



wwPDB EM Validation Summary Report ⓘ

Mar 18, 2025 – 11:22 PM JST

PDB ID : 8WLT
EMDB ID : EMD-37630
Title : Cryo-EM structure of the membrane-anchored part of the flagellar motor-hook complex in the CCW state
Authors : Tan, J.X.; Zhang, L.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2023-10-01
Resolution : 4.10 Å (reported)
Based on initial models : ., ?

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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

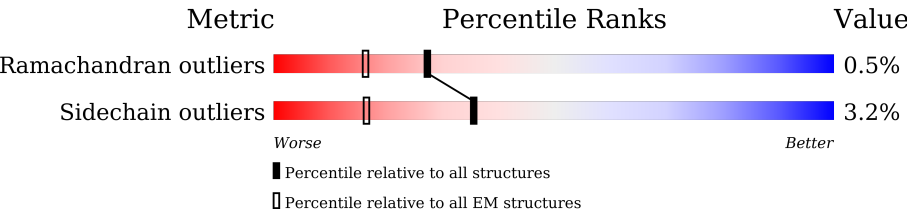
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	232	<div> <div>31%</div> <div>88%</div> <div>9%</div> </div>
1	B	232	<div> <div>31%</div> <div>88%</div> <div>9%</div> </div>
1	C	232	<div> <div>29%</div> <div>88%</div> <div>9%</div> </div>
1	D	232	<div> <div>26%</div> <div>88%</div> <div>9%</div> </div>
1	E	232	<div> <div>31%</div> <div>88%</div> <div>9%</div> </div>
1	F	232	<div> <div>30%</div> <div>88%</div> <div>9%</div> </div>
1	G	232	<div> <div>28%</div> <div>88%</div> <div>9%</div> </div>
1	H	232	<div> <div>25%</div> <div>88%</div> <div>9%</div> </div>
1	I	232	<div> <div>24%</div> <div>88%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
1	J	232	27% 88% 9%
1	K	232	27% 88% 9%
1	L	232	28% 88% 9%
1	M	232	27% 88% 9%
1	N	232	26% 88% 9%
1	O	232	29% 88% 9%
1	P	232	26% 88% 9%
1	Q	232	27% 88% 9%
1	R	232	25% 88% 9%
1	S	232	26% 88% 9%
1	T	232	27% 88% 9%
1	U	232	24% 88% 9%
1	V	232	29% 88% 9%
1	W	232	28% 88% 9%
1	X	232	28% 88% 9%
1	Y	232	28% 88% 9%
1	Z	232	26% 88% 9%
2	a	365	37% 82% 17%
2	b	365	35% 82% 17%
2	c	365	36% 82% 17%
2	d	365	36% 82% 17%
2	e	365	39% 82% 17%
2	f	365	32% 82% 17%
2	g	365	29% 82% 17%
2	h	365	30% 82% 17%

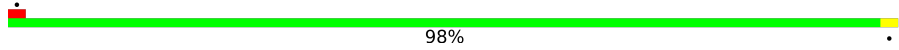
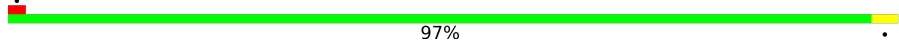
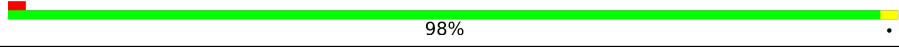
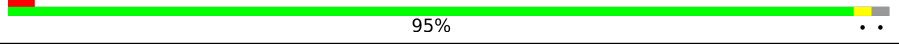
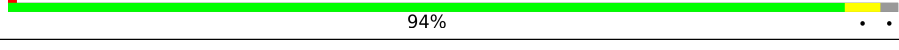
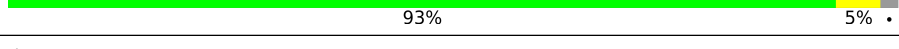
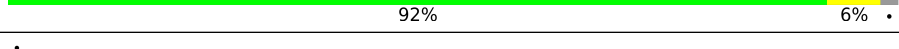
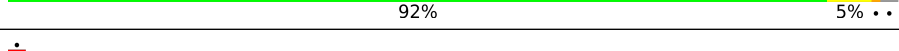
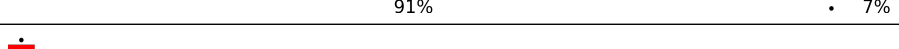
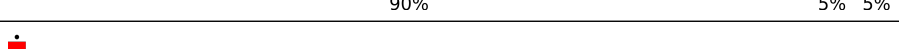
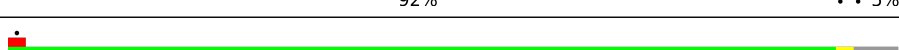
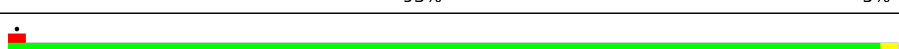
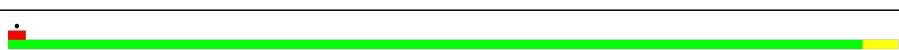
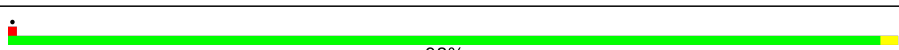
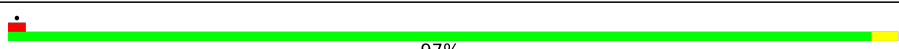


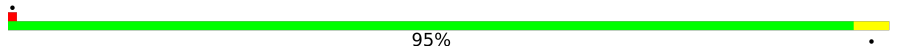
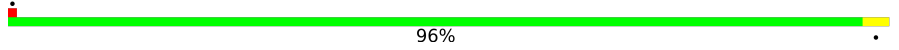
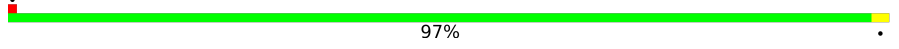
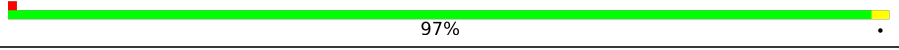
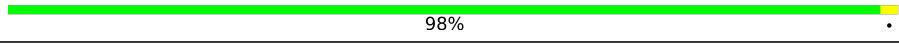
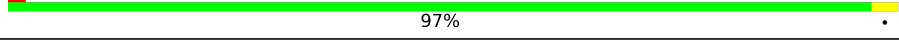
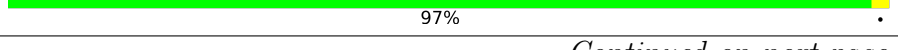

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Mol	Chain	Length	Quality of chain
2	i	365	<div> <div>31%</div> <div>82%</div> <div>17%</div> </div>
2	j	365	<div> <div>29%</div> <div>82%</div> <div>17%</div> </div>
2	k	365	<div> <div>29%</div> <div>82%</div> <div>17%</div> </div>
2	l	365	<div> <div>33%</div> <div>82%</div> <div>17%</div> </div>
2	m	365	<div> <div>30%</div> <div>82%</div> <div>17%</div> </div>
2	n	365	<div> <div>33%</div> <div>82%</div> <div>17%</div> </div>
2	o	365	<div> <div>32%</div> <div>82%</div> <div>17%</div> </div>
2	p	365	<div> <div>33%</div> <div>82%</div> <div>17%</div> </div>
2	q	365	<div> <div>34%</div> <div>82%</div> <div>17%</div> </div>
2	r	365	<div> <div>35%</div> <div>82%</div> <div>17%</div> </div>
2	s	365	<div> <div>34%</div> <div>82%</div> <div>17%</div> </div>
2	t	365	<div> <div>33%</div> <div>82%</div> <div>17%</div> </div>
2	u	365	<div> <div>37%</div> <div>82%</div> <div>17%</div> </div>
2	v	365	<div> <div>36%</div> <div>82%</div> <div>17%</div> </div>
2	w	365	<div> <div>34%</div> <div>82%</div> <div>17%</div> </div>
2	x	365	<div> <div>39%</div> <div>82%</div> <div>17%</div> </div>
2	y	365	<div> <div>41%</div> <div>82%</div> <div>17%</div> </div>
2	z	365	<div> <div>37%</div> <div>82%</div> <div>17%</div> </div>
3	0	260	<div> <div>92%</div> <div>5%</div> </div>
3	1	260	<div> <div>93%</div> </div>
3	2	260	<div> <div>98%</div> </div>
3	3	260	<div> <div>98%</div> </div>
3	4	260	<div> <div>97%</div> </div>
3	5	260	<div> <div>97%</div> </div>
3	6	260	<div> <div>97%</div> </div>

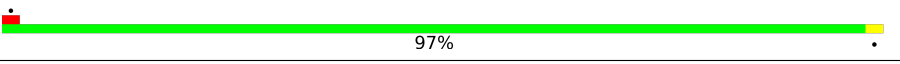
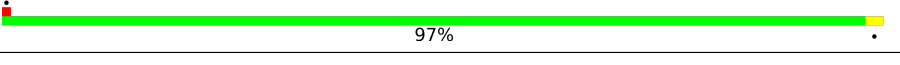
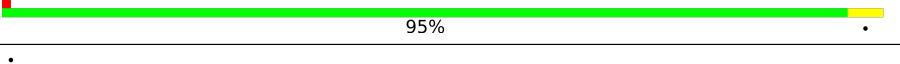
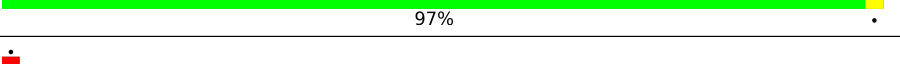
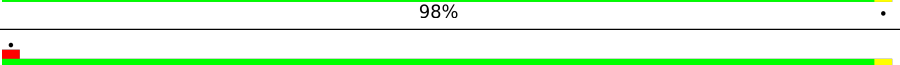
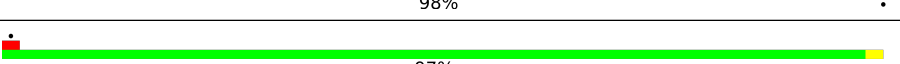
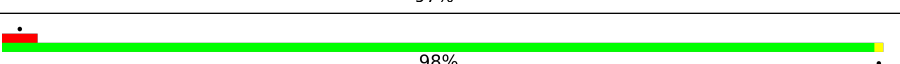
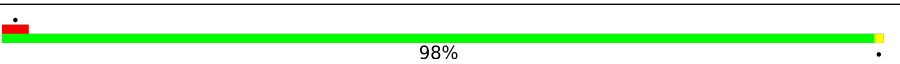
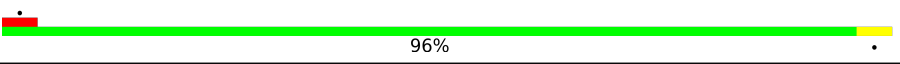
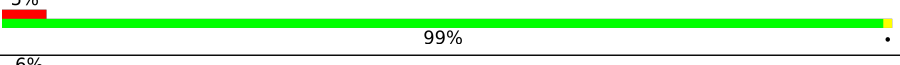
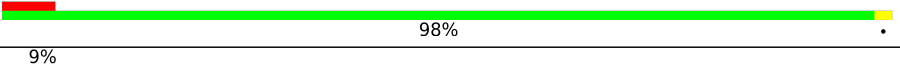
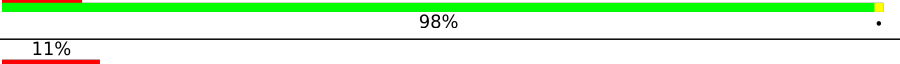
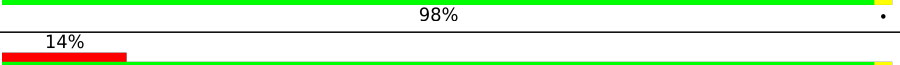
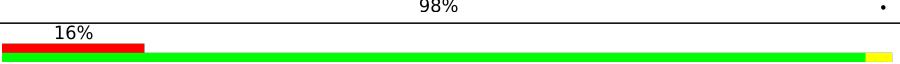
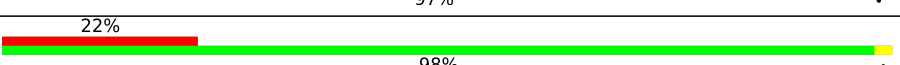
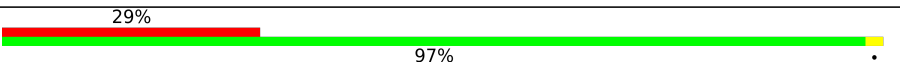
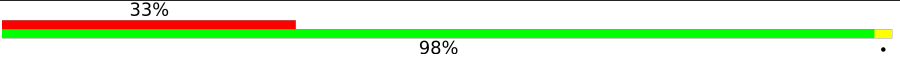
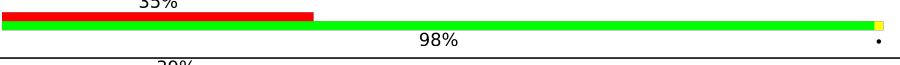
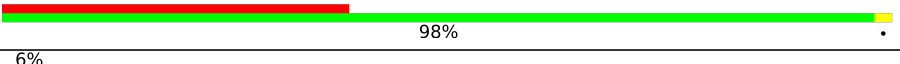
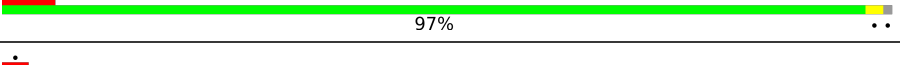
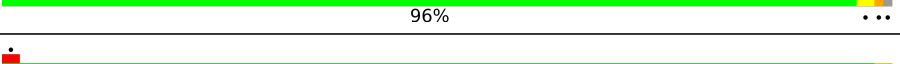
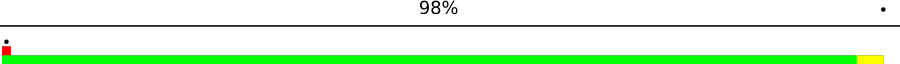
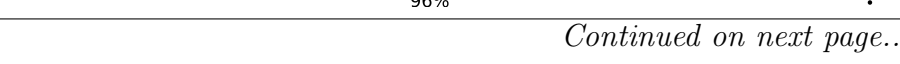


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Mol	Chain	Length	Quality of chain
3	7	260	 98%
3	8	260	 97%
3	9	260	 98%
3	AF	260	 95%
3	AG	260	 94%
3	AH	260	 93%5%
3	AI	260	 92%6%
3	AJ	260	 92%5%
3	AK	260	 91%7%
3	AL	260	 90%5%5%
3	AM	260	 92%5%
3	AN	260	 93%5%
3	ZA	260	 98%
3	ZB	260	 96%
3	ZC	260	 98%
3	ZD	260	 97%
3	ZE	260	 97%
4	ZF	403	 29%97%
4	ZG	403	 95%
4	ZH	403	 96%
4	ZI	403	 97%
4	ZJ	403	 97%
4	ZK	403	 98%
4	ZL	403	 97%
4	ZM	403	 97%

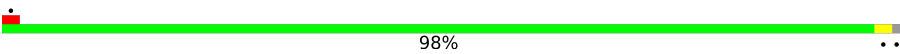



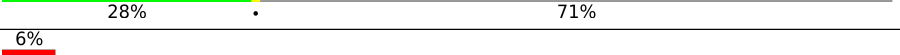
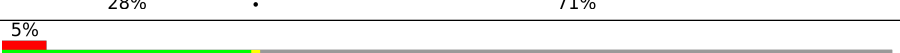









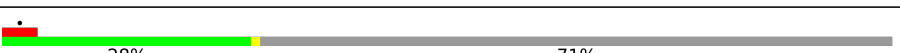





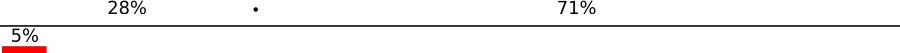



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Mol	Chain	Length	Quality of chain
4	ZN	403	 97%
4	ZO	403	 97%
4	ZP	403	 95%
4	ZQ	403	 97%
4	ZR	403	 98%
4	ZS	403	 98%
4	ZT	403	 97%
4	ZU	403	 98%
4	ZV	403	 98%
4	ZW	403	 96%
4	ZX	403	 99%
4	ZY	403	 98%
4	ZZ	403	 98%
4	Za	403	 98%
4	Zb	403	 98%
4	Zc	403	 97%
4	Zd	403	 98%
4	Ze	403	 97%
4	Zf	403	 98%
4	Zg	403	 98%
4	Zh	403	 98%
5	AA	251	 97%
5	AB	251	 96%
5	AC	251	 98%
5	AD	251	 96%

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Mol	Chain	Length	Quality of chain
5	AE	251	 98%
6	AO	560	 28% 71%
6	AP	560	 28% 71%
6	AQ	560	 28% 71%
6	AR	560	 28% 71%
6	AS	560	 28% 71%
6	AT	560	 28% 71%
6	AU	560	 28% 71%
6	AV	560	 28% 71%
6	AW	560	 28% 71%
6	AX	560	 28% 71%
6	AY	560	 28% 71%
6	AZ	560	 28% 71%
6	Aa	560	 28% 71%
6	Ac	560	 28% 71%
6	Ad	560	 28% 71%
6	Ae	560	 28% 71%
6	Af	560	 28% 71%
6	Ag	560	 28% 71%
6	Ah	560	 28% 71%
6	Ai	560	 28% 71%
6	Aj	560	 28% 71%
6	Ak	560	 28% 71%
6	Al	560	 28% 71%
6	Am	560	 28% 71%

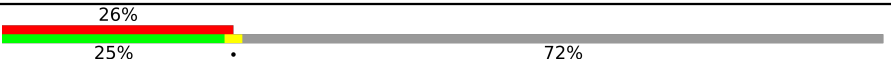


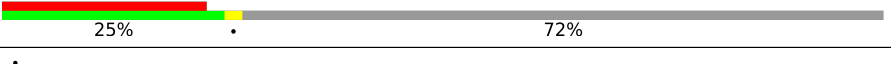



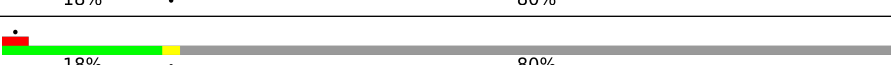
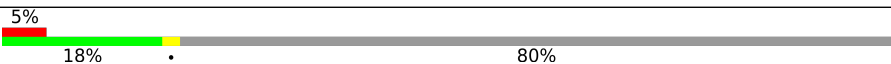

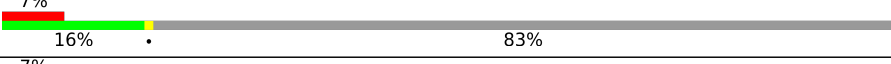




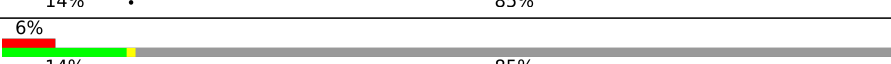









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Mol	Chain	Length	Quality of chain
6	An	560	
6	Ao	560	
6	Ap	560	
6	BG	560	
6	BH	560	
6	BI	560	
6	BJ	560	
6	BK	560	
6	BL	560	
6	BM	560	
6	BN	560	
6	BO	560	
6	BP	560	
6	BQ	560	
6	BR	560	
6	BS	560	
6	BT	560	
6	BU	560	
6	BV	560	
6	BW	560	
6	BX	560	
6	UI	560	
6	UJ	560	
6	UK	560	
6	UL	560	



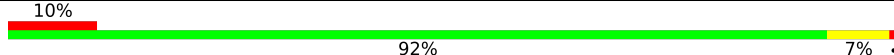
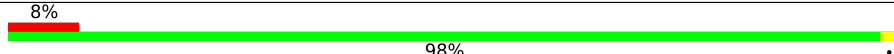
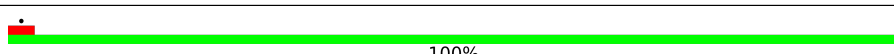
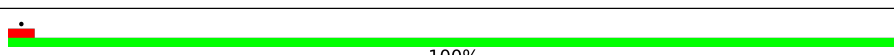
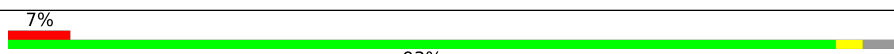
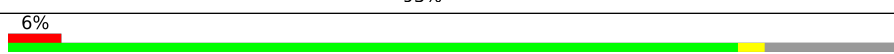

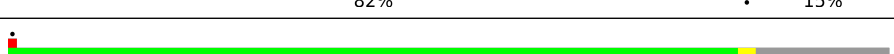
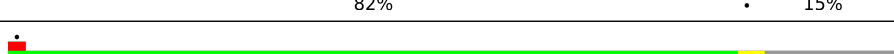
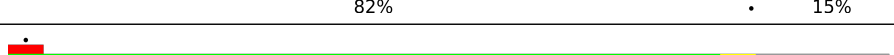
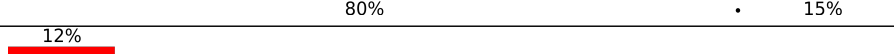
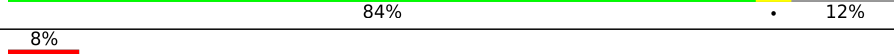





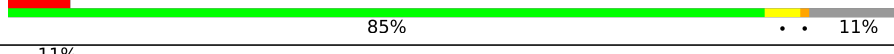
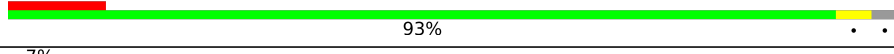
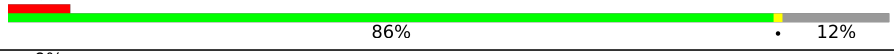


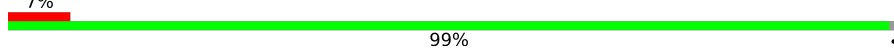
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Mol	Chain	Length	Quality of chain	
6	UM	560		
6	UN	560		
6	UO	560		
6	UP	560		
6	WA	560		
6	WB	560		
6	WC	560		
6	WD	560		
6	WE	560		
6	WF	560		
6	WG	560		
6	WH	560		
6	WI	560		
6	WJ	560		
6	WK	560		
6	WL	560		
6	WM	560		
6	WN	560		
6	WO	560		
6	WP	560		
6	WQ	560		
6	WR	560		
6	WS	560		
6	WT	560		
6	WU	560		

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Mol	Chain	Length	Quality of chain
6	WV	560	
6	WW	560	
7	Ab	89	
7	Aq	89	
7	Ar	89	
7	As	89	
8	At	264	
9	Au	245	
9	Av	245	
9	Aw	245	
9	Ax	245	
9	Ay	245	
10	A1	104	
10	A2	104	
10	A3	104	
10	A4	104	
10	A5	104	
10	Az	104	
11	A0	138	
11	A6	138	
11	A7	138	
11	A8	138	
11	A9	138	
12	BA	134	
12	BB	134	

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Mol	Chain	Length	Quality of chain
12	BC	134	<div><div>5%</div><div><div></div></div><div>98%</div><div><div></div></div><div>..</div></div>
12	BD	134	<div><div><div></div></div><div>93%</div><div>6%</div><div><div></div></div><div>.</div></div>
12	BE	134	<div><div>5%</div><div><div></div></div><div>94%</div><div><div></div></div><div><div></div></div><div>.</div></div>
12	BF	134	<div><div><div></div></div><div>94%</div><div>5%</div><div><div></div></div><div>.</div></div>

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 338664 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 L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	B	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	C	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	D	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	E	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	F	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	G	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	H	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	I	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	J	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	K	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	L	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	M	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	N	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	O	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	P	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	Q	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	S	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	T	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	U	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	V	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	W	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	X	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	Y	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	Z	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	b	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	c	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	d	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	e	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	f	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	g	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	h	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	i	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	j	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	k	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	l	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	m	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	n	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	o	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	p	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	q	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	r	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	s	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	t	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	u	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	v	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	w	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	x	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	y	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	z	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

- Molecule 3 is a protein called Flagellar basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
3	1	252	Total	C	N	O	S	0	0
			1894	1172	331	385	6		
3	2	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	4	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	5	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	6	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	7	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	8	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	9	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZA	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZB	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZC	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZD	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZE	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	AF	254	Total 1903	C 1175	N 334	O 389	S 5	0	0
3	AG	255	Total 1911	C 1181	N 335	O 390	S 5	0	0
3	AH	256	Total 1919	C 1186	N 336	O 391	S 6	0	0
3	AI	254	Total 1903	C 1175	N 334	O 389	S 5	0	0
3	AJ	255	Total 1911	C 1181	N 335	O 390	S 5	0	0
3	AK	243	Total 1823	C 1127	N 318	O 373	S 5	0	0
3	AL	248	Total 1866	C 1154	N 327	O 379	S 6	0	0
3	AM	248	Total 1866	C 1154	N 327	O 379	S 6	0	0
3	AN	248	Total 1866	C 1154	N 327	O 379	S 6	0	0

- Molecule 4 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	ZF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZH	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZI	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZJ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZK	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZL	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZM	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZN	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZO	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZP	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZQ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZR	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZS	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZT	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZU	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZV	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZW	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZX	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZY	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZZ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Za	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zb	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zc	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zd	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Ze	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zf	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zg	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zh	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AA	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
5	AB	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
5	AC	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
5	AD	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
5	AE	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

- Molecule 6 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AR	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AS	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AT	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AU	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AV	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AW	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AX	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AY	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AZ	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Aa	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ac	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ad	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ae	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Af	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ag	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ah	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ai	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Aj	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ak	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Al	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Am	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	An	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ao	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	Ap	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AO	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AP	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AQ	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	UI	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UJ	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UK	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UL	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UM	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UN	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UO	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UP	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	WA	113	Total	C	N	O	S	0	0
			849	534	148	166	1		
6	WB	111	Total	C	N	O	S	0	0
			836	526	146	163	1		
6	WC	108	Total	C	N	O	S	0	0
			812	510	142	159	1		
6	WD	110	Total	C	N	O	S	0	0
			827	522	144	160	1		
6	WE	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WF	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WG	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WH	95	Total	C	N	O	S	0	0
			703	439	126	137	1		
6	WI	95	Total	C	N	O	S	0	0
			703	439	126	137	1		
6	WJ	99	Total	C	N	O	S	0	0
			737	462	131	143	1		
6	WK	98	Total	C	N	O	S	0	0
			729	456	130	142	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	WL	85	Total	C	N	O	S	0	0
			622	389	110	122	1		
6	WM	82	Total	C	N	O	S	0	0
			596	372	107	116	1		
6	WN	84	Total	C	N	O	S	0	0
			611	380	109	121	1		
6	WO	96	Total	C	N	O	S	0	0
			714	448	127	138	1		
6	WP	100	Total	C	N	O	S	0	0
			741	464	132	144	1		
6	WQ	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WR	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WS	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WT	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WU	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WV	110	Total	C	N	O	S	0	0
			827	521	144	161	1		
6	WW	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	BG	13	Total	C	N	O		0	0
			81	50	15	16			
6	BH	16	Total	C	N	O		0	0
			103	64	19	20			
6	BI	20	Total	C	N	O		0	0
			133	83	23	27			
6	BJ	16	Total	C	N	O		0	0
			103	64	19	20			
6	BK	21	Total	C	N	O		0	0
			140	88	24	28			
6	BL	16	Total	C	N	O		0	0
			103	64	19	20			
6	BM	21	Total	C	N	O		0	0
			140	88	24	28			
6	BN	16	Total	C	N	O		0	0
			103	64	19	20			
6	BO	20	Total	C	N	O		0	0
			133	83	23	27			

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	BP	16	Total	C	N	O		0	0
			103	64	19	20			
6	BQ	21	Total	C	N	O		0	0
			140	88	24	28			
6	BR	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BS	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BT	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BU	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BV	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BW	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BX	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		

- Molecule 7 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ab	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	Aq	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	Ar	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	As	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	At	253	Total	C	N	O	S	0	0
			1945	1305	307	318	15		

- Molecule 9 is a protein called Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Au	207	Total	C	N	O	S	0	0
			1605	1072	249	272	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Av	209	Total	C	N	O	S	0	0
			1626	1086	252	276	12		
9	Aw	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
9	Ax	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
9	Ay	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 10 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Az	59	Total	C	N	O	S	0	0
			429	265	74	83	7		
10	A1	91	Total	C	N	O	S	0	0
			672	415	121	129	7		
10	A2	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
10	A3	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
10	A4	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
10	A5	92	Total	C	N	O	S	0	0
			679	420	122	130	7		

- Molecule 11 is a protein called Flagellar basal body rod protein FlgB.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A6	134	Total	C	N	O	S	0	0
			1030	633	189	203	5		
11	A7	121	Total	C	N	O	S	0	0
			942	583	172	182	5		
11	A8	125	Total	C	N	O	S	0	0
			967	598	177	187	5		
11	A9	127	Total	C	N	O	S	0	0
			982	606	182	189	5		
11	A0	123	Total	C	N	O	S	0	0
			950	588	172	185	5		

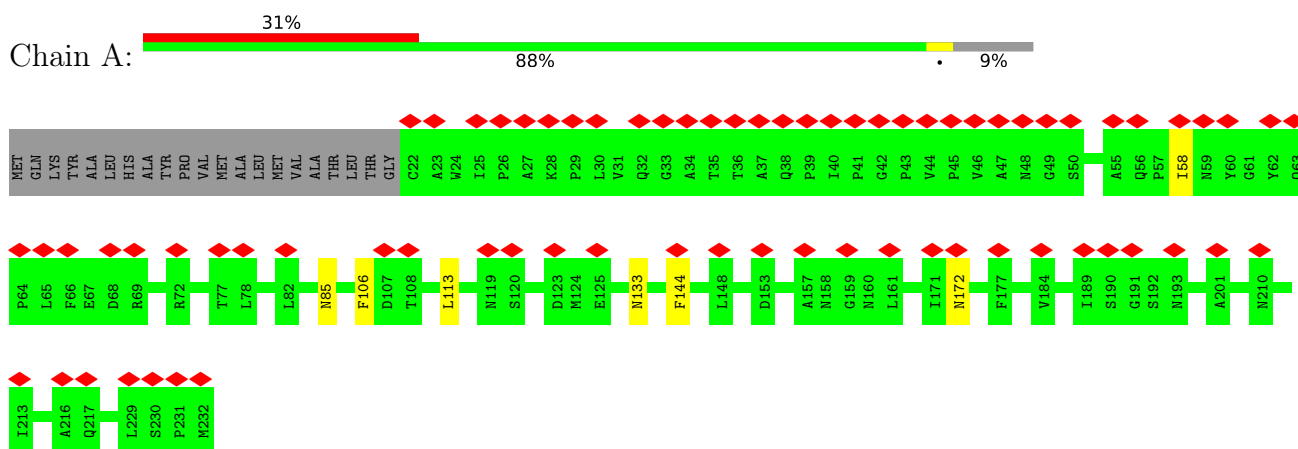
- Molecule 12 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BA	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BB	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
12	BC	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BD	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BE	131	Total	C	N	O	S	0	0
			956	595	165	191	5		
12	BF	133	Total	C	N	O	S	0	0
			969	604	167	193	5		

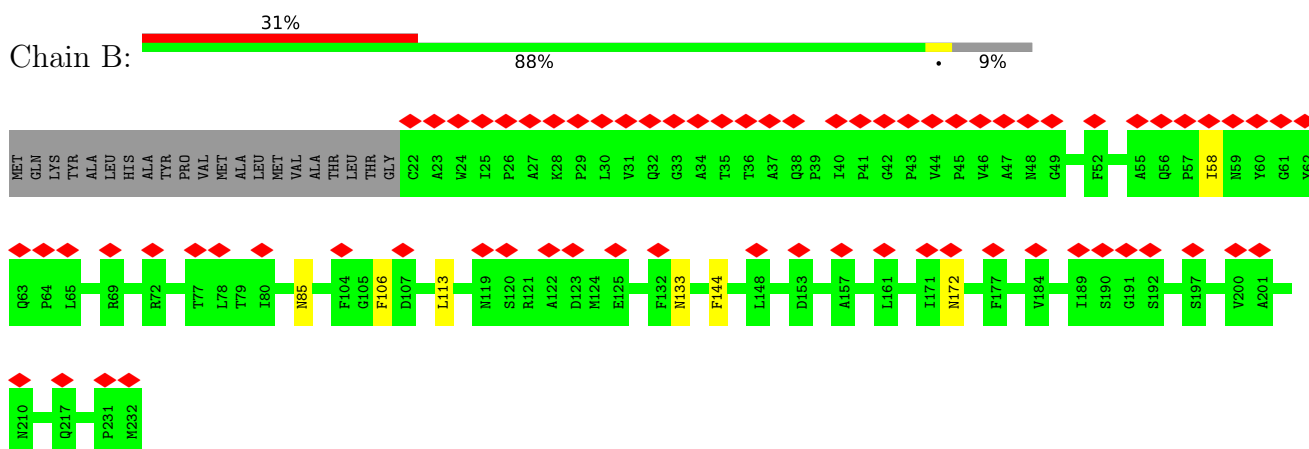
3 Residue-property plots [i](#)

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.

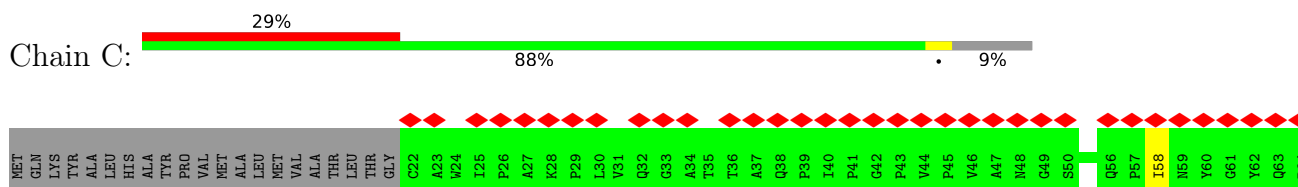
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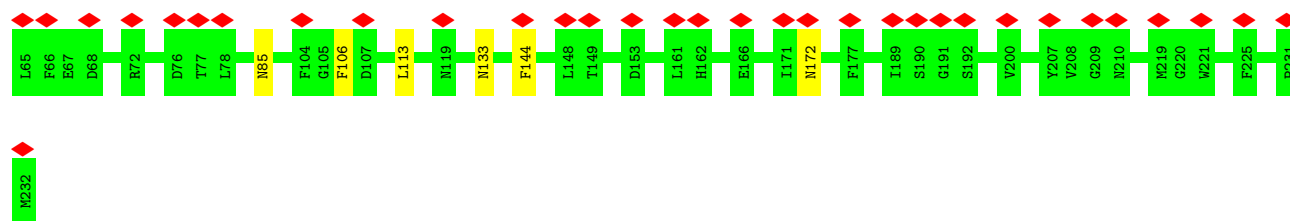


- Molecule 1: Flagellar L-ring protein



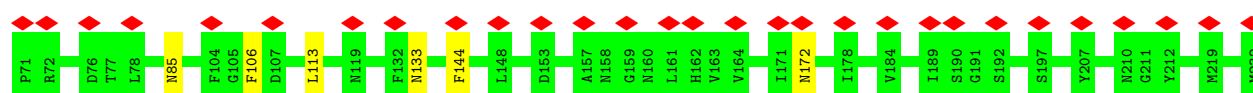
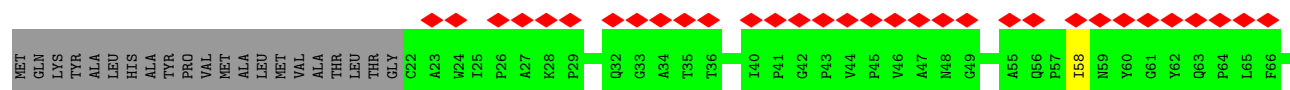
- Molecule 1: Flagellar L-ring protein





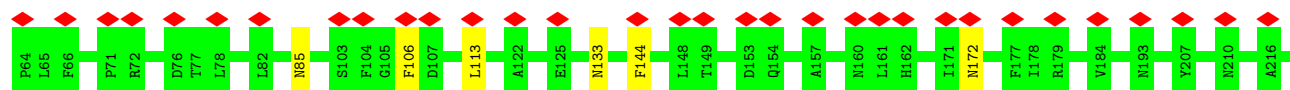
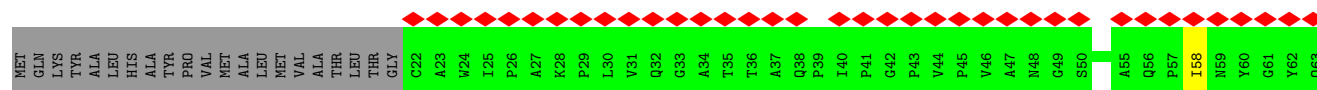
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Chain D: 26% 88% 9%



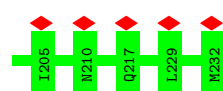
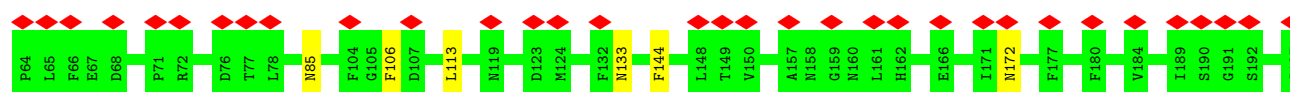
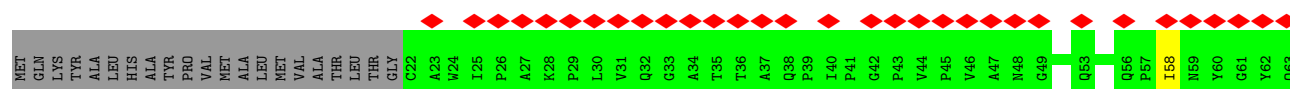
- Molecule 1: Flagellar L-ring protein

Chain E: 31% 88% 9%

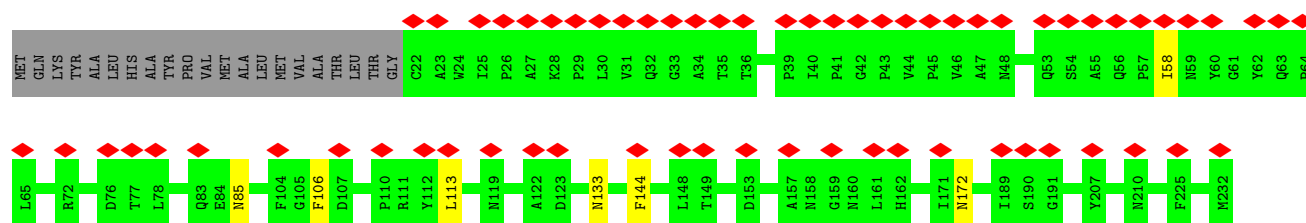


- Molecule 1: Flagellar L-ring protein

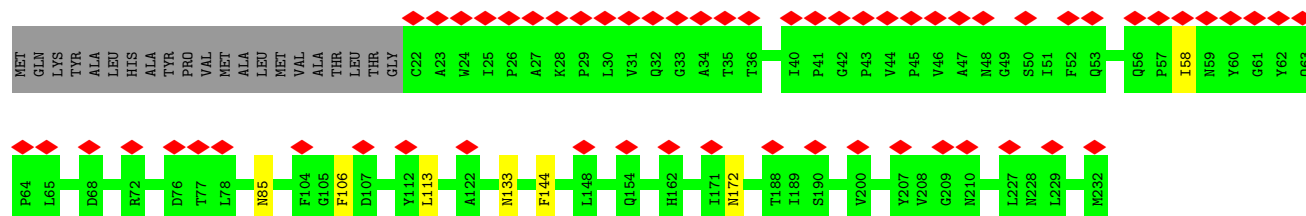
Chain F: 30% 88% 9%



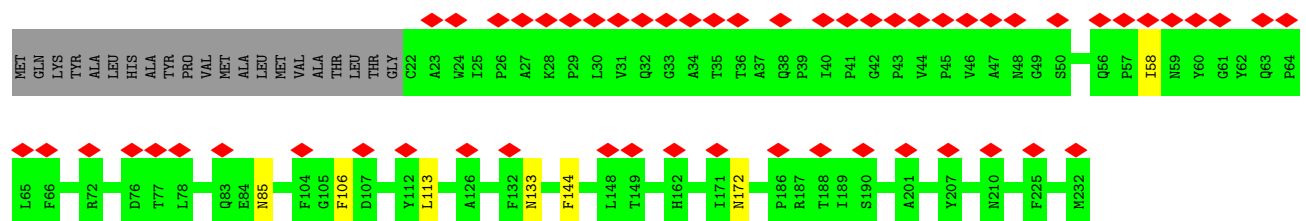
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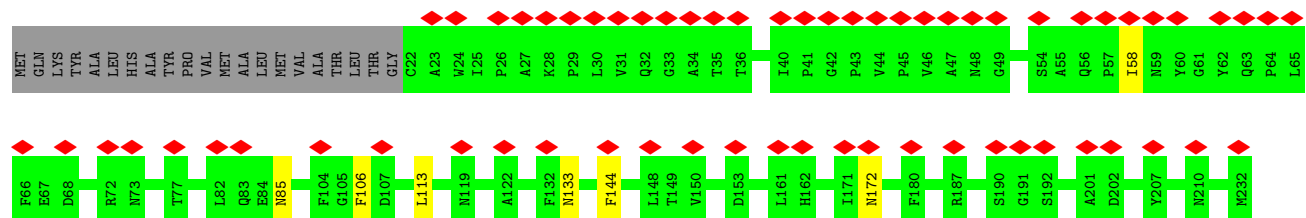
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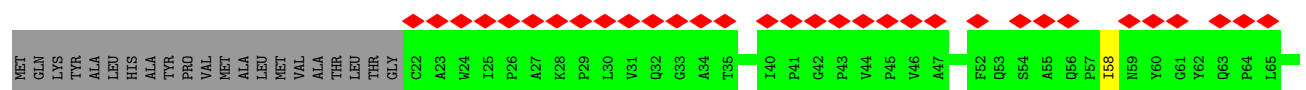
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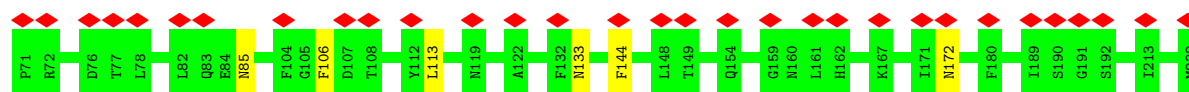


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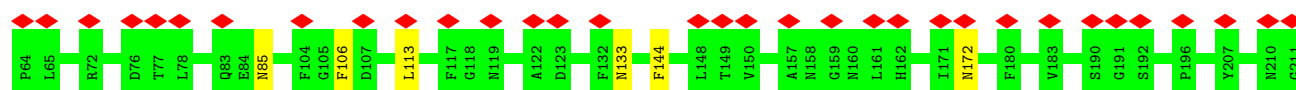
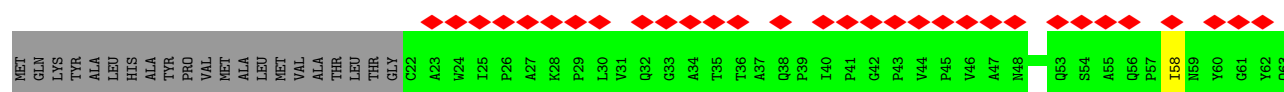
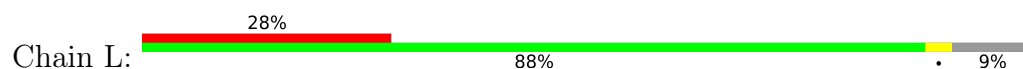


