



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:36 PM UTC

PDB ID : 8WLT / pdb_00008wlt
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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

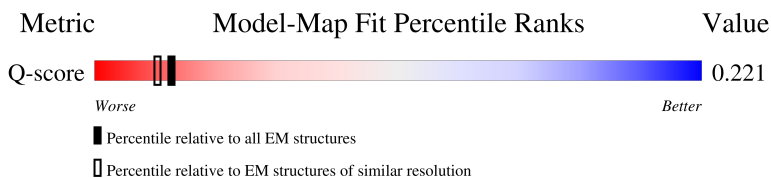
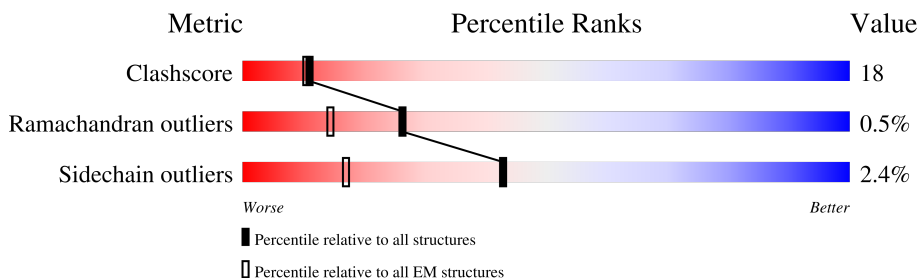
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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	
1	B	232	
1	C	232	
1	D	232	

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Mol	Chain	Length	Quality of chain
1	E	232	
1	F	232	
1	G	232	
1	H	232	
1	I	232	
1	J	232	
1	K	232	
1	L	232	
1	M	232	
1	N	232	
1	O	232	
1	P	232	
1	Q	232	
1	R	232	
1	S	232	
1	T	232	
1	U	232	
1	V	232	
1	W	232	
1	X	232	
1	Y	232	
1	Z	232	
2	a	365	
2	b	365	
2	c	365	

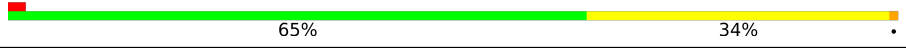
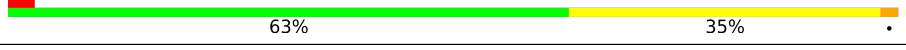
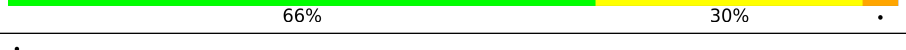
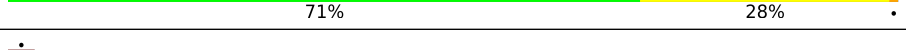
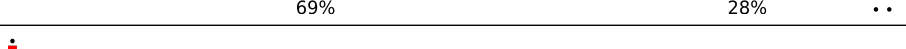
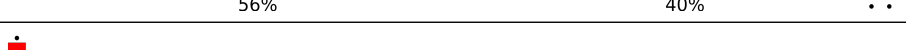
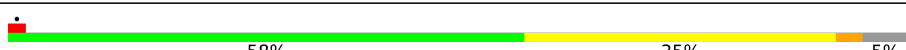
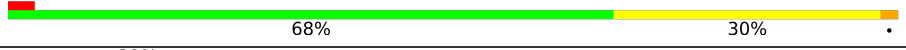
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Mol	Chain	Length	Quality of chain
2	d	365	
2	e	365	
2	f	365	
2	g	365	
2	h	365	
2	i	365	
2	j	365	
2	k	365	
2	l	365	
2	m	365	
2	n	365	
2	o	365	
2	p	365	
2	q	365	
2	r	365	
2	s	365	
2	t	365	
2	u	365	
2	v	365	
2	w	365	
2	x	365	
2	y	365	
2	z	365	
3	0	260	
3	1	260	

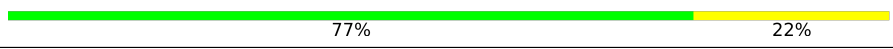
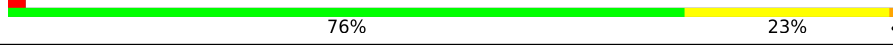
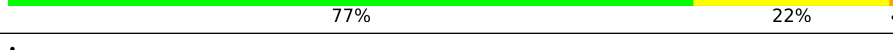
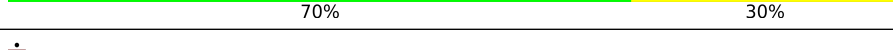
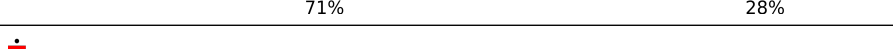
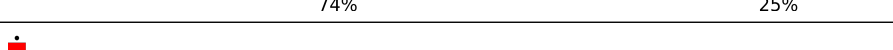
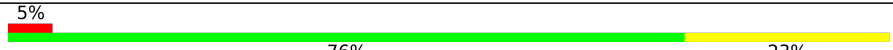
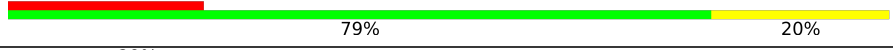
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Mol	Chain	Length	Quality of chain
3	2	260	 67% 31%
3	3	260	 65% 35%
3	4	260	 65% 34%
3	5	260	 63% 35%
3	6	260	 67% 32%
3	7	260	 66% 32%
3	8	260	 66% 30%
3	9	260	 71% 28%
3	AF	260	 69% 28%
3	AG	260	 56% 40%
3	AH	260	 62% 33%
3	AI	260	 60% 37%
3	AJ	260	 62% 33%
3	AK	260	 62% 30% 7%
3	AL	260	 57% 36% 5%
3	AM	260	 58% 35% 5%
3	AN	260	 66% 28% 5%
3	ZA	260	 65% 34%
3	ZB	260	 67% 31%
3	ZC	260	 68% 31%
3	ZD	260	 63% 35%
3	ZE	260	 68% 30%
4	ZF	403	 29% 78% 21%
4	ZG	403	 73% 25%
4	ZH	403	 76% 23%

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Mol	Chain	Length	Quality of chain
4	ZI	403	
4	ZJ	403	
4	ZK	403	
4	ZL	403	
4	ZM	403	
4	ZN	403	
4	ZO	403	
4	ZP	403	
4	ZQ	403	
4	ZR	403	
4	ZS	403	
4	ZT	403	
4	ZU	403	
4	ZV	403	
4	ZW	403	
4	ZX	403	
4	ZY	403	
4	ZZ	403	
4	Za	403	
4	Zb	403	
4	Zc	403	
4	Zd	403	
4	Ze	403	
4	Zf	403	
4	Zg	403	

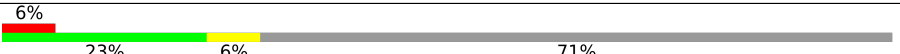
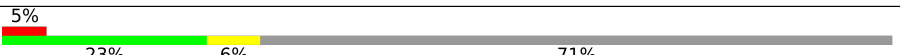
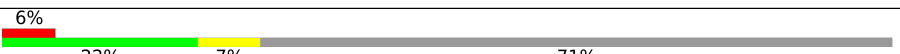
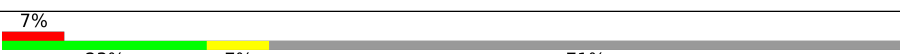
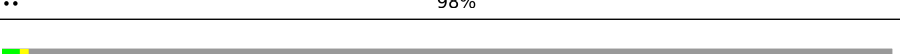
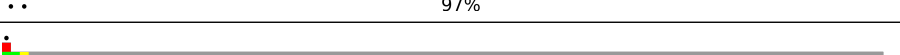
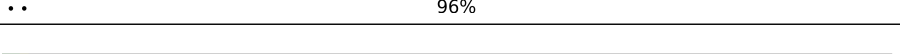
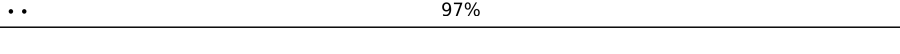
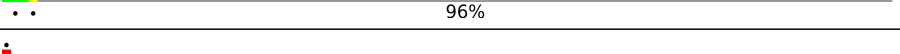
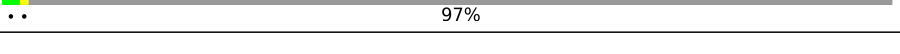
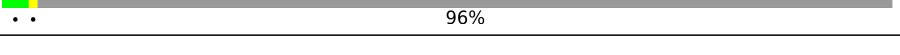
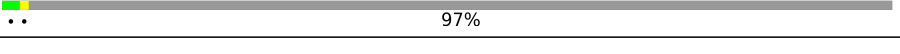
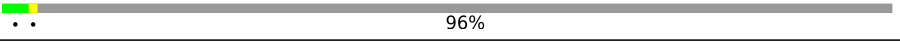
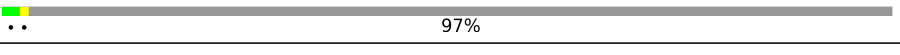
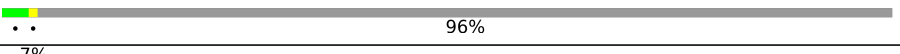
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Mol	Chain	Length	Quality of chain
4	Zh	403	
5	AA	251	
5	AB	251	
5	AC	251	
5	AD	251	
5	AE	251	
6	AO	560	
6	AP	560	
6	AQ	560	
6	AR	560	
6	AS	560	
6	AT	560	
6	AU	560	
6	AV	560	
6	AW	560	
6	AX	560	
6	AY	560	
6	AZ	560	
6	Aa	560	
6	Ac	560	
6	Ad	560	
6	Ae	560	
6	Af	560	
6	Ag	560	
6	Ah	560	

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Mol	Chain	Length	Quality of chain
6	Ai	560	 5% 23% 7% 71%
6	Aj	560	 5% 22% 7% 71%
6	Ak	560	 6% 22% 7% 71%
6	Al	560	 6% 23% 6% 71%
6	Am	560	 5% 23% 6% 71%
6	An	560	 6% 22% 7% 71%
6	Ao	560	 7% 23% 7% 71%
6	Ap	560	 6% 23% 6% 71%
6	BG	560	 98%
6	BH	560	 97%
6	BI	560	 96%
6	BJ	560	 97%
6	BK	560	 96%
6	BL	560	 97%
6	BM	560	 96%
6	BN	560	 97%
6	BO	560	 96%
6	BP	560	 97%
6	BQ	560	 96%
6	BR	560	 7% 22% 7% 71%
6	BS	560	 6% 22% 7% 71%
6	BT	560	 6% 23% 6% 71%
6	BU	560	 6% 22% 7% 71%
6	BV	560	 5% 23% 7% 71%
6	BW	560	 23% 7% 71%

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Mol	Chain	Length	Quality of chain
6	BX	560	
6	UI	560	
6	UJ	560	
6	UK	560	
6	UL	560	
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	

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Mol	Chain	Length	Quality of chain
6	WQ	560	
6	WR	560	
6	WS	560	
6	WT	560	
6	WU	560	
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	

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Mol	Chain	Length	Quality of chain
11	A7	138	 7% 59% 28% 12%
11	A8	138	 9% 54% 35% 9%
11	A9	138	 8% 61% 30% 8%
12	BA	134	 7% 72% 28% 1%
12	BB	134	 6% 63% 33% 2%
12	BC	134	 5% 62% 37% 2%
12	BD	134	 1% 58% 37% 2%
12	BE	134	 5% 57% 40% 2%
12	BF	134	 1% 56% 42% 2%

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		

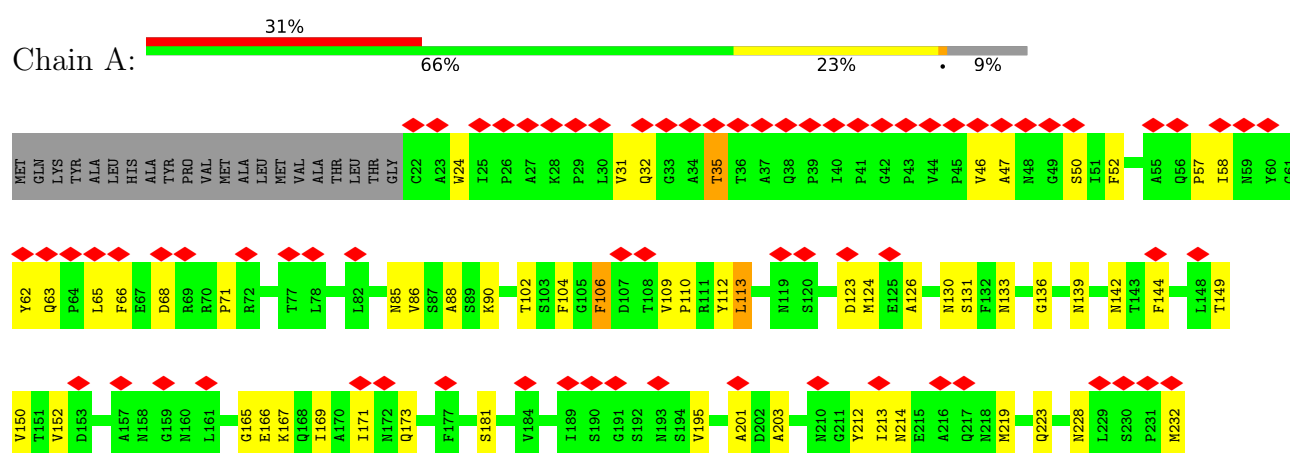
- Molecule 12 is a protein called Flagellar basal-body rod protein FlgC.

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		

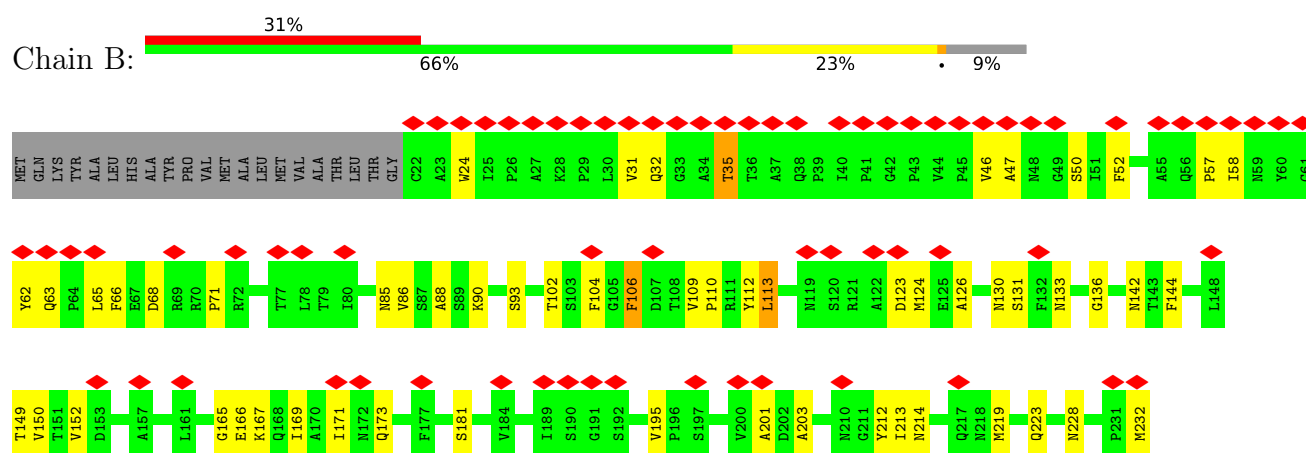
3 Residue-property plots

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

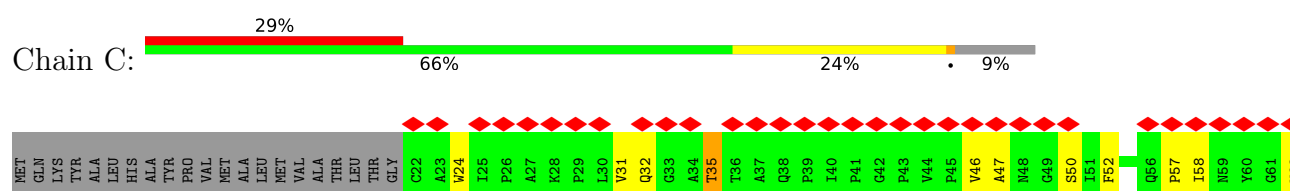
• Molecule 1: Flagellar L-ring protein

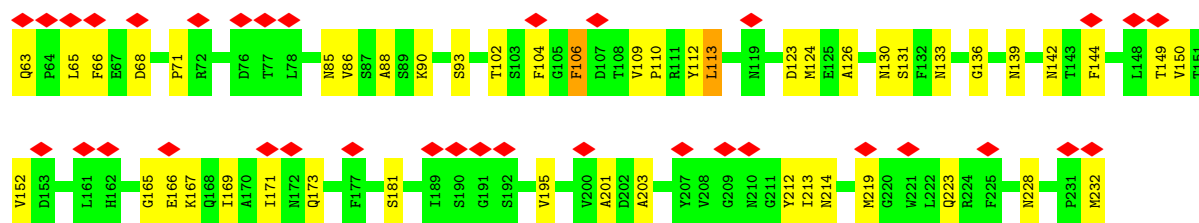


• Molecule 1: Flagellar L-ring protein

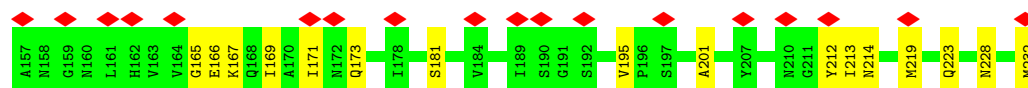


• Molecule 1: Flagellar L-ring protein

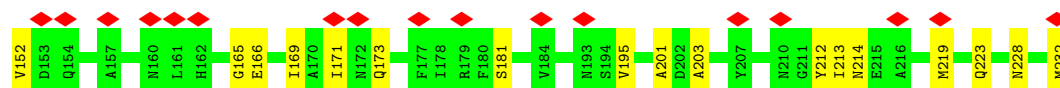




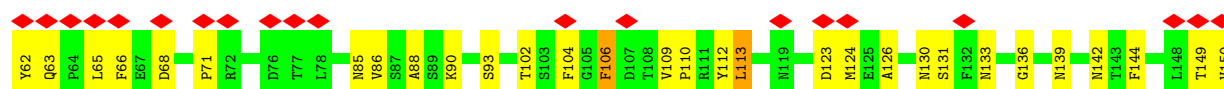
• Molecule 1: Flagellar L-ring protein

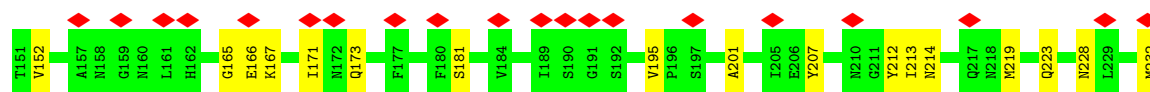


• Molecule 1: Flagellar L-ring protein

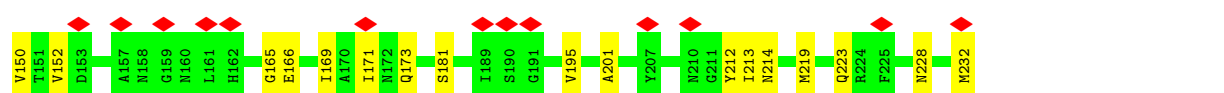
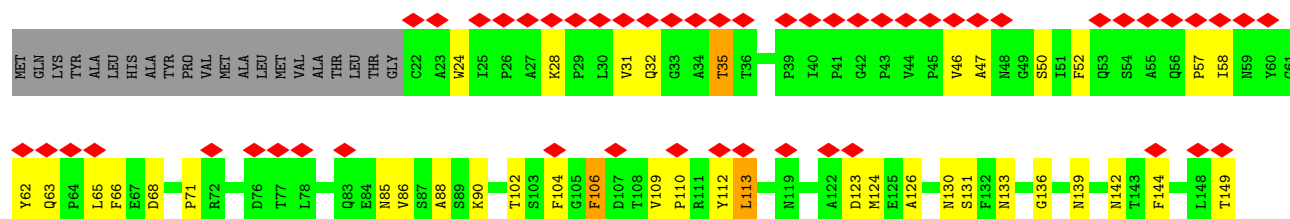


• Molecule 1: Flagellar L-ring protein

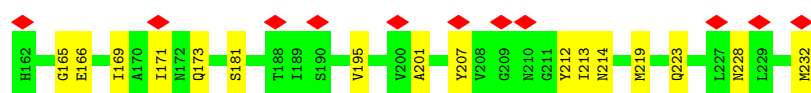
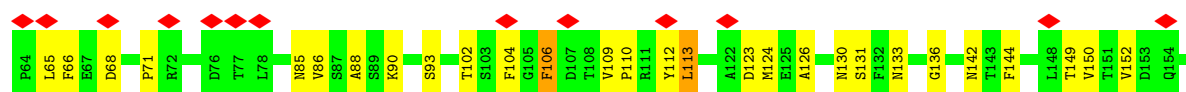




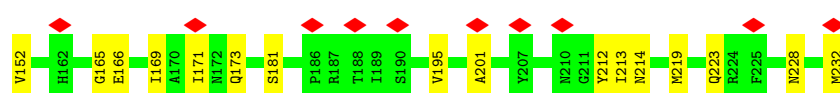
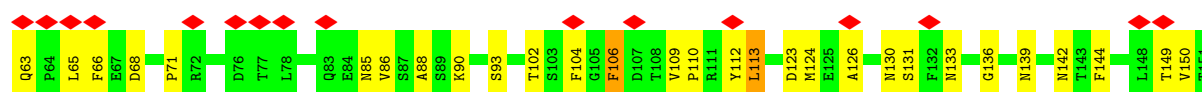
- Molecule 1: Flagellar L-ring protein



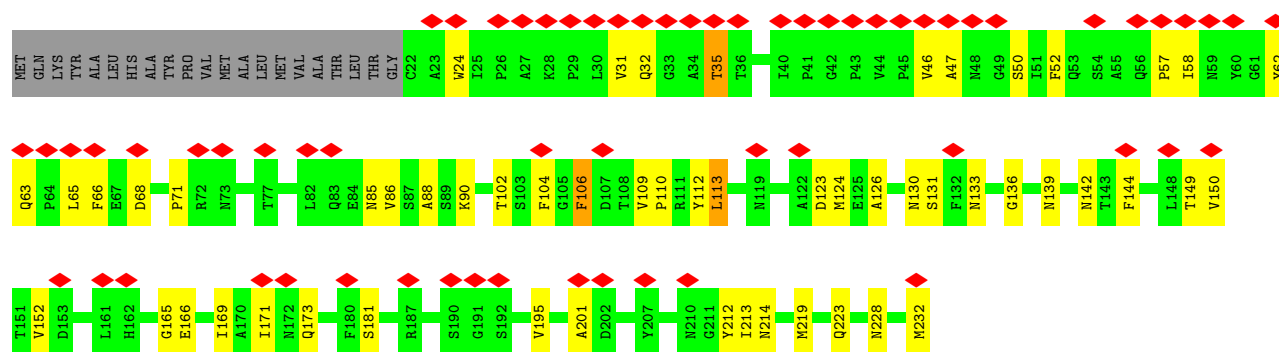
- Molecule 1: Flagellar L-ring protein



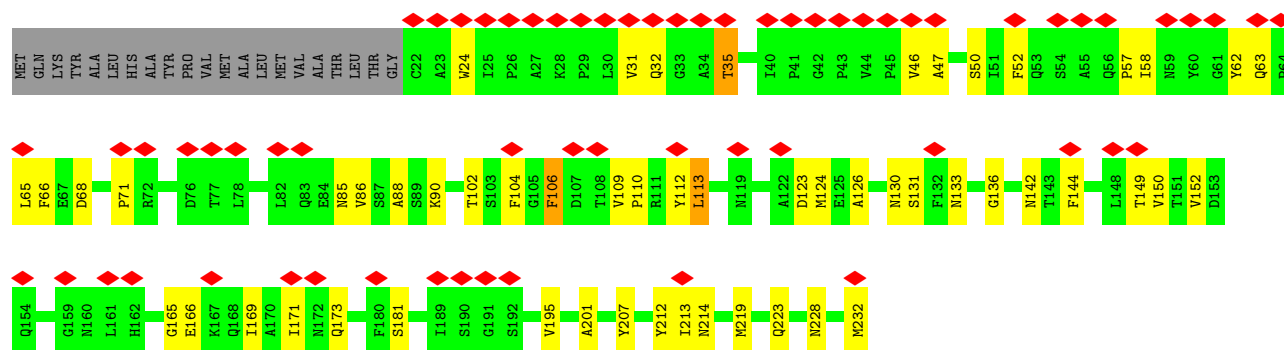
- Molecule 1: Flagellar L-ring protein



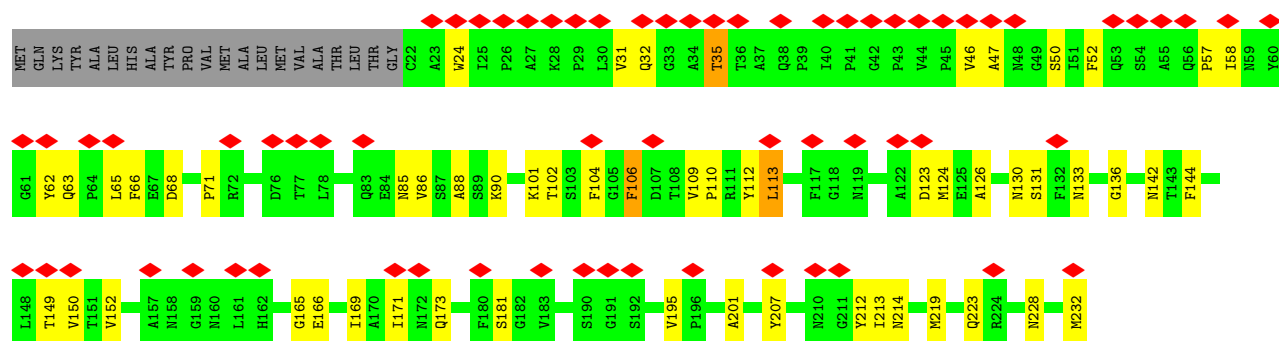
- Molecule 1: Flagellar L-ring protein



• Molecule 1: Flagellar L-ring protein

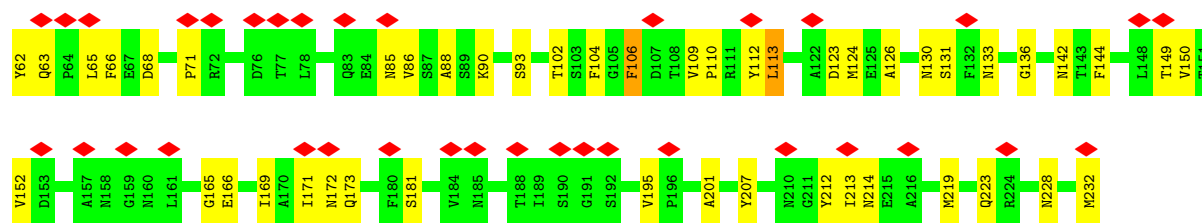


• Molecule 1: Flagellar L-ring protein

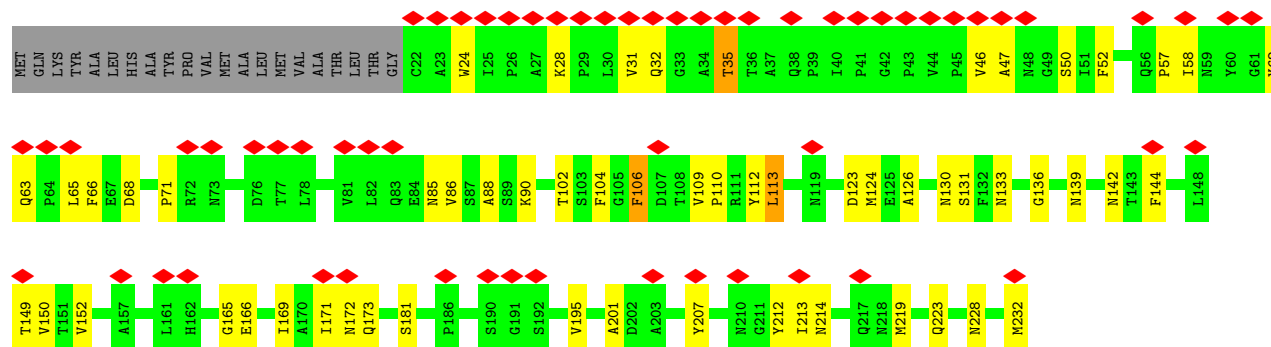


• Molecule 1: Flagellar L-ring protein

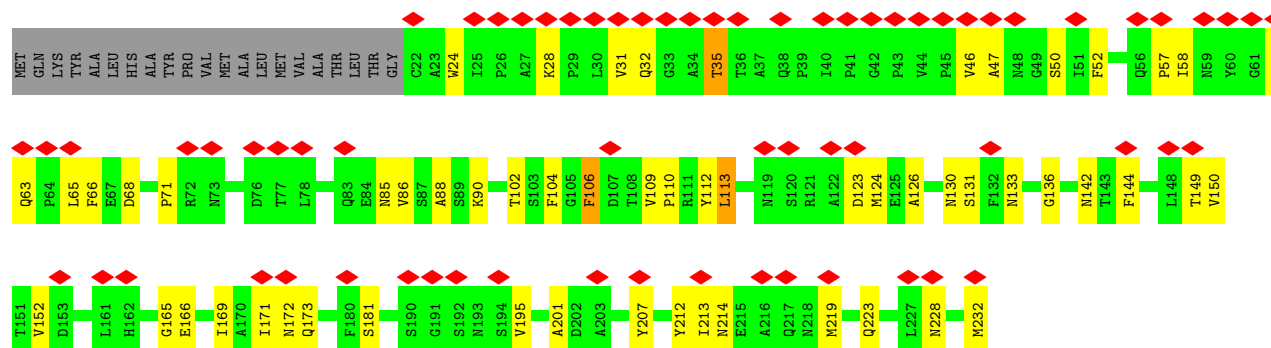




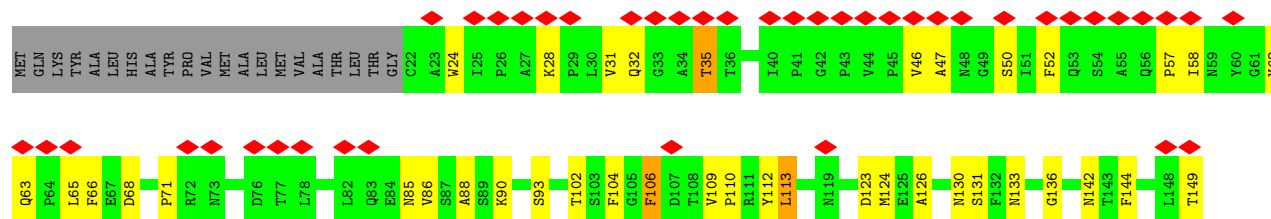
• Molecule 1: Flagellar L-ring protein

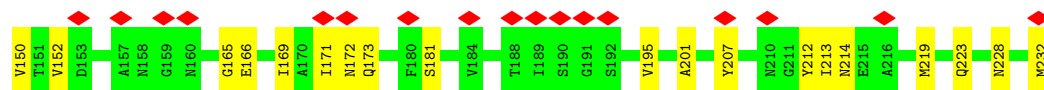


• Molecule 1: Flagellar L-ring protein

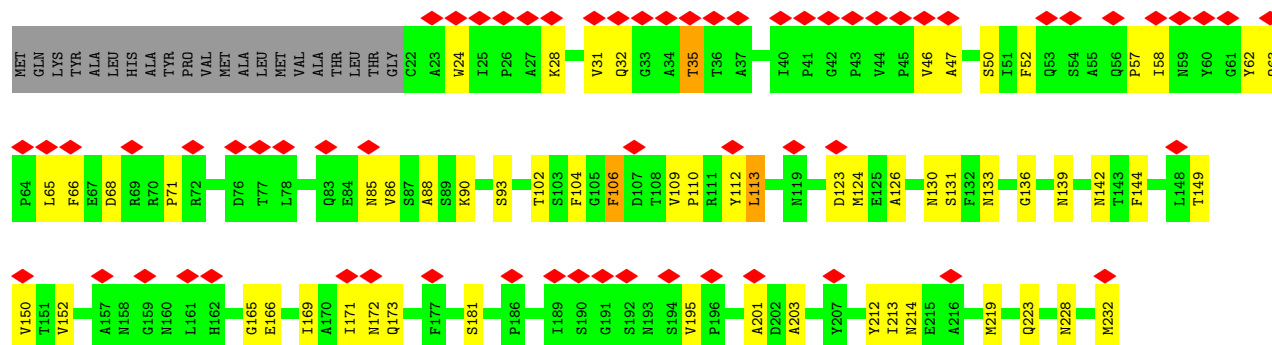


• Molecule 1: Flagellar L-ring protein

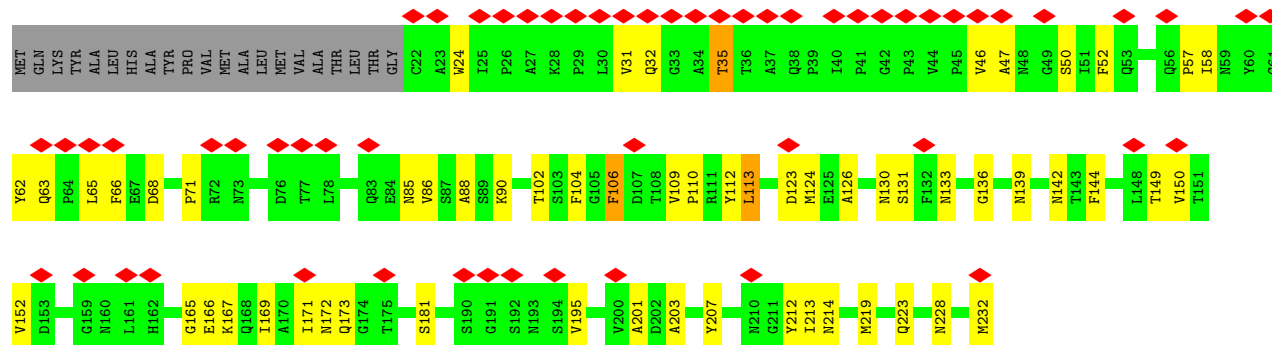




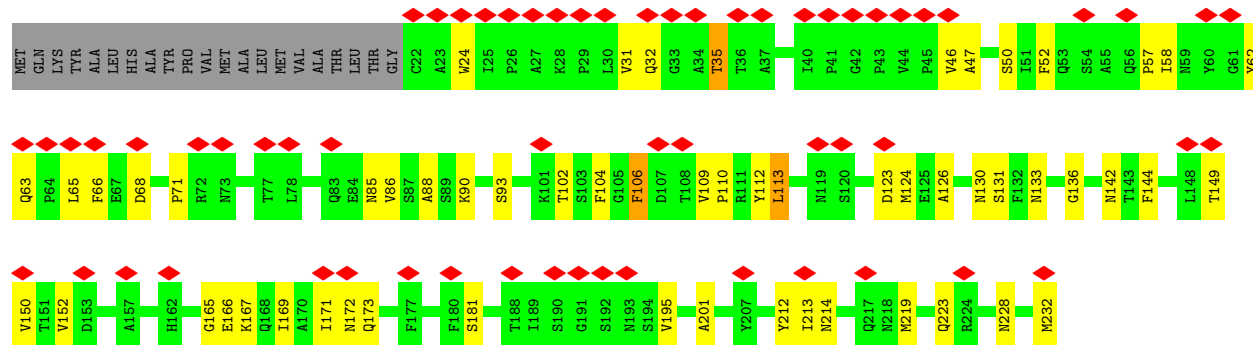
- Molecule 1: Flagellar L-ring protein



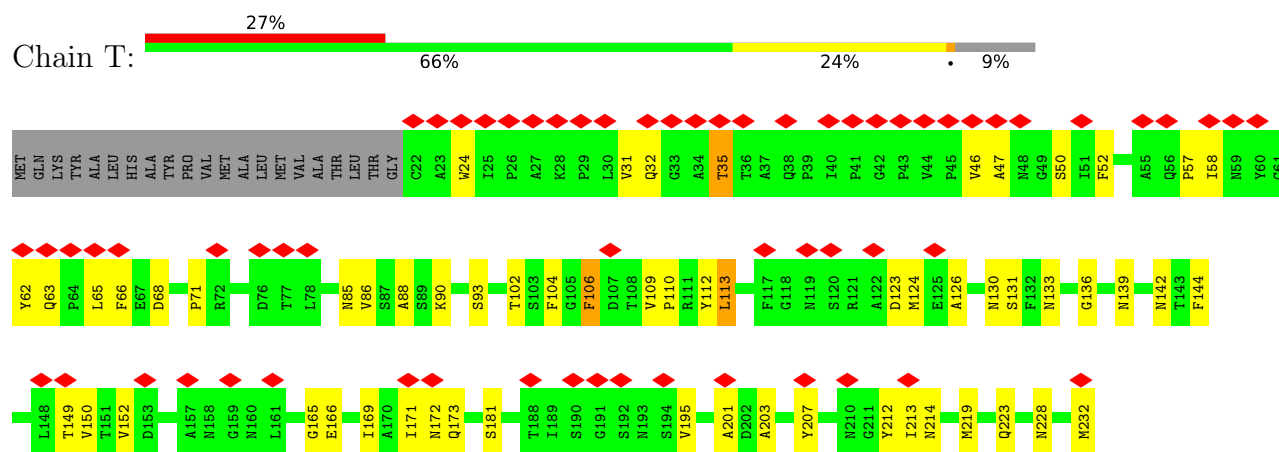
- Molecule 1: Flagellar L-ring protein



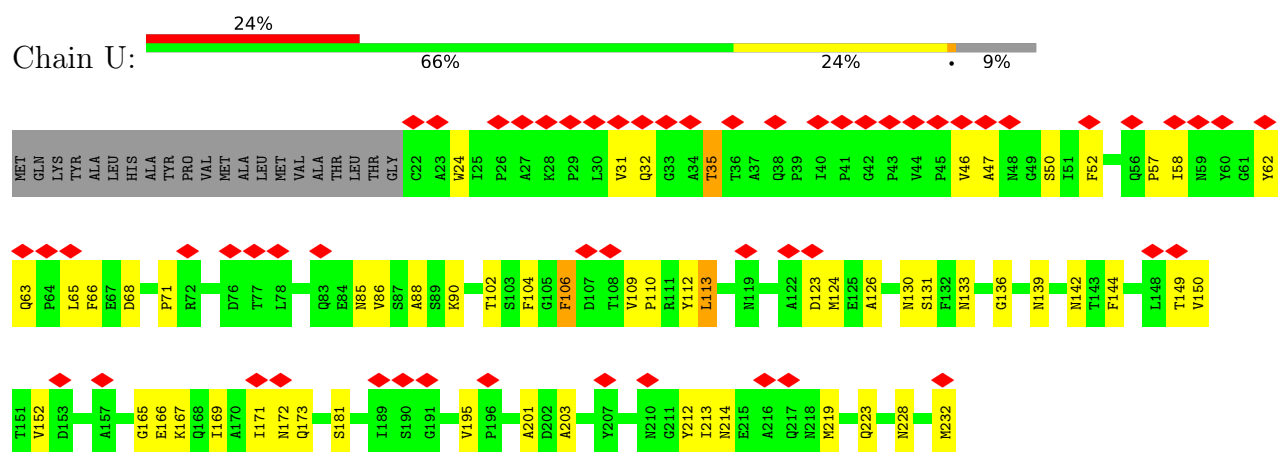
- Molecule 1: Flagellar L-ring protein



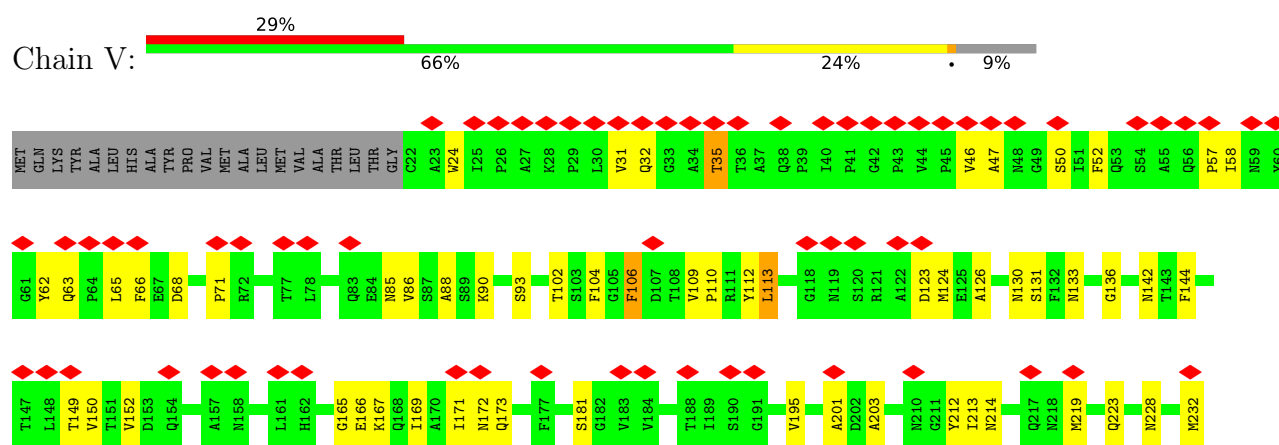
- Molecule 1: Flagellar L-ring protein



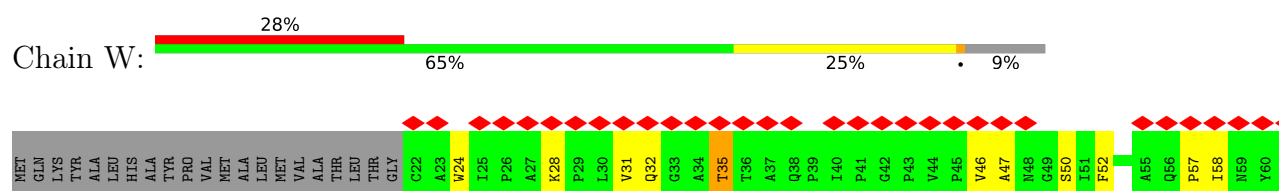
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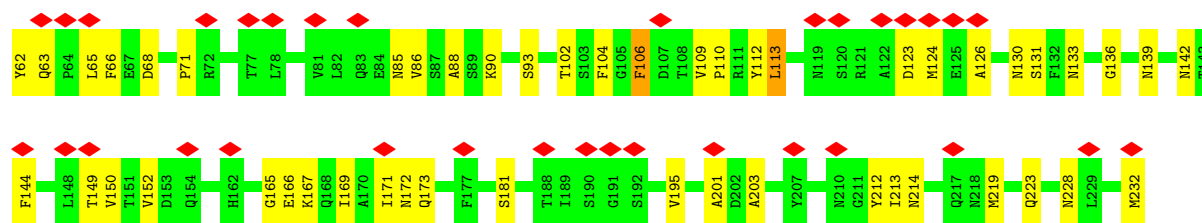


• Molecule 1: Flagellar L-ring protein

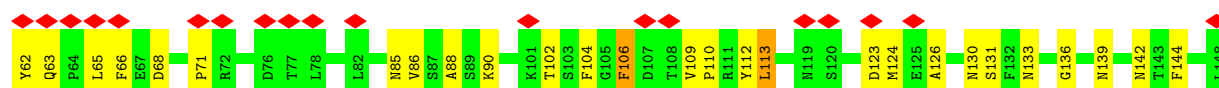


• Molecule 1: Flagellar L-ring protein

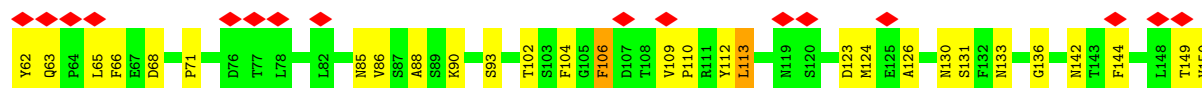




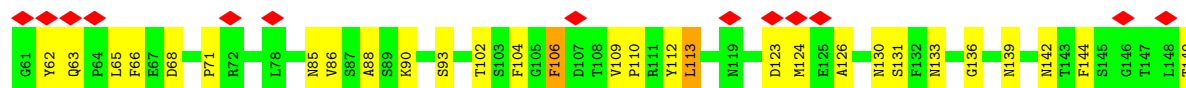
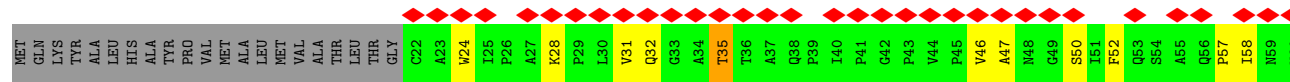
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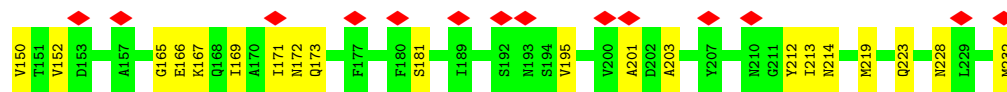


