



wwPDB EM Validation Summary Report ⓘ

Aug 17, 2026 – 12:54 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, Y.
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:

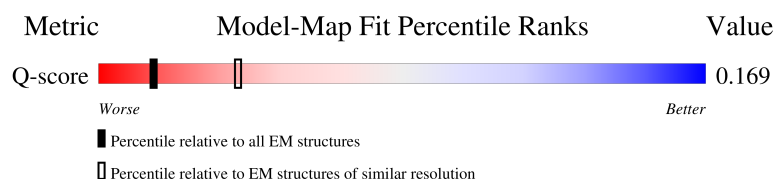
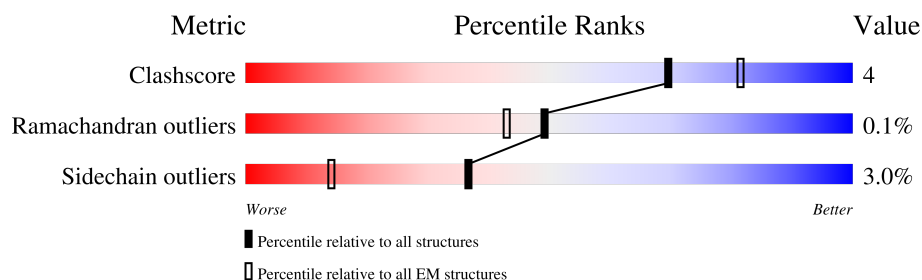
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 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.



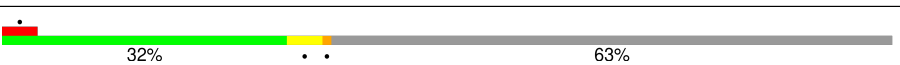
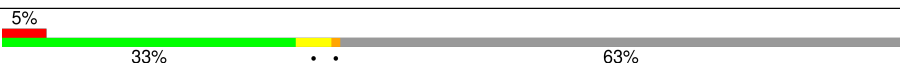
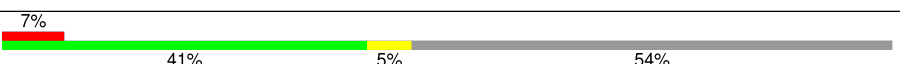
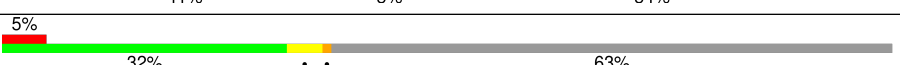
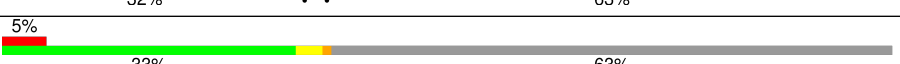
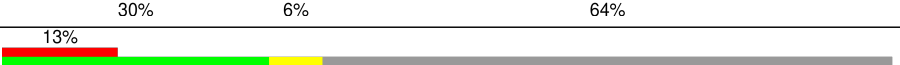
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1057 (4.50 - 5.50)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	569	
1	1	569	
1	2	569	
1	3	569	

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

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

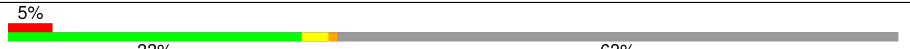
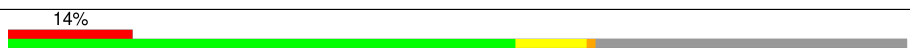
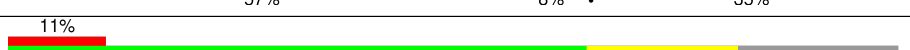
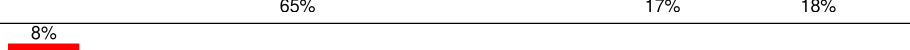
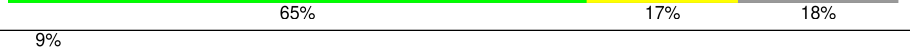
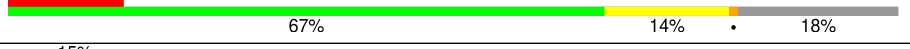
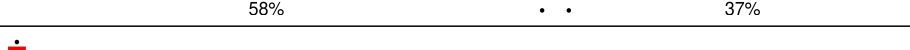
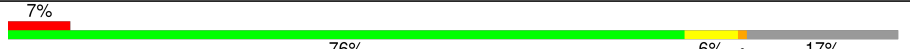
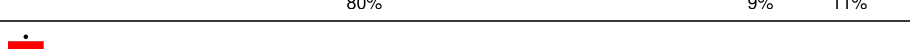
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Mol	Chain	Length	Quality of chain
1	Y	569	
1	Z	569	
1	a	569	
1	b	569	
1	c	569	
1	d	569	
1	e	569	
1	f	569	
1	g	569	
1	h	569	
1	i	569	
1	j	569	
1	k	569	
1	l	569	
1	m	569	
1	n	569	
1	o	569	
1	p	569	
1	q	569	
1	r	569	
1	s	569	
1	t	569	
1	u	569	
1	v	569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

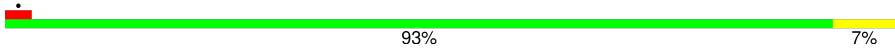
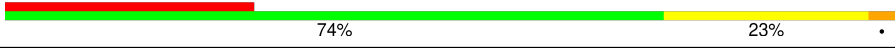
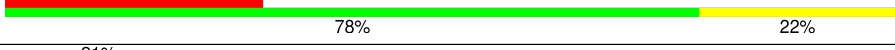
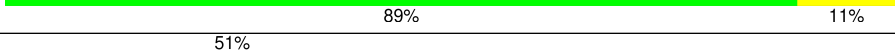
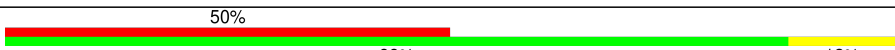
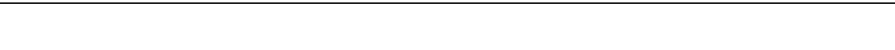
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Mol	Chain	Length	Quality of chain
1	x	569	
1	y	569	
1	z	569	
2	AX	372	
3	AY	254	
3	AZ	254	
3	Aa	254	
3	Ab	254	
3	Ac	254	
4	Ad	269	
5	Ae	111	
5	Af	111	
5	Ag	111	
5	Ah	111	
5	Ai	111	
5	Aj	111	
6	Ak	135	
6	Al	135	
6	Am	135	
6	An	135	
6	Ao	135	
7	Ap	152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

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

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 231030 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	B	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	C	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	D	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	E	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	F	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	G	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	H	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	I	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	J	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	K	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	L	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	M	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	N	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	O	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	P	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		
1	Q	262	Total	C	N	O	S	0	0
			2104	1328	365	406	5		

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

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

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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		

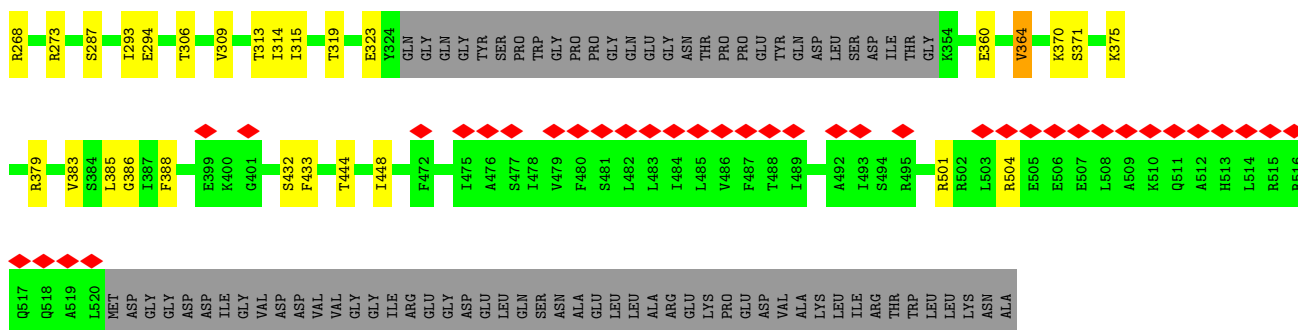
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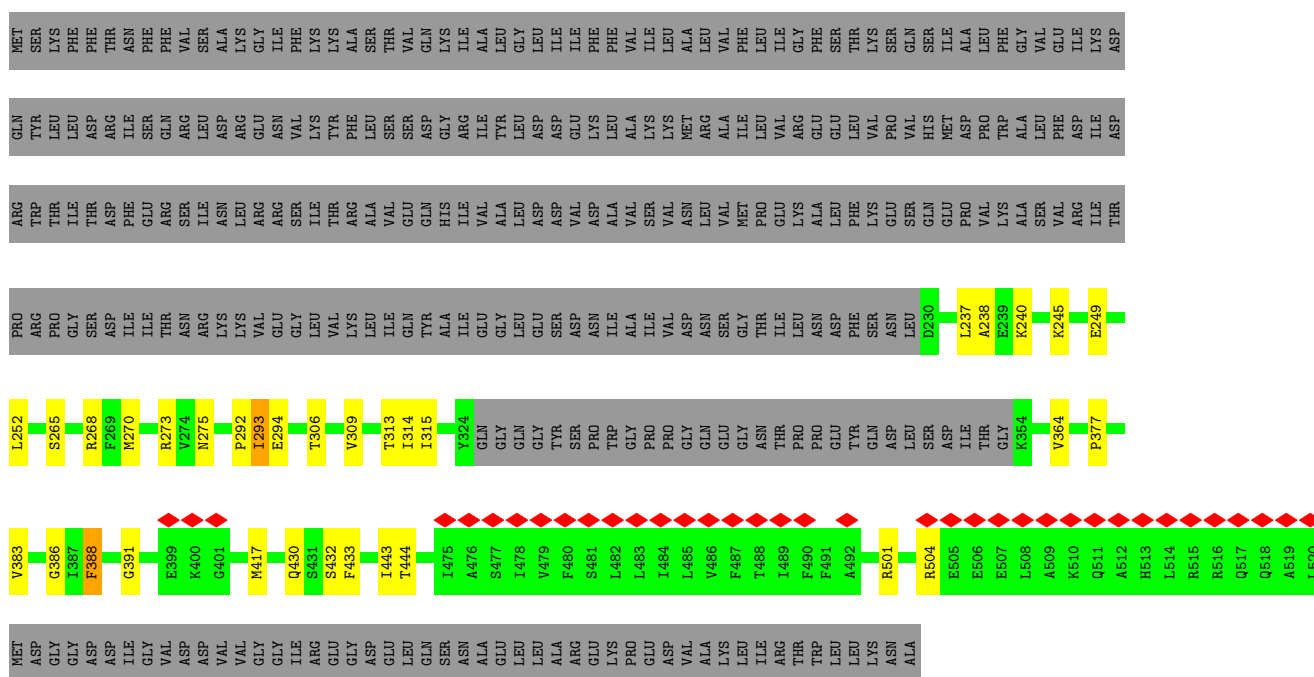
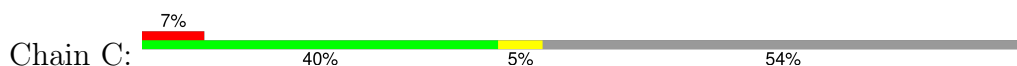
Mol	Chain	Residues	Atoms					AltConf	Trace
8	AV	87	Total	C	N	O	S	0	0
			692	471	104	113	4		
8	AW	87	Total	C	N	O	S	0	0
			692	471	104	113	4		

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

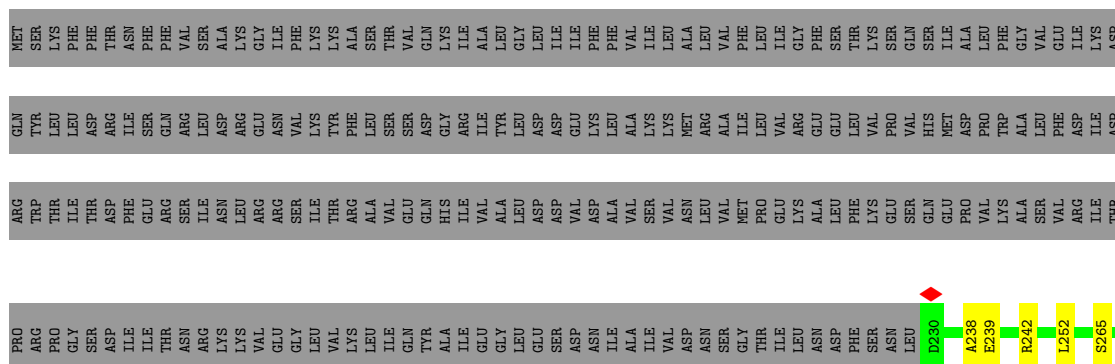
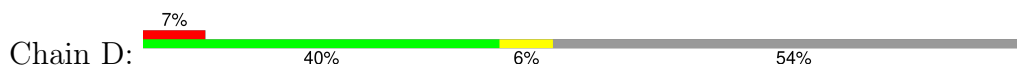
Mol	Chain	Residues	Atoms					AltConf	Trace
9	Aw	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Ax	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Ay	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	Az	697	Total	C	N	O	S	0	0
			5429	3527	875	1015	12		
9	A1	697	Total	C	N	O	S	0	0
			5429	3527	875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

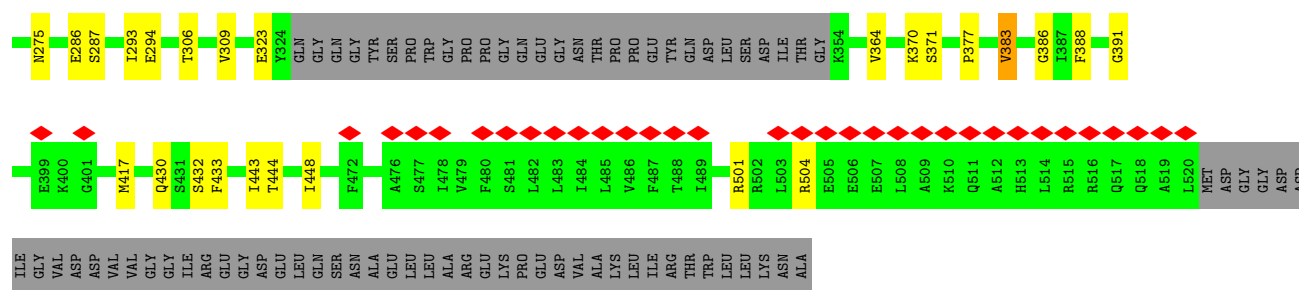


- Molecule 1: Flagellar M-ring protein

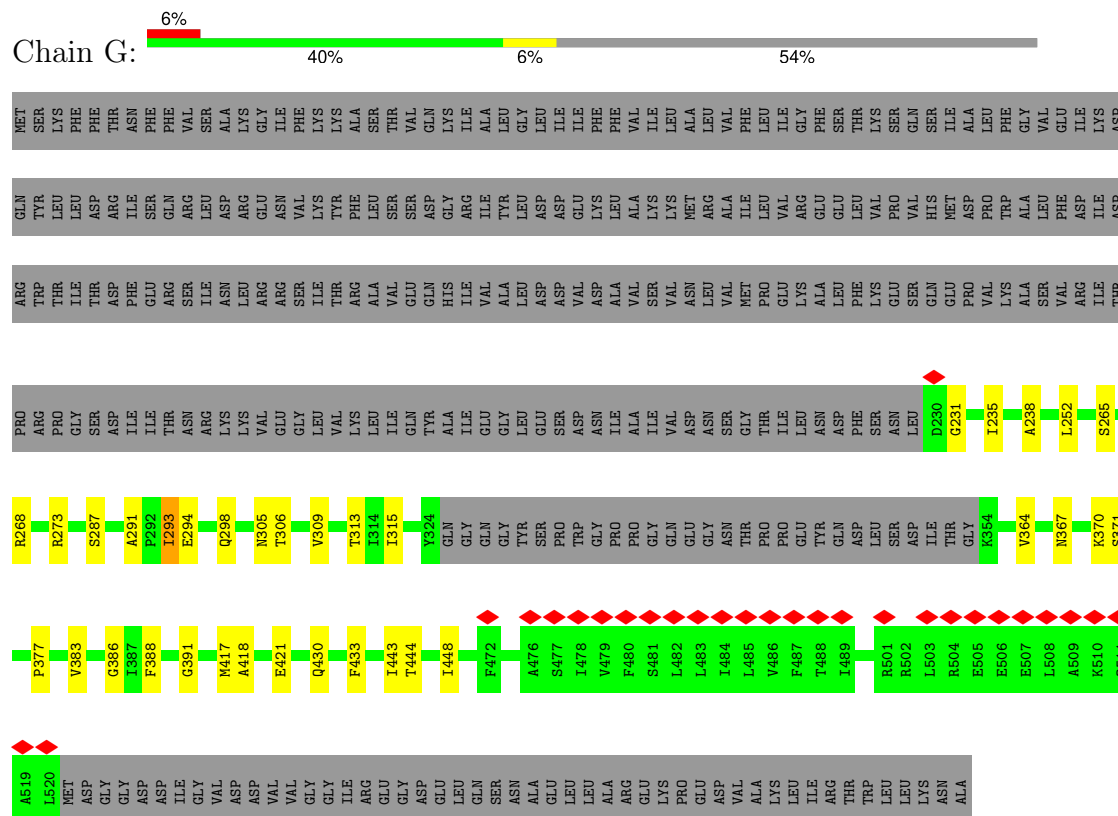


- Molecule 1: Flagellar M-ring protein

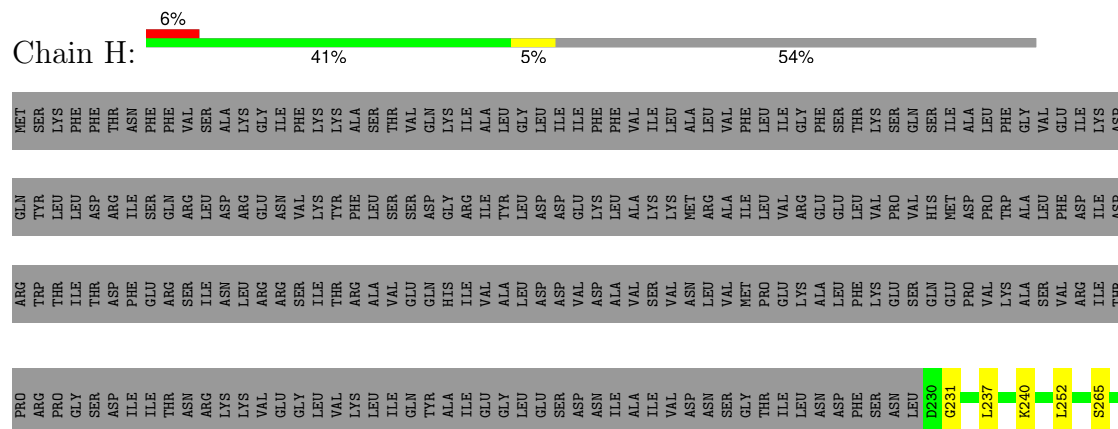


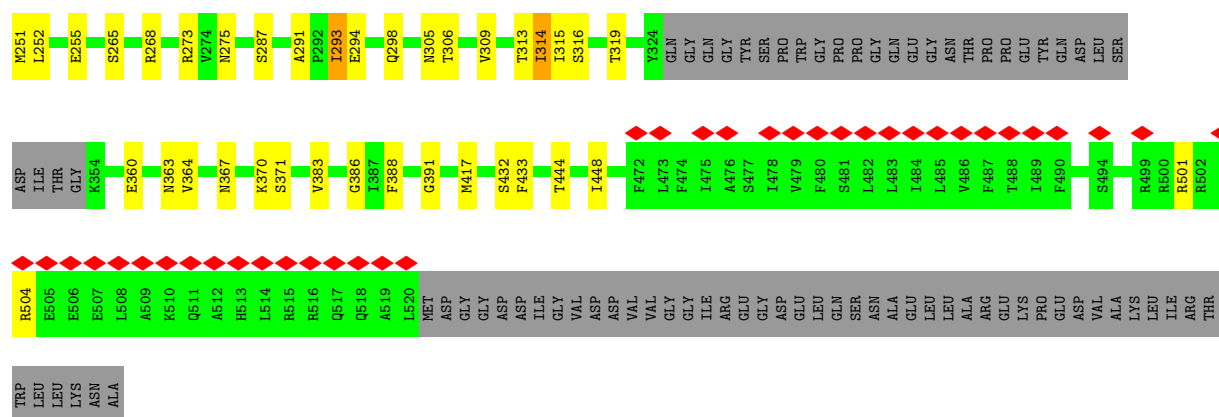


• Molecule 1: Flagellar M-ring protein

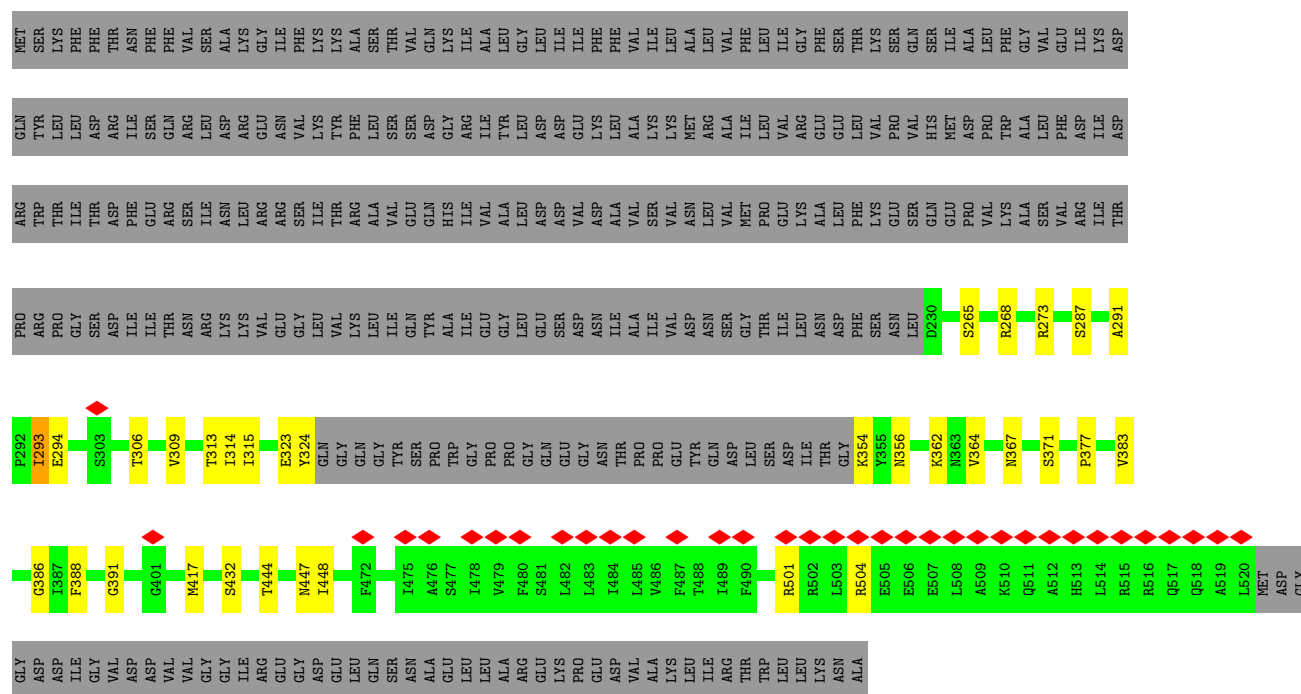
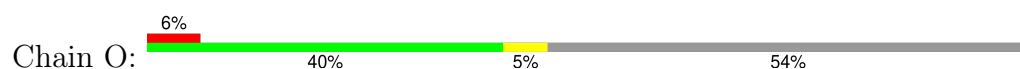


• Molecule 1: Flagellar M-ring protein

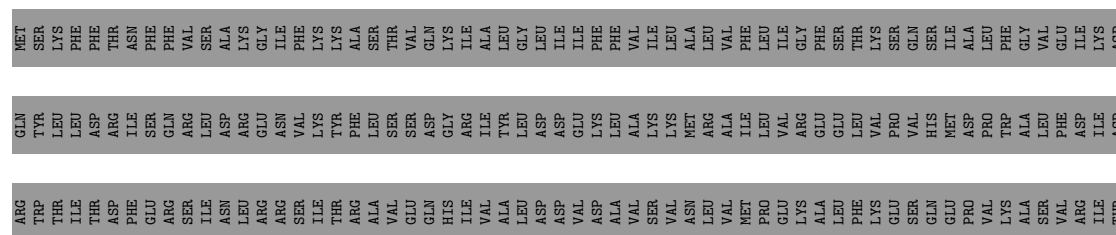
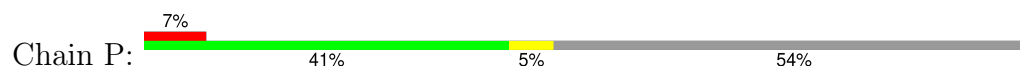


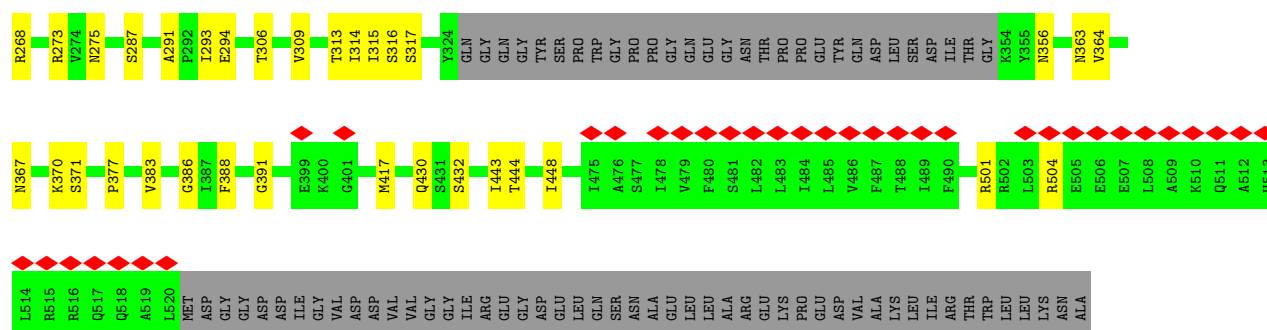


• Molecule 1: Flagellar M-ring protein

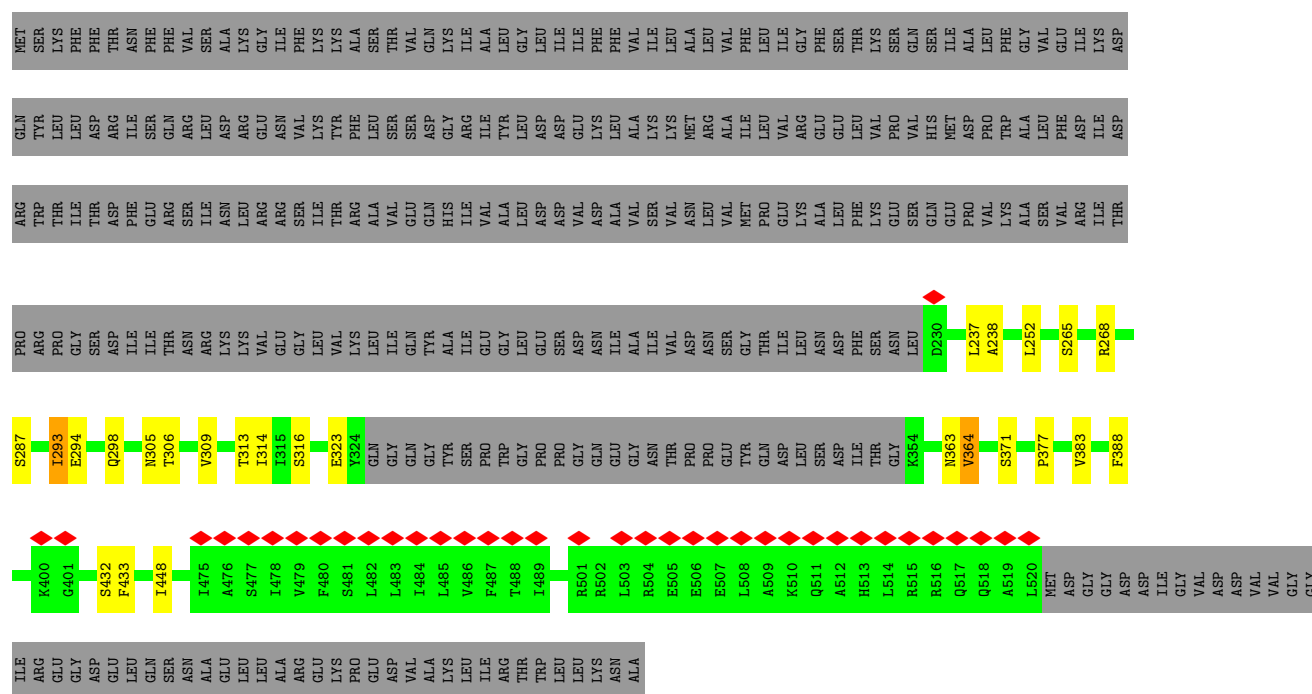


• Molecule 1: Flagellar M-ring protein

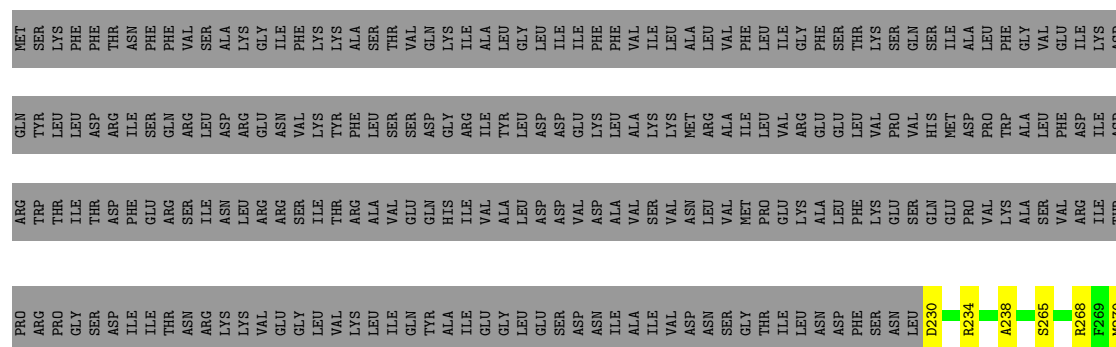
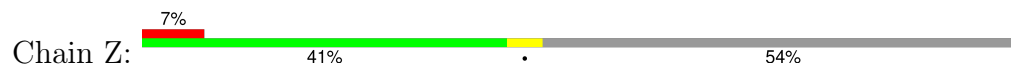


