



wwPDB EM Validation Summary Report ⓘ

Aug 17, 2026 – 04:41 PM EDT

PDB ID : 12EQ / pdb_000012eq
EMDB ID : EMD-76383
Title : Subtomogram average structure of flagellar export apparatus and MS-ring in
Borrelia burgdorferi
Authors : Yue, J.; Liu, Y.
Deposited on : 2026-03-31
Resolution : 16.00 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:

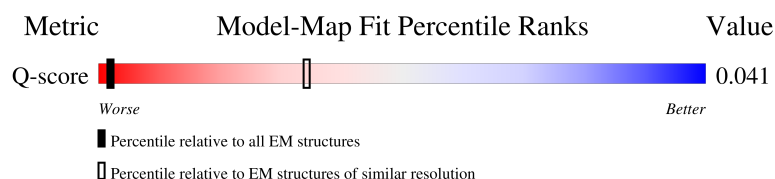
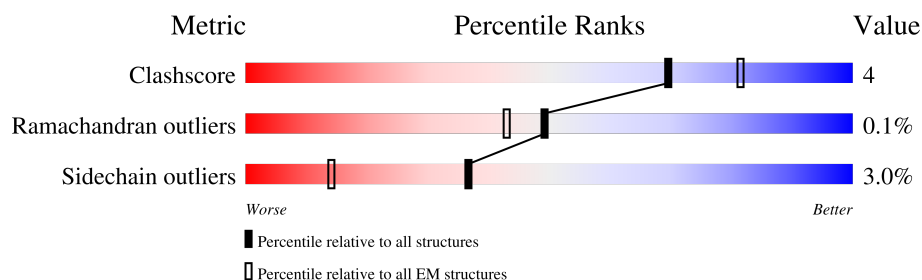
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 16.00 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	41 (15.50 - 16.50)

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	569	
1	1	569	
1	2	569	
1	3	569	

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Mol	Chain	Length	Quality of chain
1	4	569	
1	5	569	
1	6	569	
1	7	569	
1	8	569	
1	9	569	
1	A	569	
1	AA	569	
1	AB	569	
1	AC	569	
1	AD	569	
1	AE	569	
1	AF	569	
1	AG	569	
1	AH	569	
1	AI	569	
1	AJ	569	
1	AK	569	
1	AL	569	
1	AM	569	
1	AN	569	
1	AO	569	
1	AP	569	
1	AQ	569	
1	AR	569	

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Mol	Chain	Length	Quality of chain
1	AS	569	
1	AT	569	
1	B	569	
1	C	569	
1	D	569	
1	E	569	
1	F	569	
1	G	569	
1	H	569	
1	I	569	
1	J	569	
1	K	569	
1	L	569	
1	M	569	
1	N	569	
1	O	569	
1	P	569	
1	Q	569	
1	R	569	
1	S	569	
1	T	569	
1	U	569	
1	V	569	
1	W	569	
1	X	569	

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Mol	Chain	Length	Quality of chain
1	Y	569	
1	Z	569	
1	a	569	
1	b	569	
1	c	569	
1	d	569	
1	e	569	
1	f	569	
1	g	569	
1	h	569	
1	i	569	
1	j	569	
1	k	569	
1	l	569	
1	m	569	
1	n	569	
1	o	569	
1	p	569	
1	q	569	
1	r	569	
1	s	569	
1	t	569	
1	u	569	
1	v	569	
1	w	569	

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Mol	Chain	Length	Quality of chain
1	x	569	
1	y	569	
1	z	569	
2	AX	372	
3	AY	254	
3	AZ	254	
3	Aa	254	
3	Ab	254	
3	Ac	254	
4	Ad	269	
5	Ae	111	
5	Af	111	
5	Ag	111	
5	Ah	111	
5	Ai	111	
5	Aj	111	
6	Ak	135	
6	Al	135	
6	Am	135	
6	An	135	
6	Ao	135	
7	Ap	152	
7	Aq	152	
7	Ar	152	
7	As	152	

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Mol	Chain	Length	Quality of chain
7	At	152	
7	Au	152	
8	AU	87	
8	AV	87	
8	AW	87	
8	Av	87	
9	A1	697	
9	A2	697	
9	A3	697	
9	A4	697	
9	A5	697	
9	Aw	697	
9	Ax	697	
9	Ay	697	
9	Az	697	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 231030 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	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	B	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	C	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	D	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	E	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	F	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	G	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	H	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	I	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	J	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	K	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	L	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	M	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	N	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	O	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	P	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	Q	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	S	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	T	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	U	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	V	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	W	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	X	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	Y	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	Z	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	a	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	b	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	c	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	d	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	e	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	f	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	g	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	h	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	i	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	j	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	k	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	l	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	n	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	o	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	p	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	q	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	r	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	s	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	t	205	Total	C	N	O	S	0	0
			1595	1028	270	295	2		
1	u	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	v	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	w	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	x	205	Total	C	N	O	S	0	0
			1595	1028	270	295	2		
1	y	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	z	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	1	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	2	205	Total	C	N	O	S	0	0
			1595	1028	270	295	2		
1	3	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	4	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	5	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	6	205	Total	C	N	O	S	0	0
			1595	1028	270	295	2		
1	7	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	9	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	0	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	AA	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	AB	209	Total	C	N	O	S	0	0
			1632	1054	275	301	2		
1	AC	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AD	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AE	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AF	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AG	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AH	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AI	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AJ	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AK	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AL	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AM	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AN	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AO	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AP	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AQ	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AR	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AS	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		
1	AT	202	Total	C	N	O	S	0	0
			1614	1036	276	299	3		

- Molecule 2 is a protein called Flagellar biosynthetic protein FlhB.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AX	242	Total	C	N	O	S	0	0
			1988	1325	311	342	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AY	209	Total	C	N	O	S	0	0
			1665	1118	255	277	15		
3	AZ	209	Total	C	N	O	S	0	0
			1656	1114	252	275	15		
3	Aa	209	Total	C	N	O	S	0	0
			1657	1116	252	274	15		
3	Ab	209	Total	C	N	O	S	0	0
			1666	1119	255	277	15		
3	Ac	209	Total	C	N	O	S	0	0
			1676	1128	256	277	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ad	259	Total	C	N	O	S	0	0
			2083	1434	304	340	5		

- Molecule 5 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ae	70	Total	C	N	O	S	0	0
			542	342	94	104	2		
5	Af	70	Total	C	N	O	S	0	0
			542	342	94	104	2		
5	Ag	70	Total	C	N	O	S	0	0
			542	342	94	104	2		
5	Ah	70	Total	C	N	O	S	0	0
			530	333	91	104	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ai	70	Total	C	N	O	S	0	0
			542	342	94	104	2		
5	Aj	40	Total	C	N	O	S	0	0
			308	193	55	58	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Ak	112	Total	C	N	O	S	0	0
			920	577	161	177	5		
6	Al	112	Total	C	N	O	S	0	0
			920	577	161	177	5		
6	Am	112	Total	C	N	O	S	0	0
			920	577	161	177	5		
6	An	112	Total	C	N	O	S	0	0
			920	577	161	177	5		
6	Ao	112	Total	C	N	O	S	0	0
			920	577	161	177	5		

- Molecule 7 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ap	136	Total	C	N	O	S	0	0
			1030	639	187	200	4		
7	Aq	152	Total	C	N	O	S	0	0
			1153	724	201	224	4		
7	Ar	136	Total	C	N	O	S	0	0
			1034	641	188	201	4		
7	As	152	Total	C	N	O	S	0	0
			1169	732	208	225	4		
7	At	152	Total	C	N	O	S	0	0
			1169	732	208	225	4		
7	Au	152	Total	C	N	O	S	0	0
			1169	732	208	225	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Av	87	Total	C	N	O	S	0	0
			678	463	99	112	4		
8	AU	87	Total	C	N	O	S	0	0
			682	465	100	113	4		

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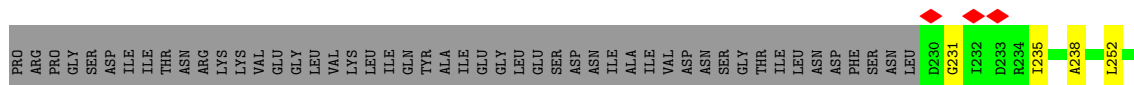
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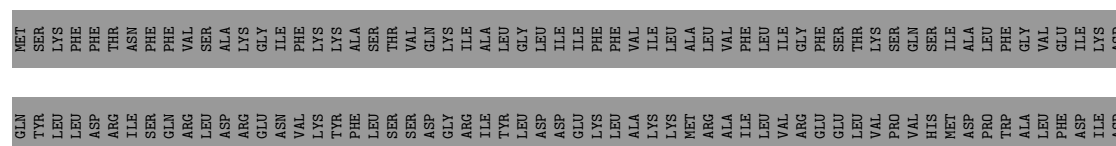
Mol	Chain	Residues	Atoms					AltConf	Trace
8	AV	87	Total	C	N	O	S	0	0
			692	471	104	113	4		
8	AW	87	Total	C	N	O	S	0	0
			692	471	104	113	4		

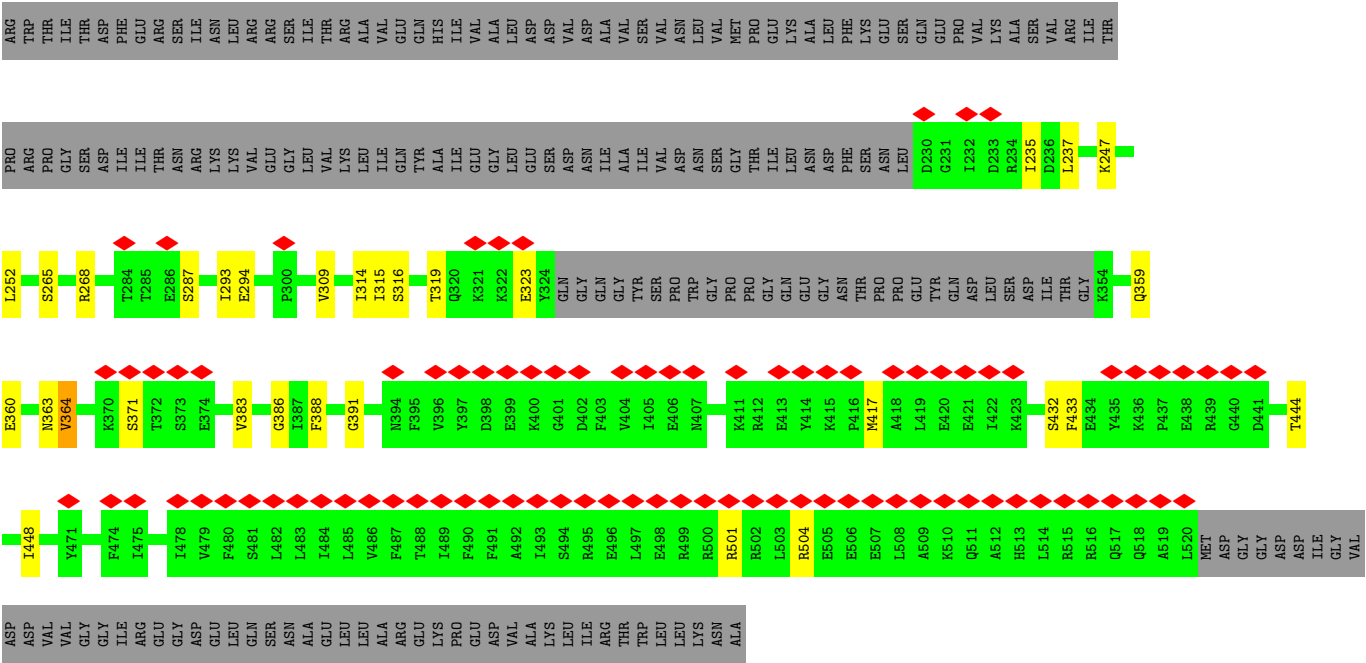
- Molecule 9 is a protein called Flagellar biosynthesis protein FlhA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aw	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Ax	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Ay	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Az	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A1	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A2	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A3	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A4	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A5	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		

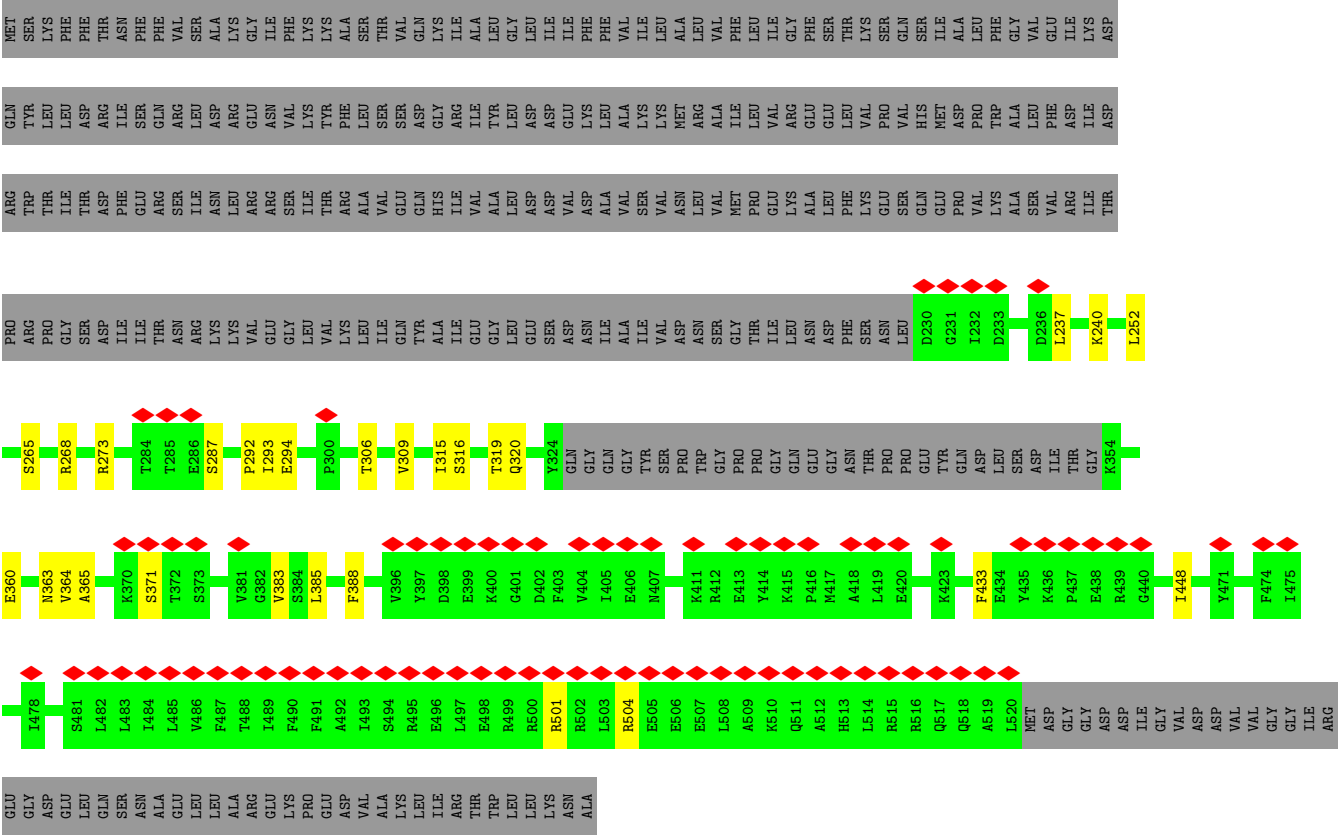
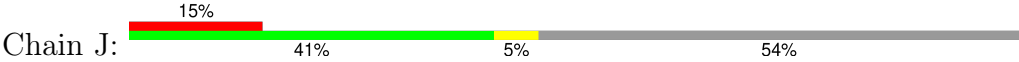




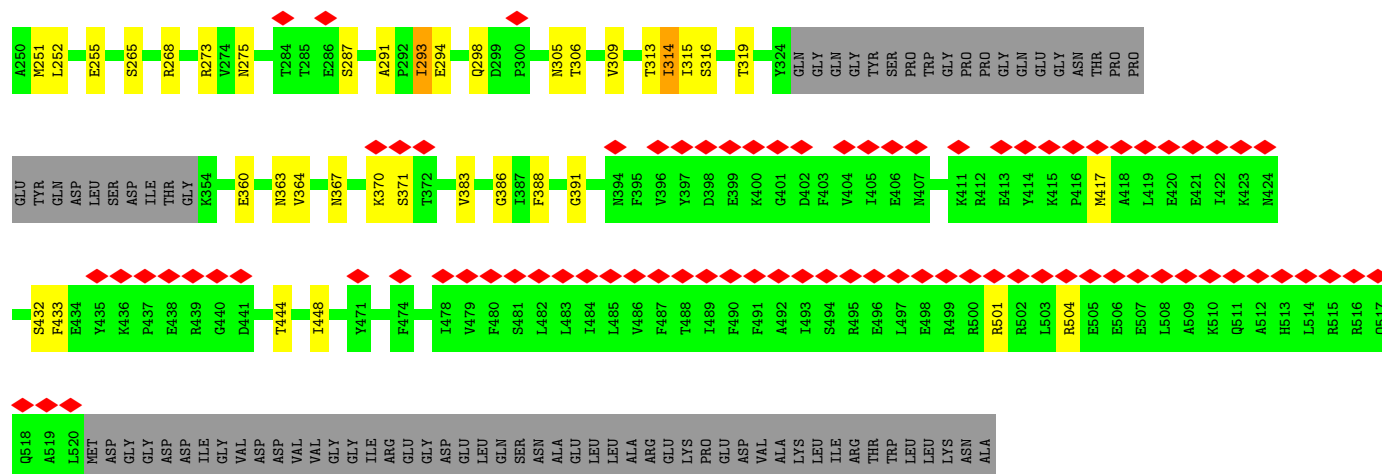




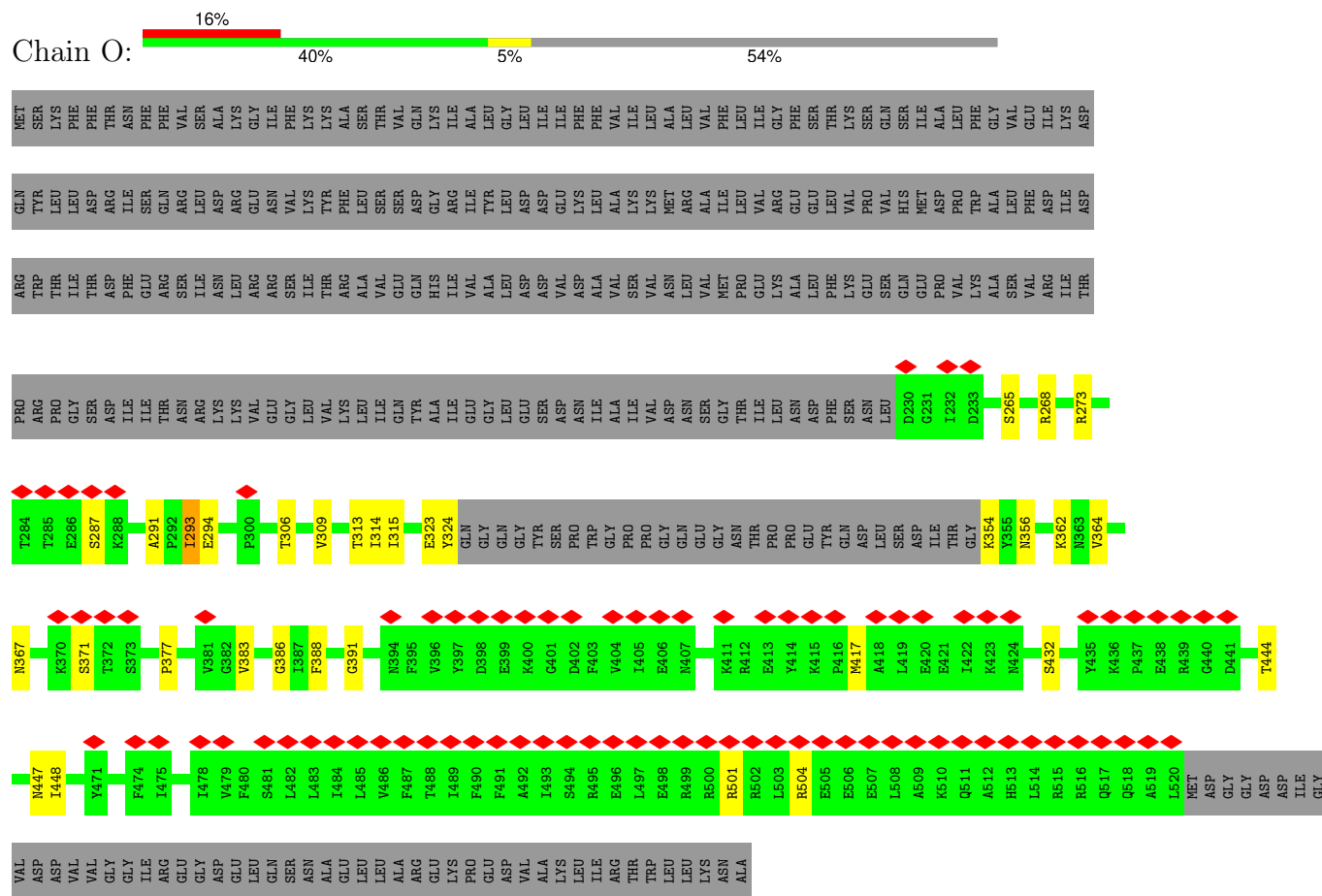
• Molecule 1: Flagellar M-ring protein



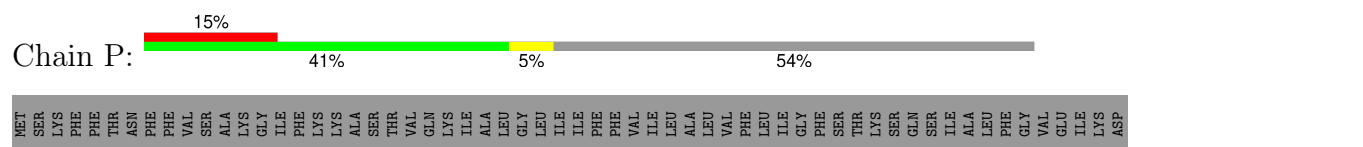
• Molecule 1: Flagellar M-ring protein

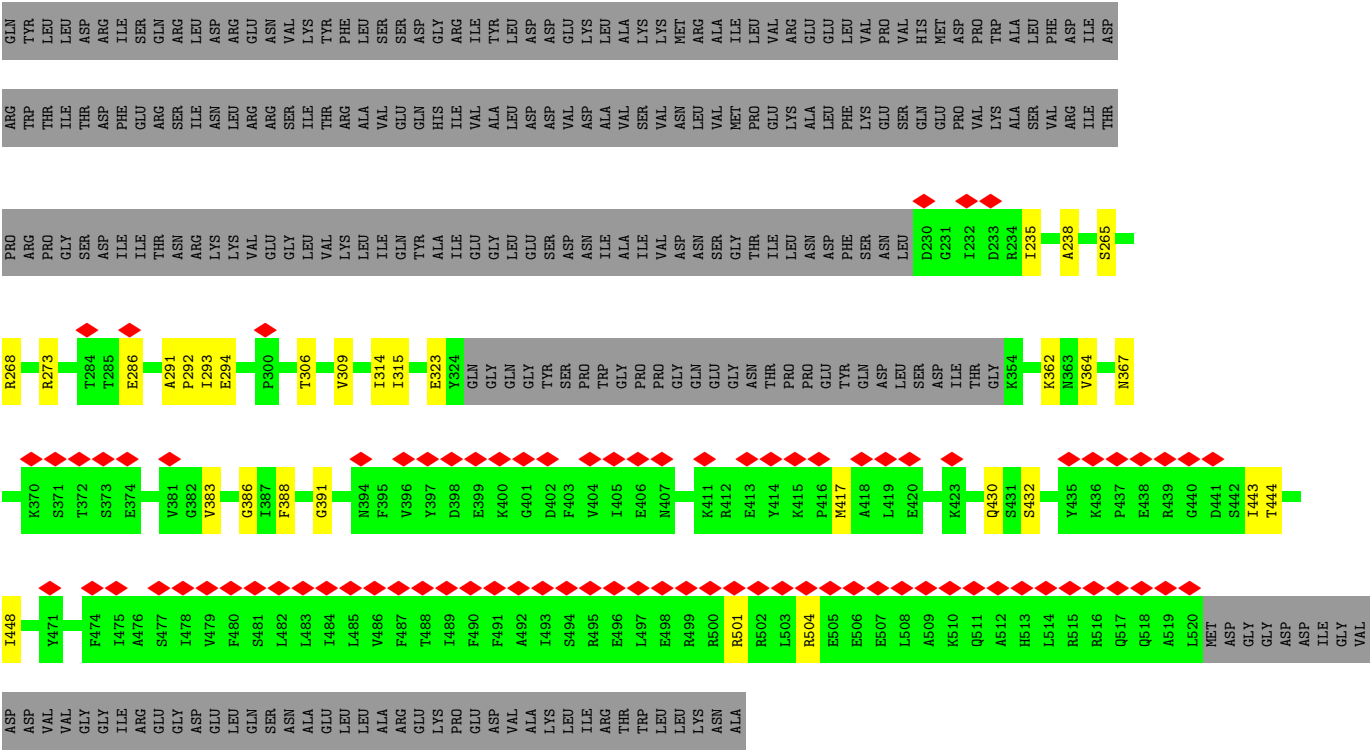


• Molecule 1: Flagellar M-ring protein

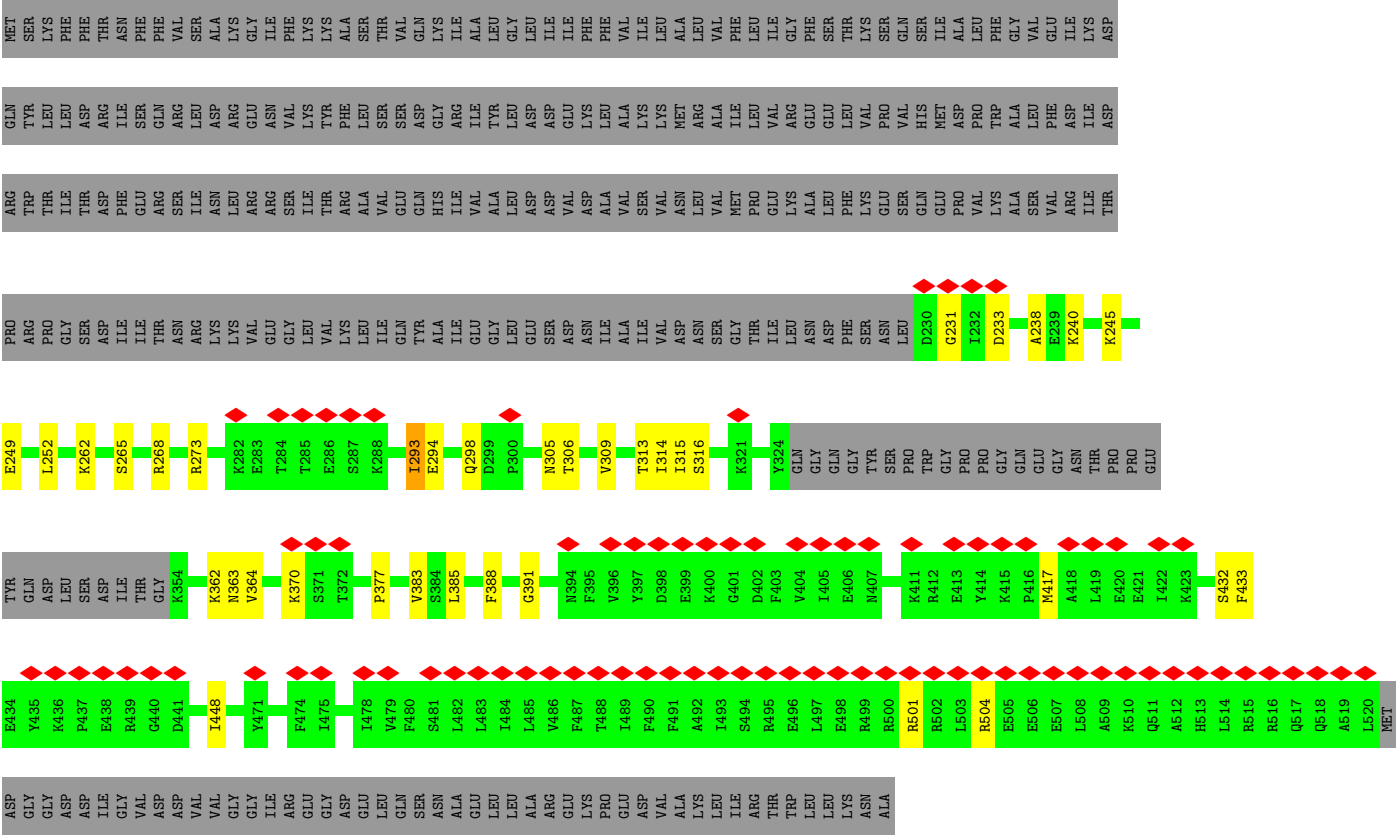
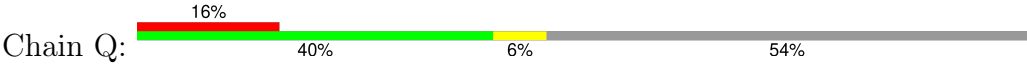


• Molecule 1: Flagellar M-ring protein



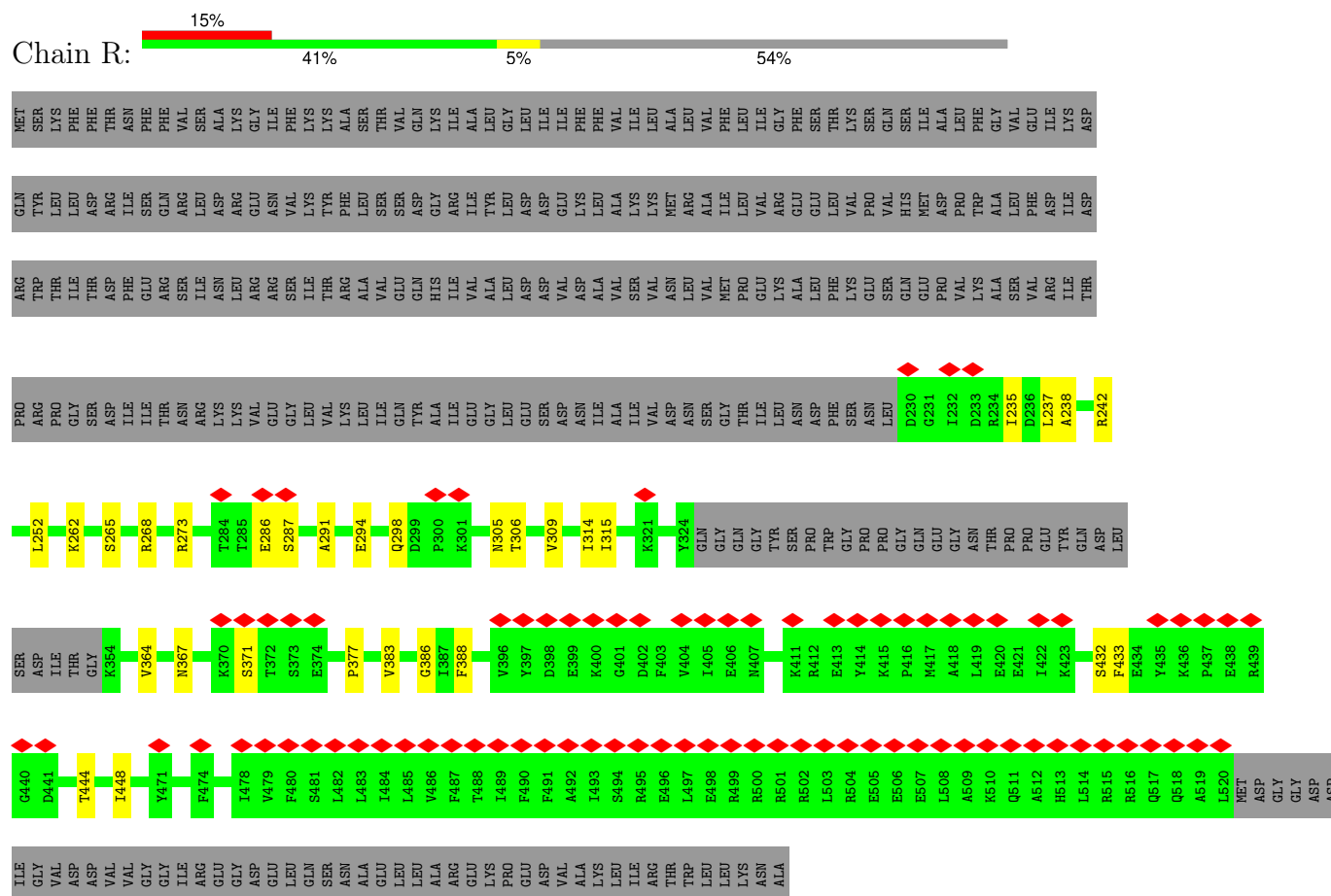


● Molecule 1: Flagellar M-ring protein



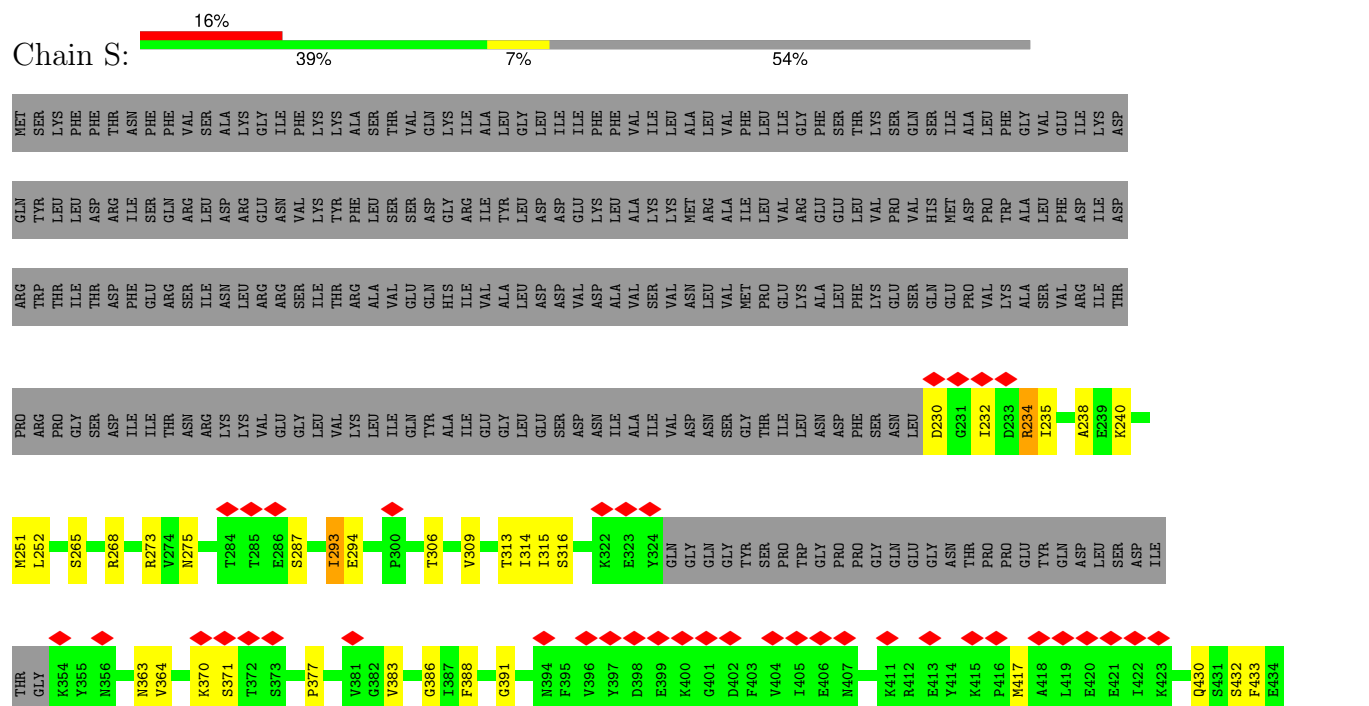
- Molecule 1: Flagellar M-ring protein

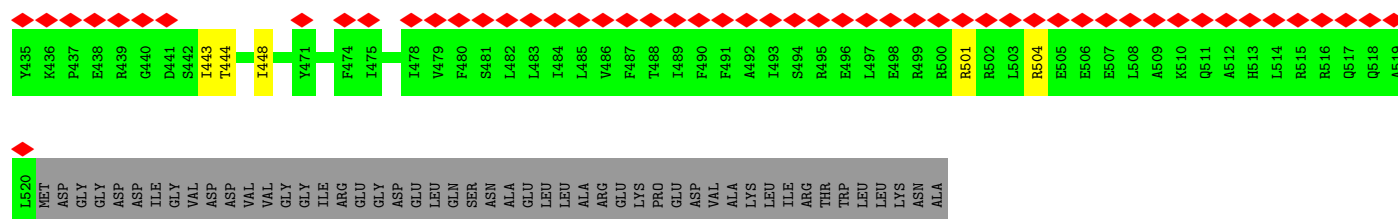
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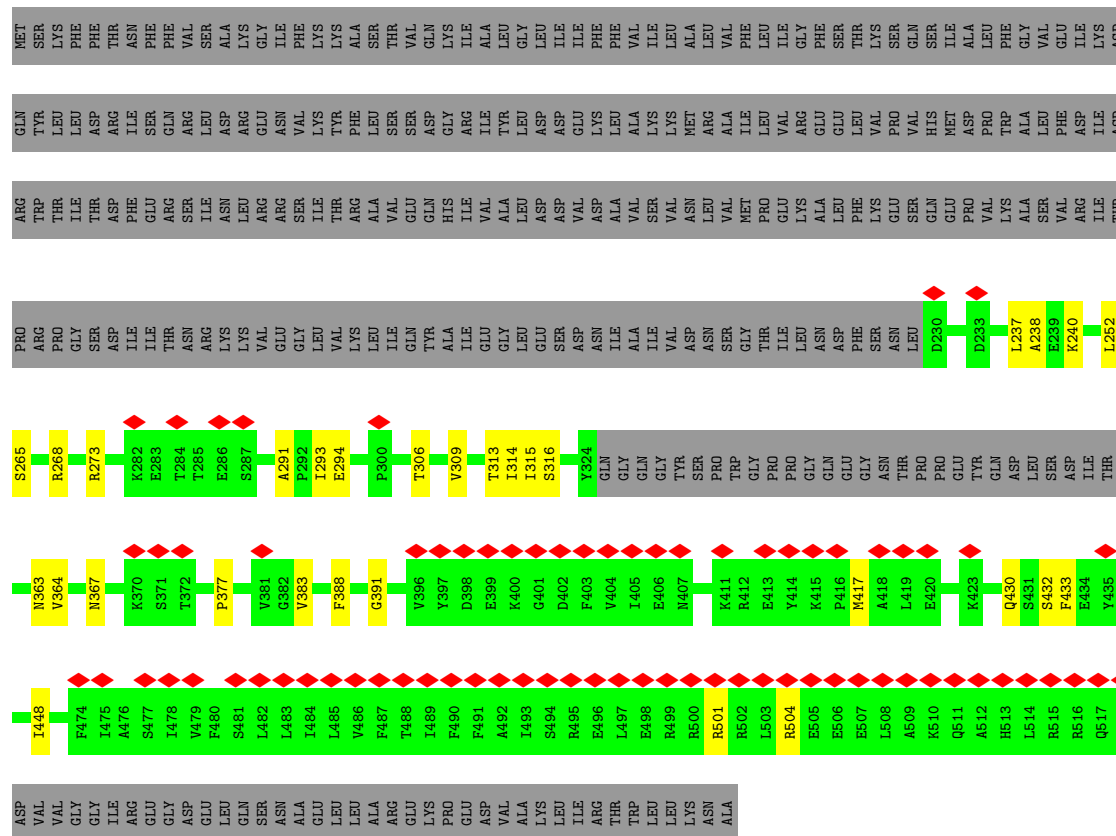
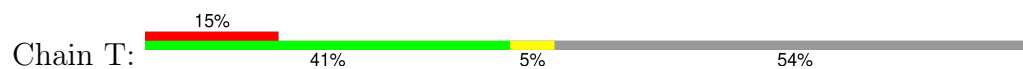
- Molecule 1: Flagellar M-ring protein

