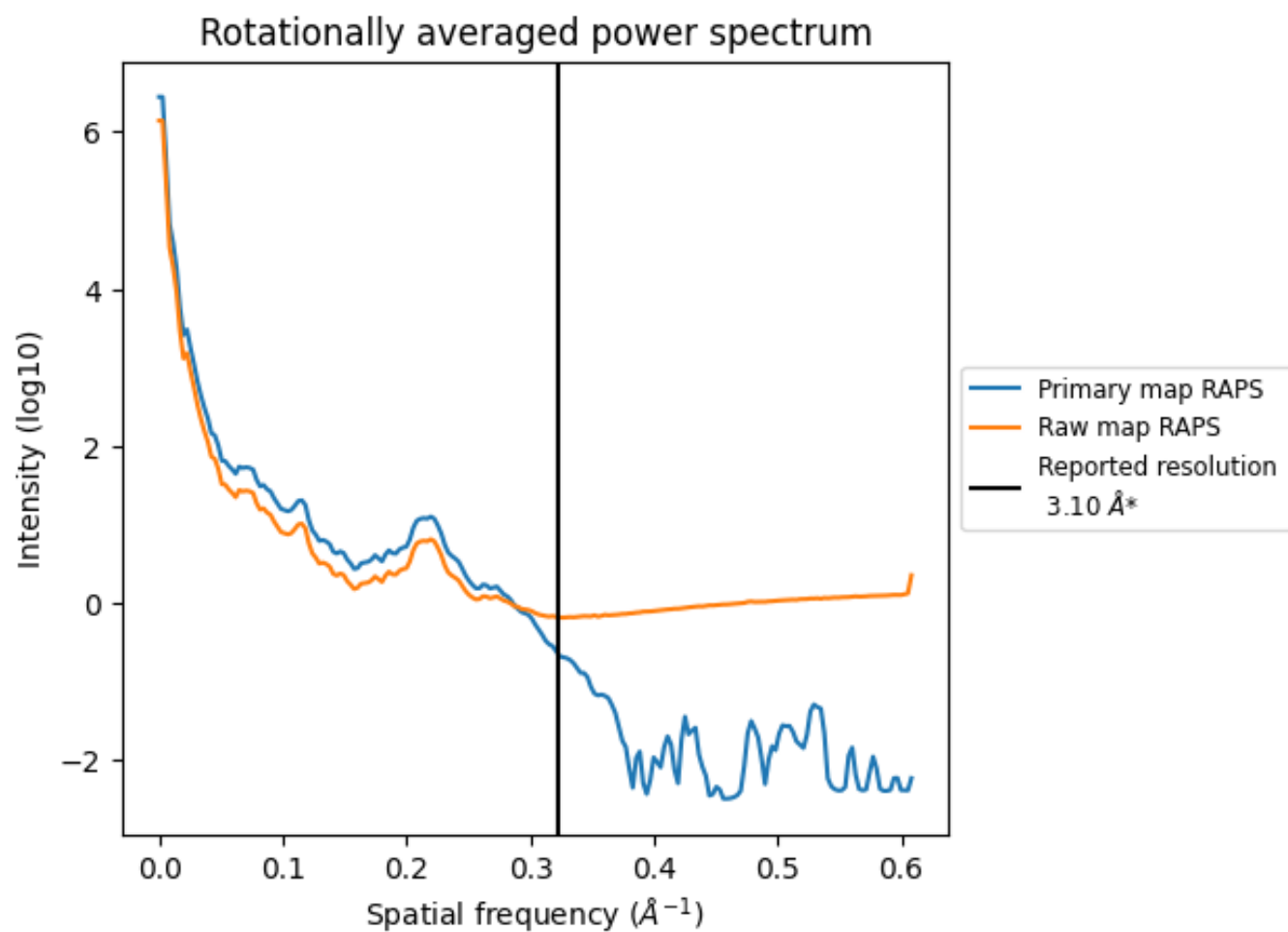
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 565 nm³; this corresponds to an approximate mass of 510 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 ⓘ