• Molecule 1: Flagellar L-ring protein

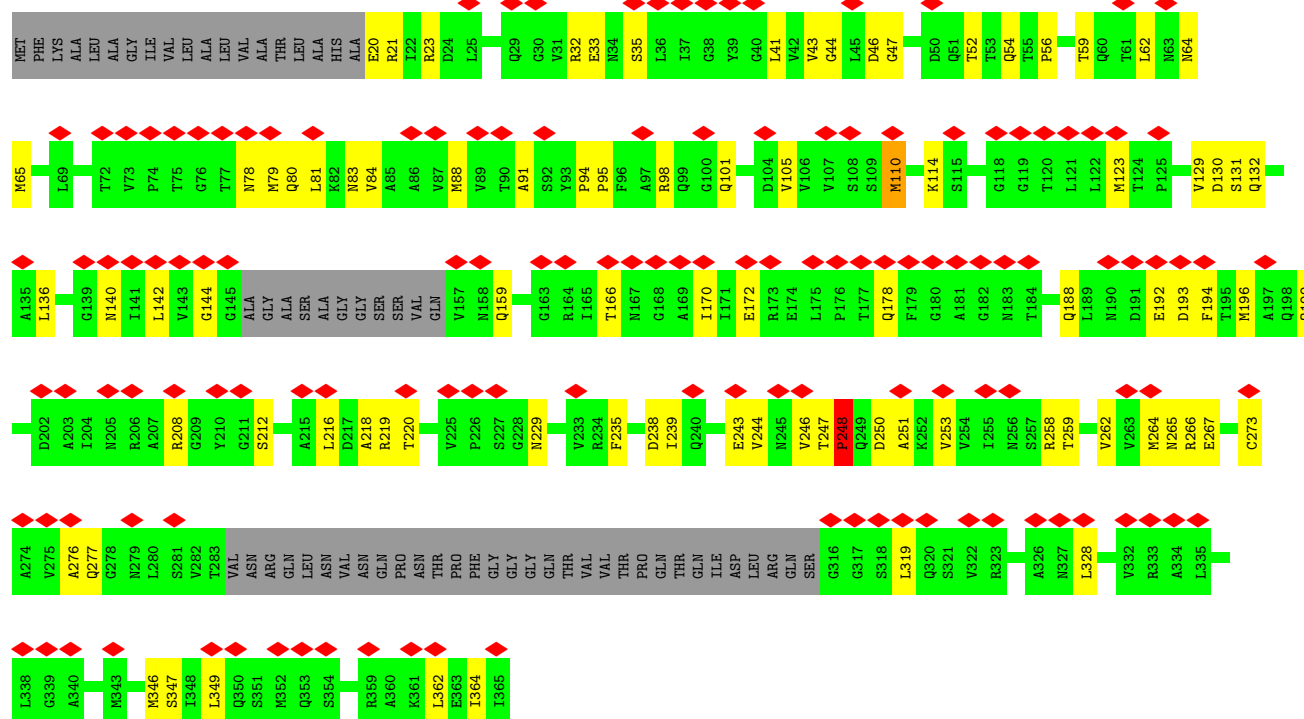


• Molecule 1: Flagellar L-ring protein

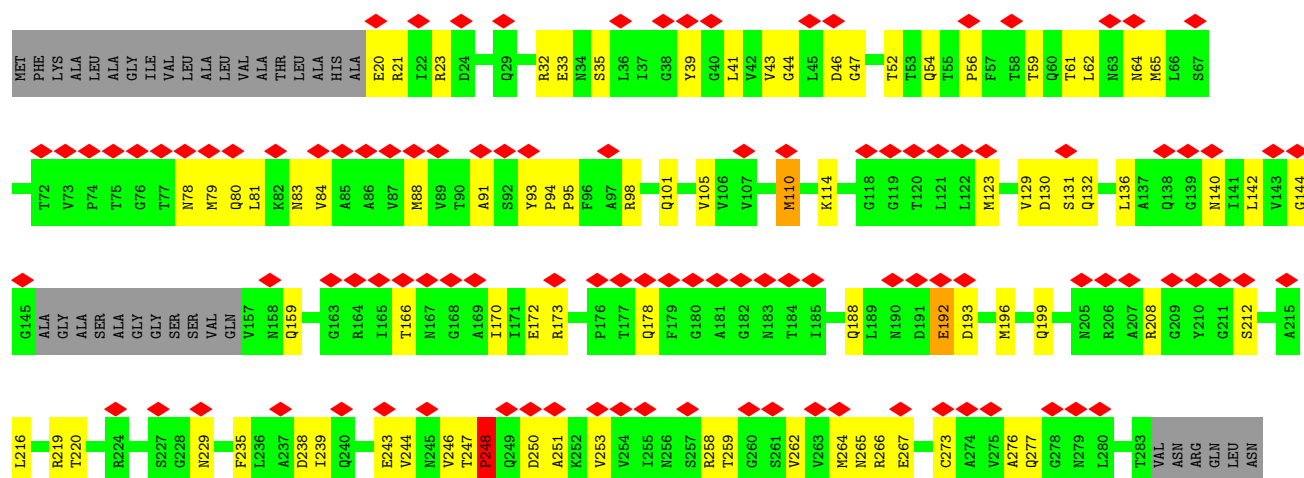


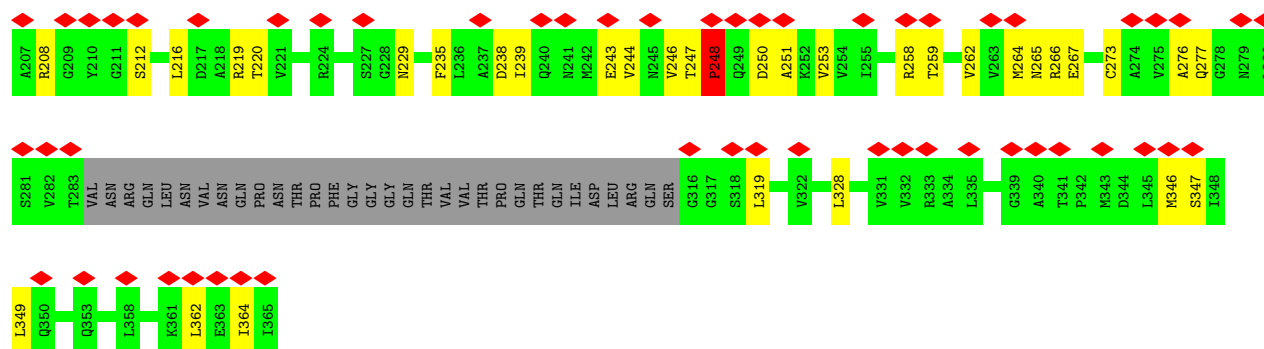


• Molecule 2: Flagellar P-ring protein

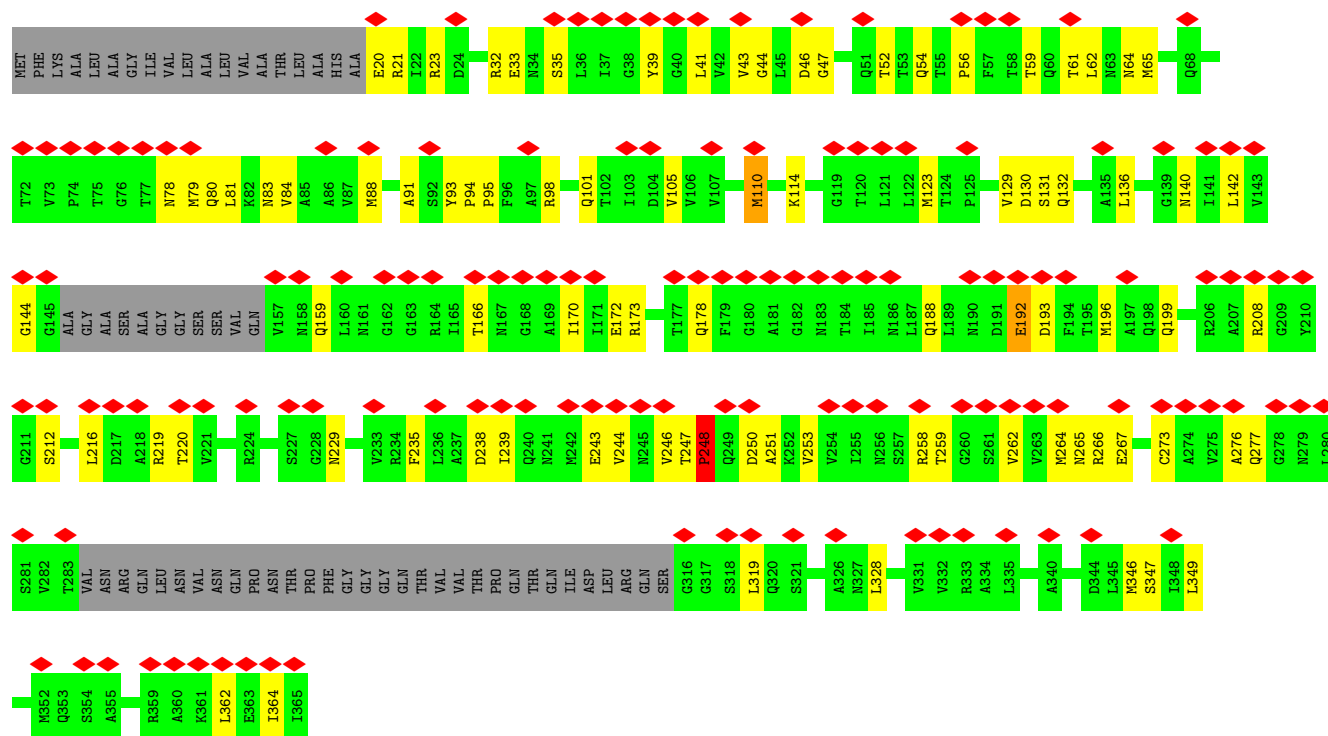


• Molecule 2: Flagellar P-ring protein

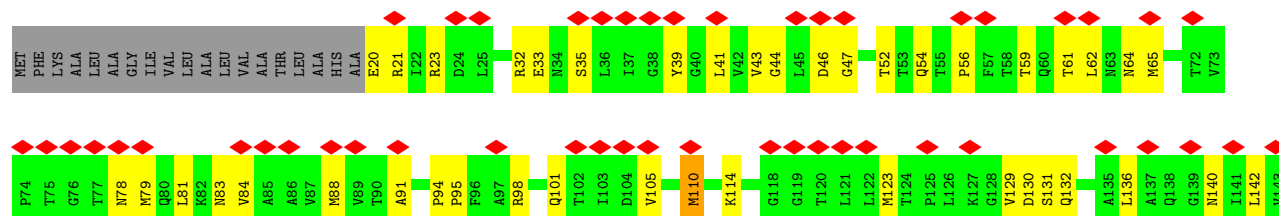


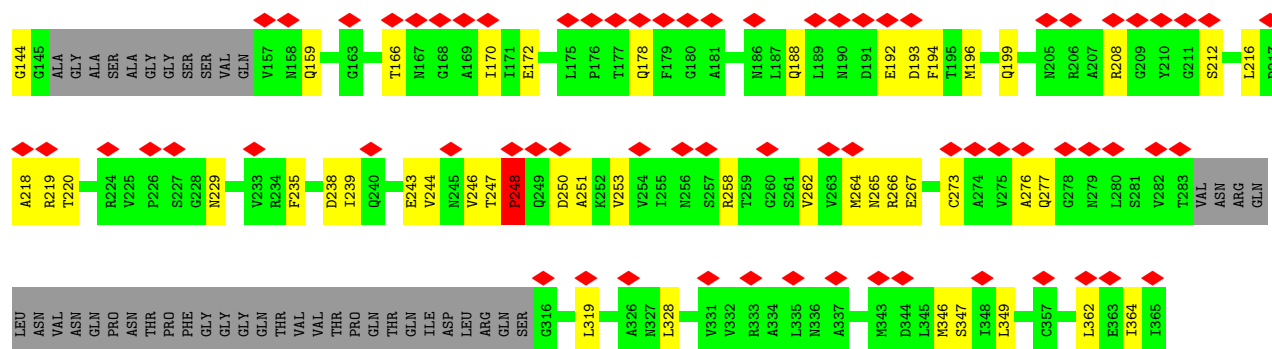


- Molecule 2: Flagellar P-ring protein

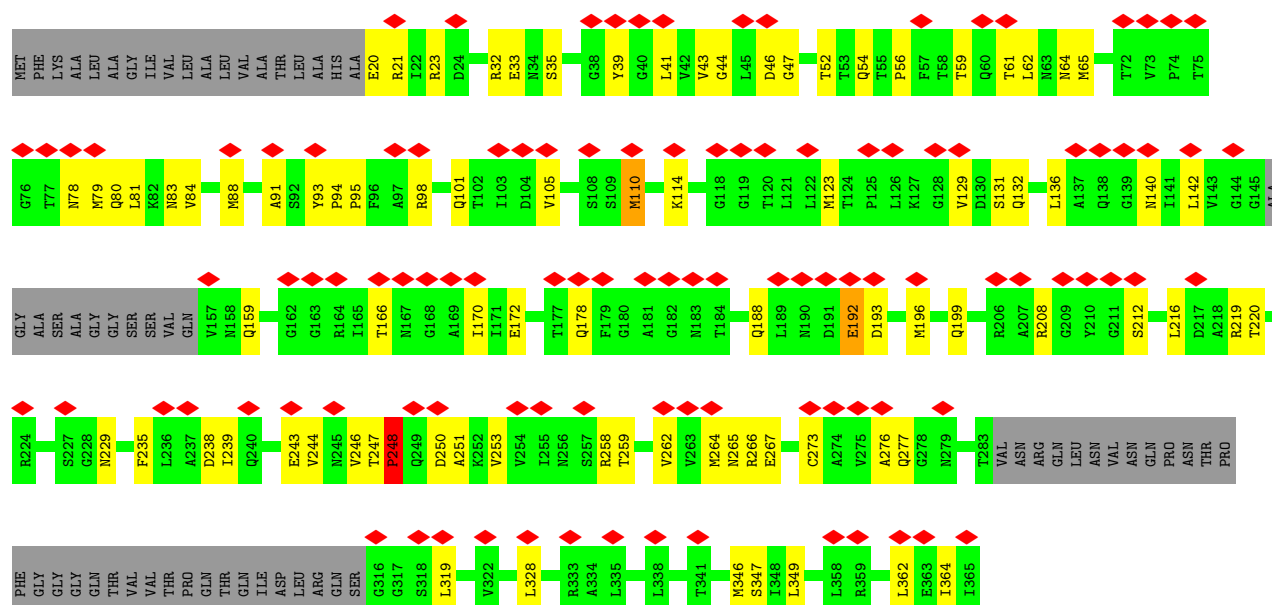


- Molecule 2: Flagellar P-ring protein

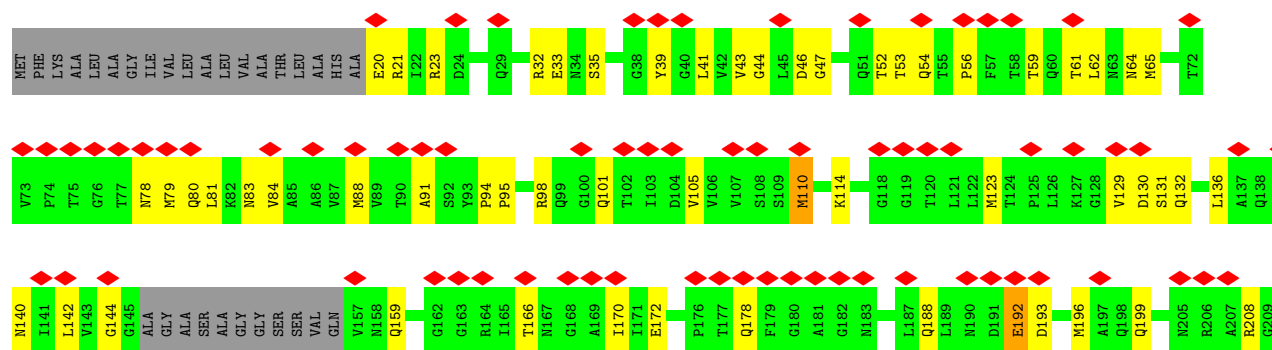


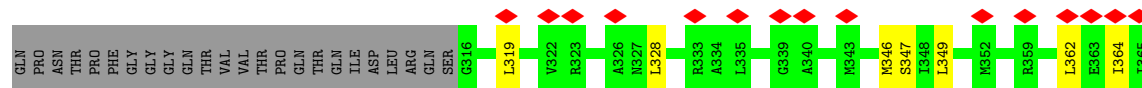


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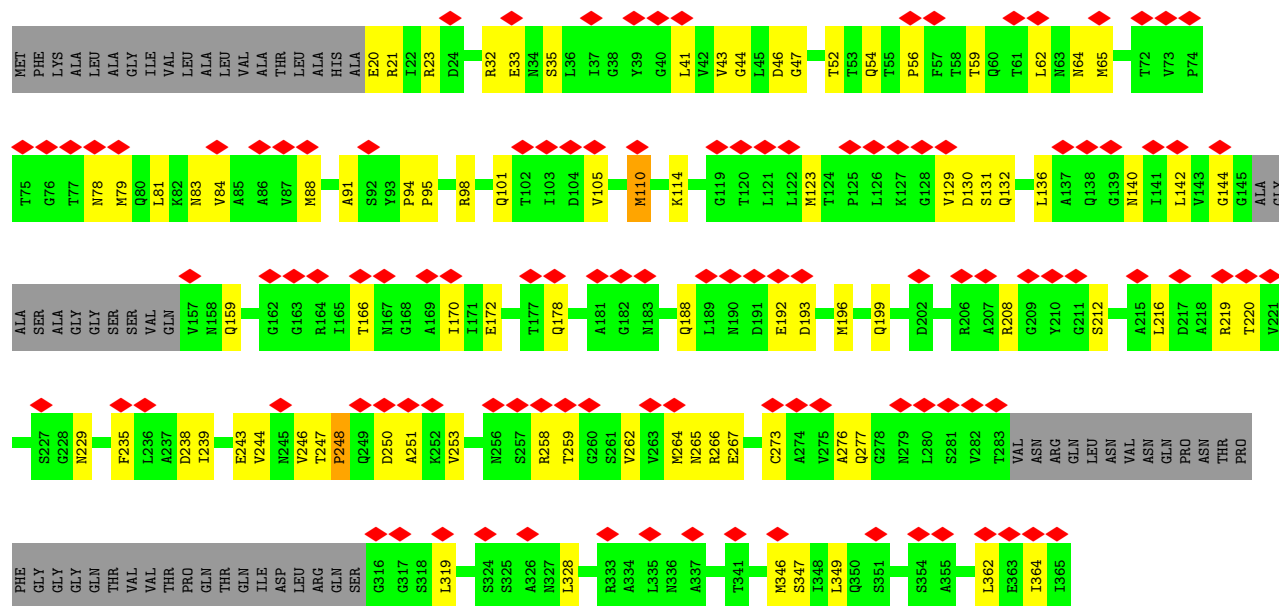


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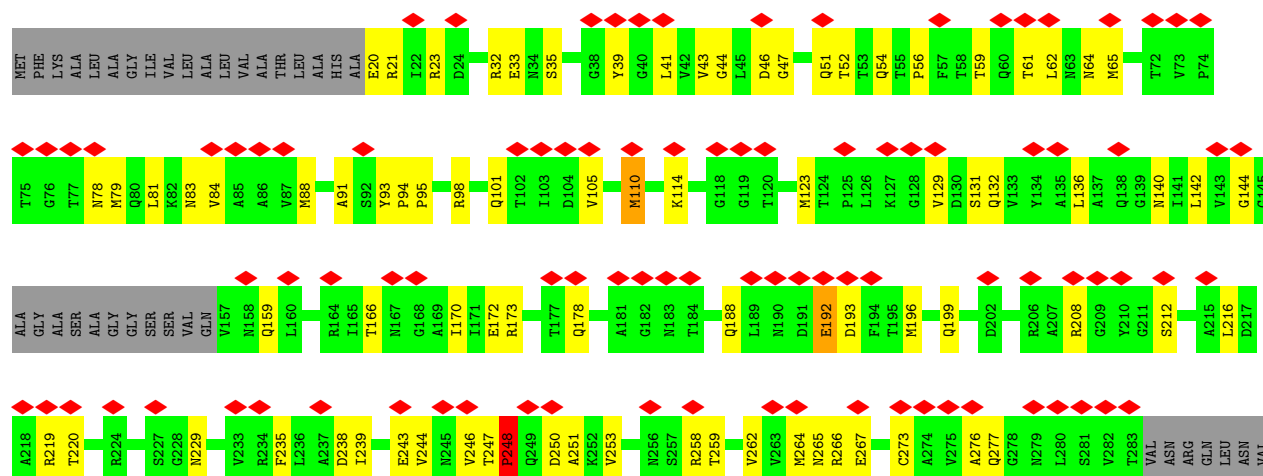


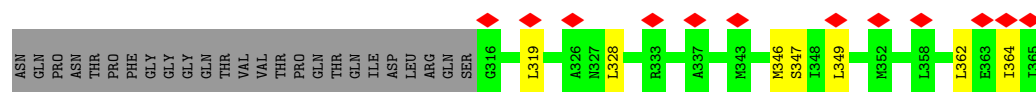


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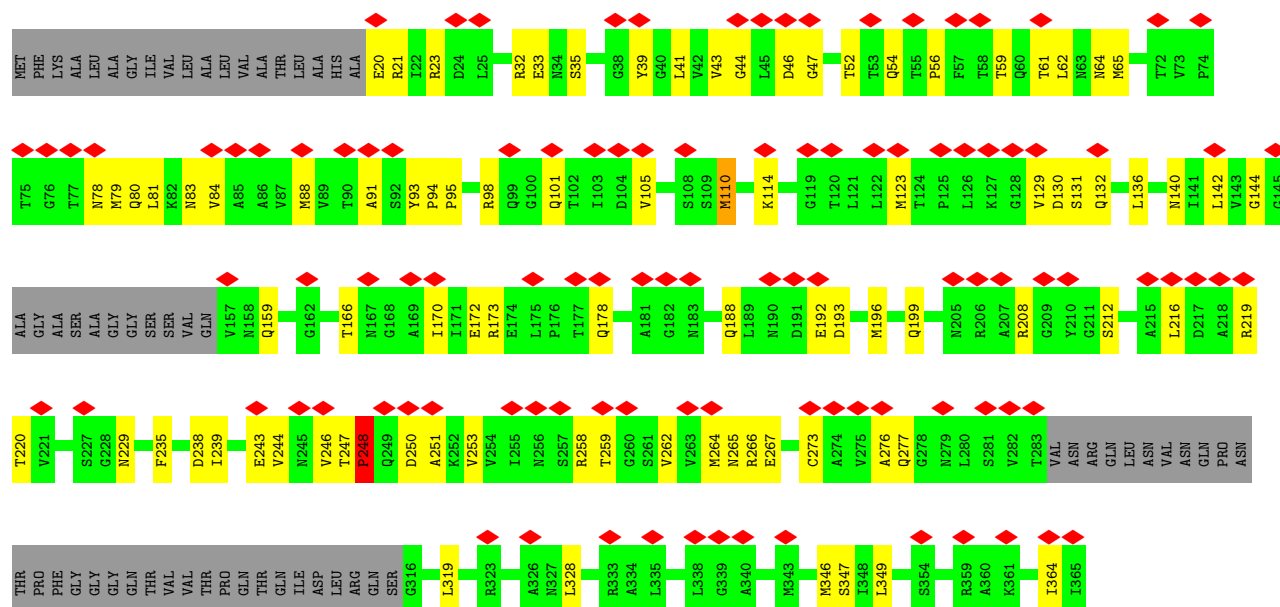


- Molecule 2: Flagellar P-ring protein

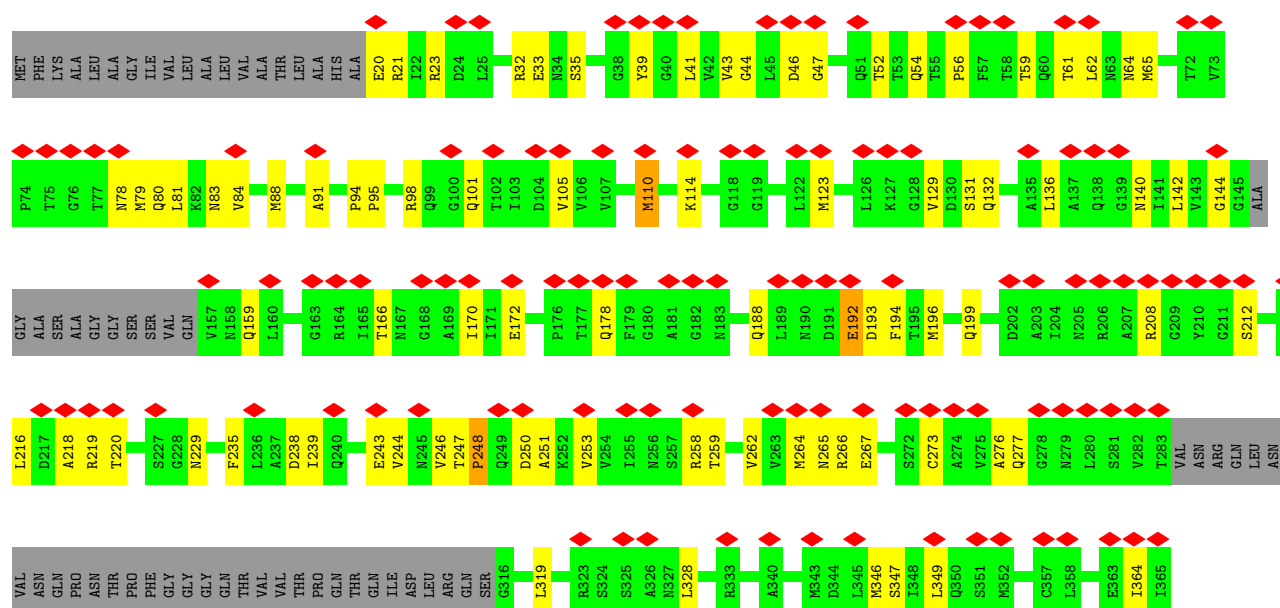




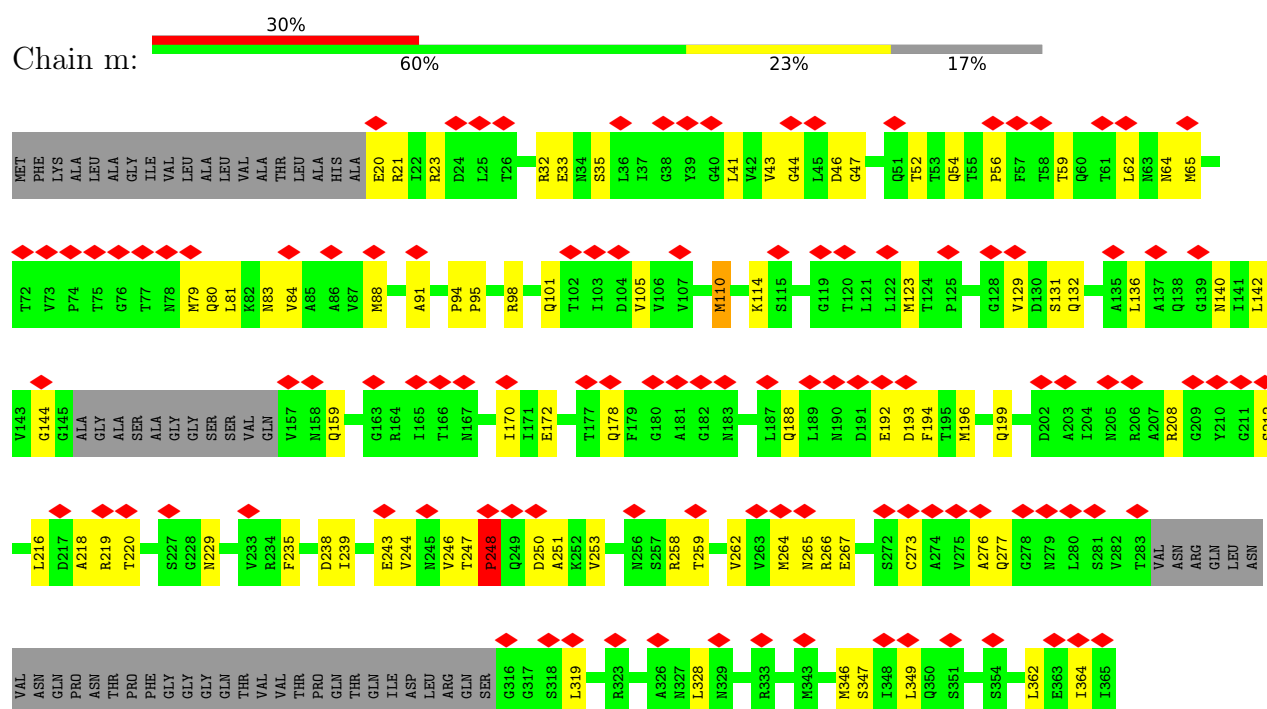
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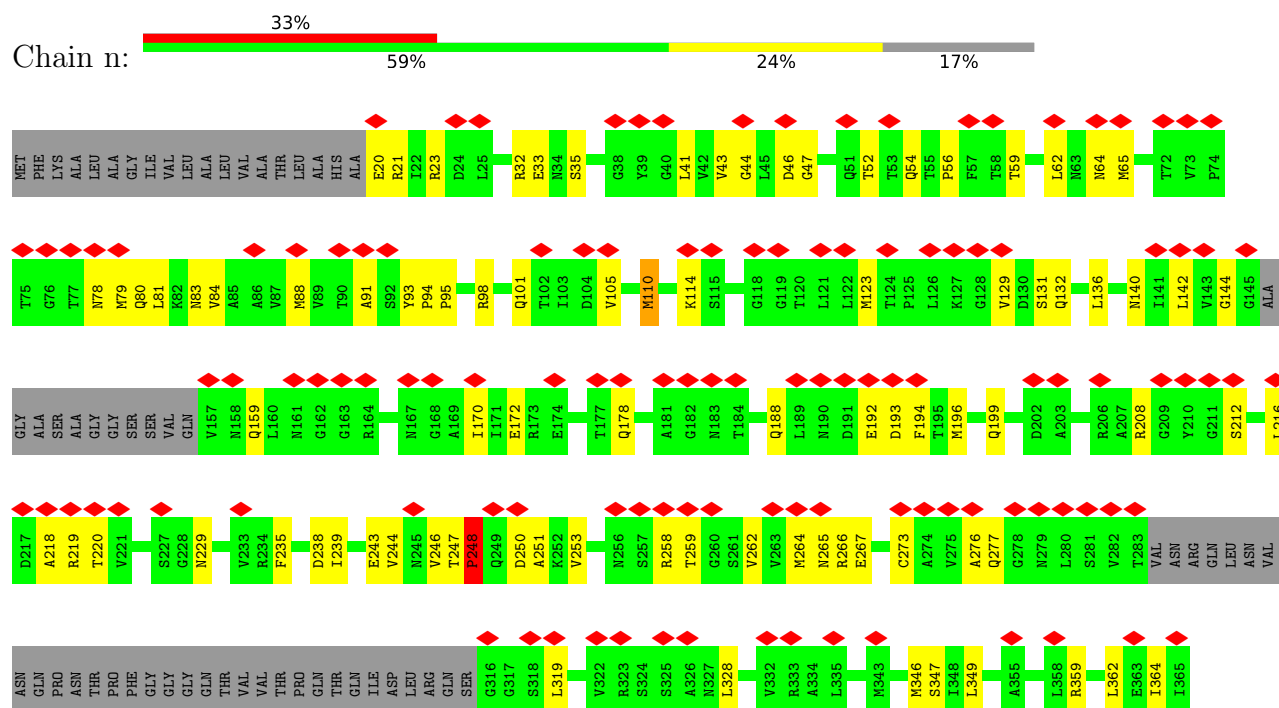
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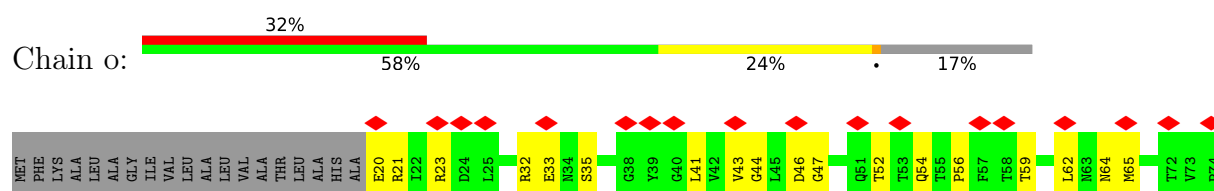
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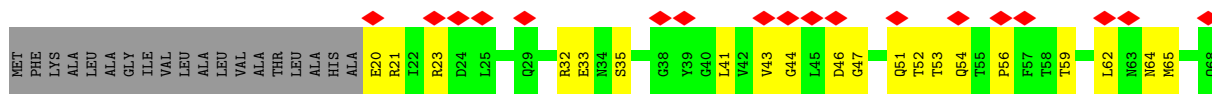


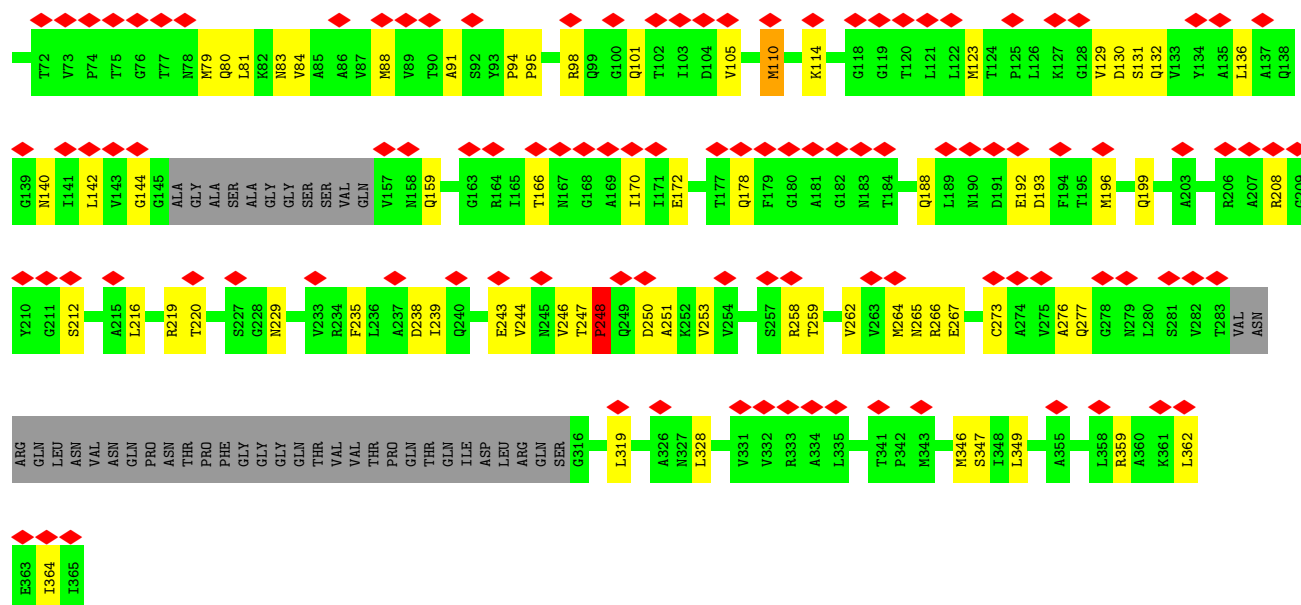
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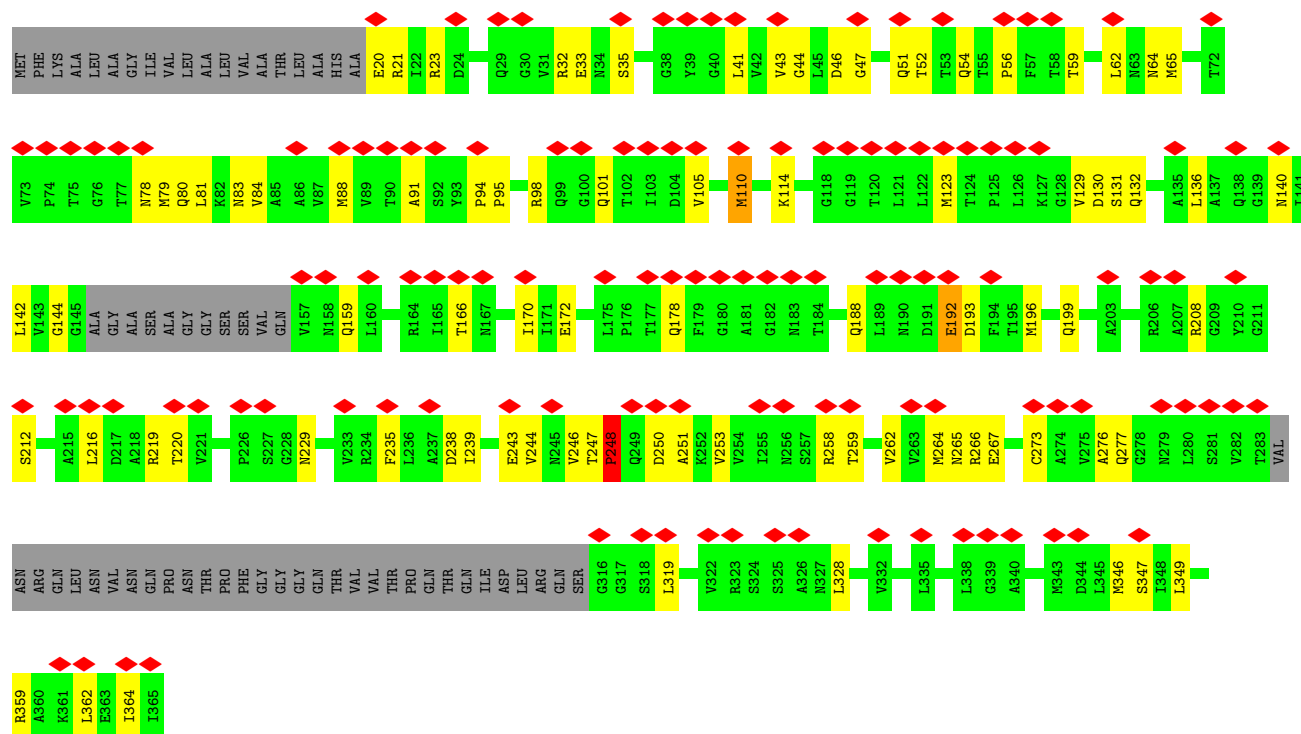
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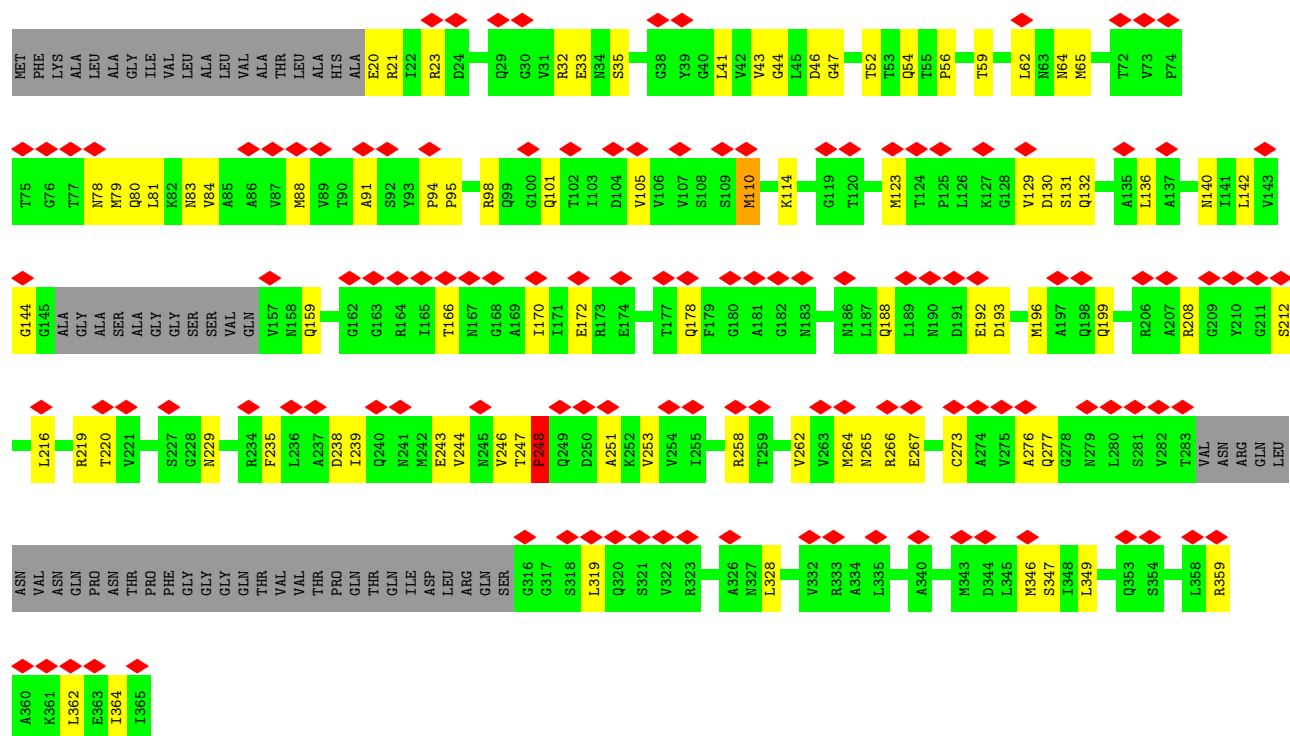


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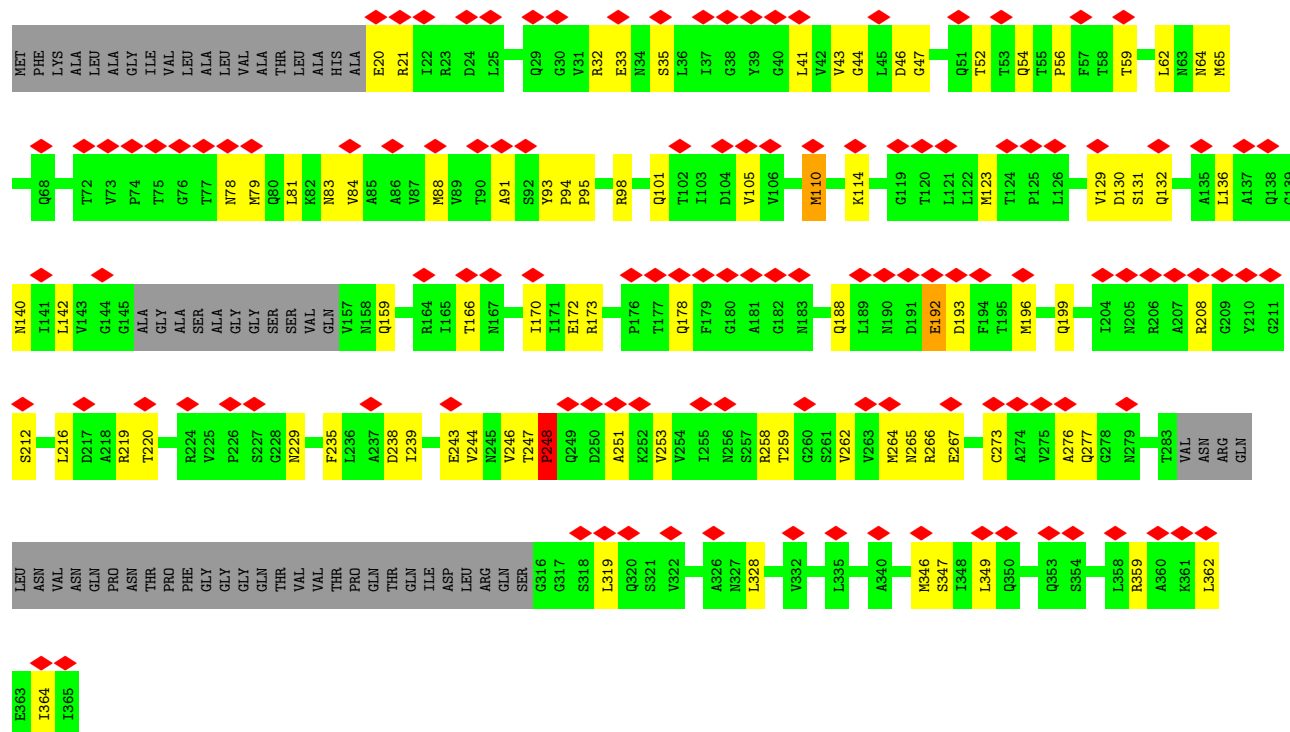