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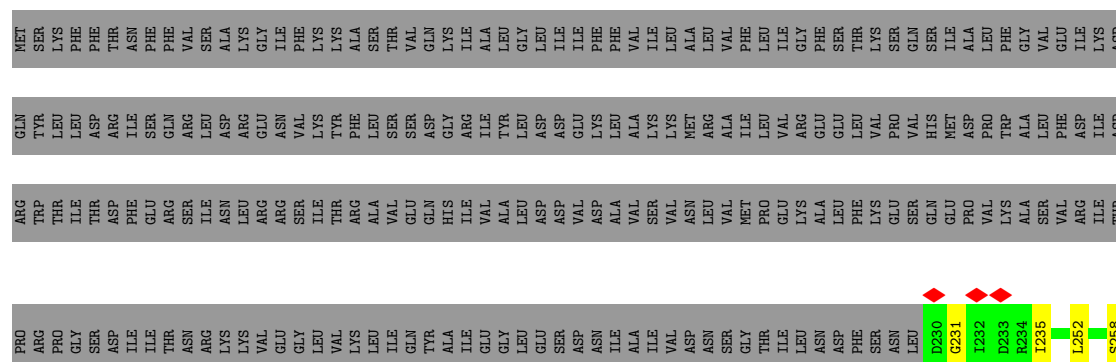
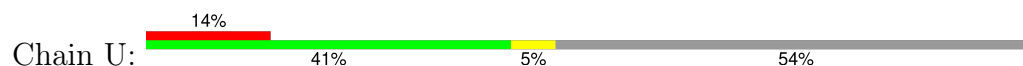


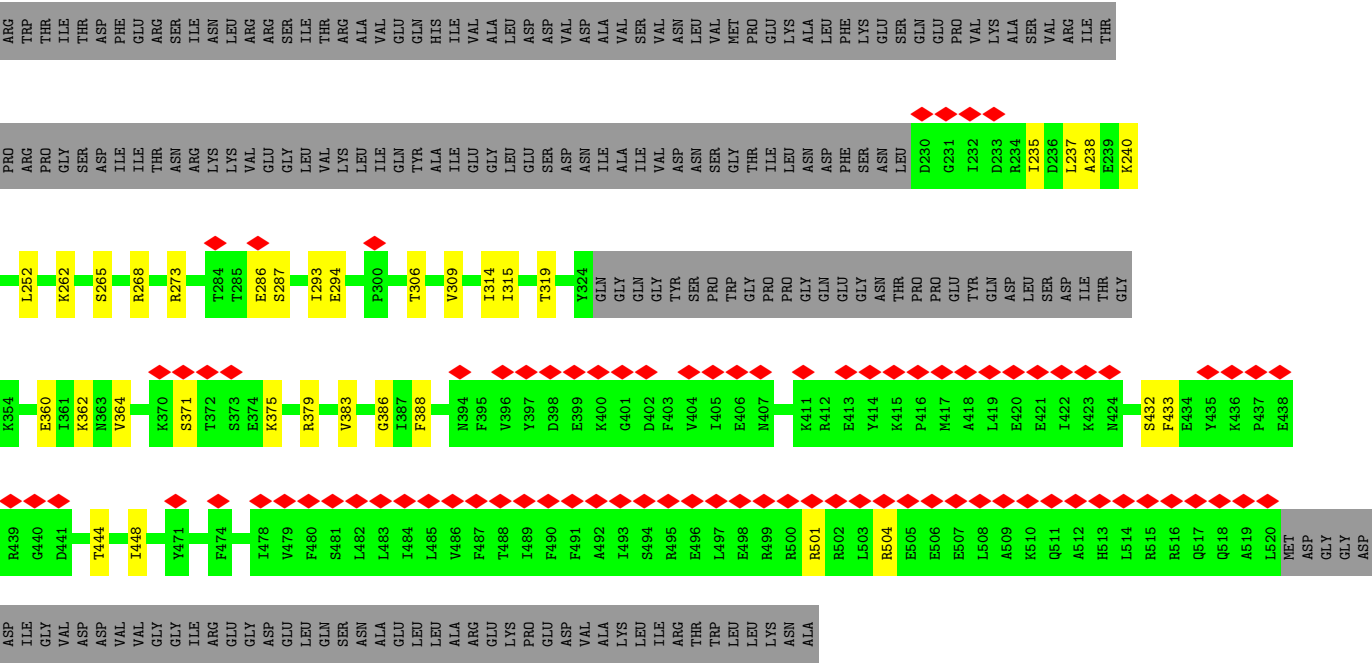


• Molecule 1: Flagellar M-ring protein

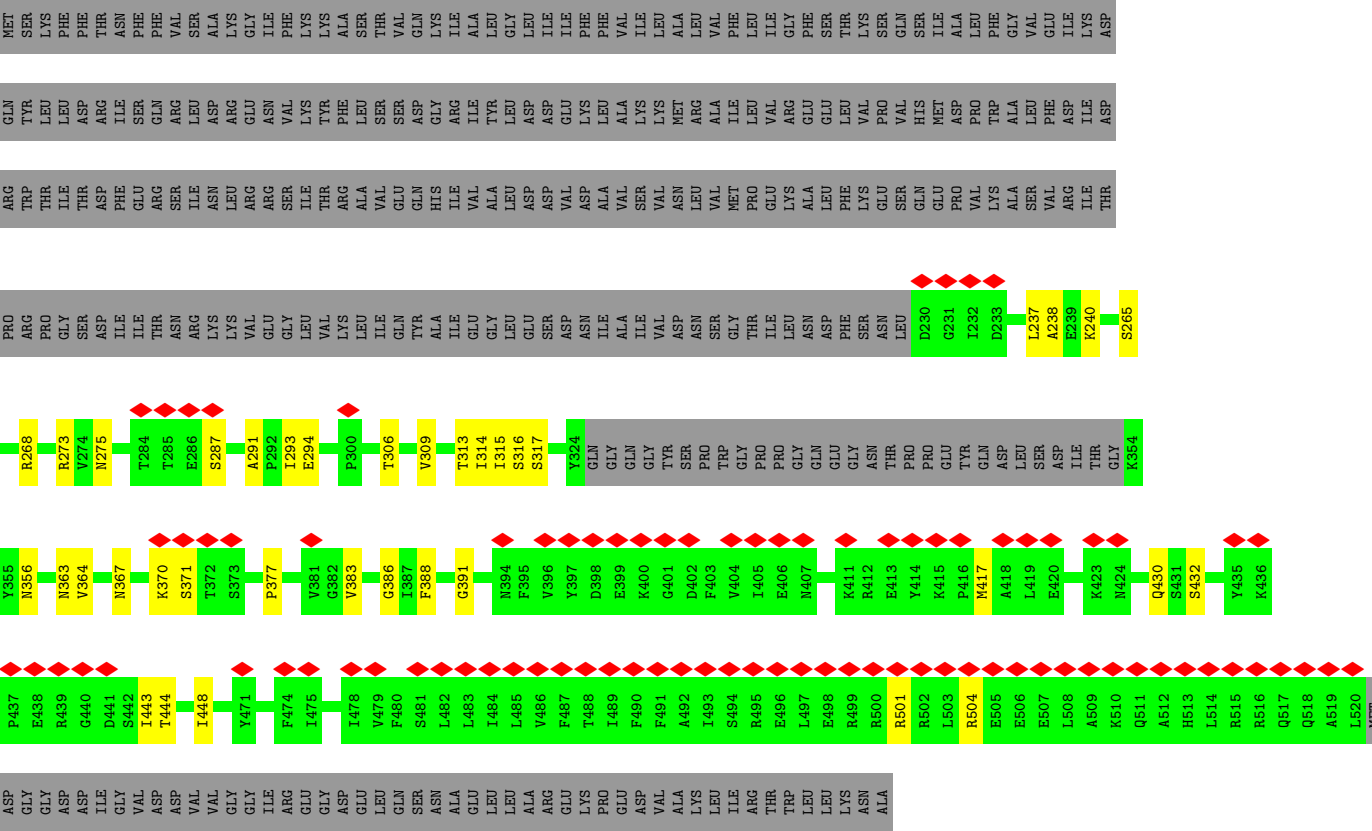
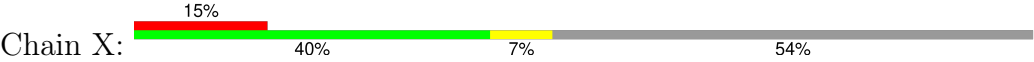


• Molecule 1: Flagellar M-ring protein

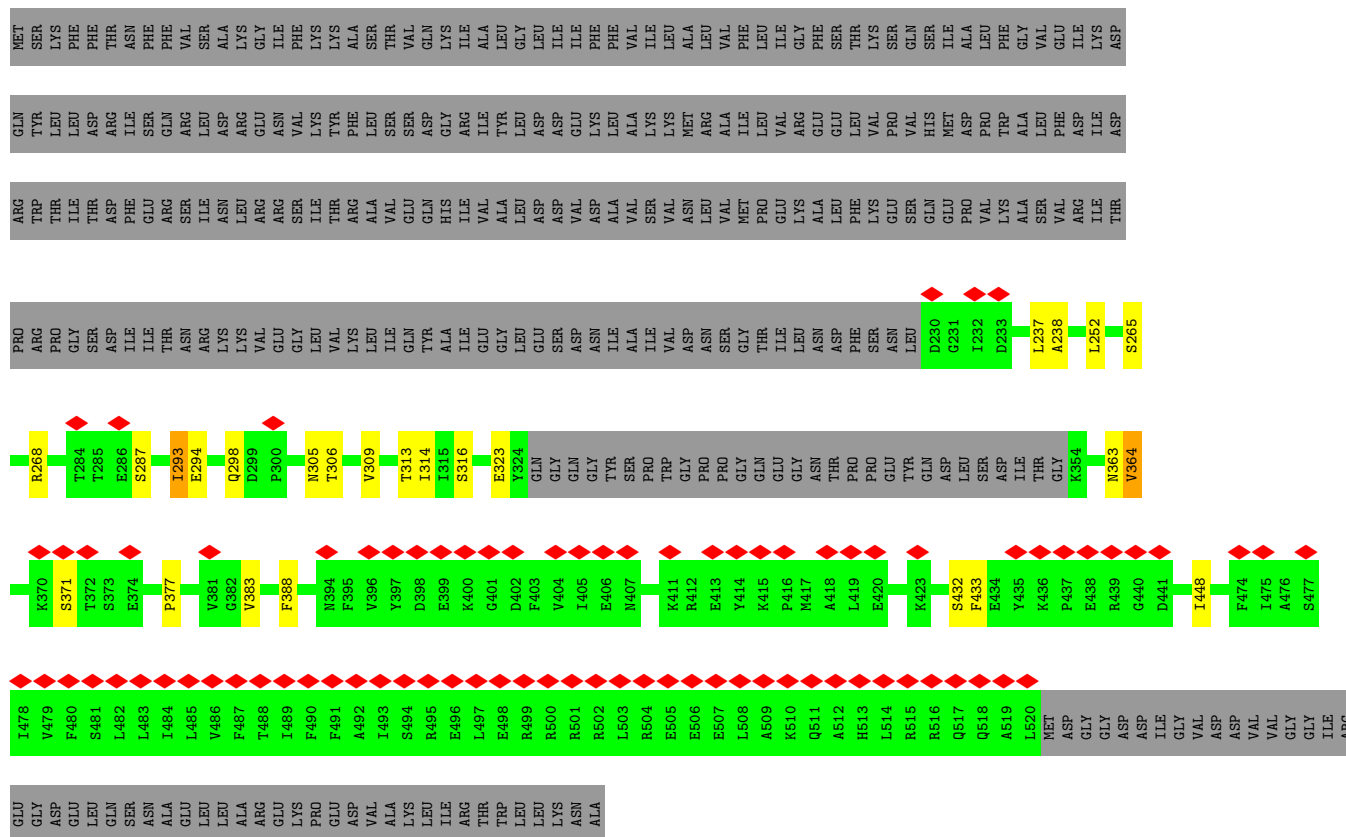




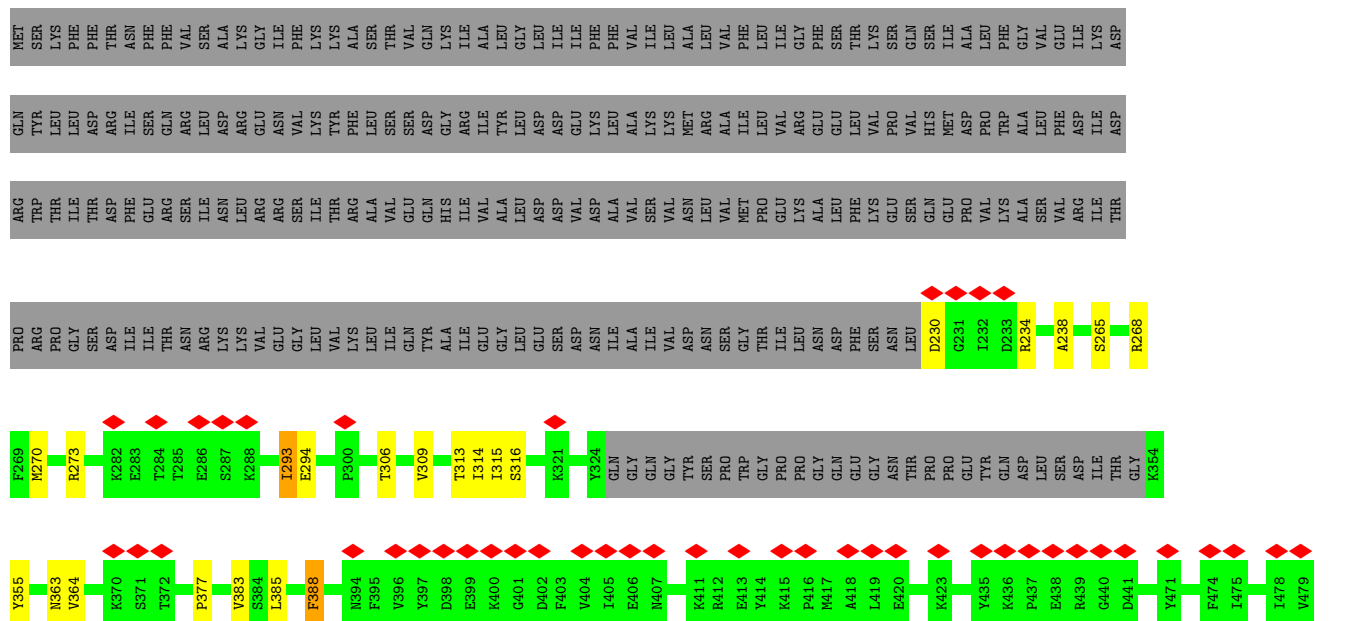
• Molecule 1: Flagellar M-ring protein

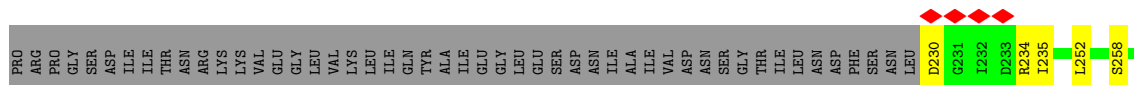


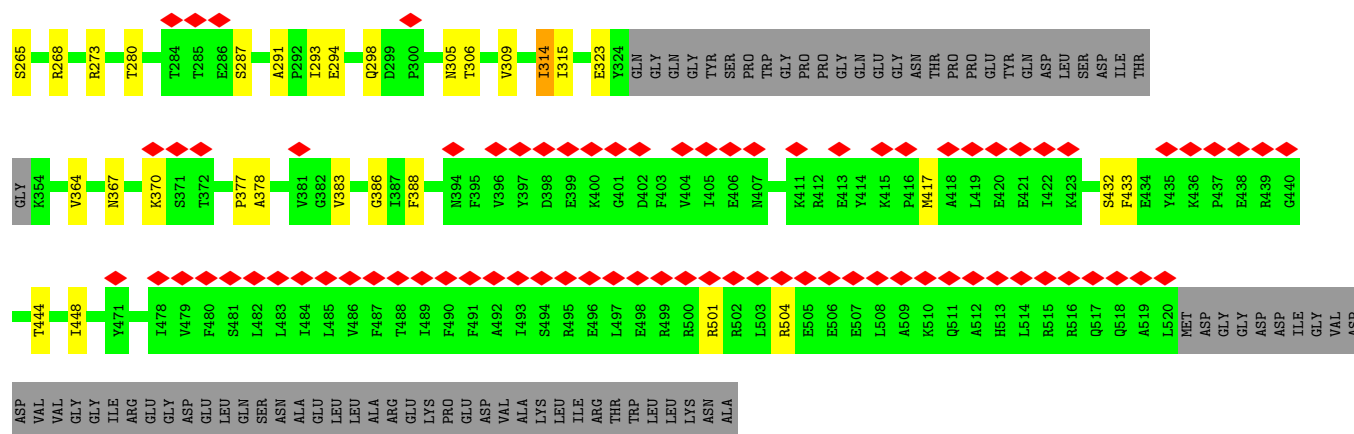
• Molecule 1: Flagellar M-ring protein



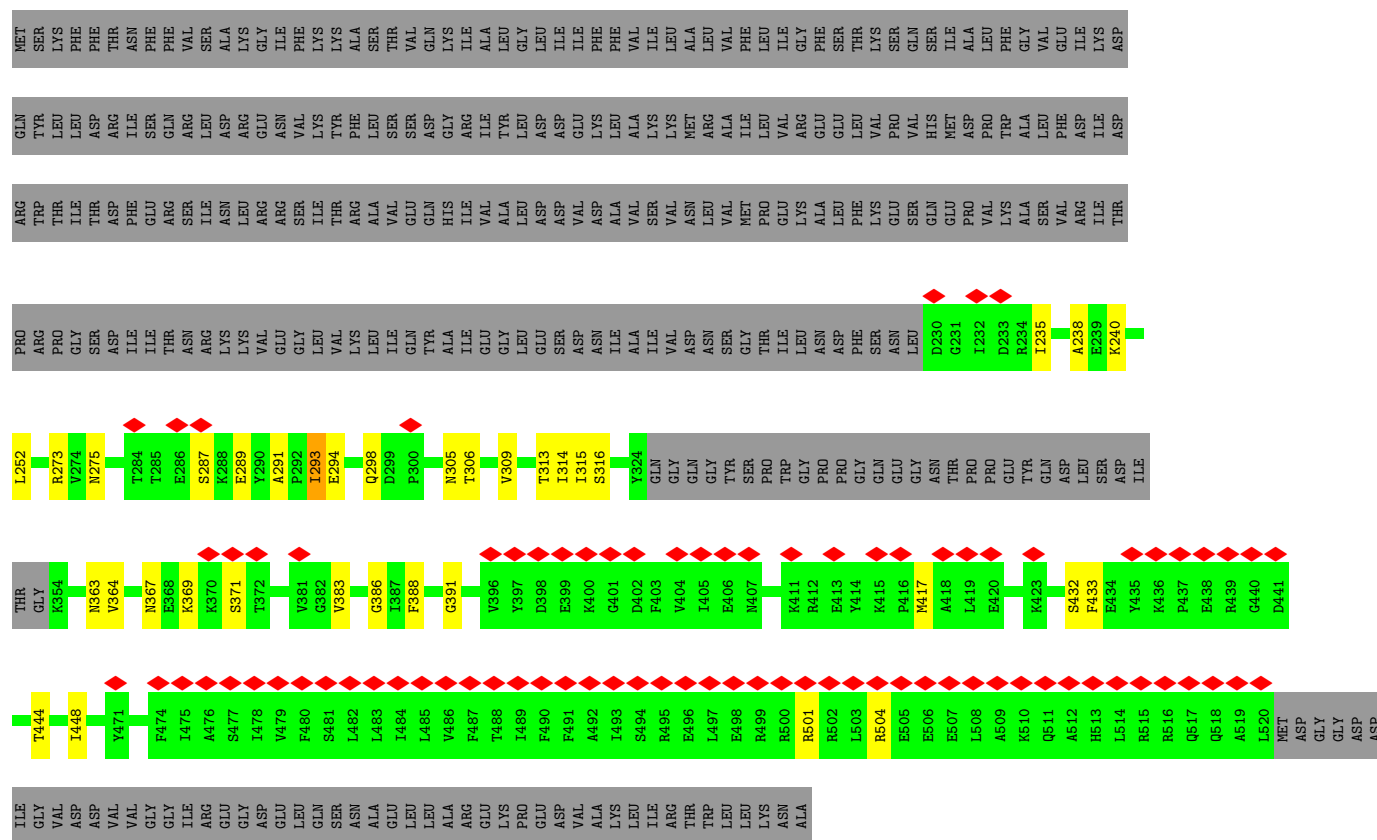
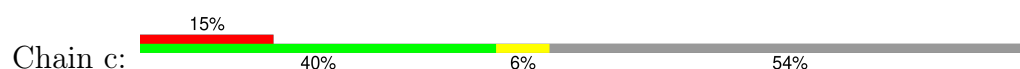
● Molecule 1: Flagellar M-ring protein



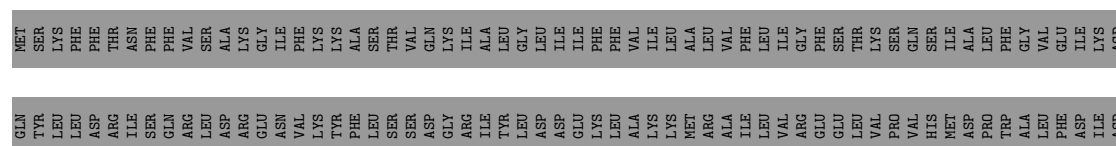
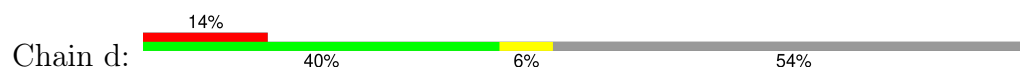


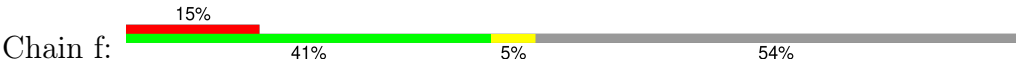


• Molecule 1: Flagellar M-ring protein



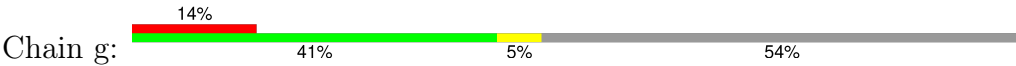
• Molecule 1: Flagellar M-ring protein



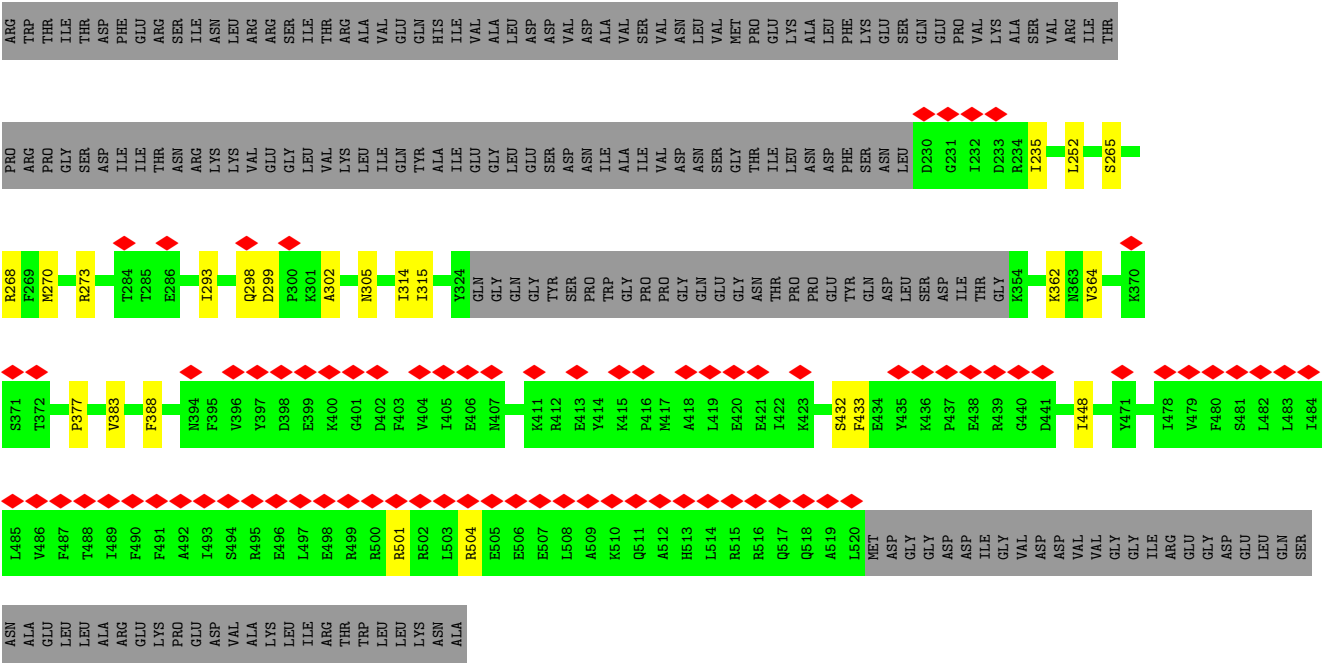


MET	GLN	ARG	PRO	S265	K370	F480	ASP
SER	TYR	TRP	ARG	R268	S371	S481	GLU
LYS	LEU	THR	PRO	R273	T372	L482	LEU
PHE	LEU	ILE	GLY	T273	P377	L483	GLN
THR	ASP	THR	SER	T284	V383	I484	ASN
ASN	ARG	PHE	ASP	T285	S384	L485	ALA
PHE	ILE	GLU	ILE	E286	V385	V486	GLU
PHE	SER	GLN	THR	I293	L386	F487	LEU
VAL	ARG	VAL	ASN	E294	G386	F488	LEU
SER	LEU	ILE	ARG	P300	I387	I488	ALA
LEU	ASP	ASN	LYS	E294	F388	T489	GLU
ALA	LEU	ASN	VAL	P300	N394	F490	LYS
LYS	GLU	LEU	VAL	T306	F395	F491	PRO
GLY	ASN	ILE	GLY	V309	V396	A492	GLU
ILE	VAL	PHE	LEU	T313	Y397	I493	ASP
PHE	THR	ALA	LYS	I314	D398	A494	VAL
SER	ARG	ALA	LEU	I315	E399	S494	LYS
THR	LEU	VAL	ILE	S316	K400	R495	LEU
THR	SER	VAL	GLN	Y324	G401	E496	LEU
GLN	GLU	GLN	TYR	GLN	D402	L497	ILE
ASP	ASP	ASP	ALA	GLY	F403	E498	ARG
ILE	ILE	VAL	ILE	TYR	V404	R499	THR
ILE	GLY	VAL	ILE	PRO	I405	R500	LEU
PHE	LEU	ALA	GLY	ASN	E406	R501	LEU
PHE	GLY	VAL	GLN	SER	M407	R502	LYS
VAL	ASP	VAL	GLY	PRO	K411	L503	ASN
ILE	GLY	VAL	ASN	TRP	R412	R504	ALA
VAL	ASP	VAL	ASN	ILE	E413	E506	
ALA	ALA	VAL	ILE	TRP	E414	E507	
LEU	LYS	VAL	VAL	PRO	K415	L508	
LEU	ASN	VAL	ASP	PRO	P416	K510	
VAL	ASN	LEU	ASN	GLY	M417	Q511	
VAL	ASP	LEU	SER	GLY	A418	A512	
VAL	ASP	LEU	ASN	THR	L419	H513	
VAL	ASP	LEU	ASN	PRO	E420	L514	
VAL	ASP	LEU	ASN	PRO	E421	R515	
VAL	ASP	LEU	ASN	PRO	I422	R516	
VAL	ASP	LEU	ASN	PRO	K423	Q517	
VAL	ASP	LEU	ASN	PRO	N424	Q518	
VAL	ASP	LEU	ASN	PRO	F433	A519	
VAL	ASP	LEU	ASN	PRO	K436	L520	
VAL	ASP	LEU	ASN	PRO	P437	MET	
VAL	ASP	LEU	ASN	PRO	E438	ASP	
VAL	ASP	LEU	ASN	PRO	R439	GLY	
VAL	ASP	LEU	ASN	PRO	G440	ASP	
VAL	ASP	LEU	ASN	PRO	D441	ILE	
VAL	ASP	LEU	ASN	PRO	T444	GLY	
VAL	ASP	LEU	ASN	PRO	I448	VAL	
VAL	ASP	LEU	ASN	PRO	Y471	GLY	
VAL	ASP	LEU	ASN	PRO	I478	ILE	
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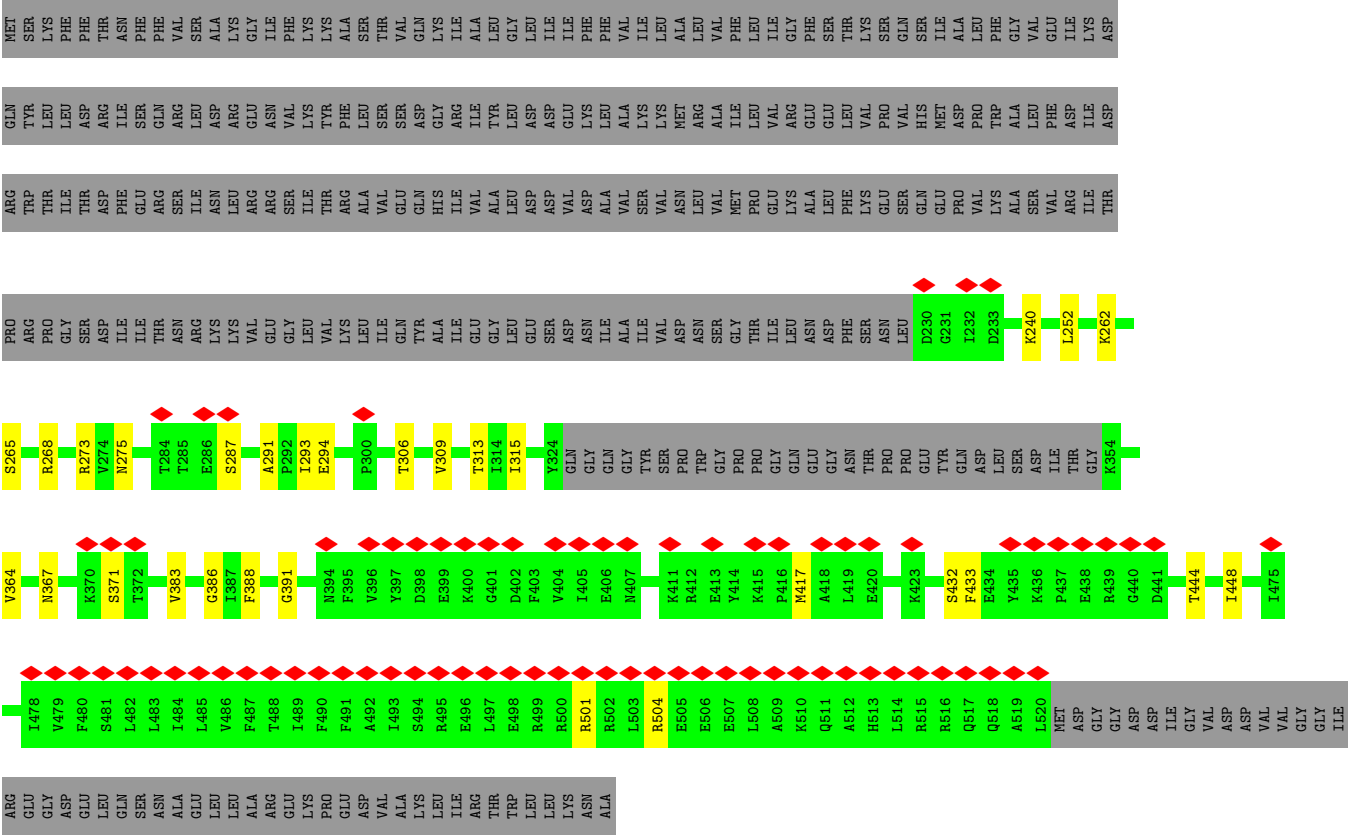
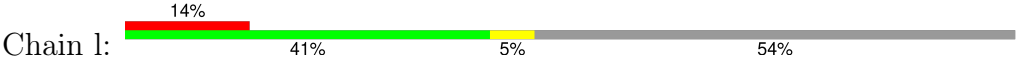
● Molecule 1: Flagellar M-ring protein



