



wwPDB EM Validation Summary Report ⓘ

May 7, 2026 – 03:15 PM JST

PDB ID : 8Z5X / pdb_00008z5x
EMDB ID : EMD-39787
Title : Cryo-EM structure of the MS ring with the proximal rod and the export apparatus (C1) within the polar flagellar motor
Authors : Zhang, L.; Tan, J.X.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2024-04-18
Resolution : 3.64 Å(reported)
Based on initial model : .

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

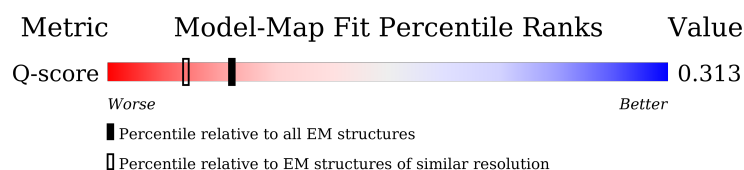
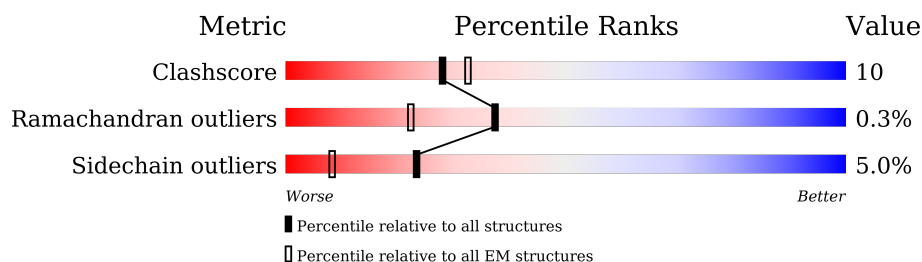
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.64 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.



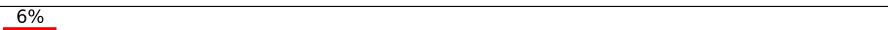
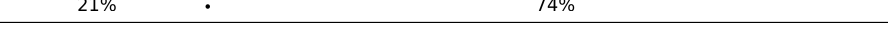
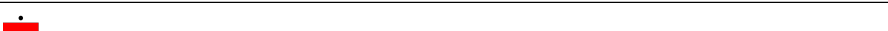
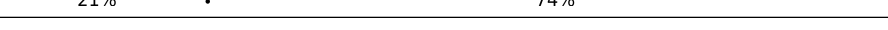
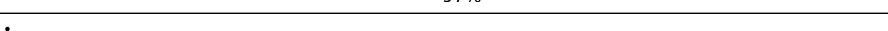
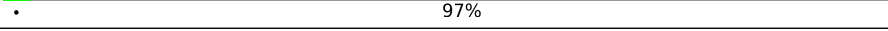
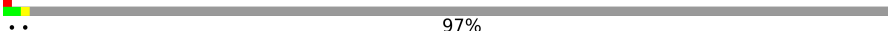
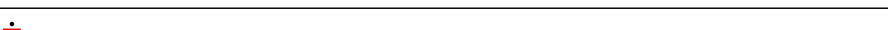
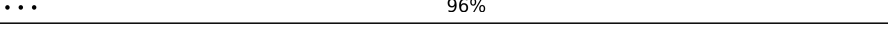
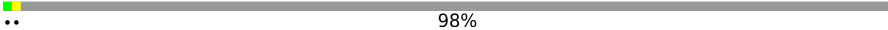
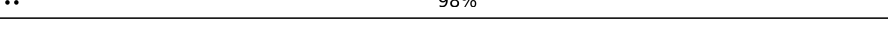
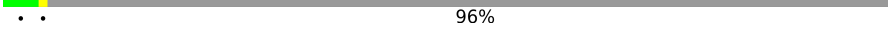
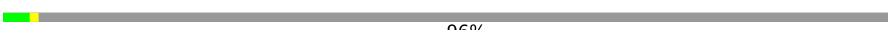
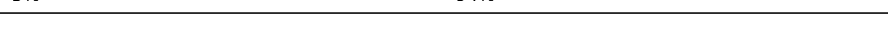
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11633 (3.14 - 4.14)

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	0	289	
1	9	289	
1	AP	289	
1	Ak	289	

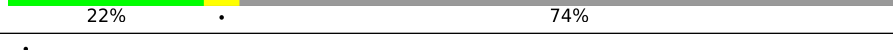
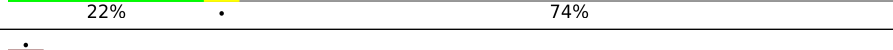
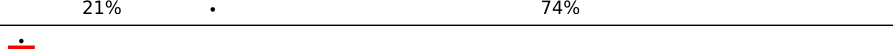
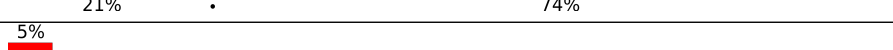
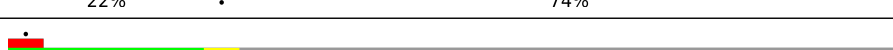
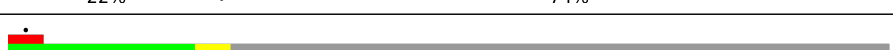
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Mol	Chain	Length	Quality of chain
1	Al	289	 54% 16% 28%
2	1	580	 7% 22% 74%
2	2	580	 6% 21% 74%
2	3	580	 21% 5% 74%
2	4	580	 5% 21% 74%
2	5	580	 21% 74%
2	A	580	 21% 74%
2	AA	580	 97%
2	AB	580	 97%
2	AC	580	 97%
2	AD	580	 97%
2	AE	580	 97%
2	AF	580	 96%
2	AG	580	 98%
2	AH	580	 98%
2	AI	580	 98%
2	AJ	580	 96%
2	AK	580	 96%
2	AL	580	 5% 94%
2	AM	580	 5% 94%
2	AN	580	 5% 94%
2	AO	580	 94%
2	B	580	 22% 74%
2	C	580	 22% 74%
2	D	580	 22% 74%

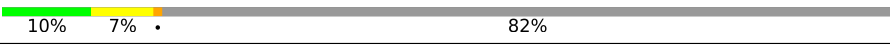
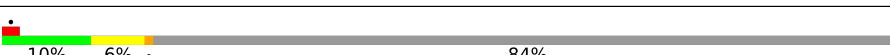
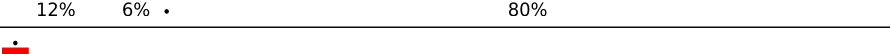
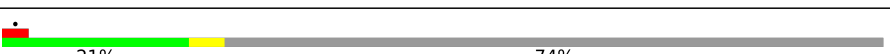
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Mol	Chain	Length	Quality of chain
2	E	580	 21% 74%
2	F	580	 21% 74%
2	G	580	 21% 74%
2	H	580	 21% 74%
2	I	580	 21% 74%
2	J	580	 21% 74%
2	K	580	 22% 74%
2	L	580	 22% 74%
2	M	580	 21% 74%
2	N	580	 21% 74%
2	O	580	 22% 74%
2	P	580	 22% 74%
2	Q	580	 21% 74%
2	R	580	 22% 74%
2	S	580	 11% 80%
2	T	580	 10% 80%
2	U	580	 12% 80%
2	V	580	 12% 80%
2	W	580	 11% 80%
2	X	580	 12% 81%
2	Y	580	 12% 80%
2	Z	580	 12% 80%
2	a	580	 13% 80%
2	b	580	 11% 84%
2	c	580	 10% 82%

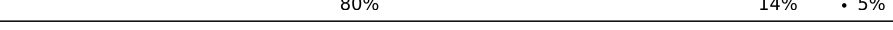
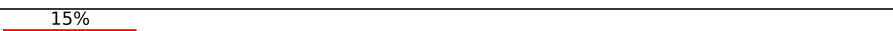
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Mol	Chain	Length	Quality of chain
2	d	580	 9% 7% 82%
2	e	580	 10% 7% 82%
2	f	580	 9% 6% 85%
2	g	580	 10% 5% 84%
2	h	580	 10% 6% 84%
2	i	580	 9% 6% 85%
2	j	580	 10% 6% 84%
2	k	580	 12% 7% 80%
2	l	580	 12% 7% 80%
2	m	580	 13% 6% 80%
2	n	580	 11% 7% 82%
2	o	580	 12% 6% 80%
2	p	580	 22% 6% 74%
2	q	580	 21% 6% 74%
2	r	580	 22% 6% 74%
2	s	580	 21% 6% 74%
2	t	580	 22% 6% 74%
2	u	580	 22% 6% 74%
2	v	580	 22% 6% 74%
2	w	580	 21% 6% 74%
2	x	580	 21% 5% 74%
2	y	580	 21% 5% 74%
2	z	580	 22% 6% 74%
3	6	89	69% 29% 2%
3	7	89	78% 22% 0%

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Mol	Chain	Length	Quality of chain
3	AQ	89	
3	AR	89	
4	8	260	
5	AS	131	
5	AT	131	
5	AU	131	
5	AV	131	
5	AW	131	
6	AX	137	
6	AY	137	
6	AZ	137	
6	Aa	137	
6	Ab	137	
6	Ac	137	
7	Ad	103	
7	Ae	103	
7	Af	103	
7	Ag	103	
7	Ah	103	
7	Ai	103	
8	Aj	376	
9	Am	13	
9	An	13	
9	Ao	13	
9	Ap	13	

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Mol	Chain	Length	Quality of chain
9	Aq	13	 38% 54% 8%
10	Ar	17	 6% 88% 12%
10	As	17	 6% 82% 18%
10	At	17	 18% 88% 12%
10	Au	17	 59% 94% 6%
10	Av	17	 18% 88% 12%
10	Aw	17	 94% 6%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 88315 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 biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	208	Total	C	N	O	S	0	0
			1608	1060	244	285	19		
1	9	207	Total	C	N	O	S	0	0
			1599	1055	243	282	19		
1	AP	208	Total	C	N	O	S	0	0
			1608	1060	244	285	19		
1	Ak	208	Total	C	N	O	S	0	0
			1608	1060	244	285	19		
1	Al	208	Total	C	N	O	S	0	0
			1608	1060	244	285	19		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	26	SER	THR	conflict	UNP A0A1W6TTE6
0	204	ASP	GLU	conflict	UNP A0A1W6TTE6
9	26	SER	THR	conflict	UNP A0A1W6TTE6
9	204	ASP	GLU	conflict	UNP A0A1W6TTE6
AP	26	SER	THR	conflict	UNP A0A1W6TTE6
AP	204	ASP	GLU	conflict	UNP A0A1W6TTE6
Ak	26	SER	THR	conflict	UNP A0A1W6TTE6
Ak	204	ASP	GLU	conflict	UNP A0A1W6TTE6
Al	26	SER	THR	conflict	UNP A0A1W6TTE6
Al	204	ASP	GLU	conflict	UNP A0A1W6TTE6

- Molecule 2 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	2	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	3	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	5	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	A	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	AA	19	Total	C	N	O	S	0	0
			135	82	23	29	1		
2	AB	19	Total	C	N	O	S	0	0
			135	82	23	29	1		
2	AC	20	Total	C	N	O	S	0	0
			139	84	24	30	1		
2	AD	19	Total	C	N	O	S	0	0
			135	82	23	29	1		
2	AE	19	Total	C	N	O	S	0	0
			135	82	23	29	1		
2	AF	23	Total	C	N	O	S	0	0
			158	97	27	33	1		
2	AG	11	Total	C	N	O		0	0
			73	46	13	14			
2	AH	11	Total	C	N	O		0	0
			73	46	13	14			
2	AI	11	Total	C	N	O		0	0
			73	46	13	14			
2	AJ	24	Total	C	N	O	S	0	0
			163	100	28	34	1		
2	AK	25	Total	C	N	O	S	0	0
			169	104	29	35	1		
2	AL	32	Total	C	N	O	S	0	0
			220	134	38	46	2		
2	AM	33	Total	C	N	O	S	0	0
			224	136	39	47	2		
2	AN	33	Total	C	N	O	S	0	0
			224	136	39	47	2		
2	AO	32	Total	C	N	O	S	0	0
			220	134	38	46	2		
2	B	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	C	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	D	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	F	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	G	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	H	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	I	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	J	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	K	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	L	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	M	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	N	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	O	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	P	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	Q	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	R	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	S	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	T	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	U	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	V	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	W	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	X	109	Total	C	N	O	S	0	0
			839	515	157	163	4		
2	Y	114	Total	C	N	O	S	0	0
			881	543	165	169	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Z	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	a	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	b	94	Total	C	N	O	S	0	0
			724	446	135	140	3		
2	c	103	Total	C	N	O	S	0	0
			803	496	153	151	3		
2	d	103	Total	C	N	O	S	0	0
			803	496	153	151	3		
2	e	103	Total	C	N	O	S	0	0
			803	496	153	151	3		
2	f	85	Total	C	N	O	S	0	0
			660	405	125	127	3		
2	g	92	Total	C	N	O	S	0	0
			704	432	132	137	3		
2	h	91	Total	C	N	O	S	0	0
			695	427	131	134	3		
2	i	89	Total	C	N	O	S	0	0
			684	420	129	132	3		
2	j	92	Total	C	N	O	S	0	0
			704	432	132	137	3		
2	k	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	l	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	m	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	n	105	Total	C	N	O	S	0	0
			802	494	147	157	4		
2	o	114	Total	C	N	O	S	0	0
			881	543	165	169	4		
2	p	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	q	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	r	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	s	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	t	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	u	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	v	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	w	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	x	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	y	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		
2	z	148	Total	C	N	O	S	0	0
			1171	719	215	235	2		

- Molecule 3 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	89	Total	C	N	O	S	0	0
			722	489	107	117	9		
3	7	89	Total	C	N	O	S	0	0
			722	489	107	117	9		
3	AQ	89	Total	C	N	O	S	0	0
			722	489	107	117	9		
3	AR	89	Total	C	N	O	S	0	0
			722	489	107	117	9		

- Molecule 4 is a protein called Flagellar biosynthetic protein FliR.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	8	242	Total	C	N	O	S	0	0
			1896	1265	295	315	21		

- Molecule 5 is a protein called Flagellar basal body rod protein FlgB.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS	109	Total	C	N	O	S	0	0
			845	523	155	166	1		
5	AT	107	Total	C	N	O	S	0	0
			835	518	153	163	1		
5	AU	109	Total	C	N	O	S	0	0
			845	523	155	166	1		
5	AV	108	Total	C	N	O	S	0	0
			837	519	154	163	1		

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Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AW	108	Total	C	N	O	S	0	0
			837	519	154	163	1		

- Molecule 6 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AX	130	Total	C	N	O	S	0	0
			983	605	168	203	7		
6	AY	130	Total	C	N	O	S	0	0
			983	605	168	203	7		
6	AZ	130	Total	C	N	O	S	0	0
			983	605	168	203	7		
6	Aa	130	Total	C	N	O	S	0	0
			983	605	168	203	7		
6	Ab	130	Total	C	N	O	S	0	0
			983	605	168	203	7		
6	Ac	130	Total	C	N	O	S	0	0
			983	605	168	203	7		

- Molecule 7 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ad	72	Total	C	N	O	S	0	0
			560	345	99	113	3		
7	Ae	80	Total	C	N	O	S	0	0
			605	372	108	122	3		
7	Af	80	Total	C	N	O	S	0	0
			605	372	108	122	3		
7	Ag	72	Total	C	N	O	S	0	0
			560	345	99	113	3		
7	Ah	72	Total	C	N	O	S	0	0
			560	345	99	113	3		
7	Ai	40	Total	C	N	O	S	0	0
			311	194	53	61	3		

- Molecule 8 is a protein called Flagellar biosynthetic protein FlhB.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Aj	71	Total	C	N	O	S	0	0
			552	370	83	95	4		

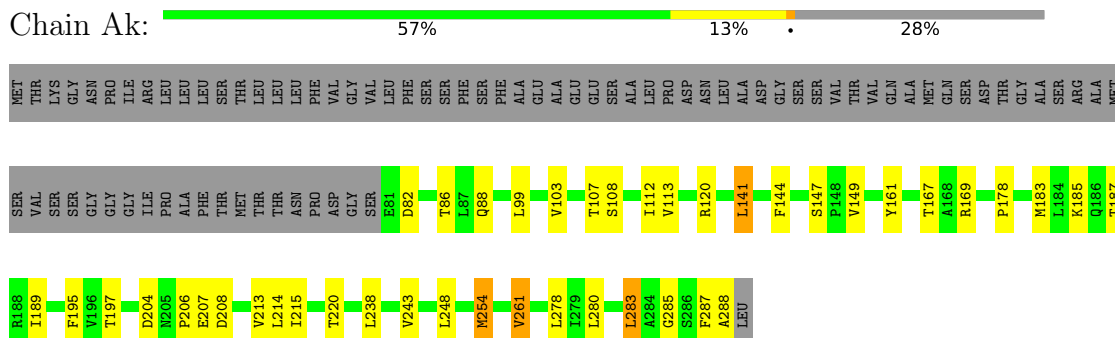
- Molecule 9 is a protein called Alanine-modelled FlgB-Dc loop.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Am	12	Total	C	N	O	0	0
			58	34	12	12		
9	An	9	Total	C	N	O	0	0
			44	26	9	9		
9	Ao	10	Total	C	N	O	0	0
			49	29	10	10		
9	Ap	10	Total	C	N	O	0	0
			49	29	10	10		
9	Aq	13	Total	C	N	O	0	0
			63	37	13	13		

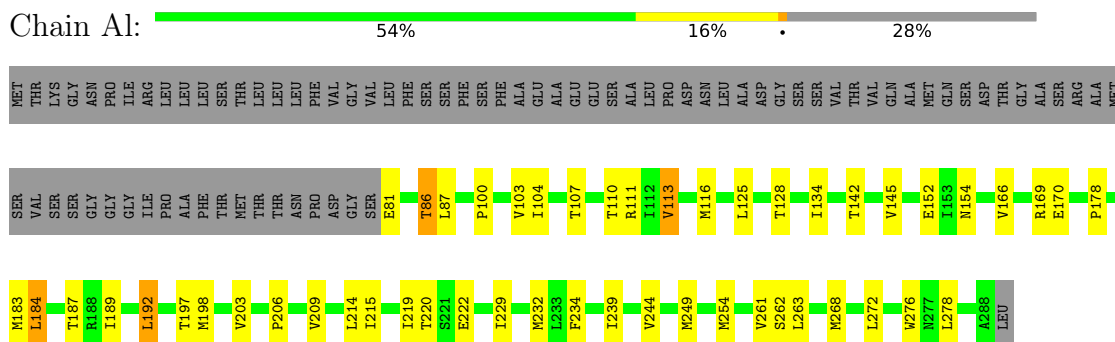
- Molecule 10 is a protein called FliE-helix 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	Ar	17	Total	C	N	O	0	0
			84	50	17	17		
10	As	17	Total	C	N	O	0	0
			84	50	17	17		
10	At	17	Total	C	N	O	0	0
			84	50	17	17		
10	Au	17	Total	C	N	O	0	0
			84	50	17	17		
10	Av	17	Total	C	N	O	0	0
			84	50	17	17		
10	Aw	17	Total	C	N	O	0	0
			84	50	17	17		

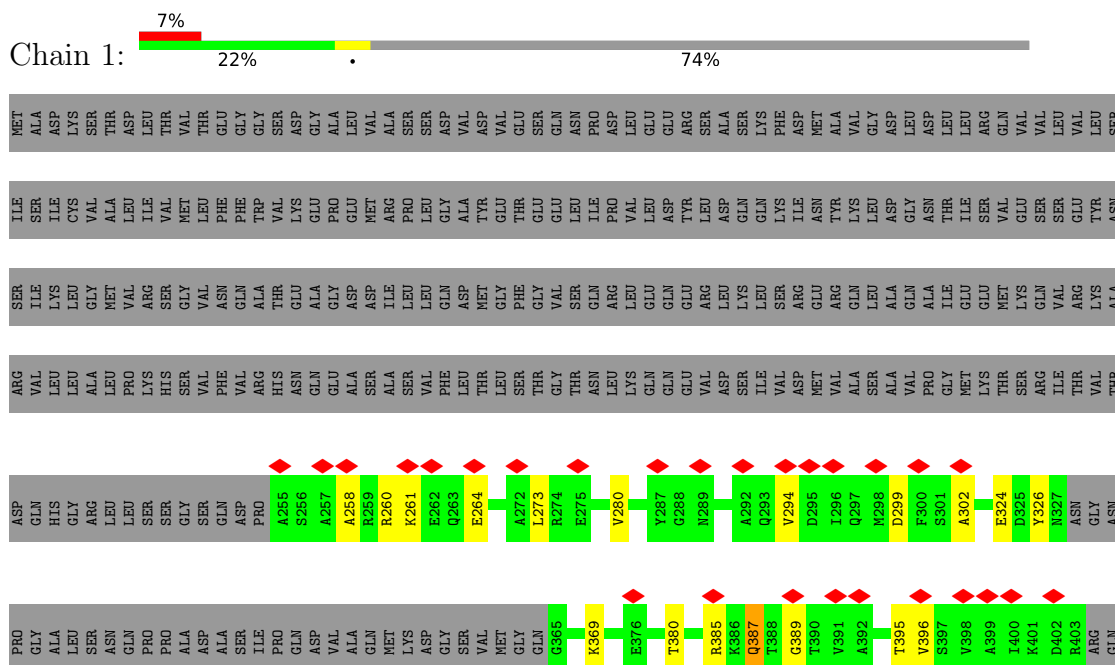
- Molecule 1: Flagellar biosynthetic protein FlpP