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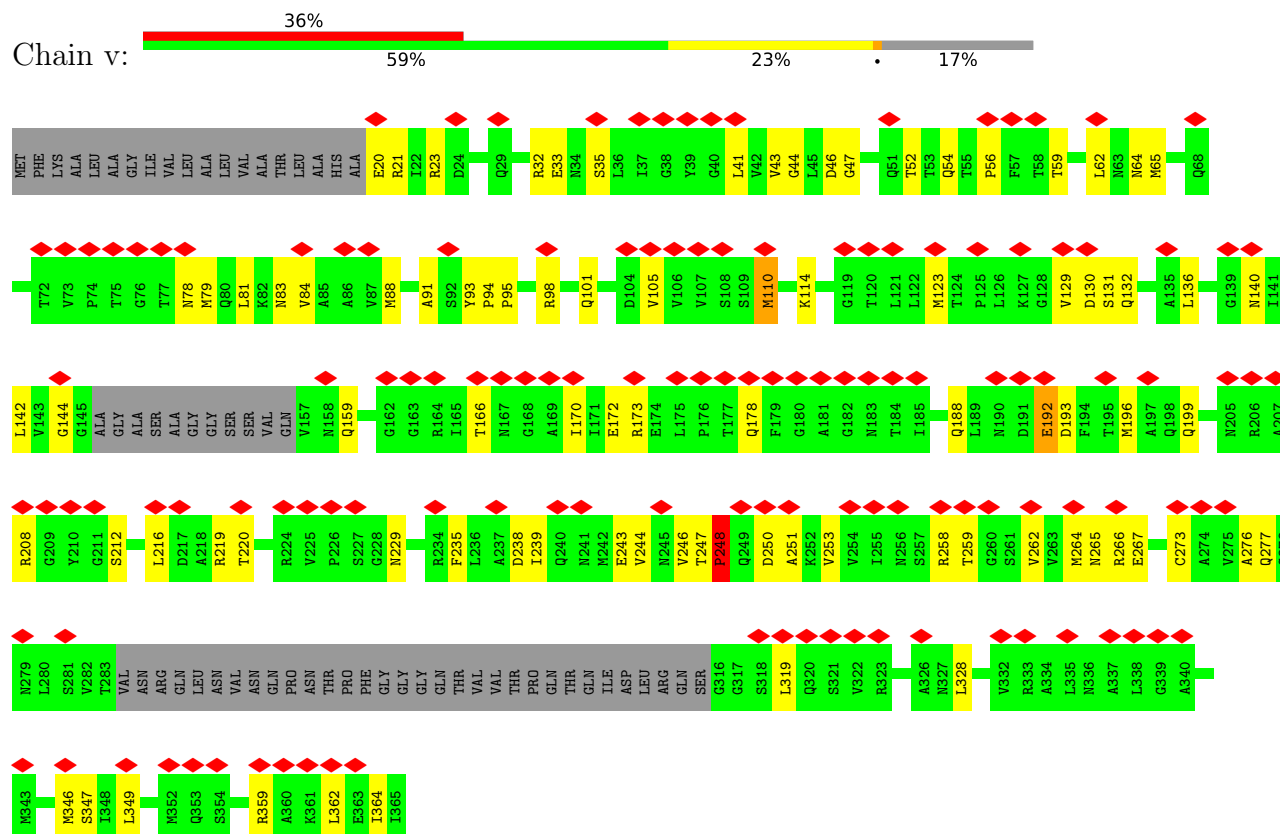




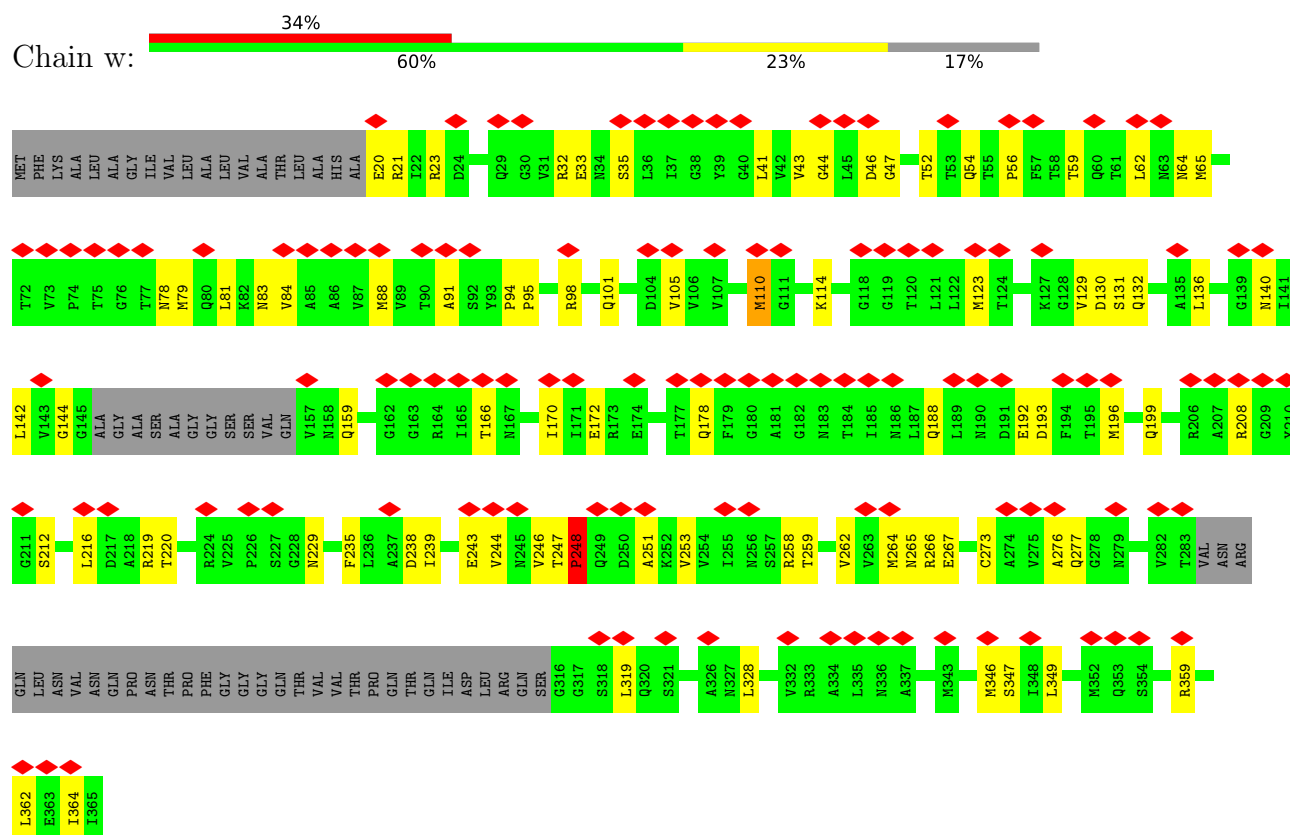
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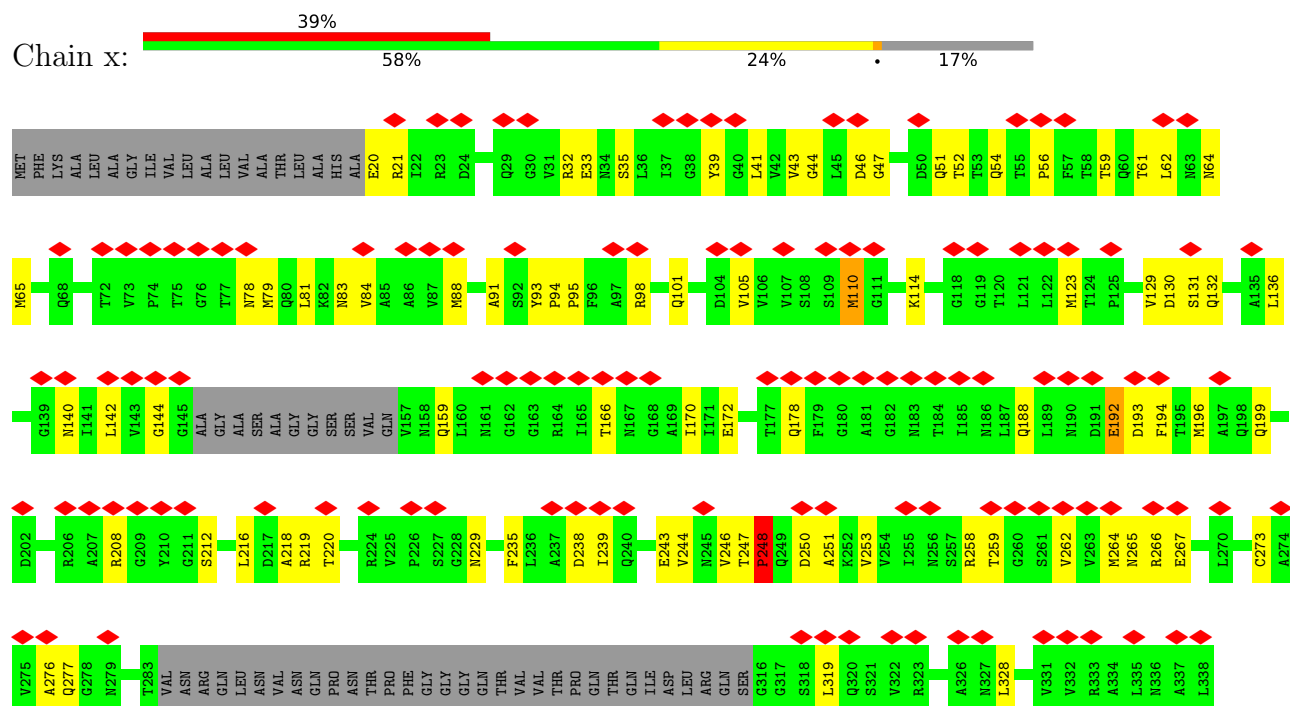
• Molecule 2: Flagellar P-ring protein

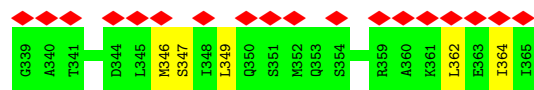


- Molecule 2: Flagellar P-ring protein

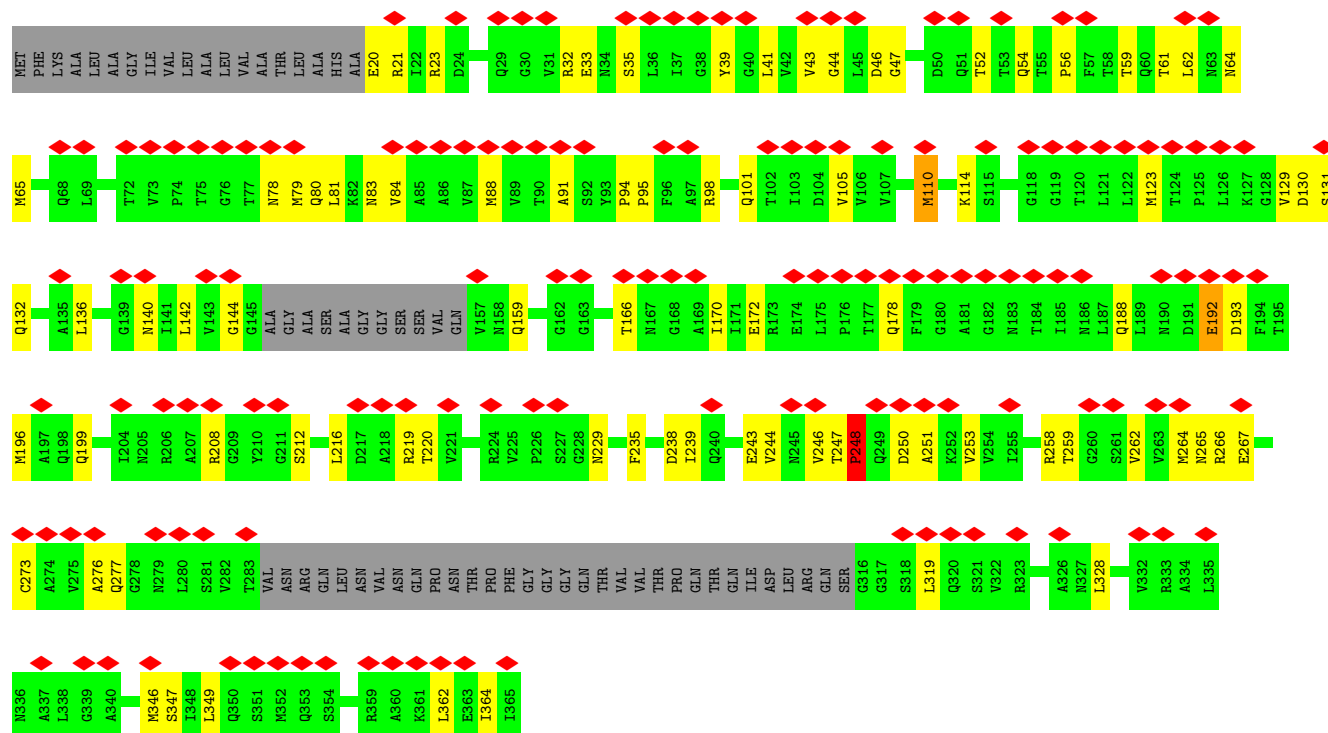
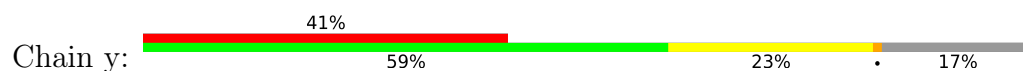


- Molecule 2: Flagellar P-ring protein

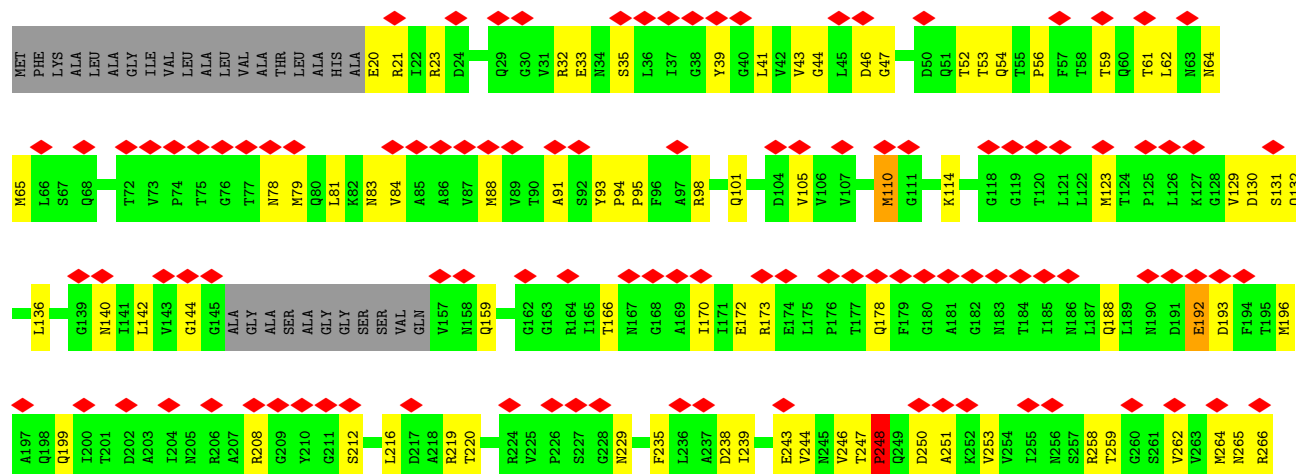


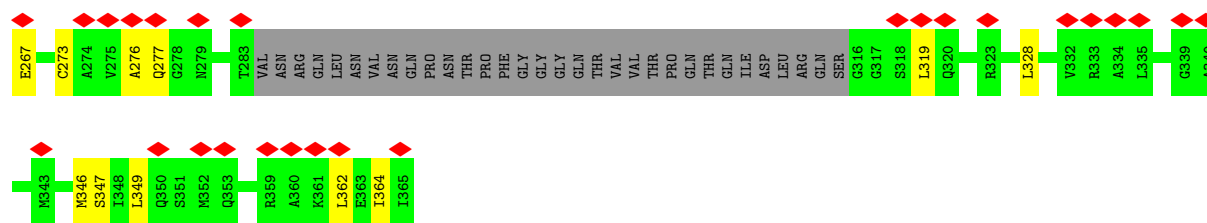


• Molecule 2: Flagellar P-ring protein



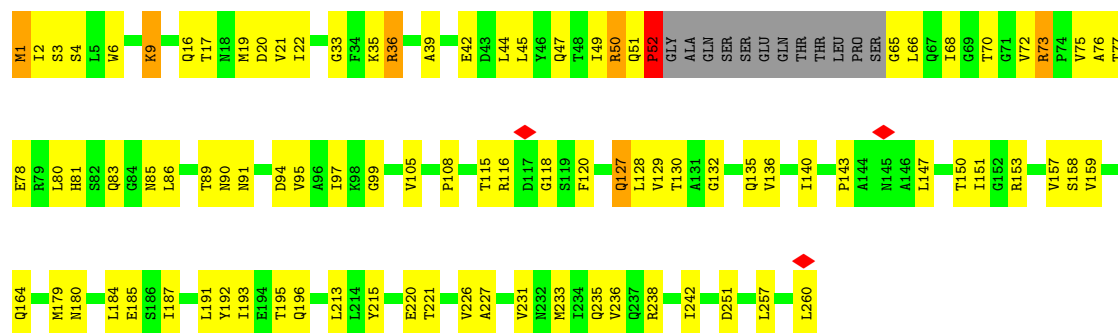
• Molecule 2: Flagellar P-ring protein





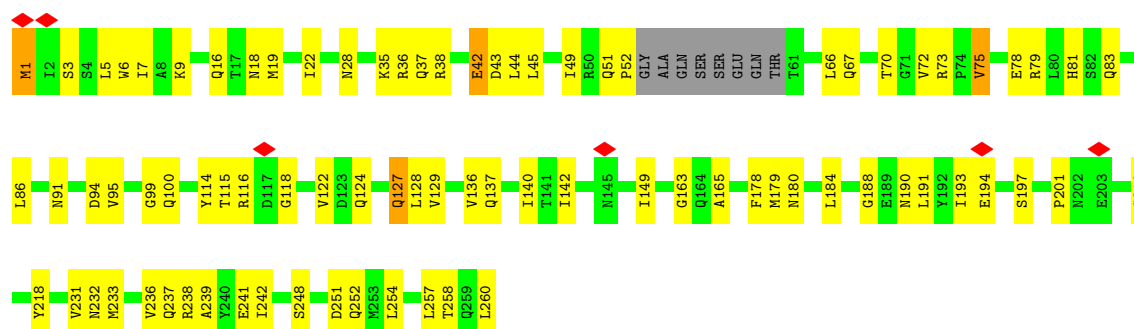
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain 0: 59% 34% 5%



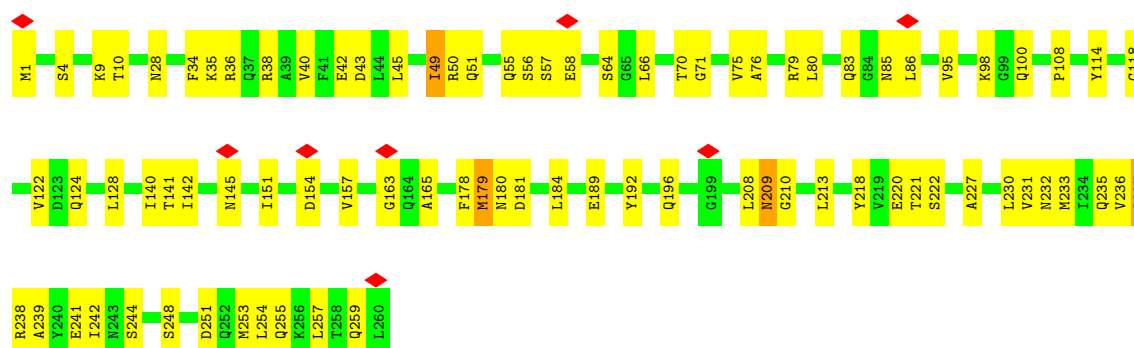
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain 1: 65% 30% 5%

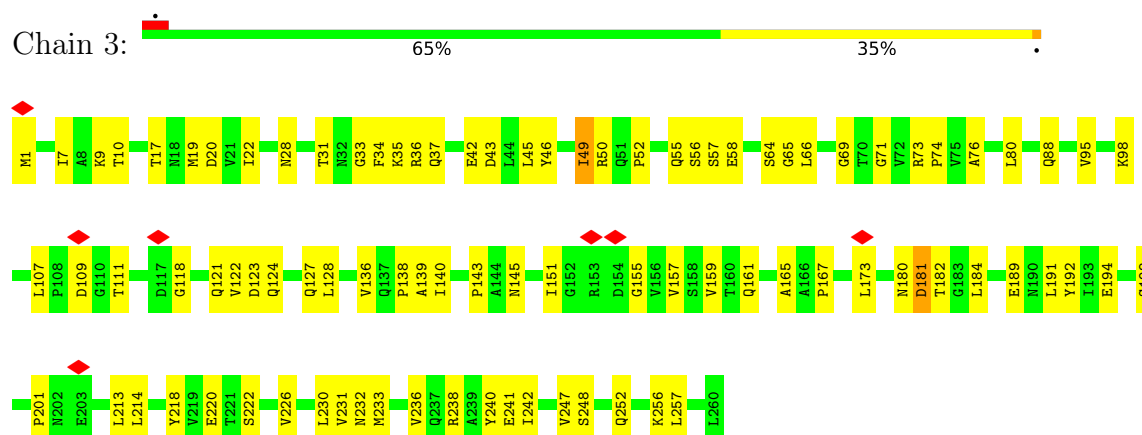


• Molecule 3: Flagellar basal-body rod protein FlgG

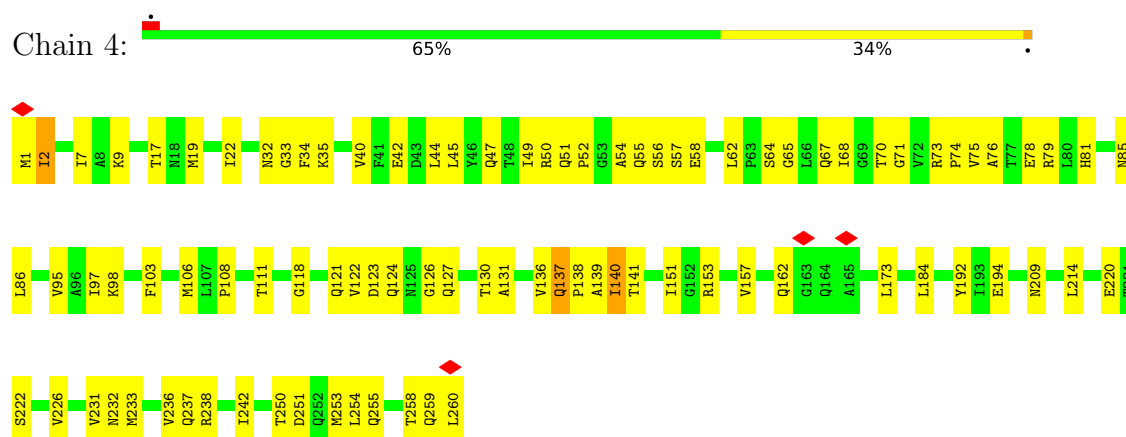
Chain 2: 67% 31% 2%



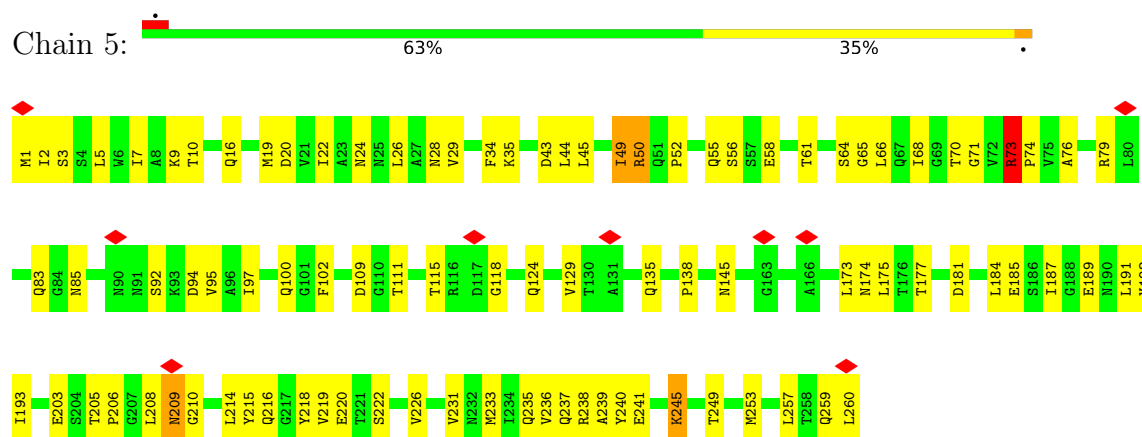
- Molecule 3: Flagellar basal-body rod protein FlgG



- Molecule 3: Flagellar basal-body rod protein FlgG

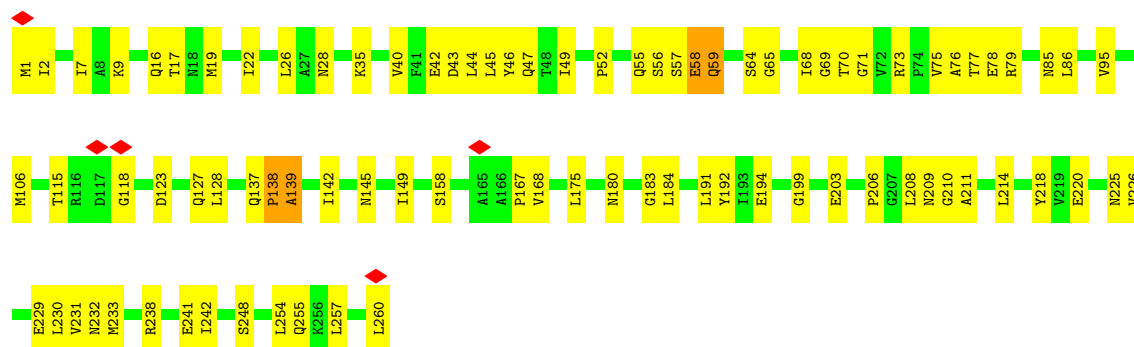


- Molecule 3: Flagellar basal-body rod protein FlgG



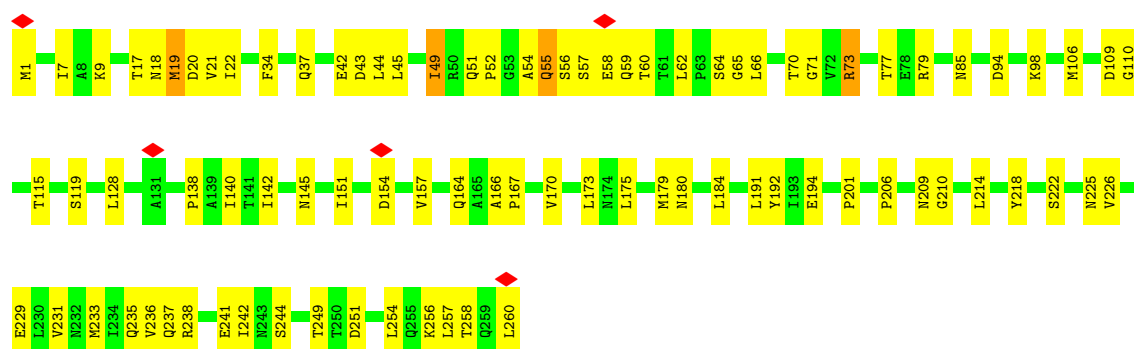
- Molecule 3: Flagellar basal-body rod protein FlgG





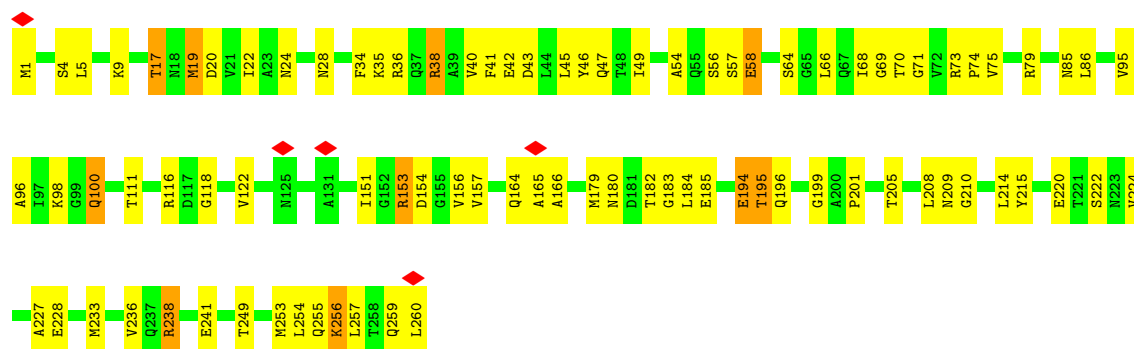
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain 7: 66% 32%



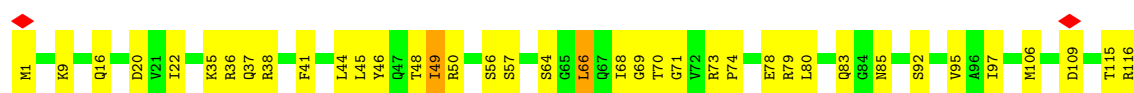
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain 8: 66% 30%



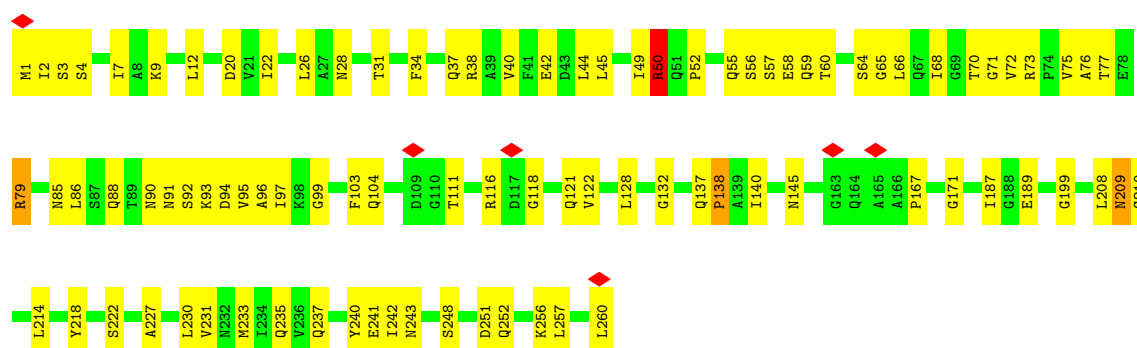
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain 9: 71% 28%

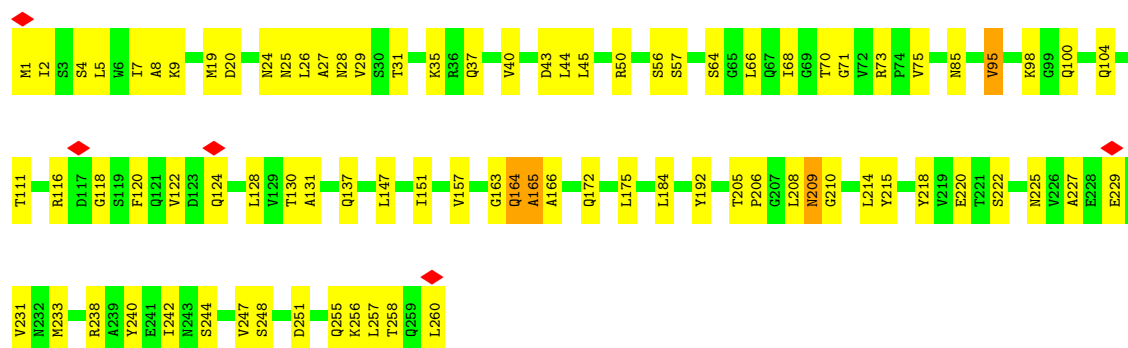




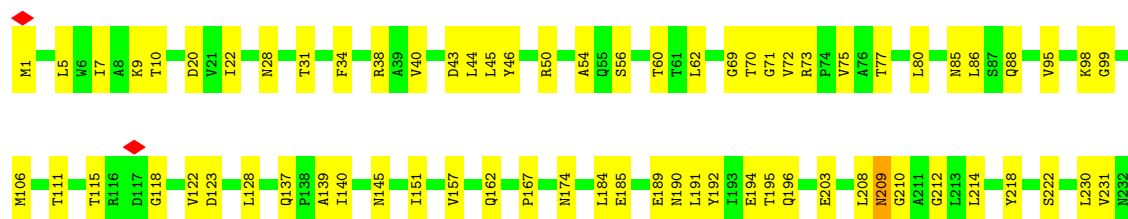
• Molecule 3: Flagellar basal-body rod protein FlgG

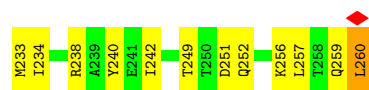


• Molecule 3: Flagellar basal-body rod protein FlgG



• Molecule 3: Flagellar basal-body rod protein FlgG

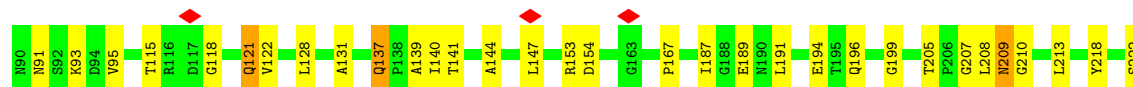
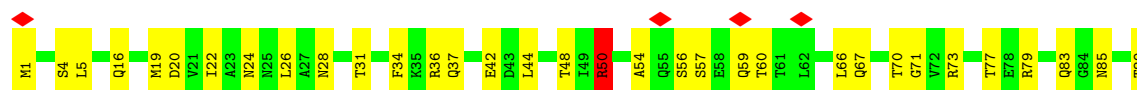




• Molecule 3: Flagellar basal-body rod protein FlgG



• Molecule 3: Flagellar basal-body rod protein FlgG

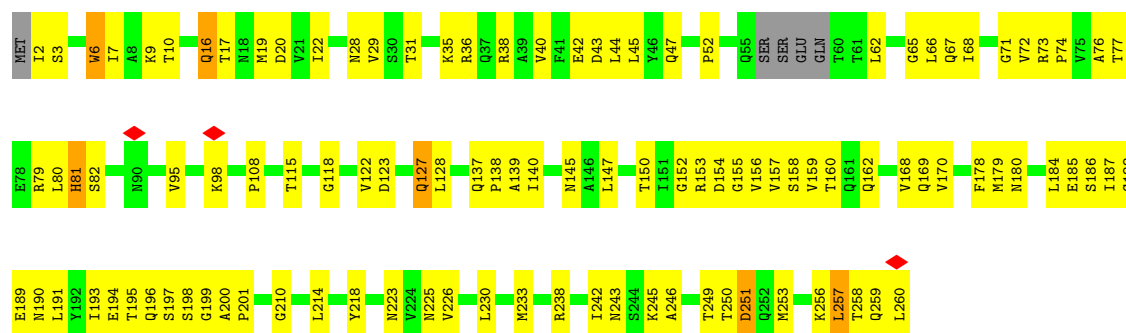


• Molecule 3: Flagellar basal-body rod protein FlgG



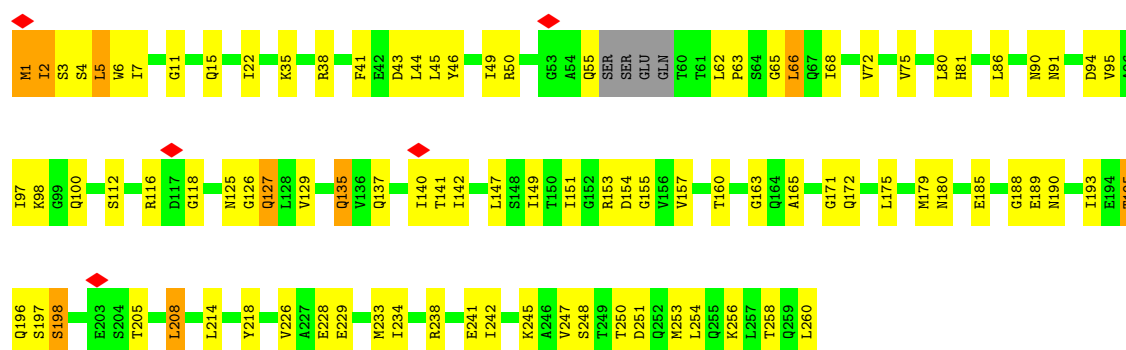
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain AG:  56% 40%



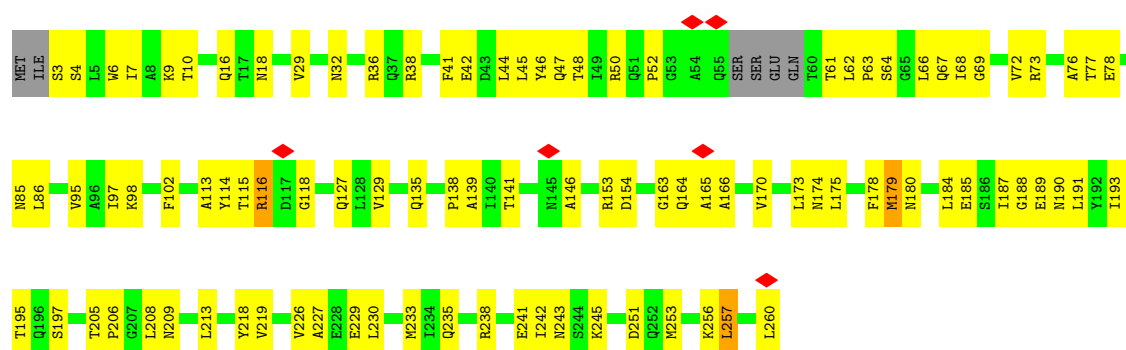
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain AH:  62% 33%



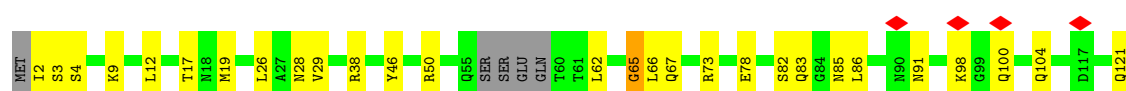
• Molecule 3: Flagellar basal-body rod protein FlgG

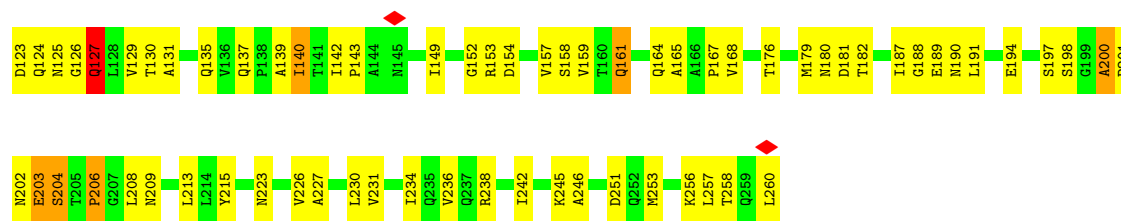
Chain AI:  60% 37%



• Molecule 3: Flagellar basal-body rod protein FlgG

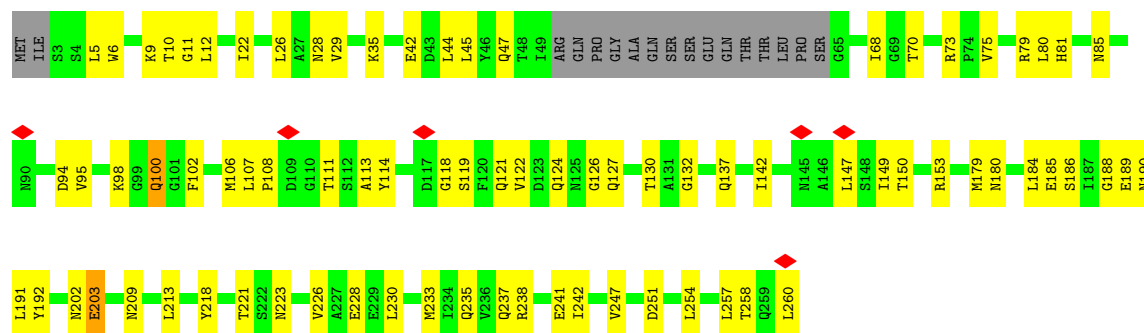
Chain AJ:  62% 33%





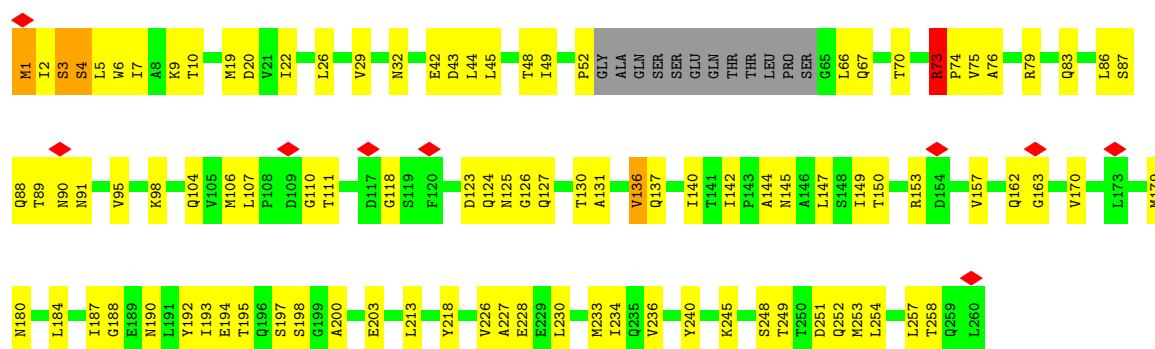
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain AK: 62% 30% 7%



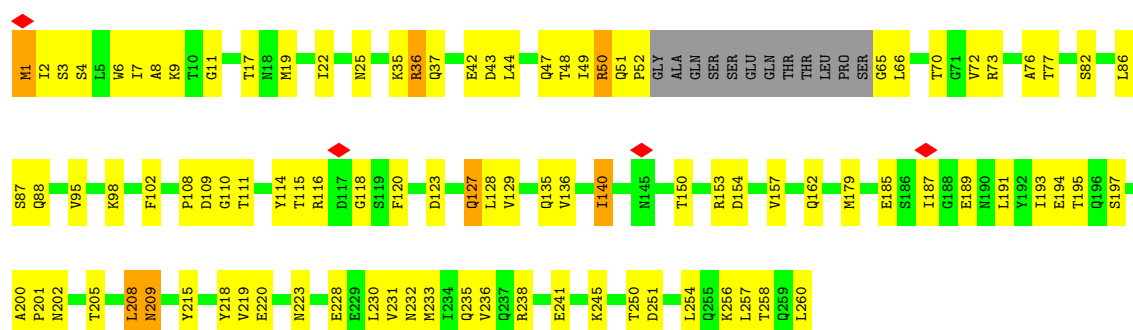
• Molecule 3: Flagellar basal-body rod protein FlgG