MET	GLN	ARG	PRO	L252	K369	F423	ASP
SER	TYR	TRP	ARG	S265	K370	S432	GLU
PHE	LEU	THR	PRO	R268	S371	F433	LEU
PHE	LEU	ILE	GLY	R273	T372	K436	GLY
ASN	ASP	THR	SER	T273	P377	P437	THR
PHE	ILE	PHE	ILE	T284	V383	E438	VAL
PHE	SER	GLU	THR	T285	G382	R439	GLU
VAL	ARG	VAL	ASN	E286	V383	G440	ILE
SER	LEU	ILE	ARG	E289	L385	D441	ILE
ALA	ASP	ALA	LYS	Q298	I387	T444	VAL
LYS	ARG	VAL	VAL	D299	F388	I448	ASP
GLY	GLU	THR	VAL	P300	N394	Y471	
ILE	ASN	ILE	GLY	T306	F395		
LYS	VAL	LYS	LEU	I314	V396		
VAL	PHE	ALA	LYS	I315	Y397		
ALA	SER	VAL	ILE	S316	D398		
SER	LEU	VAL	ALA	Y324	E399		
THR	SER	VAL	GLN	GLN	K400		
THR	VAL	VAL	GLN	TYR	G401		
THR	VAL	VAL	ASP	GLY	D402		
THR	VAL	VAL	ASP	GLY	F403		
THR	VAL	VAL	ASP	TYR	V404		
THR	VAL	VAL	ASP	ILE	I405		
THR	VAL	VAL	ASP	ILE	E406		
THR	VAL	VAL	ASP	ILE	M407		
THR	VAL	VAL	ASP	ILE	K411		
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THR	VAL	VAL	ASP	ILE	S432		
THR	VAL	VAL	ASP	ILE	F433		
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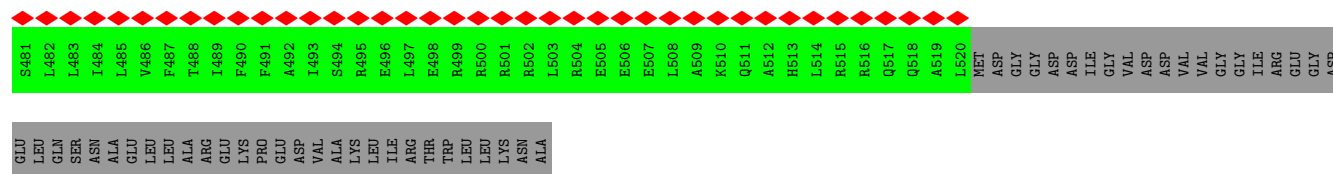


• Molecule 1: Flagellar M-ring protein

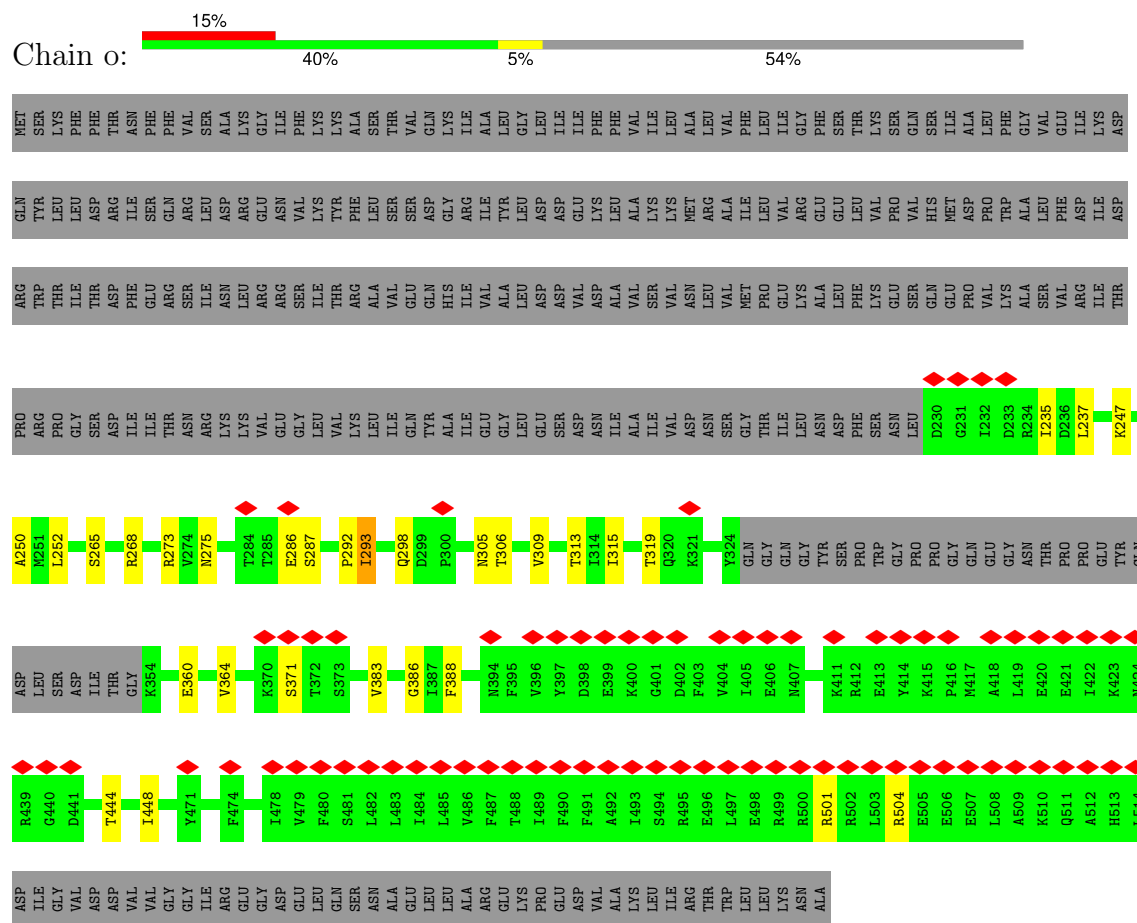


• Molecule 1: Flagellar M-ring protein

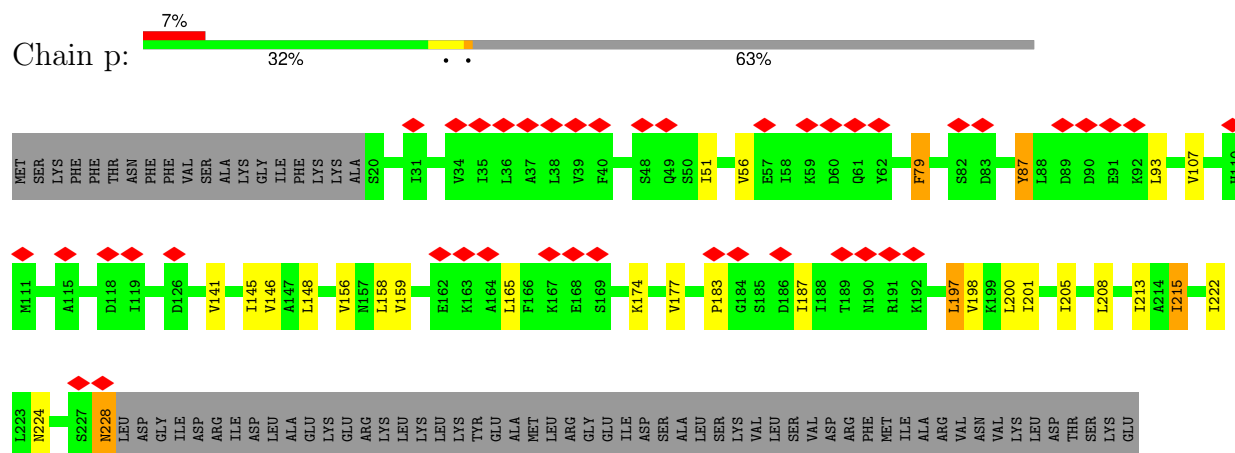




• Molecule 1: Flagellar M-ring protein

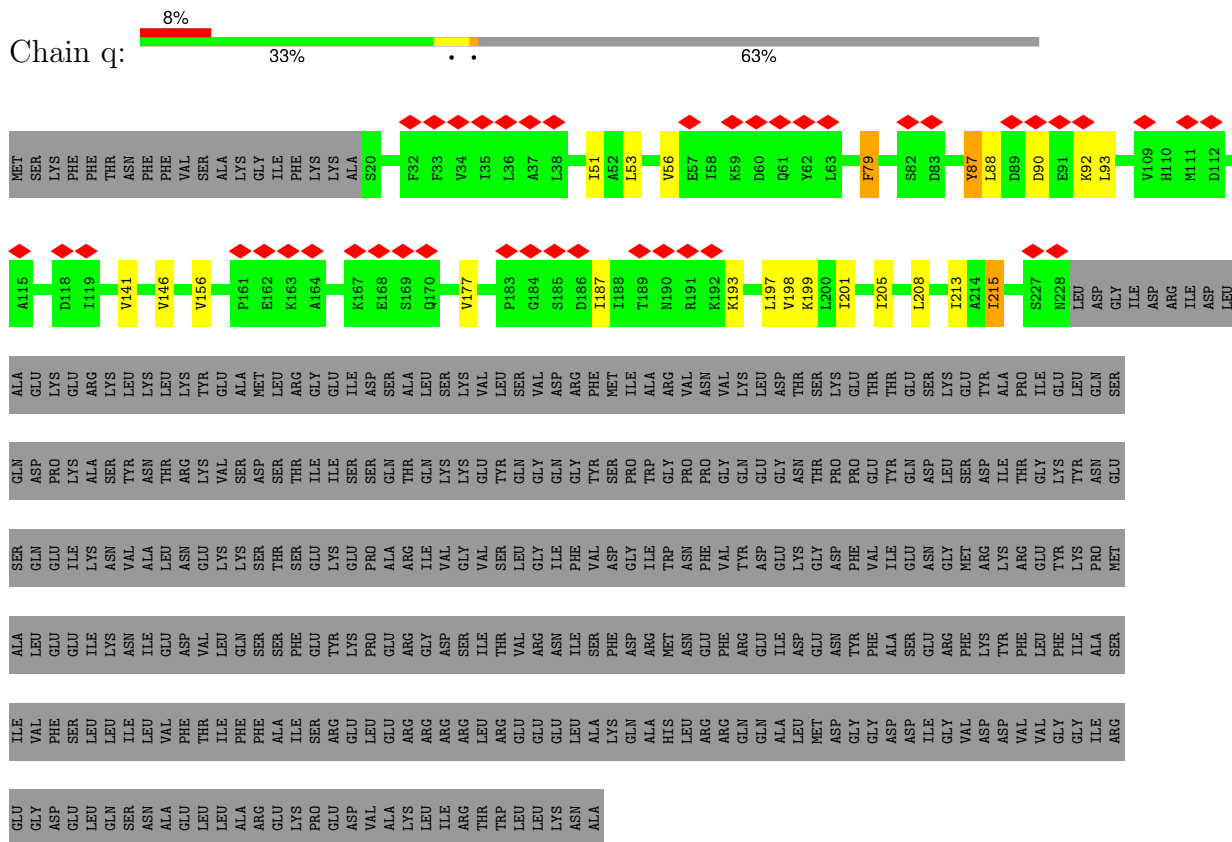


• Molecule 1: Flagellar M-ring protein

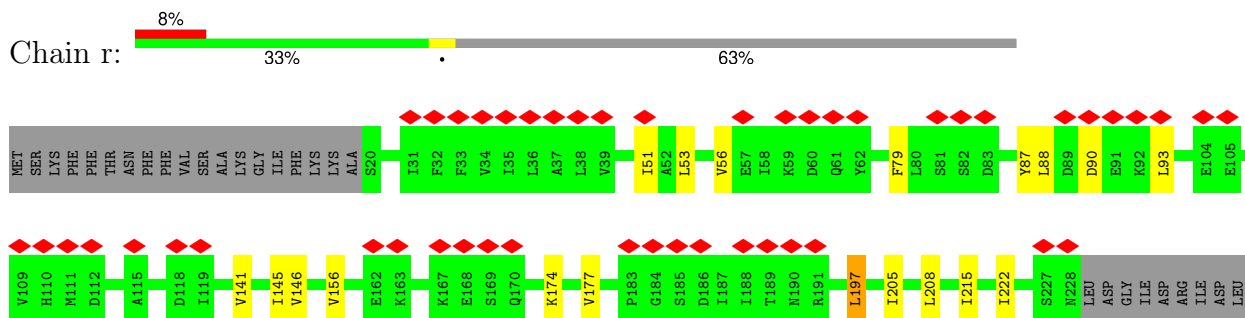


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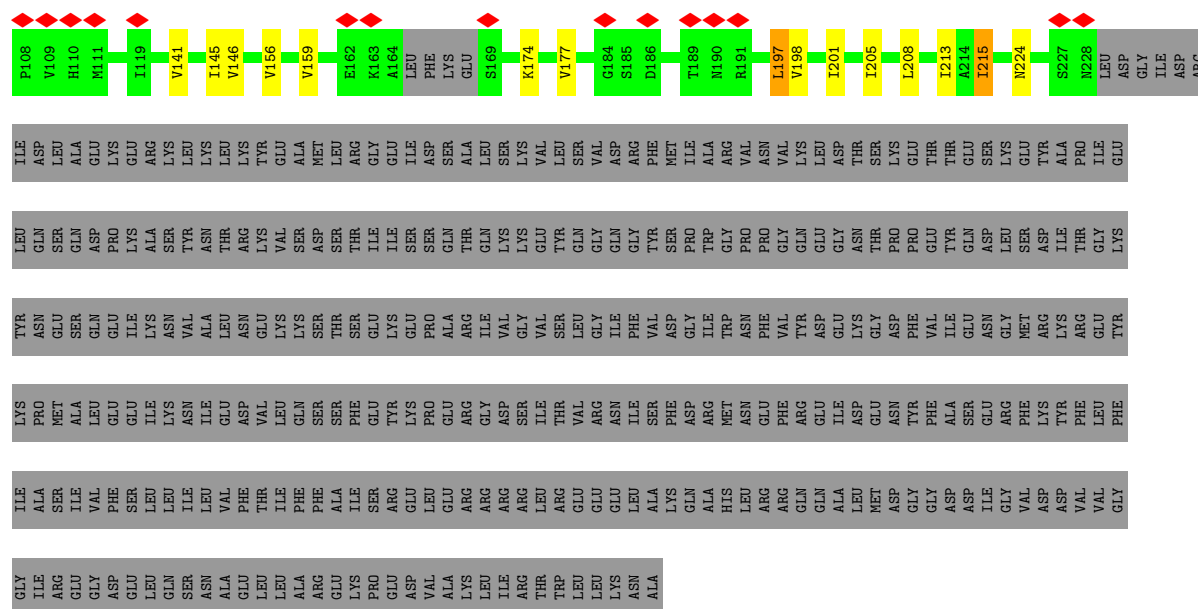
- Molecule 1: Flagellar M-ring protein



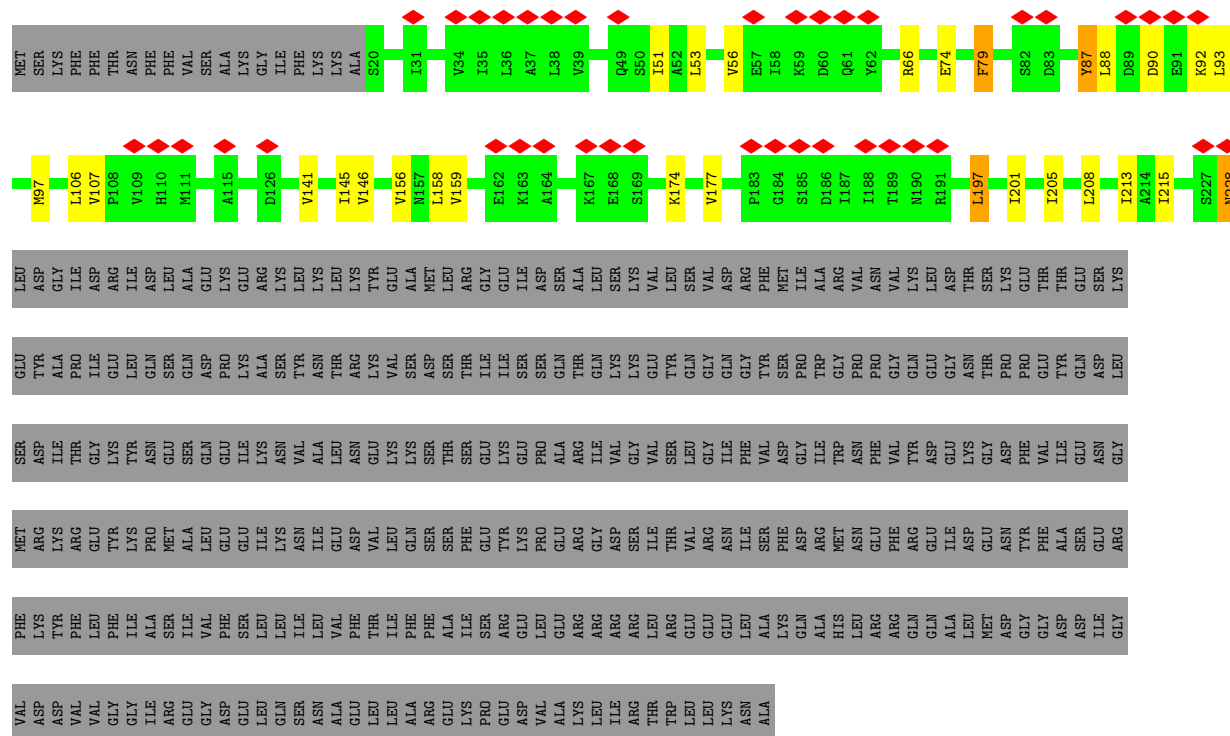
- Molecule 1: Flagellar M-ring protein



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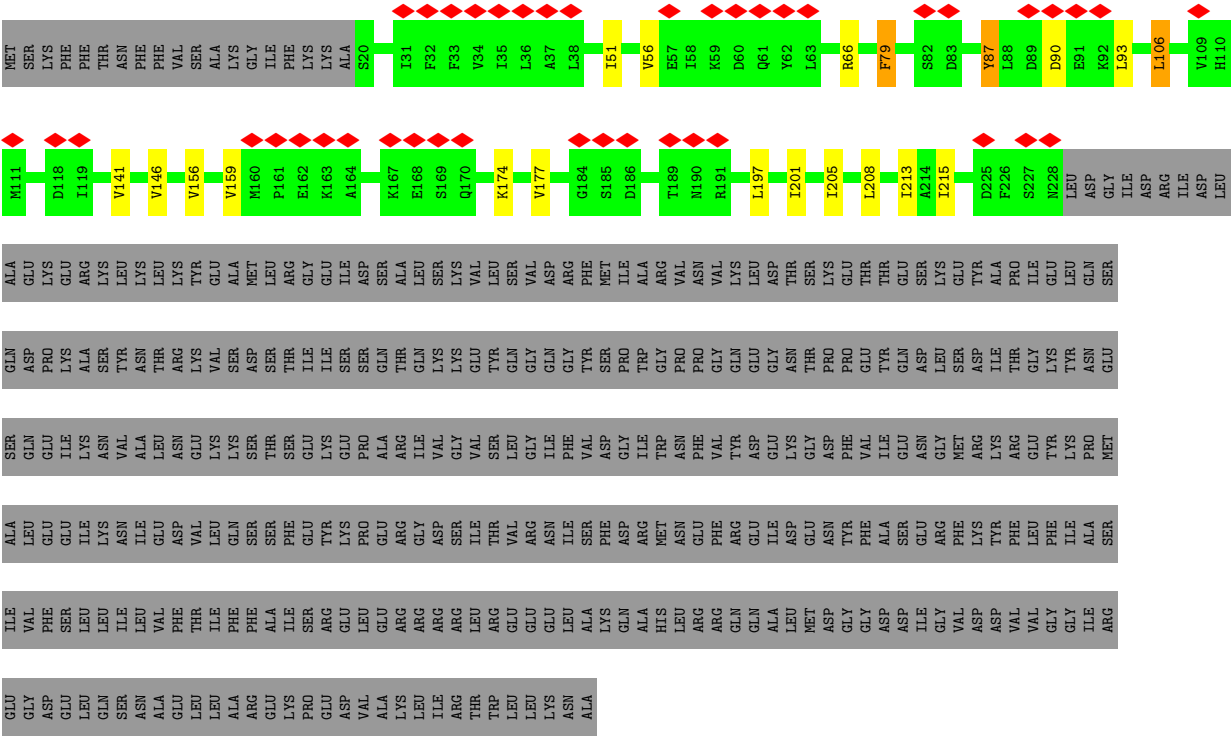


• Molecule 1: Flagellar M-ring protein

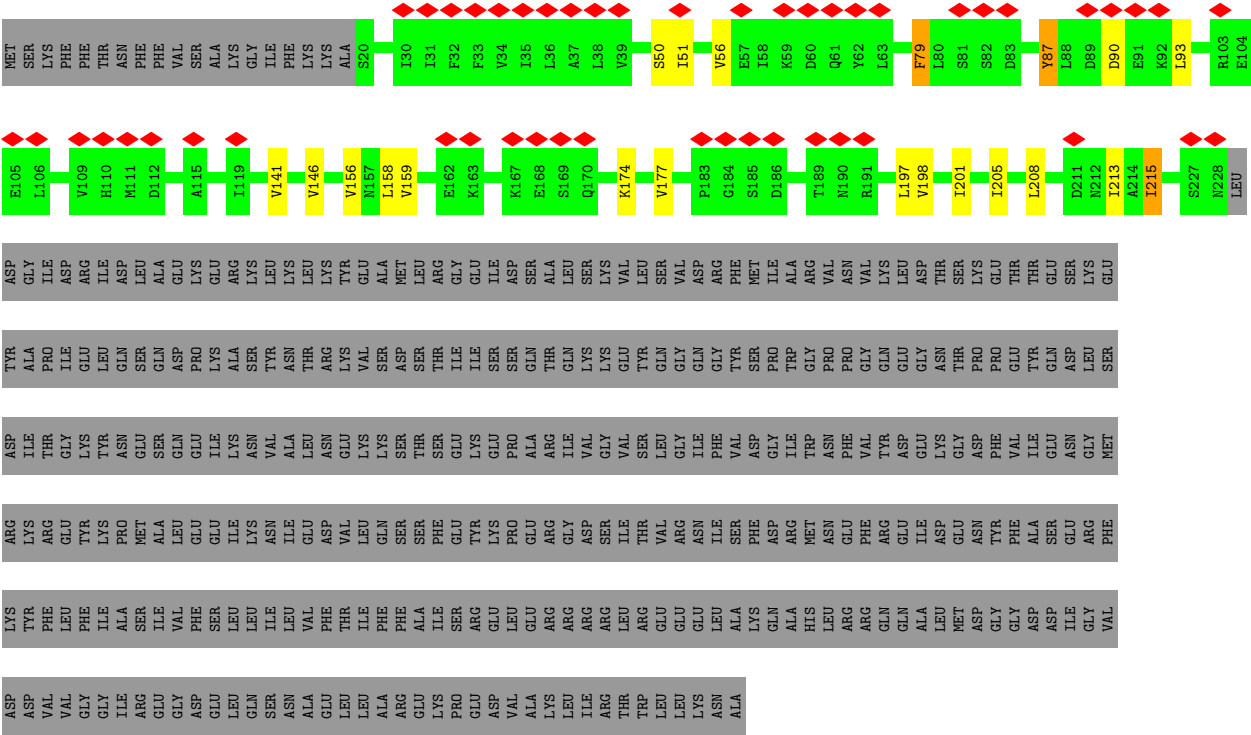


• Molecule 1: Flagellar M-ring protein

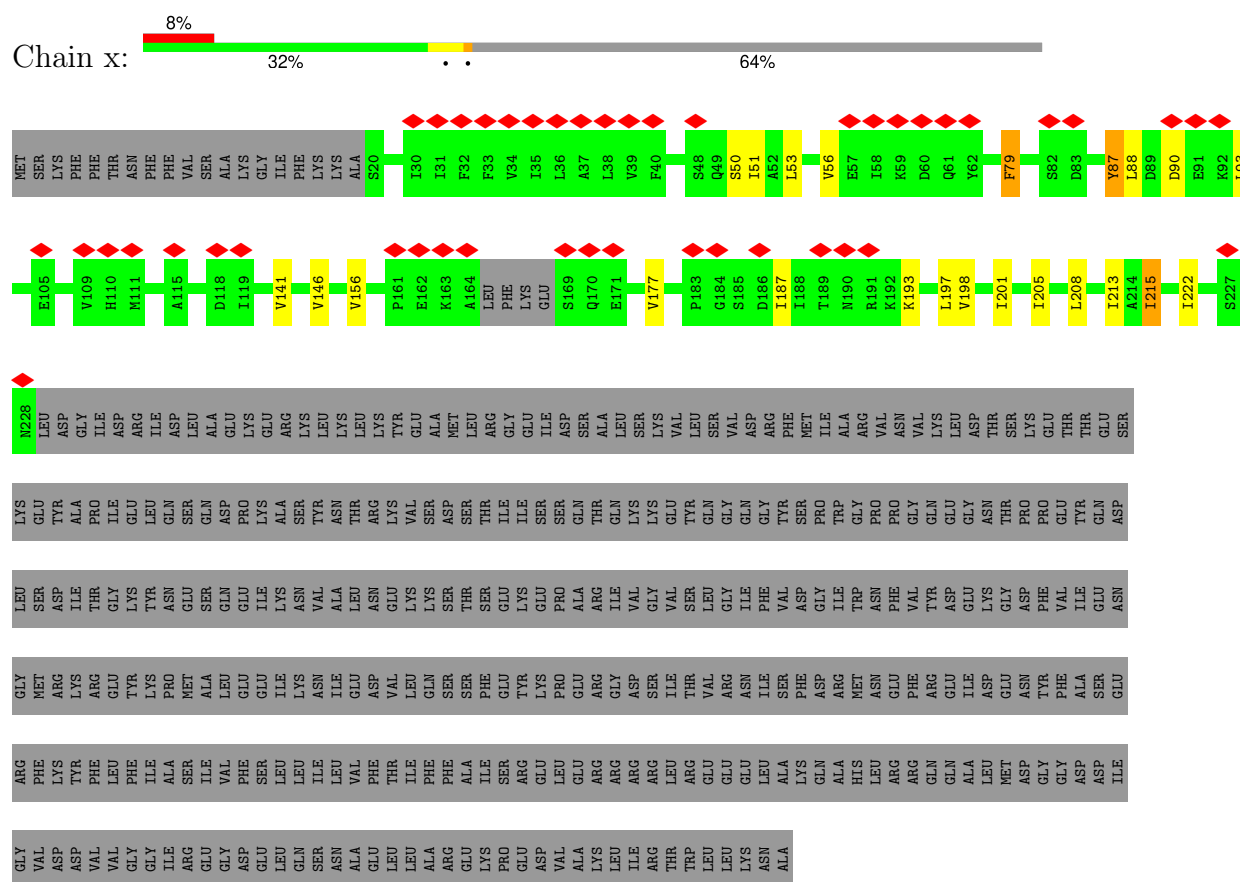




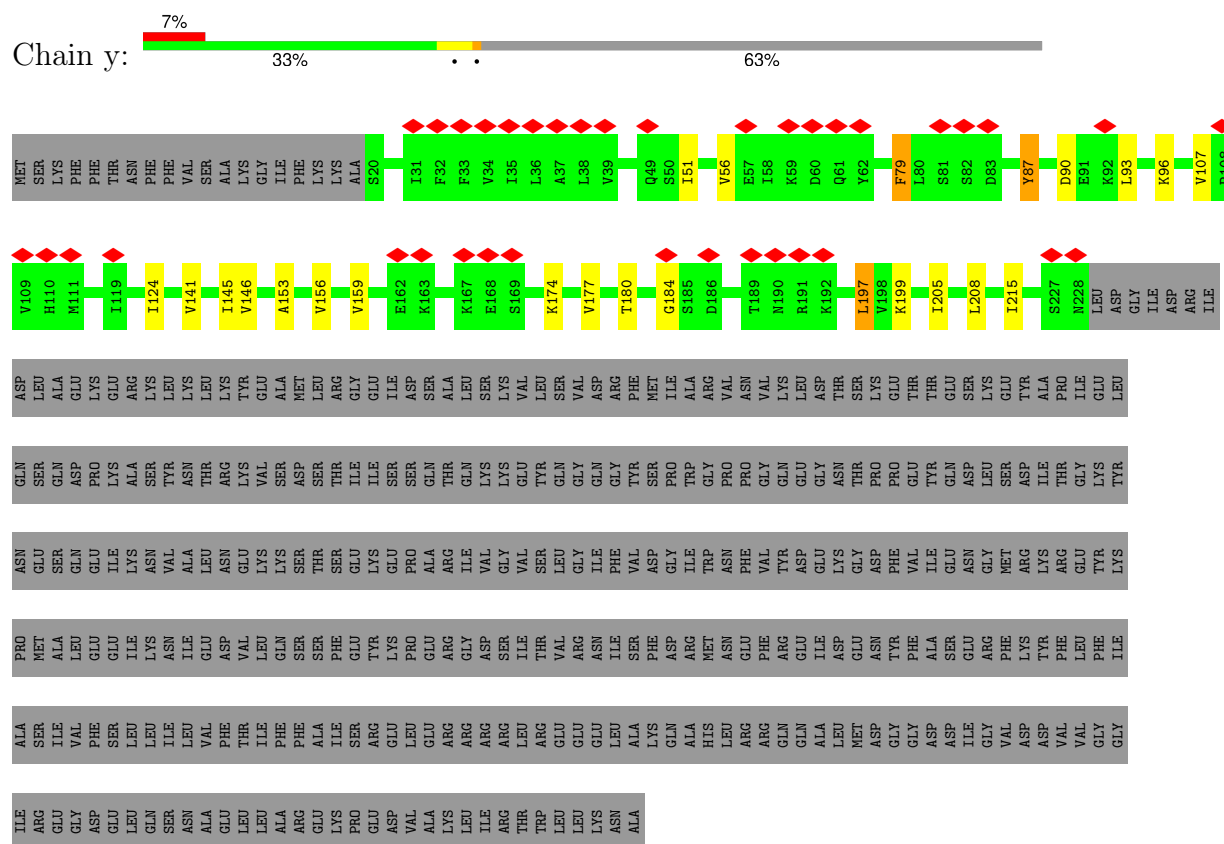
● Molecule 1: Flagellar M-ring protein



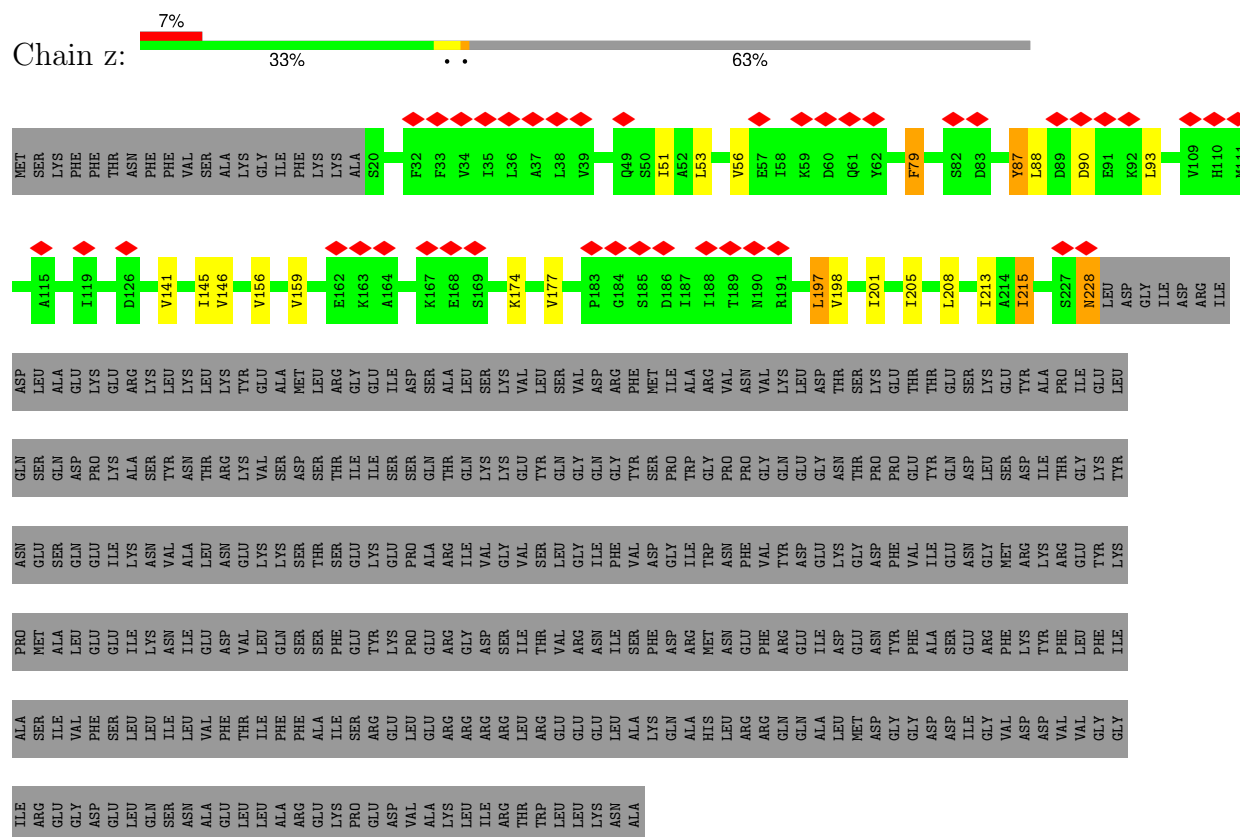
● Molecule 1: Flagellar M-ring protein



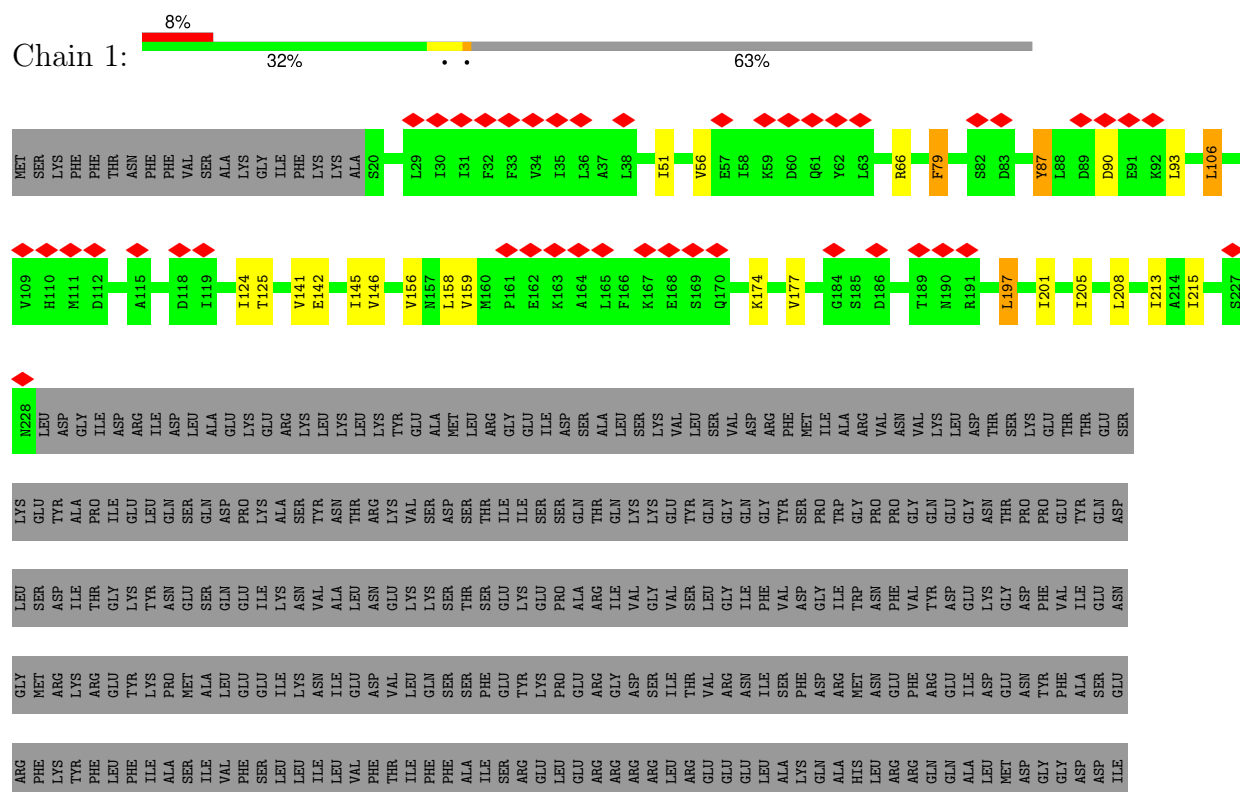
• Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein

[illegible]

- Molecule 1: Flagellar M-ring protein

[illegible]

PHE	ILE	ALA	SER	ILE	VAL	PHE	SER	LEU	LEU	LEU	VAL	PHE	THR	ILE	PHE	ALA	ALA	ILE	ILE	PRO	SER	GLU	GLU	VAL	LEU	ALA	LYS	GLN	ALA	LYS	GLN	HIS	LEU	ARG	ARG	GLN	ALA	LEU	LEU	MET	ASP	GLY	GLY	ASP	ASP	ASP	ILE	GLY	VAL	ASP	VAL	VAL
GLY	GLY	ILE	ARG	GLY	GLY	ASP	GLU	GLN	GLN	ASN	ALA	GLY	ILE	LEU	LEU	ALA	ARG	GLY	LYS	PRO	SER	ASP	GLU	VAL	LEU	ALA	LYS	LEU	ILE	ARG	ARG	THR	TRP	LEU	LEU	LYS	ASN	ALA														

● Molecule 1: Flagellar M-ring protein

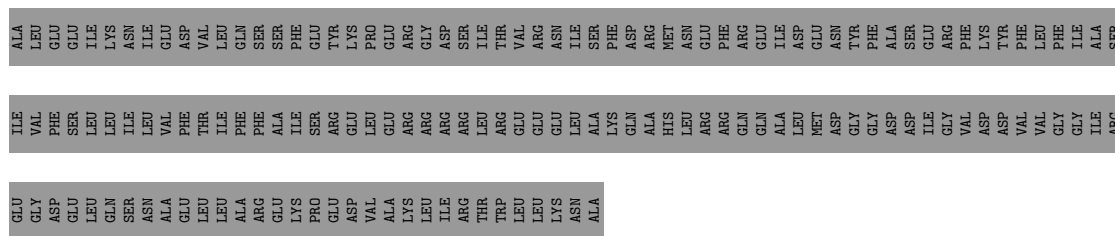


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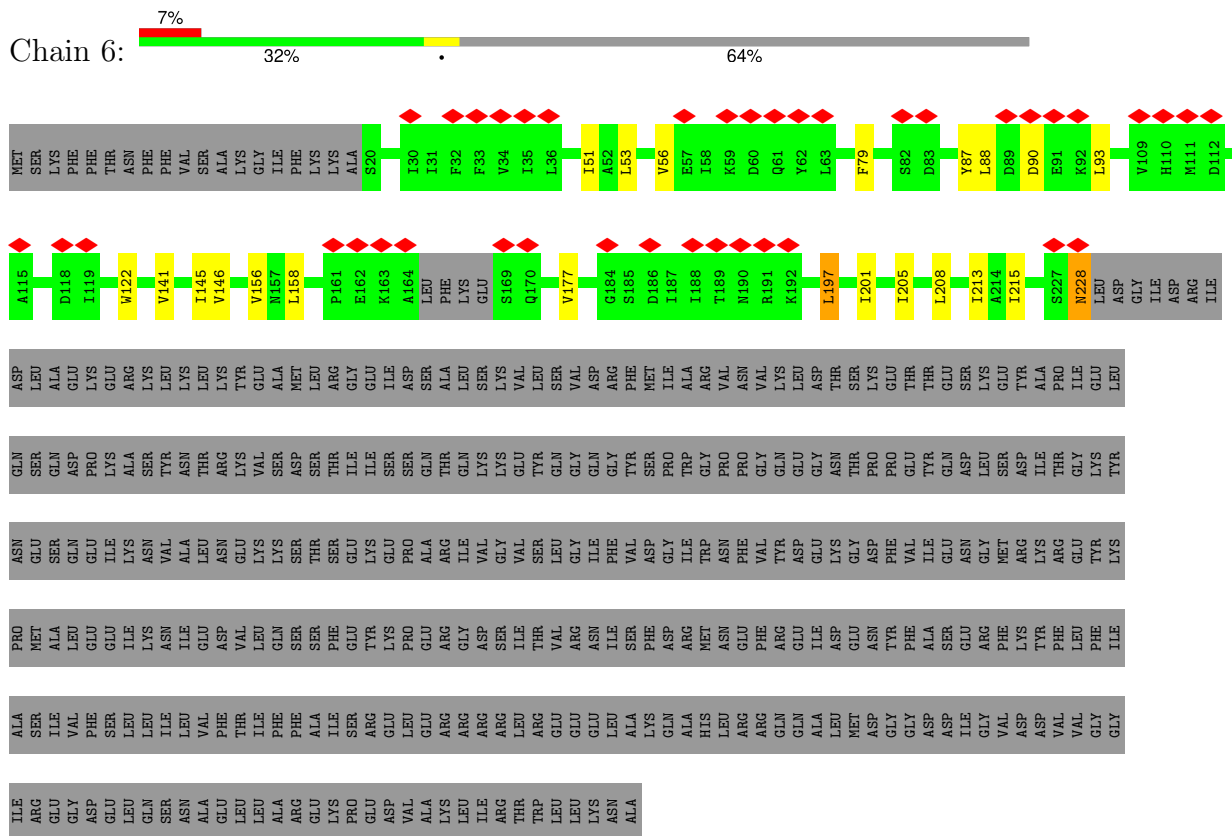
● Molecule 1: Flagellar M-ring protein



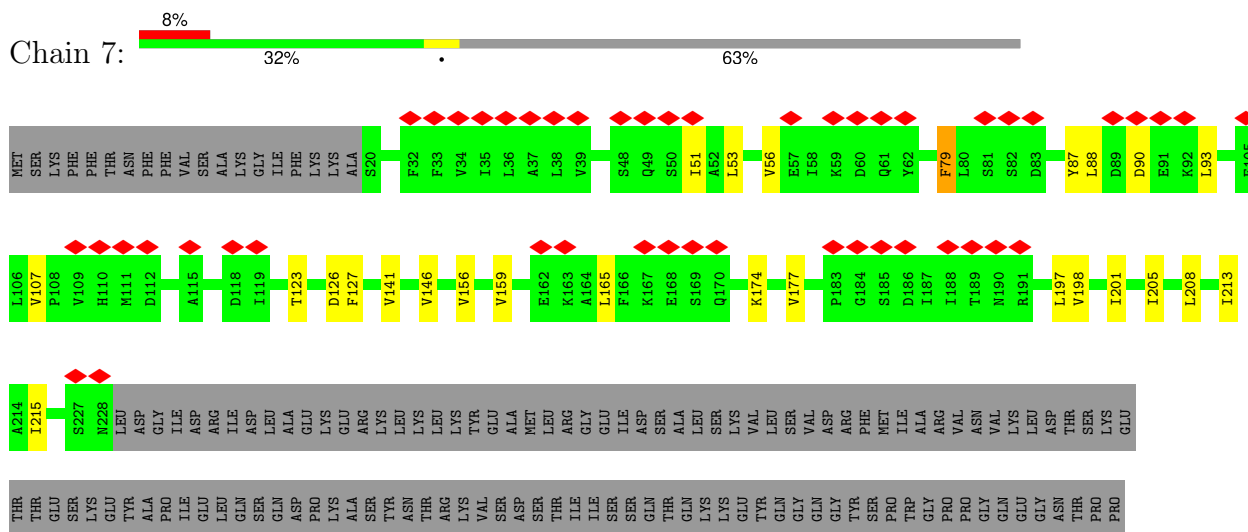
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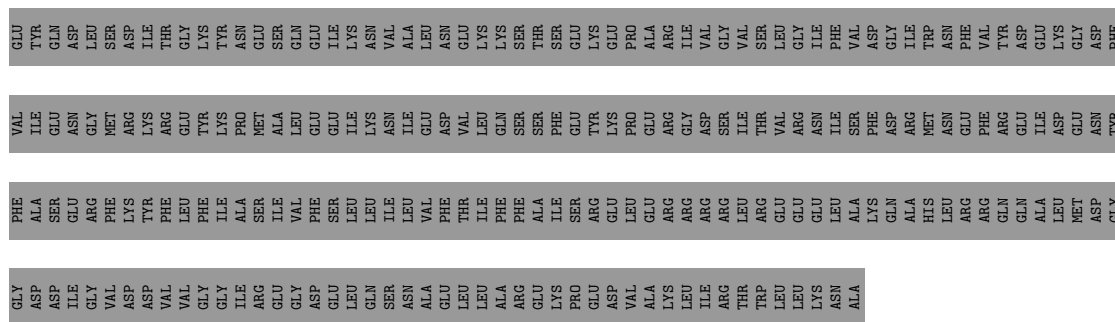


- Molecule 1: Flagellar M-ring protein

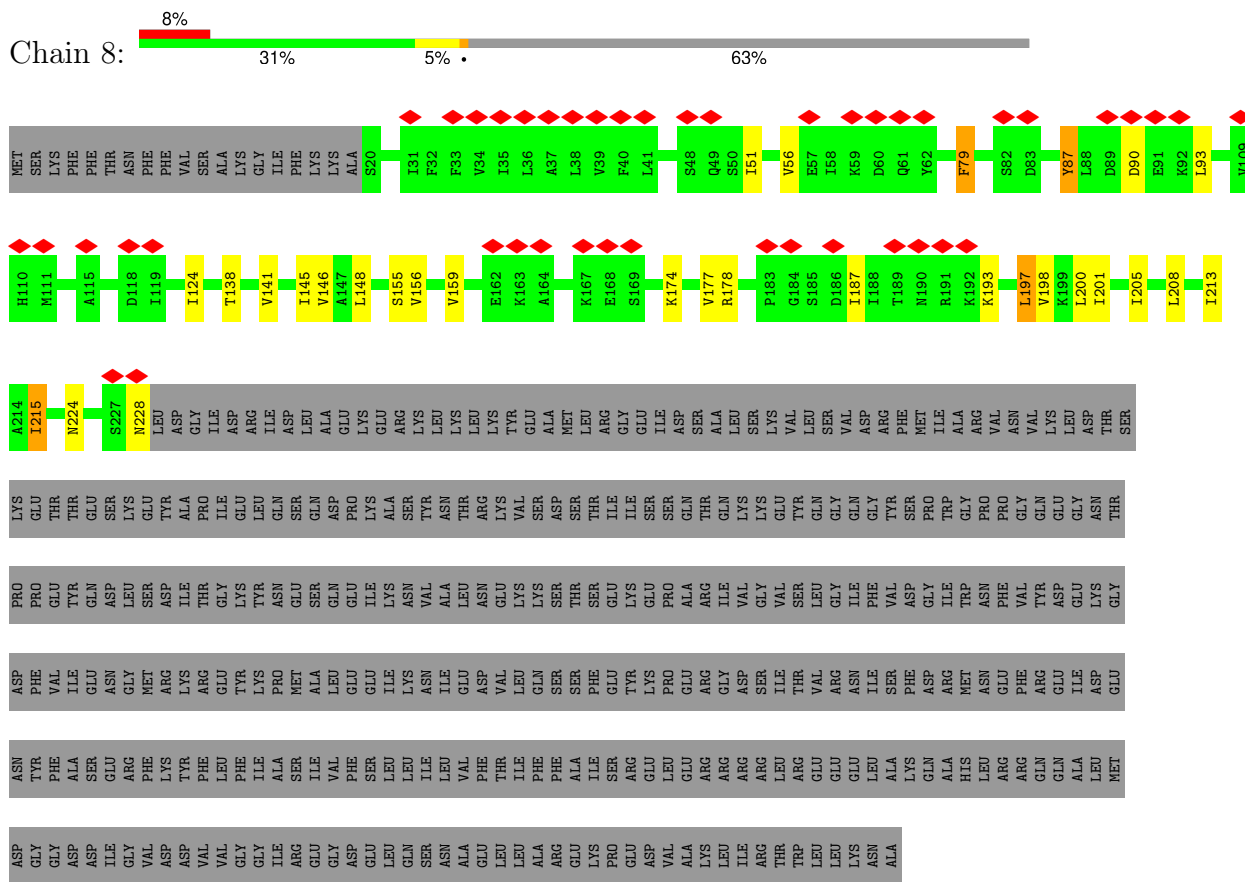


- Molecule 1: Flagellar M-ring protein

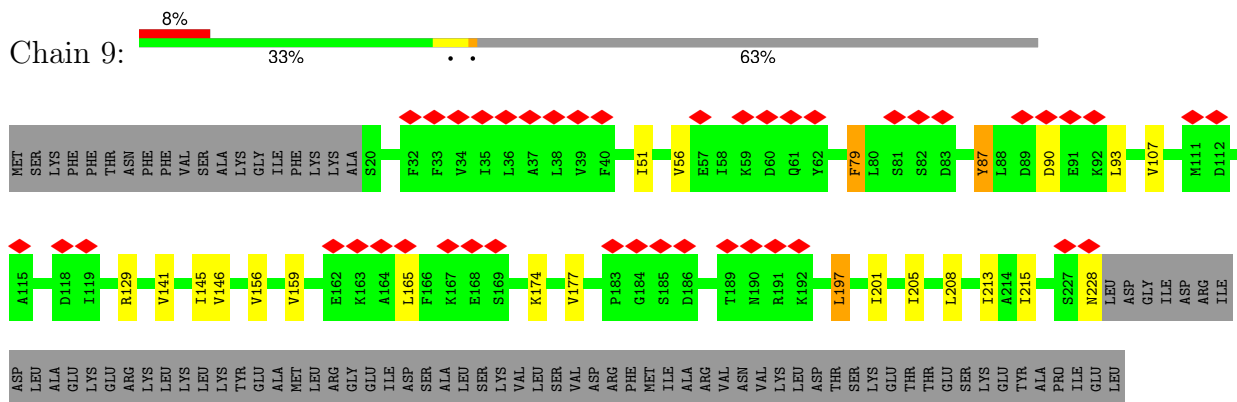


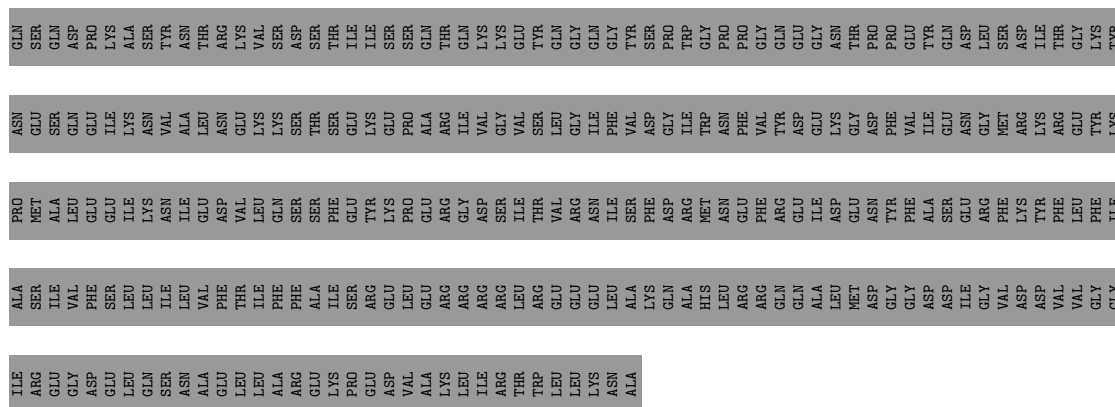


- Molecule 1: Flagellar M-ring protein

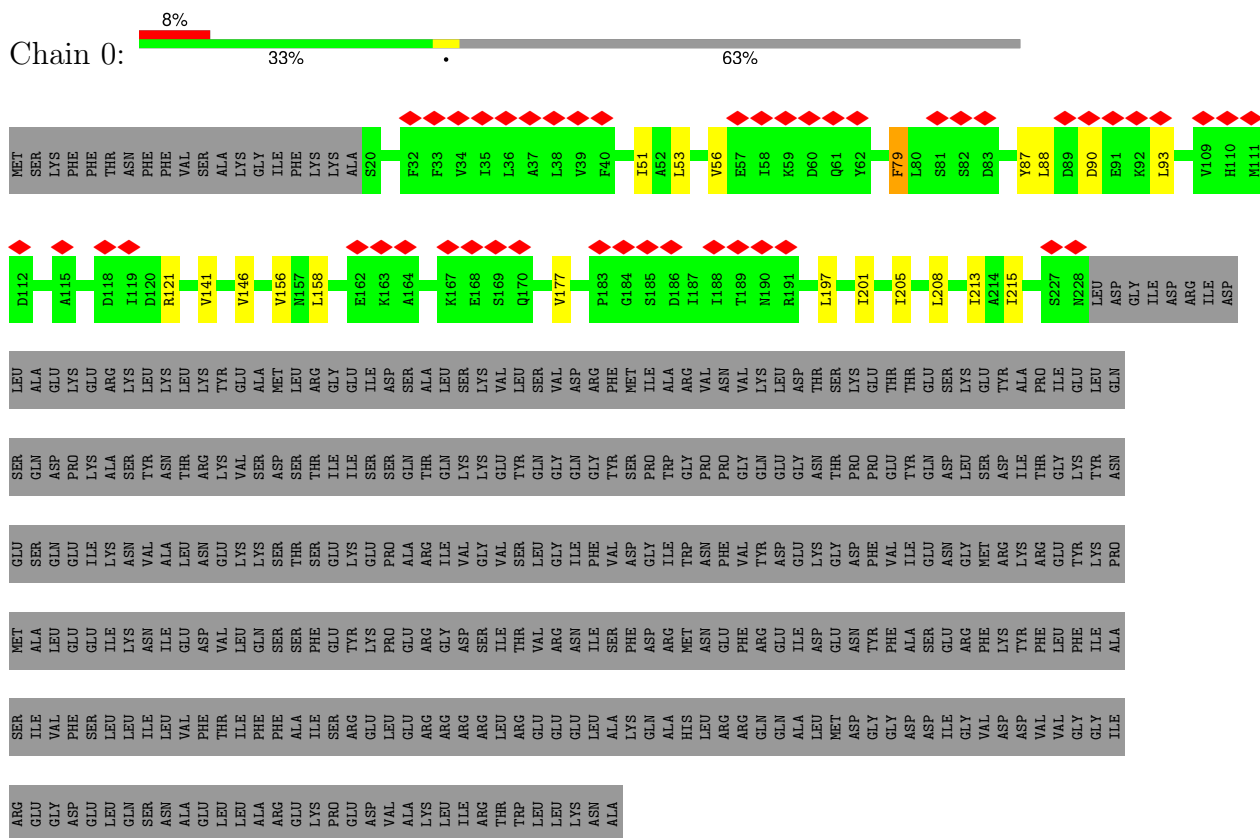


- Molecule 1: Flagellar M-ring protein

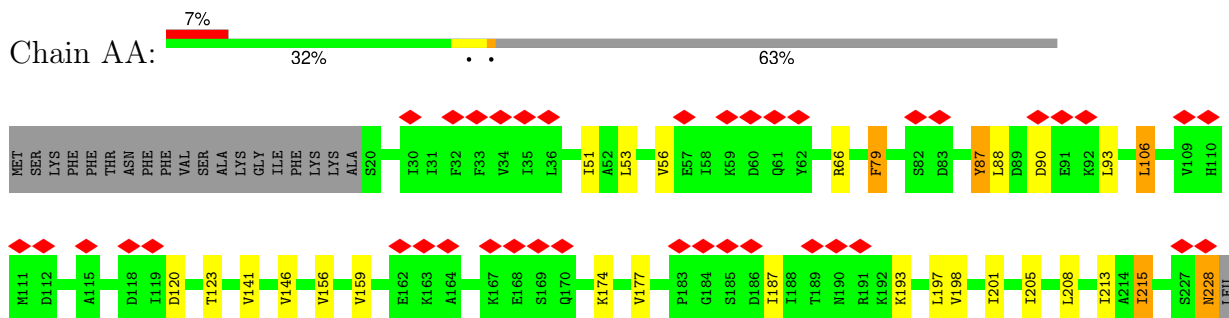


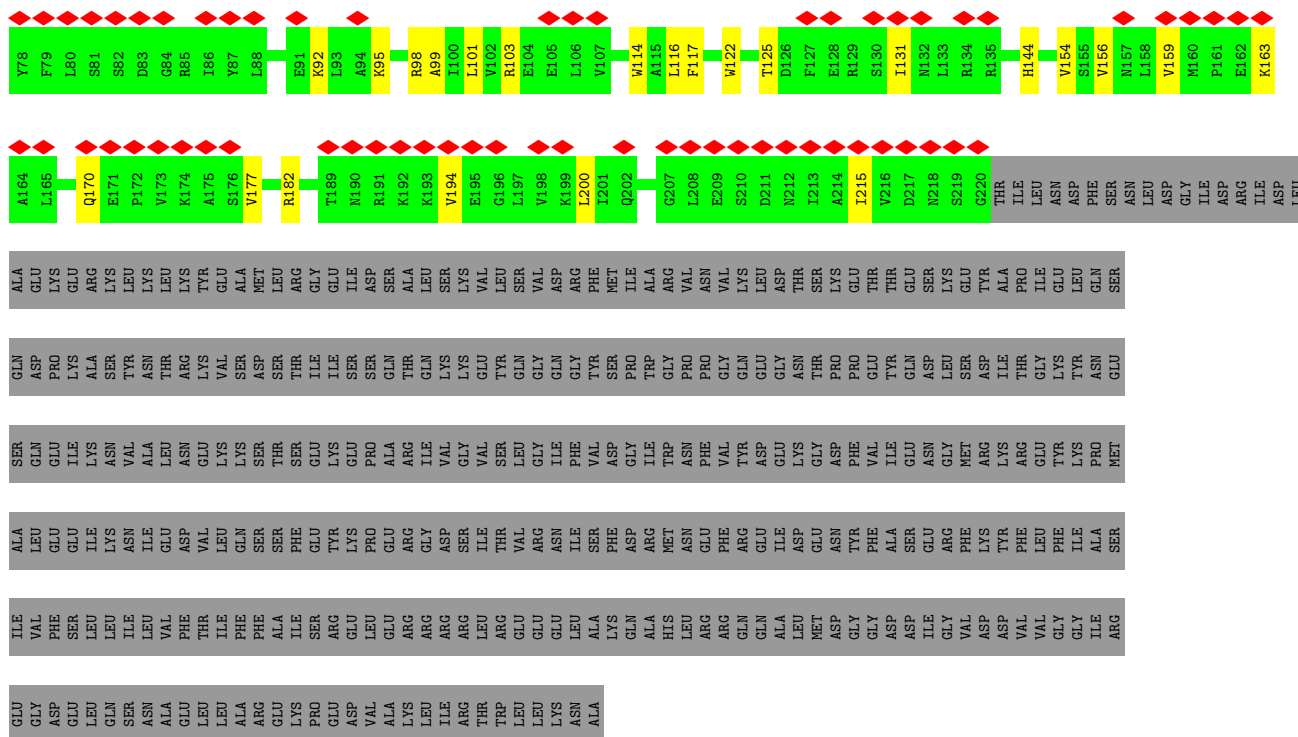


- Molecule 1: Flagellar M-ring protein

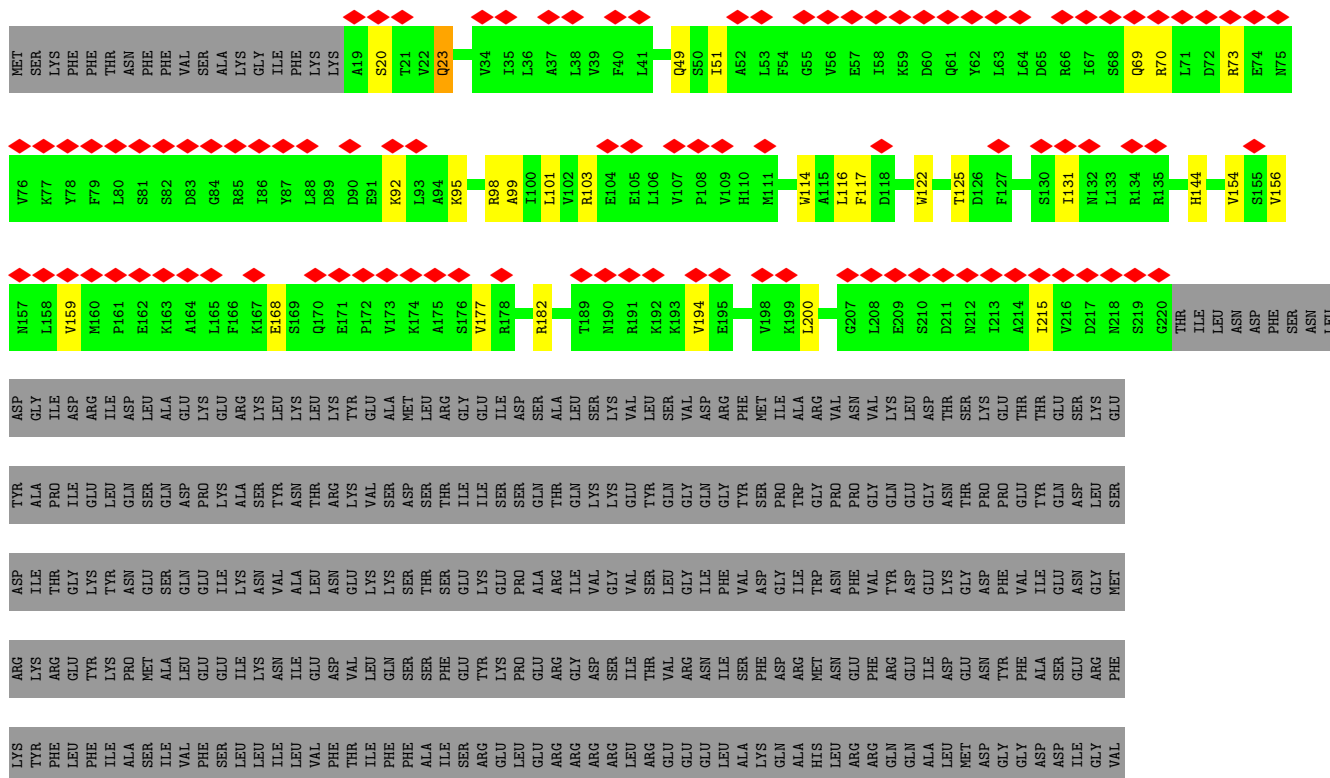


- Molecule 1: Flagellar M-ring protein

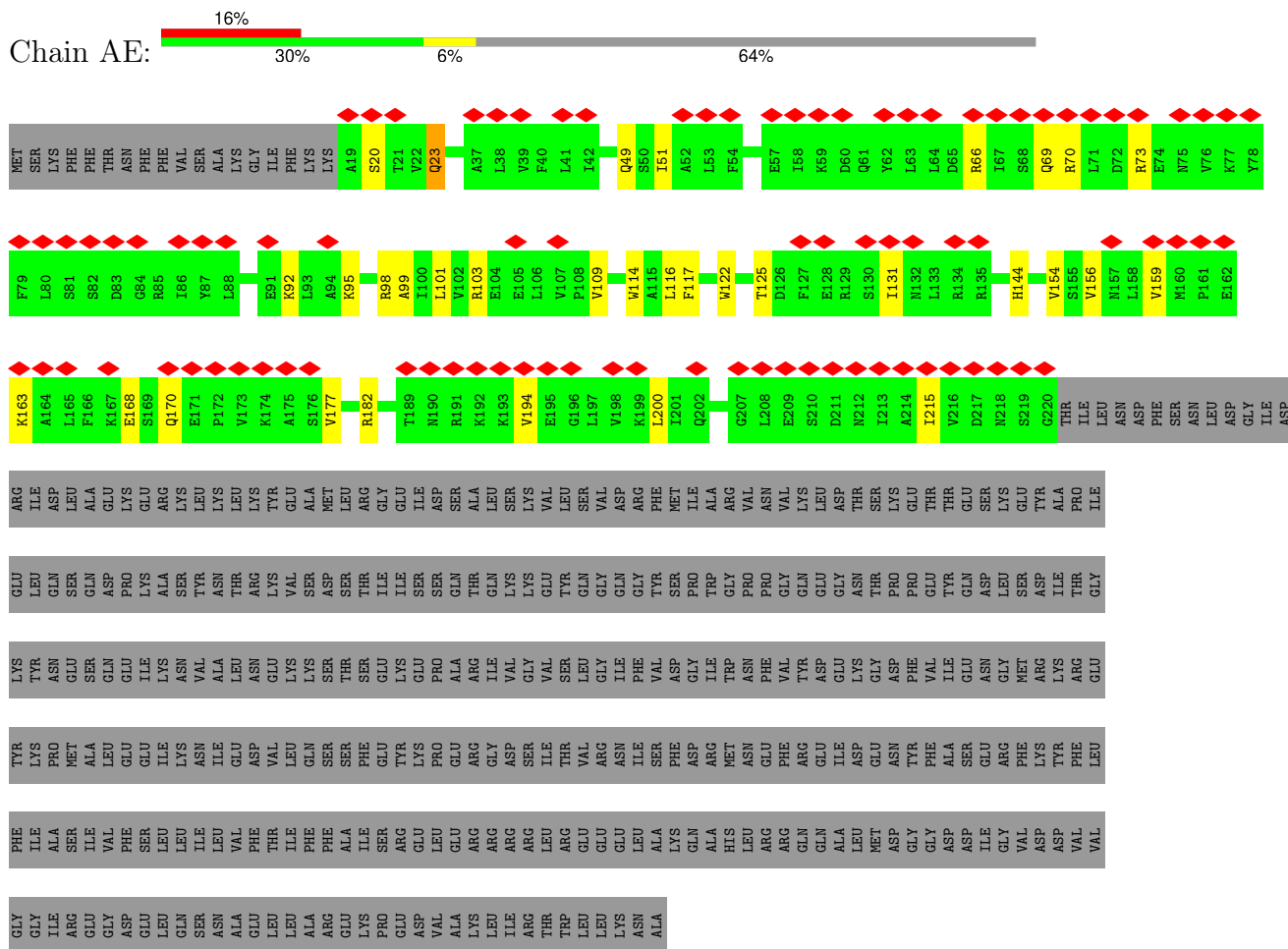




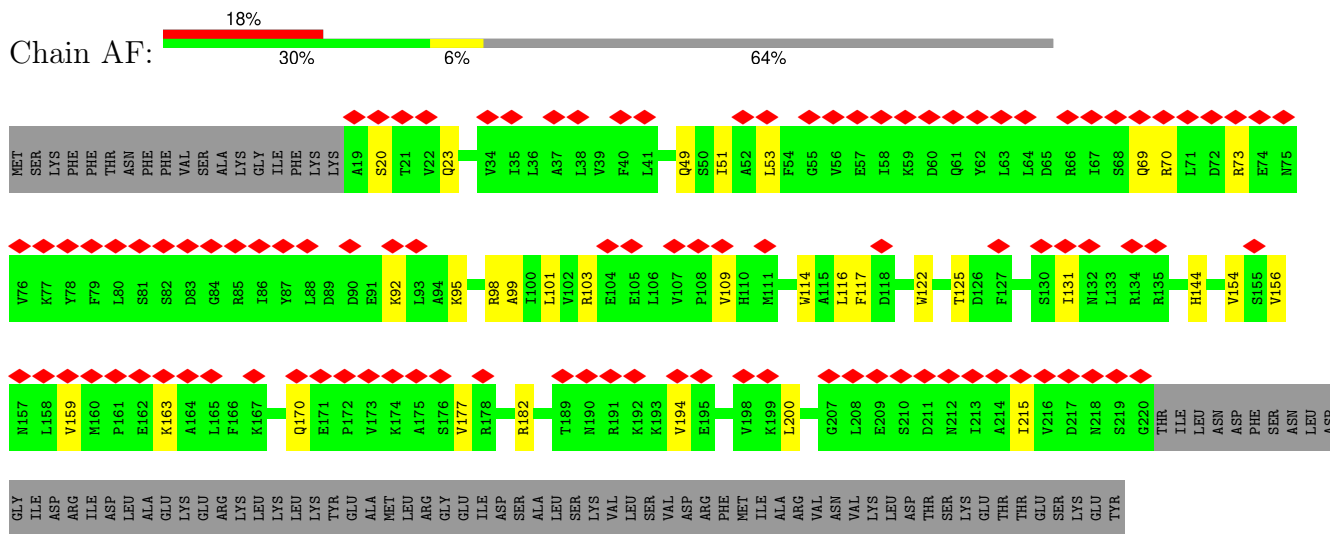
- Molecule 1: Flagellar M-ring protein

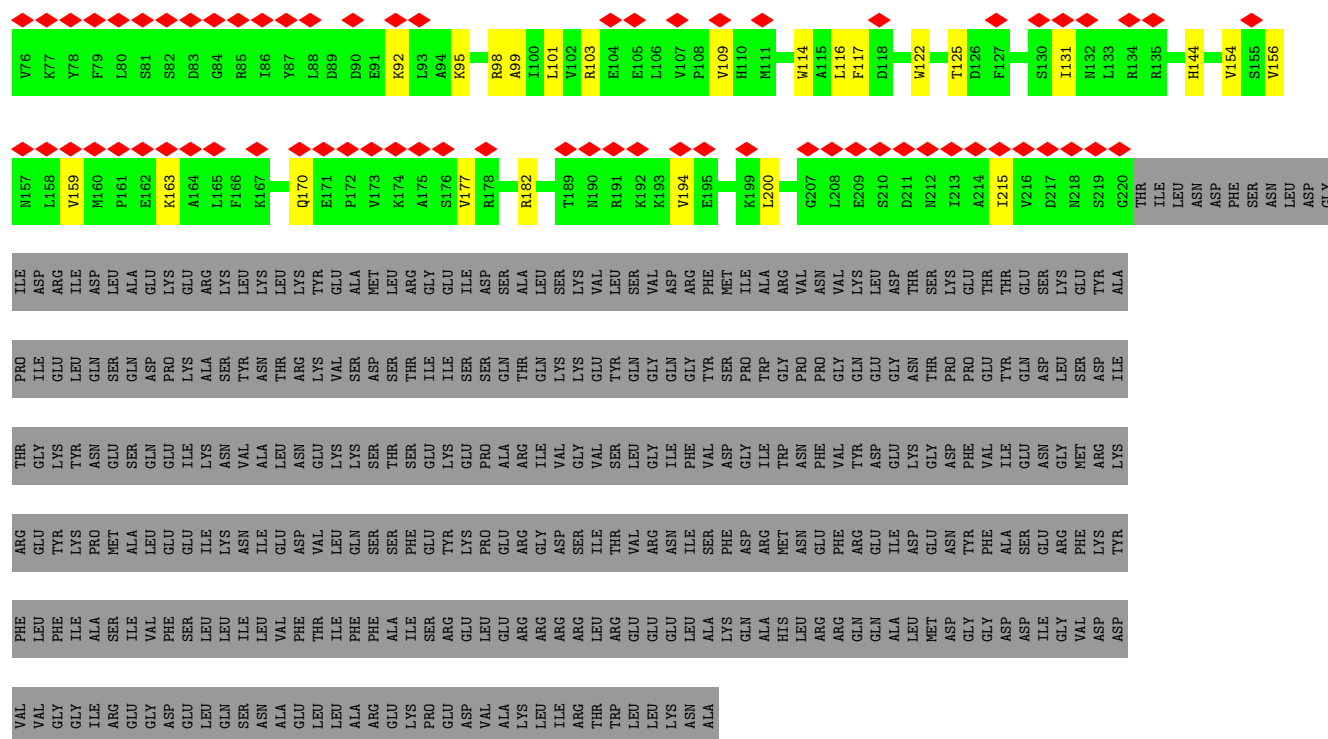


Chain AE:

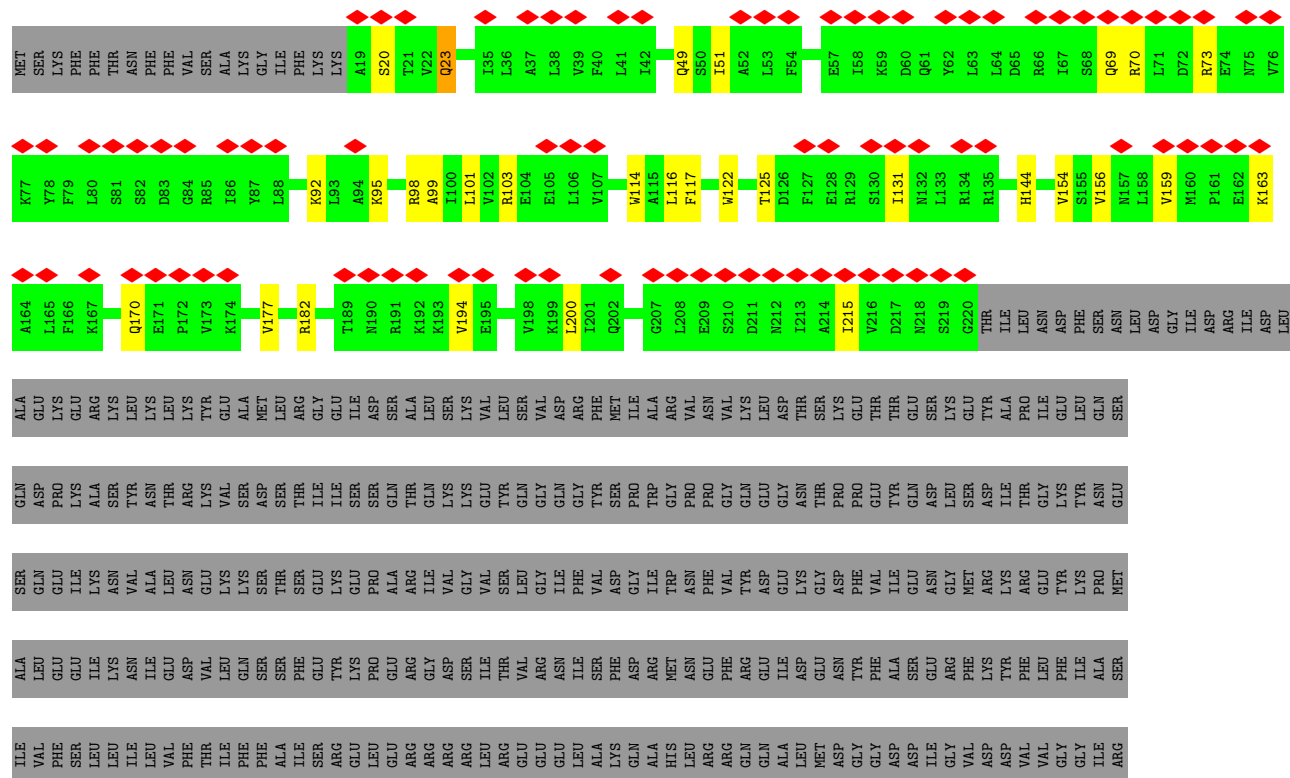


Chain AF:





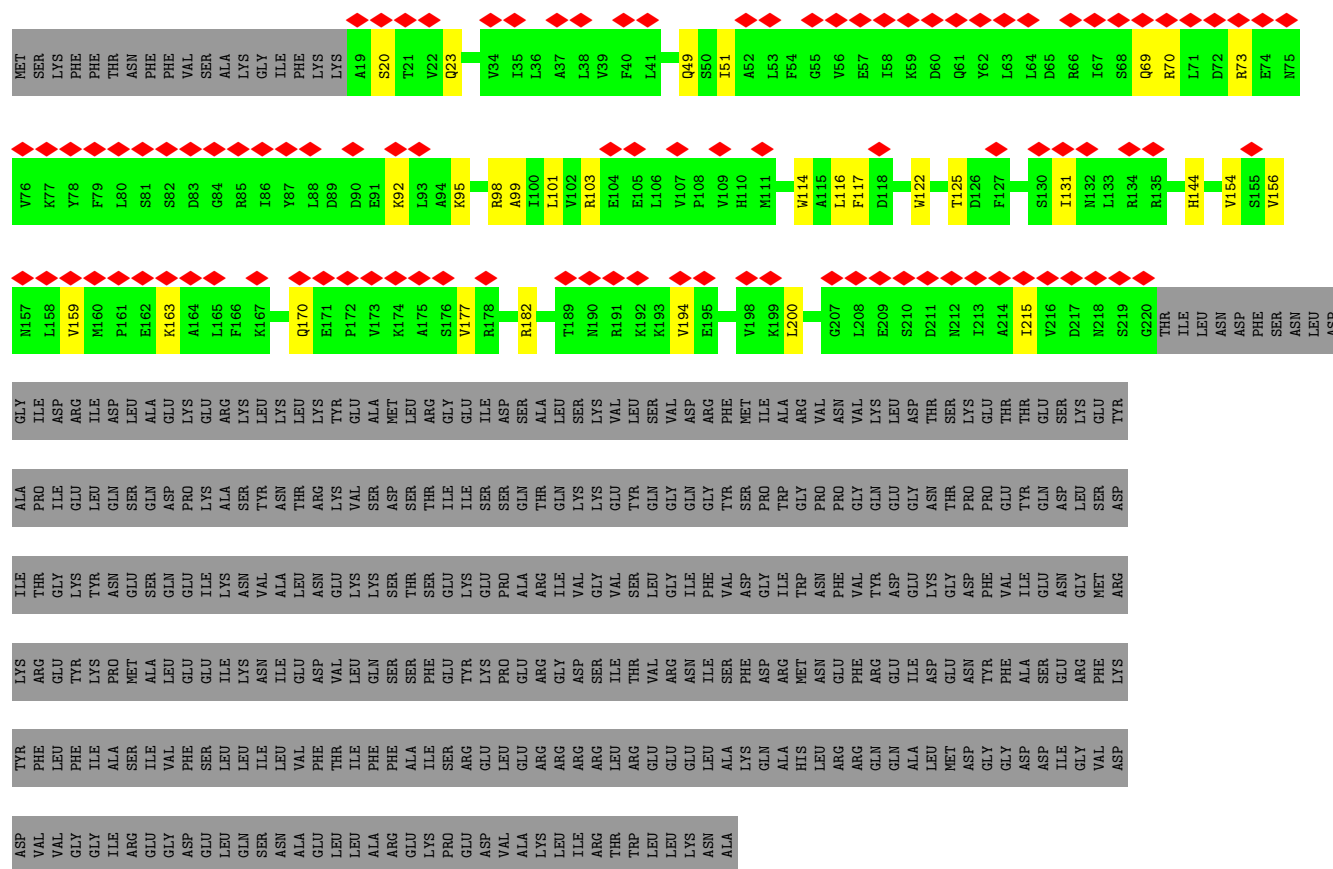
• Molecule 1: Flagellar M-ring protein



GLU
GLY
ASP
GLU
LEU
PHE
GLN
SER
ASN
ALA
GLU
LEU
LEU
ALA
ARG
GLU
LEU
PHE
LYS
PRO
GLU
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ILE
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THR
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LYS
ASN
ALA

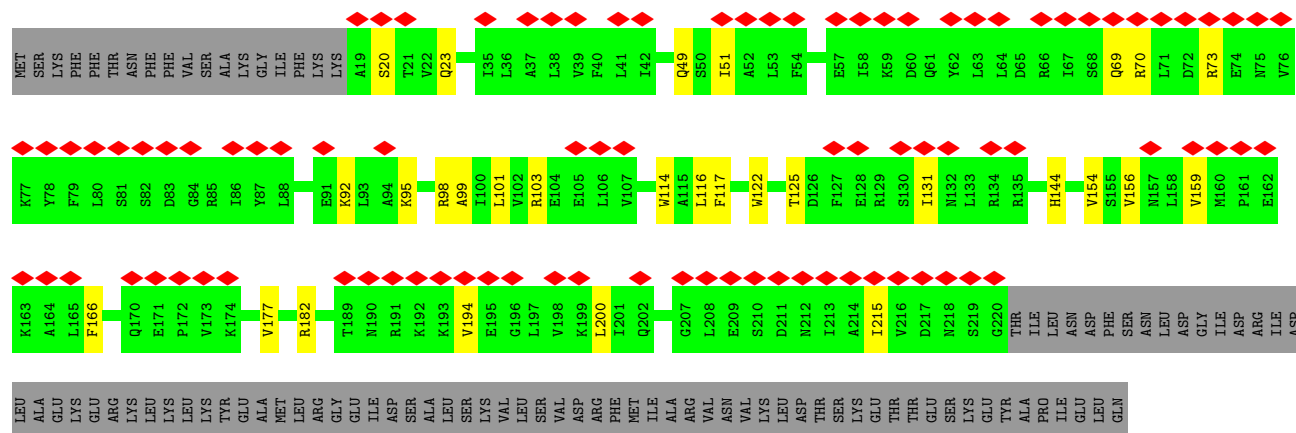
• Molecule 1: Flagellar M-ring protein

Chain AJ: 18% 30% 5% 64%



• Molecule 1: Flagellar M-ring protein

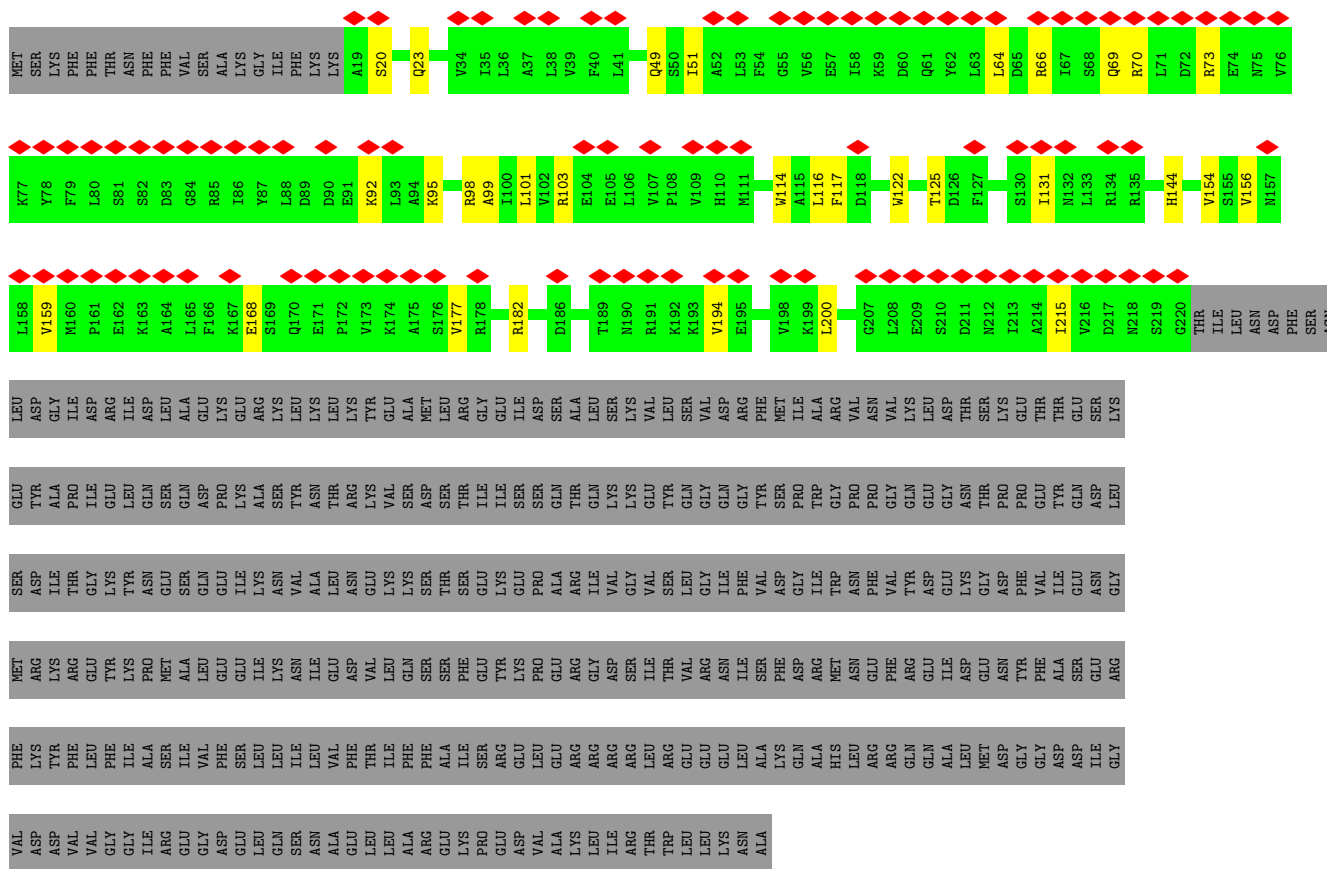
Chain AK: 16% 30% 5% 64%



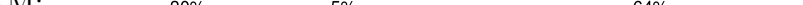
ARG	SER	MET	GLU	SER
GLU	ILE	ALA	SER	GLN
GLY	VAL	LEU	GLN	GLN
ASP	PHE	GLU	GLU	PRO
GLU	SER	ILE	ILE	LYS
LEU	LEU	ILE	LYS	ALA
GLN	LEU	LYS	ASN	SER
LEU	ILE	ASN	VAL	TYR
ASN	LEU	ILE	ALA	THR
ALA	VAL	GLU	LEU	THR
GLU	PHE	ASP	ASN	ARG
LEU	THR	VAL	GLU	LYS
LEU	ILE	LEU	LYS	VAL
ALA	PHE	GLN	LYS	SER
ARG	PHE	SER	SER	ASP
GLU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

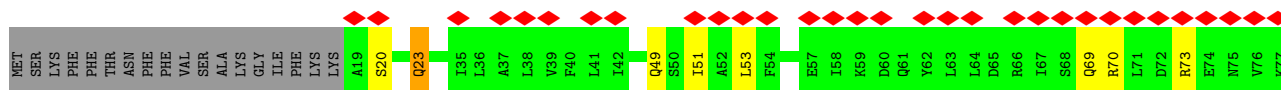
- Molecule 1: Flagellar M-ring protein

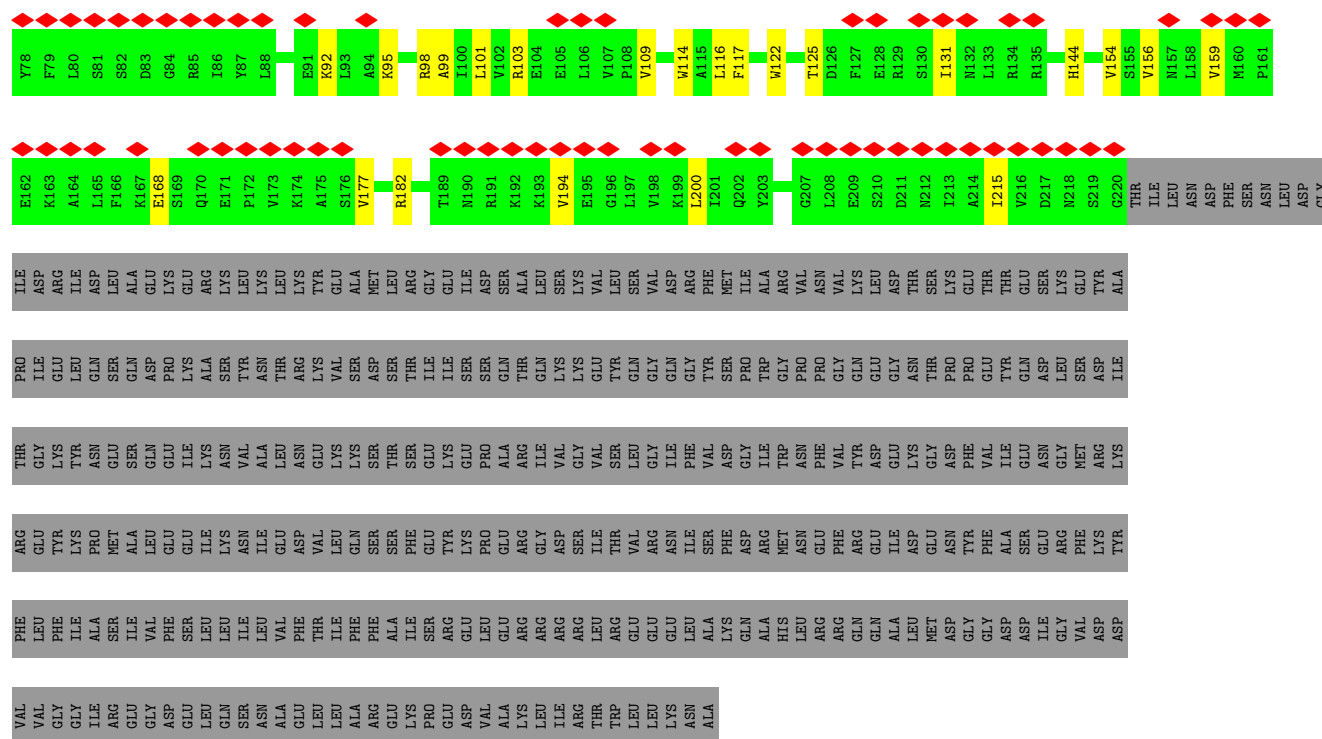
Chain AL: 18% 30% 5% 64%



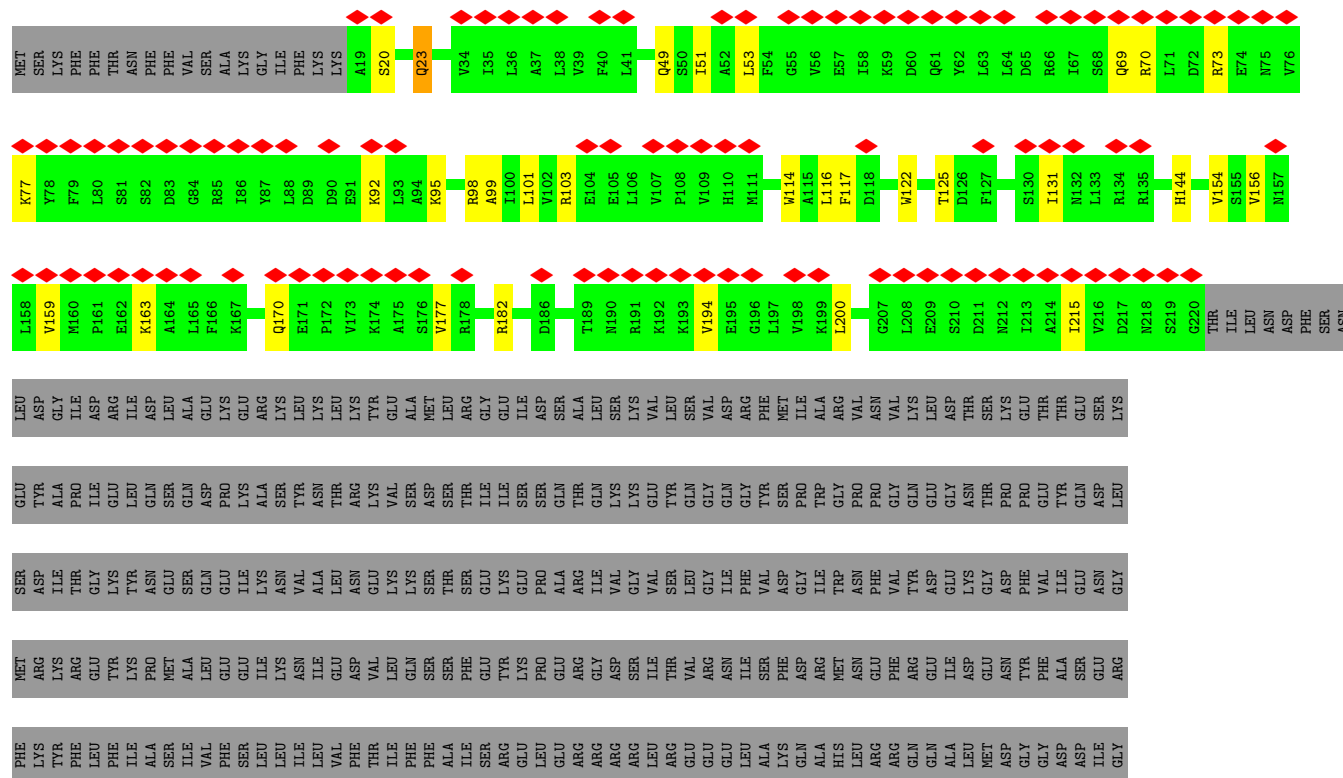
- Molecule 1: Flagellar M-ring protein

Chain AM: 





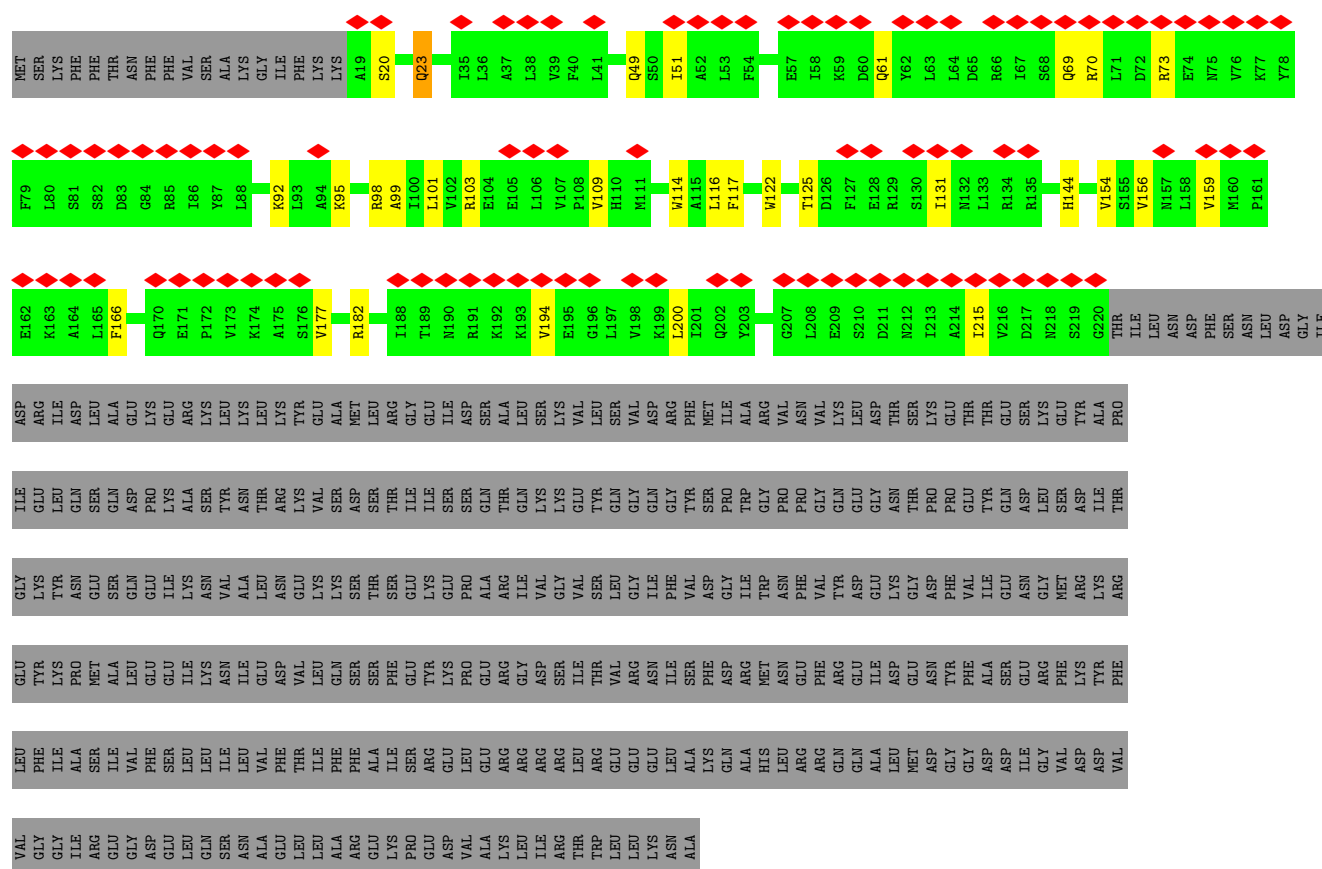
● Molecule 1: Flagellar M-ring protein



VAL ASP
VAL PHE
VAL PHE
GLY GLY
ILE ARG
GLY GLY
ASP ASP
GLY LEU
LEU GLN
SER PHE
ASN LYS
ALA ALA
GLU LEU
LEU LEU
ALA ALA
ARG ARG
GLY LYS
PRO PRO
GLU ASP
VAL VAL
ALA ALA
LYS LYS
LEU LEU
ILE ILE
ARG ARG
THR TRP
LEU LEU
LYS LYS
ASN ASN
ALA ALA

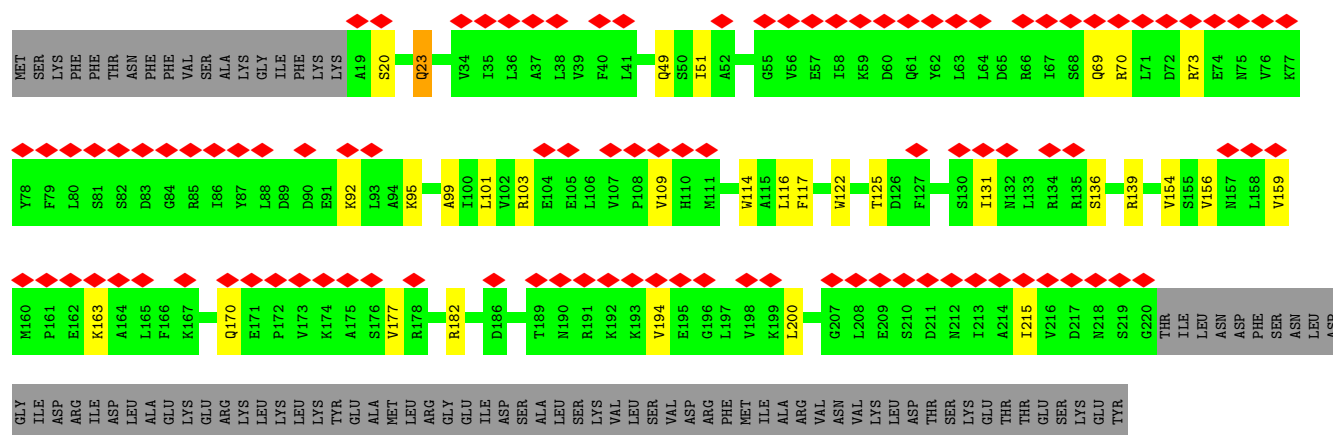
• Molecule 1: Flagellar M-ring protein

Chain AO: 17% 30% 5% 64%



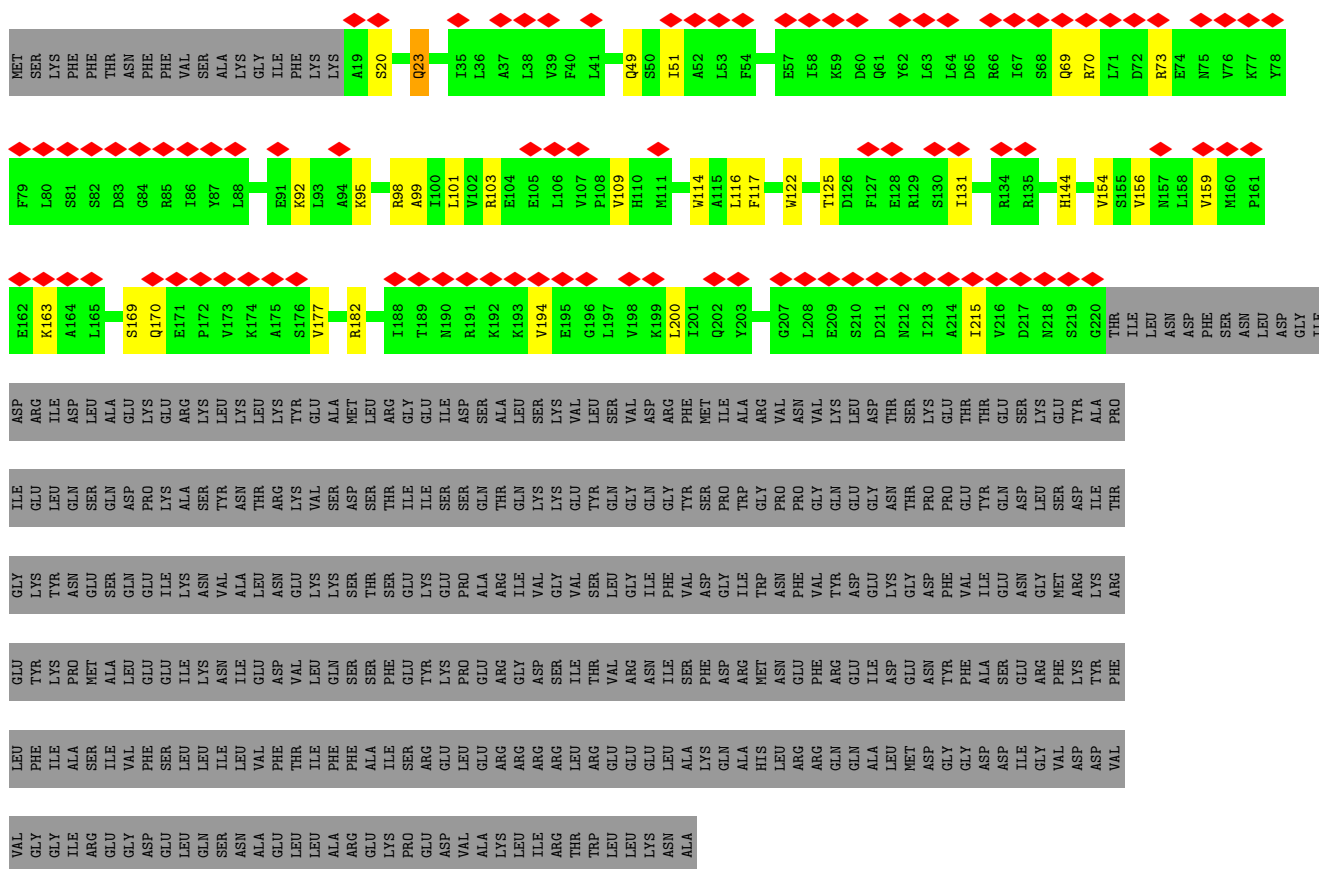
• Molecule 1: Flagellar M-ring protein

Chain AP: 18% 30% 5% 64%

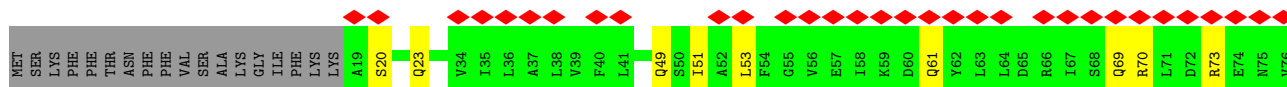


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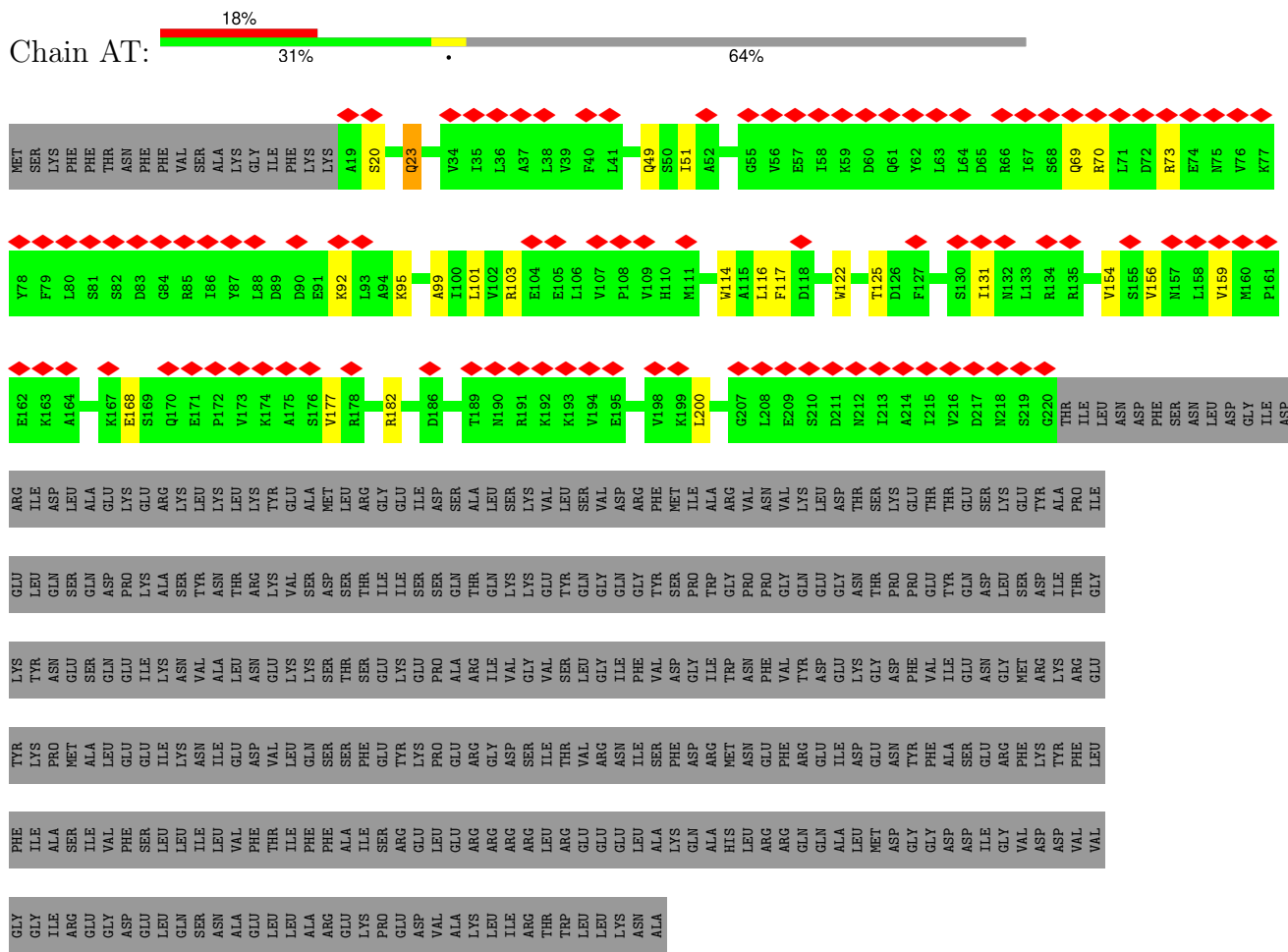
- Molecule 1: Flagellar M-ring protein