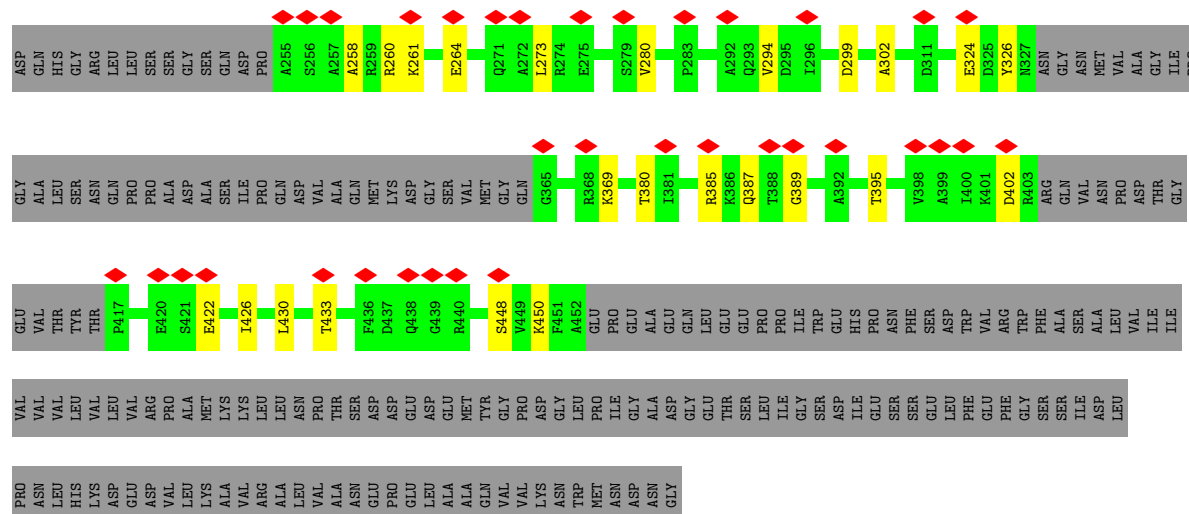


- Molecule 1: Flagellar biosynthetic protein FlhP

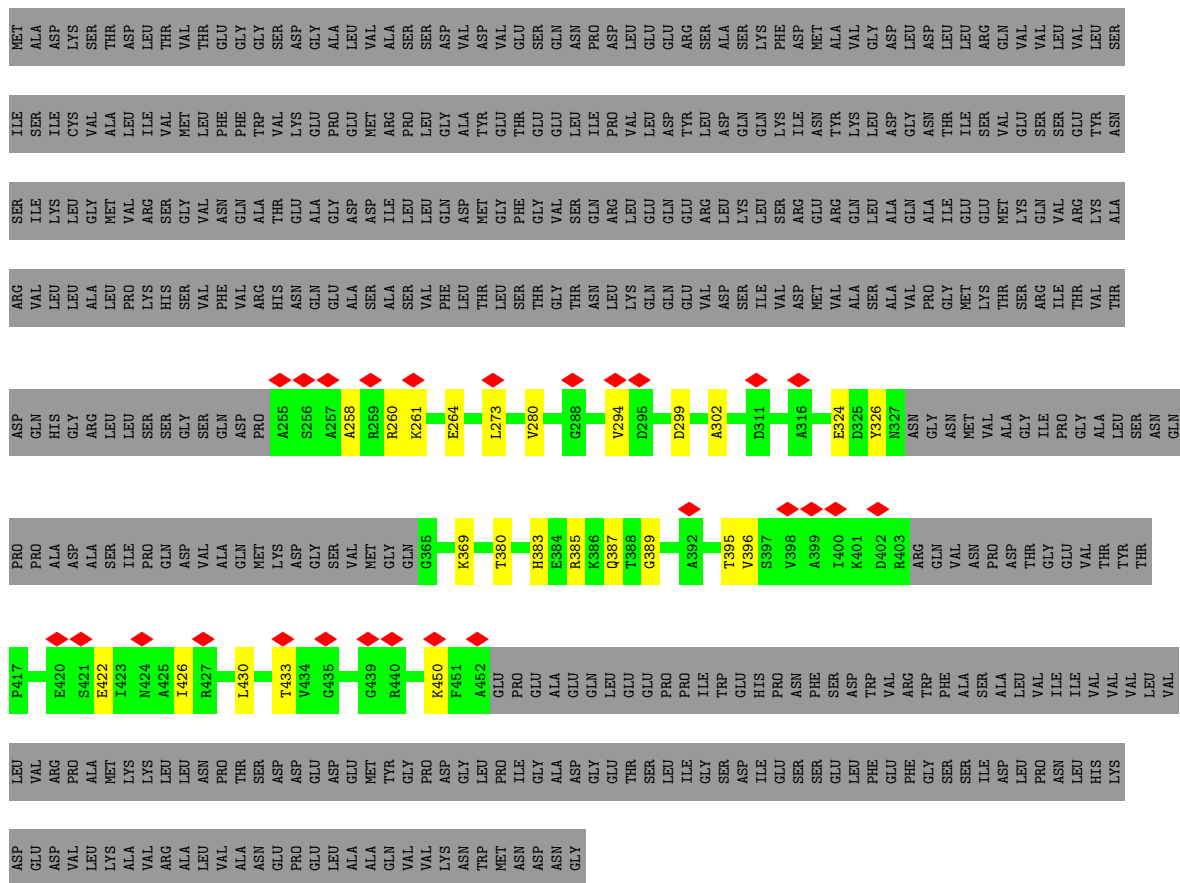


- Molecule 2: Flagellar M-ring protein

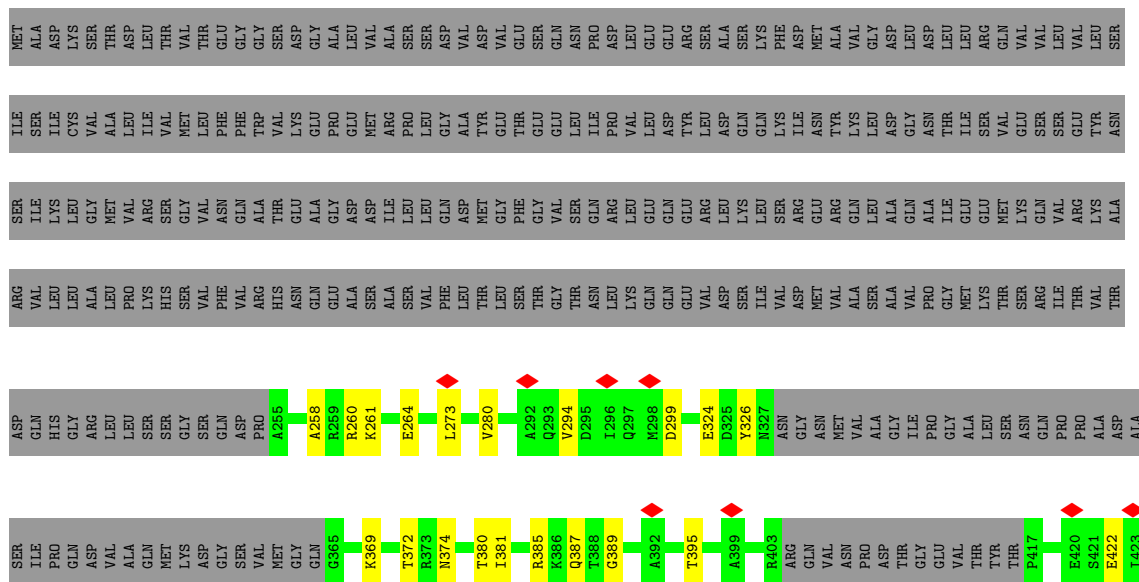


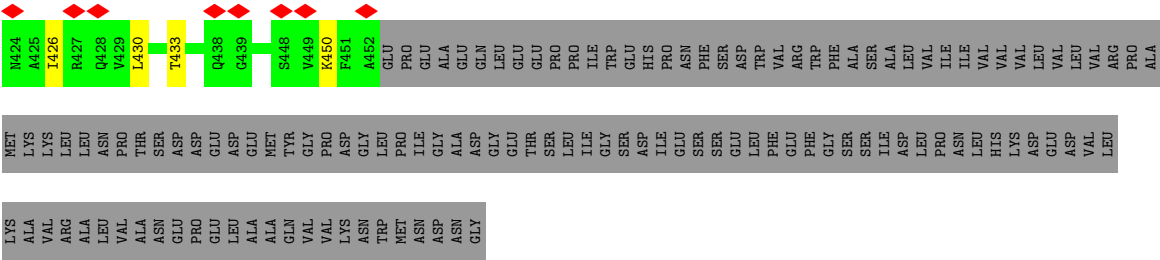




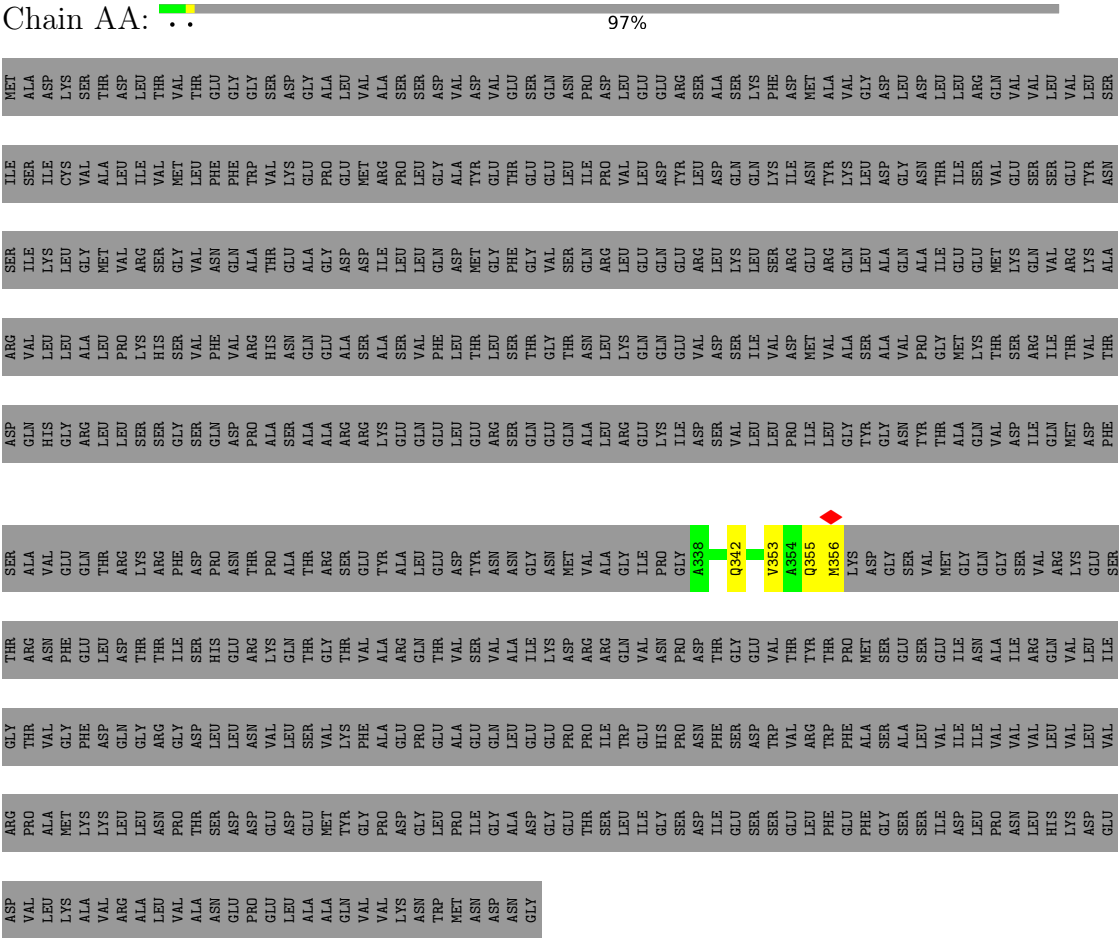


- Molecule 2: Flagellar M-ring protein

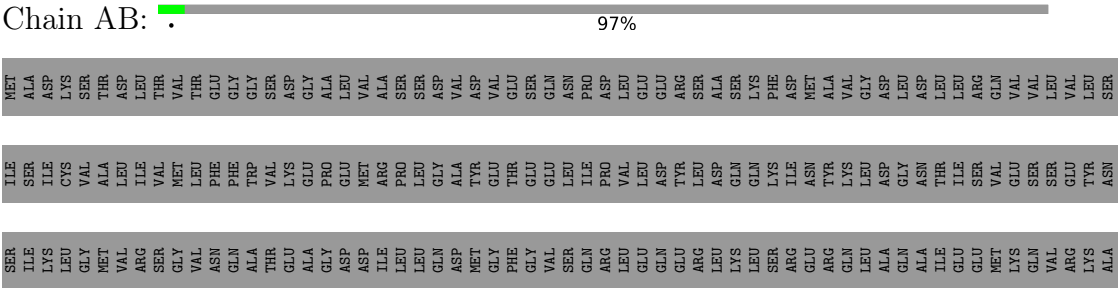




● Molecule 2: Flagellar M-ring protein



● Molecule 2: Flagellar M-ring protein



GLU	ASP	VAL	ILE	SER	SER	ASP	ARG	VAL	ARG
ASP	VAL	PRO	THR	THR	THR	ALA	ALA	VAL	GLN
VAL	PRO	ALA	THR	THR	VAL	GLN	GLN	GLY	HIS
LYS	LYS	MET	GLY	PHE	GLU	THR	THR	ARG	LEU
ALA	ALA	LYS	PHE	LEU	LEU	THR	ARG	LEU	PRO
VAL	VAL	LYS	ASP	ASP	GLN	ARG	LYS	LEU	LYS
ARG	ARG	LEU	GLN	ASP	ASP	THR	THR	SER	HIS
ALA	ALA	LEU	GLY	THR	THR	ARG	ARG	SER	SER
LEU	LEU	ASN	ARG	ILE	ILE	PRO	PRO	SER	VAL
VAL	VAL	THR	ASP	SER	HIS	ASN	THR	ASP	PHE
ASN	ASN	SER	LEU	THR	GLY	ARG	GLY	VAL	VAL
ASP	PRO	ASP	LEU	GLU	THR	THR	GLU	PRO	ARG
PRO	PRO	ASP	ASN	ARG	VAL	ALA	ALA	ALA	HIS
GLU	GLU	GLU	VAL	LYS	GLN	THR	THR	SER	ALA
LEU	LEU	ASP	LEU	GLN	GLN	LEU	LEU	ALA	GLN
ALA	ALA	GLU	SER	THR	THR	ARG	ARG	ALA	GLU
ALA	ALA	MET	VAL	GLY	GLY	SER	SER	ARG	ALA
GLN	GLN	TYR	LYS	THR	THR	GLU	GLU	ARG	ARG
VAL	VAL	GLY	PHE	VAL	VAL	ALA	ALA	LYS	ALA
VAL	VAL	PRO	GLU	ALA	ALA	LEU	LEU	GLU	VAL
ASN	ASN	ASP	GLU	ARG	GLN	LEU	LEU	THR	PHE
LYS	LYS	GLY	PRO	GLN	THR	ASP	ASP	LEU	LEU
ASN	ASN	GLY	GLU	THR	GLN	LEU	LEU	THR	THR
TRP	TRP	LEU	GLU	THR	THR	ASP	ASP	LEU	LEU
GLY	GLY	ASP	GLU	ILE	ILE	GLY	GLY	GLY	GLY
GLY	GLY	ASP	GLU	LYS	LYS	ASN	ASN	GLY	THR
GLU	GLU	GLY	GLU	THR	THR	PRO	PRO	GLY	GLN
GLU	GLU	THR	PRO	ASP	ASP	GLY	GLY	ILE	GLN
THR	THR	SER	PRO	ARG	ALA	ALA	ALA	ARG	LYS
LEU	LEU	SER	ILE	ARG	GLY	GLY	GLY	ILE	GLN
LEU	LEU	TRP	GLN	GLN	ILE	PRO	PRO	GLY	GLN
ILE	ILE	GLU	THR	ASN	GLY	THR	THR	ILE	GLU
GLY	GLY	THR	HIS	ASN	THR	A338	A338	ASP	GLU
VAL	VAL	ASP	PRO	PRO	THR	+	+	SER	VAL
ASP	ASP	ASP	ASN	ASN	THR	Q342	Q342	ASP	VAL
ILE	ILE	ILE	PHE	THR	THR	P343	P343	VAL	LEU
SER	SER	GLU	SER	GLY	GLY	+	+	LEU	ILE
ASP	ASP	SER	ASP	GLU	THR	V352	V352	PRO	ASP
THR	THR	TRP	VAL	VAL	THR	+	+	ILE	VAL
THR	THR	ARG	THR	THR	THR	D353	D353	LEU	VAL
THR	THR	THR	THR	THR	THR	+	+	ALA	ALA
PRO	PRO	PHE	PHE	PRO	PRO	A356	A356	TYR	SER
PHE	PHE	GLU	ALA	MET	MET	LYS	LYS	GLY	SER
GLY	GLY	SER	SER	SER	ASP	ASP	ASP	ASN	VAL
SER	SER	ALA	ALA	GLU	GLU	GLY	GLY	THR	THR
SER	SER	SER	LEU	SER	VAL	VAL	VAL	THR	GLY
ILE	ILE	ILE	VAL	GLU	MET	MET	MET	ALA	LYS
ASP	ASP	ASP	ILE	ILE	GLY	GLN	GLN	GLN	THR
LEU	LEU	LEU	ILE	ASN	ASN	VAL	VAL	VAL	THR
PRO	PRO	VAL	VAL	ALA	ALA	GLY	GLY	ASP	SER
ASN	ASN	ASN	VAL	ILE	ILE	GLY	GLY	ASP	THR
LEU	LEU	LEU	VAL	ARG	VAL	ARG	ARG	ILE	ILE
LEU	LEU	HIS	LEU	GLN	GLN	VAL	VAL	THR	THR
LYS	LYS	ASP	VAL	THR	LYS	THR	THR	MET	MET
ASP	ASP	THR	THR	THR	THR	ASP	ASP	THR	THR

- Molecule 2: Flagellar M-ring protein

Chain AC: 97%

[illegible]

- Molecule 2: Flagellar M-ring protein

97%

- Molecule 2: Flagellar M-ring protein

97%



[illegible]

- Molecule 2: Flagellar M-ring protein

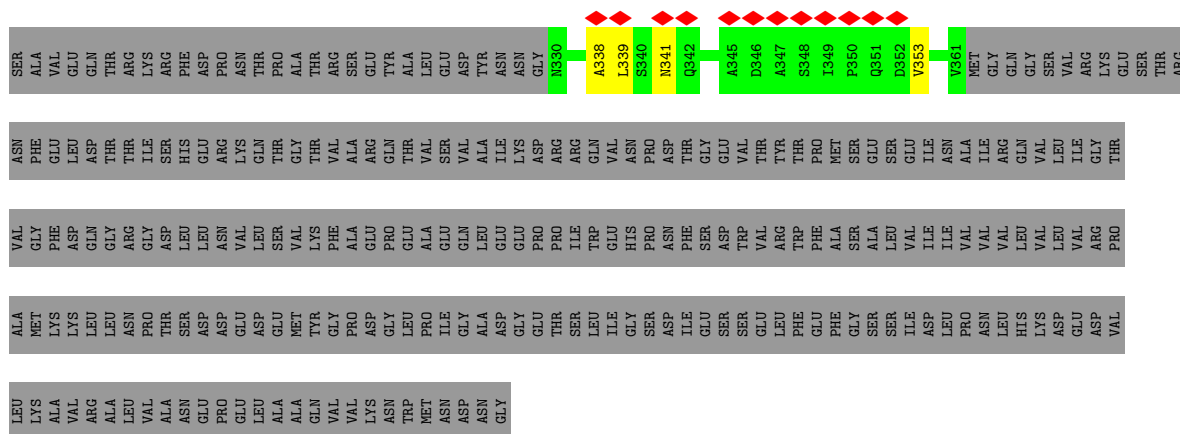
Chain AH: .. 98%

[illegible]

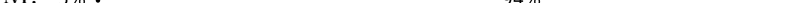
- Molecule 2: Flagellar M-ring protein

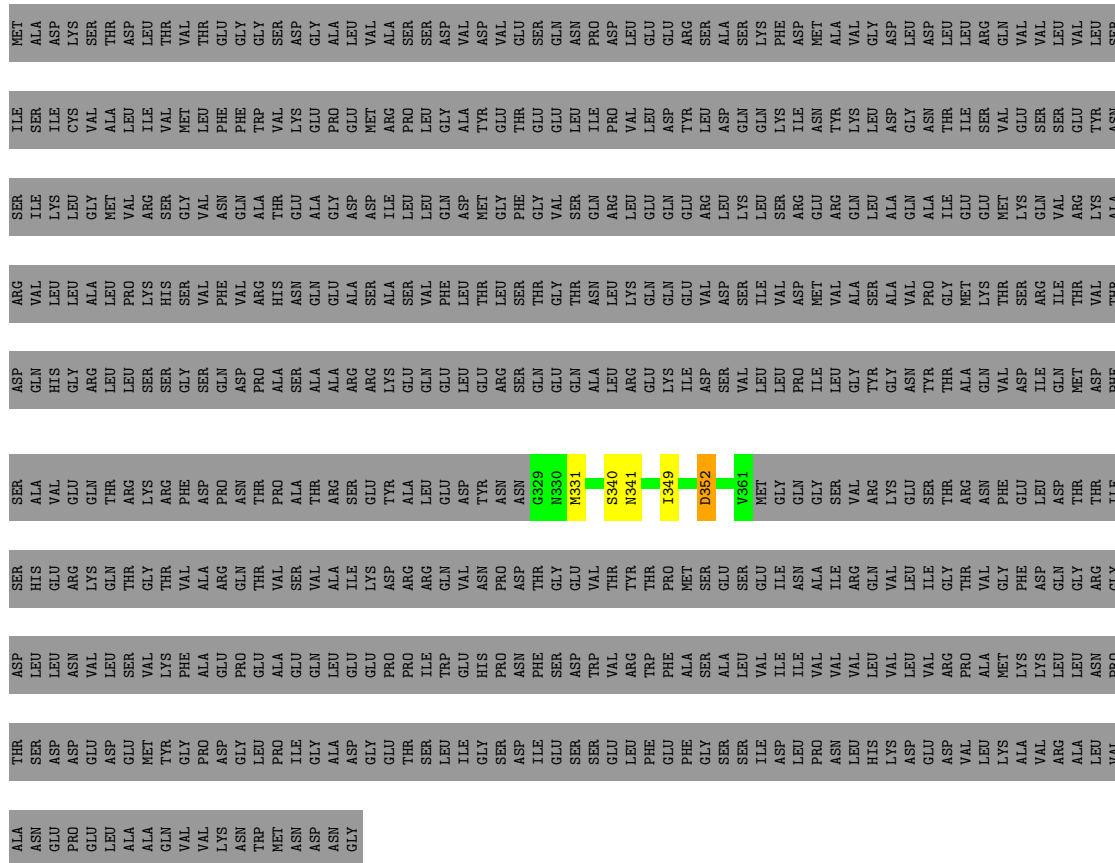
Chain AI: 98%

NET	ASP	ASP	LYS	SER	THR	ASP	LEU	THR	THR	THR	GLU	GLY	GLY	SER	SER	GLY	ALA	LEU	VAL	ALA	ALA	SER	SER	ASP	VAL	ASP	ASP	GLU	GLU	GLY	ARG	SER	ALA	ALA	VAL	VAL	LEU	LEU	ARG	GLN	VAL	VAL	LEU	VAL	LEU	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