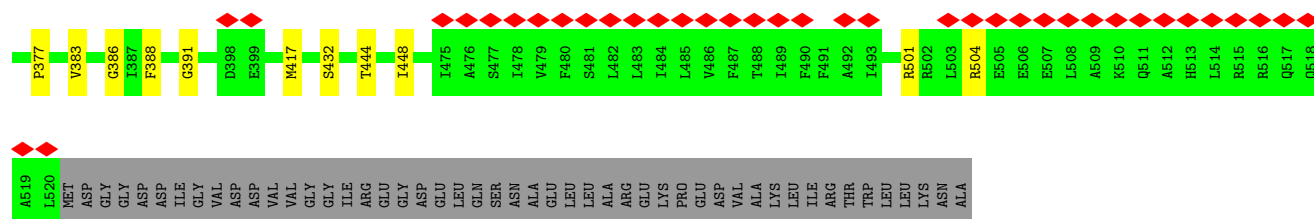


• Molecule 1: Flagellar M-ring protein

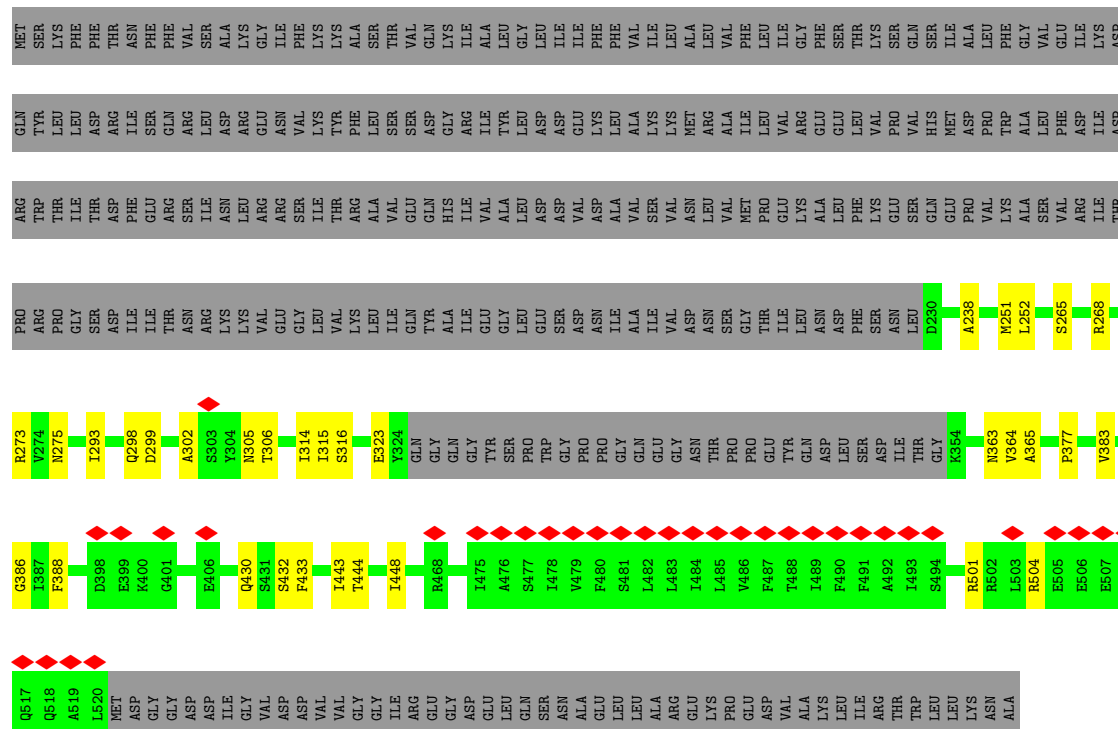
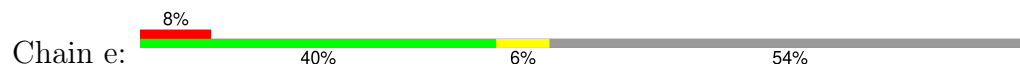


• Molecule 1: Flagellar M-ring protein

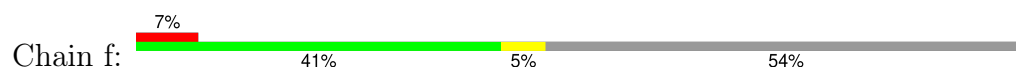


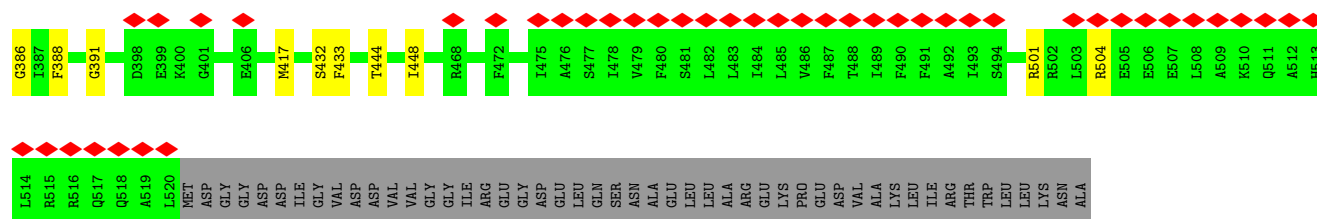


• Molecule 1: Flagellar M-ring protein

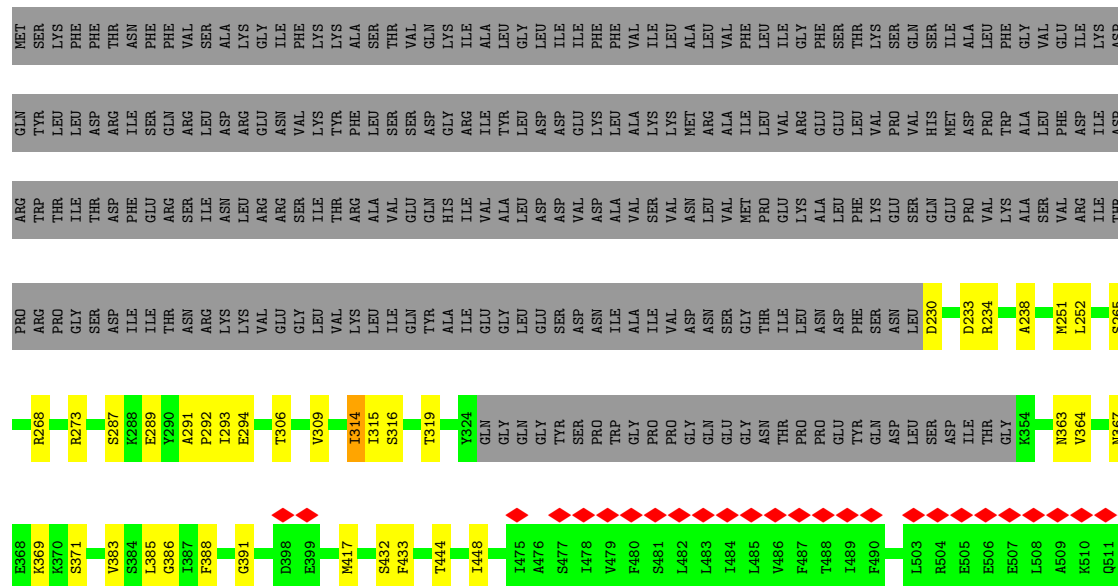
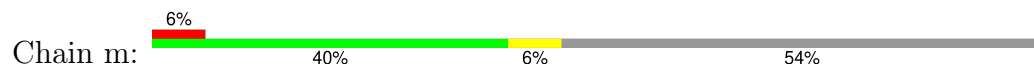


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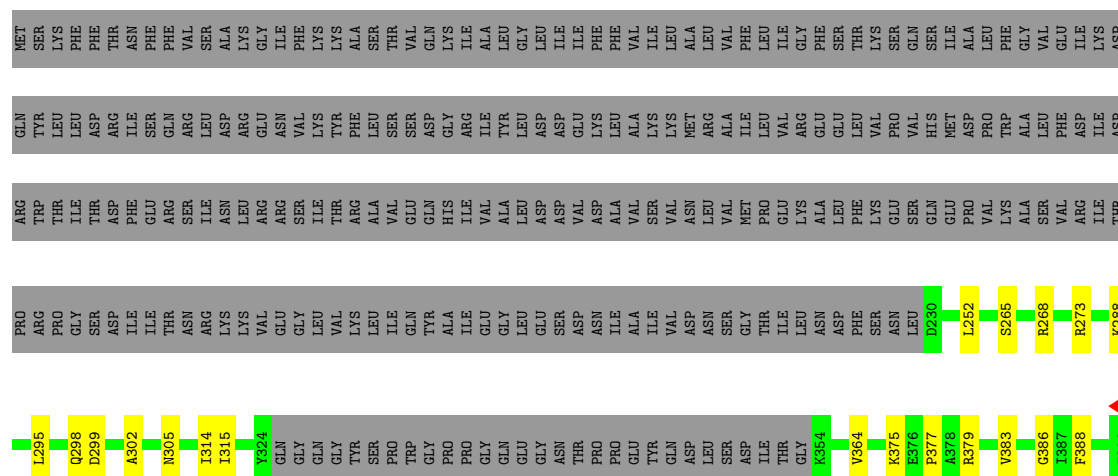
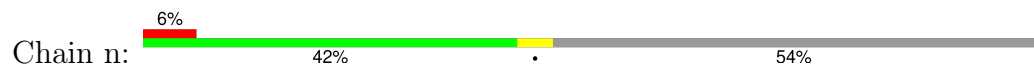


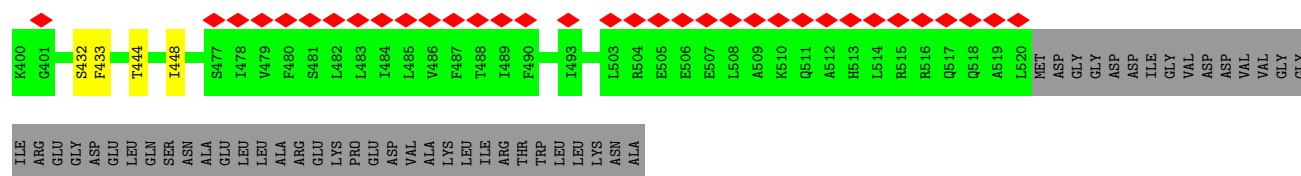


• Molecule 1: Flagellar M-ring protein

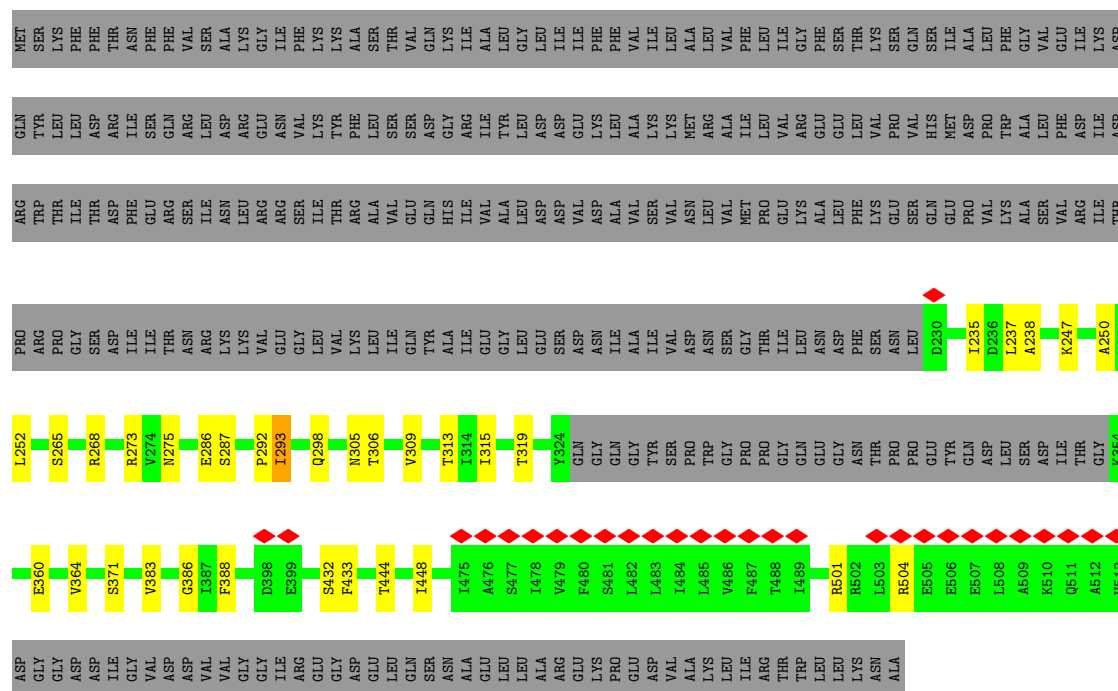
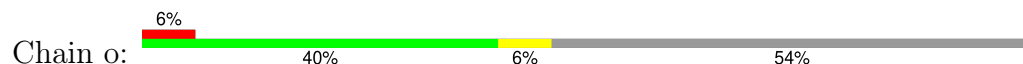


• Molecule 1: Flagellar M-ring protein

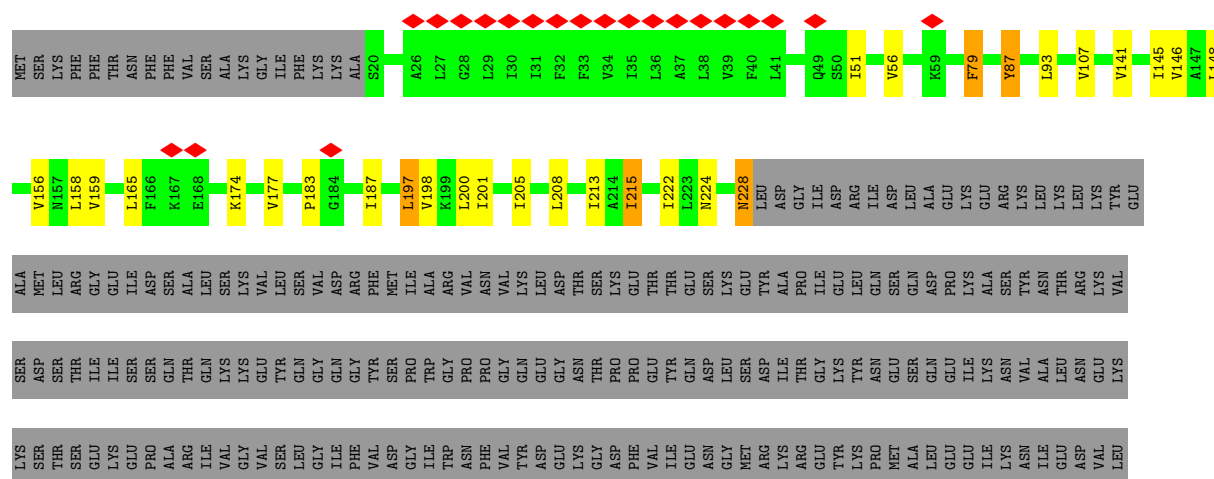




• Molecule 1: Flagellar M-ring protein

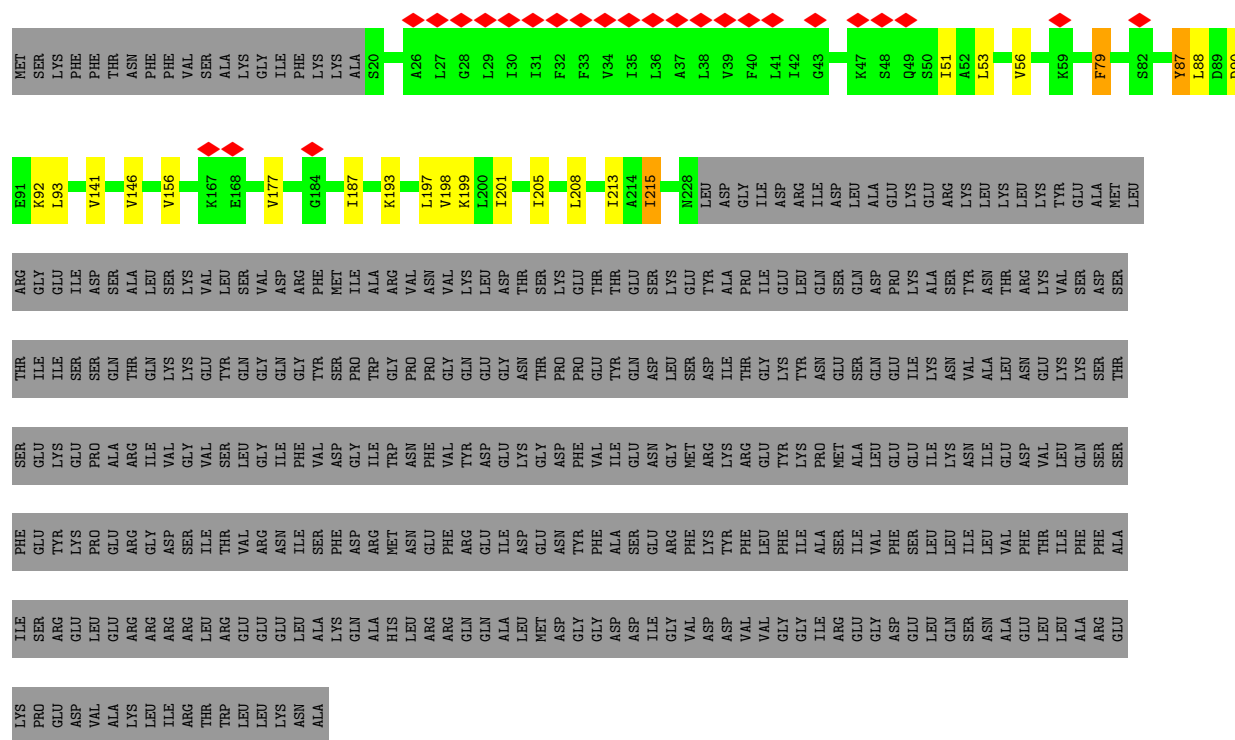


• Molecule 1: Flagellar M-ring protein



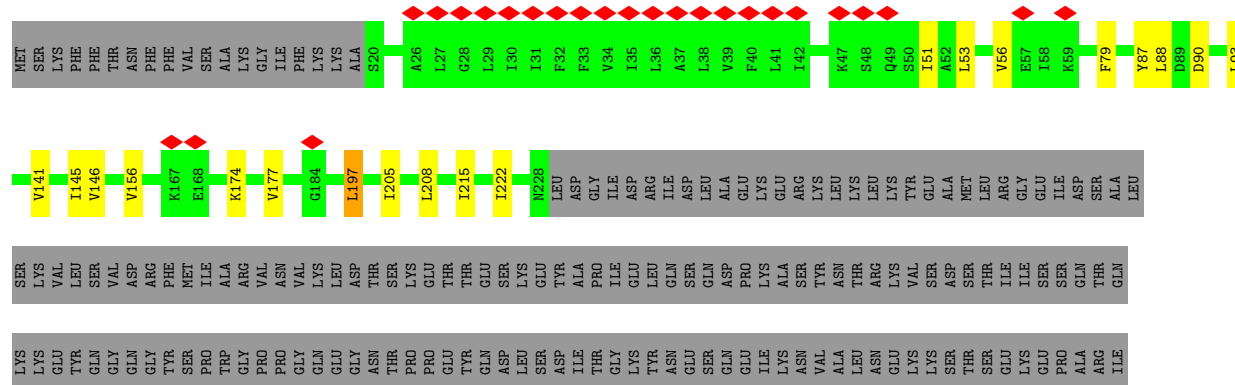
- Molecule 1: Flagellar M-ring protein

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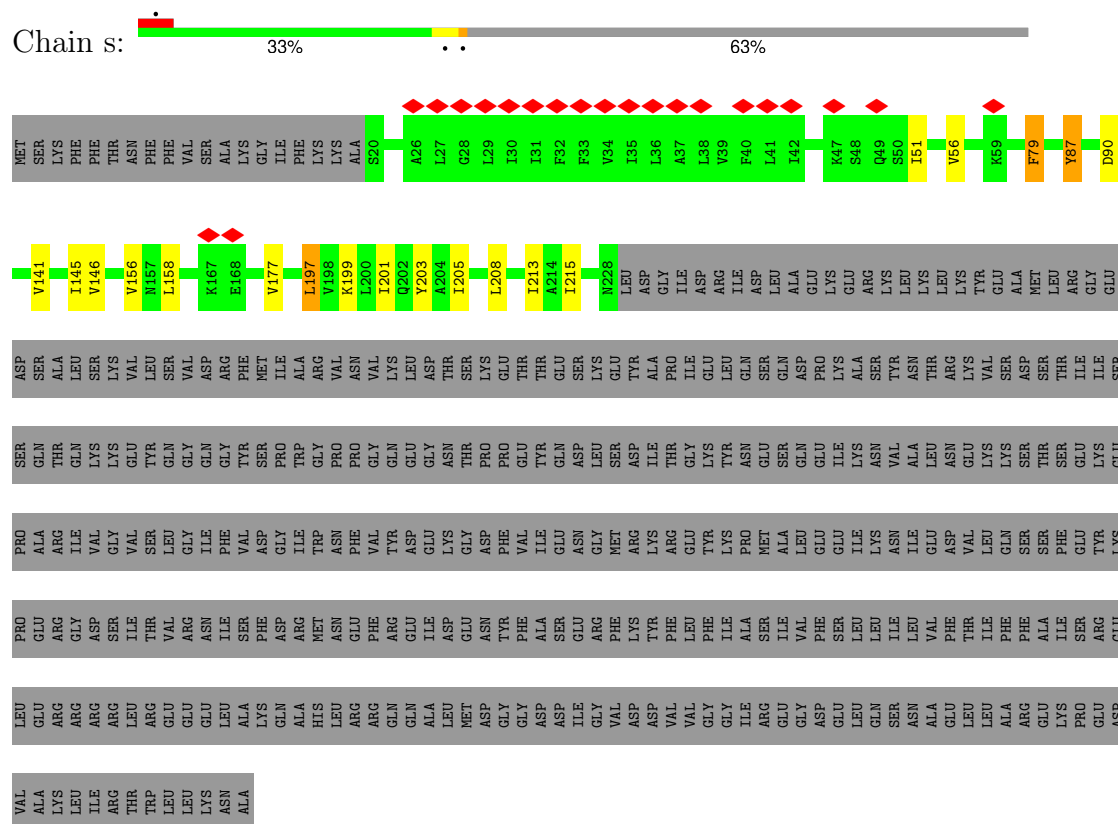
- Molecule 1: Flagellar M-ring protein

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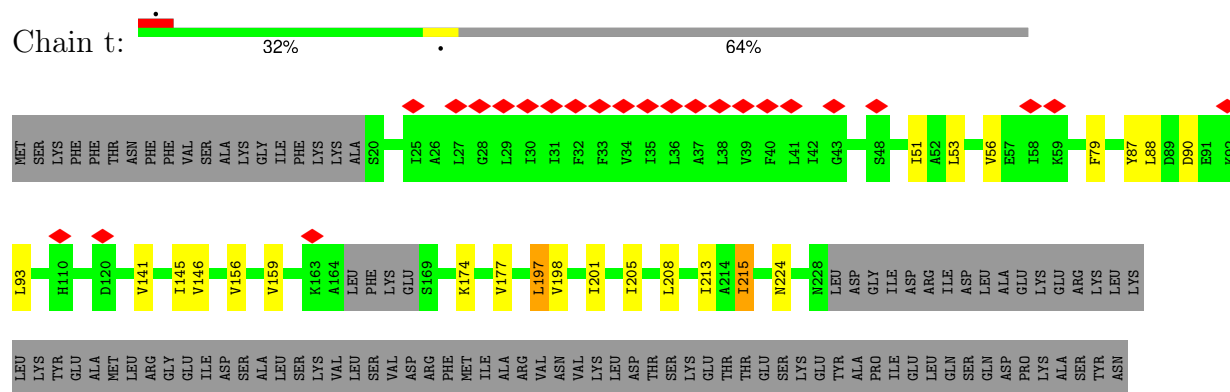


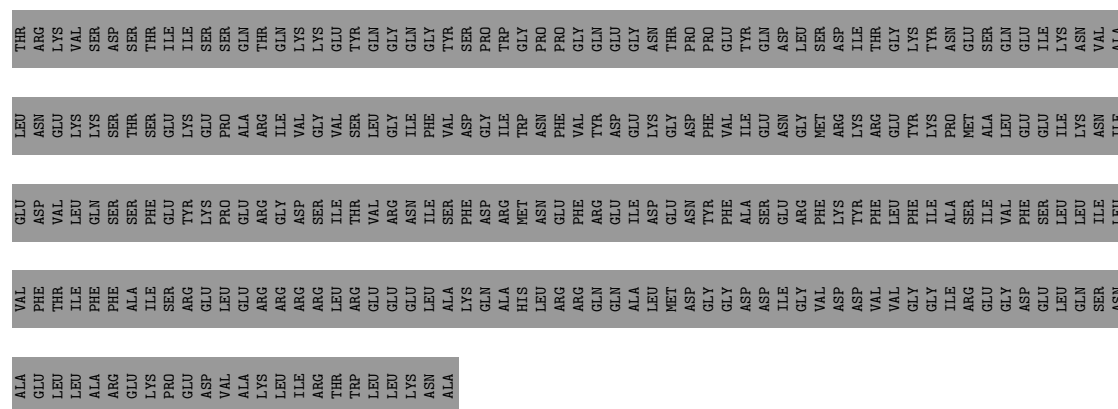
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TRP	ARG	GLU	VAL	THR	VAL
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LEU	GLU	LEU	ASN	GLY	LEU
LYS	GLU	LEU	ILE	ASN	GLY
ALA	ALA	ALA	SER	VAL	PHE
	LYS	LYS	PHE	ASP	ASP
	GLN	ALA	ASP	GLY	GLY
	ALA	ALA	ARG	ILE	ILE
	HIS	LEU	MET	TRP	TRP
	LEU	LEU	ASN	ASN	ASN
	ARG	ARG	GLU	PHE	PHE
	GLN	GLN	THR	VAL	VAL
	GLN	ALA	GLU	ARG	TYR
	ALA	LEU	ILE	ASP	ASP
	LEU	LEU	ASP	GLU	GLU
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	ASP	VAL	LYS	THR	VAL
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	GLY	GLY	LEU	LEU	LEU
	ILE	ILE	ILE	ILE	ILE
	ARG	ARG	ALA	ALA	ALA
	GLU	GLY	VAL	VAL	LEU
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	GLU	GLU	SER	GLU	GLU
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	GLN	GLN	LEU	LYS	LYS
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	GLU	GLU	THR	VAL	VAL
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	GLU	GLU	ARG	GLY	GLY
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- Molecule 1: Flagellar M-ring protein