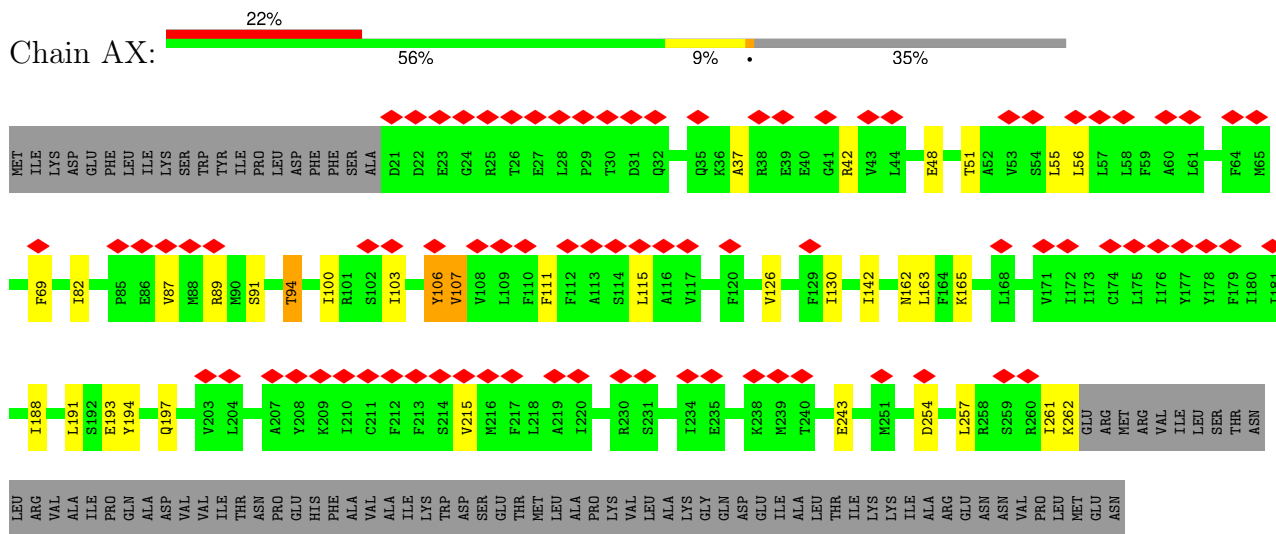
- Molecule 1: Flagellar M-ring protein

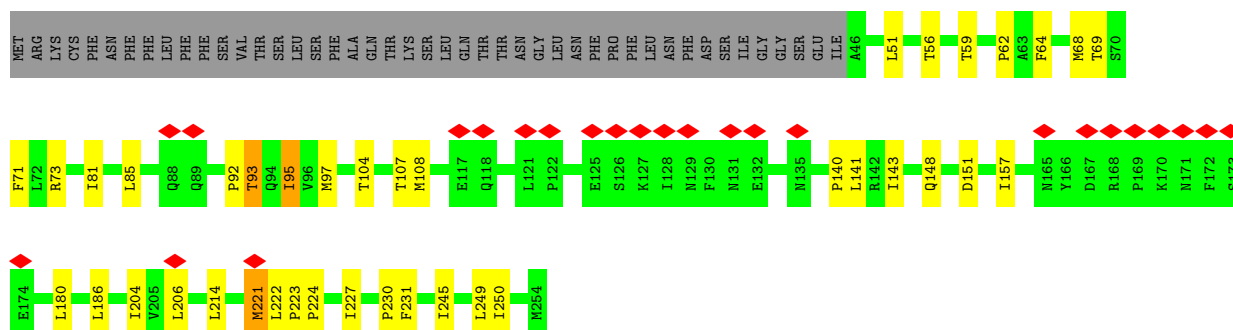


Chain AT:

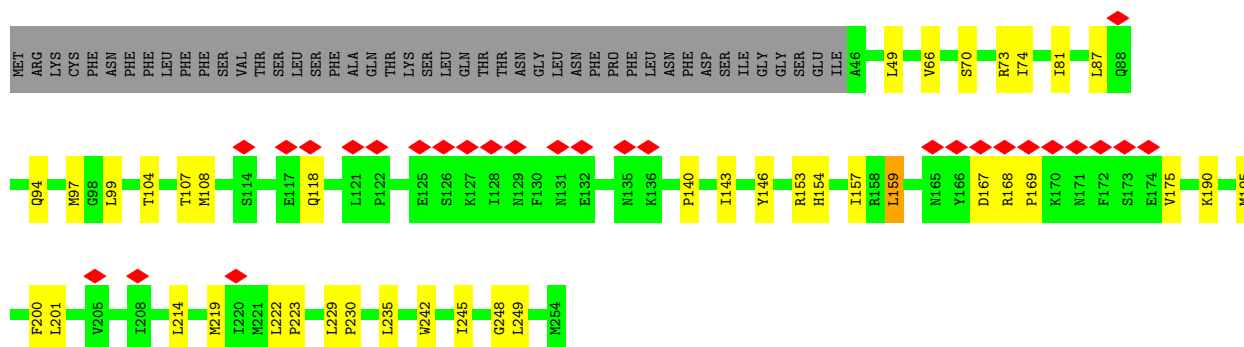


Chain AX:

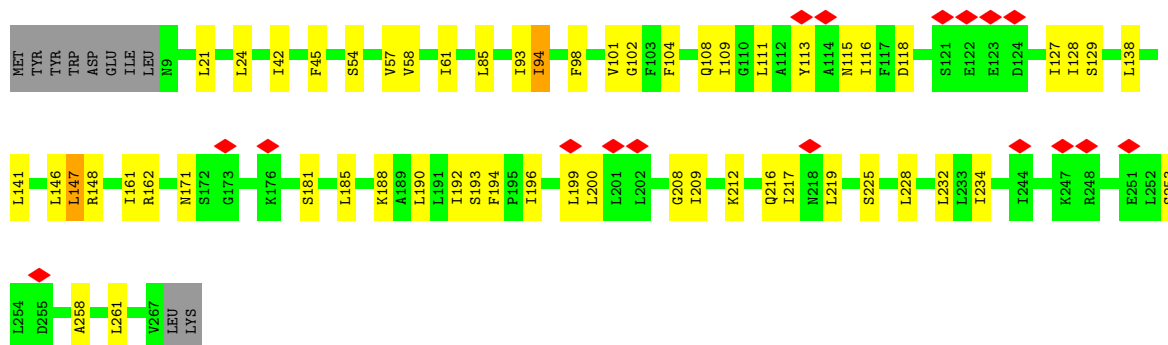
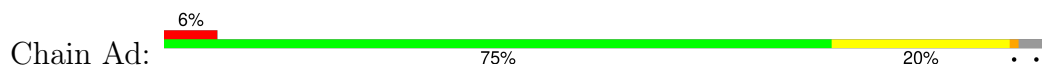




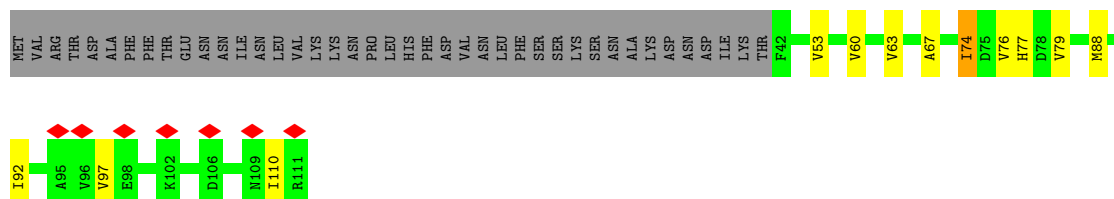
• Molecule 3: Flagellar biosynthetic protein FliP



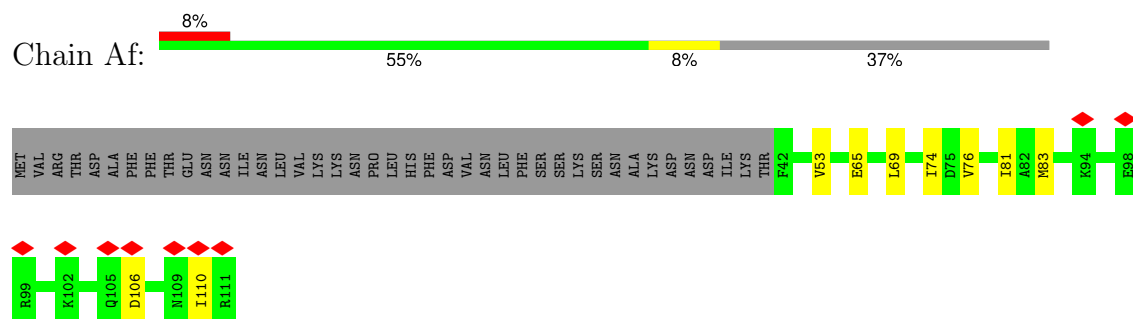
• Molecule 4: Flagellar biosynthetic protein FliR



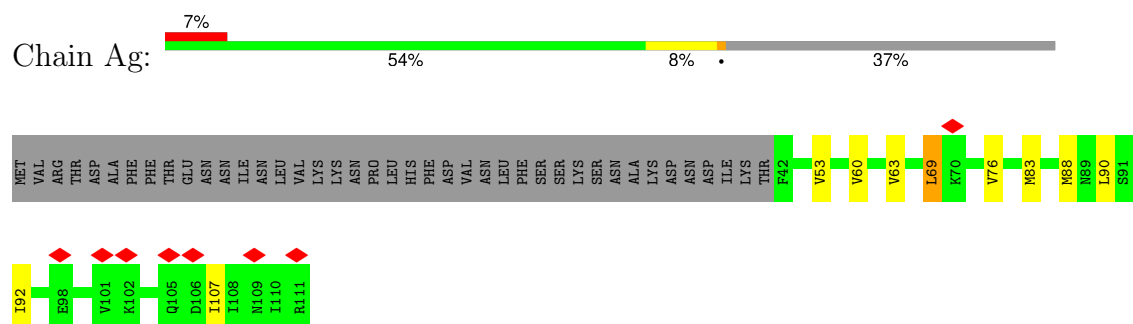
• Molecule 5: Flagellar hook-basal body complex protein FliE



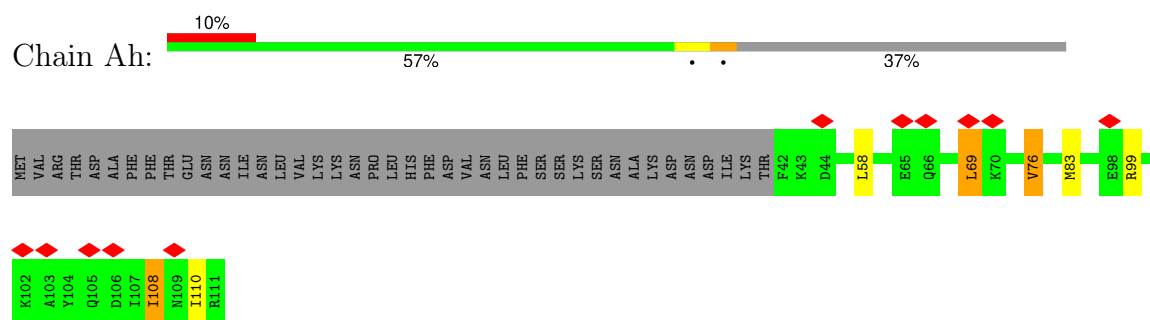
- Molecule 5: Flagellar hook-basal body complex protein FliE



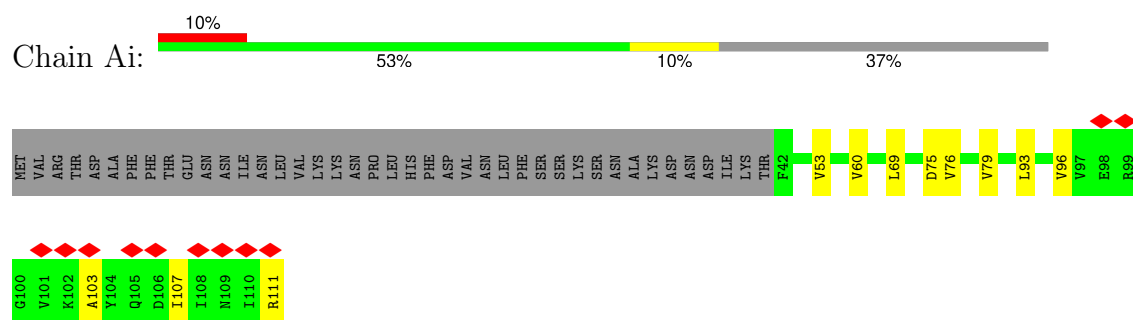
- Molecule 5: Flagellar hook-basal body complex protein FliE



- Molecule 5: Flagellar hook-basal body complex protein FliE

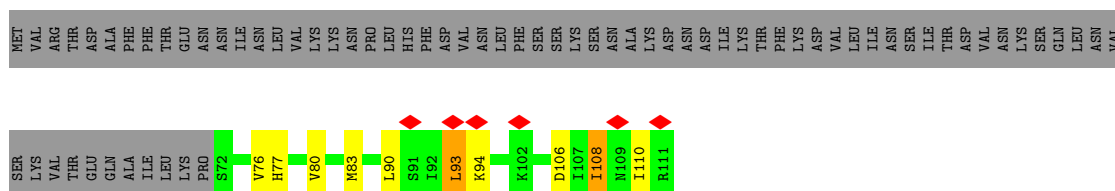


- Molecule 5: Flagellar hook-basal body complex protein FliE

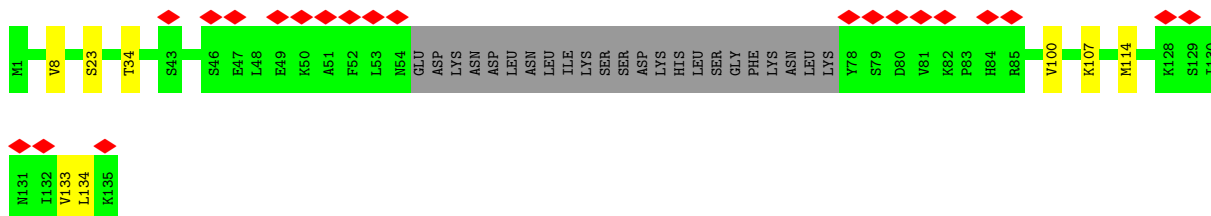
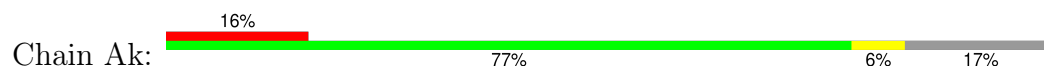


- Molecule 5: Flagellar hook-basal body complex protein FliE

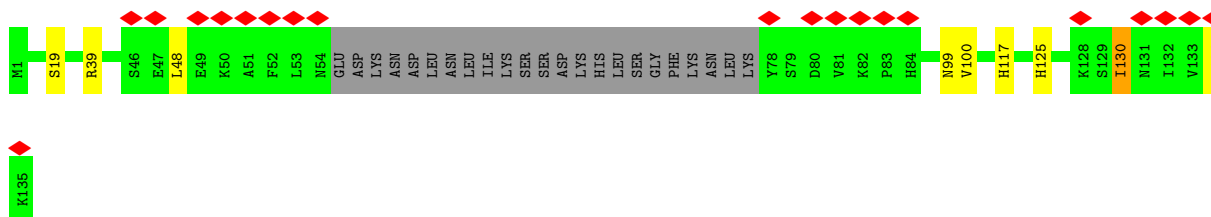
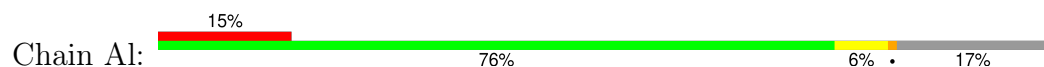




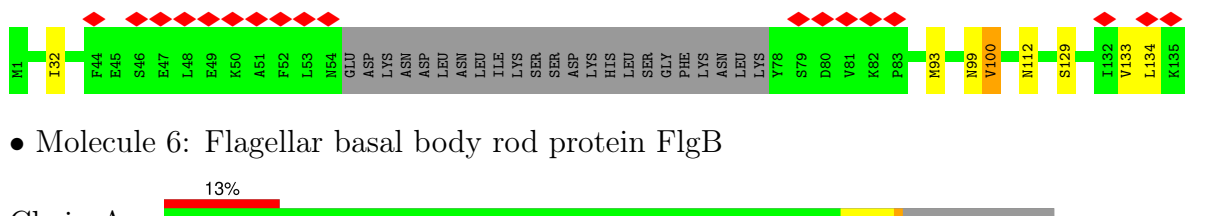
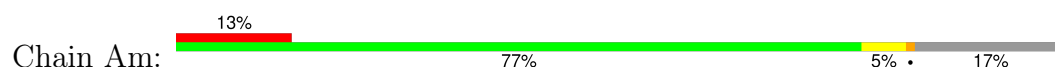
• Molecule 6: Flagellar basal body rod protein FlgB



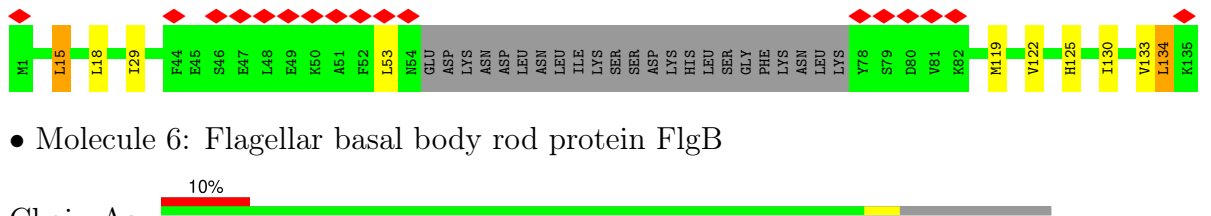
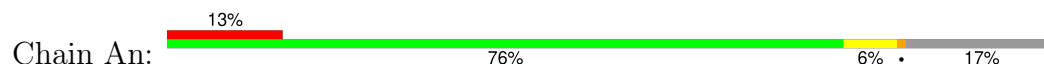
• Molecule 6: Flagellar basal body rod protein FlgB



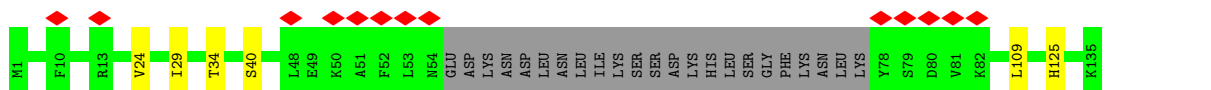
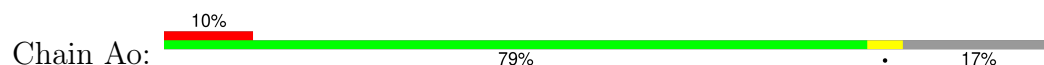
• Molecule 6: Flagellar basal body rod protein FlgB



• Molecule 6: Flagellar basal body rod protein FlgB

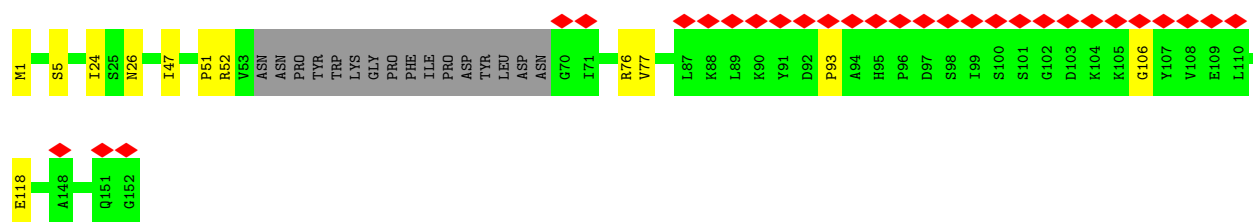


• Molecule 6: Flagellar basal body rod protein FlgB



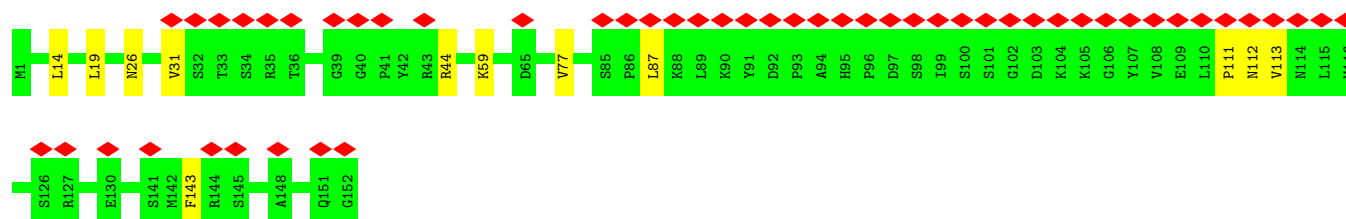
- Molecule 7: Flagellar basal-body rod protein FlgC

Chain Ap: 



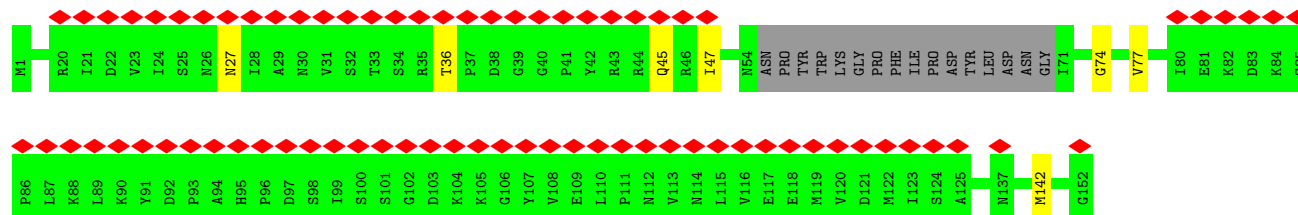
- Molecule 7: Flagellar basal-body rod protein FlgC

Chain Aq: 

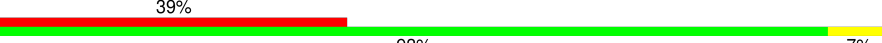


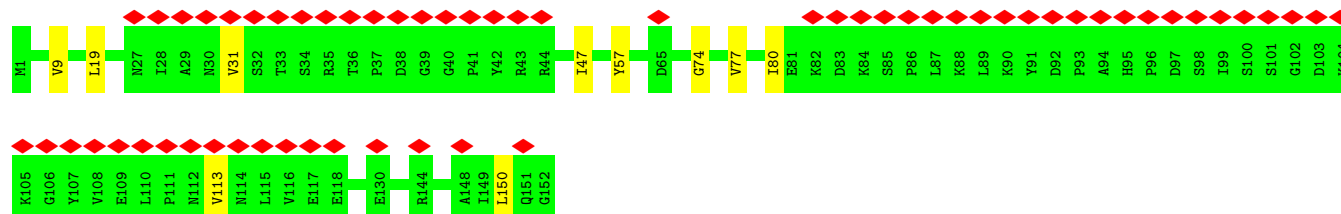
- Molecule 7: Flagellar basal-body rod protein FlgC

Chain Ar: 



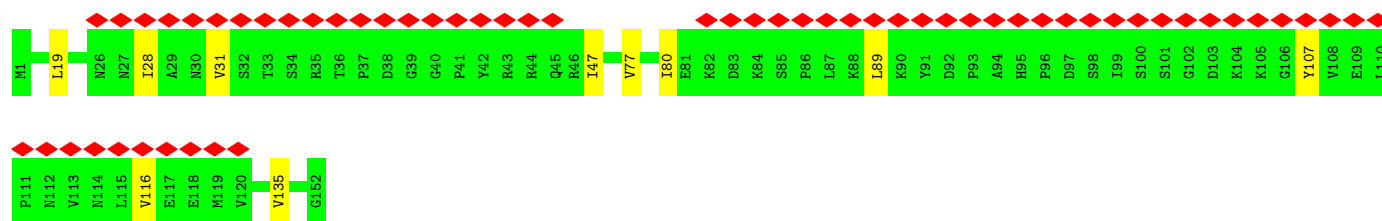
- Molecule 7: Flagellar basal-body rod protein FlgC

Chain As: 

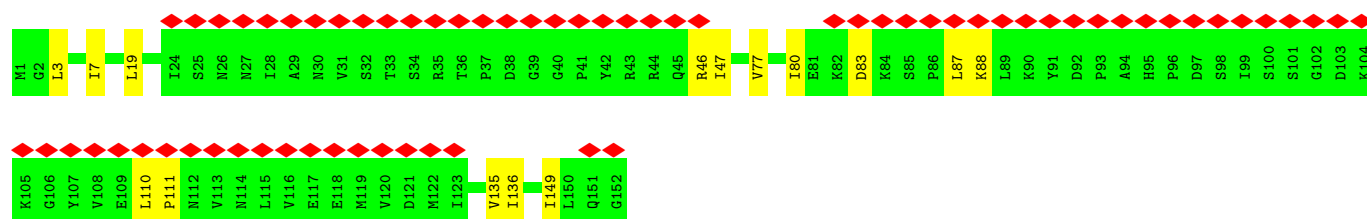
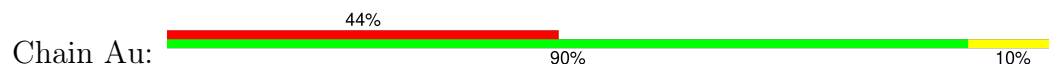


- Molecule 7: Flagellar basal-body rod protein FlgC

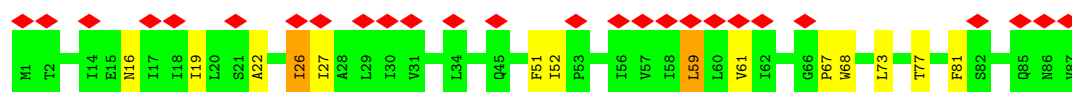
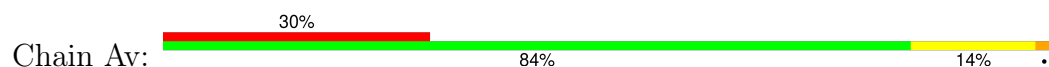
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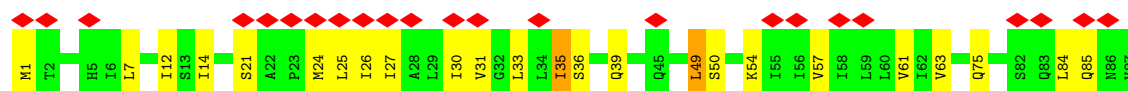
• Molecule 7: Flagellar basal-body rod protein FlgC



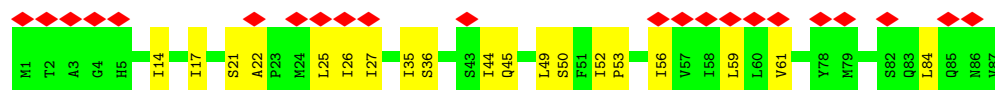
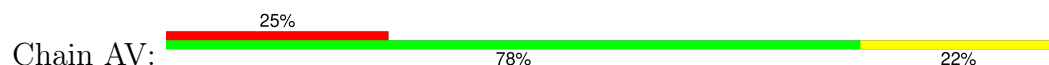
• Molecule 8: Flagellar biosynthetic protein FliQ



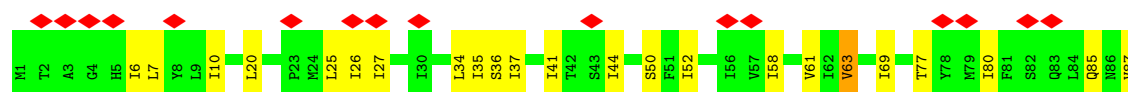
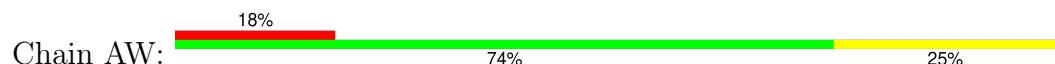
• Molecule 8: Flagellar biosynthetic protein FliQ



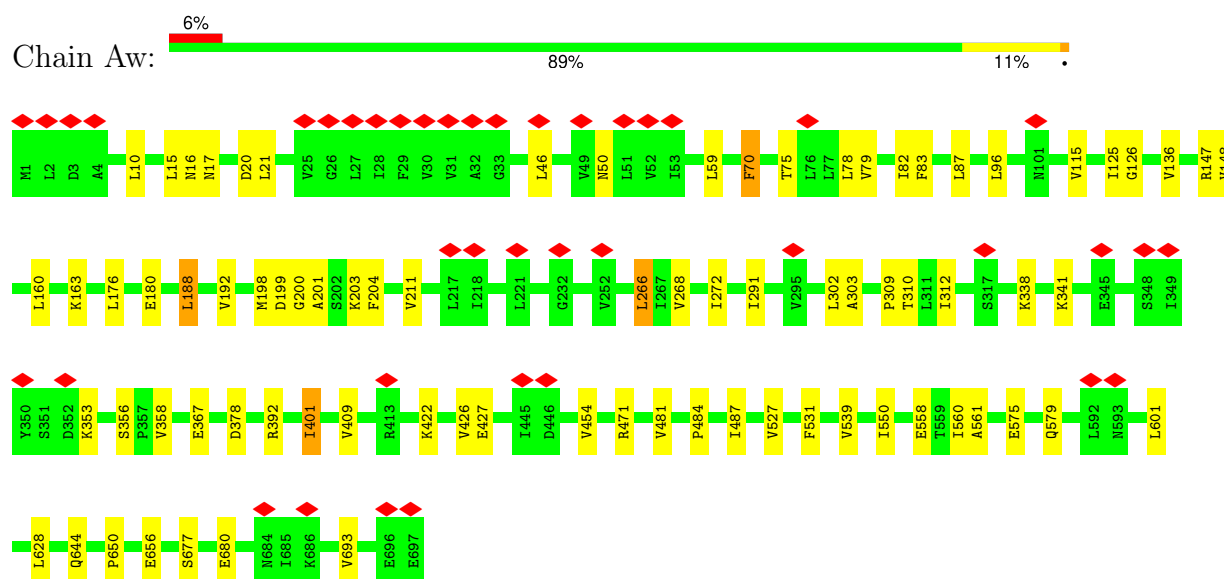
• Molecule 8: Flagellar biosynthetic protein FliQ



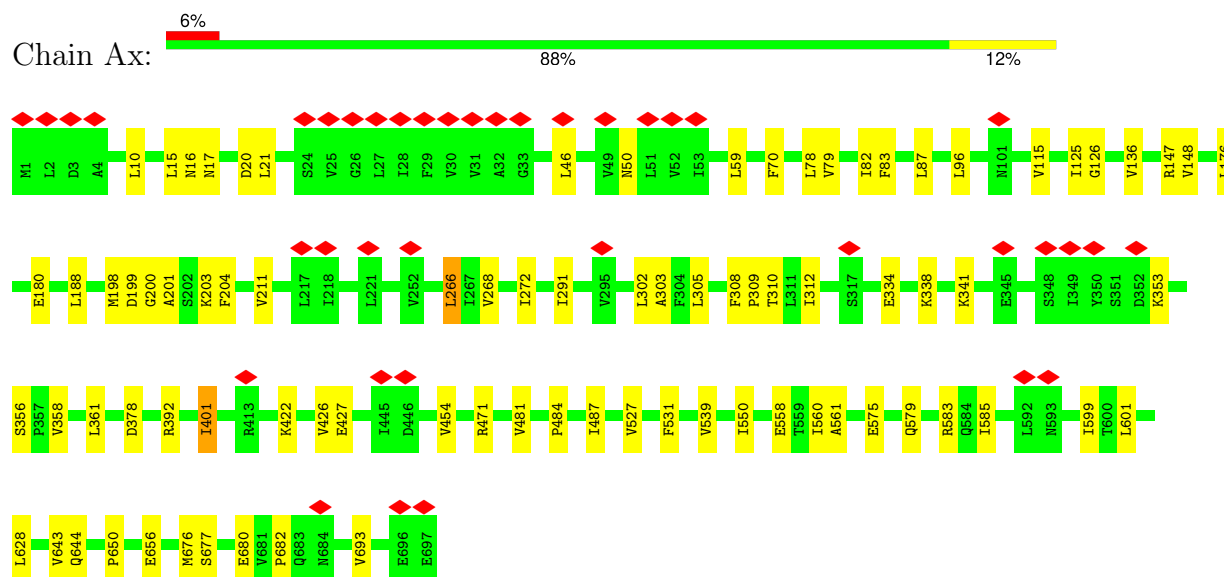
• Molecule 8: Flagellar biosynthetic protein FliQ



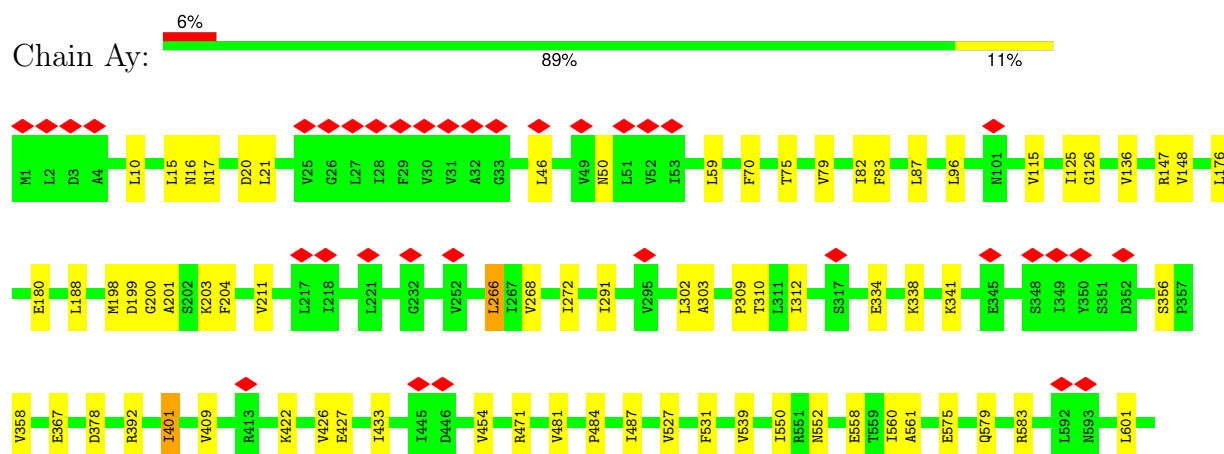
• Molecule 9: Flagellar biosynthesis protein FlhA

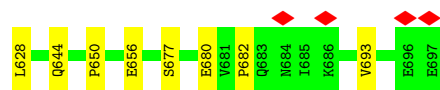


• Molecule 9: Flagellar biosynthesis protein FlhA

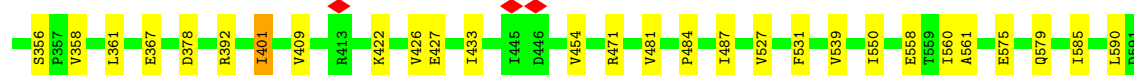
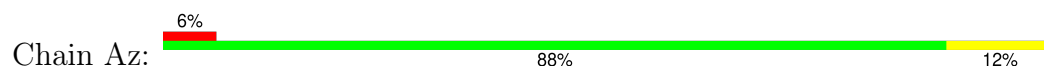


• Molecule 9: Flagellar biosynthesis protein FlhA

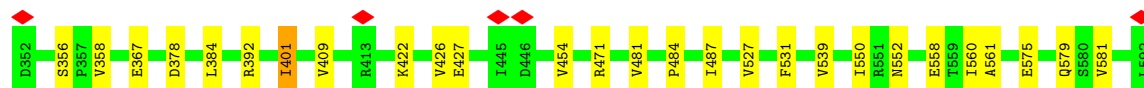
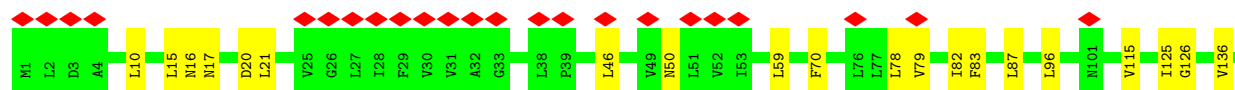
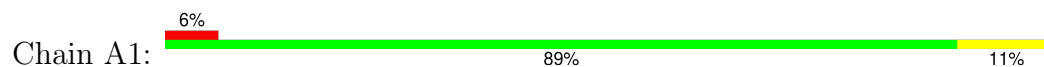




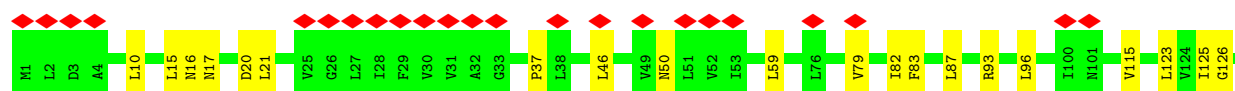
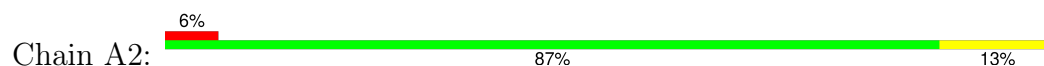
• Molecule 9: Flagellar biosynthesis protein FlhA