Chain AL: 57% 36% 5%

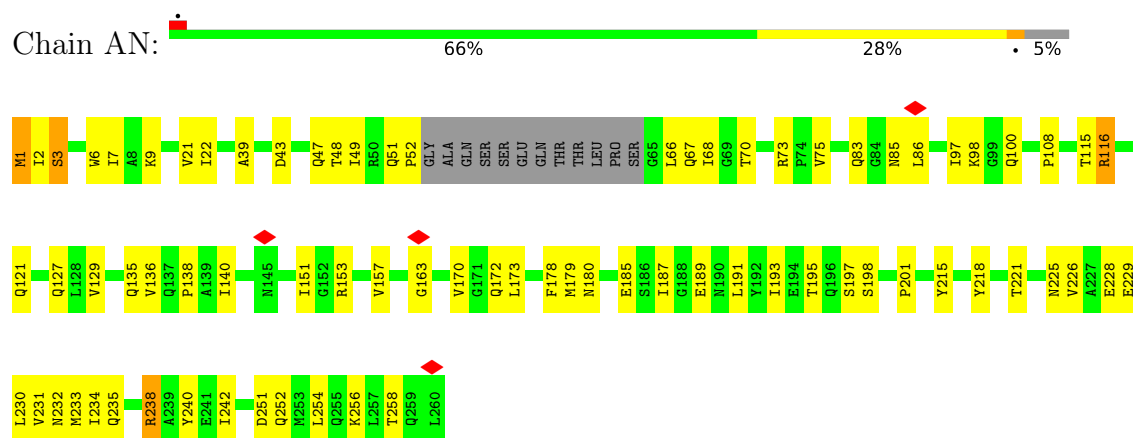


• Molecule 3: Flagellar basal-body rod protein FlgG

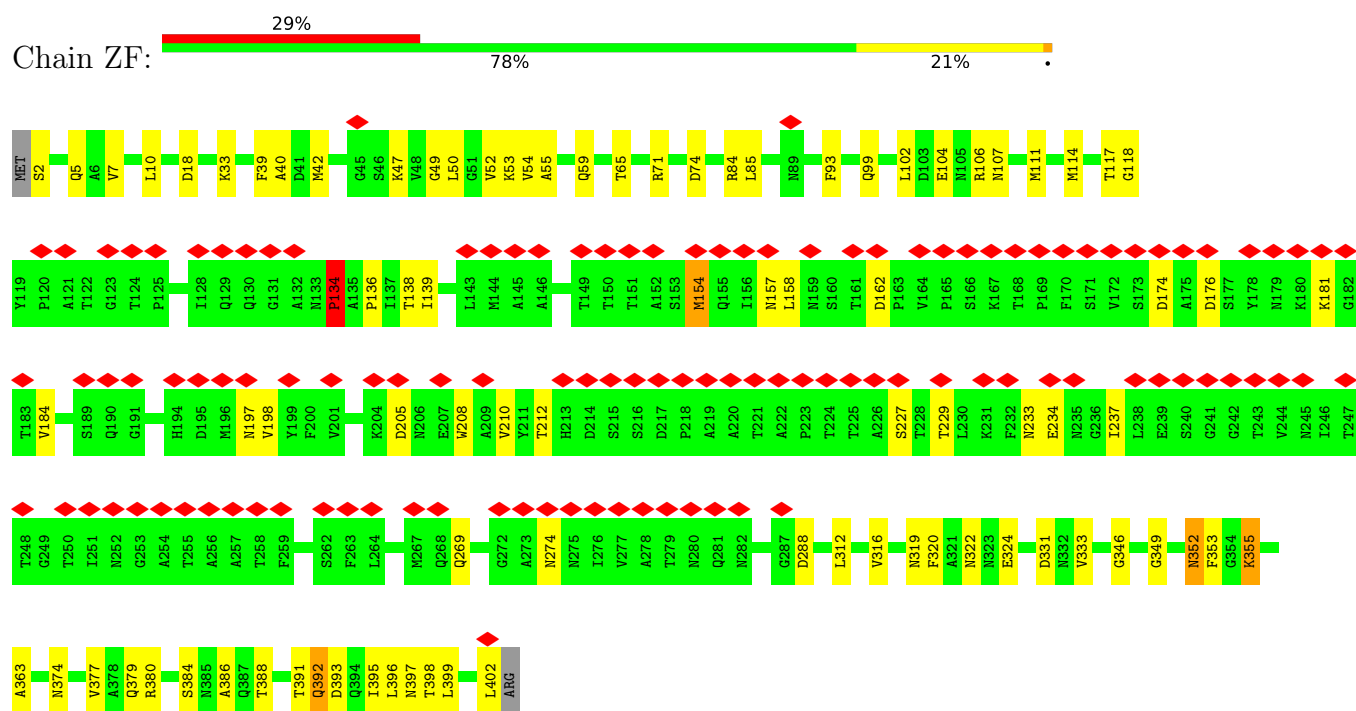
Chain AM: 58% 35% 5%



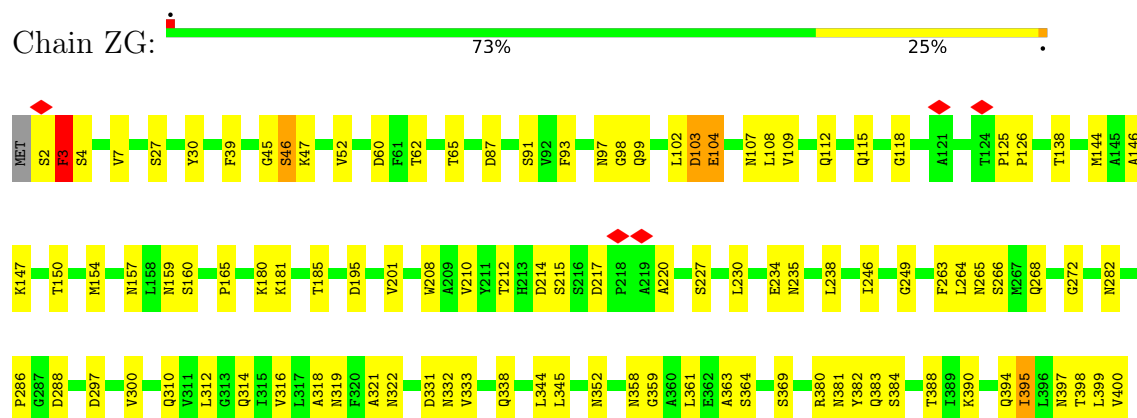
• Molecule 3: Flagellar basal-body rod protein FlgG



• Molecule 4: Flagellar hook protein FlgE



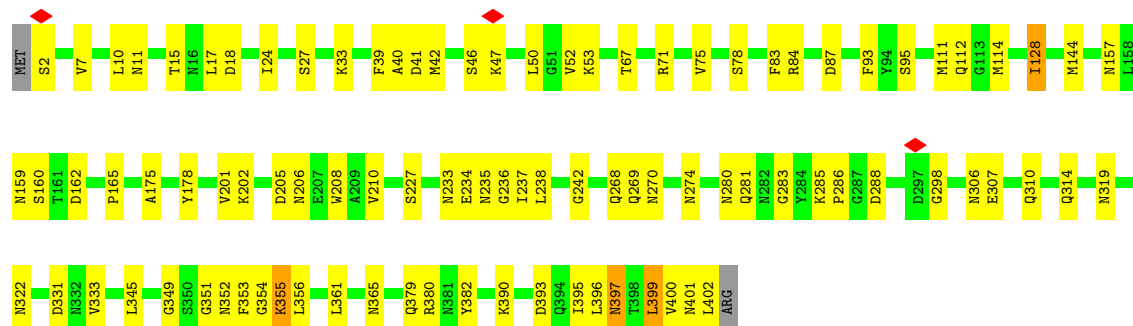
• Molecule 4: Flagellar hook protein FlgE





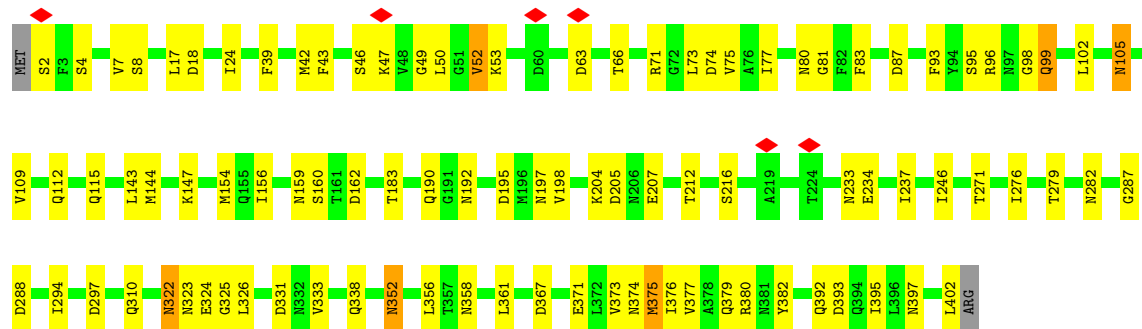
• Molecule 4: Flagellar hook protein FlgE

Chain ZH: 76% 23%



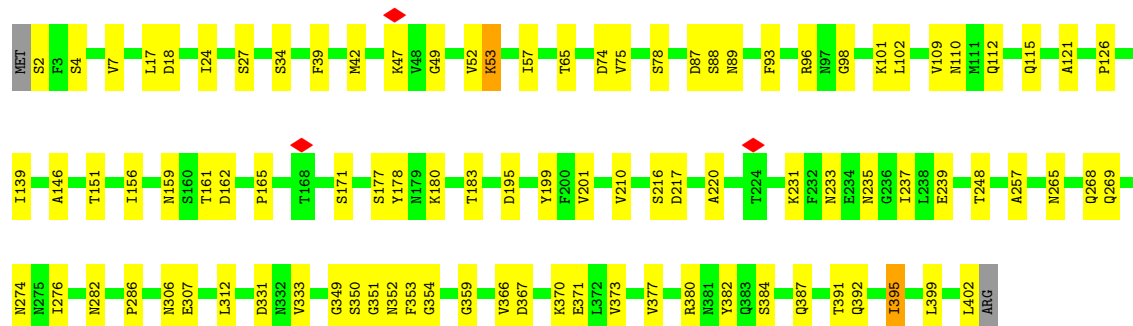
• Molecule 4: Flagellar hook protein FlgE

Chain ZI: 76% 22%



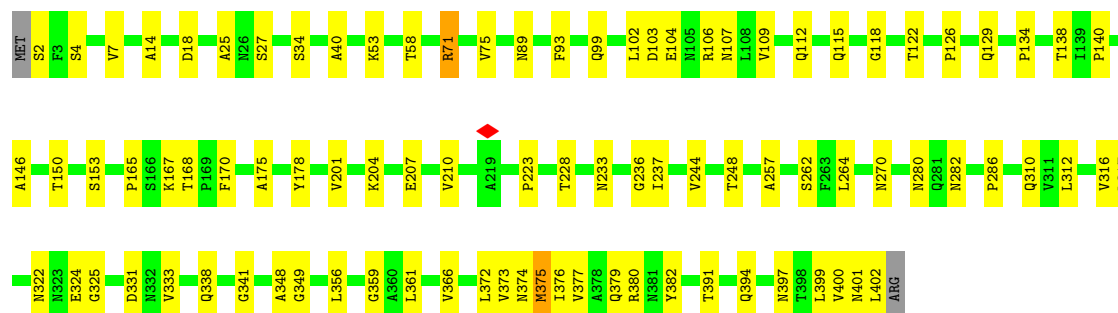
• Molecule 4: Flagellar hook protein FlgE

Chain ZJ: 76% 23%



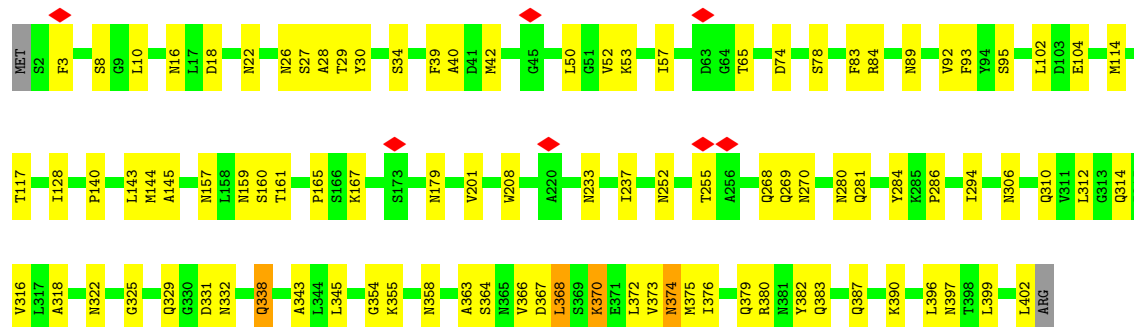
• Molecule 4: Flagellar hook protein FlgE

Chain ZK: 77% 22%



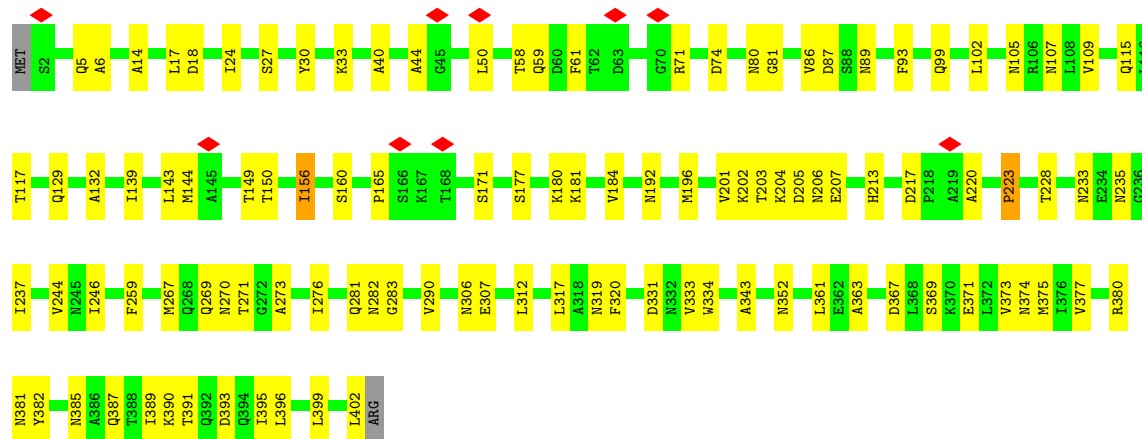
• Molecule 4: Flagellar hook protein FlgE

Chain ZL:  76% 23% .



• Molecule 4: Flagellar hook protein FlgE

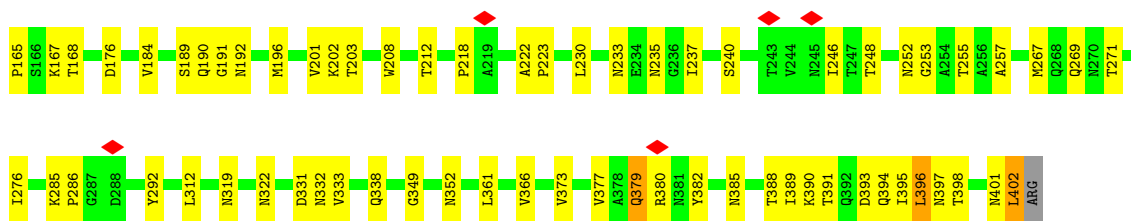
Chain ZM:  73% 26% .



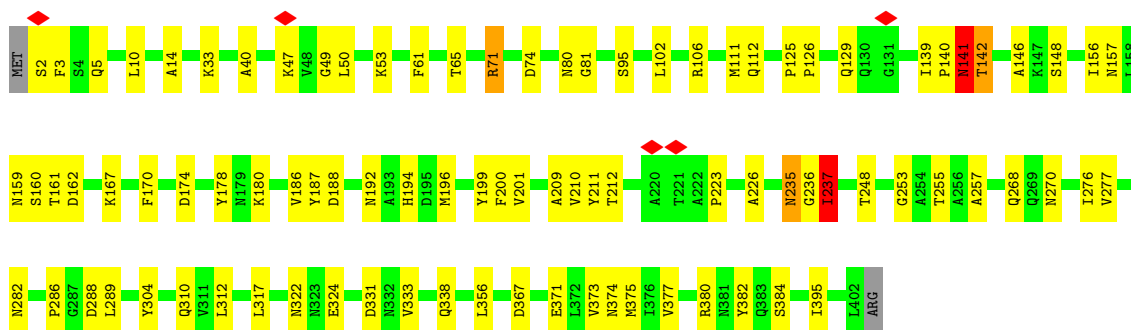
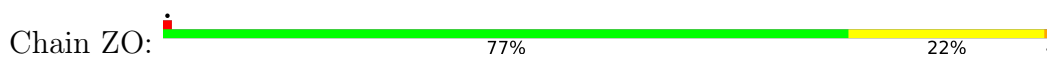
• Molecule 4: Flagellar hook protein FlgE

Chain ZN:  76% 23% .

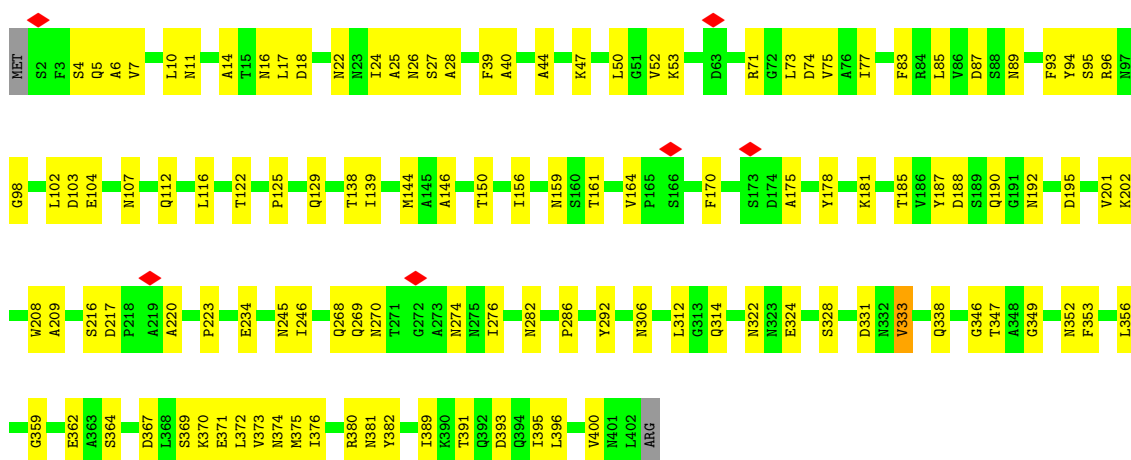




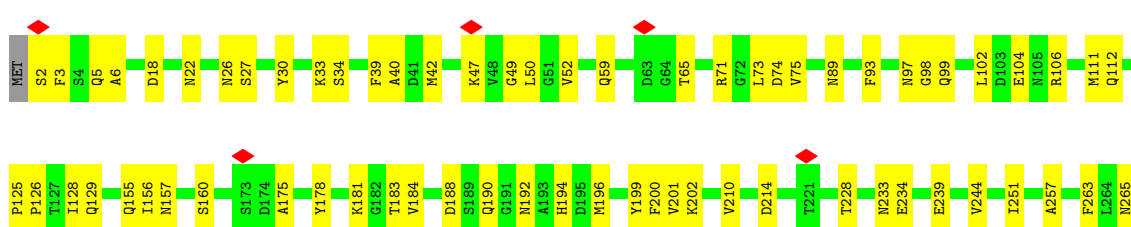
• Molecule 4: Flagellar hook protein FlgE

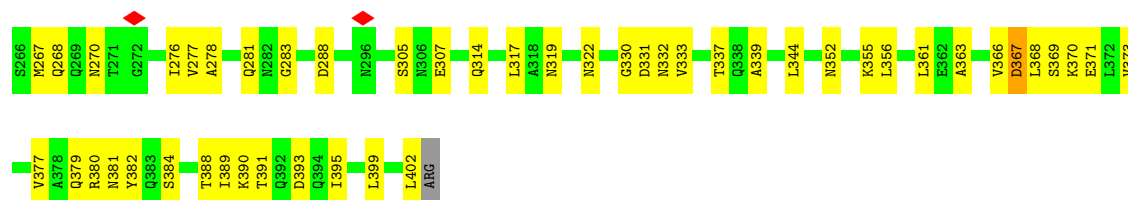


• Molecule 4: Flagellar hook protein FlgE

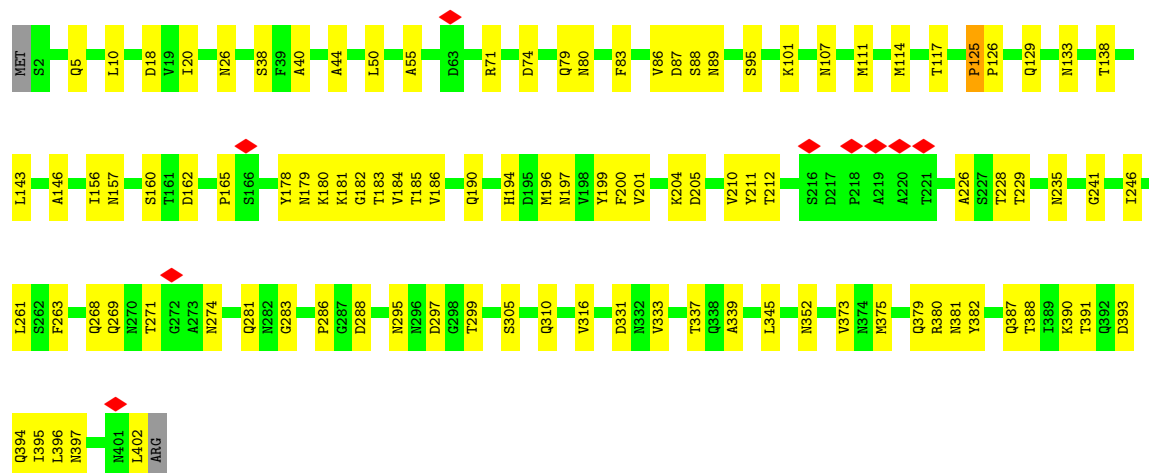
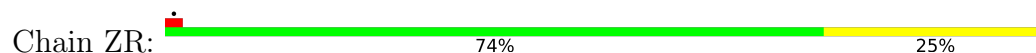


• Molecule 4: Flagellar hook protein FlgE

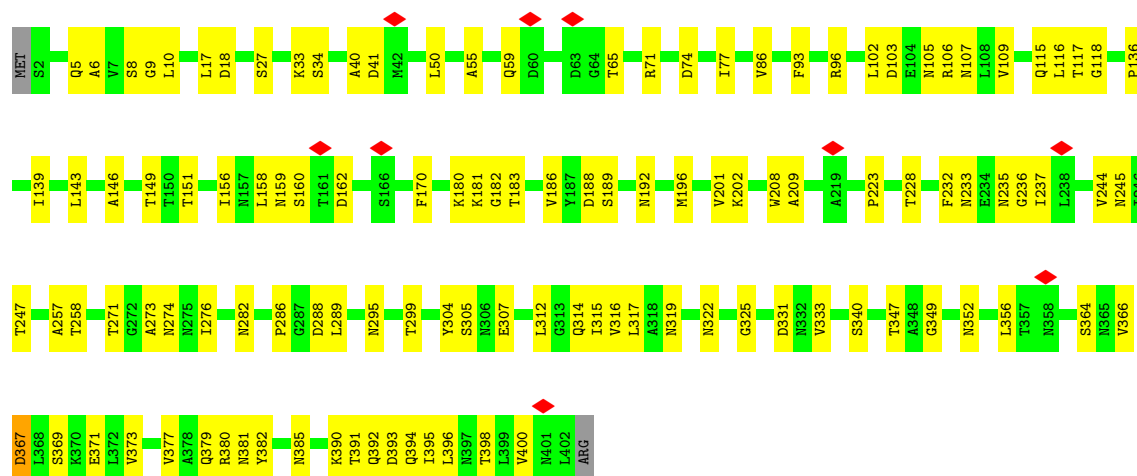




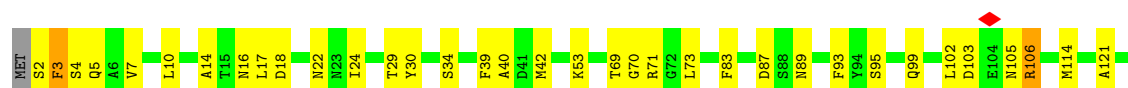
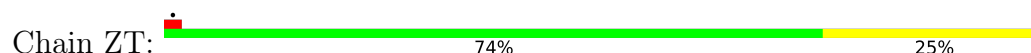
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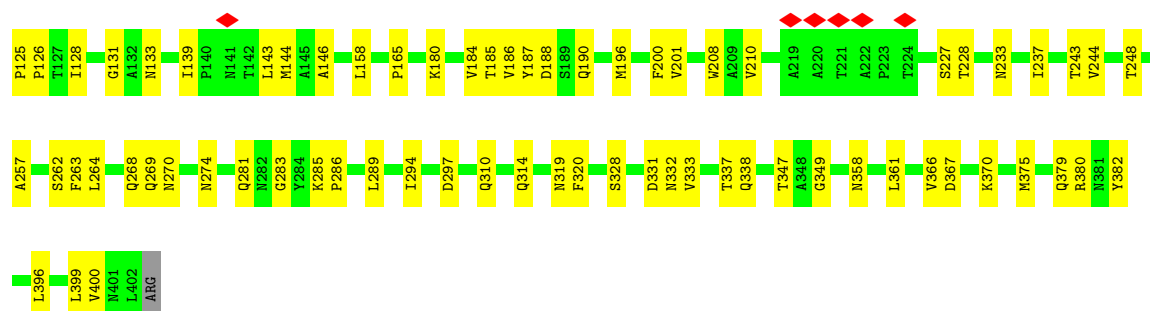


• Molecule 4: Flagellar hook protein FlgE

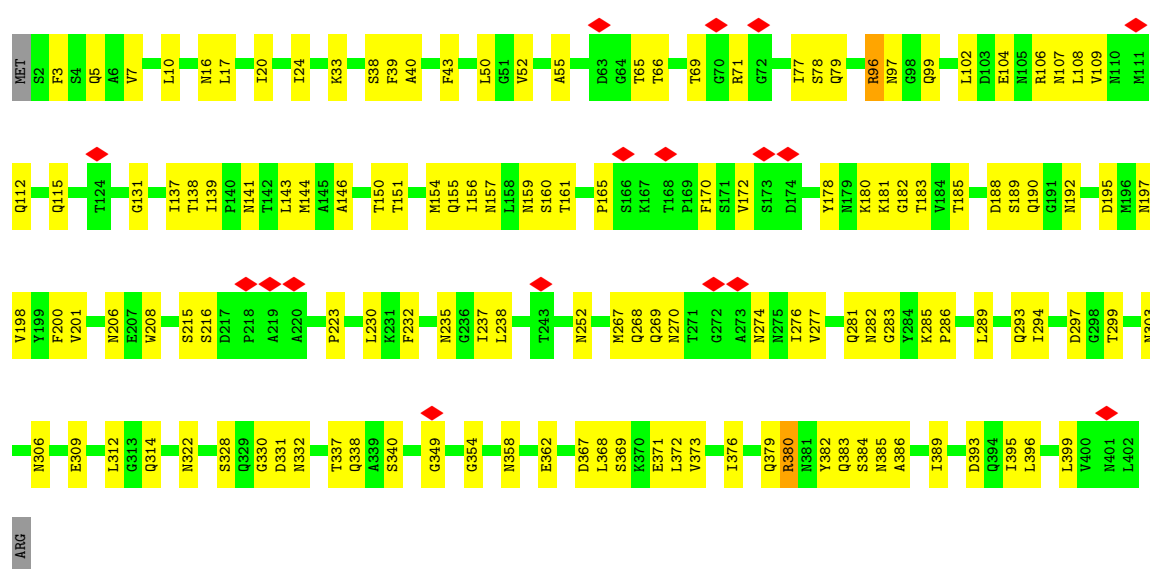


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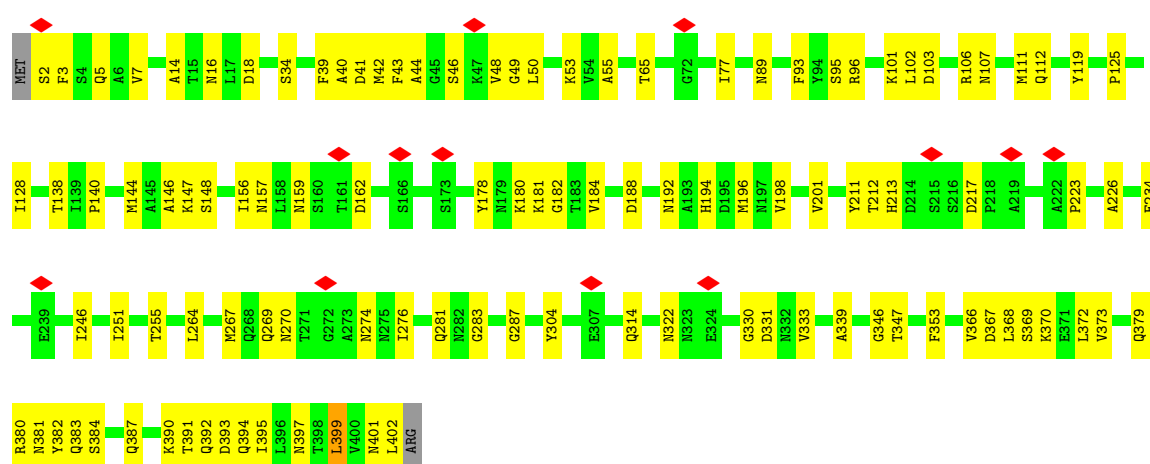
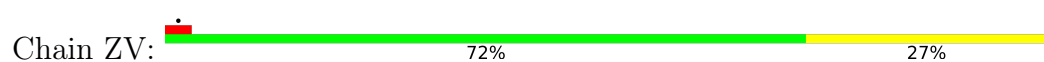




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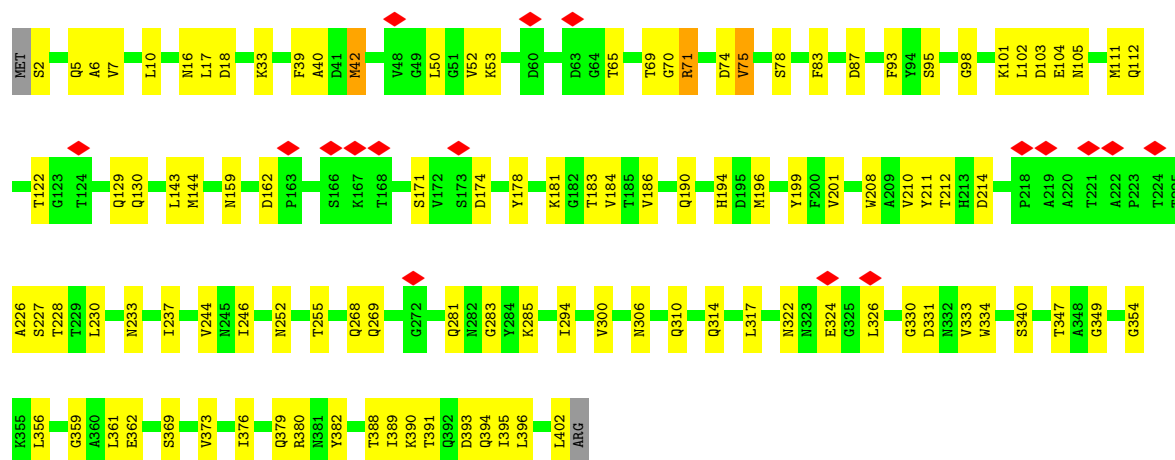


• Molecule 4: Flagellar hook protein FlgE



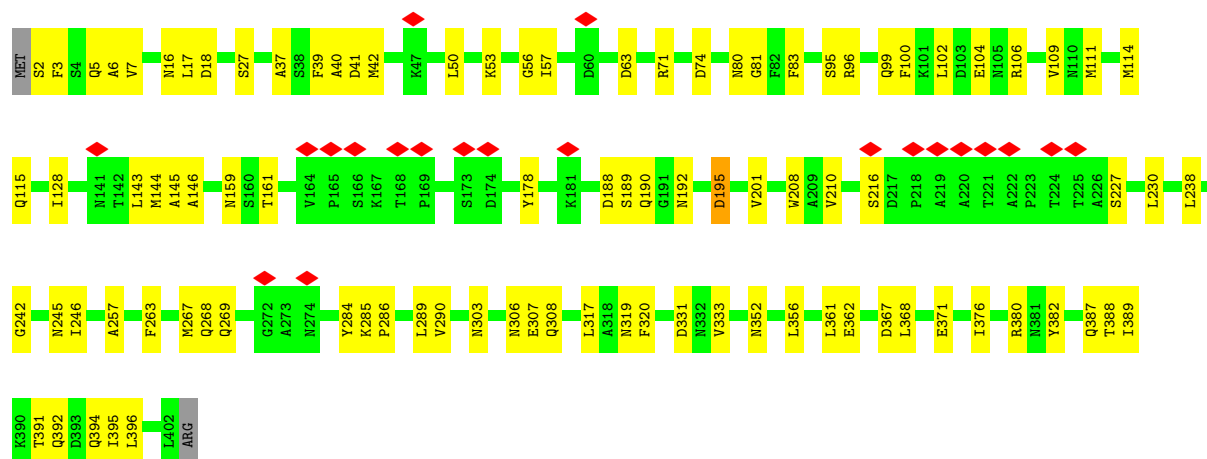
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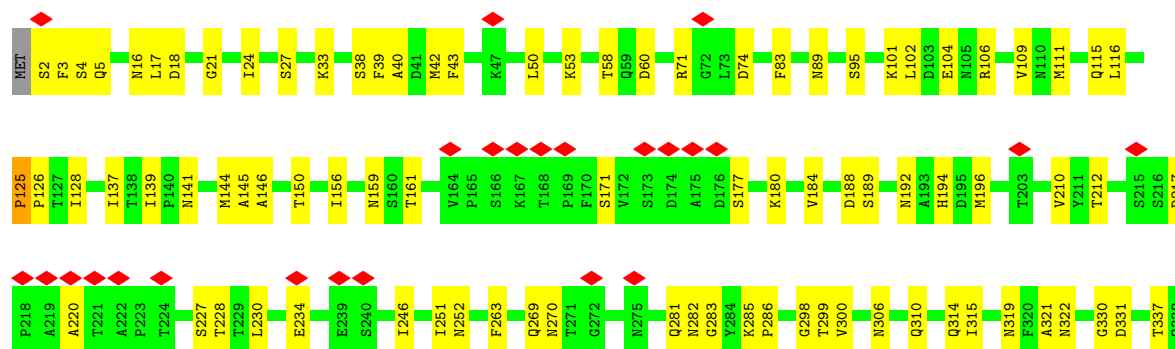
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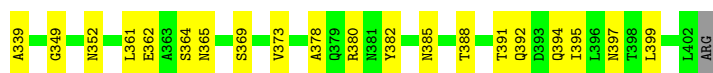
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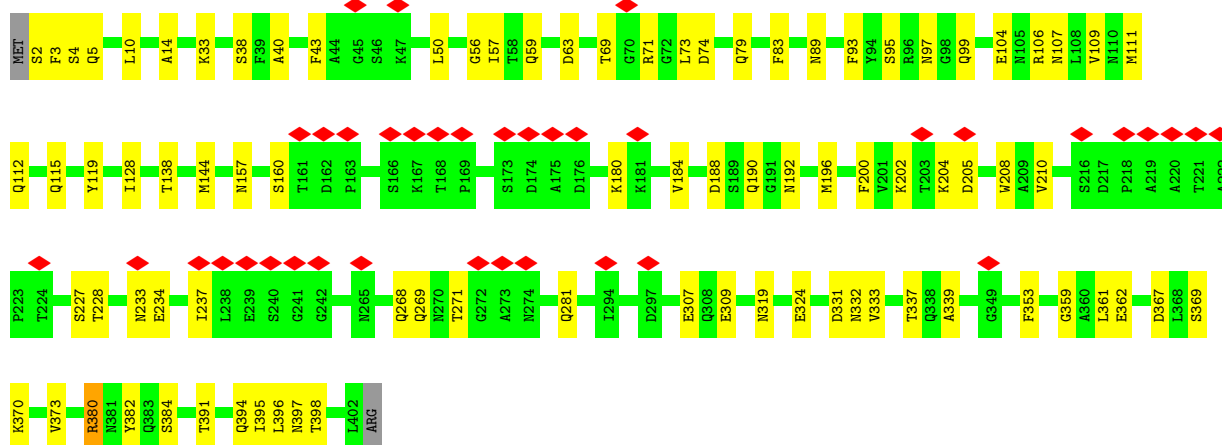
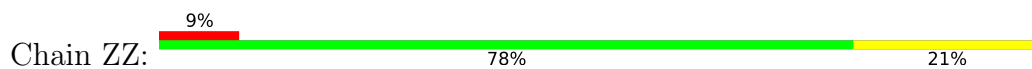
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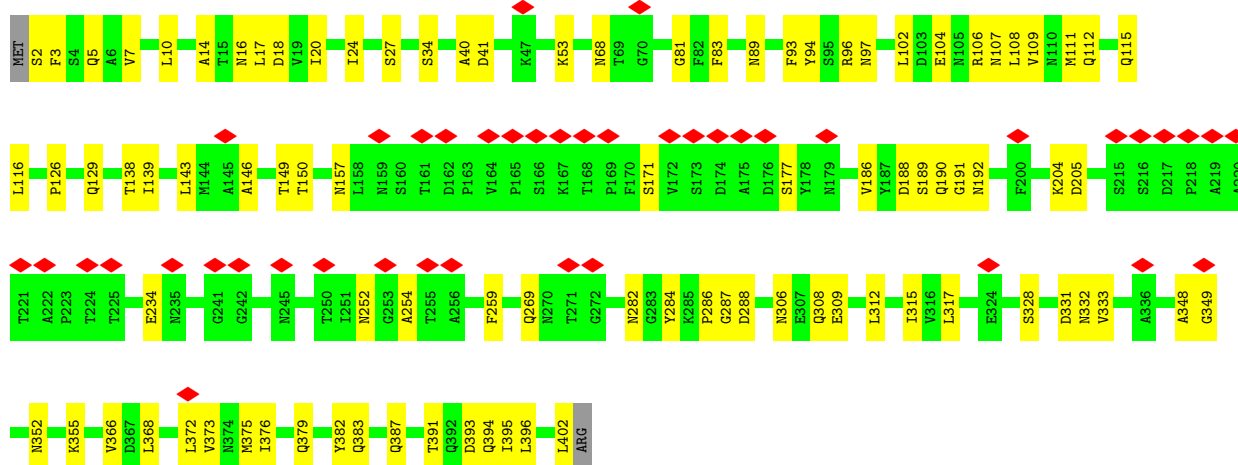
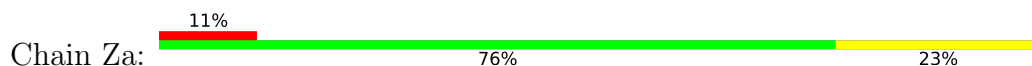




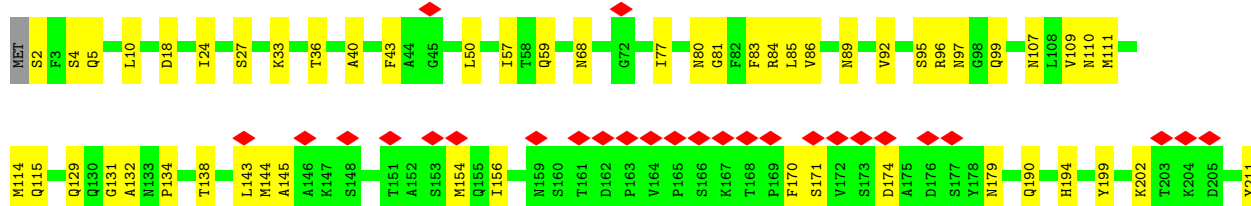
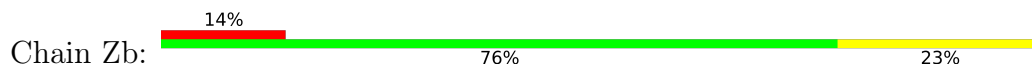
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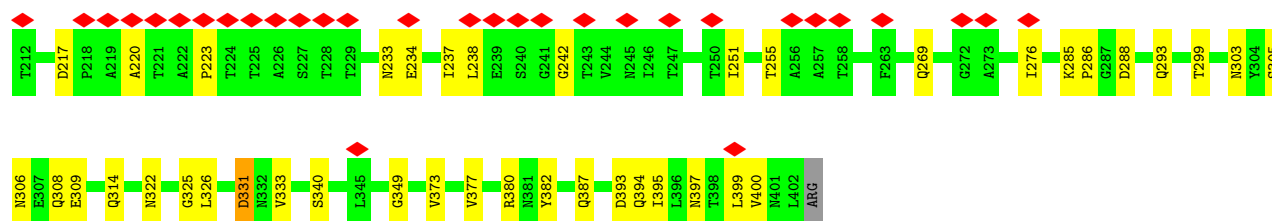


• Molecule 4: Flagellar hook protein FlgE

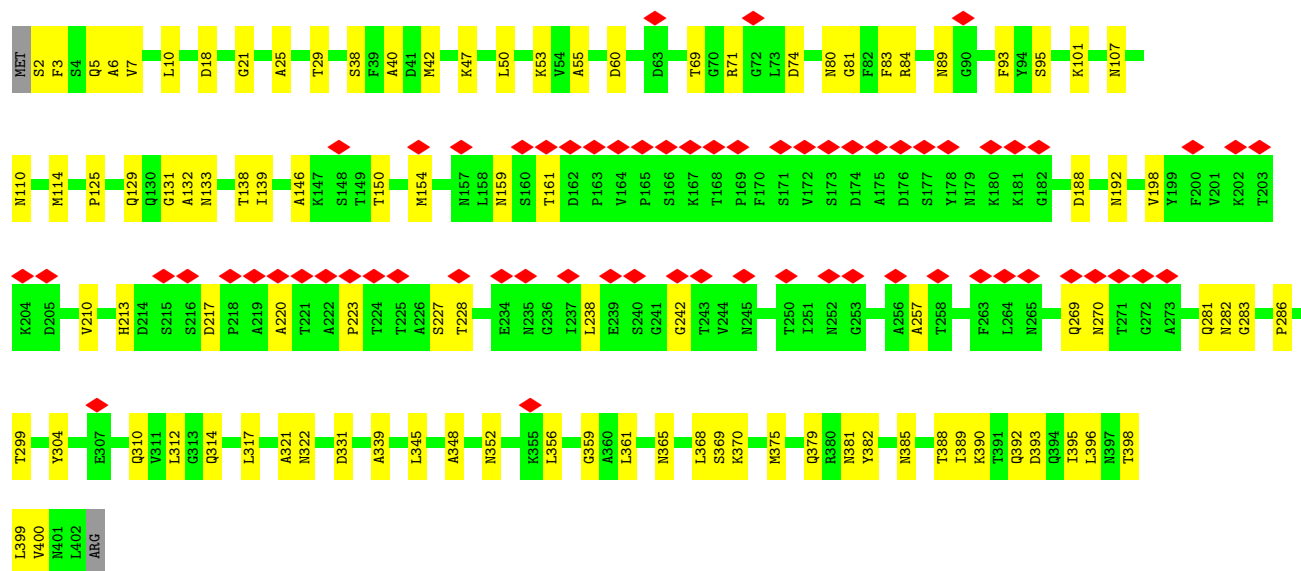
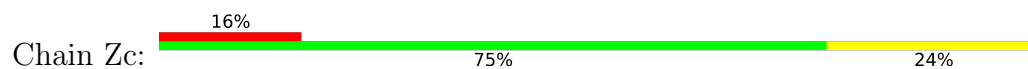


• Molecule 4: Flagellar hook protein FlgE

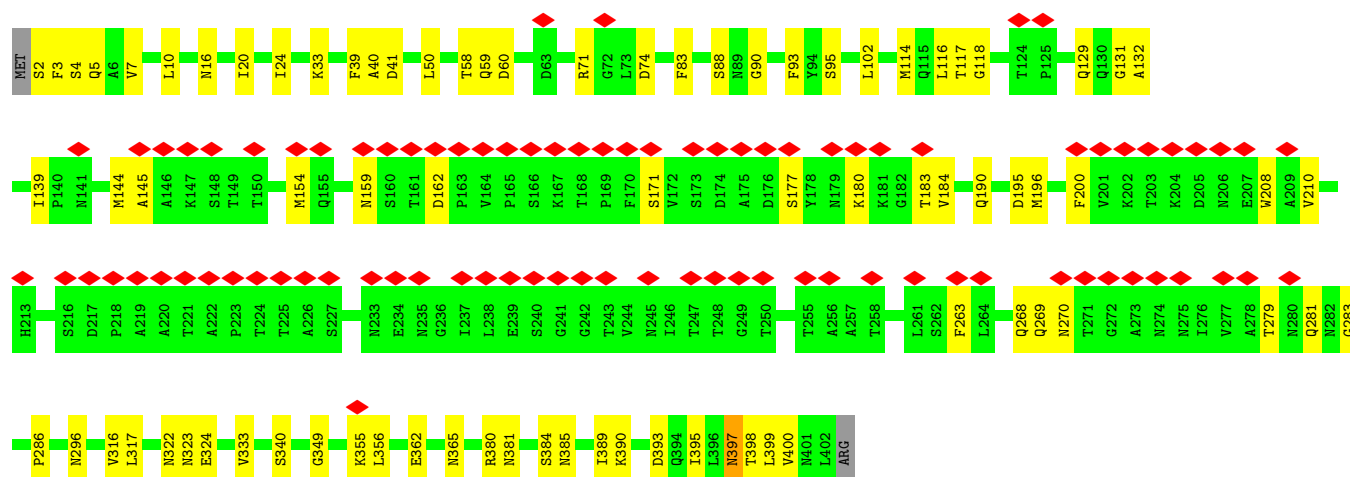
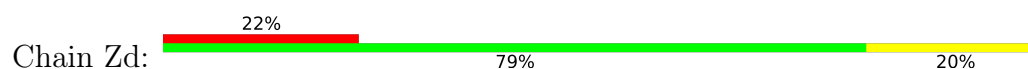