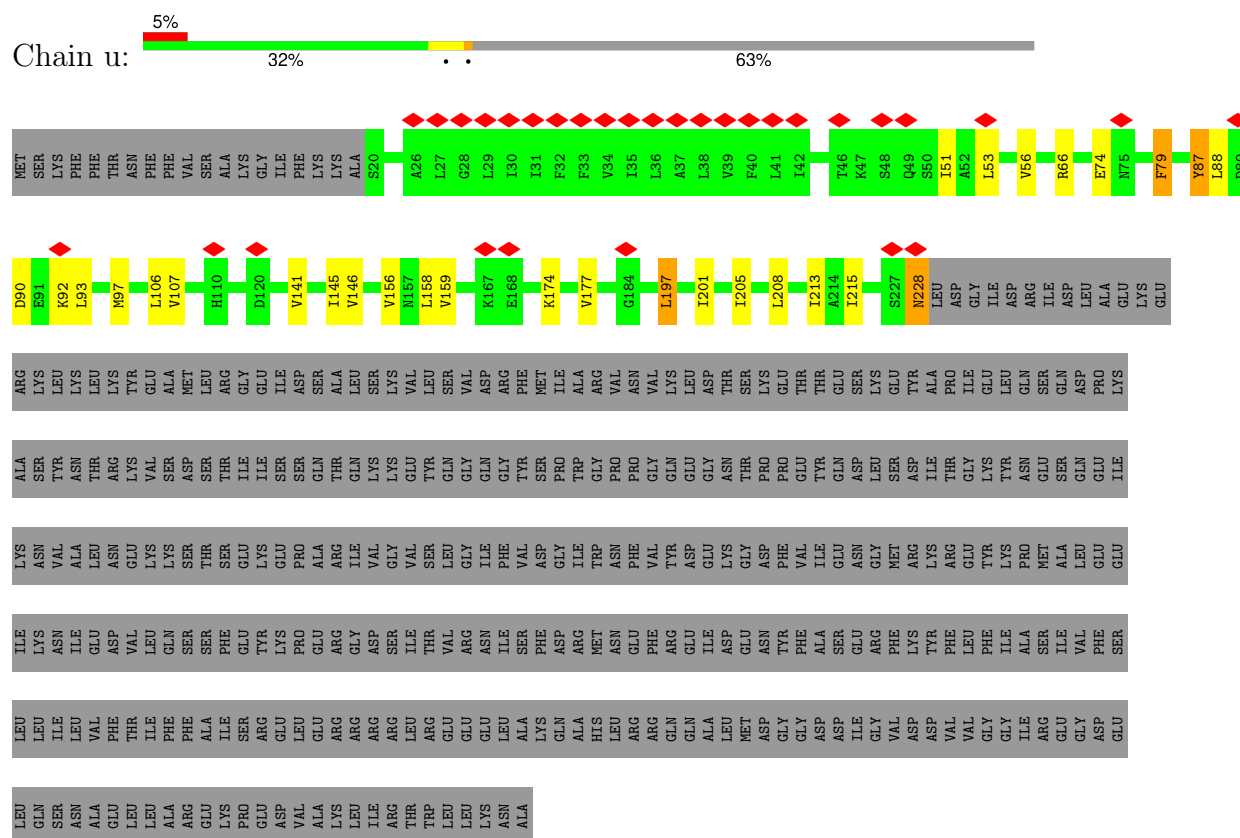


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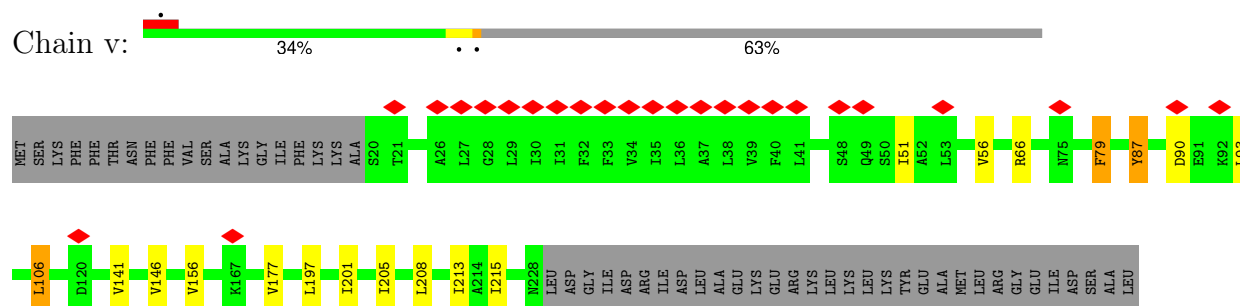




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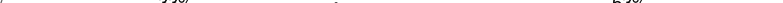


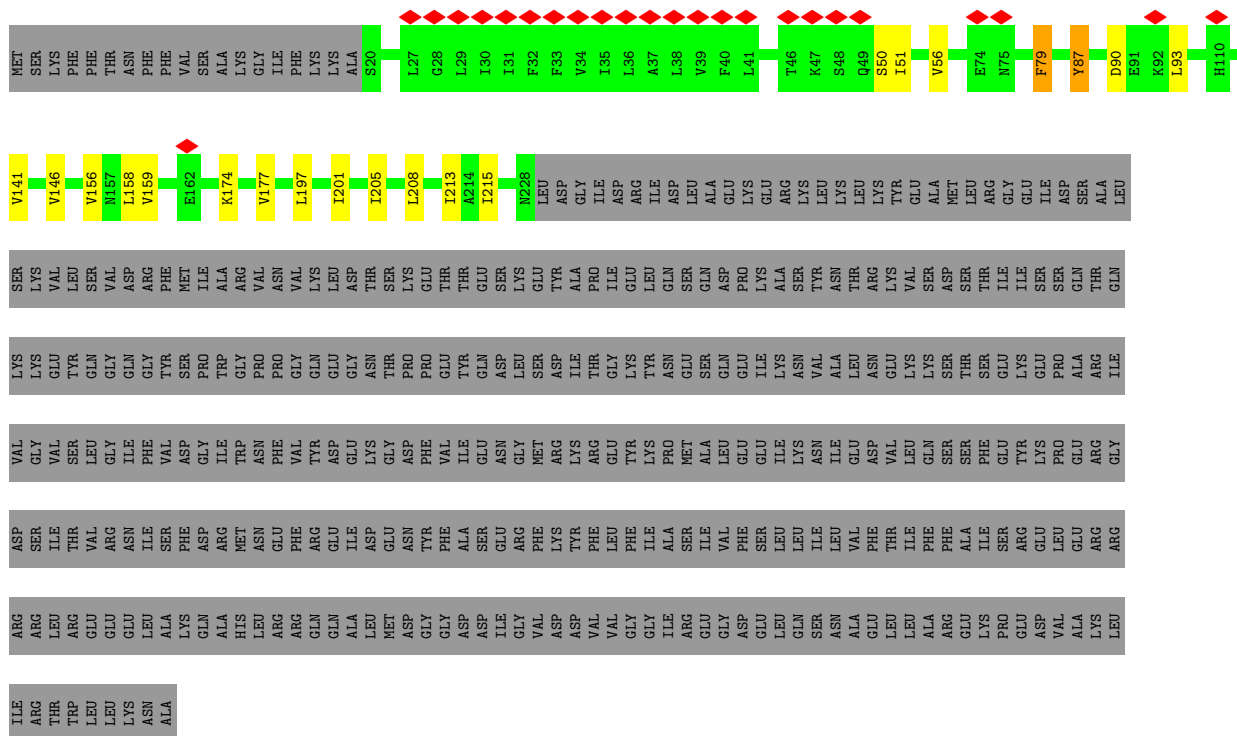
- Molecule 1: Flagellar M-ring protein



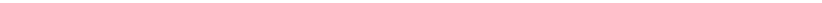
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LEU	ARG	VAL	LEU	GLN	SER
LEU	GLU	ARG	GLY	GLY	VAL
LYS	GLU	ASN	ILE	GLN	ASP
ALA	LEU	ILE	PHE	GLY	ARG
	ALA	PHE	VAL	TYR	MET
	LYS	ASP	GLY	PRO	ILE
	GLN	ASP	GLY	TRP	ALA
	HIS	MET	TRP	GLY	ARG
	LEU	ASN	ASN	PRO	VAL
	ARG	GLU	PHE	PRO	VAL
	ARG	PHE	VAL	GLN	VAL
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	GLY	TYR	PHE	PRO	GLU
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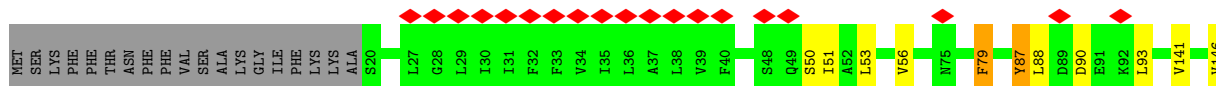
- Molecule 1: Flagellar M-ring protein

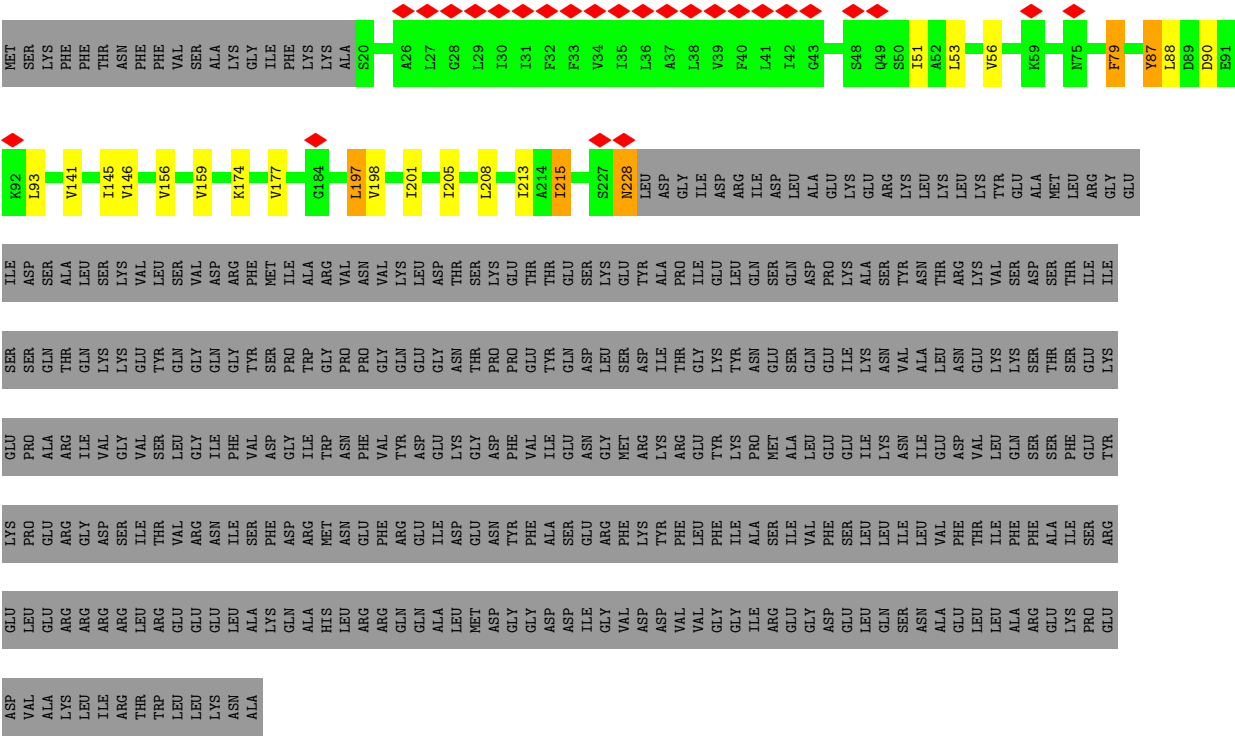
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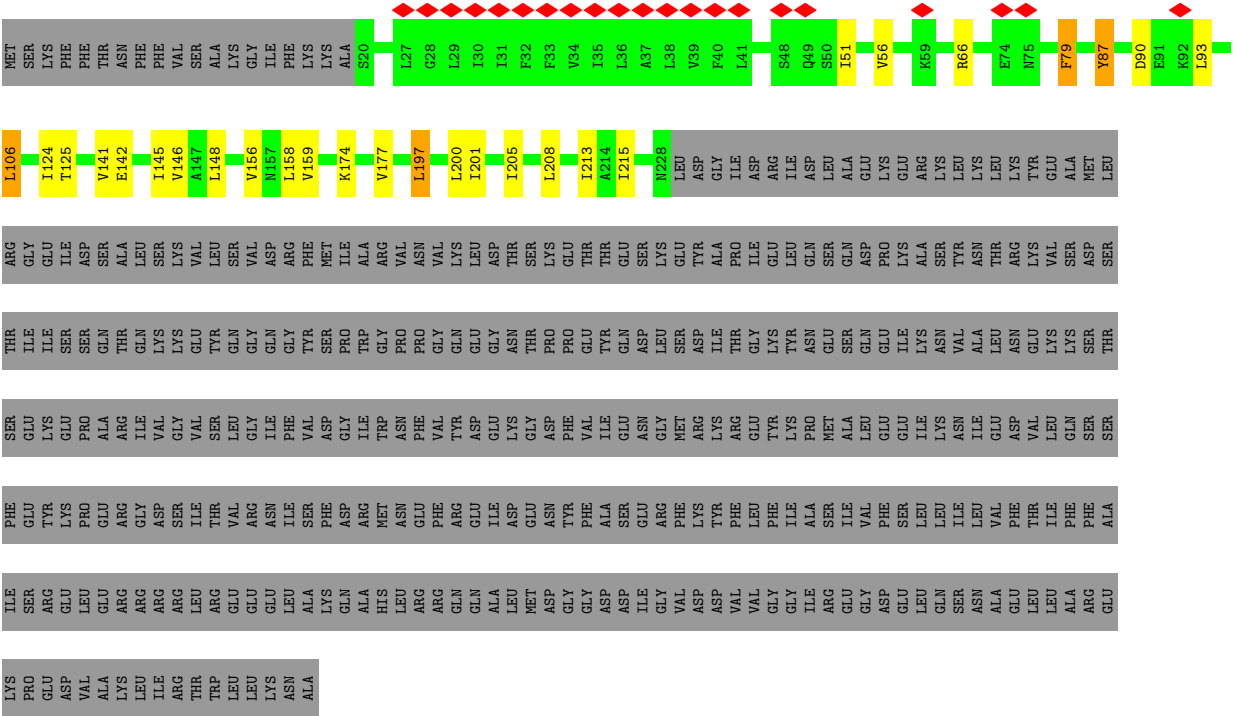
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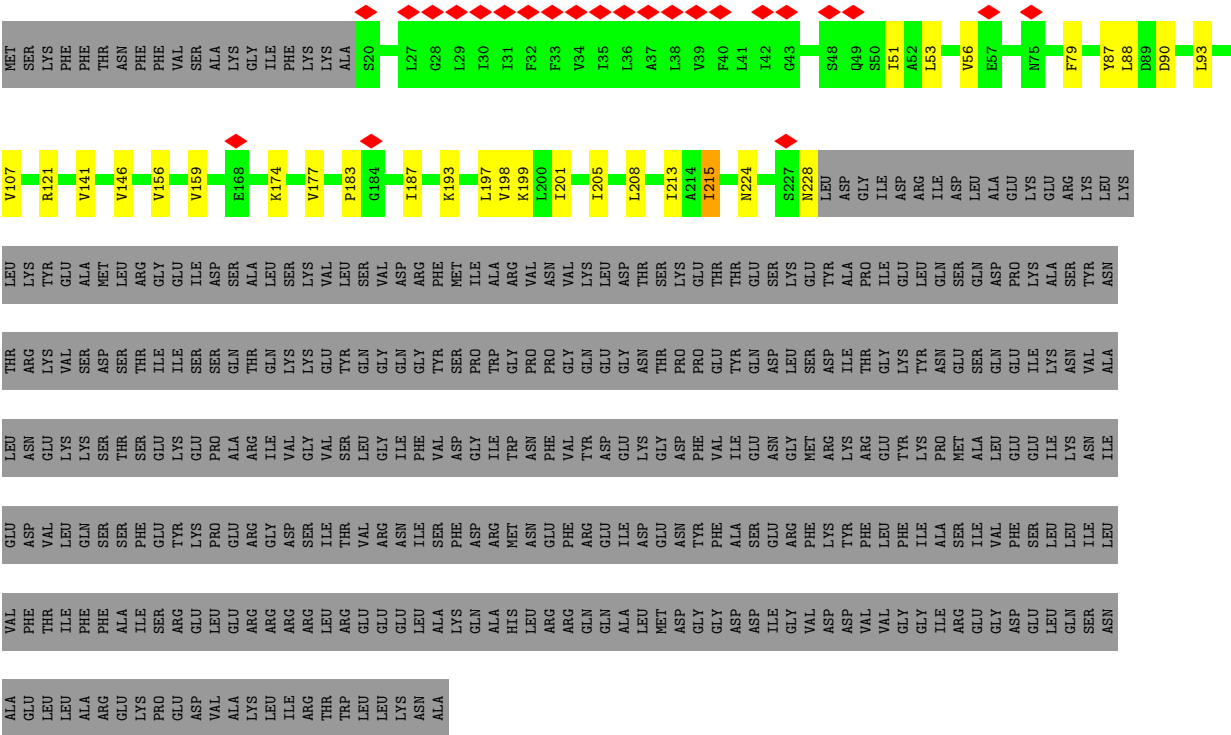


• Molecule 1: Flagellar M-ring protein

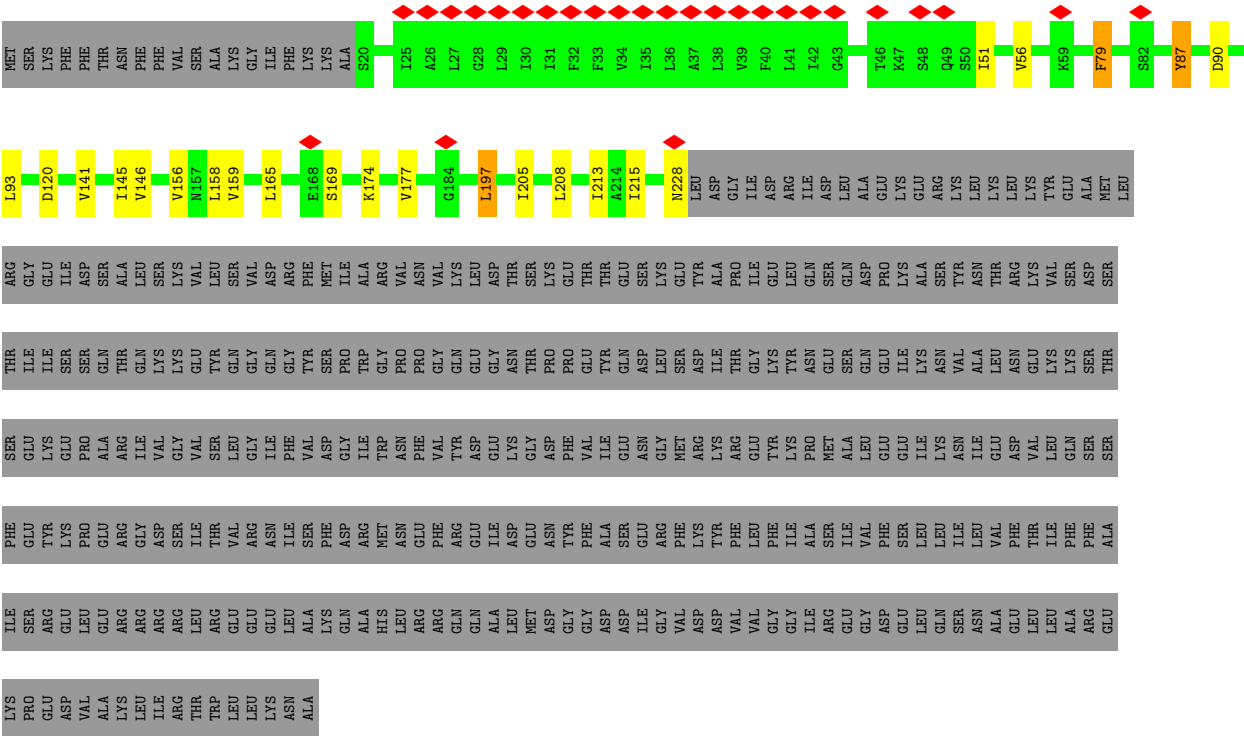


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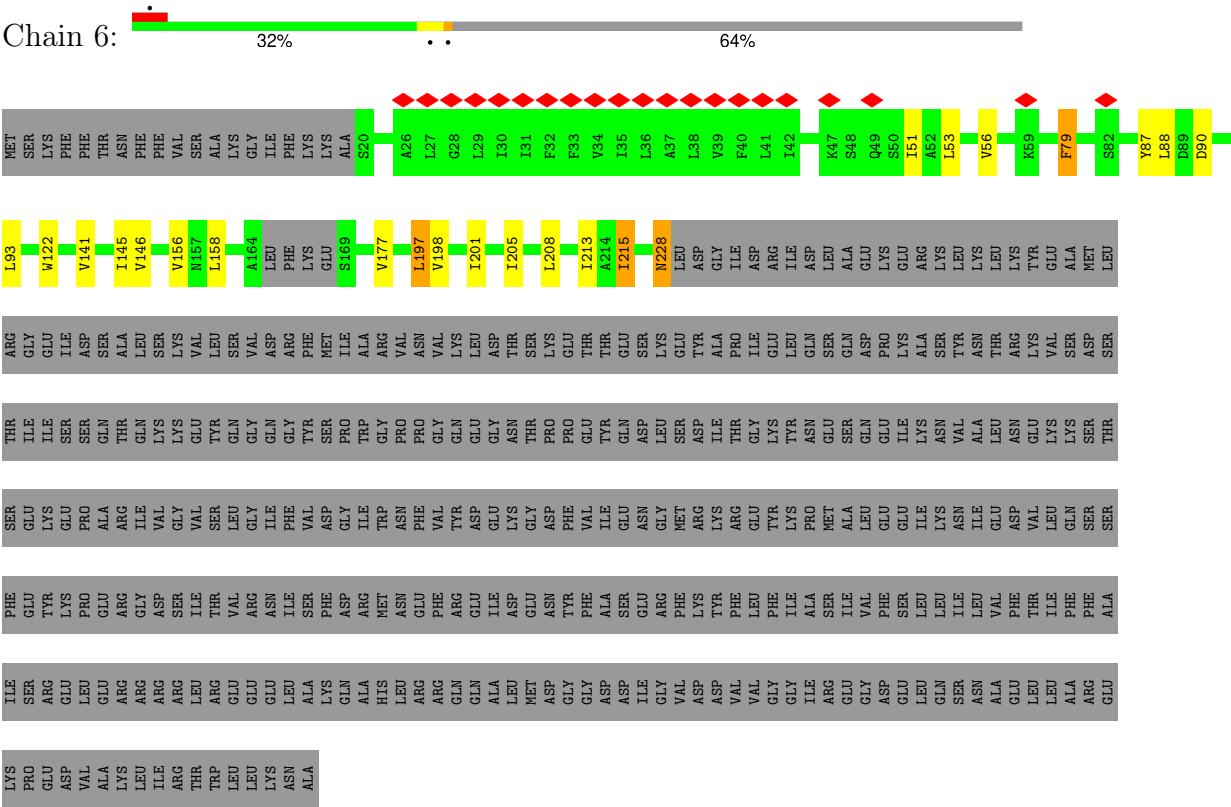




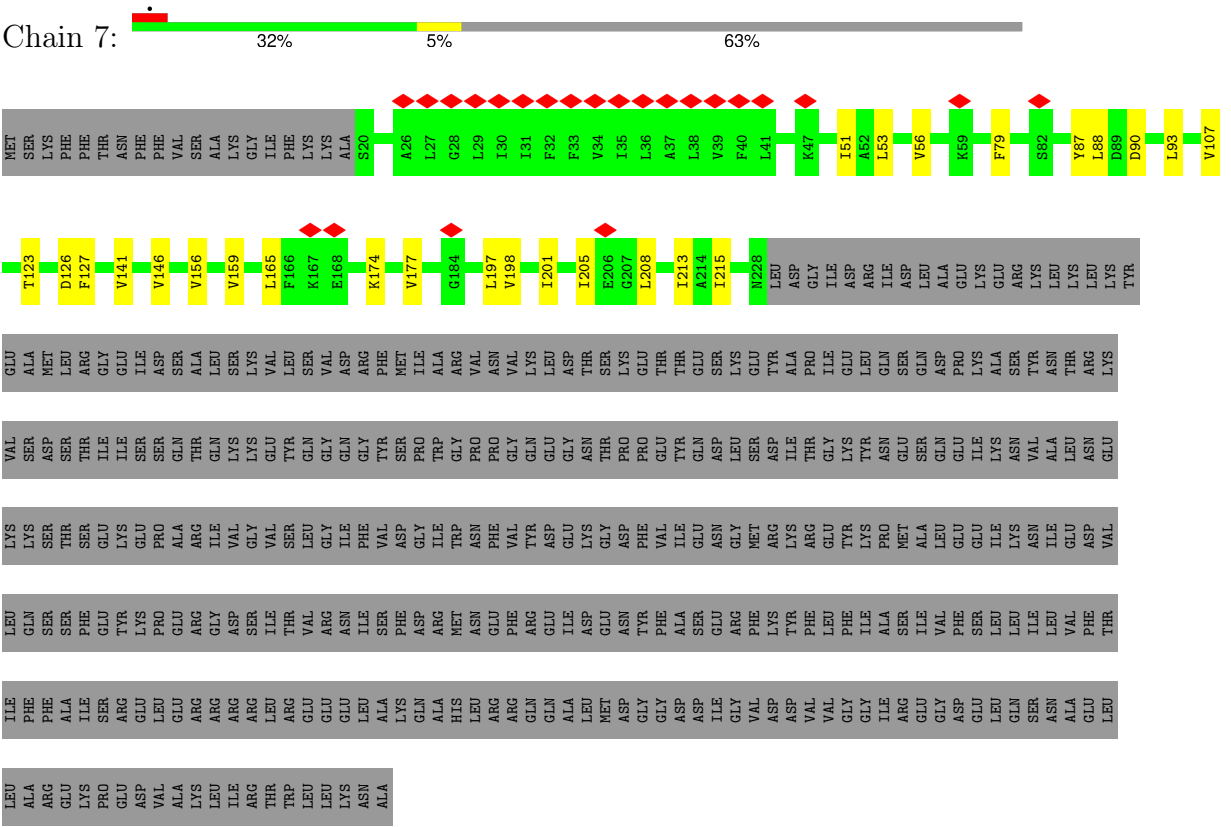
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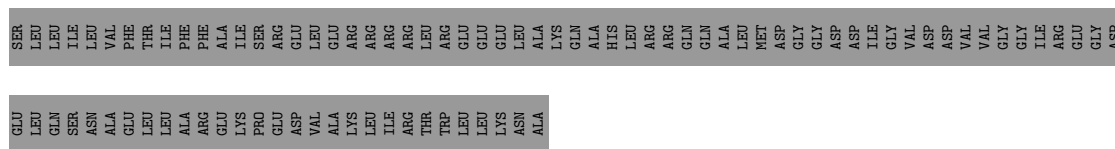