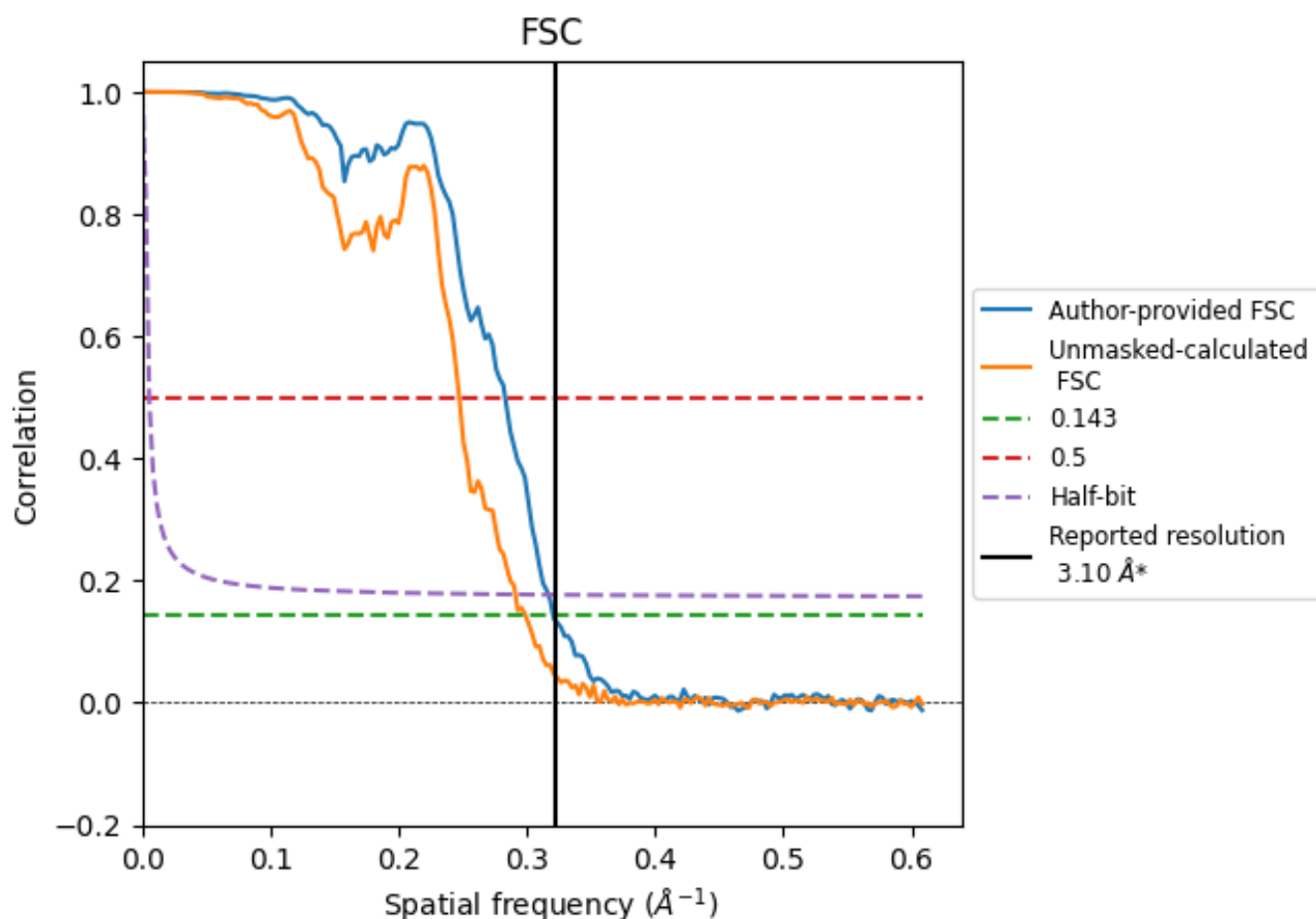


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

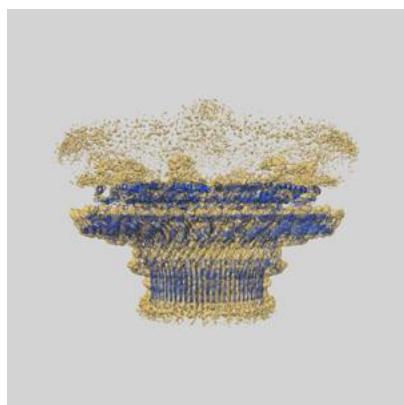
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.53	3.16
Unmasked-calculated*	3.35	4.04	3.44

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

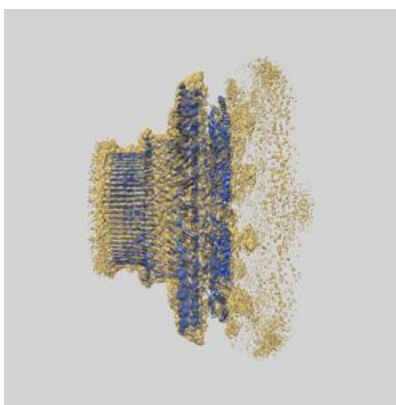
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10143 and PDB model 6SCN. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