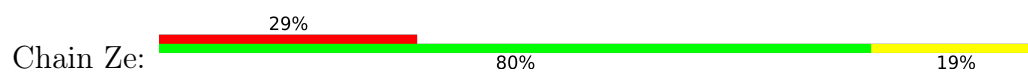
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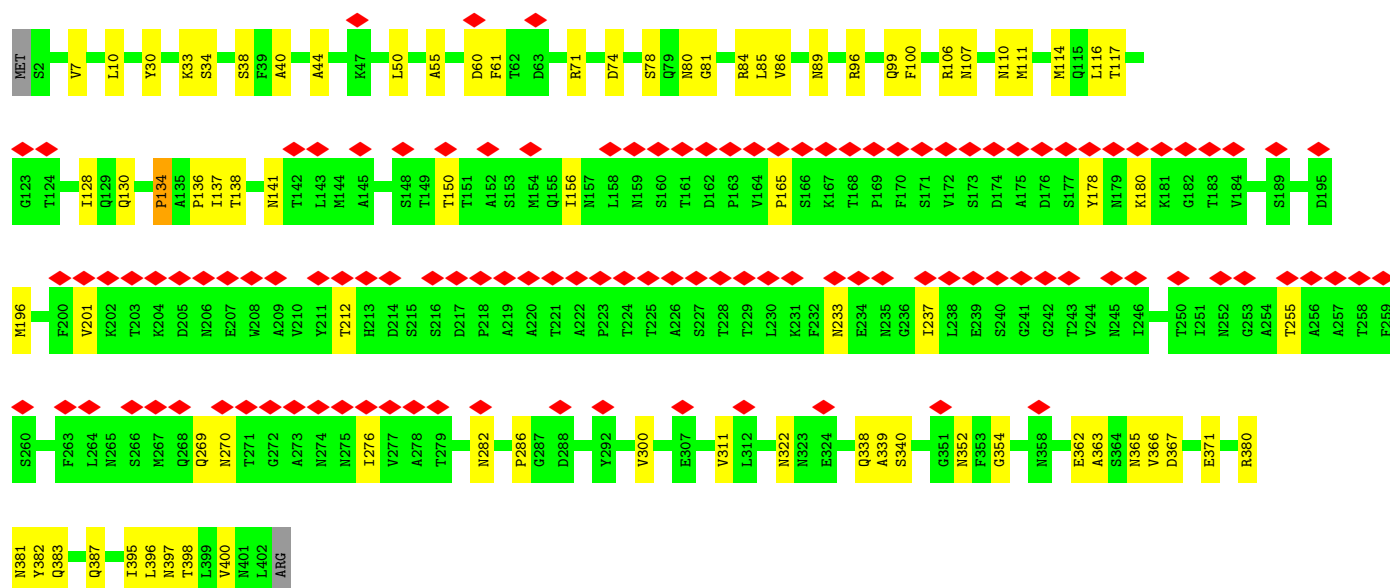


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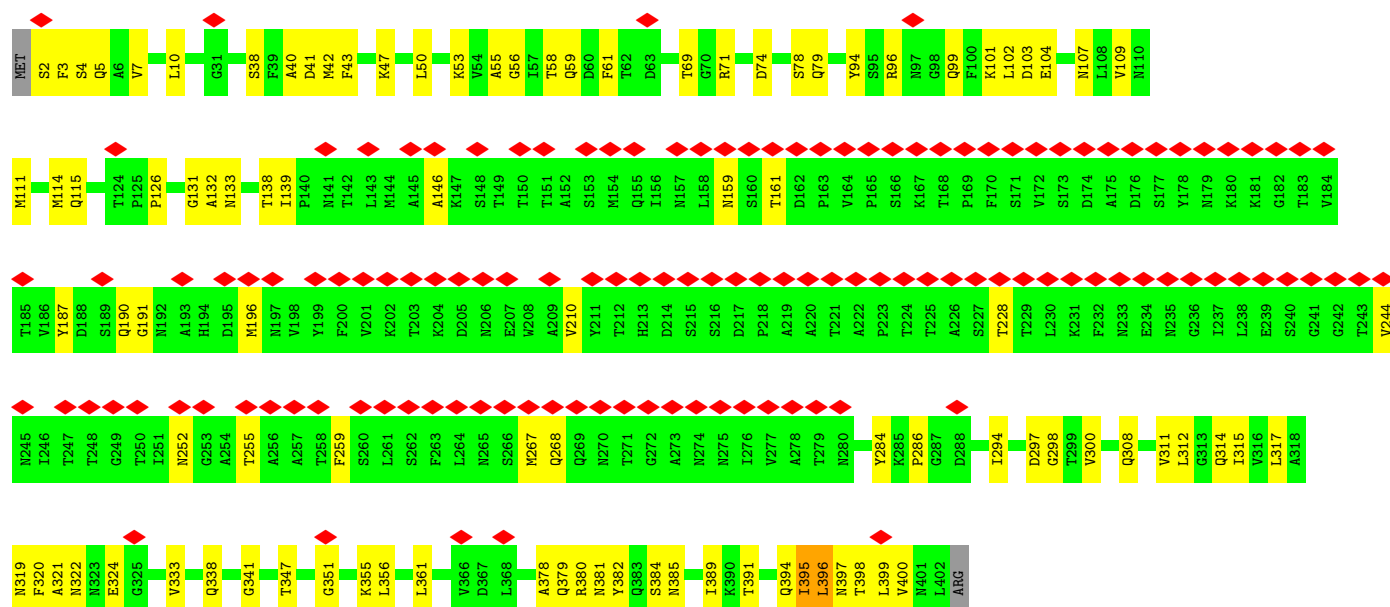
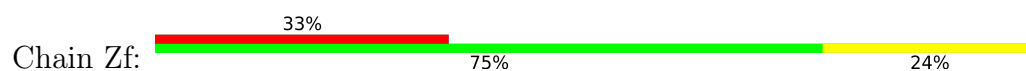


• Molecule 4: Flagellar hook protein FlgE

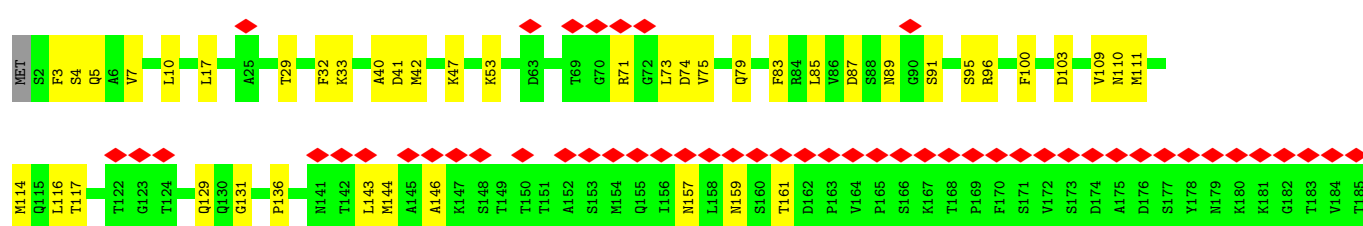
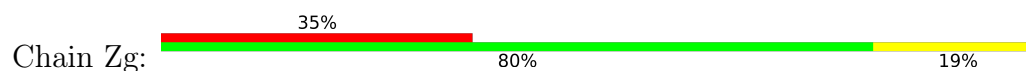


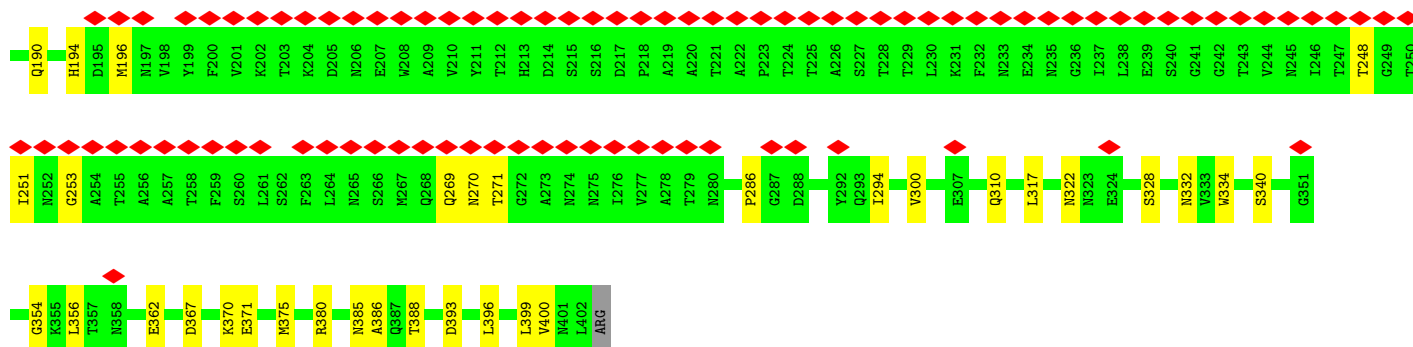


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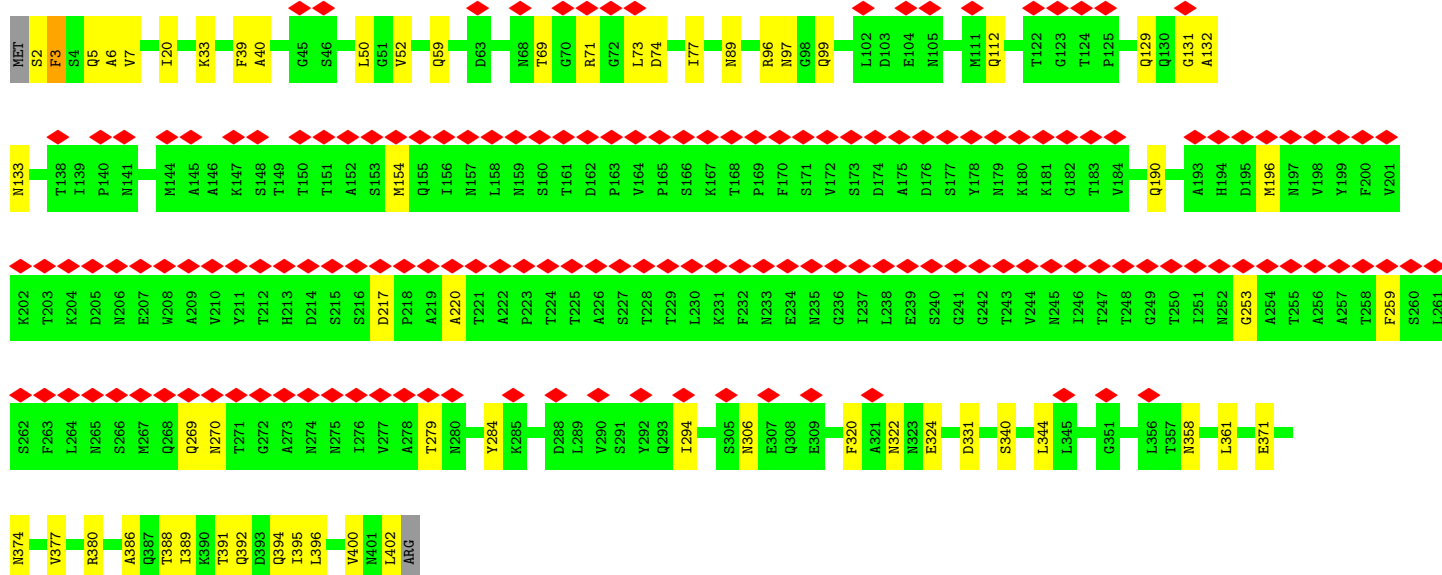
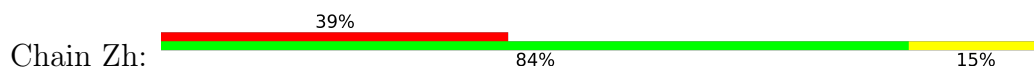


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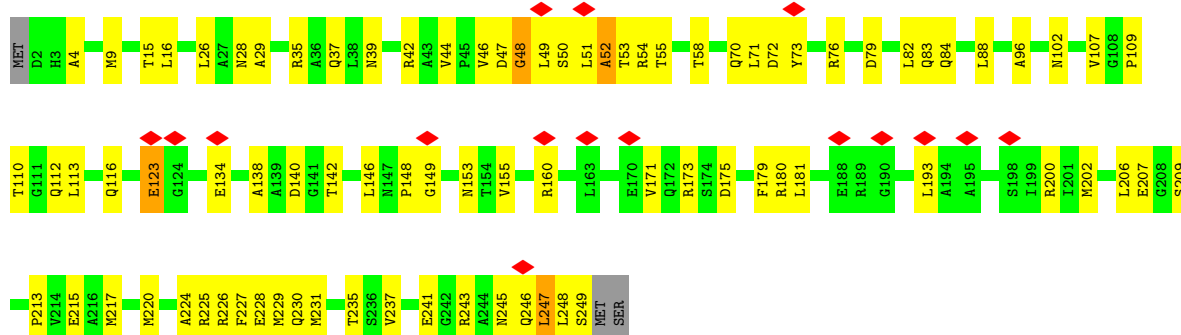




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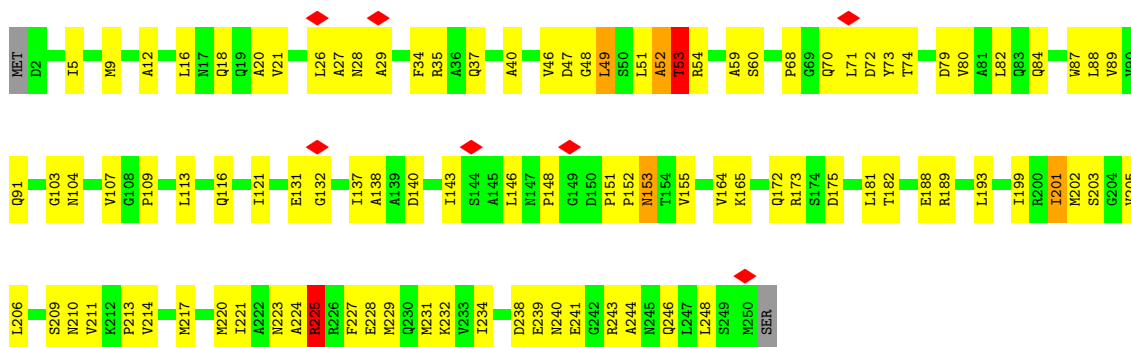


• Molecule 5: Flagellar basal-body rod protein FlgF

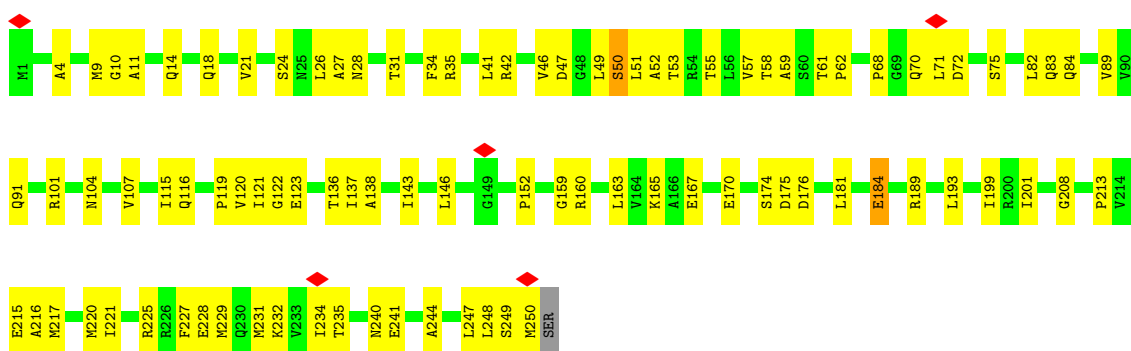


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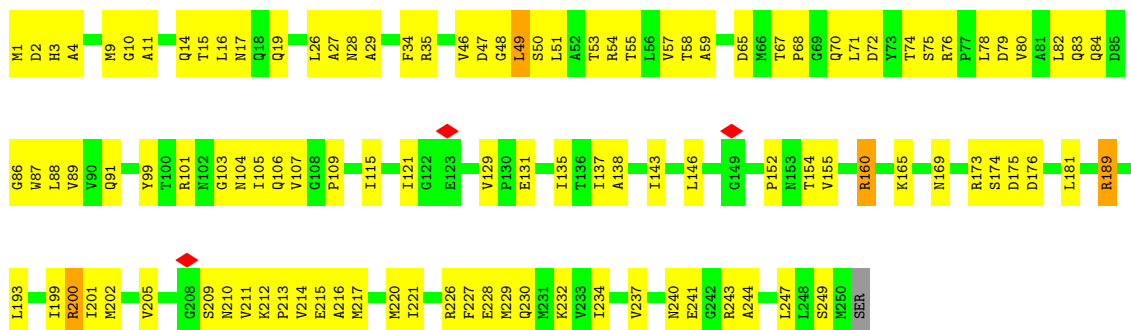




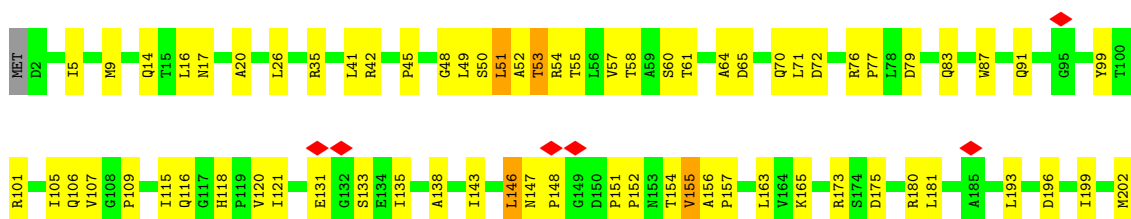
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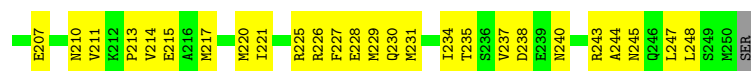


• Molecule 5: Flagellar basal-body rod protein FlgF

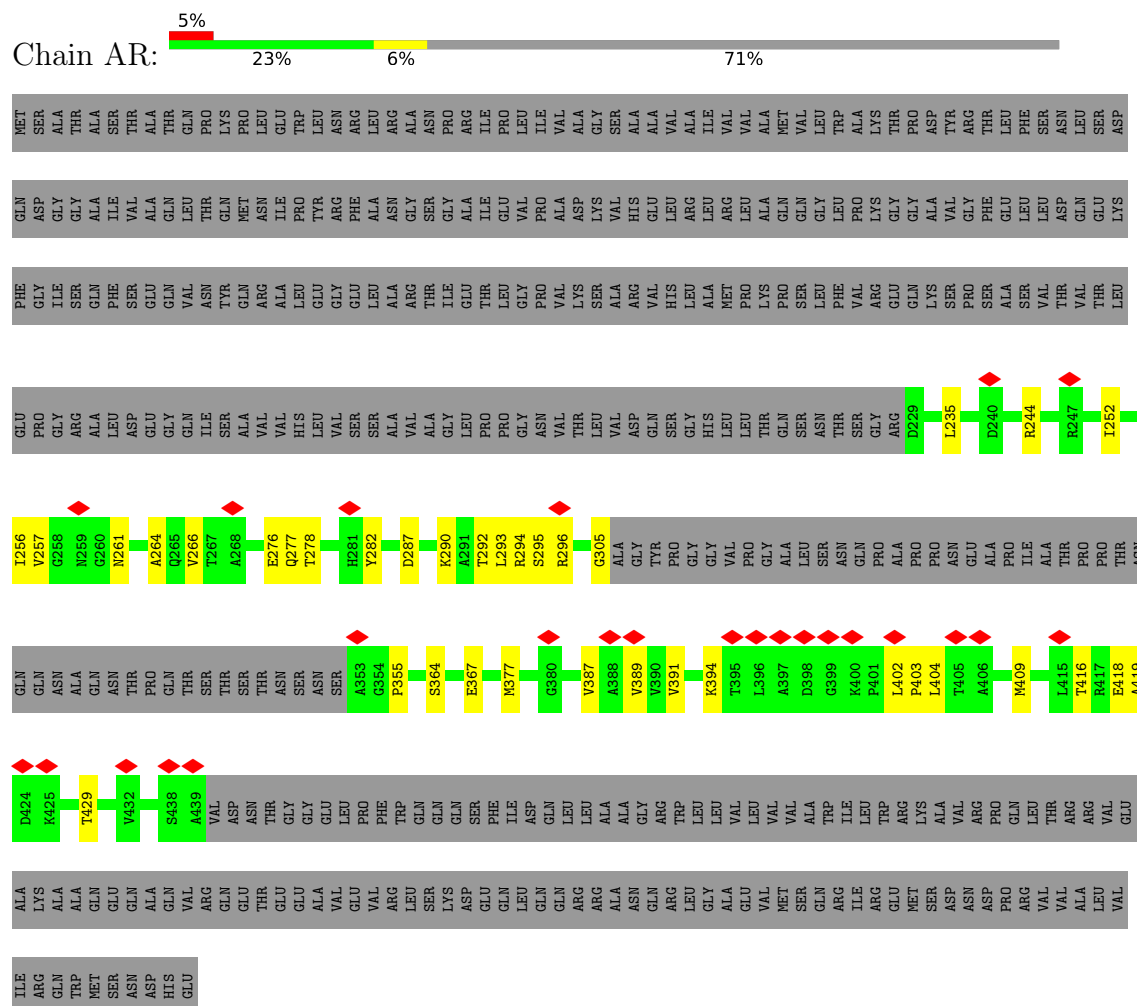


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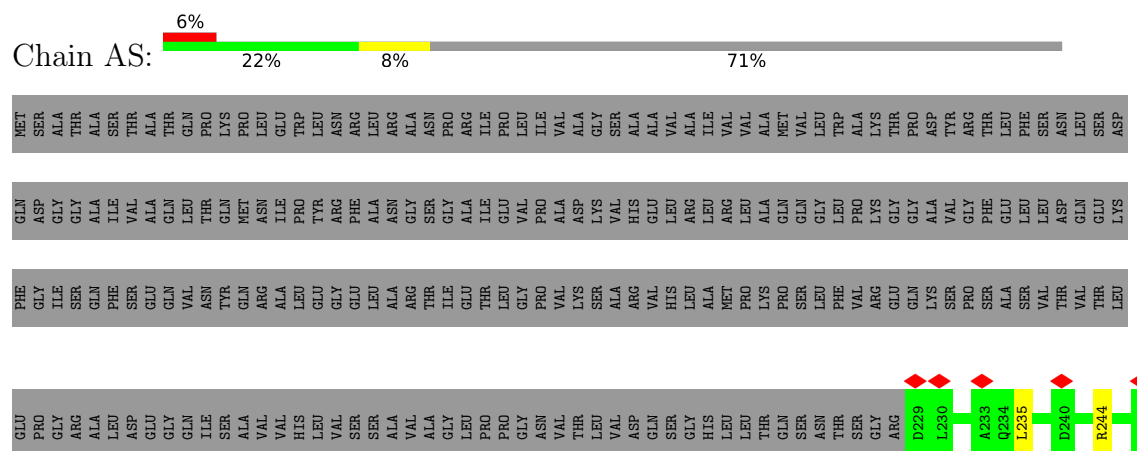




• Molecule 6: Flagellar M-ring protein

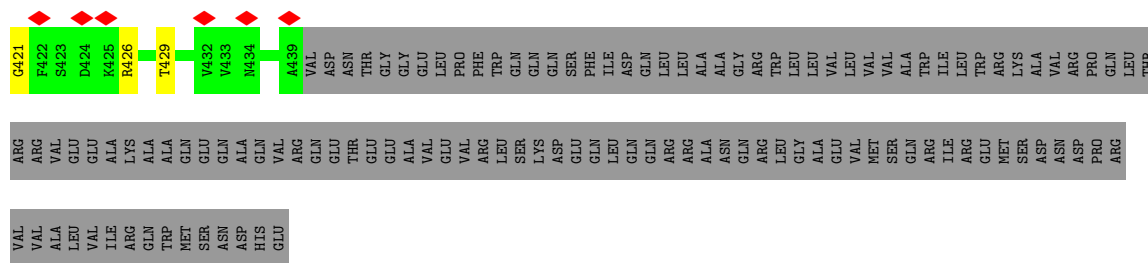


• Molecule 6: Flagellar M-ring protein

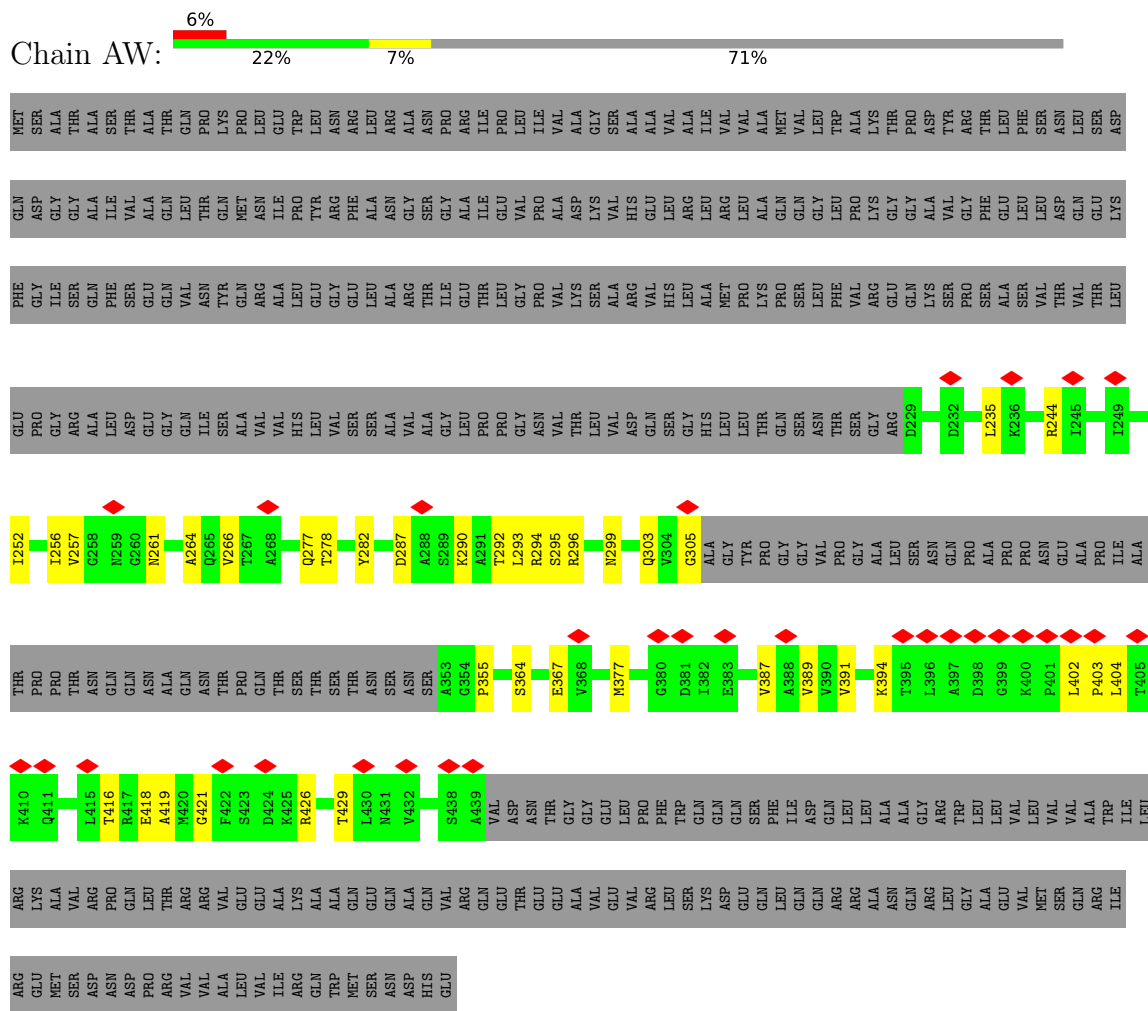




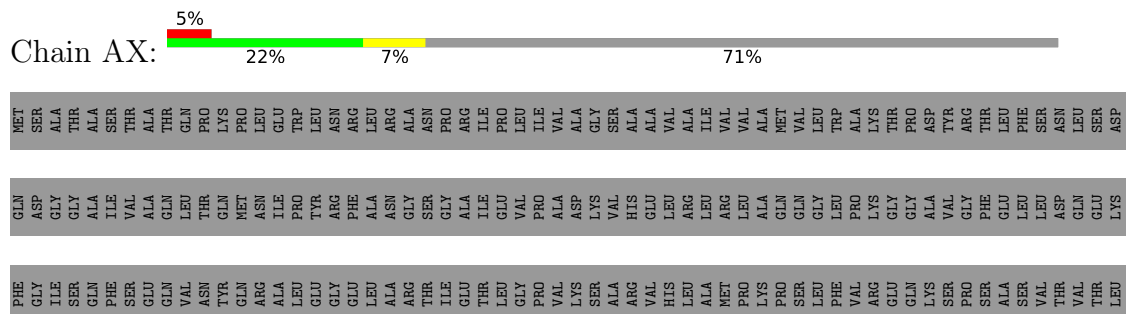




• Molecule 6: Flagellar M-ring protein



• Molecule 6: Flagellar M-ring protein







[illegible]

- Molecule 6: Flagellar M-ring protein



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

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GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLN	ILE	SER	VAL	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	GLY	LEU	PRO	PRO	GLY	ASN	VAL	THR	LEU	VAL	ASP	GLN	SER	GLY	HIS	LEU	THR	SER	GLY	ARG	D229	L235	D240	V241	E242	S243	R244	I252
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T429
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ALA GLN GLU GLN ALA VAL GLN THR LEU GLU ALA VAL GLU ARG LEU SER LYS ASP GLU GLN LEU GLN GLN ARG ARG ALA ASN GLN ARG ARG LEU GLY GLU VAL MET SER SER GLN ARG ILE ARG ARG MET GLU LEU LEU ALA GLU VAL ASP ASN PRO PRO ARG ARG VAL VAL ALA LEU ILE ILE ARG ALA

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- Molecule 6: Flagellar M-ring protein

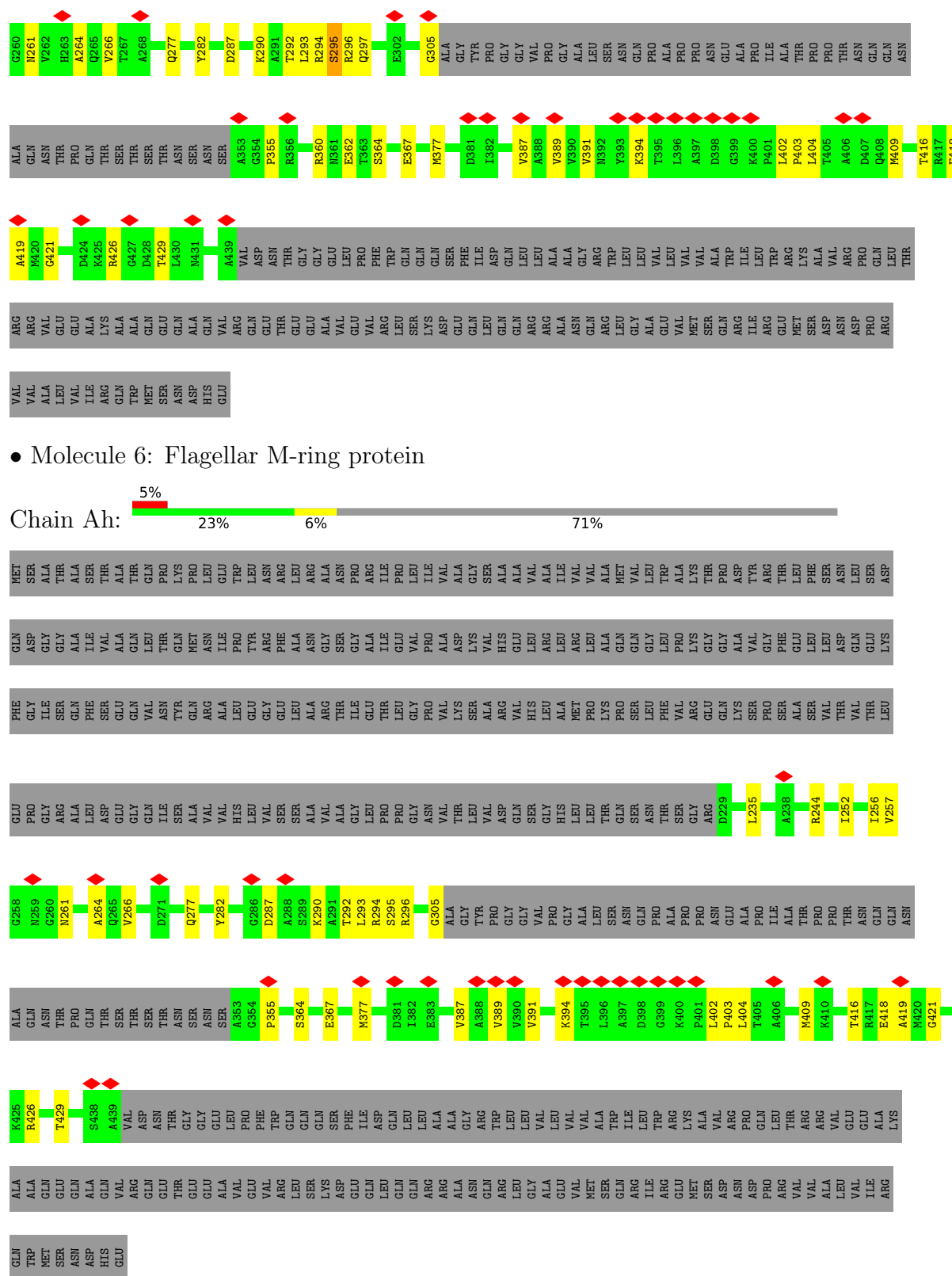


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GLN ASP GLY GLY GLY ALA ALA ILE VAL VAL LEU LEU THR THR GLN MET MET ASN ASN ILE ILE PRO PRO ARG ARG PHE PHE ALA ALA GLY GLY SER SER GLY GLY ALA ALA ILE ILE GLU GLU VAL VAL PRO PRO ASP ASP LYS LYS VAL VAL HIS HIS GLU GLU LEU LEU LEU LEU ALA ALA GLN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

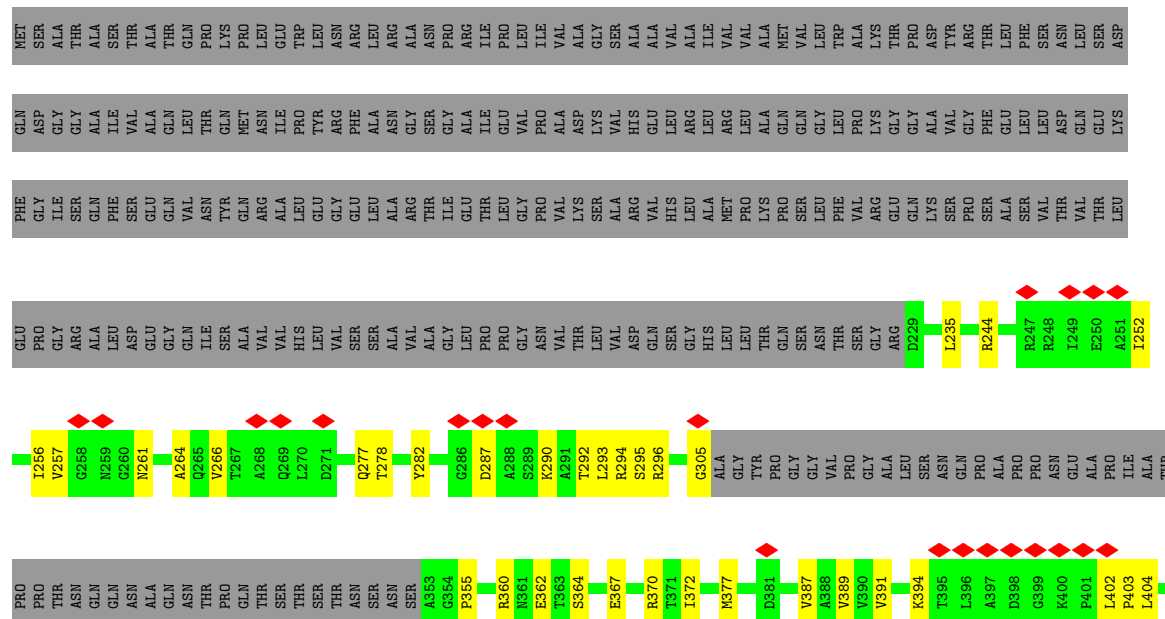
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GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	ALA	ALA	GLY	LEU	PRO	PRO	GLY	ASN	VAL	THR	LEU	VAL	VAL	ASP	GLN	SER	GLY	HIS	LEU	LEU	THR	THR	GLN	SER	ASN	THR	SER	GLY	ARG	D229	L235	R244	I252	I256	V257	G258
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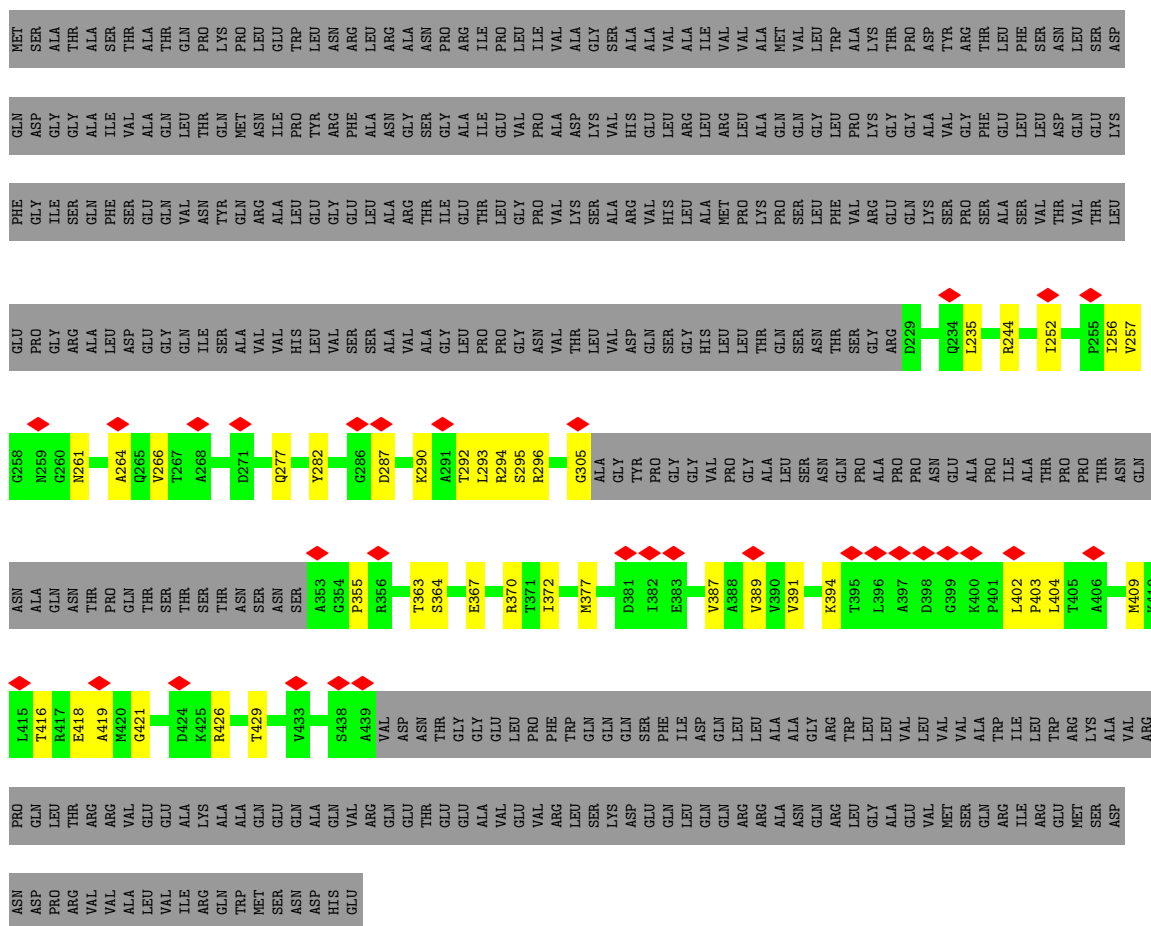