● Molecule 1: Flagellar M-ring protein

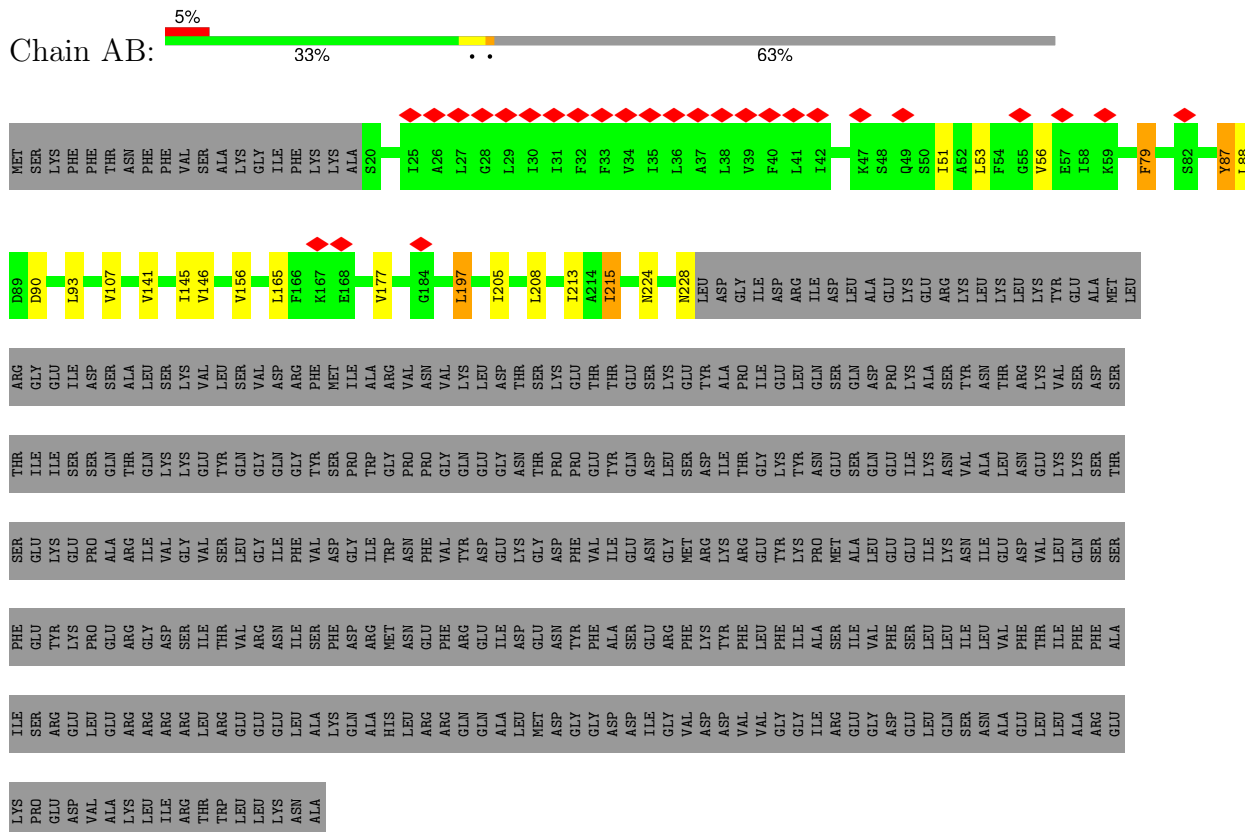


● Molecule 1: Flagellar M-ring protein

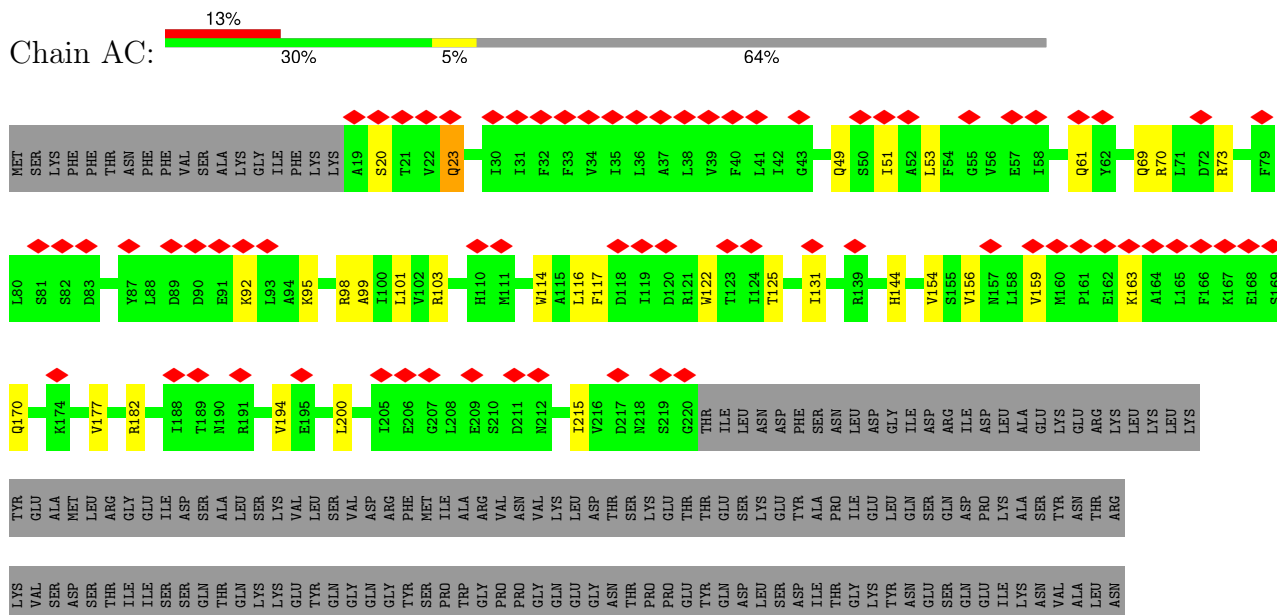


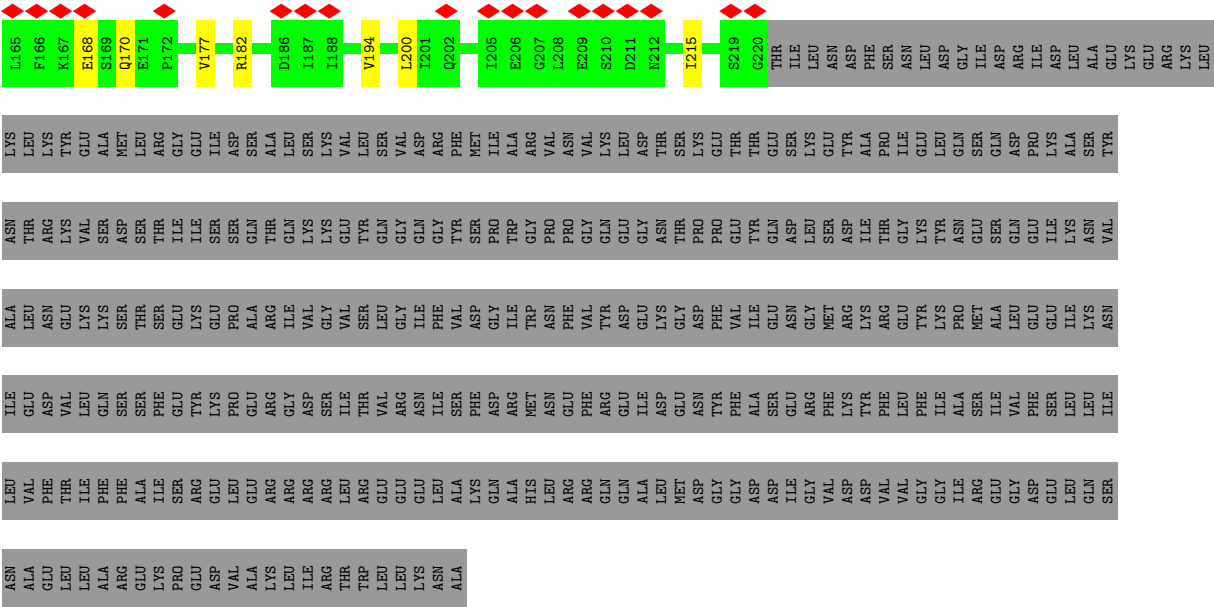


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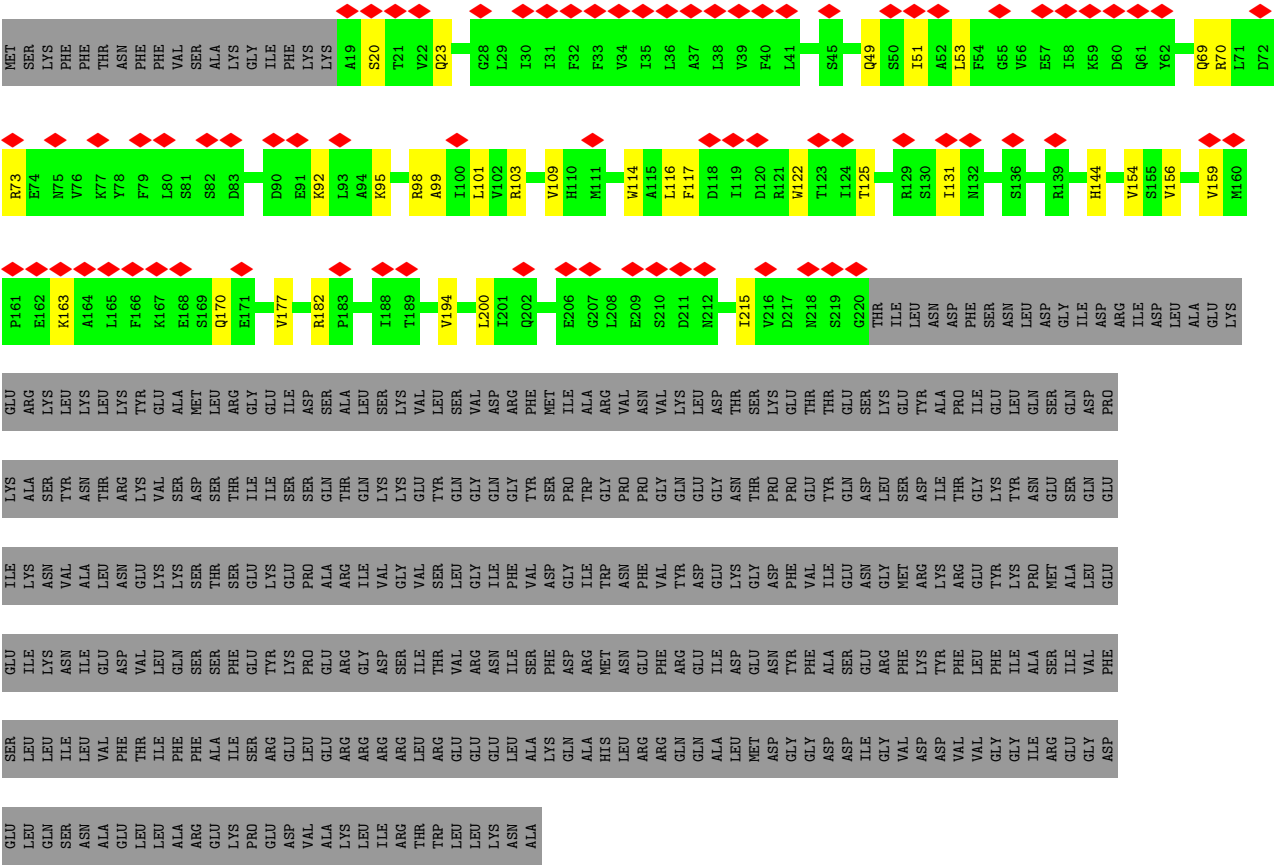


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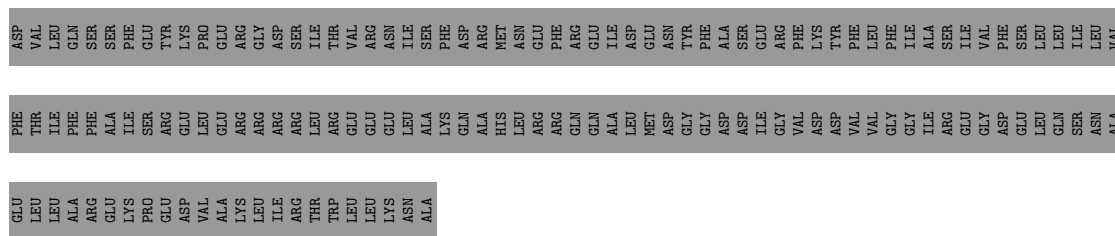


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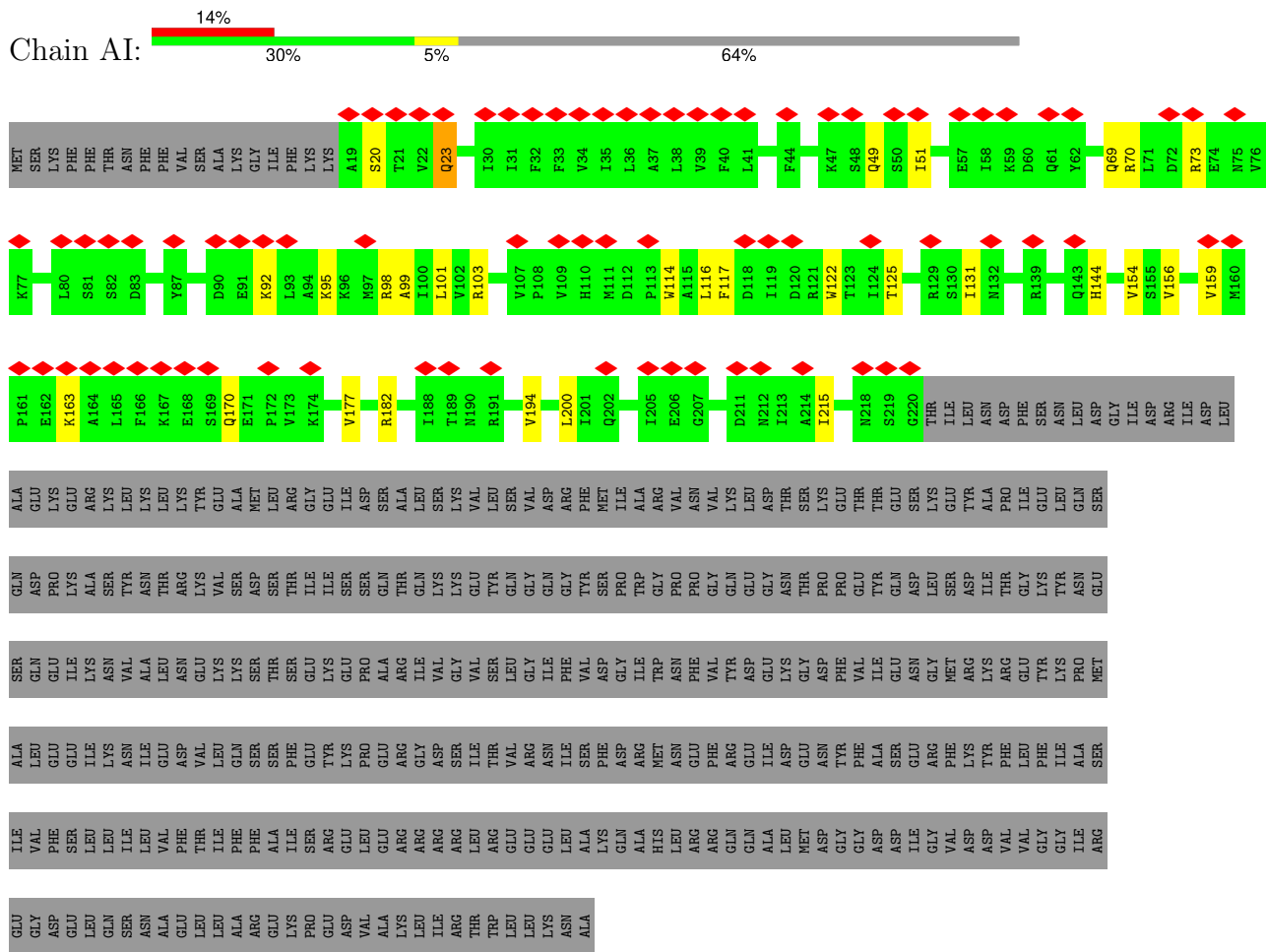


• Molecule 1: Flagellar M-ring protein

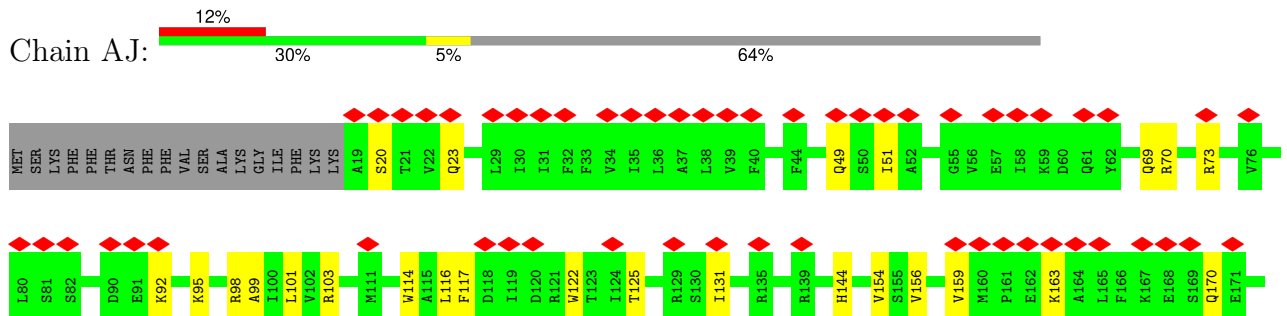


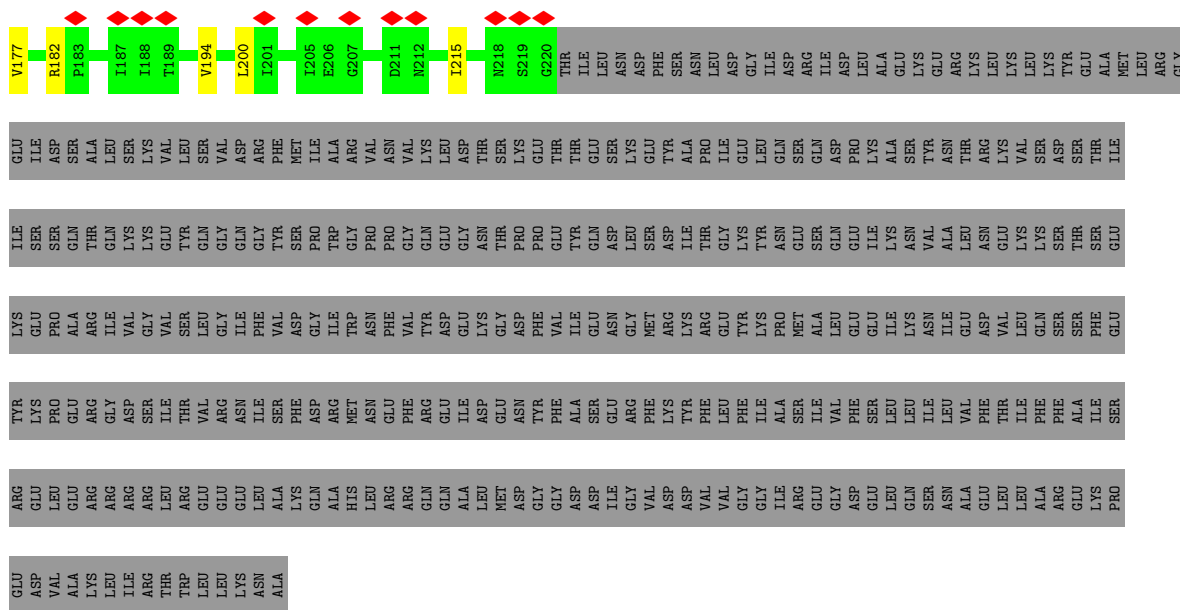


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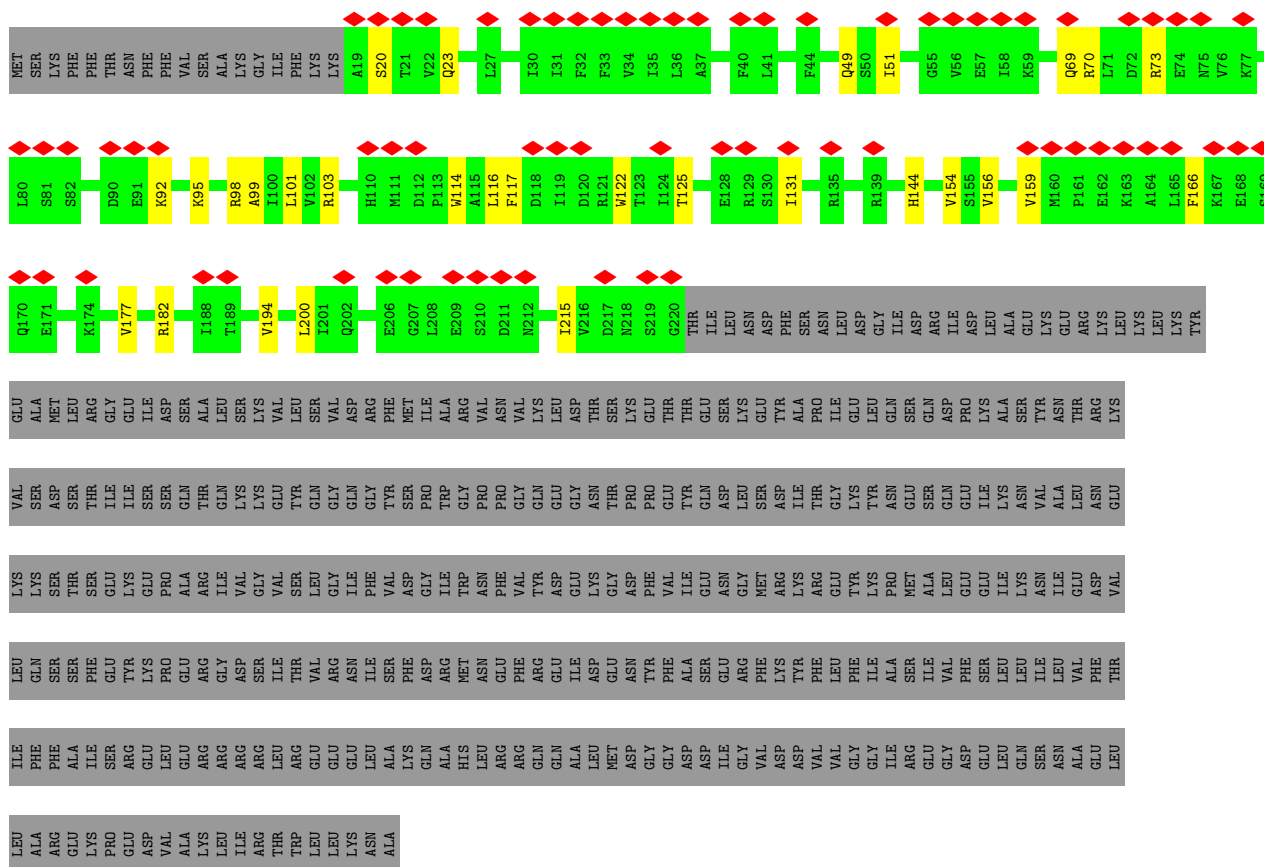


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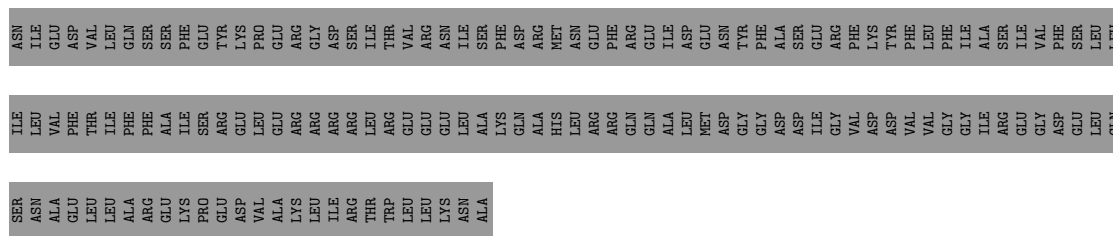


- Molecule 1: Flagellar M-ring protein

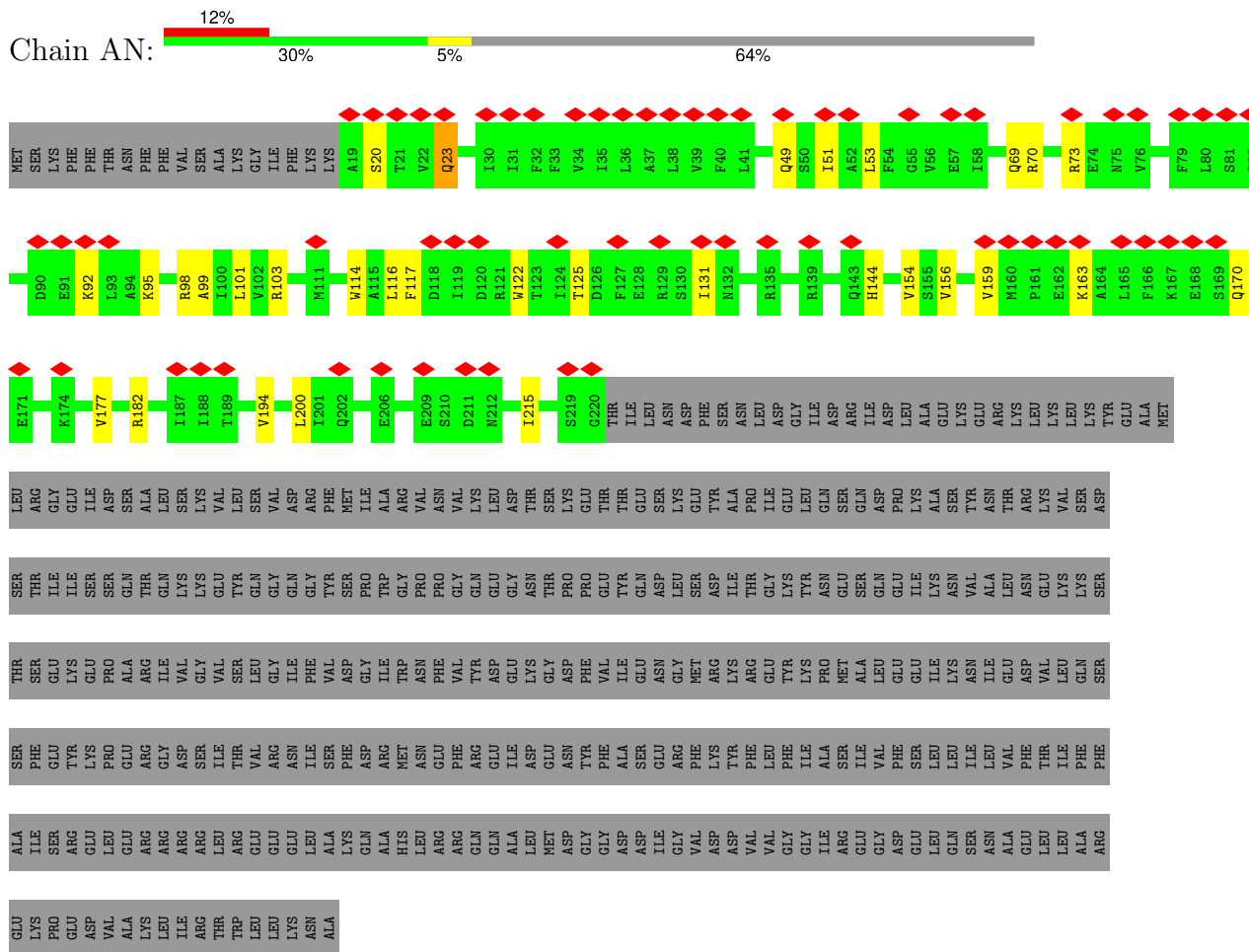


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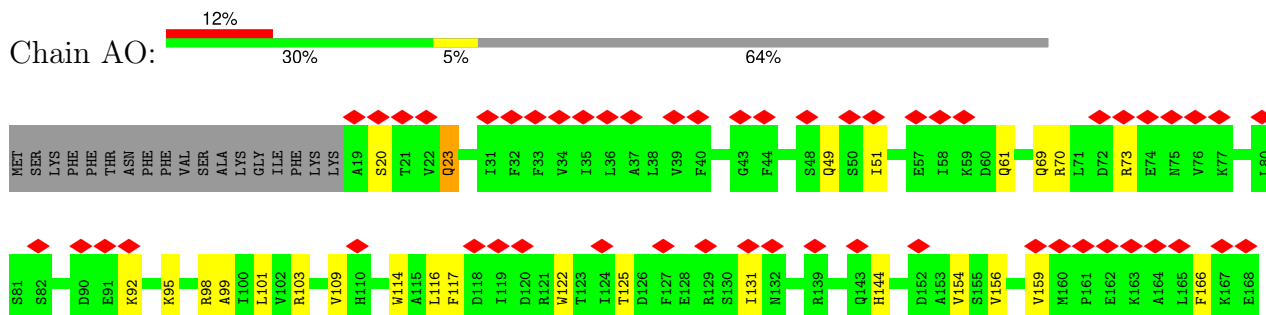