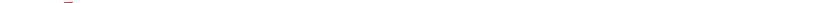


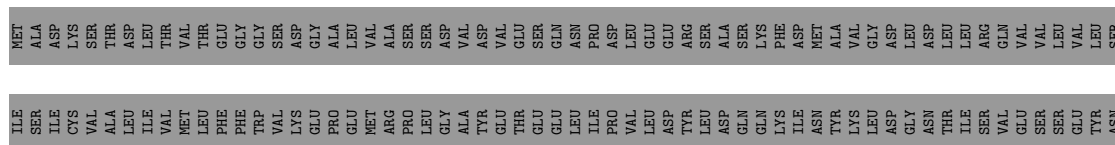
- Molecule 2: Flagellar M-ring protein

Chain AM:  5% . 94%

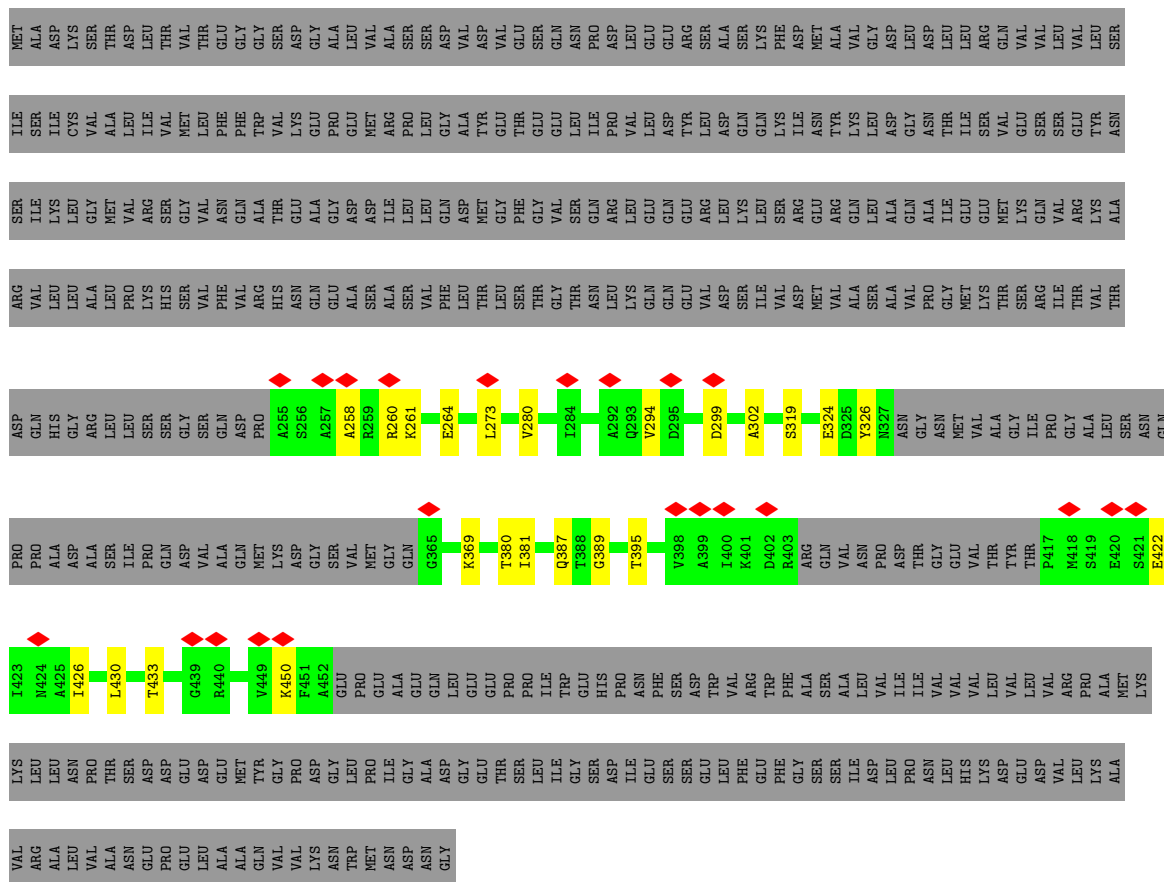


- Molecule 2: Flagellar M-ring protein

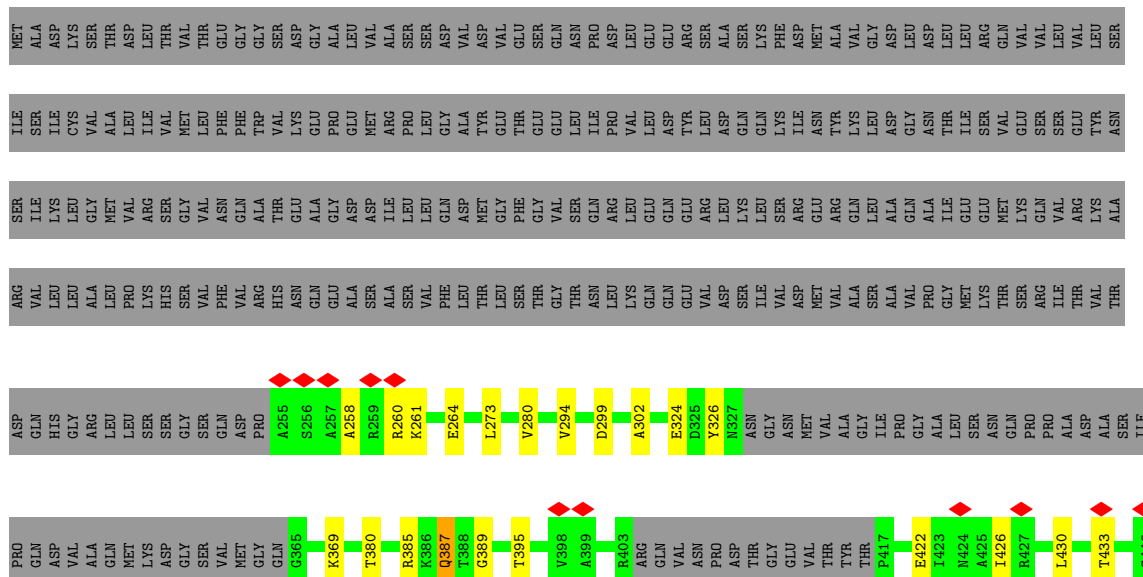
Chain AN:  5% 94%



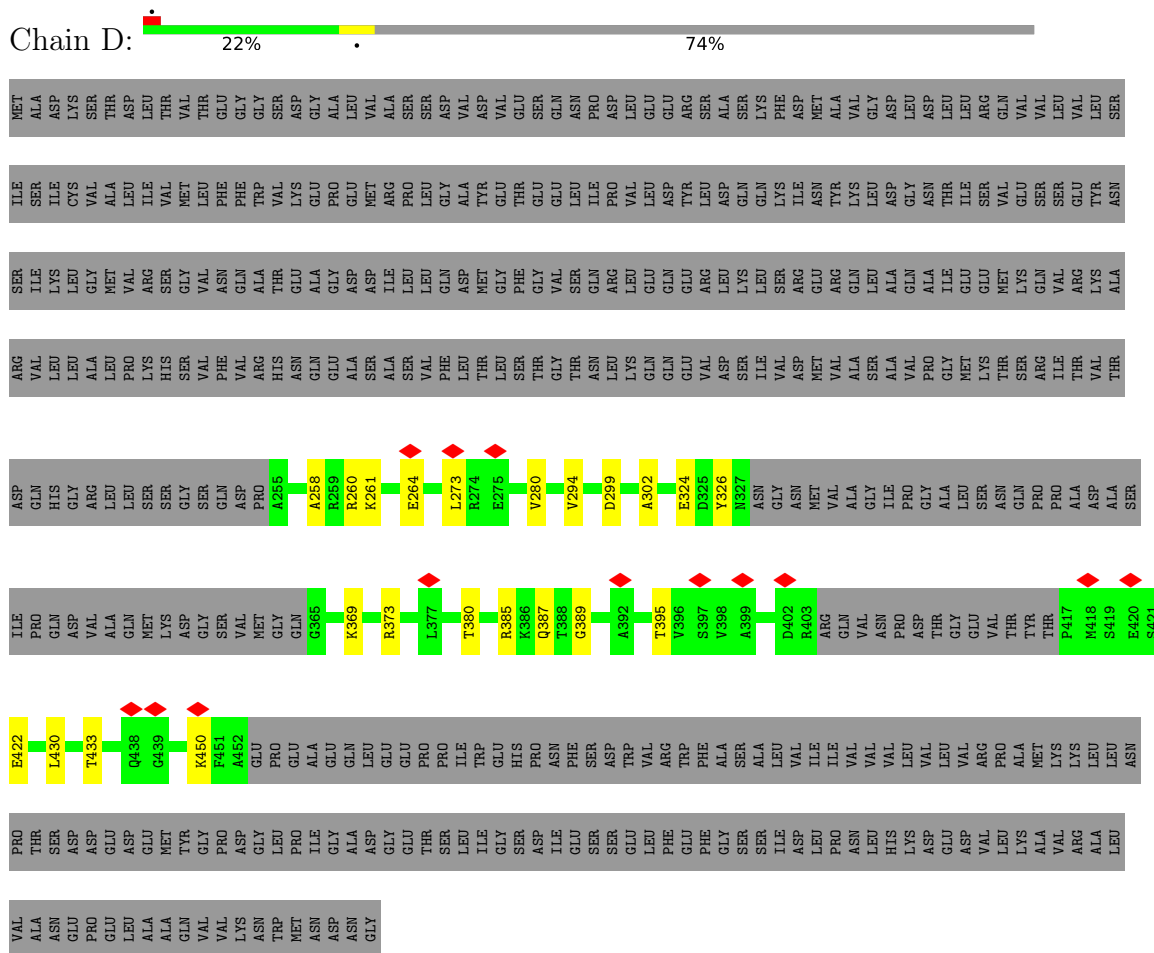
Chain B: 22% . 74%



Chain C: 22% . 74%



- Molecule 2: Flagellar M-ring protein

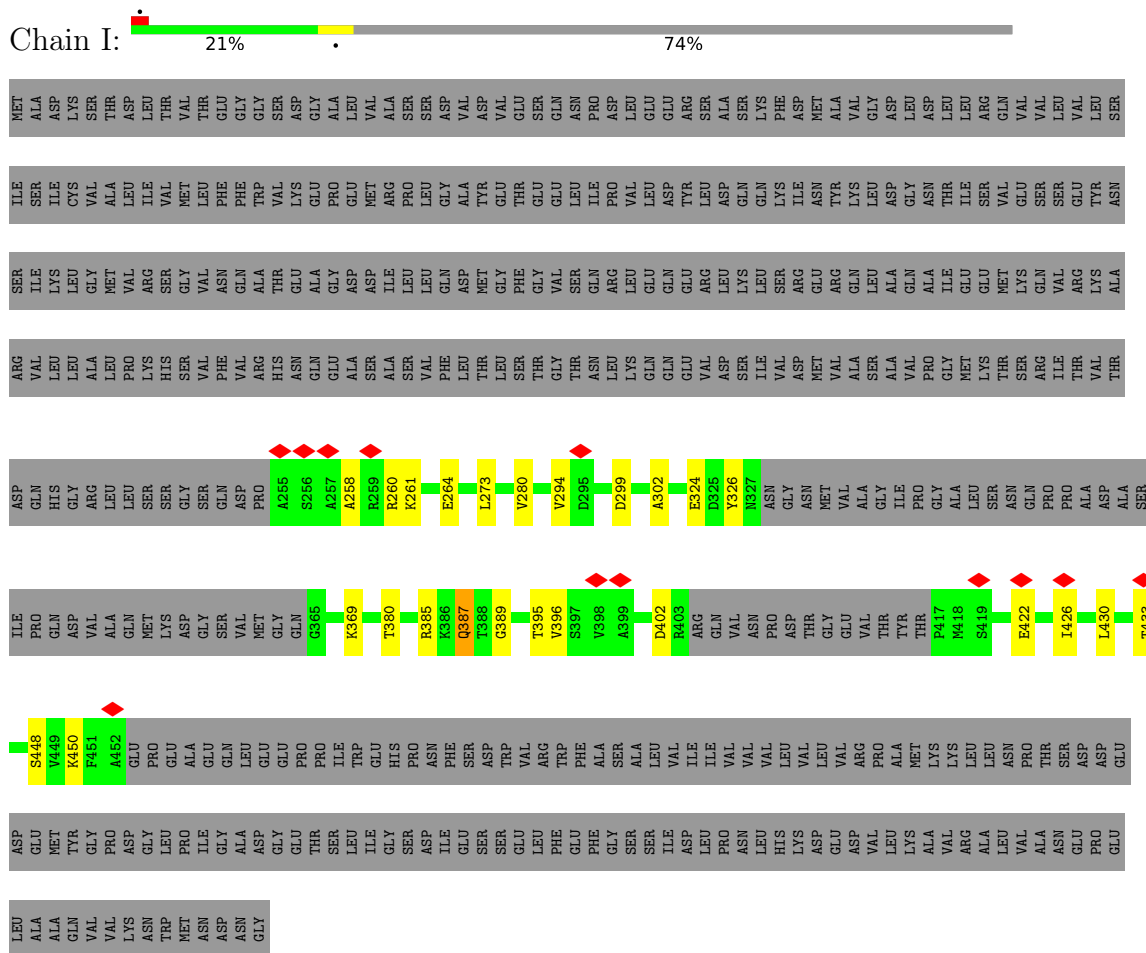


- Molecule 2: Flagellar M-ring protein





- Molecule 2: Flagellar M-ring protein

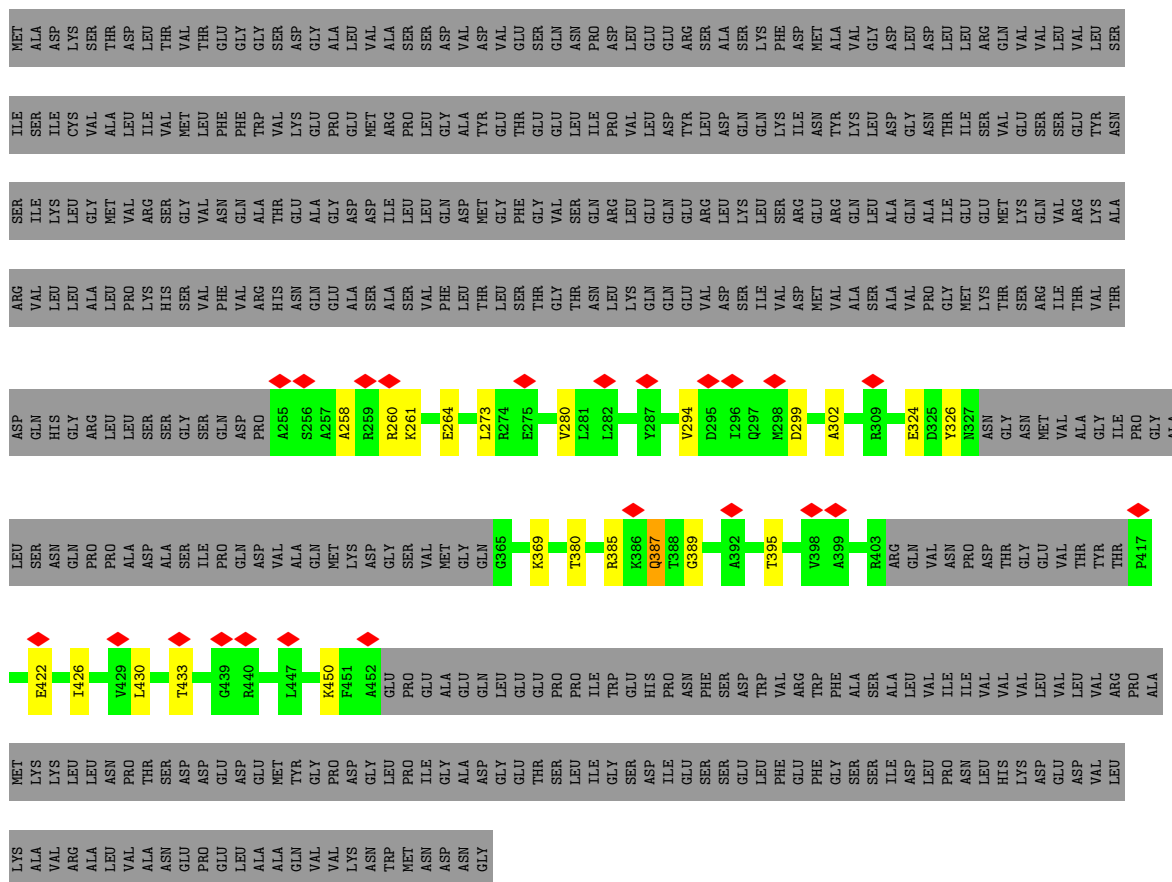


- Molecule 2: Flagellar M-ring protein

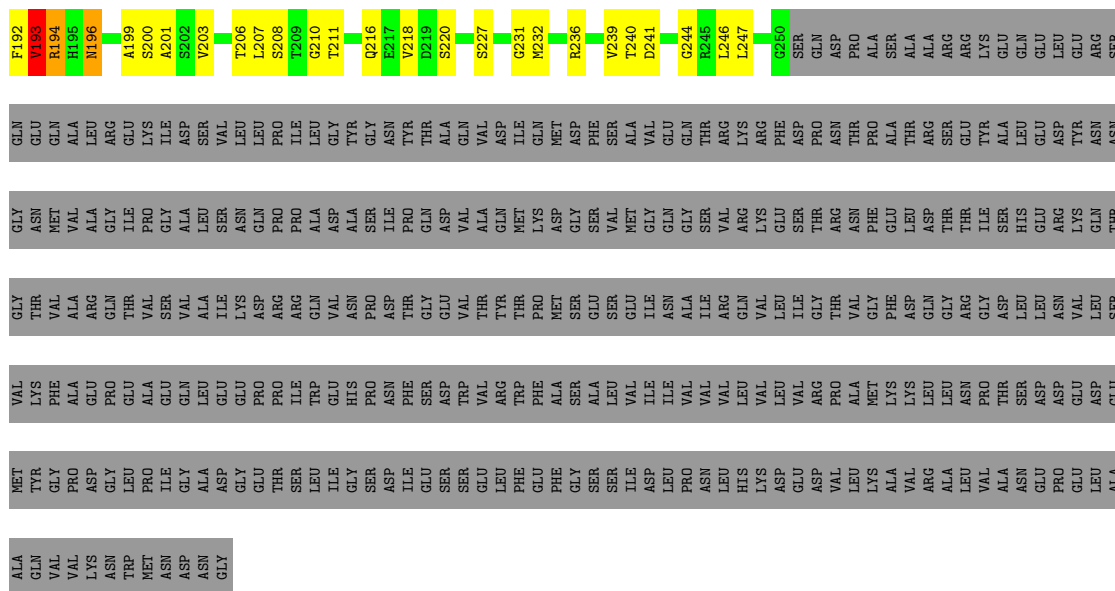




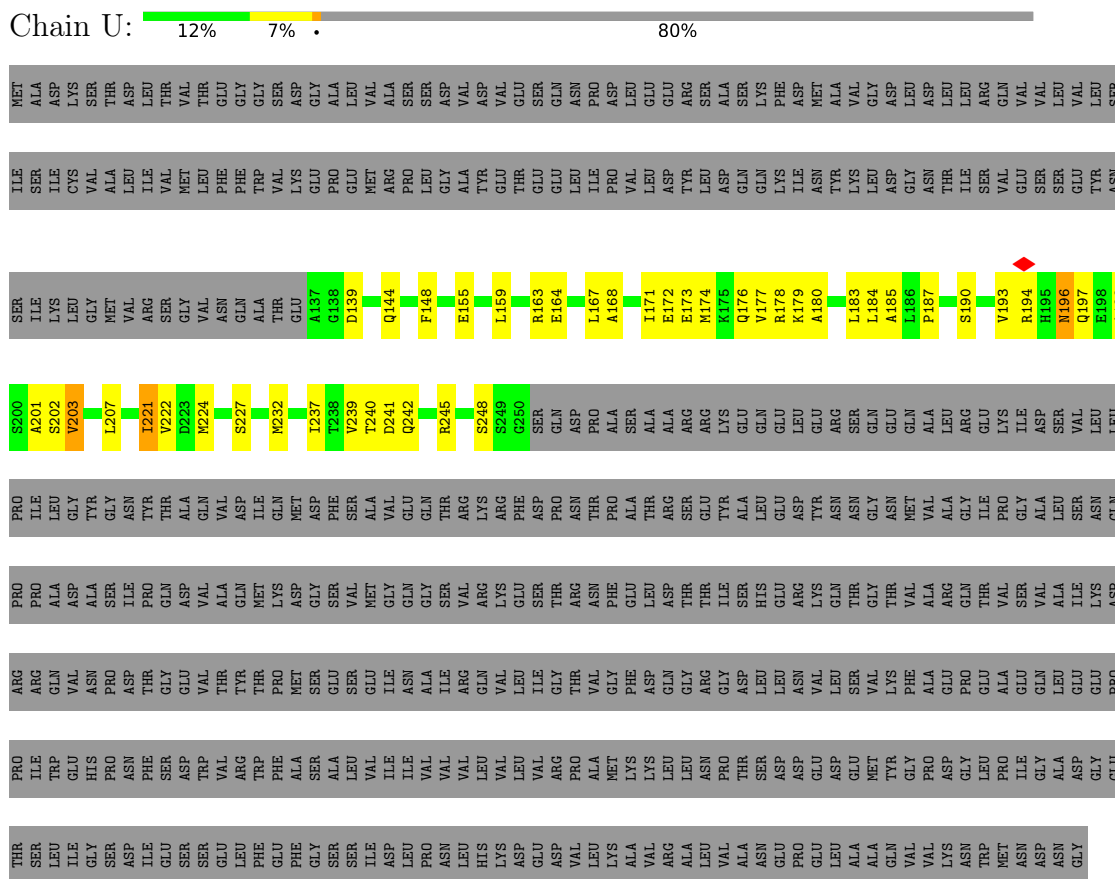
- Molecule 2: Flagellar M-ring protein



- Molecule 2: Flagellar M-ring protein

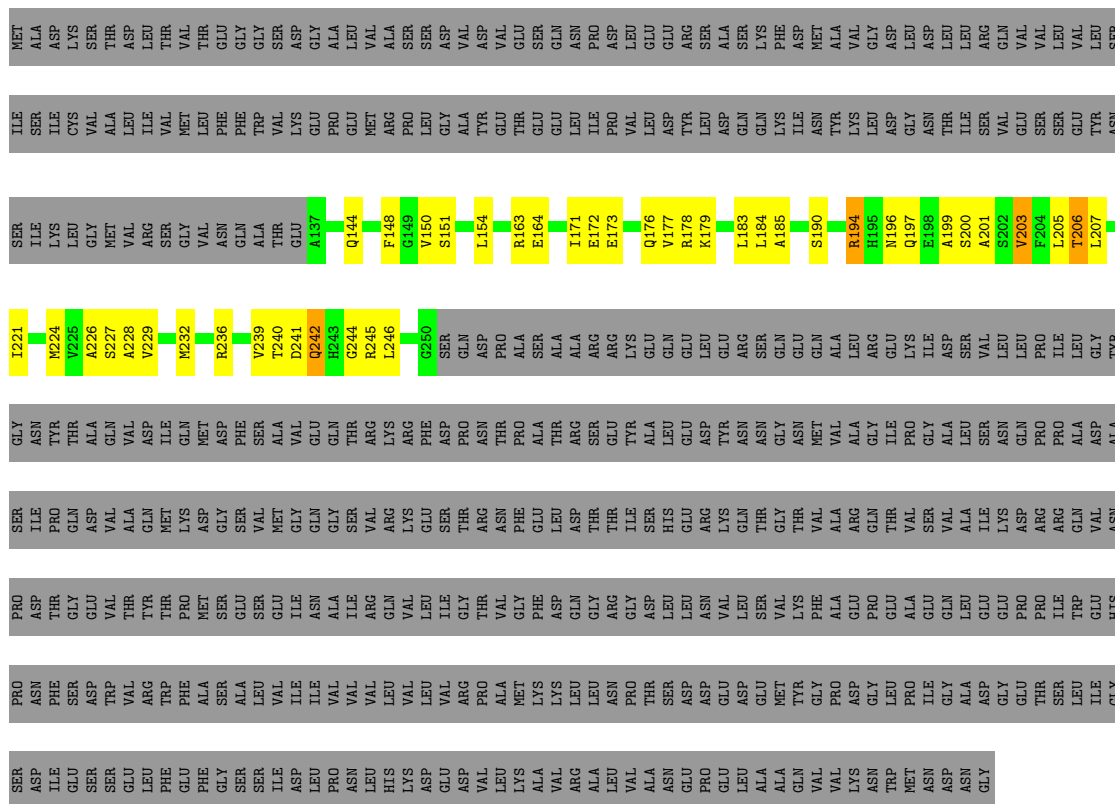


- Molecule 2: Flagellar M-ring protein

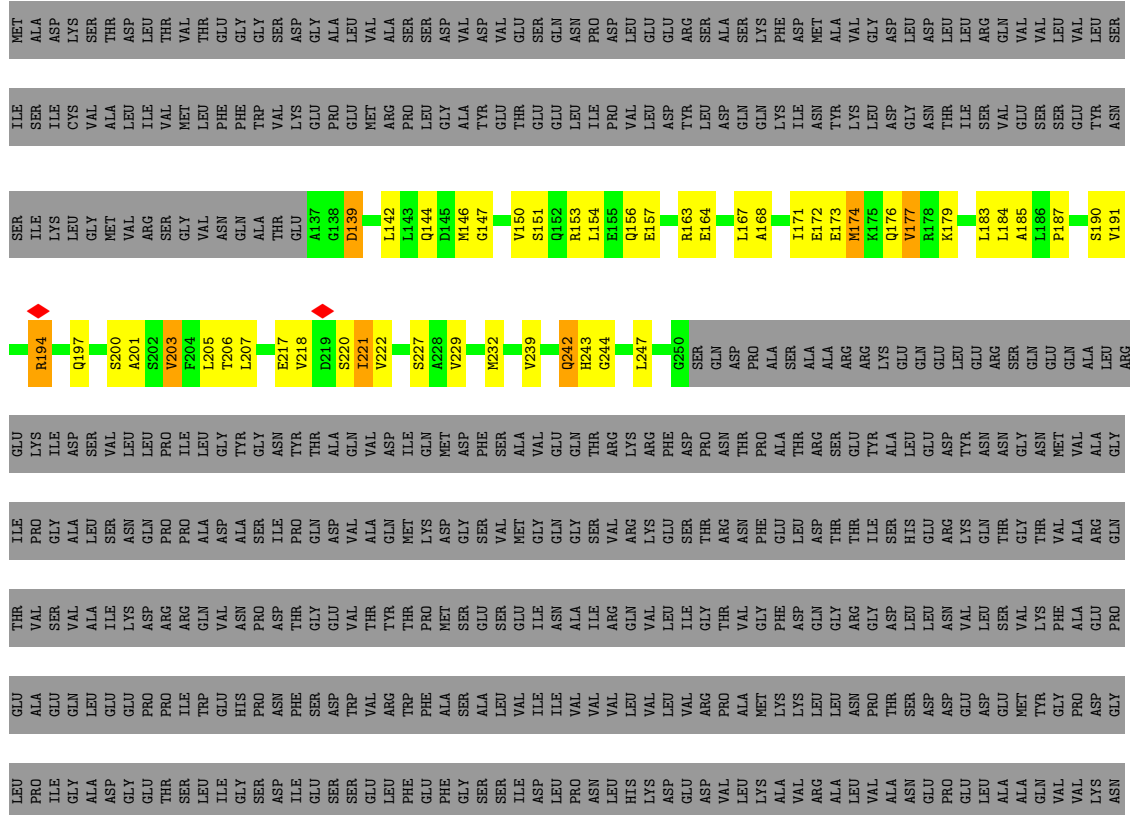


- Molecule 2: Flagellar M-ring protein





- Molecule 2: Flagellar M-ring protein







ALA	LEU	ALA	LEU	LEU	SER	A201	SER	ILE	MET
GLY	GLU	ILE	GLY	SER	VAL	S202	ILE	SER	ALA
GLU	GLY	LYS	ASN	ASN	LEU	V203	LYS	ILE	ASP
THR	PRO	ARG	GLU	GLN	LEU	T206	GLY	CYS	LYS
SER	ILE	ARG	PRO	PRO	ILE	L207	LEU	VAL	SER
LEU	TRP	GLN	ALA	LEU	LEU	S208	MET	ALA	THR
ILE	GLU	VAL	ASP	ASP	GLY		VAL	LEU	ASP
GLY	HIS	ASN	ALA	TYR	TYR	L213	ARG	ILE	LEU
SER	PRO	PRO	SER	SER	GLY	K214	SER	THR	VAL
ASP	ASN	THR	ILE	ILE	ASN	Q215	VAL	LEU	THR
ILE	PHE	THR	PRO	PRO	TYR		ASN	PHE	GLU
GLU	SER	GLY	GLN	GLN	THR	V218	GLN	PHE	GLY
SER	ASP	GLU	ASP	ASP	ALA	D219	ALA	TRP	GLY
SER	TRP	VAL	VAL	VAL	GLN	S220	THR	VAL	GLY
GLU	VAL	THR	ALA	ASP	VAL	I221	GLU	VAL	VAL
LEU	ARG	TYR	GLN	GLN	ASP	V222	ALA	GLY	GLY
PHE	TRP	THR	MET	MET	ILE		ALA	PRO	LEU
GLU	PHE	PRO	LYS	LYS	GLN	V229	ASP	GLU	ALA
PHE	ALA	MET	ASP	ASP	MET		ASP	GLU	LEU
GLY	SER	SER	GLY	GLY	ASP	M232	ILE	MET	VAL
SER	ALA	GLU	SER	PHE	ASP		LEU	ARG	ALA
SER	VAL	VAL	SER	SER	SER	I237	GLN	LEU	SER
ILE	GLU	GLU	MET	ALA	VAL		GLN	GLY	ASP
ASP	ILE	ILE	GLY	VAL	ALA	D241	ASP	ALA	VAL
LEU	ILE	ASN	GLN	GLN	GLN		MET	TYR	VAL
PRO	VAL	ALA	GLY	GLY	GLN	G244	GLY	GLU	VAL
ASN	VAL	ILE	SER	SER	THR	P245	THR	THR	GLU
LEU	VAL	ARG	VAL	VAL	ARG	L246	GLN	GLU	SER
HIS	VAL	GLN	ARG	ARG	LYS	L247	LYS	LEU	GLN
LYS	VAL	VAL	VAL	VAL	PHE		ARG	LEU	GLN
ASP	LEU	ILE	GLU	GLU	ARG	G250	THR	LEU	GLY
GLU	VAL	ILE	GLU	GLU	ASP	SER	PRO	ASP	ASP
ASP	VAL	GLU	SER	THR	PRO	GLN	ASN	LEU	GLU
VAL	PRO	THR	ASN	ASN	ASN		ASP	LEU	GLU
LEU	ALA	VAL	ASN	ASN	THR	E157	THR	ASP	GLU
LYS	MET	GLY	PHE	PHE	PRO		TYR	LEU	GLU
ALA	LYS	PHE	GLU	GLU	ALA	R163	SER	LEU	ARG
VAL	LYS	ASP	LEU	LEU	THR		ASP	LEU	ALA
ARG	LEU	GLN	ASP	ASP	ARG	L167	GLN	SER	ALA
ALA	LEU	GLY	THR	THR	SER		GLN	LYS	LYS
LEU	ASN	ARG	THR	THR	GLU	I171	LYS	PHE	PHE
VAL	PRO	GLY	ILE	ILE	TYR	E172	ILE	ASP	ALA
ALA	THR	ASP	SER	SER	ALA	E173	ASN	MET	VAL
ASN	ASN	LEU	HIS	LEU	LEU	M174	TYR	ALA	ALA
GLU	ASP	LEU	GLU	GLU	GLN	K175	LYS	VAL	VAL
PRO	ASP	ASN	ARG	ARG	ASP	Q176	GLY	GLY	GLY
GLU	VAL	VAL	LYS	LYS	TYR	V177	ASP	ASP	ASP
LEU	ASP	LEU	GLN	GLN	ASN	R178	LEU	LEU	LEU
ALA	GLU	SER	THR	THR	ASN	K179	ASN	ASP	ASP
ALA	MET	VAL	VAL	GLY	GLY	A180	THR	THR	THR
GLN	TYR	PHE	VAL	THR	ASN		ILE	ILE	LEU
VAL	GLY	LYS	GLY	MET	MET	L183	SER	ARG	ARG
VAL	PRO	ALA	ALA	VAL	VAL	L184	VAL	VAL	GLN
LYS	ASP	PRO	ARG	ALA	ALA		GLU	VAL	GLN
ASN	GLY	GLU	GLN	GLN	GLY		SER	SER	VAL
TRP	PRO	GLU	THR	THR	ILE	F192	GLY	GLY	VAL
MET	PRO	ALA	VAL	VAL	PRO	V193	LEU	SER	LEU
ASN	ILE	GLN	GLU	SER	GLY	R194	TYR	GLU	VAL
ASP	GLY	GLN	VAL	VAL	ALA		ASN	ASN	SER

Chain d: 9% 7% 82%

ASN	ASN	ARG	V191 F192	SER	ILE	MET
ASN	Gly	GLN	F198	ILE	SER	ALA
ASN	MET	GLU	A199	LEU	CYS	LYS
VAL	ALA	ALA	S200	MET	VAL	THR
ALA	LEU	LEU	A201	VAL	LEU	ASP
Gly	ARG	ARG	T206	ARG	ILE	LEU
PRO	PRO	Lys	L207	SER	VAL	THR
Gly	ILE	ILE	G210	VAL	PHE	GLU
ALA	LEU	SER	T211	ASN	PHE	GLY