• Molecule 6: Flagellar M-ring protein

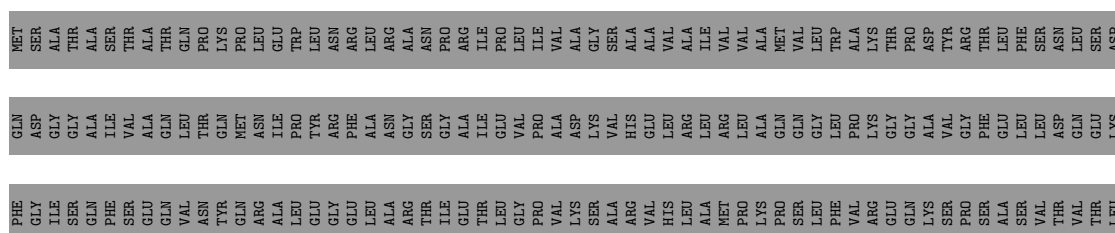




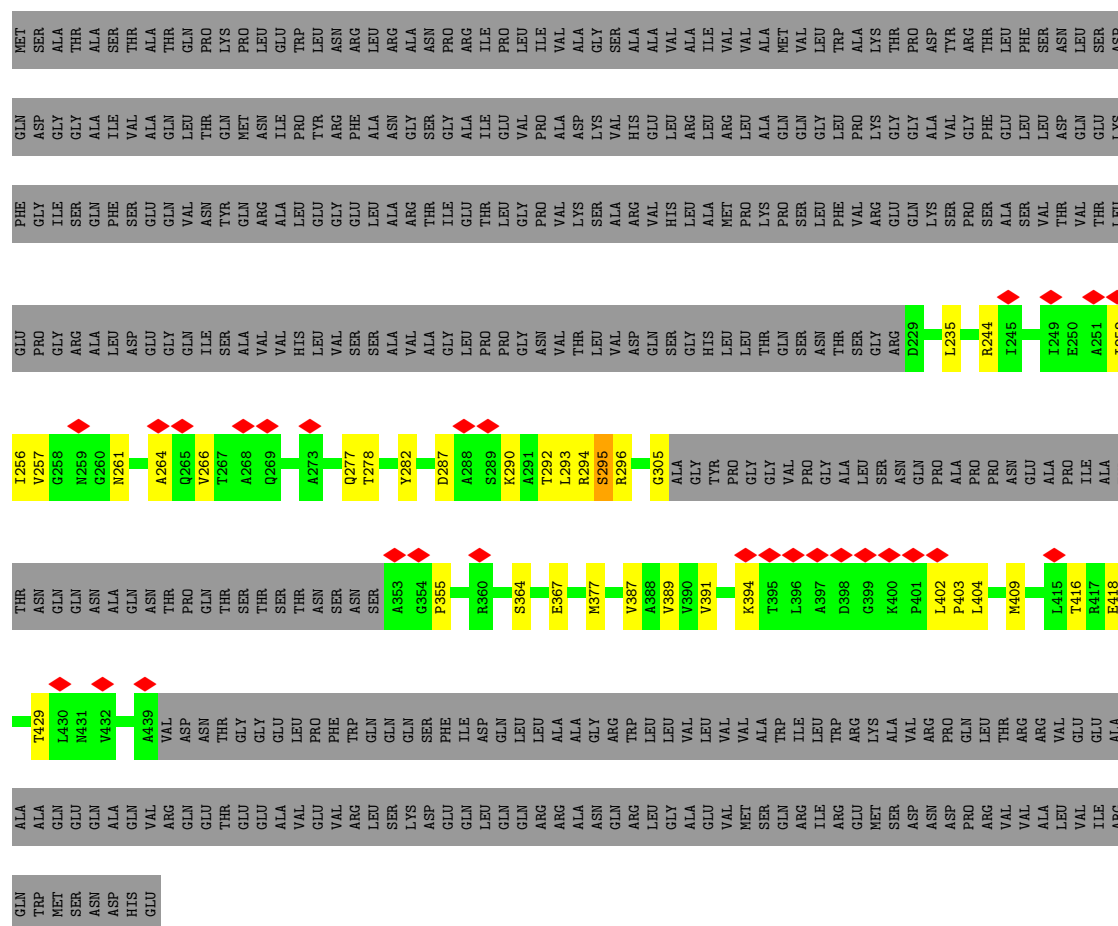
- Molecule 6: Flagellar M-ring protein

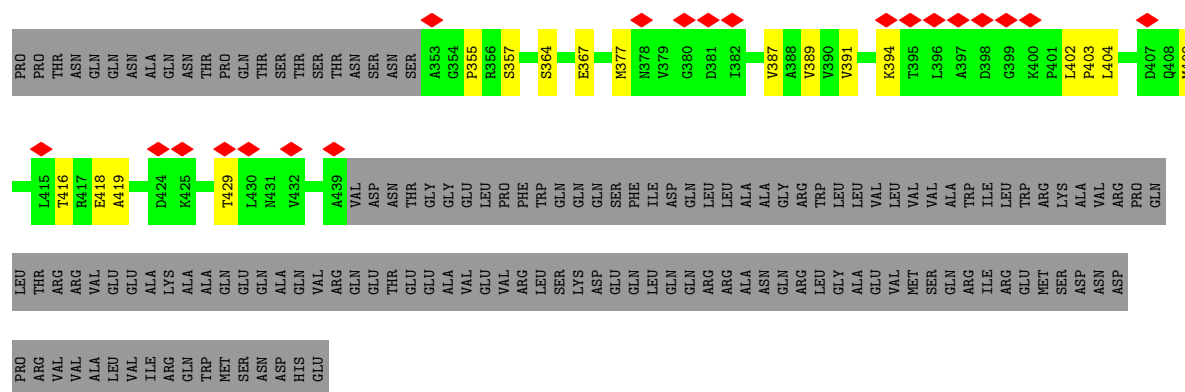


- Molecule 6: Flagellar M-ring protein

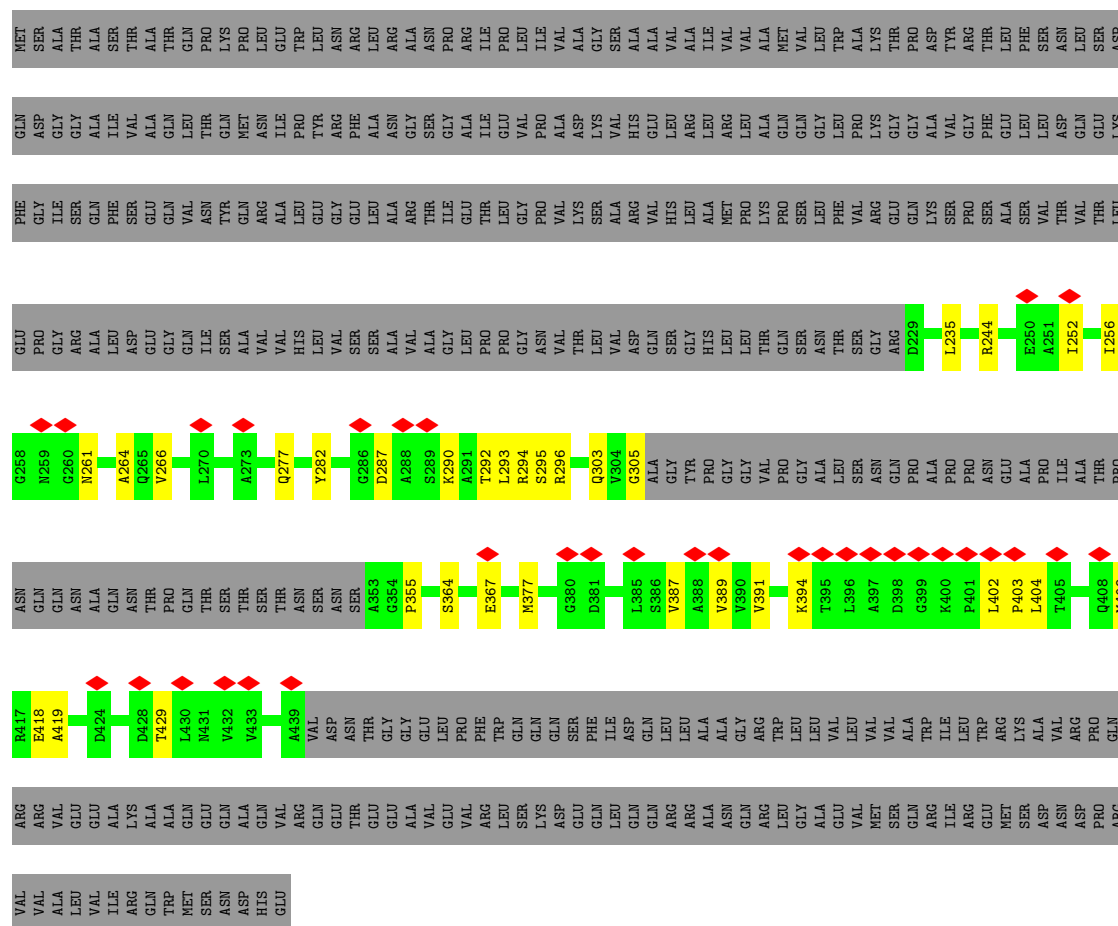


- Molecule 6: Flagellar M-ring protein

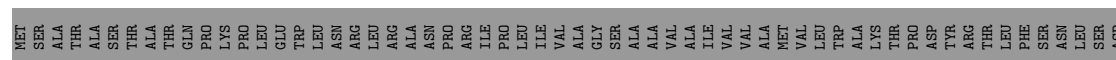


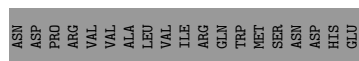


- Molecule 6: Flagellar M-ring protein

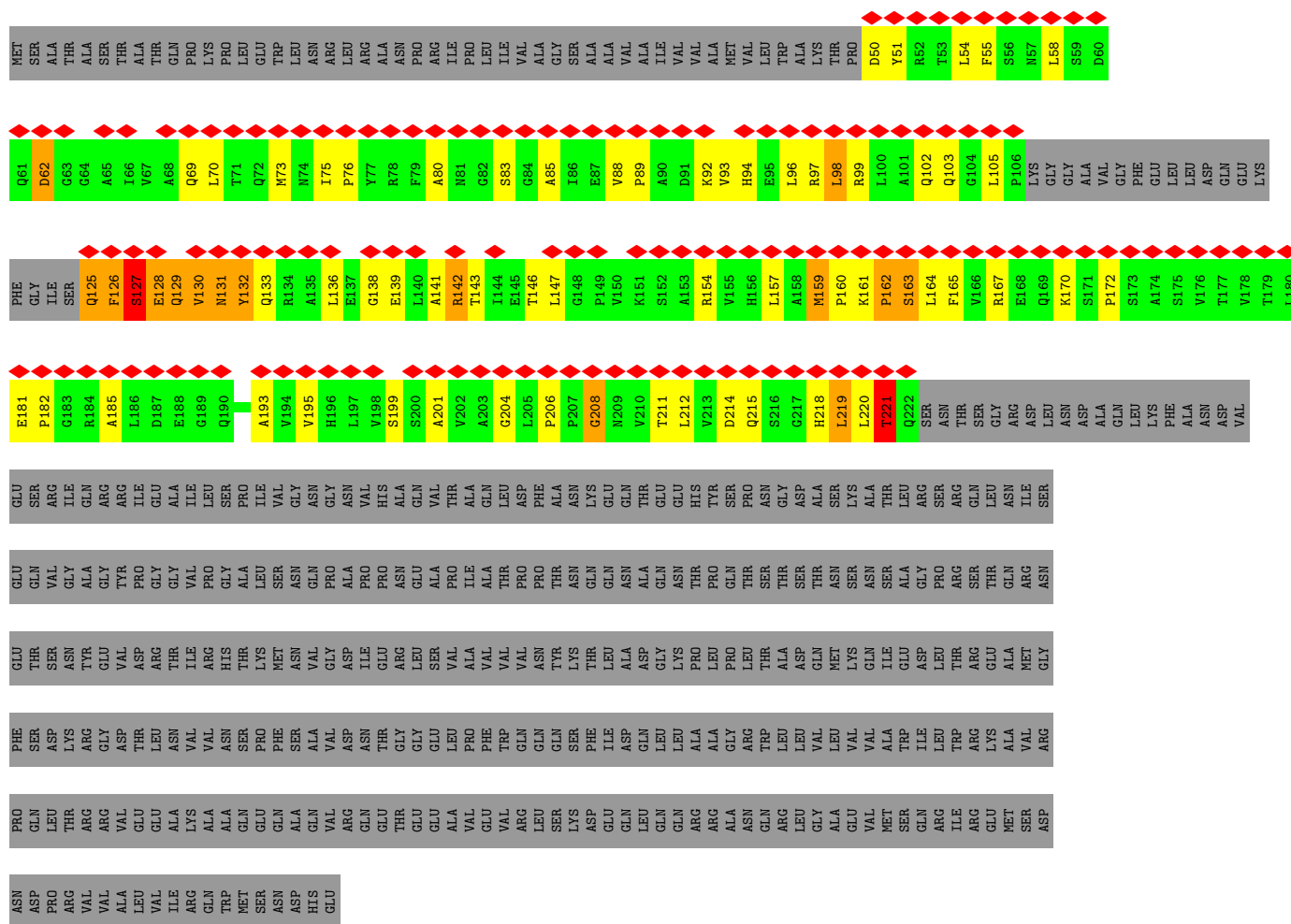


- Molecule 6: Flagellar M-ring protein

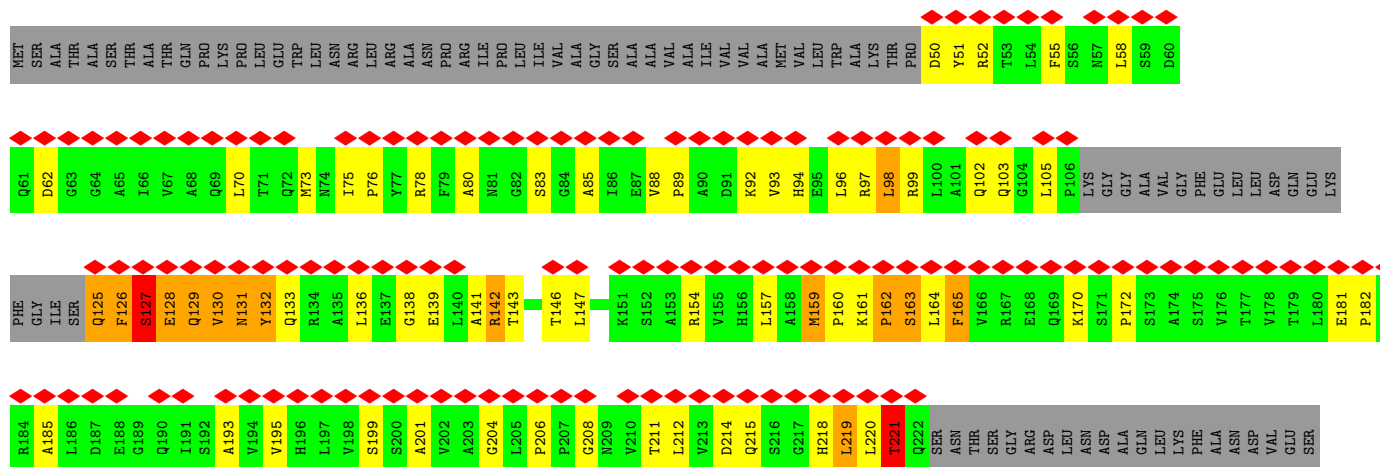




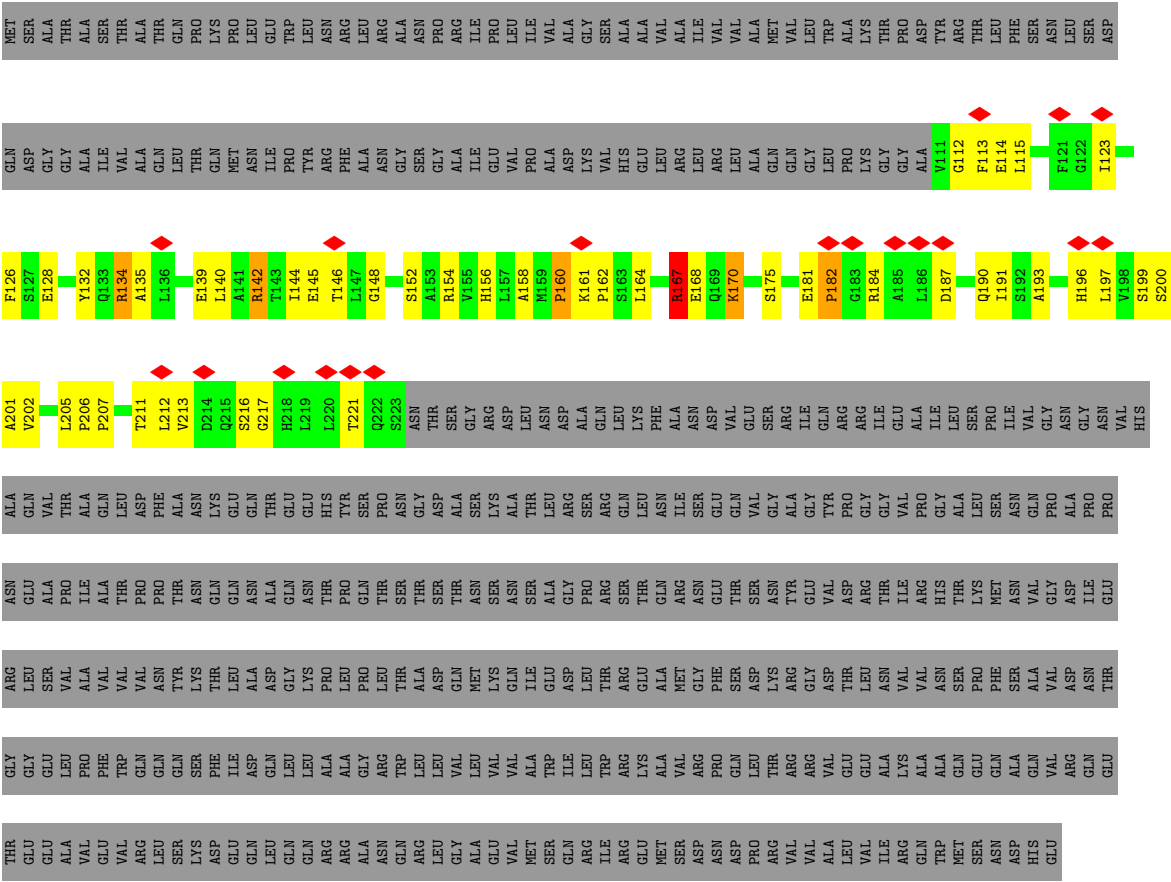




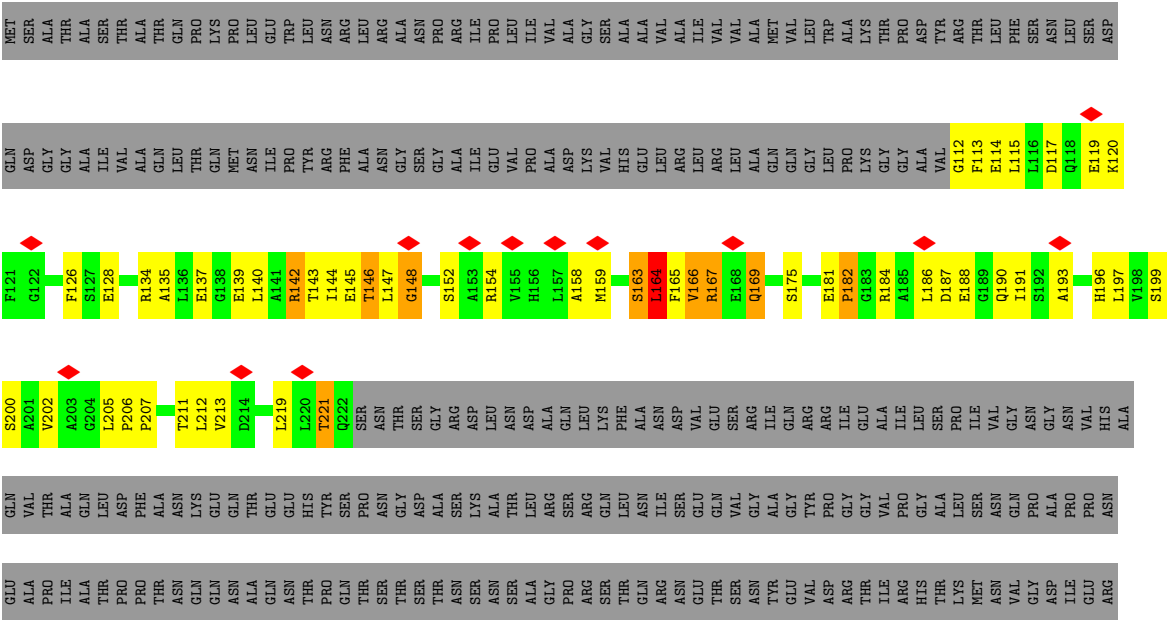
• Molecule 6: Flagellar M-ring protein

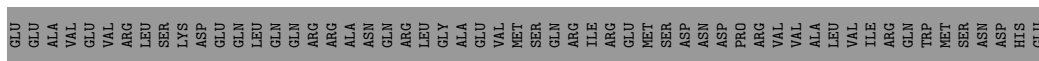


- Molecule 6: Flagellar M-ring protein

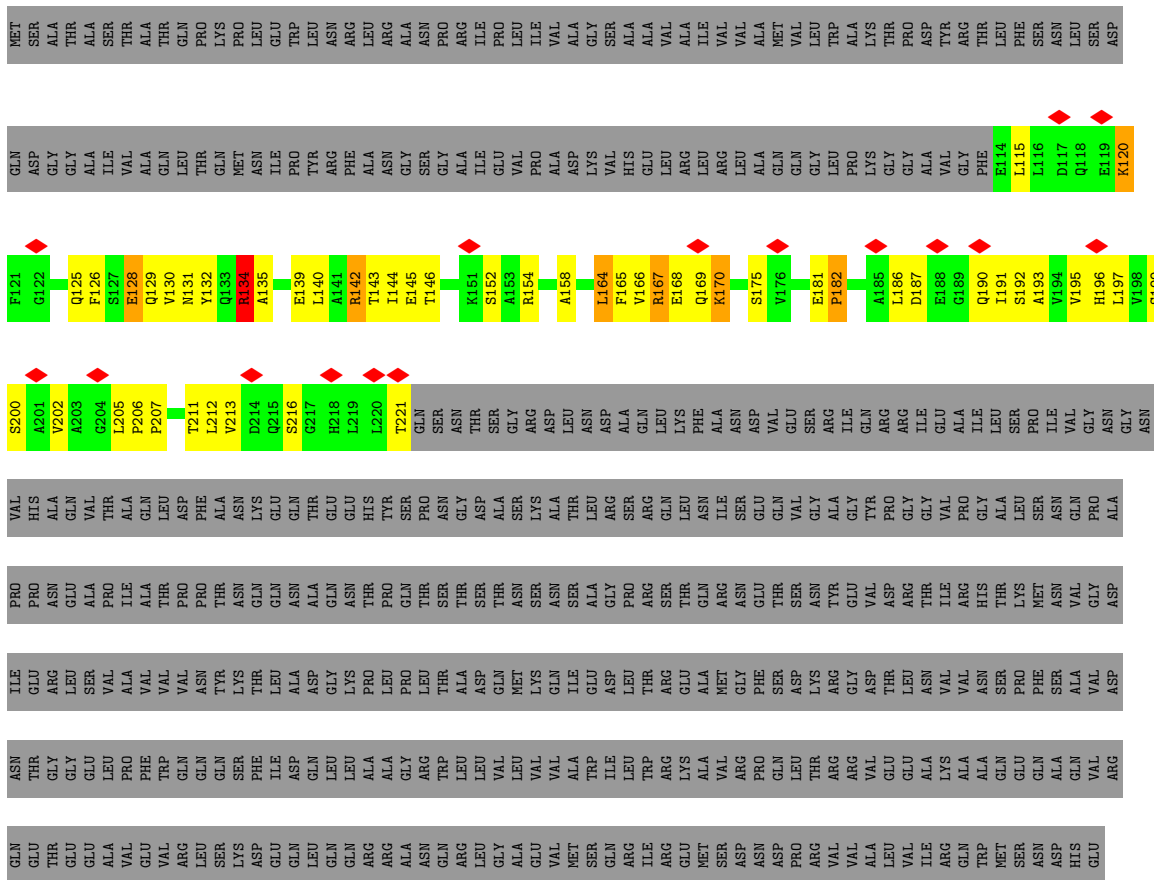


● Molecule 6: Flagellar M-ring protein

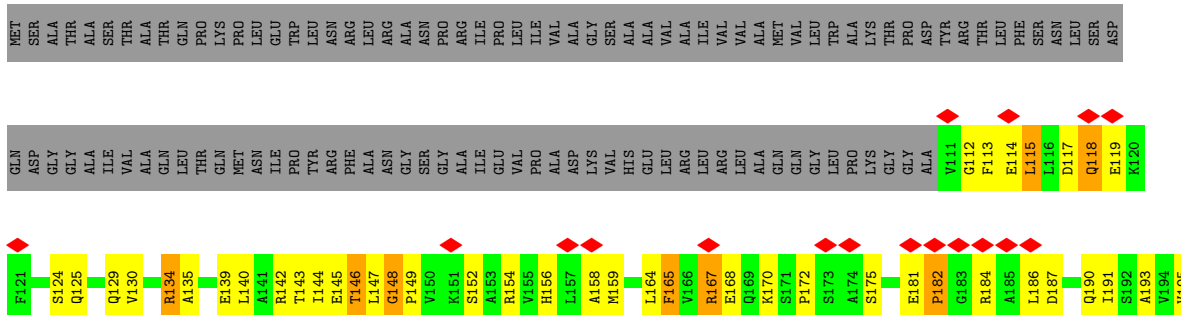




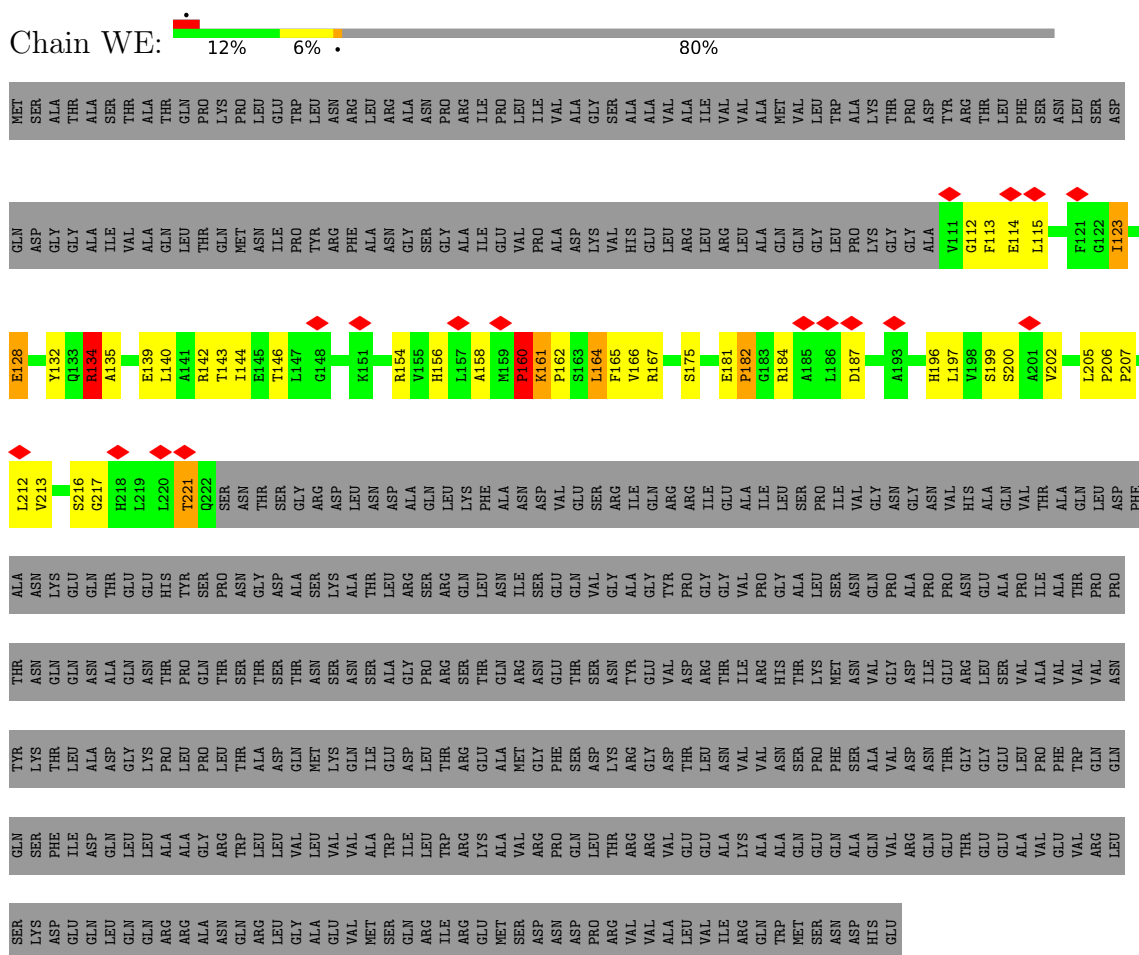
Chain WC: 10% 8% 81%



Chain WD:



- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein

[illegible]

- Molecule 6: Flagellar M-ring protein



PHE	GLY	ILE	SER	GLN	PHE	S127	E128	Q129	Y132	Q133	R134	A135	L136	E137	G138	E139	L140	A141	T142	I144	E145	T146	L147	G148	K151	S152	A153	R154	V155	H156	L157	A158	M159	P160	K161	P162	S163	L164	P165	V166	R167	E168	Q169	S171	P172	T173	A174	S175	V176	E181	P182	G183	R184	A185
NET	SER	THR	ALA	GLY	ILE	VAL	GLN	THR	GLN	MET	ASN	ILE	PRO	TVR	PHE	ARG	ALA	ASN	GLY	SER	GLY	ILE	GLU	VAL	PRO	ALA	ASP	LYS	HIS	GLU	LEU	ARG	LEU	ARG	LEU	ALA	GLN	GLY	LEU	PRO	LYS	THR	PRO	ASP	TVR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	ASP



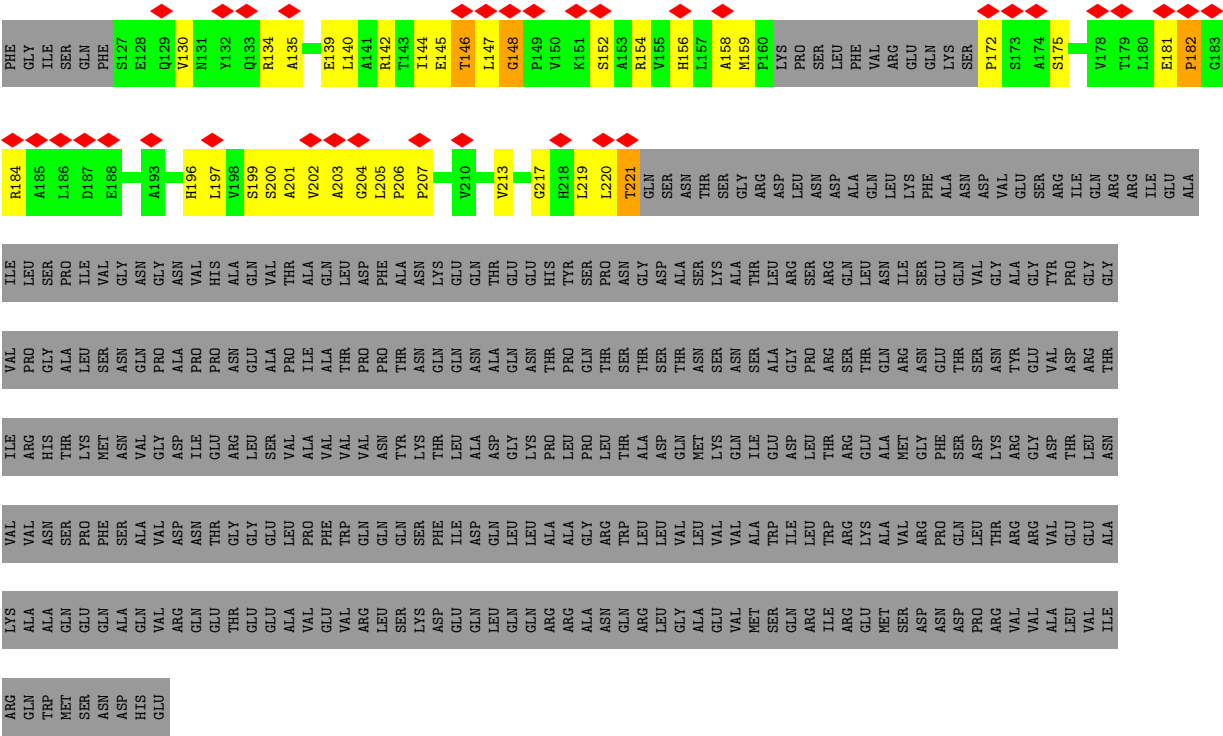
[illegible]

- Molecule 6: Flagellar M-ring protein

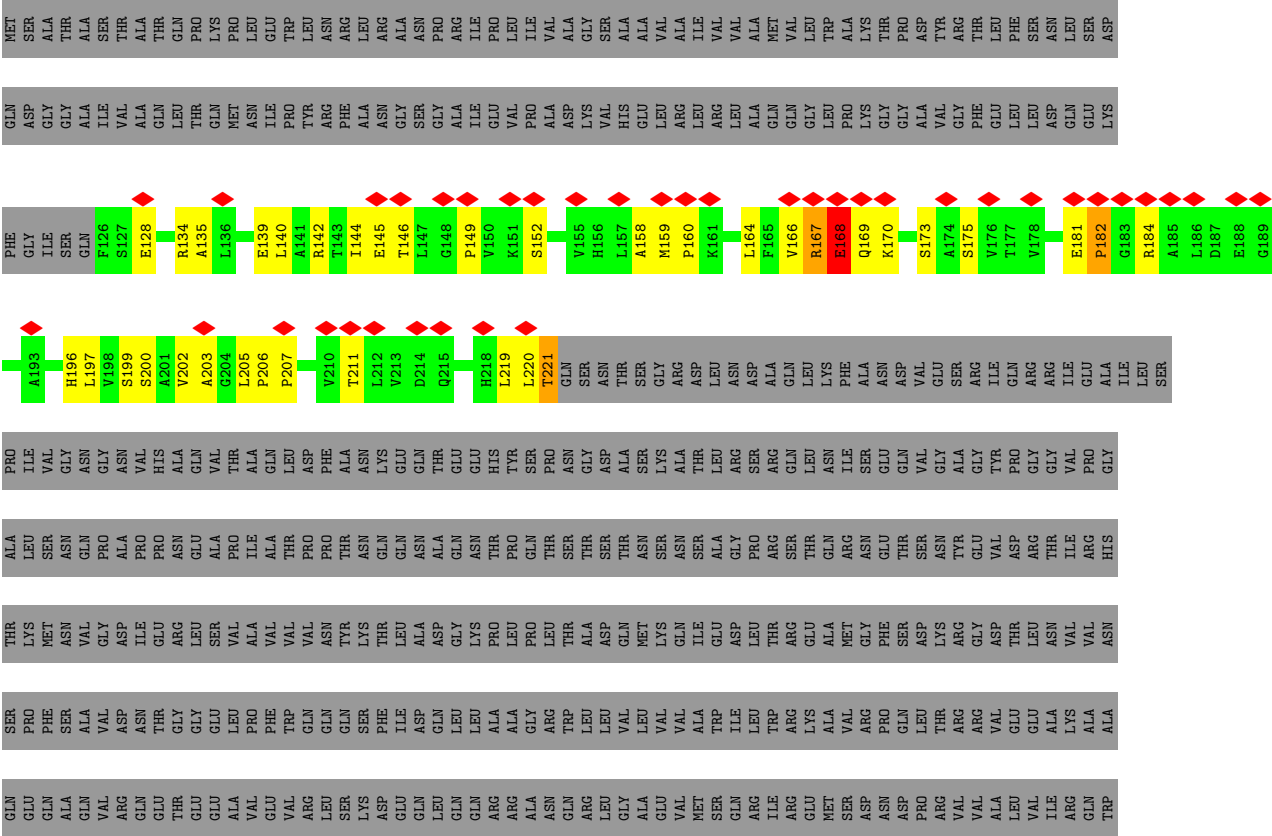
[illegible]

- Molecule 6: Flagellar M-ring protein

[illegible]



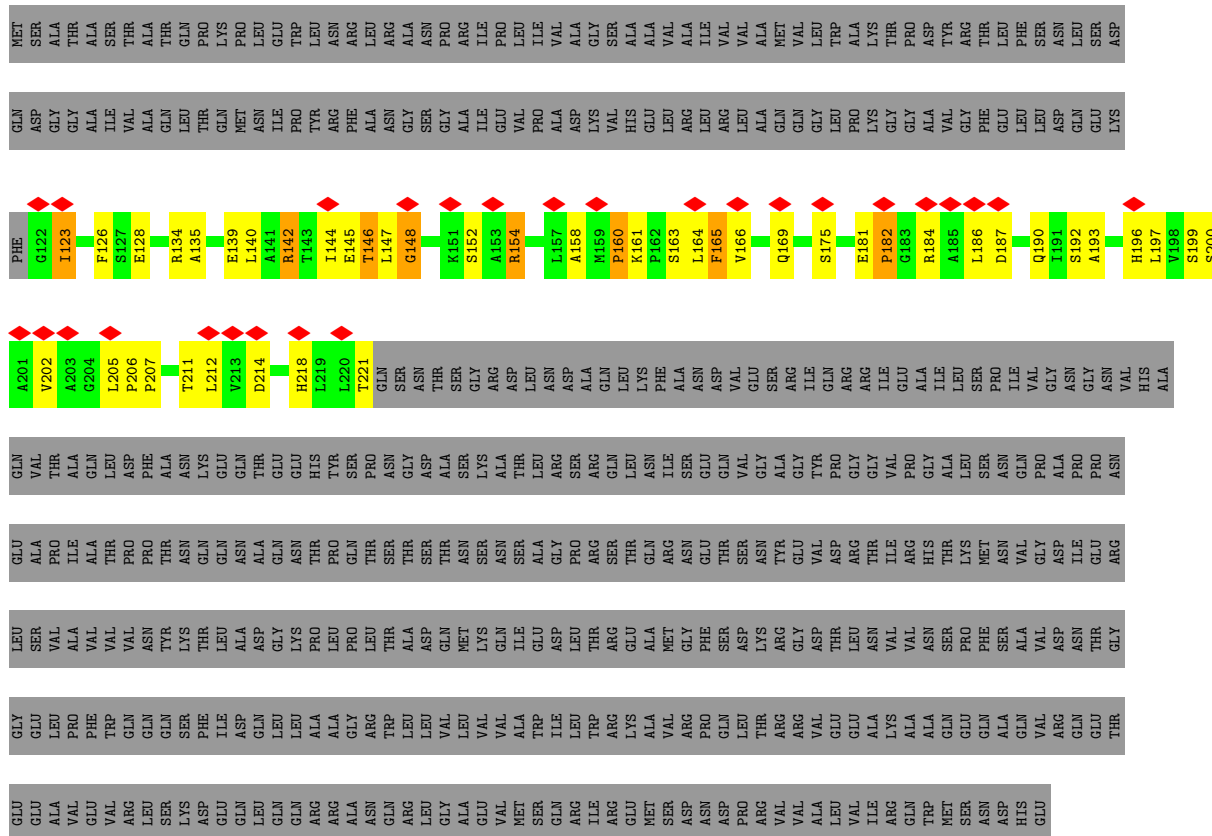
● Molecule 6: Flagellar M-ring protein



MET
SER
ASN
ASP
HIS
GLU

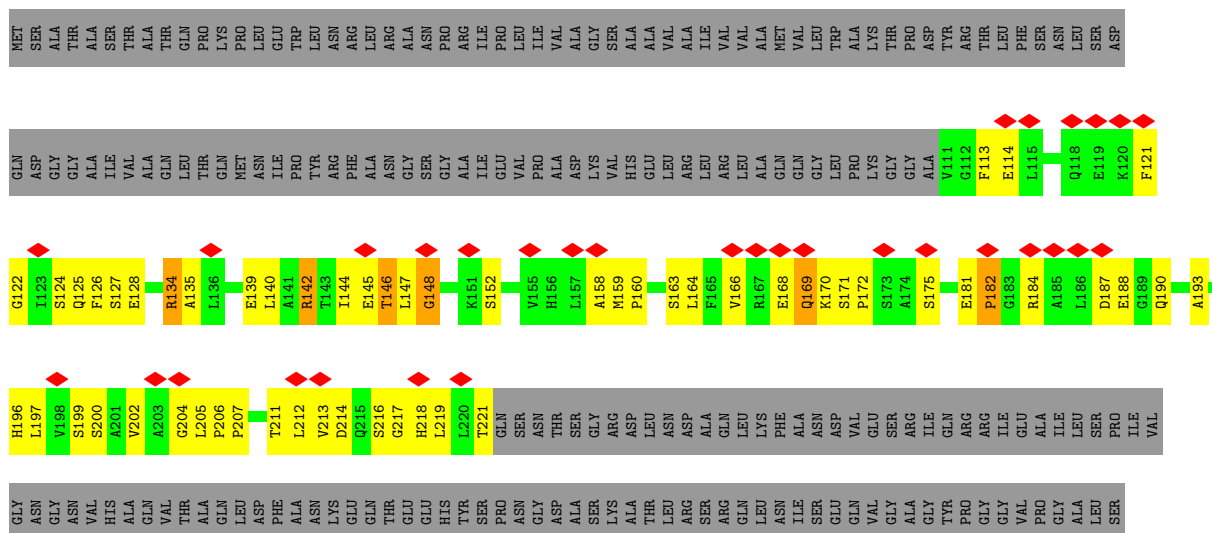
● Molecule 6: Flagellar M-ring protein

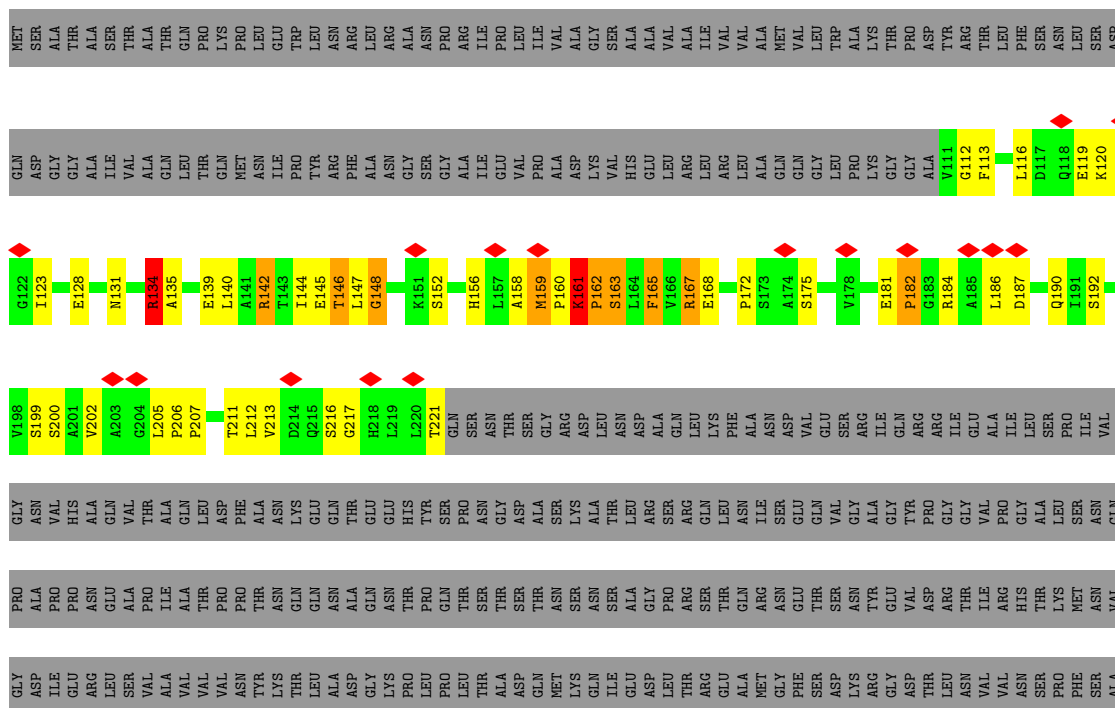
Chain WP:  5% 10% 7% 82%



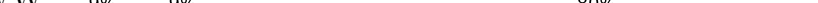
● Molecule 6: Flagellar M-ring protein

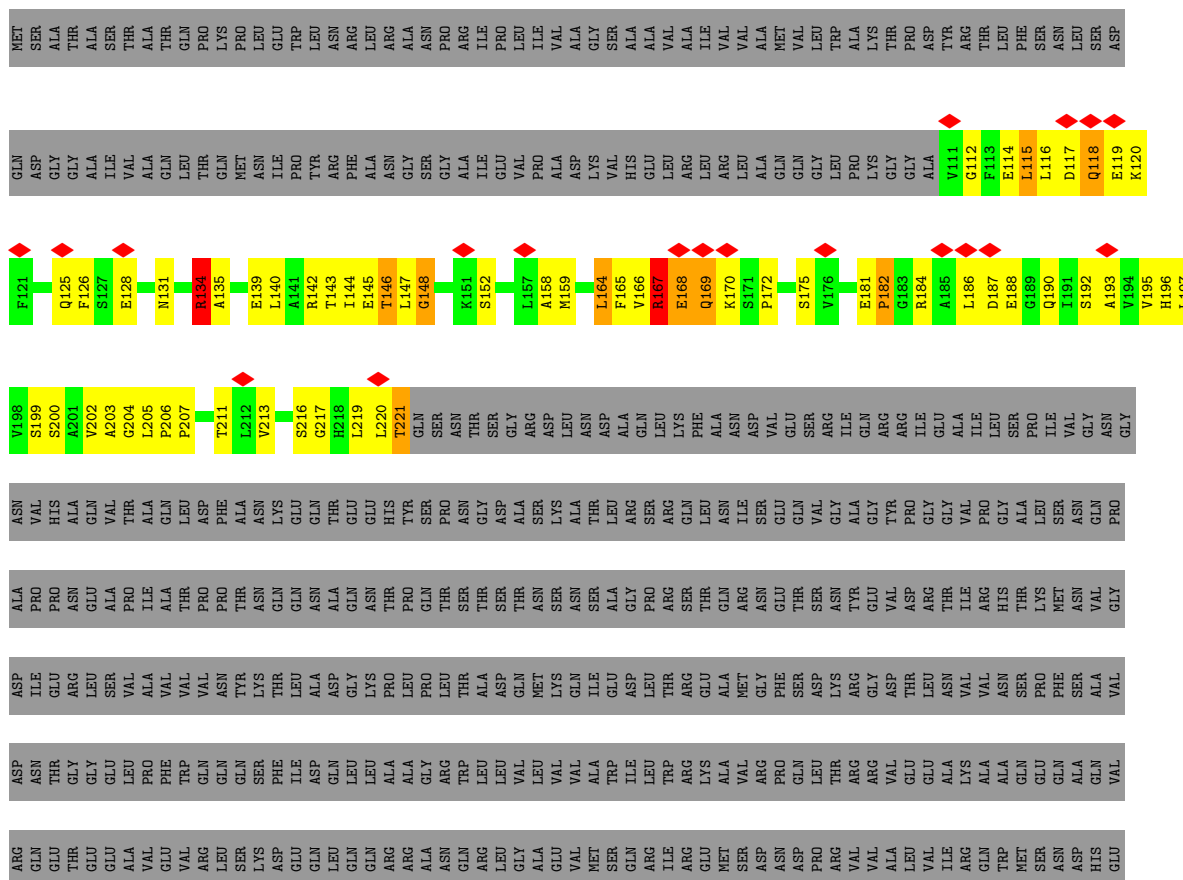
Chain WQ:  6% 10% 9% 80%





- Molecule 6: Flagellar M-ring protein

Chain WW: 



- Molecule 6: Flagellar M-ring protein

Chain BG: .. 98%

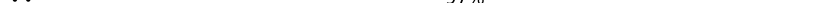
[illegible]

- Molecule 6: Flagellar M-ring protein

Chain BI: 96%

[illegible]