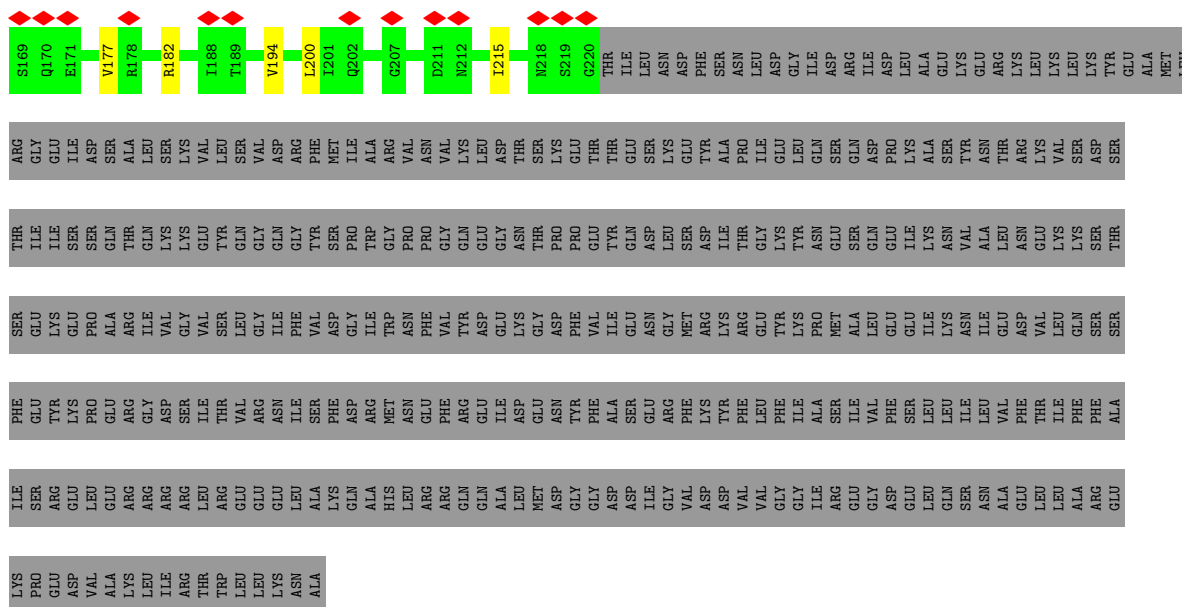


- Molecule 1: Flagellar M-ring protein

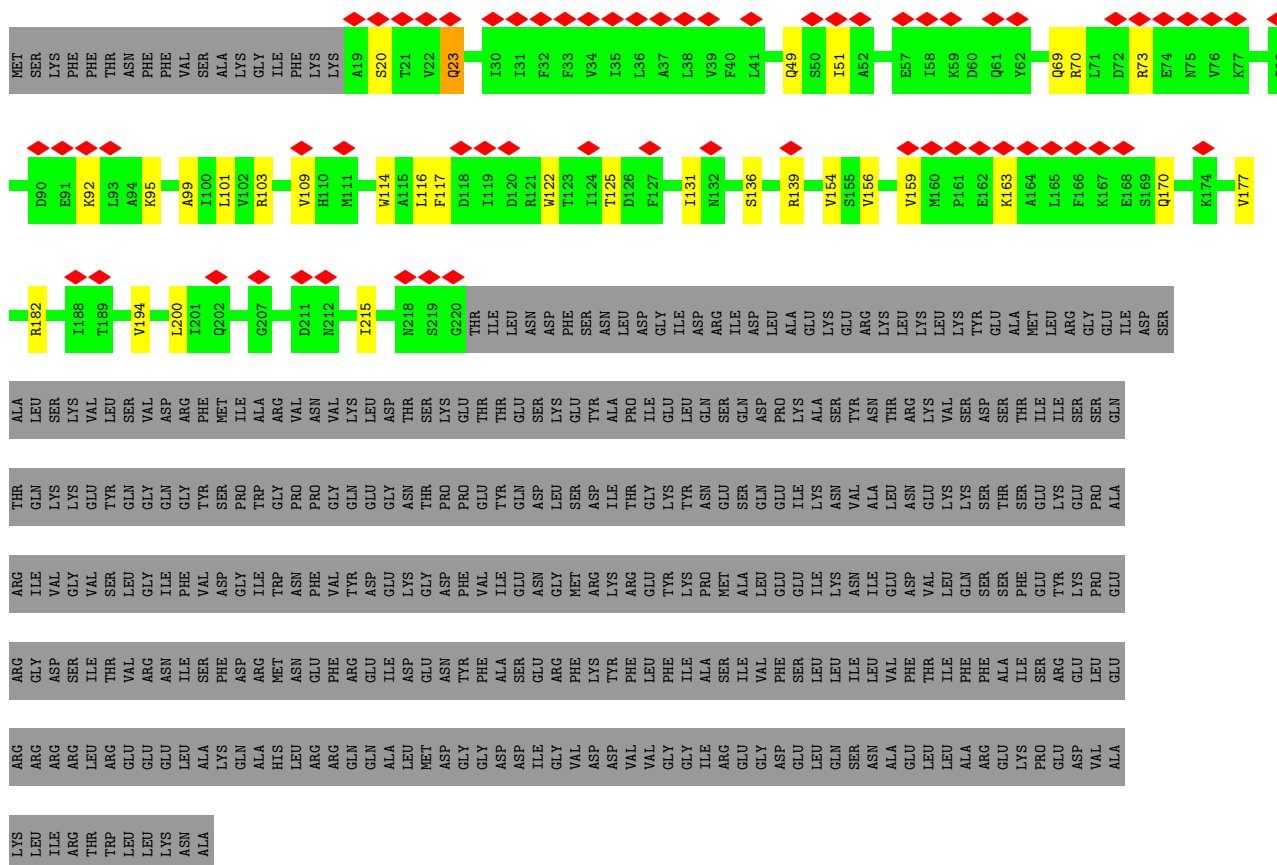


- Molecule 1: Flagellar M-ring protein

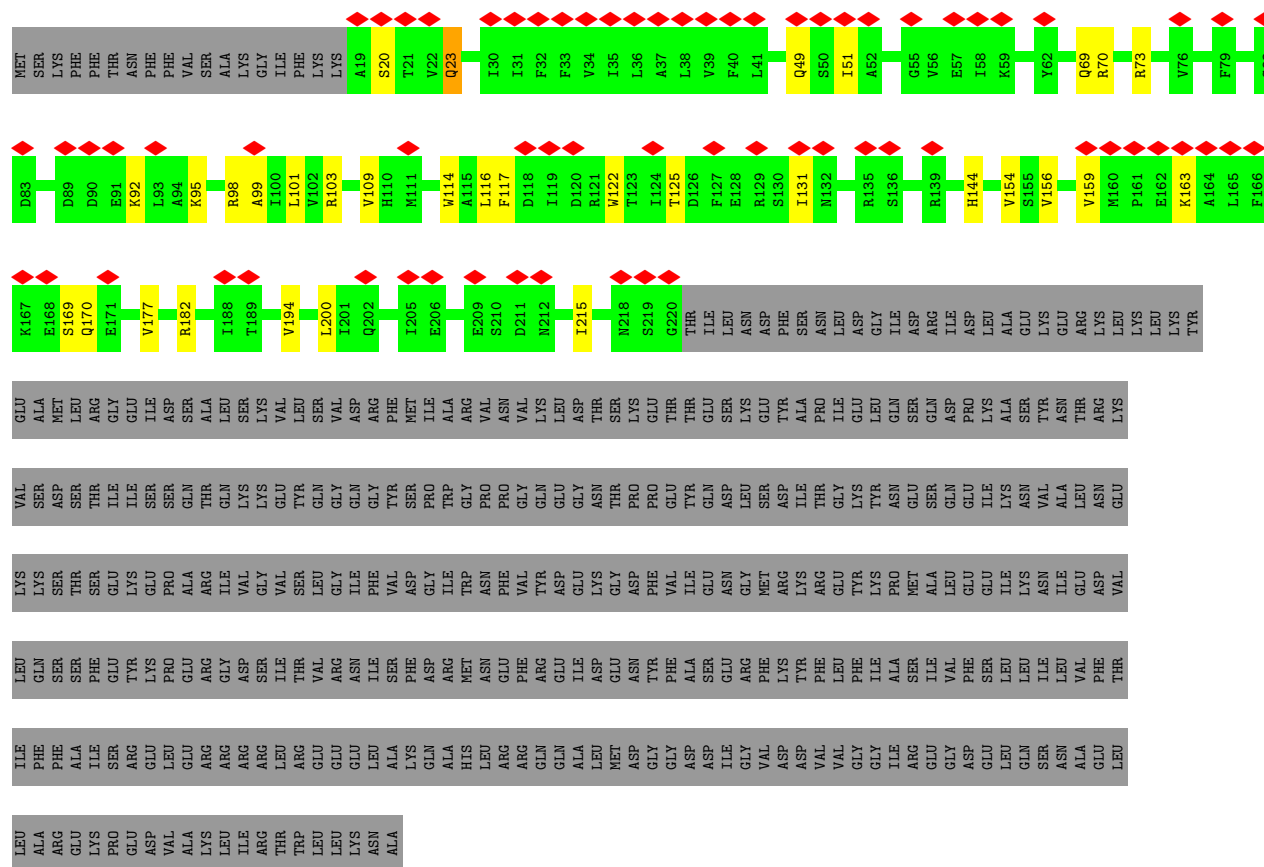




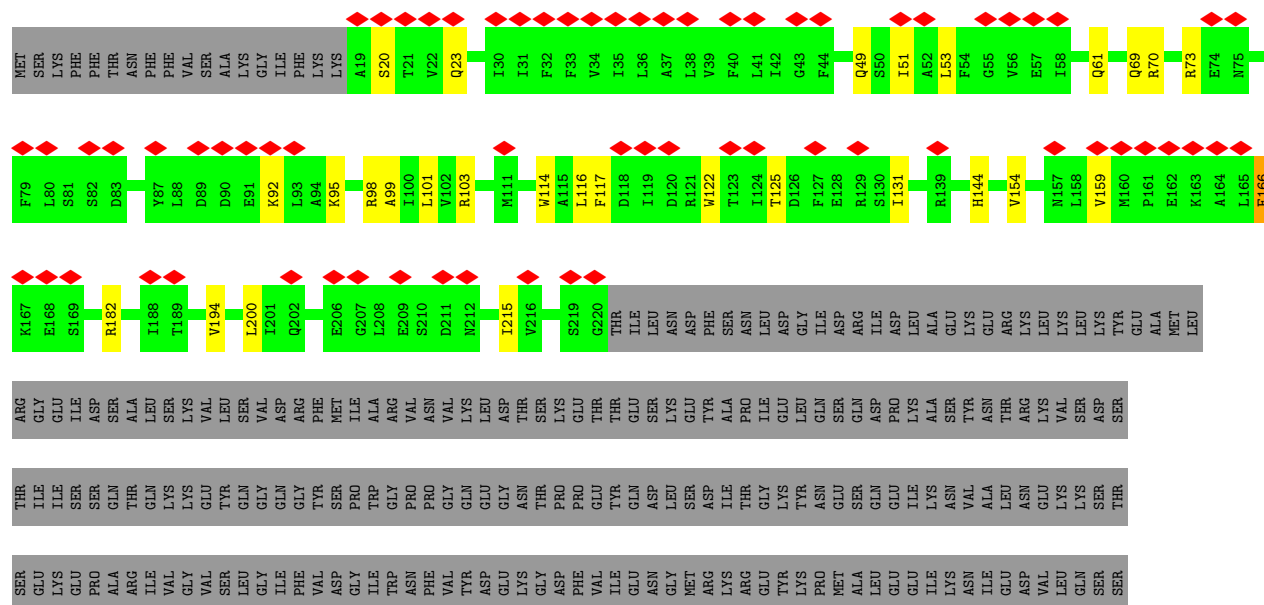
- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein

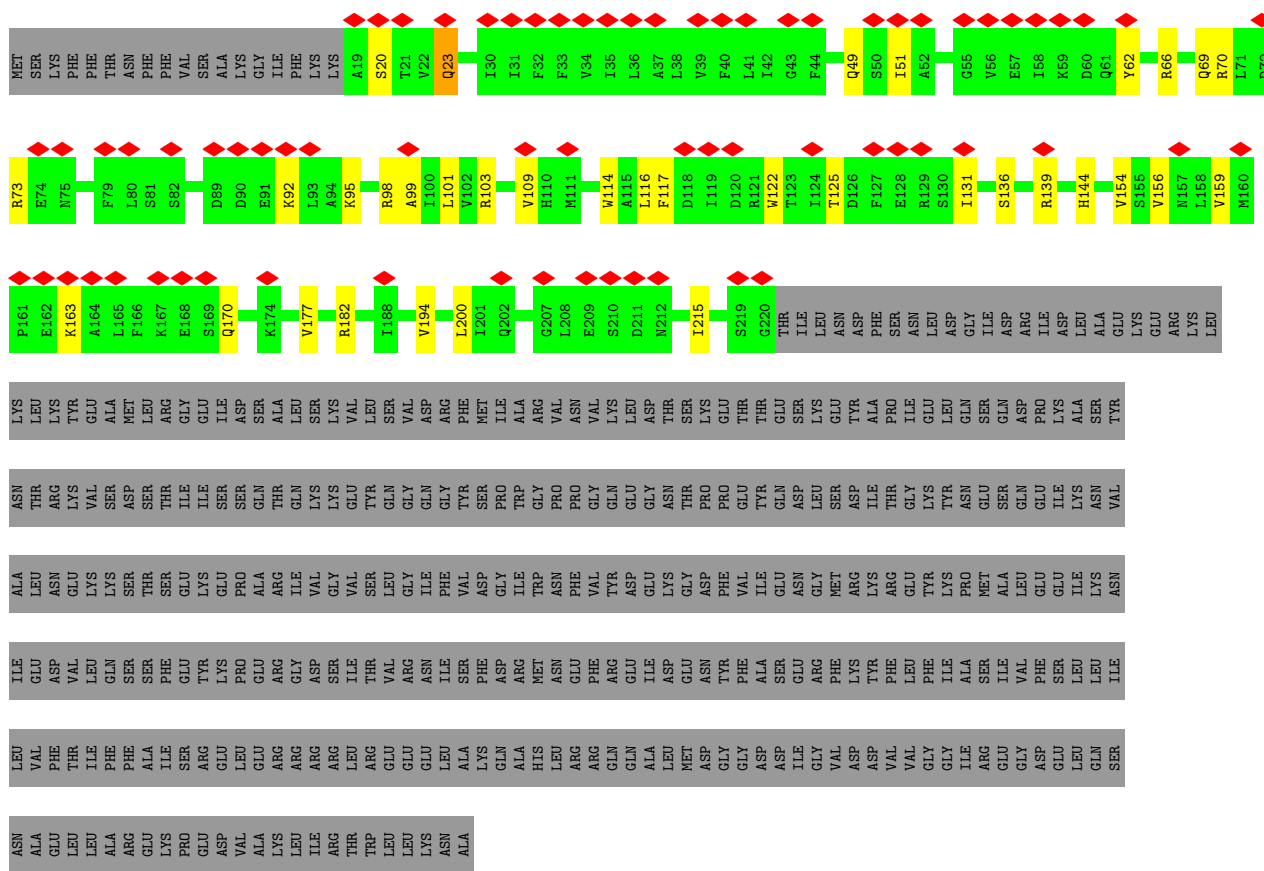


● Molecule 1: Flagellar M-ring protein

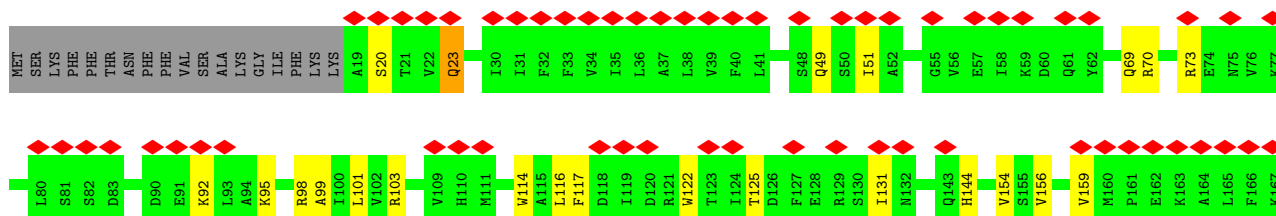


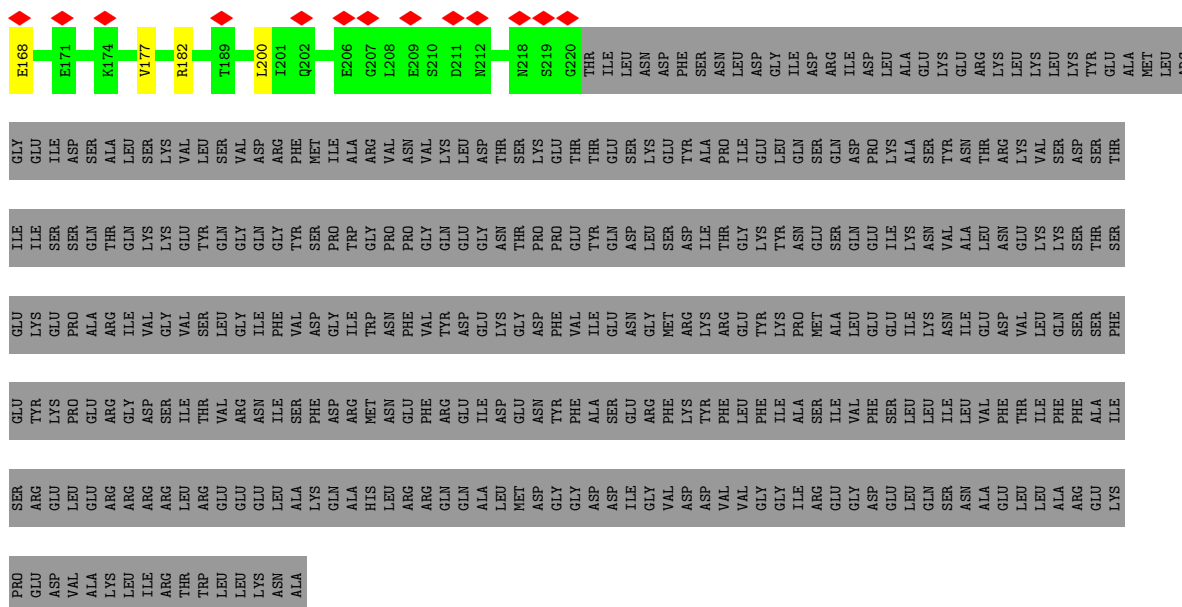
[illegible]

- Molecule 1: Flagellar M-ring protein

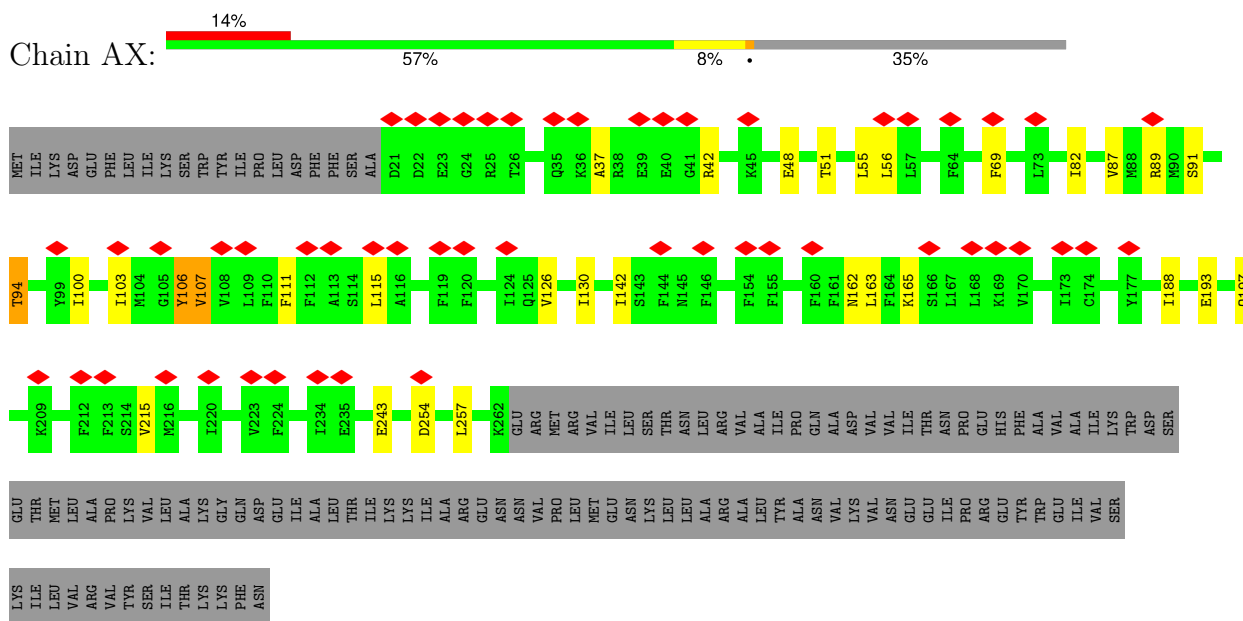


- Molecule 1: Flagellar M-ring protein

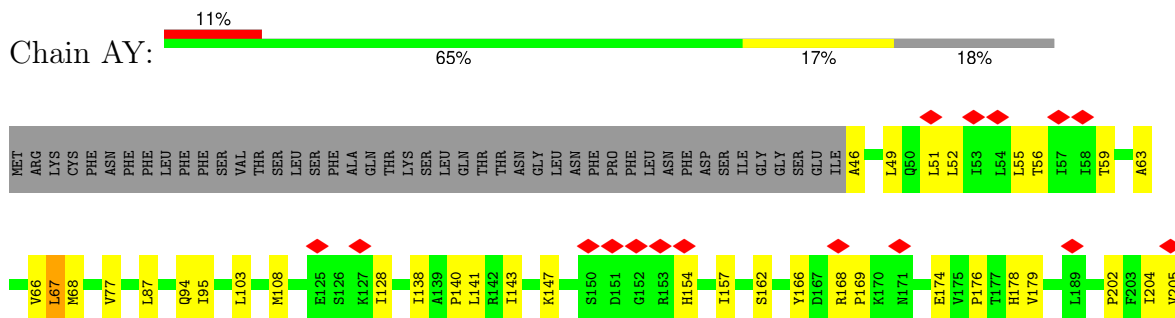


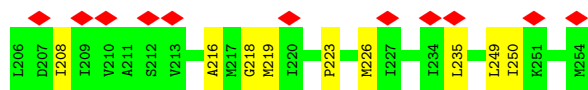


- Molecule 2: Flagellar biosynthetic protein FlhB

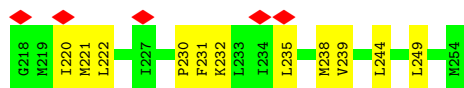
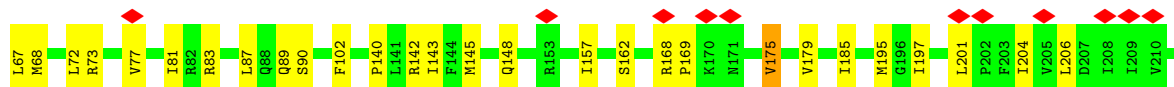
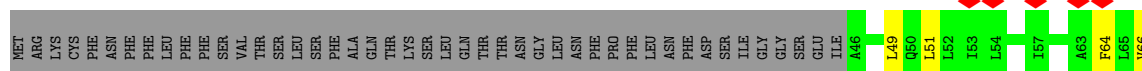


- Molecule 3: Flagellar biosynthetic protein FlhP

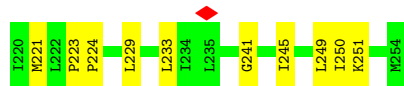
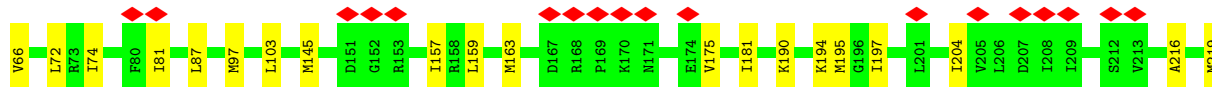
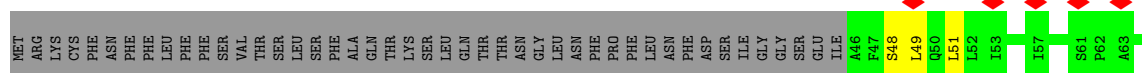




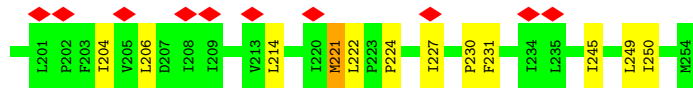
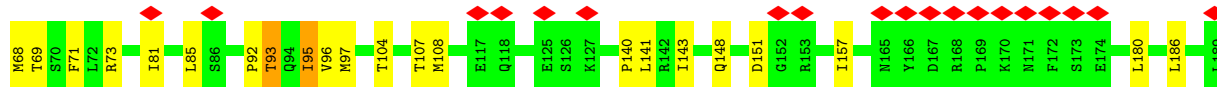
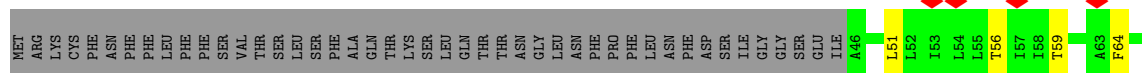
• Molecule 3: Flagellar biosynthetic protein Flp



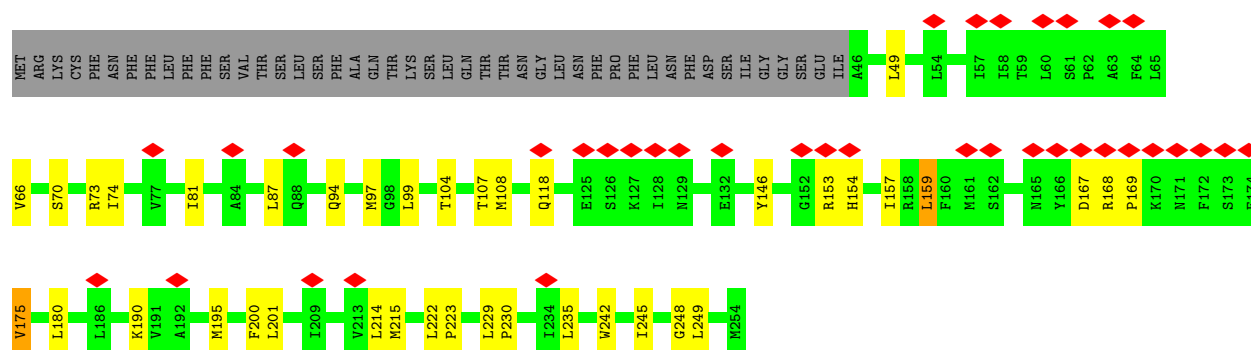
• Molecule 3: Flagellar biosynthetic protein Flp