SER	VAL	VAL	G216	ALA	TRP	GLY
ASN	LEU	LEU	Q216	THR	VAL	SER
GLN	LEU	PRO	D219	GLU	Lys	ASP
PRO	PRO	ILE	S220	ALA	GLU	Gly
ALA	LEU	LEU	I221	Gly	PRO	ALA
ASP	ASP	Gly	V222	ASP	GLU	LEU
ALA	ALA	Tyr	D223	ILE	ARG	VAL
SER	SER	Gly	S227	LEU	ALA	SER
ILE	ASN	ASN	A228	LEU	LEU	SER
PRO	PRO	Tyr	V229	GLN	Gly	ASP
GLN	ASP	ALA	M232	ASP	ALA	VAL
VAL	VAL	GLN	K233	Met	GLY	VAL
ALA	ALA	VAL	T234	F148	THR	GLU
GLN	ASP	ASP	S235	Q152	GLU	SER
MET	ILE	ILE	R236	R153	LEU	GLN
Lys	ASP	GLN	I237	ILE	LEU	ASN
Gly	Gly	MET	T238	Q156	PRO	PRO
SER	SER	ASP	V239	E157	VAL	ASP
VAL	VAL	PHE	T240	R163	LEU	GLU
MET	MET	ALA	D241	TYR	GLY	JLU
Gly	Gly	VAL	Q242	ASP	ARG	ARG
GLN	GLN	GLU	H243	L167	LEU	SER
Gly	SER	GLN	G244	A168	ASP	ALA
VAL	VAL	THR	R245	Q169	GLN	SER
ARG	ARG	ARG	L246	A170	GLN	Lys
Lys	Lys	Lys	L247	I171	Lys	PHE
ARG	ARG	ARG	G250	E172	ILE	ASP
GLU	GLU	PHE	SER	E173	ASN	Met
SER	SER	ASP	SER	M174	Tyr	ALA
THR	THR	PRO	ASN	K175	Lys	Val
ARG	ARG	ASN	GLN	Q176	Leu	Gly
ASN	ASN	THR	PRO	V177	ASP	ASP
PHE	PHE	PRO	ALA	R178	GLY	LEU
GLU	GLU	ALA	SER	K179	ASN	ASP
LEU	LEU	THR	ALA	A180	Thr	LEU
ASP	ASP	ARG	ALA	I181	ILE	LEU
THR	THR	SER	ARG	V182	SER	ARG
THR	THR	GLU	ARG	L183	VAL	GLN
ILE	ILE	Tyr	ALA	L184	GLU	VAL
SER	SER	ALA	Lys	A185	SER	VAL
HIS	HIS	LEU	GLU	K188	SER	LEU
GLU	GLU	GLU	GLN	I189	GLU	VAL
ARG	ARG	THR	LEU		Tyr	Val
ASN	ASN	THR	LEU		ASN	SER

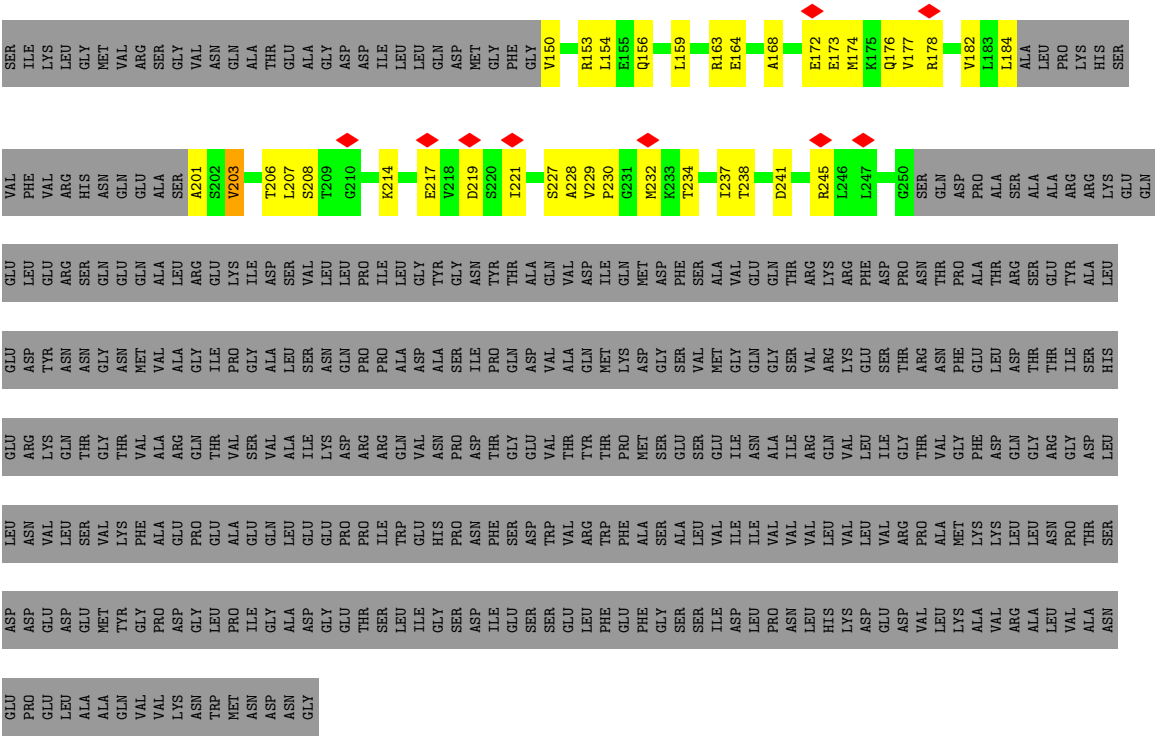
[illegible]

- Molecule 2: Flagellar M-ring protein

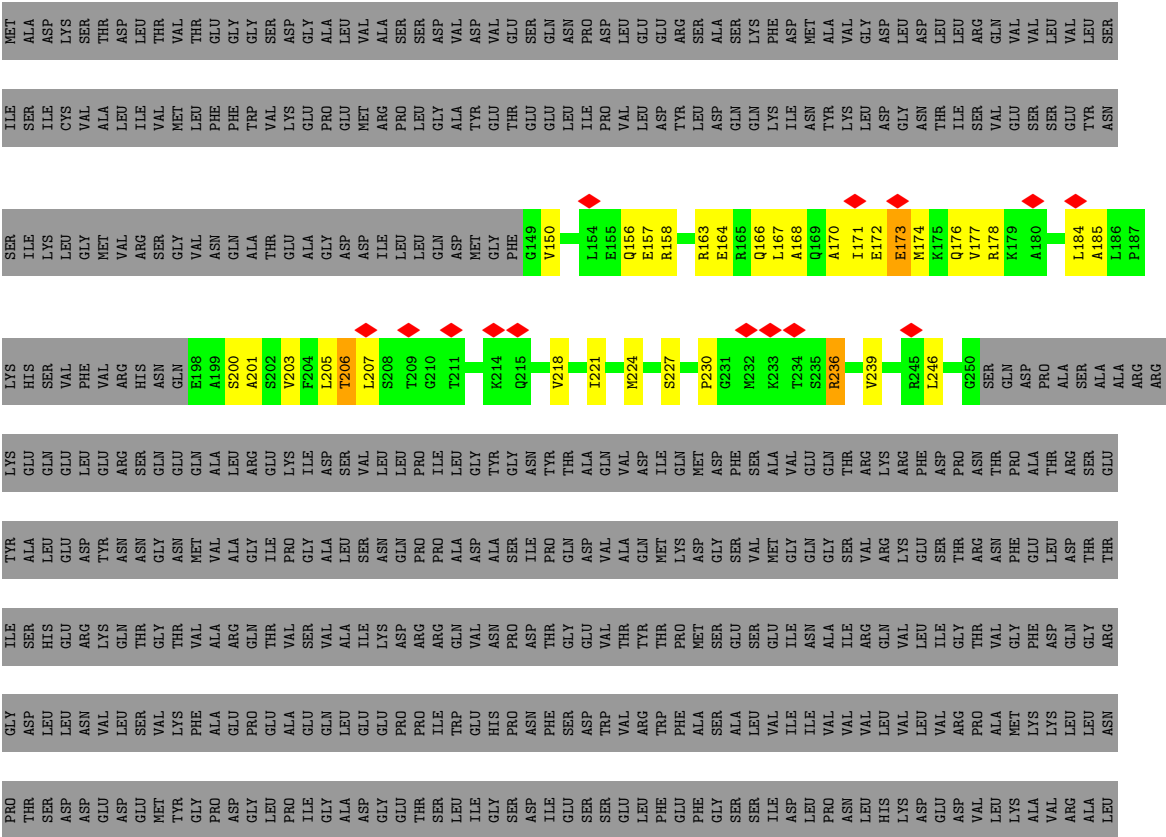
[illegible]

- Molecule 2: Flagellar M-ring protein

[illegible]



● Molecule 2: Flagellar M-ring protein



VAL	ALA	ASN	GLN	PRO	GLU	LEU	ALA	ALA	GLN	VAL	VAL	VAL	LYS	ASN	TRP	MET	ASN	ASP	ASN	GLY
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

• Molecule 2: Flagellar M-ring protein



MET	ALA	ASP	LYS	GLN	THR	ASP	LEU	THR	THR	VAL	GLN	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ILE	SER	ILE	CYS	VAL	ALA	THR	LEU	ILE	VAL	VAL	MET	LEU	PHE	PHE	TRP	VAL	LYS	GLY	ALA	ALA

SER	ILE	LYS	LEU	GLY	MET	VAL	VAL	ASN	GLN	ALA	THR	THR	ALA	GLY	ASP	ASP	GLY	GLY	PRO	ILE
G149	R153	Q156	E157	R163	L167	A168	I171	E172	E173	M174	K179	A180	R181	V182	L183	L184	A185	L186	P187	LYS

ARG	HIS	ASN	GLN	A199	S200	A201	S202	V203	T206	L207	G210	Q215	Q216	E217	V218	D219	S220	I221	M224	S227
G231	P230	G231	M232	K233	T238	L246	L247	S248	S249	G250	SER	GLN	ASP	PRO	ALA	ALA	ARG	GLY	GLU	GLN

GLU	GLN	ALA	LEU	ARG	GLY	PRO	LYS	ILE	ASP	SER	VAL	LEU	PRO	ILE	GLY	GLY	TYR	ASN	GLY	ASP
GLY	GLN	ALA	LEU	ARG	GLY	PRO	LYS	ILE	ASP	SER	VAL	LEU	PRO	ILE	GLY	GLY	TYR	ASN	GLY	ASP

ASN	MET	VAL	ALA	GLY	ILE	PRO	GLY	ALA	LEU	SER	VAL	ASN	GLN	PRO	PRO	ALA	ASP	GLY	GLY	GLY
THR	VAL	ALA	ARG	THR	THR	VAL	GLY	ALA	LEU	ILE	ASP	GLY	ALA	ASP	GLY	THR	THR	THR	THR	THR

THR	VAL	ALA	ARG	THR	THR	VAL	GLY	ALA	LEU	ILE	ASP	GLY	ALA	ASP	GLY	THR	THR	THR	THR	THR
THR	VAL	ALA	ARG	THR	THR	VAL	GLY	ALA	LEU	ILE	ASP	GLY	ALA	ASP	GLY	THR	THR	THR	THR	THR

LYS	PHE	ALA	GLY	PRO	GLY	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
LYS	PHE	ALA	GLY	PRO	GLY	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

TYR	GLY	PRO	GLY	LEU	PRO	ILE	GLY	ASP	GLY	GLY	THR	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
TYR	GLY	PRO	GLY	LEU	PRO	ILE	GLY	ASP	GLY	GLY	THR	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY

GLN	VAL	VAL	LYS	ASN	TRP	MET	ASN	GLY
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• Molecule 2: Flagellar M-ring protein



MET	ALA	ASP	LYS	SER	THR	ASP	LEU	THR	THR	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
ILE	SER	ILE	CYS	VAL	ALA	THR	LEU	ILE	VAL	VAL	MET	PHE	PHE	TRP	VAL	LYS	GLY	GLY	GLY	GLY

SER	ILE	LYS	LEU	MET	VAL	VAL	ASN	GLN	ALA	THR	THR	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
G150	S151	R152	R153	E157	R163	E164	Q166	L167	A168	E172	E173	K175	Q176	V177	R178	K179	V182	L183	L184	A185