- Molecule 6: Flagellar M-ring protein

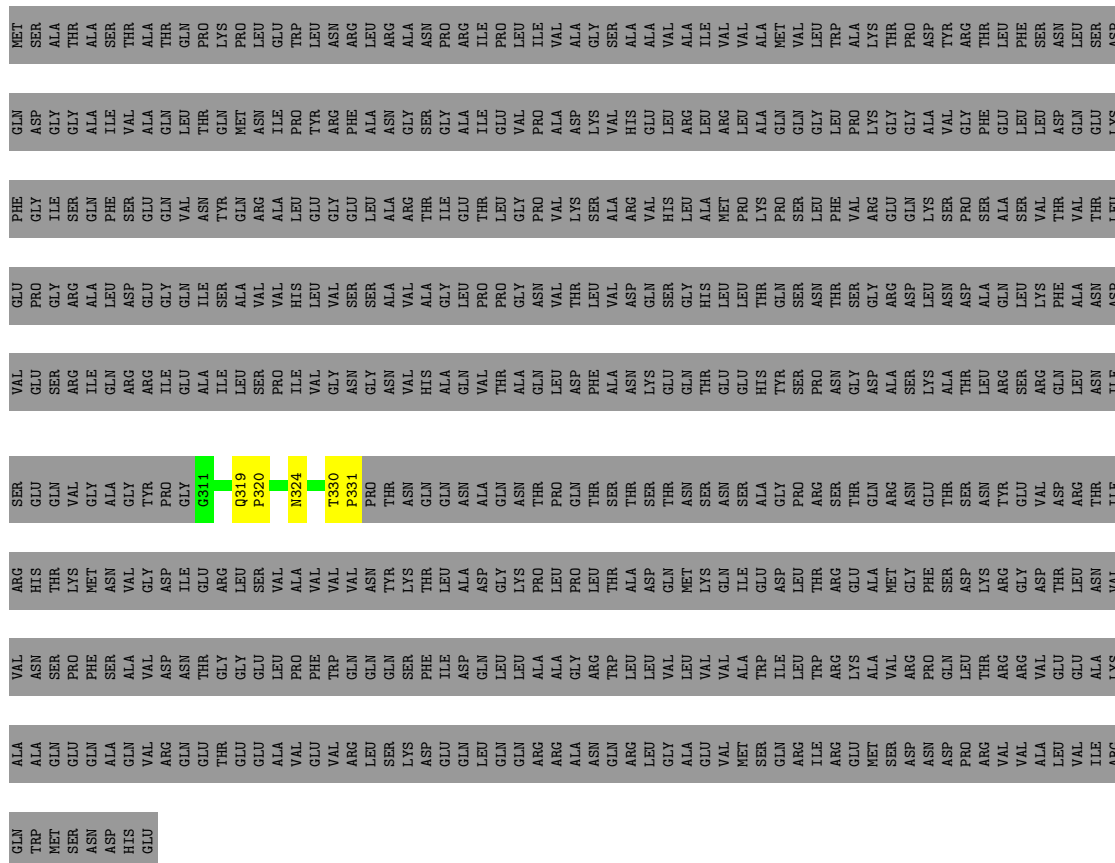
Chain BJ:  97%

[illegible]



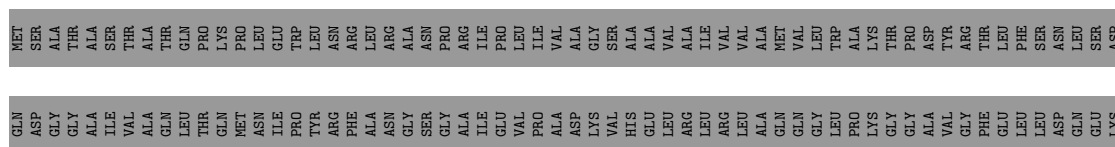
- Molecule 6: Flagellar M-ring protein

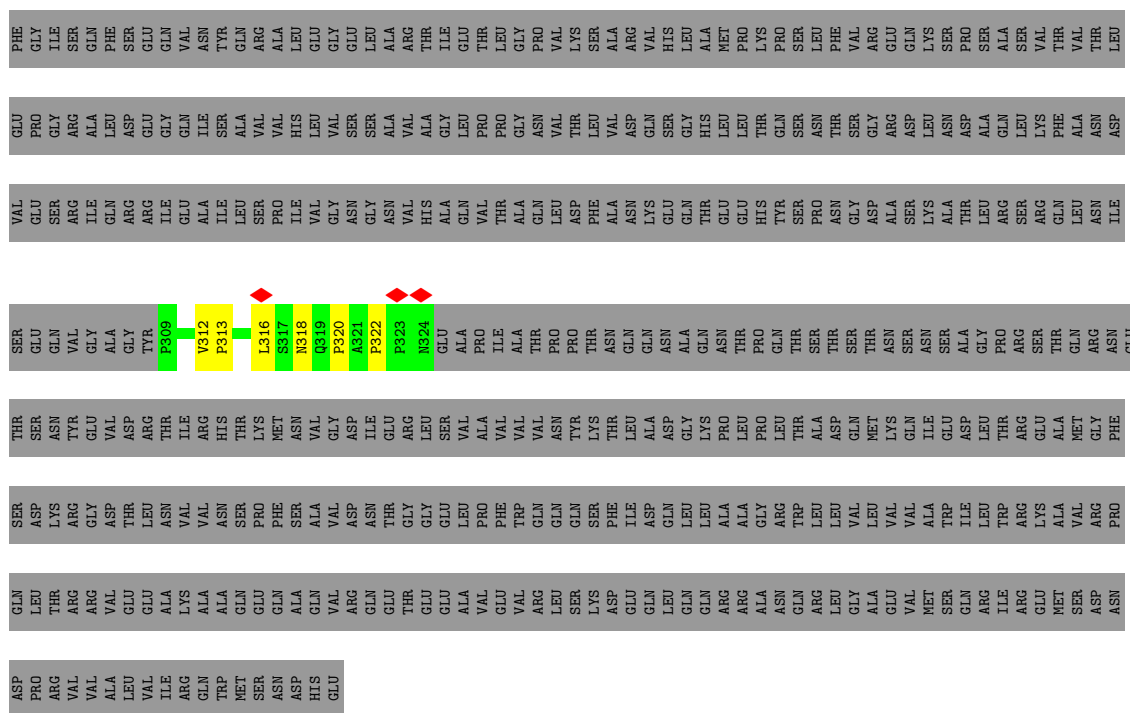
Chain BK: 96%



- Molecule 6: Flagellar M-ring protein

Chain BL:  97%





- Molecule 6: Flagellar M-ring protein

Chain BM: 96%





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

- Molecule 6: Flagellar M-ring protein

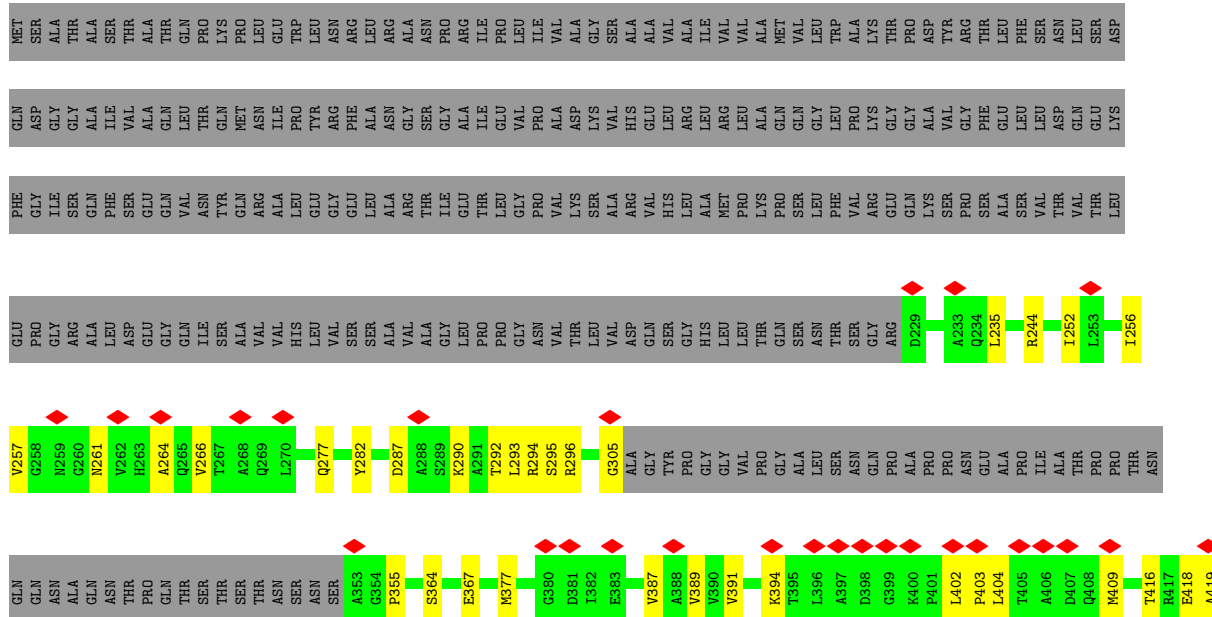
Chain BP: 97%

ARG	THR	LYS	ASN	SER	VAL	GLU	PHE	GLN	MET
VAL	ARG	ARG	TYR	GLU	GLU	PRO	GLY	ASP	SER
VAL	ARG	GLY	GLU	GLN	SER	GLY	ILE	GLY	ILE
LEU	VAL	ASP	VAL	VAL	ARG	ALA	SER	GLN	GLY
VAL	GLU	THR	ASP	GLY	ILE	ALA	PHE	ILE	SER
ILE	ALA	ASN	THR	GLY	ARG	ASP	SER	VAL	THR
LYS	LYS	VAL	ILE	TYR	ARG	GLU	GLU	ALA	ALA
VAL	ALA	ASN	HIS	G309	ILE	GLY	GLN	GLN	GLN
GLN	ALA	HIS	G310	G310	GLU	GLY	VAL	LEU	GLN
GLU	GLN	SER	THR	G311	ALA	ILE	ASN	THR	PRO
SER	GLN	PRO	LYS	V312	ILE	SER	TYR	GLN	LYS
ASN	GLN	PHE	MET	P313	LEU	ALA	GLN	MET	PRO
ASP	ALA	SER	ASN		SER	VAL	ARG	ASN	LEU
HIS	GLN	ALA	VAL		PRO	ILE	ALA	GLU	TRP
GLU	VAL	VAL	GLY	L316	VAL	LEU	GLY	PRO	LEU
	ARG	ASP	ASP	S317	GLY	VAL	GLY	TYR	ASN
	GLN	ASN	ILE		GLY	VAL	GLY	ARG	ASN
	GLU	THR	GLU	P322	ASN	SER	GLU	PHE	ARG
	THR	GLY	ARG	P323	GLY	GLY	GLU	LEU	LEU
	GLU	GLY	LEU	G324	GLU	VAL	ARG	ALA	ASN
	GLU	GLU	SER		VAL	VAL	ARG	GLY	ALA
	ALA	LEU	VAL	ALA	HIS	ALA	ILE	SER	ASN
	VAL	PHE	VAL	ILE	ALA	GLY	THR	GLY	PRO
	ARG	THR	VAL	ALA	GLN	LEU	GLU	ALA	ARG
	VAL	GLN	VAL	THR	THR	PRO	THR	ILE	PRO
	LEU	GLN	ASN	PRO	ALA	GLY	GLU	VAL	LEU
	LEU	GLN	TYR	THR	GLN	ASN	PRO	PRO	ILE
	LYS	SER	LYS	ASN	LEU	VAL	VAL	ALA	VAL
	ASP	PHE	THR	GLN	ASP	THR	LYS	ASP	ALA
	GLU	ILE	LEU	GLN	PHE	LEU	SER	GLY	SER
	GLN	ASP	ALA	ASN	ALA	VAL	ARG	HIS	ALA
	LEU	GLN	ASP	ALA	LYS	GLN	VAL	GLU	ALA
	GLN	LEU	GLY	GLN	GLU	SER	HIS	LEU	VAL
	ARG	ALA	PRO	ASN	GLN	GLY	LEU	ARG	VAL
	ALA	GLY	PRO	THR	THR	HIS	PRO	LEU	ALA
	ASN	ARG	LEU	THR	HIS	THR	LYS	ALA	ALA
	GLN	THR	THR	SER	TYR	GLN	PRO	GLN	MET
	ARG	LEU	ALA	THR	SER	THR	GLY	GLN	VAL
	LEU	LEU	ASP	THR	SER	ASN	LEU	GLY	SER
	GLY	VAL	GLN	THR	THR	THR	PHE	TRP	ALA
	ALA	LEU	MET	ASN	GLY	SER	VAL	PRO	LYS
	GLU	VAL	LYS	SER	ASP	GLY	ARG	GLY	THR
	VAL	VAL	GLN	ASN	ALA	ARG	GLU	GLY	GLY
	MET	ALA	ILE	ASN	SER	ASP	GLU	PRO	LYS
					ALA	ARG	GLY	GLY	GLY
					GLY	ASP	GLY	GLY	GLY
					ALA	THR	GLY	ALA	ALA
					GLY	ASN	LYS	VAL	TYR
					PRO	ASP	PRO	GLY	THR
					THR	LEU	SER	PHE	THR
					ARG	ALA	ALA	GLU	LEU
					THR	ARG	SER	LEU	PHE
					GLN	SER	VAL	LEU	ASN
					ARG	GLY	THR	ASP	ASN
					THR	LEU	VAL	GLN	SER
					ASN	ALA	THR	GLN	GLY
					THR	ASN	ILE	GLY	ASN
					THR	ASN	THR	GLY	SER

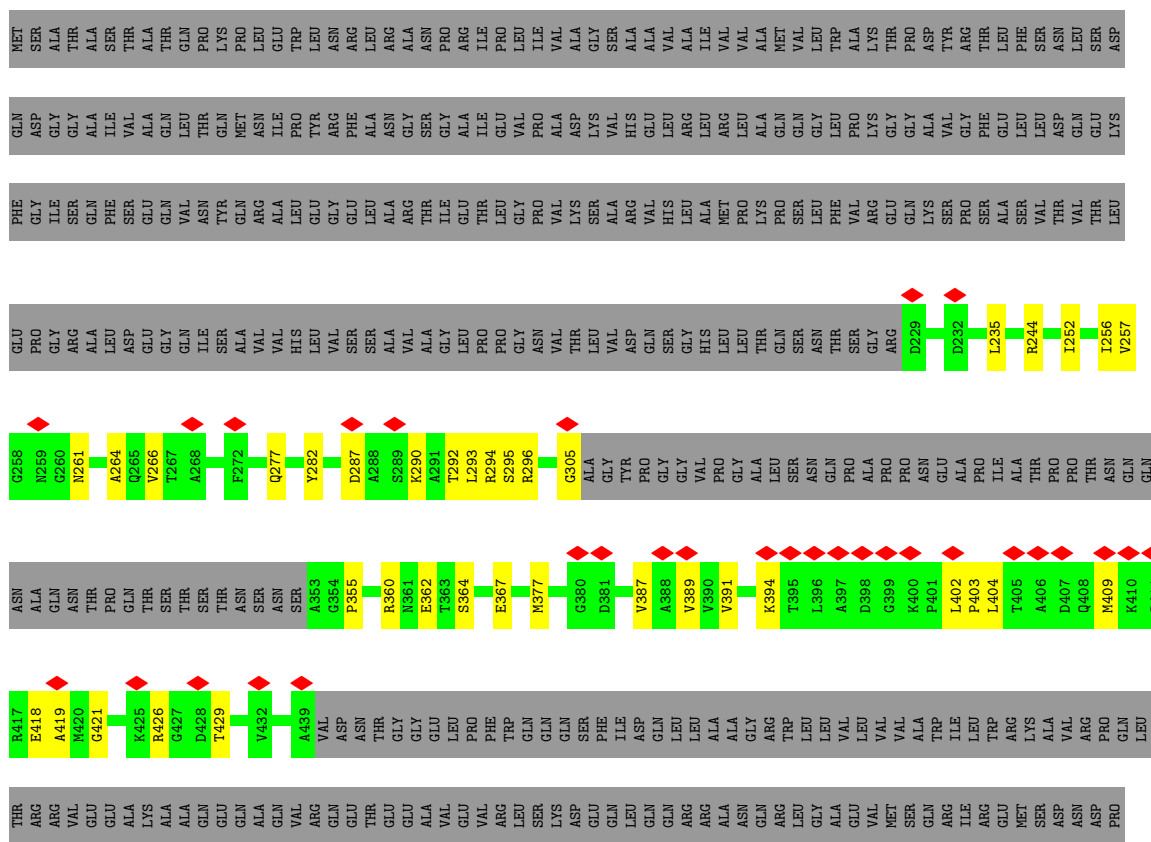
- Molecule 6: Flagellar M-ring protein

Chain BQ: 96%

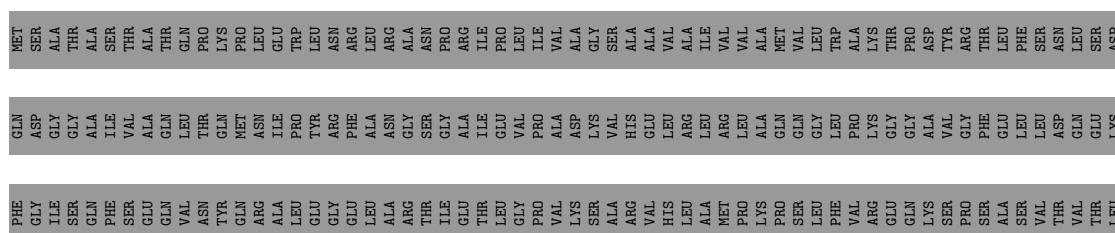
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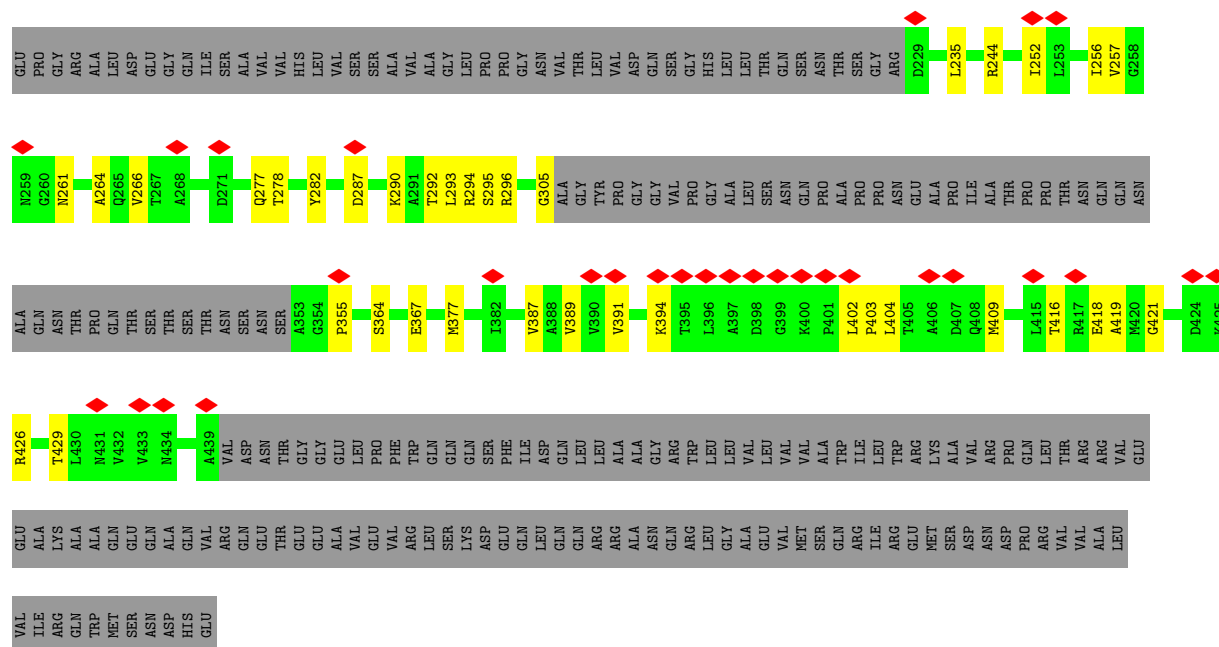


- Molecule 6: Flagellar M-ring protein

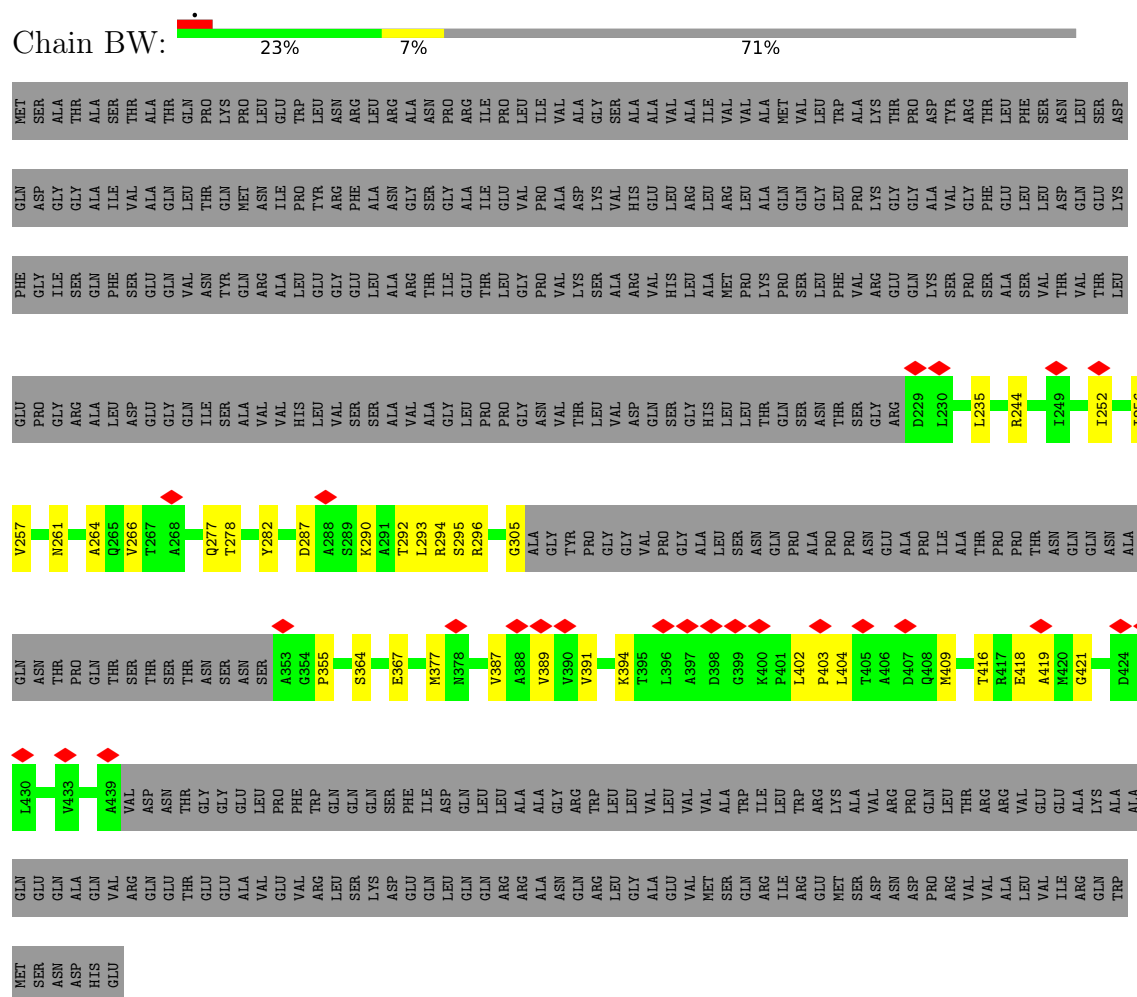


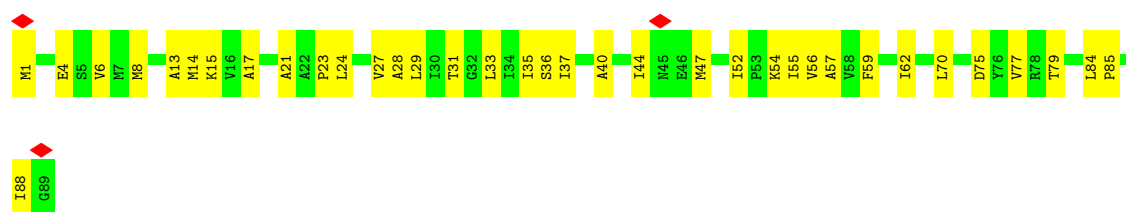
- Molecule 6: Flagellar M-ring protein



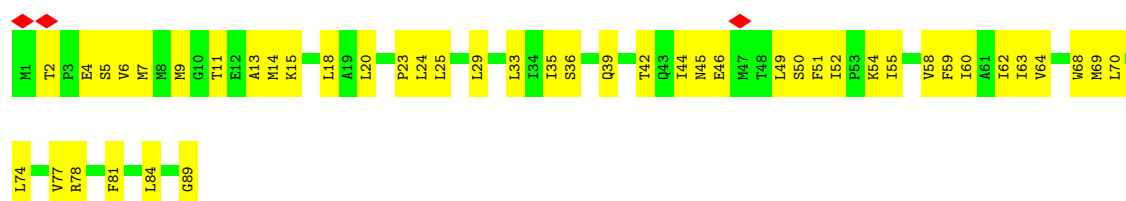


- Molecule 6: Flagellar M-ring protein

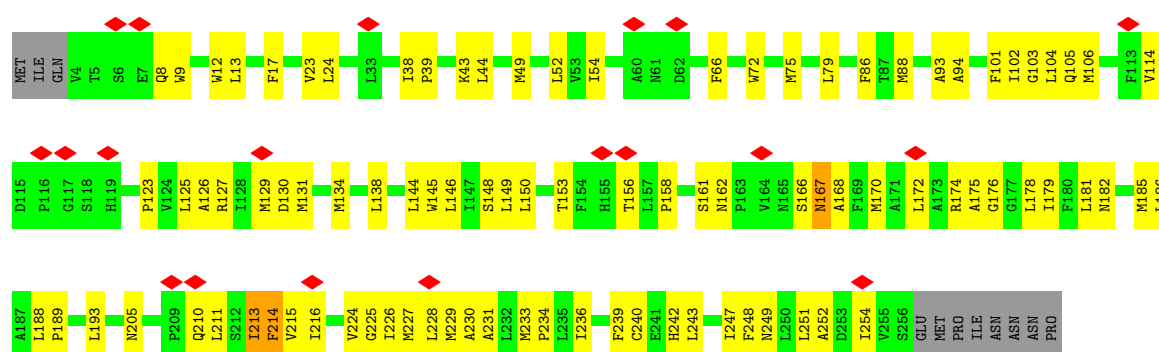




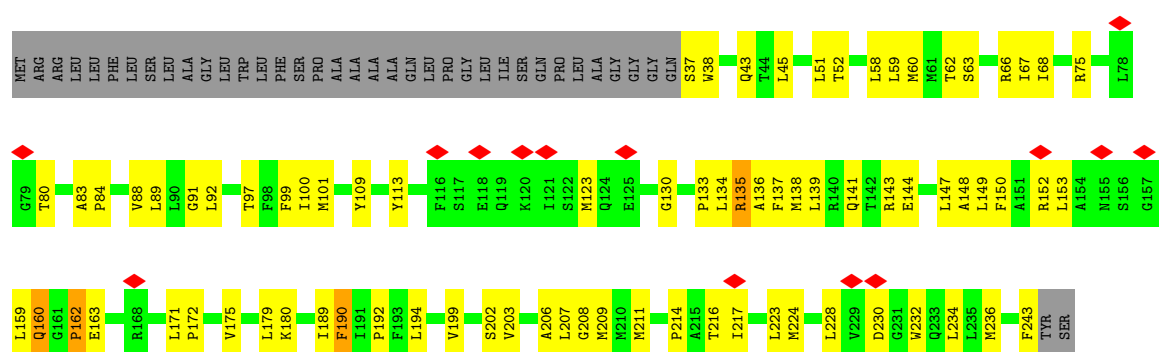
• Molecule 7: Flagellar biosynthetic protein FliQ



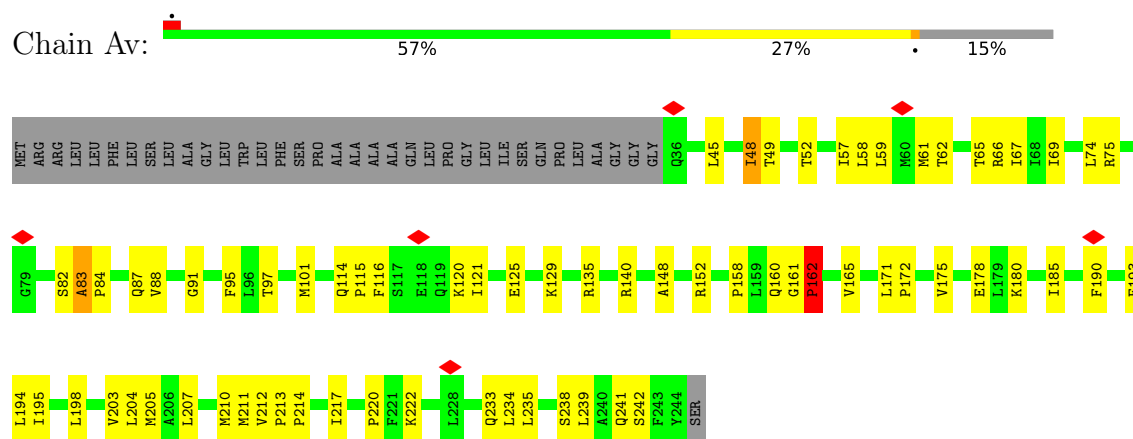
• Molecule 8: Flagellar biosynthetic protein FliR



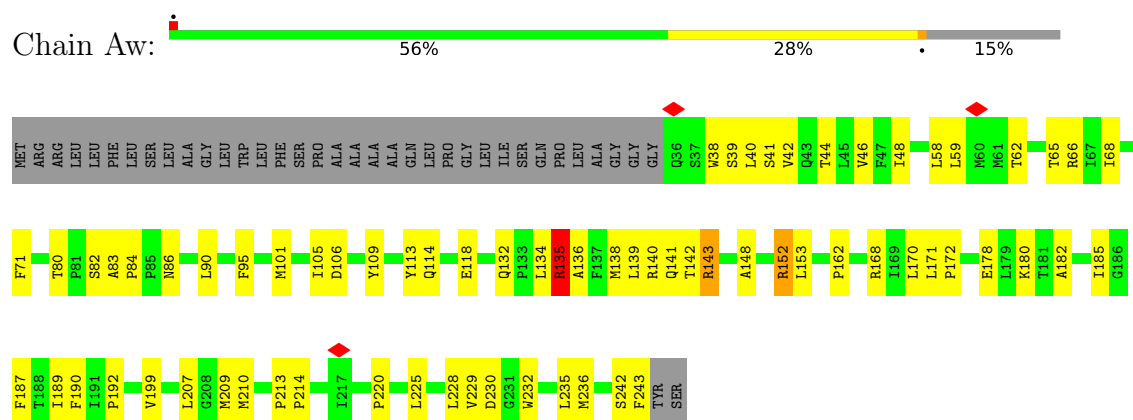
• Molecule 9: Flagellar biosynthetic protein FliP



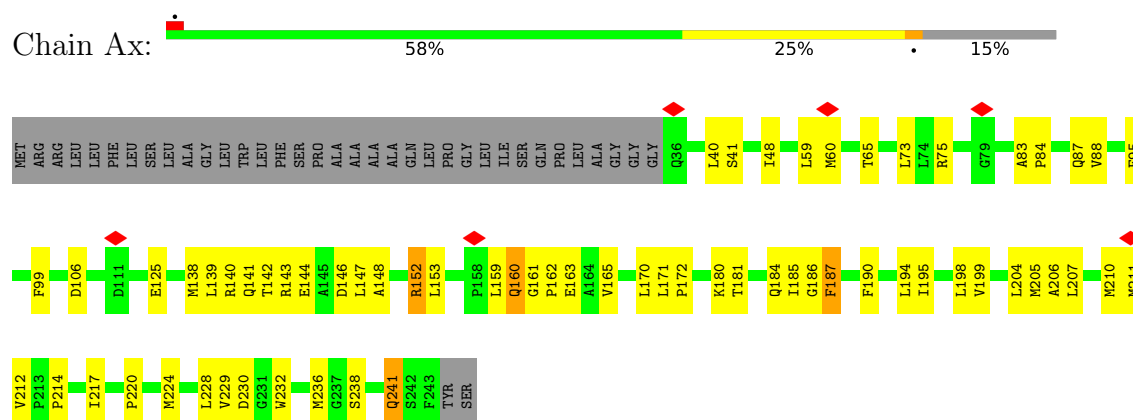
• Molecule 9: Flagellar biosynthetic protein FliP



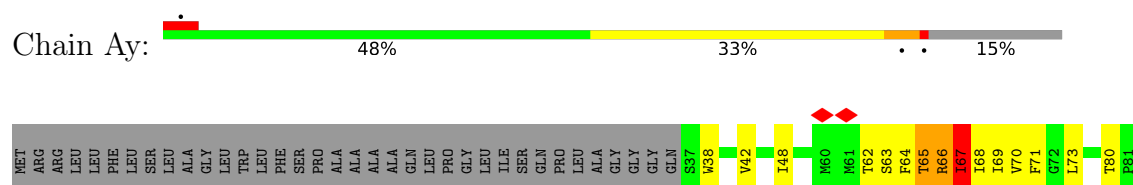
• Molecule 9: Flagellar biosynthetic protein FlpP

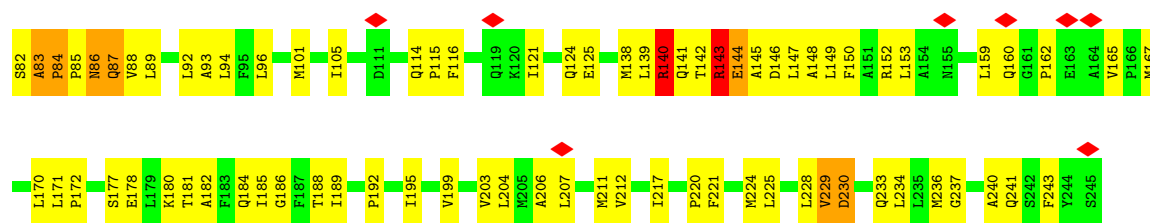


• Molecule 9: Flagellar biosynthetic protein FlpP

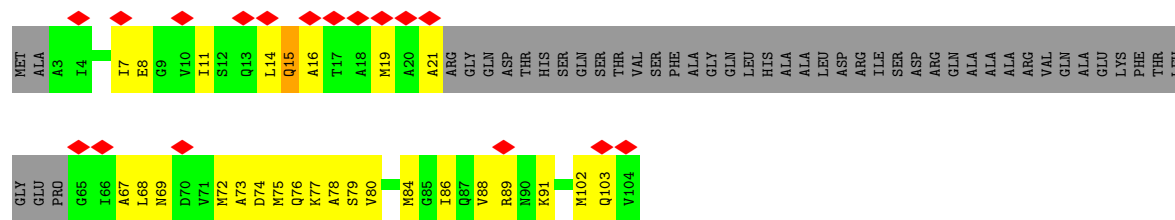
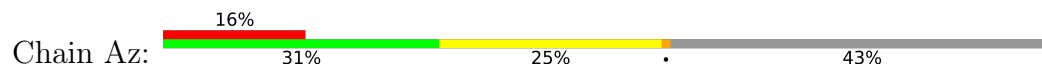


• Molecule 9: Flagellar biosynthetic protein FlpP

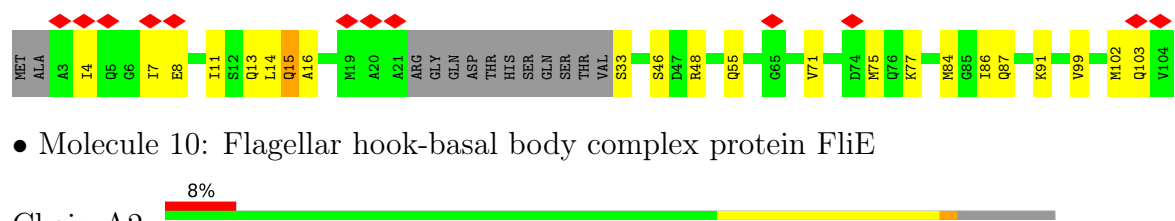




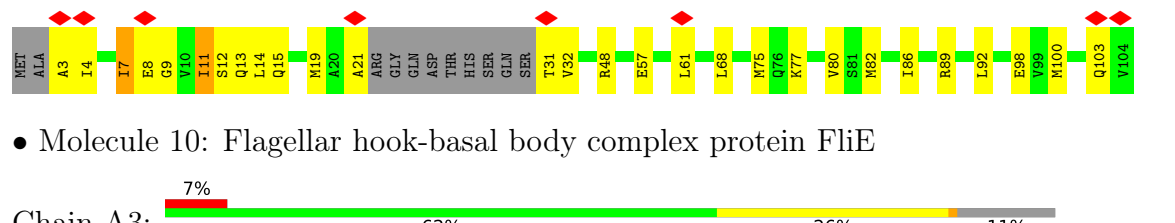
• Molecule 10: Flagellar hook-basal body complex protein FliE



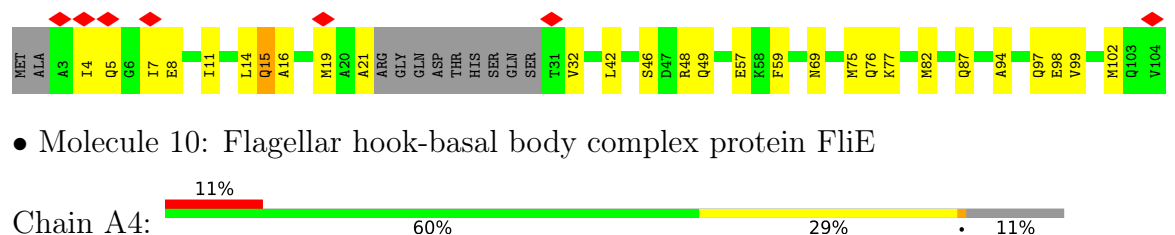
• Molecule 10: Flagellar hook-basal body complex protein FliE



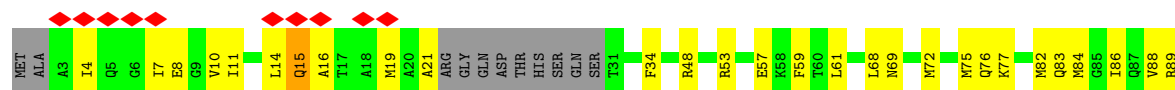
• Molecule 10: Flagellar hook-basal body complex protein FliE



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

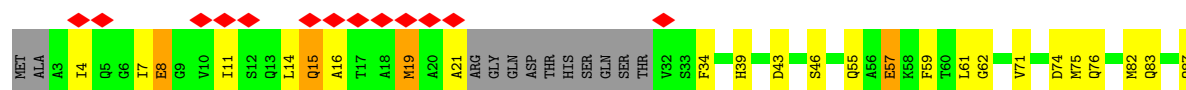


• Molecule 10: Flagellar hook-basal body complex protein FliE

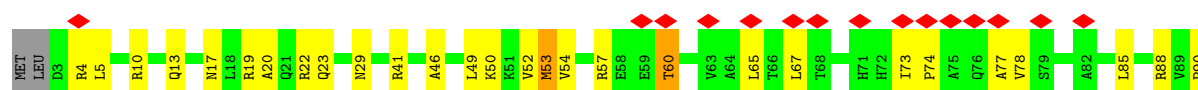




- Molecule 10: Flagellar hook-basal body complex protein FliE

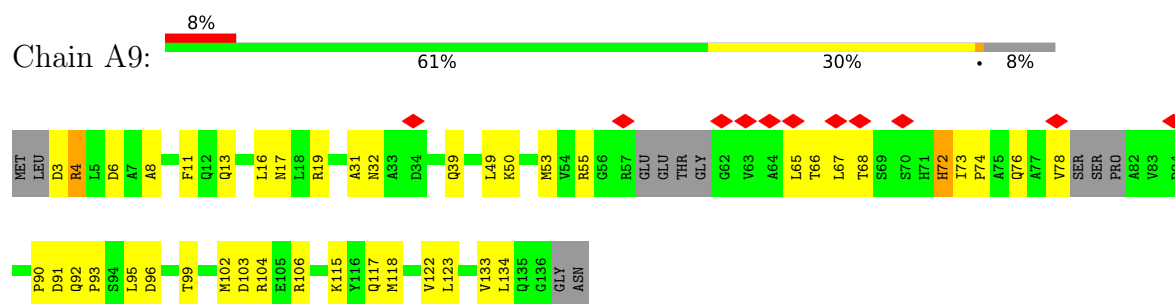


- Molecule 11: Flagellar basal body rod protein FlgB

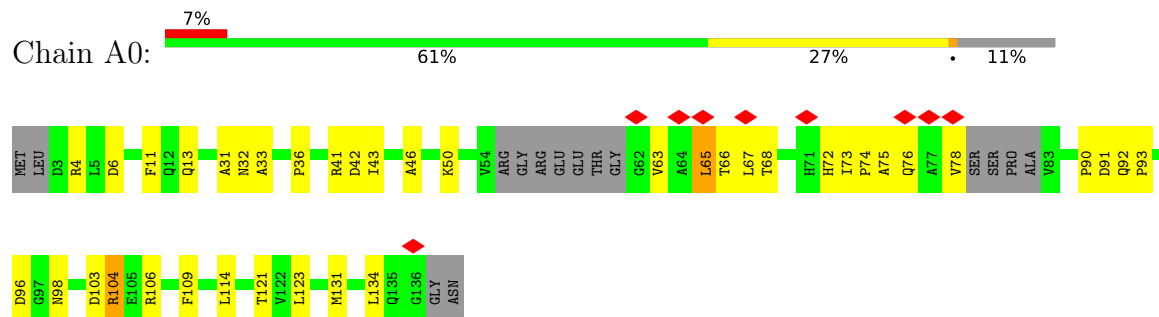


- Molecule 11: Flagellar basal body rod protein FlgB

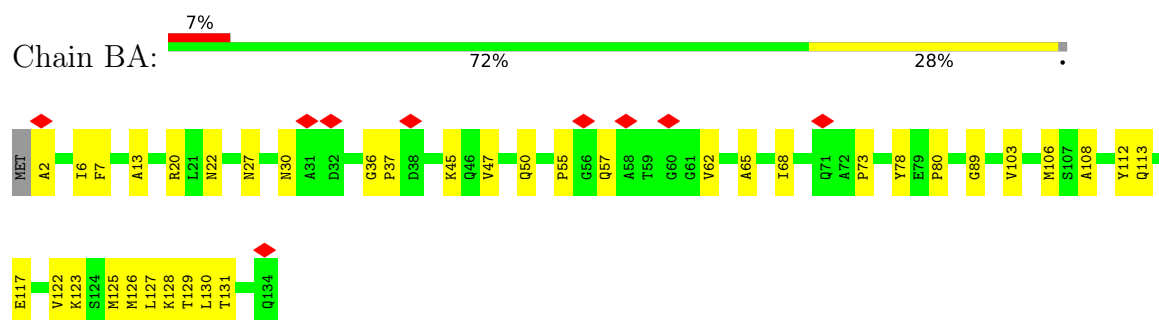




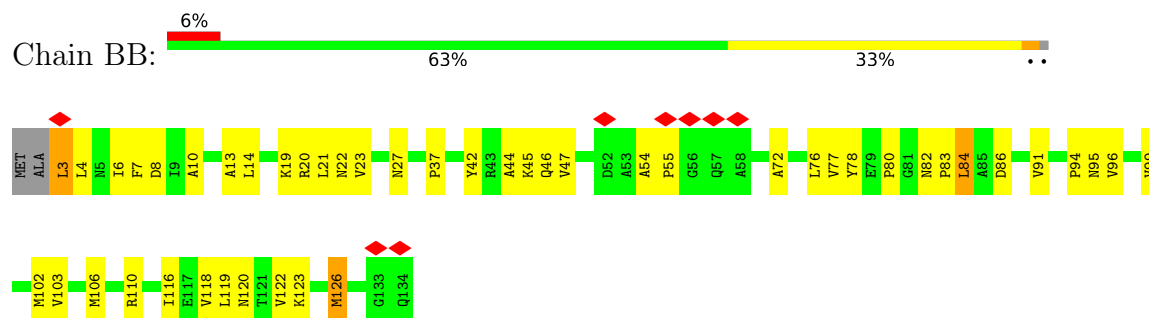
- Molecule 11: Flagellar basal body rod protein FlgB



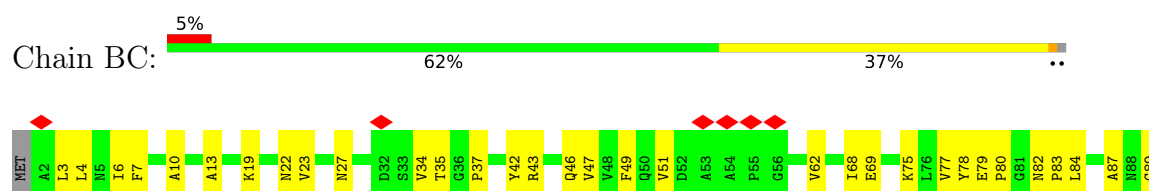
- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC