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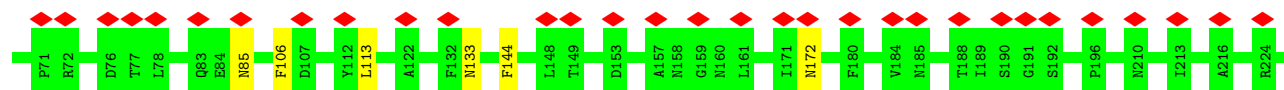
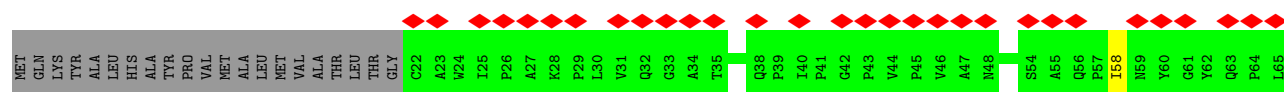
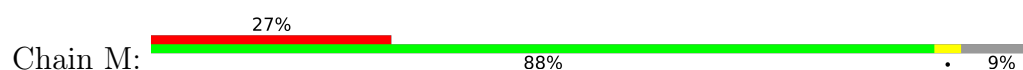




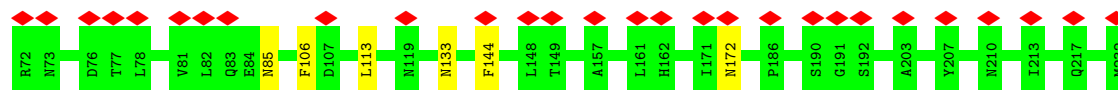
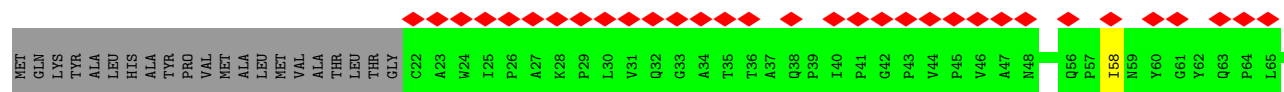
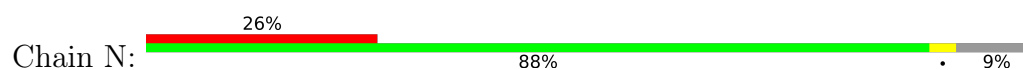
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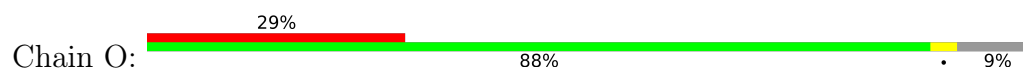
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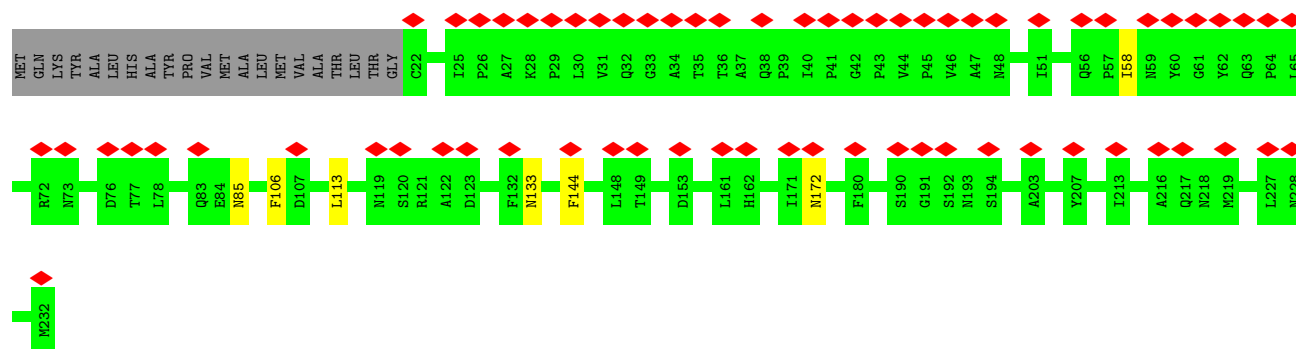


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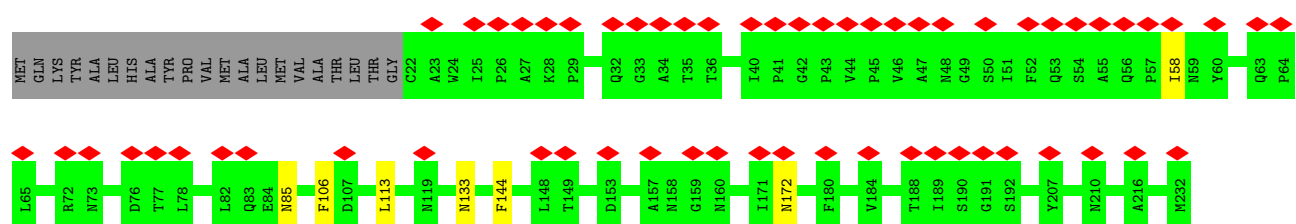
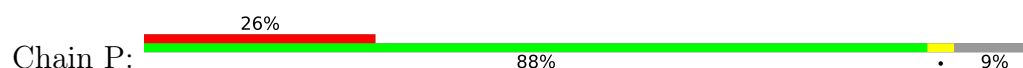


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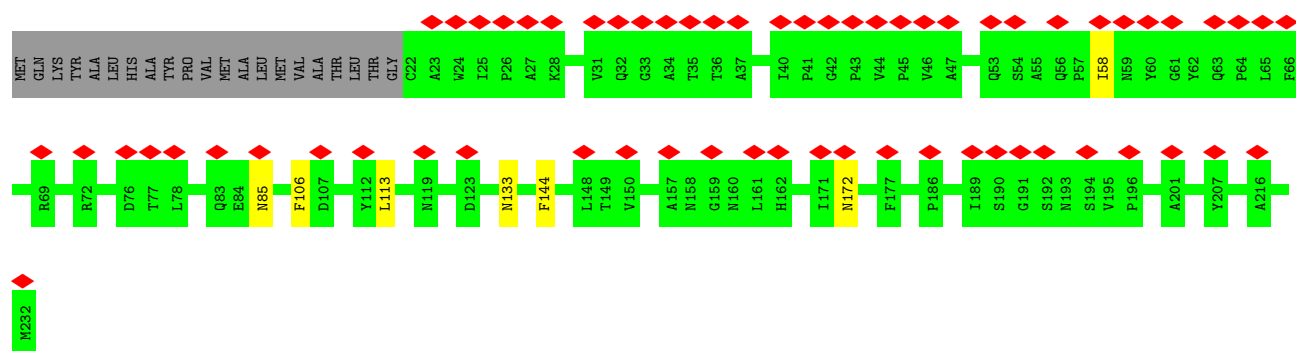
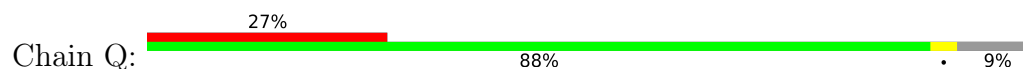




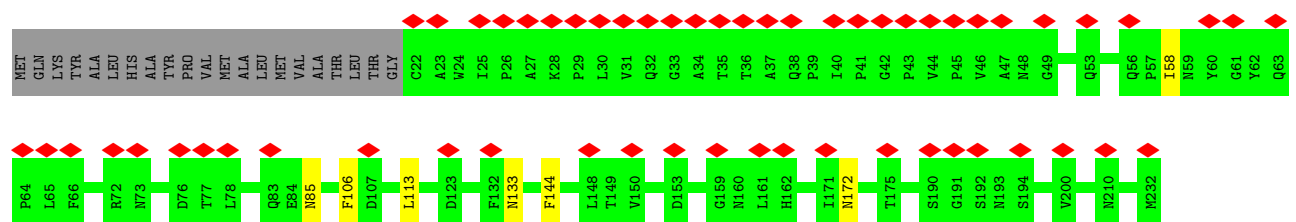
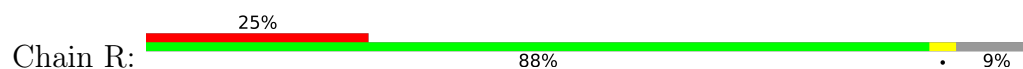
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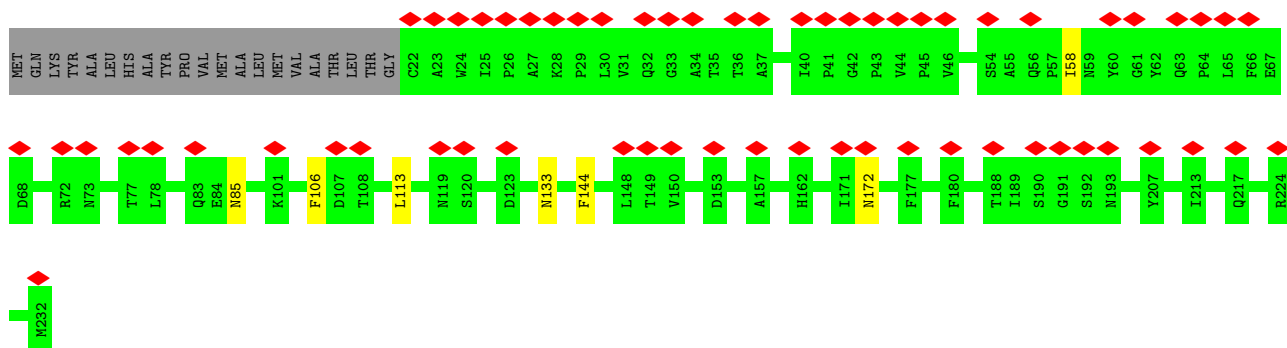
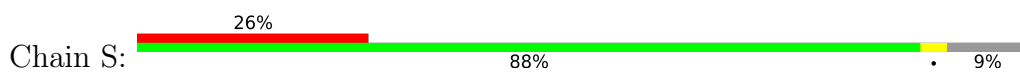
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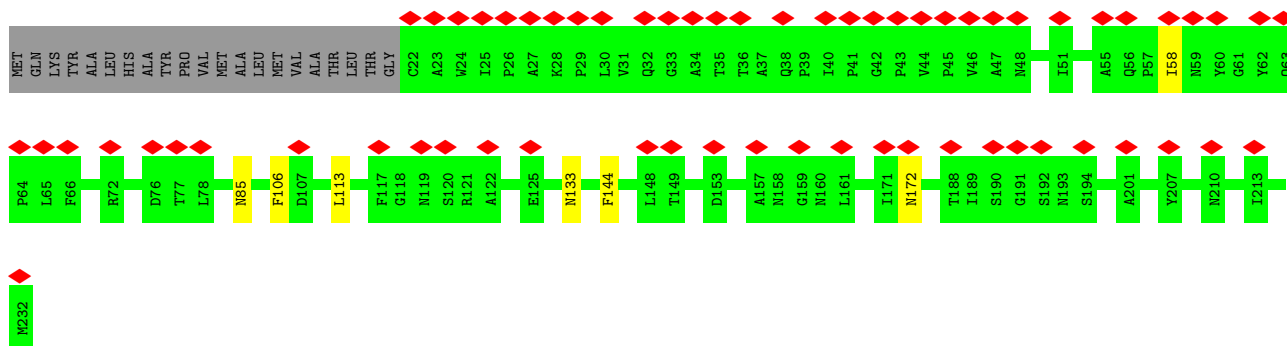
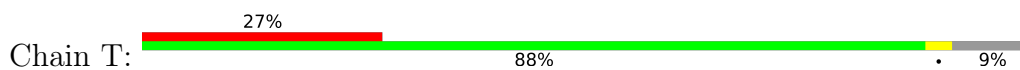
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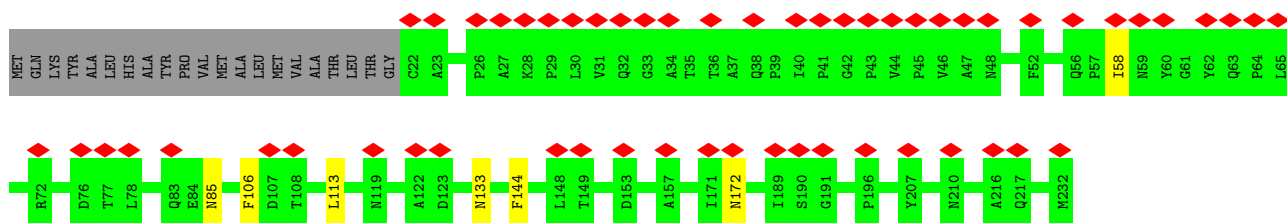
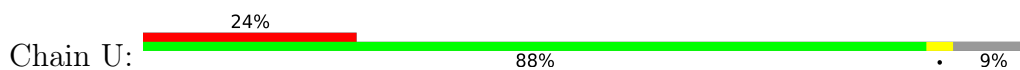
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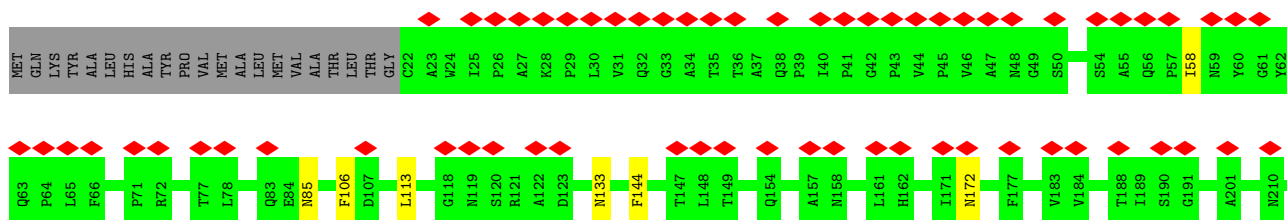
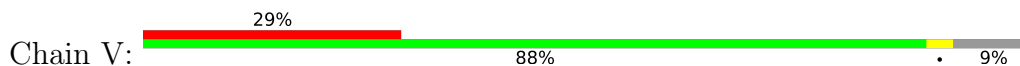
- Molecule 1: Flagellar L-ring protein

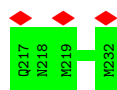


- Molecule 1: Flagellar L-ring protein

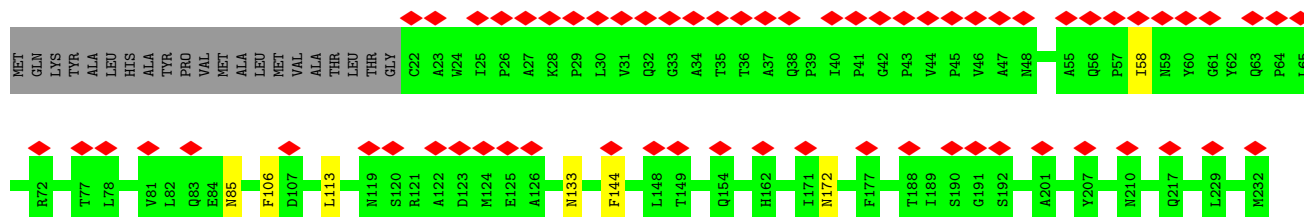
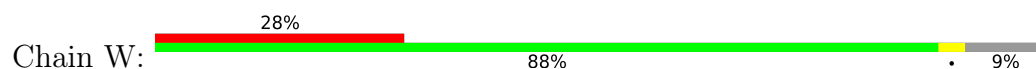


- Molecule 1: Flagellar L-ring protein

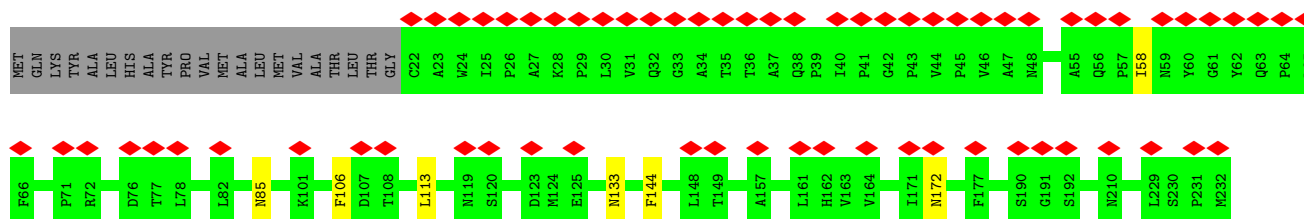
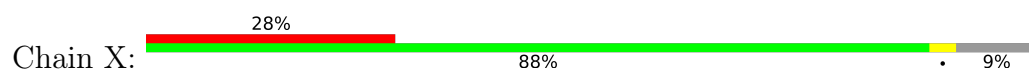




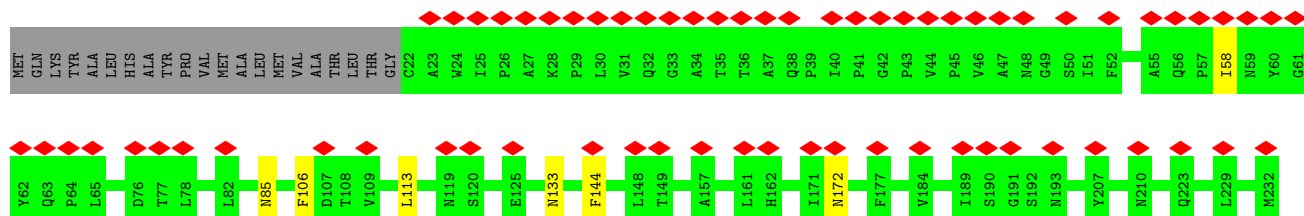
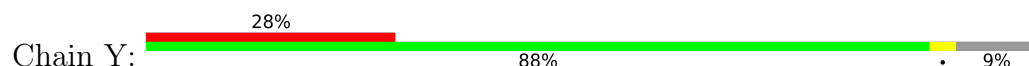
• Molecule 1: Flagellar L-ring protein



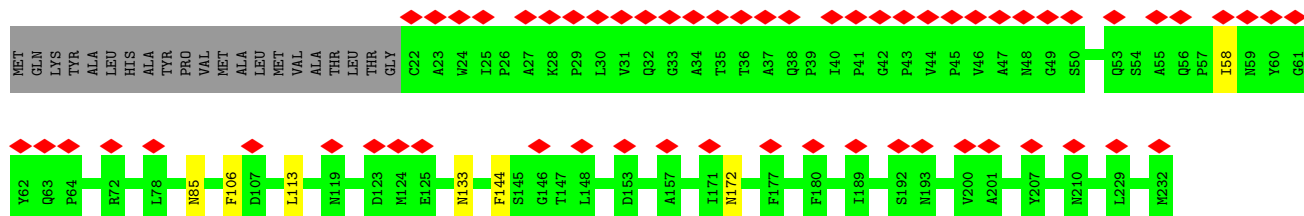
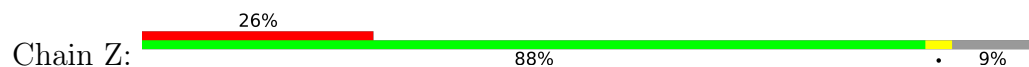
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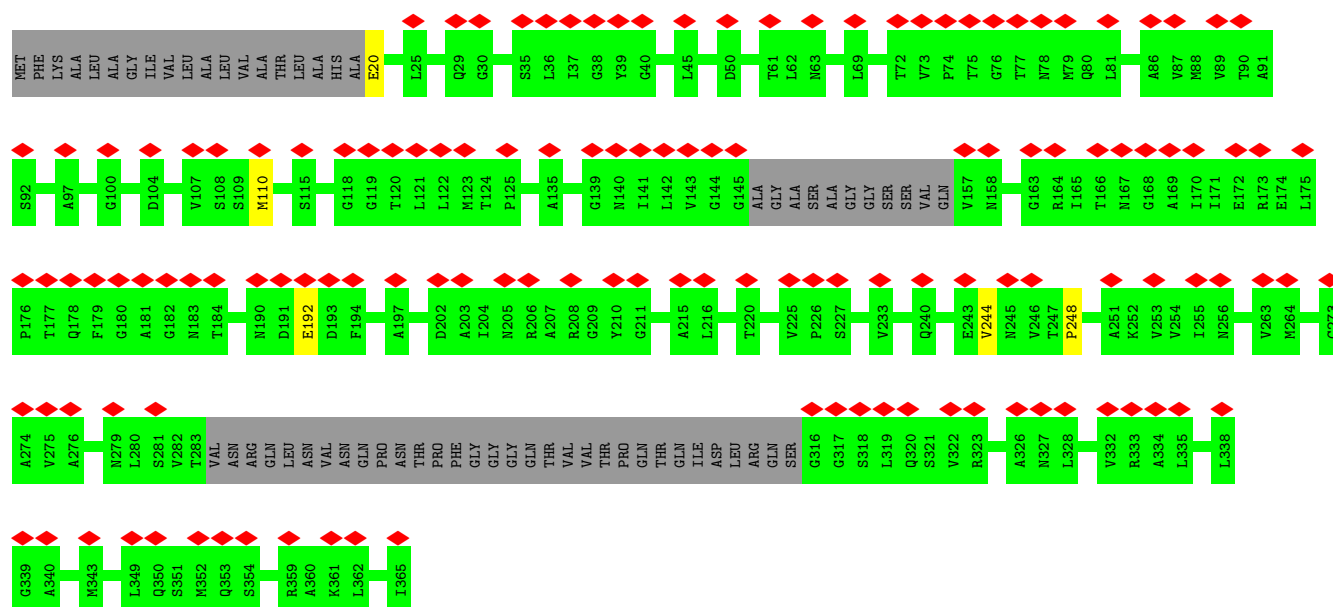
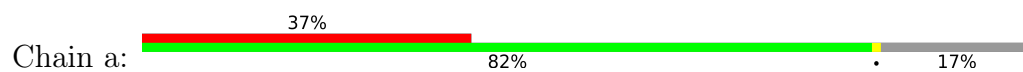
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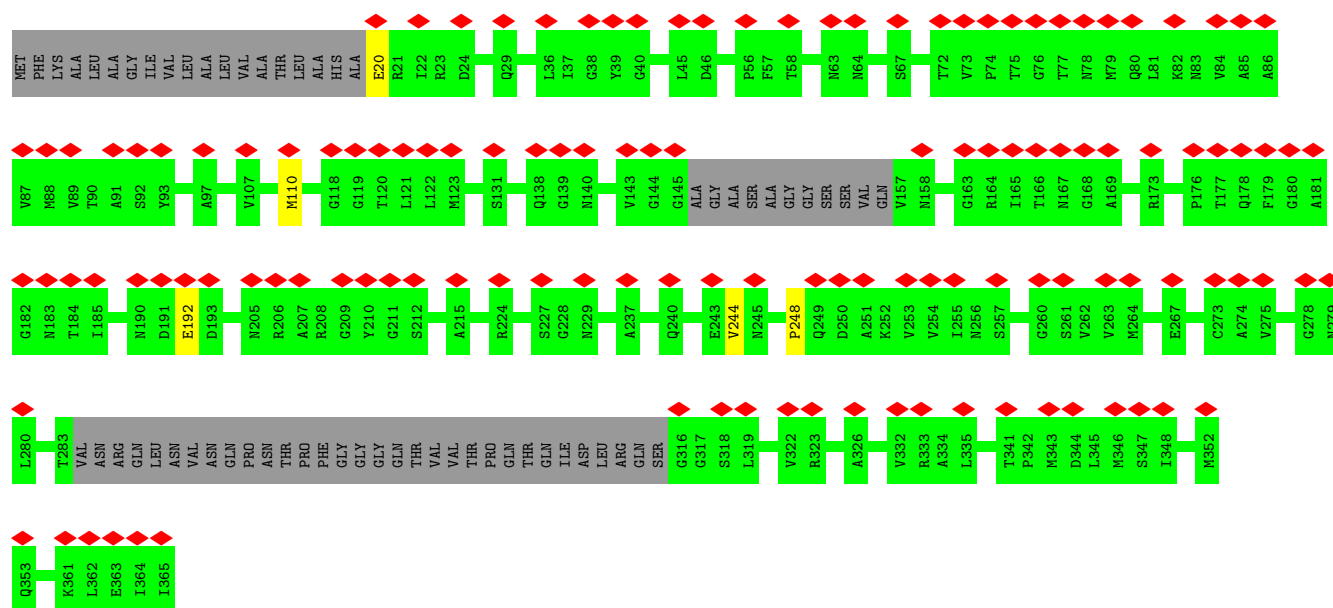
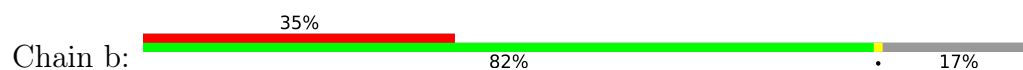
• Molecule 1: Flagellar L-ring protein



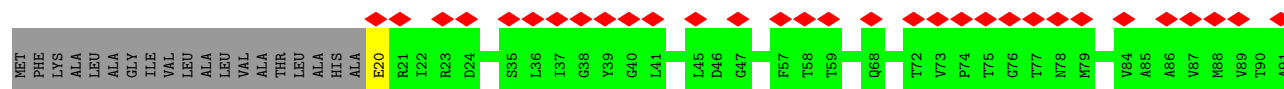
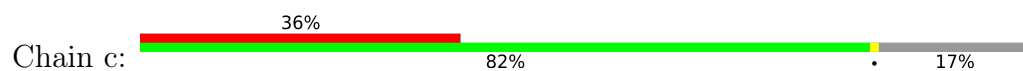
• Molecule 2: Flagellar P-ring protein

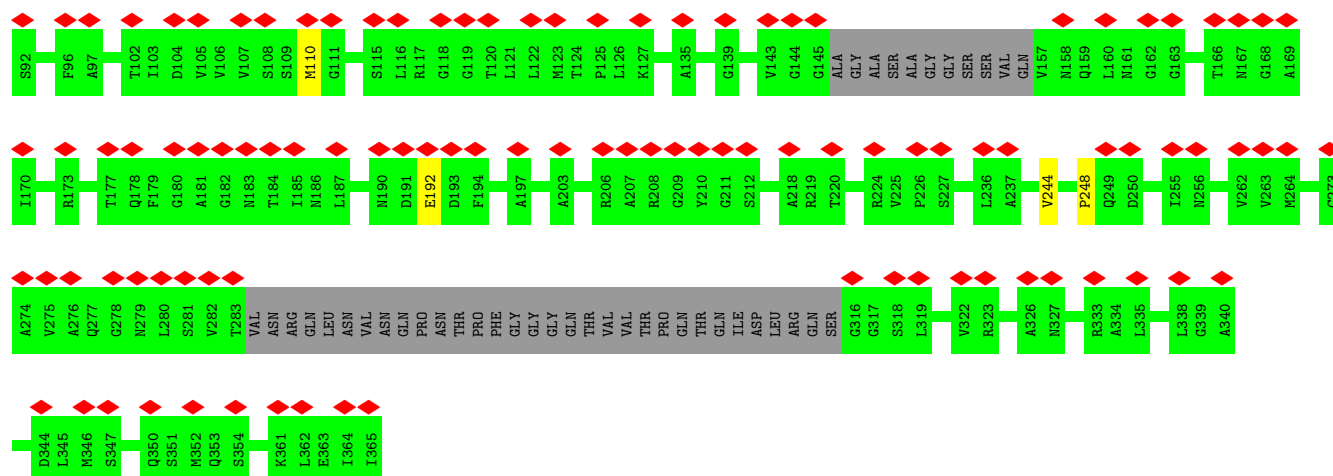


• Molecule 2: Flagellar P-ring protein



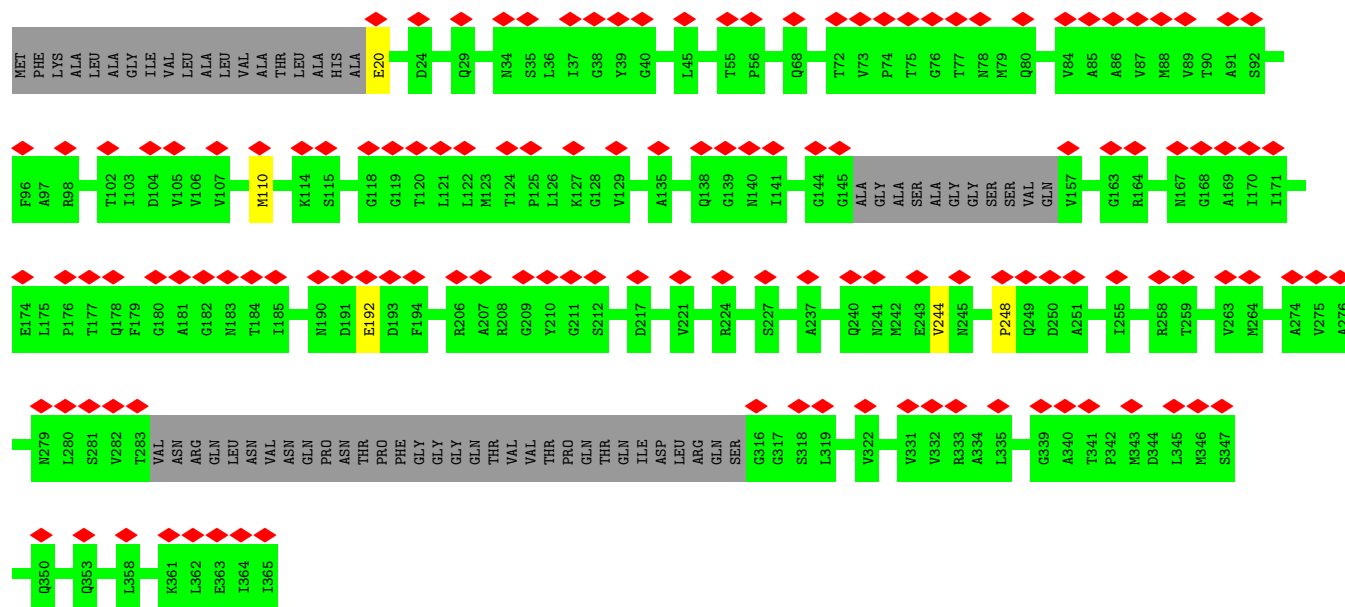
• Molecule 2: Flagellar P-ring protein





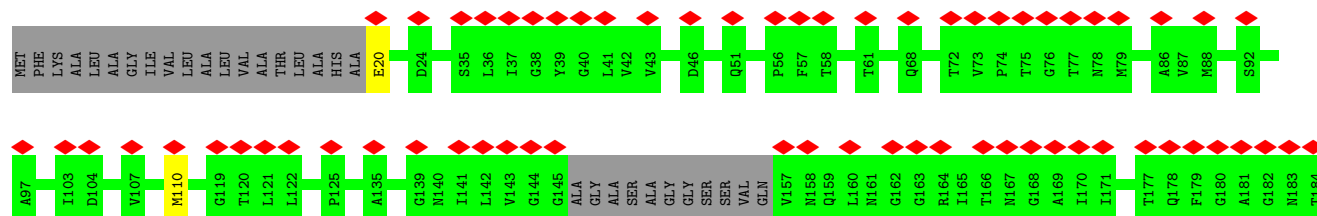
• Molecule 2: Flagellar P-ring protein

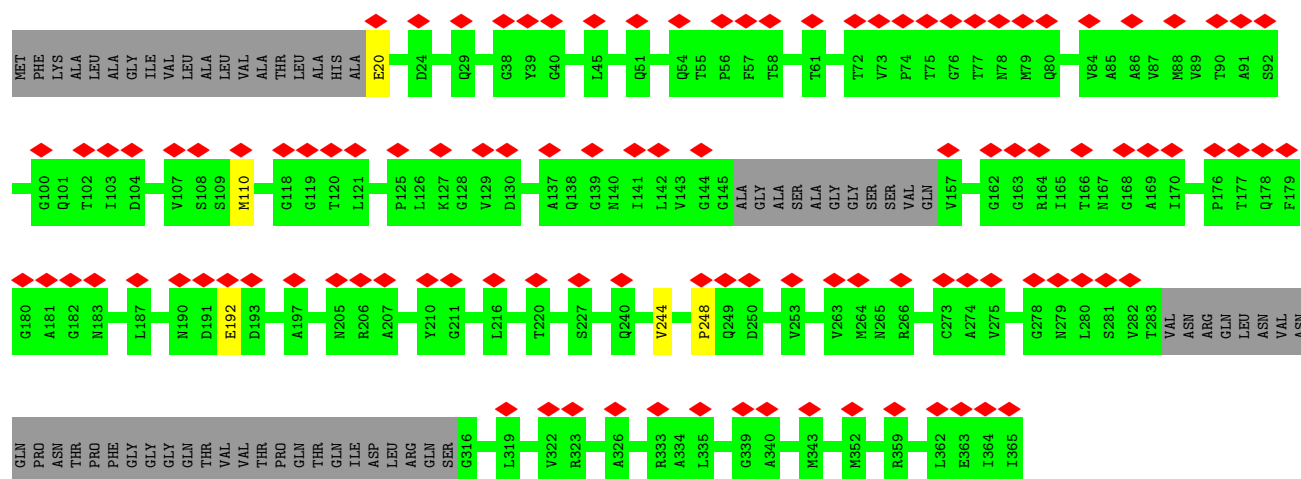
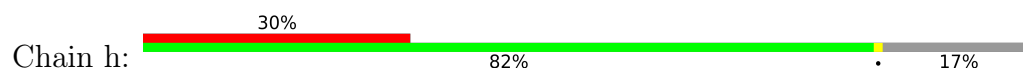
Chain d: 36% 82% 17%



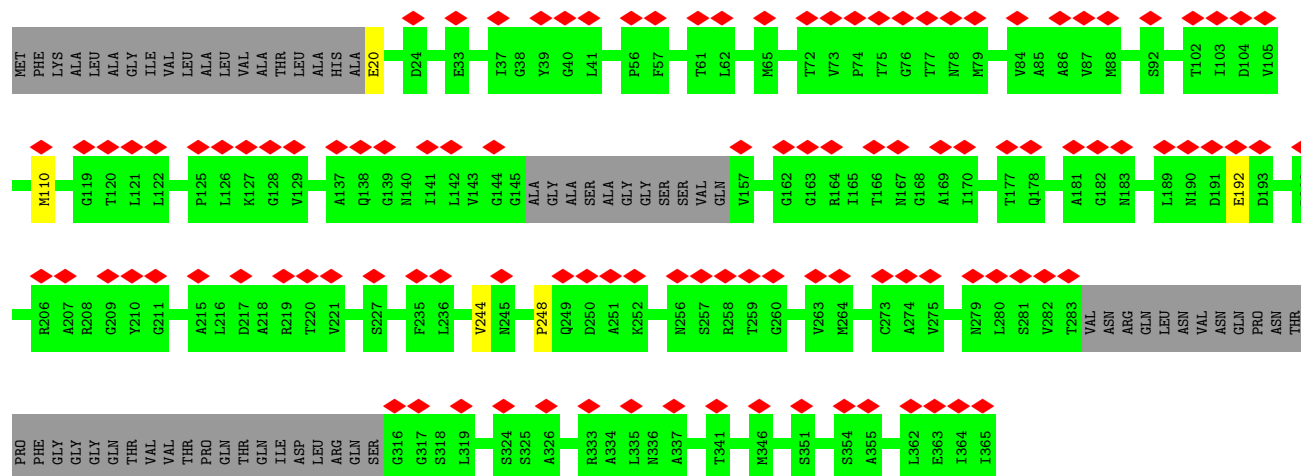
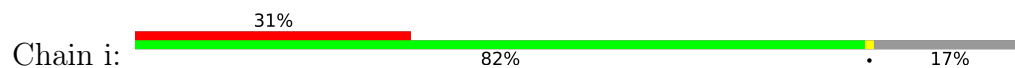
• Molecule 2: Flagellar P-ring protein

Chain e: 39% 82% 17%

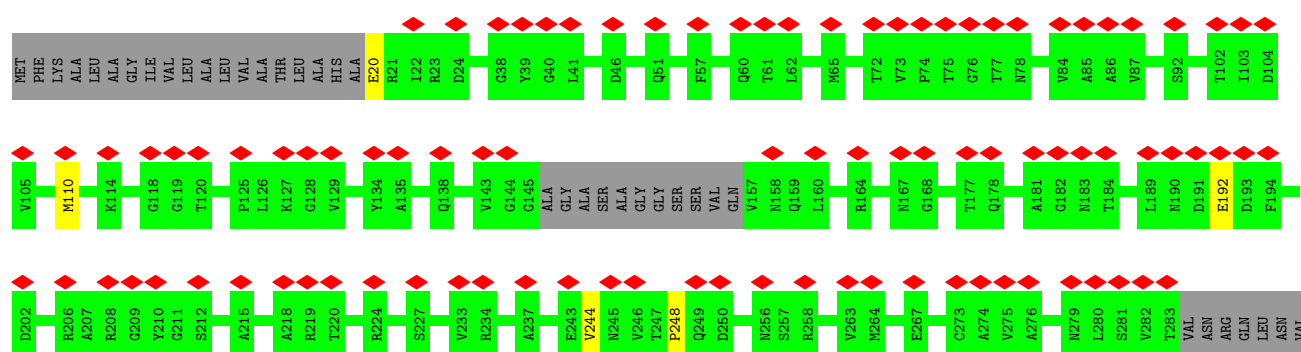
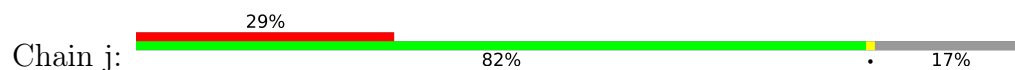


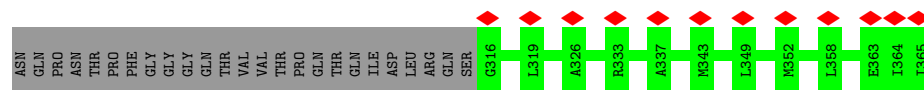


• Molecule 2: Flagellar P-ring protein

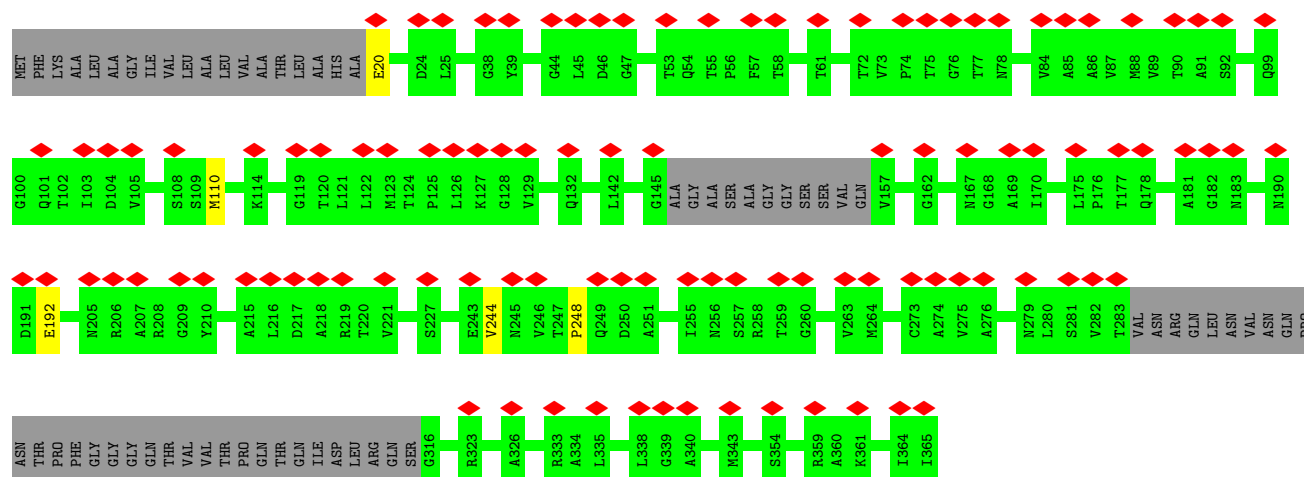
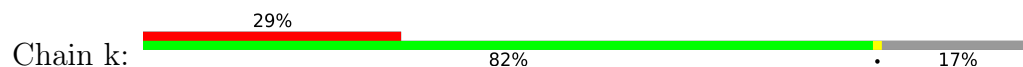


• Molecule 2: Flagellar P-ring protein

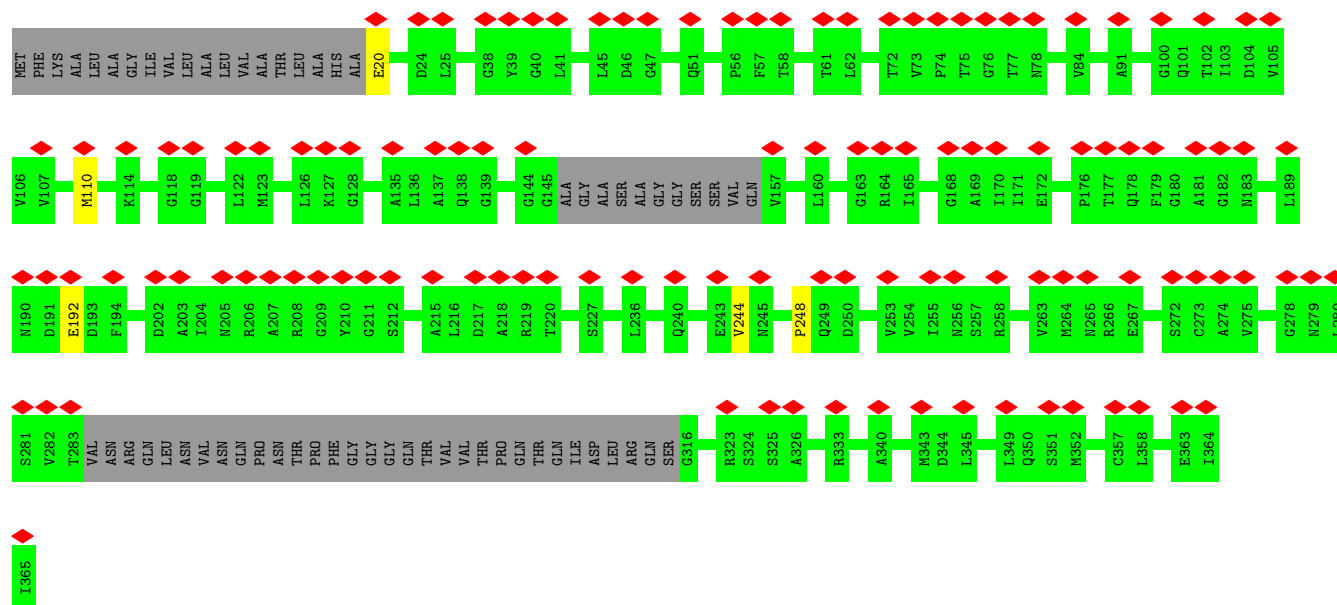
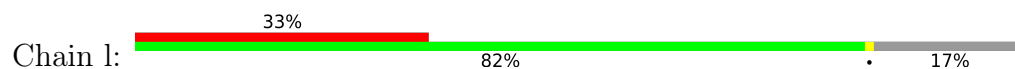




