wwPDB EM Validation Summary Report ⓘ

Oct 5, 2026 – 03:52 PM EDT

PDB ID	:	12DW / pdb_000012dw
EMDB ID	:	EMD-76349
Title	:	In situ cryo-EM structure of the export apparatus and MS-ring of the flagellar basal body from Borrelia burgdorferi
Authors	:	Yue, J.; Liu, J.
Deposited on	:	2026-03-30
Resolution	:	5.00 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:

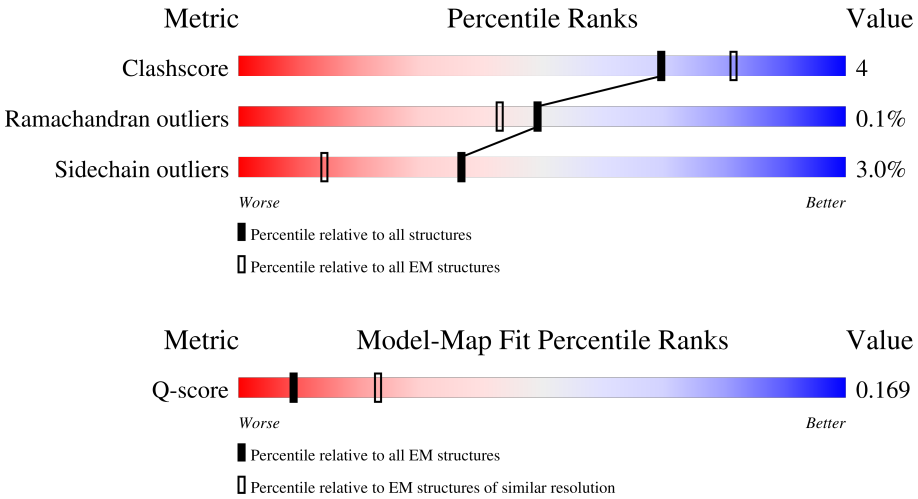
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 5.00 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	1057 (4.50 - 5.50)

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 <=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	5% 33% 63%
1	1	569	32% 63%
1	2	569	32% 64%
1	3	569	33% 63%

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Mol	Chain	Length	Quality of chain
1	4	569	32% 5% 63%
1	5	569	5% 33% 63%
1	6	569	32% 64%
1	7	569	32% 5% 63%
1	8	569	32% 63%
1	9	569	5% 33% 63%
1	A	569	7% 41% 5% 54%
1	AA	569	5% 32% 63%
1	AB	569	5% 33% 63%
1	AC	569	13% 30% 5% 64%
1	AD	569	11% 30% 5% 64%
1	AE	569	13% 30% 6% 64%
1	AF	569	13% 30% 6% 64%
1	AG	569	13% 31% 5% 64%
1	AH	569	12% 30% 6% 64%
1	AI	569	14% 30% 5% 64%
1	AJ	569	12% 30% 5% 64%
1	AK	569	12% 30% 5% 64%
1	AL	569	13% 30% 5% 64%
1	AM	569	12% 30% 5% 64%
1	AN	569	12% 30% 5% 64%
1	AO	569	12% 30% 5% 64%
1	AP	569	11% 30% 5% 64%
1	AQ	569	12% 30% 5% 64%
1	AR	569	12% 30% 5% 64%

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Mol	Chain	Length	Quality of chain
1	AS	569	12% 29% 6% 64%
1	AT	569	13% 31% 5% 64%
1	B	569	7% 40% 6% 54%
1	C	569	7% 40% 5% 54%
1	D	569	7% 40% 6% 54%
1	E	569	6% 39% 7% 54%
1	F	569	6% 41% 5% 54%
1	G	569	6% 40% 6% 54%
1	H	569	6% 41% 5% 54%
1	I	569	7% 41% 5% 54%
1	J	569	6% 41% 5% 54%
1	K	569	7% 41% 5% 54%
1	L	569	7% 40% 6% 54%
1	M	569	7% 41% 5% 54%
1	N	569	7% 38% 7% 54%
1	O	569	6% 40% 5% 54%
1	P	569	7% 41% 5% 54%
1	Q	569	6% 40% 6% 54%
1	R	569	6% 41% 5% 54%
1	S	569	7% 39% 7% 54%
1	T	569	7% 41% 5% 54%
1	U	569	7% 41% 5% 54%
1	V	569	7% 40% 5% 54%
1	W	569	6% 40% 6% 54%
1	X	569	6% 39% 7% 54%

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Mol	Chain	Length	Quality of chain
1	Y	569	7% 42% 54%
1	Z	569	7% 41% 54%
1	a	569	6% 41% 5% 54%
1	b	569	7% 40% 6% 54%
1	c	569	7% 40% 6% 54%
1	d	569	7% 40% 5% 54%
1	e	569	8% 40% 6% 54%
1	f	569	7% 41% 5% 54%
1	g	569	7% 41% 5% 54%
1	h	569	7% 41% 5% 54%
1	i	569	7% 40% 6% 54%
1	j	569	7% 41% 5% 54%
1	k	569	7% 42% 54%
1	l	569	8% 41% 5% 54%
1	m	569	6% 40% 6% 54%
1	n	569	6% 42% 54%
1	o	569	6% 40% 6% 54%
1	p	569	32% 63%
1	q	569	33% 63%
1	r	569	33% 63%
1	s	569	33% 63%
1	t	569	32% 64%
1	u	569	5% 32% 63%
1	v	569	34% 63%
1	w	569	33% 63%

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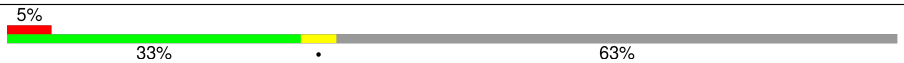
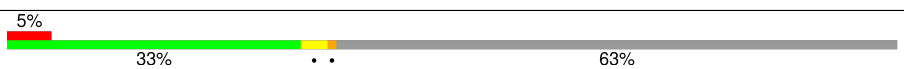
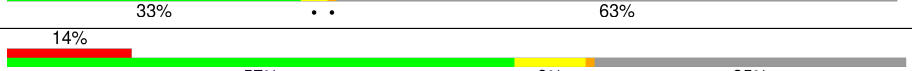
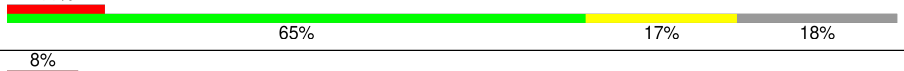
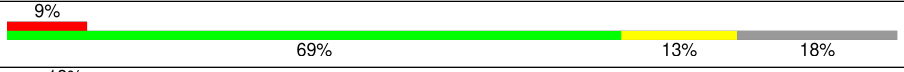
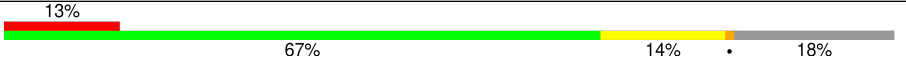
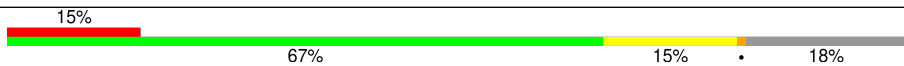
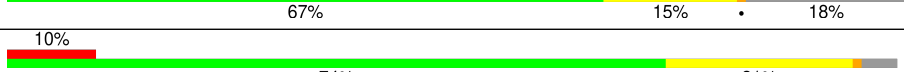
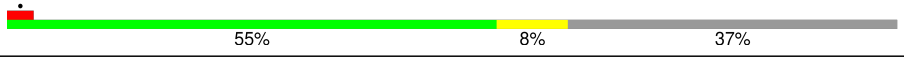
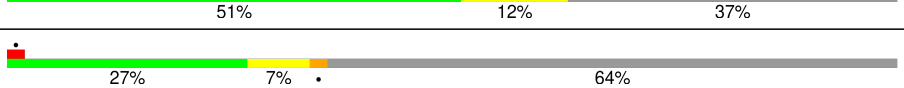
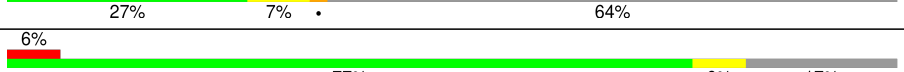
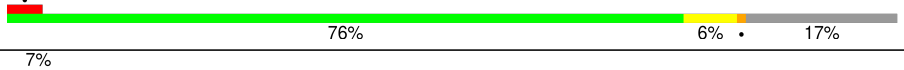
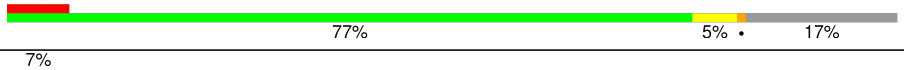
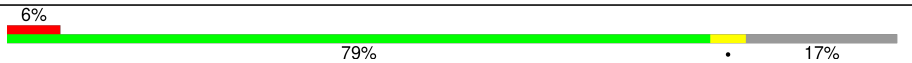
Mol	Chain	Length	Quality of chain
1	x	569	
1	y	569	
1	z	569	
2	AX	372	
3	AY	254	
3	AZ	254	
3	Aa	254	
3	Ab	254	
3	Ac	254	
4	Ad	269	
5	Ae	111	
5	Af	111	
5	Ag	111	
5	Ah	111	
5	Ai	111	
5	Aj	111	
6	Ak	135	
6	Al	135	
6	Am	135	
6	An	135	
6	Ao	135	
7	Ap	152	
7	Aq	152	
7	Ar	152	
7	As	152	

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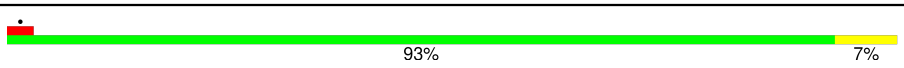
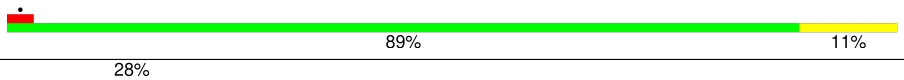
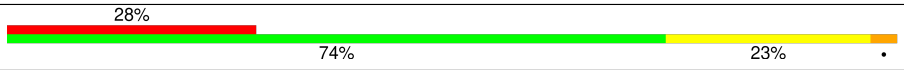
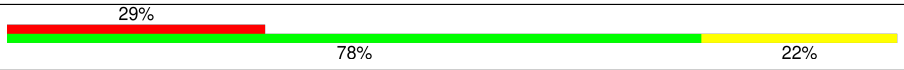
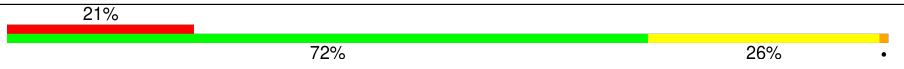
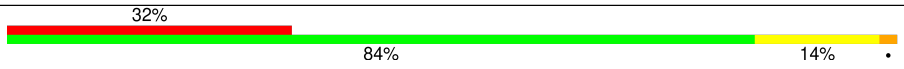
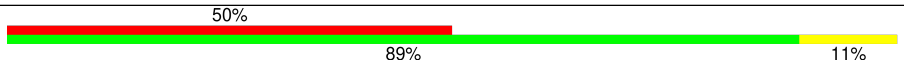
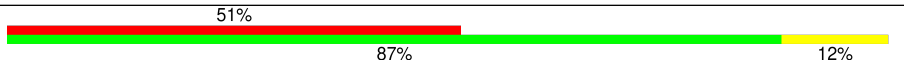
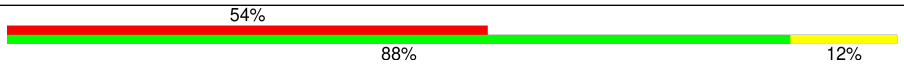
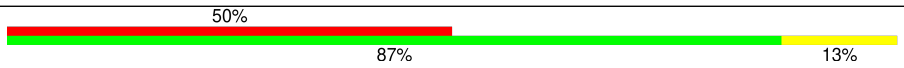
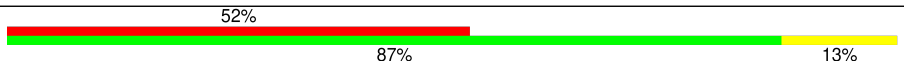
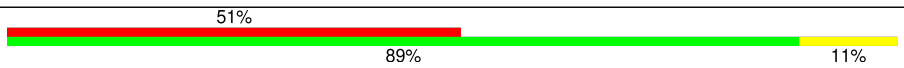
Mol	Chain	Length	Quality of chain
7	At	152	
7	Au	152	
8	AU	87	
8	AV	87	
8	AW	87	
8	Av	87	
9	A1	697	
9	A2	697	
9	A3	697	
9	A4	697	
9	A5	697	
9	Aw	697	
9	Ax	697	
9	Ay	697	
9	Az	697	

2 Entry composition (i)

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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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.

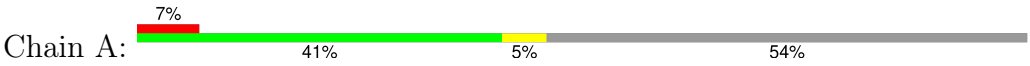
Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aw	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Ax	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Ay	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Az	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A1	697	Total	C	N	O	S	0	0
			5429	3527	875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

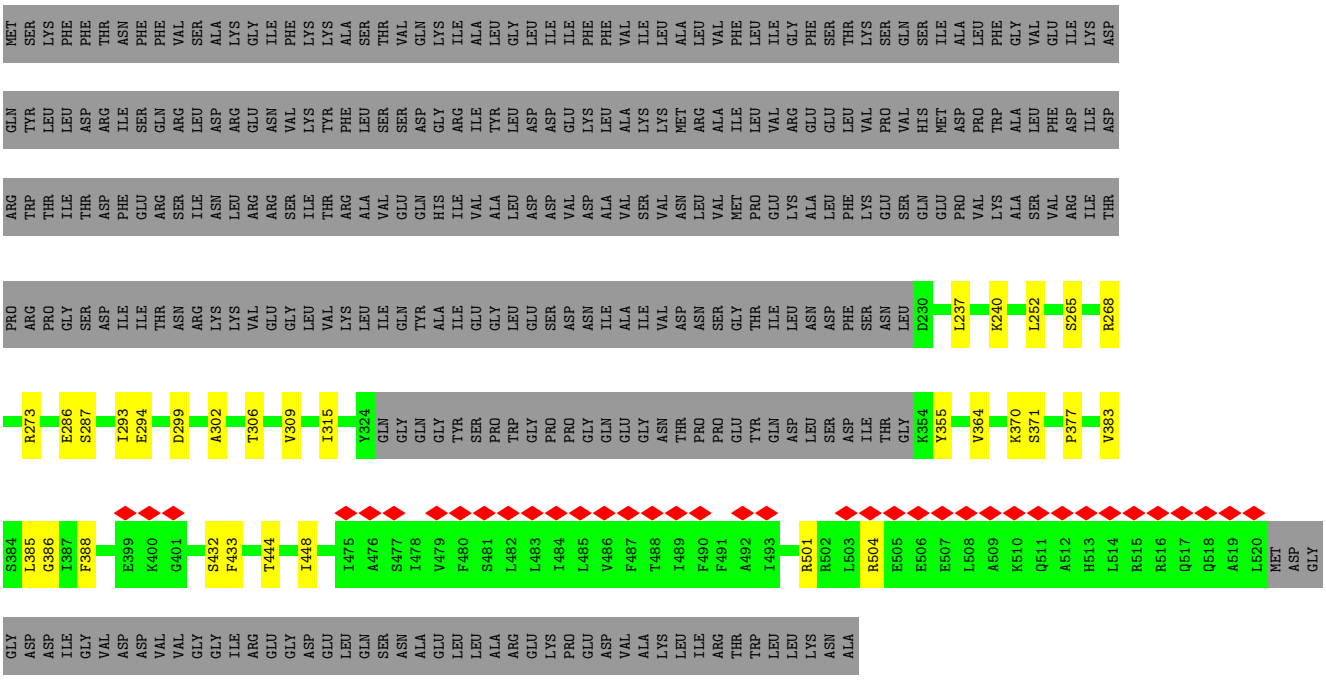
3 Residue-property plots (i)

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

• Molecule 1: Flagellar M-ring protein

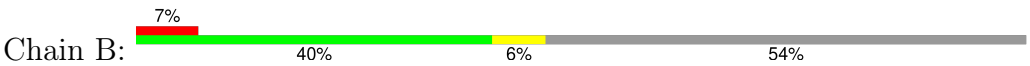
Chain A:

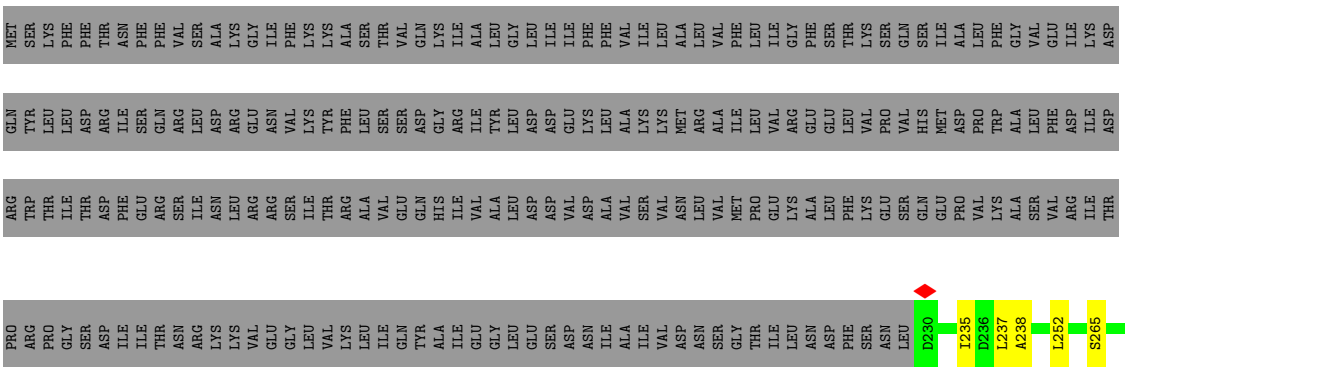


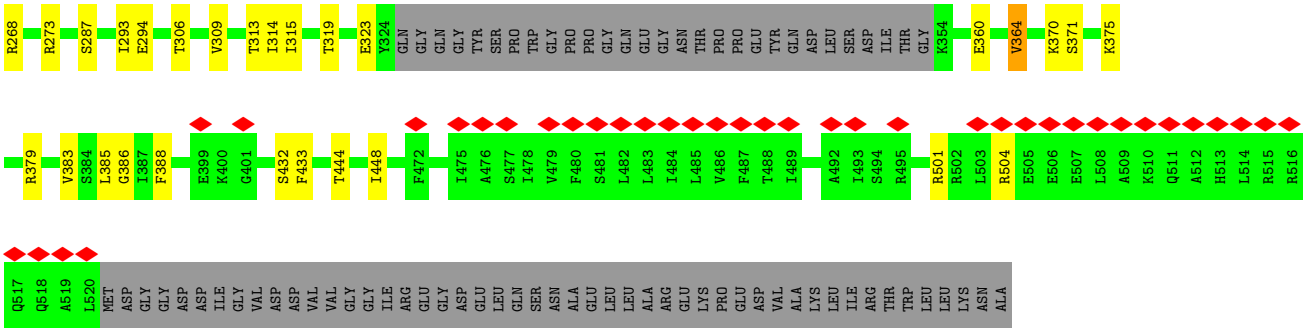


• Molecule 1: Flagellar M-ring protein

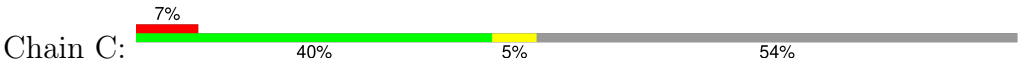
Chain B:

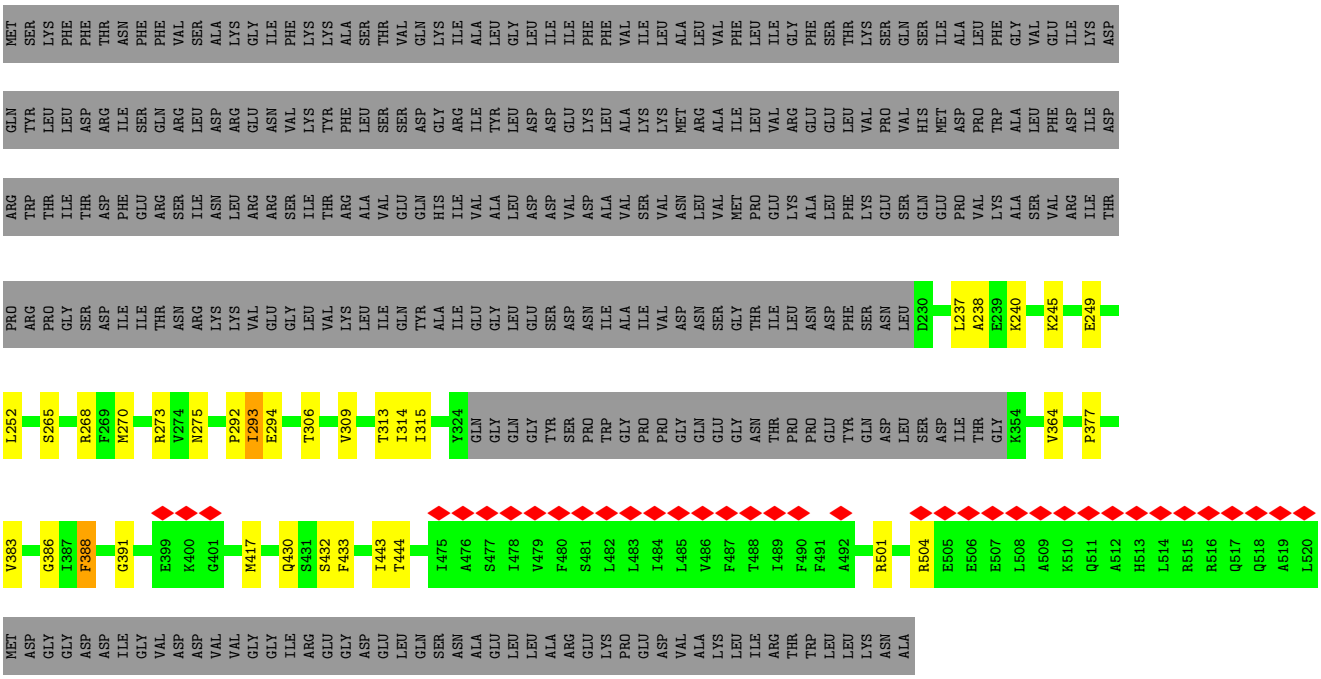




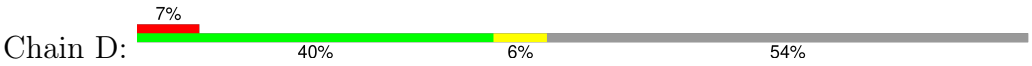


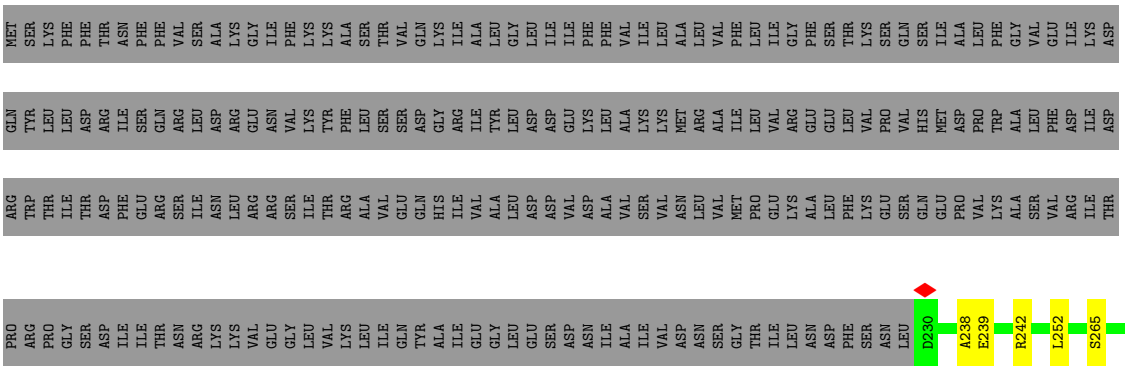
• Molecule 1: Flagellar M-ring protein

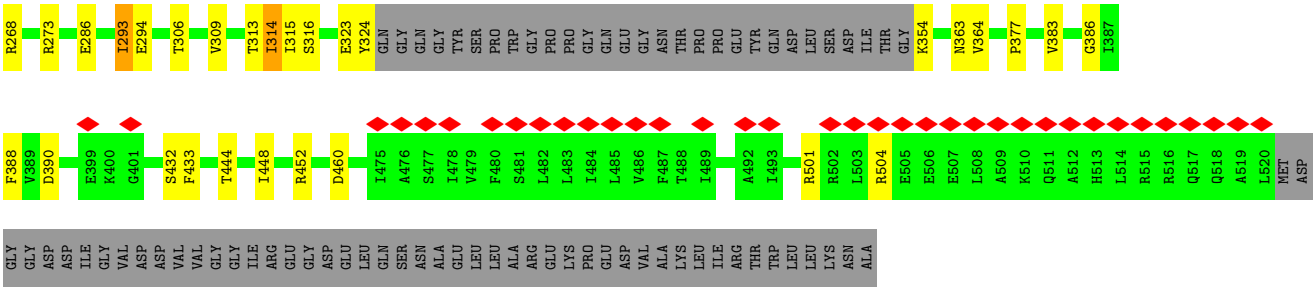




• Molecule 1: Flagellar M-ring protein



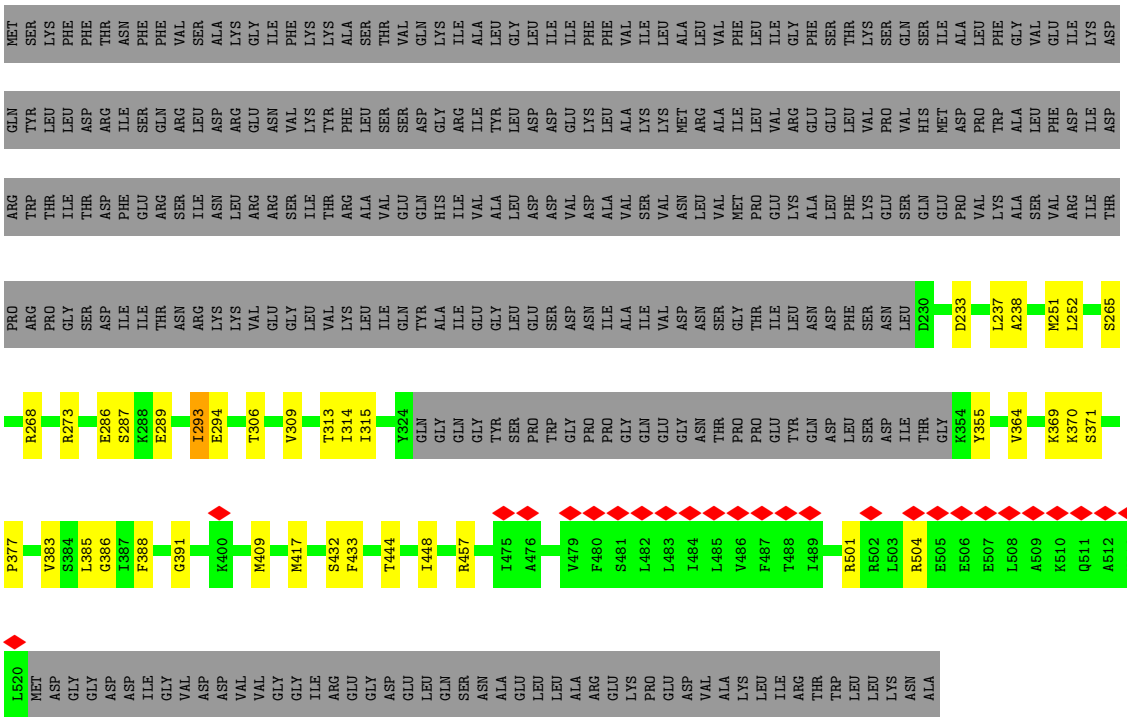




• Molecule 1: Flagellar M-ring protein

Chain E:

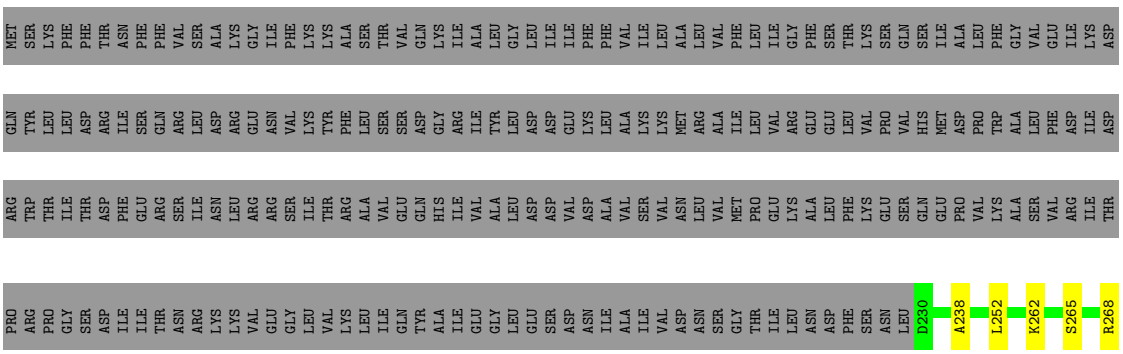


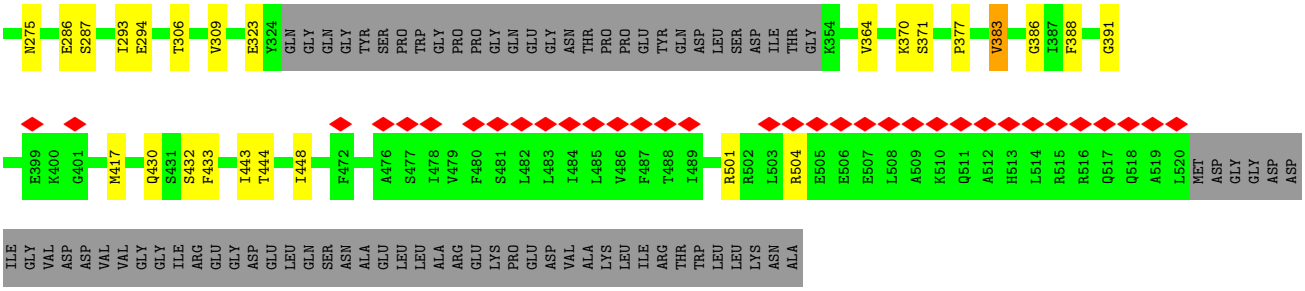


• Molecule 1: Flagellar M-ring protein

Chain F:



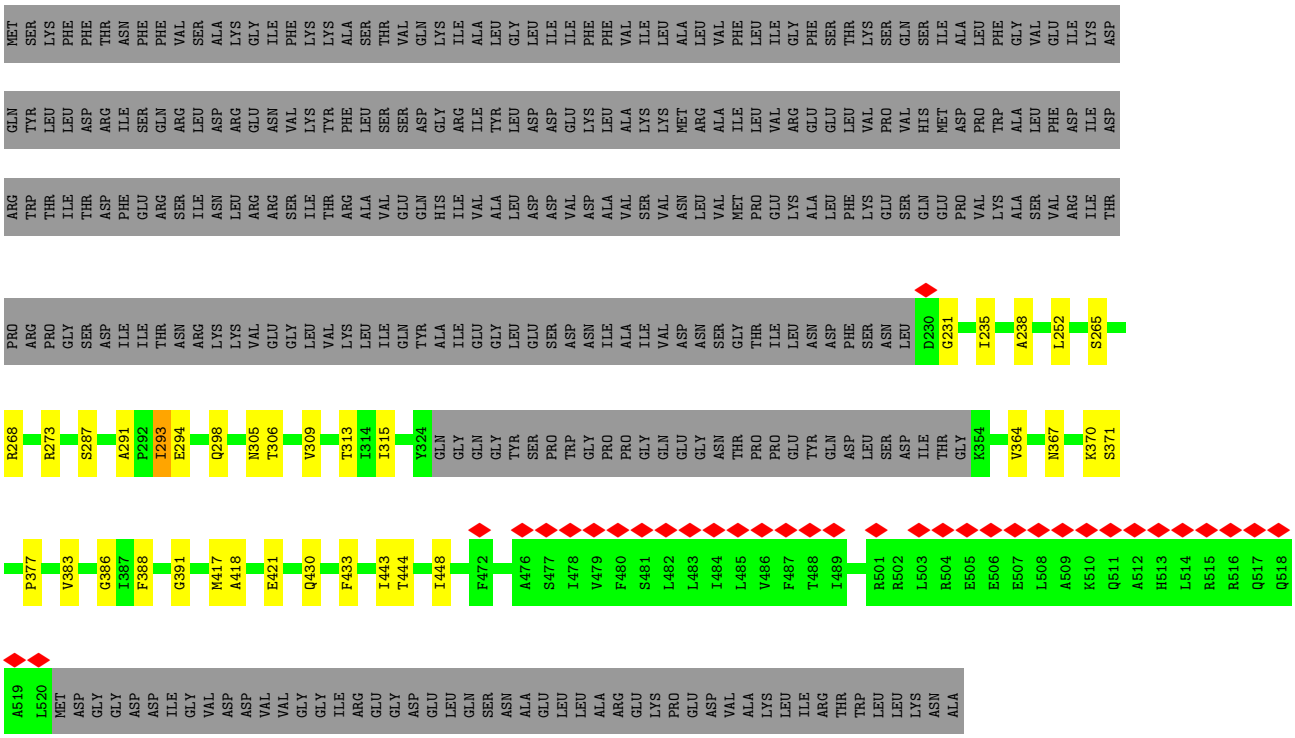




• Molecule 1: Flagellar M-ring protein

Chain G:

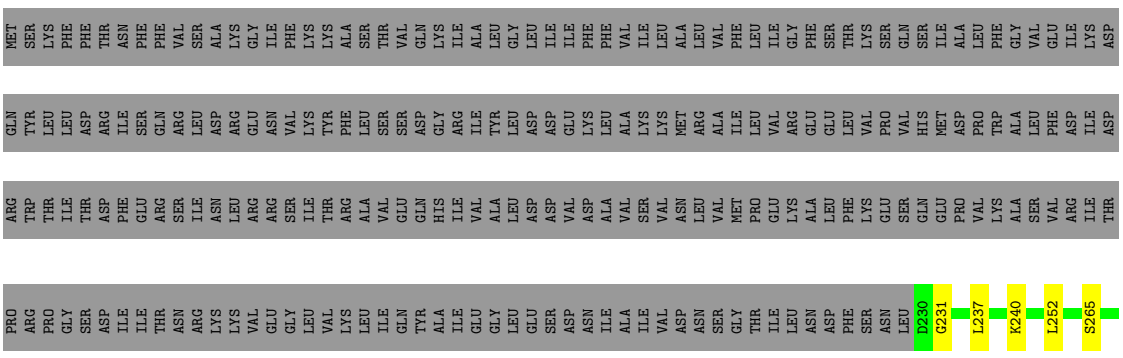


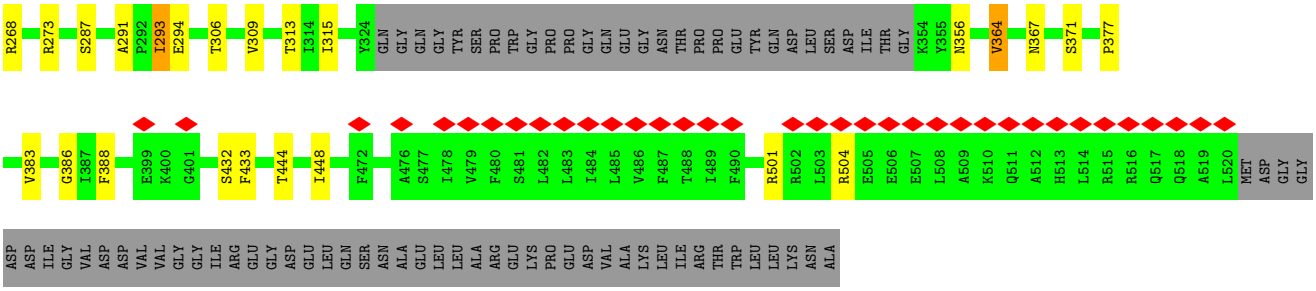


• Molecule 1: Flagellar M-ring protein

Chain H:



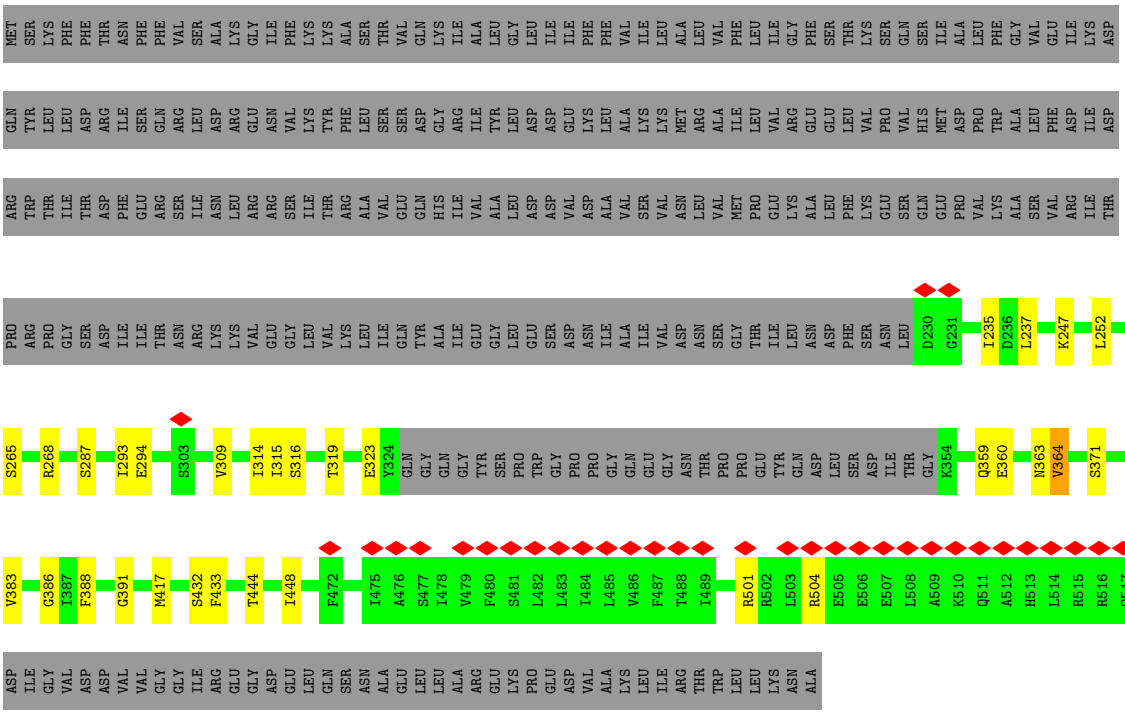




• Molecule 1: Flagellar M-ring protein

Chain I:

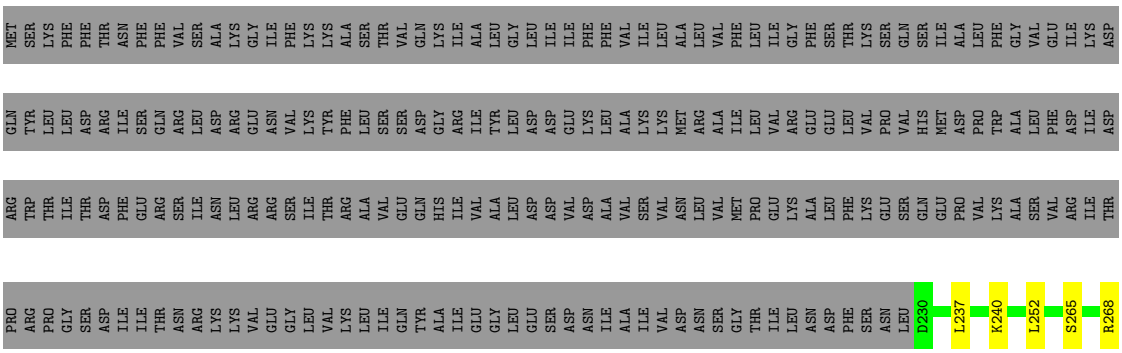


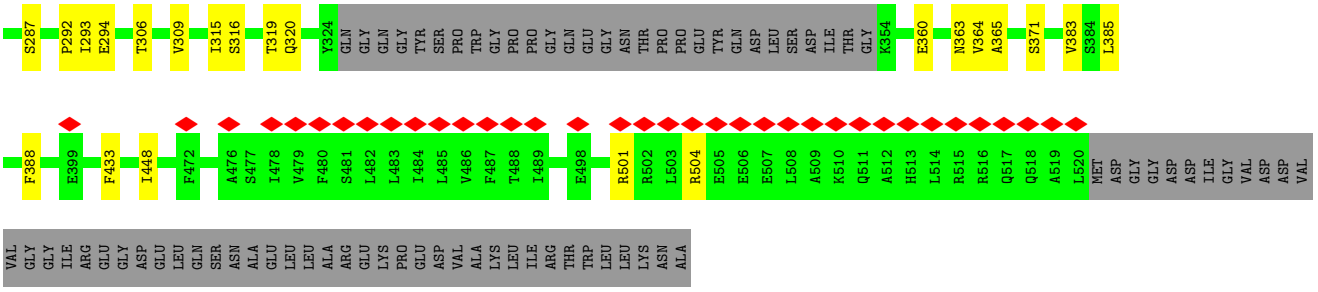


• Molecule 1: Flagellar M-ring protein

Chain J:



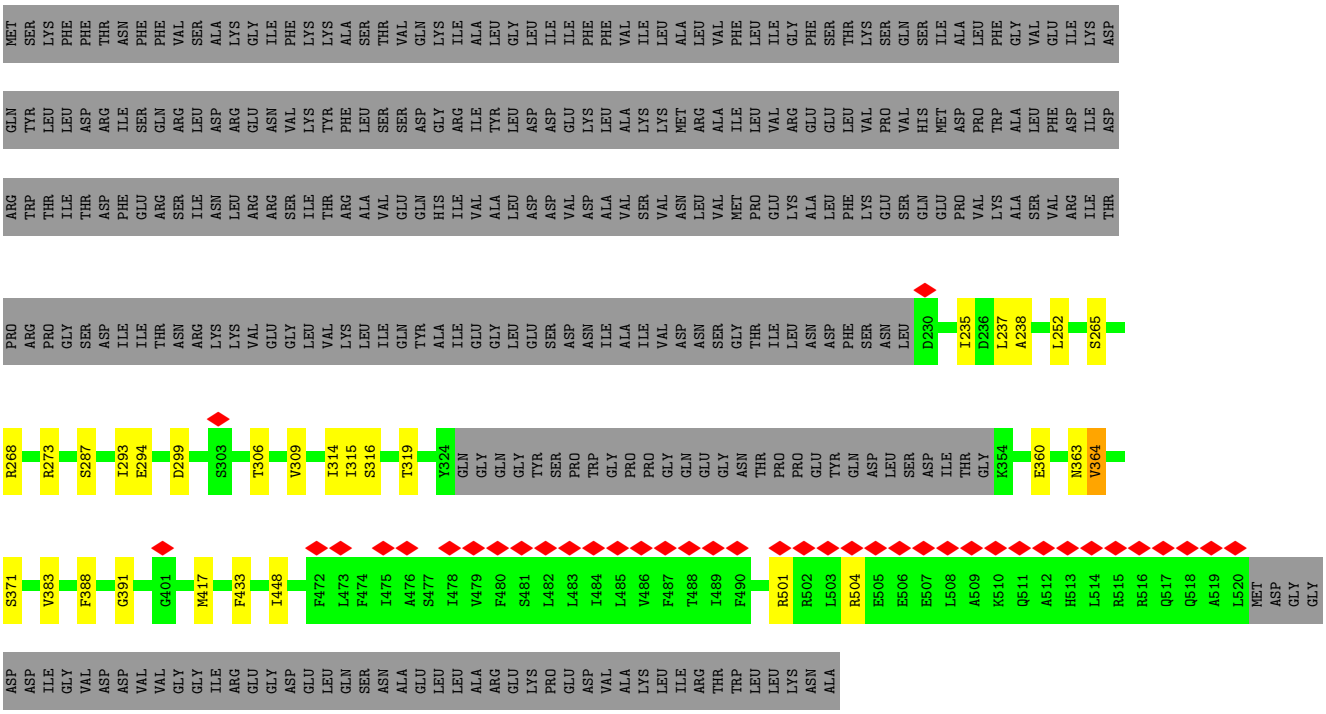




• Molecule 1: Flagellar M-ring protein

Chain K:

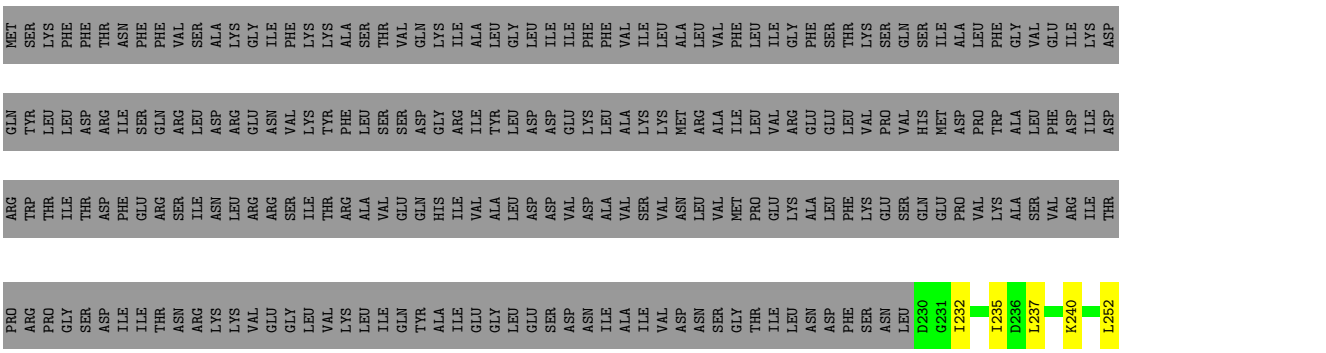


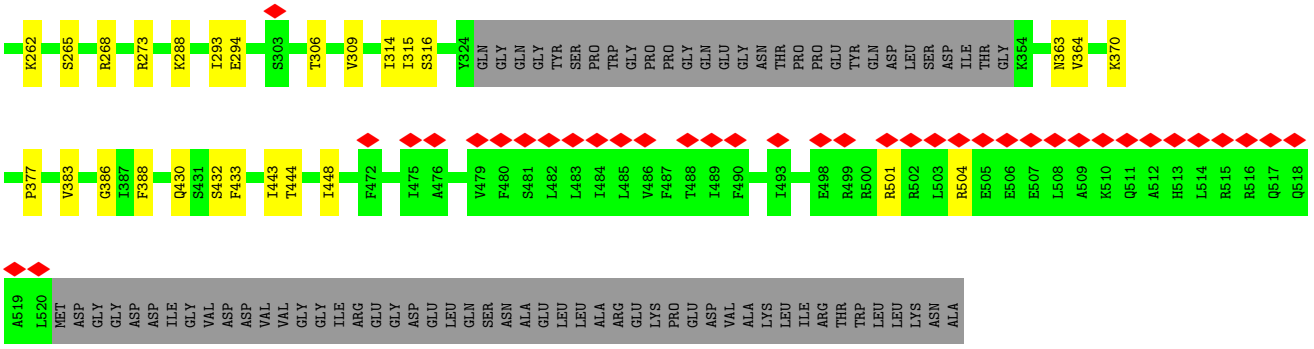


• Molecule 1: Flagellar M-ring protein

Chain L:



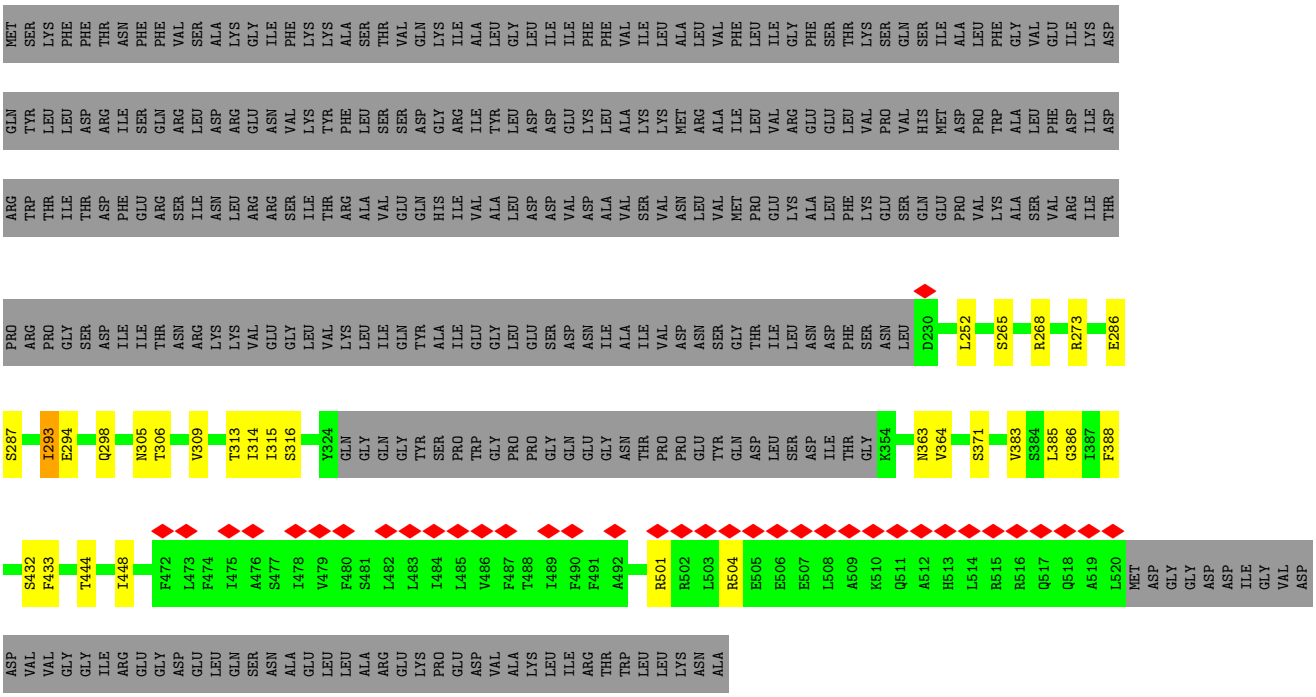




• Molecule 1: Flagellar M-ring protein

Chain M:

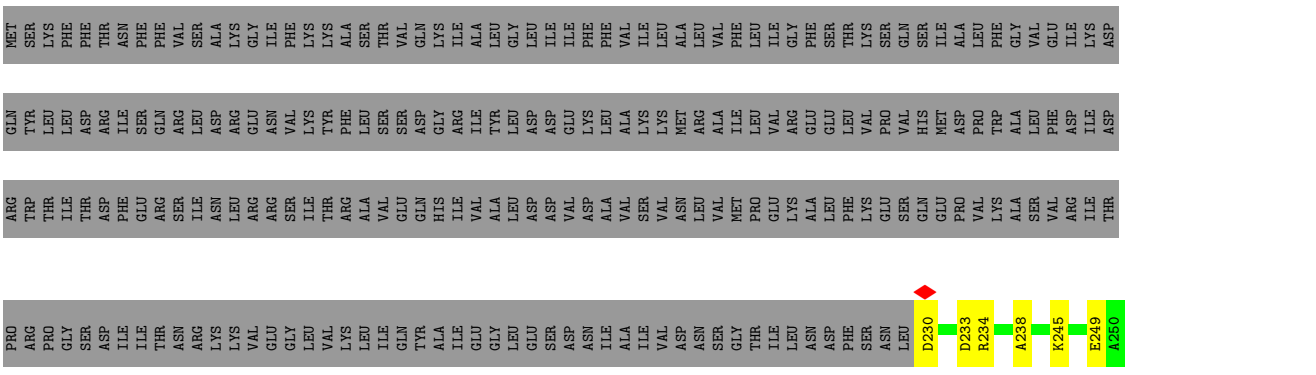




• Molecule 1: Flagellar M-ring protein

Chain N:



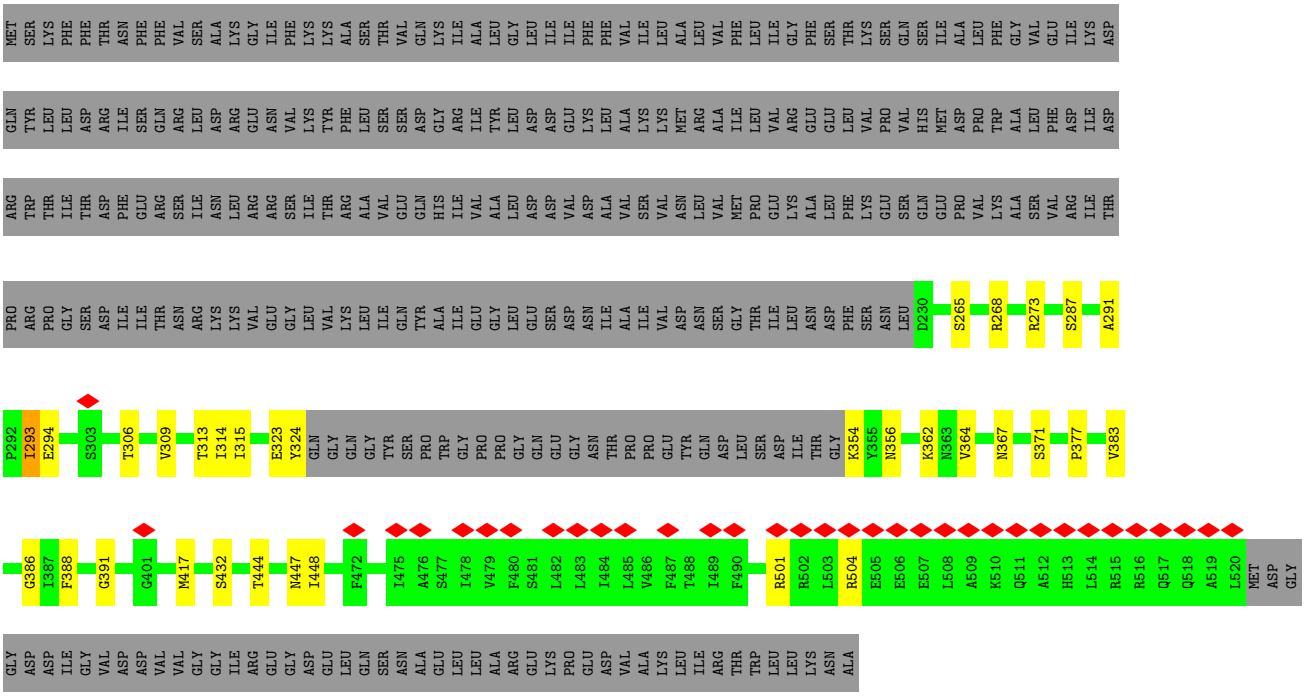




• Molecule 1: Flagellar M-ring protein

Chain O:

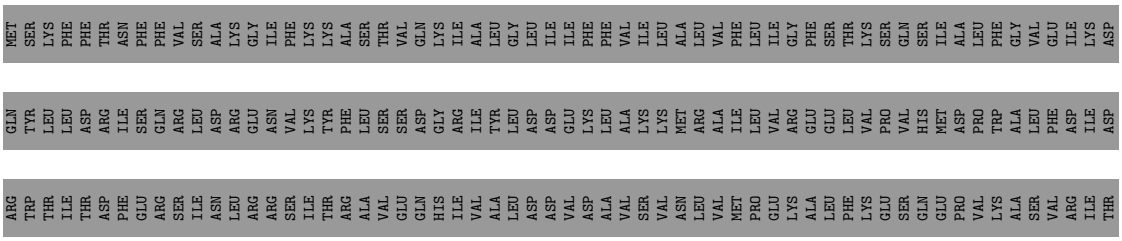


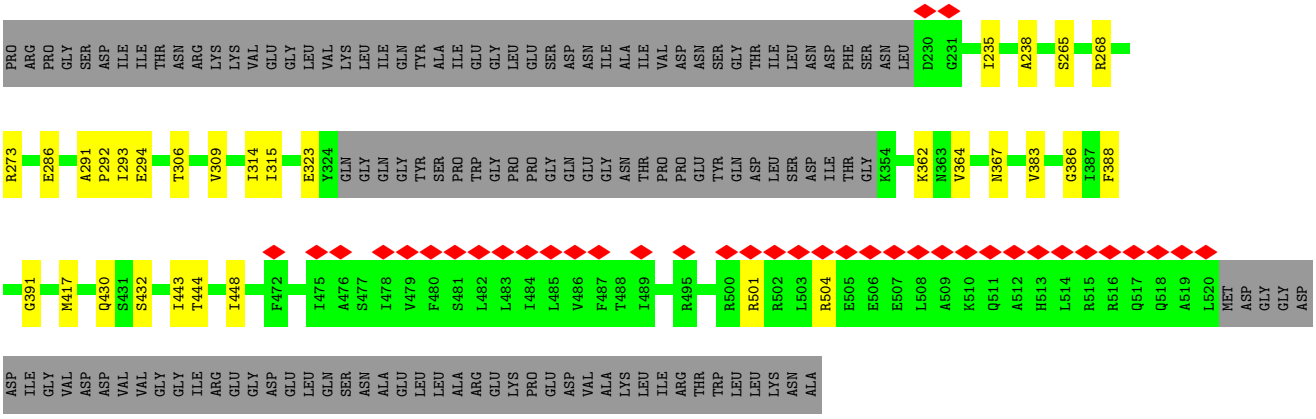


• Molecule 1: Flagellar M-ring protein

Chain P:



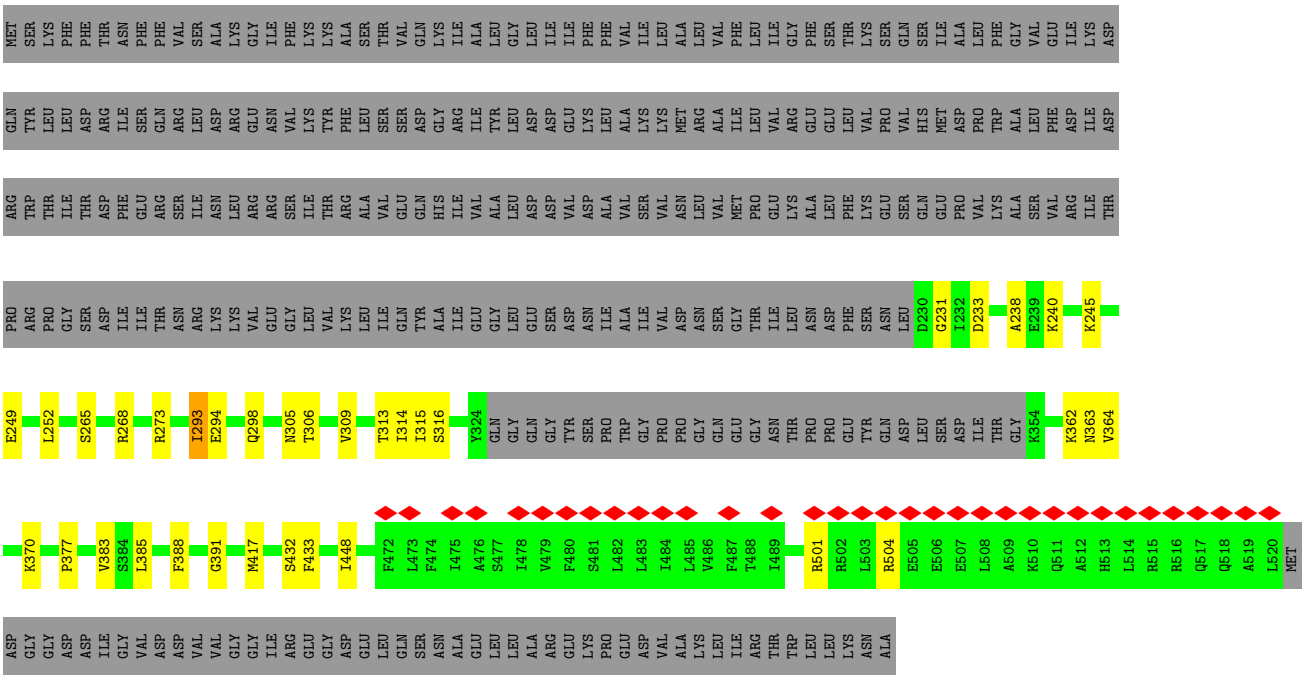




• Molecule 1: Flagellar M-ring protein

Chain Q:

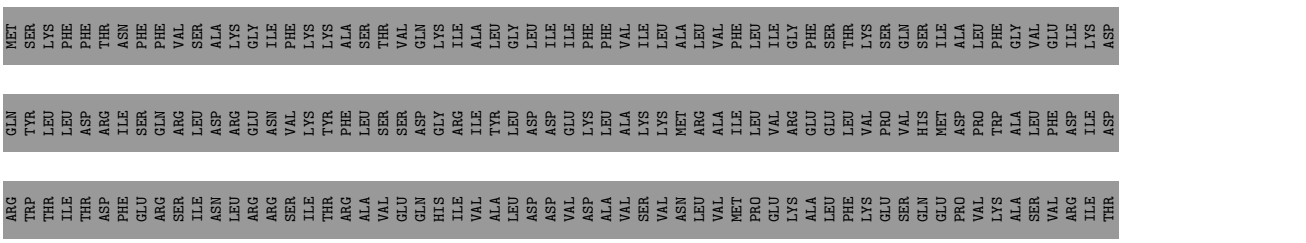


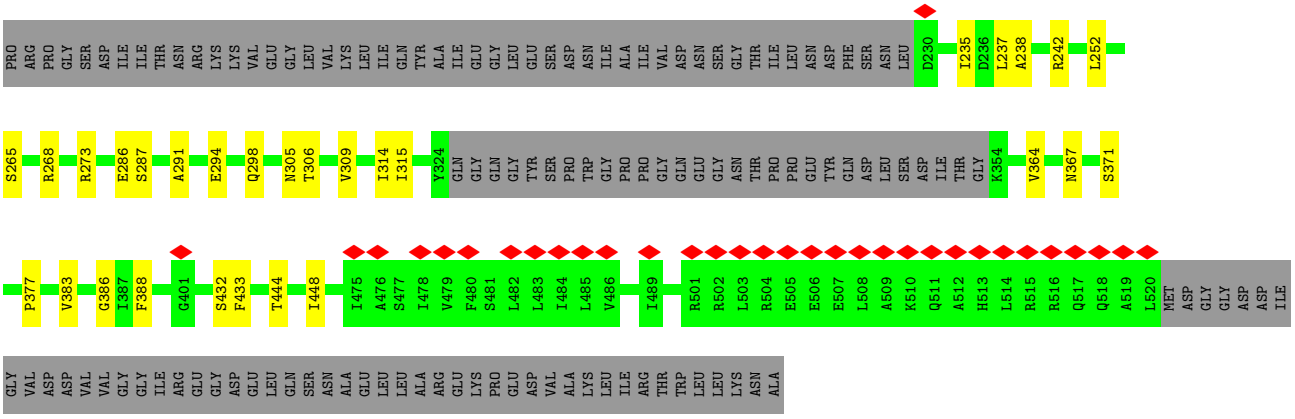


• Molecule 1: Flagellar M-ring protein

Chain R:



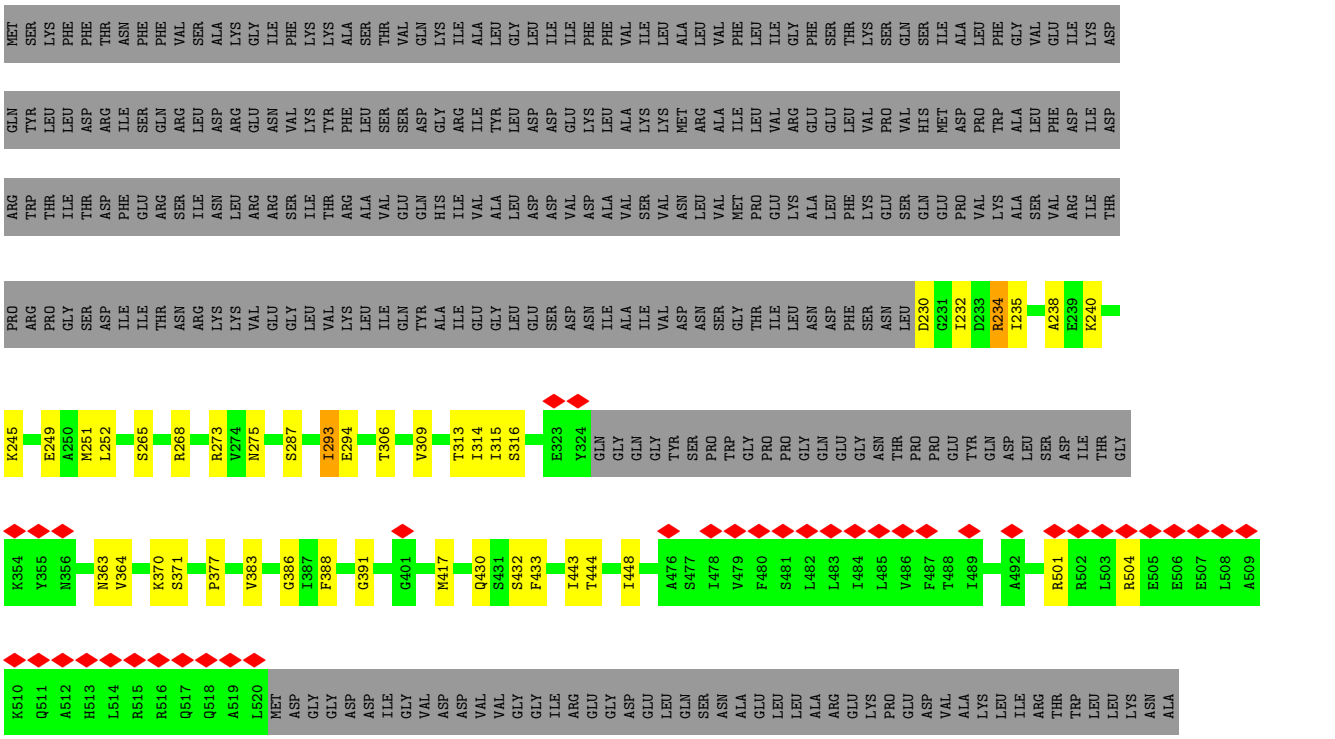




• Molecule 1: Flagellar M-ring protein

Chain S:

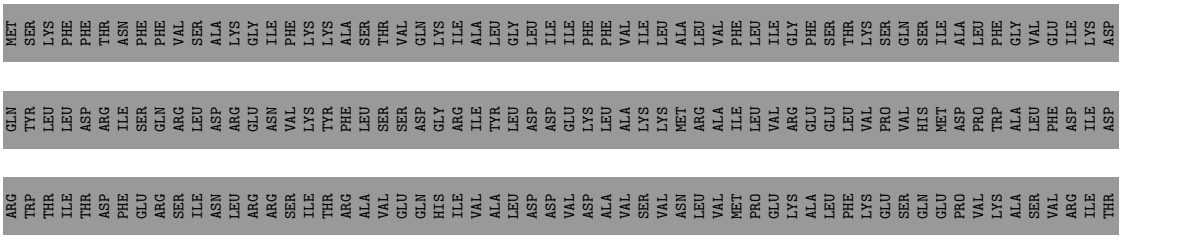


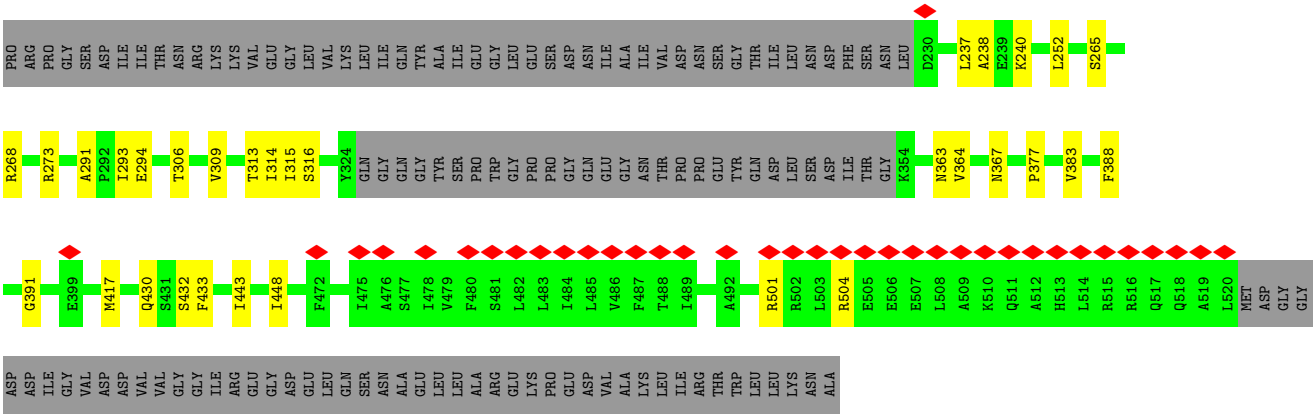


• Molecule 1: Flagellar M-ring protein

Chain T:



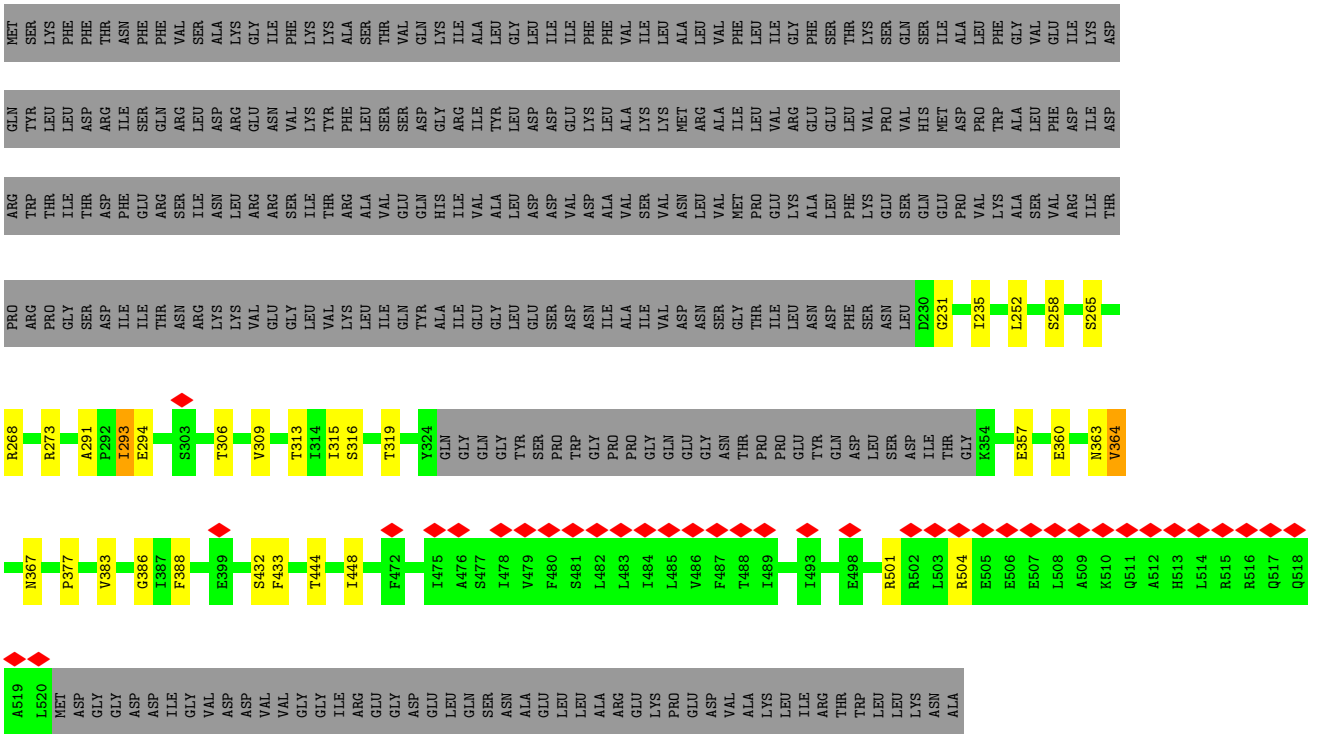




• Molecule 1: Flagellar M-ring protein

Chain U:

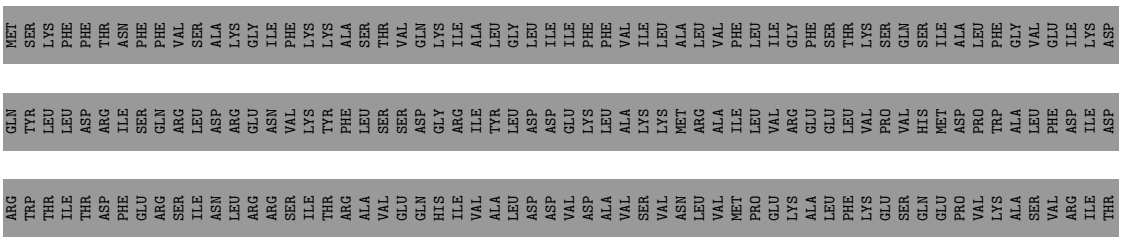


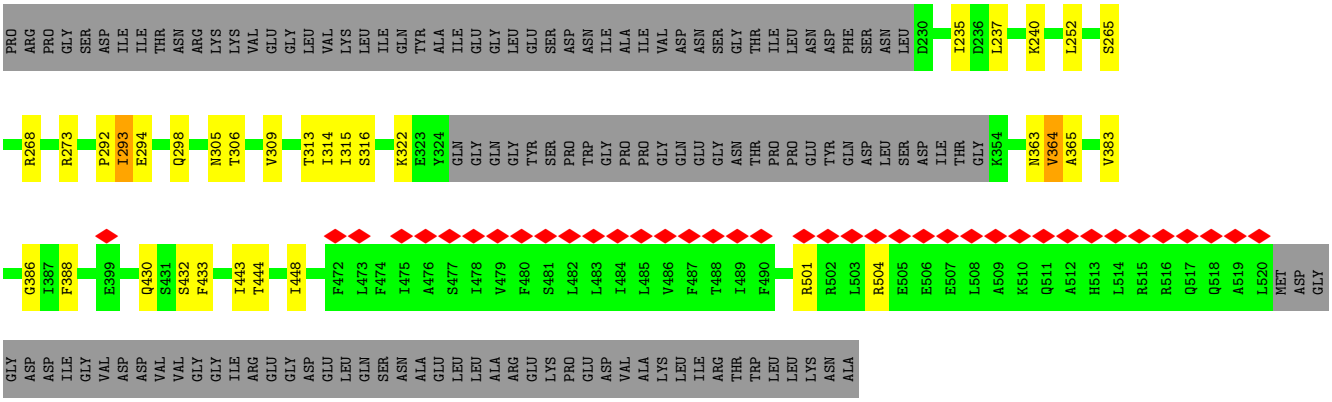


• Molecule 1: Flagellar M-ring protein

Chain V:



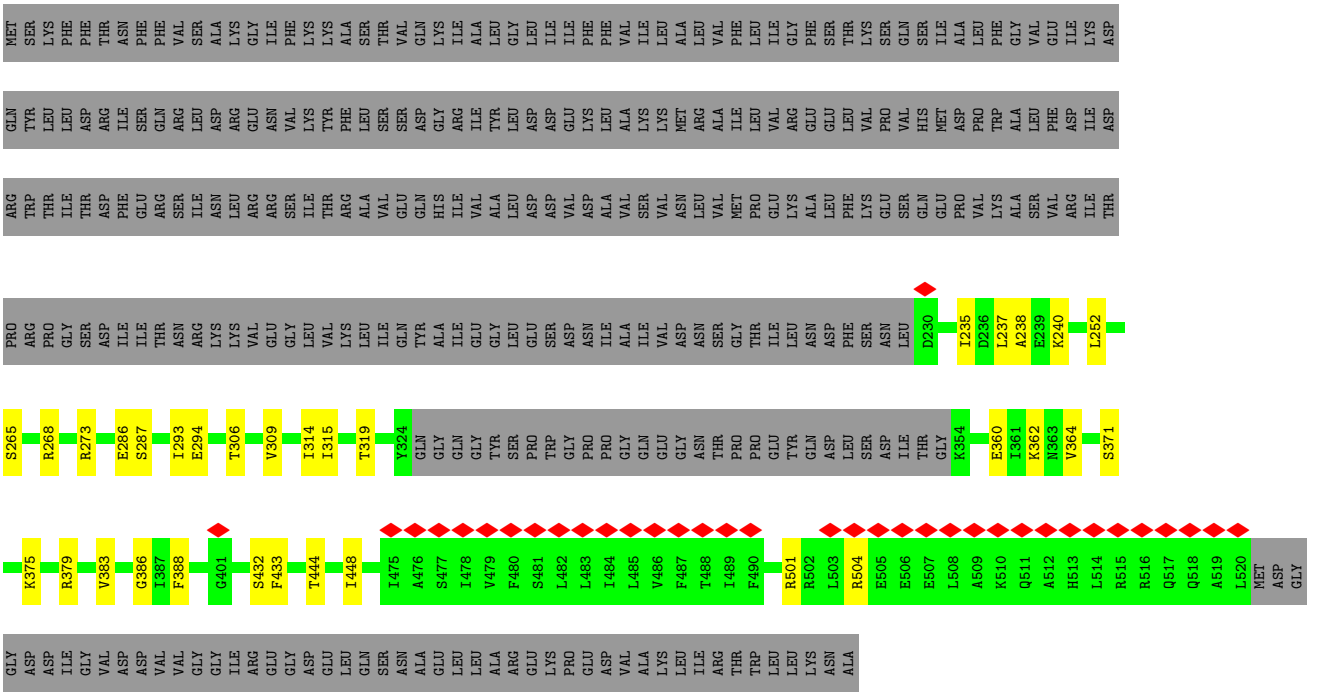




• Molecule 1: Flagellar M-ring protein

Chain W:

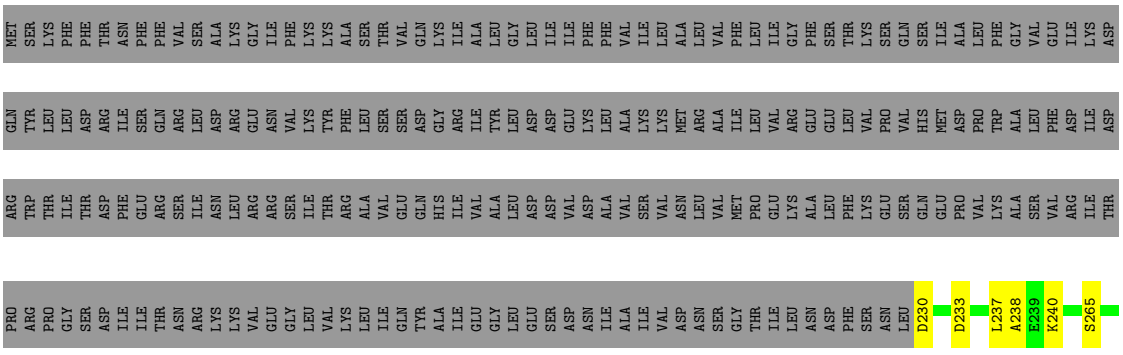


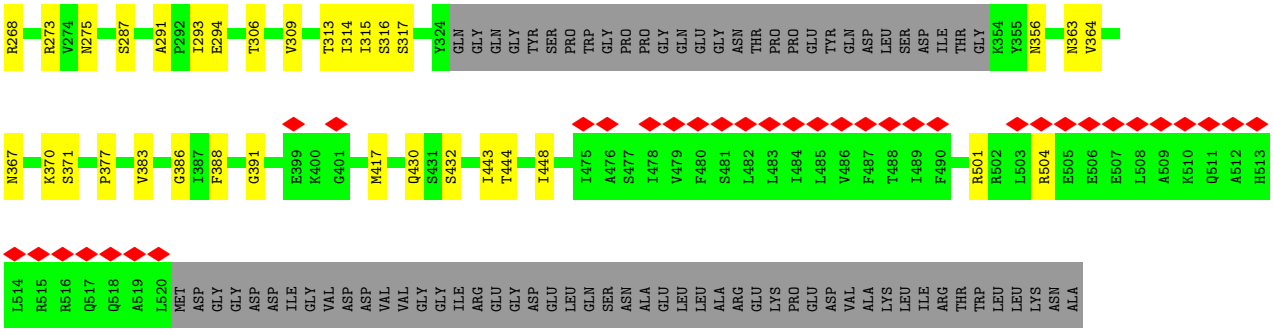


• Molecule 1: Flagellar M-ring protein

Chain X:



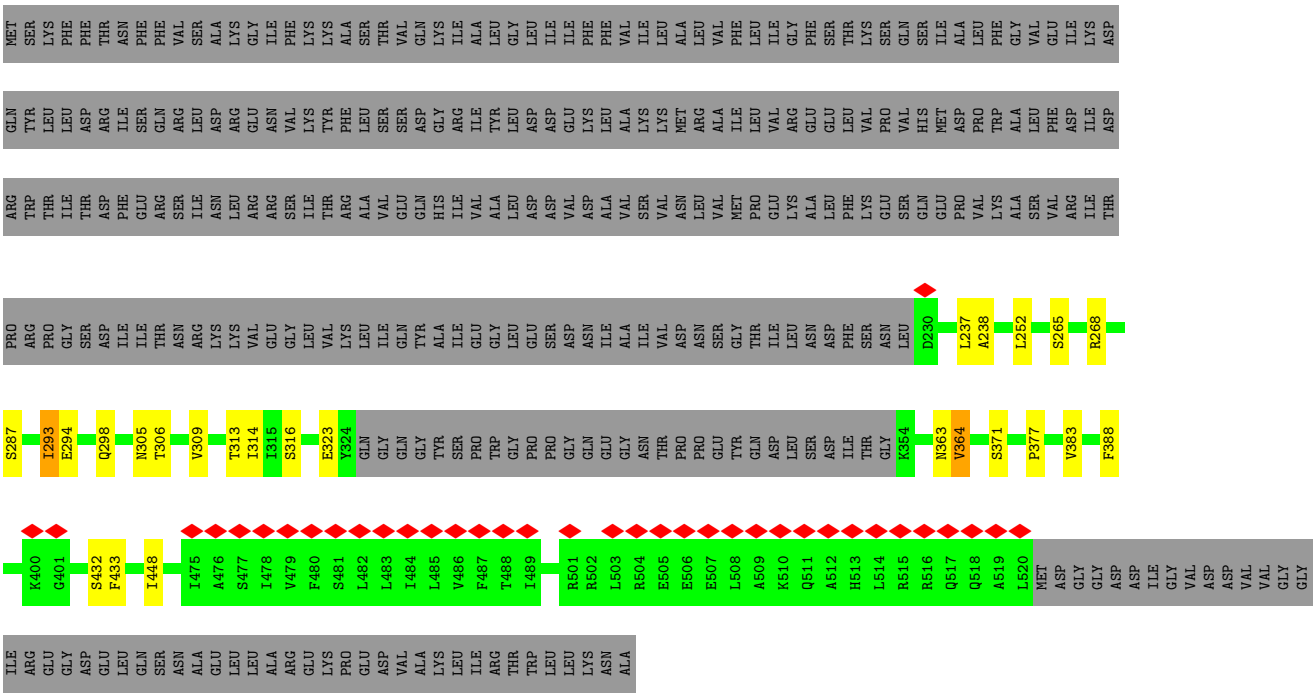




• Molecule 1: Flagellar M-ring protein

Chain Y:

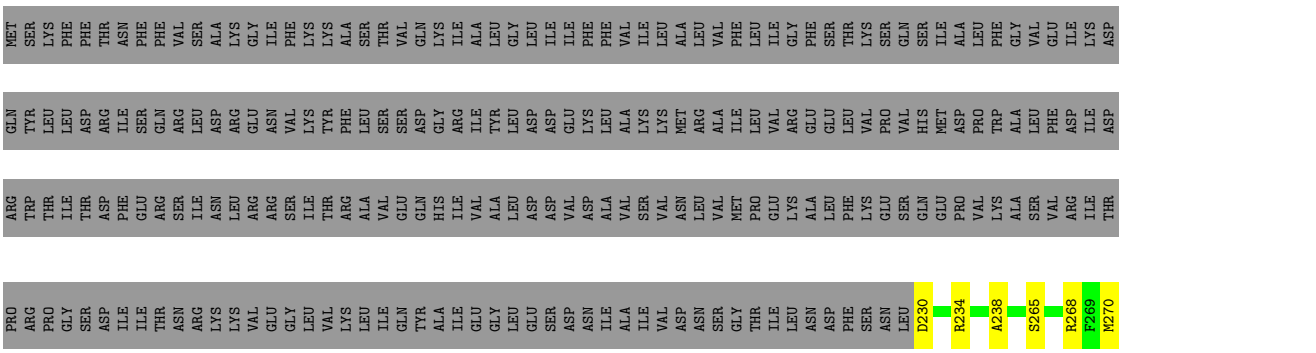


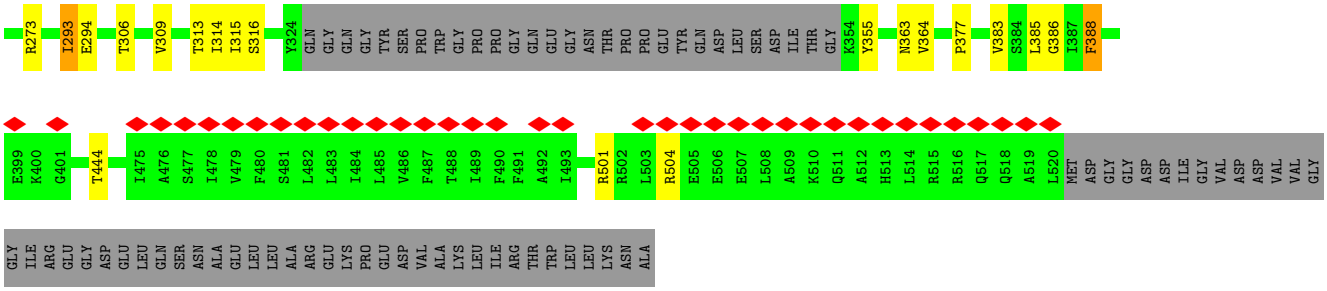


• Molecule 1: Flagellar M-ring protein

Chain Z:



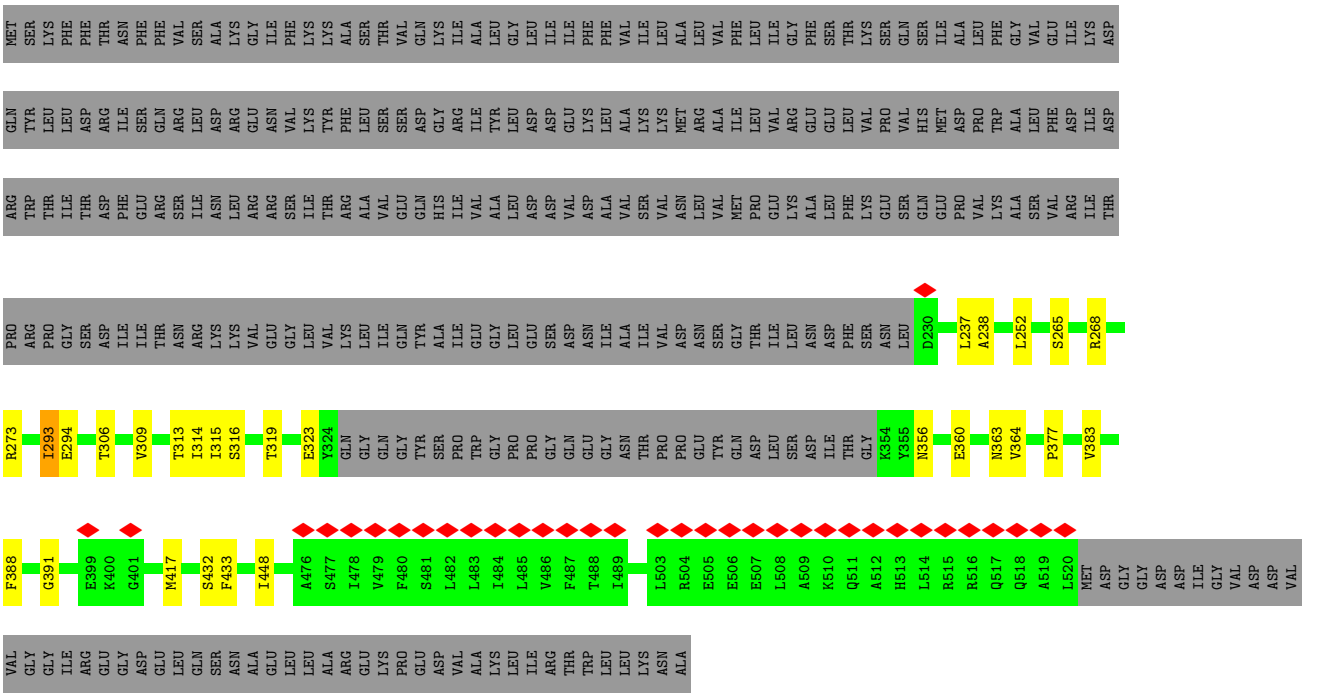




• Molecule 1: Flagellar M-ring protein

Chain a:

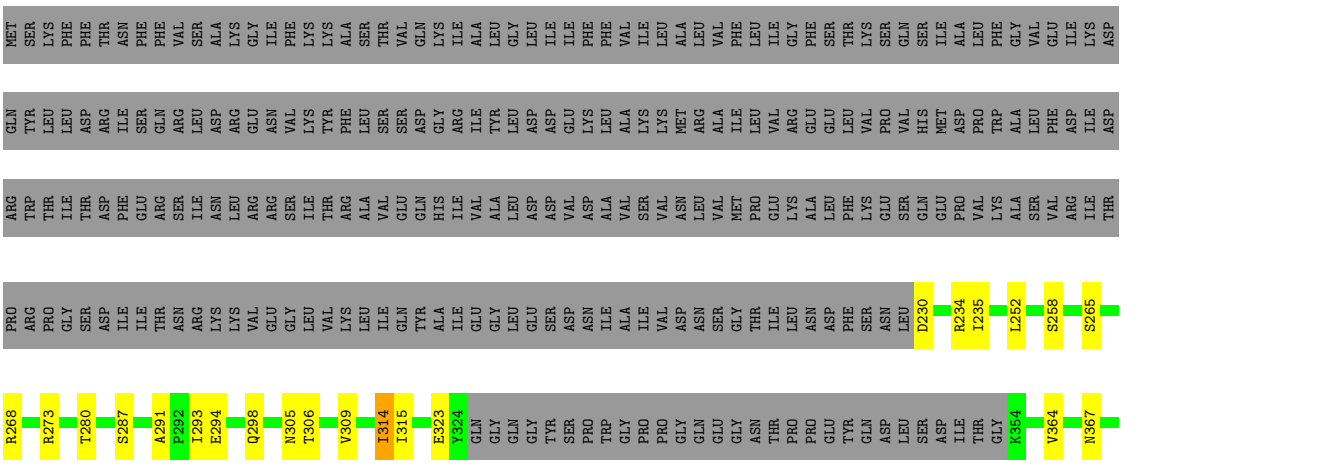


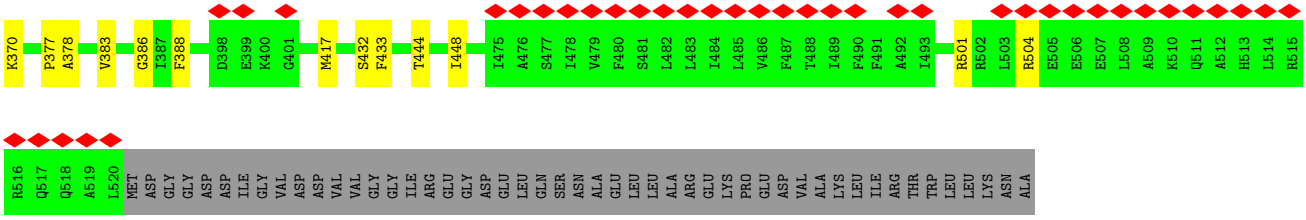


• Molecule 1: Flagellar M-ring protein

Chain b:



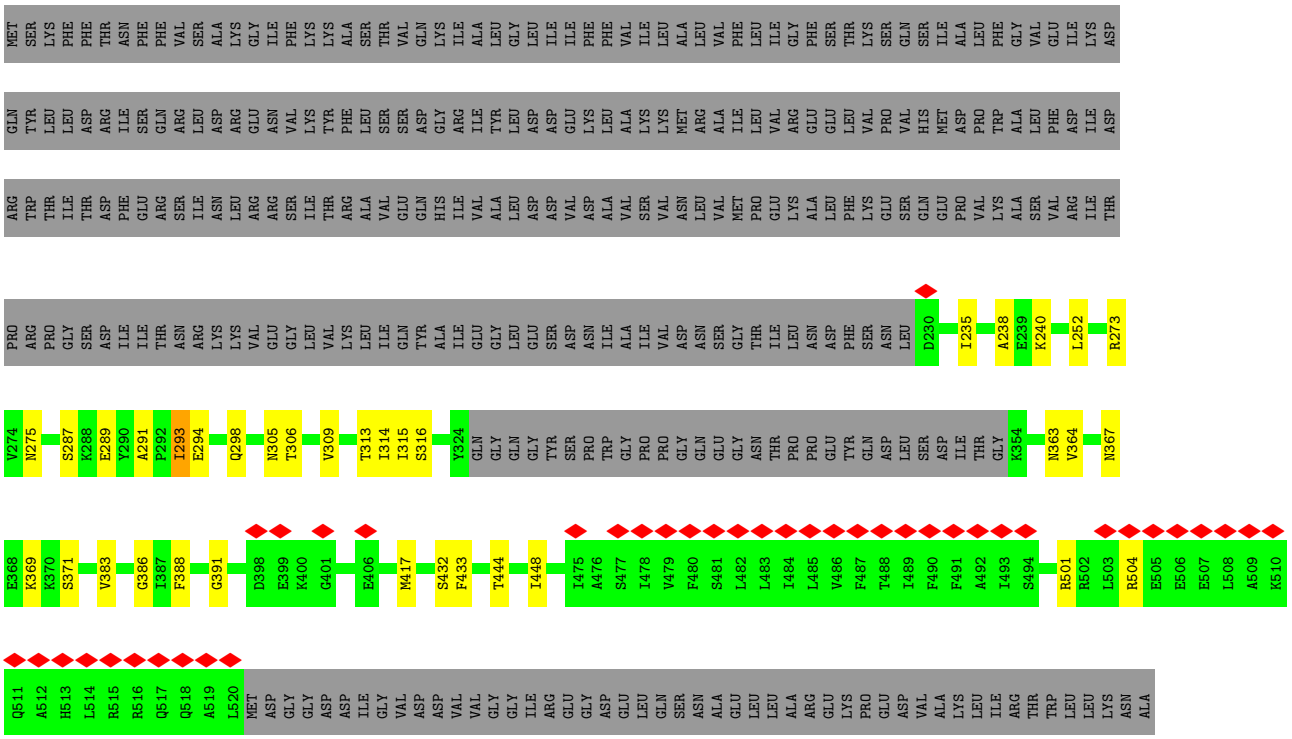




• Molecule 1: Flagellar M-ring protein

Chain c:

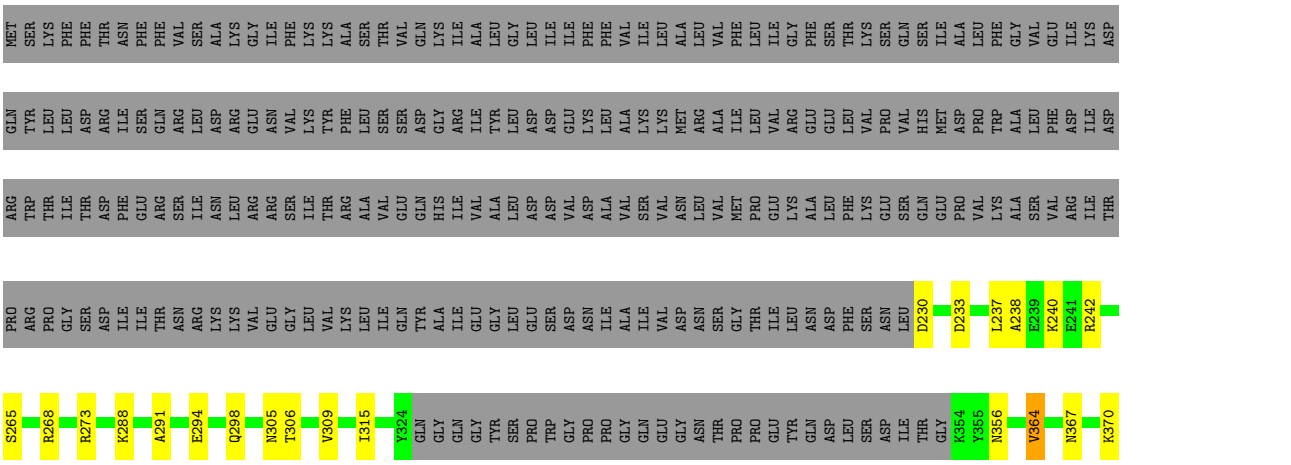


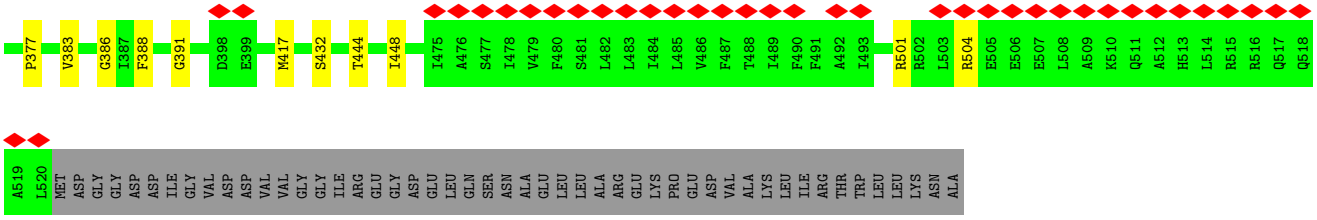


• Molecule 1: Flagellar M-ring protein

Chain d:



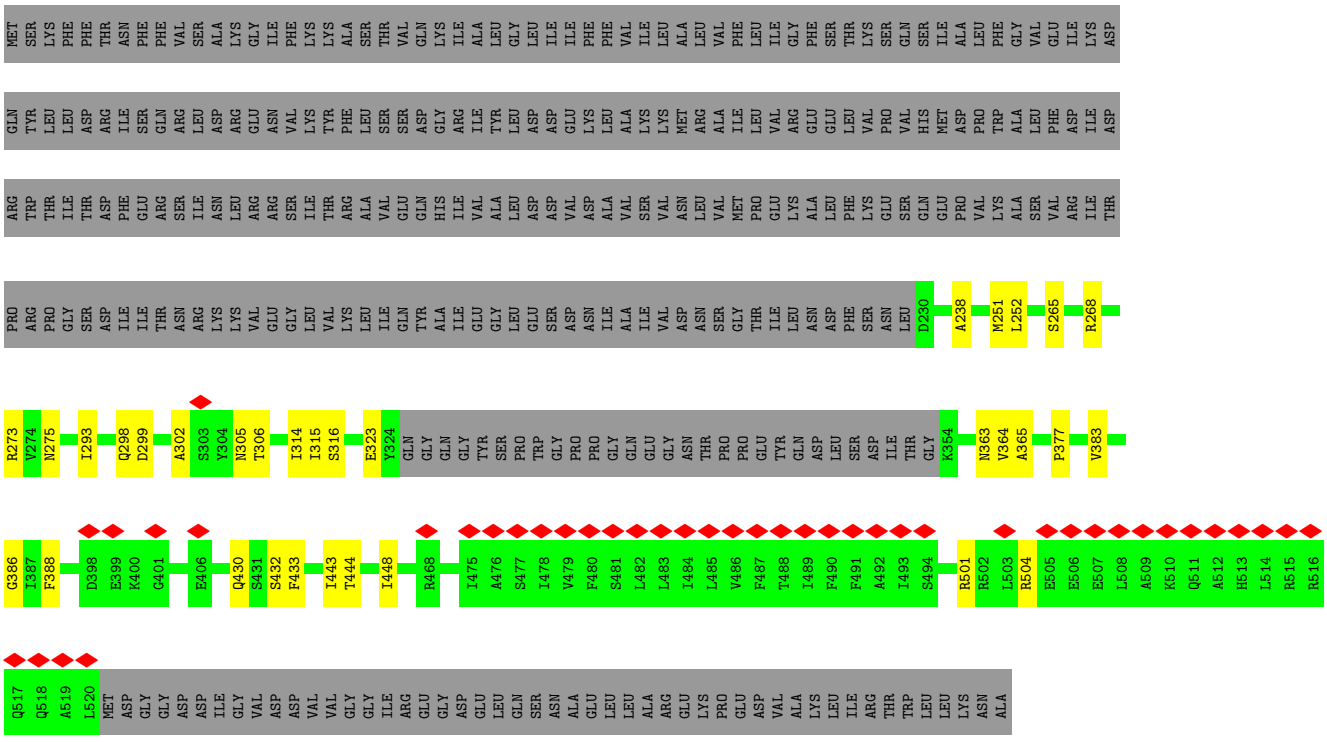




• Molecule 1: Flagellar M-ring protein

Chain e:

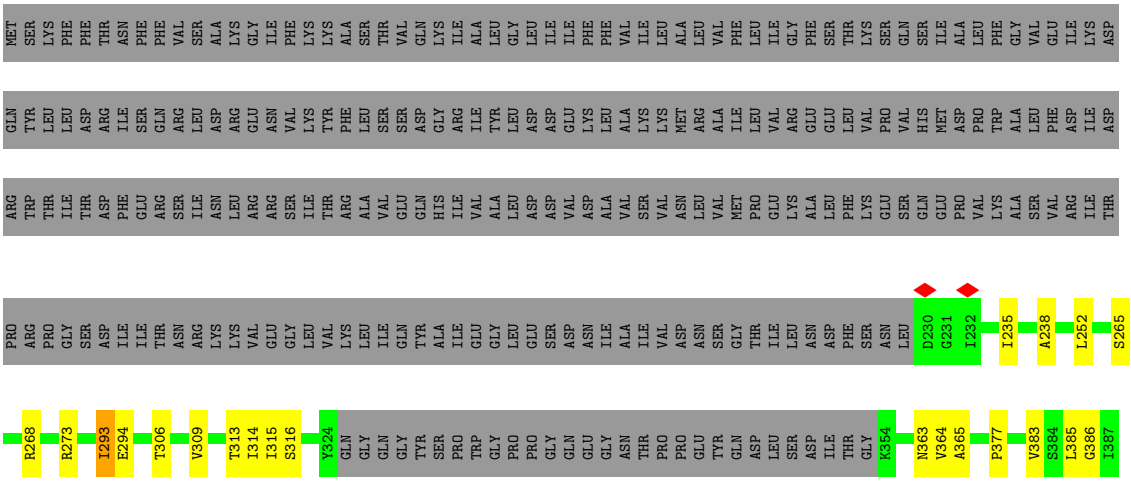


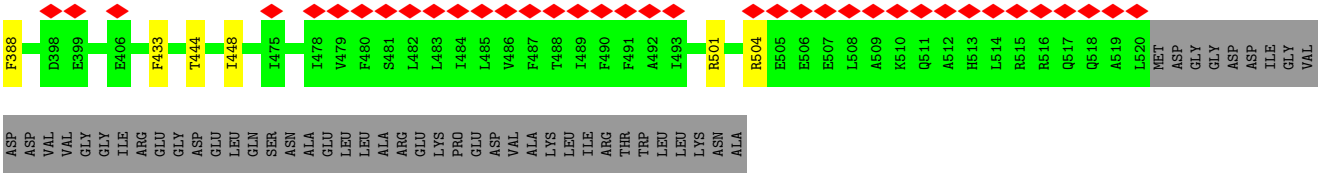


• Molecule 1: Flagellar M-ring protein

Chain f:



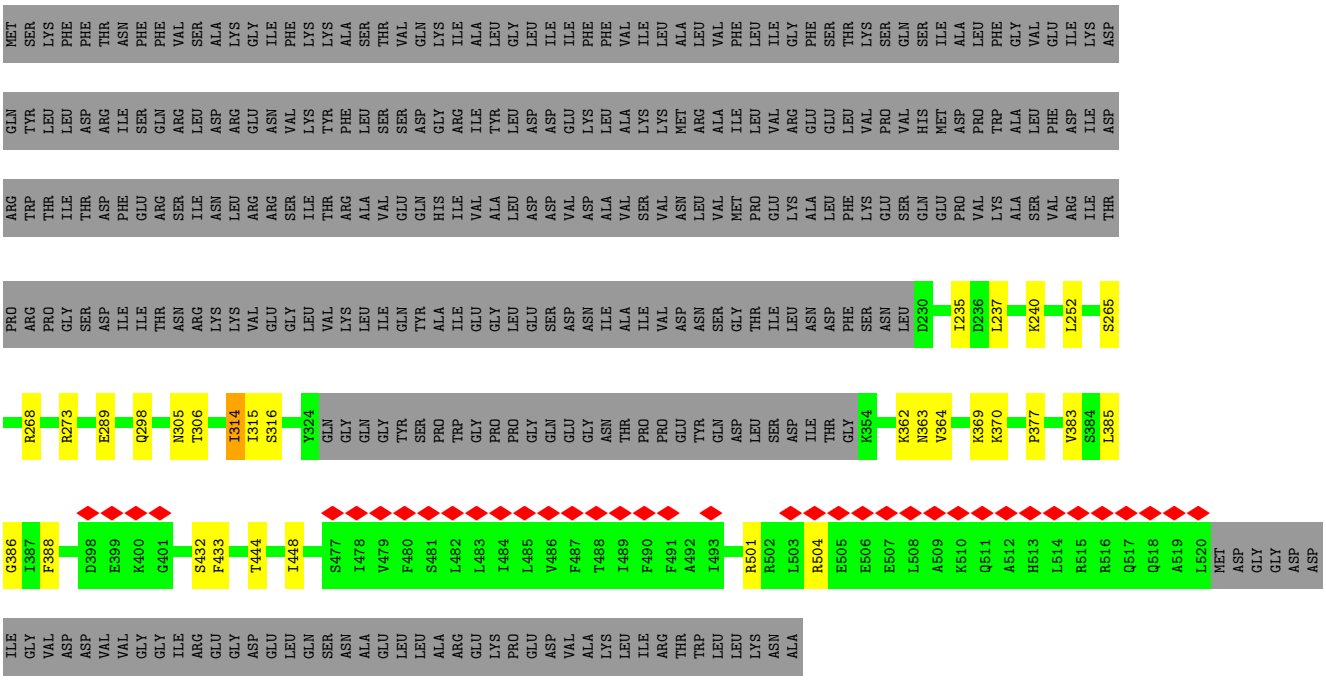




• Molecule 1: Flagellar M-ring protein

Chain g:

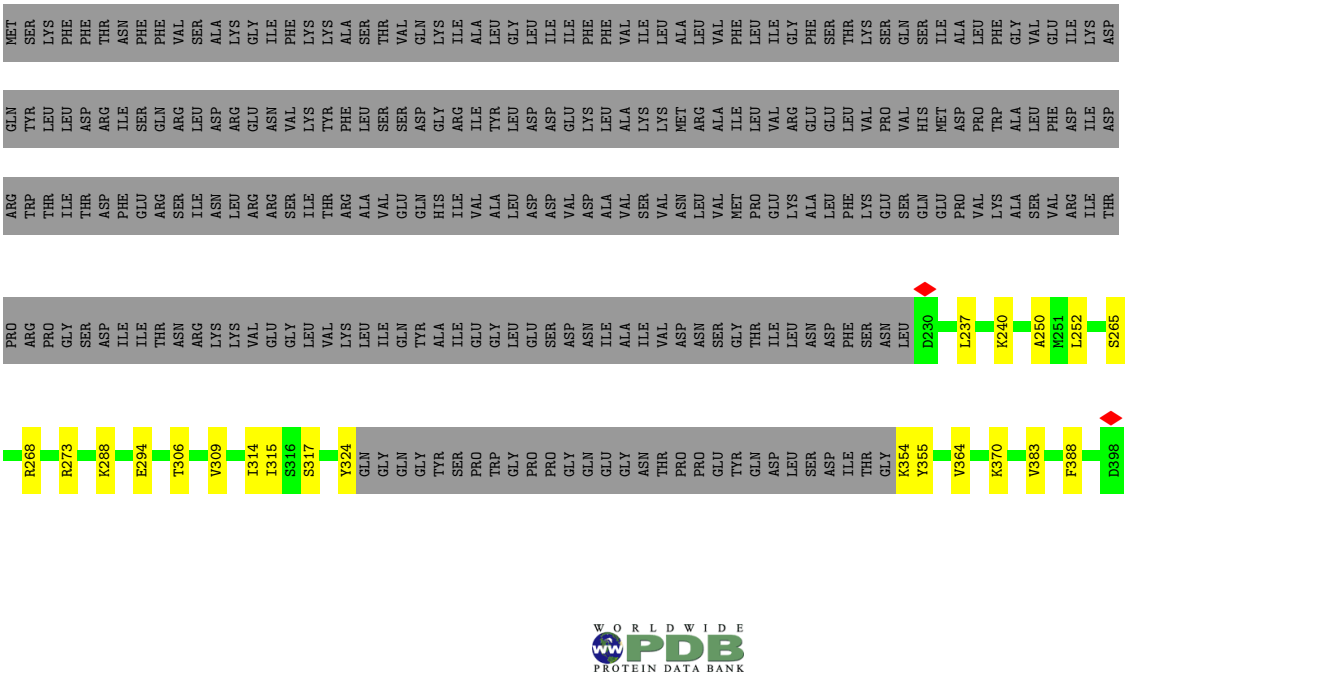


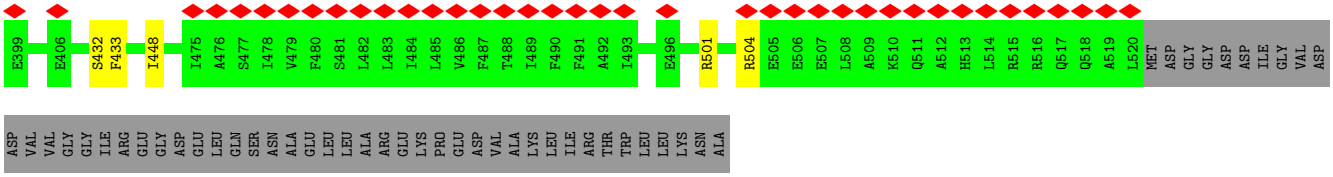


• Molecule 1: Flagellar M-ring protein

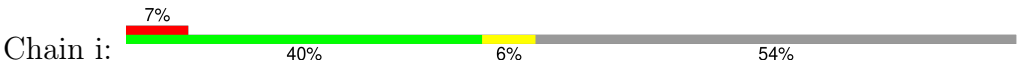
Chain h:

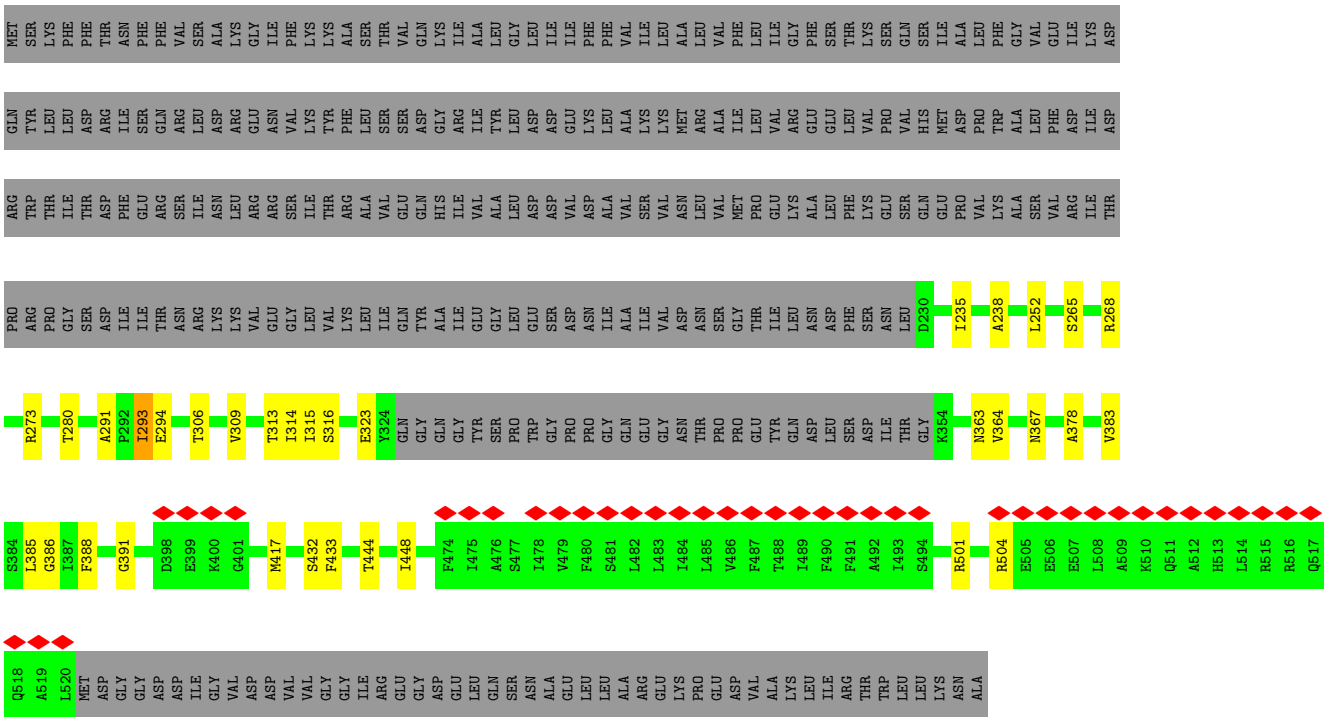




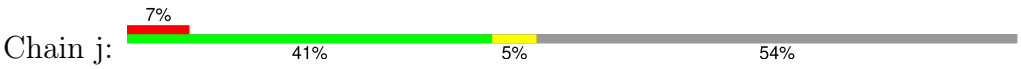


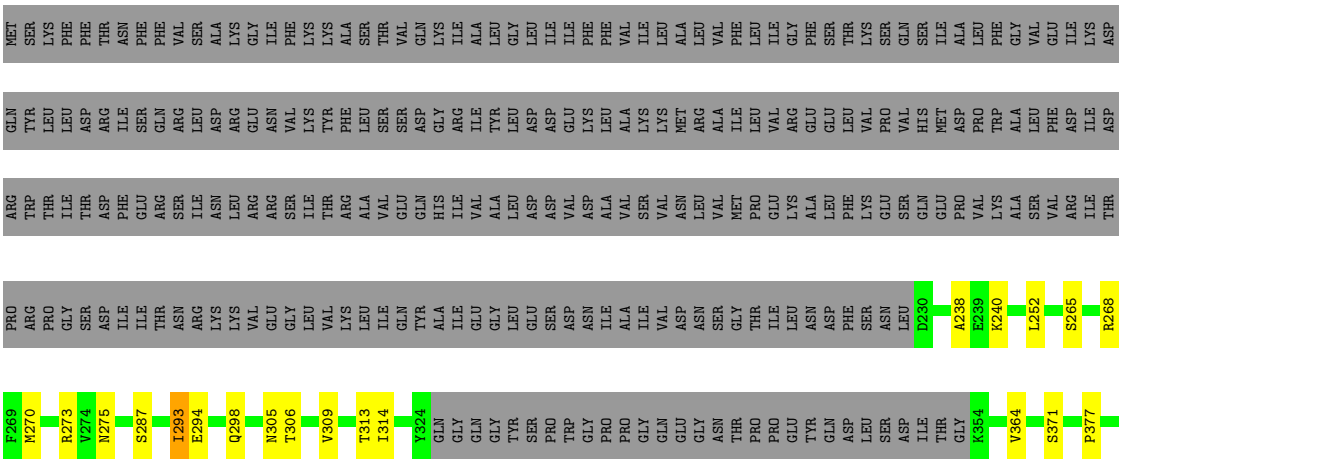
• Molecule 1: Flagellar M-ring protein

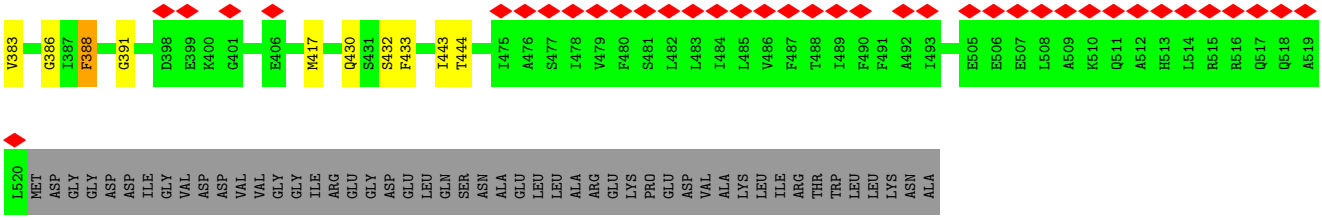




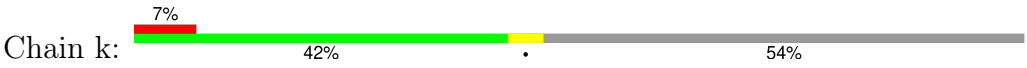
• Molecule 1: Flagellar M-ring protein

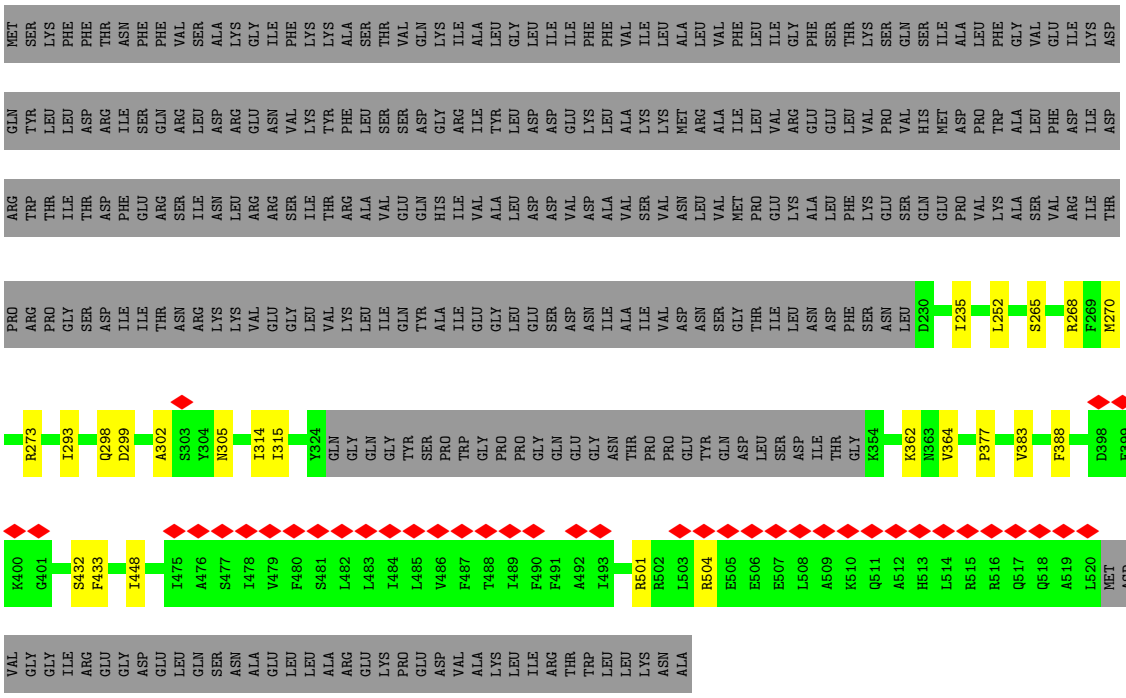




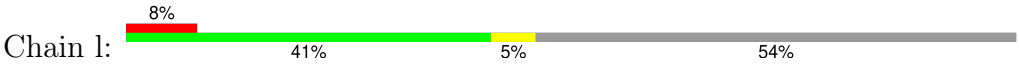


• Molecule 1: Flagellar M-ring protein

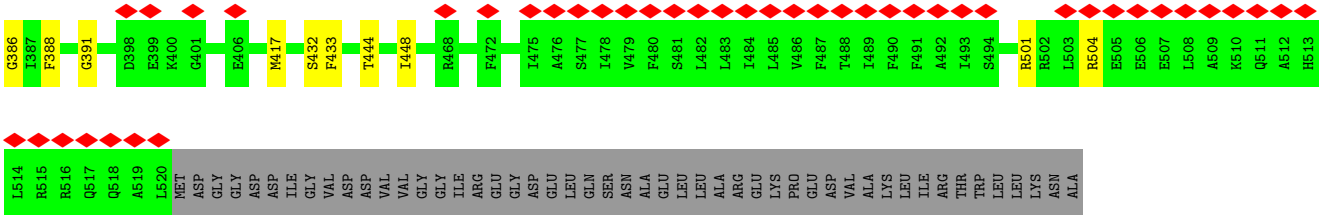




• Molecule 1: Flagellar M-ring protein



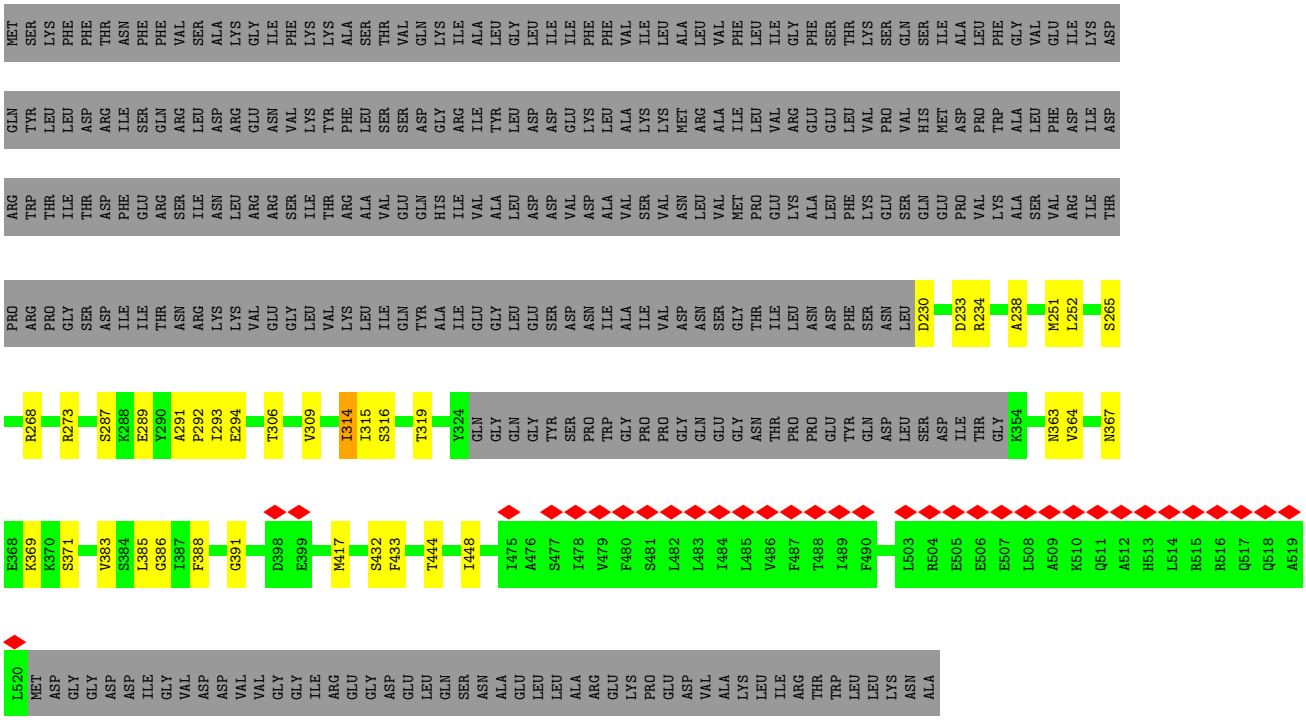




• Molecule 1: Flagellar M-ring protein

Chain m:



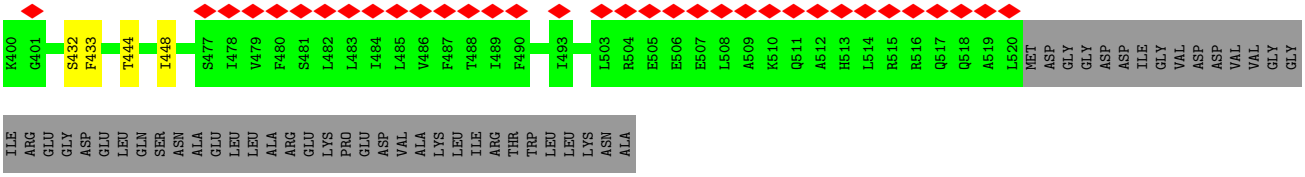


• Molecule 1: Flagellar M-ring protein

Chain n:



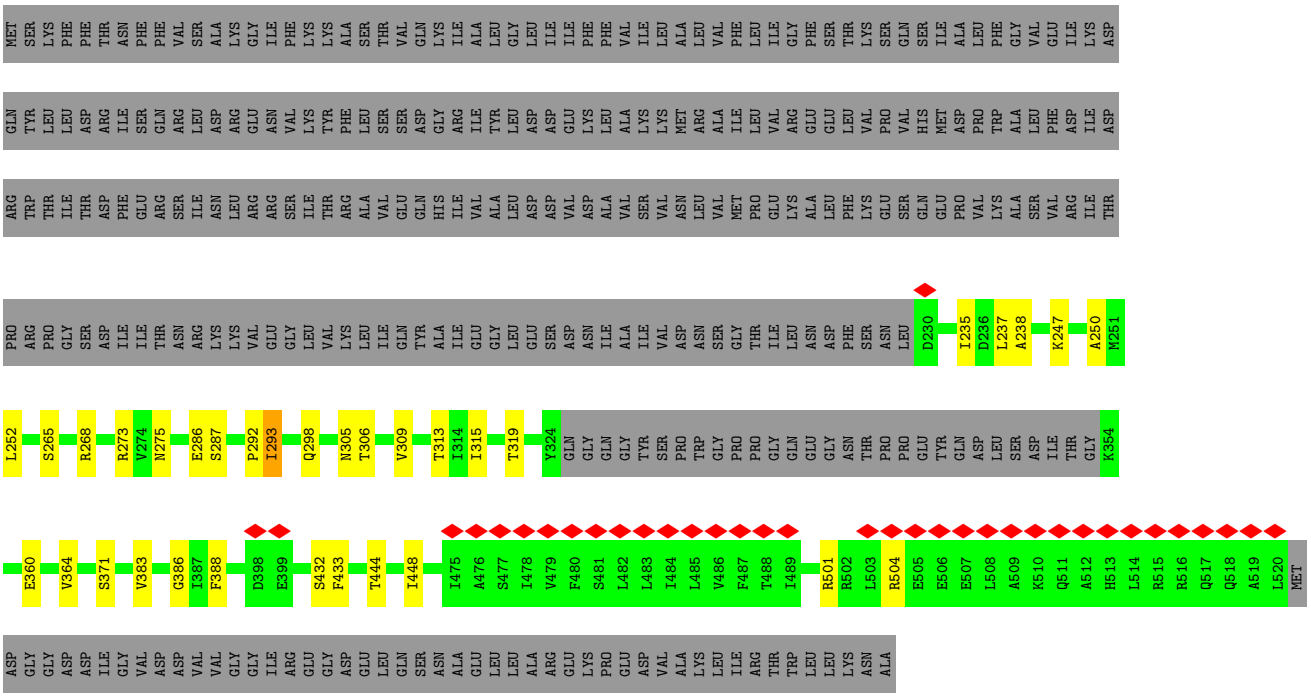




• Molecule 1: Flagellar M-ring protein

Chain o:

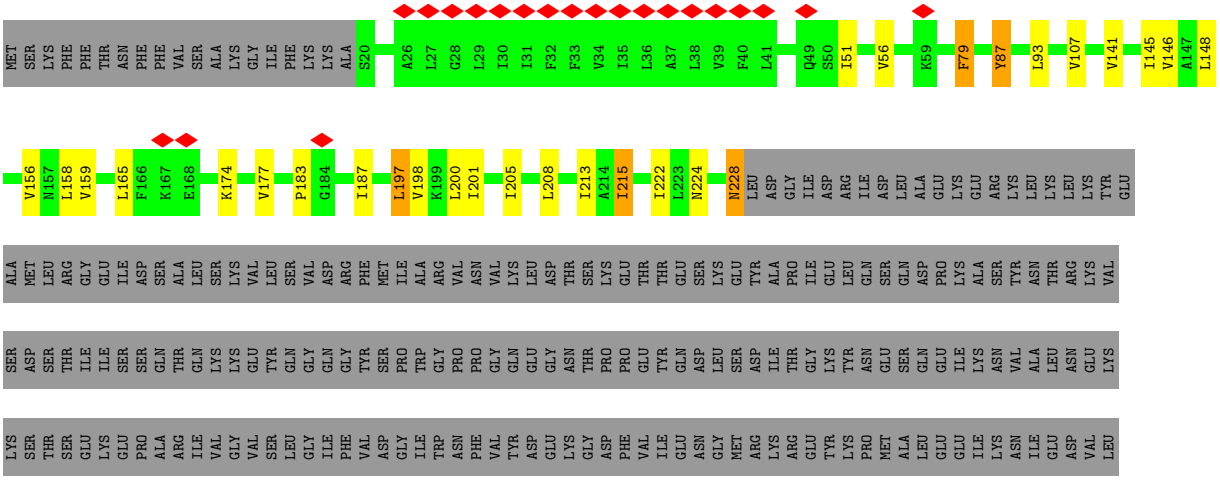


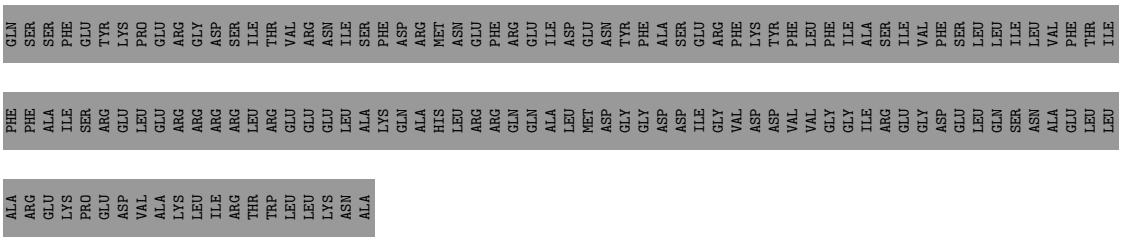


• Molecule 1: Flagellar M-ring protein

Chain p:



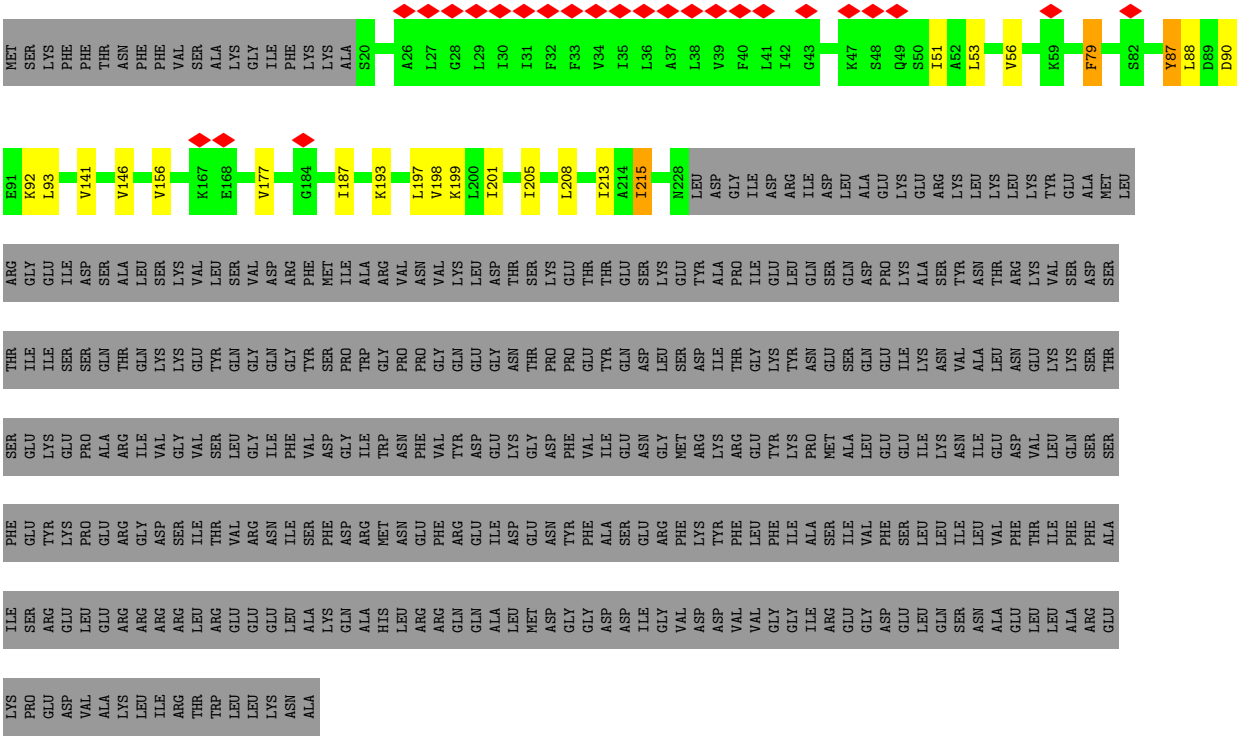




• Molecule 1: Flagellar M-ring protein

Chain q:

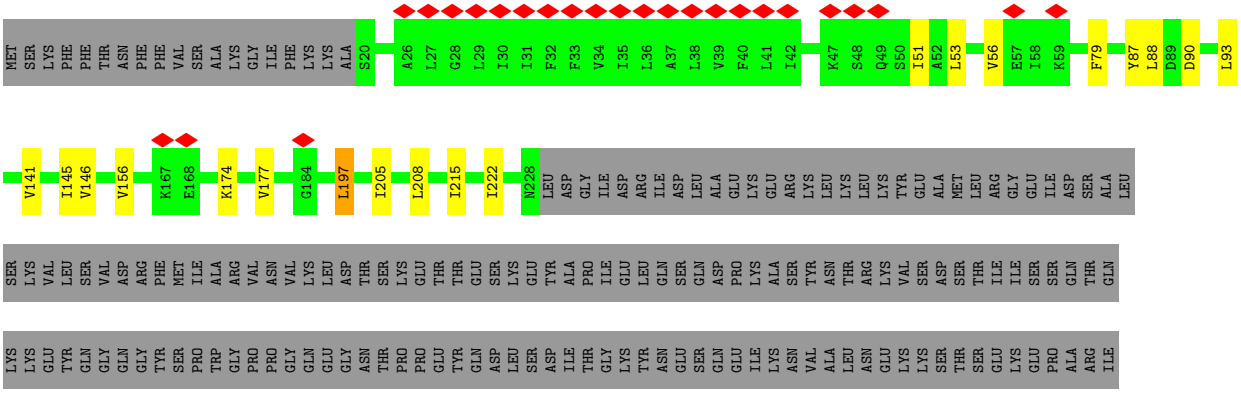


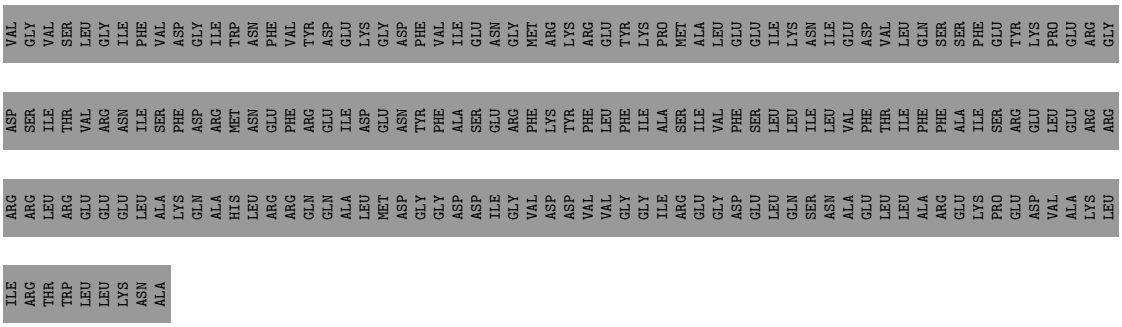


• Molecule 1: Flagellar M-ring protein

Chain r:



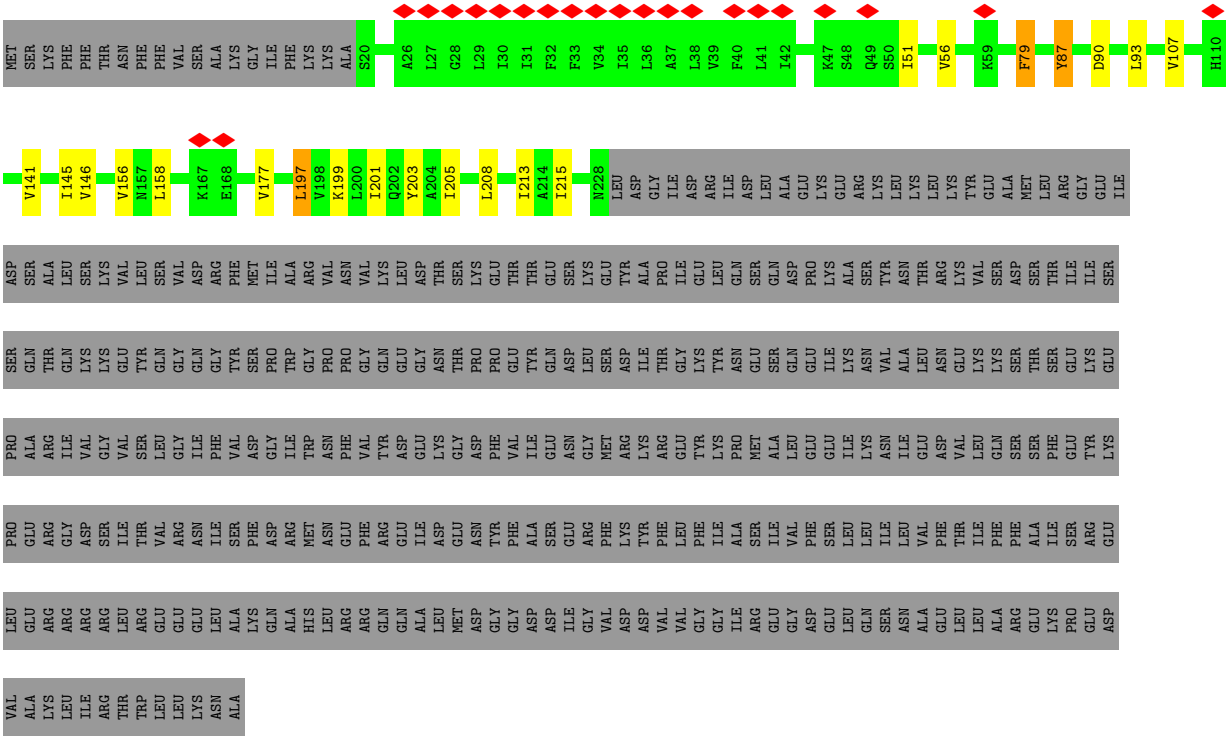




• Molecule 1: Flagellar M-ring protein

Chain s:

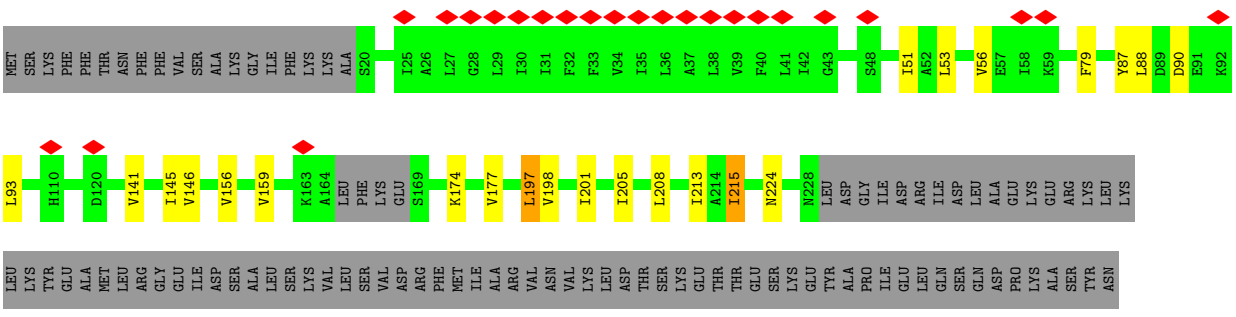


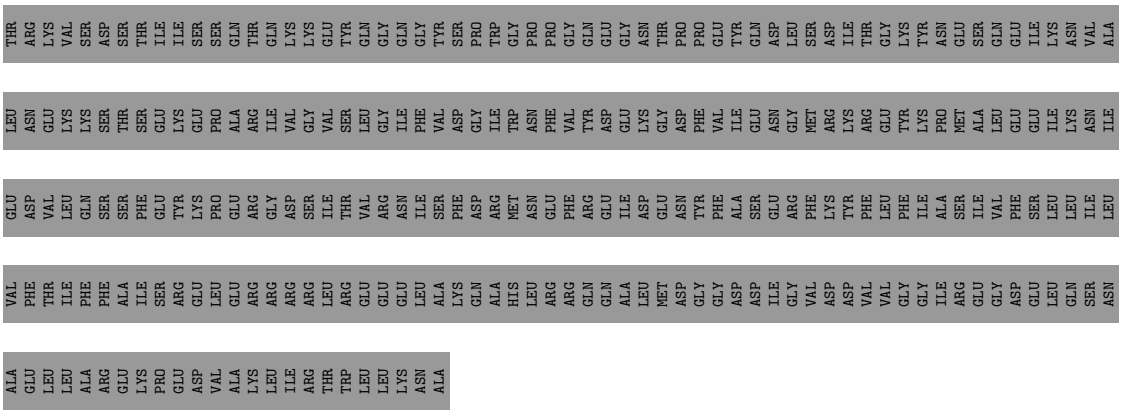


• Molecule 1: Flagellar M-ring protein

Chain t:



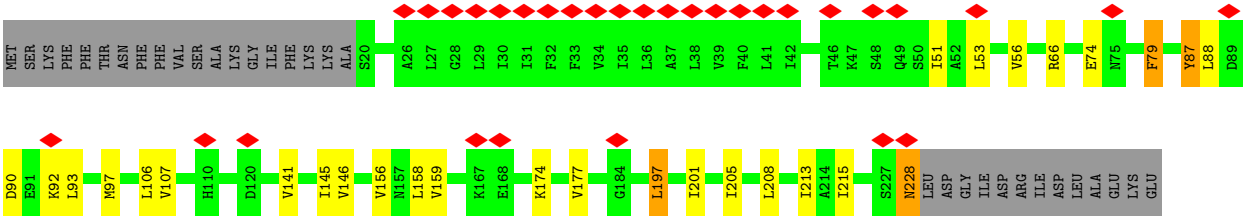




• Molecule 1: Flagellar M-ring protein

Chain u:

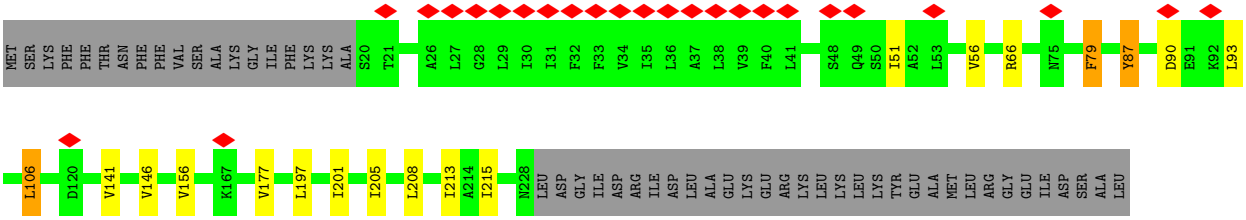


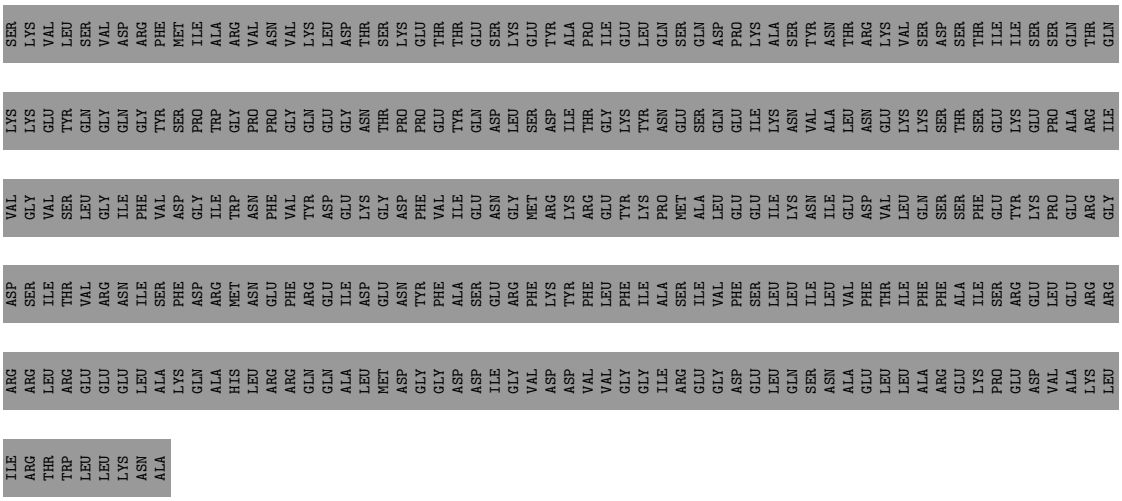


• Molecule 1: Flagellar M-ring protein

Chain v:



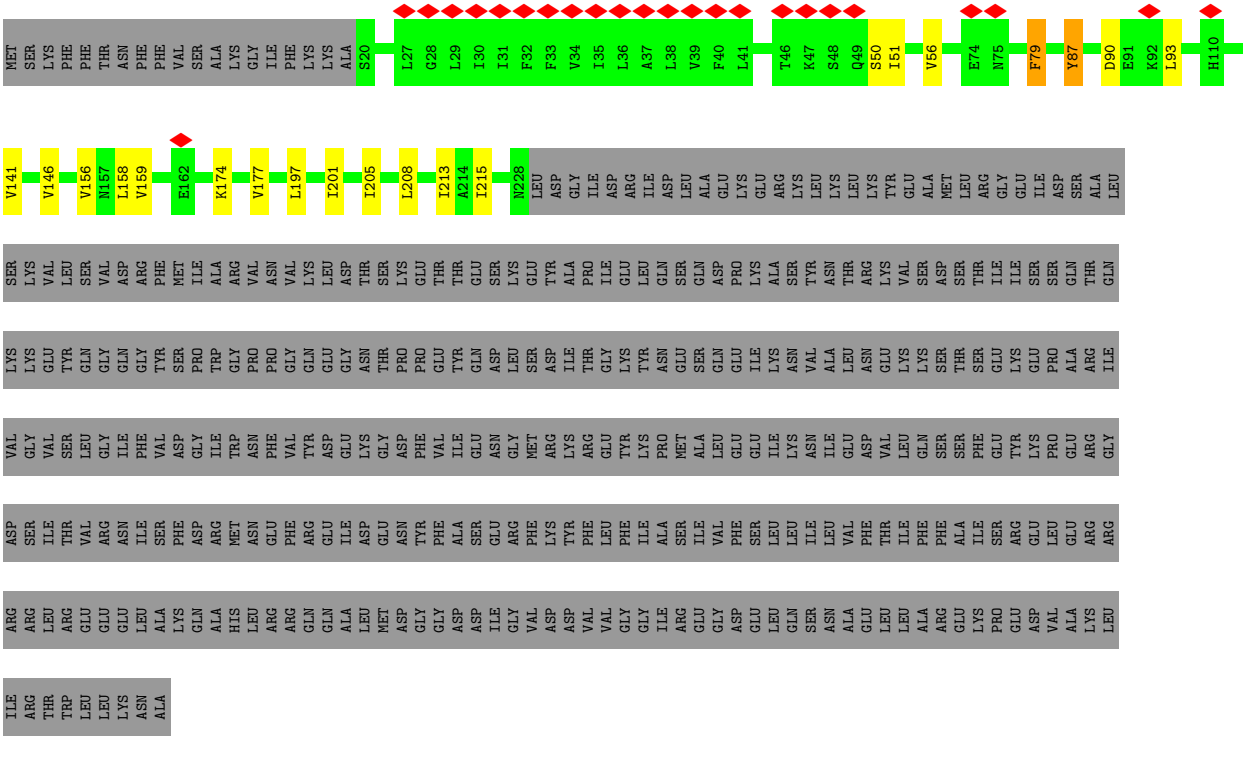




• Molecule 1: Flagellar M-ring protein

Chain w:

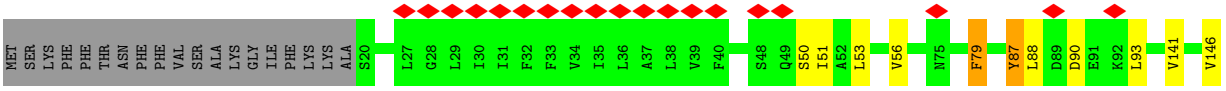


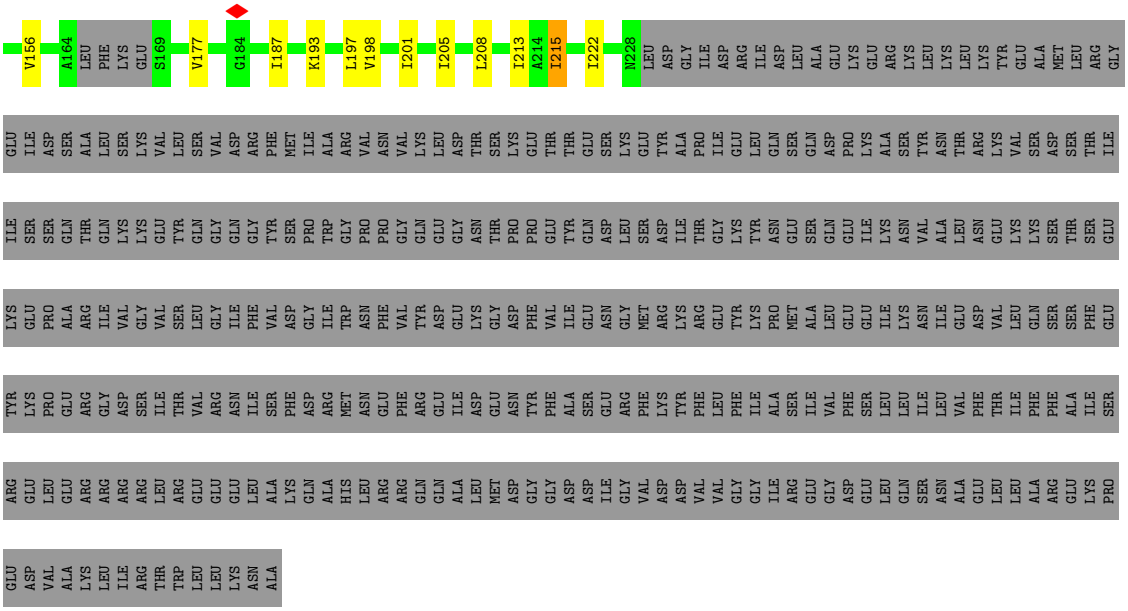


• Molecule 1: Flagellar M-ring protein

Chain x:



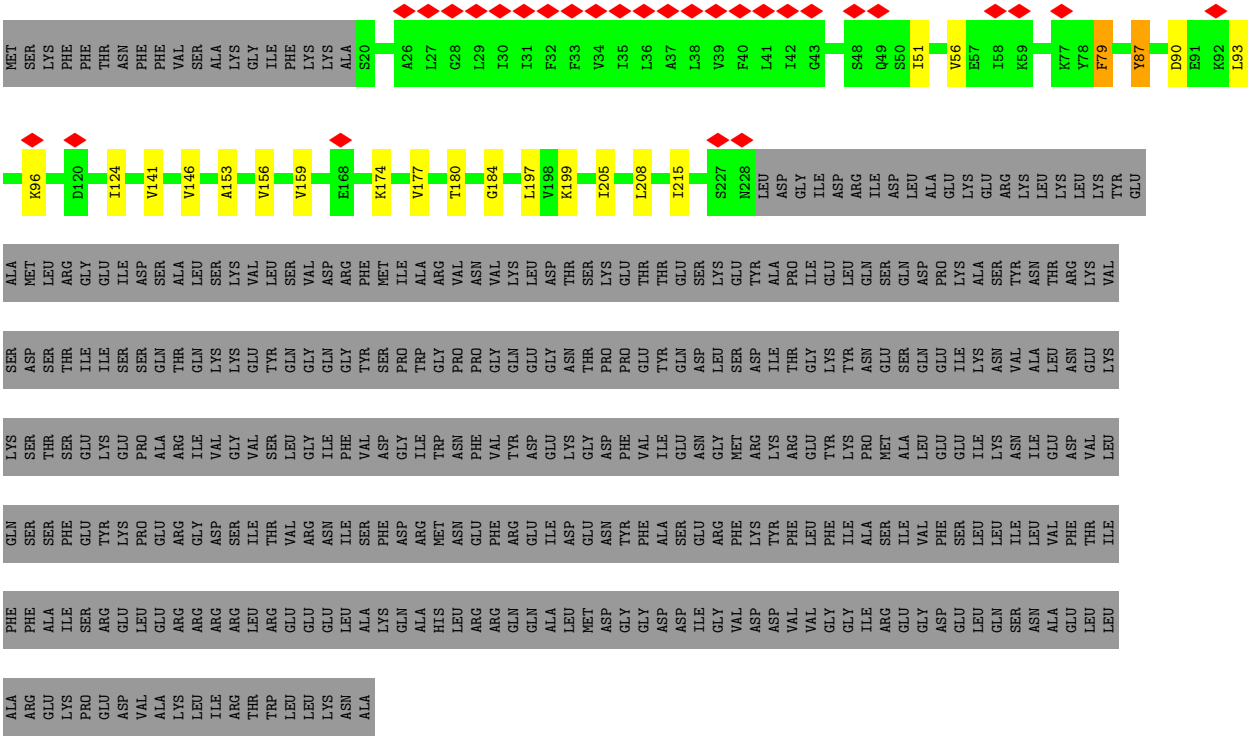




• Molecule 1: Flagellar M-ring protein

Chain y:

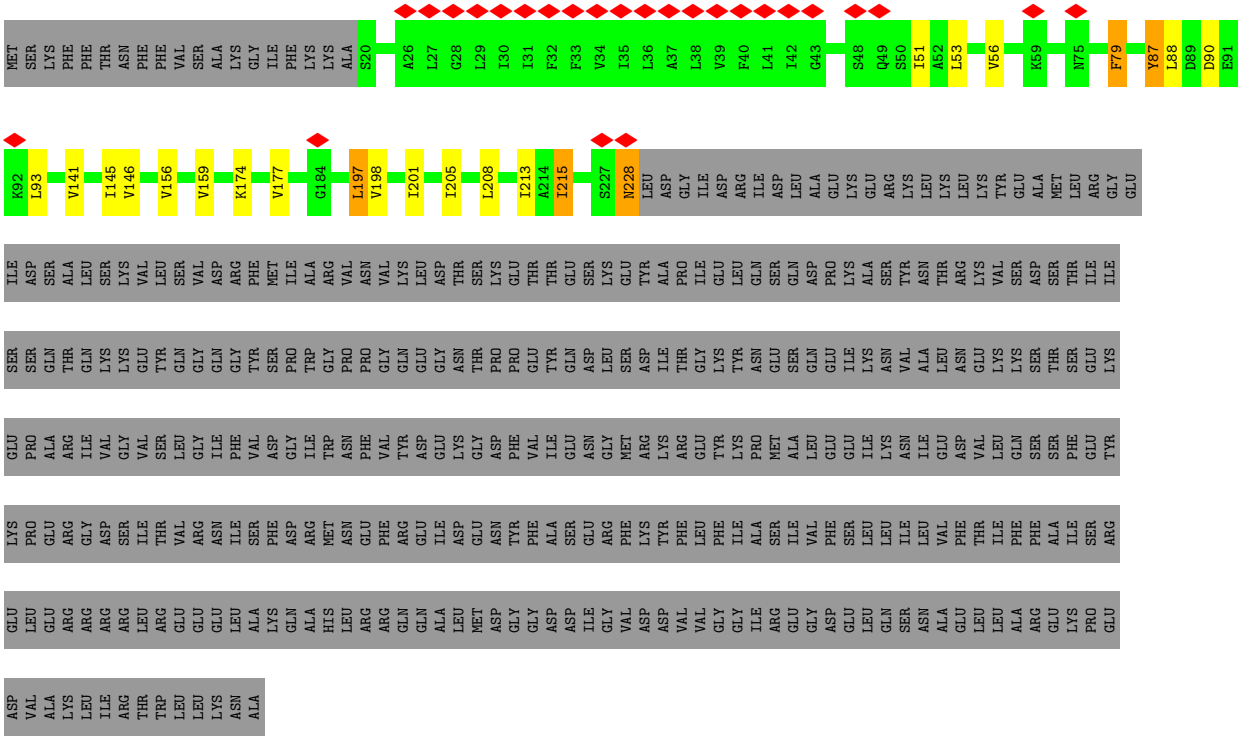




• Molecule 1: Flagellar M-ring protein

Chain z:

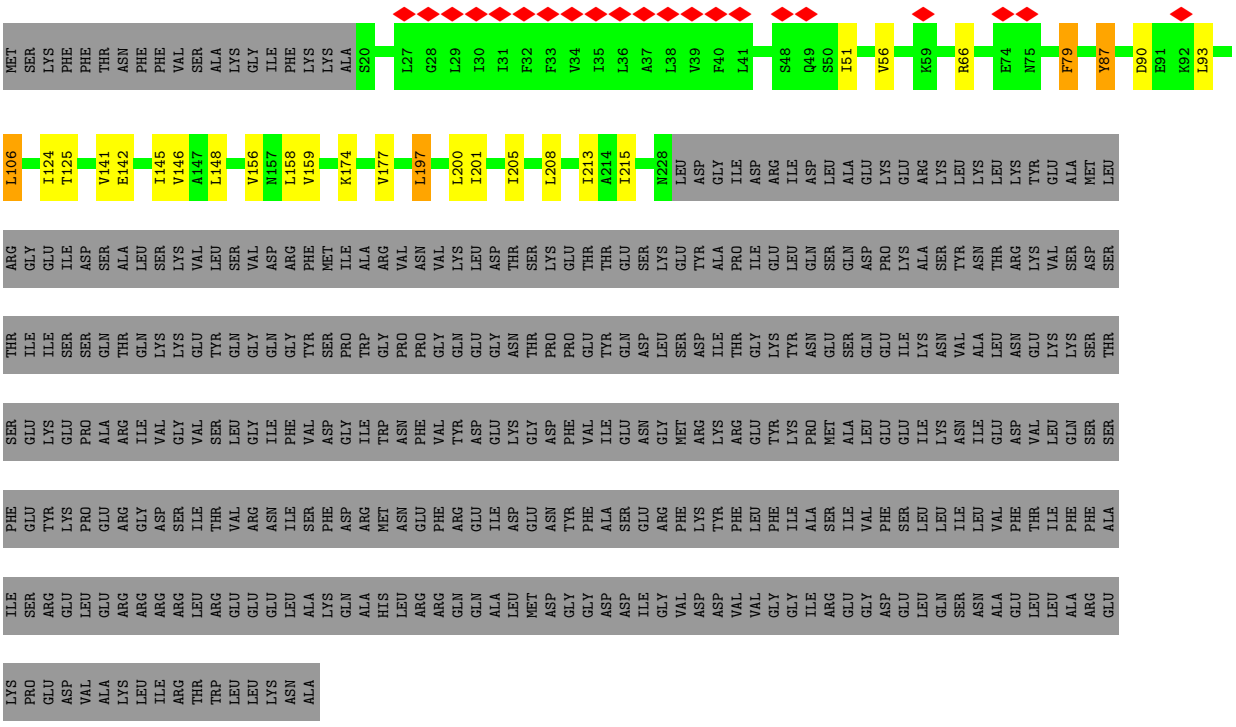




• Molecule 1: Flagellar M-ring protein

Chain 1:

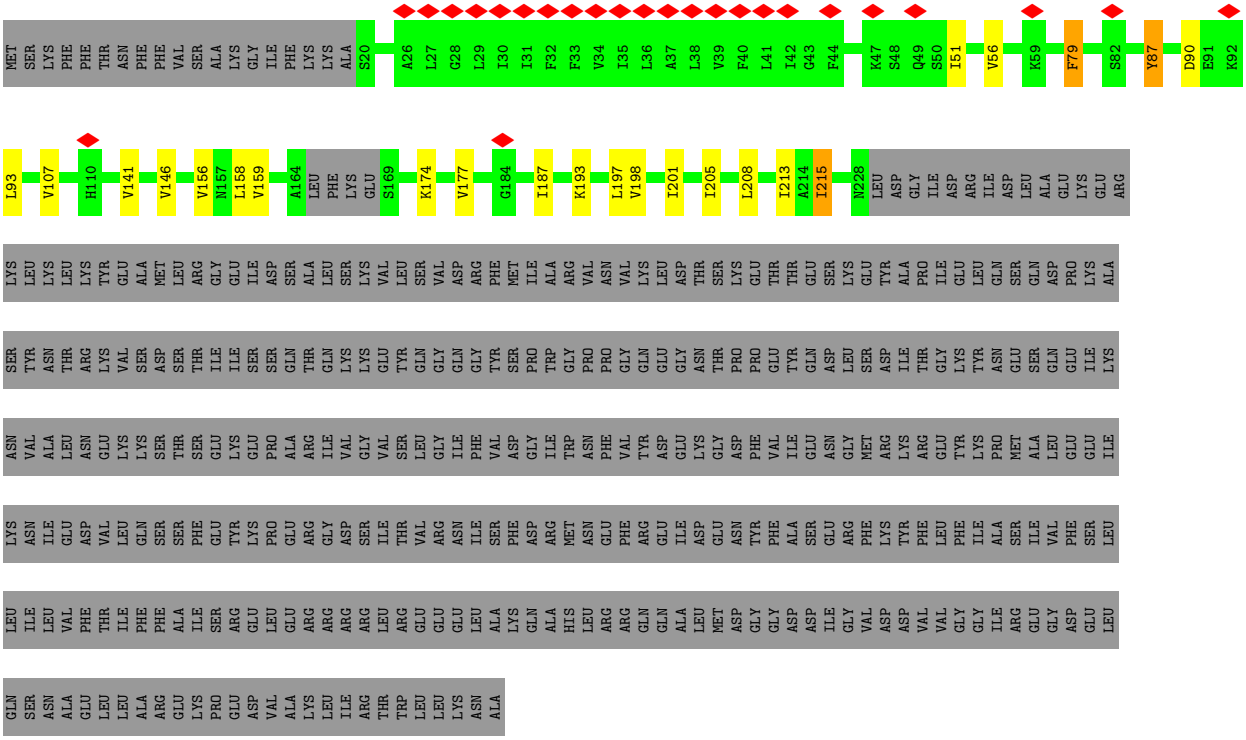




• Molecule 1: Flagellar M-ring protein

Chain 2:

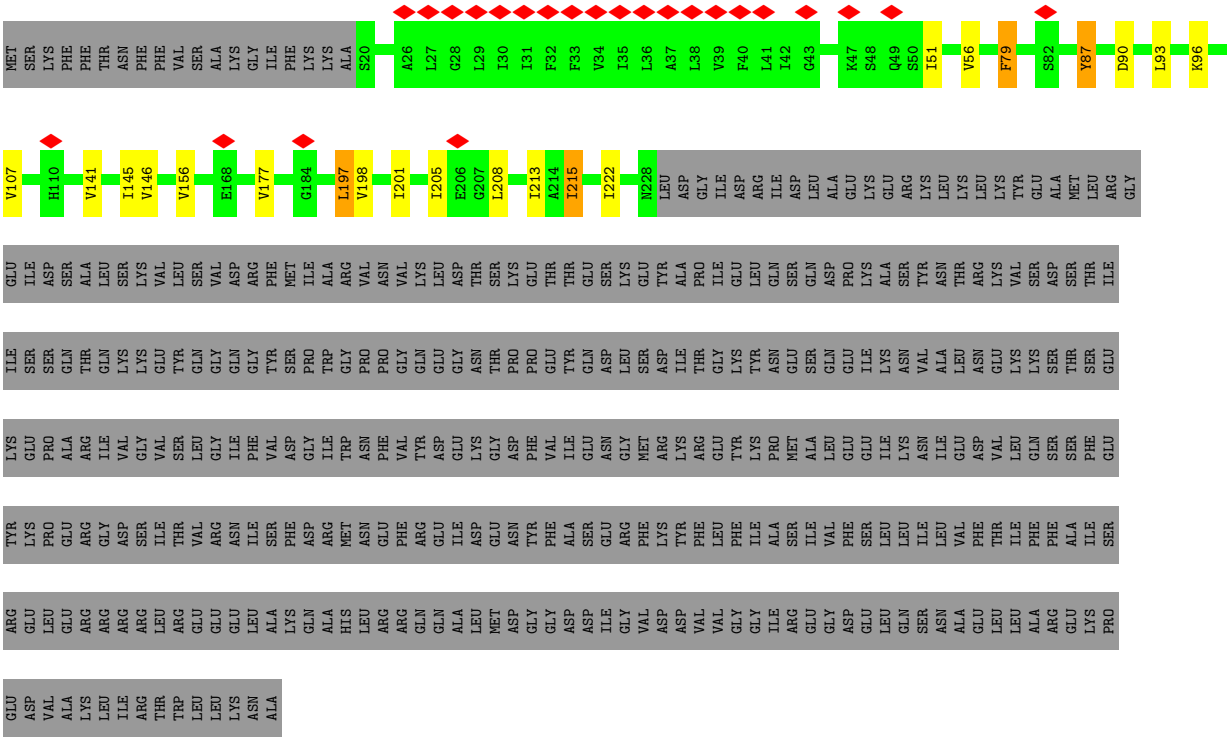




• Molecule 1: Flagellar M-ring protein

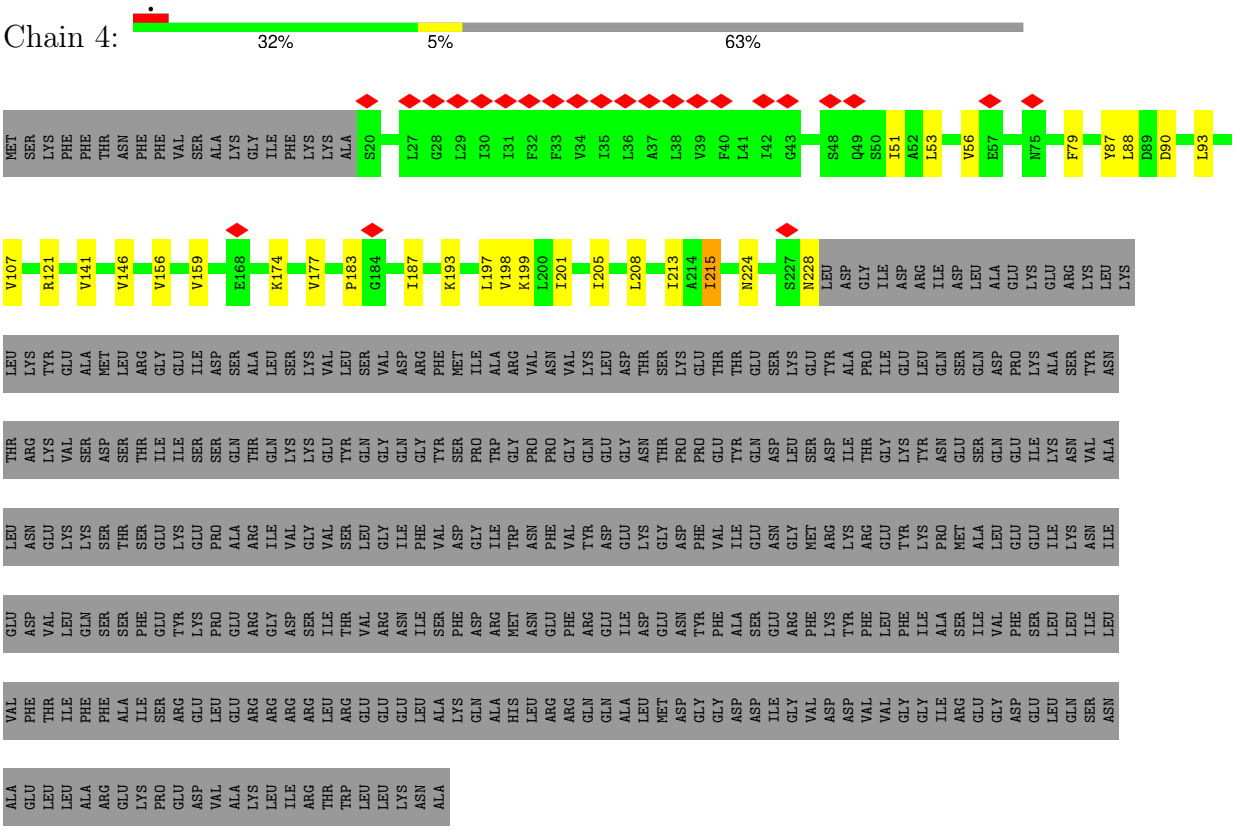
Chain 3:





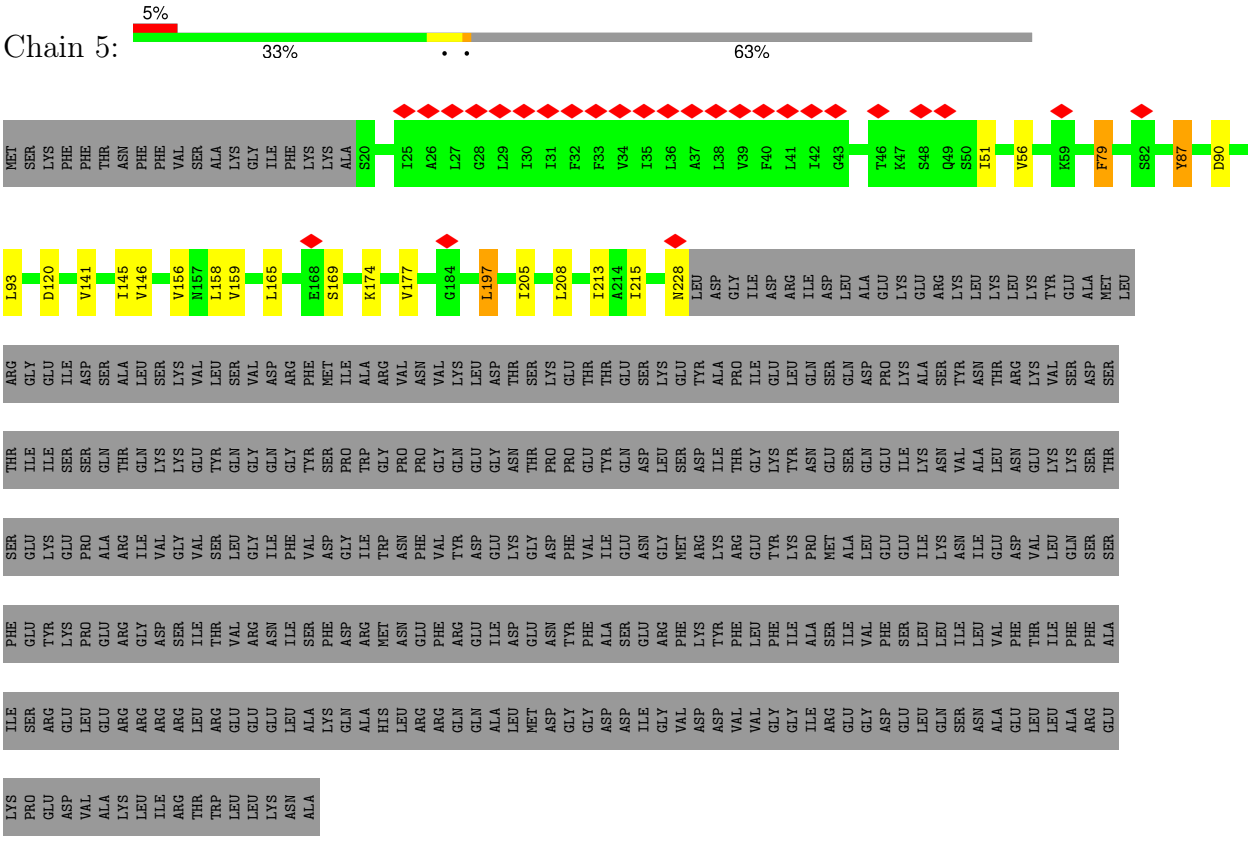
• Molecule 1: Flagellar M-ring protein

Chain 4:



• Molecule 1: Flagellar M-ring protein

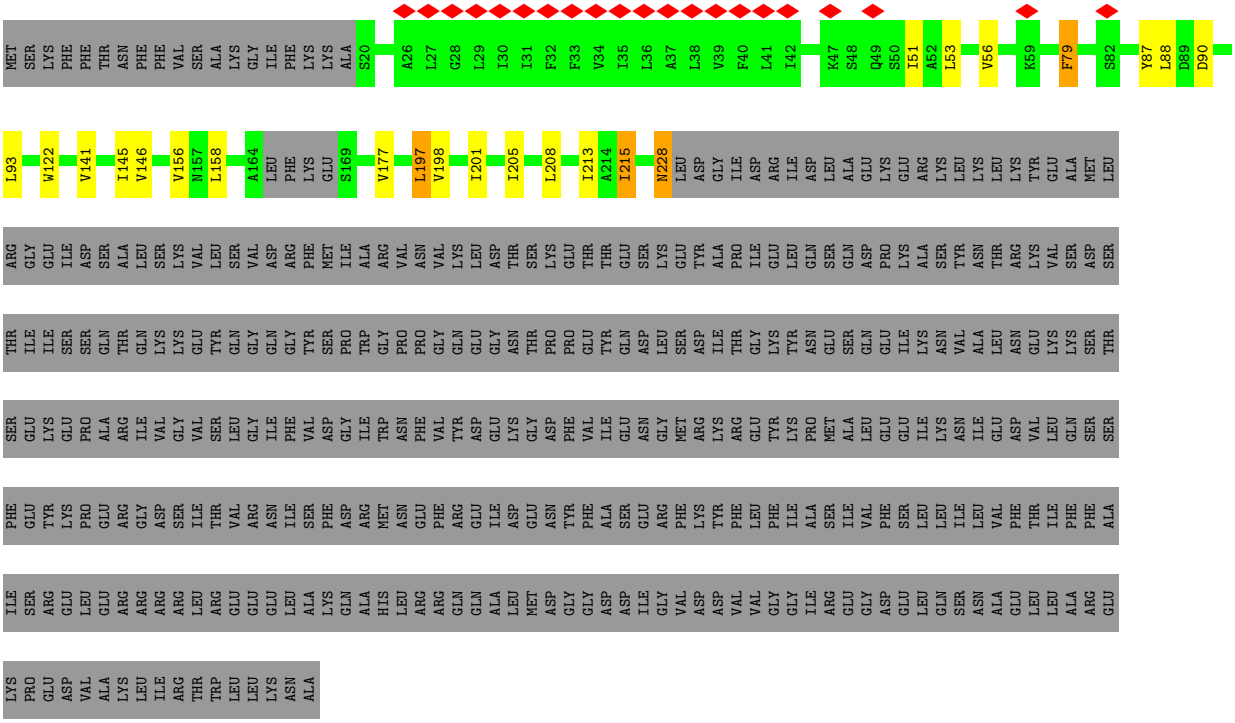
Chain 5:



• Molecule 1: Flagellar M-ring protein

Chain 6:

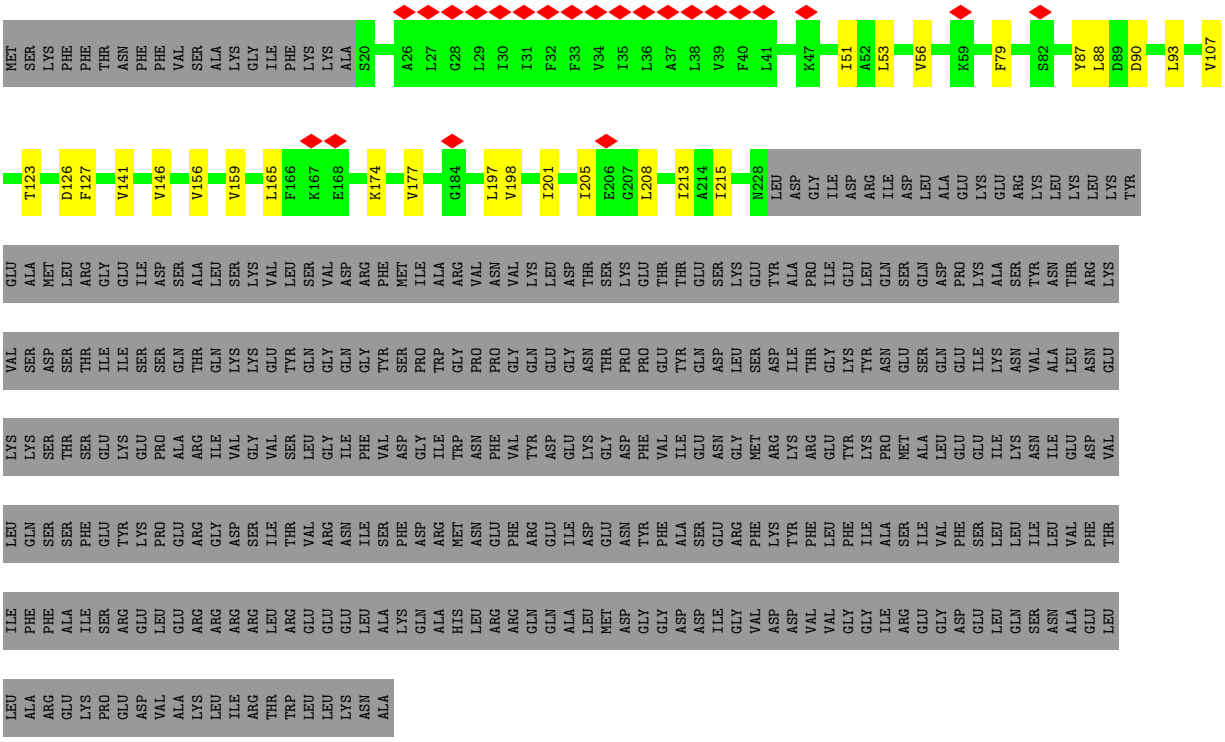




• Molecule 1: Flagellar M-ring protein

Chain 7:

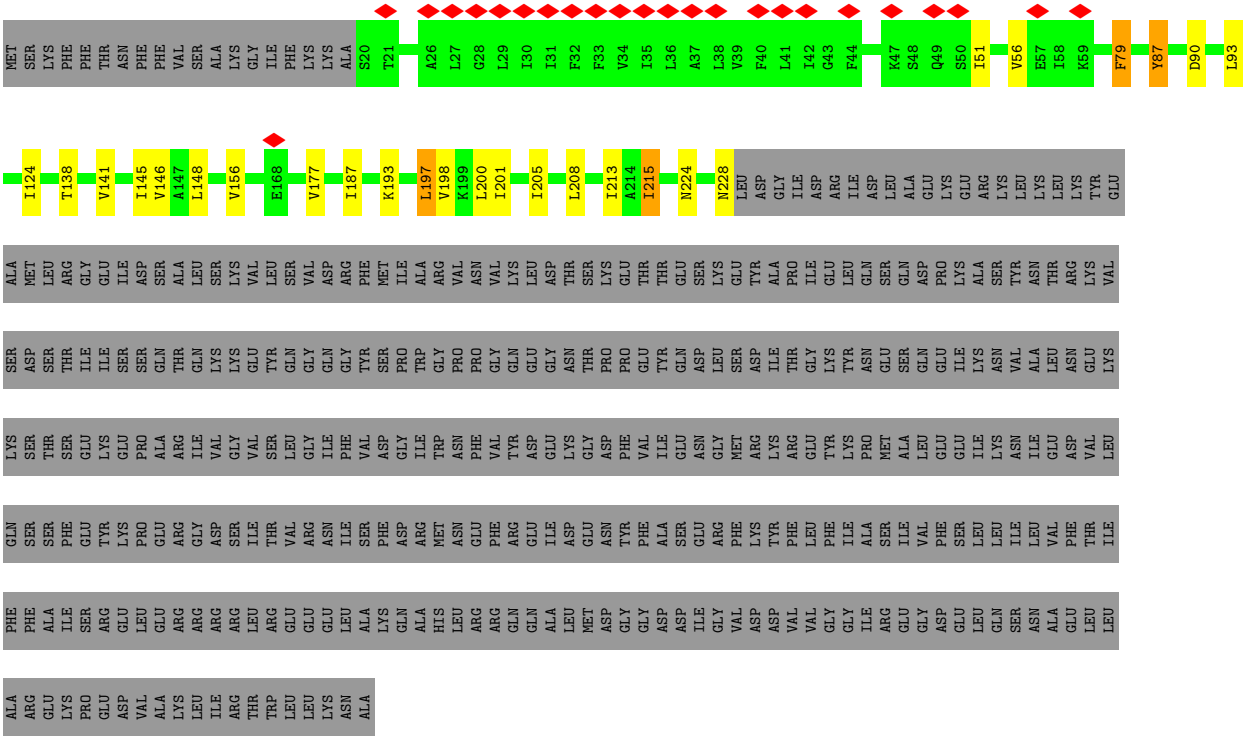




• Molecule 1: Flagellar M-ring protein

Chain 8:

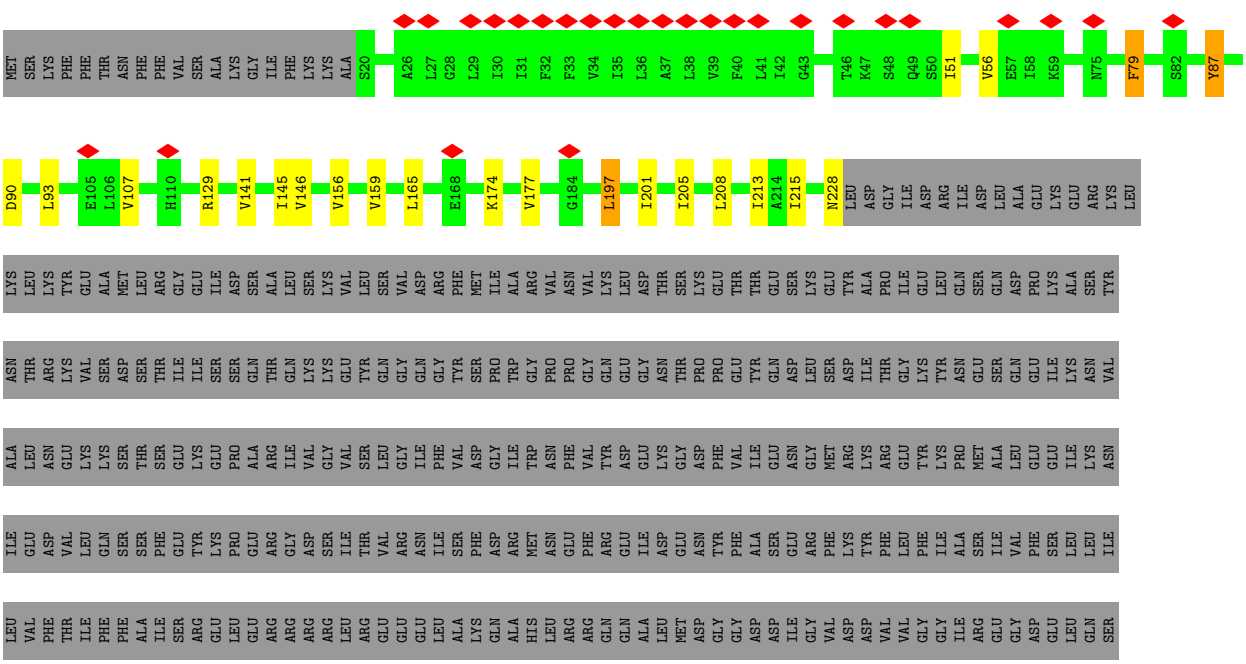




• Molecule 1: Flagellar M-ring protein

Chain 9:



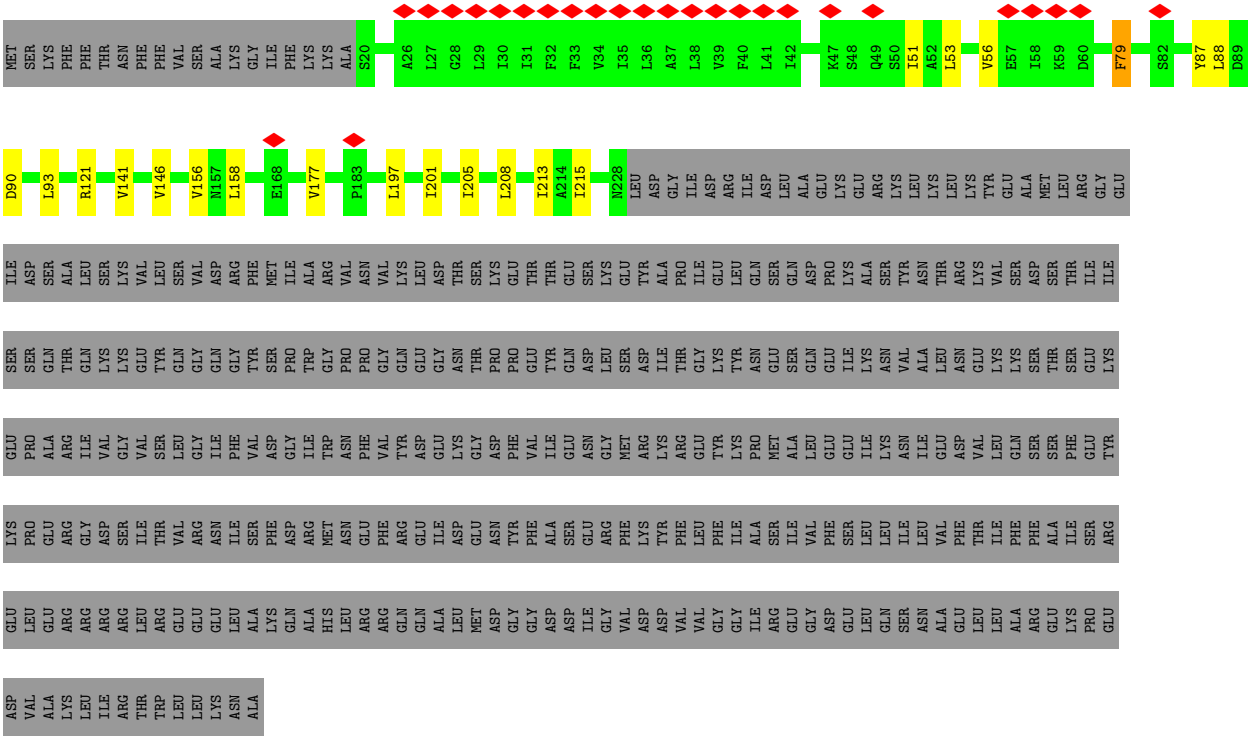




• Molecule 1: Flagellar M-ring protein

Chain 0:

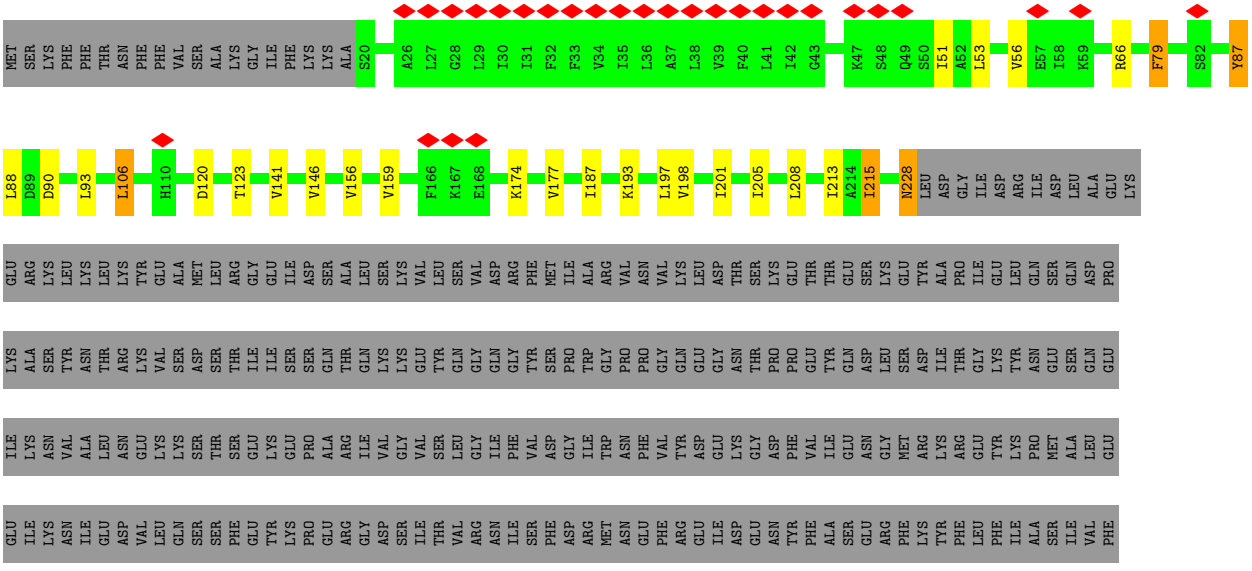


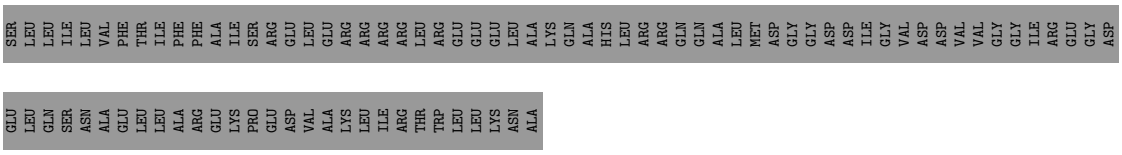


• Molecule 1: Flagellar M-ring protein

Chain AA:



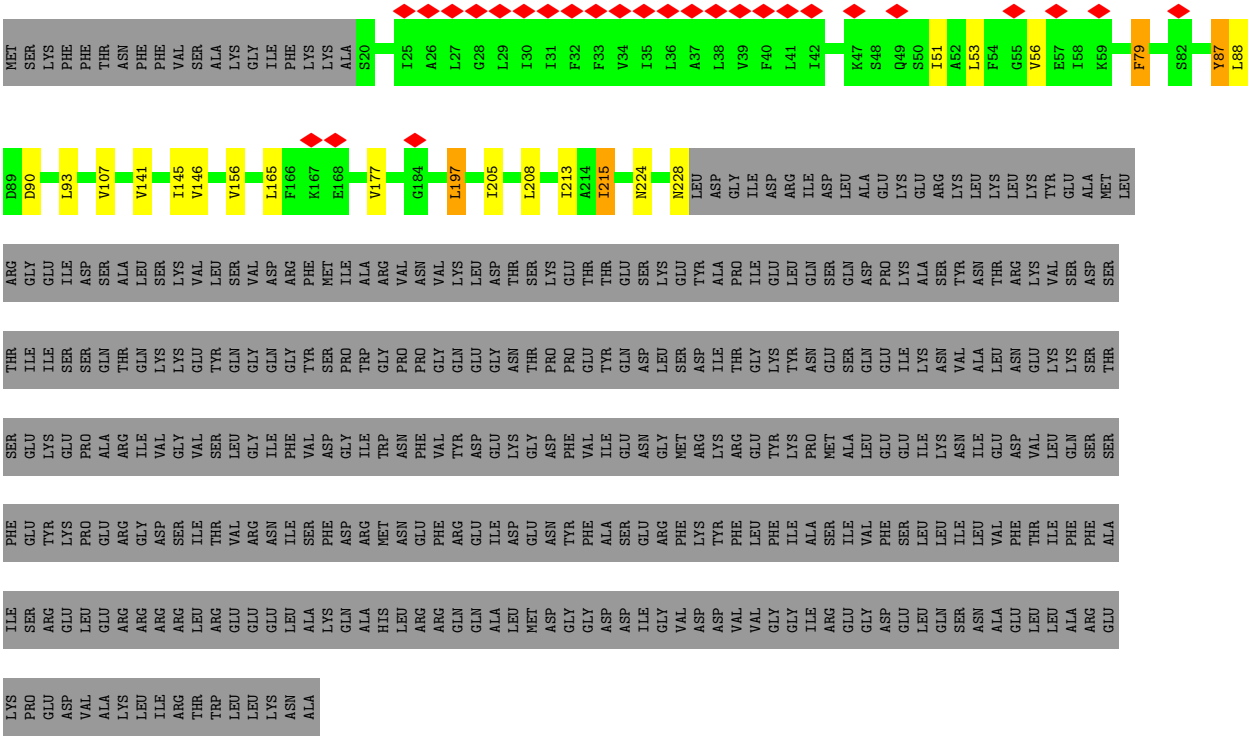




• Molecule 1: Flagellar M-ring protein

Chain AB:

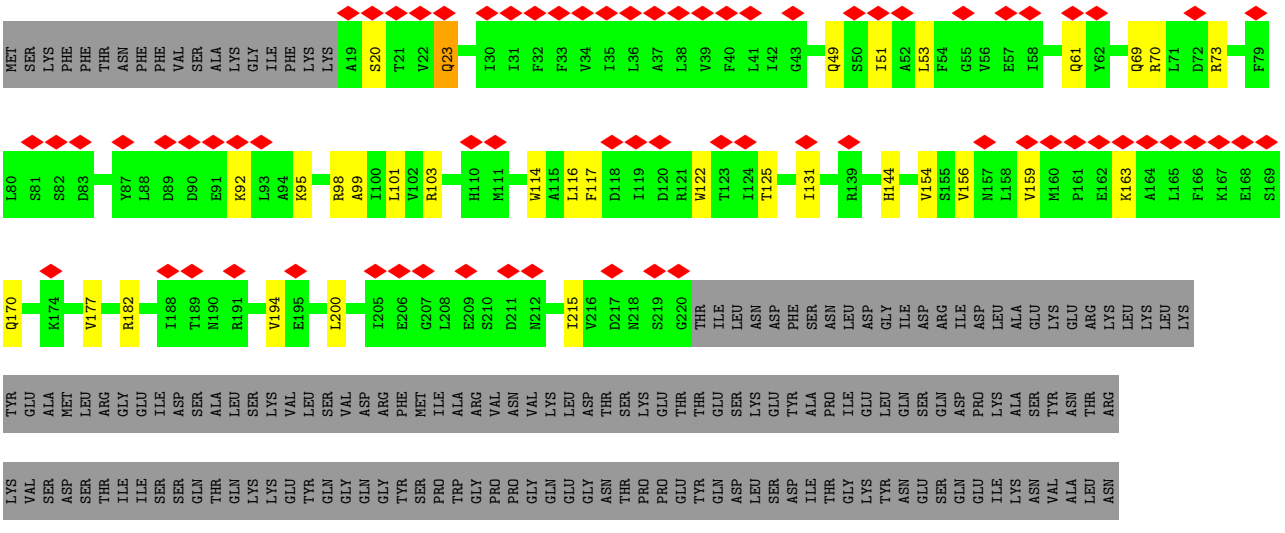


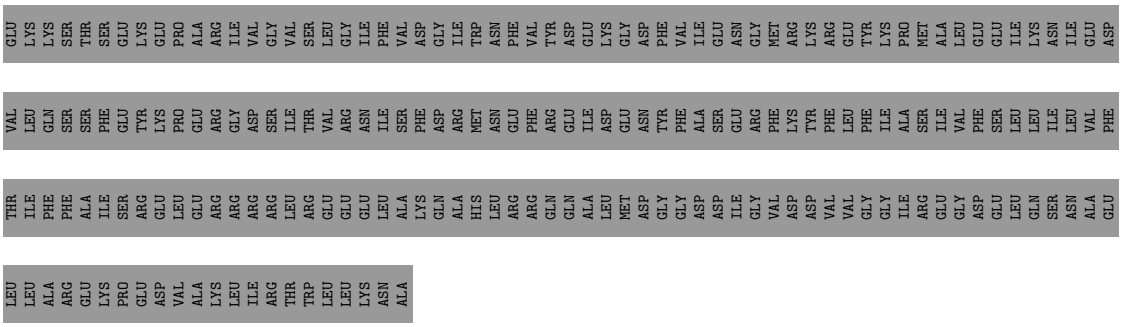


• Molecule 1: Flagellar M-ring protein

Chain AC:



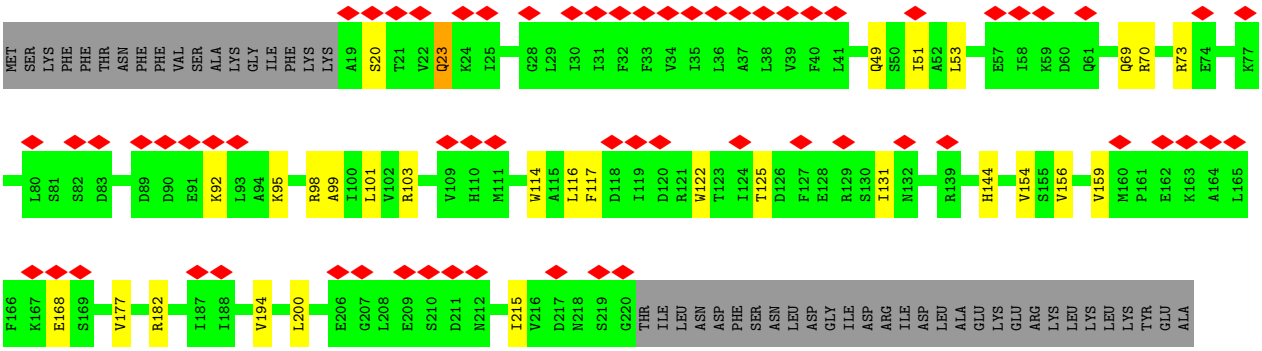




• Molecule 1: Flagellar M-ring protein

Chain AD:

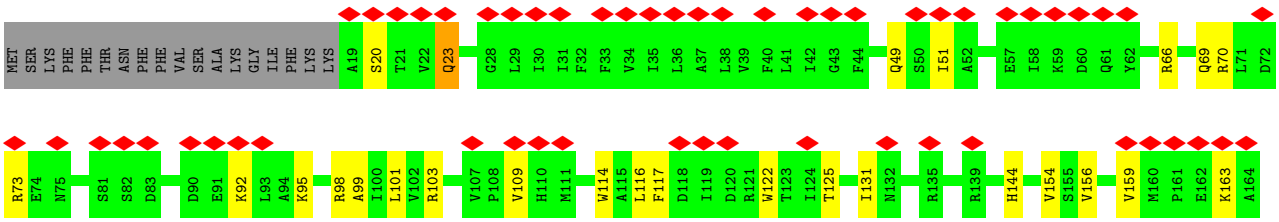


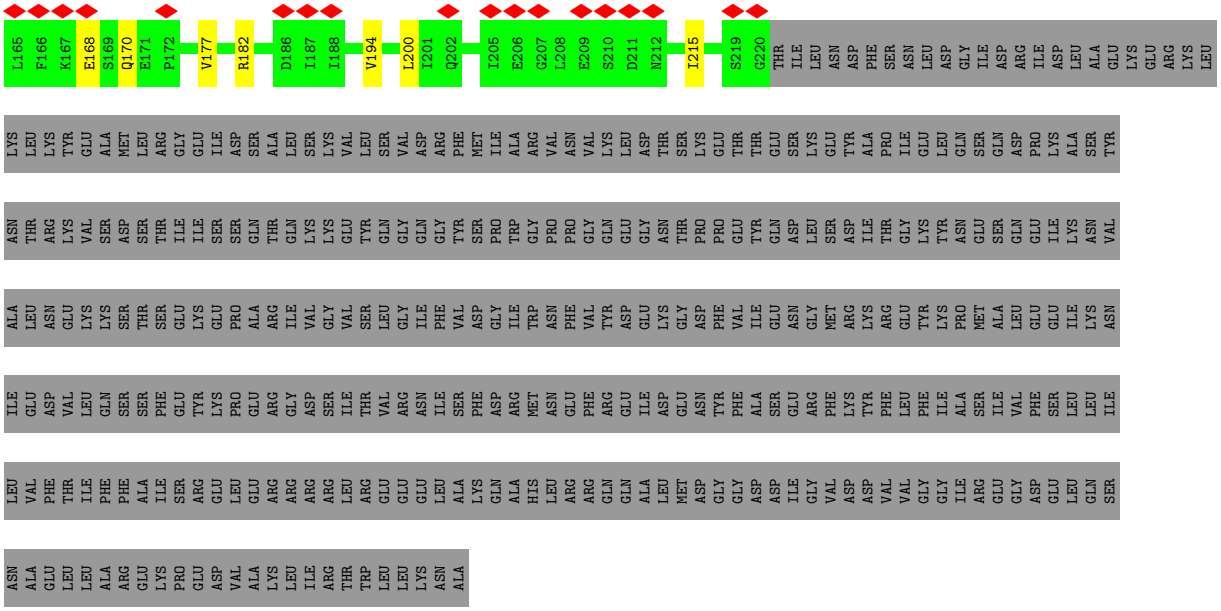


• Molecule 1: Flagellar M-ring protein

Chain AE:



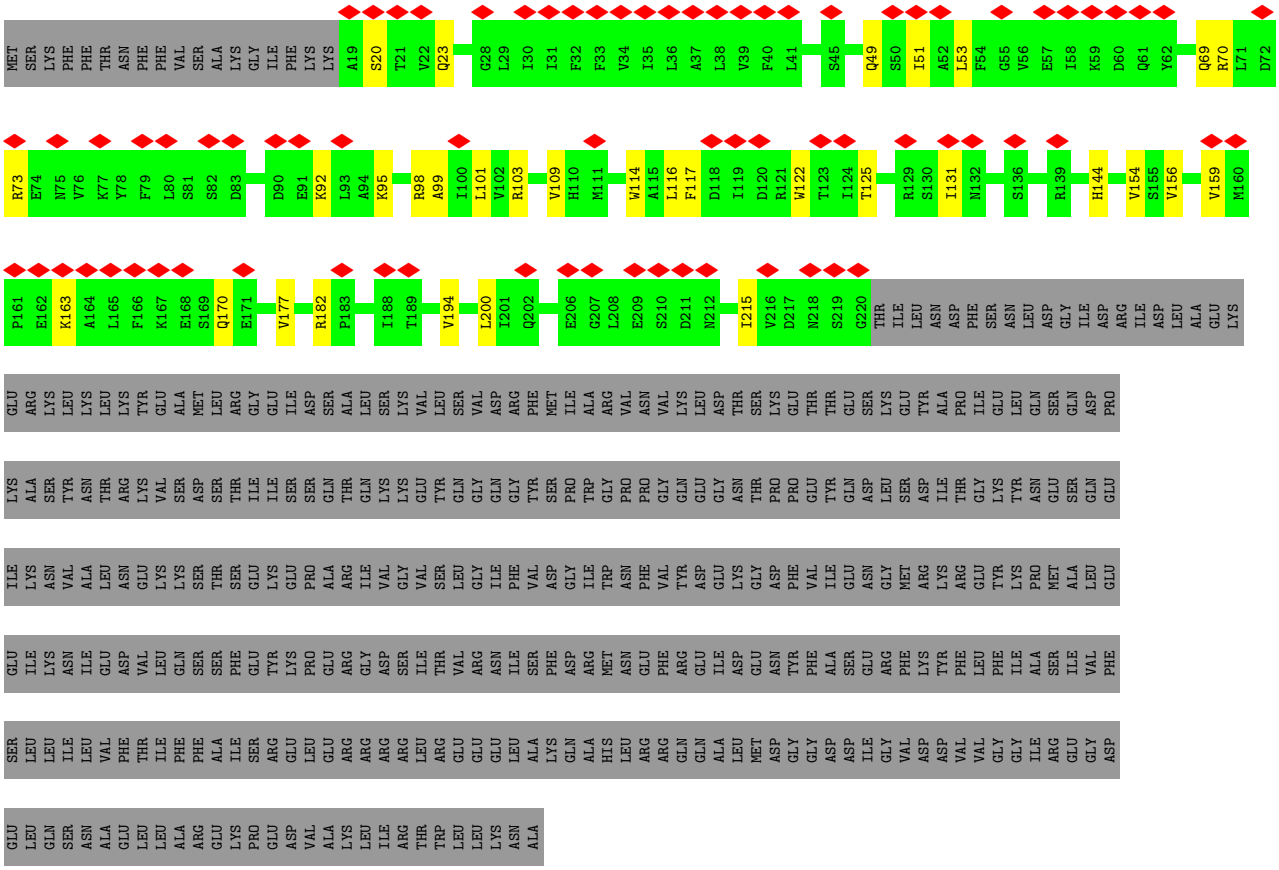




• Molecule 1: Flagellar M-ring protein

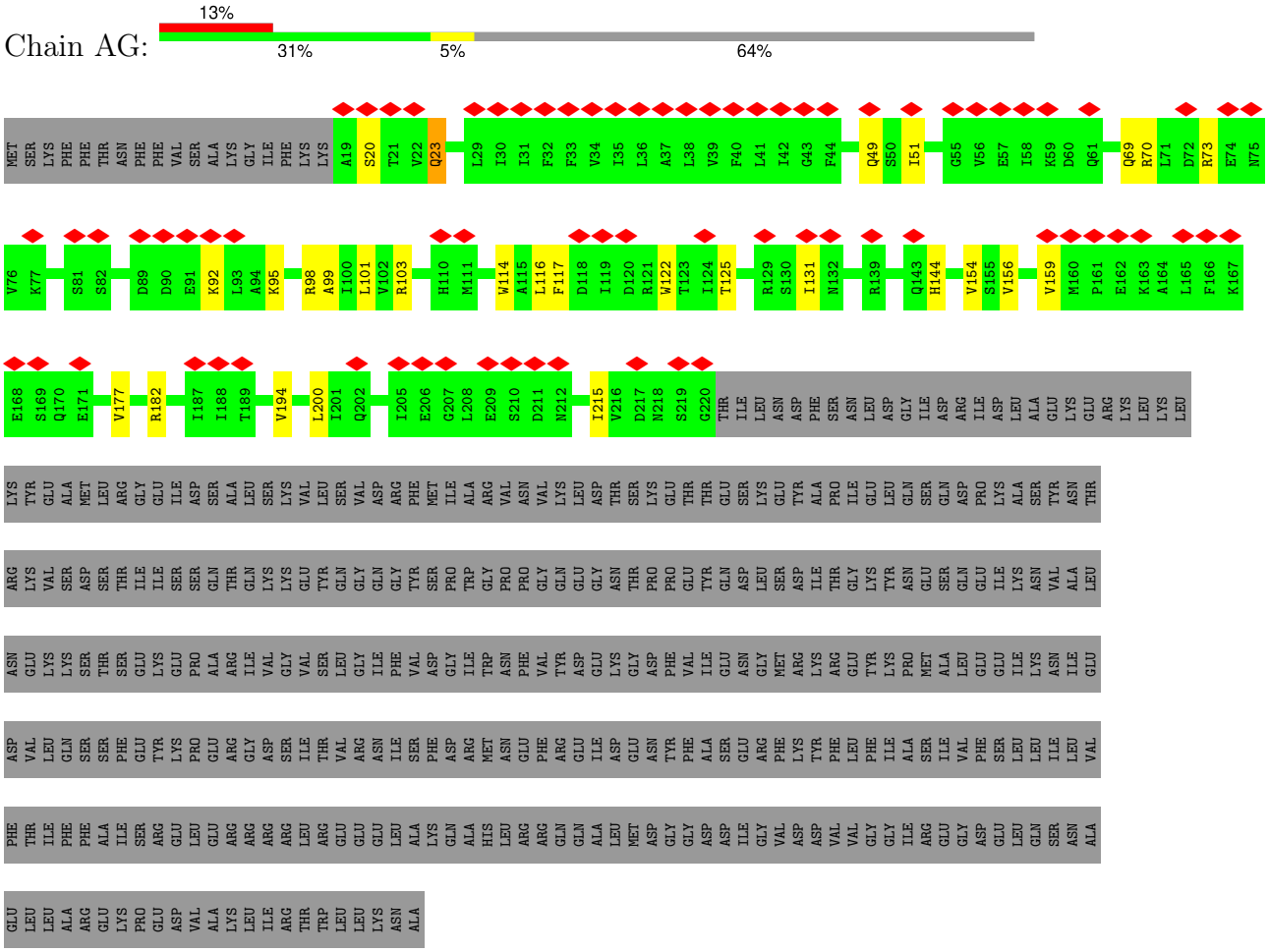
Chain AF:





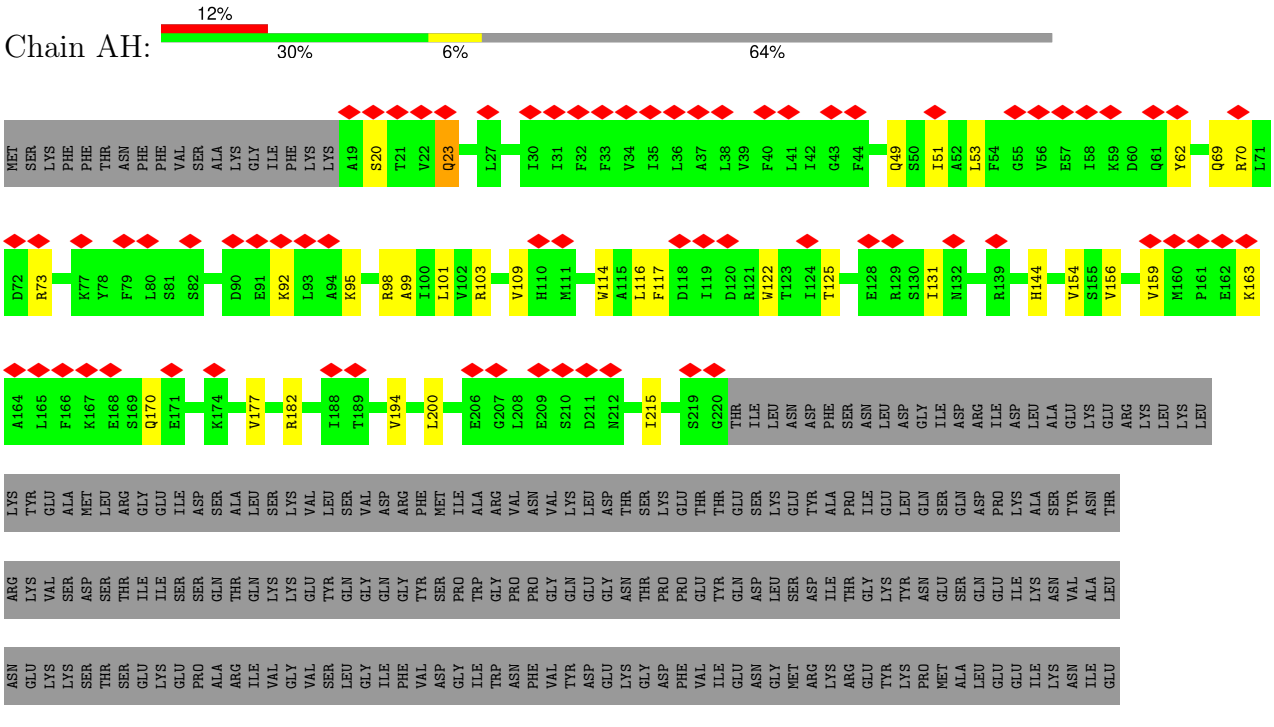
• Molecule 1: Flagellar M-ring protein

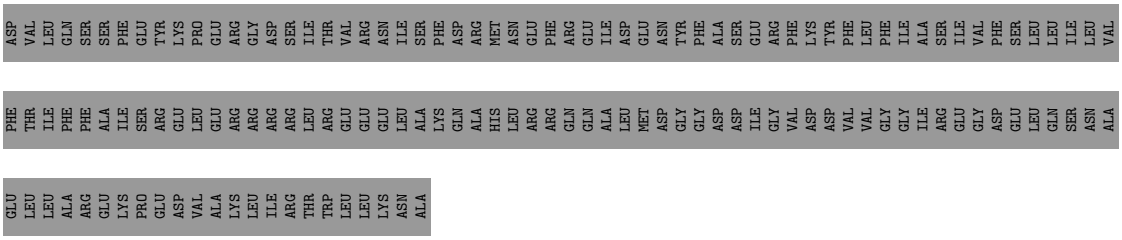
Chain AG:



• Molecule 1: Flagellar M-ring protein

Chain AH:

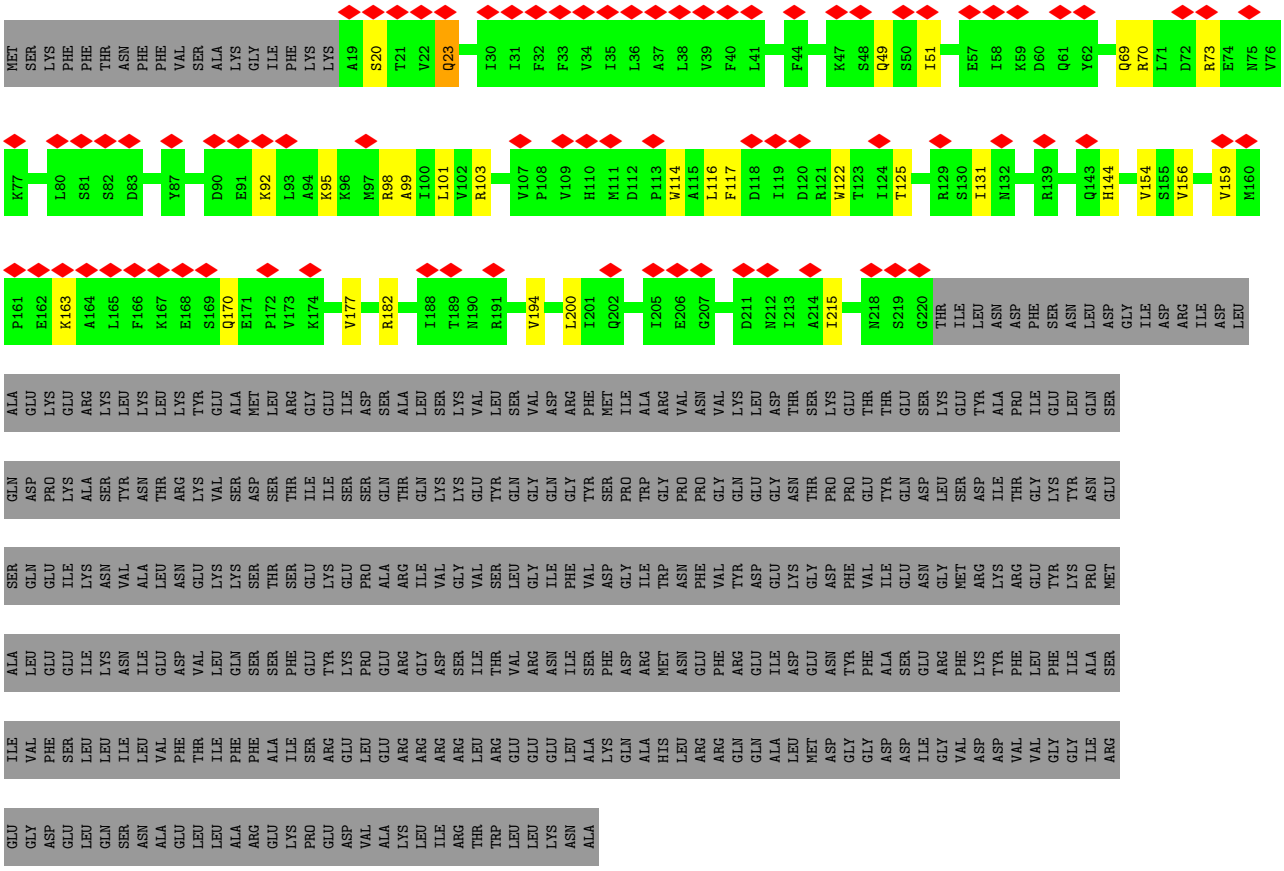




• Molecule 1: Flagellar M-ring protein

Chain AI:

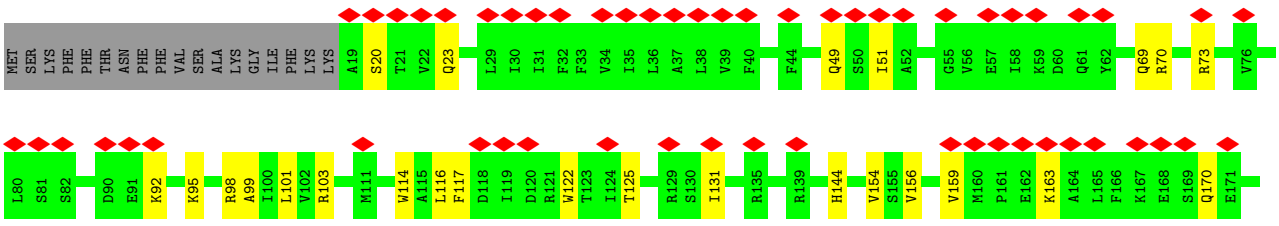


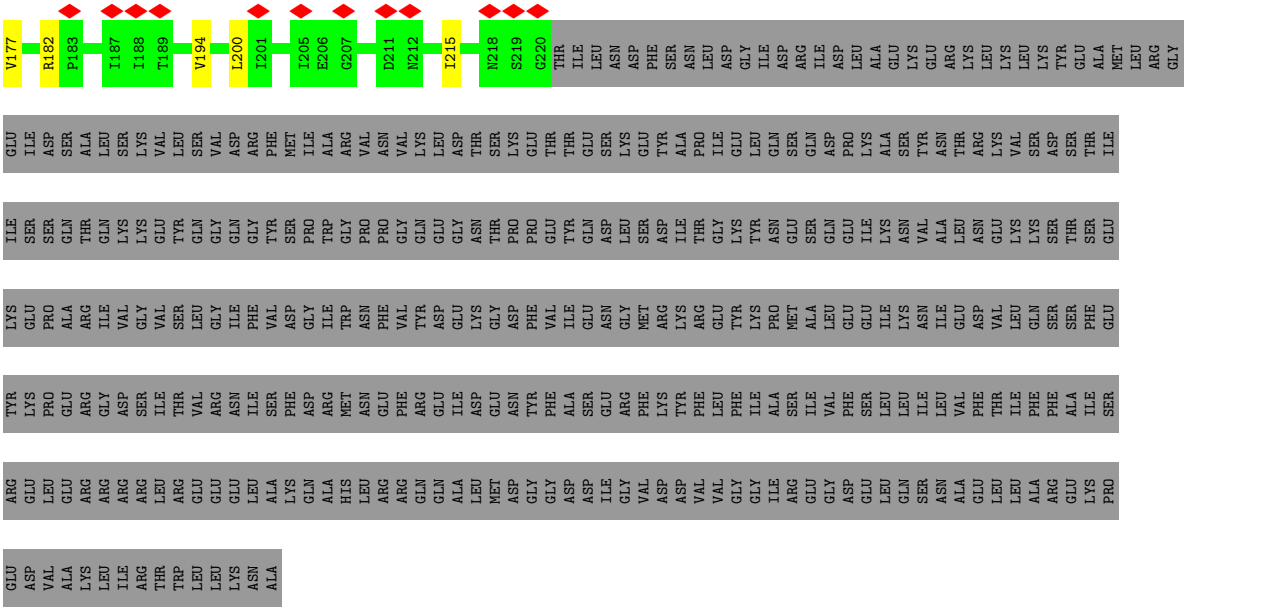


• Molecule 1: Flagellar M-ring protein

Chain AJ:



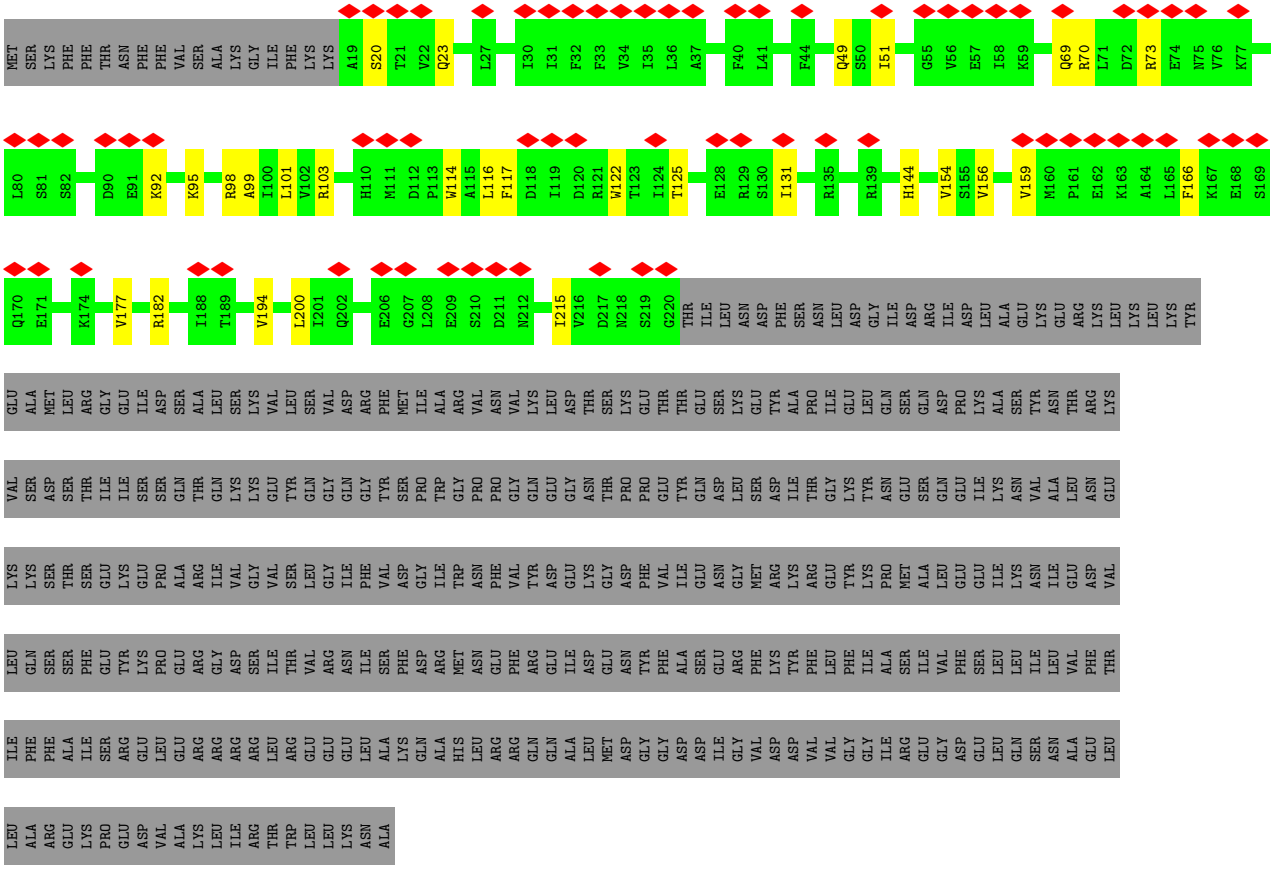




• Molecule 1: Flagellar M-ring protein

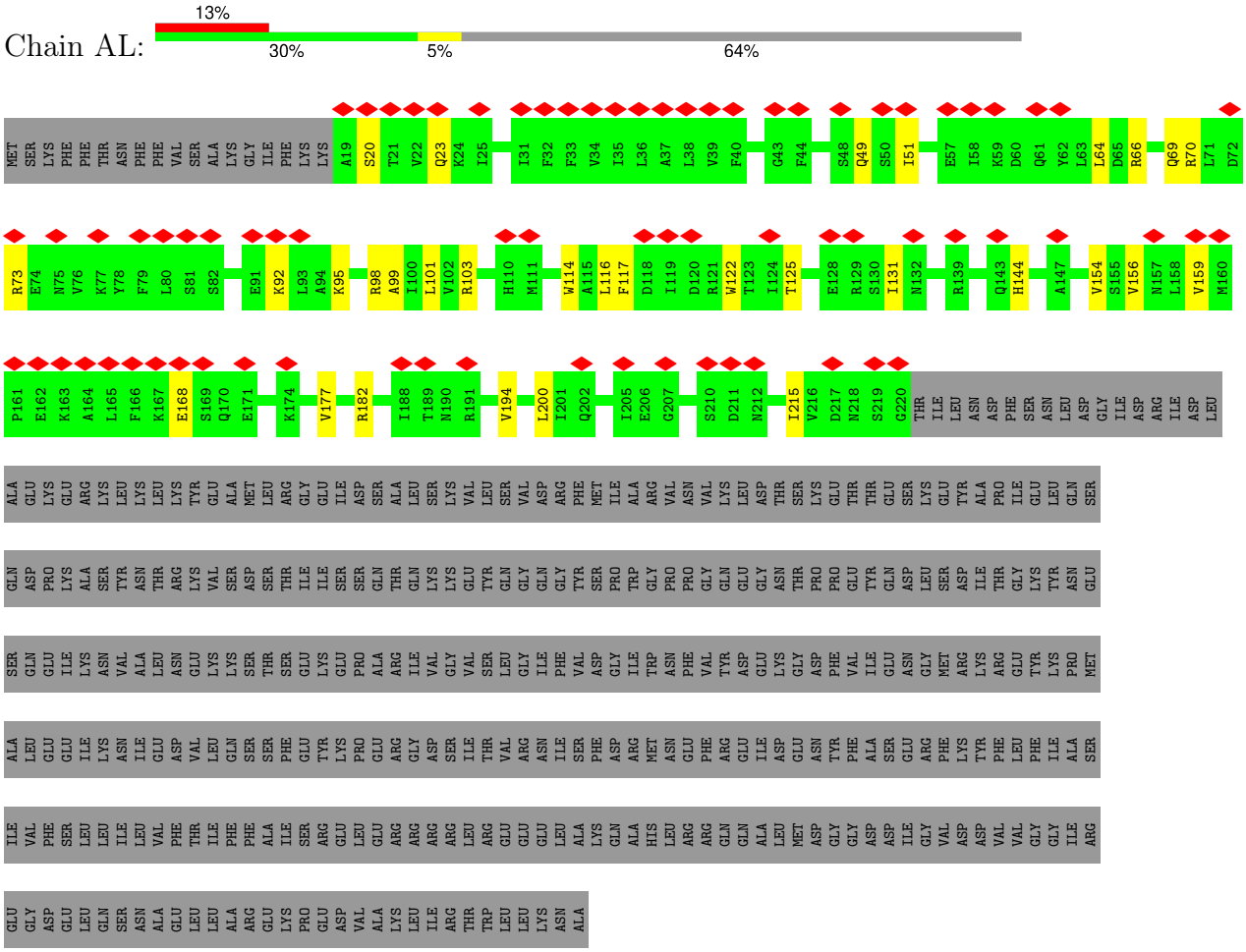
Chain AK:





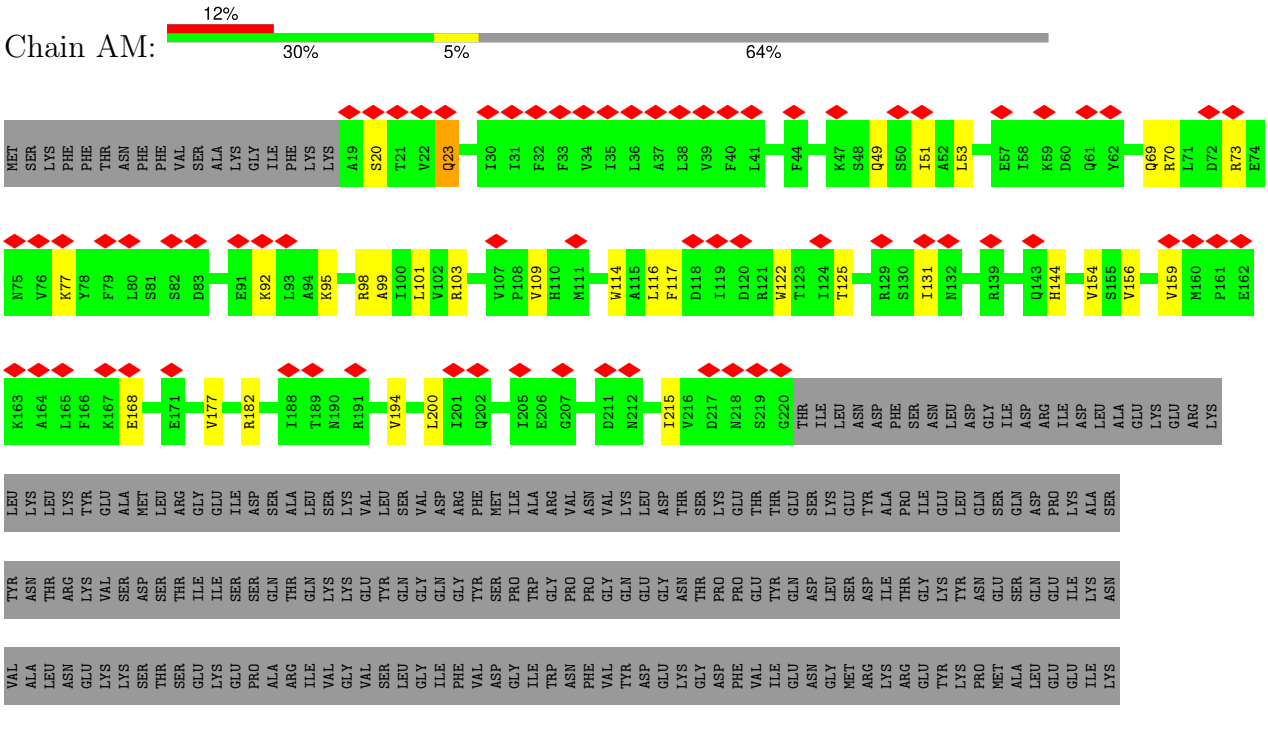
• Molecule 1: Flagellar M-ring protein

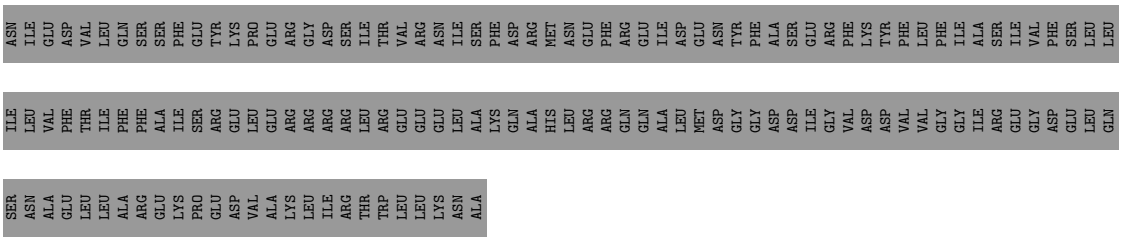
Chain AL:



• Molecule 1: Flagellar M-ring protein

Chain AM:

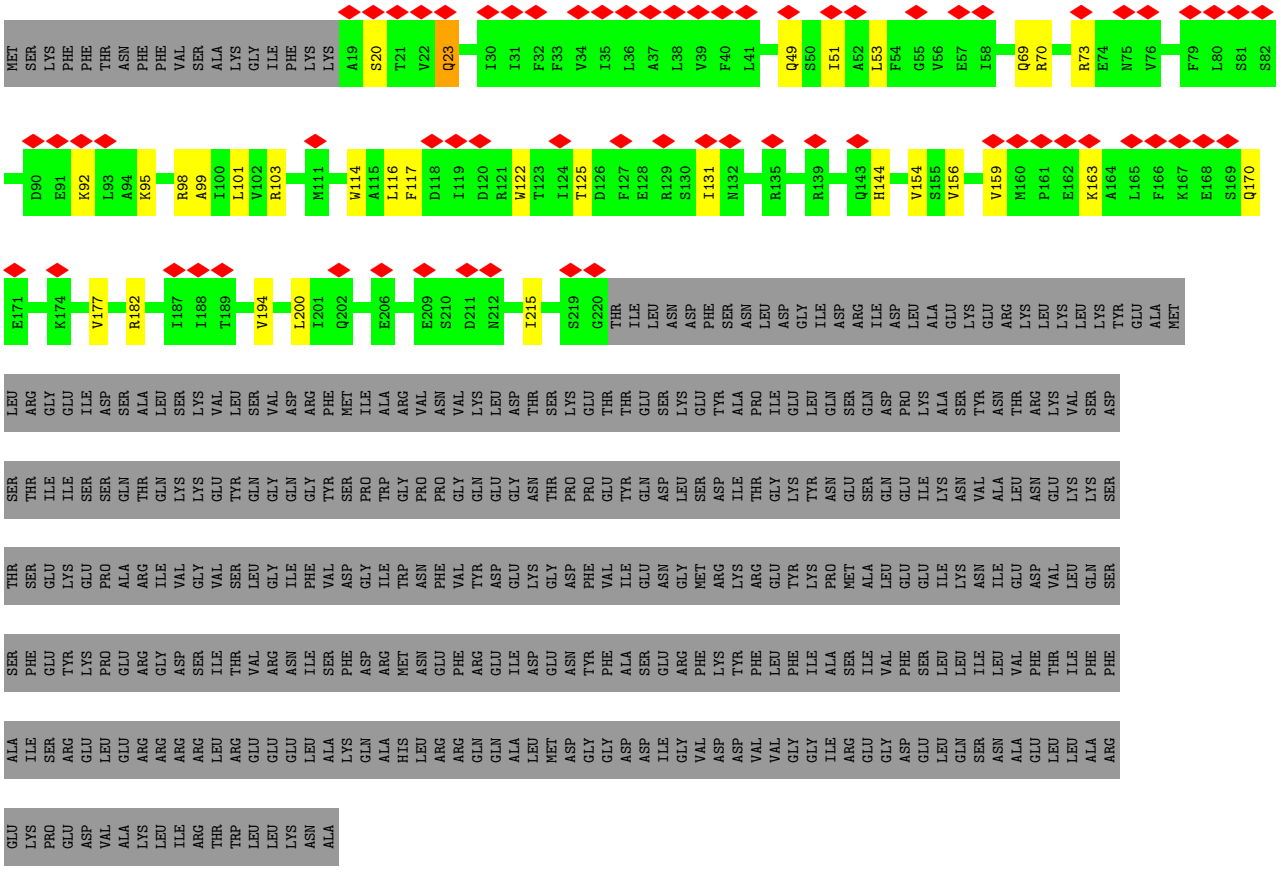




• Molecule 1: Flagellar M-ring protein

Chain AN:

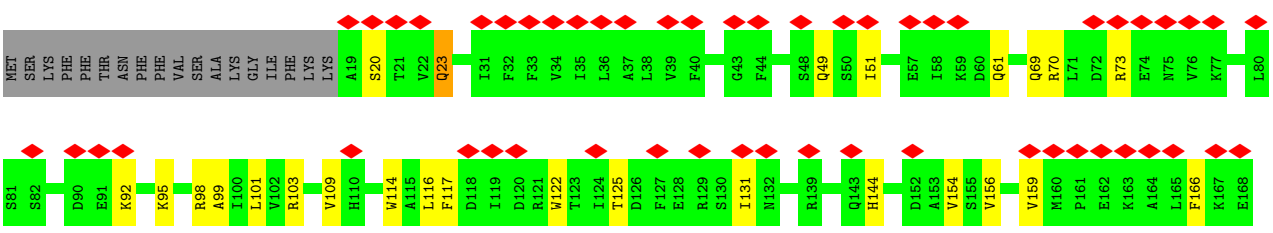


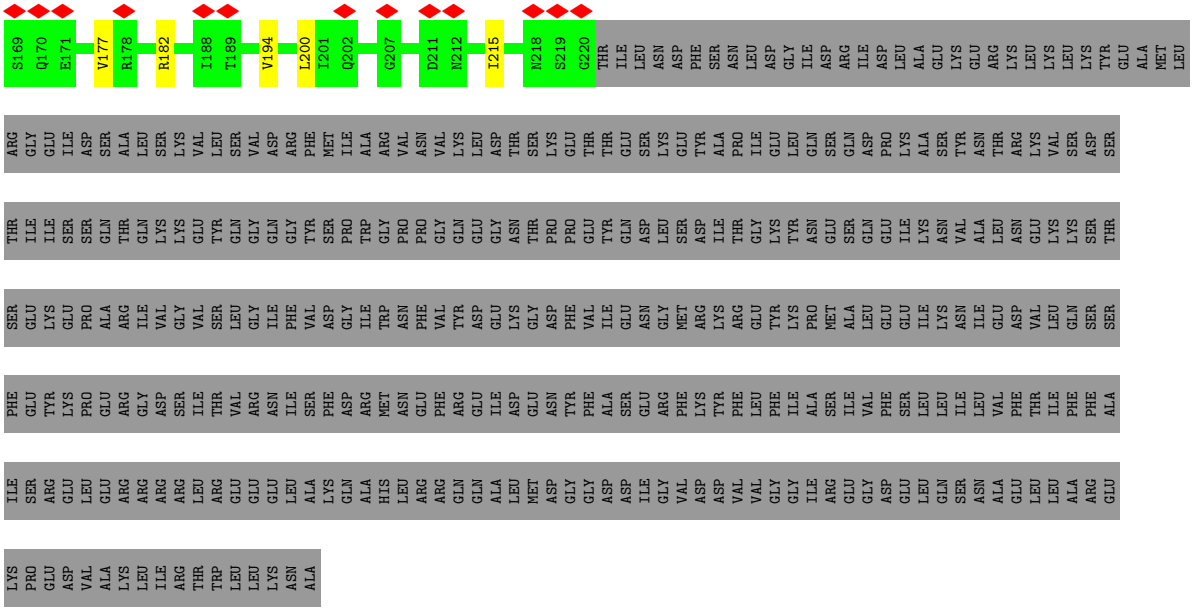


• Molecule 1: Flagellar M-ring protein

Chain AO:



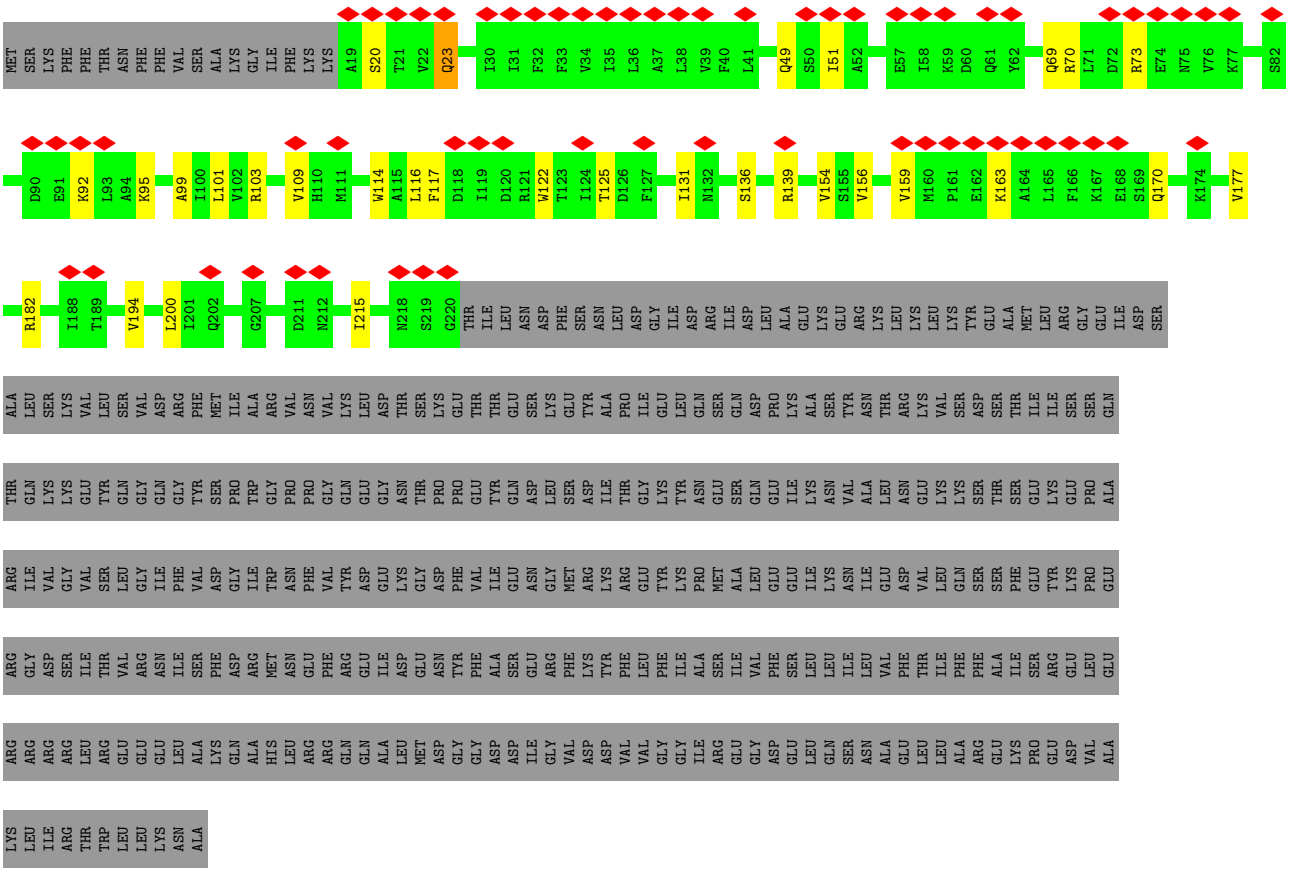




• Molecule 1: Flagellar M-ring protein

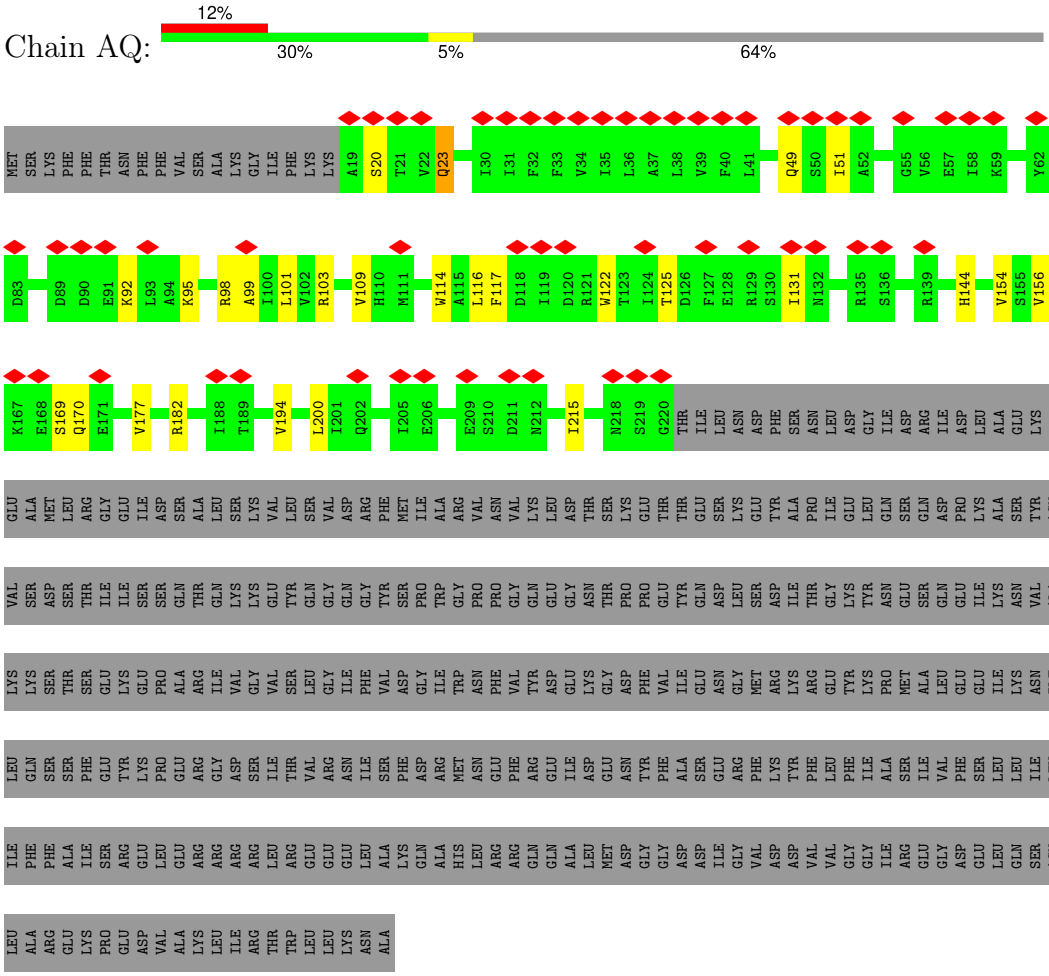
Chain AP:





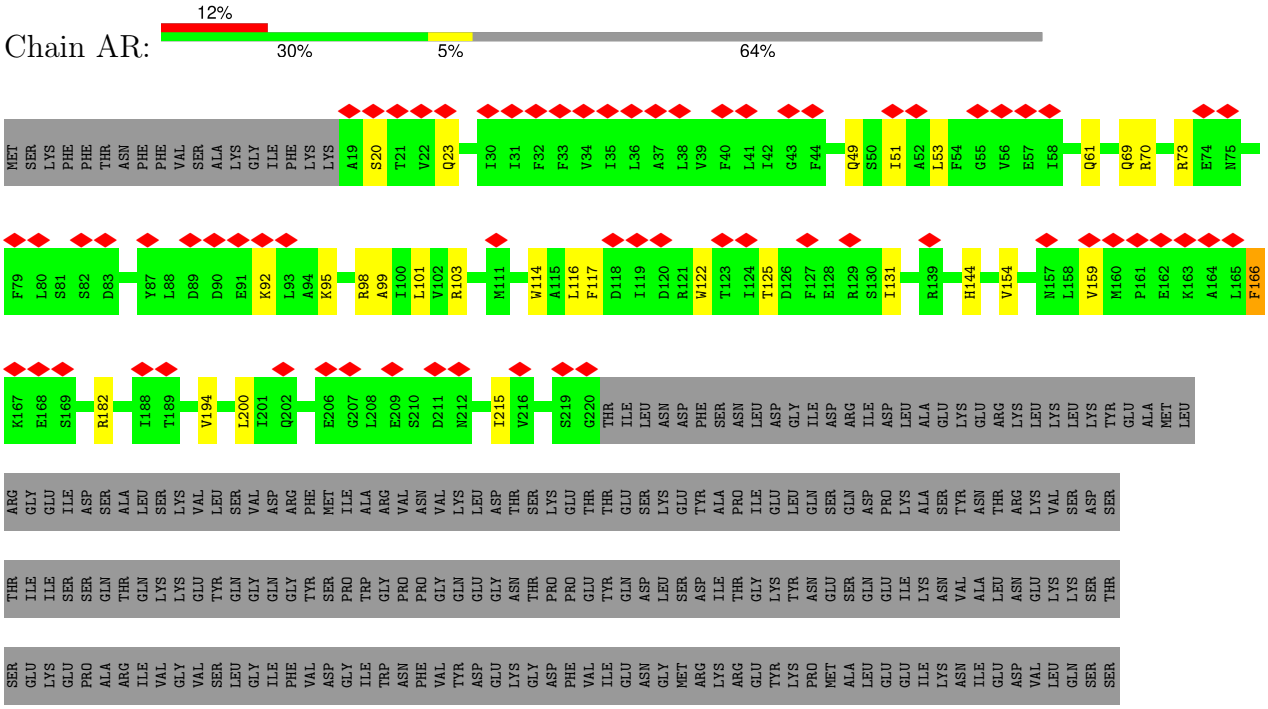
• Molecule 1: Flagellar M-ring protein

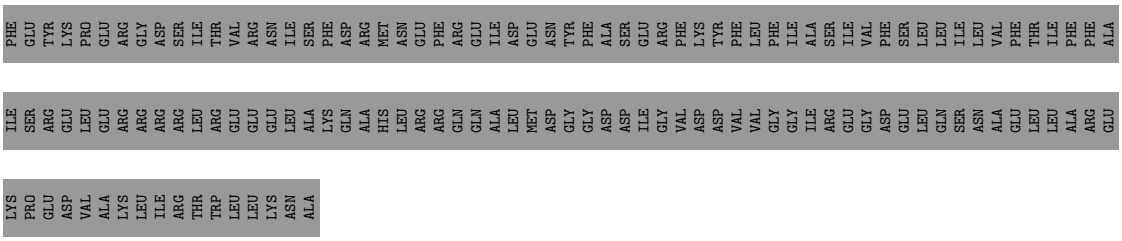
Chain AQ:



• Molecule 1: Flagellar M-ring protein

Chain AR:

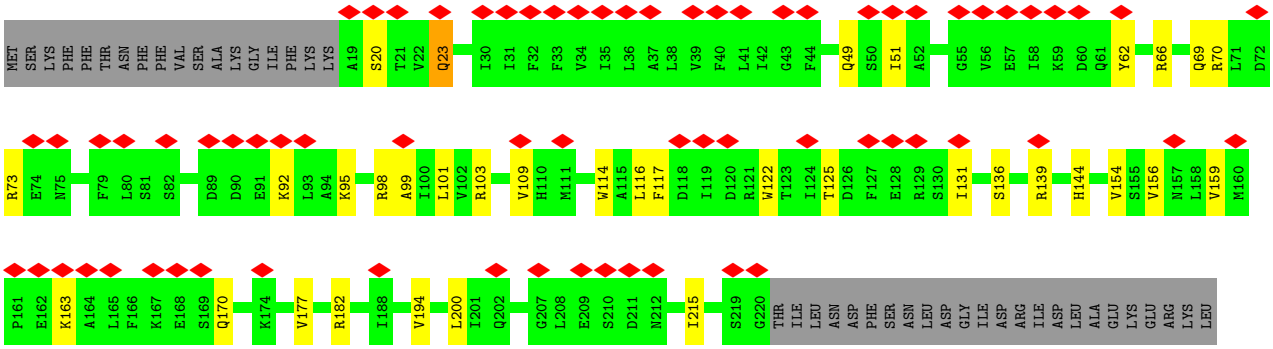




• Molecule 1: Flagellar M-ring protein

Chain AS:

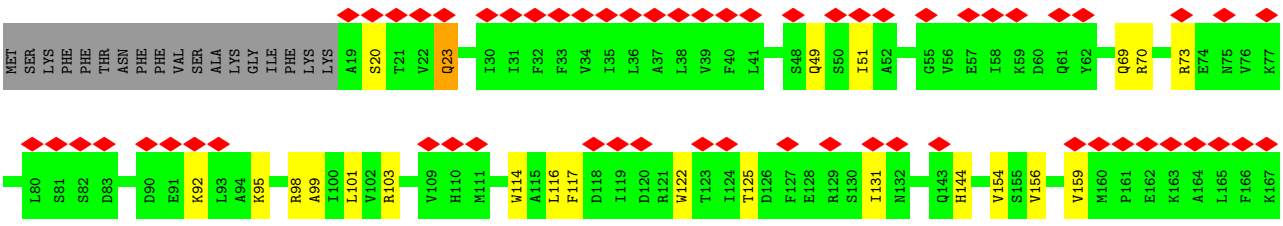


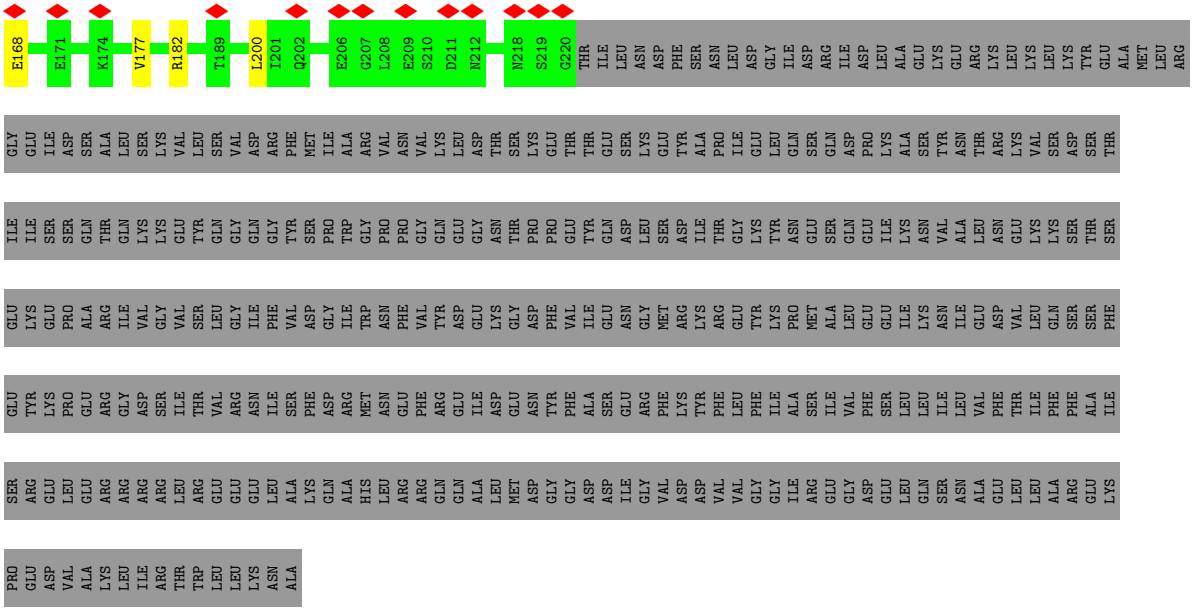


• Molecule 1: Flagellar M-ring protein

Chain AT:



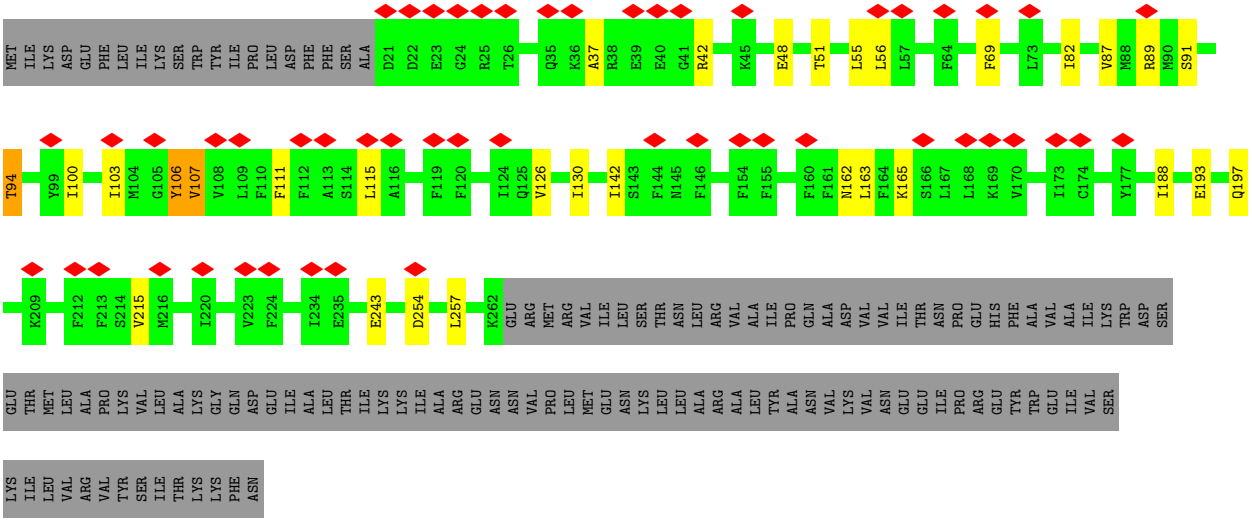




• Molecule 2: Flagellar biosynthetic protein FlhB

Chain AX:

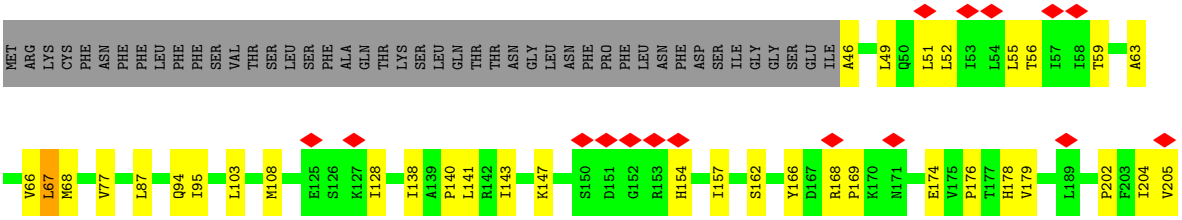


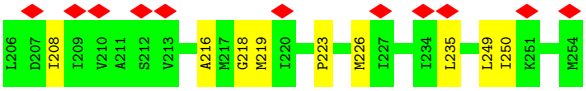


• Molecule 3: Flagellar biosynthetic protein FliP

Chain AY:



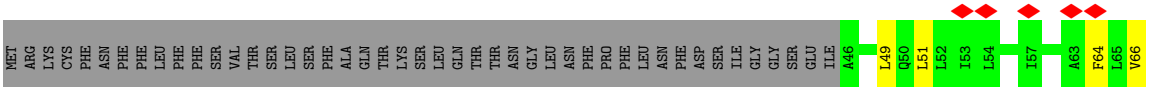




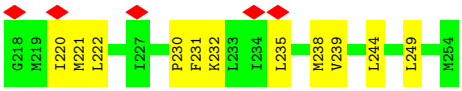
• Molecule 3: Flagellar biosynthetic protein FliP

Chain AZ:





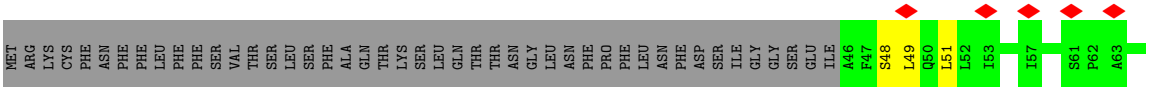


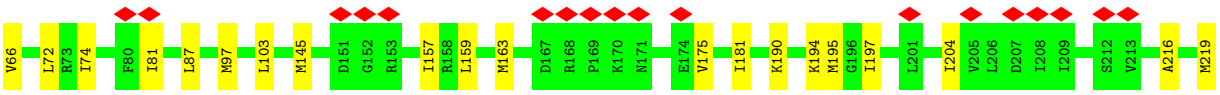


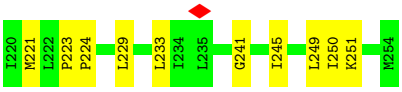
• Molecule 3: Flagellar biosynthetic protein FliP

Chain Aa:





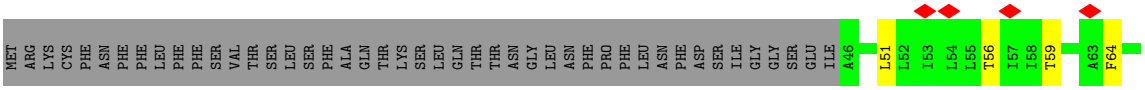


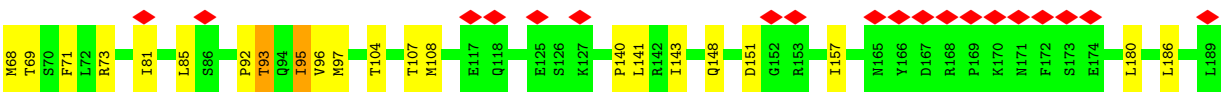


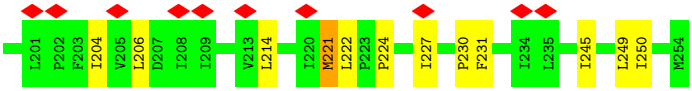
• Molecule 3: Flagellar biosynthetic protein FliP

Chain Ab:



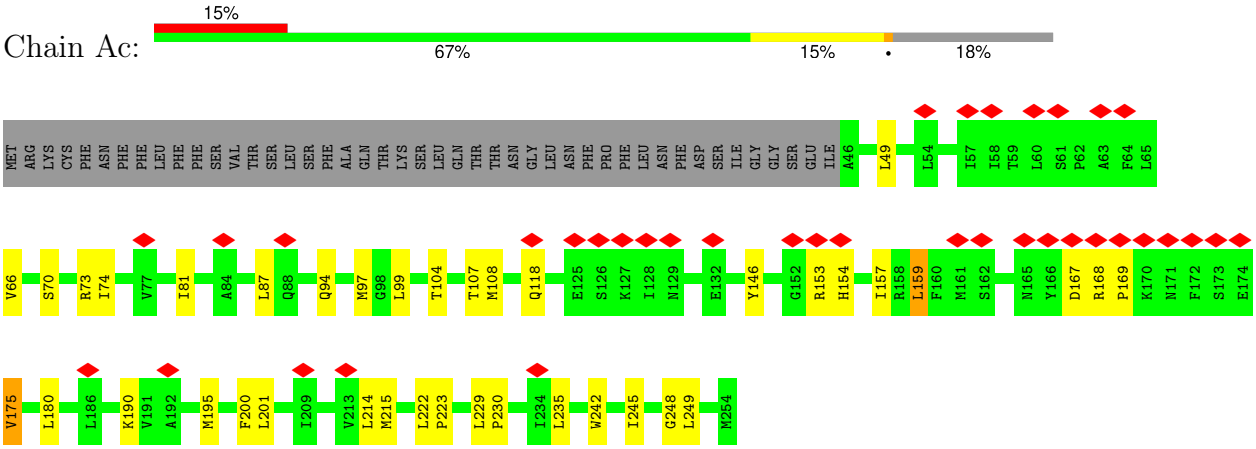






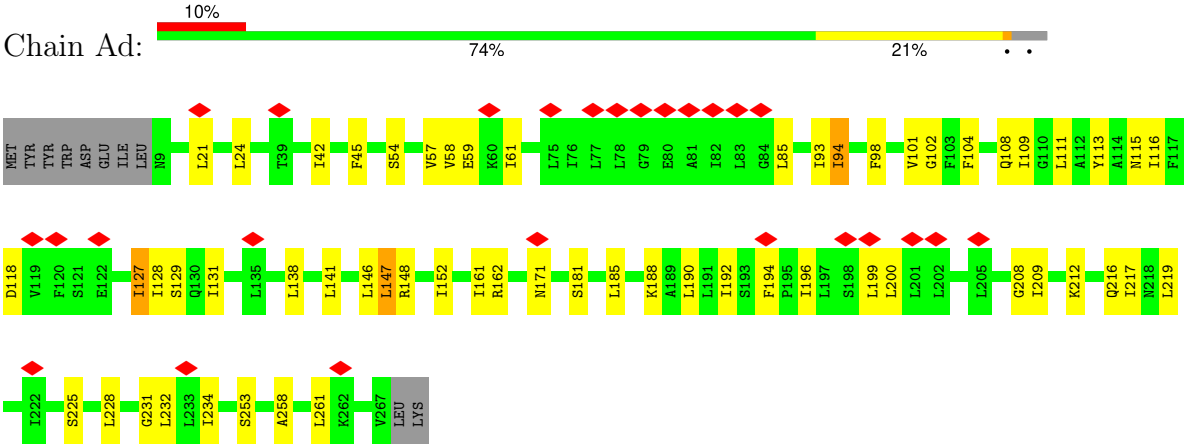
• Molecule 3: Flagellar biosynthetic protein FliP

Chain Ac:



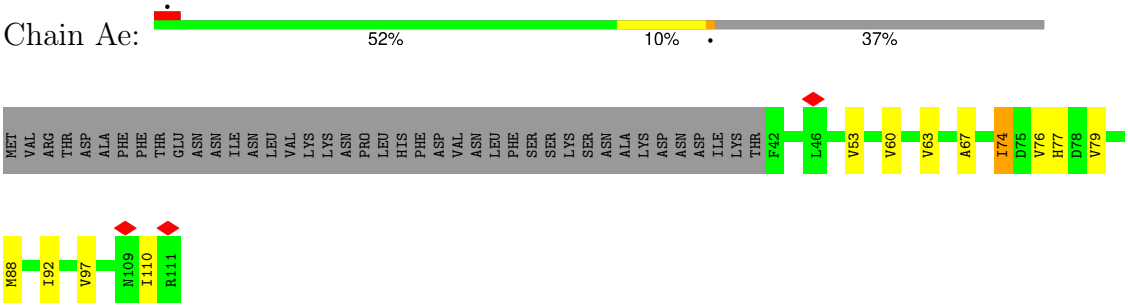
• Molecule 4: Flagellar biosynthetic protein FliR

Chain Ad:



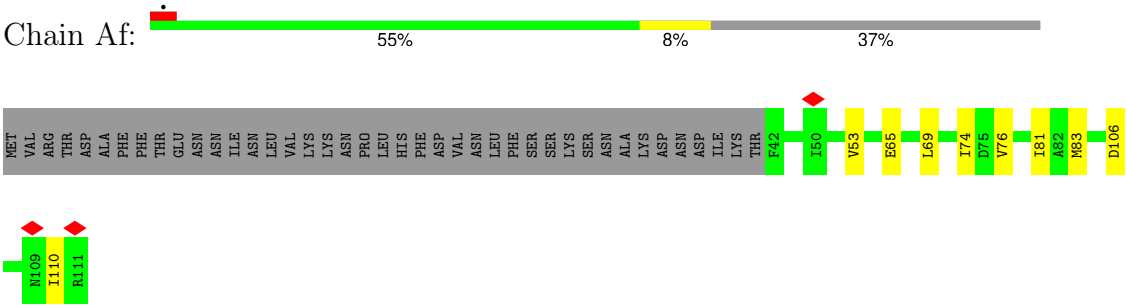
• Molecule 5: Flagellar hook-basal body complex protein FliE

Chain Ae:



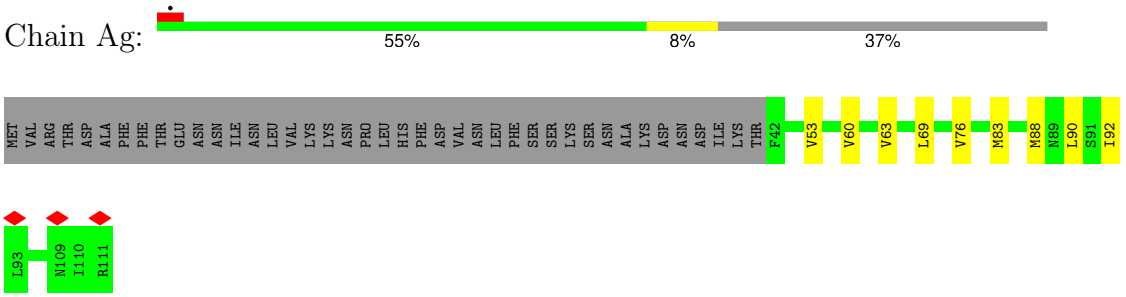
• Molecule 5: Flagellar hook-basal body complex protein FliE

Chain Af:



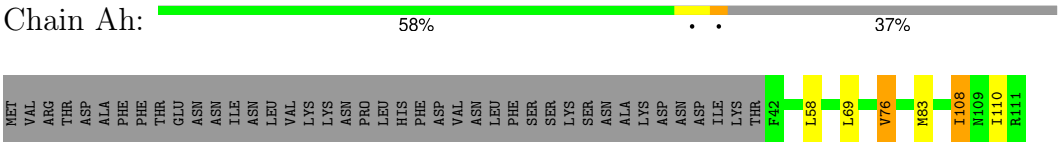
• Molecule 5: Flagellar hook-basal body complex protein FliE

Chain Ag:



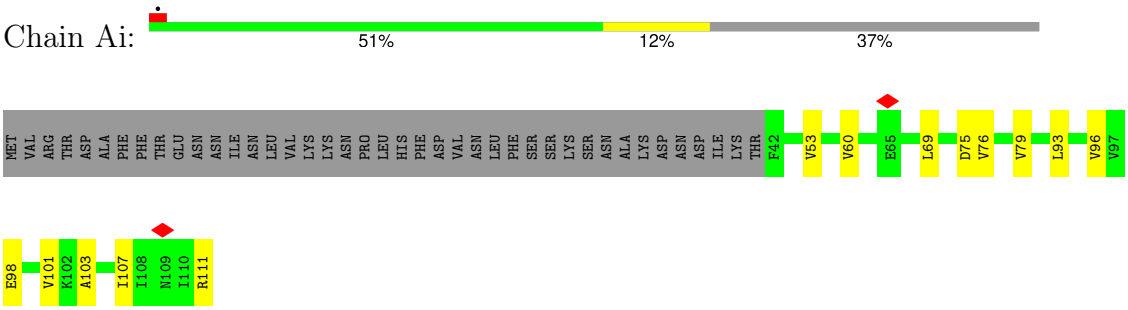
• Molecule 5: Flagellar hook-basal body complex protein FliE

Chain Ah:



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

Chain Ai:



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

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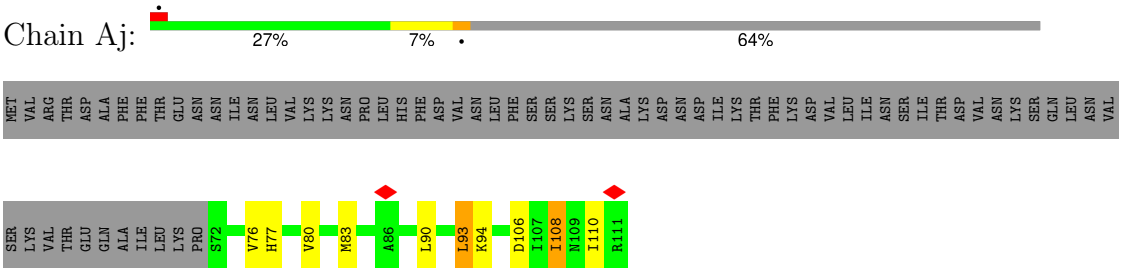
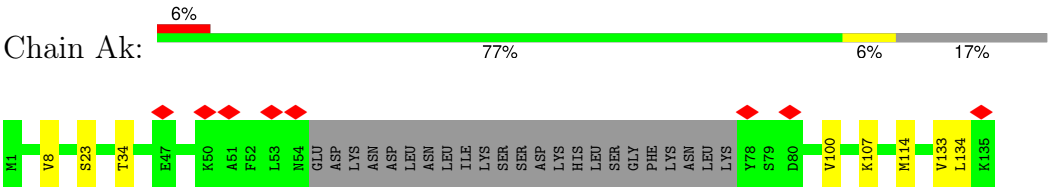


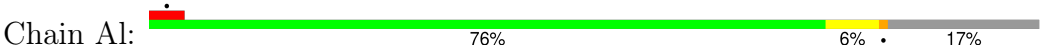
• Molecule 6: Flagellar basal body rod protein FlgB

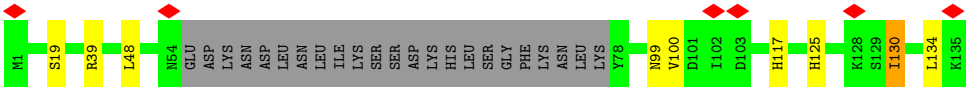
Chain Ak:



• Molecule 6: Flagellar basal body rod protein FlgB

Chain Al:

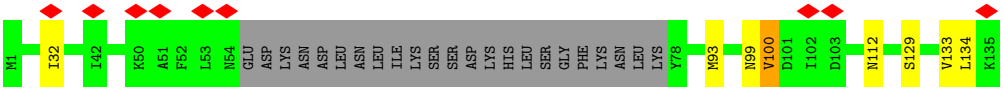




• Molecule 6: Flagellar basal body rod protein FlgB

Chain Am:

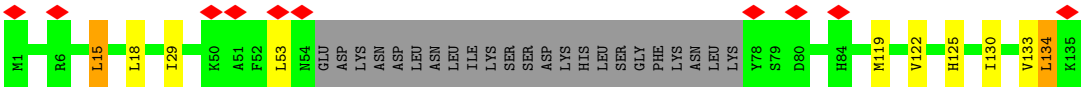




• Molecule 6: Flagellar basal body rod protein FlgB

Chain An:

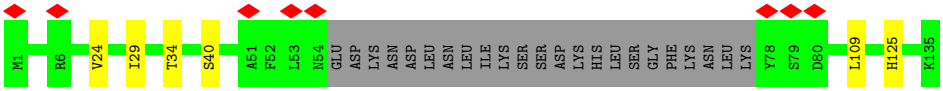




• Molecule 6: Flagellar basal body rod protein FlgB

Chain Ao:

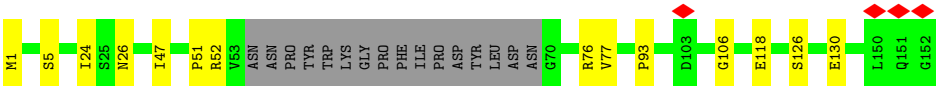




• Molecule 7: Flagellar basal-body rod protein FlgC

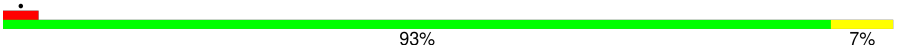
Chain Ap:

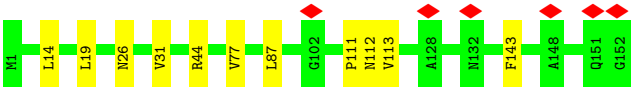




• Molecule 7: Flagellar basal-body rod protein FlgC

Chain Aq:

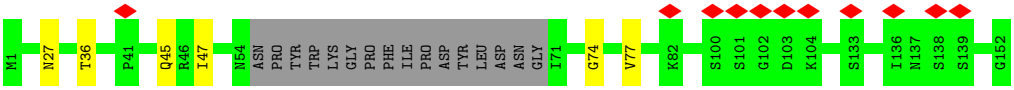




• Molecule 7: Flagellar basal-body rod protein FlgC

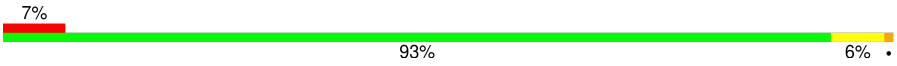
Chain Ar:

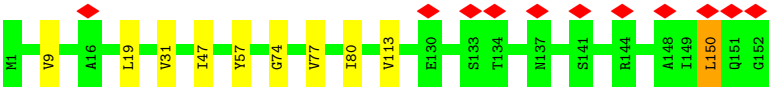




• Molecule 7: Flagellar basal-body rod protein FlgC

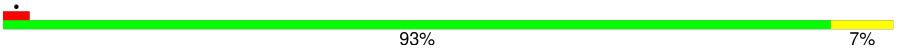
Chain As:

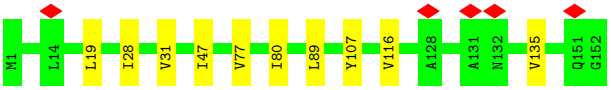




• Molecule 7: Flagellar basal-body rod protein FlgC

Chain At:

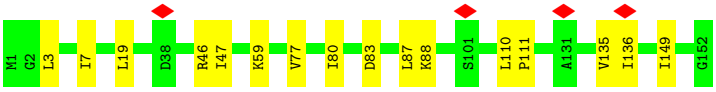




• Molecule 7: Flagellar basal-body rod protein FlgC

Chain Au:

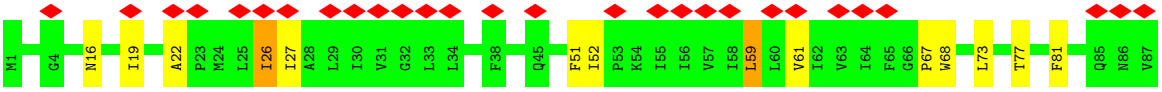




• Molecule 8: Flagellar biosynthetic protein FliQ

Chain Av:

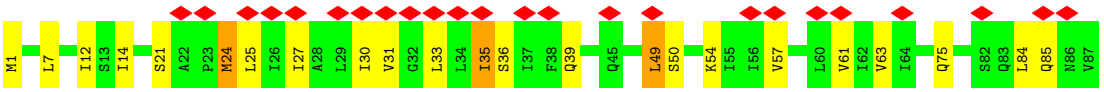




• Molecule 8: Flagellar biosynthetic protein FliQ

Chain AU:

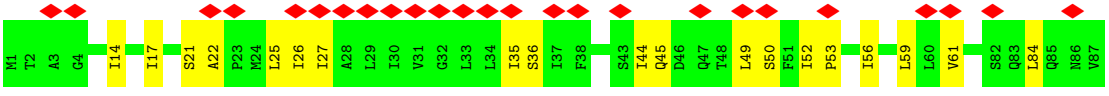




• Molecule 8: Flagellar biosynthetic protein FliQ

Chain AV:

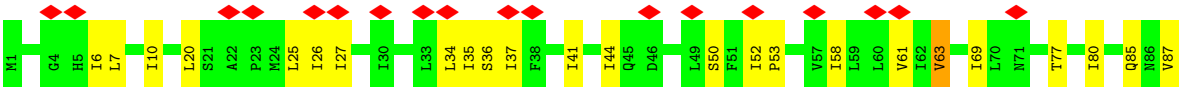




• Molecule 8: Flagellar biosynthetic protein FliQ

Chain AW:

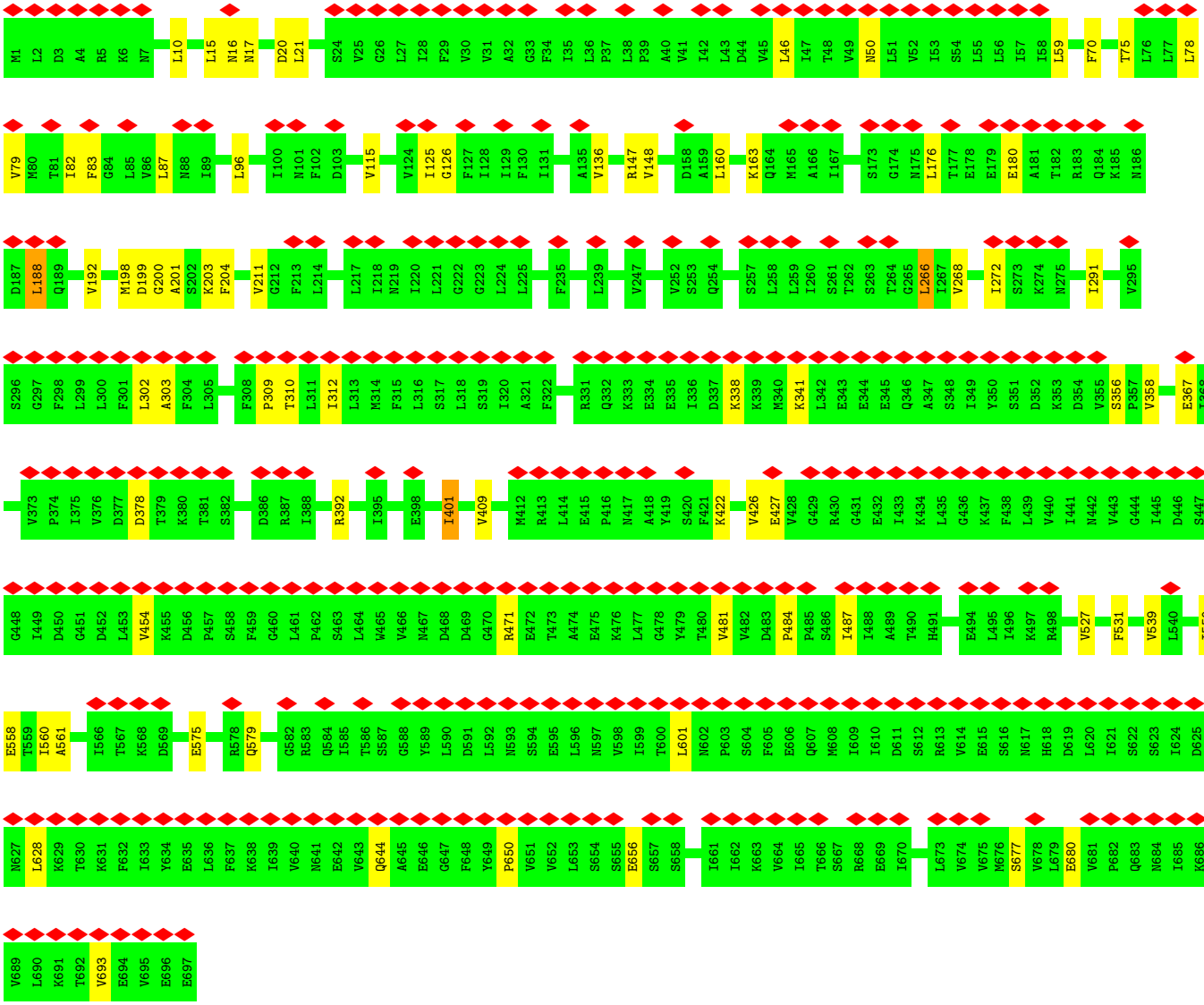




• Molecule 9: Flagellar biosynthesis protein FlhA

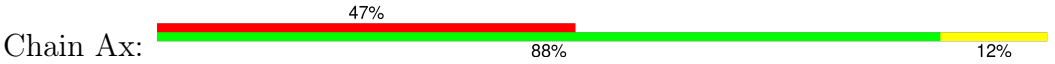
Chain Aw:

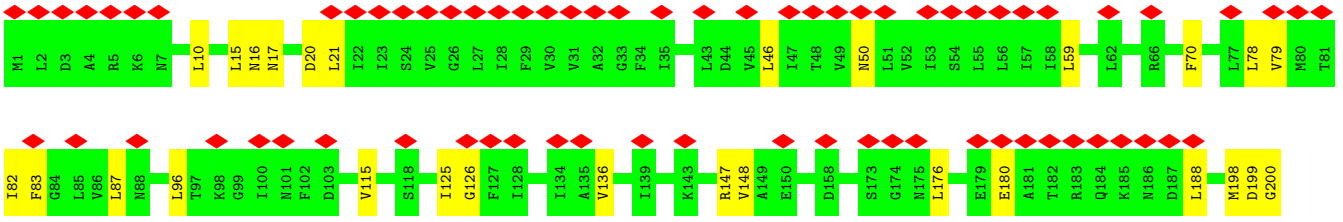


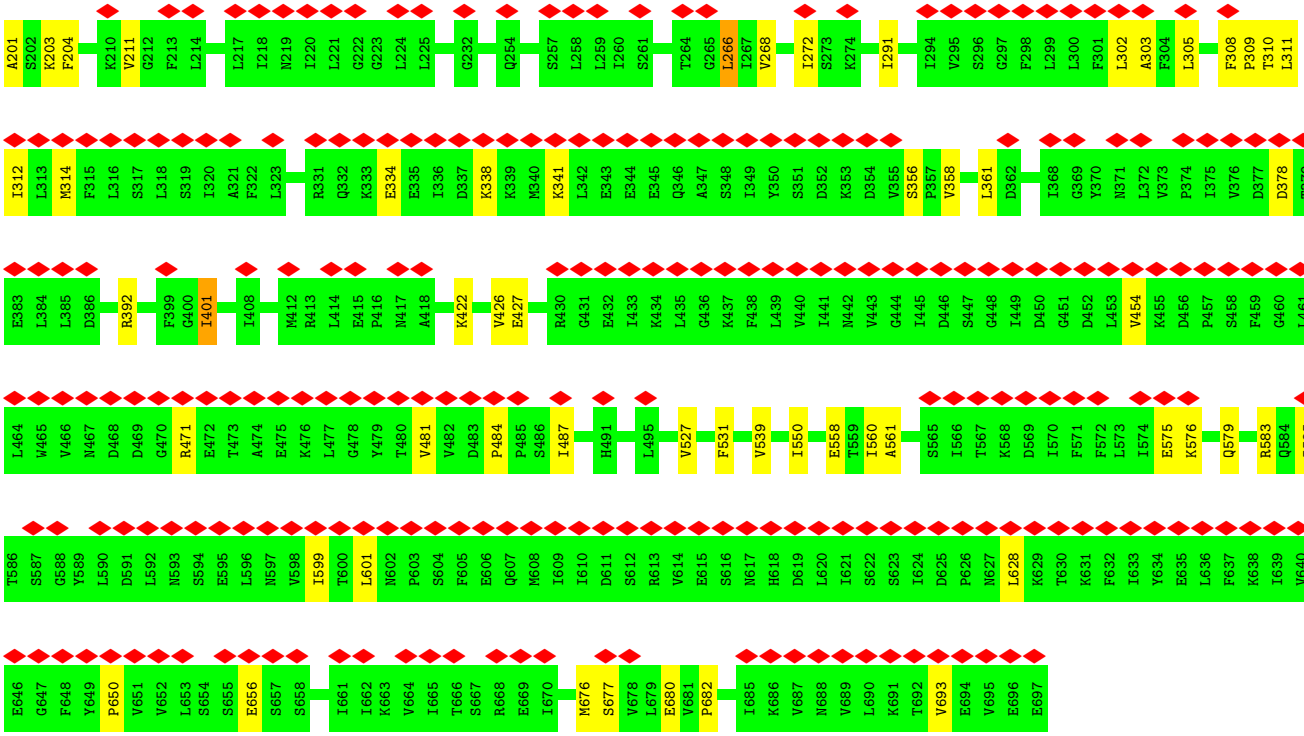


• Molecule 9: Flagellar biosynthesis protein FlhA

Chain Ax:



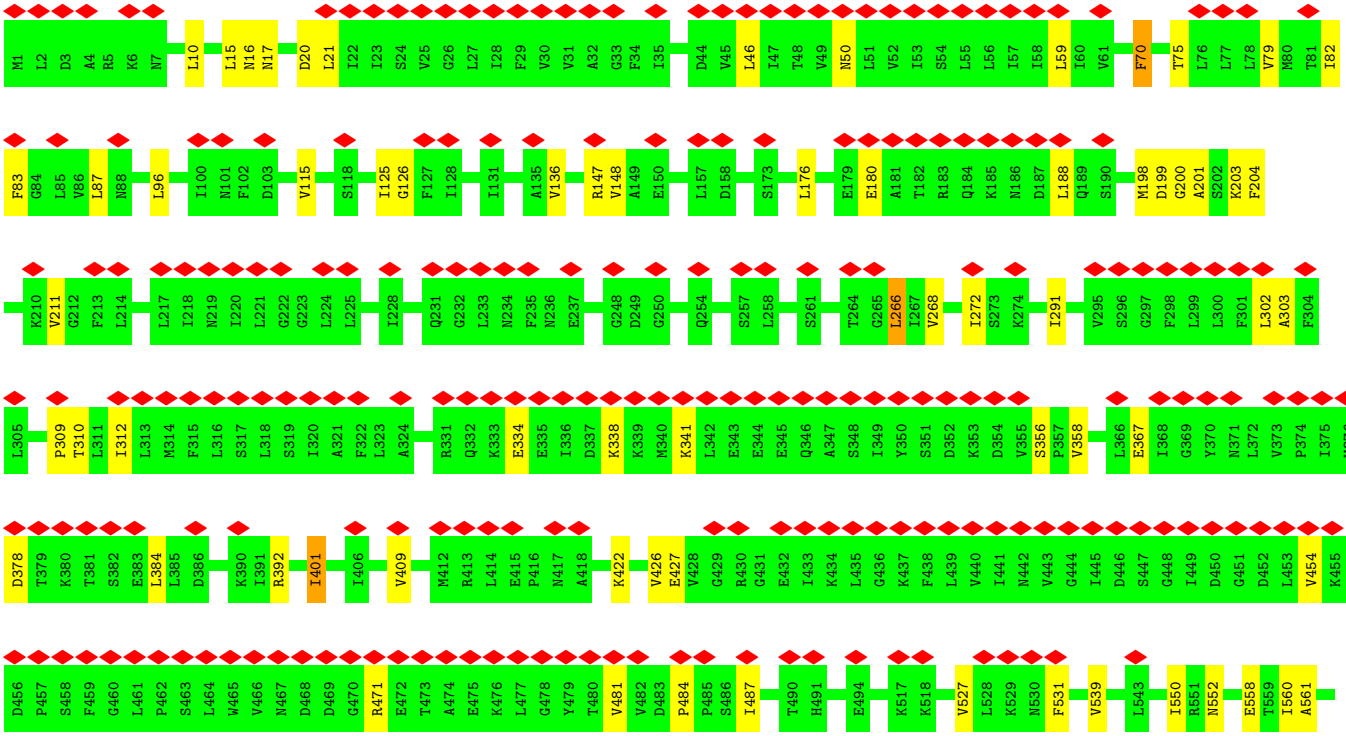


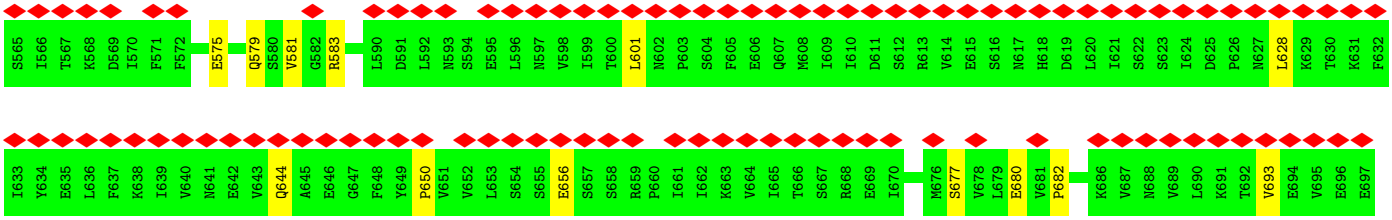


• Molecule 9: Flagellar biosynthesis protein FlhA

Chain Ay:



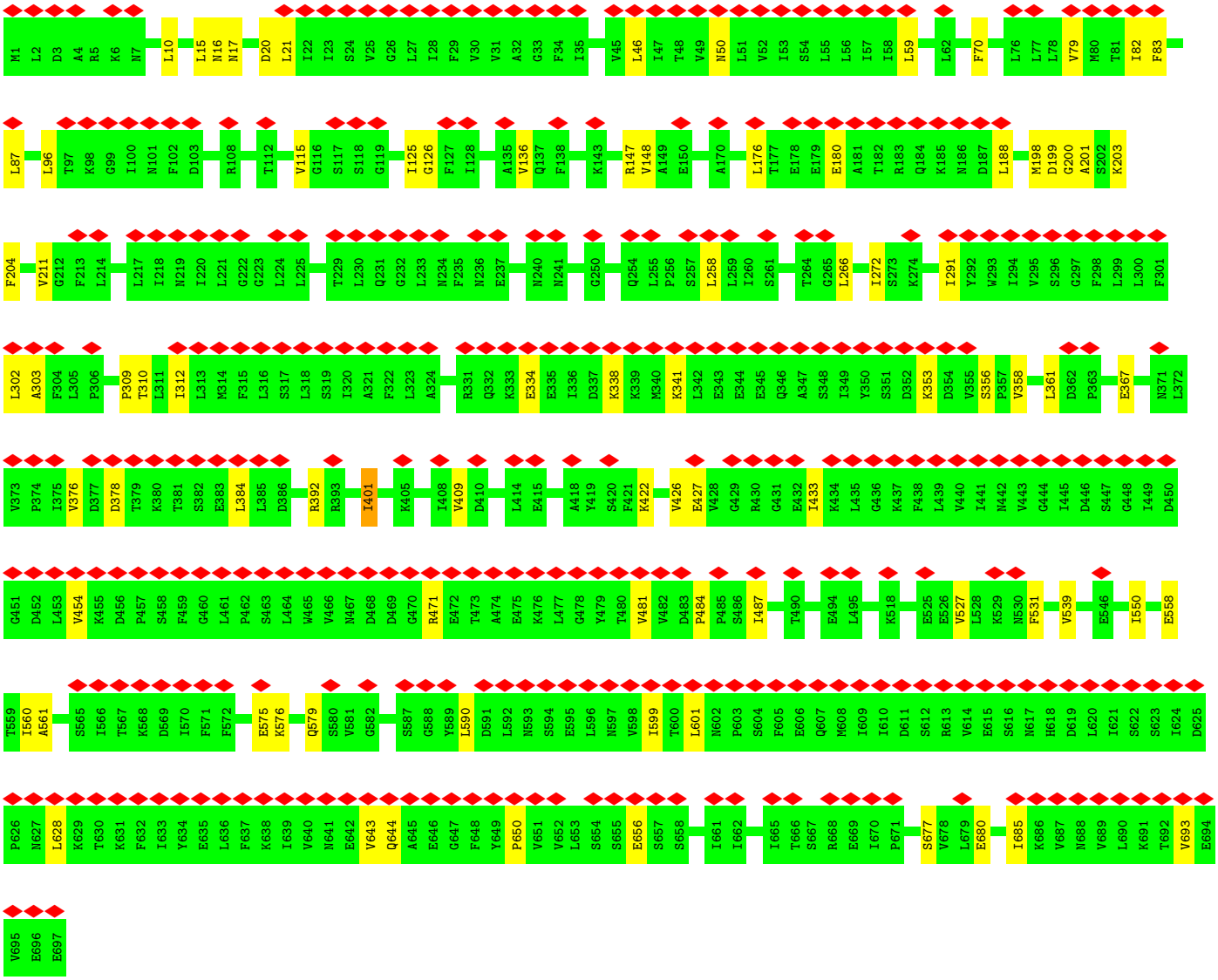




• Molecule 9: Flagellar biosynthesis protein FlhA

Chain Az:

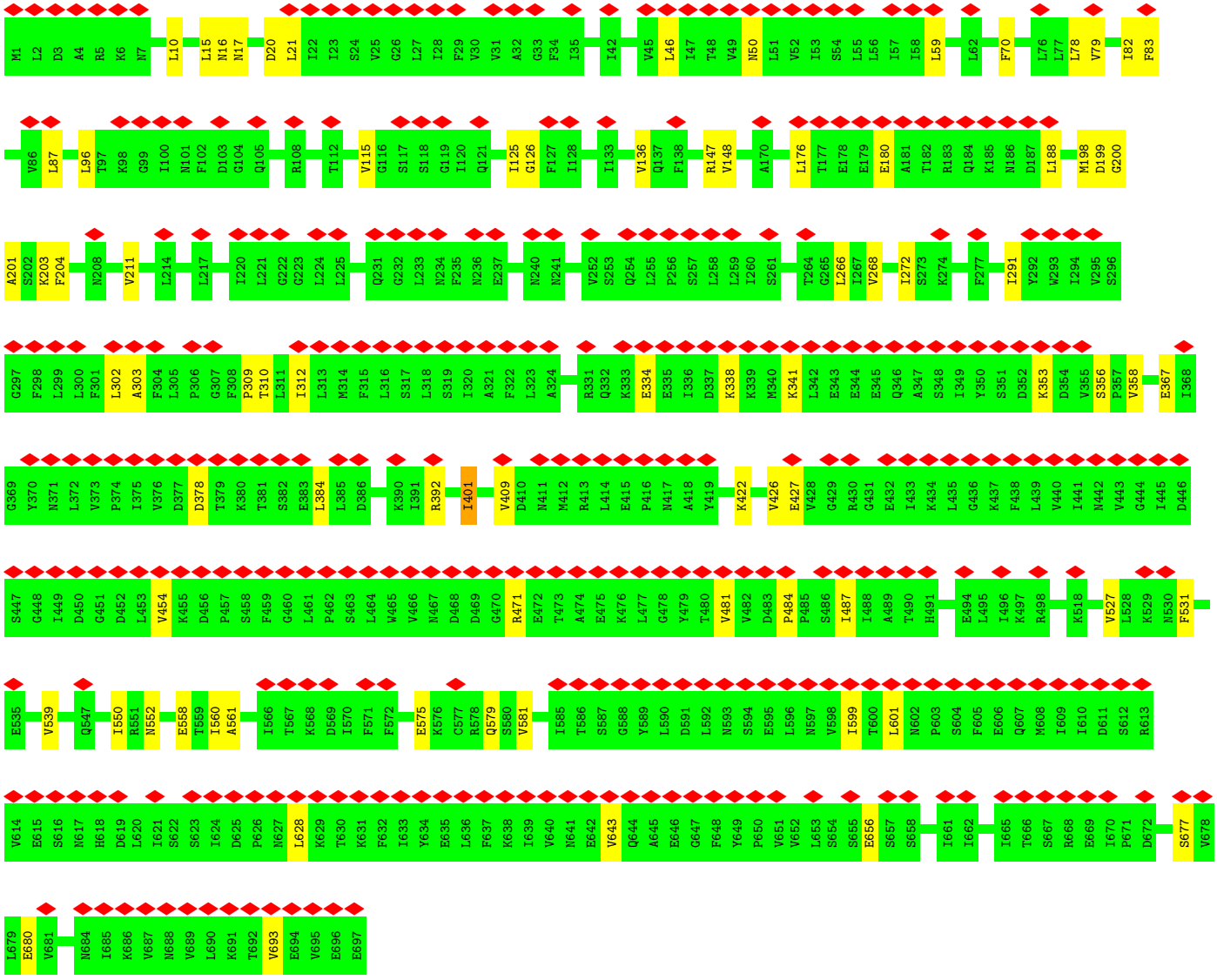




• Molecule 9: Flagellar biosynthesis protein FlhA

Chain A1:

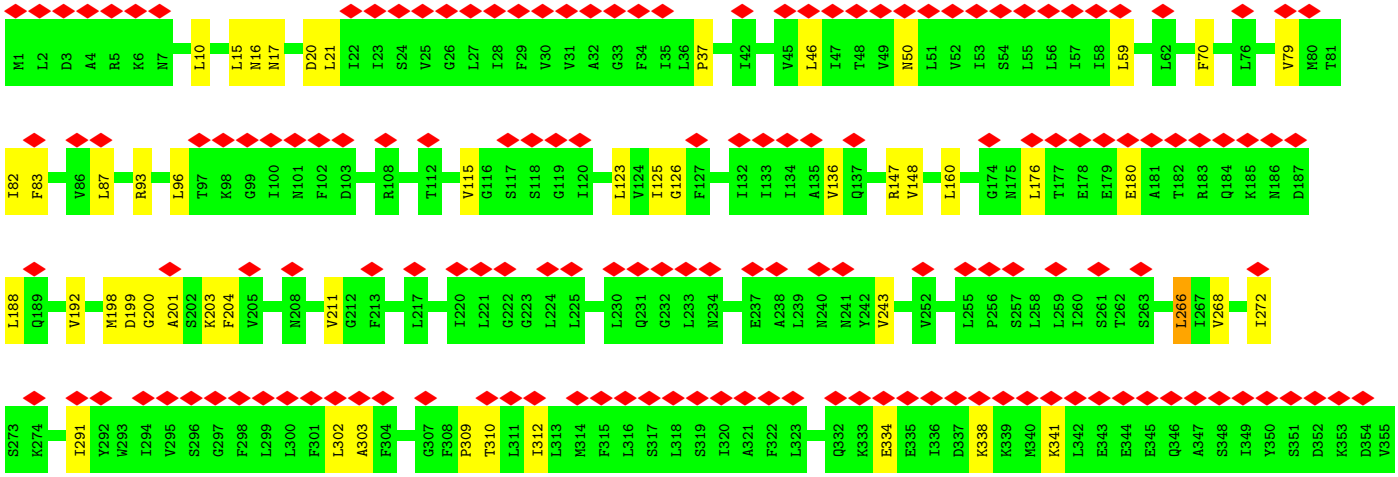


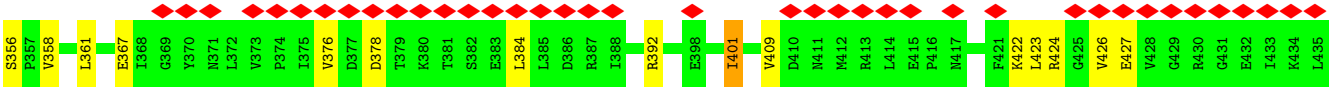


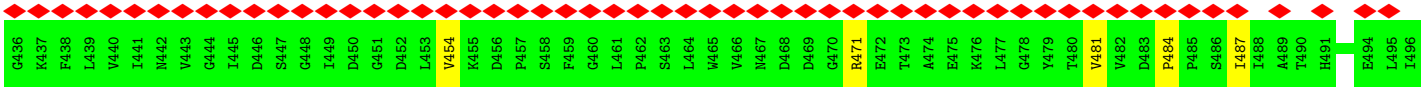
• Molecule 9: Flagellar biosynthesis protein FlhA

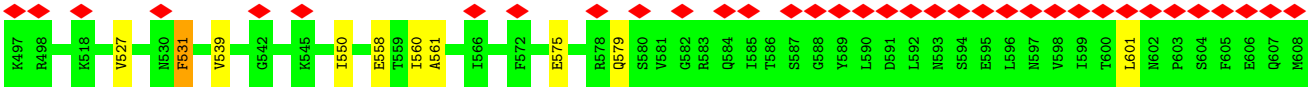
Chain A2:

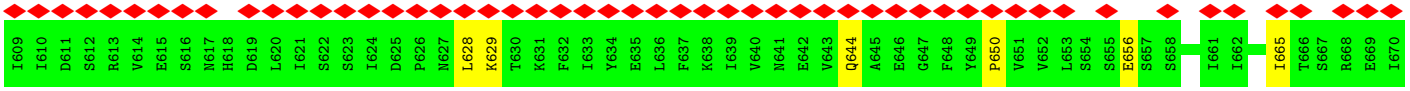


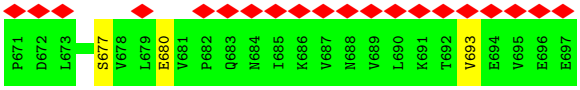








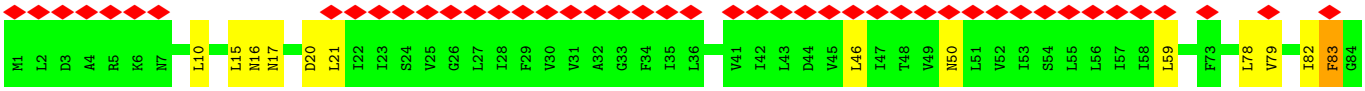


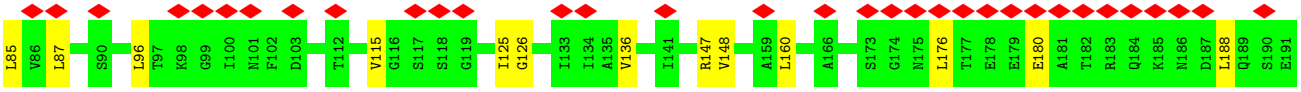


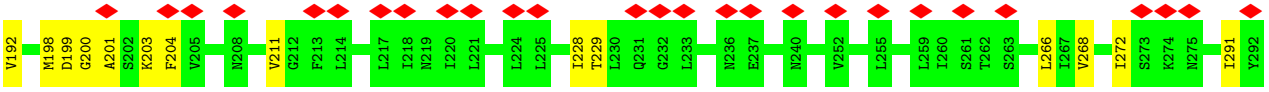
• Molecule 9: Flagellar biosynthesis protein FlhA

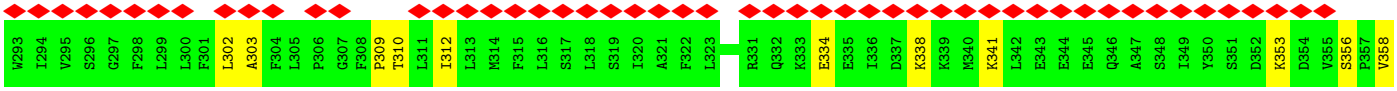
Chain A3:

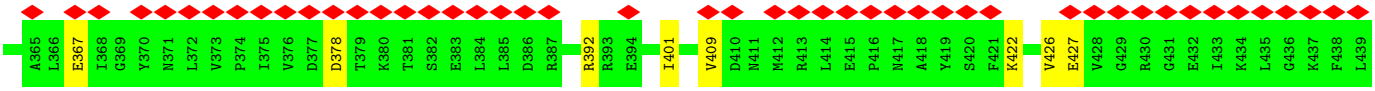


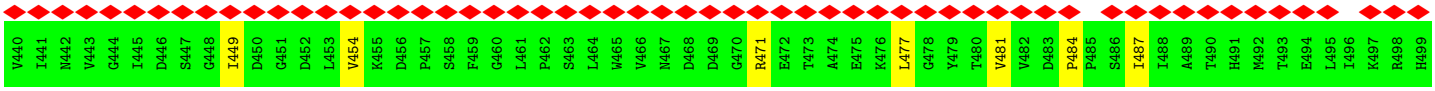


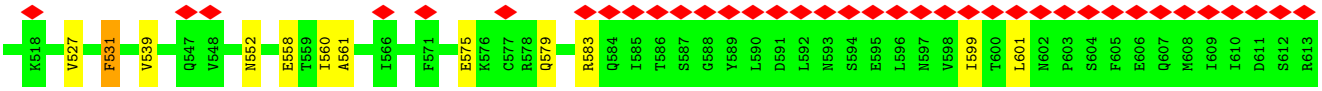


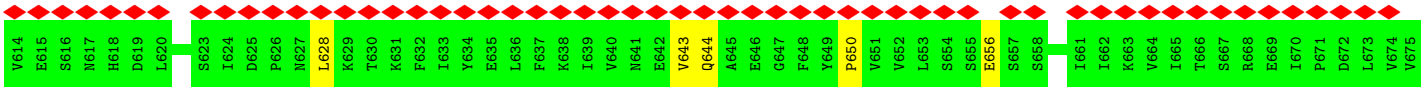


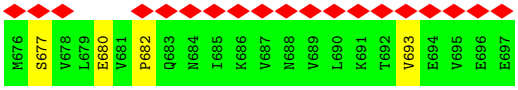






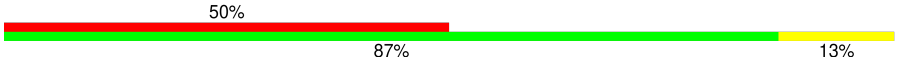


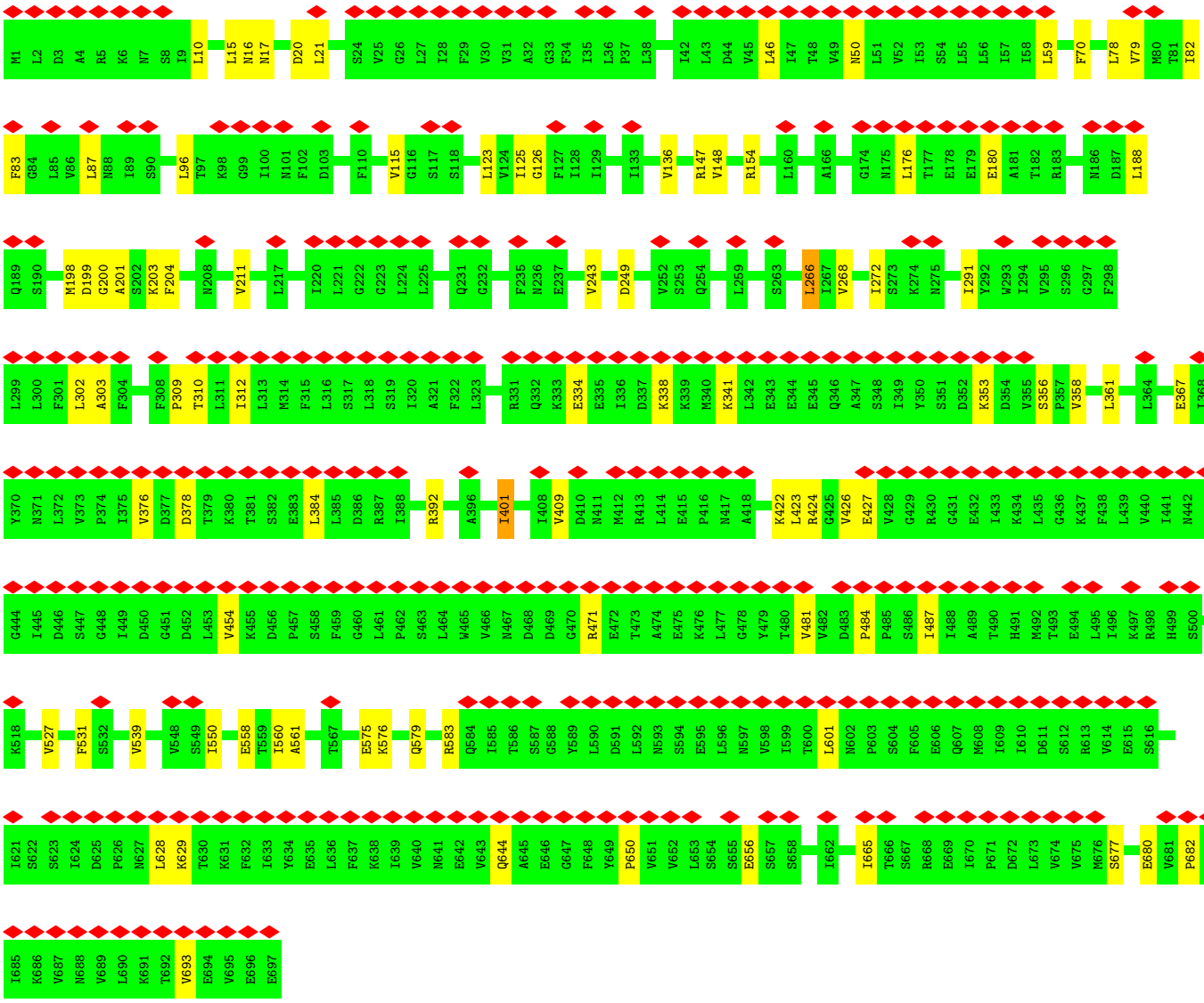




• Molecule 9: Flagellar biosynthesis protein FlhA

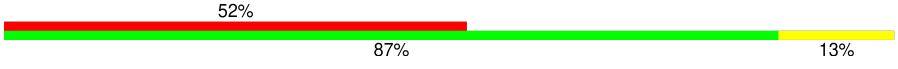
Chain A4:

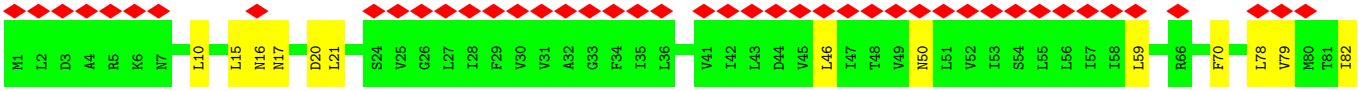


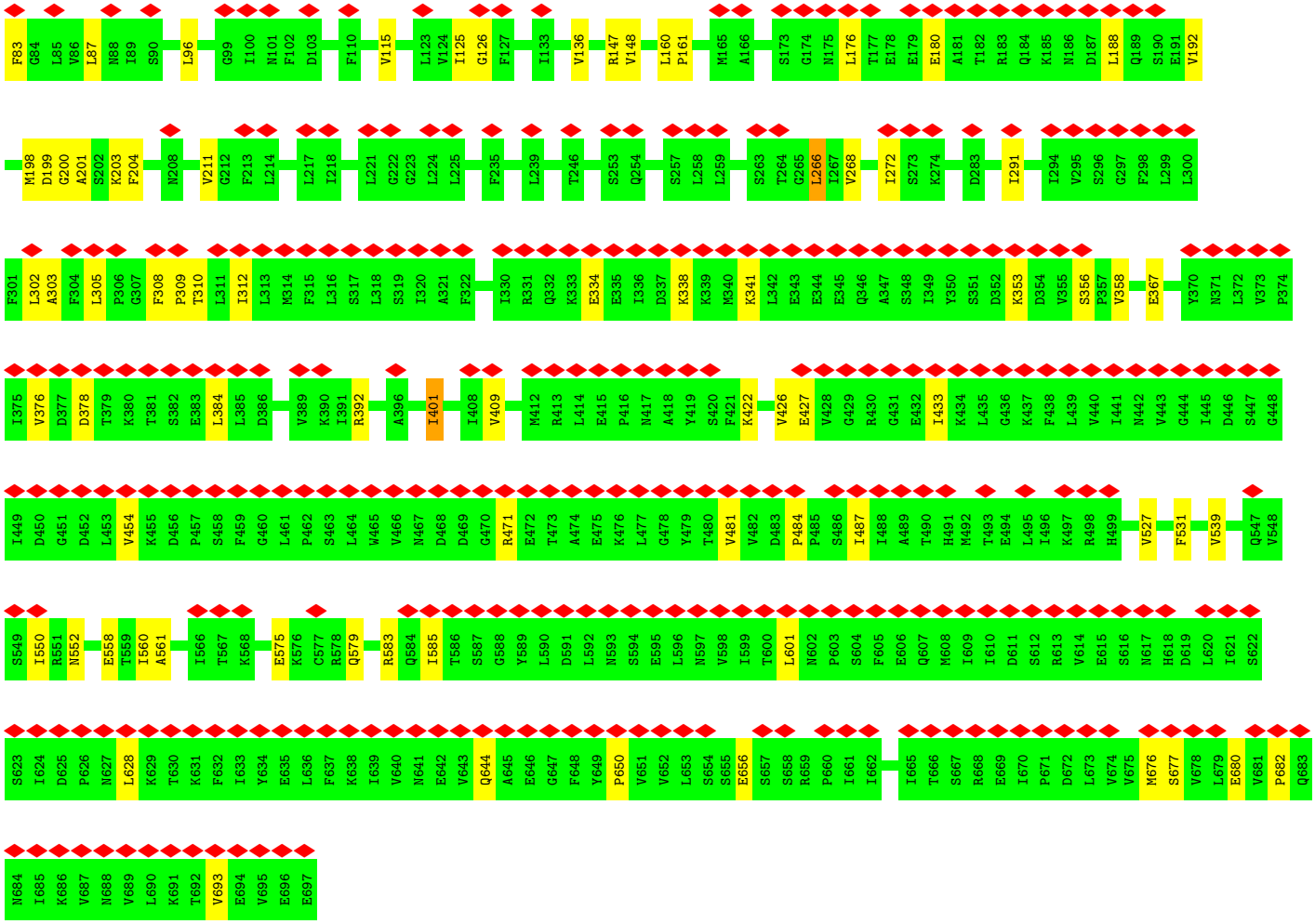


• Molecule 9: Flagellar biosynthesis protein FlhA

Chain A5:






F83 G84 L85 V86 L87 N88 I89 S90 L96 G99 I100 N101 F102 D103 F110 V115 L123 V124 I125 G126 F127 I133 V136 R147 V148 L160 P161 M165 A166 S173 G174 N175 L176 T177 E178 E179 E180 A181 T182 R183 Q184 K185 N186 D187 L188 Q189 S190 E191 V192
M198 D199 G200 A201 S202 K203 F204 N208 V211 G212 F213 L214 L217 I218 L221 G222 G223 L224 L225 F235 L239 T246 S253 Q254 S257 L258 L259 S263 T264 G265 L266 I267 V268 I272 S273 K274 D283 I291 I294 V295 S296 G297 F298 L299 L300
F301 L302 A303 F304 L305 P306 G307 F308 P309 T310 L311 I312 L313 M314 F315 L316 S317 L318 S319 I320 A321 F322 I330 R331 Q332 K333 E334 E335 I336 D337 K338 K339 M340 K341 L342 E343 E344 E345 Q346 A347 S348 I349 Y350 S351 D352 K353 D354 V355 S356 P357 V358 E367 Y370 N371 L372 V373 P374
I375 V376 D377 D378 T379 K380 T381 S382 E383 L384 L385 D386 V389 K390 I391 R392 A396 I401 I408 V409 M412 R413 L414 E415 P416 N417 A418 Y419 S420 F421 K422 V426 E427 V428 G429 R430 G431 E432 I433 K434 L435 G436 K437 F438 L439 V440 I441 N442 V443 G444 I445 D446 S447 G448
I449 D450 G451 D452 L453 V454 K455 D456 P457 S458 F459 G460 L461 P462 S463 L464 W465 V466 N467 D468 D469 G470 R471 E472 T473 A474 E475 K476 L477 G478 Y479 T480 V481 V482 D483 P484 P485 S486 I487 I488 A489 T490 H491 M492 T493 E494 L495 I496 K497 R498 H499 V527 F531 V539 Q547 V548
S549 I550 R551 N552 E558 T559 I560 A561 I566 T567 K568 E575 K576 C577 R578 Q579 R583 Q584 I585 T586 S587 G588 Y589 L590 D591 L592 N593 S594 E595 L596 N597 V598 I599 T600 L601 N602 P603 S604 F605 E606 Q607 M608 I609 I610 D611 S612 R613 V614 E615 S616 N617 H618 D619 L620 I621 S622
S623 I624 D625 P626 N627 L628 K629 T630 K631 F632 I633 Y634 E635 L636 F637 K638 I639 V640 N641 E642 V643 Q644 A645 E646 G647 F648 Y649 P650 V651 V652 L653 S654 S655 E656 S657 S658 R659 P660 I661 I662 I665 T666 S667 R668 E669 I670 P671 D672 L673 V674 V675 M676 S677 V678 L679 E680 V681 P682 Q683
N684 I685 K686 V687 N688 V689 L690 K691 T692 V693 E694 V695 E696 E697

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40949	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	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	0.767	Depositor
Minimum map value	-0.492	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	640.63995, 640.63995, 640.63995	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	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	0.18	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%)	0.36	0/2246
1	5	0.13	0/1657	0.35	0/2246
1	6	0.13	0/1618	0.34	0/2193
1	7	0.18	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	0.10	0/2132	0.24	0/2861
1	AA	0.13	0/1657	0.34	0/2246
1	AB	0.18	1/1657 (0.1%)	0.34	0/2246
1	AC	0.12	0/1638	0.36	0/2214
1	AD	0.12	0/1638	0.37	0/2214
1	AE	0.12	0/1638	0.36	0/2214
1	AF	0.12	0/1638	0.36	0/2214
1	AG	0.12	0/1638	0.37	0/2214
1	AH	0.12	0/1638	0.36	0/2214
1	AI	0.12	0/1638	0.35	0/2214
1	AJ	0.12	0/1638	0.35	0/2214
1	AK	0.12	0/1638	0.36	0/2214
1	AL	0.12	0/1638	0.37	0/2214
1	AM	0.12	0/1638	0.36	0/2214
1	AN	0.12	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	0.38	0/2214
1	AR	0.13	0/1638	0.37	0/2214
1	AS	0.12	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	0.11	0/2132	0.25	0/2861

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	E	0.11	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	0.10	0/2132	0.25	0/2861
1	M	0.10	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	0.10	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	0.10	0/2132	0.25	0/2861
1	V	0.11	0/2132	0.26	0/2861
1	W	0.11	0/2132	0.28	0/2861
1	X	0.11	0/2132	0.28	0/2861
1	Y	0.10	0/2132	0.25	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	0.27	0/2861
1	c	0.10	0/2132	0.28	0/2861
1	d	0.11	0/2132	0.27	0/2861
1	e	0.10	0/2132	0.25	0/2861
1	f	0.11	0/2132	0.27	0/2861
1	g	0.10	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	0.10	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	0.17	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	0.13	0/1657	0.35	0/2246
1	z	0.13	0/1657	0.34	0/2246
2	AX	0.13	0/2033	0.30	0/2734
3	AY	0.15	0/1706	0.35	0/2313
3	AZ	0.15	0/1696	0.33	0/2300
3	Aa	0.14	0/1697	0.34	0/2300
3	Ab	0.15	0/1706	0.36	0/2312
3	Ac	0.14	0/1717	0.32	0/2325
4	Ad	0.13	0/2135	0.32	0/2892
5	Ae	0.13	0/545	0.29	0/734
5	Af	0.12	0/545	0.26	0/734
5	Ag	0.12	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	0.10	0/936	0.27	0/1259
6	Am	0.10	0/936	0.24	0/1259
6	An	0.11	0/936	0.28	0/1259
6	Ao	0.10	0/936	0.23	0/1259
7	Ap	0.11	0/1043	0.24	0/1405
7	Aq	0.11	0/1175	0.25	0/1593
7	Ar	0.11	0/1047	0.27	0/1411
7	As	0.10	0/1191	0.25	0/1612
7	At	0.11	0/1191	0.26	0/1612
7	Au	0.10	0/1191	0.26	0/1612
8	AU	0.15	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	0.13	0/5515	0.33	0/7477
9	A2	0.13	0/5515	0.33	0/7477
9	A3	0.13	0/5515	0.33	0/7477
9	A4	0.13	0/5515	0.33	0/7477
9	A5	0.13	0/5515	0.33	0/7477
9	Aw	0.13	0/5515	0.33	0/7477
9	Ax	0.13	0/5515	0.33	0/7477
9	Ay	0.13	0/5515	0.33	0/7477
9	Az	0.13	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	5.73	1.38	1.33
1	4	107	VAL	C-N	5.68	1.38	1.33
1	AB	107	VAL	C-N	5.63	1.38	1.33
1	9	107	VAL	C-N	5.61	1.38	1.33
1	2	107	VAL	C-N	5.61	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	10	0
1	2	1595	0	1633	7	0
1	3	1632	0	1673	8	0
1	4	1632	0	1673	12	0
1	5	1632	0	1673	9	0
1	6	1595	0	1633	9	0
1	7	1632	0	1673	10	0
1	8	1632	0	1673	11	0
1	9	1632	0	1673	11	0
1	A	2104	0	2085	17	0
1	AA	1632	0	1673	12	0
1	AB	1632	0	1673	9	0
1	AC	1614	0	1677	19	0
1	AD	1614	0	1677	17	0
1	AE	1614	0	1677	18	0
1	AF	1614	0	1677	18	0
1	AG	1614	0	1677	17	0
1	AH	1614	0	1677	17	0
1	AI	1614	0	1677	18	0
1	AJ	1614	0	1677	17	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	18	0
1	AM	1614	0	1677	17	0
1	AN	1614	0	1677	18	0
1	AO	1614	0	1677	17	0
1	AP	1614	0	1677	17	0
1	AQ	1614	0	1677	18	0
1	AR	1614	0	1677	18	0
1	AS	1614	0	1677	19	0
1	AT	1614	0	1677	17	0
1	B	2104	0	2085	19	0
1	C	2104	0	2085	20	0
1	D	2104	0	2085	20	0
1	E	2104	0	2085	22	0
1	F	2104	0	2085	18	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	14	0
1	K	2104	0	2085	14	0
1	L	2104	0	2085	19	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	20	0
1	Q	2104	0	2085	21	0
1	R	2104	0	2085	18	0
1	S	2104	0	2085	29	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	18	0
1	X	2104	0	2085	23	0
1	Y	2104	0	2085	14	0
1	Z	2104	0	2085	15	0
1	a	2104	0	2085	17	0
1	b	2104	0	2085	21	0
1	c	2104	0	2085	21	0
1	d	2104	0	2085	21	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	18	0
1	k	2104	0	2085	14	0
1	l	2104	0	2085	17	0
1	m	2104	0	2085	19	0
1	n	2104	0	2085	13	0
1	o	2104	0	2085	20	0
1	p	1632	0	1673	14	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	8	0
1	u	1632	0	1673	14	0
1	v	1632	0	1673	5	0
1	w	1632	0	1673	6	0
1	x	1595	0	1633	9	0
1	y	1632	0	1673	8	0
1	z	1632	0	1673	10	0
2	AX	1988	0	2043	19	0
3	AY	1665	0	1752	30	0
3	AZ	1656	0	1740	29	0
3	Aa	1657	0	1747	24	0
3	Ab	1666	0	1755	22	0
3	Ac	1676	0	1773	23	0
4	Ad	2083	0	2194	35	0
5	Ae	542	0	579	8	0
5	Af	542	0	579	4	0
5	Ag	542	0	579	5	0
5	Ah	530	0	561	5	0
5	Ai	542	0	579	9	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	5	0
7	Ap	1030	0	1055	9	0
7	Aq	1153	0	1150	6	0
7	Ar	1034	0	1058	3	0
7	As	1169	0	1178	6	0
7	At	1169	0	1178	5	0
7	Au	1169	0	1178	10	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	17	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	47	0
9	A4	5429	0	5666	52	0
9	A5	5429	0	5666	50	0
9	Aw	5429	0	5666	42	0
9	Ax	5429	0	5666	47	0
9	Ay	5429	0	5666	44	0
9	Az	5429	0	5666	45	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	0.82
1:m:230:ASP:O	1:m:234:ARG:HB2	1.80	0.81
8:Av:22:ALA:O	8:Av:26:ILE:HB	1.82	0.79
8:AU:27:ILE:HG21	8:AU:61:VAL:HG21	1.65	0.77
1:AE:69:GLN:HE22	1:AE:73:ARG:HH21	1.37	0.70

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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%)	197 (95%)	9 (4%)	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%)	185 (92%)	14 (7%)	1 (0%)	24	63
1	AG	200/569 (35%)	186 (93%)	13 (6%)	1 (0%)	24	63
1	AH	200/569 (35%)	185 (92%)	14 (7%)	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%)	185 (92%)	14 (7%)	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%)	251 (97%)	7 (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%)	252 (98%)	6 (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%)	206 (100%)	1 (0%)	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%)	66 (97%)	2 (3%)	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%)	27879 (97%)	904 (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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	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	38
1	3	178/506 (35%)	168 (94%)	10 (6%)	19	41
1	4	178/506 (35%)	168 (94%)	10 (6%)	19	41
1	5	178/506 (35%)	166 (93%)	12 (7%)	15	37
1	6	174/506 (34%)	162 (93%)	12 (7%)	14	36
1	7	178/506 (35%)	169 (95%)	9 (5%)	21	43
1	8	178/506 (35%)	167 (94%)	11 (6%)	16	38
1	9	178/506 (35%)	168 (94%)	10 (6%)	19	41
1	A	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	AA	178/506 (35%)	166 (93%)	12 (7%)	15	37
1	AB	178/506 (35%)	168 (94%)	10 (6%)	19	41
1	AC	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AD	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AE	180/506 (36%)	173 (96%)	7 (4%)	28	50
1	AF	180/506 (36%)	174 (97%)	6 (3%)	33	55
1	AG	180/506 (36%)	175 (97%)	5 (3%)	38	59
1	AH	180/506 (36%)	172 (96%)	8 (4%)	25	47
1	AI	180/506 (36%)	175 (97%)	5 (3%)	38	59
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	59
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	50
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	50
1	AT	180/506 (36%)	175 (97%)	5 (3%)	38	59
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	72
1	G	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	H	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	I	226/506 (45%)	222 (98%)	4 (2%)	51	67
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	67
1	M	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	N	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	O	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	P	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	Q	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	R	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	S	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	T	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	U	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	V	226/506 (45%)	222 (98%)	4 (2%)	51	67
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	72
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	67
1	b	226/506 (45%)	221 (98%)	5 (2%)	45	64
1	c	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	d	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	e	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	f	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	g	226/506 (45%)	220 (97%)	6 (3%)	39	60
1	h	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	i	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	j	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	k	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	l	226/506 (45%)	224 (99%)	2 (1%)	70	77
1	m	226/506 (45%)	219 (97%)	7 (3%)	35	56
1	n	226/506 (45%)	223 (99%)	3 (1%)	61	72
1	o	226/506 (45%)	222 (98%)	4 (2%)	51	67
1	p	178/506 (35%)	166 (93%)	12 (7%)	15	37
1	q	178/506 (35%)	168 (94%)	10 (6%)	19	41
1	r	178/506 (35%)	169 (95%)	9 (5%)	21	43
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	37
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	41
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	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AZ	185/232 (80%)	179 (97%)	6 (3%)	34	55
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	45
4	Ad	236/249 (95%)	220 (93%)	16 (7%)	14	36
5	Ae	64/103 (62%)	60 (94%)	4 (6%)	16	38
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	59
6	Al	107/129 (83%)	104 (97%)	3 (3%)	38	59
6	Am	107/129 (83%)	105 (98%)	2 (2%)	50	66
6	An	107/129 (83%)	103 (96%)	4 (4%)	30	51
6	Ao	107/129 (83%)	106 (99%)	1 (1%)	70	77
7	Ap	115/130 (88%)	115 (100%)	0	100	100
7	Aq	127/130 (98%)	125 (98%)	2 (2%)	55	69
7	Ar	116/130 (89%)	115 (99%)	1 (1%)	70	77
7	As	130/130 (100%)	128 (98%)	2 (2%)	57	71
7	At	130/130 (100%)	128 (98%)	2 (2%)	57	71
7	Au	130/130 (100%)	129 (99%)	1 (1%)	73	78
8	AU	78/80 (98%)	71 (91%)	7 (9%)	9	28
8	AV	80/80 (100%)	75 (94%)	5 (6%)	16	38
8	AW	80/80 (100%)	75 (94%)	5 (6%)	16	38
8	Av	77/80 (96%)	74 (96%)	3 (4%)	28	50
9	A1	619/619 (100%)	605 (98%)	14 (2%)	44	63
9	A2	619/619 (100%)	604 (98%)	15 (2%)	43	63
9	A3	619/619 (100%)	604 (98%)	15 (2%)	43	63
9	A4	619/619 (100%)	605 (98%)	14 (2%)	44	63
9	A5	619/619 (100%)	605 (98%)	14 (2%)	44	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Aw	619/619 (100%)	604 (98%)	15 (2%)	43	63
9	Ax	619/619 (100%)	605 (98%)	14 (2%)	44	63
9	Ay	619/619 (100%)	604 (98%)	15 (2%)	43	63
9	Az	619/619 (100%)	604 (98%)	15 (2%)	43	63
All	All	25492/51170 (50%)	24717 (97%)	775 (3%)	37	57

5 of 775 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AJ	159	VAL
4	Ad	128	ILE
1	AM	53	LEU
1	AJ	154	VAL
1	AT	49	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 235 such sidechains are listed below:

Mol	Chain	Res	Type
1	AN	23	GLN
9	A3	219	ASN
3	Ac	154	HIS
9	A3	175	ASN
9	Ay	530	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

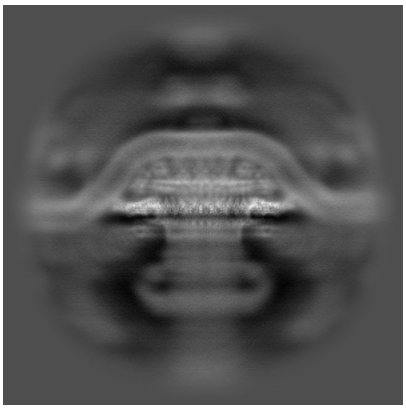
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-76349. These allow visual inspection of the internal detail of the map and identification of artifacts.