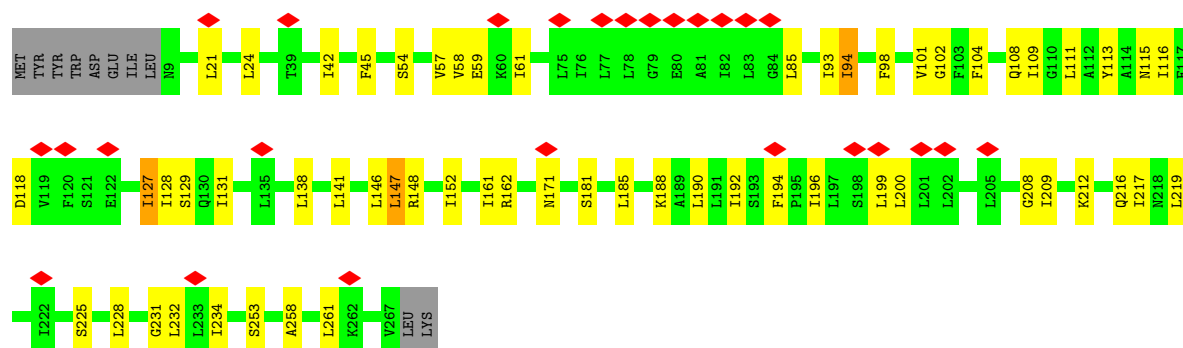
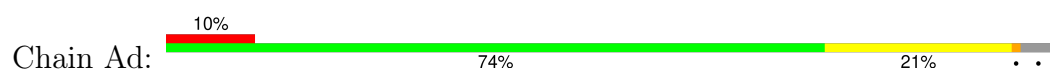
• Molecule 3: Flagellar biosynthetic protein Flp



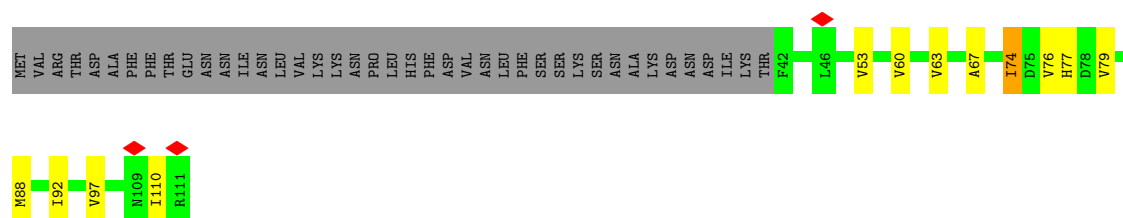
• Molecule 3: Flagellar biosynthetic protein Flp



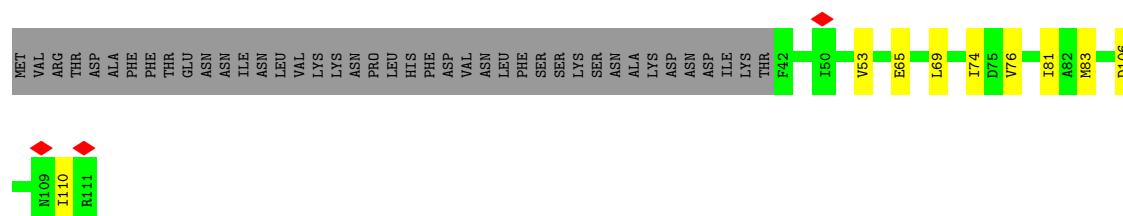
• Molecule 4: Flagellar biosynthetic protein FliR



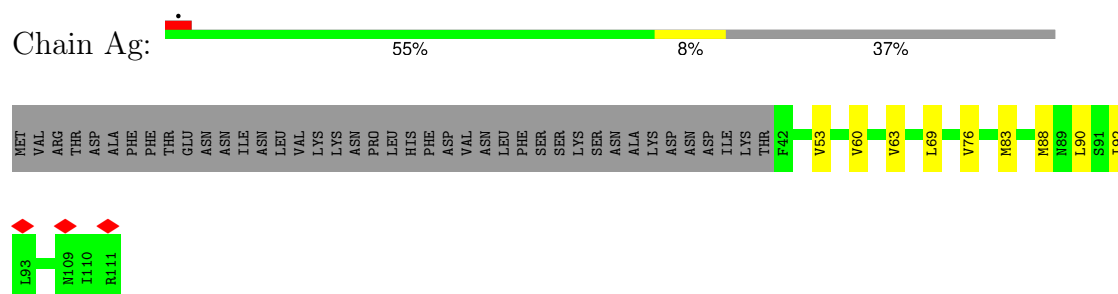
• Molecule 5: Flagellar hook-basal body complex protein FliE



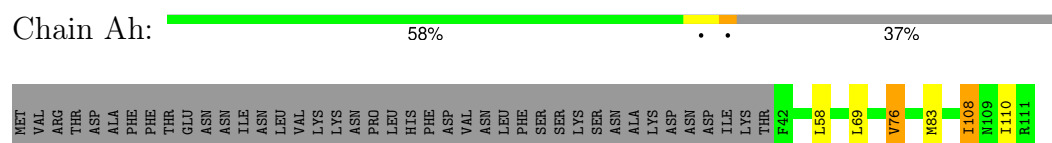
• Molecule 5: Flagellar hook-basal body complex protein FliE



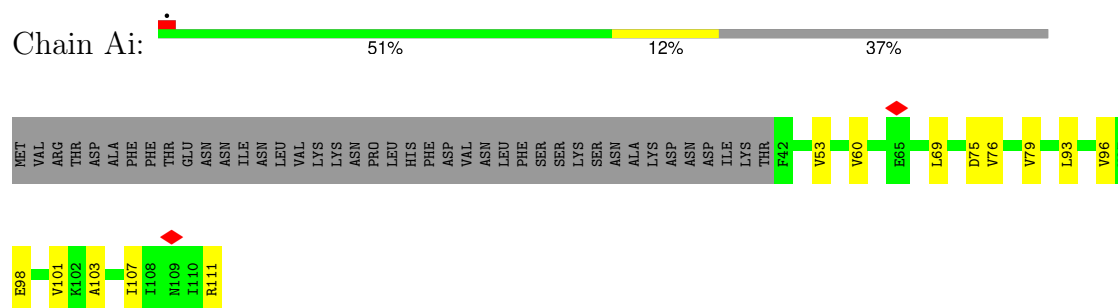
- Molecule 5: Flagellar hook-basal body complex protein FliE



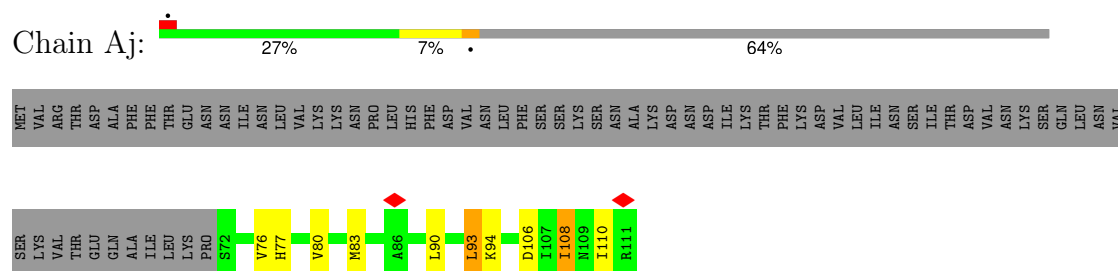
- Molecule 5: Flagellar hook-basal body complex protein FliE



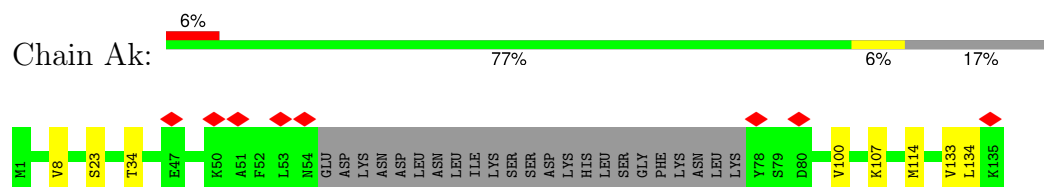
- Molecule 5: Flagellar hook-basal body complex protein FliE



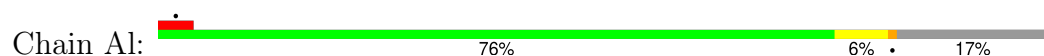
- Molecule 5: Flagellar hook-basal body complex protein FliE

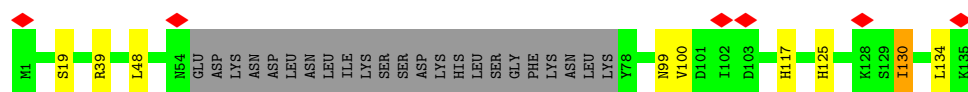


- Molecule 6: Flagellar basal body rod protein FlgB

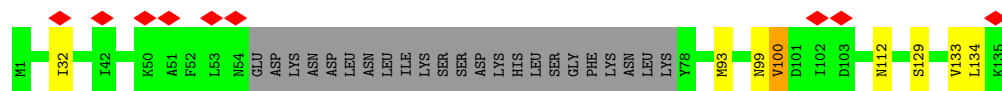
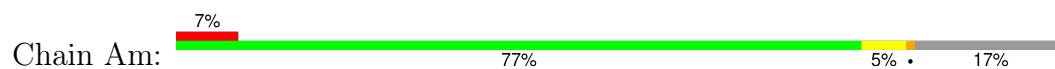


- Molecule 6: Flagellar basal body rod protein FlgB

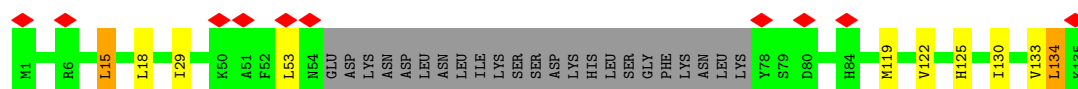
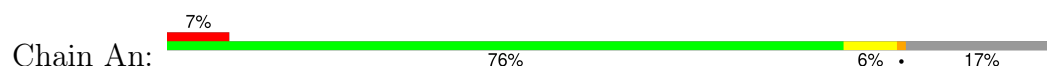




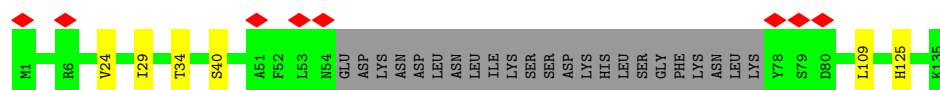
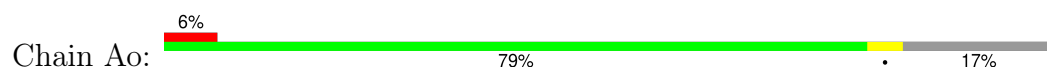
- Molecule 6: Flagellar basal body rod protein FlgB



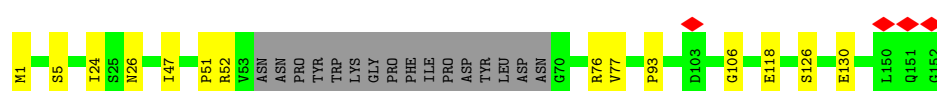
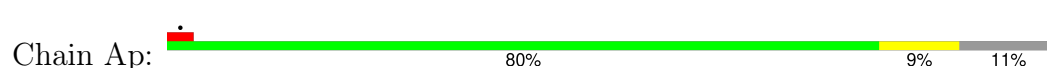
- Molecule 6: Flagellar basal body rod protein FlgB



- Molecule 6: Flagellar basal body rod protein FlgB



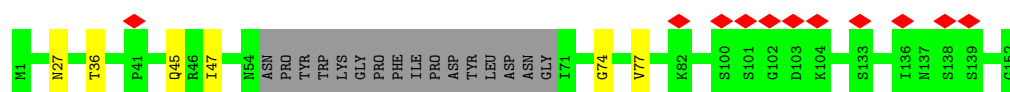
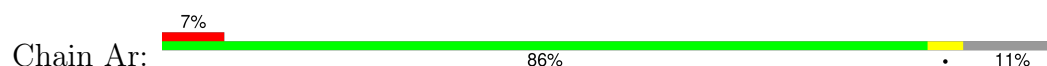
- Molecule 7: Flagellar basal-body rod protein FlgC



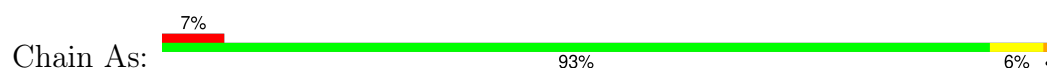
- Molecule 7: Flagellar basal-body rod protein FlgC



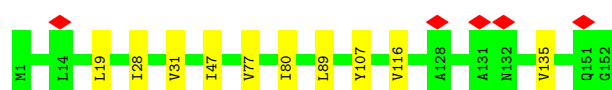
- Molecule 7: Flagellar basal-body rod protein FlgC



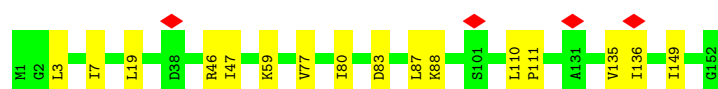
- Molecule 7: Flagellar basal-body rod protein FlgC



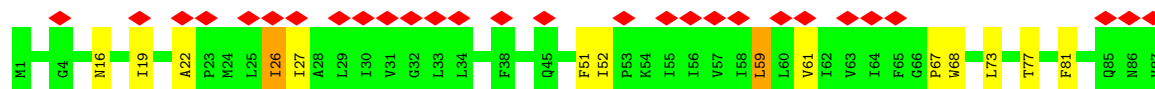
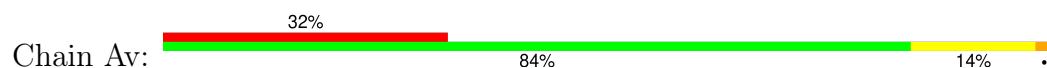
- Molecule 7: Flagellar basal-body rod protein FlgC



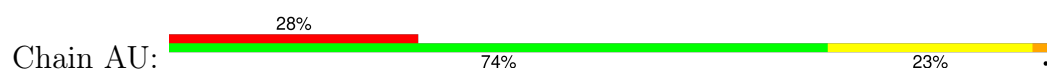
- Molecule 7: Flagellar basal-body rod protein FlgC



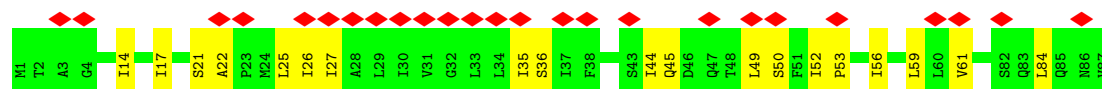
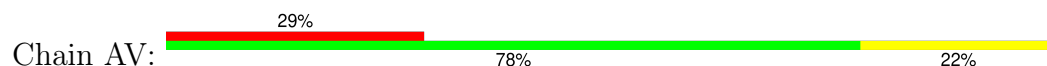
- Molecule 8: Flagellar biosynthetic protein FliQ



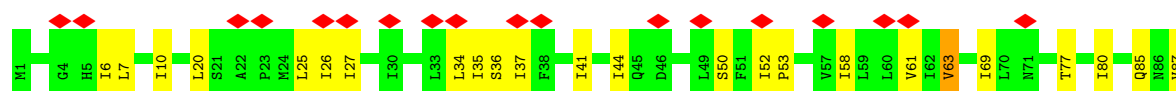
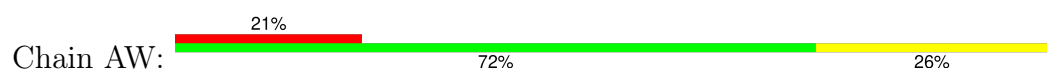
- Molecule 8: Flagellar biosynthetic protein FliQ

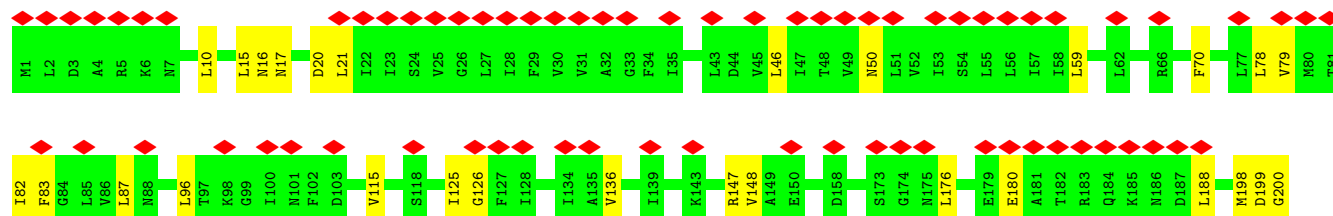


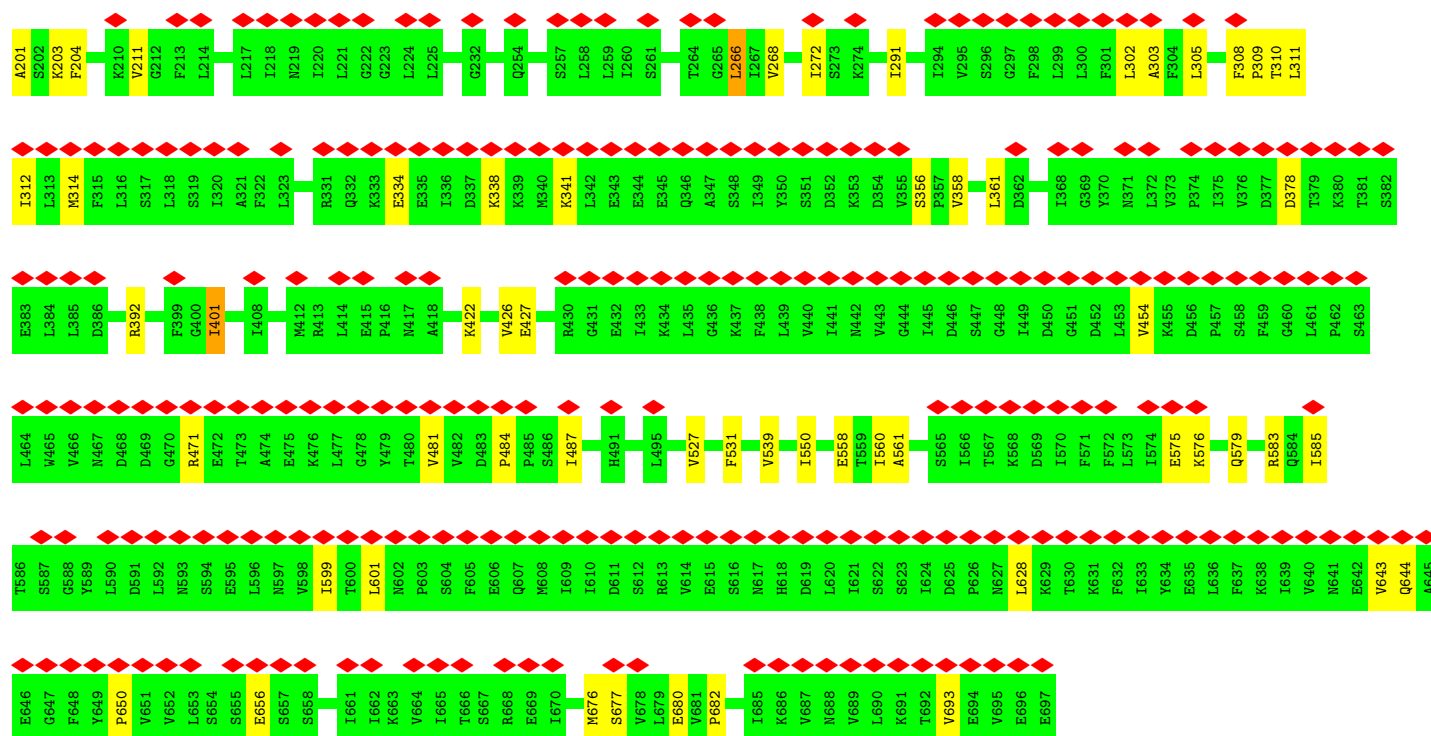
- Molecule 8: Flagellar biosynthetic protein FliQ



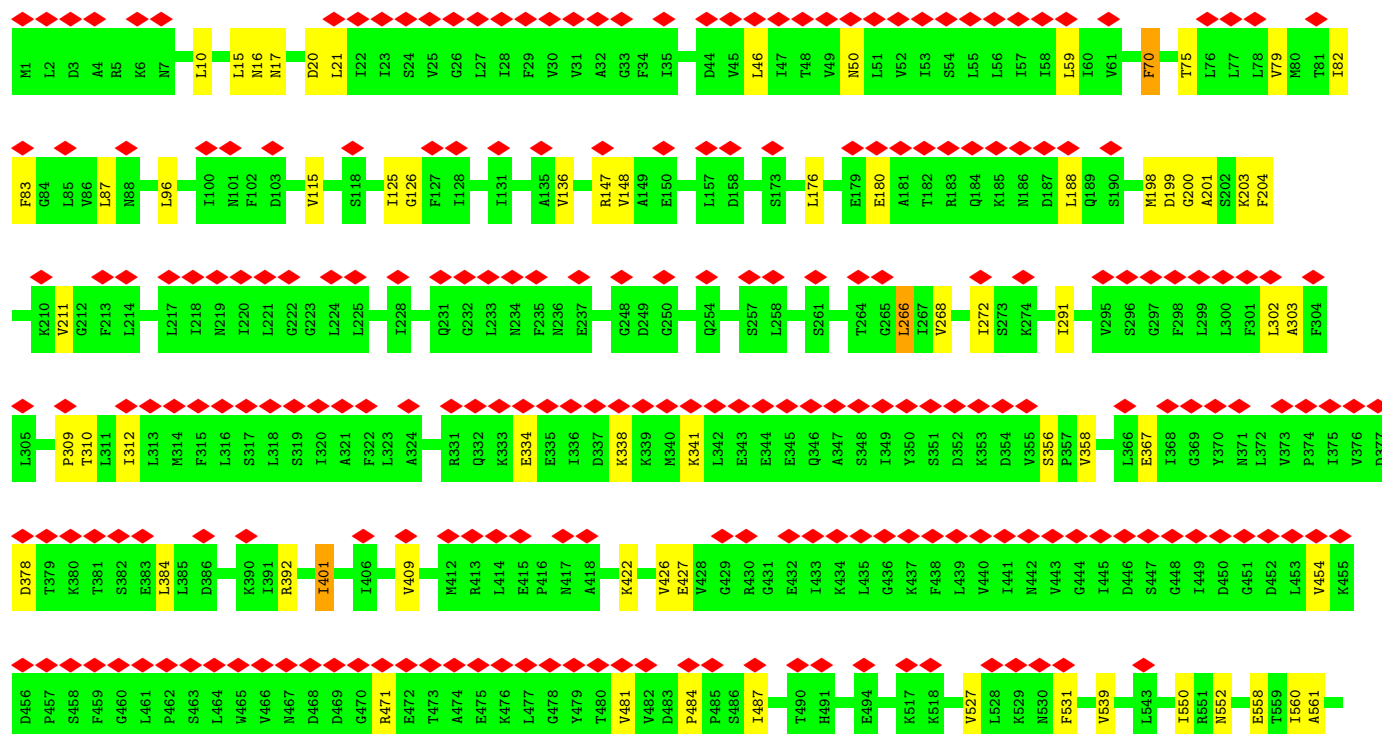
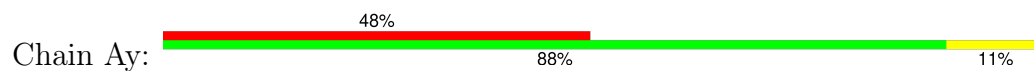
- Molecule 8: Flagellar biosynthetic protein FliQ





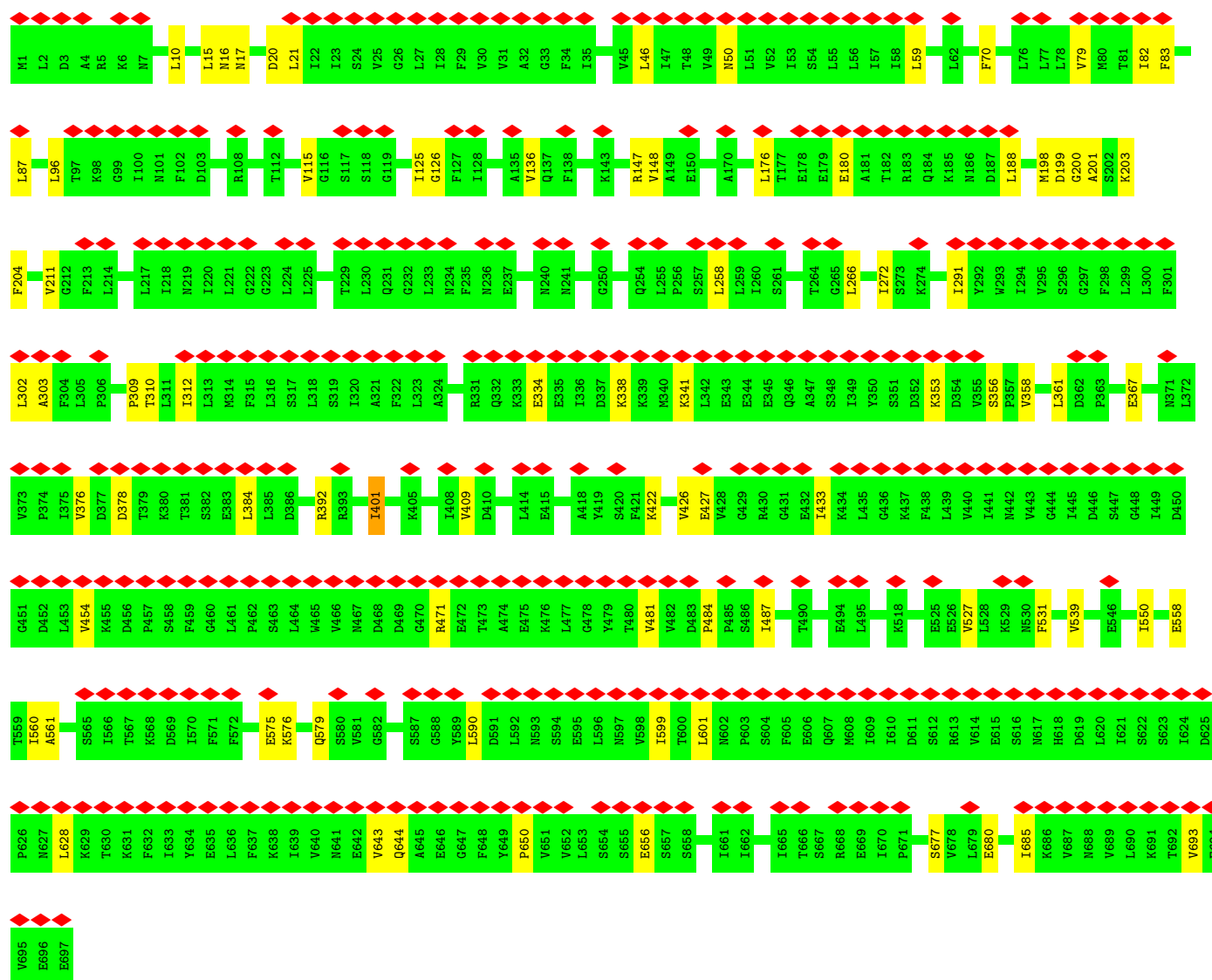
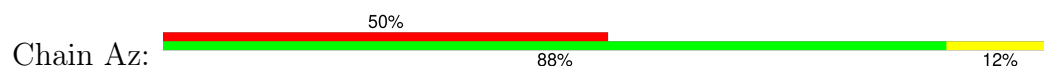