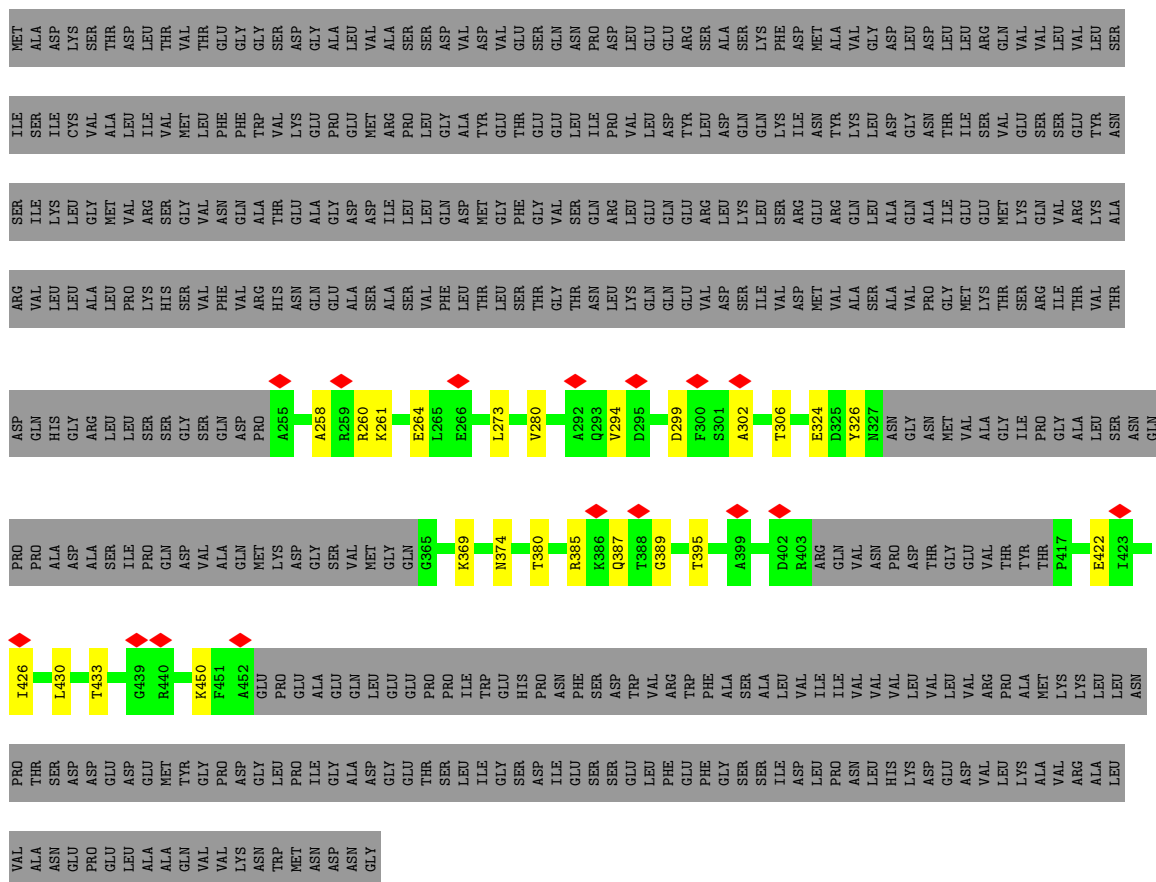
SER	VAL	PHE	ARG	HIS	ASN	GLN	A199	S200	V203	F204	L205	T206	L207	G210	T211	Q215	D219	S220	S227	P230
G231	M232	D241	Q242	H243	G244	L246	G250	SER	GLN	ASP	PRO	ALA	ALA	SER	THR	ARG	GLY	GLY	GLY	GLY

GLN	ALA	LEU	ARG	GLY	LYS	ILE	ASP	SER	VAL	LEU	LEU	LEU	PRO	ILE	THR	GLY	GLY	GLY	GLY	GLY
GLN	ALA	LEU	ARG	GLY	LYS	ILE	ASP	SER	VAL	LEU	LEU	LEU	PRO	ILE	THR	GLY	GLY	GLY	GLY	GLY

MET	ALA	ASP	ASP	LYS	SER	THR	ASP	LEU	THR	THR	GLU	GLY	GLY	SER	SER	ASP	ALA	ALA	LEU	VAL	VAL	ALA	ALA	SER	SER	SER	SER	ASP	VAL	VAL	ASP	GLU	GLU	GLU	GLU	ARG	ASP	GLY	ASP	LEU	LEU	LEU	LEU	LEU	VAL	VAL	VAL	GLN	ARG	LYS	PHE	ASP	MET	VAL	VAL	ALA	ALA	VAL	VAL	GLY	ASP	LEU	LEU	LEU	LEU	VAL	VAL	VAL	GLN	ARG	LEU	LEU	LEU	LEU	SER
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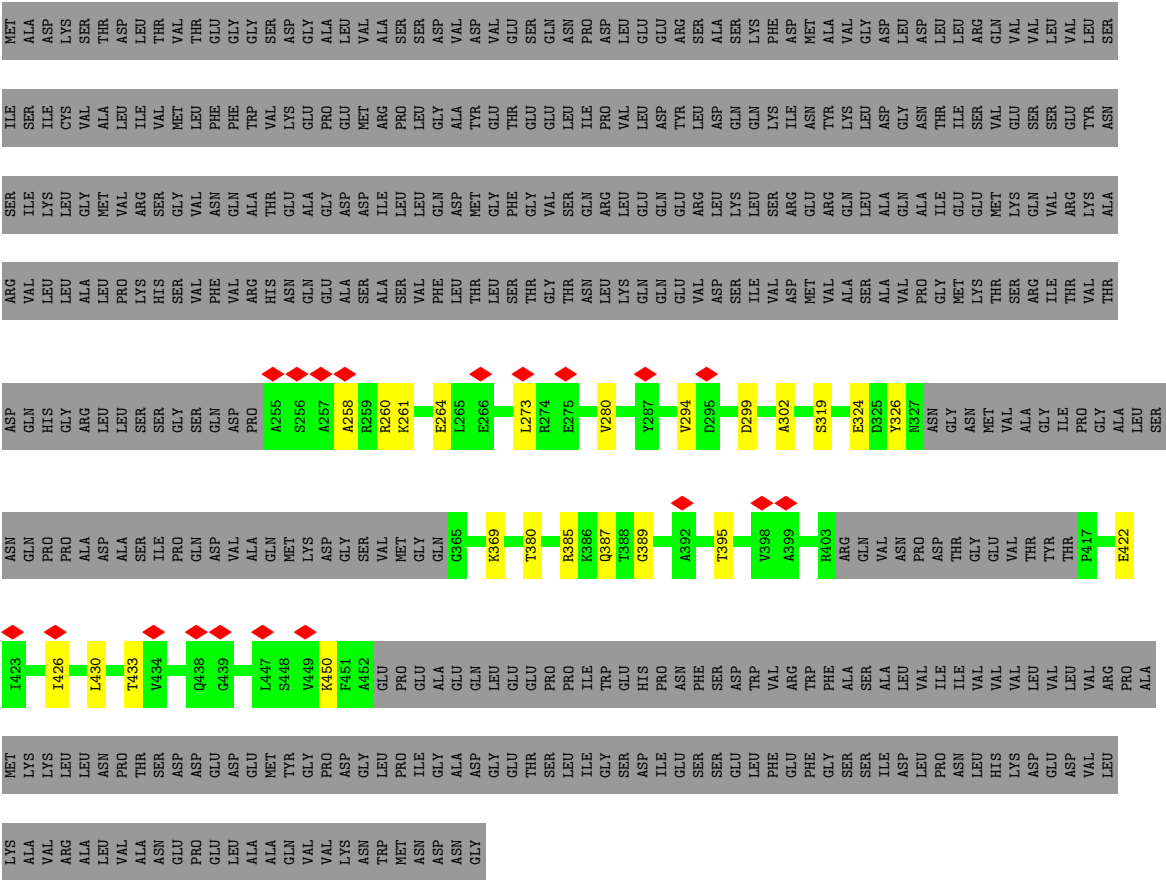


- Molecule 2: Flagellar M-ring protein

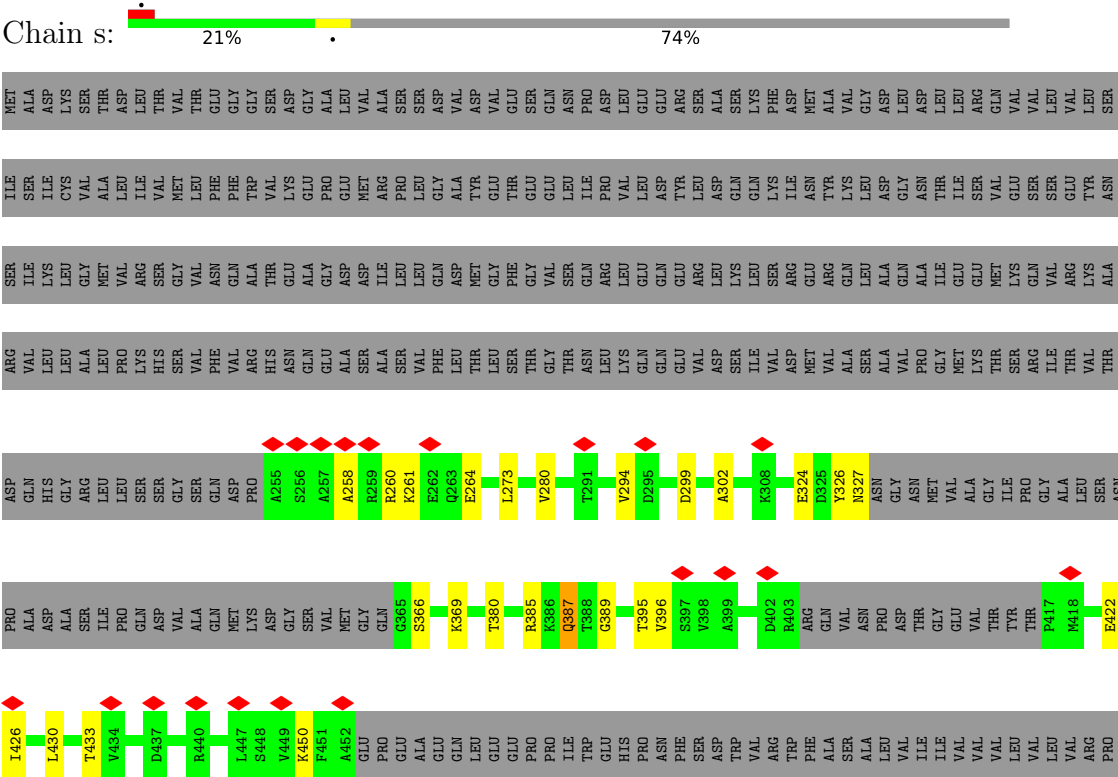


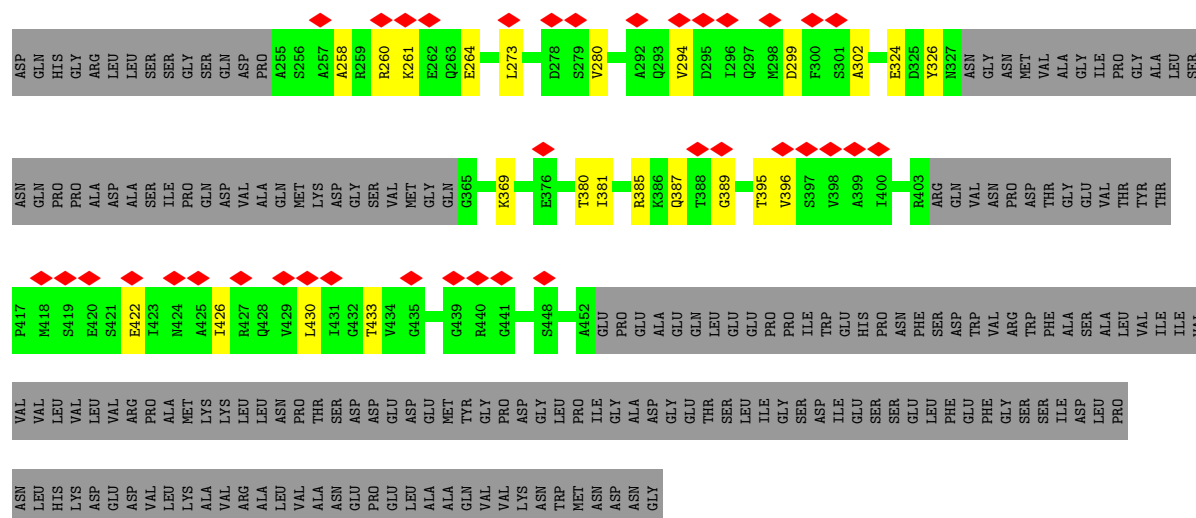
- Molecule 2: Flagellar M-ring protein





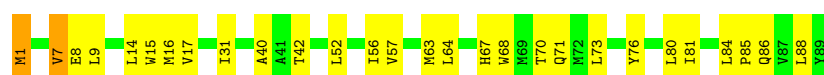
• Molecule 2: Flagellar M-ring protein





- Molecule 3: Flagellar biosynthetic protein FliQ

Chain 6: 69% 29%



- Molecule 3: Flagellar biosynthetic protein FliQ

Chain 7: 78% 22%



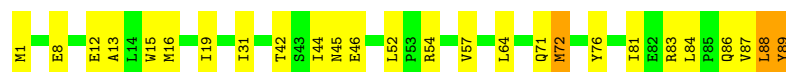
- Molecule 3: Flagellar biosynthetic protein FliQ

Chain AQ: 71% 28%



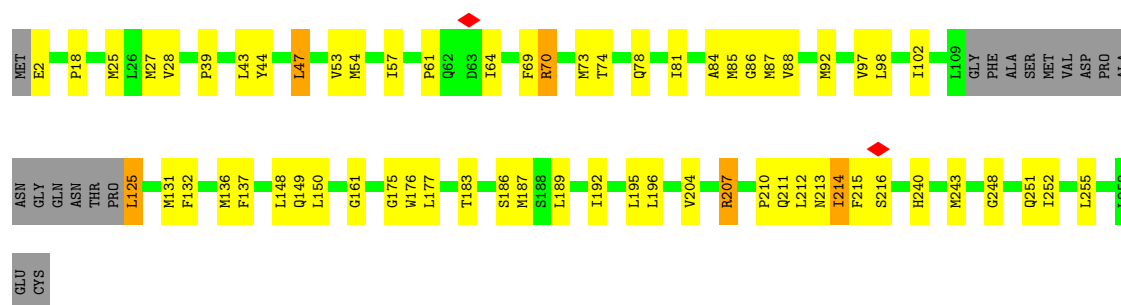
- Molecule 3: Flagellar biosynthetic protein FliQ

Chain AR: 71% 26%



- Molecule 4: Flagellar biosynthetic protein FliR

Chain 8: 69% 22% 7%



- Molecule 5: Flagellar basal body rod protein FlgB



- Molecule 5: Flagellar basal body rod protein FlgB



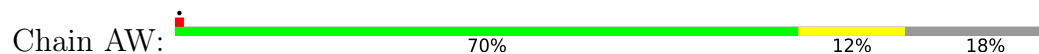
- Molecule 5: Flagellar basal body rod protein FlgB

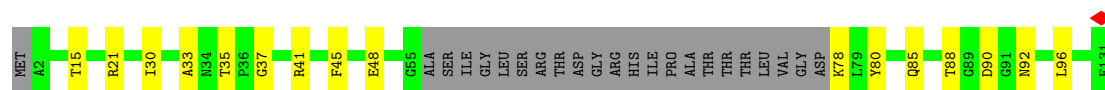


- Molecule 5: Flagellar basal body rod protein FlgB

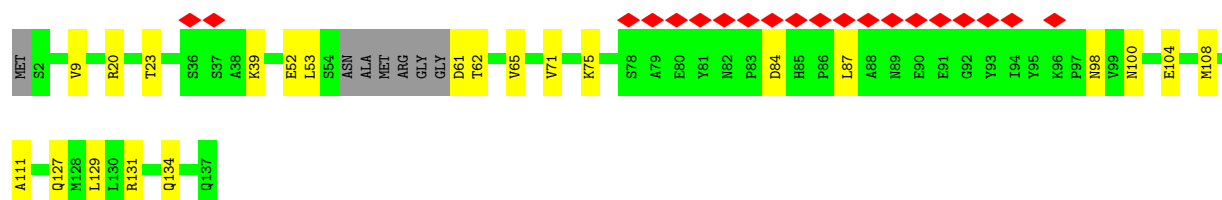
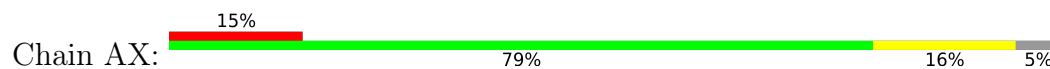


- Molecule 5: Flagellar basal body rod protein FlgB

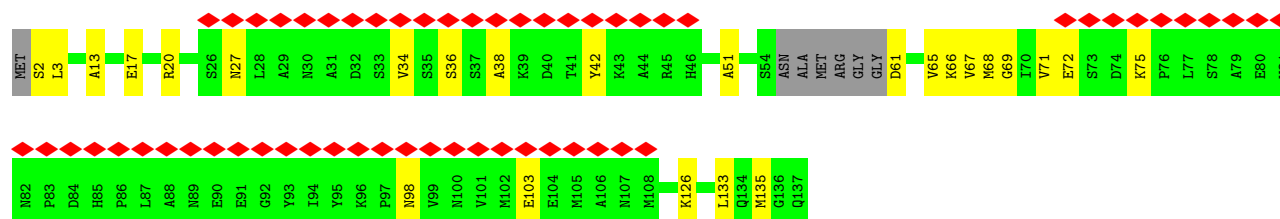
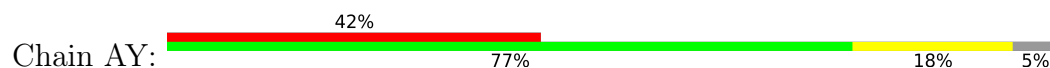




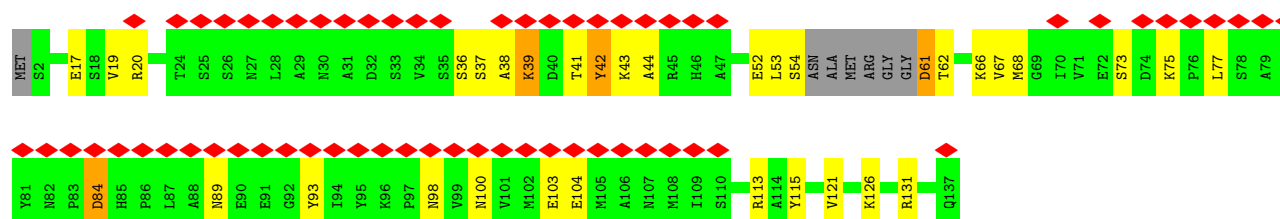
- Molecule 6: Flagellar basal-body rod protein FlgC



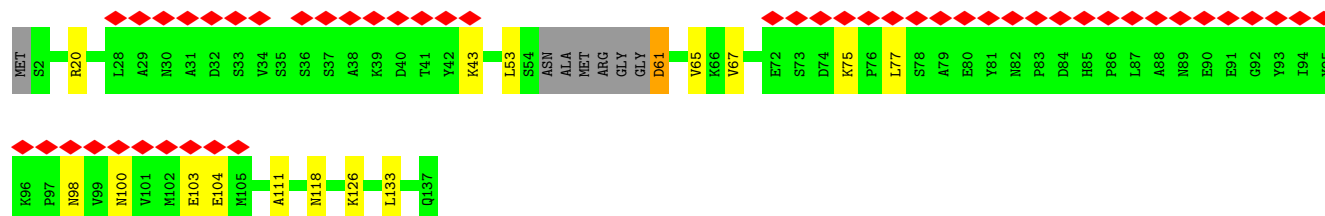
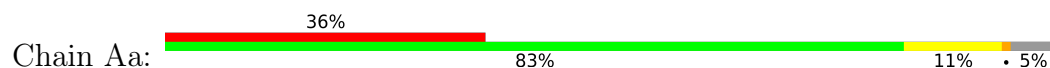
- Molecule 6: Flagellar basal-body rod protein FlgC



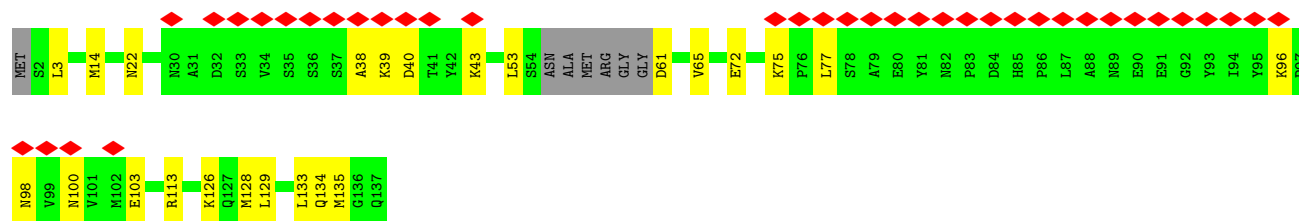
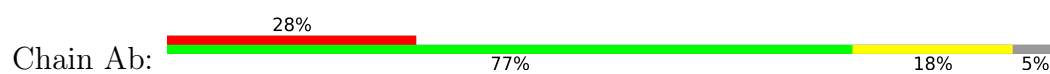
- Molecule 6: Flagellar basal-body rod protein FlgC



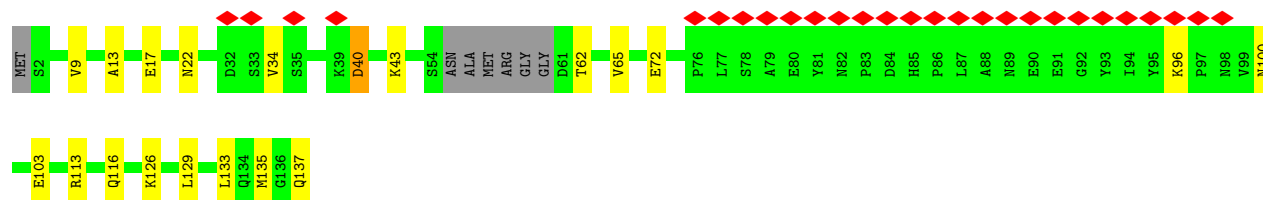
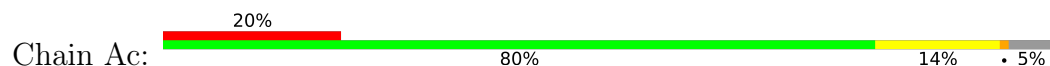
- Molecule 6: Flagellar basal-body rod protein FlgC



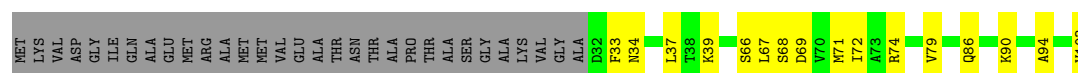
- Molecule 6: Flagellar basal-body rod protein FlgC



- Molecule 6: Flagellar basal-body rod protein FlgC



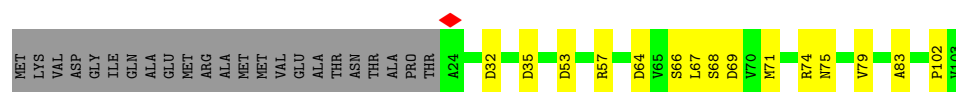
- Molecule 7: Flagellar hook-basal body complex protein FliE



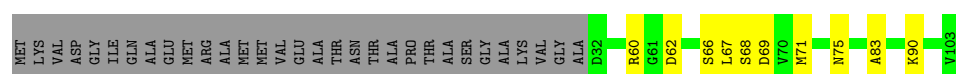
- Molecule 7: Flagellar hook-basal body complex protein FliE



- Molecule 7: Flagellar hook-basal body complex protein FliE

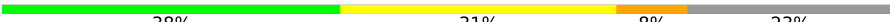


- Molecule 7: Flagellar hook-basal body complex protein FliE



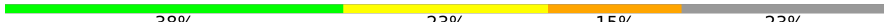
- Molecule 7: Flagellar hook-basal body complex protein FliE

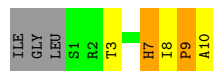
- Molecule 9: Alanine-modelled FlgB-Dc loop

Chain Ao:  38% 31% 8% 23%

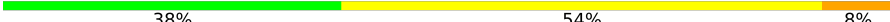


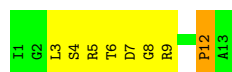
- Molecule 9: Alanine-modelled FlgB-Dc loop

Chain Ap:  38% 23% 15% 23%



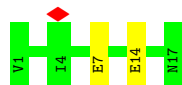
- Molecule 9: Alanine-modelled FlgB-Dc loop