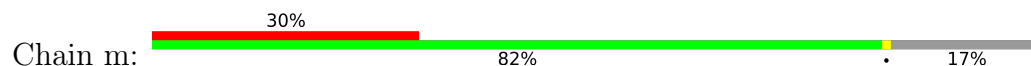
• Molecule 2: Flagellar P-ring protein

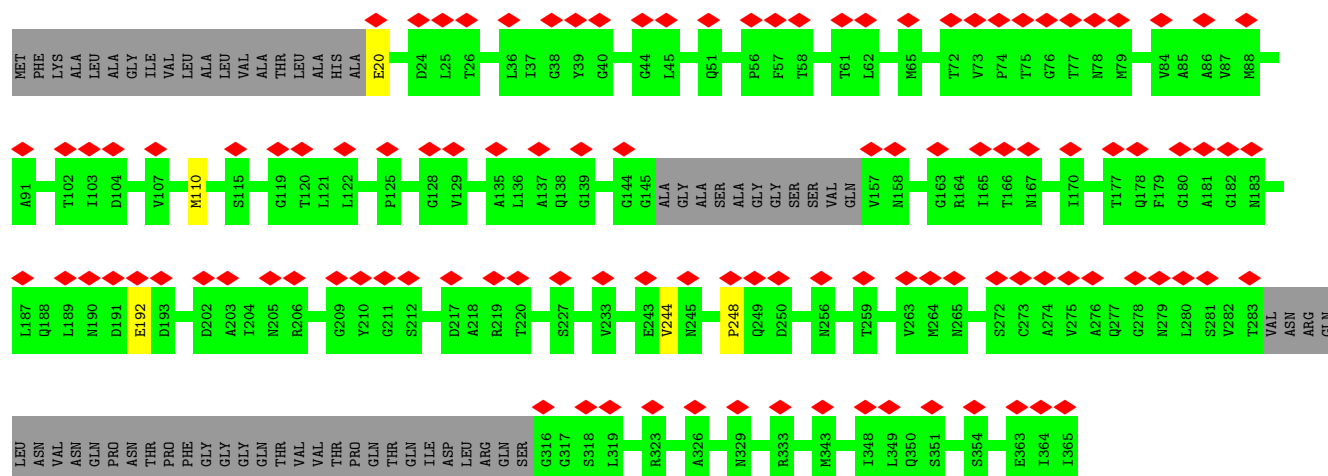


• Molecule 2: Flagellar P-ring protein

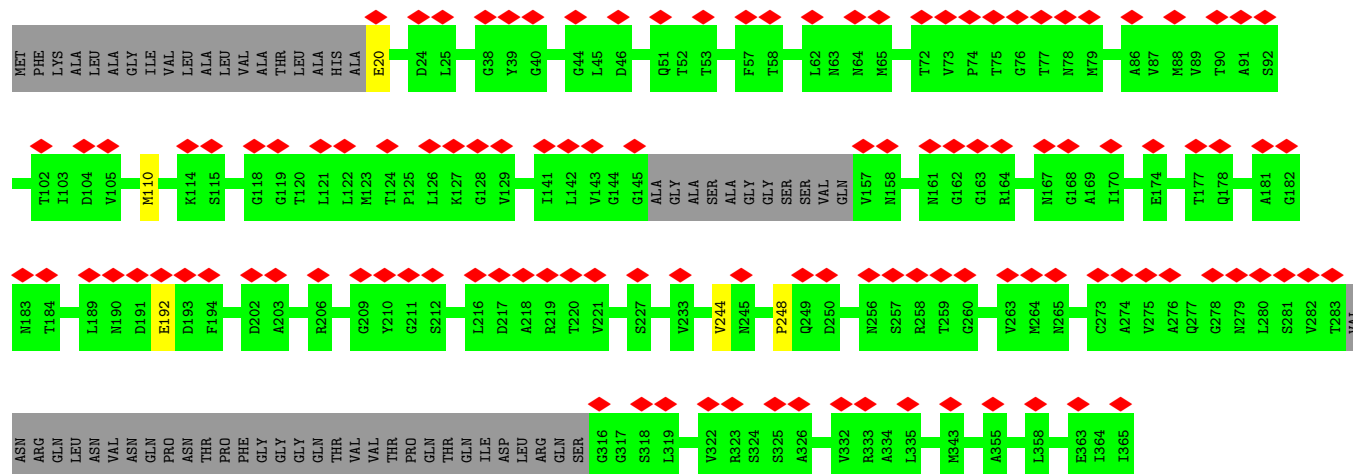
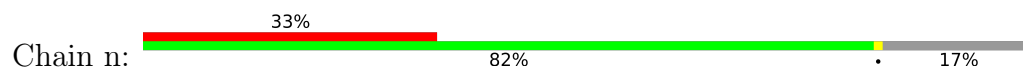


• Molecule 2: Flagellar P-ring protein

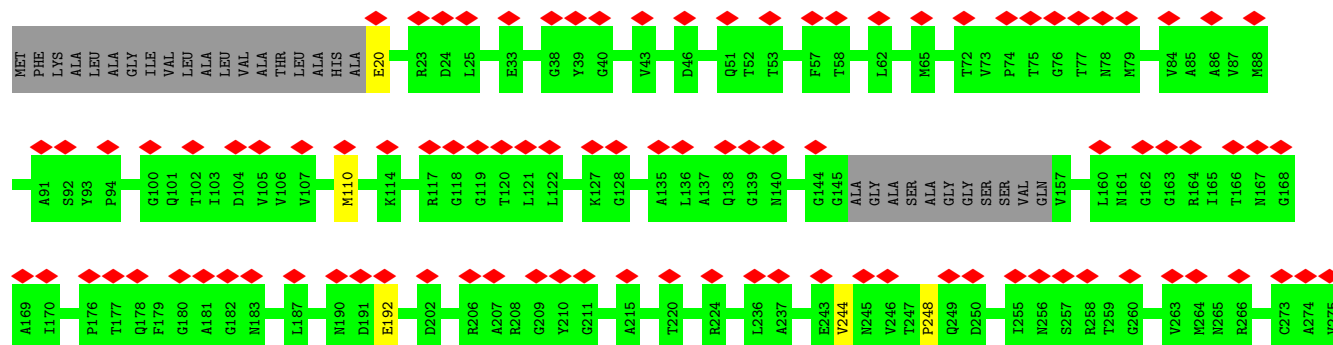
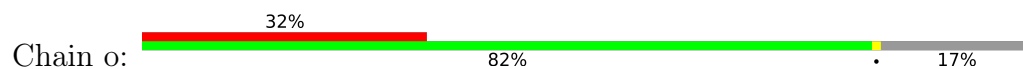


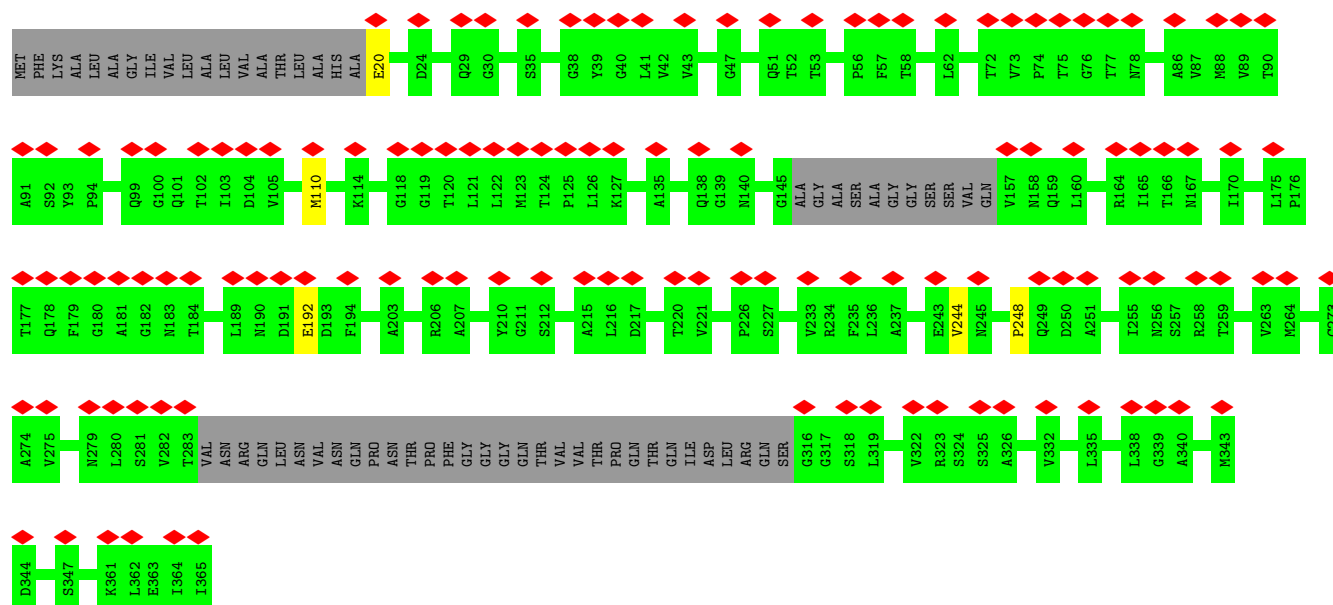


• Molecule 2: Flagellar P-ring protein



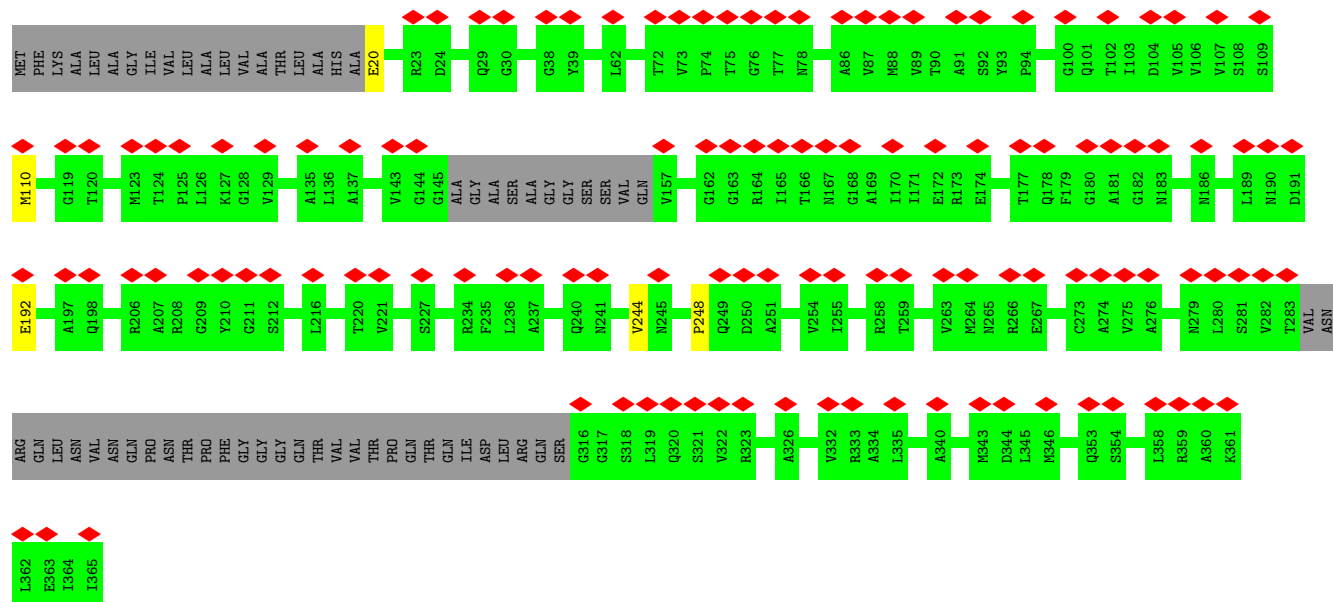
• Molecule 2: Flagellar P-ring protein





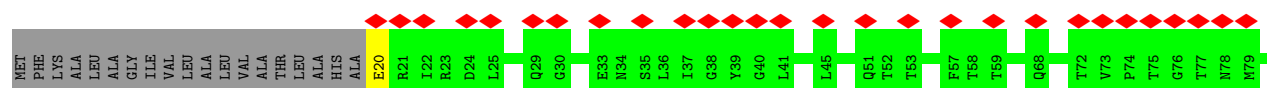
• Molecule 2: Flagellar P-ring protein

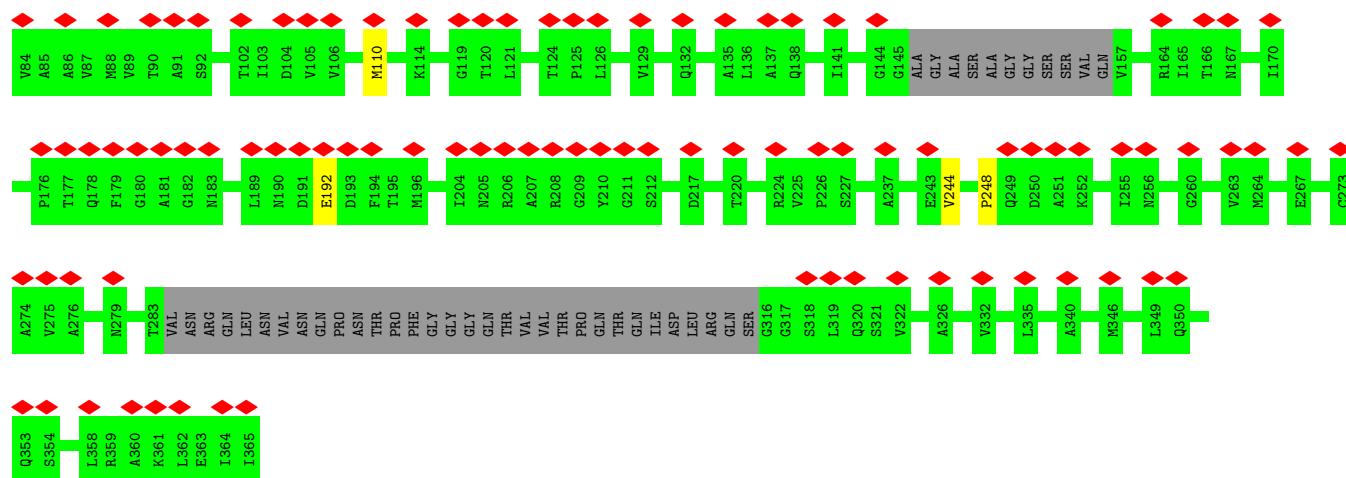
Chain s: 34% 82% 17%



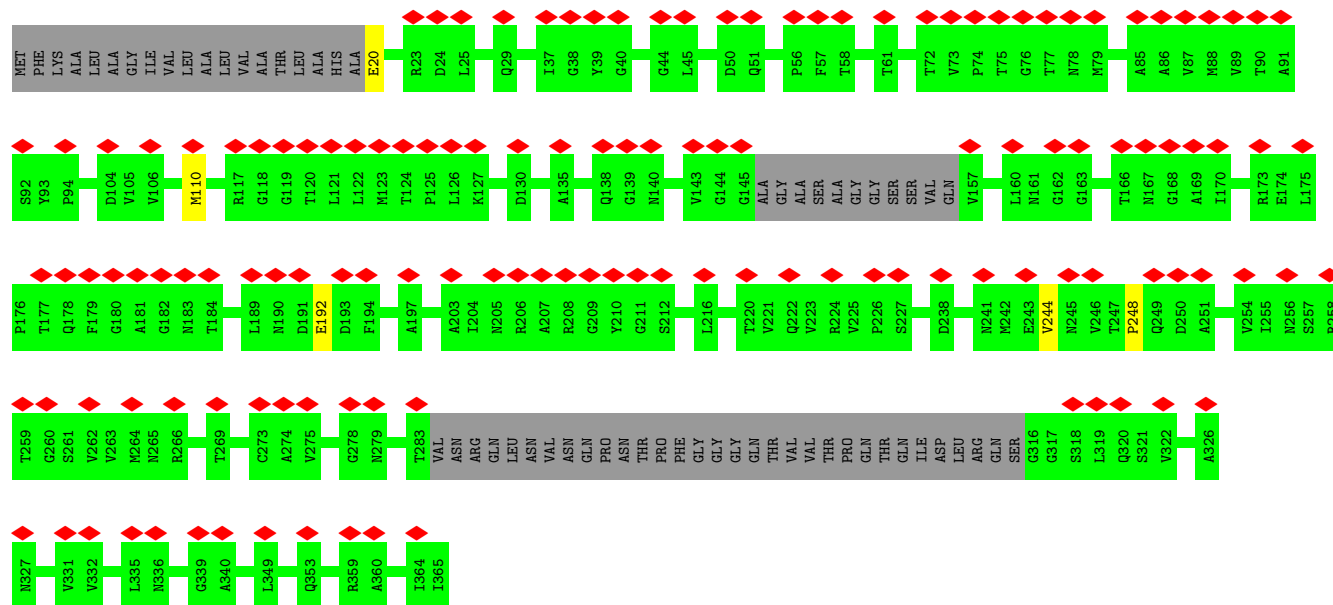
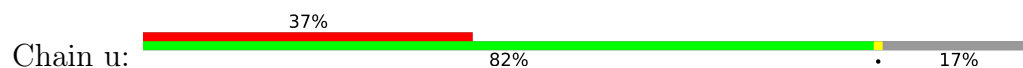
• Molecule 2: Flagellar P-ring protein

Chain t: 33% 82% 17%

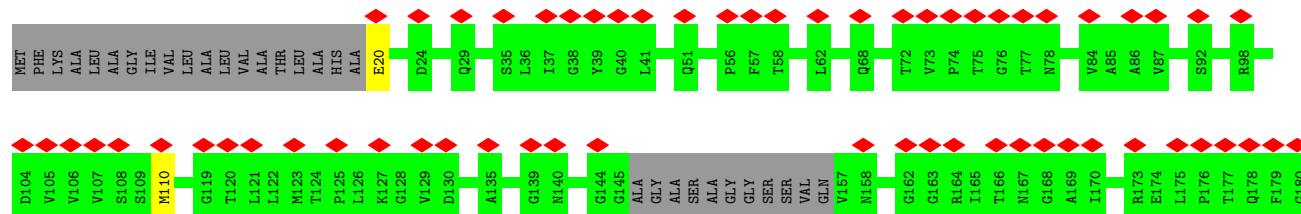
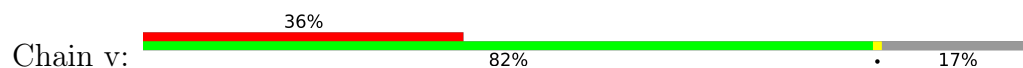


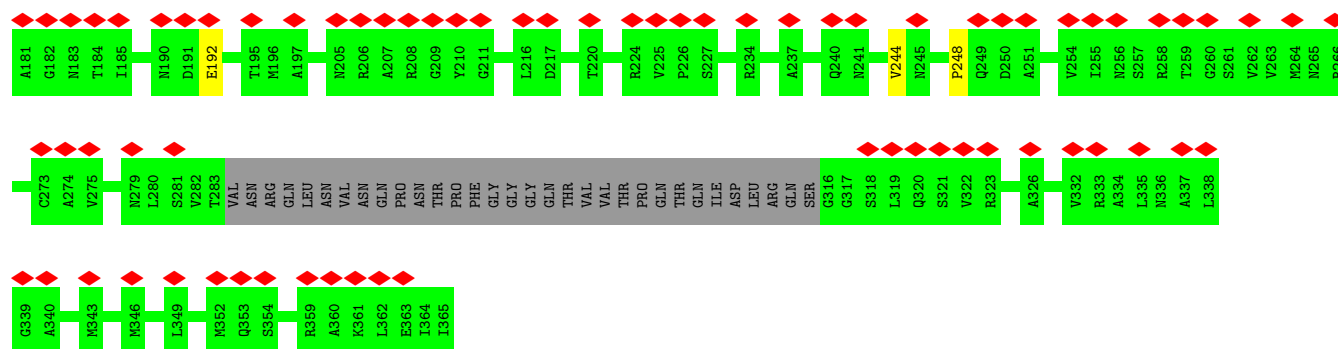


• Molecule 2: Flagellar P-ring protein

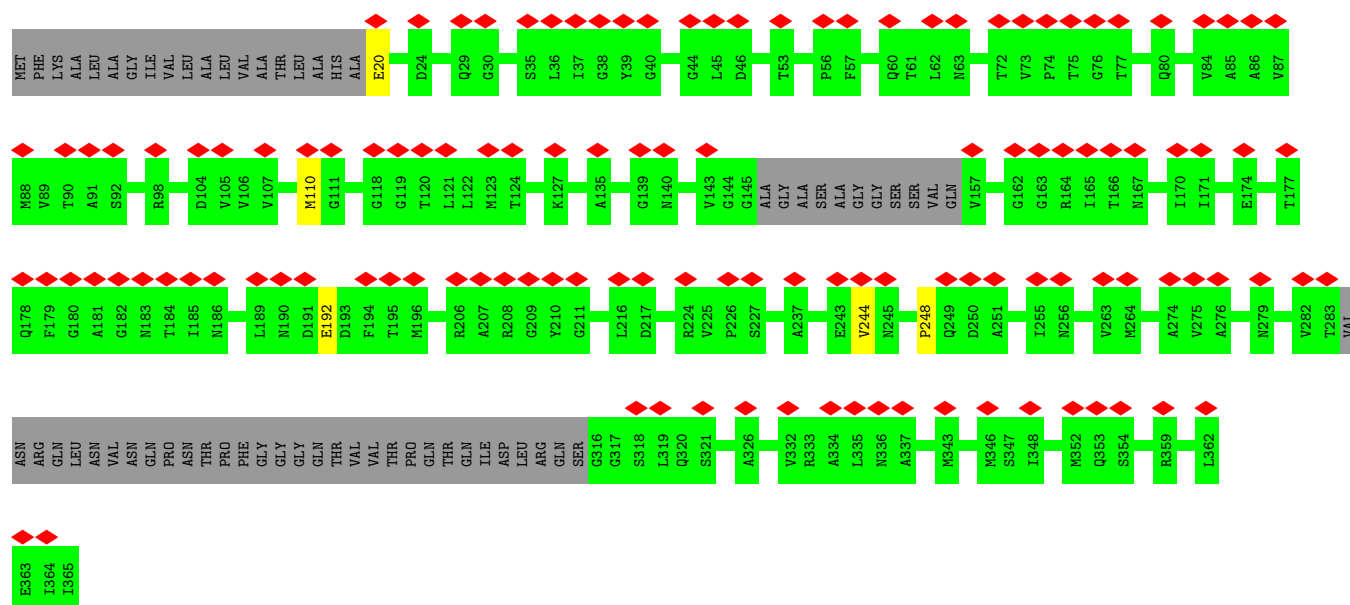
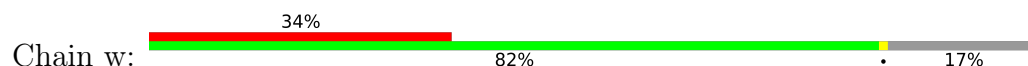


• Molecule 2: Flagellar P-ring protein

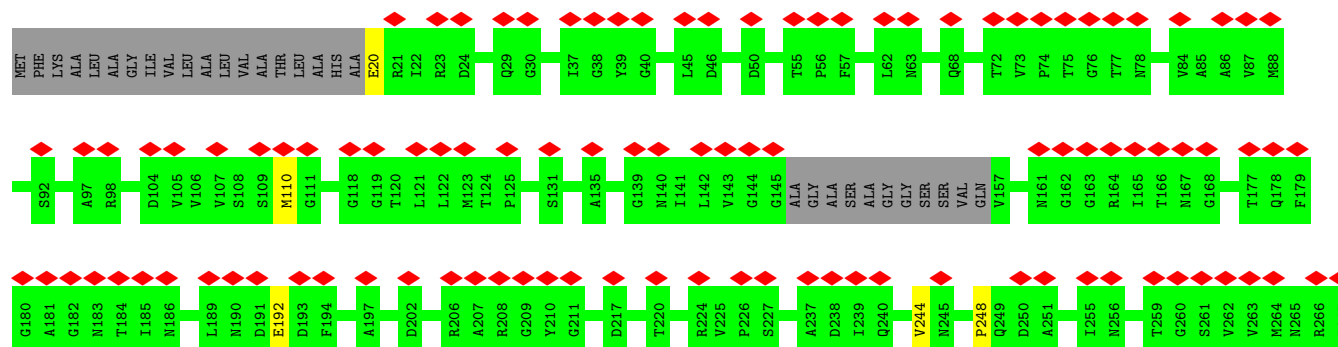
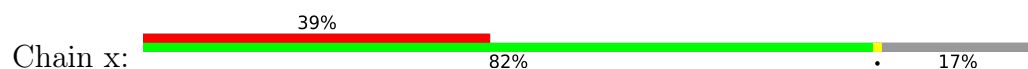


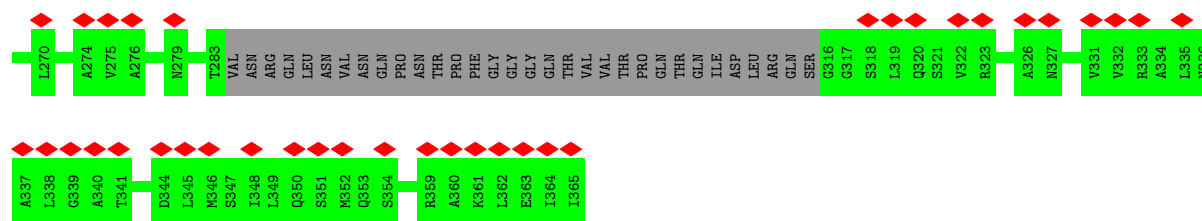


• Molecule 2: Flagellar P-ring protein

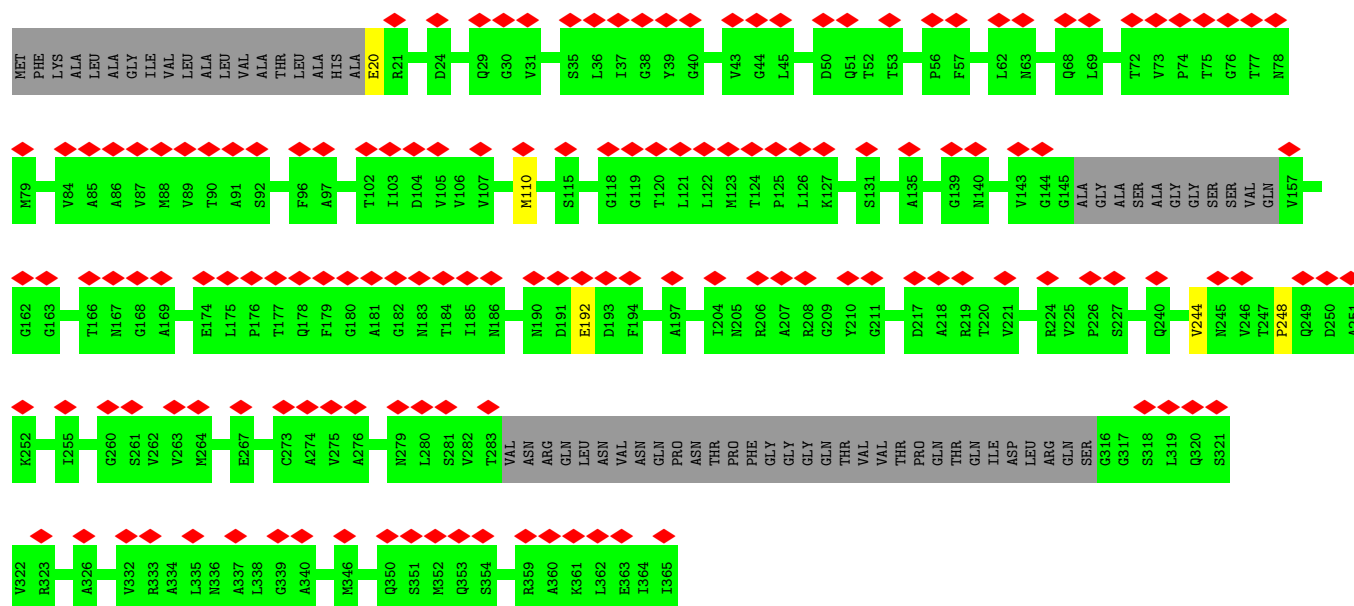
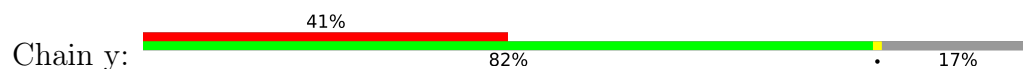


• Molecule 2: Flagellar P-ring protein

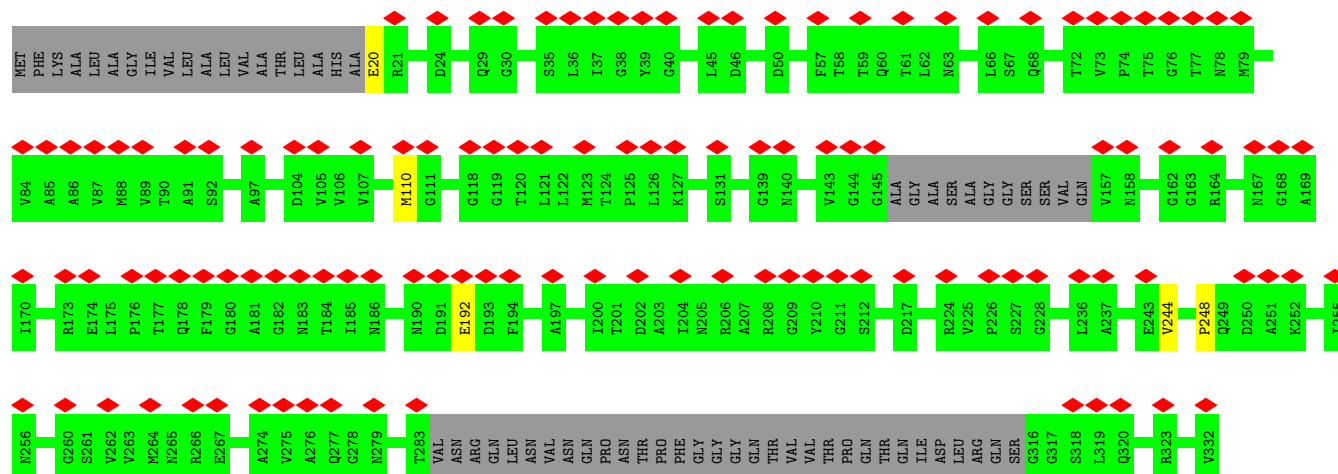
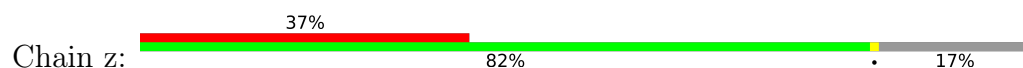


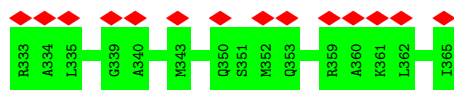


• Molecule 2: Flagellar P-ring protein

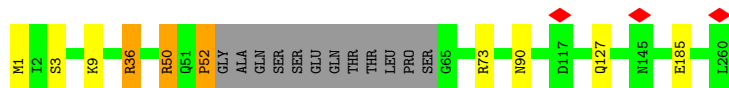


• Molecule 2: Flagellar P-ring protein

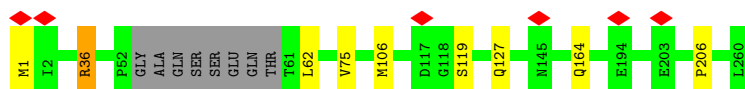




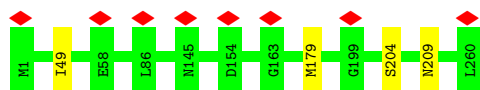
- Molecule 3: Flagellar basal-body rod protein FlgG



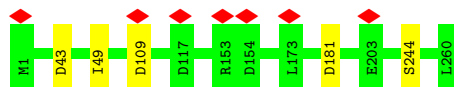
- Molecule 3: Flagellar basal-body rod protein FlgG



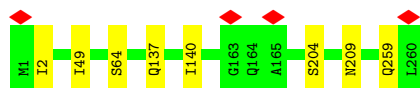
- Molecule 3: Flagellar basal-body rod protein FlgG



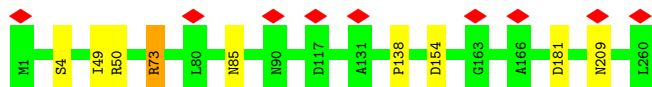
- Molecule 3: Flagellar basal-body rod protein FlgG



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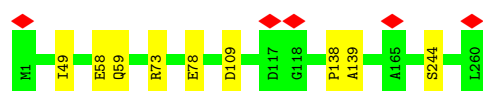


- Molecule 3: Flagellar basal-body rod protein FlgG



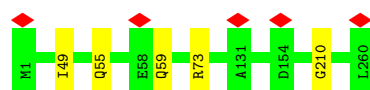
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 6:  97%



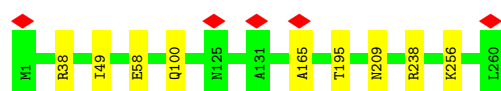
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 7:  98%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 8:  97%



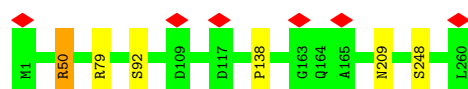
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 9:  98%



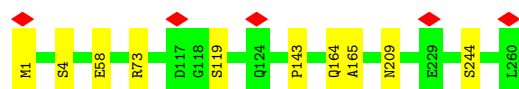
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZA:  98%



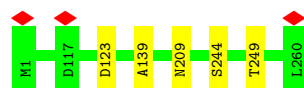
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZB:  96%



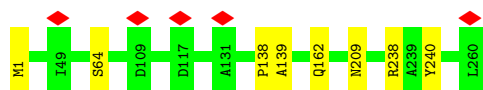
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZC:  98%



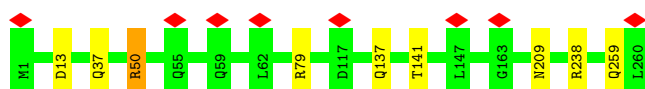
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZD:  97%



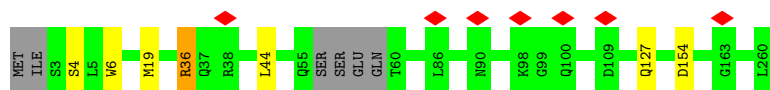
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZE:  97%



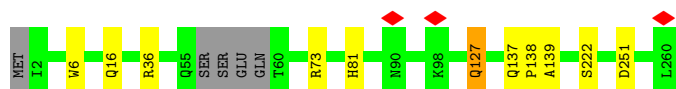
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AF:  95%



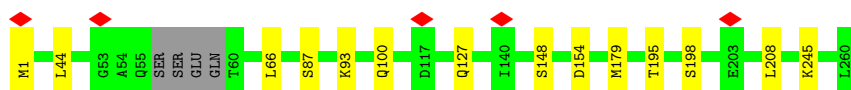
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AG:  94%



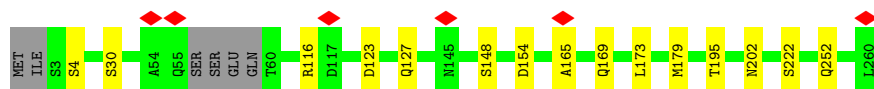
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AH:  93%



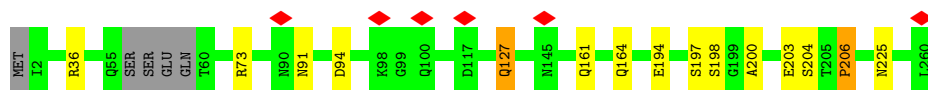
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AI:  92%



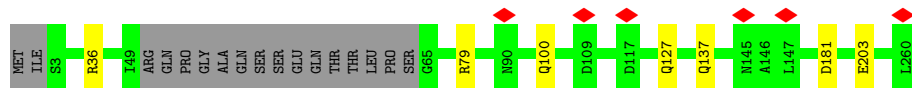
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AJ:  92%



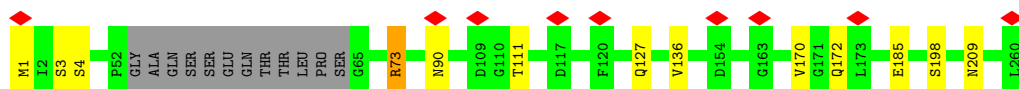
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AK: 91% 7%



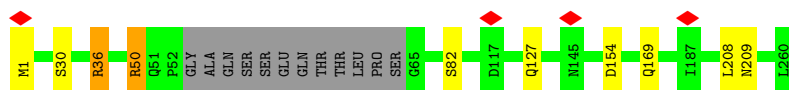
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AL: 90% 5% 5%



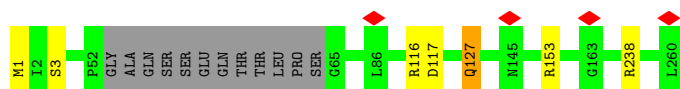
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AM: 92% 5% 5%



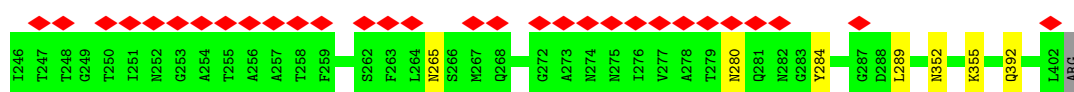
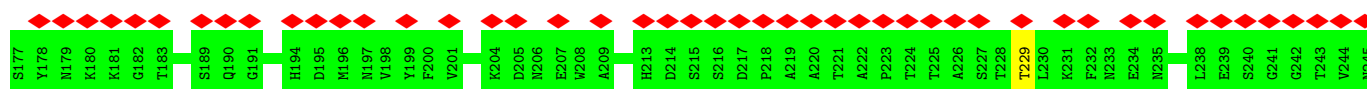
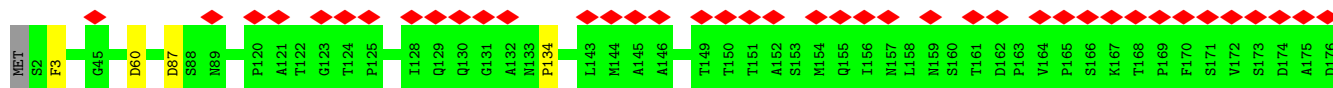
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AN: 93% 5% 5%



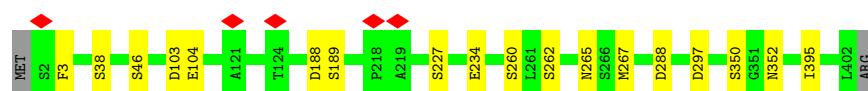
- Molecule 4: Flagellar hook protein FlgE

Chain ZF: 29% 97% 5%



- Molecule 4: Flagellar hook protein FlgE

Chain ZG:  95%



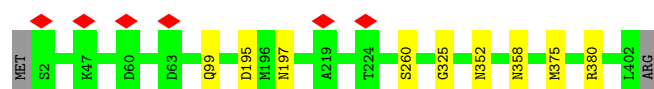
- Molecule 4: Flagellar hook protein FlgE

Chain ZH:  96%



- Molecule 4: Flagellar hook protein FlgE

Chain ZI:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZJ:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZK:  98%



- Molecule 4: Flagellar hook protein FlgE

Chain ZL:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZM:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZN:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZO:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZP:  95%



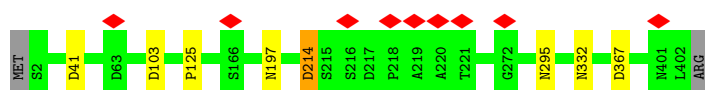
- Molecule 4: Flagellar hook protein FlgE

Chain ZQ:  97%



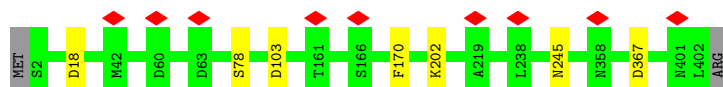
- Molecule 4: Flagellar hook protein FlgE

Chain ZR:  98%



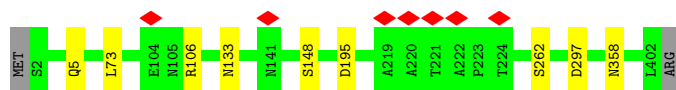
- Molecule 4: Flagellar hook protein FlgE

Chain ZS:  98%

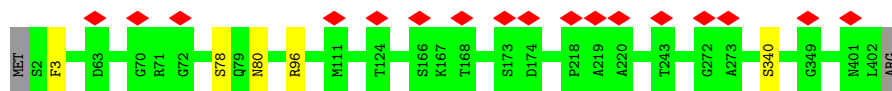


- Molecule 4: Flagellar hook protein FlgE

Chain ZT:  97%



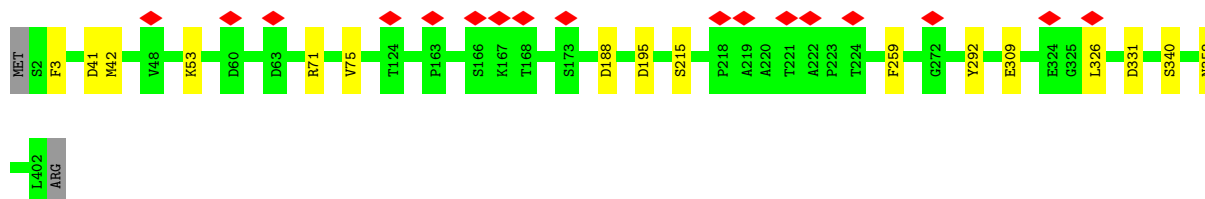
- Molecule 4: Flagellar hook protein FlgE



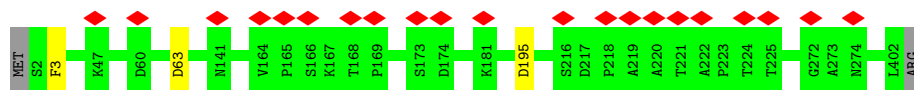
- Molecule 4: Flagellar hook protein FlgE



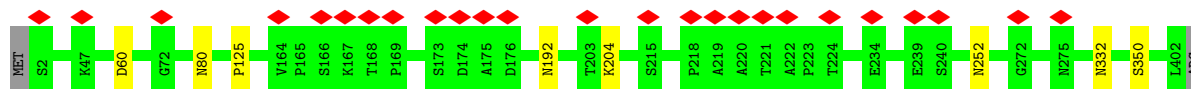
- Molecule 4: Flagellar hook protein FlgE



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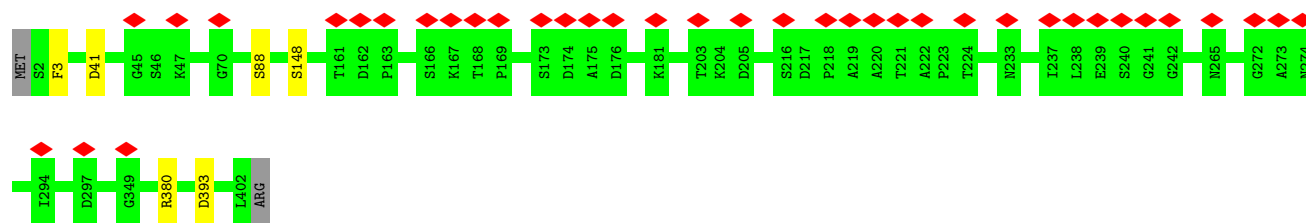