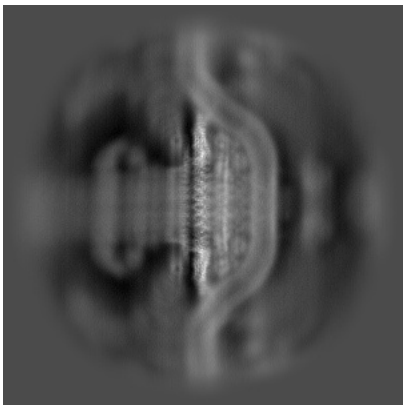
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

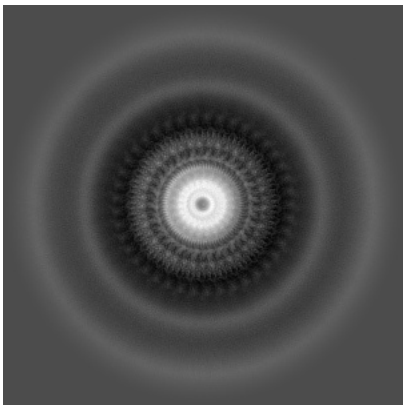
6.1.1 Primary map



X

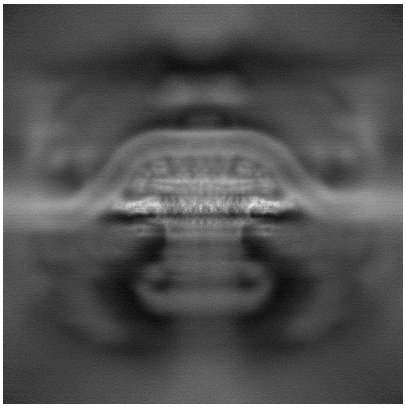


Y

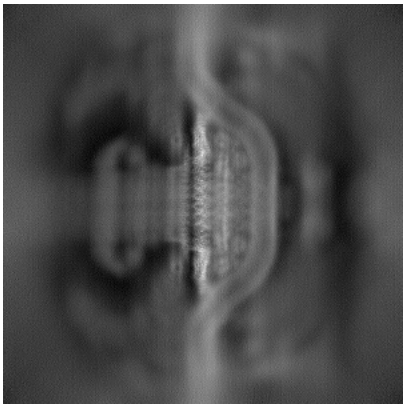


Z

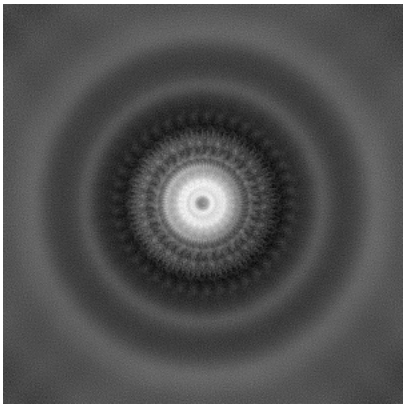
6.1.2 Raw map



X



Y

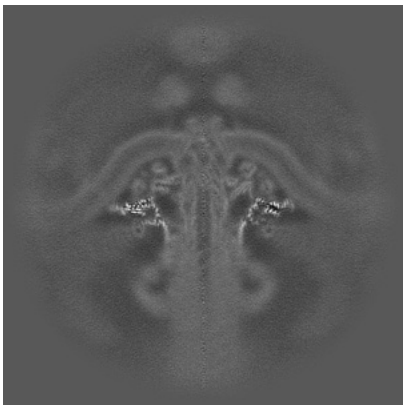


Z

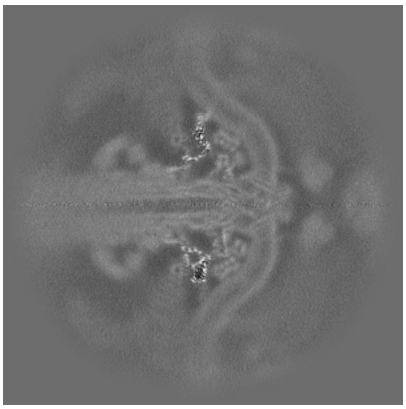
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

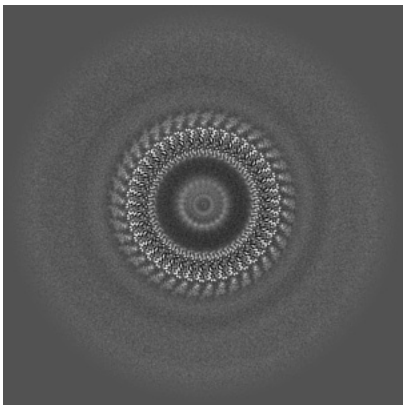
6.2.1 Primary map



X Index: 224

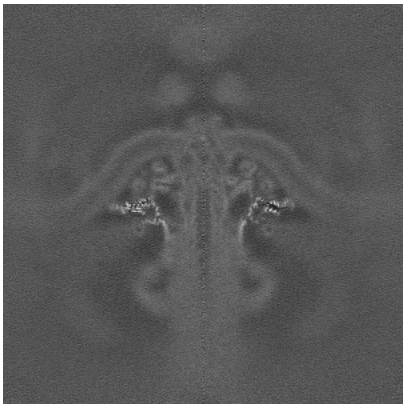


Y Index: 224

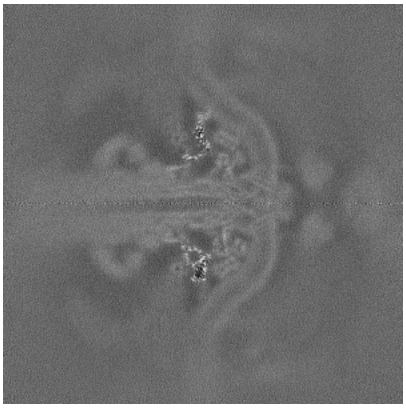


Z Index: 224

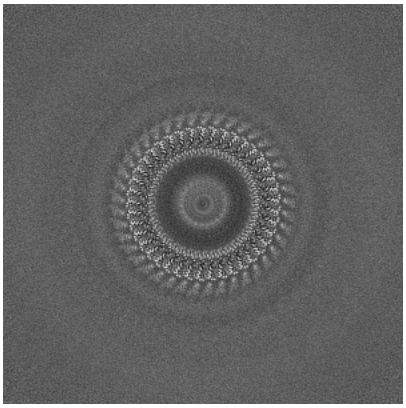
6.2.2 Raw map



X Index: 224



Y Index: 224

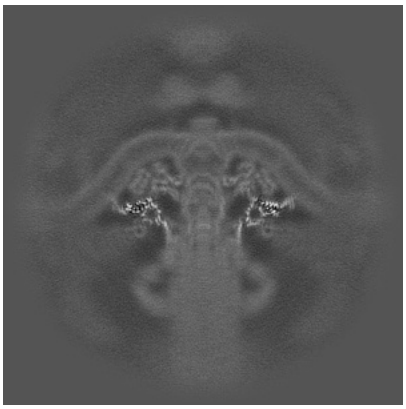


Z Index: 224

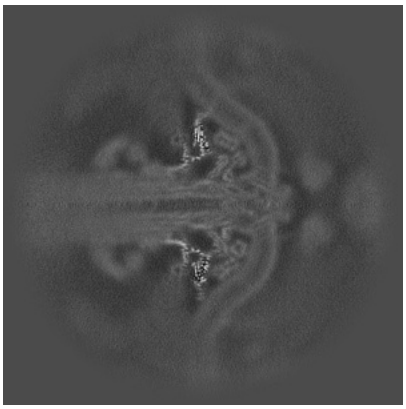
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

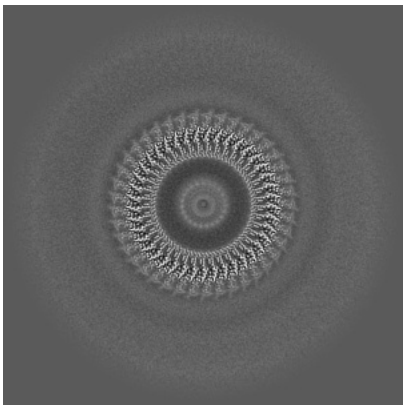
6.3.1 Primary map



X Index: 211

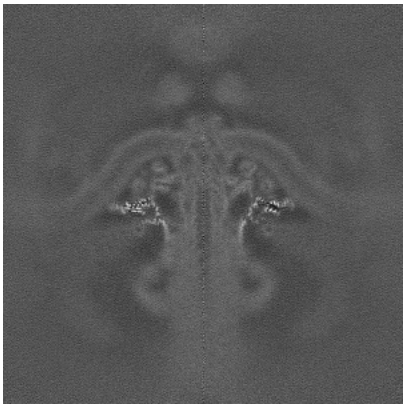


Y Index: 222

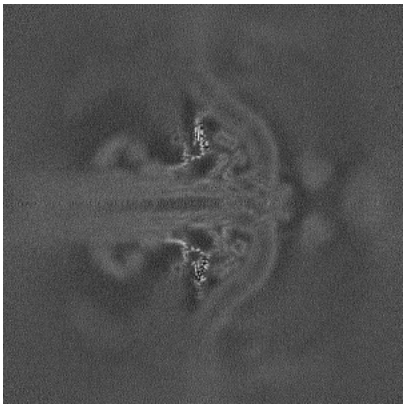


Z Index: 222

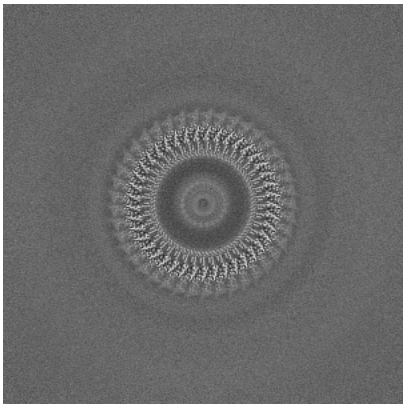
6.3.2 Raw map



X Index: 224



Y Index: 222

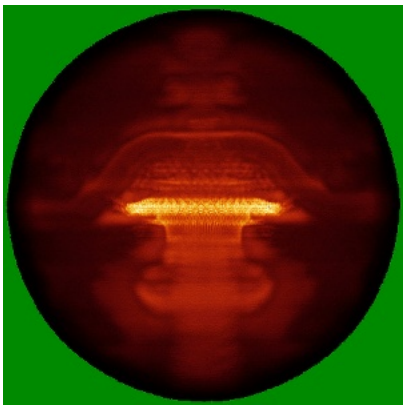


Z Index: 222

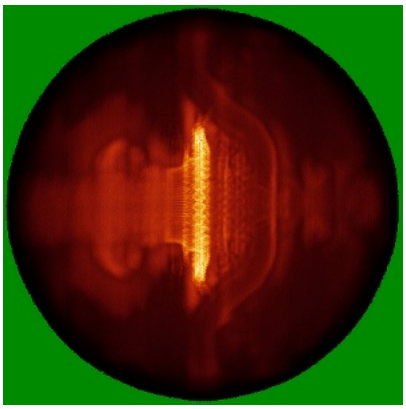
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

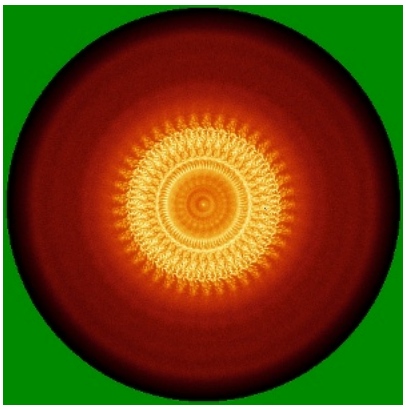
6.4.1 Primary map



X

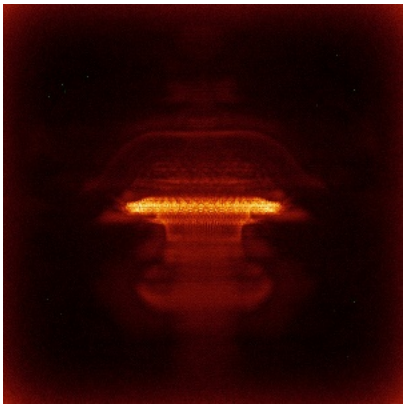


Y

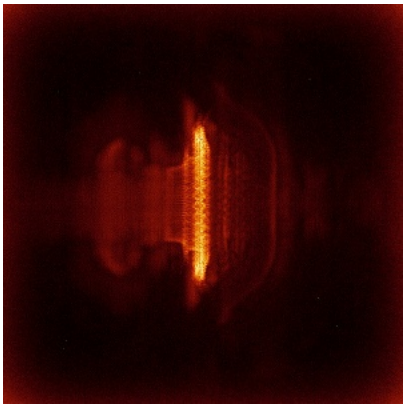


Z

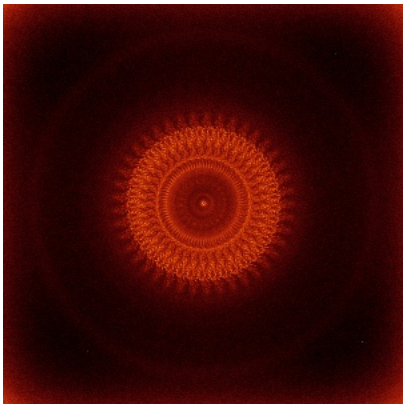
6.4.2 Raw map



X



Y

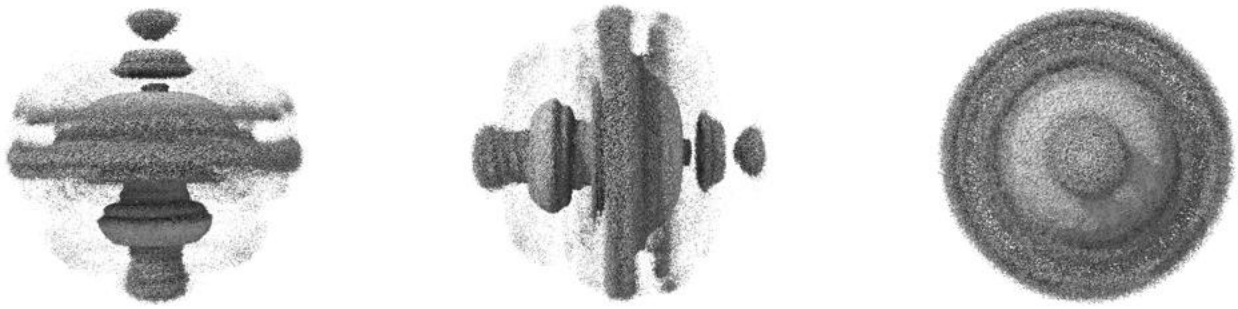


Z

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)

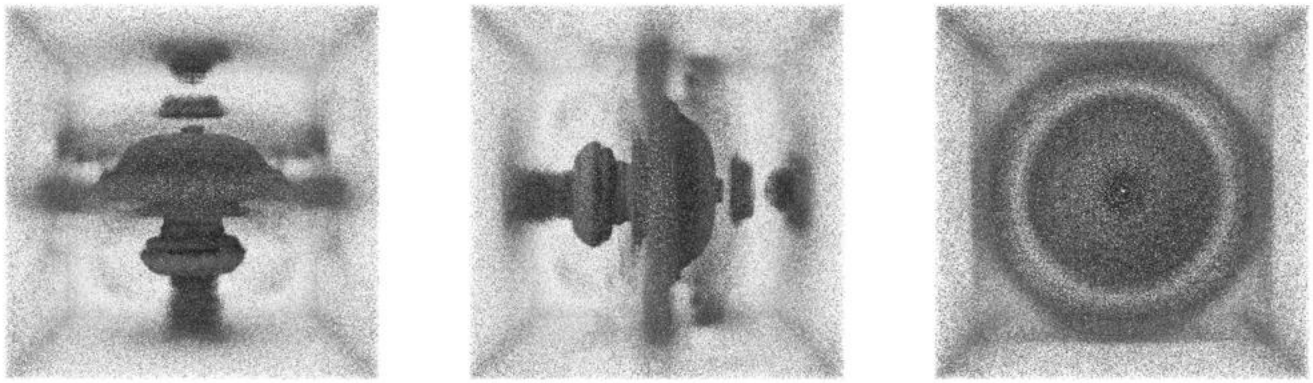
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. 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



X Y Z

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.

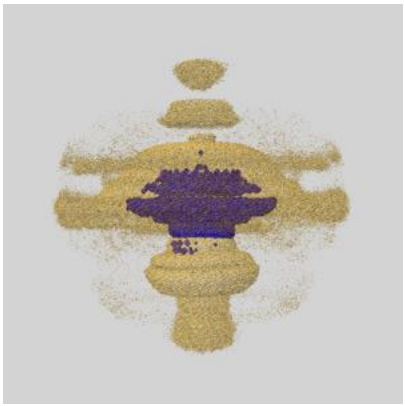
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

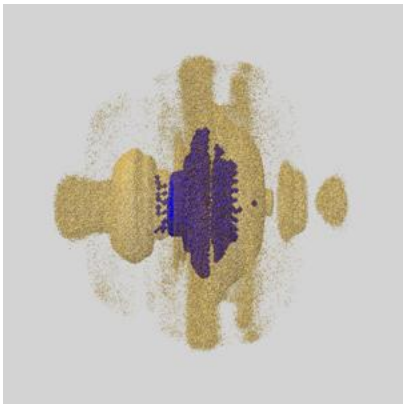
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

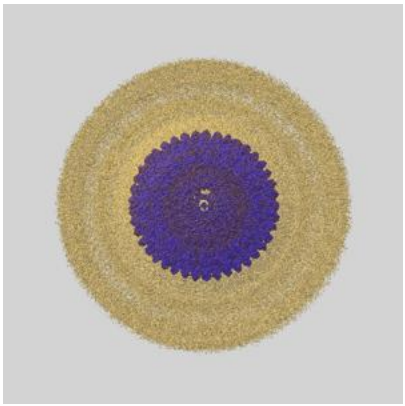
6.6.1 emd_76349_msk_1.map (i)



X



Y

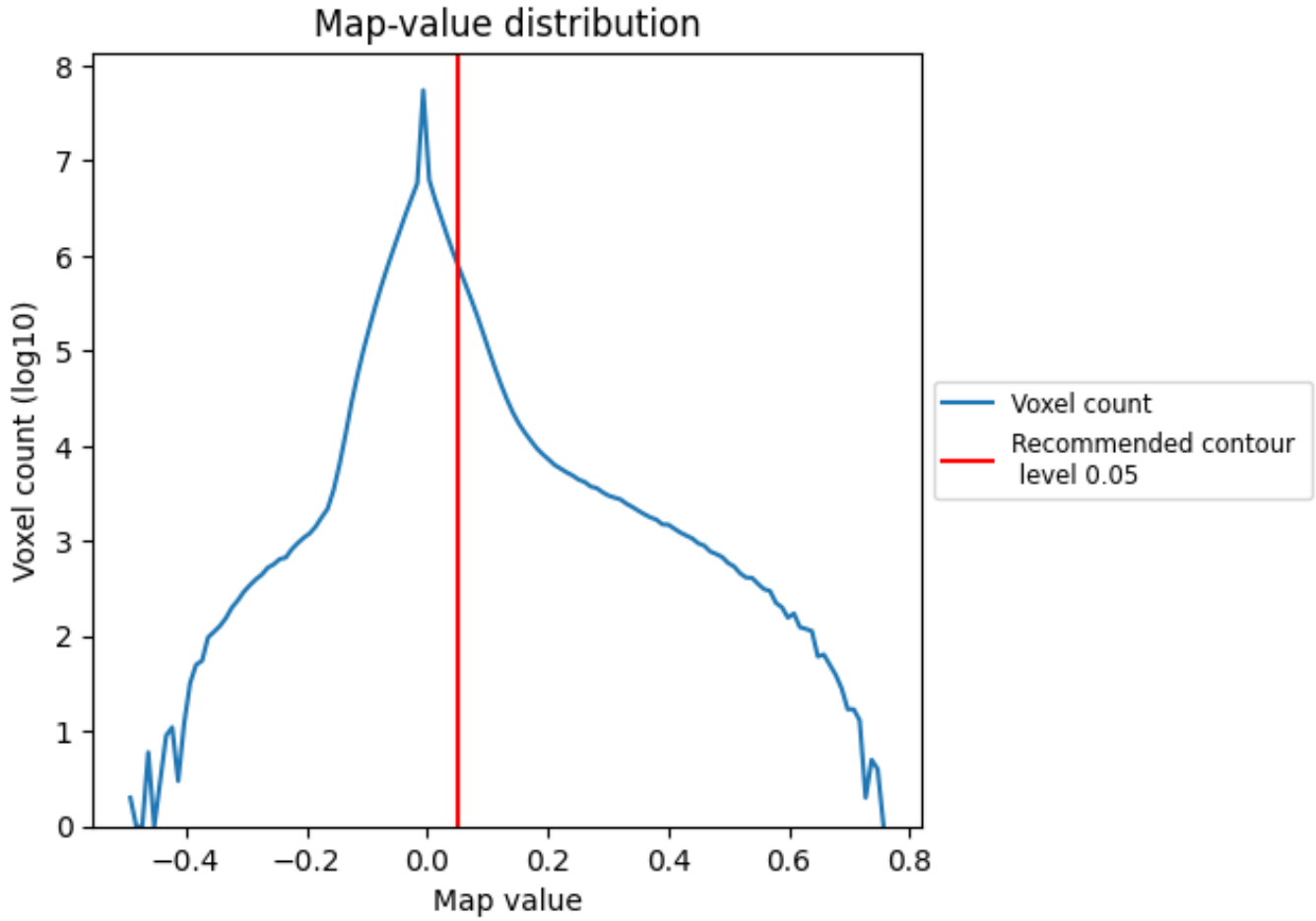


Z

7 Map analysis

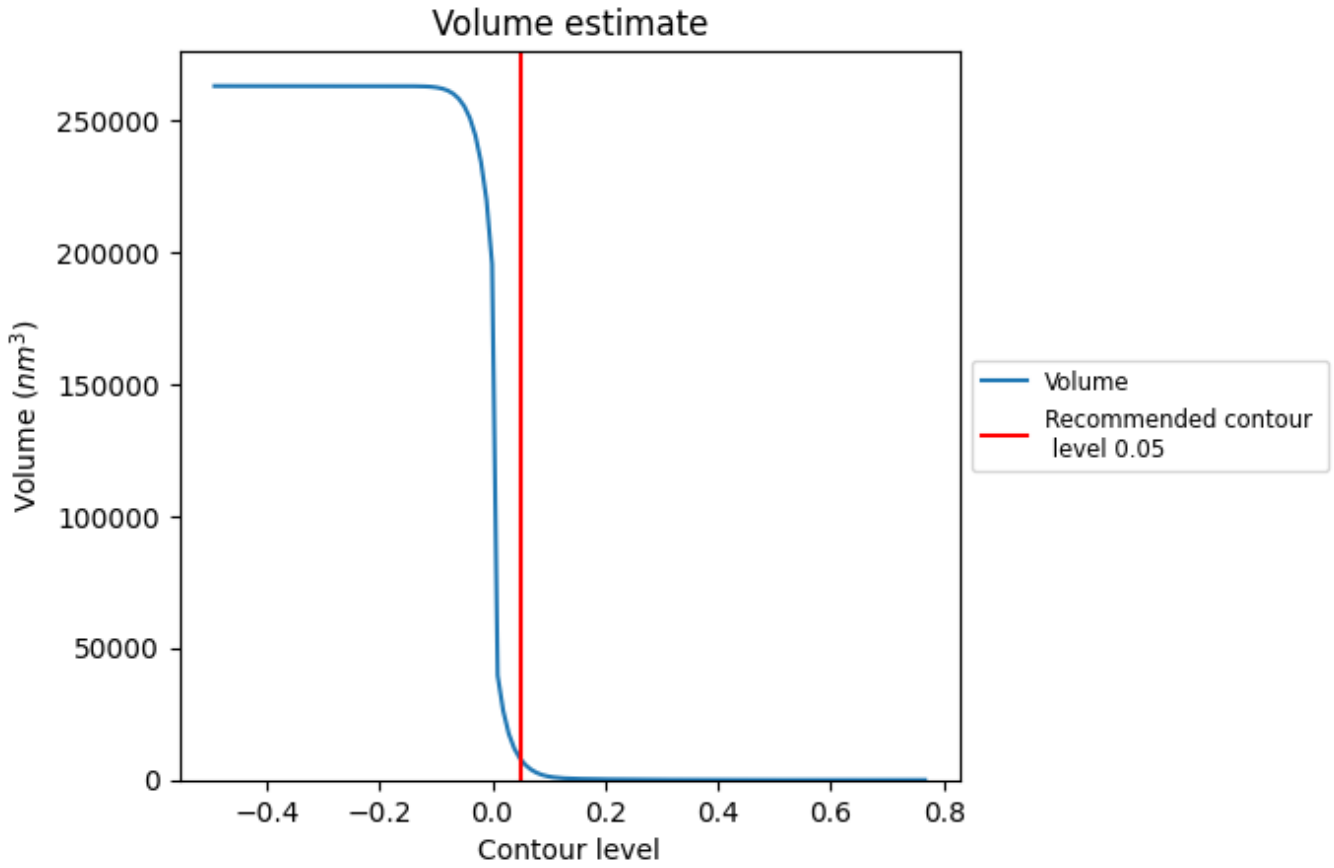
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

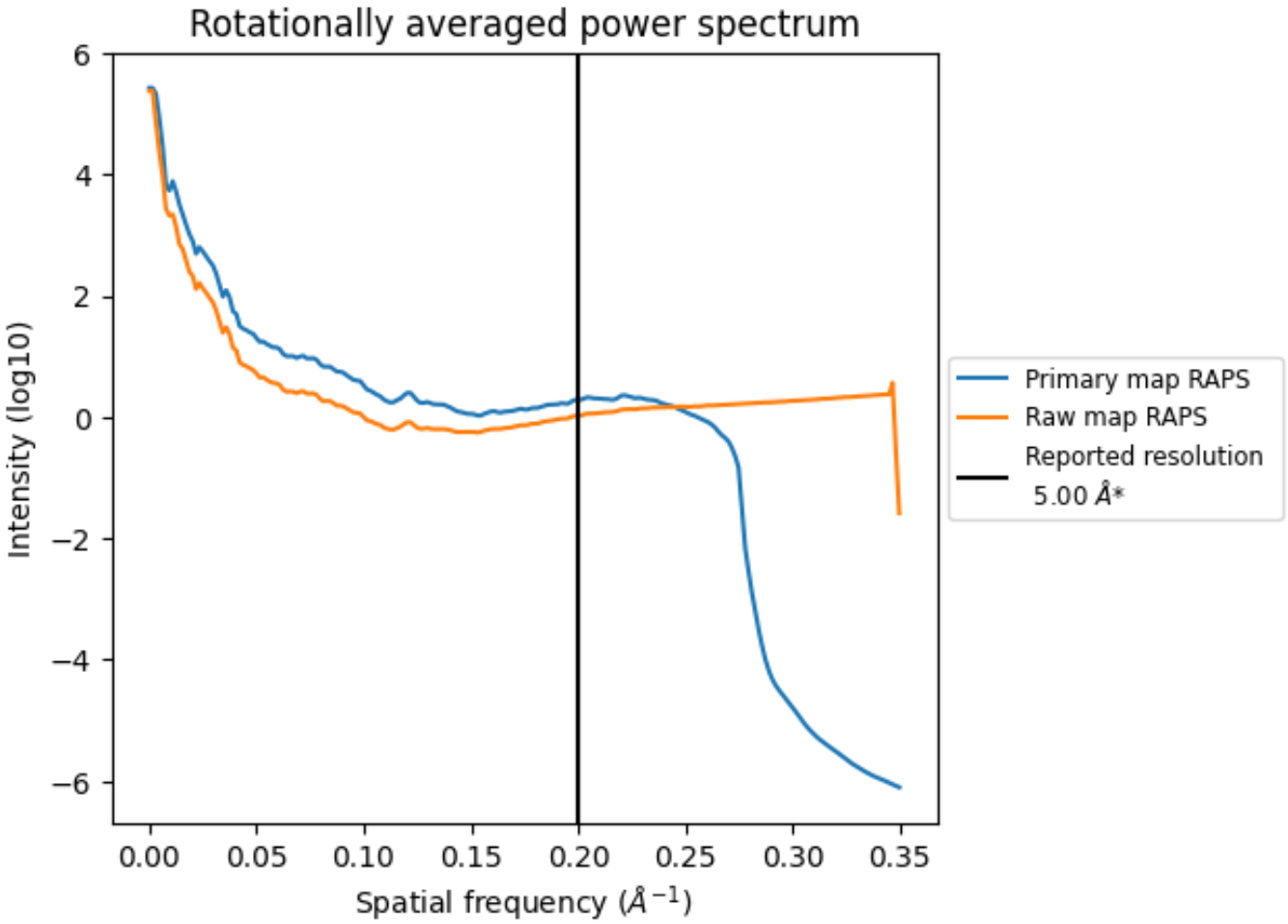
7.2 Volume estimate (i)



The volume at the recommended contour level is 7949 nm^3; this corresponds to an approximate mass of 7180 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)

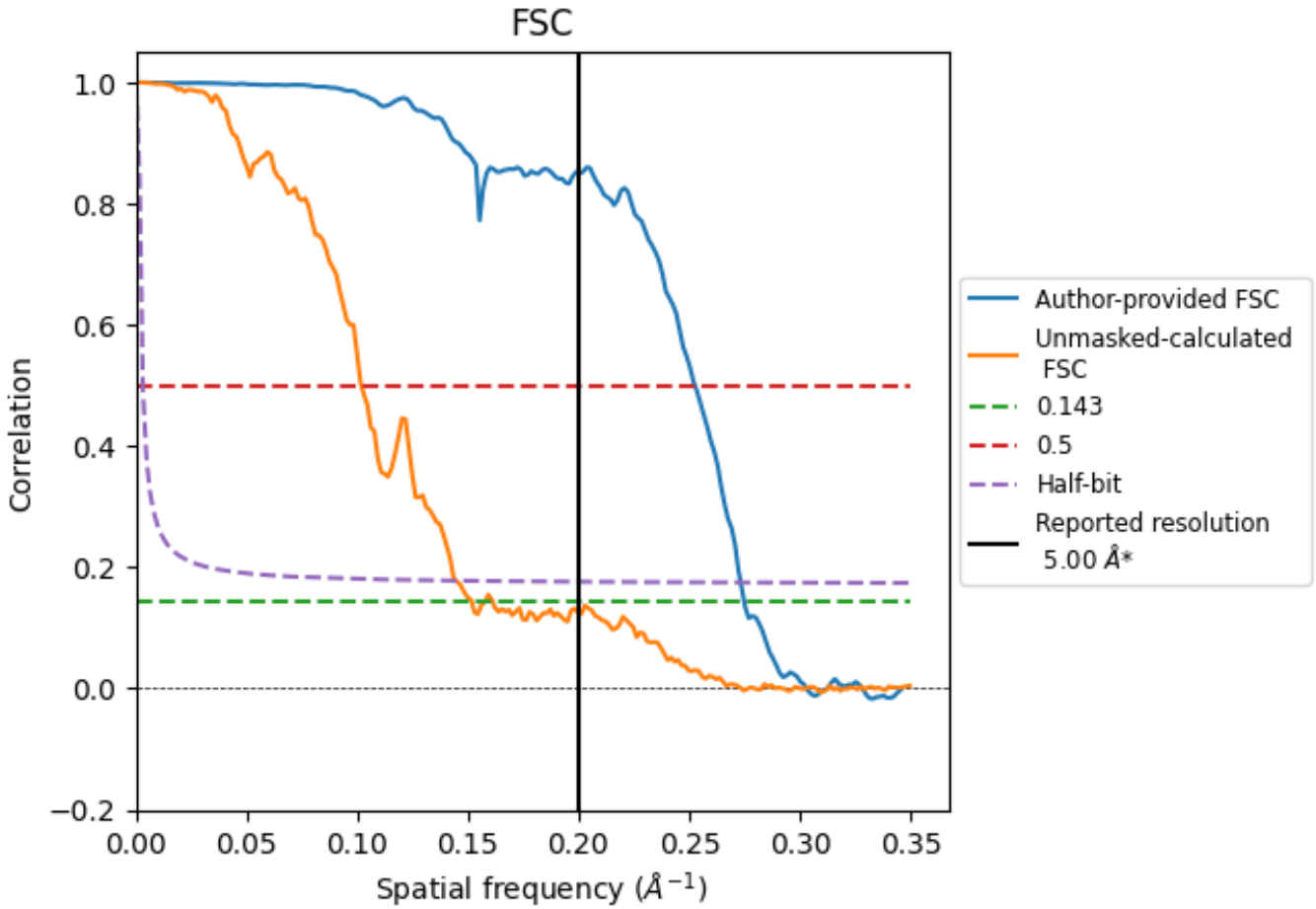


*Reported resolution corresponds to spatial frequency of 0.200 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.200 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.00	-	-
Author-provided FSC curve	3.64	3.96	3.66
Unmasked-calculated*	6.59	9.82	6.92

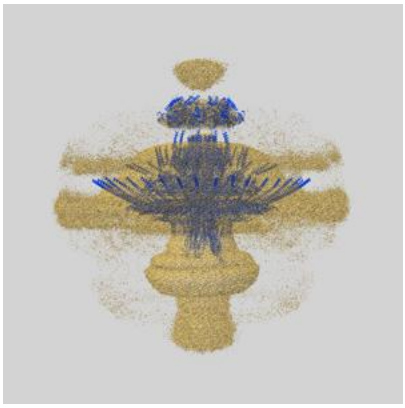
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.64 differs from the reported value 5.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.59 differs from the reported value 5.0 by more than 10 %

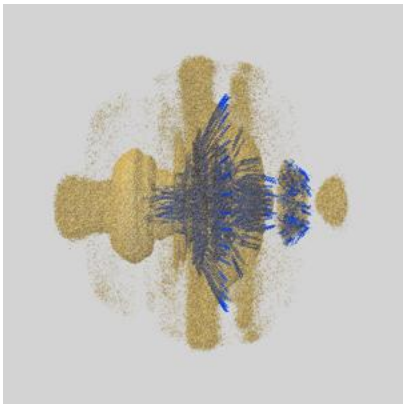
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-76349 and PDB model 12DW. Per-residue inclusion information can be found in section 3 on page 15.

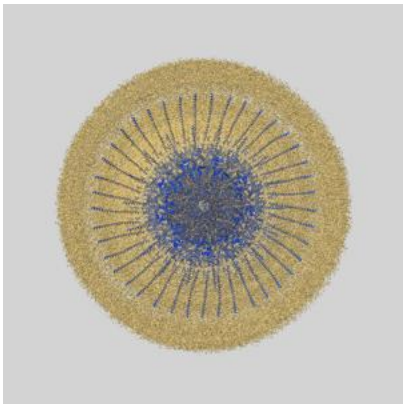
9.1 Map-model overlay



X



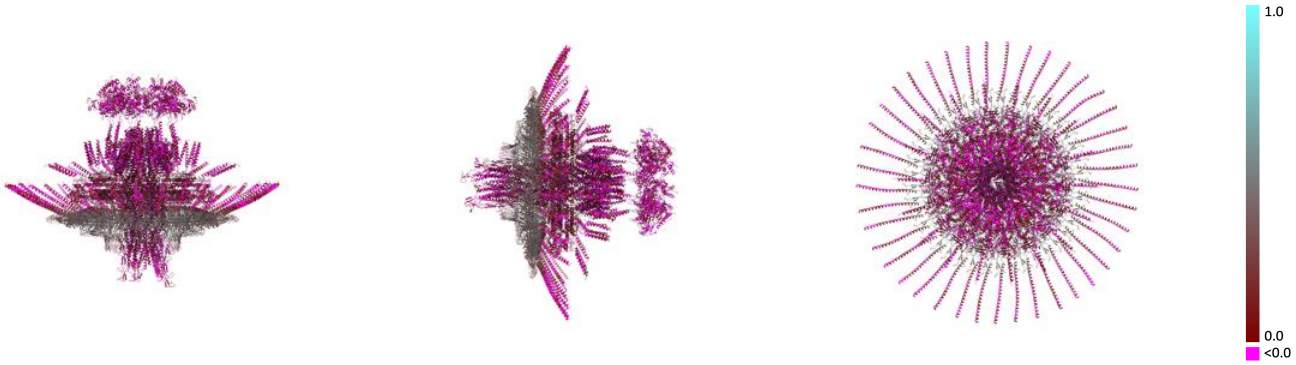
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

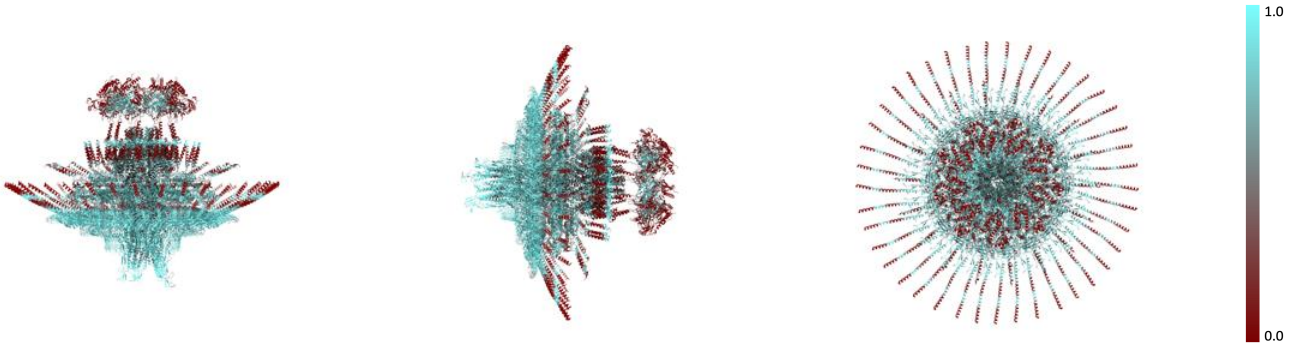
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

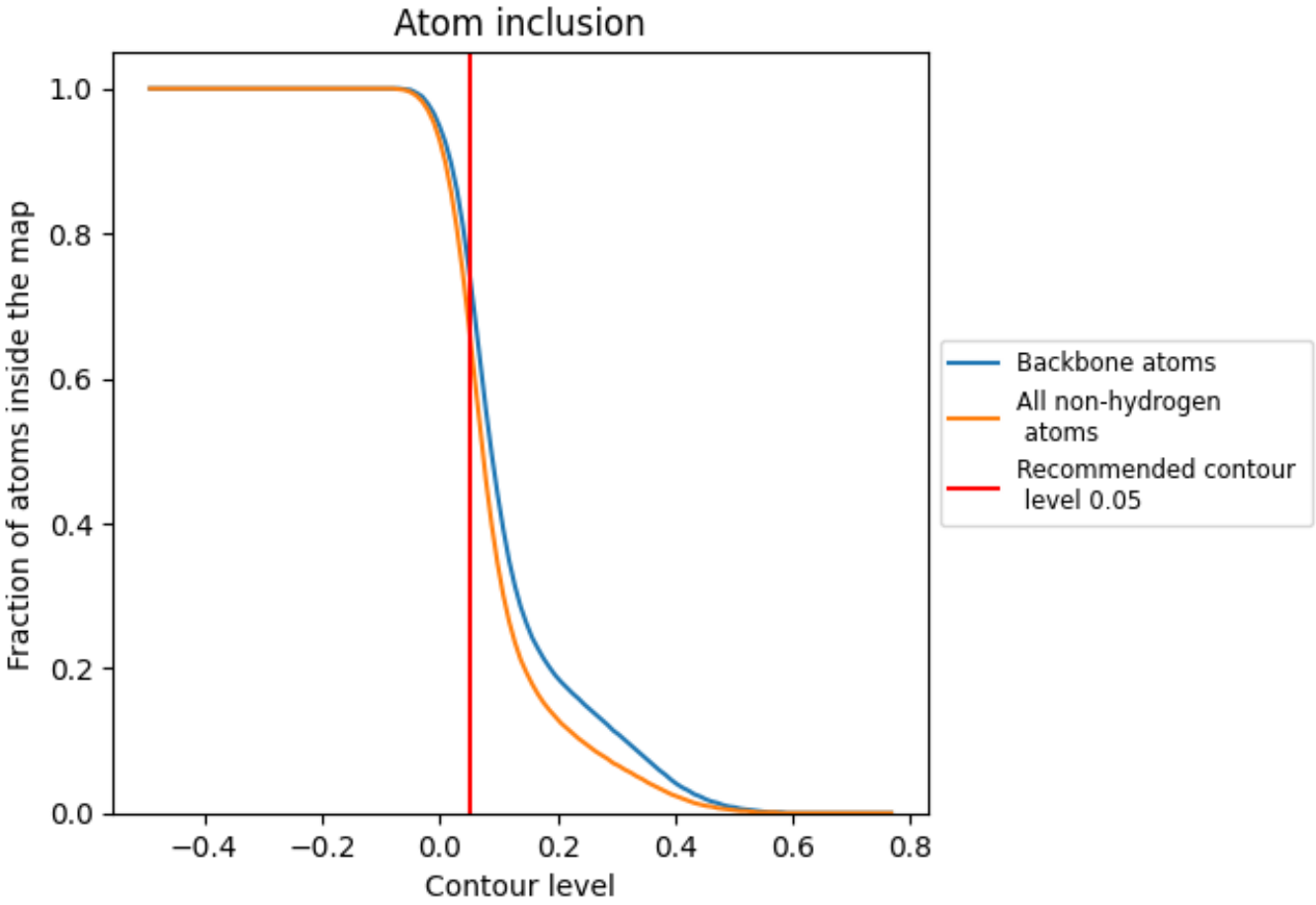
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 67% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6700	0.1690
0	0.7300	0.1840
1	0.7490	0.1900
2	0.7500	0.1780
3	0.7540	0.1860
4	0.7510	0.1760
5	0.7270	0.1720
6	0.7440	0.1840
7	0.7290	0.1730
8	0.7200	0.1850
9	0.7270	0.1740
A	0.7690	0.3260
A1	0.4290	0.0300
A2	0.4210	0.0300
A3	0.4190	0.0290
A4	0.4320	0.0220
A5	0.4290	0.0270
AA	0.7230	0.1830
AB	0.7200	0.1660
AC	0.5520	0.0600
AD	0.5750	0.0830
AE	0.5390	0.0690
AF	0.5600	0.0950
AG	0.5510	0.0760
AH	0.5490	0.0730
AI	0.5250	0.0540
AJ	0.5610	0.0930
AK	0.5400	0.0620
AL	0.5470	0.0510
AM	0.5680	0.0790
AN	0.5800	0.0730
AO	0.5820	0.0840
AP	0.5670	0.0640
AQ	0.5820	0.0780
AR	0.5680	0.0700



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Chain	Atom inclusion	Q-score
AS	0.5850	0.0890
AT	0.5650	0.0790
AU	0.6420	0.0640
AV	0.6300	0.0340
AW	0.7020	0.0640
AX	0.6650	0.0740
AY	0.7840	0.0910
AZ	0.8250	0.0920
Aa	0.7840	0.0430
Ab	0.7640	0.0710
Ac	0.7480	0.0560
Ad	0.7980	0.0770
Ae	0.8990	0.1110
Af	0.9050	0.0450
Ag	0.9050	0.0810
Ah	0.9300	0.0890
Ai	0.9030	0.0400
Aj	0.8520	0.0690
Ak	0.8810	0.0860
Al	0.8840	0.0480
Am	0.8500	0.0320
An	0.8360	0.0470
Ao	0.8900	0.0570
Ap	0.9020	0.0650
Aq	0.9080	0.0590
Ar	0.8610	0.0120
As	0.8950	0.0350
At	0.9160	0.0400
Au	0.9090	0.0340
Av	0.6300	0.0830
Aw	0.4390	0.0230
Ax	0.4490	0.0260
Ay	0.4540	0.0230
Az	0.4390	0.0240
B	0.7710	0.3120
C	0.7690	0.3140
D	0.7740	0.3310
E	0.7760	0.3190
F	0.7790	0.3340
G	0.7690	0.3170
H	0.7730	0.3240
I	0.7630	0.3130

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Chain	Atom inclusion	Q-score
J	0.7720	0.3180
K	0.7650	0.3210
L	0.7620	0.3030
M	0.7660	0.3240
N	0.7690	0.3160
O	0.7640	0.3240
P	0.7620	0.3210
Q	0.7710	0.3160
R	0.7660	0.3140
S	0.7600	0.3190
T	0.7690	0.3250
U	0.7650	0.3140
V	0.7540	0.3120
W	0.7620	0.3090
X	0.7690	0.3170
Y	0.7570	0.3100
Z	0.7610	0.3140
a	0.7600	0.3160
b	0.7480	0.3080
c	0.7530	0.3130
d	0.7600	0.3070
e	0.7450	0.3080
f	0.7560	0.3110
g	0.7630	0.3210
h	0.7500	0.2990
i	0.7440	0.2950
j	0.7550	0.3050
k	0.7510	0.3100
l	0.7520	0.3100
m	0.7670	0.3140
n	0.7720	0.3260
o	0.7570	0.3180
p	0.7350	0.1690
q	0.7340	0.1550
r	0.7510	0.1880
s	0.7430	0.1660
t	0.7440	0.1720
u	0.7370	0.1590
v	0.7440	0.1680
w	0.7460	0.1750
x	0.7590	0.1810
y	0.7370	0.1760

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Chain	Atom inclusion	Q-score
z	0.7510	0.1840