Chain Aq:  38% 54% 8%



- Molecule 10: FliE-helix 1

Chain Ar:  6% 88% 12%



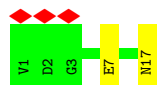
- Molecule 10: FliE-helix 1

Chain As:  6% 82% 18%



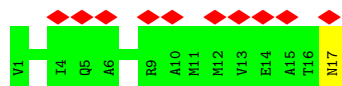
- Molecule 10: FliE-helix 1

Chain At:  18% 88% 12%



- Molecule 10: FliE-helix 1

Chain Au:  59% 94% 6%

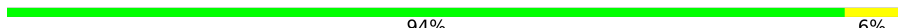


• Molecule 10: FliE-helix 1

Chain Av:  18% 88% 12%



• Molecule 10: FliE-helix 1

Chain Aw:  94% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	58418	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.065	Depositor
Minimum map value	-0.657	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	744.0, 744.0, 744.0	wwPDB
Map dimensions	620, 620, 620	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	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	0	0.16	0/1637	0.33	0/2221
1	9	0.14	0/1628	0.30	0/2209
1	AP	0.10	0/1637	0.26	0/2221
1	AK	0.11	0/1637	0.27	0/2221
1	AI	0.12	0/1637	0.28	0/2221
2	1	0.16	0/1182	0.27	0/1588
2	2	0.16	0/1182	0.27	0/1588
2	3	0.16	0/1182	0.27	0/1588
2	4	0.16	0/1182	0.27	0/1588
2	5	0.16	0/1182	0.27	0/1588
2	A	0.16	0/1182	0.27	0/1588
2	AA	0.35	0/137	0.45	0/188
2	AB	0.29	0/137	0.43	0/188
2	AC	0.14	0/141	0.31	0/193
2	AD	0.31	0/137	0.46	0/188
2	AE	0.13	0/137	0.28	0/188
2	AF	0.92	0/161	1.23	0/221
2	AG	0.16	0/75	0.32	0/103
2	AH	0.20	0/75	0.41	0/103
2	AI	0.95	0/75	1.34	0/103
2	AJ	0.37	0/166	0.57	0/228
2	AK	0.32	0/172	0.70	0/237
2	AL	0.39	0/223	0.61	0/304
2	AM	0.20	0/227	0.44	0/309
2	AN	0.24	0/227	0.49	0/309
2	AO	0.17	0/223	0.40	0/304
2	B	0.16	0/1182	0.27	0/1588
2	C	0.16	0/1182	0.27	0/1588
2	D	0.16	0/1182	0.27	0/1588
2	E	0.16	0/1182	0.27	0/1588
2	F	0.16	0/1182	0.27	0/1588
2	G	0.16	0/1182	0.27	0/1588
2	H	0.16	0/1182	0.27	0/1588
2	I	0.16	0/1182	0.27	0/1588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	J	0.16	0/1182	0.27	0/1588
2	K	0.16	0/1182	0.27	0/1588
2	L	0.16	0/1182	0.27	0/1588
2	M	0.16	0/1182	0.27	0/1588
2	N	0.16	0/1182	0.27	0/1588
2	O	0.16	0/1182	0.27	0/1588
2	P	0.16	0/1182	0.27	0/1588
2	Q	0.16	0/1182	0.27	0/1588
2	R	0.16	0/1182	0.27	0/1588
2	S	0.33	0/888	0.56	0/1192
2	T	0.30	0/888	0.44	0/1192
2	U	0.21	0/888	0.37	0/1192
2	V	0.22	0/888	0.40	0/1192
2	W	0.21	0/888	0.41	0/1192
2	X	0.23	0/844	0.41	0/1131
2	Y	0.29	0/888	0.48	0/1192
2	Z	0.29	0/888	0.44	0/1192
2	a	0.21	0/888	0.40	0/1192
2	b	0.22	0/727	0.40	0/974
2	c	0.26	0/810	0.44	0/1087
2	d	0.27	0/810	0.44	0/1087
2	e	0.16	0/810	0.38	0/1087
2	f	0.13	0/661	0.31	0/884
2	g	0.14	0/706	0.35	0/946
2	h	0.14	0/697	0.34	0/934
2	i	0.14	0/685	0.33	0/917
2	j	0.16	0/706	0.35	0/946
2	k	0.22	0/888	0.38	0/1192
2	l	0.24	0/888	0.45	0/1192
2	m	0.20	0/888	0.35	0/1192
2	n	0.19	0/805	0.37	0/1078
2	o	0.20	0/888	0.40	0/1192
2	p	0.16	0/1182	0.27	0/1588
2	q	0.16	0/1182	0.27	0/1588
2	r	0.16	0/1182	0.27	0/1588
2	s	0.16	0/1182	0.27	0/1588
2	t	0.16	0/1182	0.27	0/1588
2	u	0.16	0/1182	0.27	0/1588
2	v	0.16	0/1182	0.27	0/1588
2	w	0.16	0/1182	0.27	0/1588
2	x	0.16	0/1182	0.27	0/1588
2	y	0.16	0/1182	0.27	0/1588
2	z	0.16	0/1182	0.27	0/1588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	6	0.28	0/739	0.49	0/1005
3	7	0.16	0/739	0.33	0/1005
3	AQ	0.12	0/739	0.31	0/1005
3	AR	0.17	0/739	0.34	0/1005
4	8	0.09	0/1941	0.25	0/2631
5	AS	0.23	0/856	0.36	0/1151
5	AT	0.22	0/846	0.30	0/1138
5	AU	0.24	0/856	0.31	0/1151
5	AV	0.19	0/848	0.31	0/1140
5	AW	0.22	0/848	0.35	0/1140
6	AX	0.11	0/996	0.27	0/1348
6	AY	0.11	0/996	0.26	0/1348
6	AZ	0.30	0/996	0.46	0/1348
6	Aa	0.10	0/996	0.24	0/1348
6	Ab	0.11	0/996	0.28	0/1348
6	Ac	0.14	0/996	0.30	0/1348
7	Ad	0.32	0/564	0.43	0/759
7	Ae	0.08	0/609	0.20	0/819
7	Af	0.08	0/609	0.17	0/819
7	Ag	0.08	0/564	0.16	0/759
7	Ah	0.08	0/564	0.18	0/759
7	Ai	0.10	0/313	0.19	0/420
8	Aj	0.08	0/562	0.19	0/760
9	Am	1.13	0/57	1.46	1/77 (1.3%)
9	An	1.26	0/43	1.85	1/58 (1.7%)
9	Ao	1.22	0/48	1.61	1/65 (1.5%)
9	Ap	1.09	0/48	1.55	1/65 (1.5%)
9	Aq	1.19	0/62	1.42	1/84 (1.2%)
10	Ar	1.12	0/83	1.44	0/114
10	As	1.11	0/83	1.44	0/114
10	At	1.12	0/83	1.45	0/114
10	Au	1.11	0/83	1.45	0/114
10	Av	1.11	0/83	1.45	0/114
10	Aw	1.11	0/83	1.44	0/114
All	All	0.21	0/89262	0.35	5/120213 (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	0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	T	0	1
2	c	0	1
2	d	0	1
2	l	0	1
All	All	0	5

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	An	8	PRO	N-CA-CB	10.53	109.83	102.35
9	Ap	9	PRO	N-CA-CB	6.81	109.66	103.33
9	Am	11	PRO	N-CA-CB	6.73	110.31	103.25
9	Ao	9	PRO	N-CA-CB	6.10	109.75	103.23
9	Aq	12	PRO	N-CA-CB	5.81	109.35	103.25

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	188	ARG	Sidechain
2	T	194	ARG	Sidechain
2	c	194	ARG	Sidechain
2	d	236	ARG	Sidechain
2	l	194	ARG	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	0	1608	0	1691	45	0
1	9	1599	0	1685	42	0
1	AP	1608	0	1691	37	0
1	Ak	1608	0	1691	66	0
1	Al	1608	0	1691	55	0
2	1	1171	0	1164	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	2	1171	0	1164	13	0
2	3	1171	0	1164	15	0
2	4	1171	0	1164	16	0
2	5	1171	0	1164	14	0
2	A	1171	0	1164	20	0
2	AA	135	0	128	2	0
2	AB	135	0	128	3	0
2	AC	139	0	131	4	0
2	AD	135	0	128	7	0
2	AE	135	0	128	1	0
2	AF	158	0	152	13	0
2	AG	73	0	72	4	0
2	AH	73	0	72	3	0
2	AI	73	0	72	8	0
2	AJ	163	0	157	3	0
2	AK	169	0	164	6	0
2	AL	220	0	215	3	0
2	AM	224	0	218	4	0
2	AN	224	0	218	2	0
2	AO	220	0	215	3	0
2	B	1171	0	1164	15	0
2	C	1171	0	1164	13	0
2	D	1171	0	1164	12	0
2	E	1171	0	1164	15	0
2	F	1171	0	1164	23	0
2	G	1171	0	1164	20	0
2	H	1171	0	1164	23	0
2	I	1171	0	1164	15	0
2	J	1171	0	1164	16	0
2	K	1171	0	1164	13	0
2	L	1171	0	1164	11	0
2	M	1171	0	1164	18	0
2	N	1171	0	1164	22	0
2	O	1171	0	1164	14	0
2	P	1171	0	1164	14	0
2	Q	1171	0	1164	14	0
2	R	1171	0	1164	11	0
2	S	881	0	910	59	0
2	T	881	0	910	62	0
2	U	881	0	910	35	0
2	V	881	0	910	35	0
2	W	881	0	910	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	X	839	0	864	30	0
2	Y	881	0	910	56	0
2	Z	881	0	910	38	0
2	a	881	0	910	40	0
2	b	724	0	758	33	0
2	c	803	0	837	45	0
2	d	803	0	837	40	0
2	e	803	0	837	35	0
2	f	660	0	699	22	0
2	g	704	0	741	27	0
2	h	695	0	735	29	0
2	i	684	0	725	31	0
2	j	704	0	741	28	0
2	k	881	0	910	60	0
2	l	881	0	910	39	0
2	m	881	0	910	39	0
2	n	802	0	836	36	0
2	o	881	0	910	37	0
2	p	1171	0	1164	13	0
2	q	1171	0	1164	16	0
2	r	1171	0	1164	14	0
2	s	1171	0	1164	16	0
2	t	1171	0	1164	15	0
2	u	1171	0	1164	13	0
2	v	1171	0	1164	15	0
2	w	1171	0	1164	14	0
2	x	1171	0	1164	22	0
2	y	1171	0	1164	13	0
2	z	1171	0	1164	14	0
3	6	722	0	768	36	0
3	7	722	0	768	40	0
3	AQ	722	0	768	29	0
3	AR	722	0	768	31	0
4	8	1896	0	1968	49	0
5	AS	845	0	833	11	0
5	AT	835	0	825	18	0
5	AU	845	0	833	11	0
5	AV	837	0	829	10	0
5	AW	837	0	829	10	0
6	AX	983	0	958	12	0
6	AY	983	0	958	18	0
6	AZ	983	0	958	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Aa	983	0	958	8	0
6	Ab	983	0	958	15	0
6	Ac	983	0	958	11	0
7	Ad	560	0	561	11	0
7	Ae	605	0	609	10	0
7	Af	605	0	609	10	0
7	Ag	560	0	561	7	0
7	Ah	560	0	561	10	0
7	Ai	311	0	320	8	0
8	Aj	552	0	577	22	0
9	Am	58	0	30	7	0
9	An	44	0	23	12	0
9	Ao	49	0	25	14	0
9	Ap	49	0	25	7	0
9	Aq	63	0	32	5	0
10	Ar	84	0	46	6	0
10	As	84	0	46	3	0
10	At	84	0	46	4	0
10	Au	84	0	46	1	0
10	Av	84	0	46	2	0
10	Aw	84	0	46	4	0
All	All	88315	0	88899	1692	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 10.

The worst 5 of 1692 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:7:64:LEU:HD11	2:T:148:PHE:CE1	1.54	1.42
3:AQ:15:TRP:CD1	2:m:148:PHE:HE2	1.51	1.27
1:Ak:288:ALA:CB	2:m:192:PHE:HA	1.63	1.26
2:x:306:THR:HG21	10:At:17:ASN:CB	1.66	1.25
1:9:189:ILE:HD11	2:c:192:PHE:C	1.59	1.25

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	0	206/289 (71%)	203 (98%)	3 (2%)	0	100	100
1	9	205/289 (71%)	202 (98%)	3 (2%)	0	100	100
1	AP	206/289 (71%)	204 (99%)	2 (1%)	0	100	100
1	Ak	206/289 (71%)	202 (98%)	4 (2%)	0	100	100
1	Al	206/289 (71%)	202 (98%)	4 (2%)	0	100	100
2	1	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	2	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	3	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	4	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	5	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	A	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	AA	17/580 (3%)	17 (100%)	0	0	100	100
2	AB	17/580 (3%)	15 (88%)	2 (12%)	0	100	100
2	AC	18/580 (3%)	18 (100%)	0	0	100	100
2	AD	17/580 (3%)	17 (100%)	0	0	100	100
2	AE	17/580 (3%)	17 (100%)	0	0	100	100
2	AF	21/580 (4%)	14 (67%)	6 (29%)	1 (5%)	2	14
2	AG	9/580 (2%)	7 (78%)	2 (22%)	0	100	100
2	AH	9/580 (2%)	9 (100%)	0	0	100	100
2	AI	9/580 (2%)	8 (89%)	1 (11%)	0	100	100
2	AJ	22/580 (4%)	18 (82%)	4 (18%)	0	100	100
2	AK	23/580 (4%)	23 (100%)	0	0	100	100
2	AL	30/580 (5%)	26 (87%)	4 (13%)	0	100	100
2	AM	31/580 (5%)	31 (100%)	0	0	100	100
2	AN	31/580 (5%)	31 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AO	30/580 (5%)	30 (100%)	0	0	100	100
2	B	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	C	142/580 (24%)	139 (98%)	3 (2%)	0	100	100
2	D	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	E	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	F	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	G	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	H	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	I	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	J	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	K	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	L	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	M	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	N	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	O	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	P	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	Q	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	R	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	S	112/580 (19%)	100 (89%)	10 (9%)	2 (2%)	6	30
2	T	112/580 (19%)	99 (88%)	12 (11%)	1 (1%)	14	43
2	U	112/580 (19%)	102 (91%)	10 (9%)	0	100	100
2	V	112/580 (19%)	102 (91%)	9 (8%)	1 (1%)	14	43
2	W	112/580 (19%)	104 (93%)	7 (6%)	1 (1%)	14	43
2	X	105/580 (18%)	97 (92%)	7 (7%)	1 (1%)	12	41
2	Y	112/580 (19%)	99 (88%)	11 (10%)	2 (2%)	6	30
2	Z	112/580 (19%)	99 (88%)	12 (11%)	1 (1%)	14	43
2	a	112/580 (19%)	102 (91%)	9 (8%)	1 (1%)	14	43
2	b	90/580 (16%)	83 (92%)	6 (7%)	1 (1%)	11	40
2	c	101/580 (17%)	93 (92%)	7 (7%)	1 (1%)	12	41
2	d	101/580 (17%)	93 (92%)	8 (8%)	0	100	100
2	e	101/580 (17%)	90 (89%)	10 (10%)	1 (1%)	12	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	f	81/580 (14%)	74 (91%)	7 (9%)	0	100	100
2	g	88/580 (15%)	83 (94%)	5 (6%)	0	100	100
2	h	87/580 (15%)	82 (94%)	5 (6%)	0	100	100
2	i	85/580 (15%)	81 (95%)	4 (5%)	0	100	100
2	j	88/580 (15%)	80 (91%)	8 (9%)	0	100	100
2	k	112/580 (19%)	106 (95%)	5 (4%)	1 (1%)	14	43
2	l	112/580 (19%)	98 (88%)	13 (12%)	1 (1%)	14	43
2	m	112/580 (19%)	103 (92%)	8 (7%)	1 (1%)	14	43
2	n	101/580 (17%)	95 (94%)	5 (5%)	1 (1%)	12	41
2	o	112/580 (19%)	104 (93%)	6 (5%)	2 (2%)	6	30
2	p	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	q	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	r	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	s	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	t	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	u	142/580 (24%)	139 (98%)	3 (2%)	0	100	100
2	v	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	w	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	x	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	y	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
2	z	142/580 (24%)	138 (97%)	4 (3%)	0	100	100
3	6	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
3	7	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
3	AQ	87/89 (98%)	87 (100%)	0	0	100	100
3	AR	87/89 (98%)	86 (99%)	0	1 (1%)	11	40
4	8	238/260 (92%)	232 (98%)	6 (2%)	0	100	100
5	AS	105/131 (80%)	104 (99%)	1 (1%)	0	100	100
5	AT	103/131 (79%)	102 (99%)	1 (1%)	0	100	100
5	AU	105/131 (80%)	103 (98%)	2 (2%)	0	100	100
5	AV	104/131 (79%)	104 (100%)	0	0	100	100
5	AW	104/131 (79%)	103 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AX	126/137 (92%)	122 (97%)	4 (3%)	0	100	100
6	AY	126/137 (92%)	123 (98%)	3 (2%)	0	100	100
6	AZ	126/137 (92%)	122 (97%)	3 (2%)	1 (1%)	16	45
6	Aa	126/137 (92%)	125 (99%)	1 (1%)	0	100	100
6	Ab	126/137 (92%)	120 (95%)	6 (5%)	0	100	100
6	Ac	126/137 (92%)	121 (96%)	5 (4%)	0	100	100
7	Ad	70/103 (68%)	70 (100%)	0	0	100	100
7	Ae	78/103 (76%)	78 (100%)	0	0	100	100
7	Af	78/103 (76%)	77 (99%)	1 (1%)	0	100	100
7	Ag	70/103 (68%)	69 (99%)	1 (1%)	0	100	100
7	Ah	70/103 (68%)	69 (99%)	1 (1%)	0	100	100
7	Ai	38/103 (37%)	38 (100%)	0	0	100	100
8	Aj	69/376 (18%)	69 (100%)	0	0	100	100
9	Am	10/13 (77%)	5 (50%)	4 (40%)	1 (10%)	0	4
9	An	7/13 (54%)	2 (29%)	4 (57%)	1 (14%)	0	2
9	Ao	8/13 (62%)	8 (100%)	0	0	100	100
9	Ap	8/13 (62%)	2 (25%)	4 (50%)	2 (25%)	0	0
9	Aq	11/13 (85%)	6 (54%)	3 (27%)	2 (18%)	0	1
10	Ar	15/17 (88%)	15 (100%)	0	0	100	100
10	As	15/17 (88%)	15 (100%)	0	0	100	100
10	At	15/17 (88%)	15 (100%)	0	0	100	100
10	Au	15/17 (88%)	15 (100%)	0	0	100	100
10	Av	15/17 (88%)	15 (100%)	0	0	100	100
10	Aw	15/17 (88%)	15 (100%)	0	0	100	100
All	All	11000/46459 (24%)	10564 (96%)	408 (4%)	28 (0%)	37	64

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	152	GLN
9	Am	11	PRO
9	Ap	7	HIS
9	Aq	7	ASP
2	T	193	VAL

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	0	182/247 (74%)	176 (97%)	6 (3%)	33	54
1	9	181/247 (73%)	175 (97%)	6 (3%)	33	54
1	AP	182/247 (74%)	177 (97%)	5 (3%)	39	57
1	Ak	182/247 (74%)	175 (96%)	7 (4%)	29	51
1	Al	182/247 (74%)	175 (96%)	7 (4%)	29	51
2	1	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	2	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	3	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	4	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	5	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	A	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	AA	15/500 (3%)	14 (93%)	1 (7%)	15	40
2	AB	15/500 (3%)	14 (93%)	1 (7%)	15	40
2	AC	15/500 (3%)	15 (100%)	0	100	100
2	AD	15/500 (3%)	14 (93%)	1 (7%)	15	40
2	AE	15/500 (3%)	15 (100%)	0	100	100
2	AF	17/500 (3%)	13 (76%)	4 (24%)	1	5
2	AG	8/500 (2%)	8 (100%)	0	100	100
2	AH	8/500 (2%)	7 (88%)	1 (12%)	4	20
2	AI	8/500 (2%)	8 (100%)	0	100	100
2	AJ	17/500 (3%)	16 (94%)	1 (6%)	18	42
2	AK	18/500 (4%)	15 (83%)	3 (17%)	2	12
2	AL	24/500 (5%)	23 (96%)	1 (4%)	26	49
2	AM	24/500 (5%)	23 (96%)	1 (4%)	26	49
2	AN	24/500 (5%)	22 (92%)	2 (8%)	10	33
2	AO	24/500 (5%)	23 (96%)	1 (4%)	26	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	C	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	D	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	E	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	F	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	G	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	H	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	I	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	J	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	K	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	L	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	M	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	N	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	O	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	P	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	Q	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	R	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	S	98/500 (20%)	86 (88%)	12 (12%)	5	20
2	T	98/500 (20%)	84 (86%)	14 (14%)	3	16
2	U	98/500 (20%)	89 (91%)	9 (9%)	8	30
2	V	98/500 (20%)	88 (90%)	10 (10%)	7	27
2	W	98/500 (20%)	86 (88%)	12 (12%)	5	20
2	X	93/500 (19%)	85 (91%)	8 (9%)	10	32
2	Y	98/500 (20%)	89 (91%)	9 (9%)	8	30
2	Z	98/500 (20%)	89 (91%)	9 (9%)	8	30
2	a	98/500 (20%)	93 (95%)	5 (5%)	21	45
2	b	81/500 (16%)	78 (96%)	3 (4%)	30	52
2	c	90/500 (18%)	84 (93%)	6 (7%)	15	40
2	d	90/500 (18%)	81 (90%)	9 (10%)	7	28
2	e	90/500 (18%)	78 (87%)	12 (13%)	4	18
2	f	75/500 (15%)	71 (95%)	4 (5%)	20	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	g	79/500 (16%)	72 (91%)	7 (9%)	9	31
2	h	78/500 (16%)	73 (94%)	5 (6%)	16	40
2	i	77/500 (15%)	72 (94%)	5 (6%)	15	40
2	j	79/500 (16%)	73 (92%)	6 (8%)	12	36
2	k	98/500 (20%)	88 (90%)	10 (10%)	7	27
2	l	98/500 (20%)	88 (90%)	10 (10%)	7	27
2	m	98/500 (20%)	91 (93%)	7 (7%)	13	38
2	n	89/500 (18%)	83 (93%)	6 (7%)	15	40
2	o	98/500 (20%)	93 (95%)	5 (5%)	21	45
2	p	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	q	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	r	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	s	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	t	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	u	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	v	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	w	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	x	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	y	128/500 (26%)	123 (96%)	5 (4%)	28	51
2	z	128/500 (26%)	123 (96%)	5 (4%)	28	51
3	6	80/80 (100%)	75 (94%)	5 (6%)	16	41
3	7	80/80 (100%)	79 (99%)	1 (1%)	61	69
3	AQ	80/80 (100%)	77 (96%)	3 (4%)	29	51
3	AR	80/80 (100%)	76 (95%)	4 (5%)	22	46
4	8	204/218 (94%)	194 (95%)	10 (5%)	22	46
5	AS	89/106 (84%)	88 (99%)	1 (1%)	65	71
5	AT	88/106 (83%)	86 (98%)	2 (2%)	44	61
5	AU	89/106 (84%)	86 (97%)	3 (3%)	32	53
5	AV	88/106 (83%)	85 (97%)	3 (3%)	32	53
5	AW	88/106 (83%)	88 (100%)	0	100	100
6	AX	111/115 (96%)	106 (96%)	5 (4%)	24	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	AY	111/115 (96%)	107 (96%)	4 (4%)	31	52
6	AZ	111/115 (96%)	103 (93%)	8 (7%)	13	37
6	Aa	111/115 (96%)	106 (96%)	5 (4%)	24	48
6	Ab	111/115 (96%)	105 (95%)	6 (5%)	20	44
6	Ac	111/115 (96%)	106 (96%)	5 (4%)	24	48
7	Ad	63/84 (75%)	59 (94%)	4 (6%)	16	41
7	Ae	66/84 (79%)	64 (97%)	2 (3%)	36	55
7	Af	66/84 (79%)	63 (96%)	3 (4%)	24	48
7	Ag	63/84 (75%)	62 (98%)	1 (2%)	55	65
7	Ah	63/84 (75%)	63 (100%)	0	100	100
7	Ai	36/84 (43%)	35 (97%)	1 (3%)	38	57
8	Aj	58/317 (18%)	55 (95%)	3 (5%)	21	45
All	All	9652/39814 (24%)	9172 (95%)	480 (5%)	23	46

5 of 480 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	P	422	GLU
2	s	395	THR
2	V	242	GLN
2	r	395	THR
2	y	395	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 242 such sidechains are listed below:

Mol	Chain	Res	Type
2	I	445	ASN
2	t	305	GLN
2	R	327	ASN
2	s	387	GLN
2	y	305	GLN

5.3.3 RNA ⓘ

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.