- Molecule 4: Flagellar hook protein FlgE

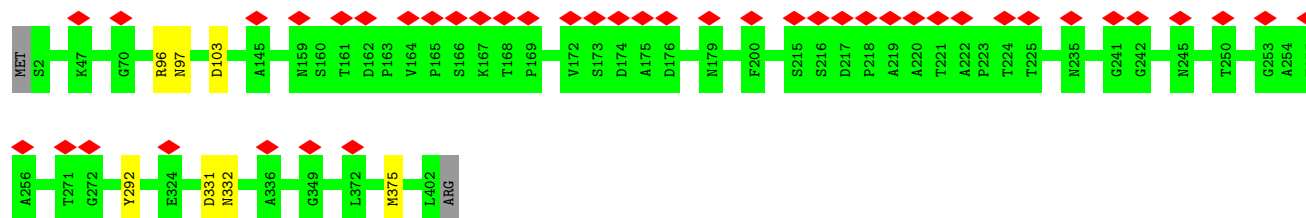


- Molecule 4: Flagellar hook protein FlgE

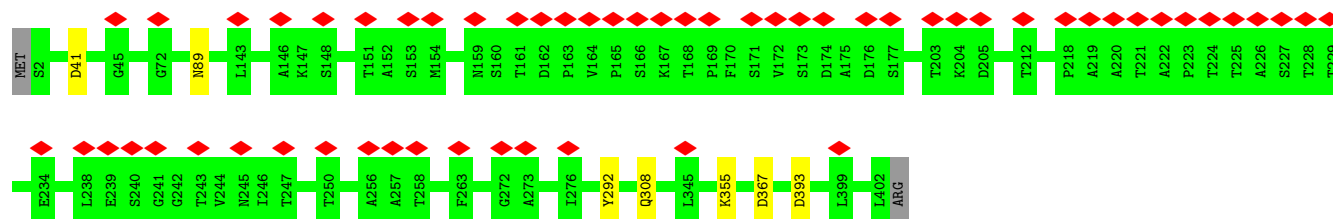




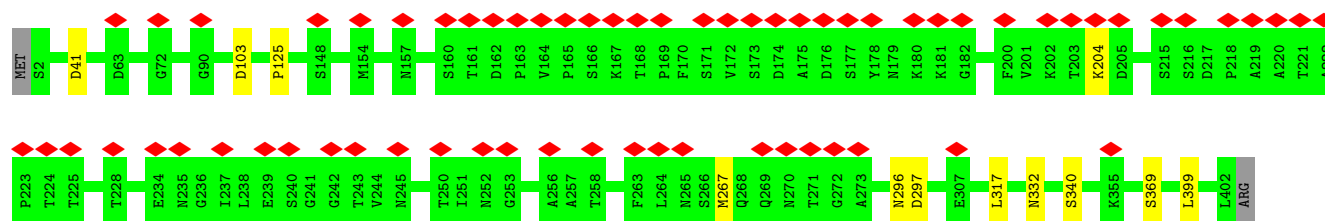
• Molecule 4: Flagellar hook protein FlgE



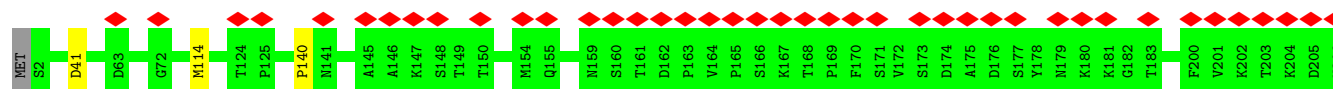
• Molecule 4: Flagellar hook protein FlgE

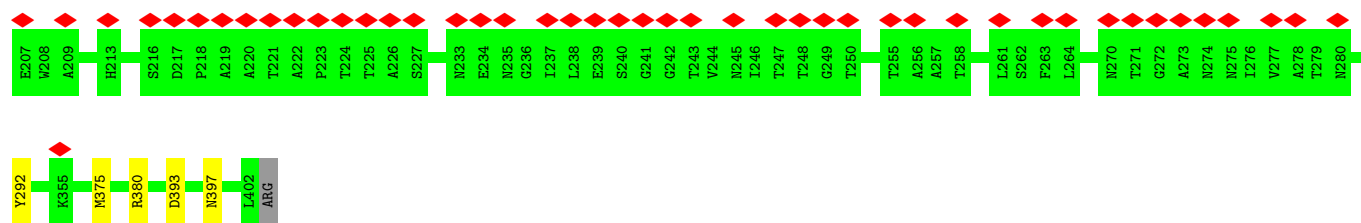


• Molecule 4: Flagellar hook protein FlgE

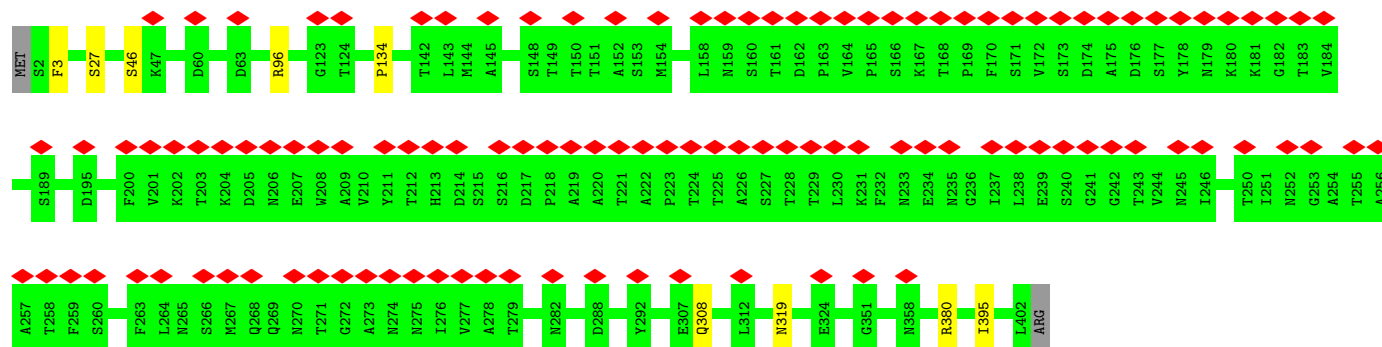


• Molecule 4: Flagellar hook protein FlgE

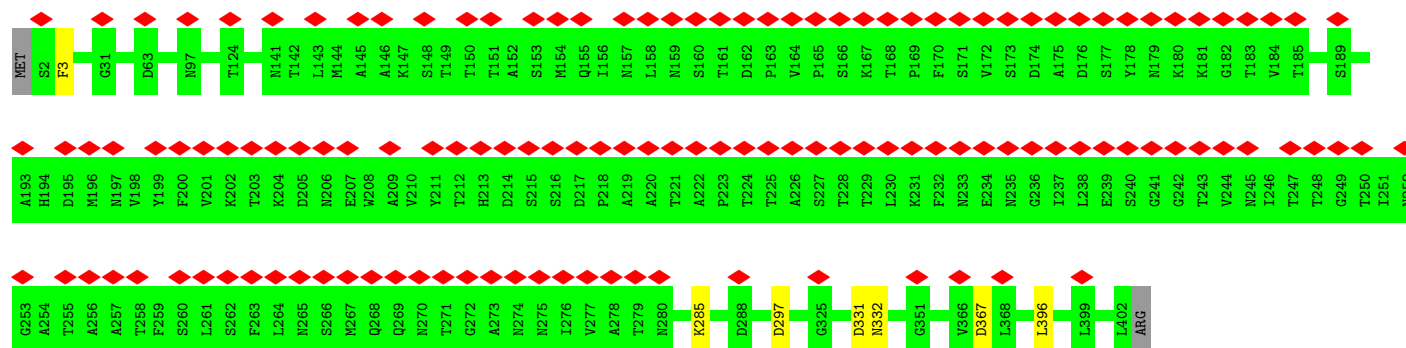




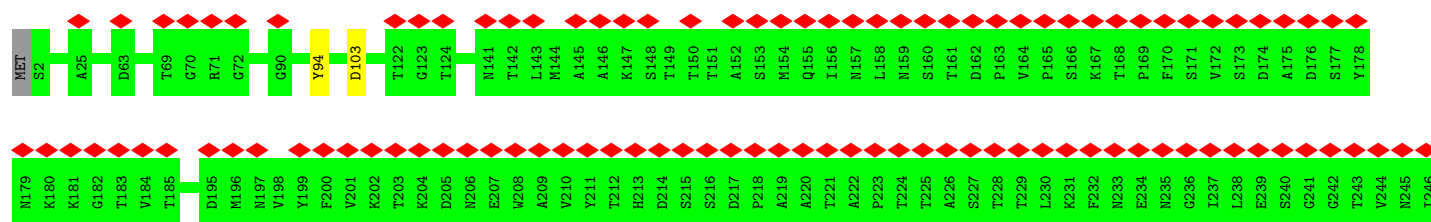
• Molecule 4: Flagellar hook protein FlgE

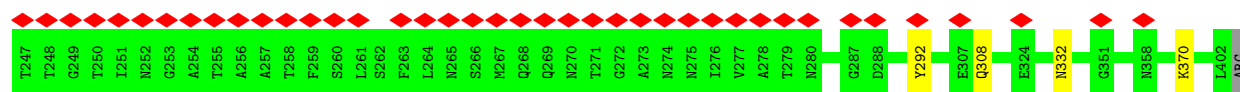


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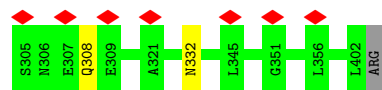
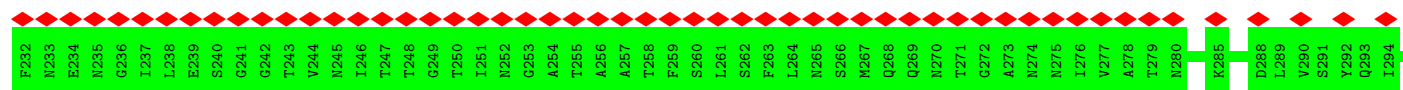
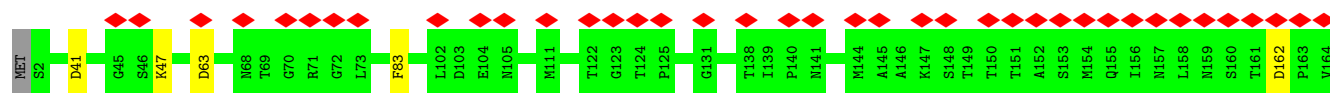
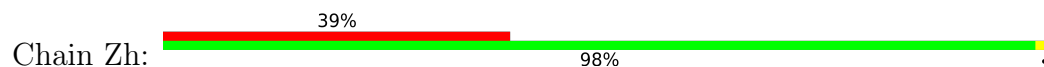


• Molecule 4: Flagellar hook protein FlgE

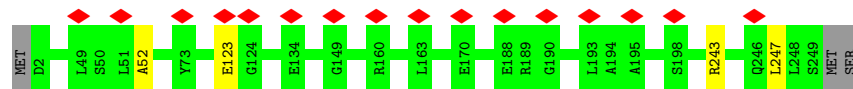




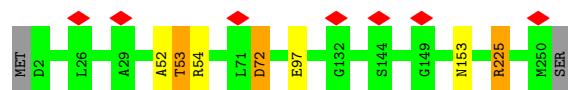
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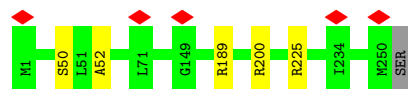
• Molecule 5: Flagellar basal-body rod protein FlgF



• Molecule 5: Flagellar basal-body rod protein FlgF

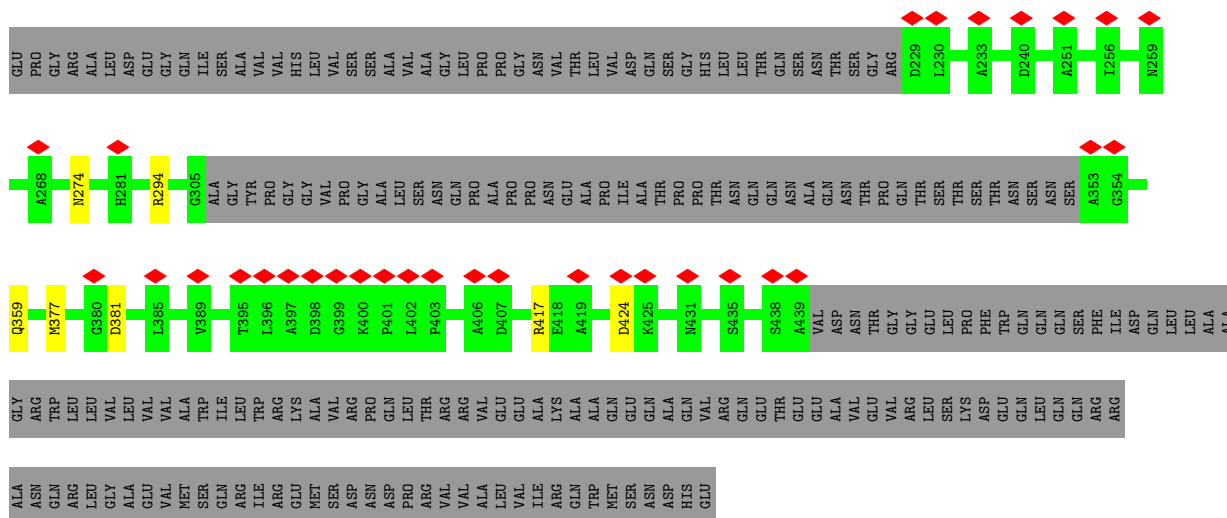


• Molecule 5: Flagellar basal-body rod protein FlgF

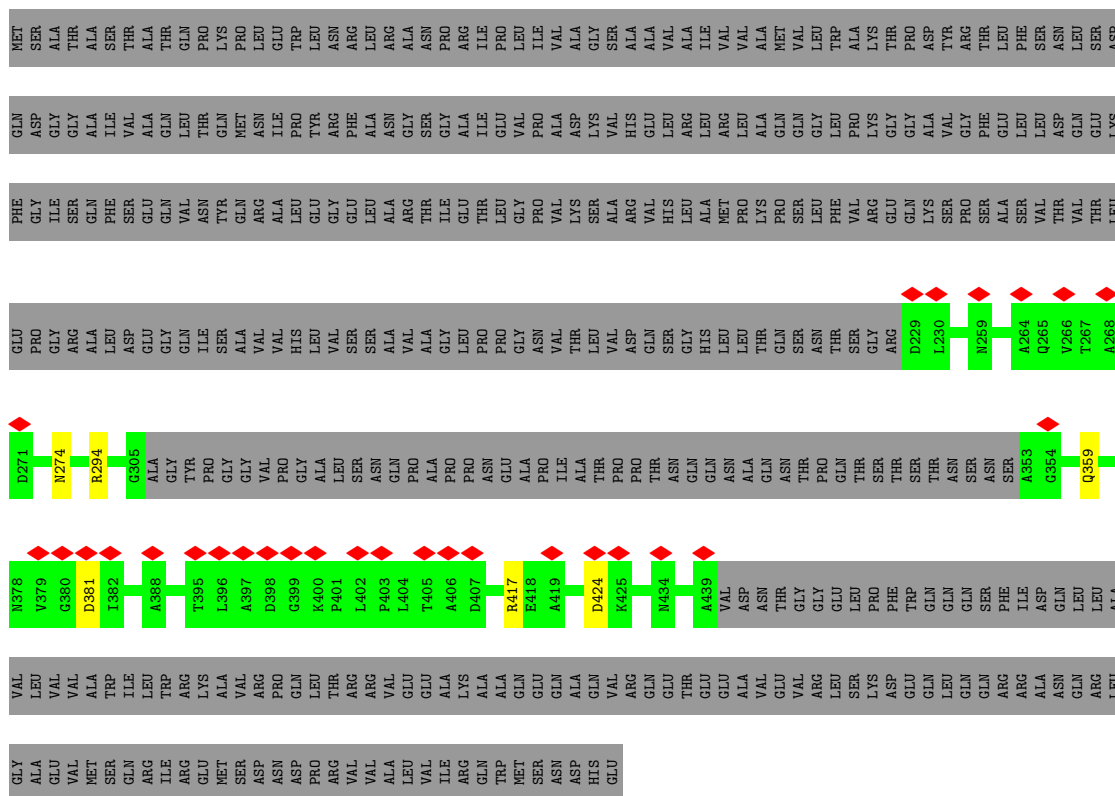


• Molecule 5: Flagellar basal-body rod protein FlgF

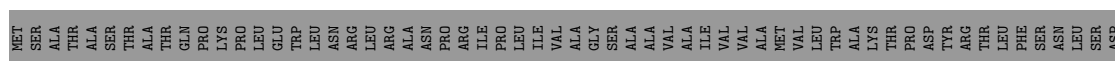




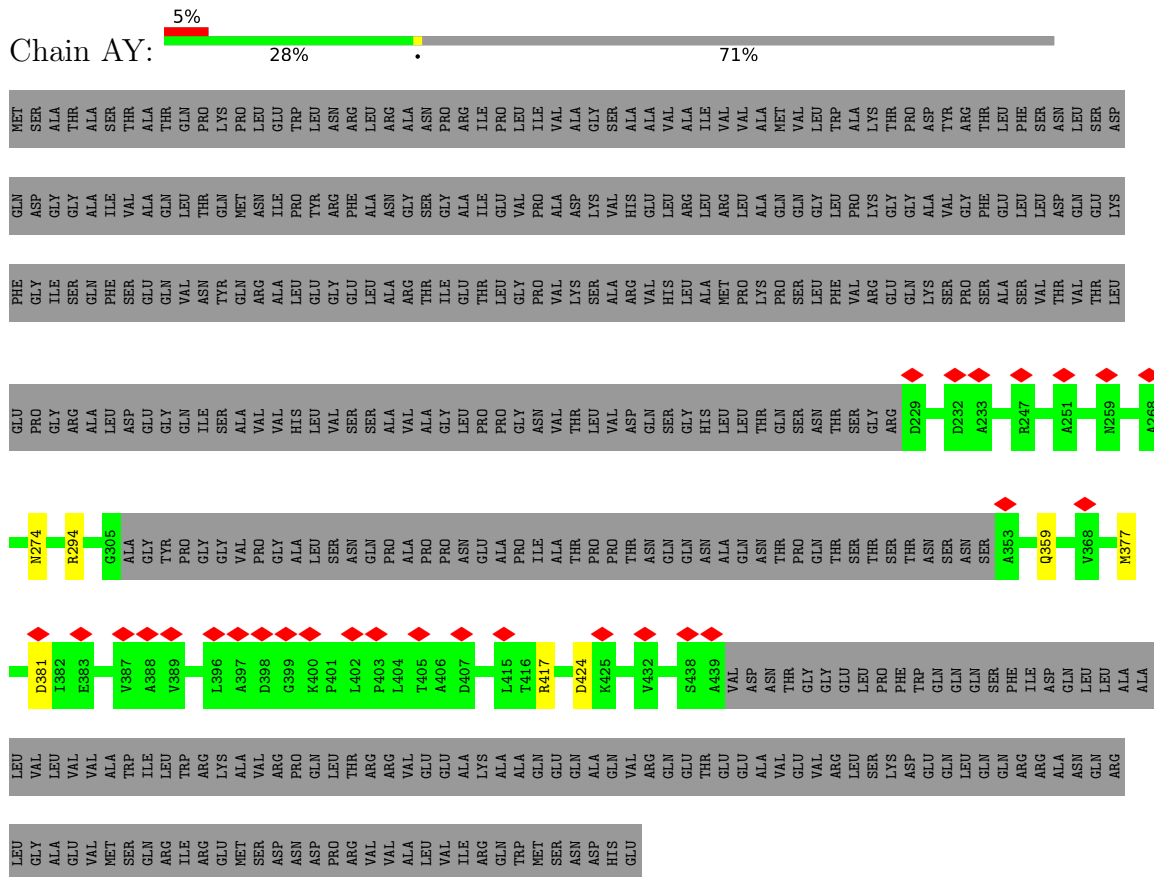
- Molecule 6: Flagellar M-ring protein



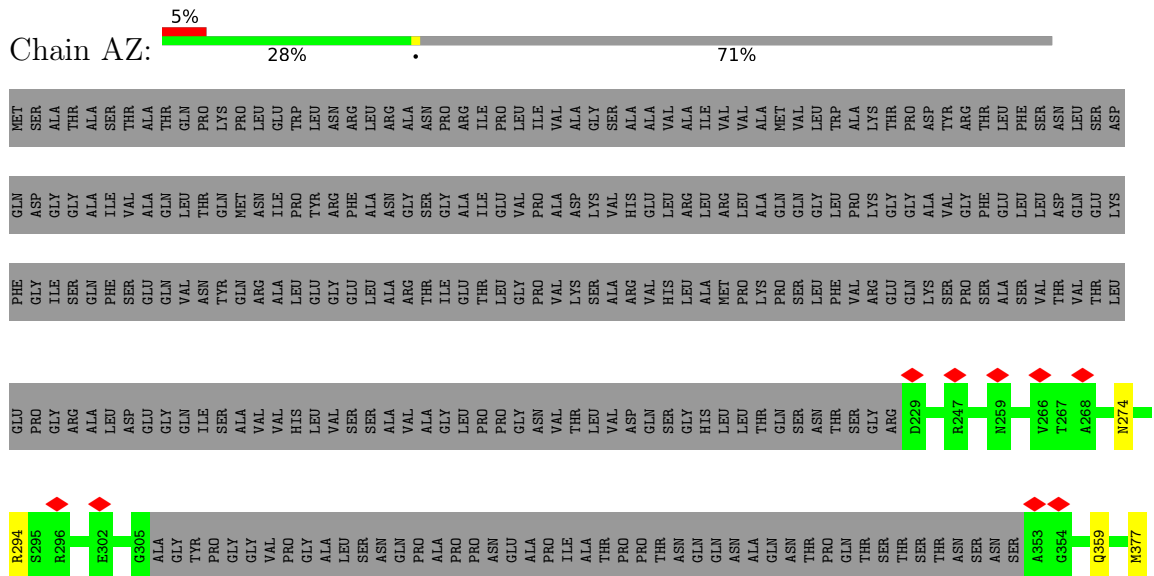
- Molecule 6: Flagellar M-ring protein

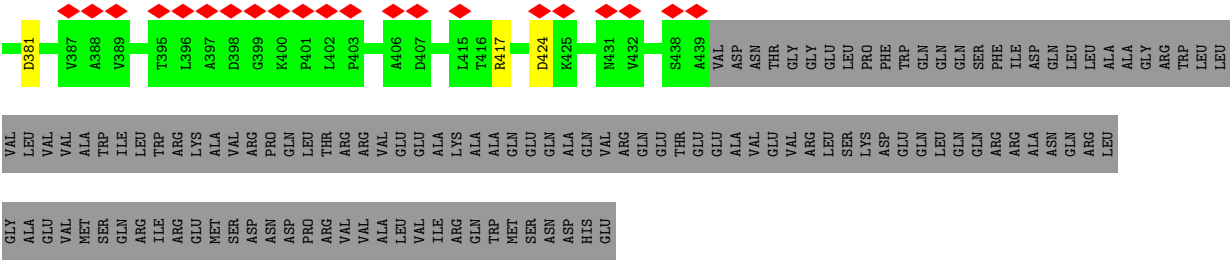


- Molecule 6: Flagellar M-ring protein

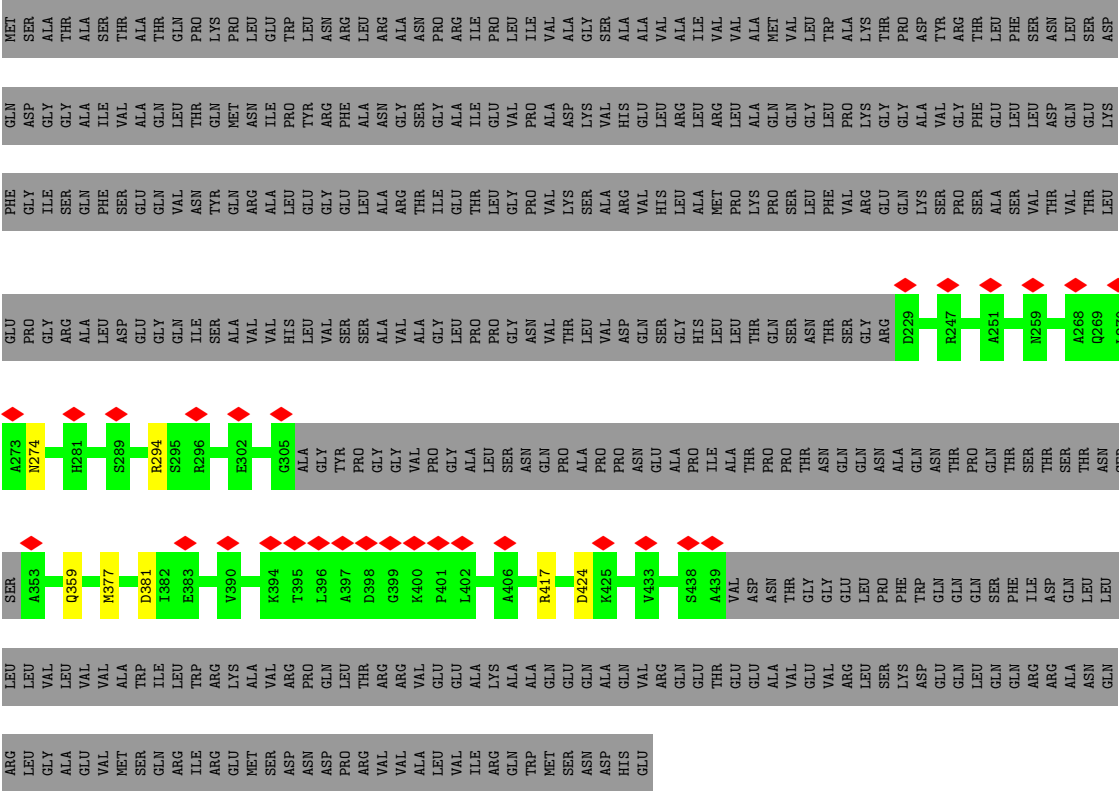


- Molecule 6: Flagellar M-ring protein

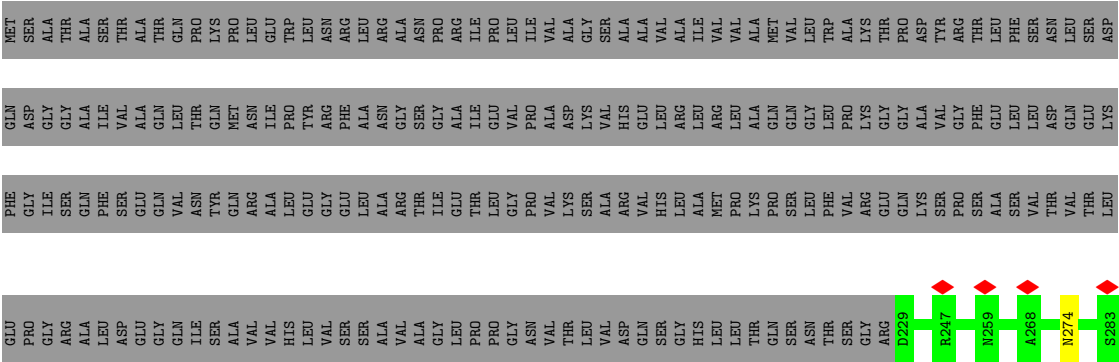


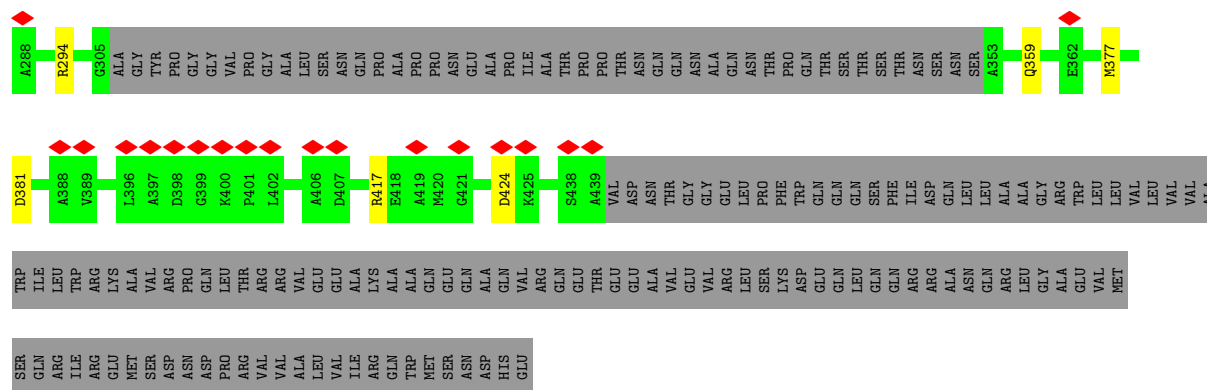


● Molecule 6: Flagellar M-ring protein

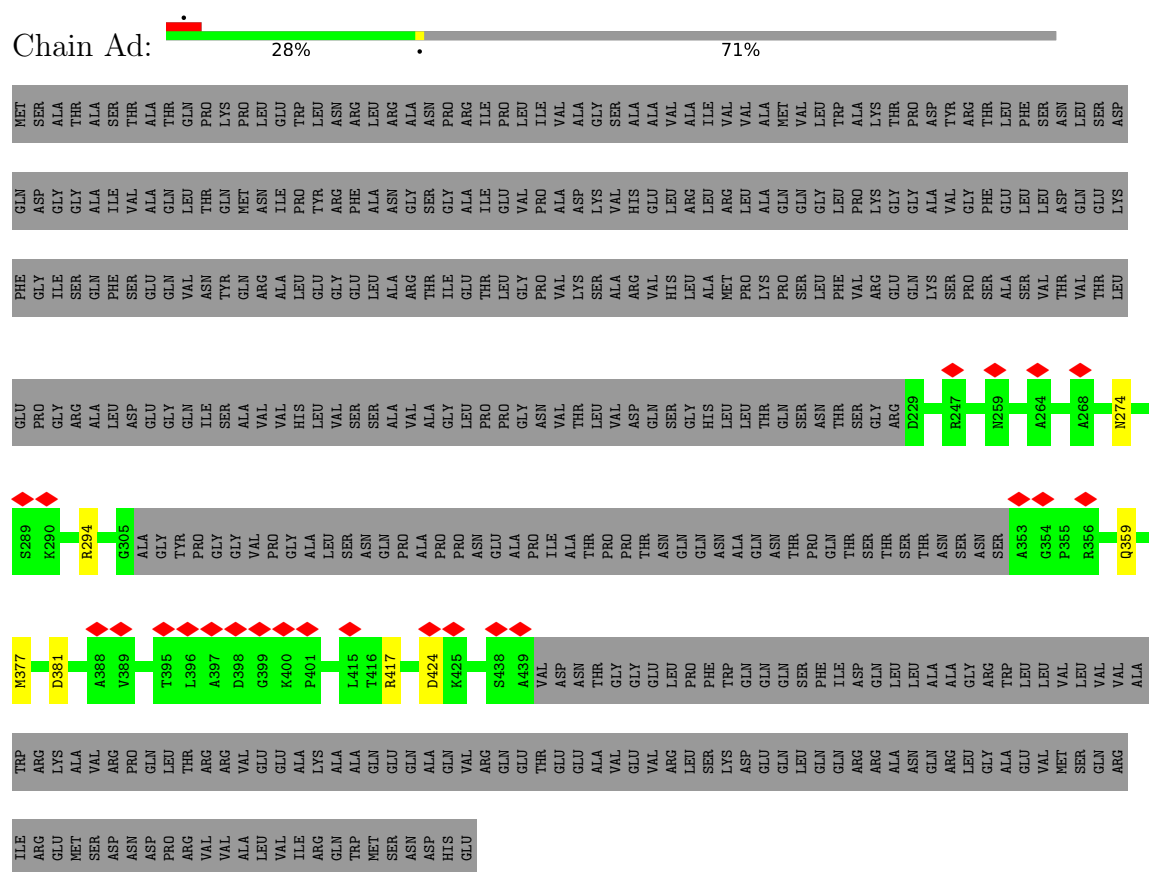


● Molecule 6: Flagellar M-ring protein

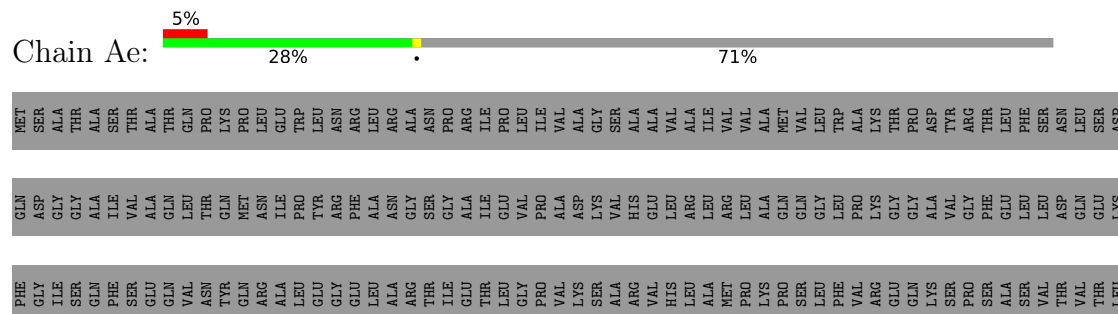


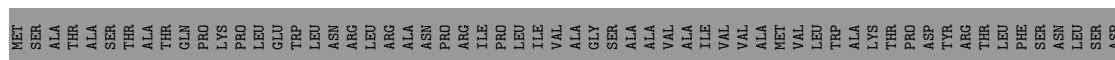


- Molecule 6: Flagellar M-ring protein

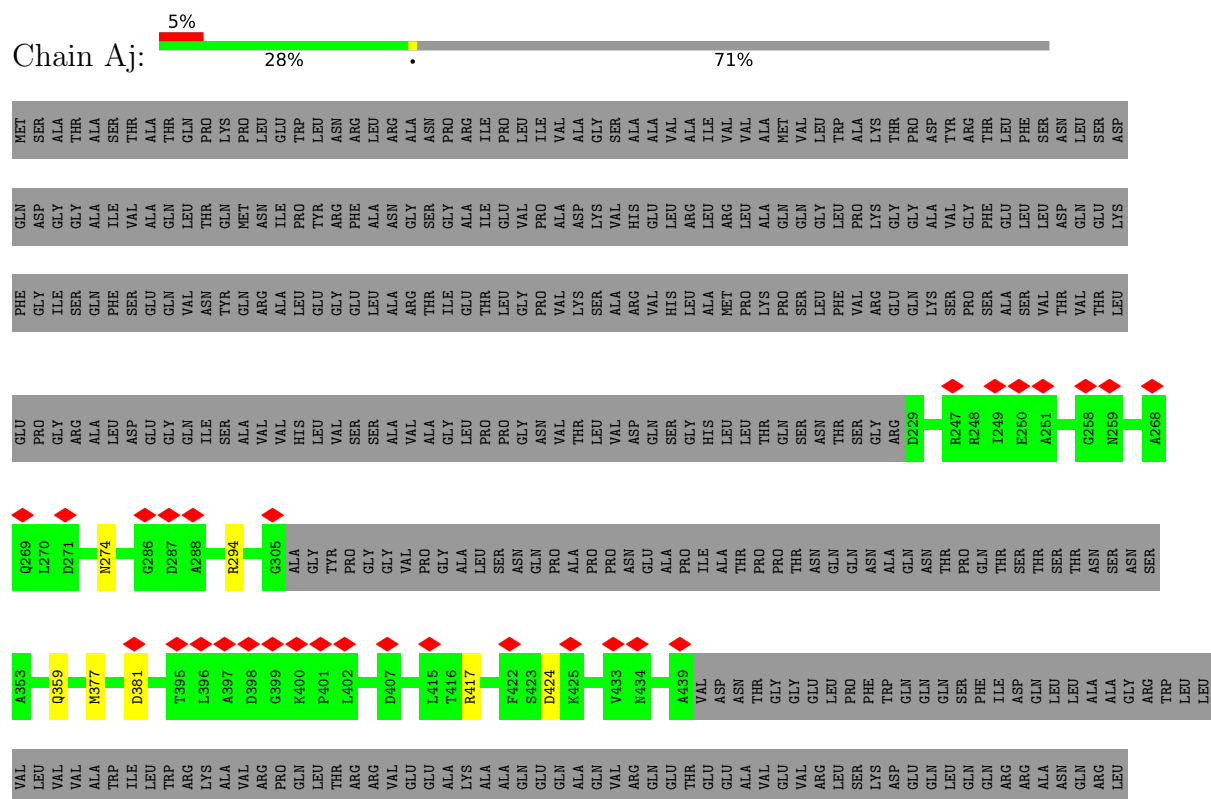


- Molecule 6: Flagellar M-ring protein









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• Molecule 6: Flagellar M-ring protein



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• Molecule 6: Flagellar M-ring protein



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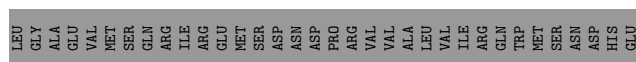
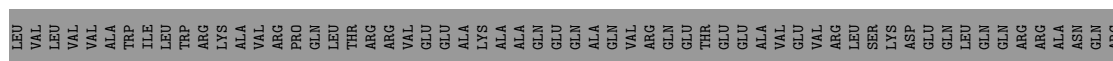
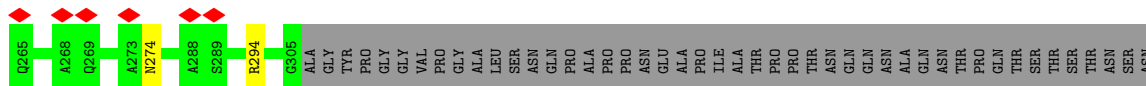
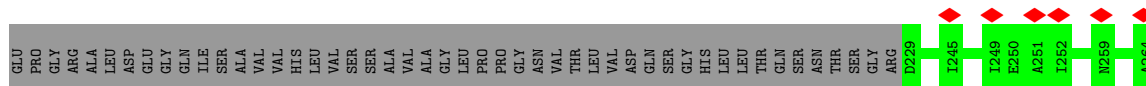
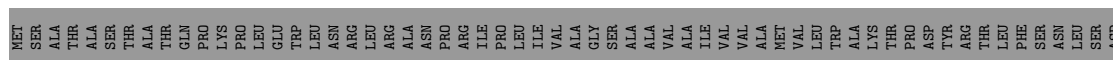
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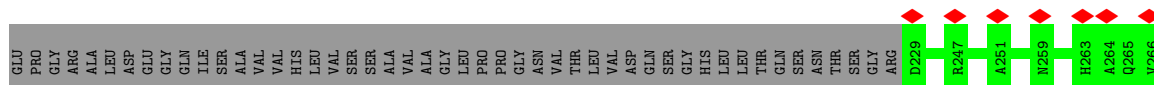
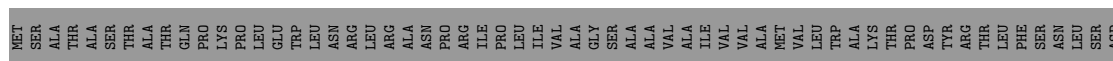
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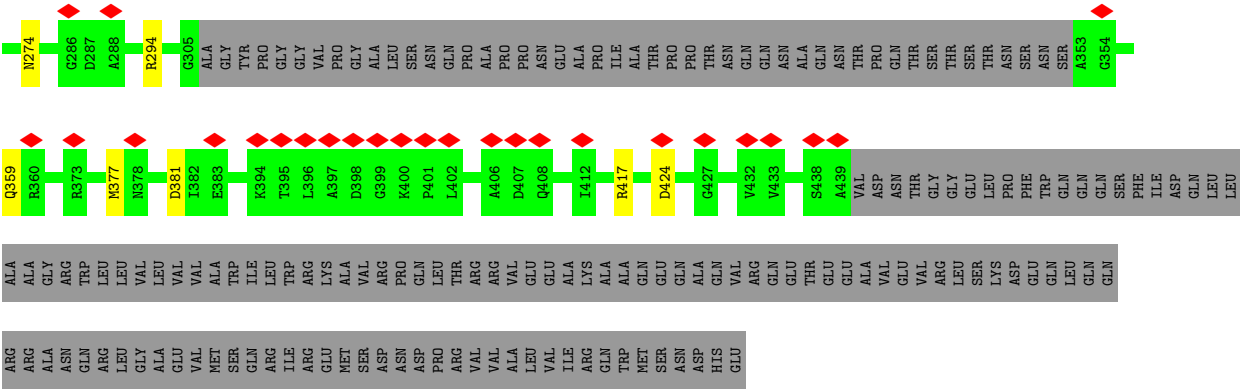
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- Molecule 6: Flagellar M-ring protein