• Molecule 9: Flagellar biosynthesis protein FlhA

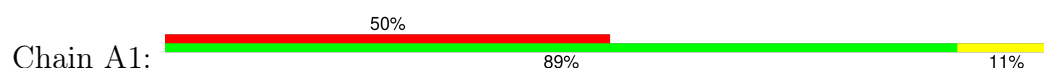


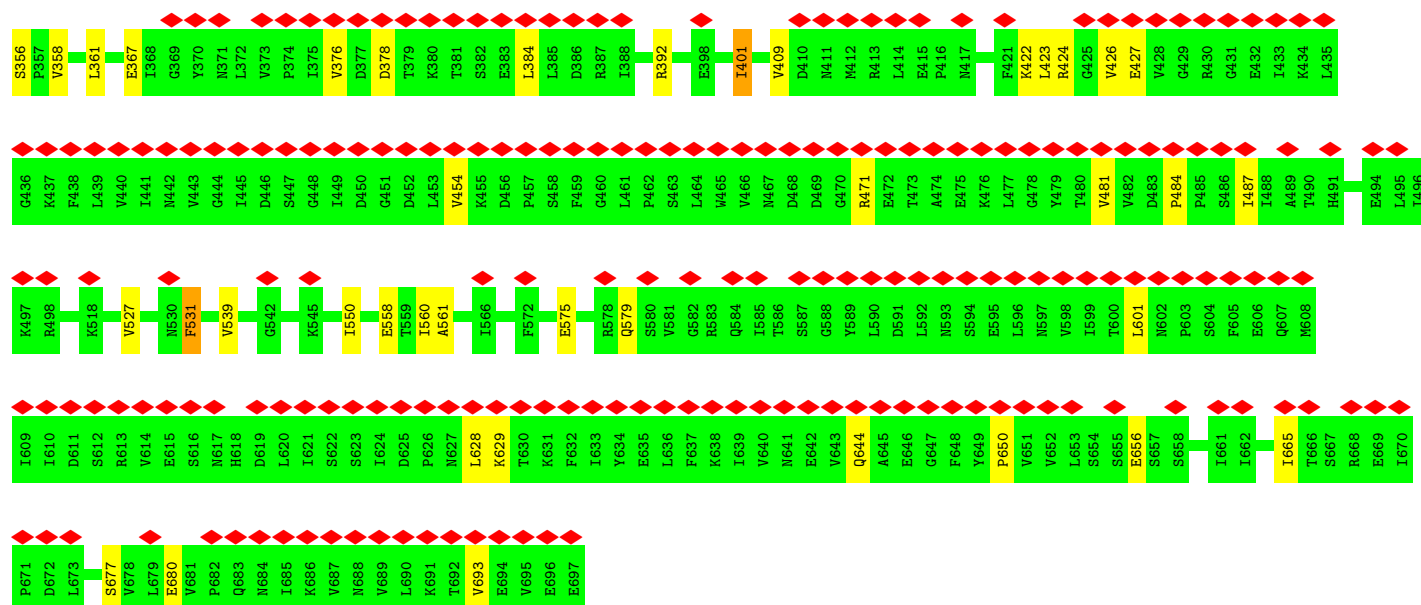


• Molecule 9: Flagellar biosynthesis protein FlhA

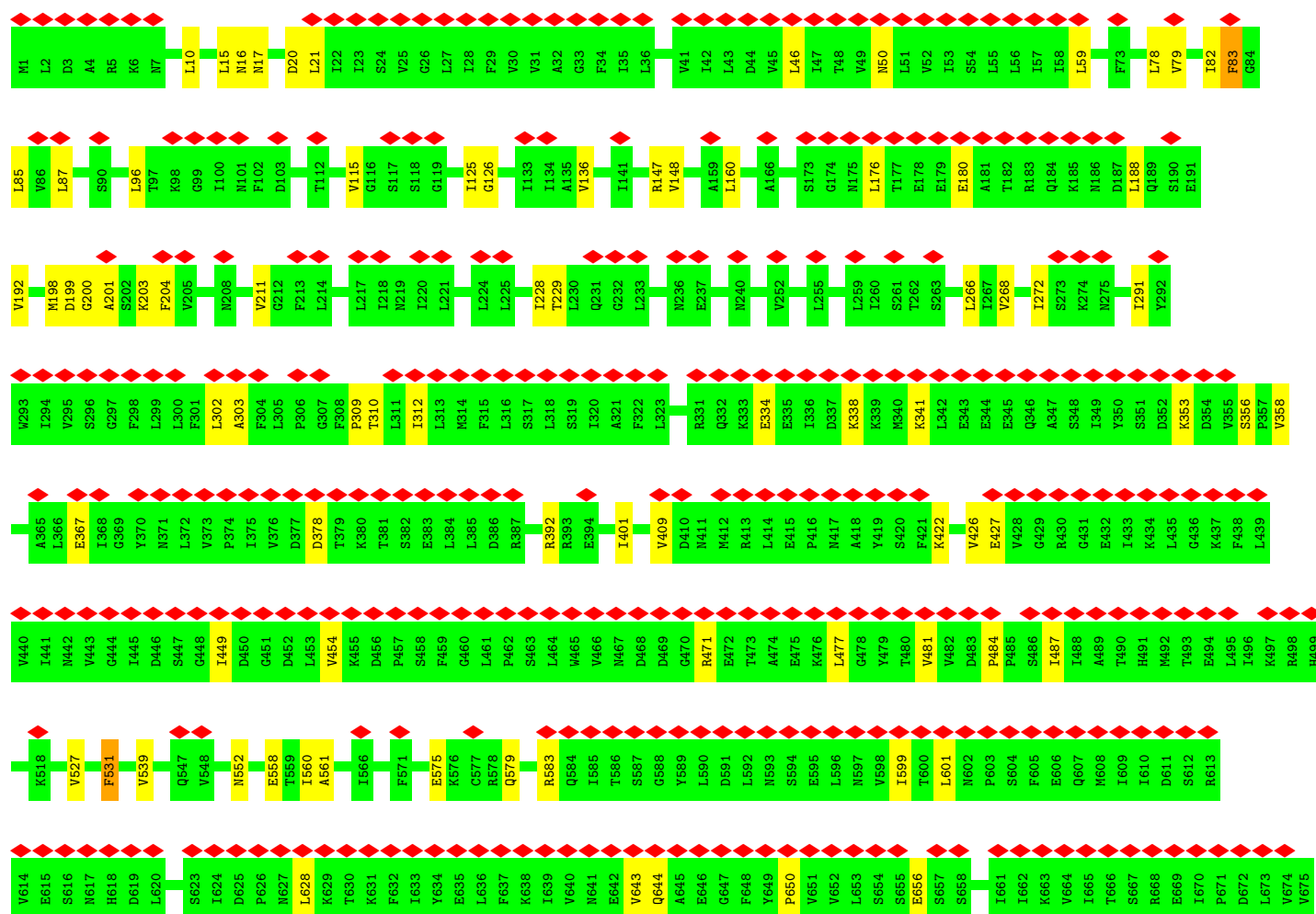


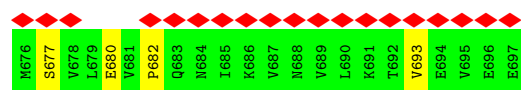
• Molecule 9: Flagellar biosynthesis protein FlhA



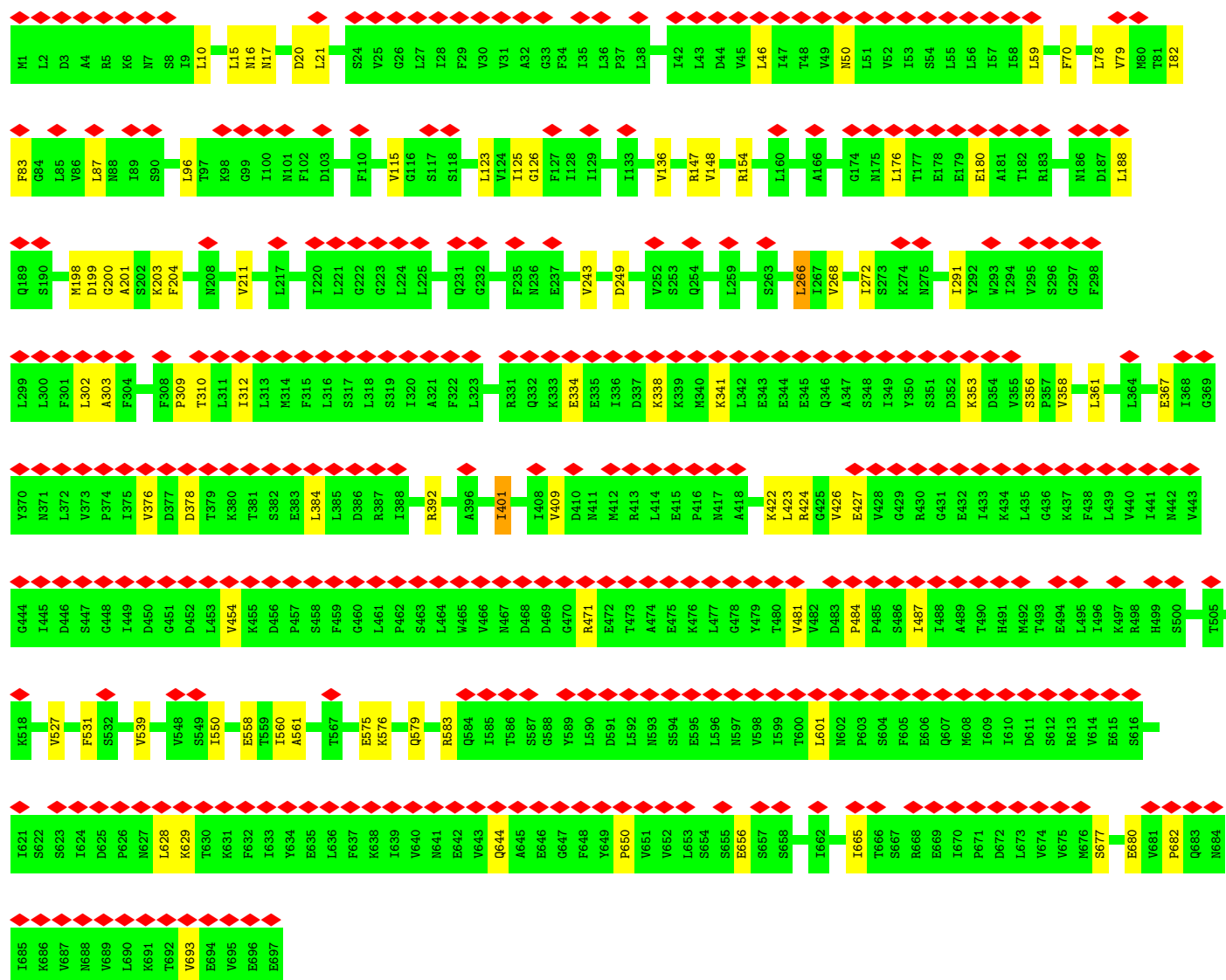
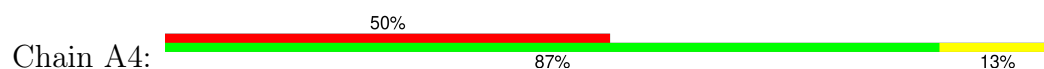


• Molecule 9: Flagellar biosynthesis protein FlhA

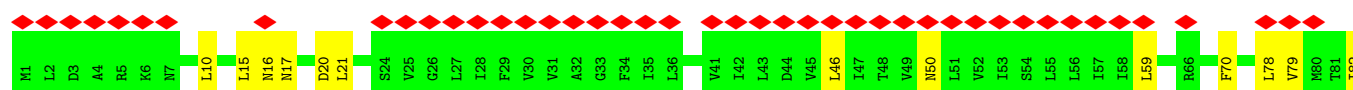
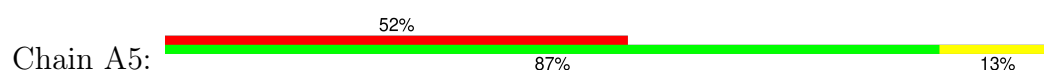


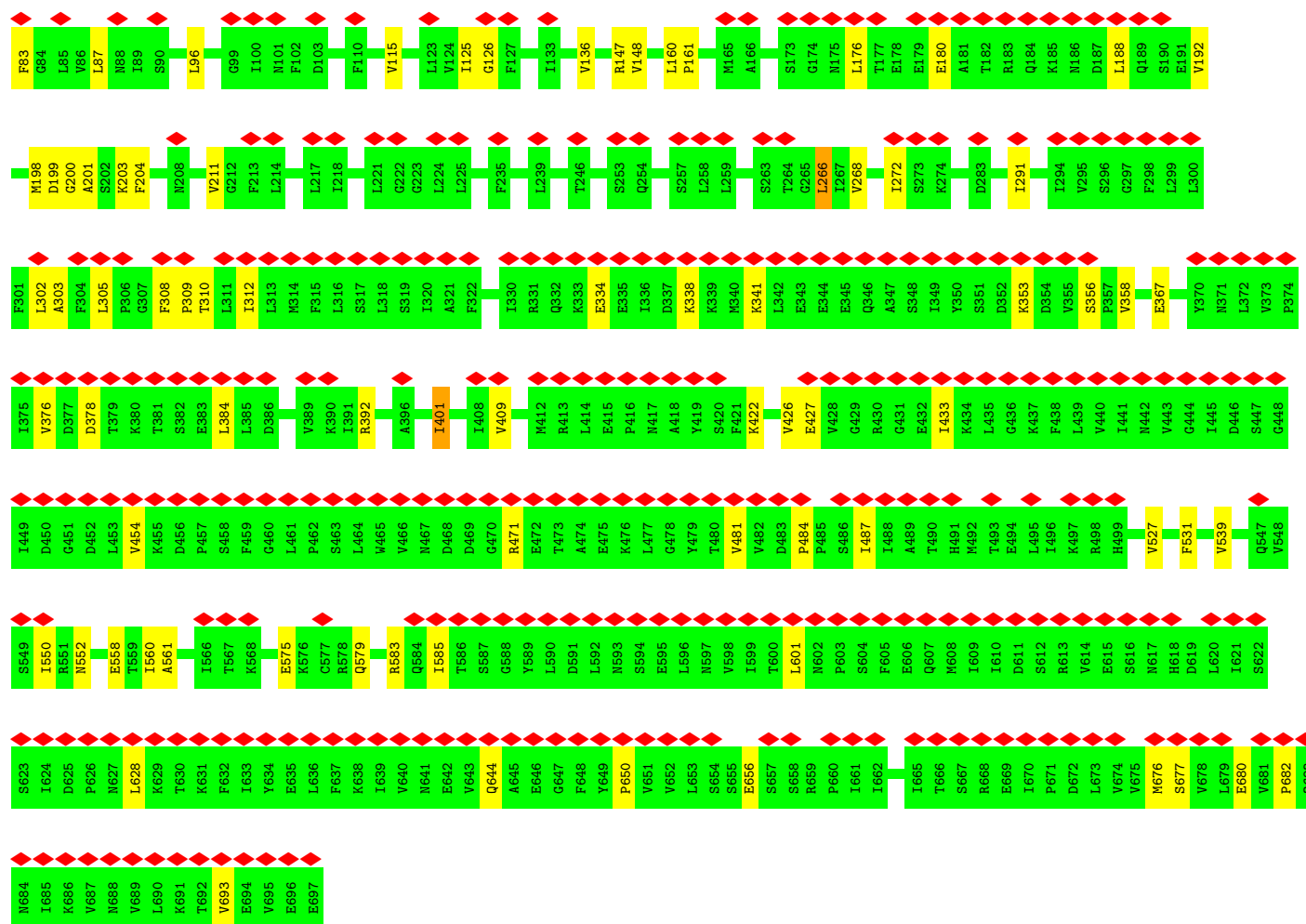


• Molecule 9: Flagellar biosynthesis protein FlhA



• Molecule 9: Flagellar biosynthesis protein FlhA





4 Experimental information

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 ($e^-/\text{\AA}^2$)	1.75	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	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 ⓘ

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 ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	207/569 (36%)	201 (97%)	5 (2%)	1 (0%)	24	63
1	1	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	2	201/569 (35%)	195 (97%)	5 (2%)	1 (0%)	24	63
1	3	207/569 (36%)	200 (97%)	6 (3%)	1 (0%)	24	63
1	4	207/569 (36%)	198 (96%)	8 (4%)	1 (0%)	24	63
1	5	207/569 (36%)	198 (96%)	8 (4%)	1 (0%)	24	63
1	6	201/569 (35%)	194 (96%)	6 (3%)	1 (0%)	24	63
1	7	207/569 (36%)	199 (96%)	7 (3%)	1 (0%)	24	63
1	8	207/569 (36%)	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 ⓘ

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 ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

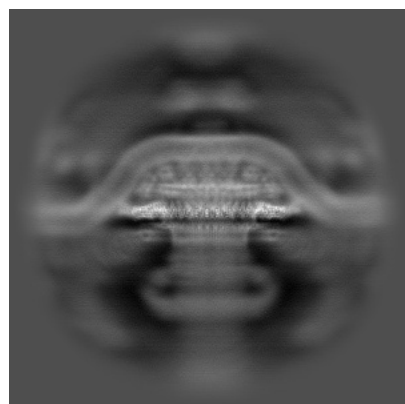
6 Map visualisation [i](#)

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

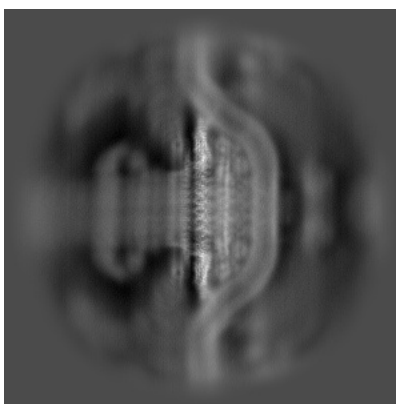
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

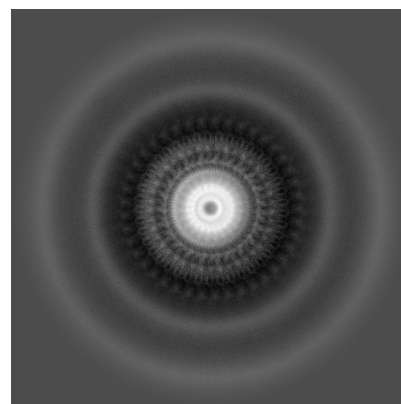
6.1.1 Primary map



X

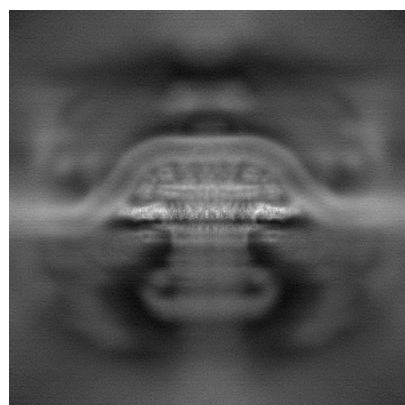


Y

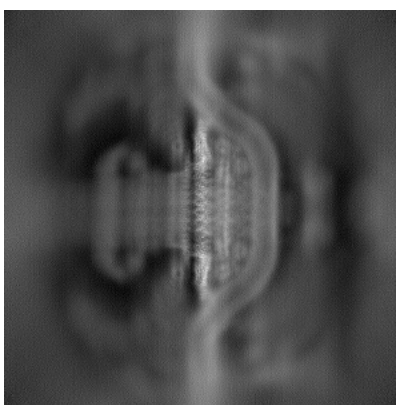


Z

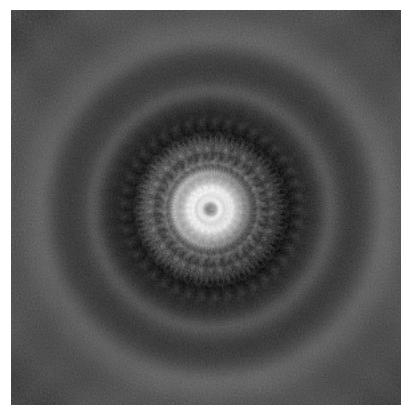
6.1.2 Raw map



X



Y

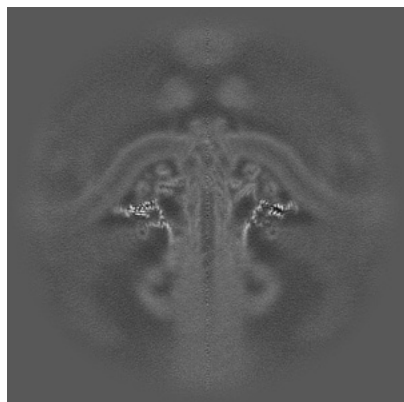


Z

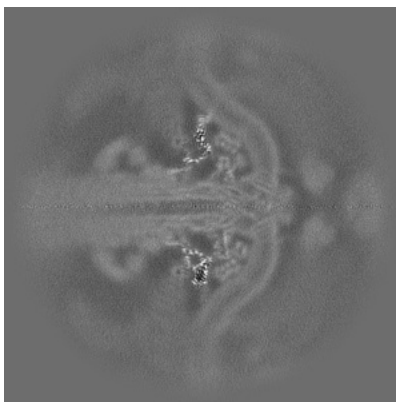
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

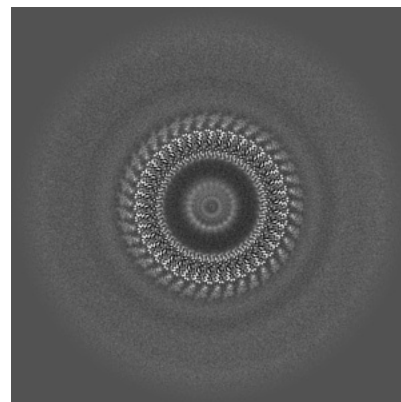
6.2.1 Primary map



X Index: 224

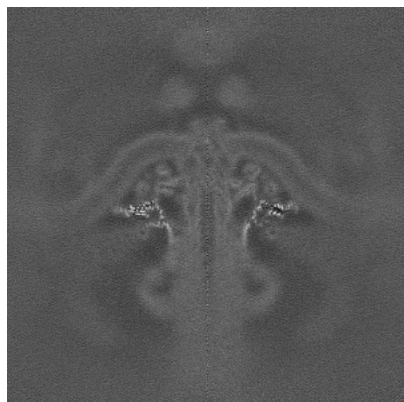


Y Index: 224

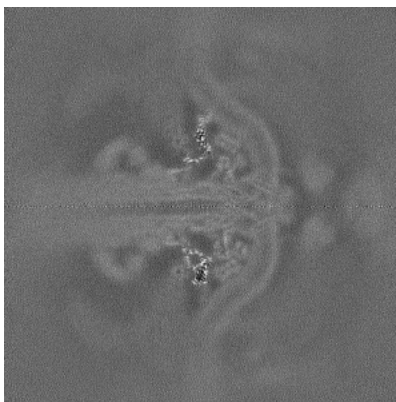


Z Index: 224

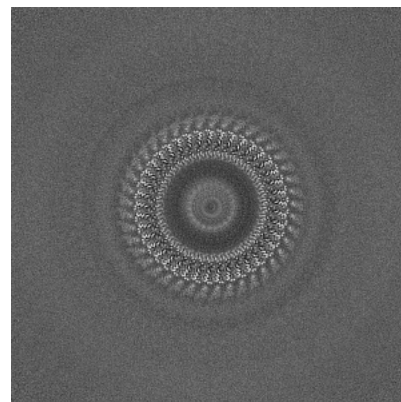
6.2.2 Raw map



X Index: 224



Y Index: 224

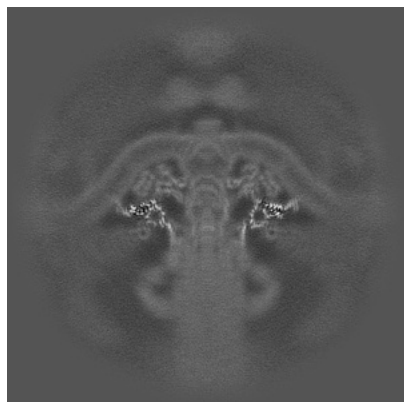


Z Index: 224

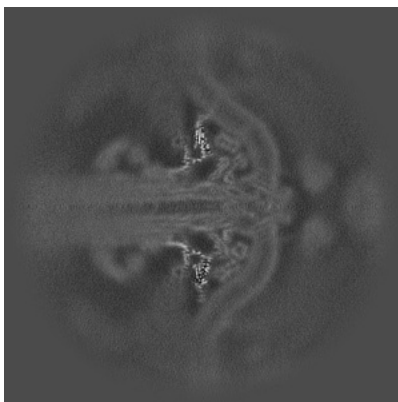
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

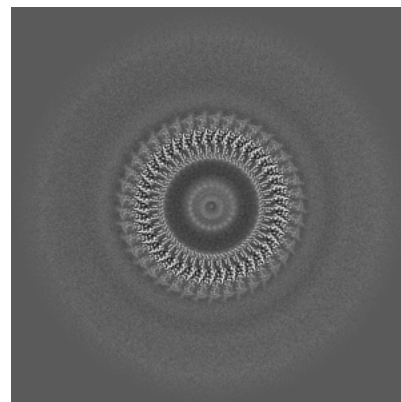
6.3.1 Primary map



X Index: 211

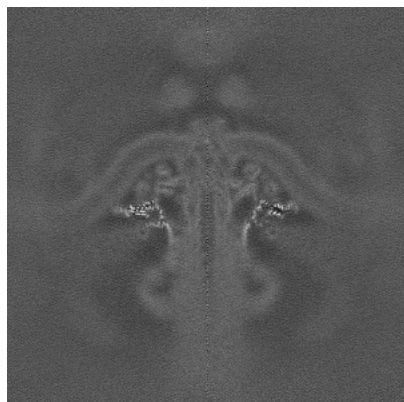


Y Index: 222

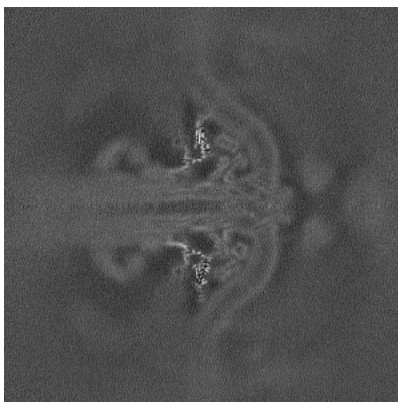


Z Index: 222

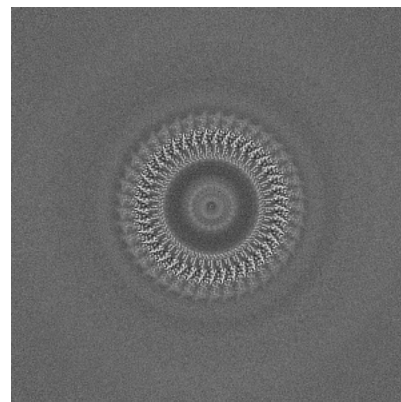
6.3.2 Raw map



X Index: 224



Y Index: 222

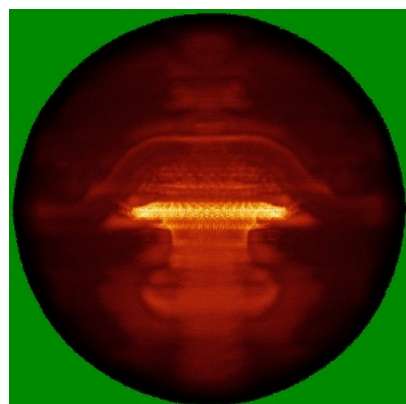


Z Index: 222

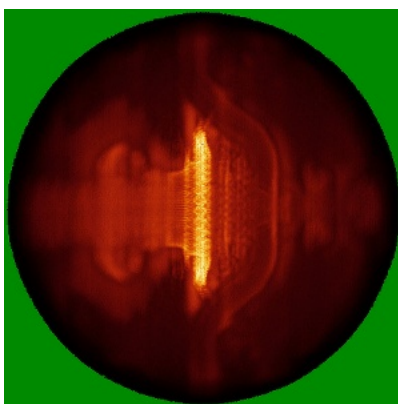
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

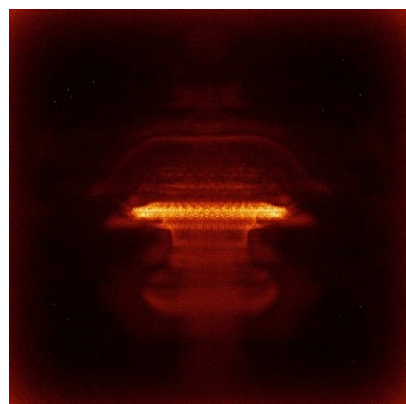


Y

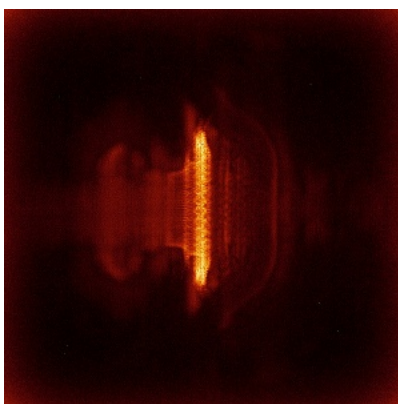


Z

6.4.2 Raw map



X



Y



Z

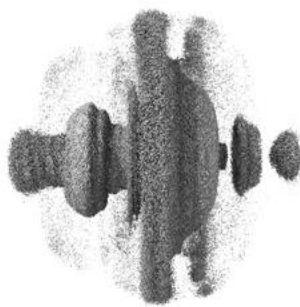
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

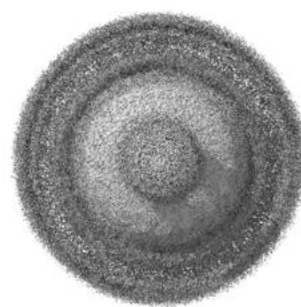
6.5.1 Primary map



X



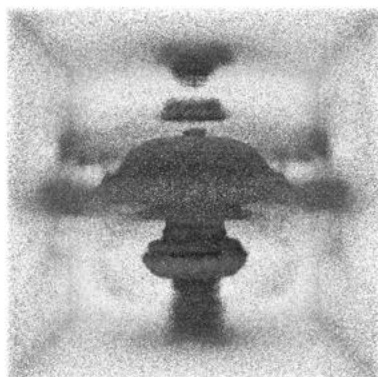
Y



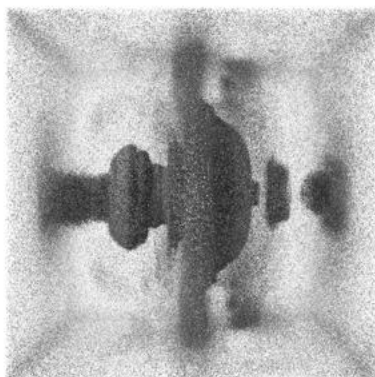
Z

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.