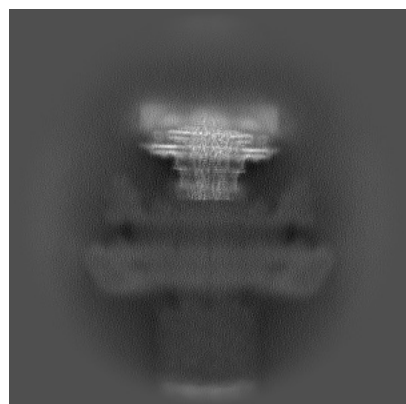
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39787. These allow visual inspection of the internal detail of the map and identification of artifacts.

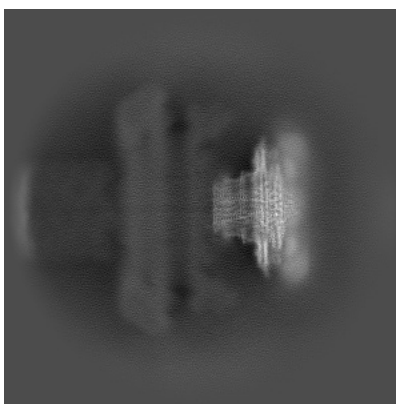
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

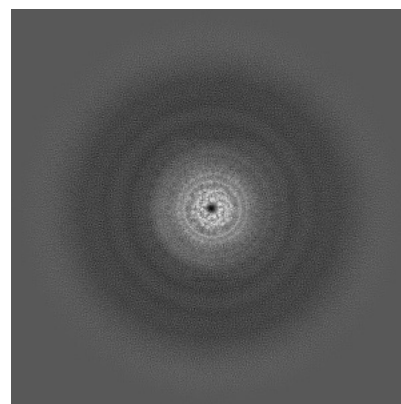
6.1.1 Primary map



X

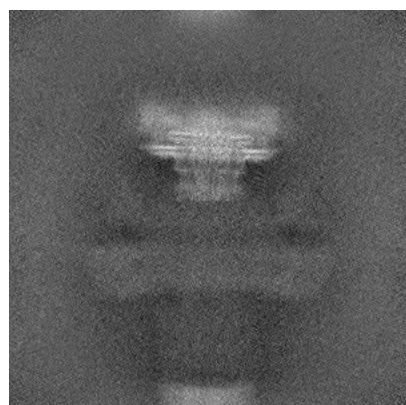


Y

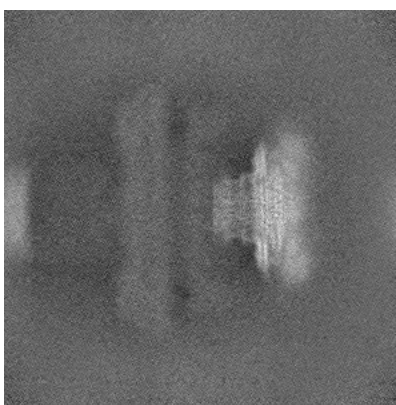


Z

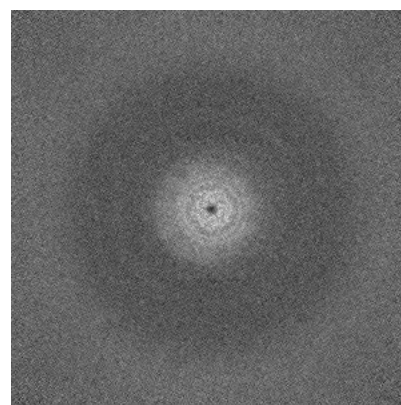
6.1.2 Raw map



X



Y

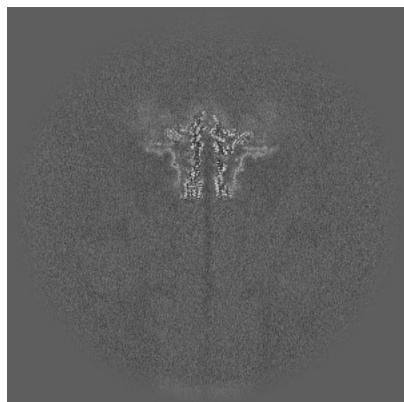


Z

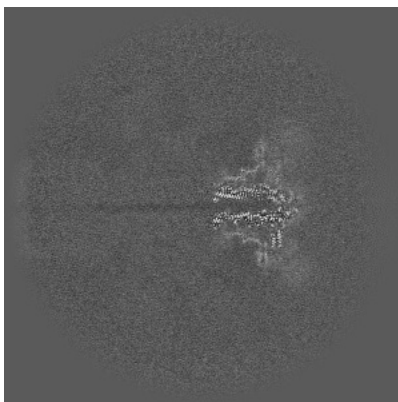
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

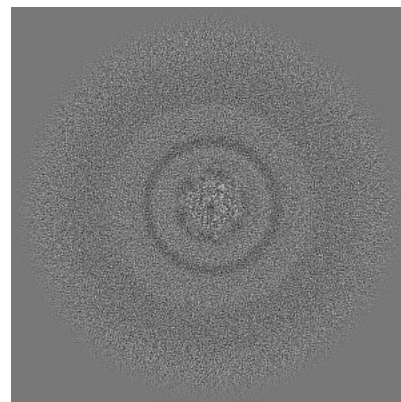
6.2.1 Primary map



X Index: 310



Y Index: 310

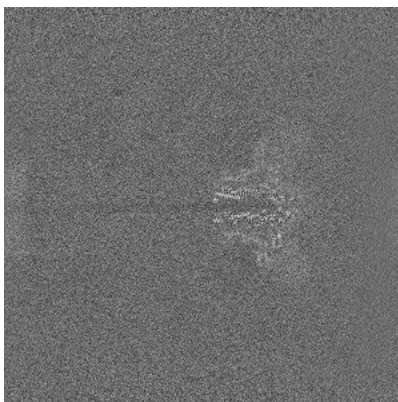


Z Index: 310

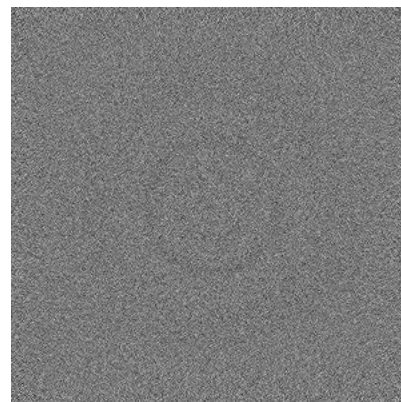
6.2.2 Raw map



X Index: 310



Y Index: 310



Z Index: 310

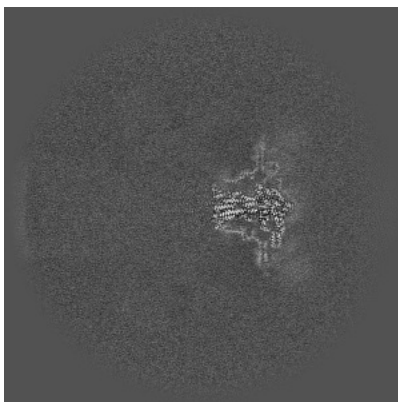
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

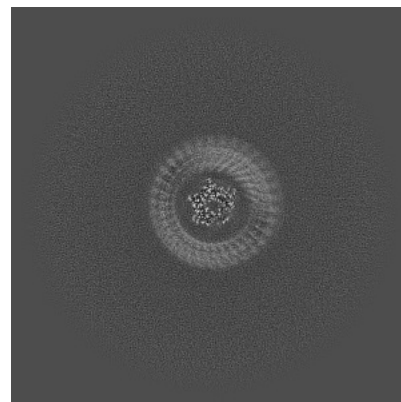
6.3.1 Primary map



X Index: 301

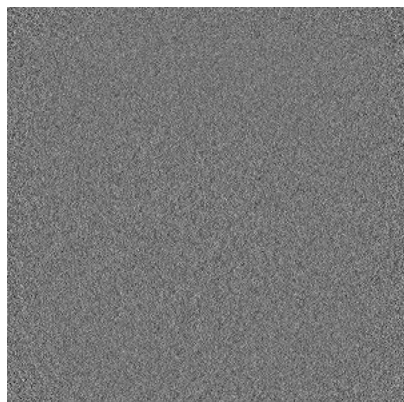


Y Index: 325

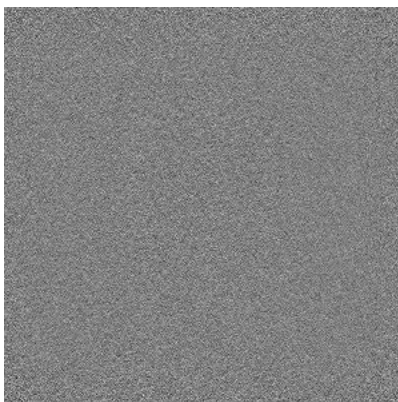


Z Index: 399

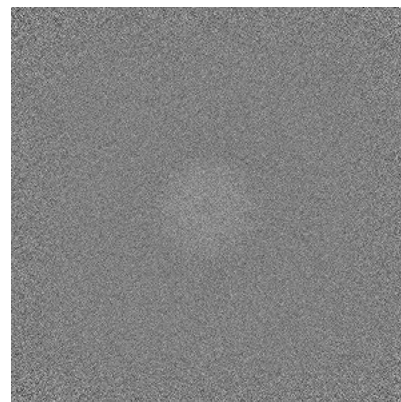
6.3.2 Raw map



X Index: 0



Y Index: 0

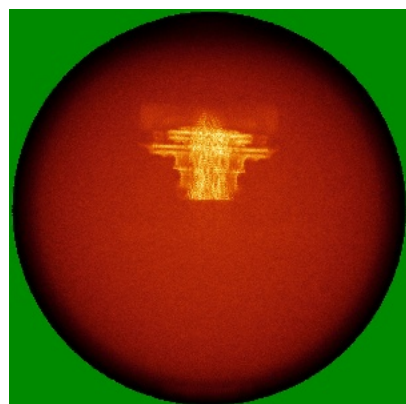


Z Index: 0

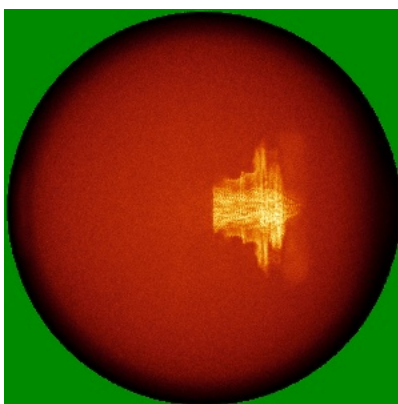
The images above show the largest variance slices of the map in three orthogonal directions.

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

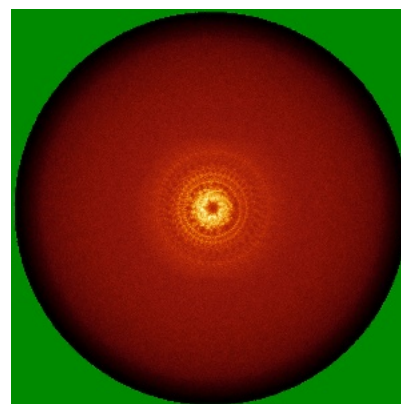
6.4.1 Primary map



X

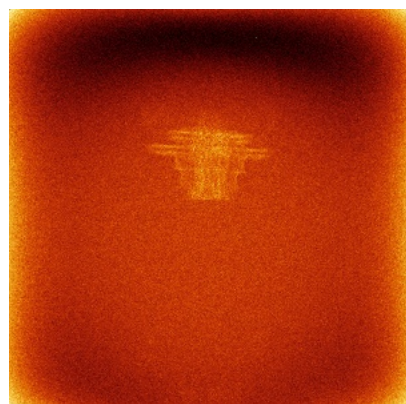


Y

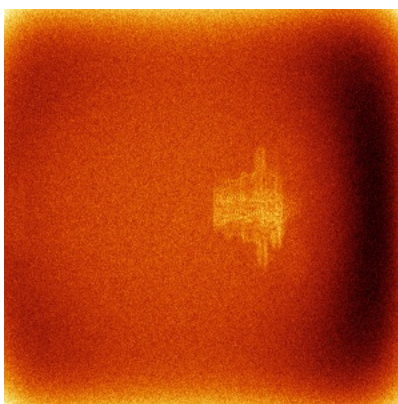


Z

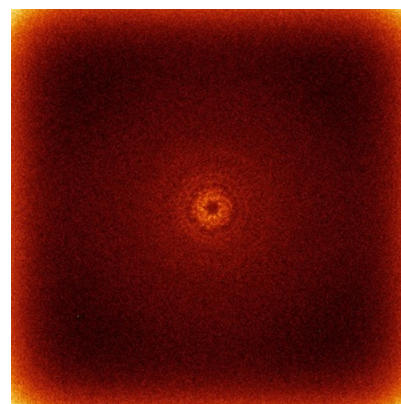
6.4.2 Raw map



X



Y

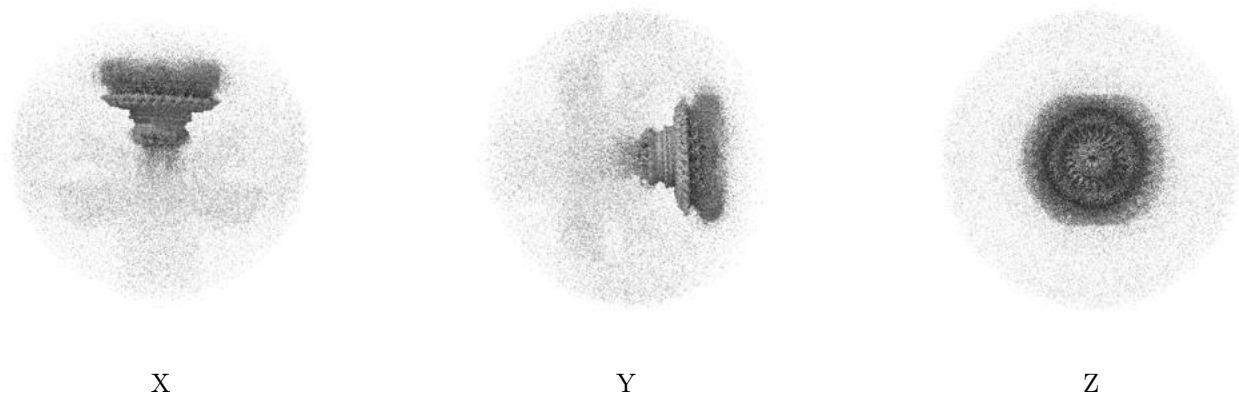


Z

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.

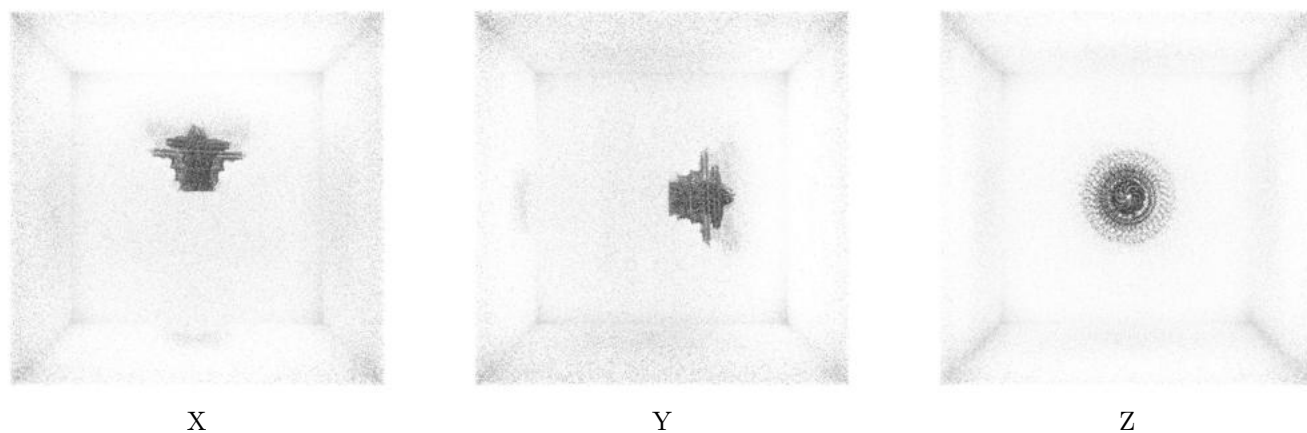
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

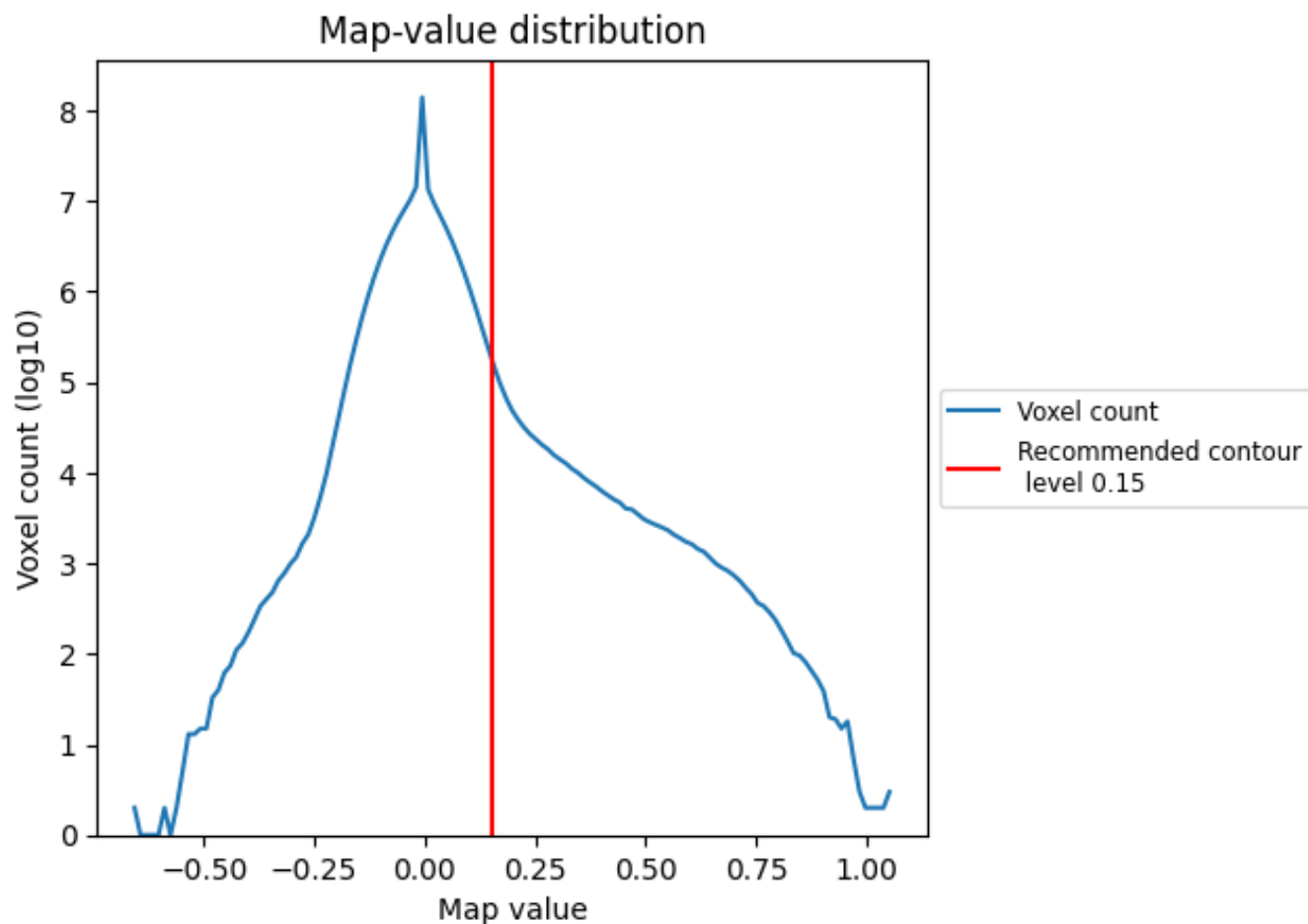
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

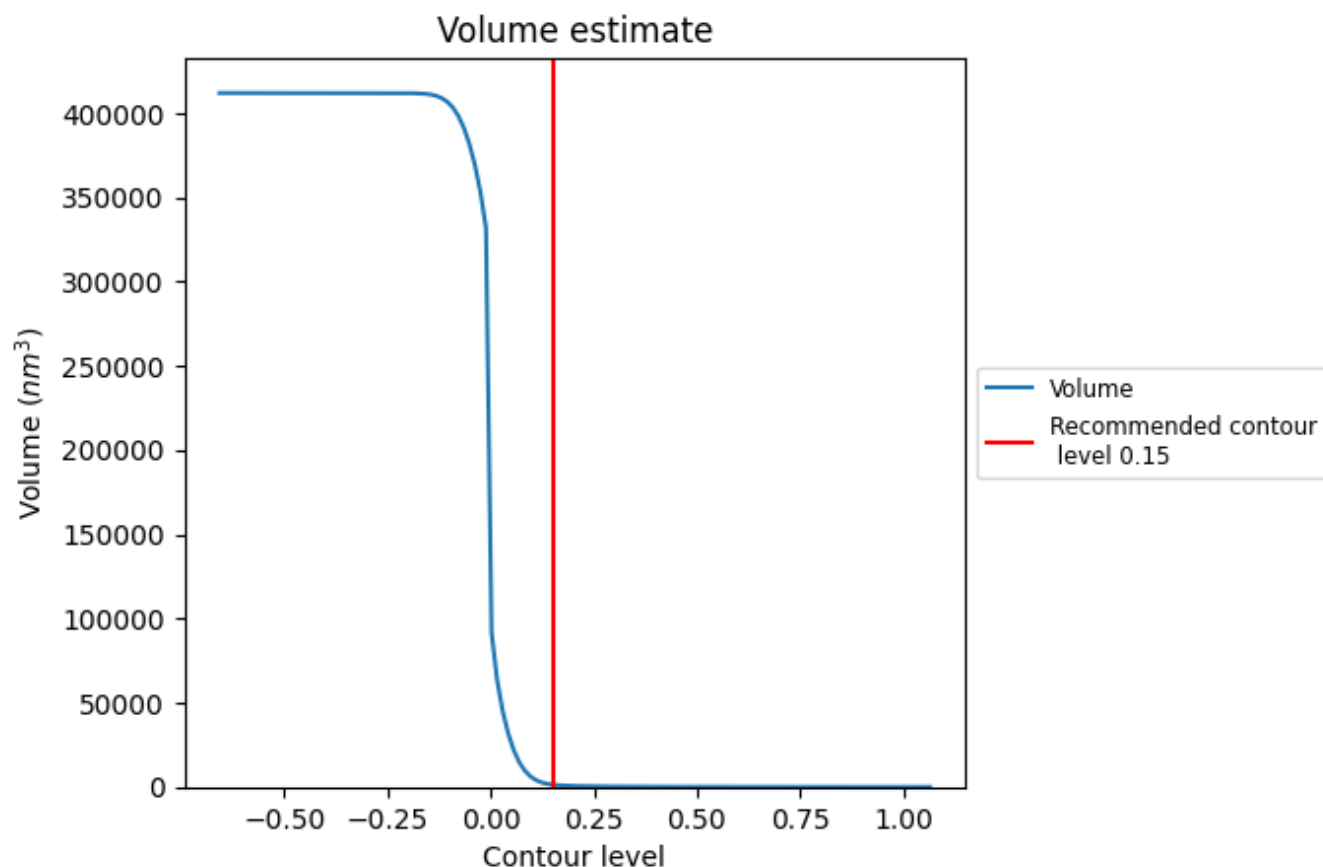
This section contains the results of statistical analysis of the map.