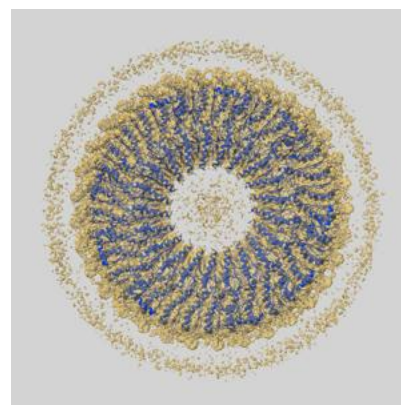
9.1 Map-model overlay [i](#)



X



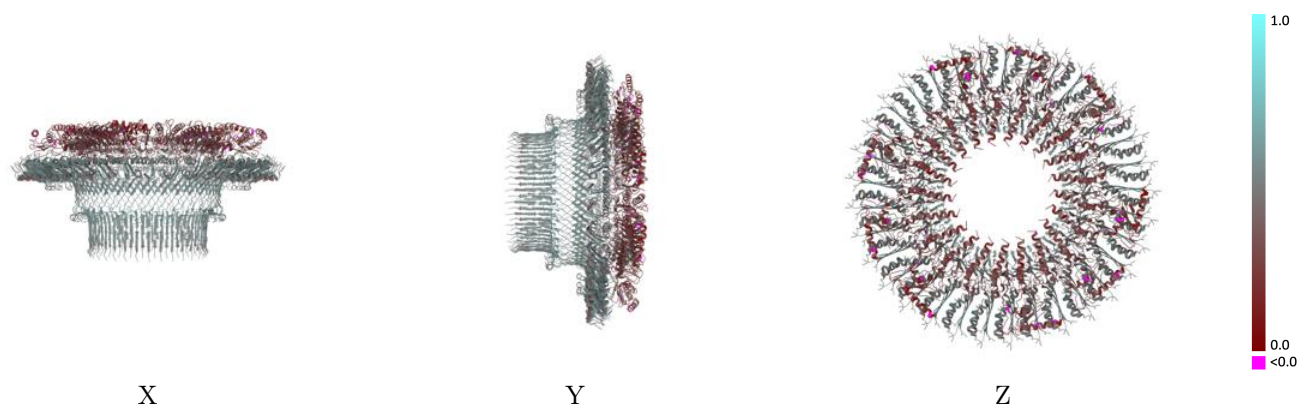
Y



Z

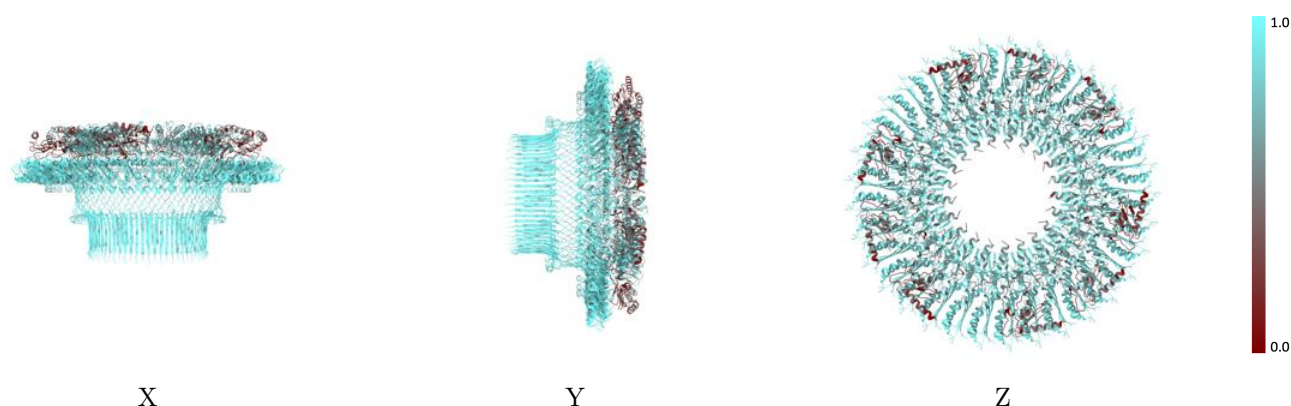
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