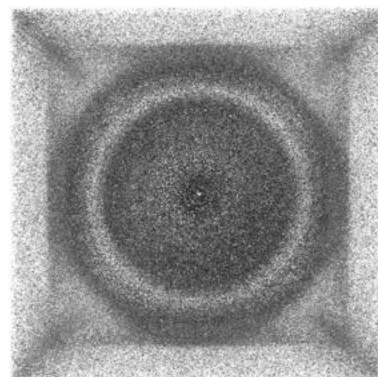
6.5.2 Raw map



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

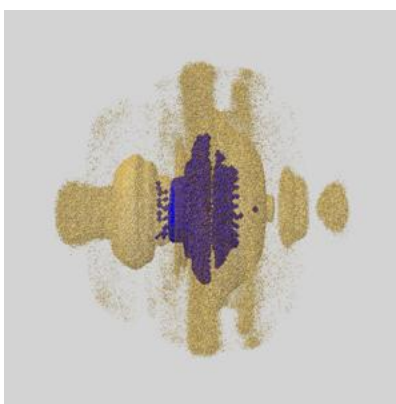
A mask typically either:

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

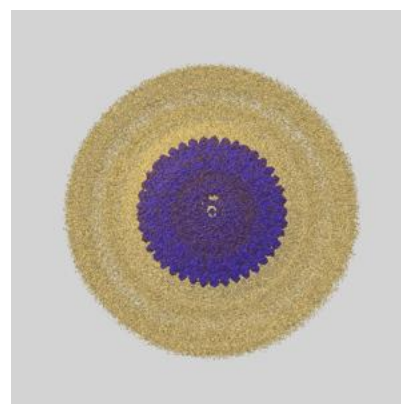
6.6.1 emd_76349_msk_1.map [i](#)



X



Y

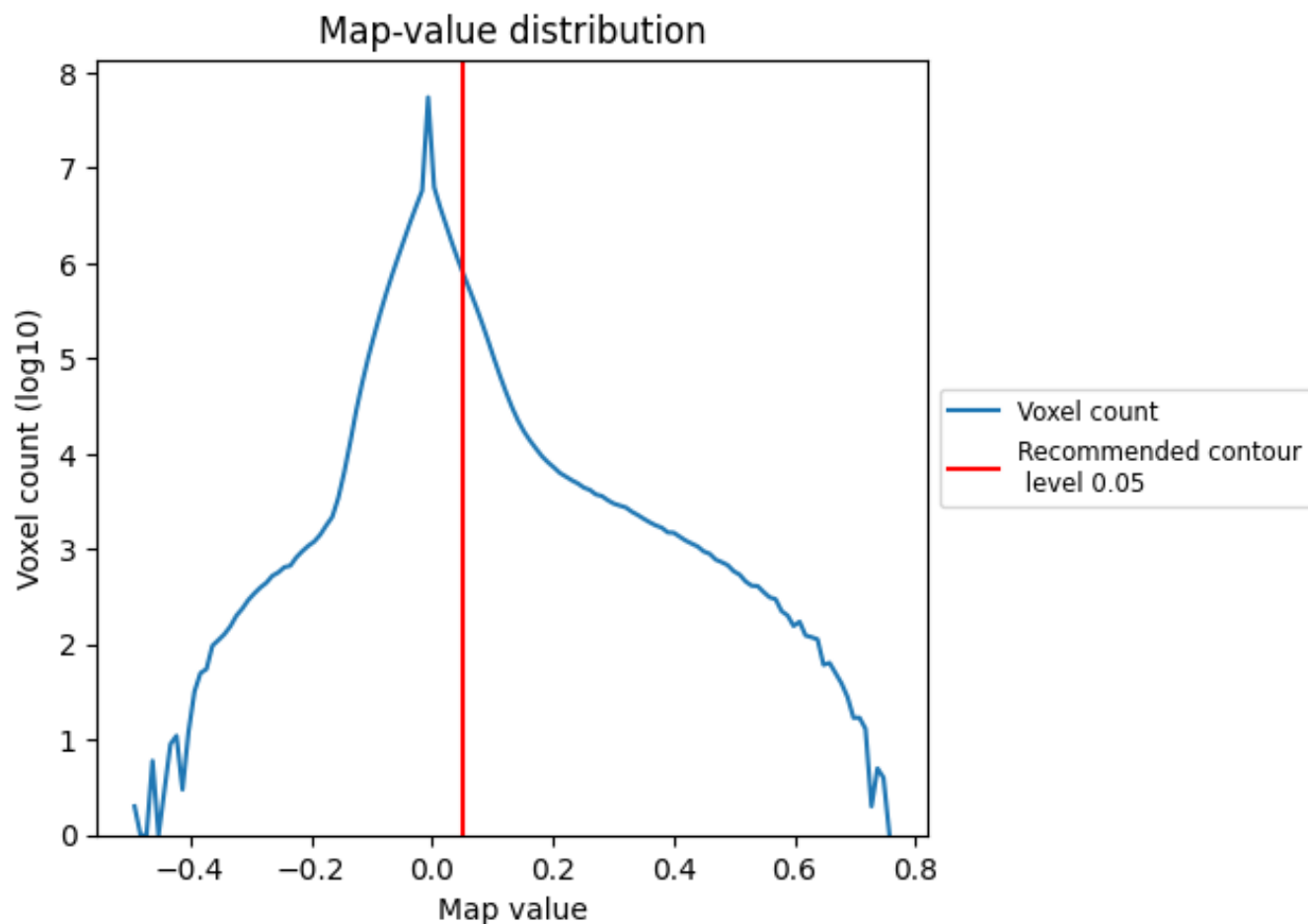


Z

7 Map analysis [i](#)

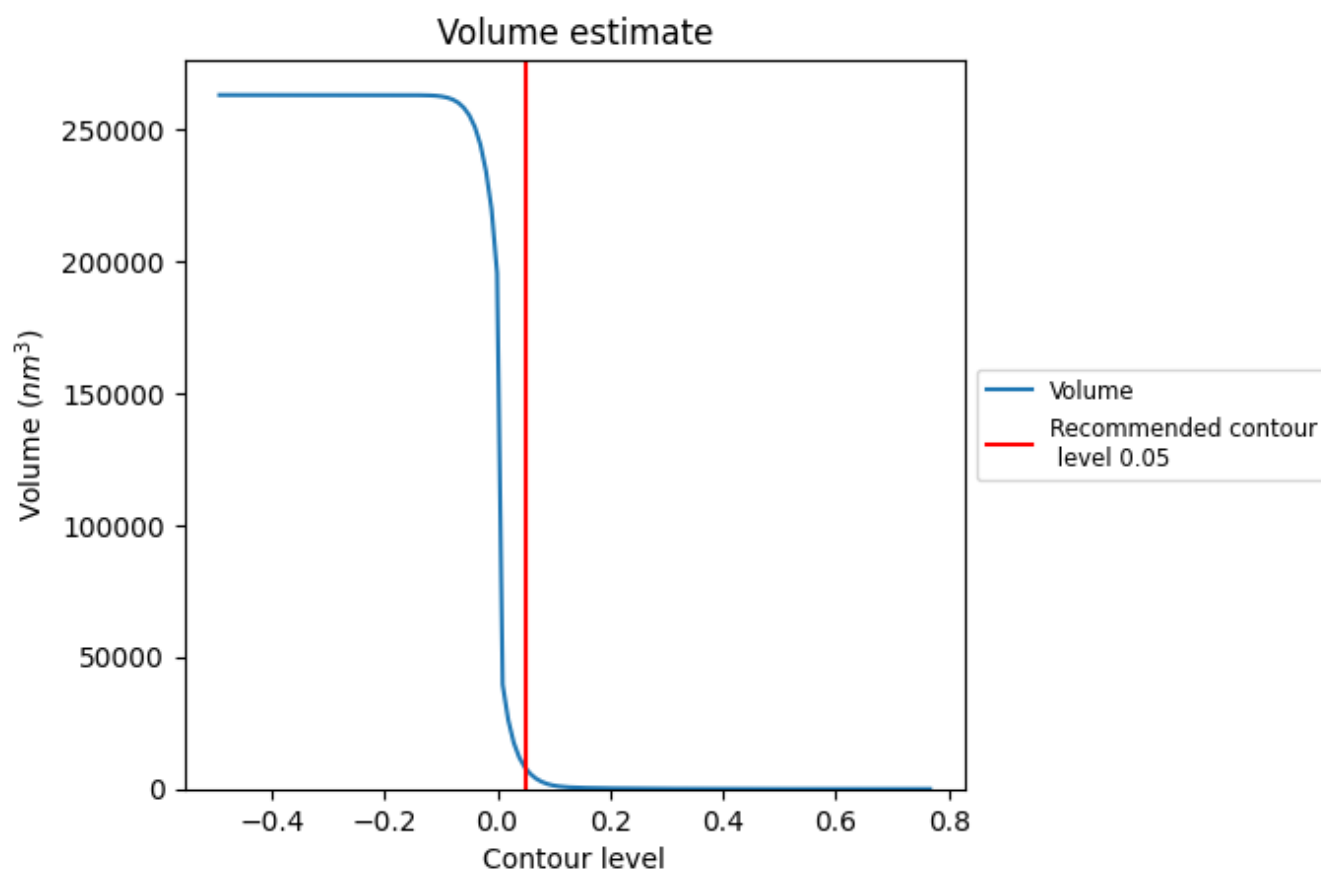
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

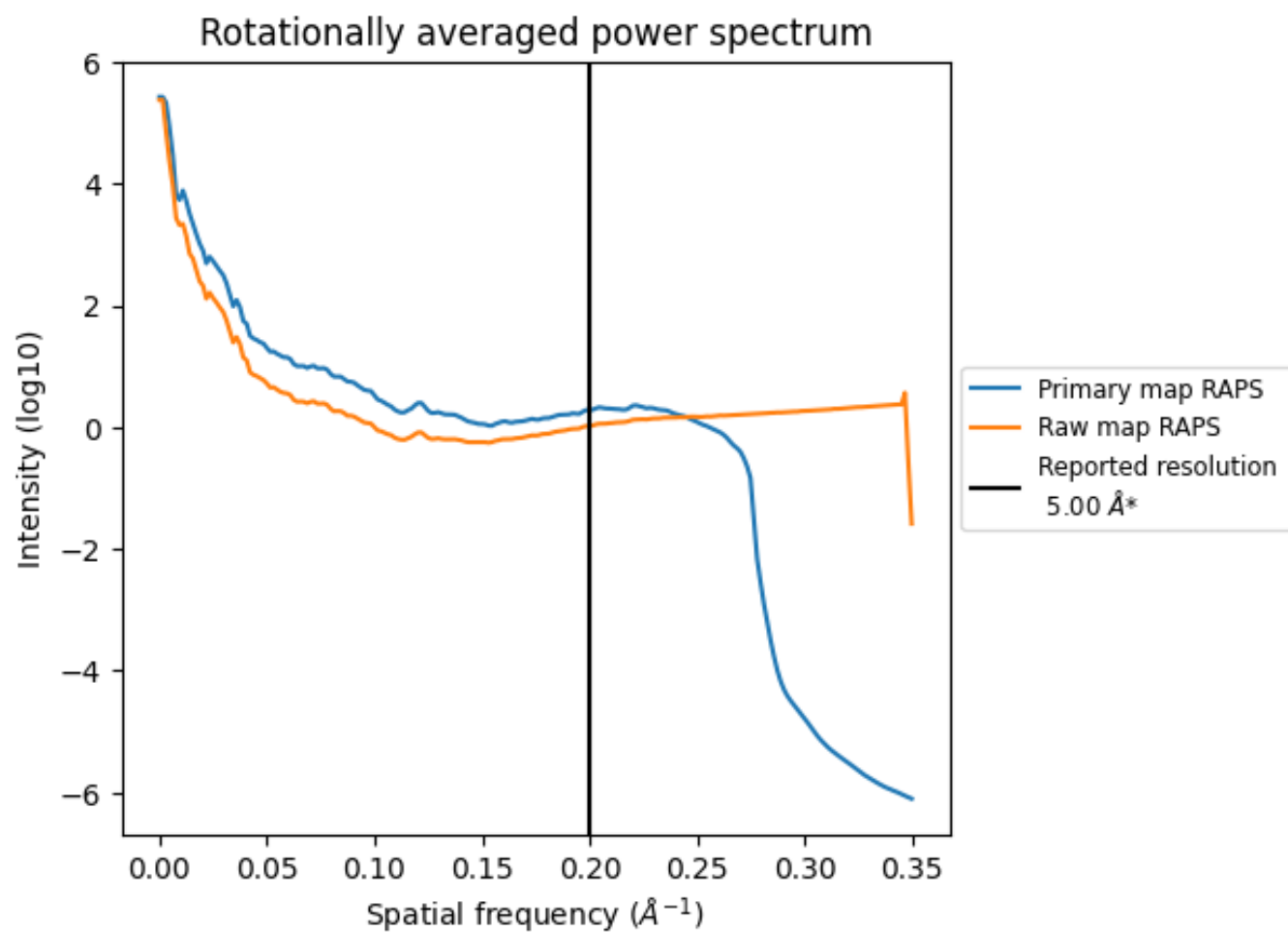
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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 ⓘ

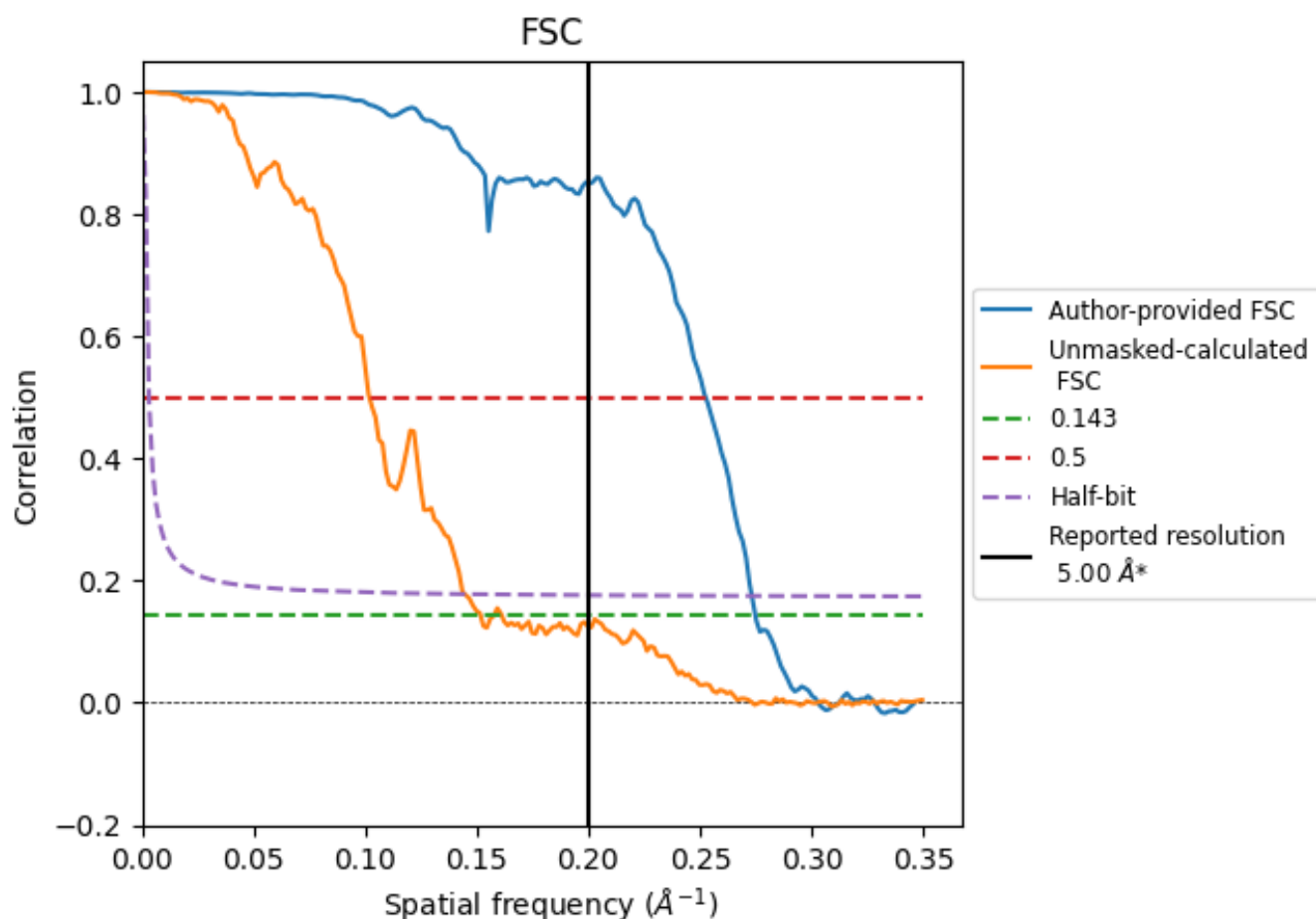


*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.200 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

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

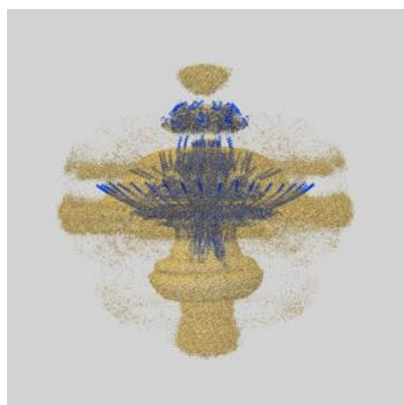
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.64 differs from the reported value 5.0 by more than 10 %

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 %

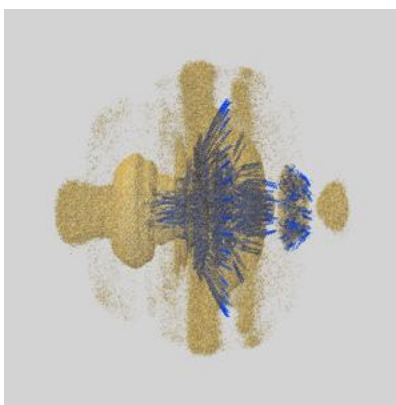
9 Map-model fit [i](#)

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](#).

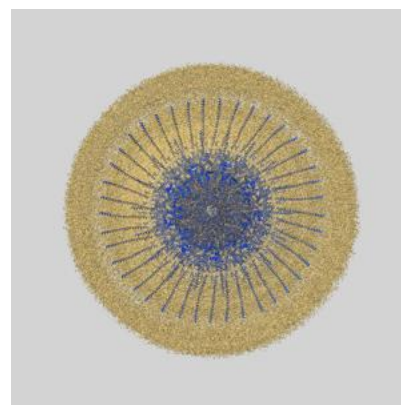
9.1 Map-model overlay [i](#)



X



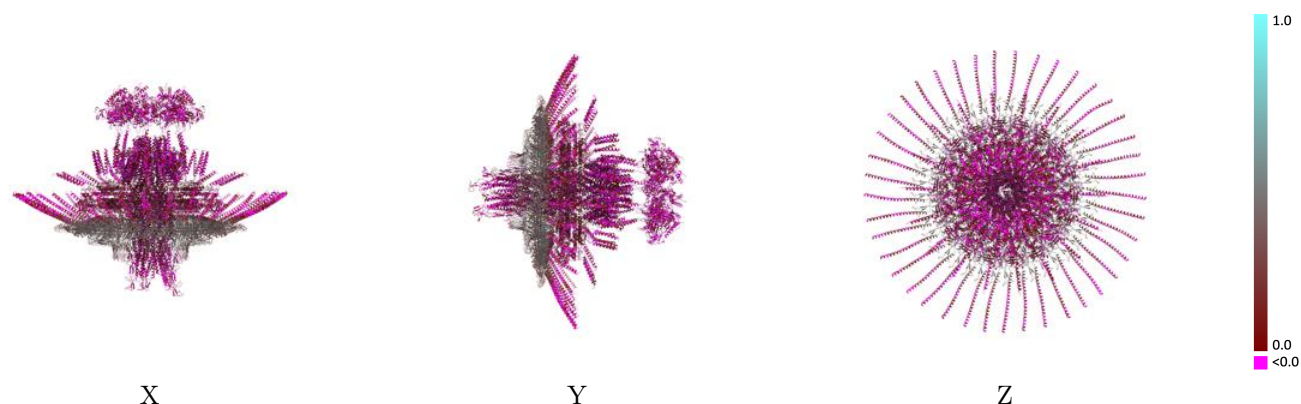
Y



Z

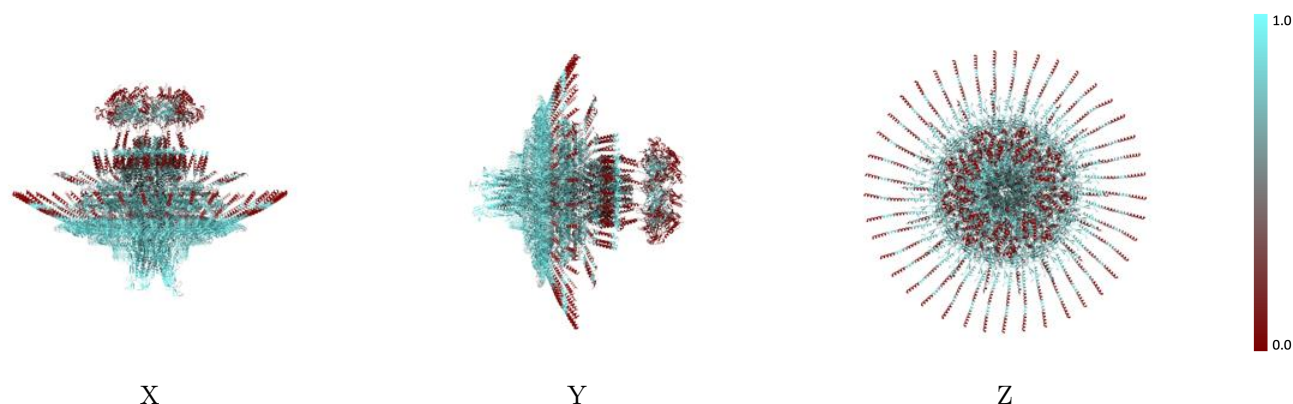
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



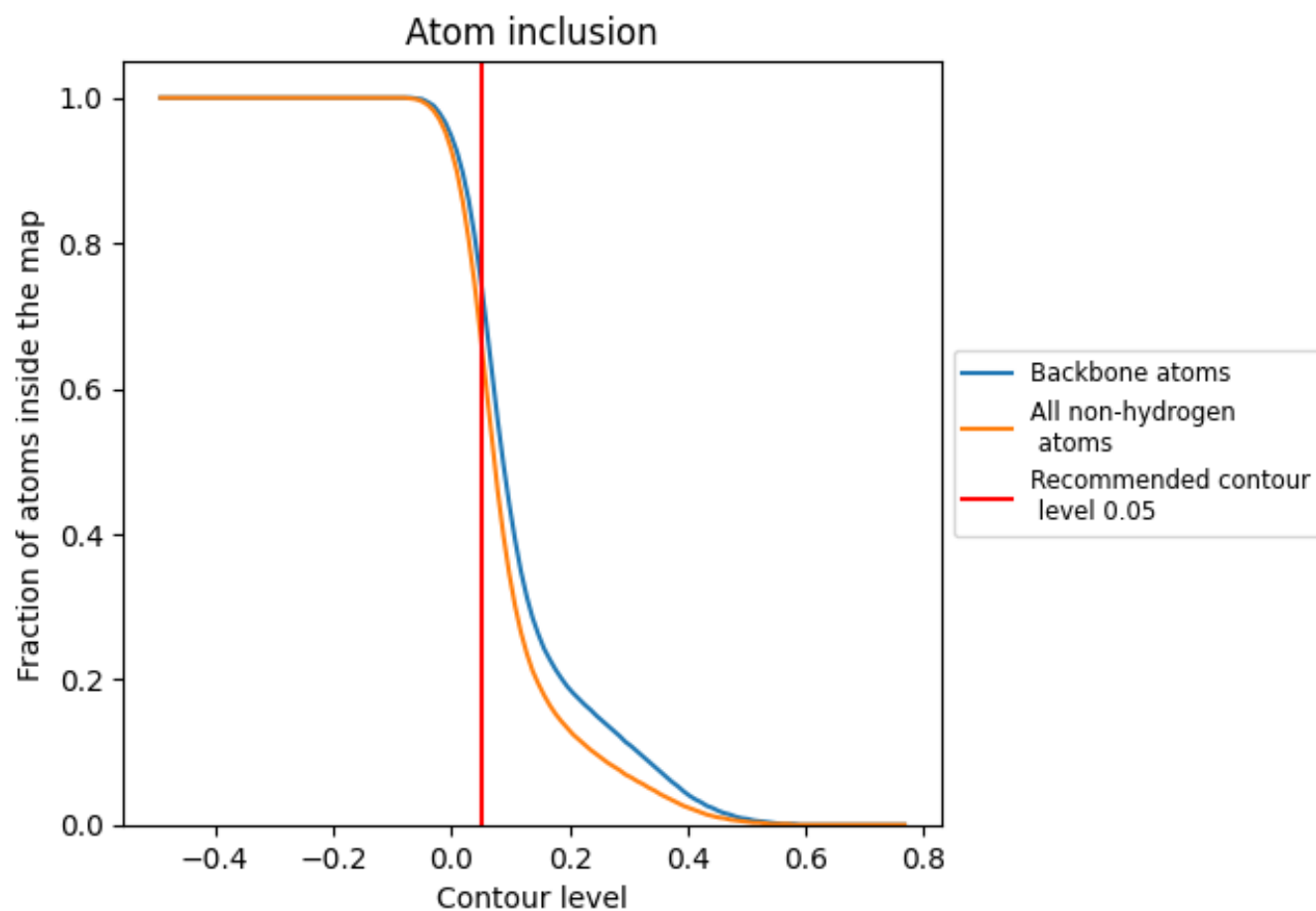
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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