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.

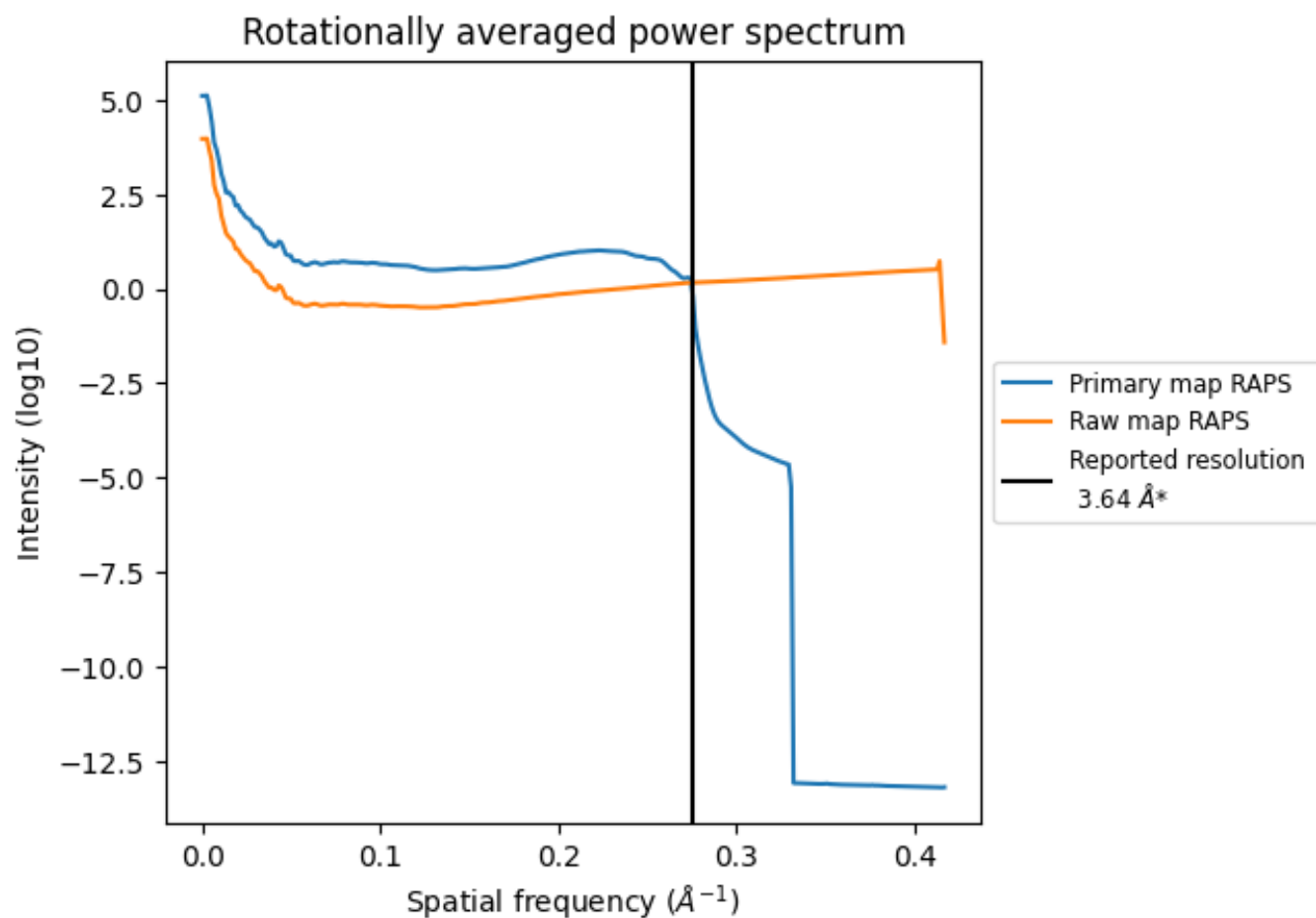
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1347 nm³; this corresponds to an approximate mass of 1217 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 ⓘ

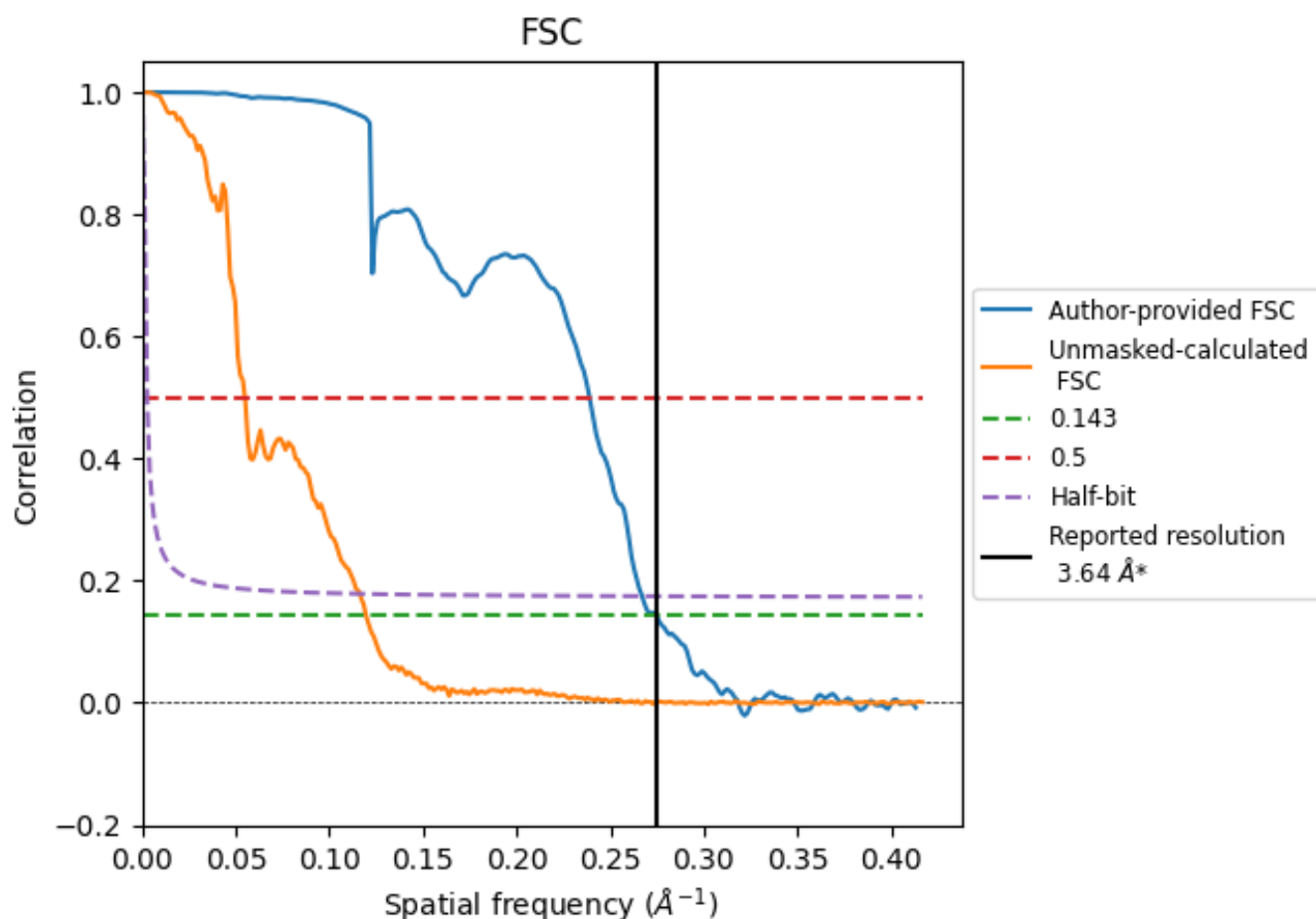


*Reported resolution corresponds to spatial frequency of 0.275 $\text{\AA}^{-1}$

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 0.275 Å⁻¹

8.2 Resolution estimates [i](#)

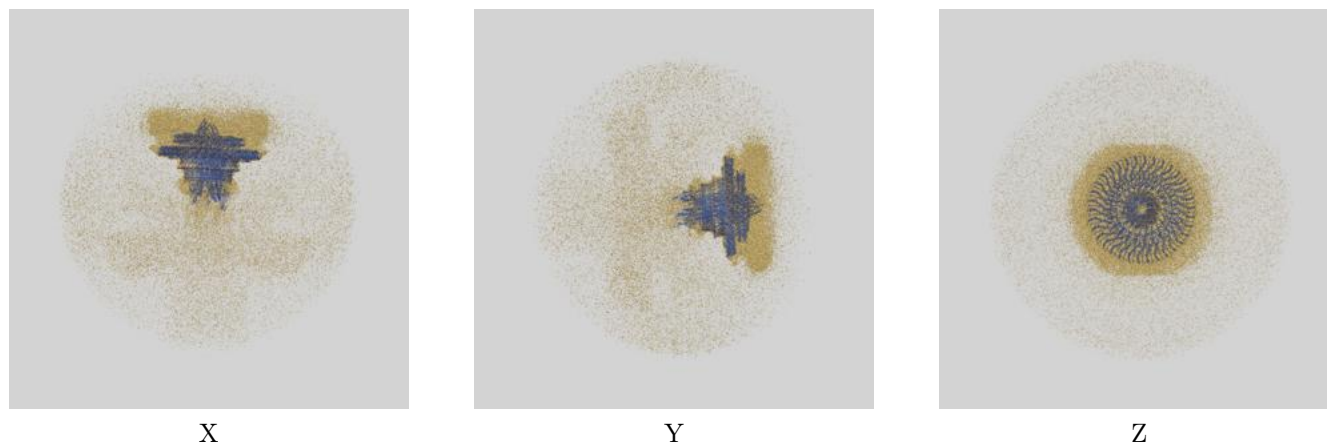
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.64	-	-
Author-provided FSC curve	3.64	4.18	3.74
Unmasked-calculated*	8.36	18.25	8.61

*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 8.36 differs from the reported value 3.64 by more than 10 %

9 Map-model fit [i](#)

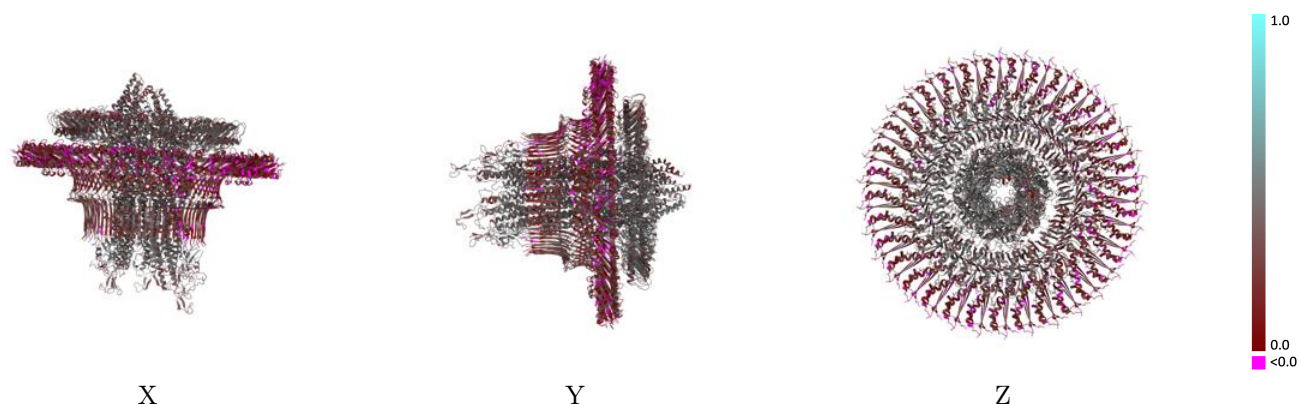
This section contains information regarding the fit between EMDB map EMD-39787 and PDB model 8Z5X. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



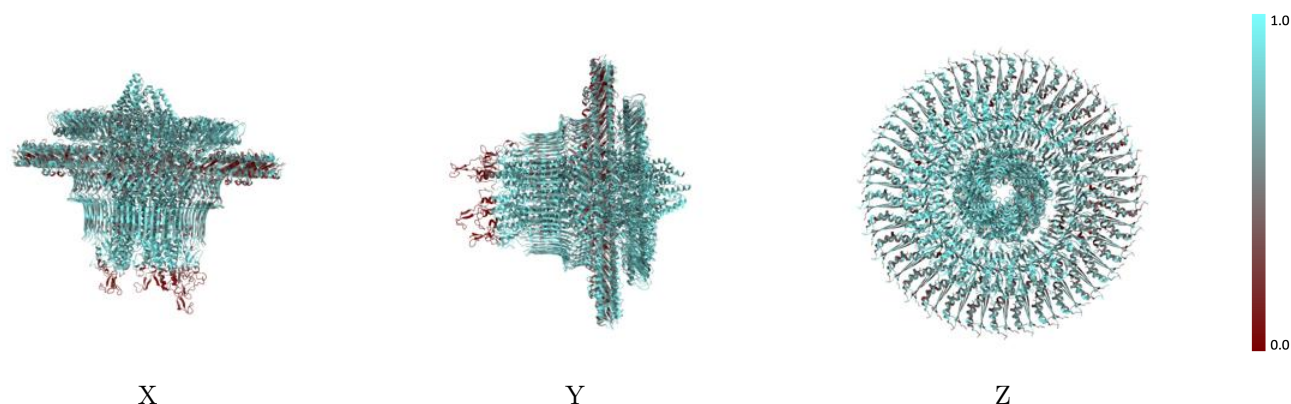
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



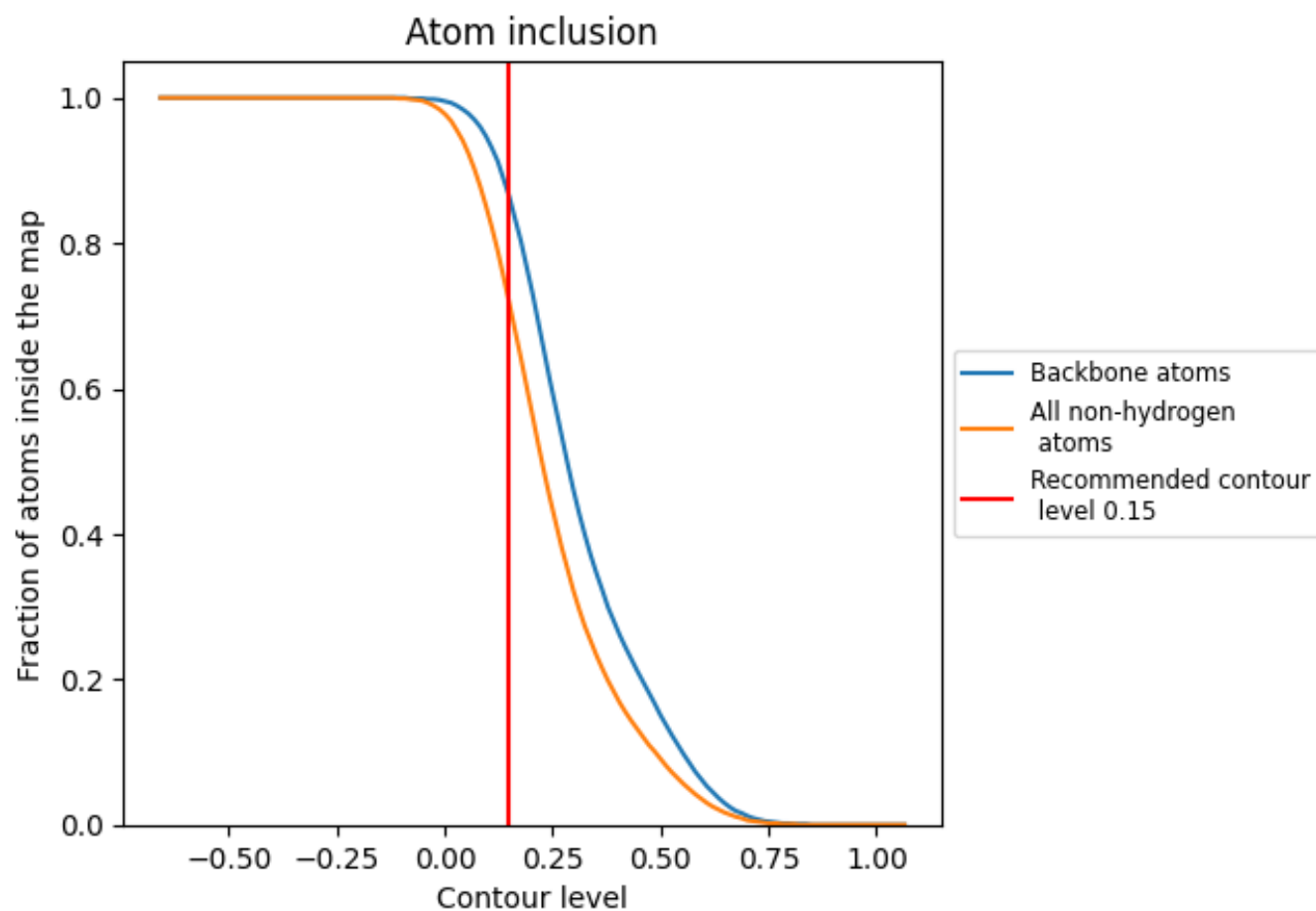
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 72% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7190	 0.3130
0	 0.8340	 0.4560
1	 0.5490	 0.1320
2	 0.5810	 0.1440
3	 0.5950	 0.1420
4	 0.6080	 0.1490
5	 0.6270	 0.1720
6	 0.8260	 0.4330
7	 0.8380	 0.4440
8	 0.8250	 0.4280
9	 0.8130	 0.4360
A	 0.6660	 0.1800
AA	 0.7330	 0.4000
AB	 0.8220	 0.4370
AC	 0.5830	 0.3990
AD	 0.4960	 0.4030
AE	 0.4370	 0.3600
AF	 0.4870	 0.3450
AG	 0.9040	 0.4450
AH	 0.8630	 0.4310
AI	 0.7120	 0.4150
AJ	 0.2090	 0.2870
AK	 0.7570	 0.3960
AL	 0.4860	 0.3860
AM	 0.8210	 0.4250
AN	 0.6470	 0.4030
AO	 0.7540	 0.4190
AP	 0.8290	 0.4360
AQ	 0.8230	 0.4190
AR	 0.8550	 0.4520
AS	 0.8350	 0.4550
AT	 0.8230	 0.4250
AU	 0.8510	 0.4530
AV	 0.8590	 0.4660
AW	 0.8690	 0.4640



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Chain	Atom inclusion	Q-score
AX	 0.7080	 0.4220
AY	 0.4880	 0.4020
AZ	 0.4640	 0.4000
Aa	 0.5470	 0.4250
Ab	 0.6300	 0.4300
Ac	 0.6800	 0.4300
Ad	 0.8440	 0.4550
Ae	 0.8220	 0.4310
Af	 0.8310	 0.4280
Ag	 0.8440	 0.4410
Ah	 0.8480	 0.4420
Ai	 0.8430	 0.4390
Aj	 0.7250	 0.3240
Ak	 0.8450	 0.4520
Al	 0.8550	 0.4620
Am	 0.7930	 0.3750
An	 0.6820	 0.3520
Ao	 0.8980	 0.4520
Ap	 0.9800	 0.4690
Aq	 0.9210	 0.4960
Ar	 0.8090	 0.2940
As	 0.8210	 0.2520
At	 0.7620	 0.3190
Au	 0.4640	 0.2320
Av	 0.7140	 0.2490
Aw	 0.8570	 0.2880
B	 0.6490	 0.1720
C	 0.7020	 0.2210
D	 0.6900	 0.2250
E	 0.6970	 0.2200
F	 0.6960	 0.2260
G	 0.7180	 0.2320
H	 0.6960	 0.2070
I	 0.7080	 0.2190
J	 0.7050	 0.2240
K	 0.6590	 0.1990
L	 0.6510	 0.1890
M	 0.6670	 0.1870
N	 0.6510	 0.1690
O	 0.6400	 0.1550
P	 0.6490	 0.1560
Q	 0.6450	 0.1840

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Chain	Atom inclusion	Q-score
R	 0.6620	 0.1890
S	 0.8370	 0.4330
T	 0.8490	 0.4330
U	 0.8130	 0.4140
V	 0.8380	 0.4280
W	 0.8120	 0.4110
X	 0.8210	 0.4340
Y	 0.8340	 0.4440
Z	 0.8360	 0.4340
a	 0.7880	 0.4320
b	 0.7910	 0.4060
c	 0.7830	 0.4040
d	 0.7440	 0.3840
e	 0.7070	 0.3480
f	 0.6490	 0.3160
g	 0.6160	 0.3140
h	 0.6700	 0.3140
i	 0.7190	 0.3300
j	 0.7540	 0.3610
k	 0.8530	 0.4330
l	 0.8390	 0.4400
m	 0.8080	 0.4170
n	 0.8130	 0.4120
o	 0.7880	 0.3920
p	 0.6650	 0.2010
q	 0.6670	 0.2000
r	 0.6460	 0.1900
s	 0.6630	 0.2040
t	 0.6420	 0.1830
u	 0.6540	 0.1960
v	 0.5910	 0.1520
w	 0.5960	 0.1680
x	 0.6250	 0.1830
y	 0.6050	 0.1790
z	 0.6000	 0.1520