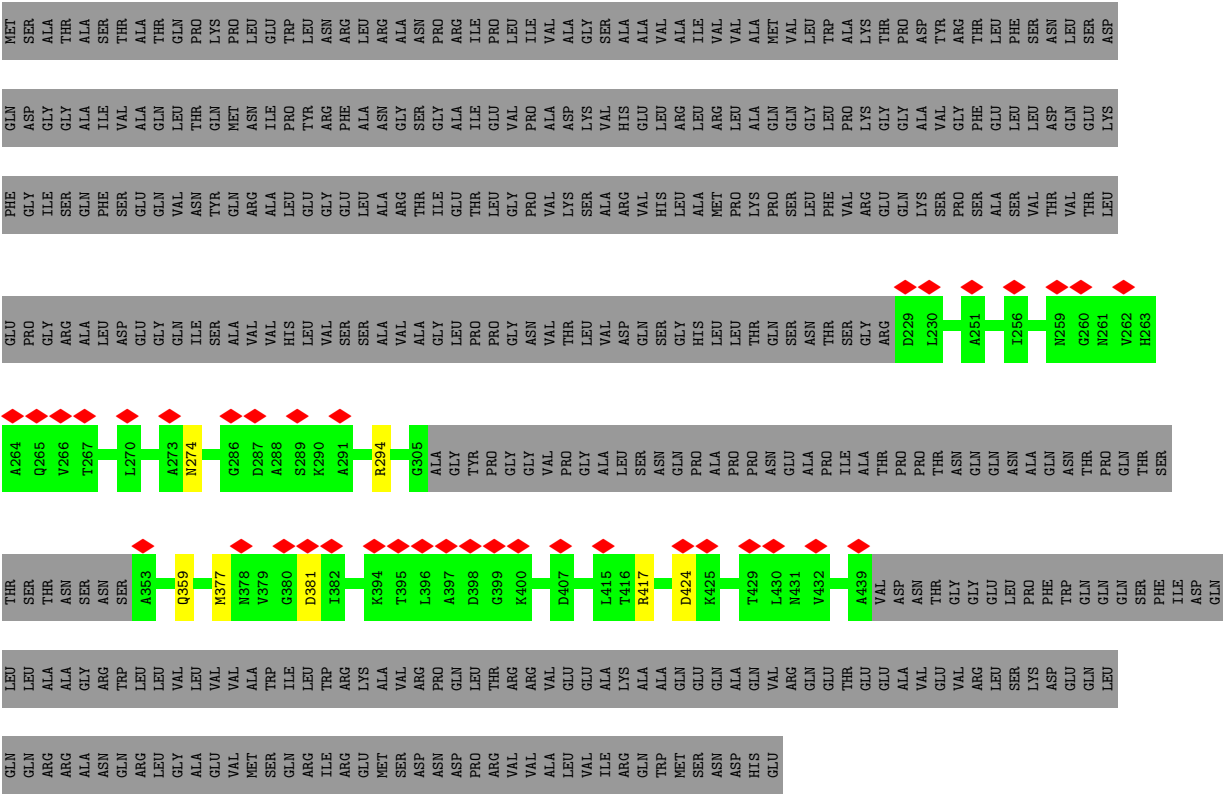


- Molecule 6: Flagellar M-ring protein

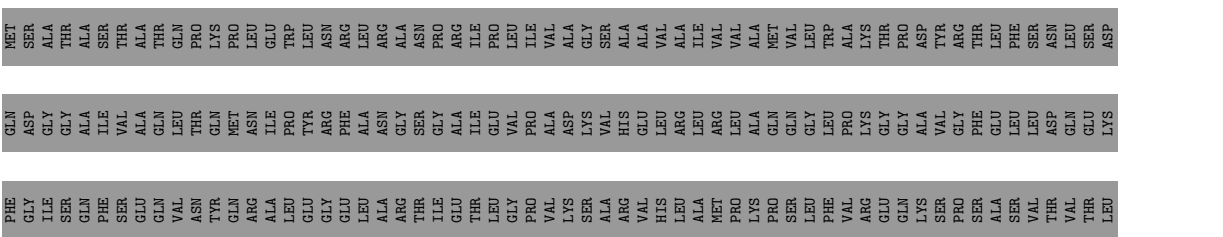


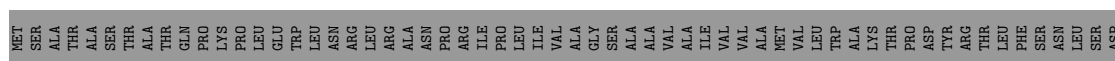


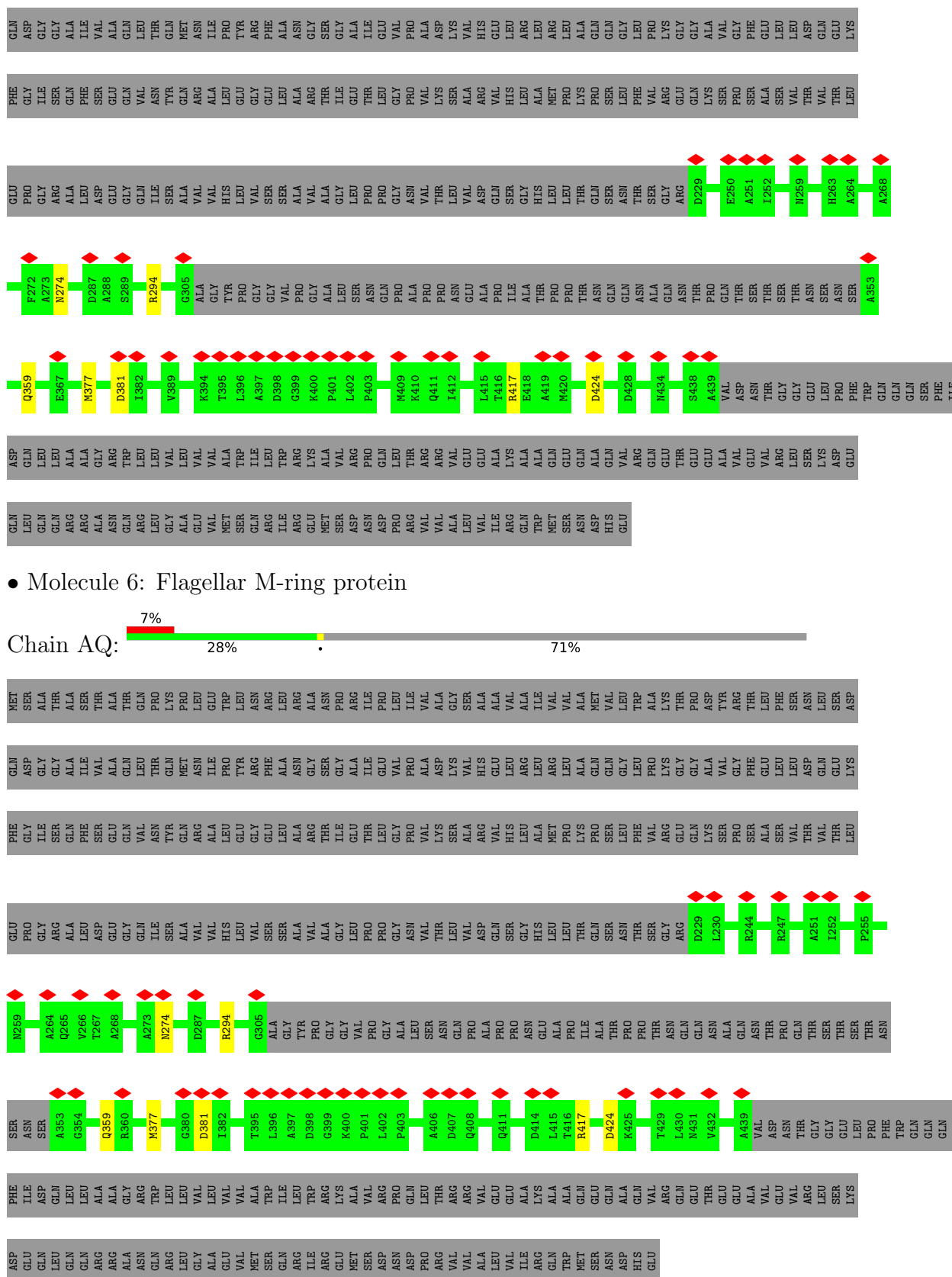
• Molecule 6: Flagellar M-ring protein



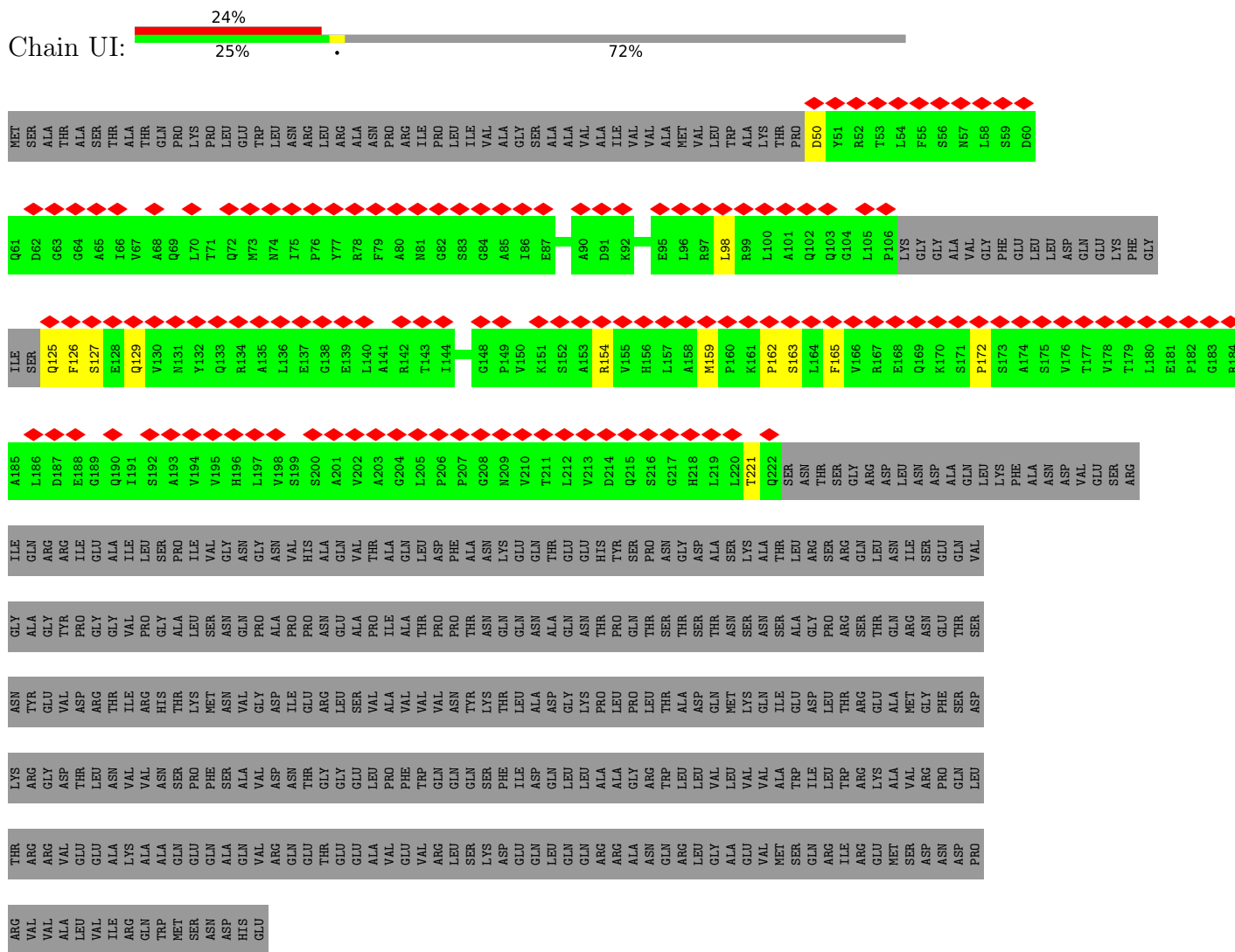
• Molecule 6: Flagellar M-ring protein



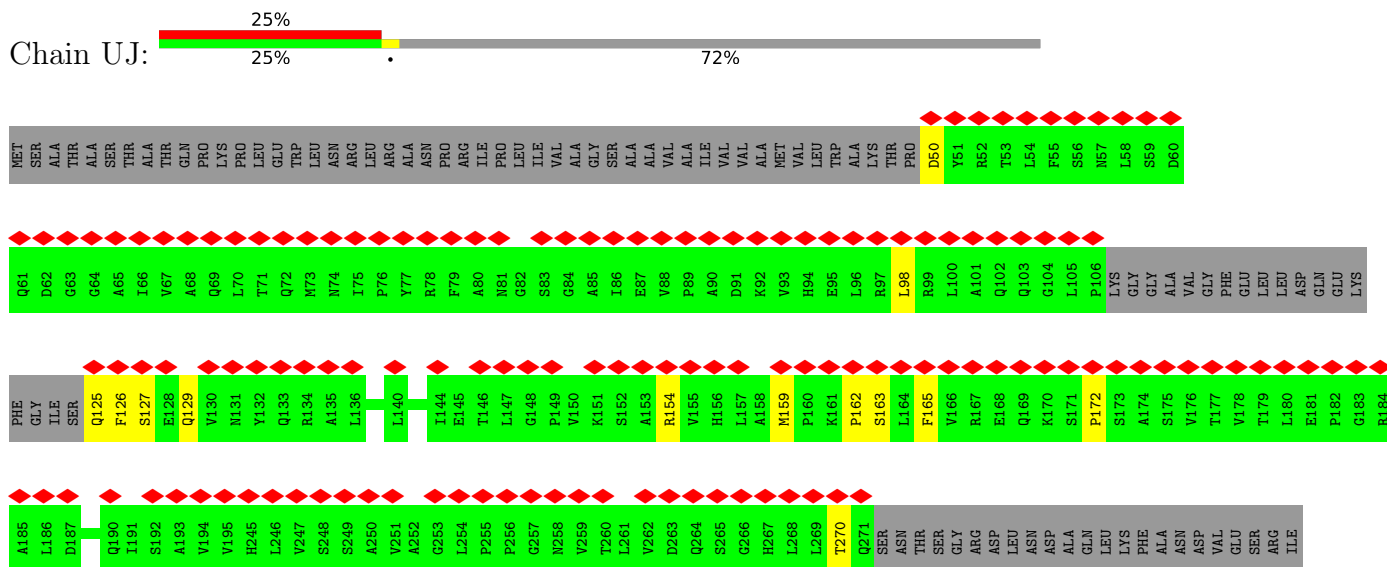




- Molecule 6: Flagellar M-ring protein



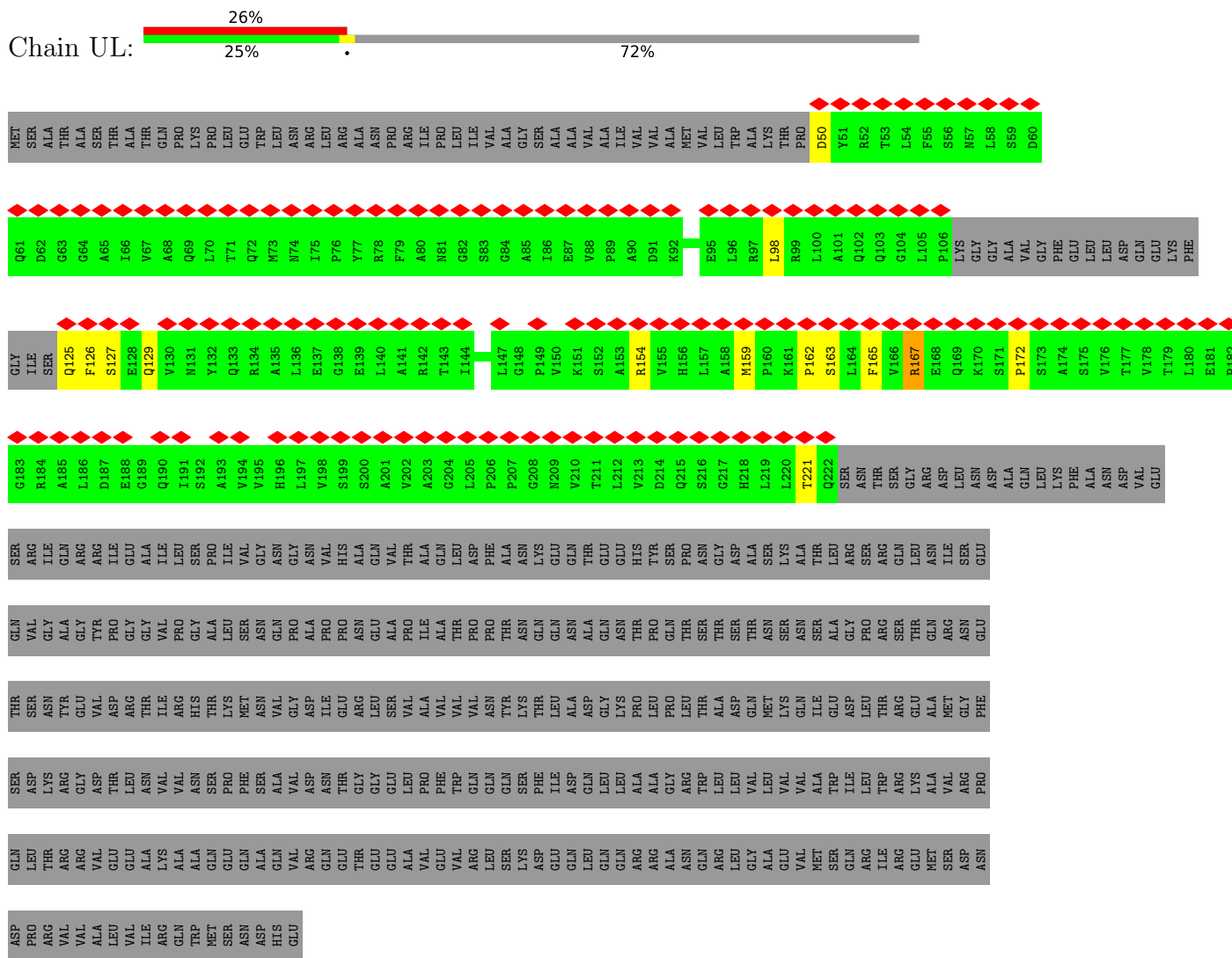
- Molecule 6: Flagellar M-ring protein



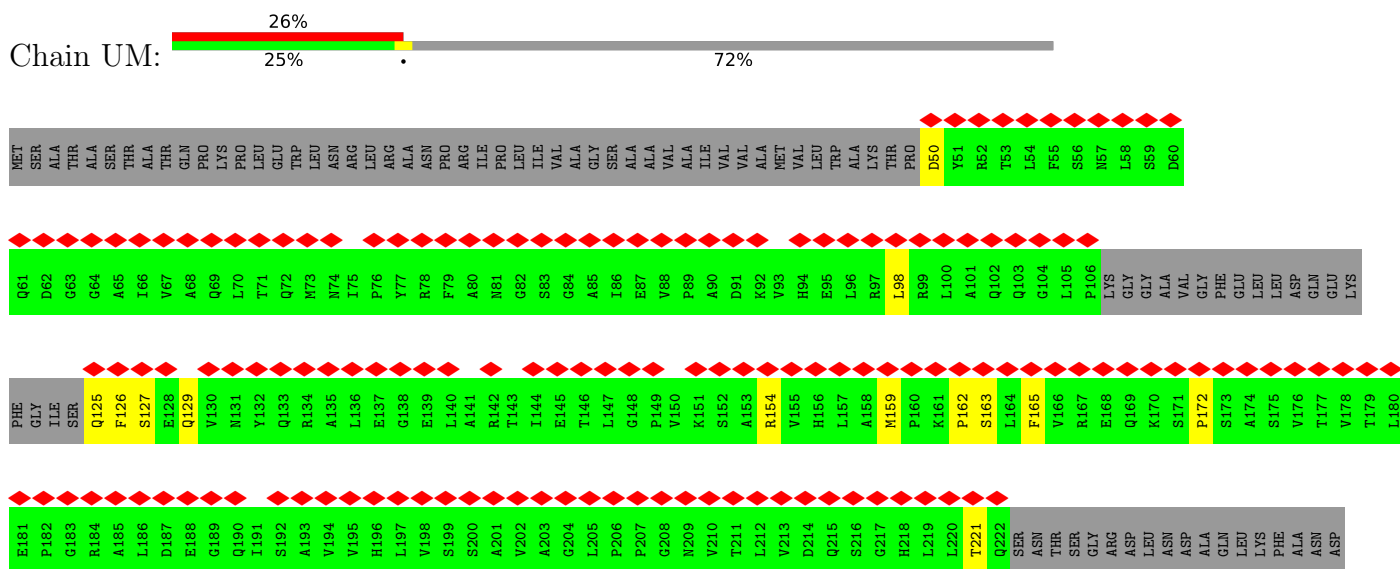
- Molecule 6: Flagellar M-ring protein

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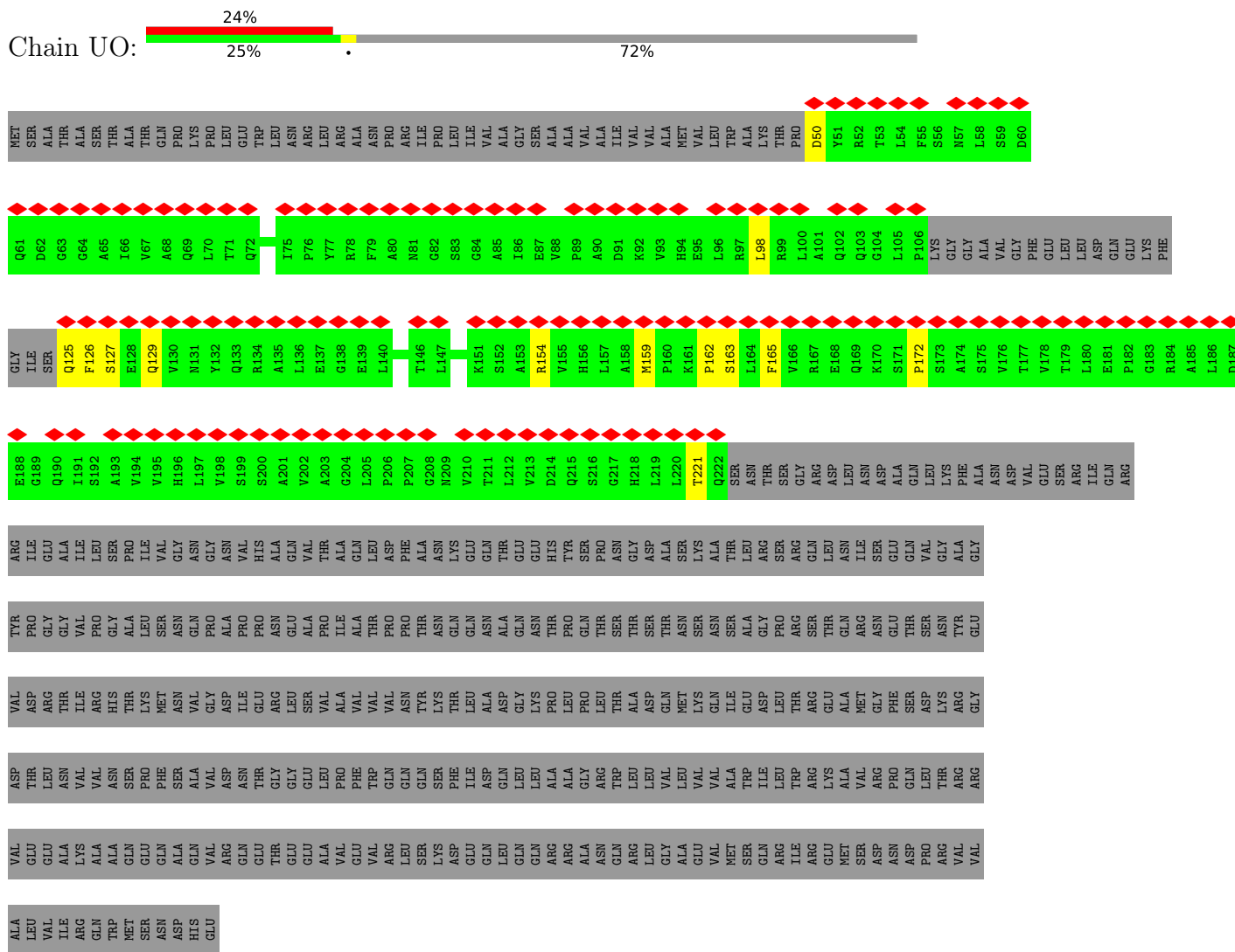
- Molecule 6: Flagellar M-ring protein



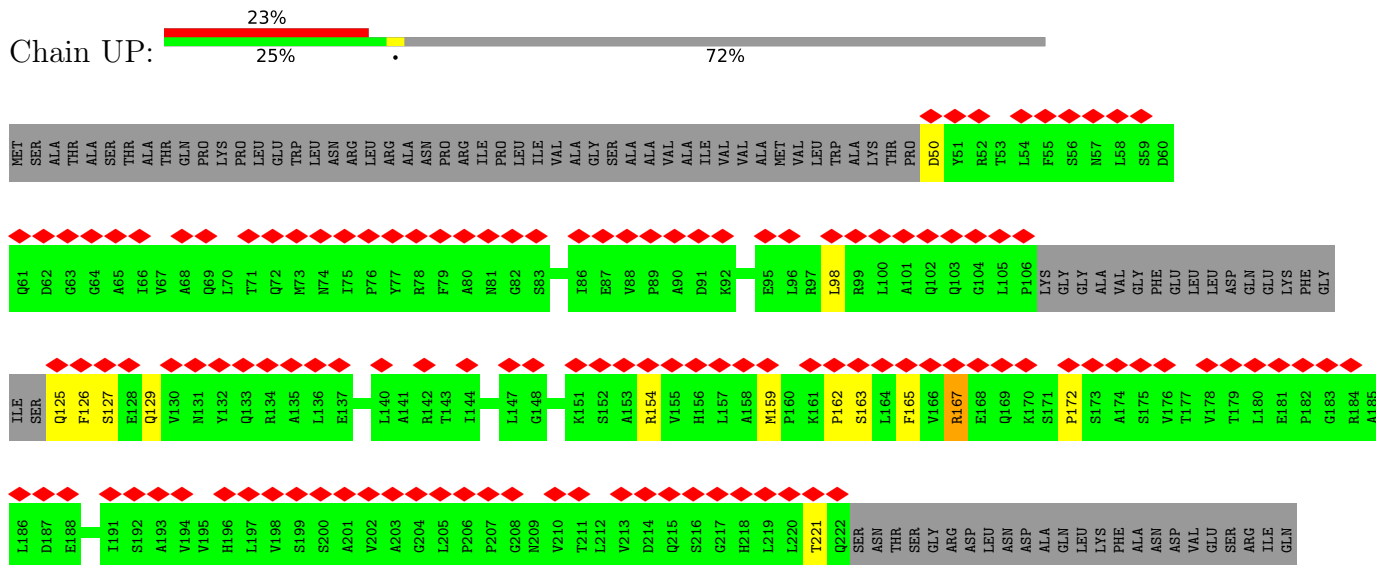
- Molecule 6: Flagellar M-ring protein







- Molecule 6: Flagellar M-ring protein



VAL	ARG	GLY	GLU
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- Molecule 6: Flagellar M-ring protein



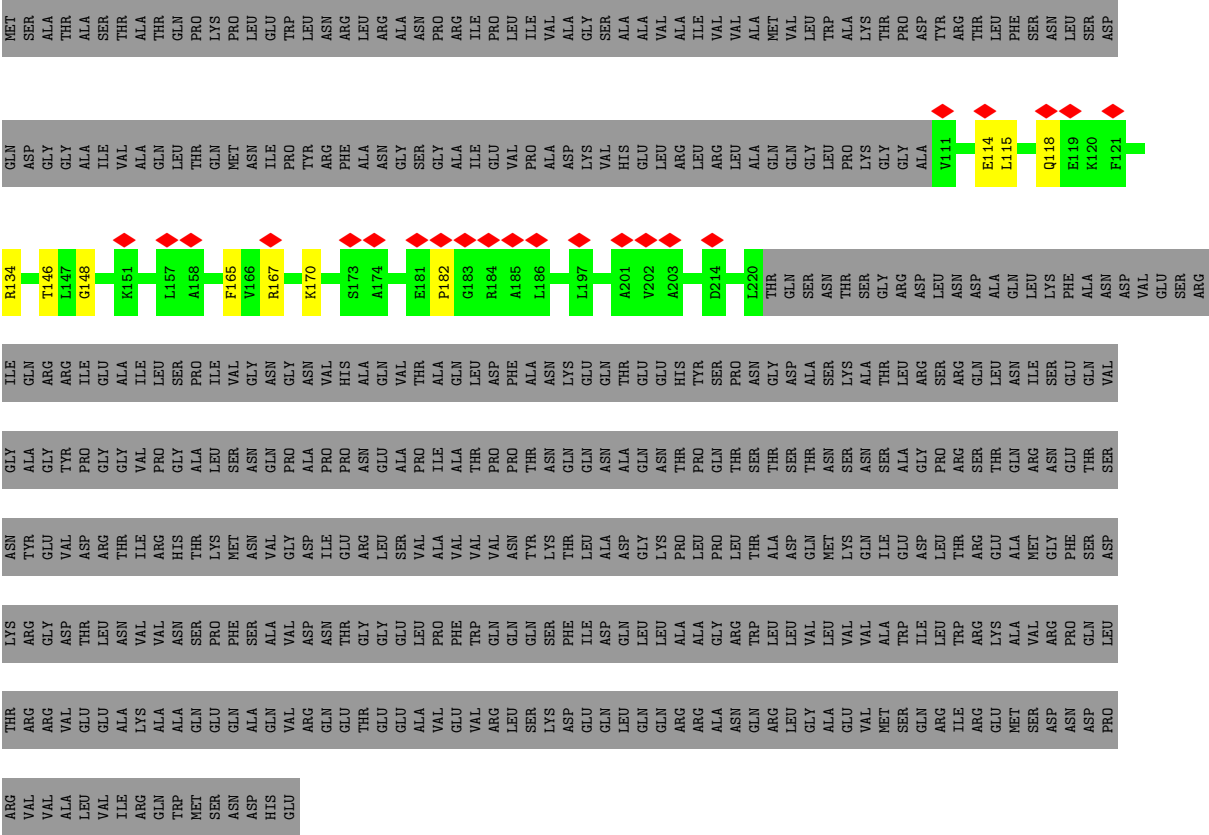
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VAL	VAL	ASP	VAL	TYR	ARG	ALA	ALA	GLY
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	ARG	ALA	PRO	THR	TYR	ARG	ARG	VAL
	ALA	ALA	LEU	ASN	SER	LEU	LEU	VAL
	ASN	ARG	PRO	GLN	SER	ARG	ARG	VAL
	GLN	TRP	LEU	THR	PRO	LEU	LEU	VAL
	ARG	LEU	ALA	THR	GLY	ALA	ALA	VAL
	LEU	LEU	ASP	THR	ASP	GLN	GLN	VAL
	GLY	VAL	GLN	THR	ALA	ASN	GLY	VAL
	ALA	LEU	MET	ASN	SER	LEU	LEU	TRP
	VAL	VAL	LYS	SER	LYS	PRO	ALA	ALA
	VAL	VAL	GLN	ASN	ALA	PRO	PRO	ALA
	MET	ALA	ILE	SER	THR	GLY	GLY	LYS
	SER	TRP	GLU	ALA	LEU	ARG	THR	THR
	GLN	ILE	ASP	GLY	ARG	ASP	ALA	ASP
	ARG	LEU	LEU	PRO	SER	LEU	ASP	TYR
	ILE	TRP	THR	THR	ARG	ASN	V111	ARG
	ARG	ARG	GLU	ARG	GLN	ASP	G112	THR
	GLU	LYS	GLU	THR	LEU	ALA	F113	LEU
	MET	ALA	ALA	GLN	ASN	GLN	E114	PHE
	SER	VAL	MET	ARG	ILE	LEU	LEU	SER
	ASP	ARG	GLY	ASN	SER	LYS	F121	ASN
	ASN	PHE	GLU	PHE	GLU	PHE	G122	LEU
	ASP	GLN	THR	THR	GLN	ALA	I123	SER
	PRO	LEU	ASP	ASP	VAL	ASN	E128	ASP
						VAL	VAL	
						GLU	GLU	
						SER	SER	

- Molecule 6: Flagellar M-ring protein

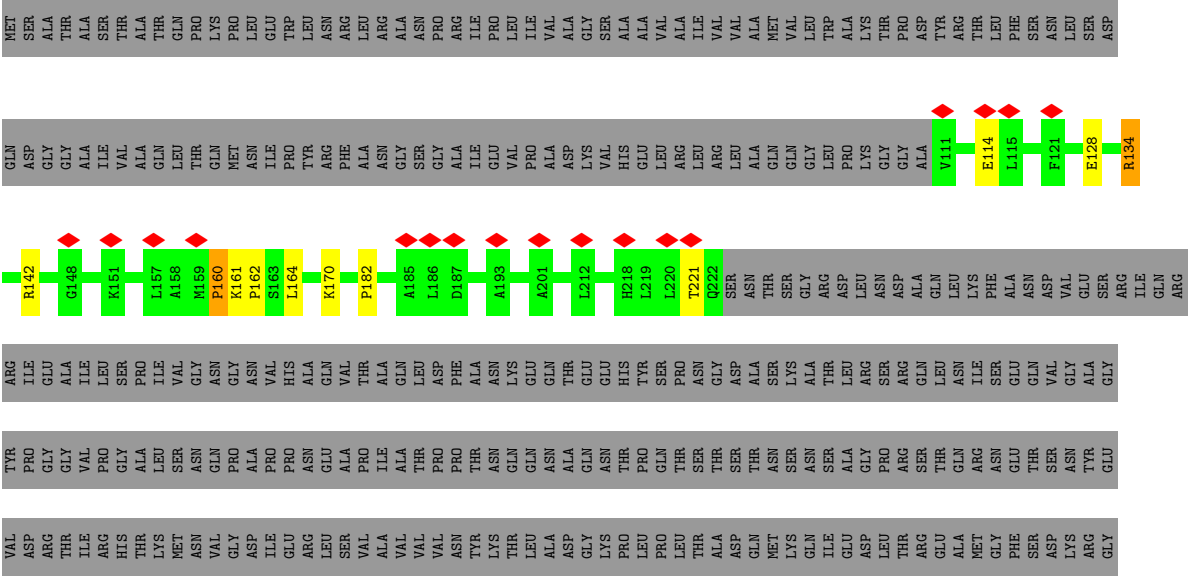


MET	ALA	THR	SER	THR	ALA	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	ARG	LEU	ALA	ALA	ASN	PRO	ARG	ILE	PRO	PRO	LEU	ILE	VAL	ALA	GLY	ALA	SER	ALA	ALA	VAL	VAL	ALA	ALA	ILE	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	THR	ALA	LYS	PRO	ASP	TYP	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	SER
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• Molecule 6: Flagellar M-ring protein



• Molecule 6: Flagellar M-ring protein



[illegible]

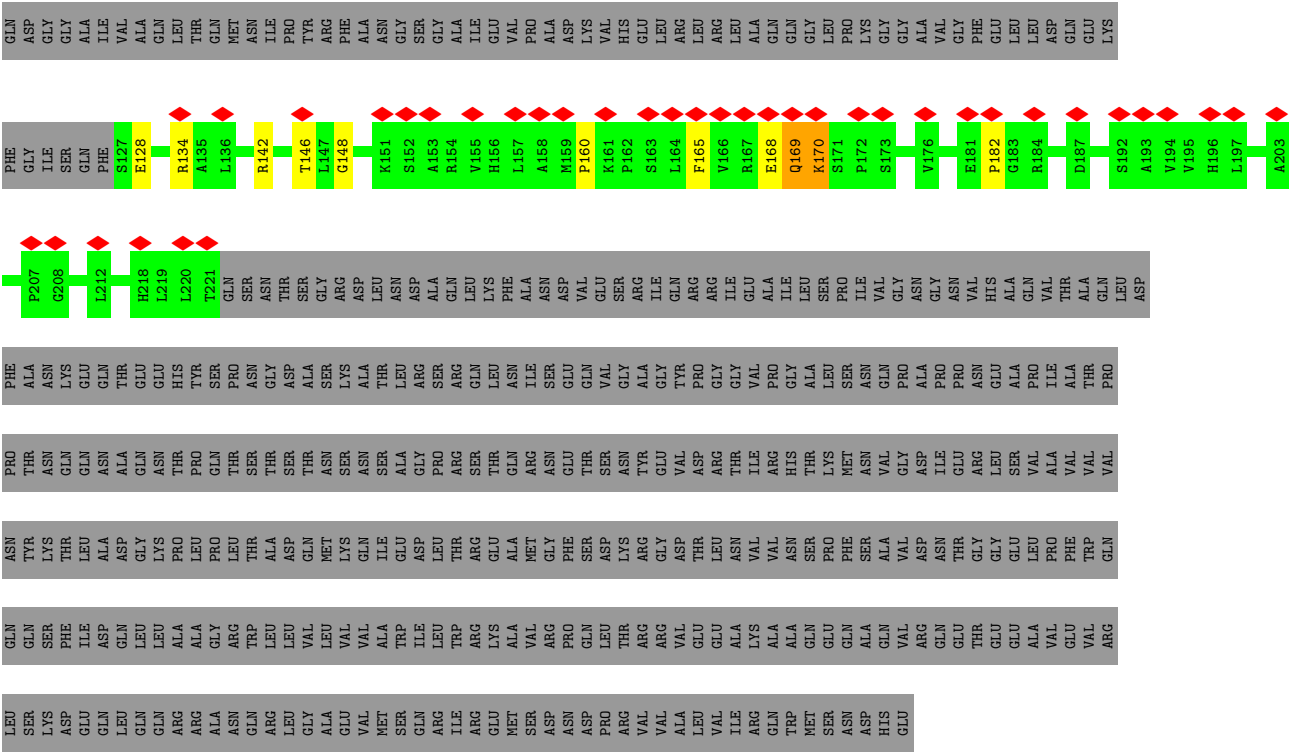
- Molecule 6: Flagellar M-ring protein

[illegible]

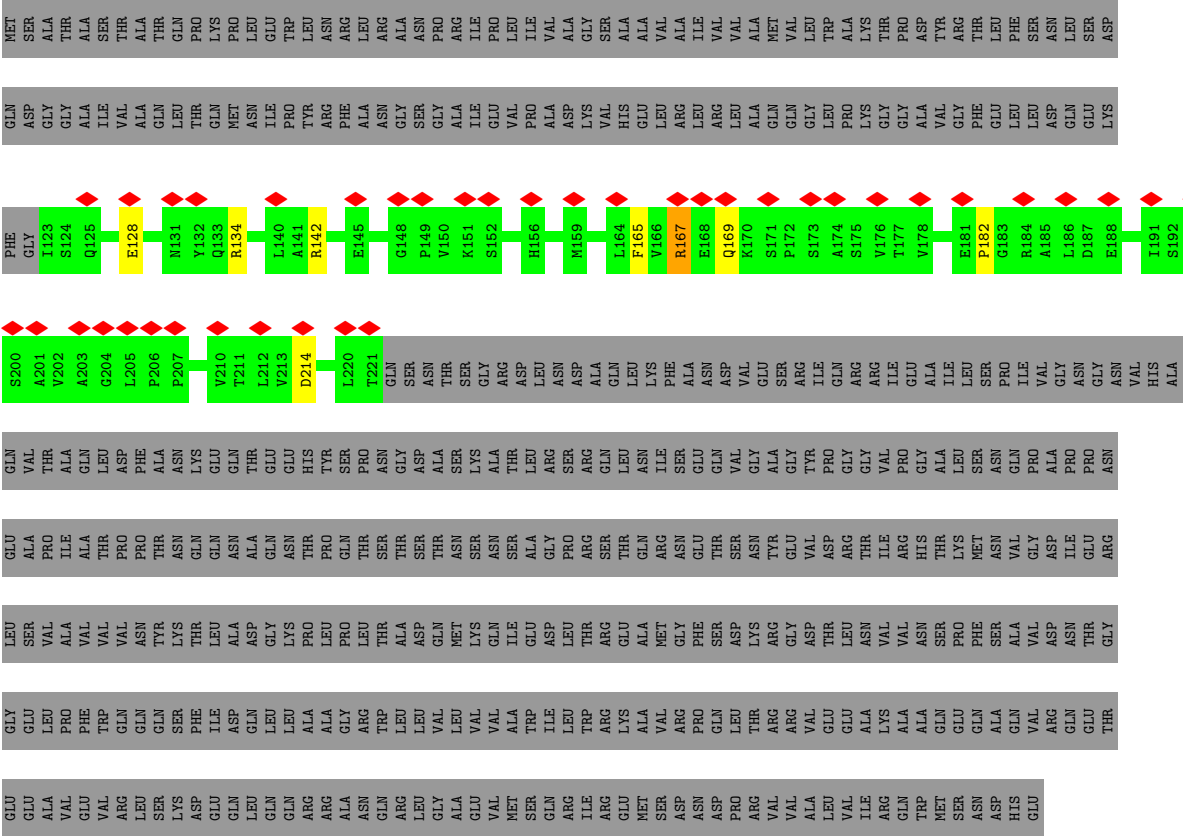
- Molecule 6: Flagellar M-ring protein



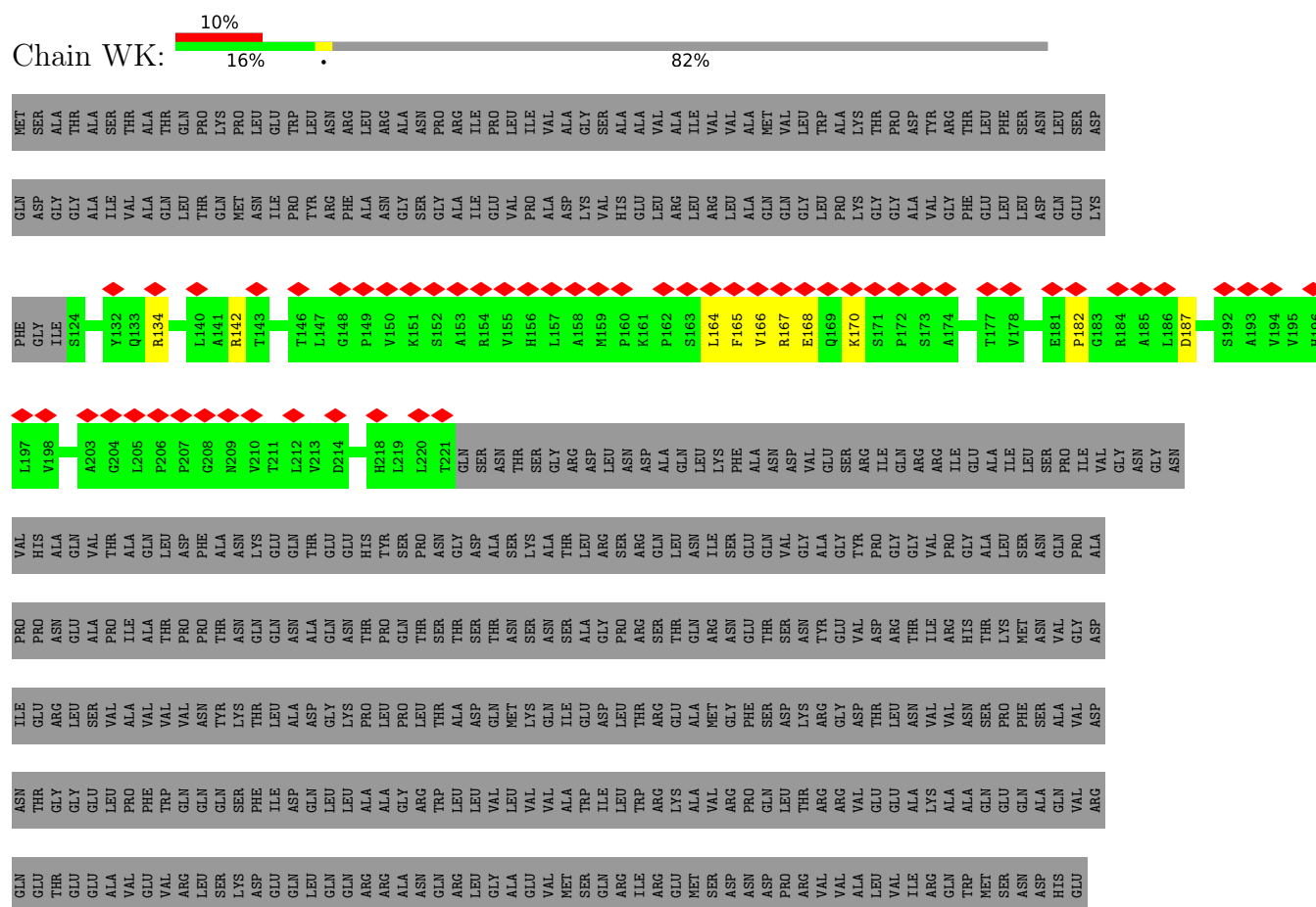
MET	SER	ALA	THR	ALA	SER	THR	THR	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	LEU	ARG	ALA	ALA	ASN	PRO	ARG	ILE	PRO	LEU	ILE	VAL	ALA	GLY	SER	ALA	ALA	VAL	VAL	ALA	ILE	VAL	VAL	VAL	VAL	MET	VAL	LEU	LEU	TRP	TRP	ALA	ALA	LYS	THR	THR	PRO	ASP	TYS	ARG	THR	LEU	PHE	SER	ASN	LEU	LEU	SER	ASP
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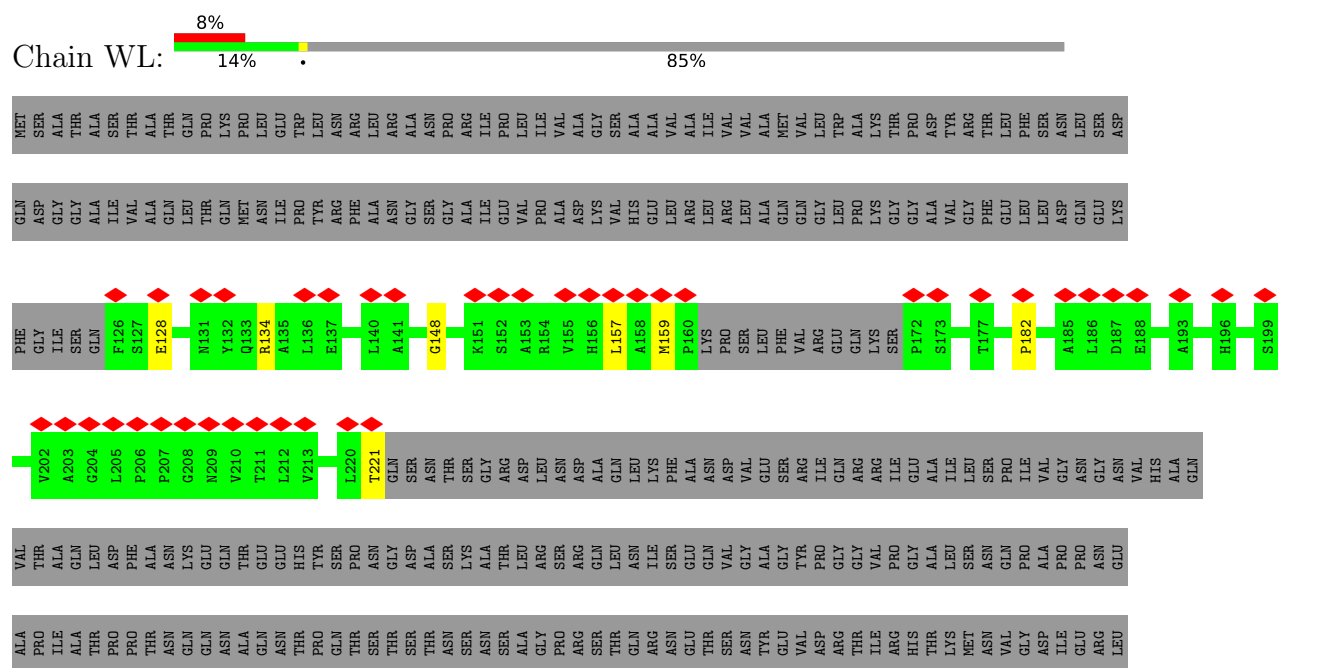
● Molecule 6: Flagellar M-ring protein