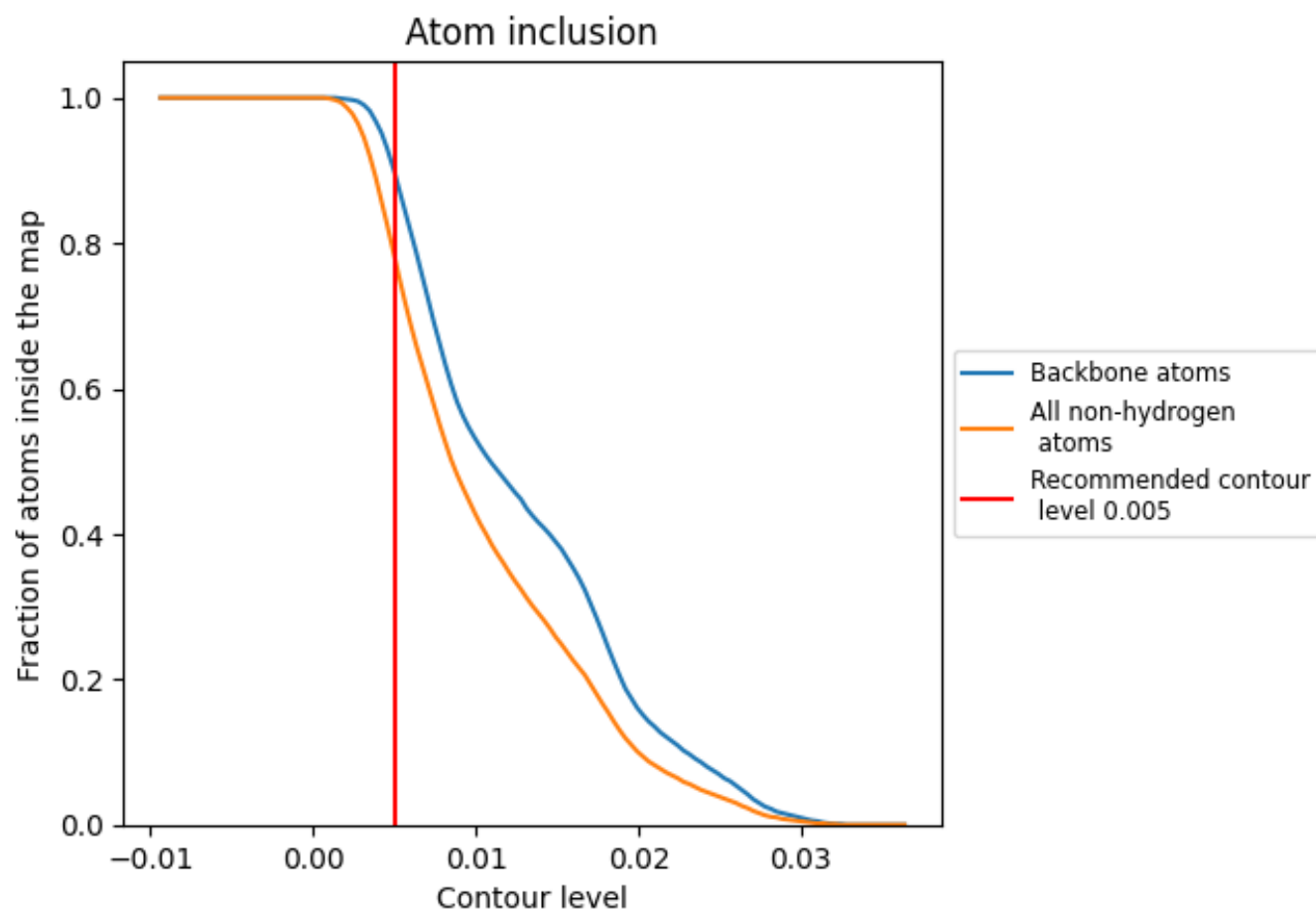
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 78% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7810	 0.4300
A	 0.8120	 0.4280
B	 0.6620	 0.3990
C	 0.8120	 0.4270
D	 0.8090	 0.4390
E	 0.6910	 0.4140
F	 0.8120	 0.4320
G	 0.8190	 0.4300
H	 0.6730	 0.4120
I	 0.8230	 0.4280
J	 0.8210	 0.4340
K	 0.9060	 0.5080
L	 0.8120	 0.4270
M	 0.6610	 0.4000
N	 0.8160	 0.4290
O	 0.8120	 0.4350
P	 0.6910	 0.4160
Q	 0.8120	 0.4340
R	 0.8200	 0.4330
S	 0.6710	 0.4150
T	 0.8190	 0.4300
U	 0.8250	 0.4360
V	 0.9080	 0.5080
W	 0.8110	 0.4280
X	 0.6590	 0.4040
Y	 0.8120	 0.4290
Z	 0.8120	 0.4390
a	 0.6890	 0.4150
b	 0.8110	 0.4320
c	 0.8190	 0.4330
d	 0.6720	 0.4130
e	 0.8180	 0.4280
f	 0.8210	 0.4330
g	 0.9060	 0.5090