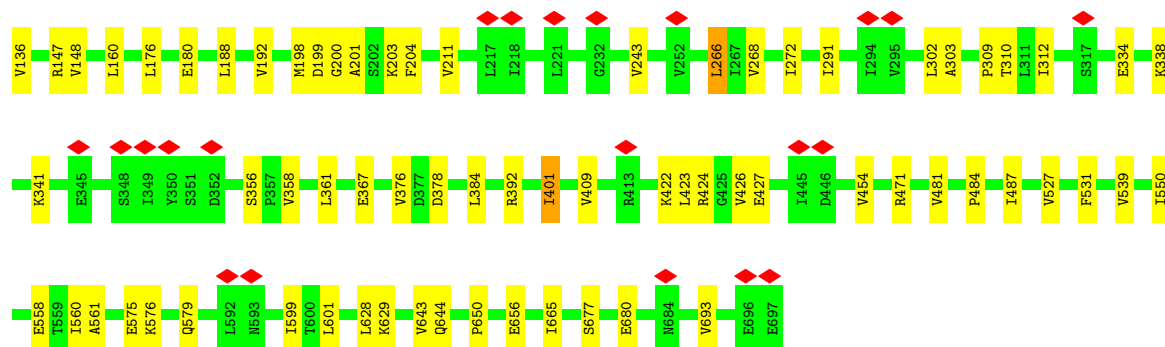


• Molecule 9: Flagellar biosynthesis protein FlhA

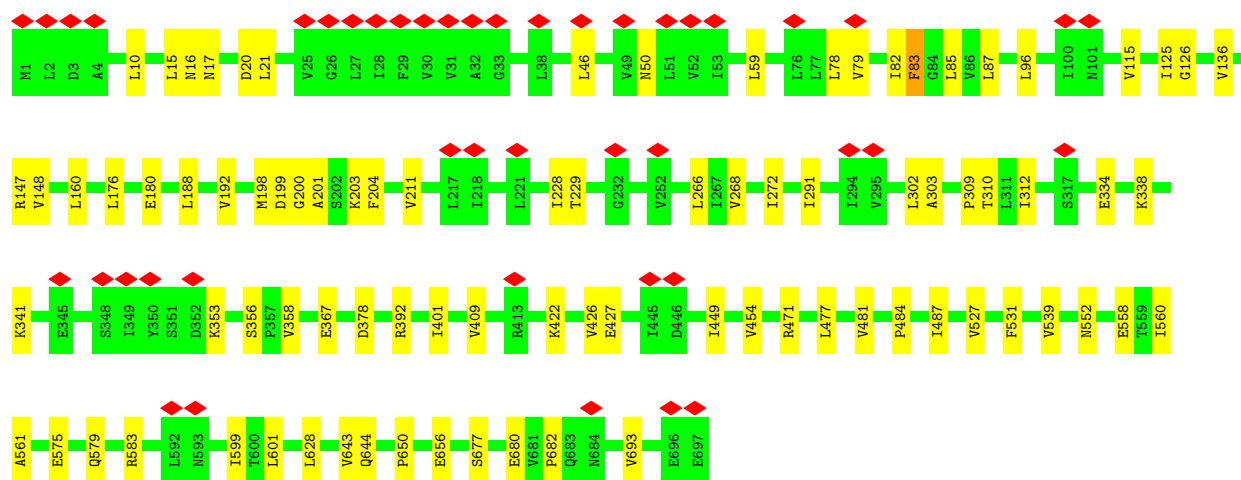
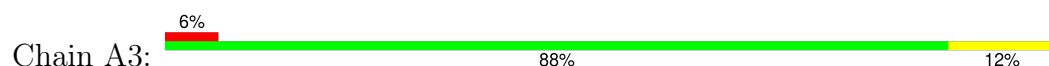


• Molecule 9: Flagellar biosynthesis protein FlhA

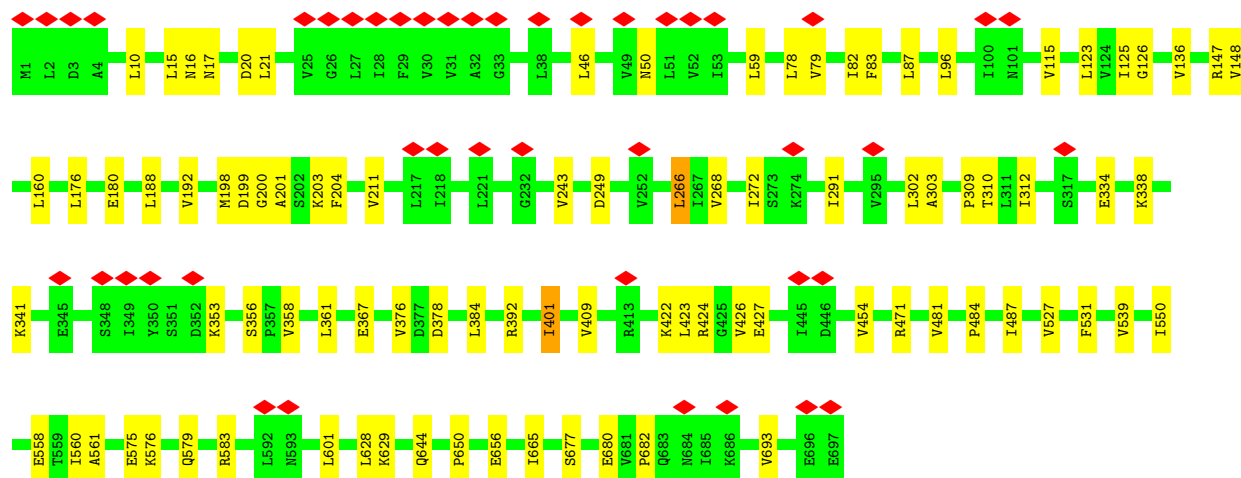
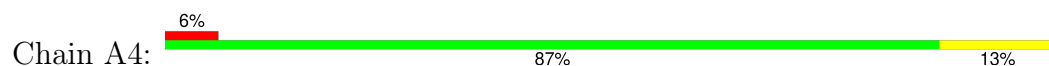




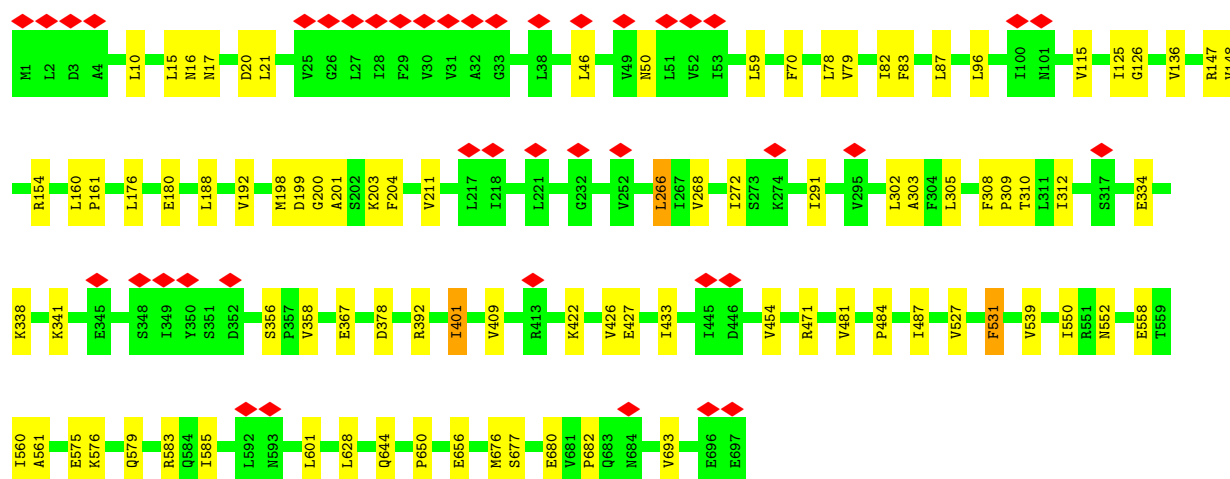
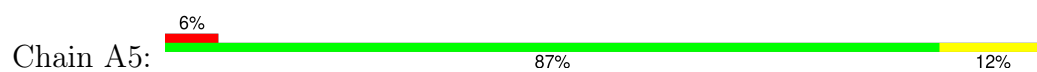
• Molecule 9: Flagellar biosynthesis protein FlhA



• Molecule 9: Flagellar biosynthesis protein FlhA



• Molecule 9: Flagellar biosynthesis protein FlhA



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C9	Depositor
Number of subtomograms used	4322	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.75	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	7.842	Depositor
Minimum map value	-5.454	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.342	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	691.2, 691.2, 691.2	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.7, 2.7, 2.7	Depositor

5 Model quality

5.1 Standard geometry

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	0.13	0/1657	0.34	0/2246
1	1	0.13	0/1657	0.34	0/2246
1	2	0.19	1/1618 (0.1%)	0.35	0/2193
1	3	0.18	1/1657 (0.1%)	0.35	0/2246
1	4	0.19	1/1657 (0.1%)	0.37	0/2246
1	5	0.13	0/1657	0.35	0/2246
1	6	0.13	0/1618	0.34	0/2193
1	7	0.19	1/1657 (0.1%)	0.36	0/2246
1	8	0.13	0/1657	0.35	0/2246
1	9	0.18	1/1657 (0.1%)	0.35	0/2246
1	A	0.11	0/2132	0.24	0/2861
1	AA	0.13	0/1657	0.34	0/2246
1	AB	0.13	0/1657	0.34	0/2246
1	AC	0.12	0/1638	0.36	0/2214
1	AD	0.13	0/1638	0.37	0/2214
1	AE	0.13	0/1638	0.36	0/2214
1	AF	0.13	0/1638	0.36	0/2214
1	AG	0.13	0/1638	0.37	0/2214
1	AH	0.13	0/1638	0.35	0/2214
1	AI	0.12	0/1638	0.35	0/2214
1	AJ	0.13	0/1638	0.35	0/2214
1	AK	0.13	0/1638	0.36	0/2214
1	AL	0.13	0/1638	0.37	0/2214
1	AM	0.12	0/1638	0.36	0/2214
1	AN	0.13	0/1638	0.36	0/2214
1	AO	0.12	0/1638	0.35	0/2214
1	AP	0.12	0/1638	0.36	0/2214
1	AQ	0.12	0/1638	0.37	0/2214
1	AR	0.13	0/1638	0.37	0/2214
1	AS	0.13	0/1638	0.37	0/2214
1	AT	0.12	0/1638	0.37	0/2214
1	B	0.11	0/2132	0.26	0/2861
1	C	0.11	0/2132	0.27	0/2861
1	D	0.12	0/2132	0.25	0/2861

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	E	0.12	0/2132	0.27	0/2861
1	F	0.11	0/2132	0.27	0/2861
1	G	0.11	0/2132	0.26	0/2861
1	H	0.11	0/2132	0.26	0/2861
1	I	0.11	0/2132	0.24	0/2861
1	J	0.11	0/2132	0.27	0/2861
1	K	0.11	0/2132	0.24	0/2861
1	L	0.11	0/2132	0.25	0/2861
1	M	0.11	0/2132	0.26	0/2861
1	N	0.11	0/2132	0.28	0/2861
1	O	0.11	0/2132	0.25	0/2861
1	P	0.11	0/2132	0.26	0/2861
1	Q	0.11	0/2132	0.26	0/2861
1	R	0.11	0/2132	0.27	0/2861
1	S	0.11	0/2132	0.26	0/2861
1	T	0.11	0/2132	0.27	0/2861
1	U	0.11	0/2132	0.25	0/2861
1	V	0.11	0/2132	0.26	0/2861
1	W	0.12	0/2132	0.28	0/2861
1	X	0.12	0/2132	0.28	0/2861
1	Y	0.11	0/2132	0.26	0/2861
1	Z	0.11	0/2132	0.27	0/2861
1	a	0.11	0/2132	0.26	0/2861
1	b	0.11	0/2132	0.28	0/2861
1	c	0.11	0/2132	0.28	0/2861
1	d	0.11	0/2132	0.27	0/2861
1	e	0.11	0/2132	0.25	0/2861
1	f	0.11	0/2132	0.27	0/2861
1	g	0.11	0/2132	0.27	0/2861
1	h	0.12	0/2132	0.28	0/2861
1	i	0.11	0/2132	0.26	0/2861
1	j	0.11	0/2132	0.26	0/2861
1	k	0.11	0/2132	0.26	0/2861
1	l	0.11	0/2132	0.27	0/2861
1	m	0.11	0/2132	0.27	0/2861
1	n	0.11	0/2132	0.25	0/2861
1	o	0.11	0/2132	0.26	0/2861
1	p	0.18	1/1657 (0.1%)	0.34	0/2246
1	q	0.13	0/1657	0.34	0/2246
1	r	0.12	0/1657	0.35	0/2246
1	s	0.18	1/1657 (0.1%)	0.35	0/2246
1	t	0.13	0/1618	0.36	0/2193
1	u	0.18	1/1657 (0.1%)	0.34	0/2246

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	v	0.13	0/1657	0.33	0/2246
1	w	0.13	0/1657	0.33	0/2246
1	x	0.12	0/1618	0.35	0/2193
1	y	0.19	1/1657 (0.1%)	0.35	0/2246
1	z	0.13	0/1657	0.34	0/2246
2	AX	0.13	0/2033	0.31	0/2734
3	AY	0.16	0/1706	0.35	0/2313
3	AZ	0.15	0/1696	0.33	0/2300
3	Aa	0.15	0/1697	0.34	0/2300
3	Ab	0.16	0/1706	0.36	0/2312
3	Ac	0.15	0/1717	0.32	0/2325
4	Ad	0.13	0/2135	0.32	0/2892
5	Ae	0.13	0/545	0.30	0/734
5	Af	0.13	0/545	0.26	0/734
5	Ag	0.13	0/545	0.28	0/734
5	Ah	0.13	0/532	0.30	0/718
5	Ai	0.13	0/545	0.29	0/734
5	Aj	0.12	0/309	0.29	0/414
6	Ak	0.11	0/936	0.25	0/1259
6	Al	0.11	0/936	0.27	0/1259
6	Am	0.11	0/936	0.24	0/1259
6	An	0.11	0/936	0.28	0/1259
6	Ao	0.11	0/936	0.23	0/1259
7	Ap	0.11	0/1043	0.24	0/1405
7	Aq	0.12	0/1175	0.26	0/1593
7	Ar	0.12	0/1047	0.27	0/1411
7	As	0.11	0/1191	0.25	0/1612
7	At	0.11	0/1191	0.27	0/1612
7	Au	0.10	0/1191	0.26	0/1612
8	AU	0.16	0/694	0.35	0/946
8	AV	0.15	0/704	0.34	0/957
8	AW	0.15	0/704	0.32	0/957
8	Av	0.17	0/690	0.34	0/941
9	A1	0.14	0/5515	0.33	0/7477
9	A2	0.14	0/5515	0.33	0/7477
9	A3	0.14	0/5515	0.33	0/7477
9	A4	0.14	0/5515	0.33	0/7477
9	A5	0.14	0/5515	0.33	0/7477
9	Aw	0.14	0/5515	0.33	0/7477
9	Ax	0.14	0/5515	0.33	0/7477
9	Ay	0.14	0/5515	0.33	0/7477
9	Az	0.14	0/5515	0.33	0/7477
All	All	0.13	9/234507 (0.0%)	0.31	0/316477

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	7	107	VAL	C-N	5.75	1.38	1.33
1	4	107	VAL	C-N	5.74	1.38	1.33
1	2	107	VAL	C-N	5.71	1.38	1.33
1	9	107	VAL	C-N	5.61	1.38	1.33
1	y	107	VAL	C-N	5.59	1.38	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1632	0	1673	6	0
1	1	1632	0	1673	9	0
1	2	1595	0	1633	7	0
1	3	1632	0	1673	8	0
1	4	1632	0	1673	10	0
1	5	1632	0	1673	8	0
1	6	1595	0	1633	7	0
1	7	1632	0	1673	11	0
1	8	1632	0	1673	14	0
1	9	1632	0	1673	12	0
1	A	2104	0	2085	18	0
1	AA	1632	0	1673	12	0
1	AB	1632	0	1673	9	0
1	AC	1614	0	1677	18	0
1	AD	1614	0	1677	18	0
1	AE	1614	0	1677	18	0
1	AF	1614	0	1677	18	0
1	AG	1614	0	1677	16	0
1	AH	1614	0	1677	17	0
1	AI	1614	0	1677	17	0
1	AJ	1614	0	1677	18	0
1	AK	1614	0	1677	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AL	1614	0	1677	19	0
1	AM	1614	0	1677	17	0
1	AN	1614	0	1677	19	0
1	AO	1614	0	1677	18	0
1	AP	1614	0	1677	17	0
1	AQ	1614	0	1677	18	0
1	AR	1614	0	1677	17	0
1	AS	1614	0	1677	16	0
1	AT	1614	0	1677	16	0
1	B	2104	0	2085	19	0
1	C	2104	0	2085	20	0
1	D	2104	0	2085	21	0
1	E	2104	0	2085	21	0
1	F	2104	0	2085	17	0
1	G	2104	0	2085	20	0
1	H	2104	0	2085	18	0
1	I	2104	0	2085	18	0
1	J	2104	0	2085	15	0
1	K	2104	0	2085	15	0
1	L	2104	0	2085	17	0
1	M	2104	0	2085	16	0
1	N	2104	0	2085	27	0
1	O	2104	0	2085	20	0
1	P	2104	0	2085	19	0
1	Q	2104	0	2085	22	0
1	R	2104	0	2085	19	0
1	S	2104	0	2085	28	0
1	T	2104	0	2085	19	0
1	U	2104	0	2085	19	0
1	V	2104	0	2085	21	0
1	W	2104	0	2085	19	0
1	X	2104	0	2085	22	0
1	Y	2104	0	2085	14	0
1	Z	2104	0	2085	14	0
1	a	2104	0	2085	17	0
1	b	2104	0	2085	20	0
1	c	2104	0	2085	21	0
1	d	2104	0	2085	22	0
1	e	2104	0	2085	19	0
1	f	2104	0	2085	16	0
1	g	2104	0	2085	17	0
1	h	2104	0	2085	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	i	2104	0	2085	18	0
1	j	2104	0	2085	19	0
1	k	2104	0	2085	14	0
1	l	2104	0	2085	17	0
1	m	2104	0	2085	20	0
1	n	2104	0	2085	13	0
1	o	2104	0	2085	19	0
1	p	1632	0	1673	15	0
1	q	1632	0	1673	9	0
1	r	1632	0	1673	6	0
1	s	1632	0	1673	7	0
1	t	1595	0	1633	9	0
1	u	1632	0	1673	14	0
1	v	1632	0	1673	6	0
1	w	1632	0	1673	7	0
1	x	1595	0	1633	10	0
1	y	1632	0	1673	10	0
1	z	1632	0	1673	9	0
2	AX	1988	0	2043	22	0
3	AY	1665	0	1752	31	0
3	AZ	1656	0	1740	29	0
3	Aa	1657	0	1747	24	0
3	Ab	1666	0	1755	23	0
3	Ac	1676	0	1773	23	0
4	Ad	2083	0	2194	32	0
5	Ae	542	0	579	8	0
5	Af	542	0	579	4	0
5	Ag	542	0	579	7	0
5	Ah	530	0	561	7	0
5	Ai	542	0	579	8	0
5	Aj	308	0	327	7	0
6	Ak	920	0	896	6	0
6	Al	920	0	896	6	0
6	Am	920	0	896	5	0
6	An	920	0	896	11	0
6	Ao	920	0	896	4	0
7	Ap	1030	0	1055	8	0
7	Aq	1153	0	1150	7	0
7	Ar	1034	0	1058	4	0
7	As	1169	0	1178	5	0
7	At	1169	0	1178	5	0
7	Au	1169	0	1178	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AU	682	0	749	14	0
8	AV	692	0	771	10	0
8	AW	692	0	771	16	0
8	Av	678	0	743	12	0
9	A1	5429	0	5666	44	0
9	A2	5429	0	5666	47	0
9	A3	5429	0	5666	46	0
9	A4	5429	0	5666	50	0
9	A5	5429	0	5666	51	0
9	Aw	5429	0	5666	43	0
9	Ax	5429	0	5666	46	0
9	Ay	5429	0	5666	43	0
9	Az	5429	0	5666	44	0
All	All	231030	0	235503	1684	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 4.

The worst 5 of 1684 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)
4:Ad:54:SER:O	4:Ad:58:VAL:HB	1.78	0.83
1:m:230:ASP:O	1:m:234:ARG:HB2	1.80	0.81
8:Av:22:ALA:O	8:Av:26:ILE:HB	1.83	0.78
8:AU:27:ILE:HG21	8:AU:61:VAL:HG21	1.65	0.77
3:AZ:64:PHE:O	3:AZ:68:MET:HB3	1.90	0.71

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	207/569 (36%)	201 (97%)	5 (2%)	1 (0%)	24	63
1	1	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	2	201/569 (35%)	195 (97%)	5 (2%)	1 (0%)	24	63
1	3	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	4	207/569 (36%)	198 (96%)	8 (4%)	1 (0%)	24	63
1	5	207/569 (36%)	198 (96%)	8 (4%)	1 (0%)	24	63
1	6	201/569 (35%)	194 (96%)	6 (3%)	1 (0%)	24	63
1	7	207/569 (36%)	199 (96%)	7 (3%)	1 (0%)	24	63
1	8	207/569 (36%)	196 (95%)	10 (5%)	1 (0%)	24	63
1	9	207/569 (36%)	199 (96%)	7 (3%)	1 (0%)	24	63
1	A	258/569 (45%)	253 (98%)	5 (2%)	0	100	100
1	AA	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	AB	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	AC	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AD	200/569 (35%)	184 (92%)	15 (8%)	1 (0%)	24	63
1	AE	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AF	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	AG	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	AH	200/569 (35%)	184 (92%)	15 (8%)	1 (0%)	24	63
1	AI	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AJ	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AK	200/569 (35%)	184 (92%)	15 (8%)	1 (0%)	24	63
1	AL	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	AM	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AN	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AO	200/569 (35%)	184 (92%)	15 (8%)	1 (0%)	24	63
1	AP	200/569 (35%)	184 (92%)	15 (8%)	1 (0%)	24	63
1	AQ	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	AR	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	AS	200/569 (35%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AT	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	B	258/569 (45%)	250 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	D	258/569 (45%)	253 (98%)	5 (2%)	0	100	100
1	E	258/569 (45%)	248 (96%)	10 (4%)	0	100	100
1	F	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	G	258/569 (45%)	246 (95%)	12 (5%)	0	100	100
1	H	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	I	258/569 (45%)	252 (98%)	6 (2%)	0	100	100
1	J	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	K	258/569 (45%)	255 (99%)	3 (1%)	0	100	100
1	L	258/569 (45%)	253 (98%)	5 (2%)	0	100	100
1	M	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	N	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	O	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	P	258/569 (45%)	249 (96%)	9 (4%)	0	100	100
1	Q	258/569 (45%)	249 (96%)	9 (4%)	0	100	100
1	R	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	S	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	T	258/569 (45%)	249 (96%)	9 (4%)	0	100	100
1	U	258/569 (45%)	254 (98%)	4 (2%)	0	100	100
1	V	258/569 (45%)	249 (96%)	9 (4%)	0	100	100
1	W	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	X	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	Y	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	Z	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	a	258/569 (45%)	252 (98%)	6 (2%)	0	100	100
1	b	258/569 (45%)	249 (96%)	9 (4%)	0	100	100
1	c	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	d	258/569 (45%)	252 (98%)	6 (2%)	0	100	100
1	e	258/569 (45%)	255 (99%)	3 (1%)	0	100	100
1	f	258/569 (45%)	250 (97%)	8 (3%)	0	100	100
1	g	258/569 (45%)	251 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	h	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	i	258/569 (45%)	249 (96%)	9 (4%)	0	100	100
1	j	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	k	258/569 (45%)	251 (97%)	7 (3%)	0	100	100
1	l	258/569 (45%)	252 (98%)	6 (2%)	0	100	100
1	m	258/569 (45%)	248 (96%)	10 (4%)	0	100	100
1	n	258/569 (45%)	253 (98%)	5 (2%)	0	100	100
1	o	258/569 (45%)	248 (96%)	10 (4%)	0	100	100
1	p	207/569 (36%)	200 (97%)	7 (3%)	0	100	100
1	q	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	r	207/569 (36%)	199 (96%)	7 (3%)	1 (0%)	24	63
1	s	207/569 (36%)	201 (97%)	5 (2%)	1 (0%)	24	63
1	t	201/569 (35%)	194 (96%)	6 (3%)	1 (0%)	24	63
1	u	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	v	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	w	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	x	201/569 (35%)	194 (96%)	6 (3%)	1 (0%)	24	63
1	y	207/569 (36%)	201 (97%)	5 (2%)	1 (0%)	24	63
1	z	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
2	AX	240/372 (64%)	236 (98%)	3 (1%)	1 (0%)	30	67
3	AY	207/254 (82%)	205 (99%)	2 (1%)	0	100	100
3	AZ	207/254 (82%)	201 (97%)	6 (3%)	0	100	100
3	Aa	207/254 (82%)	201 (97%)	6 (3%)	0	100	100
3	Ab	207/254 (82%)	202 (98%)	5 (2%)	0	100	100
3	Ac	207/254 (82%)	204 (99%)	3 (1%)	0	100	100
4	Ad	257/269 (96%)	248 (96%)	9 (4%)	0	100	100
5	Ae	68/111 (61%)	65 (96%)	3 (4%)	0	100	100
5	Af	68/111 (61%)	67 (98%)	1 (2%)	0	100	100
5	Ag	68/111 (61%)	68 (100%)	0	0	100	100
5	Ah	68/111 (61%)	67 (98%)	1 (2%)	0	100	100
5	Ai	68/111 (61%)	66 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Aj	38/111 (34%)	37 (97%)	1 (3%)	0	100	100
6	Ak	108/135 (80%)	107 (99%)	1 (1%)	0	100	100
6	Al	108/135 (80%)	106 (98%)	2 (2%)	0	100	100
6	Am	108/135 (80%)	107 (99%)	1 (1%)	0	100	100
6	An	108/135 (80%)	105 (97%)	3 (3%)	0	100	100
6	Ao	108/135 (80%)	104 (96%)	4 (4%)	0	100	100
7	Ap	132/152 (87%)	132 (100%)	0	0	100	100
7	Aq	150/152 (99%)	145 (97%)	5 (3%)	0	100	100
7	Ar	132/152 (87%)	128 (97%)	4 (3%)	0	100	100
7	As	150/152 (99%)	148 (99%)	2 (1%)	0	100	100
7	At	150/152 (99%)	148 (99%)	2 (1%)	0	100	100
7	Au	150/152 (99%)	147 (98%)	3 (2%)	0	100	100
8	AU	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
8	AV	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
8	AW	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
8	Av	85/87 (98%)	82 (96%)	3 (4%)	0	100	100
9	A1	695/697 (100%)	680 (98%)	15 (2%)	0	100	100
9	A2	695/697 (100%)	680 (98%)	15 (2%)	0	100	100
9	A3	695/697 (100%)	680 (98%)	15 (2%)	0	100	100
9	A4	695/697 (100%)	680 (98%)	15 (2%)	0	100	100
9	A5	695/697 (100%)	681 (98%)	14 (2%)	0	100	100
9	Aw	695/697 (100%)	679 (98%)	16 (2%)	0	100	100
9	Ax	695/697 (100%)	681 (98%)	14 (2%)	0	100	100
9	Ay	695/697 (100%)	680 (98%)	15 (2%)	0	100	100
9	Az	695/697 (100%)	680 (98%)	15 (2%)	0	100	100
All	All	28824/57443 (50%)	27875 (97%)	908 (3%)	41 (0%)	49	83

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AC	131	ILE
1	AD	131	ILE
1	AE	131	ILE

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Mol	Chain	Res	Type
1	AF	131	ILE
1	AG	131	ILE

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	178/506 (35%)	167 (94%)	11 (6%)	16	38
1	1	178/506 (35%)	165 (93%)	13 (7%)	13	34
1	2	174/506 (34%)	163 (94%)	11 (6%)	16	37
1	3	178/506 (35%)	168 (94%)	10 (6%)	19	40
1	4	178/506 (35%)	169 (95%)	9 (5%)	21	42
1	5	178/506 (35%)	166 (93%)	12 (7%)	15	36
1	6	174/506 (34%)	162 (93%)	12 (7%)	14	36
1	7	178/506 (35%)	169 (95%)	9 (5%)	21	42
1	8	178/506 (35%)	167 (94%)	11 (6%)	16	38
1	9	178/506 (35%)	168 (94%)	10 (6%)	19	40
1	A	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	AA	178/506 (35%)	166 (93%)	12 (7%)	15	36
1	AB	178/506 (35%)	168 (94%)	10 (6%)	19	40
1	AC	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AD	180/506 (36%)	175 (97%)	5 (3%)	38	60
1	AE	180/506 (36%)	173 (96%)	7 (4%)	28	49
1	AF	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AG	180/506 (36%)	175 (97%)	5 (3%)	38	60
1	AH	180/506 (36%)	172 (96%)	8 (4%)	25	47
1	AI	180/506 (36%)	175 (97%)	5 (3%)	38	60
1	AJ	180/506 (36%)	176 (98%)	4 (2%)	45	64
1	AK	180/506 (36%)	176 (98%)	4 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AL	180/506 (36%)	175 (97%)	5 (3%)	38	60
1	AM	180/506 (36%)	172 (96%)	8 (4%)	25	47
1	AN	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AO	180/506 (36%)	173 (96%)	7 (4%)	28	49
1	AP	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AQ	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AR	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AS	180/506 (36%)	173 (96%)	7 (4%)	28	49
1	AT	180/506 (36%)	175 (97%)	5 (3%)	38	60
1	B	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	C	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	D	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	E	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	F	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	G	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	H	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	I	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	J	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	K	226/506 (45%)	219 (97%)	7 (3%)	35	56
1	L	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	M	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	N	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	O	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	P	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	Q	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	R	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	S	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	T	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	U	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	V	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	W	226/506 (45%)	221 (98%)	5 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	Y	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	Z	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	a	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	b	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	c	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	d	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	e	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	f	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	g	226/506 (45%)	220 (97%)	6 (3%)	39	61
1	h	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	i	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	j	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	k	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	l	226/506 (45%)	224 (99%)	2 (1%)	70	79
1	m	226/506 (45%)	219 (97%)	7 (3%)	35	56
1	n	226/506 (45%)	223 (99%)	3 (1%)	61	74
1	o	226/506 (45%)	222 (98%)	4 (2%)	51	68
1	p	178/506 (35%)	166 (93%)	12 (7%)	15	36
1	q	178/506 (35%)	168 (94%)	10 (6%)	19	40
1	r	178/506 (35%)	169 (95%)	9 (5%)	21	42
1	s	178/506 (35%)	167 (94%)	11 (6%)	16	38
1	t	174/506 (34%)	164 (94%)	10 (6%)	18	40
1	u	178/506 (35%)	166 (93%)	12 (7%)	15	36
1	v	178/506 (35%)	167 (94%)	11 (6%)	16	38
1	w	178/506 (35%)	167 (94%)	11 (6%)	16	38
1	x	174/506 (34%)	164 (94%)	10 (6%)	18	40
1	y	178/506 (35%)	168 (94%)	10 (6%)	19	40
1	z	178/506 (35%)	167 (94%)	11 (6%)	16	38
2	AX	217/335 (65%)	208 (96%)	9 (4%)	27	49
3	AY	187/232 (81%)	182 (97%)	5 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AZ	185/232 (80%)	179 (97%)	6 (3%)	34	56
3	Aa	185/232 (80%)	181 (98%)	4 (2%)	45	64
3	Ab	187/232 (81%)	180 (96%)	7 (4%)	30	51
3	Ac	189/232 (82%)	180 (95%)	9 (5%)	23	44
4	Ad	236/249 (95%)	220 (93%)	16 (7%)	14	36
5	Ae	64/103 (62%)	60 (94%)	4 (6%)	16	37
5	Af	64/103 (62%)	59 (92%)	5 (8%)	11	32
5	Ag	64/103 (62%)	59 (92%)	5 (8%)	11	32
5	Ah	62/103 (60%)	58 (94%)	4 (6%)	15	37
5	Ai	64/103 (62%)	62 (97%)	2 (3%)	35	56
5	Aj	35/103 (34%)	32 (91%)	3 (9%)	10	29
6	Ak	107/129 (83%)	104 (97%)	3 (3%)	38	60
6	Al	107/129 (83%)	104 (97%)	3 (3%)	38	60
6	Am	107/129 (83%)	105 (98%)	2 (2%)	50	67
6	An	107/129 (83%)	103 (96%)	4 (4%)	30	51
6	Ao	107/129 (83%)	106 (99%)	1 (1%)	70	79
7	Ap	115/130 (88%)	115 (100%)	0	100	100
7	Aq	127/130 (98%)	125 (98%)	2 (2%)	55	70
7	Ar	116/130 (89%)	115 (99%)	1 (1%)	70	79
7	As	130/130 (100%)	128 (98%)	2 (2%)	57	72
7	At	130/130 (100%)	128 (98%)	2 (2%)	57	72
7	Au	130/130 (100%)	129 (99%)	1 (1%)	73	80
8	AU	78/80 (98%)	71 (91%)	7 (9%)	9	27
8	AV	80/80 (100%)	75 (94%)	5 (6%)	16	37
8	AW	80/80 (100%)	75 (94%)	5 (6%)	16	37
8	Av	77/80 (96%)	74 (96%)	3 (4%)	28	49
9	A1	619/619 (100%)	605 (98%)	14 (2%)	44	64
9	A2	619/619 (100%)	604 (98%)	15 (2%)	43	64
9	A3	619/619 (100%)	604 (98%)	15 (2%)	43	64
9	A4	619/619 (100%)	605 (98%)	14 (2%)	44	64
9	A5	619/619 (100%)	605 (98%)	14 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Aw	619/619 (100%)	604 (98%)	15 (2%)	43	64
9	Ax	619/619 (100%)	605 (98%)	14 (2%)	44	64
9	Ay	619/619 (100%)	604 (98%)	15 (2%)	43	64
9	Az	619/619 (100%)	604 (98%)	15 (2%)	43	64
All	All	25492/51170 (50%)	24718 (97%)	774 (3%)	37	57

5 of 774 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AK	49	GLN
4	Ad	147	LEU
1	AM	109	VAL
1	AJ	159	VAL
1	AT	51	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 232 such sidechains are listed below:

Mol	Chain	Res	Type
1	AN	144	HIS
9	A4	175	ASN
4	Ad	96	ASN
9	A3	584	GLN
9	Az	175	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76383. 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](#)

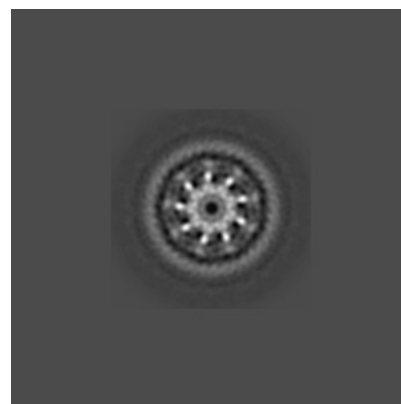
6.1.1 Primary map



X



Y

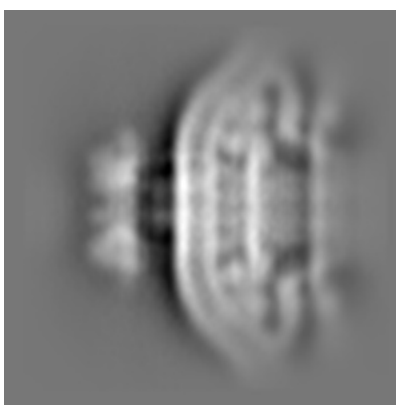


Z

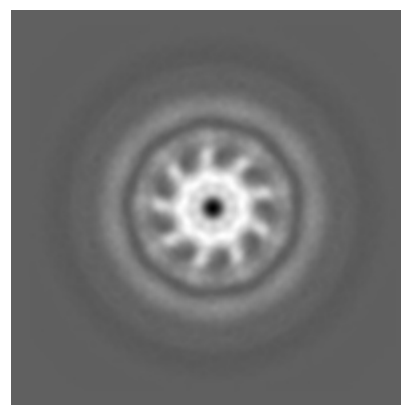
6.1.2 Raw map



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: 128

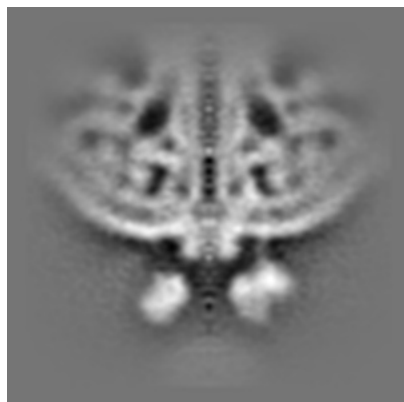


Y Index: 128



Z Index: 128

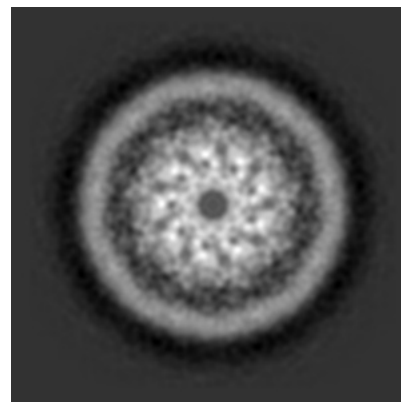
6.2.2 Raw map



X Index: 50



Y Index: 50

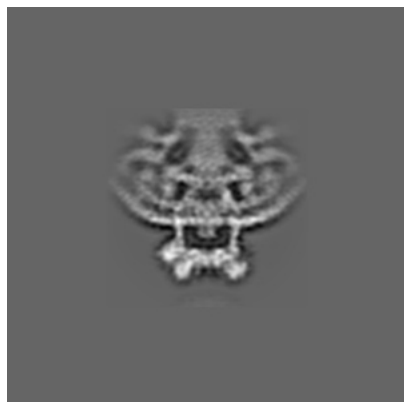


Z Index: 50

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: 138



Y Index: 116

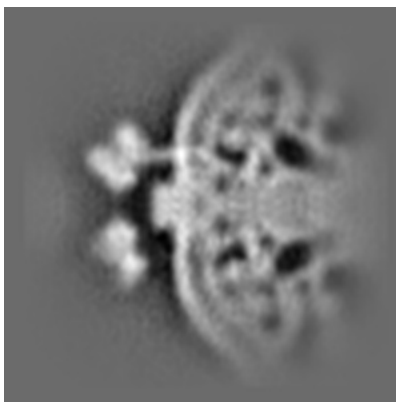


Z Index: 119

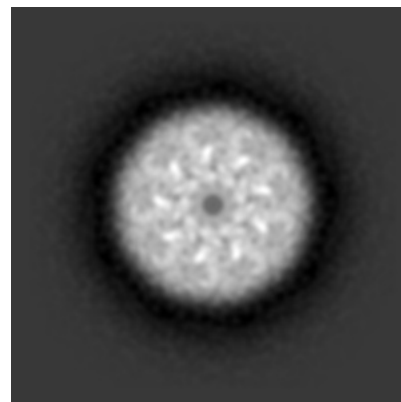
6.3.2 Raw map



X Index: 46



Y Index: 54

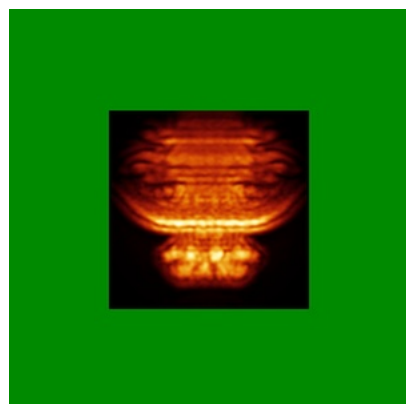


Z Index: 44

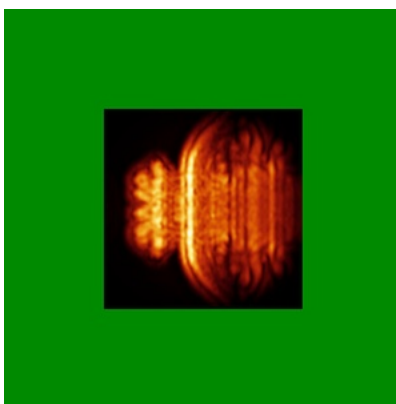
The images above show the largest variance slices of the map in three orthogonal directions.