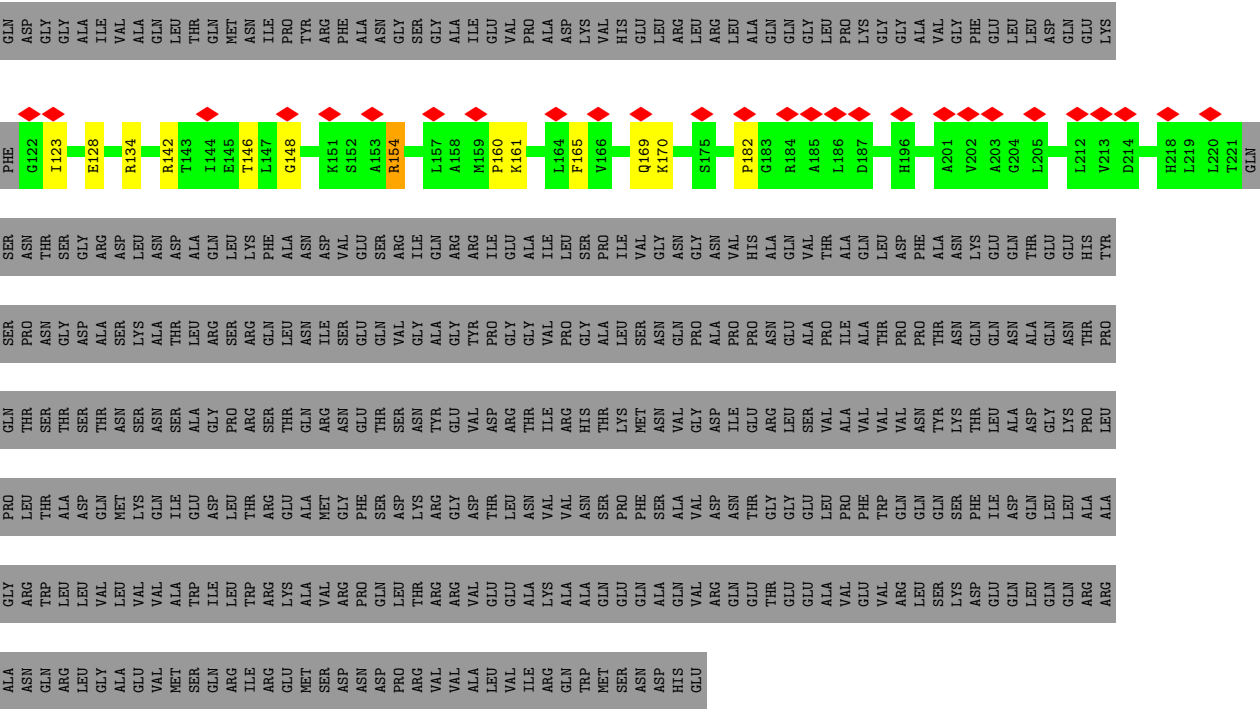
● Molecule 6: Flagellar M-ring protein



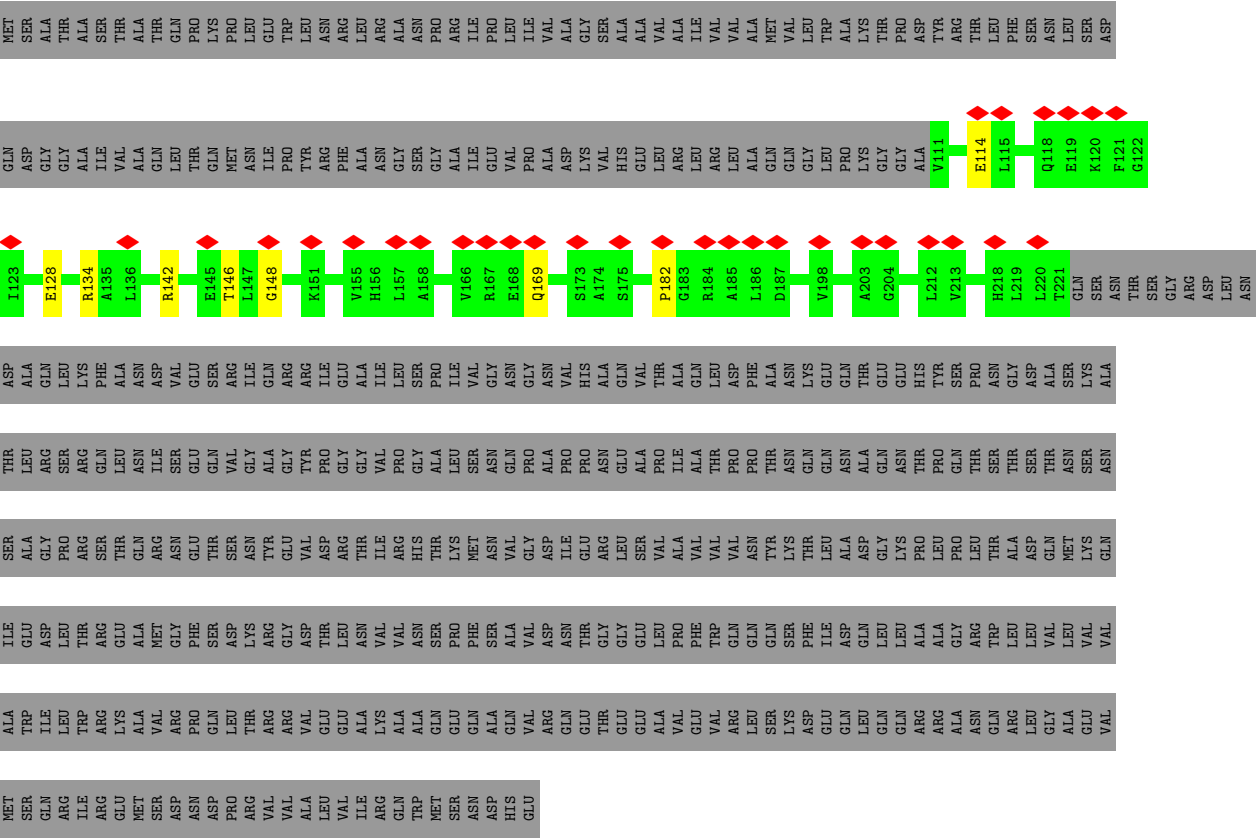
● Molecule 6: Flagellar M-ring protein



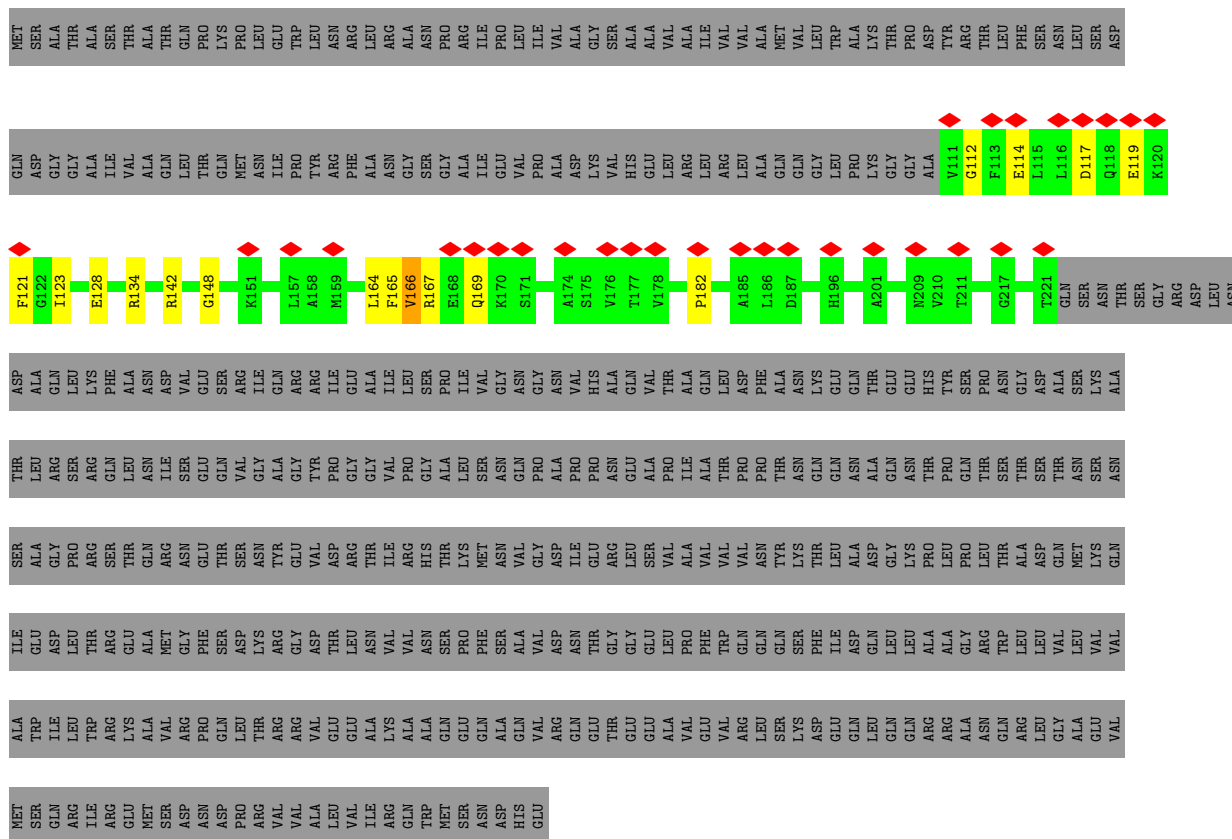
PHE	GLY	ILE	SER	GLN	PHE	SI27	E128	Q129	Y132	Q133	R134	A135	T146	L147	G148	P149	V150	K151	S152	H156	A158	M159	P160	L161	P172	S173	A174	V178	T179	L180	E181	P182	G183	R184	A185	L186	D187	E188	A193	L197	V199					
NET	SER	THR	ALA	ALA	SER	THR	ALA	THR	GLN	PRO	PRO	GLU	TRP	LEU	ASN	ARG	ASN	ARG	ILE	PRO	LEU	VAL	ALA	GLY	SER	ALA	ALA	VAL	ALA	THR	PRO	ASP	THR	ARG	LEU	PHE	SER	ASN	LEU	SER	ASP					
GLN	ASP	GLY	GLY	ALA	ILE	VAL	ALA	GLN	THR	GLN	MET	ASN	ILE	PRO	TYR	PHE	ARG	ALA	ASN	GLY	GLY	ALA	ILE	VAL	GLU	HIS	GLU	LEU	ARG	LEU	ARG	LEU	ALA	GLN	GLY	GLY	ALA	VAL	PHE	GLY	LEU	LEU	ASP	GLN	GLU	LYS



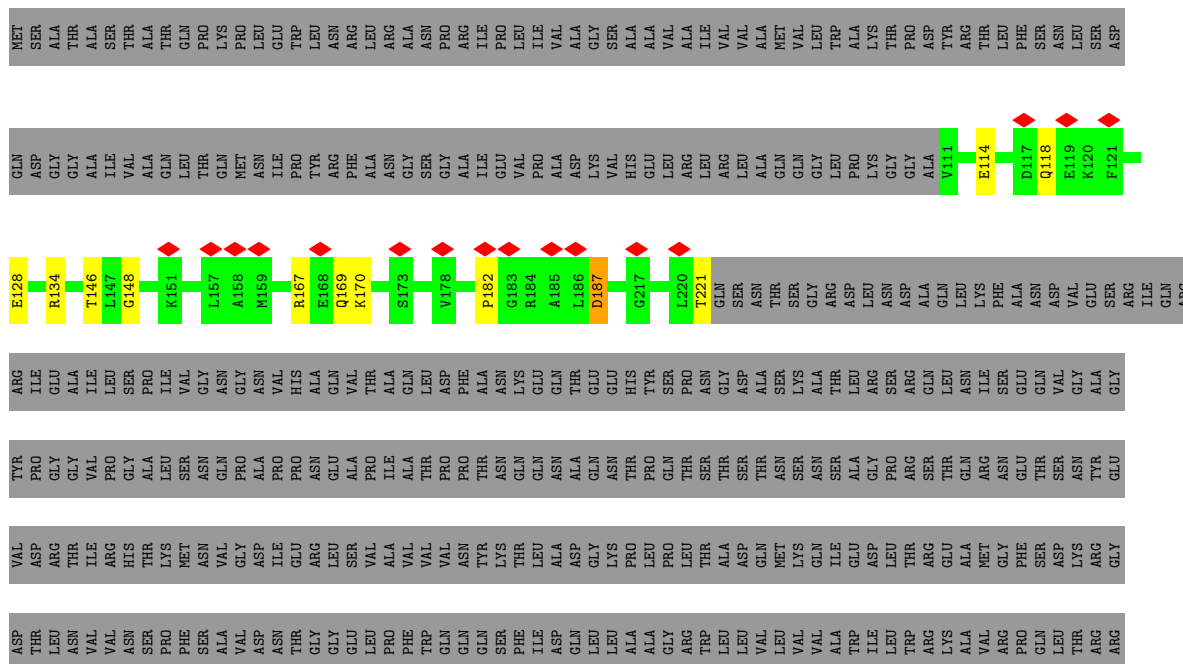
• Molecule 6: Flagellar M-ring protein

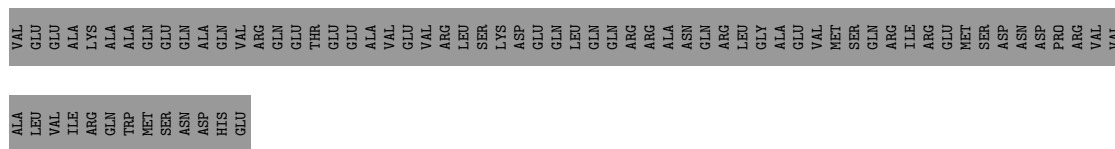


• Molecule 6: Flagellar M-ring protein

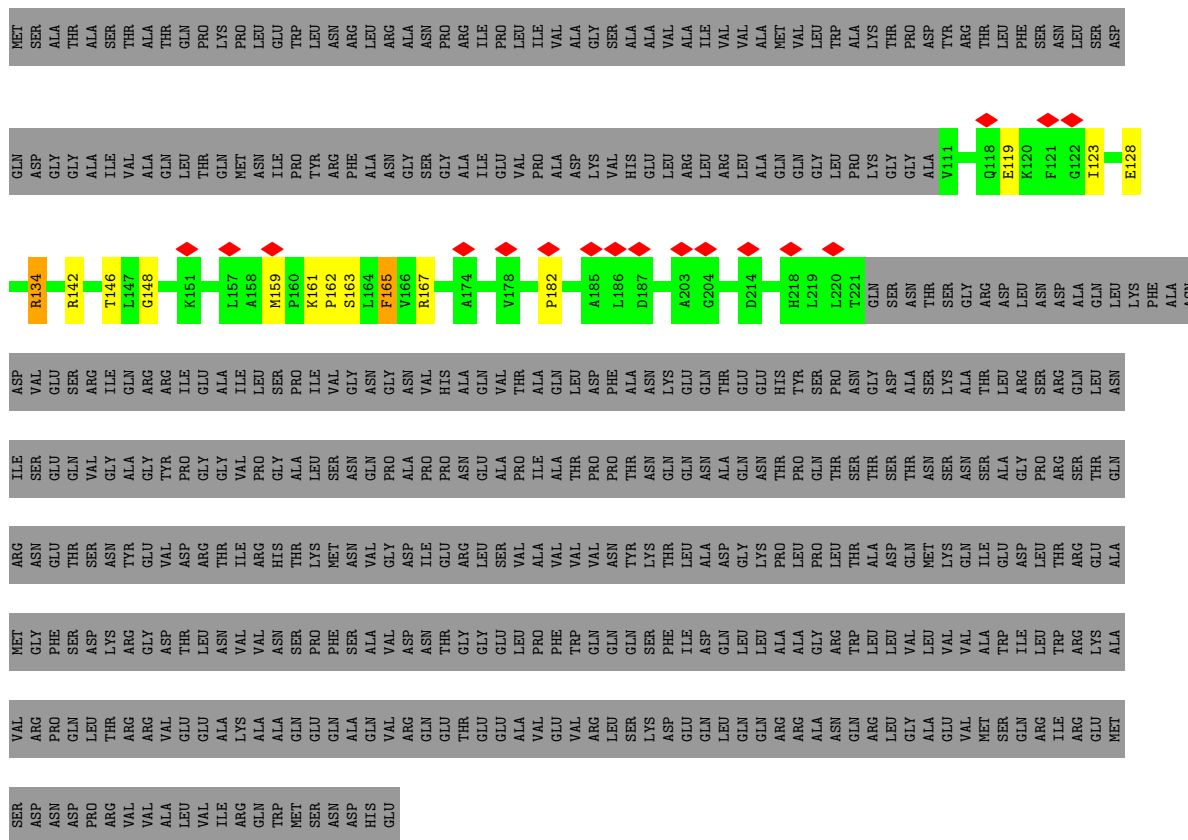


Chain WS: 18% 80%

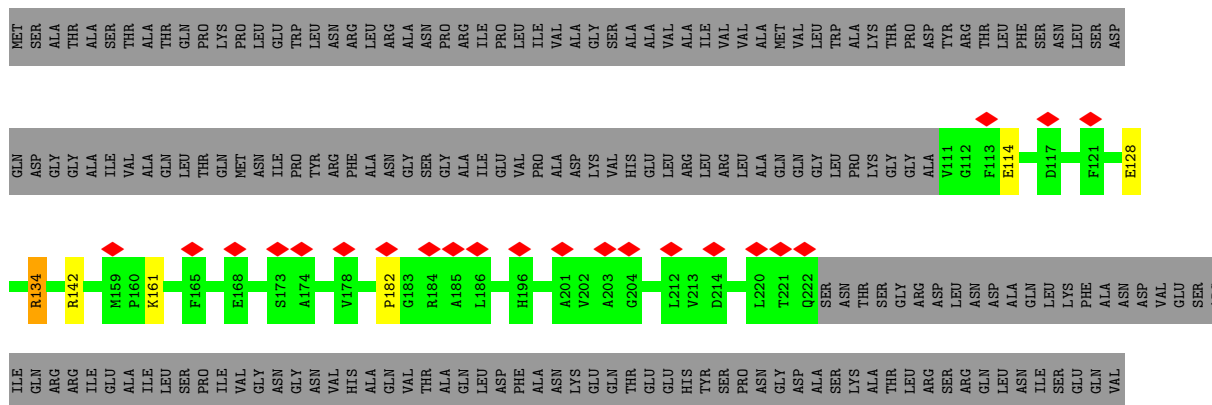


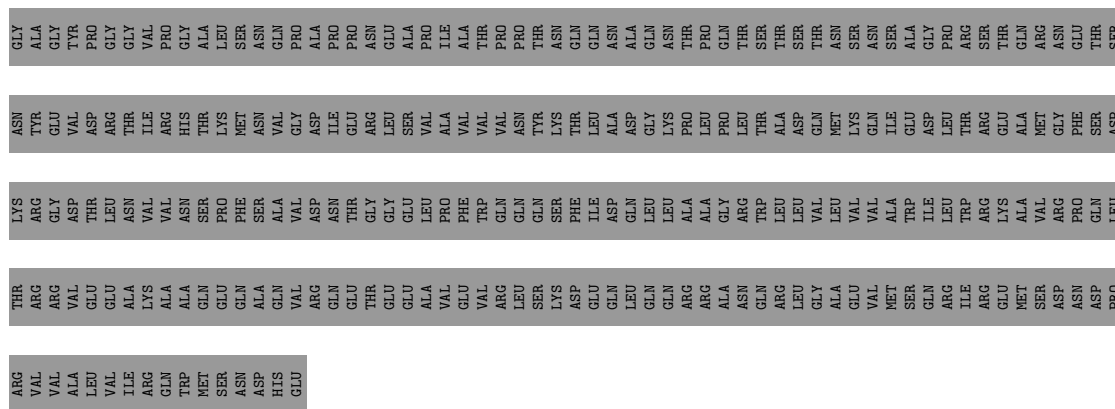


- Molecule 6: Flagellar M-ring protein

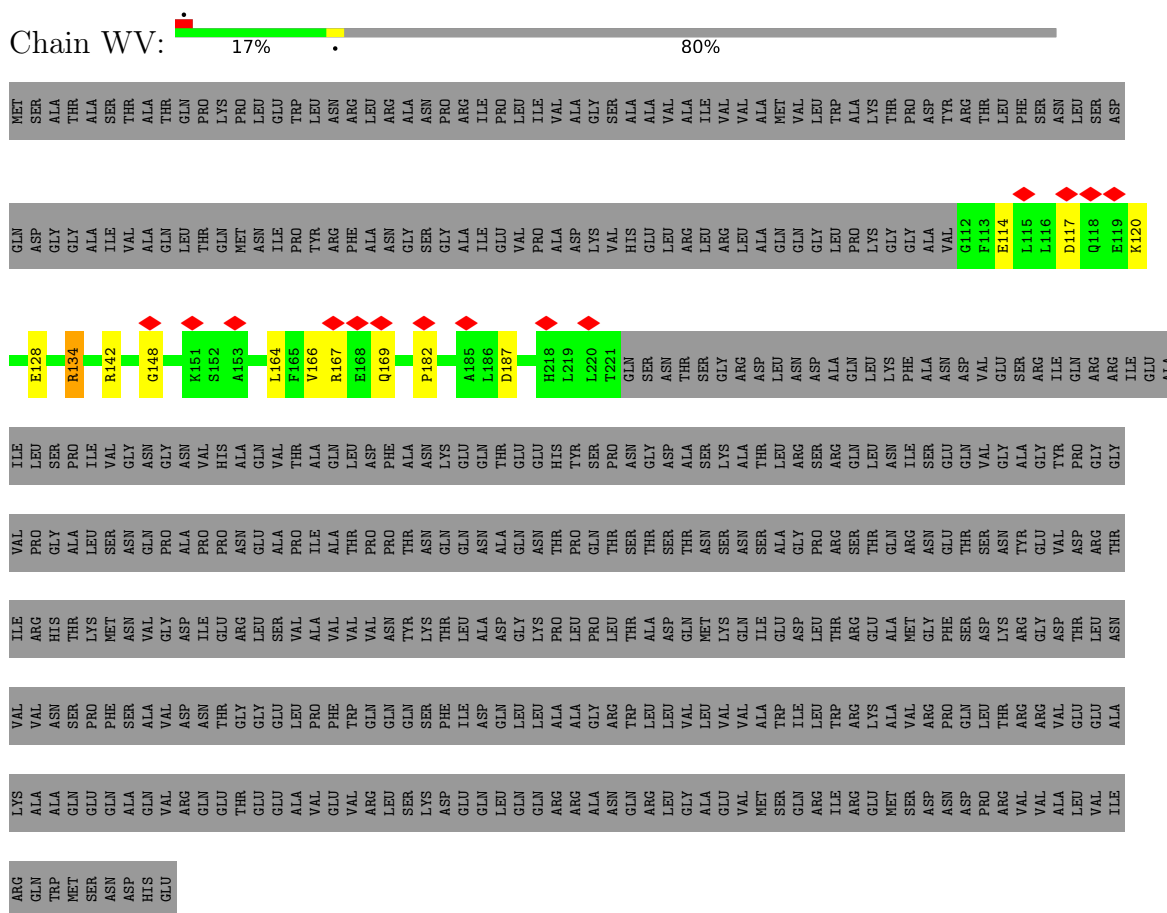


- Molecule 6: Flagellar M-ring protein

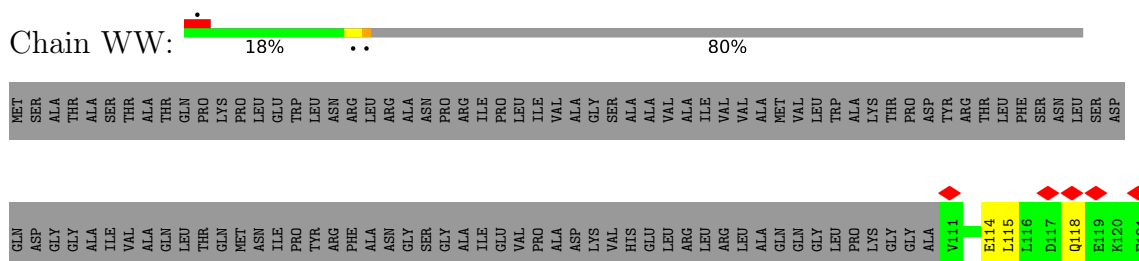




- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein



97%

SER
 GLN
 VAL
 GLY
 ALA
 GLY
 TYR
 P309
 P323
 N324
 ALA
 ALA
 ILE
 ALA
 THR
 PRO
 PRO
 THR
 ASN
 GLN
 GLN
 ASN
 ALA
 GLN
 ASN
 THR
 PRO
 GLN
 THR
 SER
 THR
 SER
 THR
 ASN
 SER
 ASN
 SER
 SER
 ALA
 GLY
 PRO
 ARG
 SER
 THR
 THR
 GLN
 ARG
 ASN
 ASN
 GLU
 THR
 SER
 ASN
 TYR
 GLU
 VAL
 ASP
 ARG
 THR
 ILE

96%

SER	GLN	GLU	VAL	GLY	ALA	GLY	TYR	PRO	GLY	G311	A315	L316	S317	N318	D319	T330	PRO	PRO	THR	ASN	GLN	GLN	GLN	ASN	ALA	ALA	GLN	ASN	THR	THR	PRO	GLN	THR	SER	THR	SER	THR	THR	ASN	SER	SER	ALA	GLY	PRO	PRO	ARG	SER	THR	GLN	ARG	ASN	GLU	THR	SER	ASN	TYR	GLU	VAL	ASP	THR	ARG	THR
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[illegible]

- Molecule 6: Flagellar M-ring protein

Chain BJ: 97%

[illegible]

- Molecule 6: Flagellar M-ring protein

Chain BK: 96%

[illegible]



WORLD WIDE
PDB
PROTEIN DATA BANK

[illegible]

- Molecule 6: Flagellar M-ring protein

Chain BQ:  96%

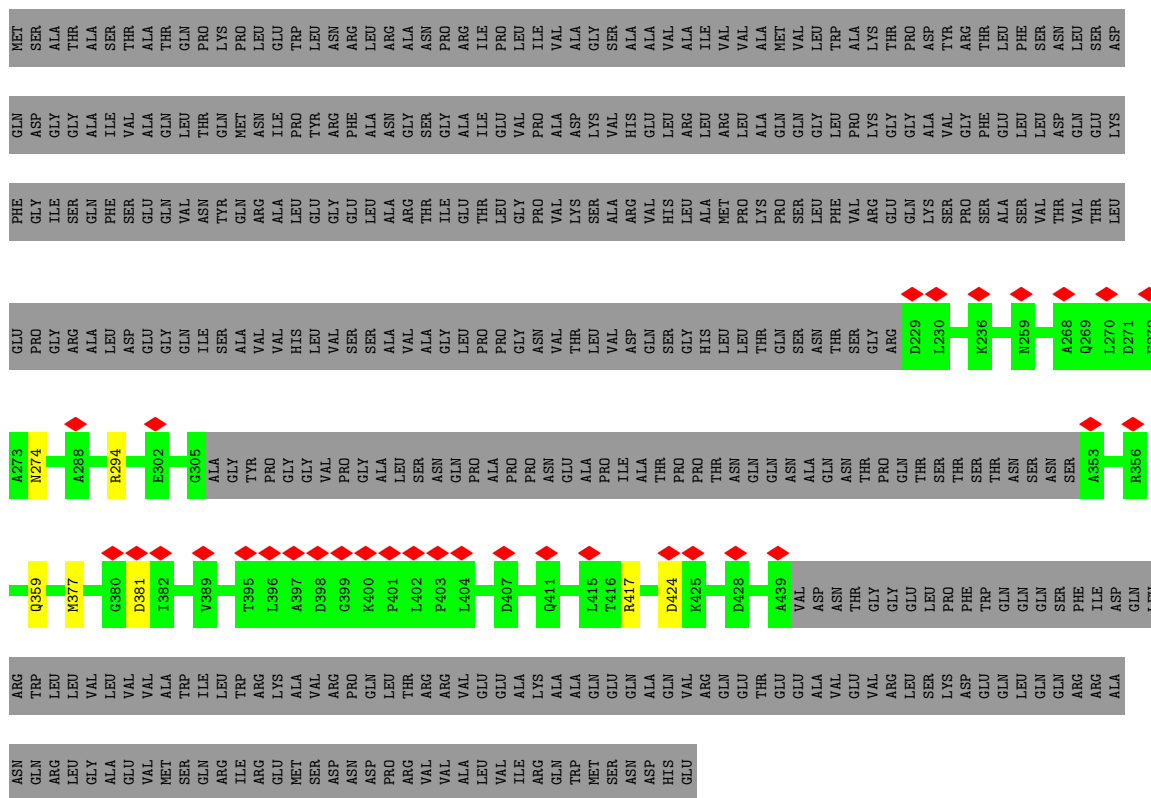
[illegible]

- Molecule 6: Flagellar M-ring protein

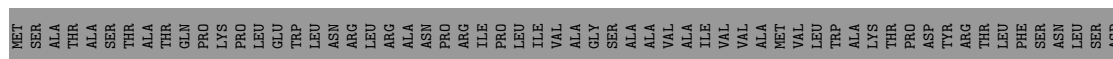
Chain BR: 

[illegible]

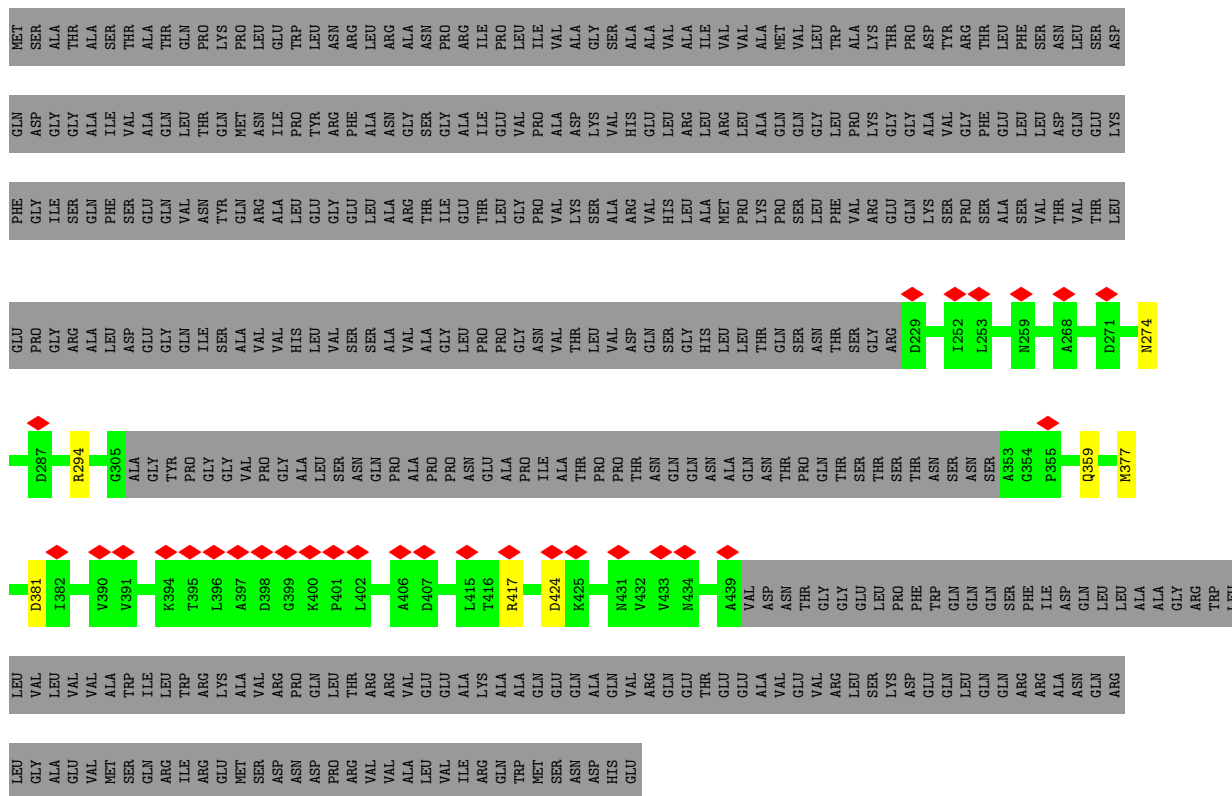
- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein

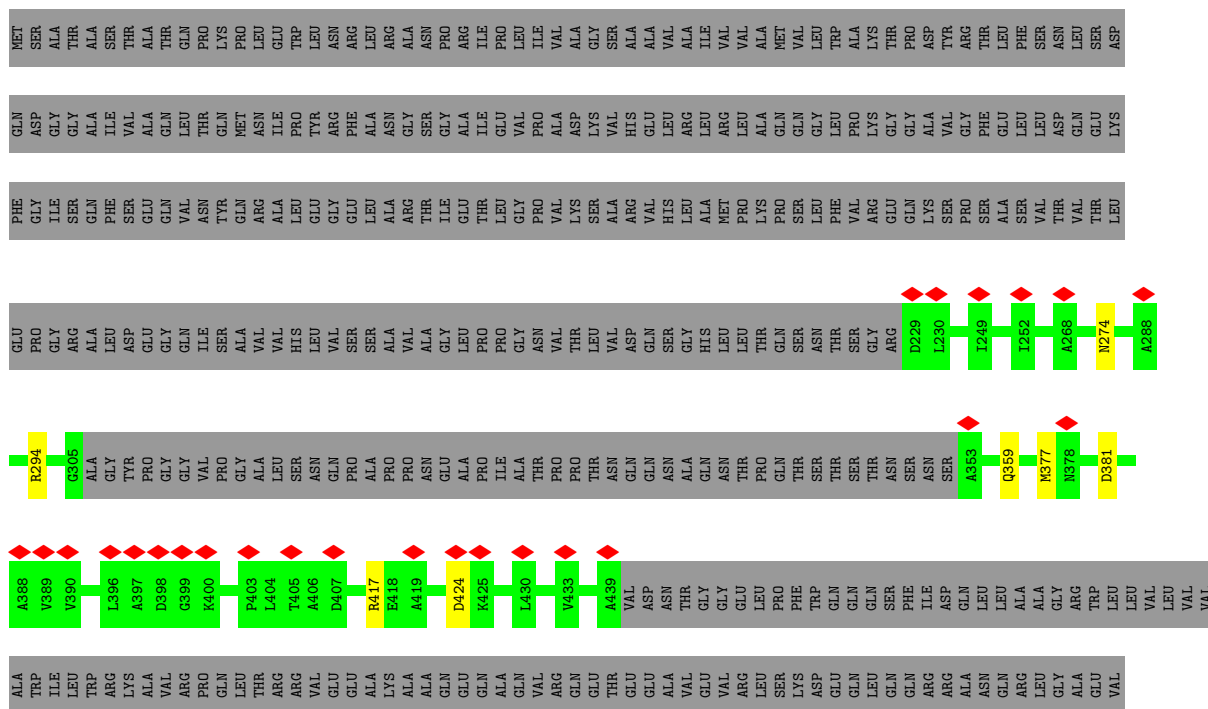


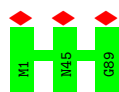
Chain BV: 



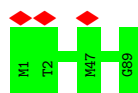
- Molecule 6: Flagellar M-ring protein

Chain BW:  28% 71%

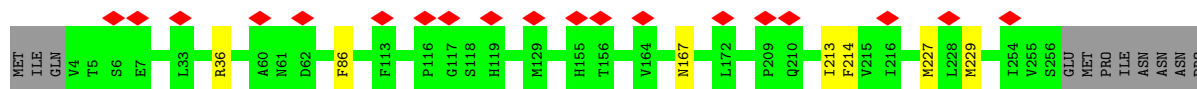




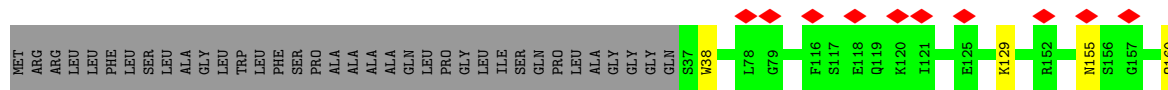
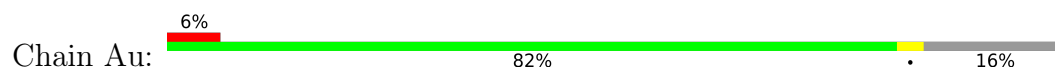
- Molecule 7: Flagellar biosynthetic protein FliQ



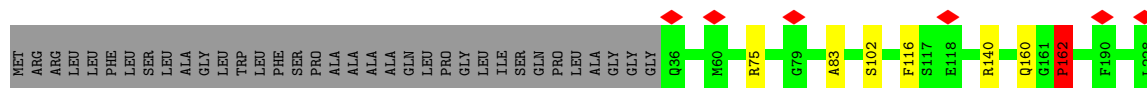
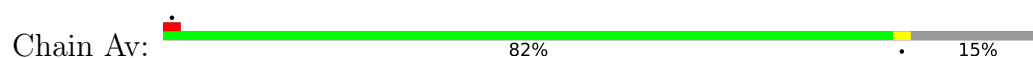
- Molecule 8: Flagellar biosynthetic protein FliR



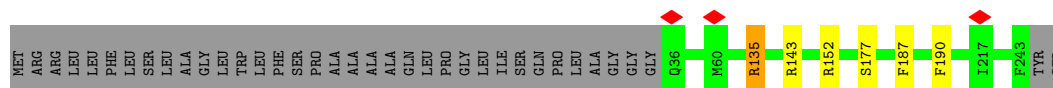
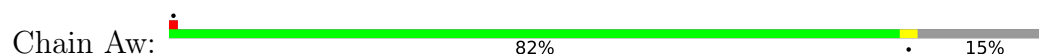
- Molecule 9: Flagellar biosynthetic protein FliP




- Molecule 9: Flagellar biosynthetic protein FliP

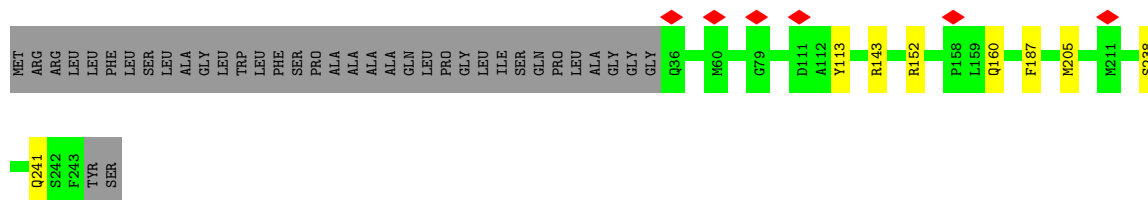


- Molecule 9: Flagellar biosynthetic protein FliP




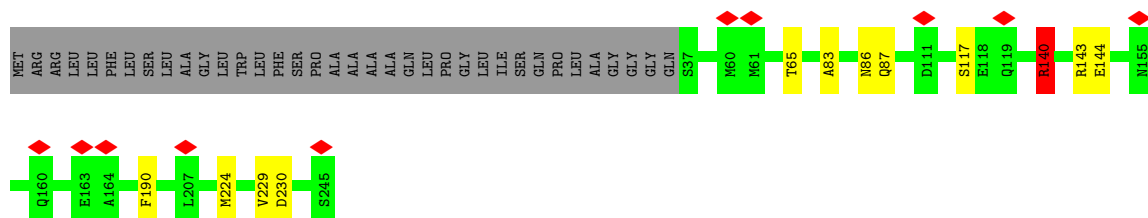
- Molecule 9: Flagellar biosynthetic protein FliP

Chain Ax:  82% 15%



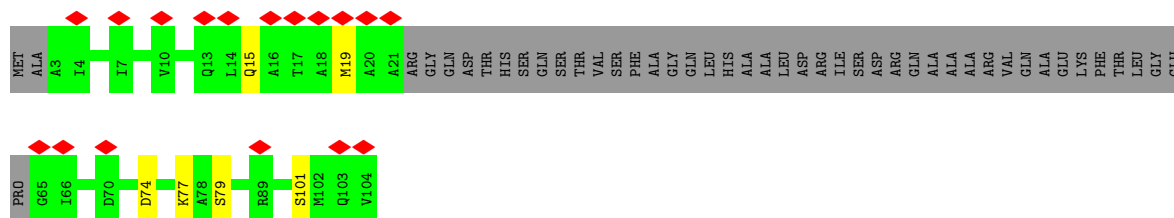
- Molecule 9: Flagellar biosynthetic protein FliP

Chain Ay:  80% 15%




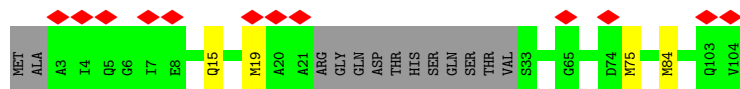
- Molecule 10: Flagellar hook-basal body complex protein FliE

Chain Az:  16% 51% 6% 43%




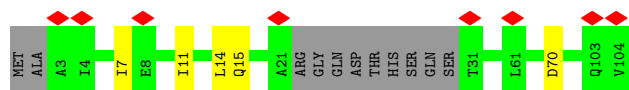
- Molecule 10: Flagellar hook-basal body complex protein FliE

Chain A1:  12% 84% 12%




- Molecule 10: Flagellar hook-basal body complex protein FliE

Chain A2:  8% 85% 5% 11%

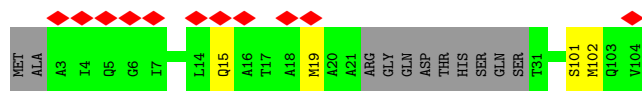
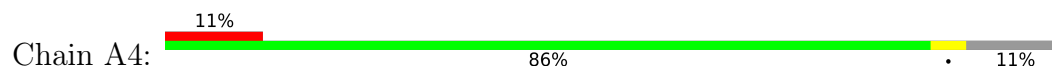


- Molecule 10: Flagellar hook-basal body complex protein FliE

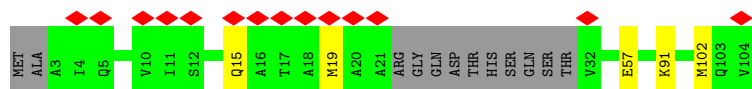
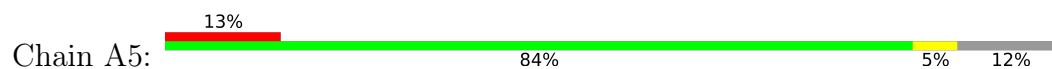
Chain A3:  7% 86% 11%



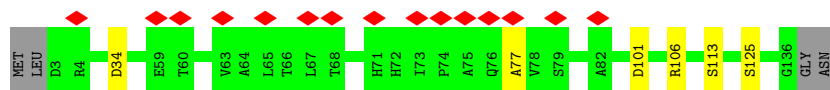
- Molecule 10: Flagellar hook-basal body complex protein FliE



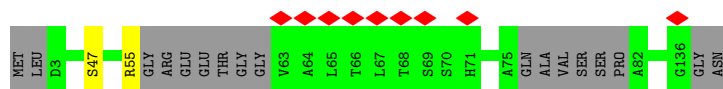
- Molecule 10: Flagellar hook-basal body complex protein FliE



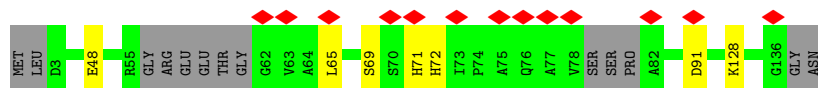
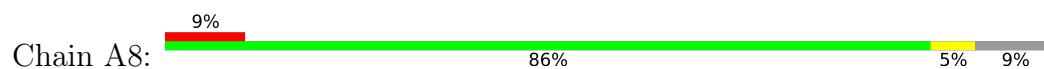
- Molecule 11: Flagellar basal body rod protein FlgB



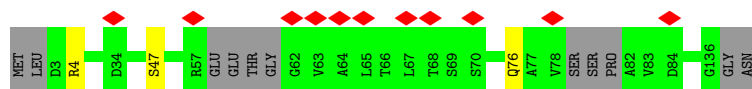
- Molecule 11: Flagellar basal body rod protein FlgB



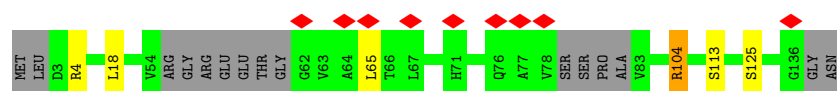
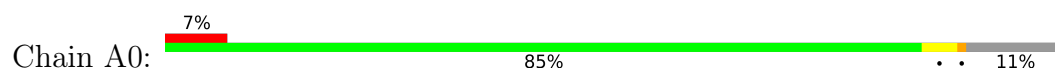
- Molecule 11: Flagellar basal body rod protein FlgB



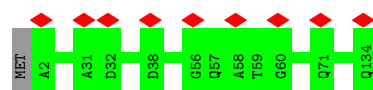
- Molecule 11: Flagellar basal body rod protein FlgB



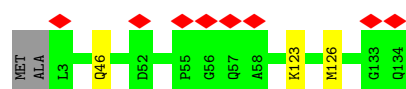
- Molecule 11: Flagellar basal body rod protein FlgB



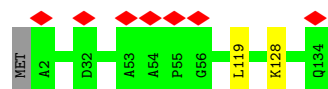
- Molecule 12: Flagellar basal-body rod protein FlgC



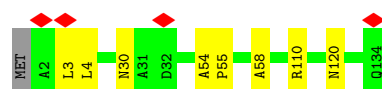
- Molecule 12: Flagellar basal-body rod protein FlgC



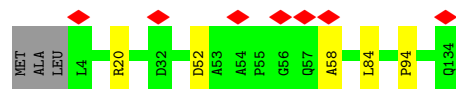
- Molecule 12: Flagellar basal-body rod protein FlgC



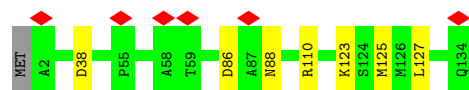
- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11858	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.637	Depositor
Minimum map value	-0.797	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	681.984, 681.984, 681.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.332, 1.332, 1.332	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	A	0.30	0/1613	0.51	0/2194
1	B	0.30	0/1613	0.51	0/2194
1	C	0.30	0/1613	0.51	0/2194
1	D	0.29	0/1613	0.51	0/2194
1	E	0.29	0/1613	0.51	0/2194
1	F	0.30	0/1613	0.51	0/2194
1	G	0.29	0/1613	0.51	0/2194
1	H	0.29	0/1613	0.51	0/2194
1	I	0.30	0/1613	0.51	0/2194
1	J	0.30	0/1613	0.51	0/2194
1	K	0.29	0/1613	0.51	0/2194
1	L	0.30	0/1613	0.51	0/2194
1	M	0.30	0/1613	0.51	0/2194
1	N	0.29	0/1613	0.51	0/2194
1	O	0.29	0/1613	0.51	0/2194
1	P	0.30	0/1613	0.51	0/2194
1	Q	0.30	0/1613	0.51	0/2194
1	R	0.30	0/1613	0.51	0/2194
1	S	0.29	0/1613	0.51	0/2194
1	T	0.29	0/1613	0.51	0/2194
1	U	0.30	0/1613	0.51	0/2194
1	V	0.29	0/1613	0.51	0/2194
1	W	0.29	0/1613	0.51	0/2194
1	X	0.30	0/1613	0.51	0/2194
1	Y	0.30	0/1613	0.51	0/2194
1	Z	0.29	0/1613	0.51	0/2194
2	a	0.31	0/2243	0.55	0/3041
2	b	0.31	0/2243	0.54	0/3041
2	c	0.31	0/2243	0.55	0/3041
2	d	0.31	0/2243	0.55	0/3041
2	e	0.30	0/2243	0.55	0/3041
2	f	0.30	0/2243	0.55	0/3041
2	g	0.31	0/2243	0.55	0/3041
2	h	0.31	0/2243	0.55	0/3041

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	i	0.31	0/2243	0.55	0/3041
2	j	0.31	0/2243	0.55	0/3041
2	k	0.30	0/2243	0.55	0/3041
2	l	0.30	0/2243	0.55	0/3041
2	m	0.30	0/2243	0.55	0/3041
2	n	0.31	0/2243	0.55	0/3041
2	o	0.30	0/2243	0.55	0/3041
2	p	0.31	0/2243	0.55	0/3041
2	q	0.31	0/2243	0.54	0/3041
2	r	0.30	0/2243	0.54	0/3041
2	s	0.30	0/2243	0.55	0/3041
2	t	0.30	0/2243	0.55	0/3041
2	u	0.30	0/2243	0.54	0/3041
2	v	0.31	0/2243	0.55	0/3041
2	w	0.30	0/2243	0.55	0/3041
2	x	0.31	0/2243	0.55	0/3041
2	y	0.31	0/2243	0.55	0/3041
2	z	0.31	0/2243	0.55	0/3041
3	0	0.33	0/1888	0.54	1/2564 (0.0%)
3	1	0.31	0/1917	0.51	0/2605
3	2	0.29	0/1973	0.51	0/2682
3	3	0.28	0/1973	0.52	0/2682
3	4	0.28	0/1973	0.51	0/2682
3	5	0.33	0/1973	0.52	0/2682
3	6	0.32	0/1973	0.54	0/2682
3	7	0.32	0/1973	0.53	0/2682
3	8	0.33	0/1973	0.56	0/2682
3	9	0.30	0/1973	0.53	1/2682 (0.0%)
3	AF	0.34	0/1926	0.53	0/2618
3	AG	0.38	0/1934	0.59	0/2629
3	AH	0.39	0/1942	0.56	0/2639
3	AI	0.35	0/1926	0.58	1/2618 (0.0%)
3	AJ	0.34	0/1934	0.54	0/2629
3	AK	0.34	0/1844	0.51	0/2505
3	AL	0.33	0/1888	0.52	0/2564
3	AM	0.33	0/1888	0.56	1/2564 (0.0%)
3	AN	0.31	0/1888	0.51	0/2564
3	ZA	0.31	0/1973	0.53	0/2682
3	ZB	0.29	0/1973	0.49	0/2682
3	ZC	0.34	0/1973	0.54	0/2682
3	ZD	0.31	0/1973	0.52	0/2682
3	ZE	0.30	0/1973	0.51	1/2682 (0.0%)
4	ZF	0.28	0/2991	0.49	0/4076

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ZG	0.34	0/2991	0.52	1/4076 (0.0%)
4	ZH	0.29	0/2991	0.50	0/4076
4	ZI	0.30	0/2991	0.51	0/4076
4	ZJ	0.31	0/2991	0.49	0/4076
4	ZK	0.29	0/2991	0.50	0/4076
4	ZL	0.29	0/2991	0.49	0/4076
4	ZM	0.29	0/2991	0.53	1/4076 (0.0%)
4	ZN	0.28	0/2991	0.51	0/4076
4	ZO	0.30	0/2991	0.50	0/4076
4	ZP	0.28	0/2991	0.50	1/4076 (0.0%)
4	ZQ	0.29	0/2991	0.51	0/4076
4	ZR	0.30	1/2991 (0.0%)	0.55	3/4076 (0.1%)
4	ZS	0.29	0/2991	0.52	1/4076 (0.0%)
4	ZT	0.29	0/2991	0.48	0/4076
4	ZU	0.29	0/2991	0.50	0/4076
4	ZV	0.50	4/2991 (0.1%)	0.67	6/4076 (0.1%)
4	ZW	0.27	0/2991	0.49	0/4076
4	ZX	0.28	0/2991	0.48	0/4076
4	ZY	0.30	1/2991 (0.0%)	0.55	2/4076 (0.0%)
4	ZZ	0.26	0/2991	0.46	0/4076
4	Za	0.28	0/2991	0.49	0/4076
4	Zb	0.30	0/2991	0.49	0/4076
4	Zc	0.29	0/2991	0.52	2/4076 (0.0%)
4	Zd	0.30	0/2991	0.51	0/4076
4	Ze	0.28	0/2991	0.48	0/4076
4	Zf	0.27	0/2991	0.48	0/4076
4	Zg	0.28	0/2991	0.49	0/4076
4	Zh	0.28	0/2991	0.48	0/4076
5	AA	0.32	0/1828	0.56	0/2492
5	AB	0.33	0/1836	0.56	2/2502 (0.1%)
5	AC	0.37	0/1844	0.57	0/2512
5	AD	0.33	0/1844	0.57	0/2512
5	AE	0.33	0/1836	0.58	0/2502
6	AO	0.27	0/1289	0.53	0/1741
6	AP	0.27	0/1289	0.53	0/1741
6	AQ	0.26	0/1289	0.53	0/1741
6	AR	0.27	0/1289	0.53	0/1741
6	AS	0.27	0/1289	0.53	0/1741
6	AT	0.27	0/1289	0.53	0/1741
6	AU	0.27	0/1289	0.53	0/1741
6	AV	0.27	0/1289	0.53	0/1741
6	AW	0.27	0/1289	0.53	0/1741
6	AX	0.27	0/1289	0.53	0/1741

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	AY	0.27	0/1289	0.53	0/1741
6	AZ	0.27	0/1289	0.53	0/1741
6	Aa	0.27	0/1289	0.53	0/1741
6	Ac	0.27	0/1289	0.53	0/1741
6	Ad	0.27	0/1289	0.53	0/1741
6	Ae	0.27	0/1289	0.53	0/1741
6	Af	0.27	0/1289	0.53	0/1741
6	Ag	0.27	0/1289	0.53	0/1741
6	Ah	0.27	0/1289	0.53	0/1741
6	Ai	0.27	0/1289	0.53	0/1741
6	Aj	0.27	0/1289	0.53	0/1741
6	Ak	0.26	0/1289	0.53	0/1741
6	Al	0.27	0/1289	0.53	0/1741
6	Am	0.27	0/1289	0.53	0/1741
6	An	0.27	0/1289	0.53	0/1741
6	Ao	0.27	0/1289	0.53	0/1741
6	Ap	0.27	0/1289	0.53	0/1741
6	BG	0.46	0/83	0.87	1/114 (0.9%)
6	BH	0.26	0/107	0.38	0/148
6	BI	0.31	0/137	0.49	0/191
6	BJ	0.28	0/107	0.57	0/148
6	BK	0.40	0/145	0.55	0/203
6	BL	0.33	0/107	0.51	0/148
6	BM	0.26	0/145	0.43	0/203
6	BN	0.30	0/107	0.38	0/148
6	BO	0.33	0/137	0.70	0/191
6	BP	0.30	0/107	0.37	0/148
6	BQ	0.29	0/145	0.45	0/203
6	BR	0.27	0/1289	0.52	0/1741
6	BS	0.27	0/1289	0.53	0/1741
6	BT	0.27	0/1289	0.53	0/1741
6	BU	0.27	0/1289	0.53	0/1741
6	BV	0.27	0/1289	0.53	0/1741
6	BW	0.27	0/1289	0.53	0/1741
6	BX	0.27	0/1289	0.53	0/1741
6	UI	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UJ	0.84	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UK	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UL	0.82	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UM	0.84	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UN	0.84	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UO	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UP	0.84	2/1191 (0.2%)	0.82	4/1618 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	WA	0.60	0/863	0.72	1/1172 (0.1%)
6	WB	0.59	0/850	0.69	0/1154
6	WC	0.59	0/825	0.68	0/1121
6	WD	0.61	0/841	0.68	0/1142
6	WE	0.60	0/857	0.71	0/1164
6	WF	0.60	0/848	0.69	0/1152
6	WG	0.60	0/857	0.68	0/1164
6	WH	0.60	0/714	0.69	0/973
6	WI	0.59	0/714	0.74	0/973
6	WJ	0.61	0/749	0.72	1/1020 (0.1%)
6	WK	0.60	0/741	0.69	0/1009
6	WL	0.60	0/631	0.70	0/860
6	WM	0.59	0/604	0.70	0/824
6	WN	0.60	0/619	0.70	0/844
6	WO	0.60	0/726	0.72	1/989 (0.1%)
6	WP	0.60	0/753	0.69	0/1025
6	WQ	0.60	0/848	0.69	0/1152
6	WR	0.60	0/848	0.69	0/1152
6	WS	0.61	0/848	0.69	0/1152
6	WT	0.60	0/848	0.71	0/1152
6	WU	0.60	0/857	0.67	0/1164
6	WV	0.61	0/841	0.69	0/1142
6	WW	0.60	0/848	0.70	0/1152
7	Ab	0.45	0/681	0.67	1/930 (0.1%)
7	Aq	0.32	0/681	0.53	0/930
7	Ar	0.28	0/681	0.50	0/930
7	As	0.26	0/681	0.48	0/930
8	At	0.31	0/1994	0.52	0/2724
9	Au	0.36	0/1643	0.62	2/2237 (0.1%)
9	Av	0.30	0/1665	0.49	1/2267 (0.0%)
9	Aw	0.30	0/1652	0.50	0/2249
9	Ax	0.29	0/1652	0.47	0/2249
9	Ay	0.33	0/1662	0.52	0/2263
10	A1	0.36	0/675	0.49	0/905
10	A2	0.36	0/689	0.52	0/925
10	A3	0.36	0/689	0.50	0/925
10	A4	0.37	0/689	0.53	0/925
10	A5	0.40	0/682	0.52	0/915
10	Az	0.43	0/428	0.57	0/572
11	A0	0.34	0/959	0.50	0/1293
11	A6	0.37	0/1042	0.56	0/1408
11	A7	0.33	0/951	0.50	0/1282
11	A8	0.35	0/976	0.56	0/1316

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	A9	0.35	0/991	0.54	0/1335
12	BA	0.30	0/981	0.47	0/1334
12	BB	0.29	0/976	0.50	0/1327
12	BC	0.34	0/981	0.50	0/1334
12	BD	0.33	0/981	0.62	0/1334
12	BE	0.29	0/968	0.48	0/1316
12	BF	0.36	0/981	0.52	0/1334
All	All	0.35	22/343249 (0.0%)	0.55	64/466323 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	0	0	2
3	1	0	1
3	5	0	2
3	7	0	1
3	8	0	2
3	AF	0	1
3	AI	0	1
3	AK	0	1
3	AL	0	1
3	AM	0	2
3	AN	0	3
3	ZA	0	2
3	ZD	0	1
3	ZE	0	3
4	ZI	0	1
4	ZK	0	1
4	ZO	0	1
4	ZT	0	1
4	ZU	0	1
4	ZW	0	1
4	ZZ	0	1
4	Zd	0	1
4	Ze	0	1
5	AA	0	1
5	AB	0	2
5	AD	0	1
6	UI	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	UJ	0	2
6	UK	0	3
6	UL	0	3
6	UM	0	2
6	UN	0	2
6	UO	0	2
6	UP	0	3
6	WA	0	3
6	WB	0	4
6	WC	0	3
6	WD	0	1
6	WE	0	2
6	WF	0	3
6	WG	0	3
6	WI	0	1
6	WJ	0	3
6	WK	0	2
6	WL	0	2
6	WM	0	1
6	WN	0	1
6	WO	0	1
6	WP	0	3
6	WQ	0	2
6	WR	0	3
6	WS	0	1
6	WT	0	2
6	WU	0	2
6	WV	0	3
6	WW	0	2
9	Aw	0	2
9	Ay	0	2
11	A0	0	1
11	A6	0	1
11	A7	0	1
11	A9	0	1
12	BD	0	1
12	BF	0	1
All	All	0	113

The worst 5 of 22 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	ZV	140	PRO	CG-CD	-16.11	0.97	1.50
4	ZV	125	PRO	CG-CD	-10.15	1.17	1.50
6	UM	172	PRO	N-CD	-9.55	1.34	1.47
6	UL	172	PRO	N-CD	-9.54	1.34	1.47
6	UI	172	PRO	N-CD	-9.50	1.34	1.47

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	ZV	140	PRO	N-CD-CG	-17.33	77.21	103.20
4	ZR	125	PRO	CA-N-CD	-13.96	91.96	111.50
4	ZY	125	PRO	CA-N-CD	-13.33	92.84	111.50
4	ZV	125	PRO	CA-N-CD	-13.27	92.93	111.50
9	Au	162	PRO	CA-N-CD	-11.97	94.75	111.50

There are no chirality outliers.

5 of 113 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	0	36	ARG	Sidechain
3	0	50	ARG	Sidechain
3	1	36	ARG	Sidechain
3	5	50	ARG	Sidechain
3	5	73	ARG	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	A	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	B	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	C	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	D	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	E	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	F	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	G	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	H	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	I	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	J	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	K	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	L	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	M	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	N	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	O	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	P	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	Q	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	R	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	S	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	T	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	U	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	V	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	W	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	X	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	Y	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
1	Z	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	62
2	a	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	b	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	c	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	d	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	e	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	f	297/365 (81%)	288 (97%)	9 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	g	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	h	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	i	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	j	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	k	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	l	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	m	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	n	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	o	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	p	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	q	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	r	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	s	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	t	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	u	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	v	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	w	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	x	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
2	y	297/365 (81%)	289 (97%)	8 (3%)	0	100	100
2	z	297/365 (81%)	288 (97%)	9 (3%)	0	100	100
3	0	244/260 (94%)	236 (97%)	5 (2%)	3 (1%)	11	44
3	1	248/260 (95%)	238 (96%)	9 (4%)	1 (0%)	30	67
3	2	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	53
3	3	258/260 (99%)	247 (96%)	9 (4%)	2 (1%)	16	53
3	4	258/260 (99%)	245 (95%)	11 (4%)	2 (1%)	16	53
3	5	258/260 (99%)	240 (93%)	15 (6%)	3 (1%)	11	44
3	6	258/260 (99%)	244 (95%)	10 (4%)	4 (2%)	8	39
3	7	258/260 (99%)	244 (95%)	11 (4%)	3 (1%)	11	44
3	8	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	11	44
3	9	258/260 (99%)	244 (95%)	13 (5%)	1 (0%)	30	67
3	AF	250/260 (96%)	238 (95%)	11 (4%)	1 (0%)	30	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	AG	251/260 (96%)	234 (93%)	14 (6%)	3 (1%)	11	44
3	AH	252/260 (97%)	234 (93%)	16 (6%)	2 (1%)	16	53
3	AI	250/260 (96%)	239 (96%)	9 (4%)	2 (1%)	16	53
3	AJ	251/260 (96%)	235 (94%)	10 (4%)	6 (2%)	5	30
3	AK	239/260 (92%)	231 (97%)	7 (3%)	1 (0%)	30	67
3	AL	244/260 (94%)	229 (94%)	10 (4%)	5 (2%)	6	34
3	AM	244/260 (94%)	234 (96%)	9 (4%)	1 (0%)	30	67
3	AN	244/260 (94%)	239 (98%)	4 (2%)	1 (0%)	30	67
3	ZA	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	11	44
3	ZB	258/260 (99%)	242 (94%)	13 (5%)	3 (1%)	11	44
3	ZC	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	53
3	ZD	258/260 (99%)	237 (92%)	18 (7%)	3 (1%)	11	44
3	ZE	258/260 (99%)	243 (94%)	14 (5%)	1 (0%)	30	67
4	ZF	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZG	399/403 (99%)	388 (97%)	10 (2%)	1 (0%)	37	71
4	ZH	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
4	ZI	399/403 (99%)	387 (97%)	10 (2%)	2 (0%)	25	62
4	ZJ	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZK	399/403 (99%)	387 (97%)	11 (3%)	1 (0%)	37	71
4	ZL	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	37	71
4	ZM	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZN	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZO	399/403 (99%)	381 (96%)	15 (4%)	3 (1%)	16	53
4	ZP	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	37	71
4	ZQ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
4	ZR	399/403 (99%)	391 (98%)	8 (2%)	0	100	100
4	ZS	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	ZT	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
4	ZU	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZV	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	ZW	399/403 (99%)	380 (95%)	18 (4%)	1 (0%)	37	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	ZX	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZY	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
4	ZZ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
4	Za	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	37	71
4	Zb	399/403 (99%)	392 (98%)	7 (2%)	0	100	100
4	Zc	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	Zd	399/403 (99%)	384 (96%)	15 (4%)	0	100	100
4	Ze	399/403 (99%)	385 (96%)	13 (3%)	1 (0%)	37	71
4	Zf	399/403 (99%)	386 (97%)	13 (3%)	0	100	100
4	Zg	399/403 (99%)	383 (96%)	16 (4%)	0	100	100
4	Zh	399/403 (99%)	391 (98%)	8 (2%)	0	100	100
5	AA	246/251 (98%)	238 (97%)	7 (3%)	1 (0%)	30	67
5	AB	247/251 (98%)	242 (98%)	4 (2%)	1 (0%)	30	67
5	AC	248/251 (99%)	233 (94%)	13 (5%)	2 (1%)	16	53
5	AD	248/251 (99%)	235 (95%)	13 (5%)	0	100	100
5	AE	247/251 (98%)	236 (96%)	9 (4%)	2 (1%)	16	53
6	AO	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AP	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AQ	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AR	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AS	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AT	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AU	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AV	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AW	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AX	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AY	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AZ	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Aa	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ac	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ad	160/560 (29%)	158 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Ae	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Af	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ag	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ah	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ai	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Aj	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ak	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Al	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Am	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	An	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ao	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ap	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BG	11/560 (2%)	9 (82%)	2 (18%)	0	100	100
6	BH	14/560 (2%)	12 (86%)	2 (14%)	0	100	100
6	BI	18/560 (3%)	18 (100%)	0	0	100	100
6	BJ	14/560 (2%)	14 (100%)	0	0	100	100
6	BK	19/560 (3%)	17 (90%)	2 (10%)	0	100	100
6	BL	14/560 (2%)	13 (93%)	1 (7%)	0	100	100
6	BM	19/560 (3%)	19 (100%)	0	0	100	100
6	BN	14/560 (2%)	14 (100%)	0	0	100	100
6	BO	18/560 (3%)	18 (100%)	0	0	100	100
6	BP	14/560 (2%)	14 (100%)	0	0	100	100
6	BQ	19/560 (3%)	19 (100%)	0	0	100	100
6	BR	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BS	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BT	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BU	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BV	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BW	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BX	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	UI	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	UJ	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42
6	UK	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42
6	UL	151/560 (27%)	142 (94%)	7 (5%)	2 (1%)	10	42
6	UM	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42
6	UN	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42
6	UO	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42
6	UP	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	42
6	WA	111/560 (20%)	99 (89%)	9 (8%)	3 (3%)	4	28
6	WB	109/560 (20%)	94 (86%)	10 (9%)	5 (5%)	2	20
6	WC	106/560 (19%)	96 (91%)	9 (8%)	1 (1%)	14	50
6	WD	108/560 (19%)	99 (92%)	4 (4%)	5 (5%)	2	20
6	WE	110/560 (20%)	98 (89%)	8 (7%)	4 (4%)	3	23
6	WF	109/560 (20%)	98 (90%)	8 (7%)	3 (3%)	4	27
6	WG	110/560 (20%)	98 (89%)	10 (9%)	2 (2%)	7	36
6	WH	93/560 (17%)	86 (92%)	5 (5%)	2 (2%)	5	32
6	WI	93/560 (17%)	82 (88%)	5 (5%)	6 (6%)	1	15
6	WJ	97/560 (17%)	89 (92%)	7 (7%)	1 (1%)	13	48
6	WK	96/560 (17%)	84 (88%)	9 (9%)	3 (3%)	3	26
6	WL	81/560 (14%)	75 (93%)	4 (5%)	2 (2%)	4	30
6	WM	78/560 (14%)	72 (92%)	4 (5%)	2 (3%)	4	29
6	WN	80/560 (14%)	75 (94%)	2 (2%)	3 (4%)	2	22
6	WO	94/560 (17%)	85 (90%)	7 (7%)	2 (2%)	5	33
6	WP	98/560 (18%)	87 (89%)	6 (6%)	5 (5%)	1	18
6	WQ	109/560 (20%)	100 (92%)	5 (5%)	4 (4%)	2	23
6	WR	109/560 (20%)	94 (86%)	8 (7%)	7 (6%)	1	15
6	WS	109/560 (20%)	96 (88%)	7 (6%)	6 (6%)	1	18
6	WT	109/560 (20%)	97 (89%)	5 (5%)	7 (6%)	1	15
6	WU	110/560 (20%)	101 (92%)	8 (7%)	1 (1%)	14	50
6	WV	108/560 (19%)	97 (90%)	9 (8%)	2 (2%)	6	35
6	WW	109/560 (20%)	95 (87%)	9 (8%)	5 (5%)	2	20
7	Ab	87/89 (98%)	81 (93%)	4 (5%)	2 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	Aq	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
7	Ar	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
7	As	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
8	At	251/264 (95%)	233 (93%)	16 (6%)	2 (1%)	16	53
9	Au	205/245 (84%)	197 (96%)	8 (4%)	0	100	100
9	Av	207/245 (84%)	199 (96%)	6 (3%)	2 (1%)	13	48
9	Aw	206/245 (84%)	201 (98%)	5 (2%)	0	100	100
9	Ax	206/245 (84%)	199 (97%)	6 (3%)	1 (0%)	25	62
9	Ay	207/245 (84%)	192 (93%)	10 (5%)	5 (2%)	5	30
10	A1	87/104 (84%)	87 (100%)	0	0	100	100
10	A2	89/104 (86%)	87 (98%)	2 (2%)	0	100	100
10	A3	89/104 (86%)	89 (100%)	0	0	100	100
10	A4	89/104 (86%)	89 (100%)	0	0	100	100
10	A5	88/104 (85%)	88 (100%)	0	0	100	100
10	Az	55/104 (53%)	52 (94%)	3 (6%)	0	100	100
11	A0	117/138 (85%)	115 (98%)	2 (2%)	0	100	100
11	A6	132/138 (96%)	127 (96%)	4 (3%)	1 (1%)	16	53
11	A7	115/138 (83%)	114 (99%)	1 (1%)	0	100	100
11	A8	119/138 (86%)	116 (98%)	3 (2%)	0	100	100
11	A9	121/138 (88%)	119 (98%)	2 (2%)	0	100	100
12	BA	131/134 (98%)	122 (93%)	9 (7%)	0	100	100
12	BB	130/134 (97%)	123 (95%)	7 (5%)	0	100	100
12	BC	131/134 (98%)	124 (95%)	7 (5%)	0	100	100
12	BD	131/134 (98%)	121 (92%)	7 (5%)	3 (2%)	5	31
12	BE	129/134 (96%)	123 (95%)	5 (4%)	1 (1%)	16	53
12	BF	131/134 (98%)	124 (95%)	7 (5%)	0	100	100
All	All	44706/81227 (55%)	43140 (96%)	1350 (3%)	216 (0%)	27	62

5 of 216 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	209	ASN
3	4	140	ILE

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Mol	Chain	Res	Type
3	5	209	ASN
3	6	139	ALA
3	8	209	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	B	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	C	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	D	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	E	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	F	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	G	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	H	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	I	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	J	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	K	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	L	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	M	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	N	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	O	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	P	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	Q	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	R	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	S	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	T	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	U	170/186 (91%)	164 (96%)	6 (4%)	31	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	V	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	W	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	X	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	Y	170/186 (91%)	164 (96%)	6 (4%)	31	53
1	Z	170/186 (91%)	164 (96%)	6 (4%)	31	53
2	a	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	b	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	c	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	d	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	e	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	f	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	g	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	h	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	i	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	j	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	k	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	l	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	m	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	n	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	o	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	p	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	q	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	r	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	s	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	t	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	u	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	v	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	w	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	x	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	y	248/294 (84%)	243 (98%)	5 (2%)	50	68
2	z	248/294 (84%)	243 (98%)	5 (2%)	50	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	0	205/215 (95%)	198 (97%)	7 (3%)	32	54
3	1	209/215 (97%)	201 (96%)	8 (4%)	28	51
3	2	215/215 (100%)	213 (99%)	2 (1%)	75	83
3	3	215/215 (100%)	212 (99%)	3 (1%)	62	76
3	4	215/215 (100%)	209 (97%)	6 (3%)	38	59
3	5	215/215 (100%)	210 (98%)	5 (2%)	45	64
3	6	215/215 (100%)	210 (98%)	5 (2%)	45	64
3	7	215/215 (100%)	214 (100%)	1 (0%)	86	90
3	8	215/215 (100%)	211 (98%)	4 (2%)	52	69
3	9	215/215 (100%)	212 (99%)	3 (1%)	62	76
3	AF	209/215 (97%)	203 (97%)	6 (3%)	37	58
3	AG	210/215 (98%)	201 (96%)	9 (4%)	25	48
3	AH	211/215 (98%)	199 (94%)	12 (6%)	17	41
3	AI	209/215 (97%)	198 (95%)	11 (5%)	19	43
3	AJ	210/215 (98%)	199 (95%)	11 (5%)	19	43
3	AK	200/215 (93%)	195 (98%)	5 (2%)	42	62
3	AL	205/215 (95%)	197 (96%)	8 (4%)	27	50
3	AM	205/215 (95%)	197 (96%)	8 (4%)	27	50
3	AN	205/215 (95%)	201 (98%)	4 (2%)	50	68
3	ZA	215/215 (100%)	213 (99%)	2 (1%)	75	83
3	ZB	215/215 (100%)	208 (97%)	7 (3%)	33	55
3	ZC	215/215 (100%)	212 (99%)	3 (1%)	62	76
3	ZD	215/215 (100%)	211 (98%)	4 (2%)	52	69
3	ZE	215/215 (100%)	210 (98%)	5 (2%)	45	64
4	ZF	321/323 (99%)	309 (96%)	12 (4%)	29	52
4	ZG	321/323 (99%)	305 (95%)	16 (5%)	20	44
4	ZH	321/323 (99%)	308 (96%)	13 (4%)	27	50
4	ZI	321/323 (99%)	315 (98%)	6 (2%)	52	69
4	ZJ	321/323 (99%)	312 (97%)	9 (3%)	38	59
4	ZK	321/323 (99%)	315 (98%)	6 (2%)	52	69
4	ZL	321/323 (99%)	311 (97%)	10 (3%)	35	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	ZM	321/323 (99%)	312 (97%)	9 (3%)	38	59
4	ZN	321/323 (99%)	311 (97%)	10 (3%)	35	56
4	ZO	321/323 (99%)	313 (98%)	8 (2%)	42	62
4	ZP	321/323 (99%)	306 (95%)	15 (5%)	22	46
4	ZQ	321/323 (99%)	312 (97%)	9 (3%)	38	59
4	ZR	321/323 (99%)	314 (98%)	7 (2%)	47	65
4	ZS	321/323 (99%)	315 (98%)	6 (2%)	52	69
4	ZT	321/323 (99%)	313 (98%)	8 (2%)	42	62
4	ZU	321/323 (99%)	317 (99%)	4 (1%)	67	79
4	ZV	321/323 (99%)	317 (99%)	4 (1%)	67	79
4	ZW	321/323 (99%)	307 (96%)	14 (4%)	24	47
4	ZX	321/323 (99%)	318 (99%)	3 (1%)	75	83
4	ZY	321/323 (99%)	314 (98%)	7 (2%)	47	65
4	ZZ	321/323 (99%)	316 (98%)	5 (2%)	58	74
4	Za	321/323 (99%)	315 (98%)	6 (2%)	52	69
4	Zb	321/323 (99%)	314 (98%)	7 (2%)	47	65
4	Zc	321/323 (99%)	310 (97%)	11 (3%)	32	54
4	Zd	321/323 (99%)	314 (98%)	7 (2%)	47	65
4	Ze	321/323 (99%)	314 (98%)	7 (2%)	47	65
4	Zf	321/323 (99%)	314 (98%)	7 (2%)	47	65
4	Zg	321/323 (99%)	315 (98%)	6 (2%)	52	69
4	Zh	321/323 (99%)	314 (98%)	7 (2%)	47	65
5	AA	190/193 (98%)	188 (99%)	2 (1%)	70	80
5	AB	191/193 (99%)	186 (97%)	5 (3%)	41	61
5	AC	192/193 (100%)	189 (98%)	3 (2%)	58	74
5	AD	192/193 (100%)	185 (96%)	7 (4%)	30	53
5	AE	191/193 (99%)	189 (99%)	2 (1%)	73	81
6	AO	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AP	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AQ	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AR	141/467 (30%)	134 (95%)	7 (5%)	20	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	AS	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AT	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AU	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AV	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AW	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AX	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AY	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	AZ	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Aa	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ac	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ad	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ae	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Af	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ag	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ah	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ai	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Aj	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ak	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Al	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Am	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	An	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ao	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	Ap	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BG	8/467 (2%)	6 (75%)	2 (25%)	0	3
6	BH	11/467 (2%)	10 (91%)	1 (9%)	7	26
6	BI	14/467 (3%)	12 (86%)	2 (14%)	2	15
6	BJ	11/467 (2%)	11 (100%)	0	100	100
6	BK	15/467 (3%)	15 (100%)	0	100	100
6	BL	11/467 (2%)	11 (100%)	0	100	100
6	BM	15/467 (3%)	15 (100%)	0	100	100
6	BN	11/467 (2%)	11 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	BO	14/467 (3%)	13 (93%)	1 (7%)	12	34
6	BP	11/467 (2%)	11 (100%)	0	100	100
6	BQ	15/467 (3%)	14 (93%)	1 (7%)	13	36
6	BR	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BS	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BT	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BU	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BV	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BW	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	BX	141/467 (30%)	134 (95%)	7 (5%)	20	44
6	UI	128/467 (27%)	123 (96%)	5 (4%)	27	50
6	UJ	128/467 (27%)	123 (96%)	5 (4%)	27	50
6	UK	128/467 (27%)	123 (96%)	5 (4%)	27	50
6	UL	128/467 (27%)	122 (95%)	6 (5%)	22	46
6	UM	128/467 (27%)	123 (96%)	5 (4%)	27	50
6	UN	128/467 (27%)	123 (96%)	5 (4%)	27	50
6	UO	128/467 (27%)	123 (96%)	5 (4%)	27	50
6	UP	128/467 (27%)	122 (95%)	6 (5%)	22	46
6	WA	95/467 (20%)	91 (96%)	4 (4%)	25	49
6	WB	93/467 (20%)	87 (94%)	6 (6%)	14	37
6	WC	91/467 (20%)	83 (91%)	8 (9%)	8	28
6	WD	92/467 (20%)	88 (96%)	4 (4%)	25	48
6	WE	94/467 (20%)	87 (93%)	7 (7%)	11	33
6	WF	93/467 (20%)	86 (92%)	7 (8%)	11	33
6	WG	94/467 (20%)	87 (93%)	7 (7%)	11	33
6	WH	79/467 (17%)	75 (95%)	4 (5%)	20	43
6	WI	79/467 (17%)	73 (92%)	6 (8%)	11	32
6	WJ	83/467 (18%)	79 (95%)	4 (5%)	21	45
6	WK	82/467 (18%)	77 (94%)	5 (6%)	15	39
6	WL	69/467 (15%)	66 (96%)	3 (4%)	25	48
6	WM	66/467 (14%)	65 (98%)	1 (2%)	60	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	WN	68/467 (15%)	66 (97%)	2 (3%)	37	58
6	WO	80/467 (17%)	76 (95%)	4 (5%)	20	44
6	WP	83/467 (18%)	77 (93%)	6 (7%)	12	34
6	WQ	93/467 (20%)	91 (98%)	2 (2%)	47	65
6	WR	93/467 (20%)	86 (92%)	7 (8%)	11	33
6	WS	93/467 (20%)	87 (94%)	6 (6%)	14	37
6	WT	93/467 (20%)	86 (92%)	7 (8%)	11	33
6	WU	94/467 (20%)	90 (96%)	4 (4%)	25	48
6	WV	92/467 (20%)	83 (90%)	9 (10%)	6	23
6	WW	93/467 (20%)	85 (91%)	8 (9%)	8	29
7	Ab	74/74 (100%)	68 (92%)	6 (8%)	9	31
7	Aq	74/74 (100%)	72 (97%)	2 (3%)	40	61
7	Ar	74/74 (100%)	74 (100%)	0	100	100
7	As	74/74 (100%)	74 (100%)	0	100	100
8	At	210/221 (95%)	205 (98%)	5 (2%)	44	63
9	Au	177/204 (87%)	171 (97%)	6 (3%)	32	54
9	Av	179/204 (88%)	173 (97%)	6 (3%)	32	54
9	Aw	178/204 (87%)	173 (97%)	5 (3%)	38	59
9	Ax	178/204 (87%)	171 (96%)	7 (4%)	27	50
9	Ay	179/204 (88%)	172 (96%)	7 (4%)	27	50
10	A1	68/79 (86%)	64 (94%)	4 (6%)	16	40
10	A2	70/79 (89%)	65 (93%)	5 (7%)	12	34
10	A3	70/79 (89%)	66 (94%)	4 (6%)	17	41
10	A4	70/79 (89%)	66 (94%)	4 (6%)	17	41
10	A5	69/79 (87%)	64 (93%)	5 (7%)	12	34
10	Az	45/79 (57%)	39 (87%)	6 (13%)	3	17
11	A0	102/113 (90%)	96 (94%)	6 (6%)	16	40
11	A6	110/113 (97%)	106 (96%)	4 (4%)	30	53
11	A7	101/113 (89%)	100 (99%)	1 (1%)	73	81
11	A8	103/113 (91%)	96 (93%)	7 (7%)	13	36
11	A9	104/113 (92%)	102 (98%)	2 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	BA	104/105 (99%)	104 (100%)	0	100	100
12	BB	104/105 (99%)	101 (97%)	3 (3%)	37	58
12	BC	104/105 (99%)	102 (98%)	2 (2%)	52	69
12	BD	104/105 (99%)	100 (96%)	4 (4%)	28	51
12	BE	103/105 (98%)	99 (96%)	4 (4%)	27	50
12	BF	104/105 (99%)	98 (94%)	6 (6%)	17	40
All	All	37084/66670 (56%)	35882 (97%)	1202 (3%)	36	55

5 of 1202 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	A2	7	ILE
6	BG	317	SER
11	A8	72	HIS
10	A1	84	MET
6	WF	120	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 984 such sidechains are listed below:

Mol	Chain	Res	Type
4	ZF	392	GLN
8	At	205	ASN
4	ZR	269	GLN
6	AP	299	ASN
6	WJ	169	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

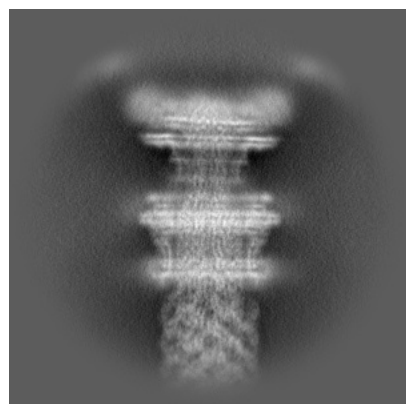
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37630. These allow visual inspection of the internal detail of the map and identification of artifacts.