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

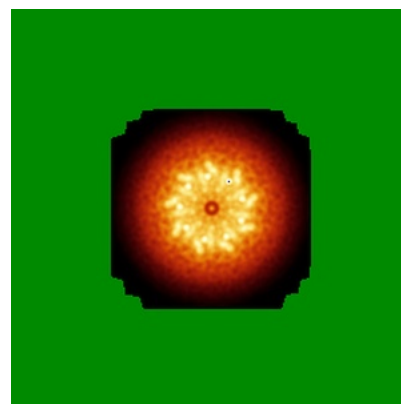
6.4.1 Primary map



X

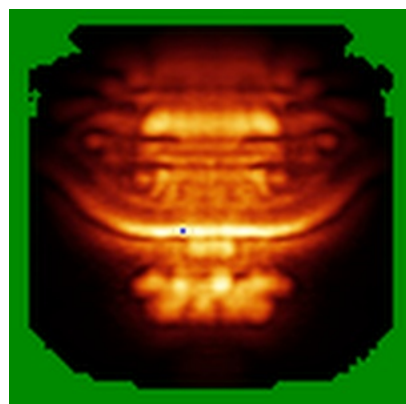


Y

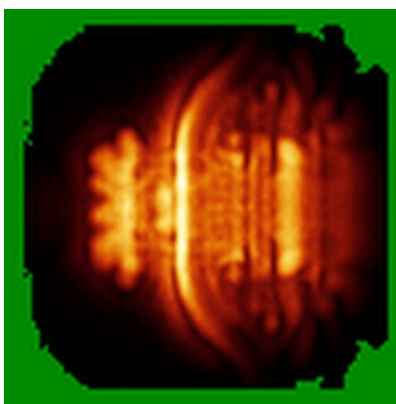


Z

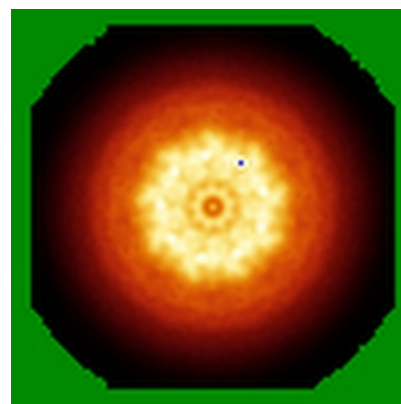
6.4.2 Raw map



X



Y

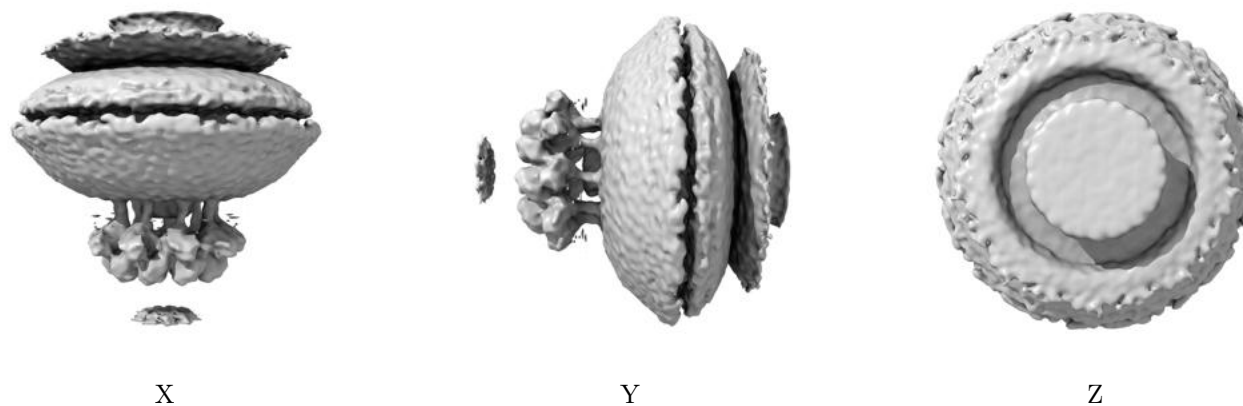


Z

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.

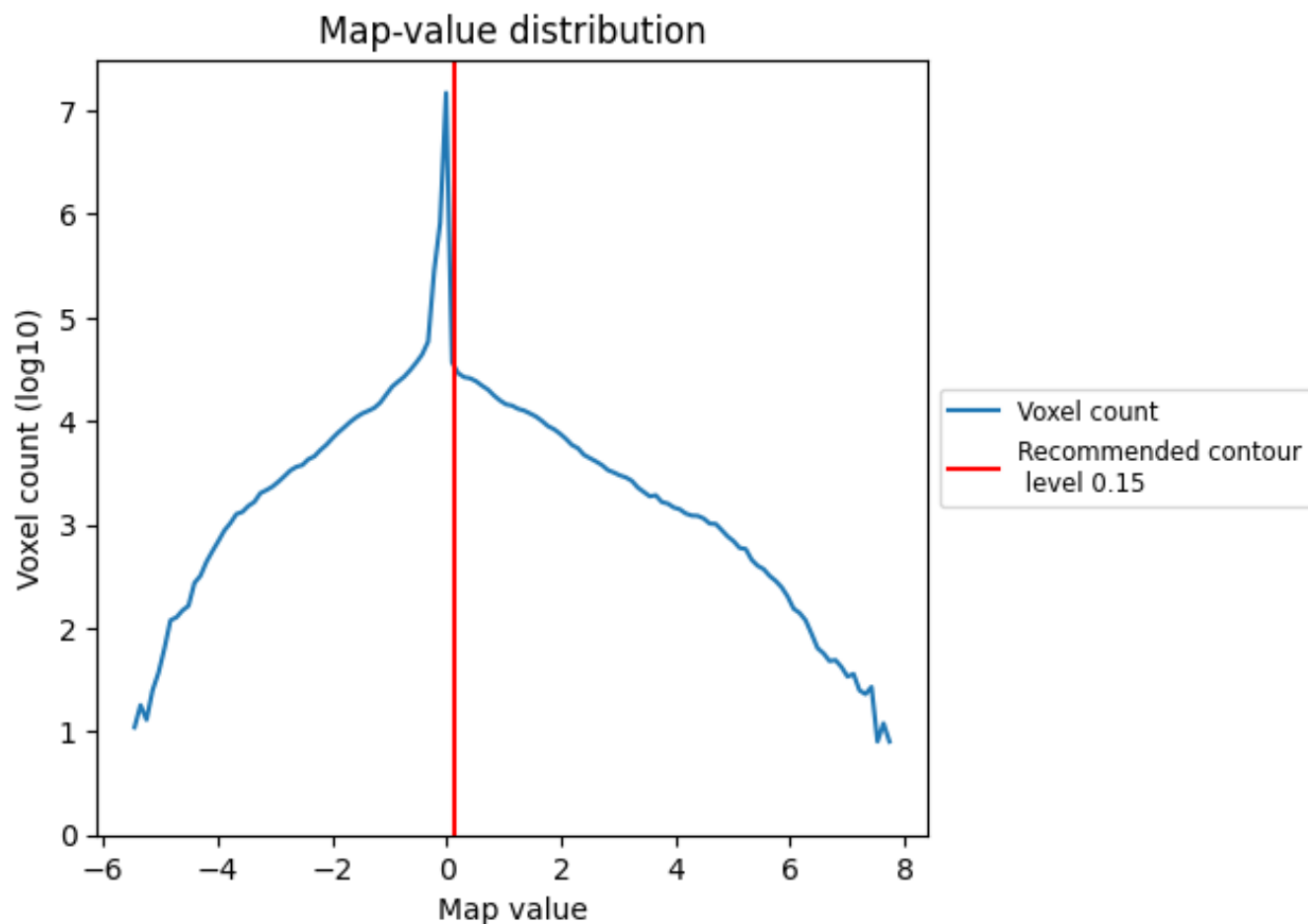
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

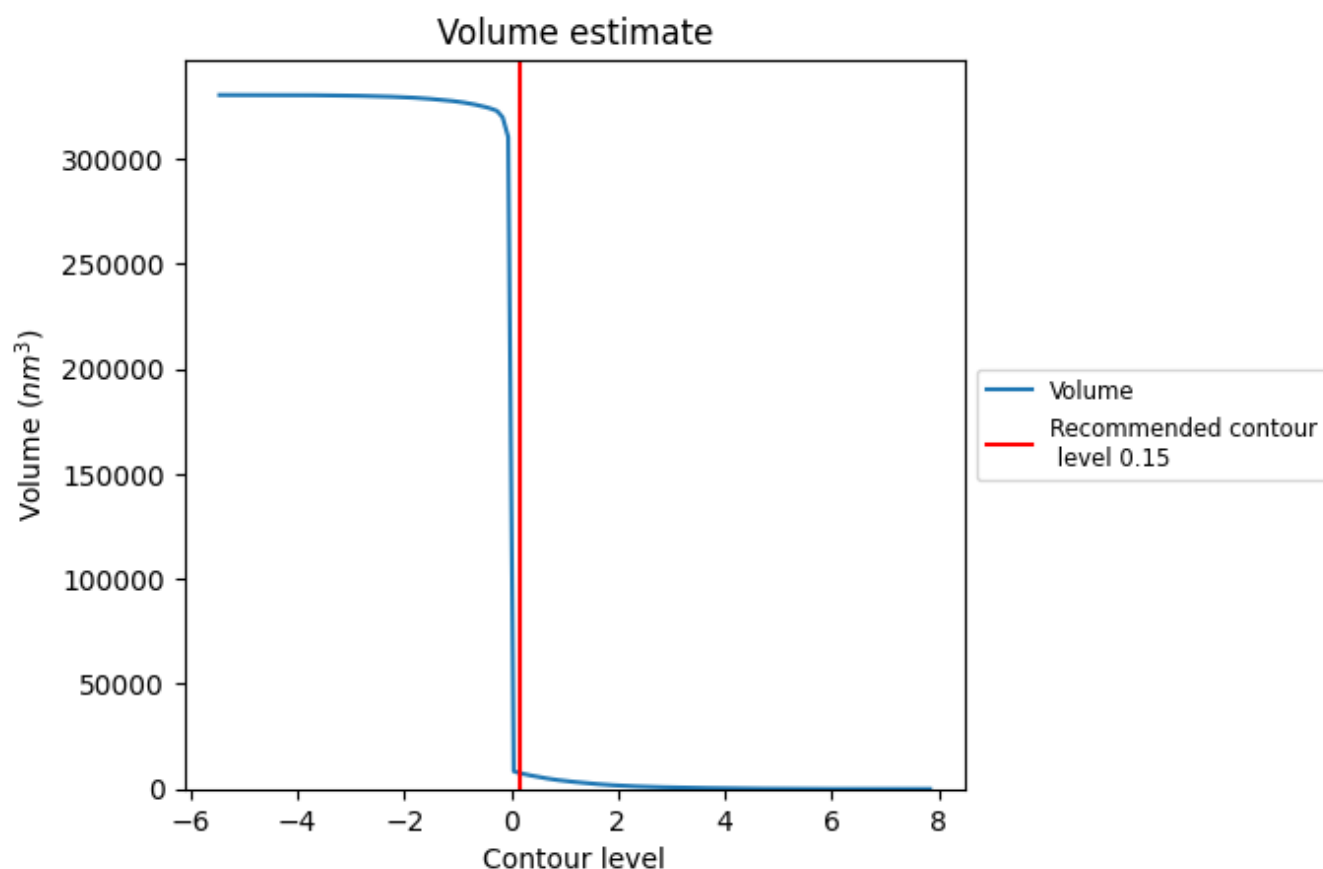
This section contains the results of statistical analysis of the map.

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.

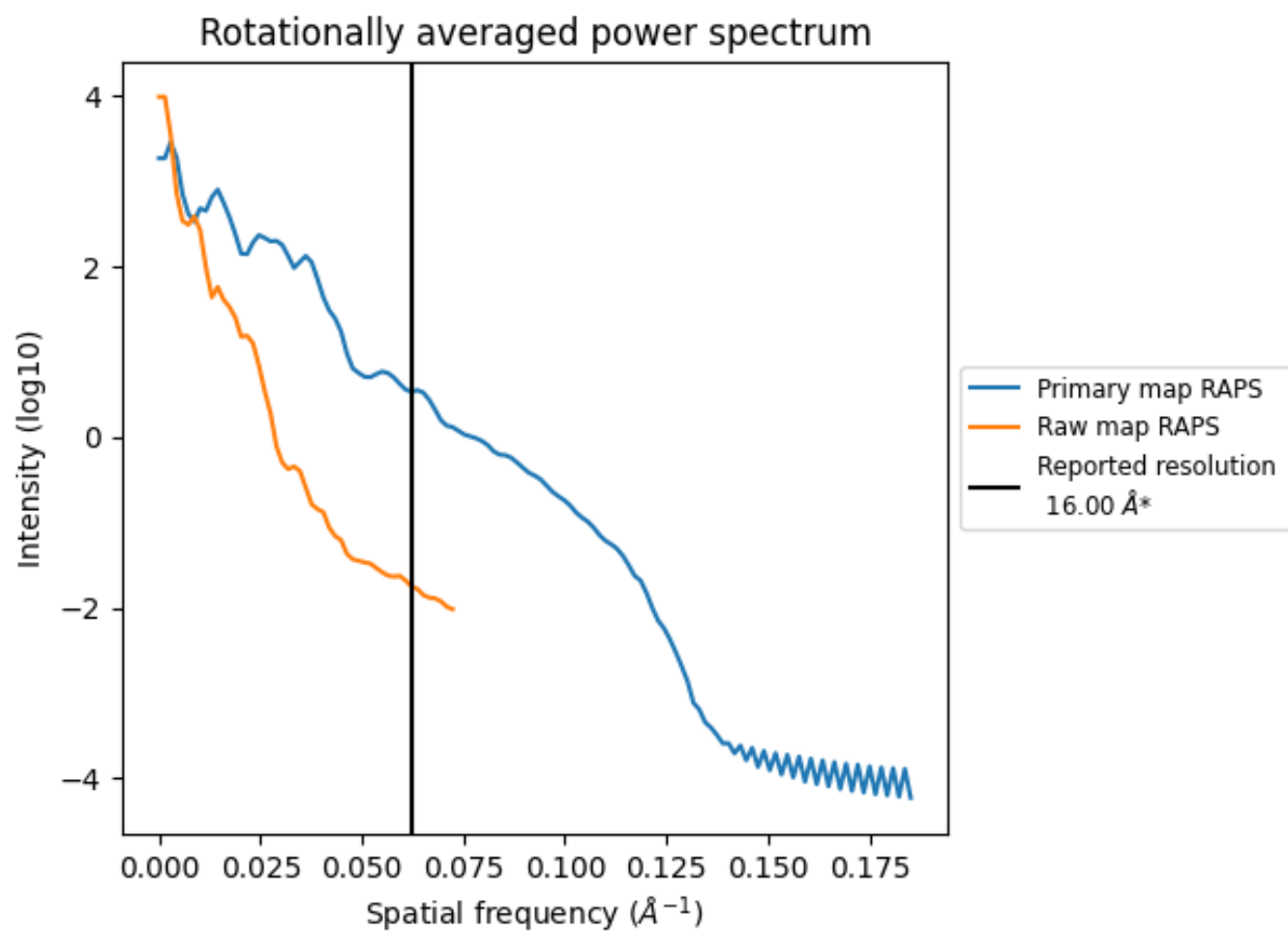
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 7631 nm^3 ; this corresponds to an approximate mass of 6894 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

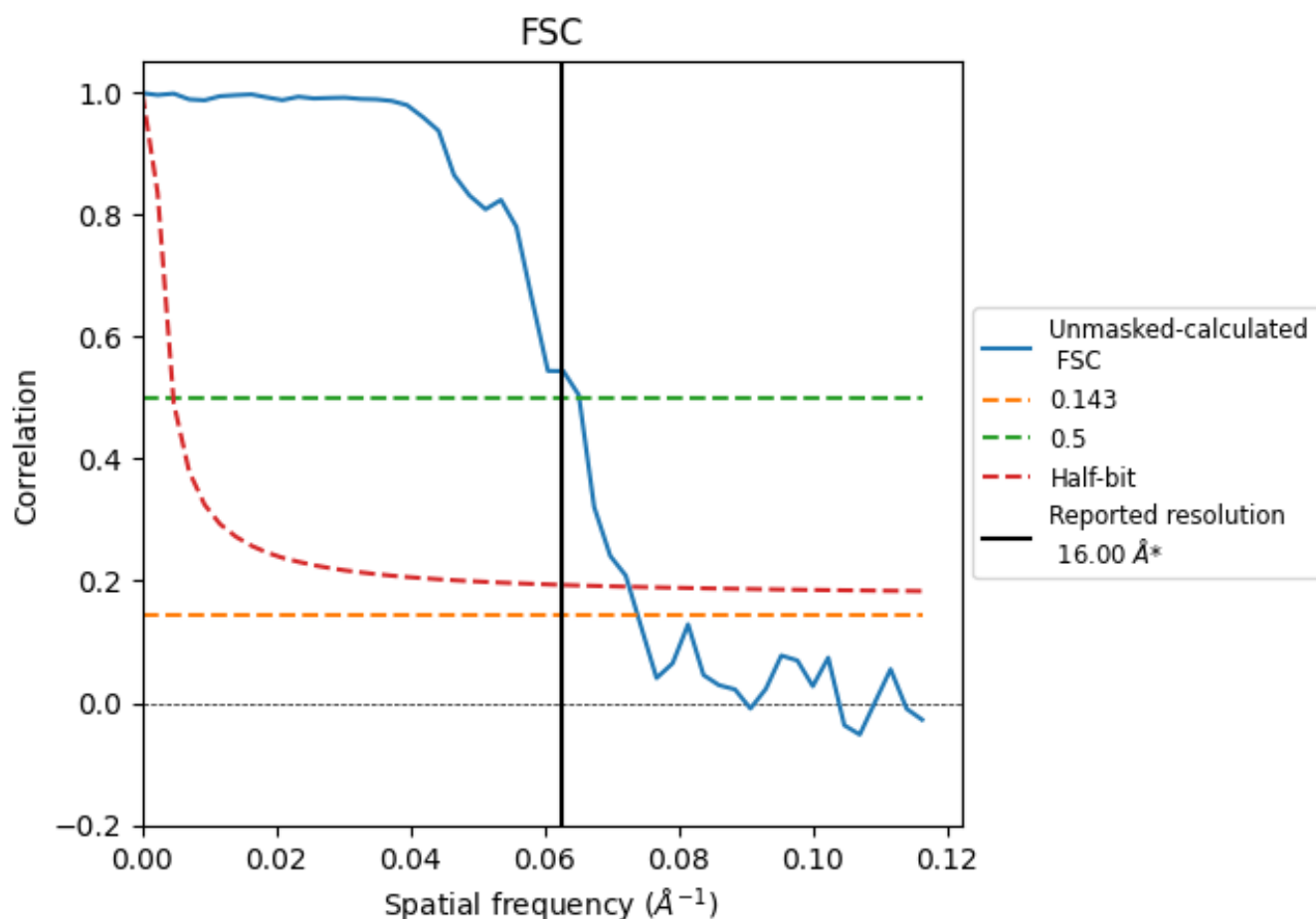


*Reported resolution corresponds to spatial frequency of 0.062 Å⁻¹

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 0.062 Å⁻¹

8.2 Resolution estimates [i](#)

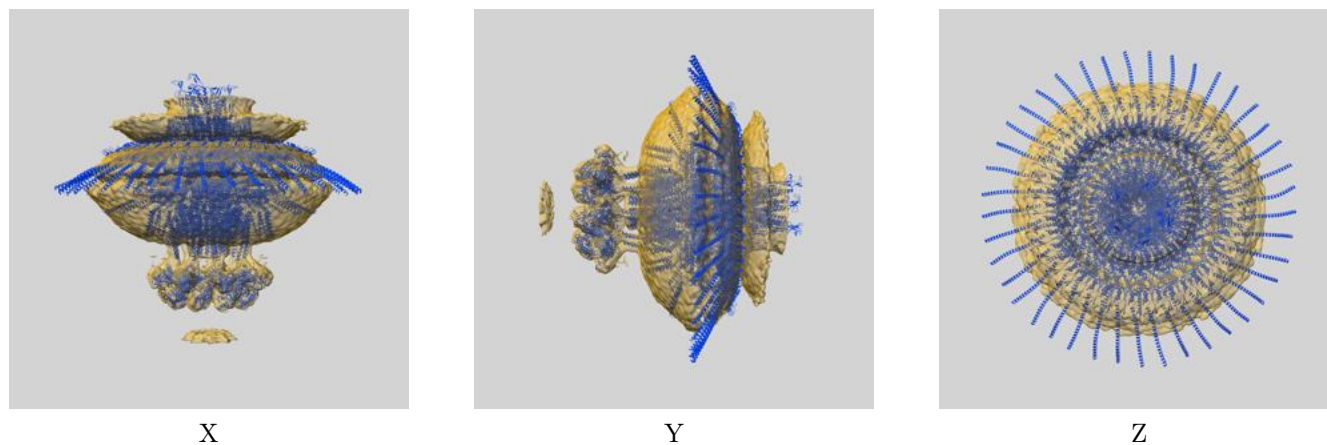
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	16.00	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	13.53	15.34	13.77

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

9 Map-model fit [i](#)

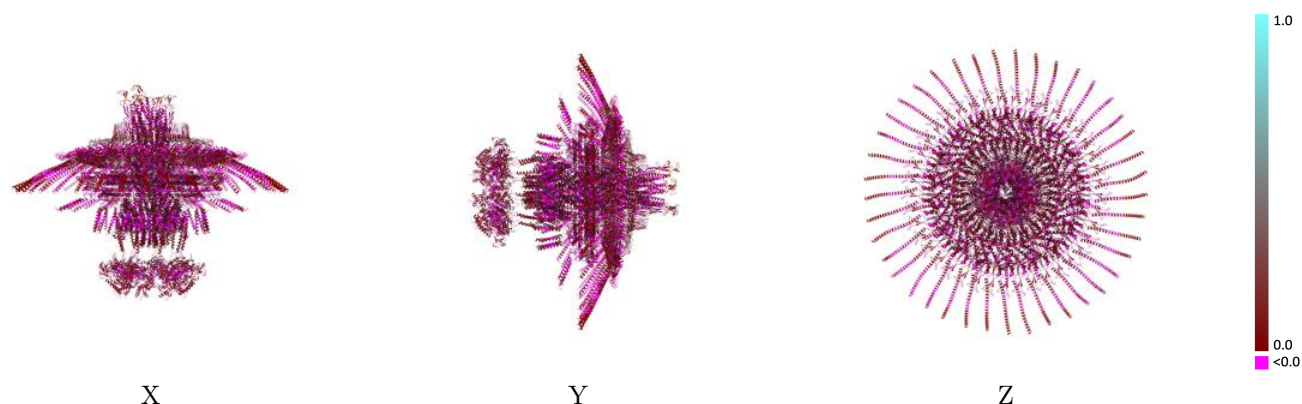
This section contains information regarding the fit between EMDB map EMD-76383 and PDB model 12EQ. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



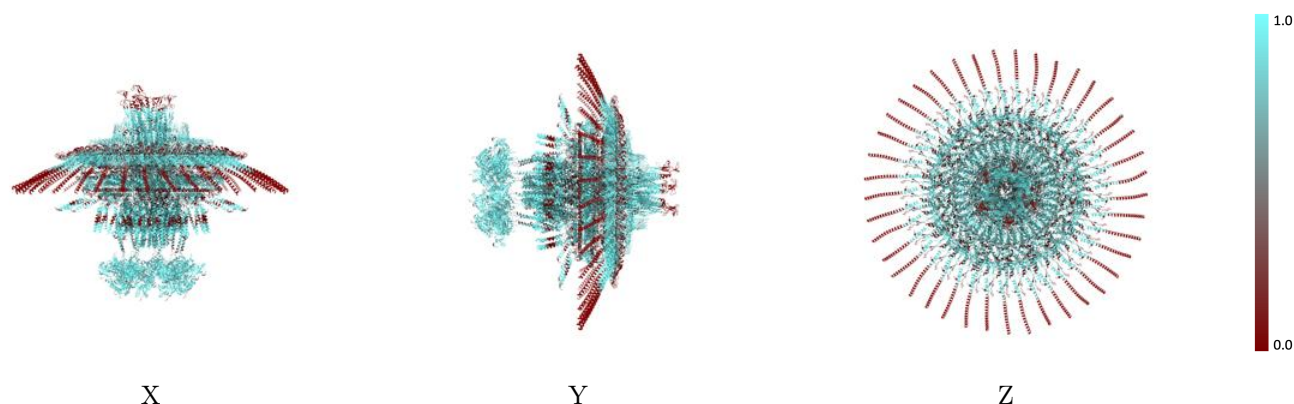
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



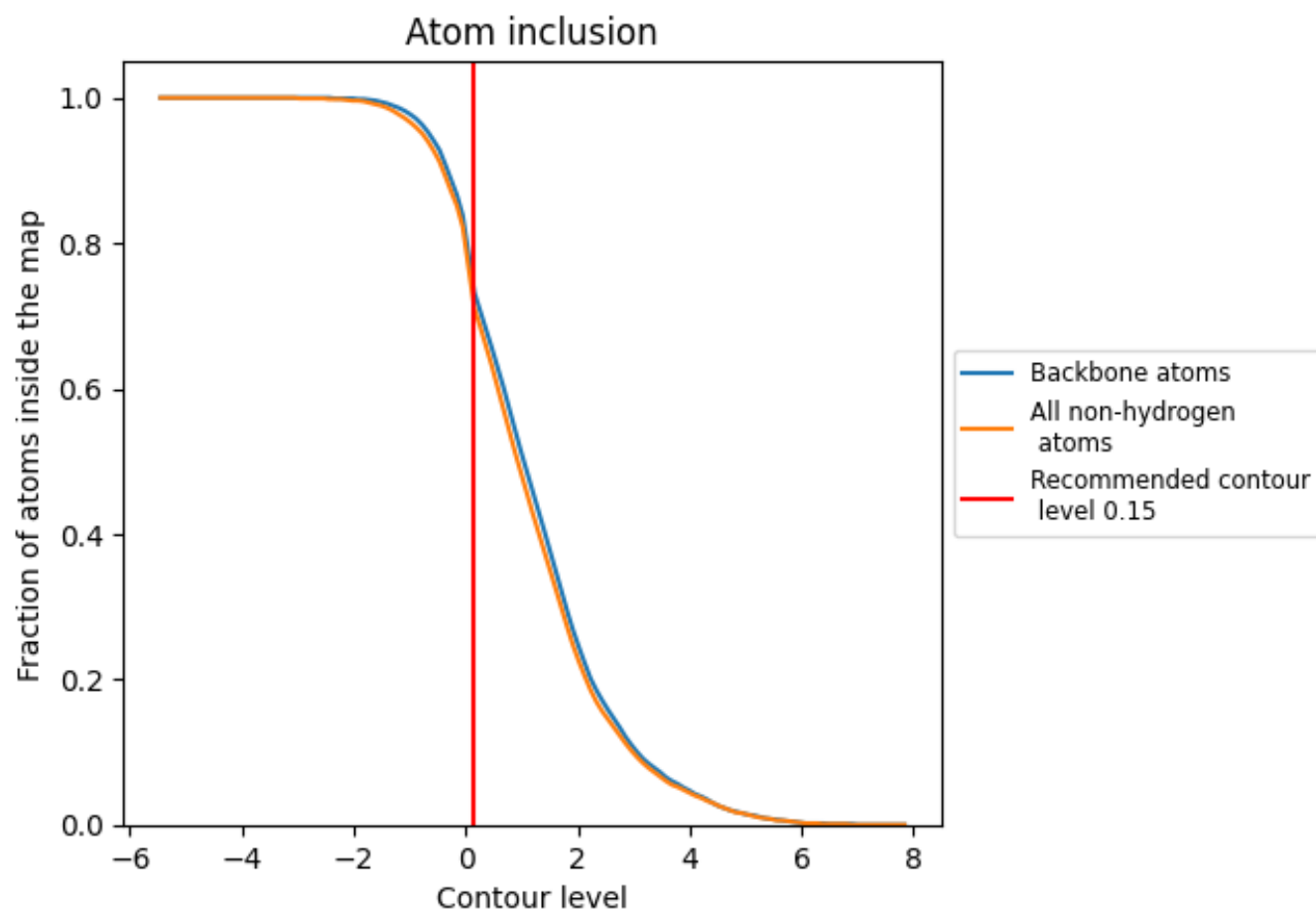
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 73% of all backbone atoms, 71% 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	 0.7120	 0.0410
0	 0.7500	 0.0450
1	 0.7740	 0.0480
2	 0.7620	 0.0550
3	 0.7590	 0.0470
4	 0.7800	 0.0570
5	 0.7620	 0.0530
6	 0.7870	 0.0520
7	 0.7550	 0.0580
8	 0.7510	 0.0470
9	 0.7730	 0.0530
A	 0.6370	 0.0450
A1	 0.8910	 0.0540
A2	 0.8910	 0.0540
A3	 0.8910	 0.0530
A4	 0.8920	 0.0530
A5	 0.8910	 0.0520
AA	 0.7800	 0.0550
AB	 0.7710	 0.0540
AC	 0.5280	 0.0170
AD	 0.4740	 0.0050
AE	 0.5400	 0.0180
AF	 0.4780	 0.0050
AG	 0.5430	 0.0150
AH	 0.4820	 0.0050
AI	 0.5420	 0.0190
AJ	 0.4800	 0.0100
AK	 0.5350	 0.0200
AL	 0.4820	 0.0050
AM	 0.5270	 0.0180
AN	 0.4760	 0.0090
AO	 0.5230	 0.0210
AP	 0.4820	 0.0060
AQ	 0.5270	 0.0150
AR	 0.4750	 0.0060



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Chain	Atom inclusion	Q-score
AS	0.5240	0.0160
AT	0.4800	0.0070
AU	0.7080	0.0040
AV	0.7180	0.0100
AW	0.7830	0.0030
AX	0.6200	0.0330
AY	0.8900	0.0330
AZ	0.9130	0.0320
Aa	0.8990	0.0470
Ab	0.8600	0.0170
Ac	0.8530	0.0330
Ad	0.9130	0.0370
Ae	0.8620	0.0510
Af	0.8510	0.0620
Ag	0.8530	0.0500
Ah	0.8050	0.0380
Ai	0.8160	0.0330
Aj	0.7760	0.0310
Ak	0.7970	0.0200
Al	0.8150	0.0210
Am	0.8210	0.0270
An	0.8330	0.0330
Ao	0.8690	0.0180
Ap	0.7690	0.0140
Aq	0.6510	-0.0060
Ar	0.4210	0.0000
As	0.5910	-0.0010
At	0.6010	0.0270
Au	0.5520	0.0100
Av	0.6520	0.0180
Aw	0.8920	0.0530
Ax	0.8930	0.0540
Ay	0.8930	0.0530
Az	0.8920	0.0530
B	0.6340	0.0490
C	0.6370	0.0480
D	0.6400	0.0440
E	0.6270	0.0380
F	0.6370	0.0390
G	0.6390	0.0510
H	0.6260	0.0470
I	0.6160	0.0440

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Chain	Atom inclusion	Q-score
J	 0.6390	 0.0470
K	 0.6260	 0.0500
L	 0.6460	 0.0480
M	 0.6370	 0.0430
N	 0.6250	 0.0410
O	 0.6220	 0.0400
P	 0.6310	 0.0490
Q	 0.6220	 0.0410
R	 0.6280	 0.0460
S	 0.6060	 0.0420
T	 0.6290	 0.0440
U	 0.6450	 0.0510
V	 0.6380	 0.0440
W	 0.6240	 0.0420
X	 0.6280	 0.0420
Y	 0.6320	 0.0520
Z	 0.6280	 0.0420
a	 0.6250	 0.0430
b	 0.6310	 0.0430
c	 0.6290	 0.0370
d	 0.6450	 0.0510
e	 0.6370	 0.0480
f	 0.6310	 0.0430
g	 0.6400	 0.0370
h	 0.6360	 0.0530
i	 0.6290	 0.0440
j	 0.6260	 0.0420
k	 0.6290	 0.0400
l	 0.6330	 0.0350
m	 0.6450	 0.0520
n	 0.6420	 0.0490
o	 0.6210	 0.0390
p	 0.7710	 0.0560
q	 0.7700	 0.0540
r	 0.7450	 0.0460
s	 0.7740	 0.0520
t	 0.7940	 0.0490
u	 0.7760	 0.0540
v	 0.7790	 0.0530
w	 0.7430	 0.0470
x	 0.7660	 0.0430
y	 0.7850	 0.0510

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Chain	Atom inclusion	Q-score
z	 0.7720	 0.0510