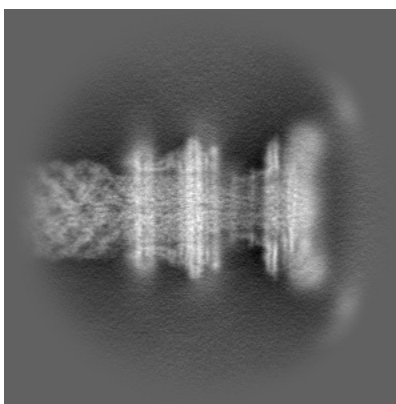
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

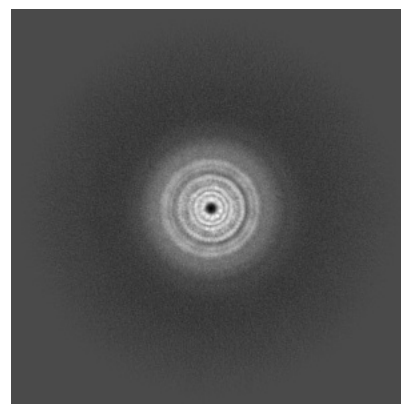
6.1.1 Primary map



X

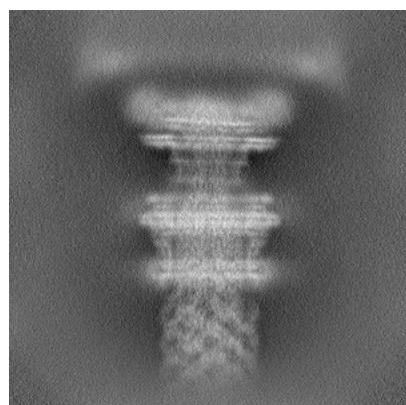


Y

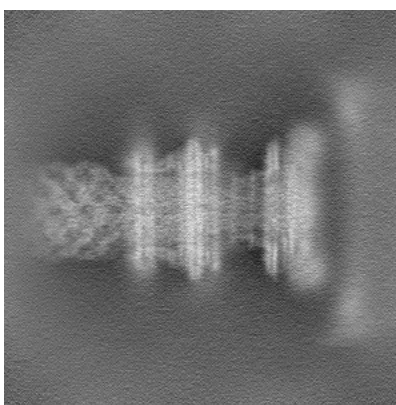


Z

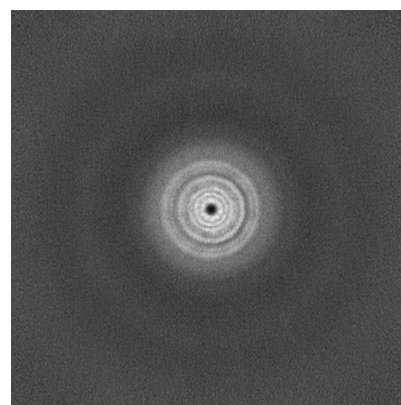
6.1.2 Raw map



X



Y

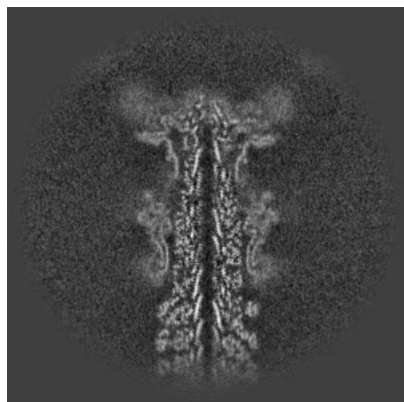


Z

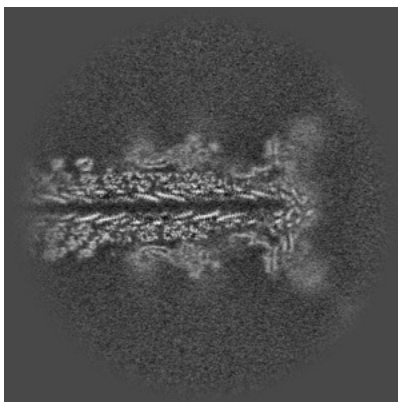
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

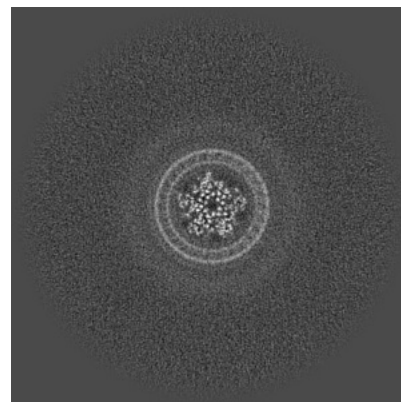
6.2.1 Primary map



X Index: 256

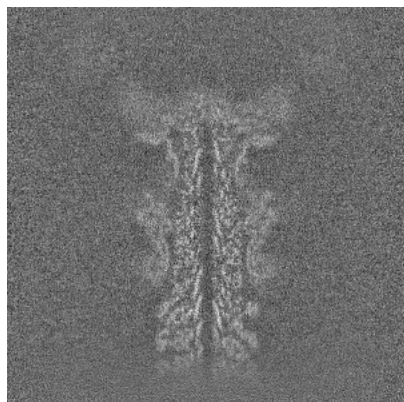


Y Index: 256

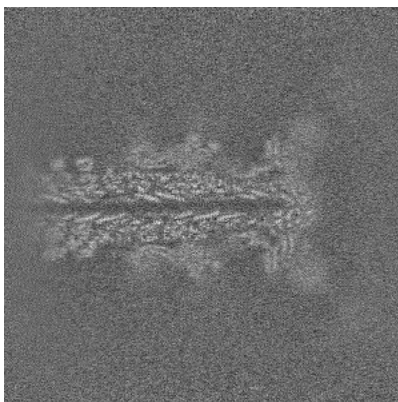


Z Index: 256

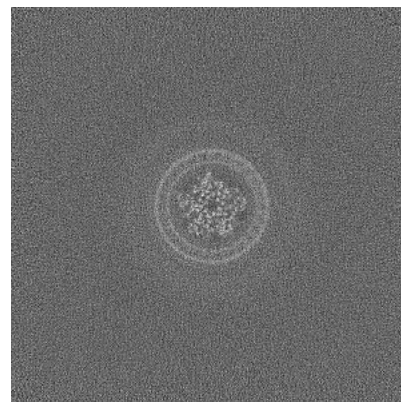
6.2.2 Raw map



X Index: 256



Y Index: 256

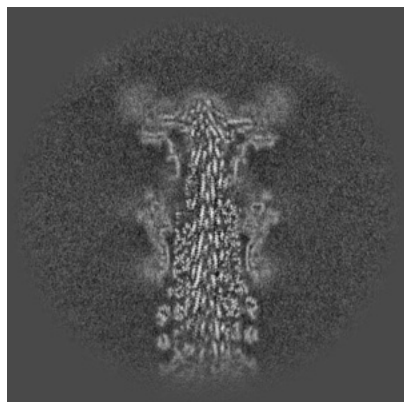


Z Index: 256

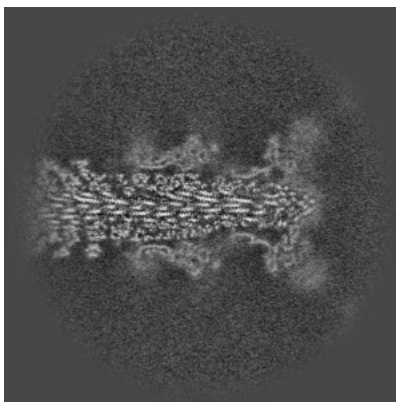
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

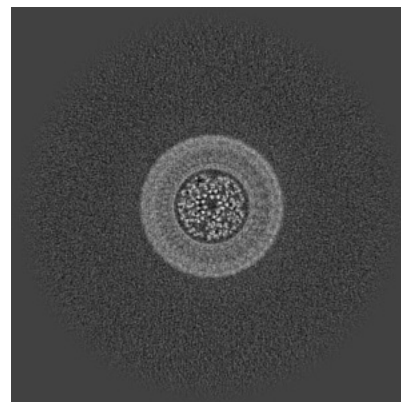
6.3.1 Primary map



X Index: 247

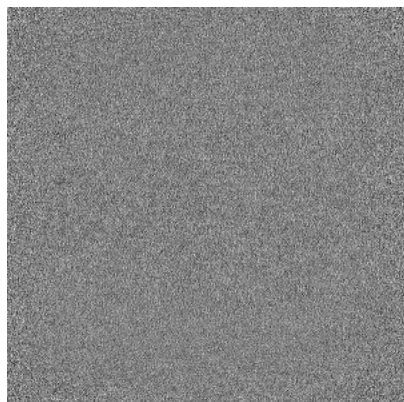


Y Index: 246

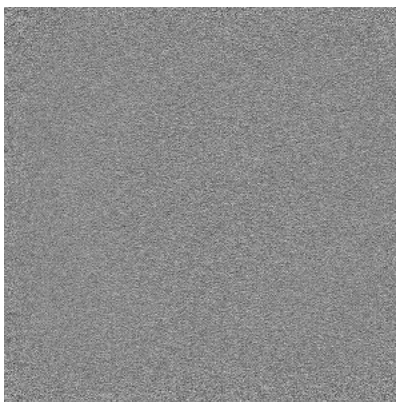


Z Index: 239

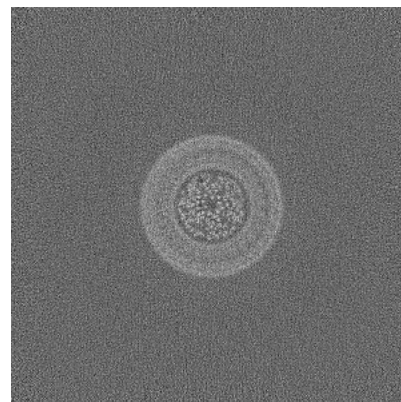
6.3.2 Raw map



X Index: 0



Y Index: 0

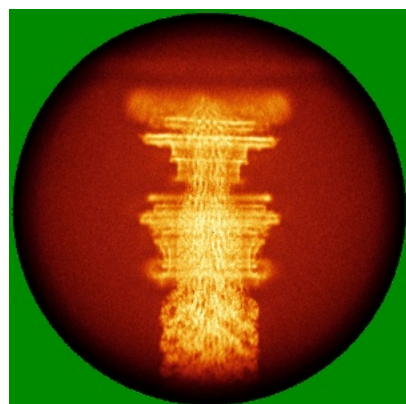


Z Index: 240

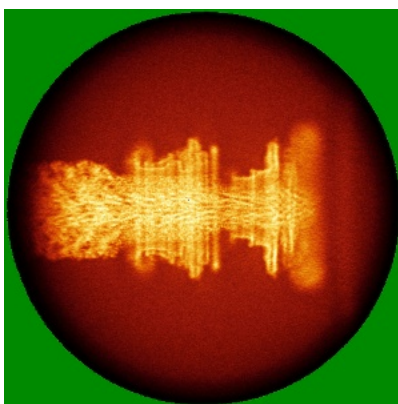
The images above show the largest variance slices of the map in three orthogonal directions.

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

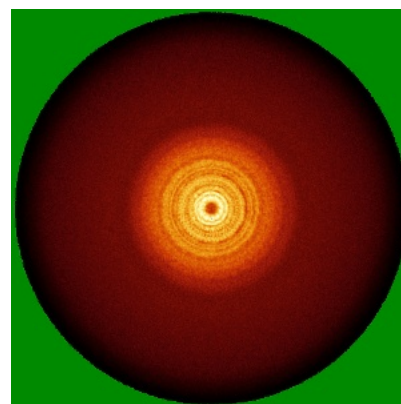
6.4.1 Primary map



X

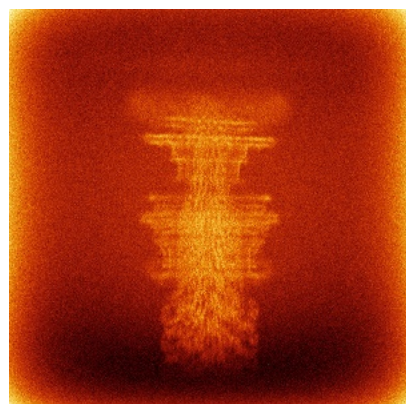


Y

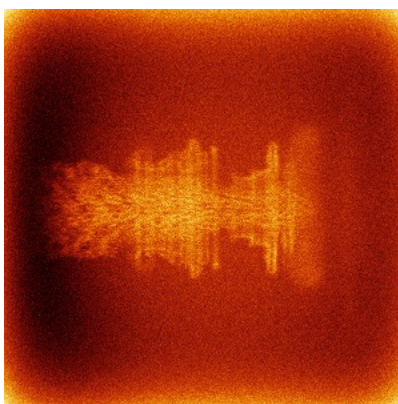


Z

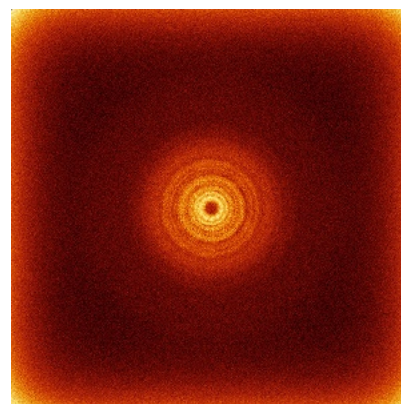
6.4.2 Raw map



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](#)

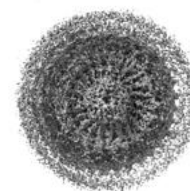
6.5.1 Primary map



X



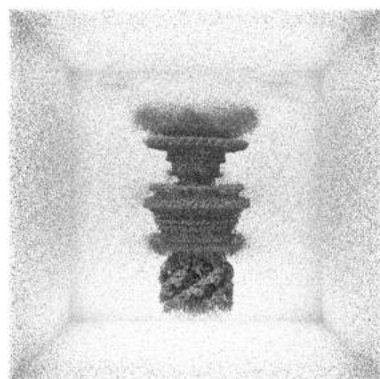
Y



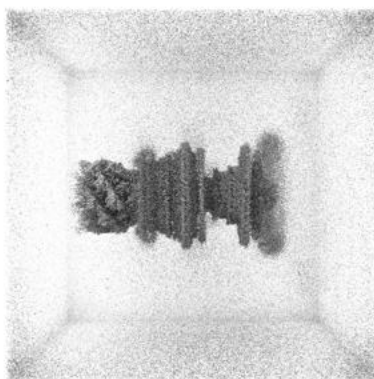
Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

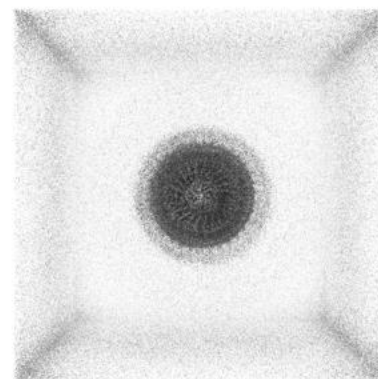
6.5.2 Raw map



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.

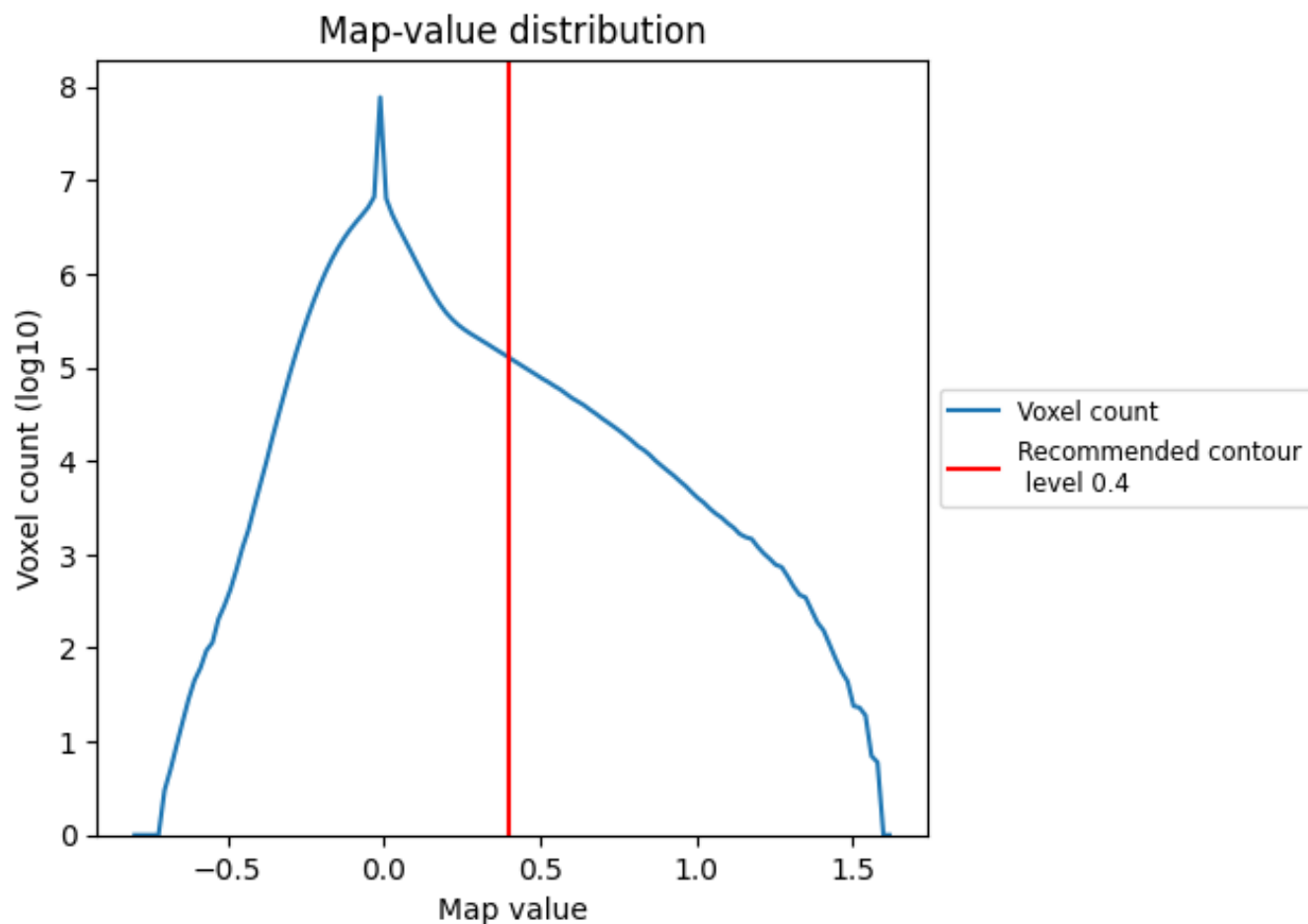
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

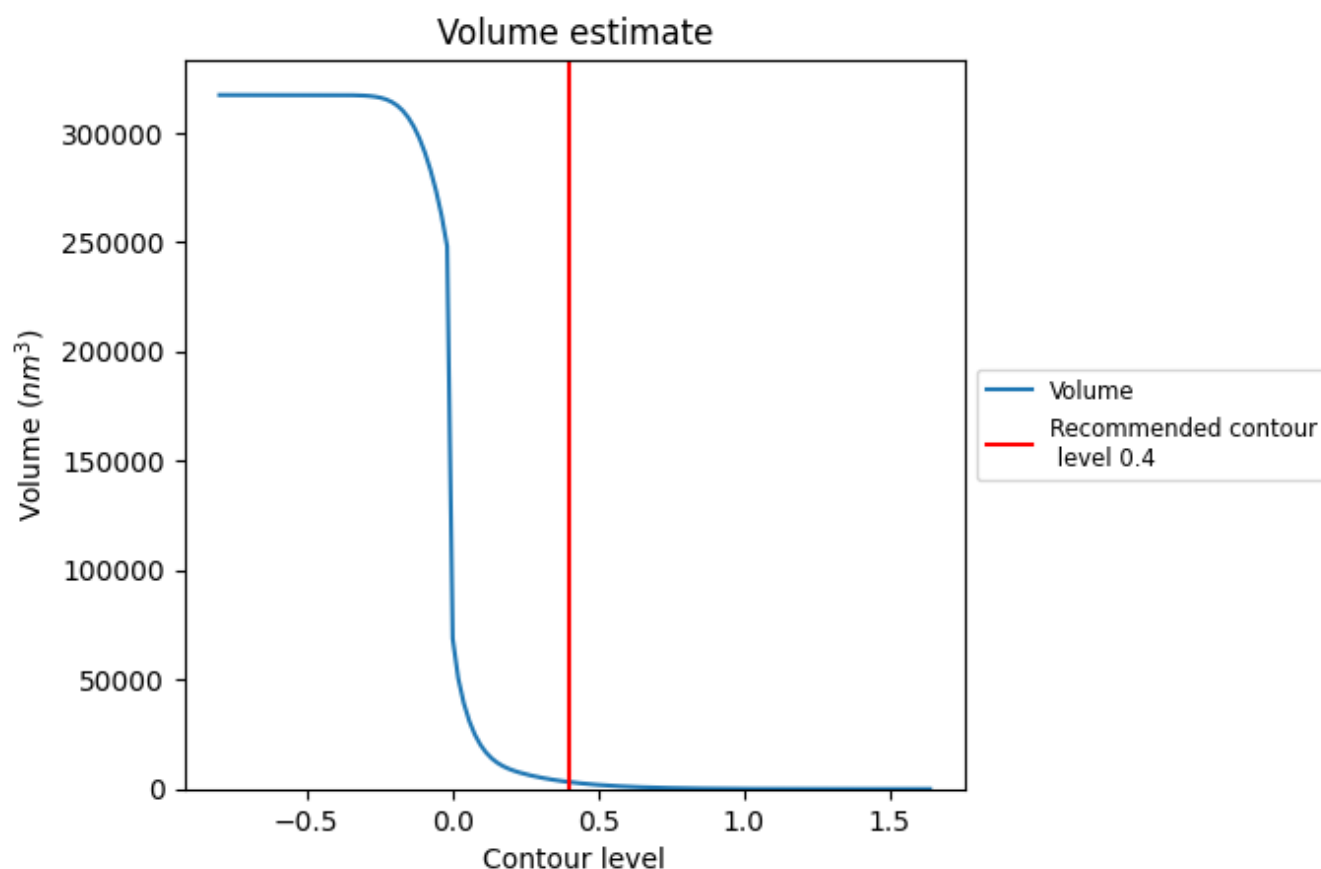
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

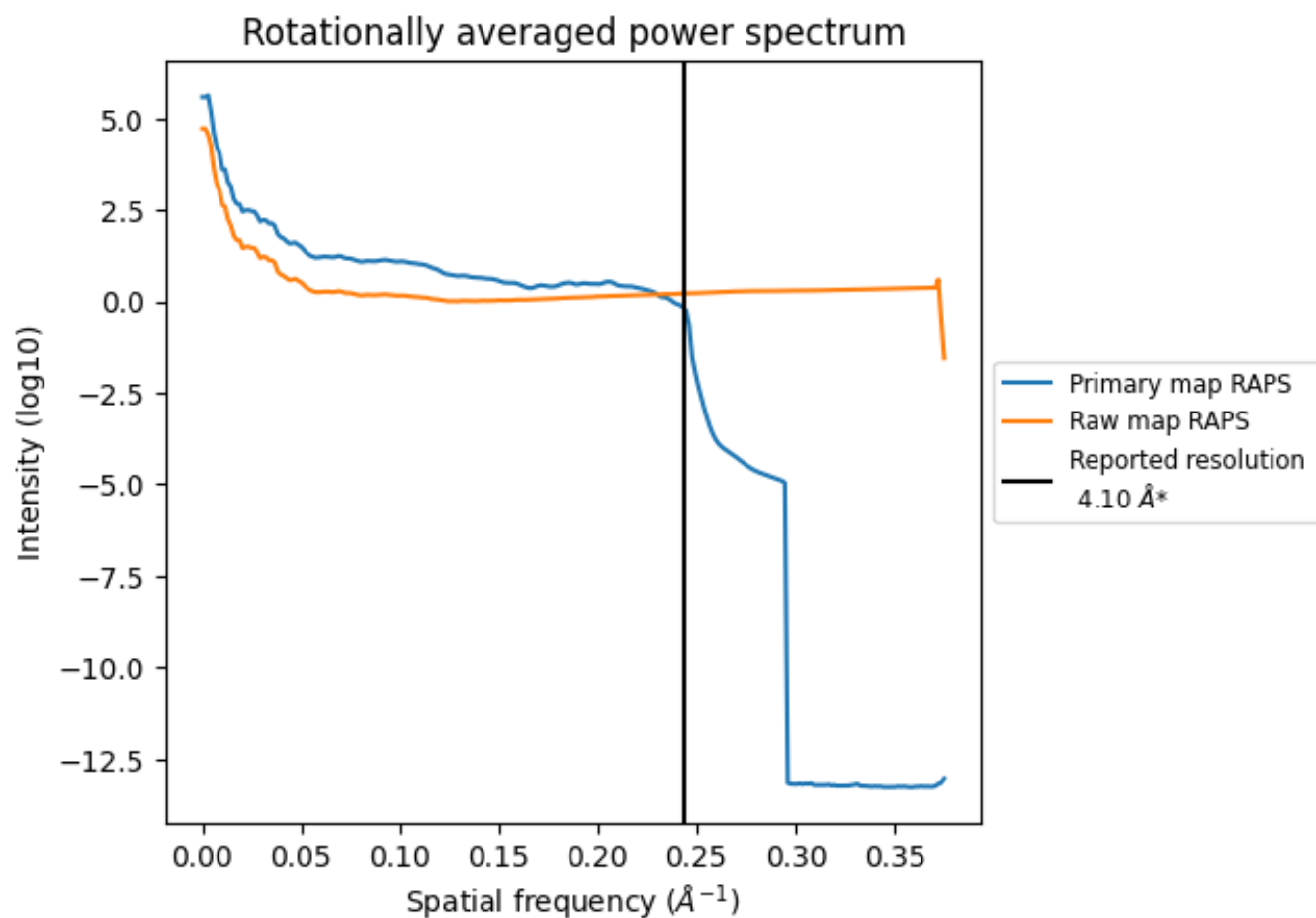
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3185 nm^3 ; this corresponds to an approximate mass of 2877 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 ⓘ

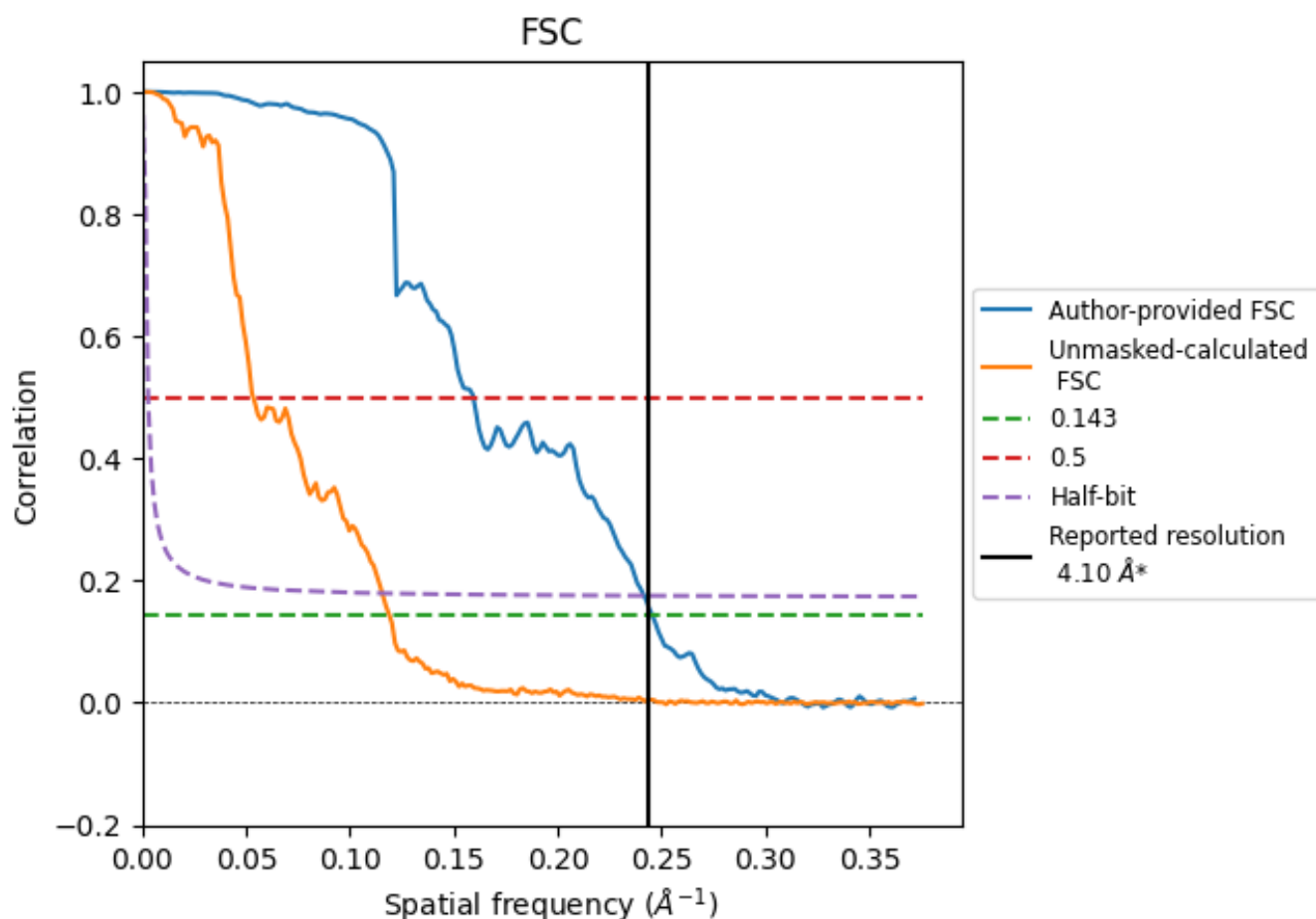


*Reported resolution corresponds to spatial frequency of 0.244 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.244 \AA^{-1}

8.2 Resolution estimates [i](#)

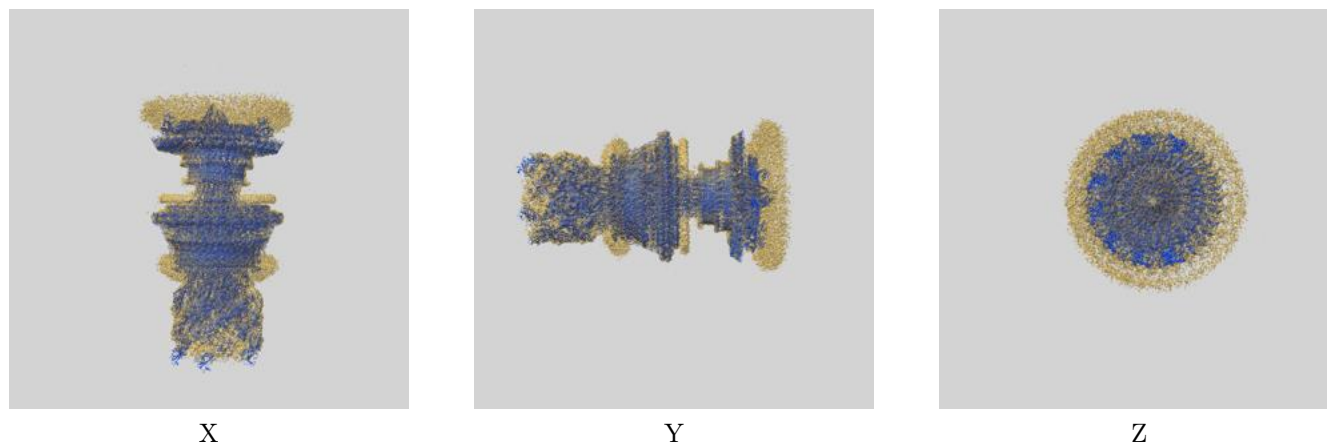
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.07	6.28	4.14
Unmasked-calculated*	8.41	18.73	8.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.41 differs from the reported value 4.1 by more than 10 %

9 Map-model fit [i](#)

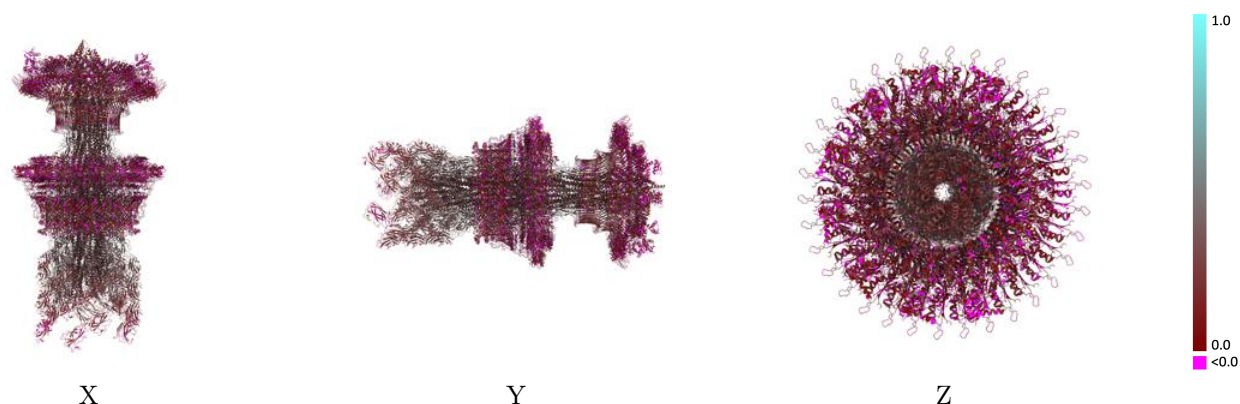
This section contains information regarding the fit between EMDB map EMD-37630 and PDB model 8WLT. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



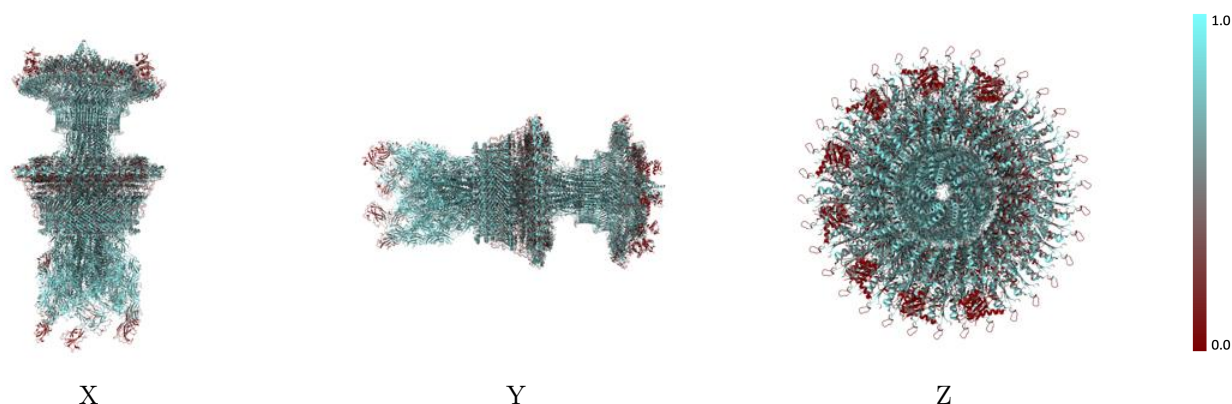
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



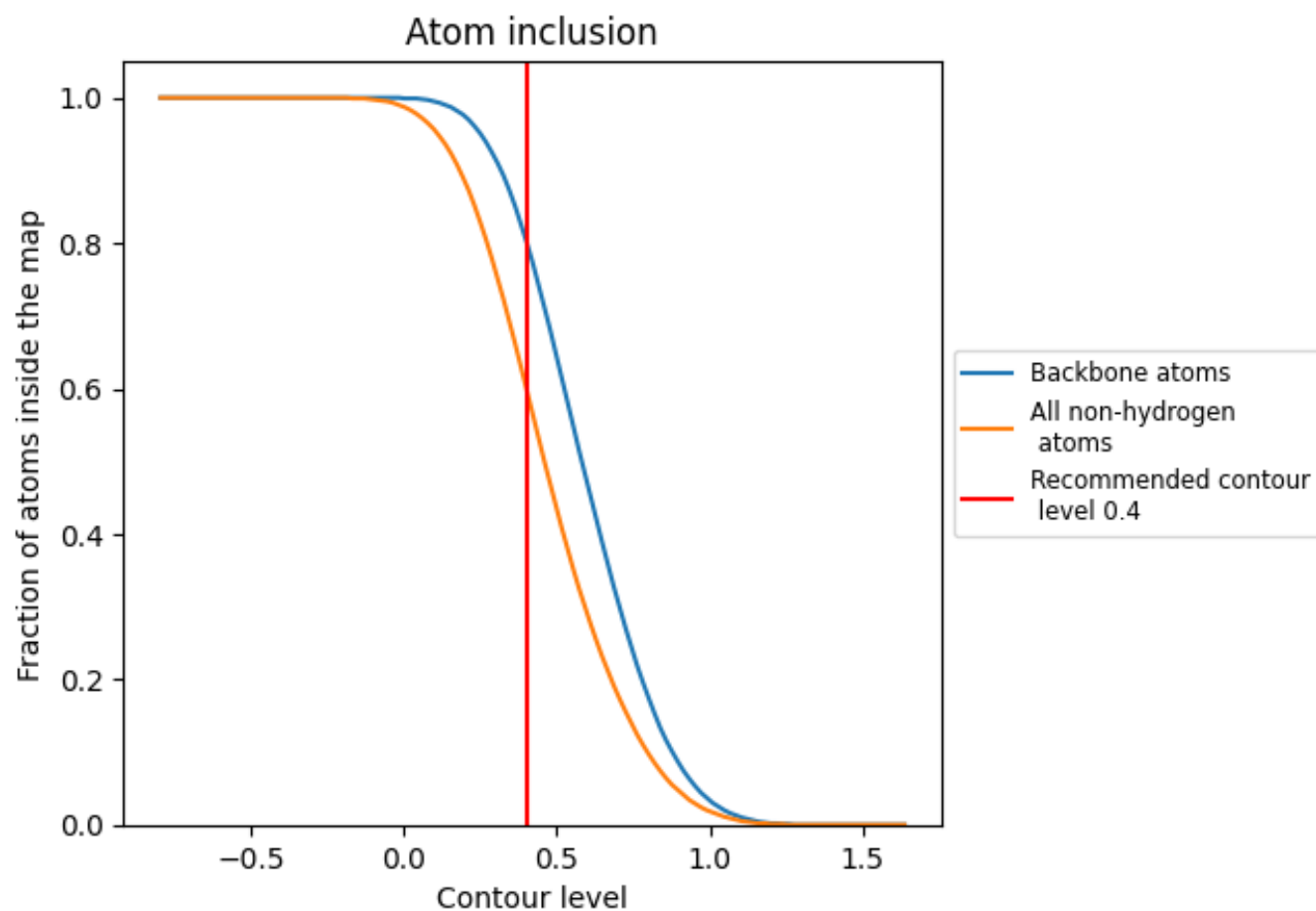
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 60% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6010	 0.2210
0	 0.6940	 0.3430
1	 0.6920	 0.3390
2	 0.6780	 0.3430
3	 0.6990	 0.3360
4	 0.7050	 0.3390
5	 0.6890	 0.3410
6	 0.7000	 0.3430
7	 0.7050	 0.3460
8	 0.7000	 0.3440
9	 0.6990	 0.3440
A	 0.5000	 0.1420
A0	 0.6570	 0.3040
A1	 0.6240	 0.2630
A2	 0.6620	 0.2750
A3	 0.6410	 0.2660
A4	 0.6090	 0.2540
A5	 0.6020	 0.2560
A6	 0.6260	 0.2980
A7	 0.6680	 0.2990
A8	 0.6560	 0.2990
A9	 0.6780	 0.2950
AA	 0.6770	 0.3340
AB	 0.7270	 0.3410
AC	 0.7260	 0.3560
AD	 0.7180	 0.3410
AE	 0.7100	 0.3340
AF	 0.6820	 0.3310
AG	 0.7090	 0.3440
AH	 0.7040	 0.3490
AI	 0.7050	 0.3470
AJ	 0.6920	 0.3430
AK	 0.6950	 0.3430
AL	 0.6840	 0.3310
AM	 0.6980	 0.3480























































































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Chain	Atom inclusion	Q-score
AN	 0.6980	 0.3400
AO	 0.6000	 0.1490
AP	 0.5970	 0.1380
AQ	 0.5990	 0.1500
AR	 0.6430	 0.1560
AS	 0.6100	 0.1490
AT	 0.6400	 0.1730
AU	 0.6380	 0.1670
AV	 0.6220	 0.1490
AW	 0.6150	 0.1550
AX	 0.6250	 0.1600
AY	 0.6250	 0.1370
AZ	 0.6350	 0.1560
Aa	 0.6330	 0.1520
Ab	 0.5990	 0.2220
Ac	 0.6450	 0.1550
Ad	 0.6390	 0.1510
Ae	 0.6260	 0.1520
Af	 0.6320	 0.1300
Ag	 0.6360	 0.1470
Ah	 0.6350	 0.1320
Ai	 0.6330	 0.1440
Aj	 0.6180	 0.1450
Ak	 0.6020	 0.1370
Al	 0.6030	 0.1530
Am	 0.6070	 0.1450
An	 0.6020	 0.1370
Ao	 0.5850	 0.1270
Ap	 0.5980	 0.1500
Aq	 0.6660	 0.2410
Ar	 0.6660	 0.2290
As	 0.6500	 0.2090
At	 0.6460	 0.2490
Au	 0.6580	 0.2420
Av	 0.6730	 0.2690
Aw	 0.6880	 0.2770
Ax	 0.6800	 0.2750
Ay	 0.6610	 0.2730
Az	 0.5230	 0.2200
B	 0.4930	 0.1220
BA	 0.6650	 0.3090
BB	 0.6940	 0.3290





















































































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Chain	Atom inclusion	Q-score
BC	 0.7000	 0.3350
BD	 0.6860	 0.3390
BE	 0.6960	 0.3350
BF	 0.6890	 0.3090
BG	 0.5430	 0.3200
BH	 0.6410	 0.3630
BI	 0.6240	 0.3380
BJ	 0.7670	 0.3940
BK	 0.7360	 0.3660
BL	 0.6800	 0.3550
BM	 0.7290	 0.3910
BN	 0.6800	 0.3410
BO	 0.7520	 0.4020
BP	 0.6700	 0.3130
BQ	 0.6500	 0.3280
BR	 0.5940	 0.1420
BS	 0.5910	 0.1320
BT	 0.6110	 0.1480
BU	 0.6150	 0.1570
BV	 0.6070	 0.1450
BW	 0.6270	 0.1610
BX	 0.6100	 0.1560
C	 0.5140	 0.1440
D	 0.5180	 0.1420
E	 0.5030	 0.1370
F	 0.5050	 0.1320
G	 0.5180	 0.1380
H	 0.5290	 0.1420
I	 0.5420	 0.1350
J	 0.5330	 0.1450
K	 0.5290	 0.1490
L	 0.5400	 0.1490
M	 0.5420	 0.1610
N	 0.5320	 0.1480
O	 0.5220	 0.1300
P	 0.5240	 0.1450
Q	 0.5360	 0.1470
R	 0.5220	 0.1420
S	 0.5400	 0.1290
T	 0.5110	 0.1390
U	 0.5270	 0.1470
UI	 0.1300	 0.0680





















































































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Chain	Atom inclusion	Q-score
UJ	 0.1340	 0.0770
UK	 0.1080	 0.0850
UL	 0.1020	 0.0320
UM	 0.0690	 0.0500
UN	 0.1330	 0.0700
UO	 0.1360	 0.0810
UP	 0.1950	 0.0760
V	 0.5270	 0.1490
W	 0.5200	 0.1430
WA	 0.6210	 0.1920
WB	 0.6410	 0.2010
WC	 0.6490	 0.2210
WD	 0.6120	 0.1780
WE	 0.6320	 0.1860
WF	 0.5930	 0.1650
WG	 0.5140	 0.1550
WH	 0.4740	 0.1420
WI	 0.4840	 0.1480
WJ	 0.4820	 0.1460
WK	 0.3380	 0.1160
WL	 0.3880	 0.1150
WM	 0.4870	 0.1190
WN	 0.4520	 0.1200
WO	 0.4240	 0.1050
WP	 0.5660	 0.1610
WQ	 0.5480	 0.1810
WR	 0.5700	 0.1690
WS	 0.6120	 0.2160
WT	 0.6190	 0.1870
WU	 0.5990	 0.2010
WV	 0.6180	 0.2050
WW	 0.6090	 0.1940
X	 0.5190	 0.1620
Y	 0.5070	 0.1390
Z	 0.5150	 0.1530
ZA	 0.7070	 0.3440
ZB	 0.7120	 0.3440
ZC	 0.7230	 0.3510
ZD	 0.7050	 0.3420
ZE	 0.6980	 0.3410
ZF	 0.5380	 0.2920
ZG	 0.7300	 0.3270























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Chain	Atom inclusion	Q-score
ZH	 0.7480	 0.3250
ZI	 0.7530	 0.3290
ZJ	 0.7500	 0.3260
ZK	 0.7630	 0.3230
ZL	 0.7550	 0.3280
ZM	 0.7440	 0.3180
ZN	 0.7530	 0.3170
ZO	 0.7570	 0.3160
ZP	 0.7510	 0.3160
ZQ	 0.7460	 0.3080
ZR	 0.7440	 0.3050
ZS	 0.7540	 0.3060
ZT	 0.7450	 0.3010
ZU	 0.7320	 0.2980
ZV	 0.7400	 0.2950
ZW	 0.7290	 0.2830
ZX	 0.7140	 0.2830
ZY	 0.7090	 0.2760
ZZ	 0.6810	 0.2700
Za	 0.6710	 0.2720
Zb	 0.6320	 0.2480
Zc	 0.6290	 0.2530
Zd	 0.5790	 0.2460
Ze	 0.5240	 0.2320
Zf	 0.5060	 0.2320
Zg	 0.4670	 0.2100
Zh	 0.4390	 0.2040
a	 0.4680	 0.1160
b	 0.4770	 0.1300
c	 0.4540	 0.1230
d	 0.4850	 0.1250
e	 0.4730	 0.1230
f	 0.4860	 0.1360
g	 0.5150	 0.1260
h	 0.5190	 0.1440
i	 0.5260	 0.1450
j	 0.5220	 0.1390
k	 0.5320	 0.1400
l	 0.5100	 0.1340
m	 0.5050	 0.1400
n	 0.4890	 0.1230
o	 0.5040	 0.1430

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Chain	Atom inclusion	Q-score
p	 0.5020	 0.1290
q	 0.4840	 0.1170
r	 0.4790	 0.1220
s	 0.4910	 0.1180
t	 0.4890	 0.1330
u	 0.4570	 0.1090
v	 0.4730	 0.1200
w	 0.4790	 0.1150
x	 0.4520	 0.1060
y	 0.4510	 0.1040
z	 0.4600	 0.1200