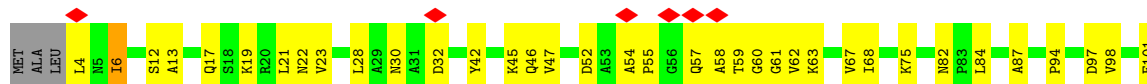




- Molecule 12: Flagellar basal-body rod protein FlgC



- 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	0.20	0/1613	0.31	0/2194
1	B	0.20	0/1613	0.31	0/2194
1	C	0.20	0/1613	0.31	0/2194
1	D	0.20	0/1613	0.31	0/2194
1	E	0.20	0/1613	0.32	0/2194
1	F	0.20	0/1613	0.32	0/2194
1	G	0.20	0/1613	0.31	0/2194
1	H	0.20	0/1613	0.32	0/2194
1	I	0.20	0/1613	0.31	0/2194
1	J	0.20	0/1613	0.31	0/2194
1	K	0.20	0/1613	0.32	0/2194
1	L	0.20	0/1613	0.31	0/2194
1	M	0.20	0/1613	0.31	0/2194
1	N	0.20	0/1613	0.32	0/2194
1	O	0.20	0/1613	0.32	0/2194
1	P	0.20	0/1613	0.31	0/2194
1	Q	0.20	0/1613	0.31	0/2194
1	R	0.20	0/1613	0.31	0/2194
1	S	0.20	0/1613	0.31	0/2194
1	T	0.20	0/1613	0.31	0/2194
1	U	0.20	0/1613	0.31	0/2194
1	V	0.20	0/1613	0.31	0/2194
1	W	0.20	0/1613	0.32	0/2194
1	X	0.20	0/1613	0.32	0/2194
1	Y	0.20	0/1613	0.32	0/2194
1	Z	0.20	0/1613	0.32	0/2194
2	a	0.27	0/2243	0.45	1/3041 (0.0%)
2	b	0.27	0/2243	0.45	1/3041 (0.0%)
2	c	0.27	0/2243	0.45	1/3041 (0.0%)
2	d	0.27	0/2243	0.45	1/3041 (0.0%)
2	e	0.27	0/2243	0.45	1/3041 (0.0%)
2	f	0.27	0/2243	0.45	1/3041 (0.0%)
2	g	0.27	0/2243	0.45	1/3041 (0.0%)
2	h	0.27	0/2243	0.45	1/3041 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	i	0.27	0/2243	0.45	1/3041 (0.0%)
2	j	0.27	0/2243	0.45	1/3041 (0.0%)
2	k	0.27	0/2243	0.45	1/3041 (0.0%)
2	l	0.27	0/2243	0.45	1/3041 (0.0%)
2	m	0.27	0/2243	0.45	1/3041 (0.0%)
2	n	0.27	0/2243	0.45	1/3041 (0.0%)
2	o	0.27	0/2243	0.45	1/3041 (0.0%)
2	p	0.27	0/2243	0.45	1/3041 (0.0%)
2	q	0.27	0/2243	0.45	1/3041 (0.0%)
2	r	0.27	0/2243	0.45	1/3041 (0.0%)
2	s	0.27	0/2243	0.45	1/3041 (0.0%)
2	t	0.27	0/2243	0.45	1/3041 (0.0%)
2	u	0.27	0/2243	0.45	1/3041 (0.0%)
2	v	0.27	0/2243	0.45	1/3041 (0.0%)
2	w	0.27	0/2243	0.45	1/3041 (0.0%)
2	x	0.27	0/2243	0.45	1/3041 (0.0%)
2	y	0.27	0/2243	0.45	1/3041 (0.0%)
2	z	0.27	0/2243	0.45	1/3041 (0.0%)
3	0	0.34	0/1888	0.61	3/2564 (0.1%)
3	1	0.29	0/1917	0.54	0/2605
3	2	0.25	0/1973	0.53	1/2682 (0.0%)
3	3	0.22	0/1973	0.50	0/2682
3	4	0.22	0/1973	0.47	0/2682
3	5	0.36	0/1973	0.59	0/2682
3	6	0.34	0/1973	0.65	0/2682
3	7	0.34	0/1973	0.59	2/2682 (0.1%)
3	8	0.35	0/1973	0.68	3/2682 (0.1%)
3	9	0.29	0/1973	0.54	0/2682
3	AF	0.39	0/1926	0.64	0/2618
3	AG	0.47	0/1934	0.77	3/2629 (0.1%)
3	AH	0.48	0/1942	0.73	3/2639 (0.1%)
3	AI	0.38	0/1926	0.67	3/2618 (0.1%)
3	AJ	0.41	0/1934	0.65	1/2629 (0.0%)
3	AK	0.36	0/1844	0.63	0/2505
3	AL	0.36	0/1888	0.59	0/2564
3	AM	0.36	0/1888	0.66	2/2564 (0.1%)
3	AN	0.30	0/1888	0.55	1/2564 (0.0%)
3	ZA	0.32	0/1973	0.57	0/2682
3	ZB	0.26	0/1973	0.49	0/2682
3	ZC	0.40	0/1973	0.67	0/2682
3	ZD	0.33	0/1973	0.61	0/2682
3	ZE	0.29	0/1973	0.54	0/2682
4	ZF	0.23	0/2991	0.46	1/4076 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ZG	0.35	1/2991 (0.0%)	0.59	4/4076 (0.1%)
4	ZH	0.26	0/2991	0.49	1/4076 (0.0%)
4	ZI	0.29	0/2991	0.51	1/4076 (0.0%)
4	ZJ	0.27	0/2991	0.48	0/4076
4	ZK	0.27	0/2991	0.51	0/4076
4	ZL	0.25	0/2991	0.46	0/4076
4	ZM	0.22	0/2991	0.49	1/4076 (0.0%)
4	ZN	0.21	0/2991	0.46	1/4076 (0.0%)
4	ZO	0.27	0/2991	0.50	1/4076 (0.0%)
4	ZP	0.21	0/2991	0.43	1/4076 (0.0%)
4	ZQ	0.23	0/2991	0.48	0/4076
4	ZR	0.22	1/2991 (0.0%)	0.47	2/4076 (0.0%)
4	ZS	0.22	0/2991	0.44	0/4076
4	ZT	0.24	0/2991	0.46	1/4076 (0.0%)
4	ZU	0.23	0/2991	0.45	0/4076
4	ZV	0.48	4/2991 (0.1%)	0.65	7/4076 (0.2%)
4	ZW	0.19	0/2991	0.43	0/4076
4	ZX	0.19	0/2991	0.41	0/4076
4	ZY	0.24	1/2991 (0.0%)	0.47	2/4076 (0.0%)
4	ZZ	0.15	0/2991	0.37	0/4076
4	Za	0.21	0/2991	0.43	1/4076 (0.0%)
4	Zb	0.28	0/2991	0.49	1/4076 (0.0%)
4	Zc	0.24	0/2991	0.49	3/4076 (0.1%)
4	Zd	0.27	0/2991	0.51	1/4076 (0.0%)
4	Ze	0.25	0/2991	0.48	0/4076
4	Zf	0.21	0/2991	0.45	0/4076
4	Zg	0.23	0/2991	0.46	0/4076
4	Zh	0.21	0/2991	0.42	1/4076 (0.0%)
5	AA	0.33	0/1828	0.57	1/2492 (0.0%)
5	AB	0.36	0/1836	0.62	1/2502 (0.0%)
5	AC	0.42	0/1844	0.62	0/2512
5	AD	0.36	0/1844	0.63	0/2512
5	AE	0.35	0/1836	0.57	0/2502
6	AO	0.23	0/1289	0.44	1/1741 (0.1%)
6	AP	0.23	0/1289	0.44	1/1741 (0.1%)
6	AQ	0.23	0/1289	0.44	1/1741 (0.1%)
6	AR	0.23	0/1289	0.44	1/1741 (0.1%)
6	AS	0.23	0/1289	0.44	1/1741 (0.1%)
6	AT	0.23	0/1289	0.44	1/1741 (0.1%)
6	AU	0.23	0/1289	0.44	1/1741 (0.1%)
6	AV	0.23	0/1289	0.44	1/1741 (0.1%)
6	AW	0.23	0/1289	0.44	1/1741 (0.1%)
6	AX	0.23	0/1289	0.44	1/1741 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	AY	0.24	0/1289	0.44	1/1741 (0.1%)
6	AZ	0.23	0/1289	0.44	1/1741 (0.1%)
6	Aa	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ac	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ad	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ae	0.23	0/1289	0.44	1/1741 (0.1%)
6	Af	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ag	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ah	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ai	0.23	0/1289	0.44	1/1741 (0.1%)
6	Aj	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ak	0.23	0/1289	0.44	1/1741 (0.1%)
6	Al	0.23	0/1289	0.44	1/1741 (0.1%)
6	Am	0.23	0/1289	0.44	1/1741 (0.1%)
6	An	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ao	0.23	0/1289	0.44	1/1741 (0.1%)
6	Ap	0.23	0/1289	0.44	1/1741 (0.1%)
6	BG	0.58	0/83	1.24	2/114 (1.8%)
6	BH	0.16	0/107	0.37	0/148
6	BI	0.27	0/137	0.51	0/191
6	BJ	0.21	0/107	0.45	0/148
6	BK	0.48	0/145	0.69	0/203
6	BL	0.23	0/107	0.57	0/148
6	BM	0.14	0/145	0.29	0/203
6	BN	0.17	0/107	0.42	0/148
6	BO	0.35	0/137	0.93	0/191
6	BP	0.17	0/107	0.30	0/148
6	BQ	0.26	0/145	0.44	0/203
6	BR	0.23	0/1289	0.44	1/1741 (0.1%)
6	BS	0.23	0/1289	0.44	1/1741 (0.1%)
6	BT	0.22	0/1289	0.44	1/1741 (0.1%)
6	BU	0.23	0/1289	0.44	1/1741 (0.1%)
6	BV	0.23	0/1289	0.44	1/1741 (0.1%)
6	BW	0.23	0/1289	0.44	1/1741 (0.1%)
6	BX	0.23	0/1289	0.44	1/1741 (0.1%)
6	UI	1.26	19/1191 (1.6%)	1.29	19/1618 (1.2%)
6	UJ	1.27	20/1191 (1.7%)	1.29	18/1618 (1.1%)
6	UK	1.26	19/1191 (1.6%)	1.29	19/1618 (1.2%)
6	UL	1.24	18/1191 (1.5%)	1.30	19/1618 (1.2%)
6	UM	1.27	20/1191 (1.7%)	1.29	19/1618 (1.2%)
6	UN	1.27	20/1191 (1.7%)	1.28	18/1618 (1.1%)
6	UO	1.26	19/1191 (1.6%)	1.28	19/1618 (1.2%)
6	UP	1.27	20/1191 (1.7%)	1.28	19/1618 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	WA	0.89	0/863	1.20	2/1172 (0.2%)
6	WB	0.91	0/850	1.21	1/1154 (0.1%)
6	WC	0.88	0/825	1.15	0/1121
6	WD	0.91	0/841	1.16	0/1142
6	WE	0.88	0/857	1.17	1/1164 (0.1%)
6	WF	0.89	0/848	1.17	0/1152
6	WG	0.89	0/857	1.16	0/1164
6	WH	0.90	0/714	1.15	1/973 (0.1%)
6	WI	0.87	0/714	1.20	2/973 (0.2%)
6	WJ	0.90	0/749	1.19	1/1020 (0.1%)
6	WK	0.90	0/741	1.16	0/1009
6	WL	0.89	0/631	1.16	1/860 (0.1%)
6	WM	0.88	0/604	1.15	1/824 (0.1%)
6	WN	0.89	0/619	1.17	1/844 (0.1%)
6	WO	0.89	0/726	1.19	3/989 (0.3%)
6	WP	0.89	0/753	1.15	0/1025
6	WQ	0.90	0/848	1.19	0/1152
6	WR	0.89	0/848	1.14	0/1152
6	WS	0.92	0/848	1.19	1/1152 (0.1%)
6	WT	0.89	0/848	1.18	0/1152
6	WU	0.89	0/857	1.16	1/1164 (0.1%)
6	WV	0.91	0/841	1.17	0/1142
6	WW	0.90	0/848	1.19	2/1152 (0.2%)
7	Ab	0.63	0/681	1.02	4/930 (0.4%)
7	Aq	0.33	0/681	0.60	0/930
7	Ar	0.24	0/681	0.53	1/930 (0.1%)
7	As	0.19	0/681	0.45	0/930
8	At	0.29	0/1994	0.52	0/2724
9	Au	0.32	0/1643	0.64	5/2237 (0.2%)
9	Av	0.27	0/1665	0.46	2/2267 (0.1%)
9	Aw	0.24	0/1652	0.48	3/2249 (0.1%)
9	Ax	0.24	0/1652	0.45	0/2249
9	Ay	0.36	0/1662	0.62	4/2263 (0.2%)
10	A1	0.42	0/675	0.64	0/905
10	A2	0.43	0/689	0.70	0/925
10	A3	0.42	0/689	0.64	0/925
10	A4	0.42	0/689	0.66	0/925
10	A5	0.48	0/682	0.71	0/915
10	Az	0.54	0/428	0.89	0/572
11	A0	0.40	0/959	0.53	0/1293
11	A6	0.45	0/1042	0.67	2/1408 (0.1%)
11	A7	0.37	0/951	0.51	0/1282
11	A8	0.41	0/976	0.60	0/1316

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	A9	0.41	0/991	0.65	3/1335 (0.2%)
12	BA	0.22	0/981	0.41	0/1334
12	BB	0.24	0/976	0.48	0/1327
12	BC	0.35	0/981	0.55	0/1334
12	BD	0.32	0/981	0.65	1/1334 (0.1%)
12	BE	0.24	0/968	0.43	0/1316
12	BF	0.40	0/981	0.55	1/1334 (0.1%)
All	All	0.40	162/343249 (0.0%)	0.58	310/466323 (0.1%)

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 162 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	-15.66	0.97	1.50
6	UJ	125	GLN	C-N	13.71	1.51	1.33
6	UK	125	GLN	C-N	13.59	1.51	1.33
6	UO	125	GLN	C-N	13.55	1.51	1.33
6	UP	125	GLN	C-N	13.54	1.51	1.33

The worst 5 of 310 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	ZV	125	PRO	N-CD-CG	-14.57	86.32	103.80
4	ZR	125	PRO	CA-N-CD	-13.96	91.96	111.50
6	UL	126	PHE	O-C-N	13.88	136.83	122.12
6	UO	126	PHE	O-C-N	13.87	136.82	122.12

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](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1580	0	1534	99	0
1	B	1580	0	1534	100	0
1	C	1580	0	1534	104	0
1	D	1580	0	1534	101	0
1	E	1580	0	1534	105	0
1	F	1580	0	1534	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1580	0	1534	100	0
1	H	1580	0	1534	102	0
1	I	1580	0	1534	102	0
1	J	1580	0	1534	102	0
1	K	1580	0	1534	104	0
1	L	1580	0	1534	110	0
1	M	1580	0	1534	105	0
1	N	1580	0	1534	106	0
1	O	1580	0	1534	103	0
1	P	1580	0	1534	102	0
1	Q	1580	0	1534	105	0
1	R	1580	0	1534	106	0
1	S	1580	0	1534	102	0
1	T	1580	0	1534	104	0
1	U	1580	0	1534	102	0
1	V	1580	0	1534	101	0
1	W	1580	0	1534	103	0
1	X	1580	0	1534	101	0
1	Y	1580	0	1534	100	0
1	Z	1580	0	1534	101	0
2	a	2228	0	2265	137	0
2	b	2228	0	2265	138	0
2	c	2228	0	2265	140	0
2	d	2228	0	2265	134	0
2	e	2228	0	2265	137	0
2	f	2228	0	2265	136	0
2	g	2228	0	2265	133	0
2	h	2228	0	2265	130	0
2	i	2228	0	2265	129	0
2	j	2228	0	2265	133	0
2	k	2228	0	2265	132	0
2	l	2228	0	2265	131	0
2	m	2228	0	2265	134	0
2	n	2228	0	2265	132	0
2	o	2228	0	2265	133	0
2	p	2228	0	2265	138	0
2	q	2228	0	2265	135	0
2	r	2228	0	2265	141	0
2	s	2228	0	2265	135	0
2	t	2228	0	2265	130	0
2	u	2228	0	2265	131	0
2	v	2228	0	2265	133	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	w	2228	0	2265	133	0
2	x	2228	0	2265	135	0
2	y	2228	0	2265	136	0
2	z	2228	0	2265	129	0
3	0	1866	0	1848	134	0
3	1	1894	0	1878	129	0
3	2	1949	0	1926	104	0
3	3	1949	0	1926	91	0
3	4	1949	0	1926	114	0
3	5	1949	0	1926	117	0
3	6	1949	0	1926	112	0
3	7	1949	0	1926	89	0
3	8	1949	0	1926	114	0
3	9	1949	0	1926	92	0
3	AF	1903	0	1878	145	0
3	AG	1911	0	1889	189	0
3	AH	1919	0	1901	151	0
3	AI	1903	0	1878	177	0
3	AJ	1911	0	1889	193	0
3	AK	1823	0	1797	131	0
3	AL	1866	0	1848	156	0
3	AM	1866	0	1848	161	0
3	AN	1866	0	1848	106	0
3	ZA	1949	0	1926	148	0
3	ZB	1949	0	1926	117	0
3	ZC	1949	0	1926	101	0
3	ZD	1949	0	1926	124	0
3	ZE	1949	0	1926	103	0
4	ZF	2947	0	2839	103	0
4	ZG	2947	0	2839	103	0
4	ZH	2947	0	2839	131	0
4	ZI	2947	0	2839	122	0
4	ZJ	2947	0	2839	101	0
4	ZK	2947	0	2839	80	0
4	ZL	2947	0	2839	96	0
4	ZM	2947	0	2839	90	0
4	ZN	2947	0	2839	101	0
4	ZO	2947	0	2839	88	0
4	ZP	2947	0	2839	118	0
4	ZQ	2947	0	2839	135	0
4	ZR	2947	0	2839	100	0
4	ZS	2947	0	2839	116	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	ZT	2947	0	2839	108	0
4	ZU	2947	0	2839	149	0
4	ZV	2947	0	2839	118	0
4	ZW	2947	0	2839	111	0
4	ZX	2947	0	2839	94	0
4	ZY	2947	0	2839	109	0
4	ZZ	2947	0	2839	90	0
4	Za	2947	0	2839	104	0
4	Zb	2947	0	2839	97	0
4	Zc	2947	0	2839	98	0
4	Zd	2947	0	2839	84	0
4	Ze	2947	0	2839	55	0
4	Zf	2947	0	2839	111	0
4	Zg	2947	0	2839	69	0
4	Zh	2947	0	2839	68	0
5	AA	1804	0	1791	187	0
5	AB	1812	0	1800	226	0
5	AC	1820	0	1812	167	0
5	AD	1820	0	1812	213	0
5	AE	1812	0	1800	239	0
6	AO	1275	0	1254	31	0
6	AP	1275	0	1254	39	0
6	AQ	1275	0	1254	34	0
6	AR	1275	0	1254	33	0
6	AS	1275	0	1254	60	0
6	AT	1275	0	1254	42	0
6	AU	1275	0	1254	29	0
6	AV	1275	0	1254	43	0
6	AW	1275	0	1254	40	0
6	AX	1275	0	1254	50	0
6	AY	1275	0	1254	54	0
6	AZ	1275	0	1254	33	0
6	Aa	1275	0	1254	29	0
6	Ac	1275	0	1254	31	0
6	Ad	1275	0	1254	44	0
6	Ae	1275	0	1254	46	0
6	Af	1275	0	1254	47	0
6	Ag	1275	0	1254	45	0
6	Ah	1275	0	1254	31	0
6	Ai	1275	0	1254	36	0
6	Aj	1275	0	1254	55	0
6	Ak	1275	0	1254	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Al	1275	0	1254	43	0
6	Am	1275	0	1254	40	0
6	An	1275	0	1254	40	0
6	Ao	1275	0	1254	40	0
6	Ap	1275	0	1254	29	0
6	BG	81	0	78	11	0
6	BH	103	0	99	5	0
6	BI	133	0	129	11	0
6	BJ	103	0	99	3	0
6	BK	140	0	136	10	0
6	BL	103	0	99	11	0
6	BM	140	0	136	11	0
6	BN	103	0	99	15	0
6	BO	133	0	129	11	0
6	BP	103	0	99	9	0
6	BQ	140	0	136	6	0
6	BR	1275	0	1254	46	0
6	BS	1275	0	1254	34	0
6	BT	1275	0	1254	29	0
6	BU	1275	0	1254	30	0
6	BV	1275	0	1254	35	0
6	BW	1275	0	1254	36	0
6	BX	1275	0	1254	52	0
6	UI	1172	0	1181	67	0
6	UJ	1172	0	1181	81	0
6	UK	1172	0	1181	78	0
6	UL	1172	0	1181	72	0
6	UM	1172	0	1181	69	0
6	UN	1172	0	1181	73	0
6	UO	1172	0	1181	68	0
6	UP	1172	0	1181	68	0
6	WA	849	0	860	80	0
6	WB	836	0	846	83	0
6	WC	812	0	826	61	0
6	WD	827	0	840	105	0
6	WE	843	0	855	96	0
6	WF	834	0	847	64	0
6	WG	843	0	855	76	0
6	WH	703	0	722	67	0
6	WI	703	0	722	77	0
6	WJ	737	0	755	91	0
6	WK	729	0	744	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	WL	622	0	632	61	0
6	WM	596	0	612	47	0
6	WN	611	0	623	59	0
6	WO	714	0	731	48	0
6	WP	741	0	758	70	0
6	WQ	834	0	847	70	0
6	WR	834	0	847	64	0
6	WS	834	0	847	86	0
6	WT	834	0	847	71	0
6	WU	843	0	855	67	0
6	WV	827	0	838	66	0
6	WW	834	0	847	96	0
7	Ab	670	0	739	73	0
7	Aq	670	0	739	53	0
7	Ar	670	0	739	51	0
7	As	670	0	739	88	0
8	At	1945	0	2063	136	0
9	Au	1605	0	1701	88	0
9	Av	1626	0	1718	90	0
9	Aw	1614	0	1709	87	0
9	Ax	1614	0	1709	117	0
9	Ay	1623	0	1715	149	0
10	A1	672	0	684	62	0
10	A2	686	0	700	73	0
10	A3	686	0	700	54	0
10	A4	686	0	700	66	0
10	A5	679	0	693	66	0
10	Az	429	0	445	57	0
11	A0	950	0	946	79	0
11	A6	1030	0	1025	50	0
11	A7	942	0	943	92	0
11	A8	967	0	968	94	0
11	A9	982	0	984	80	0
12	BA	969	0	981	53	0
12	BB	964	0	976	98	0
12	BC	969	0	981	77	0
12	BD	969	0	981	81	0
12	BE	956	0	965	85	0
12	BF	969	0	981	106	0
All	All	338664	0	335363	12325	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

The worst 5 of 12325 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AE:228:GLU:CB	3:AK:258:THR:HG21	1.27	1.63
5:AB:202:MET:HE1	3:AM:73:ARG:CD	1.40	1.49
5:AD:74:THR:HG21	3:AI:38:ARG:NH1	1.18	1.48
3:6:56:SER:HA	5:AE:138:ALA:CB	1.40	1.48
5:AE:231:MET:HE3	3:AJ:257:LEU:CA	1.40	1.48

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	51/232 (22%)	50 (98%)	1 (2%)	0	100	100
1	M	117/232 (50%)	114 (97%)	2 (2%)	1 (1%)	14	49
1	N	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	O	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	P	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	Q	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	R	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	S	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	T	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	U	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	V	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	W	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	X	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
1	Y	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Z	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	24	61
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
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%)	10	42
3	1	248/260 (95%)	238 (96%)	9 (4%)	1 (0%)	30	65
3	2	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	52
3	3	258/260 (99%)	247 (96%)	9 (4%)	2 (1%)	16	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	4	258/260 (99%)	245 (95%)	11 (4%)	2 (1%)	16	52
3	5	258/260 (99%)	240 (93%)	15 (6%)	3 (1%)	10	42
3	6	258/260 (99%)	244 (95%)	10 (4%)	4 (2%)	7	37
3	7	258/260 (99%)	244 (95%)	11 (4%)	3 (1%)	10	42
3	8	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	10	42
3	9	258/260 (99%)	244 (95%)	13 (5%)	1 (0%)	30	65
3	AF	250/260 (96%)	238 (95%)	11 (4%)	1 (0%)	30	65
3	AG	251/260 (96%)	234 (93%)	14 (6%)	3 (1%)	10	42
3	AH	252/260 (97%)	234 (93%)	16 (6%)	2 (1%)	16	52
3	AI	250/260 (96%)	239 (96%)	9 (4%)	2 (1%)	16	52
3	AJ	251/260 (96%)	235 (94%)	10 (4%)	6 (2%)	4	30
3	AK	239/260 (92%)	231 (97%)	7 (3%)	1 (0%)	30	65
3	AL	244/260 (94%)	229 (94%)	10 (4%)	5 (2%)	6	33
3	AM	244/260 (94%)	234 (96%)	9 (4%)	1 (0%)	30	65
3	AN	244/260 (94%)	239 (98%)	4 (2%)	1 (0%)	30	65
3	ZA	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	10	42
3	ZB	258/260 (99%)	242 (94%)	13 (5%)	3 (1%)	10	42
3	ZC	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	52
3	ZD	258/260 (99%)	237 (92%)	18 (7%)	3 (1%)	10	42
3	ZE	258/260 (99%)	243 (94%)	14 (5%)	1 (0%)	30	65
4	ZF	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZG	399/403 (99%)	388 (97%)	10 (2%)	1 (0%)	36	70
4	ZH	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
4	ZI	399/403 (99%)	387 (97%)	10 (2%)	2 (0%)	24	61
4	ZJ	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZK	399/403 (99%)	387 (97%)	11 (3%)	1 (0%)	36	70
4	ZL	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	36	70
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	52
4	ZP	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	36	70

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	36	70
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%)	36	70
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%)	36	70
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	65
5	AB	247/251 (98%)	242 (98%)	4 (2%)	1 (0%)	30	65
5	AC	248/251 (99%)	233 (94%)	13 (5%)	2 (1%)	16	52
5	AD	248/251 (99%)	235 (95%)	13 (5%)	0	100	100
5	AE	247/251 (98%)	236 (96%)	9 (4%)	2 (1%)	16	52
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	9	41
6	UJ	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	9	41
6	UK	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	9	41
6	UL	151/560 (27%)	142 (94%)	7 (5%)	2 (1%)	9	41
6	UM	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	9	41
6	UN	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	9	41
6	UO	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	9	41
6	UP	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	9	41
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	19
6	WC	106/560 (19%)	96 (91%)	9 (8%)	1 (1%)	14	49
6	WD	108/560 (19%)	99 (92%)	4 (4%)	5 (5%)	2	19
6	WE	110/560 (20%)	98 (89%)	8 (7%)	4 (4%)	2	22
6	WF	109/560 (20%)	98 (90%)	8 (7%)	3 (3%)	4	27
6	WG	110/560 (20%)	98 (89%)	10 (9%)	2 (2%)	6	35
6	WH	93/560 (17%)	86 (92%)	5 (5%)	2 (2%)	5	31
6	WI	93/560 (17%)	82 (88%)	5 (5%)	6 (6%)	1	15
6	WJ	97/560 (17%)	89 (92%)	7 (7%)	1 (1%)	12	46
6	WK	96/560 (17%)	84 (88%)	9 (9%)	3 (3%)	3	25
6	WL	81/560 (14%)	75 (93%)	4 (5%)	2 (2%)	4	29
6	WM	78/560 (14%)	72 (92%)	4 (5%)	2 (3%)	4	28
6	WN	80/560 (14%)	75 (94%)	2 (2%)	3 (4%)	2	21
6	WO	94/560 (17%)	85 (90%)	7 (7%)	2 (2%)	5	32
6	WP	98/560 (18%)	87 (89%)	6 (6%)	5 (5%)	1	17
6	WQ	109/560 (20%)	100 (92%)	5 (5%)	4 (4%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	17
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	49
6	WV	108/560 (19%)	97 (90%)	9 (8%)	2 (2%)	6	34
6	WW	109/560 (20%)	95 (87%)	9 (8%)	5 (5%)	2	19
7	Ab	87/89 (98%)	81 (93%)	4 (5%)	2 (2%)	5	31
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	52
9	Au	205/245 (84%)	197 (96%)	8 (4%)	0	100	100
9	Av	207/245 (84%)	199 (96%)	6 (3%)	2 (1%)	12	46
9	Aw	206/245 (84%)	201 (98%)	5 (2%)	0	100	100
9	Ax	206/245 (84%)	199 (97%)	6 (3%)	1 (0%)	24	61
9	Ay	207/245 (84%)	192 (93%)	10 (5%)	5 (2%)	4	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	52
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	BE	129/134 (96%)	123 (95%)	5 (4%)	1 (1%)	16	52
12	BF	131/134 (98%)	124 (95%)	7 (5%)	0	100	100
All	All	42157/78675 (54%)	40652 (96%)	1301 (3%)	204 (0%)	26	61

5 of 204 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	209	ASN
3	4	140	ILE
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%)	161 (95%)	9 (5%)	20	44
1	B	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	C	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	D	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	E	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	F	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	G	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	H	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	I	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	J	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	K	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	L	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	M	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	N	170/186 (91%)	161 (95%)	9 (5%)	20	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	P	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	Q	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	R	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	S	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	T	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	U	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	V	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	W	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	X	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	Y	170/186 (91%)	161 (95%)	9 (5%)	20	44
1	Z	170/186 (91%)	161 (95%)	9 (5%)	20	44
2	a	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	b	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	c	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	d	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	e	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	f	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	g	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	h	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	i	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	j	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	k	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	l	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	m	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	n	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	o	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	p	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	q	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	r	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	s	248/294 (84%)	241 (97%)	7 (3%)	38	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	t	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	u	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	v	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	w	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	x	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	y	248/294 (84%)	241 (97%)	7 (3%)	38	59
2	z	248/294 (84%)	241 (97%)	7 (3%)	38	59
3	0	205/215 (95%)	199 (97%)	6 (3%)	37	58
3	1	209/215 (97%)	206 (99%)	3 (1%)	59	71
3	2	215/215 (100%)	214 (100%)	1 (0%)	81	82
3	3	215/215 (100%)	214 (100%)	1 (0%)	81	82
3	4	215/215 (100%)	212 (99%)	3 (1%)	59	71
3	5	215/215 (100%)	211 (98%)	4 (2%)	50	67
3	6	215/215 (100%)	212 (99%)	3 (1%)	59	71
3	7	215/215 (100%)	214 (100%)	1 (0%)	81	82
3	8	215/215 (100%)	209 (97%)	6 (3%)	38	59
3	9	215/215 (100%)	213 (99%)	2 (1%)	70	76
3	AF	209/215 (97%)	207 (99%)	2 (1%)	68	76
3	AG	210/215 (98%)	202 (96%)	8 (4%)	29	51
3	AH	211/215 (98%)	204 (97%)	7 (3%)	33	55
3	AI	209/215 (97%)	203 (97%)	6 (3%)	37	58
3	AJ	210/215 (98%)	204 (97%)	6 (3%)	37	58
3	AK	200/215 (93%)	196 (98%)	4 (2%)	48	66
3	AL	205/215 (95%)	202 (98%)	3 (2%)	57	70
3	AM	205/215 (95%)	200 (98%)	5 (2%)	43	63
3	AN	205/215 (95%)	201 (98%)	4 (2%)	48	66
3	ZA	215/215 (100%)	214 (100%)	1 (0%)	81	82
3	ZB	215/215 (100%)	213 (99%)	2 (1%)	70	76
3	ZC	215/215 (100%)	212 (99%)	3 (1%)	59	71
3	ZD	215/215 (100%)	208 (97%)	7 (3%)	33	55
3	ZE	215/215 (100%)	210 (98%)	5 (2%)	44	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	ZF	321/323 (99%)	315 (98%)	6 (2%)	50	67
4	ZG	321/323 (99%)	315 (98%)	6 (2%)	50	67
4	ZH	321/323 (99%)	316 (98%)	5 (2%)	55	69
4	ZI	321/323 (99%)	316 (98%)	5 (2%)	55	69
4	ZJ	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZK	321/323 (99%)	319 (99%)	2 (1%)	78	80
4	ZL	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZM	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZN	321/323 (99%)	317 (99%)	4 (1%)	63	73
4	ZO	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZP	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZQ	321/323 (99%)	319 (99%)	2 (1%)	78	80
4	ZR	321/323 (99%)	320 (100%)	1 (0%)	86	85
4	ZS	321/323 (99%)	320 (100%)	1 (0%)	86	85
4	ZT	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZU	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	ZV	321/323 (99%)	319 (99%)	2 (1%)	78	80
4	ZW	321/323 (99%)	320 (100%)	1 (0%)	86	85
4	ZX	321/323 (99%)	319 (99%)	2 (1%)	78	80
4	ZY	321/323 (99%)	321 (100%)	0	100	100
4	ZZ	321/323 (99%)	321 (100%)	0	100	100
4	Za	321/323 (99%)	320 (100%)	1 (0%)	86	85
4	Zb	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	Zc	321/323 (99%)	318 (99%)	3 (1%)	70	76
4	Zd	321/323 (99%)	320 (100%)	1 (0%)	86	85
4	Ze	321/323 (99%)	319 (99%)	2 (1%)	78	80
4	Zf	321/323 (99%)	319 (99%)	2 (1%)	78	80
4	Zg	321/323 (99%)	320 (100%)	1 (0%)	86	85
4	Zh	321/323 (99%)	321 (100%)	0	100	100
5	AA	190/193 (98%)	186 (98%)	4 (2%)	47	65
5	AB	191/193 (99%)	186 (97%)	5 (3%)	40	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AC	192/193 (100%)	191 (100%)	1 (0%)	81	82
5	AD	192/193 (100%)	188 (98%)	4 (2%)	47	65
5	AE	191/193 (99%)	186 (97%)	5 (3%)	40	61
6	AO	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AP	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AQ	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AR	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AS	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AT	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AU	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AV	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AW	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AX	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AY	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	AZ	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Aa	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ac	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ad	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ae	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Af	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ag	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ah	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ai	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Aj	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ak	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Al	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Am	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	An	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ao	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	Ap	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BG	8/467 (2%)	7 (88%)	1 (12%)	4	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	BH	11/467 (2%)	11 (100%)	0	100	100
6	BI	14/467 (3%)	12 (86%)	2 (14%)	3	16
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
6	BO	14/467 (3%)	13 (93%)	1 (7%)	13	37
6	BP	11/467 (2%)	11 (100%)	0	100	100
6	BQ	15/467 (3%)	14 (93%)	1 (7%)	15	39
6	BR	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BS	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BT	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BU	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BV	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BW	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	BX	141/467 (30%)	140 (99%)	1 (1%)	76	79
6	UI	128/467 (27%)	122 (95%)	6 (5%)	23	47
6	UJ	128/467 (27%)	121 (94%)	7 (6%)	19	44
6	UK	128/467 (27%)	122 (95%)	6 (5%)	23	47
6	UL	128/467 (27%)	122 (95%)	6 (5%)	23	47
6	UM	128/467 (27%)	122 (95%)	6 (5%)	23	47
6	UN	128/467 (27%)	122 (95%)	6 (5%)	23	47
6	UO	128/467 (27%)	122 (95%)	6 (5%)	23	47
6	UP	128/467 (27%)	121 (94%)	7 (6%)	19	44
6	WA	95/467 (20%)	91 (96%)	4 (4%)	26	49
6	WB	93/467 (20%)	86 (92%)	7 (8%)	12	35
6	WC	91/467 (20%)	83 (91%)	8 (9%)	9	31
6	WD	92/467 (20%)	88 (96%)	4 (4%)	26	49
6	WE	94/467 (20%)	87 (93%)	7 (7%)	13	35
6	WF	93/467 (20%)	84 (90%)	9 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	WG	94/467 (20%)	85 (90%)	9 (10%)	8	27
6	WH	79/467 (17%)	75 (95%)	4 (5%)	21	45
6	WI	79/467 (17%)	75 (95%)	4 (5%)	21	45
6	WJ	83/467 (18%)	80 (96%)	3 (4%)	31	53
6	WK	82/467 (18%)	76 (93%)	6 (7%)	13	36
6	WL	69/467 (15%)	67 (97%)	2 (3%)	37	58
6	WM	66/467 (14%)	64 (97%)	2 (3%)	36	57
6	WN	68/467 (15%)	66 (97%)	2 (3%)	37	58
6	WO	80/467 (17%)	76 (95%)	4 (5%)	22	45
6	WP	83/467 (18%)	80 (96%)	3 (4%)	31	53
6	WQ	93/467 (20%)	90 (97%)	3 (3%)	34	56
6	WR	93/467 (20%)	85 (91%)	8 (9%)	10	32
6	WS	93/467 (20%)	89 (96%)	4 (4%)	26	49
6	WT	93/467 (20%)	86 (92%)	7 (8%)	12	35
6	WU	94/467 (20%)	88 (94%)	6 (6%)	16	40
6	WV	92/467 (20%)	82 (89%)	10 (11%)	6	23
6	WW	93/467 (20%)	85 (91%)	8 (9%)	10	32
7	Ab	74/74 (100%)	67 (90%)	7 (10%)	8	27
7	Aq	74/74 (100%)	72 (97%)	2 (3%)	39	60
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%)	209 (100%)	1 (0%)	81	82
9	Au	177/204 (87%)	174 (98%)	3 (2%)	53	68
9	Av	179/204 (88%)	175 (98%)	4 (2%)	45	64
9	Aw	178/204 (87%)	176 (99%)	2 (1%)	65	74
9	Ax	178/204 (87%)	174 (98%)	4 (2%)	45	64
9	Ay	179/204 (88%)	174 (97%)	5 (3%)	38	59
10	A1	68/79 (86%)	65 (96%)	3 (4%)	25	48
10	A2	70/79 (89%)	68 (97%)	2 (3%)	37	58
10	A3	70/79 (89%)	66 (94%)	4 (6%)	18	43
10	A4	70/79 (89%)	68 (97%)	2 (3%)	37	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	A5	69/79 (87%)	63 (91%)	6 (9%)	9	31
10	Az	45/79 (57%)	43 (96%)	2 (4%)	25	48
11	A0	102/113 (90%)	100 (98%)	2 (2%)	48	66
11	A6	110/113 (97%)	106 (96%)	4 (4%)	31	53
11	A7	101/113 (89%)	101 (100%)	0	100	100
11	A8	103/113 (91%)	98 (95%)	5 (5%)	22	46
11	A9	104/113 (92%)	103 (99%)	1 (1%)	68	76
12	BA	104/105 (99%)	104 (100%)	0	100	100
12	BB	104/105 (99%)	100 (96%)	4 (4%)	29	51
12	BC	104/105 (99%)	102 (98%)	2 (2%)	50	67
12	BD	104/105 (99%)	100 (96%)	4 (4%)	29	51
12	BE	103/105 (98%)	101 (98%)	2 (2%)	50	67
12	BF	104/105 (99%)	102 (98%)	2 (2%)	50	67
All	All	37084/66670 (56%)	36199 (98%)	885 (2%)	43	63

5 of 885 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	ZE	141	THR
3	AI	173	LEU
6	BQ	318	ASN
6	WK	164	LEU
4	ZH	71	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1360 such sidechains are listed below:

Mol	Chain	Res	Type
5	AE	240	ASN
6	Ak	303	GLN
3	AH	259	GLN
5	AE	153	ASN
6	AU	231	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

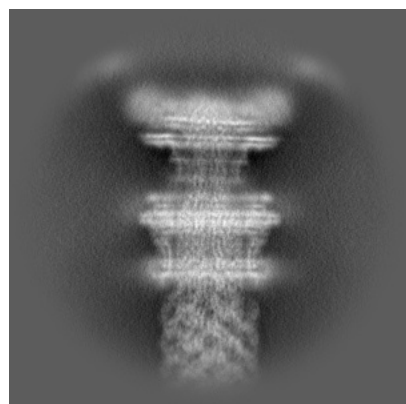
6 Map visualisation [i](#)

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

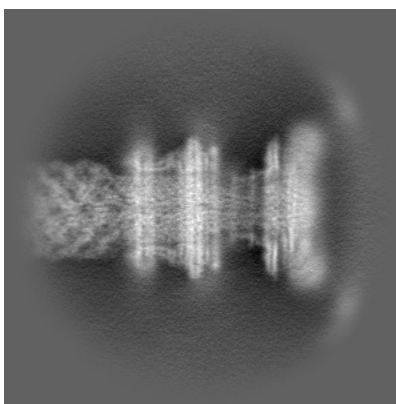
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

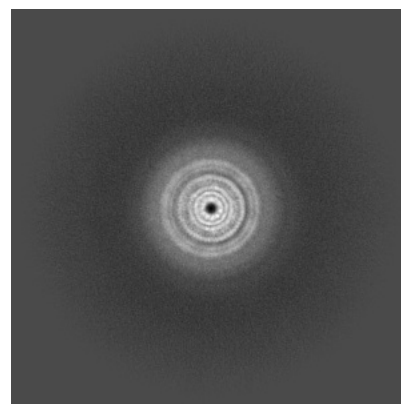
6.1.1 Primary map



X

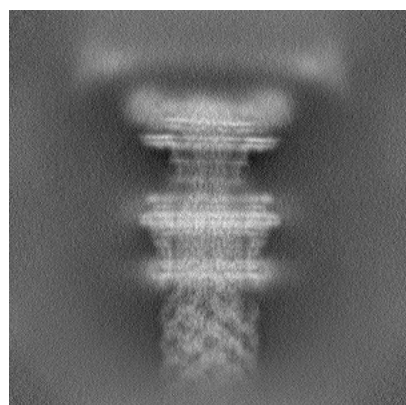


Y

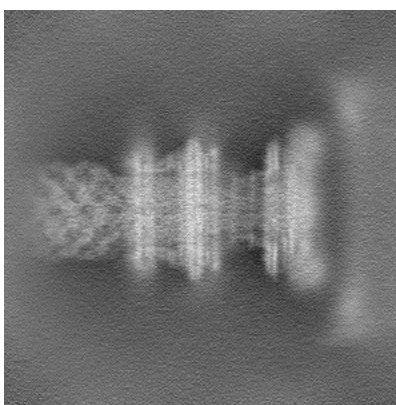


Z

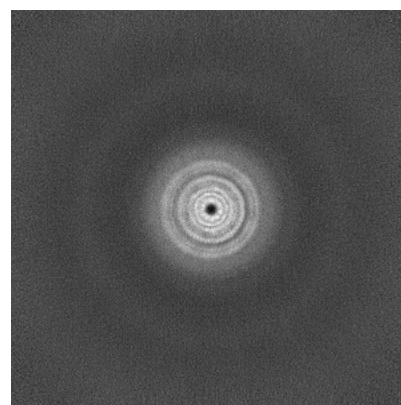
6.1.2 Raw map



X



Y

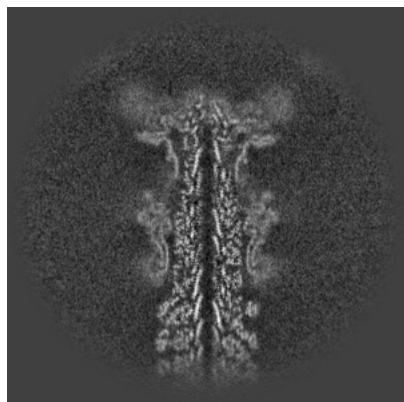


Z

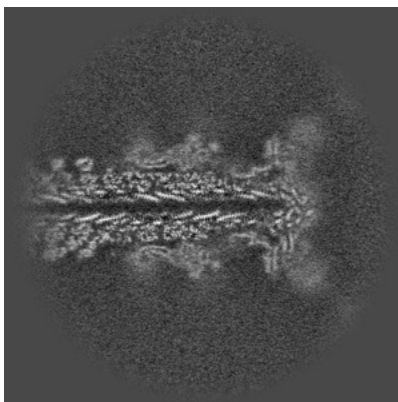
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

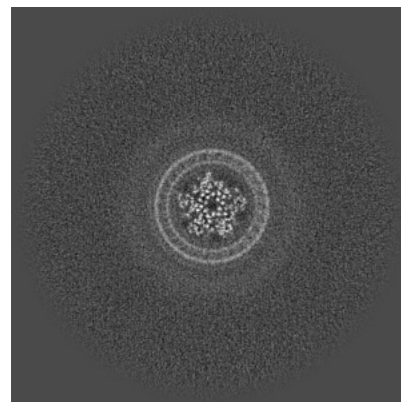
6.2.1 Primary map



X Index: 256

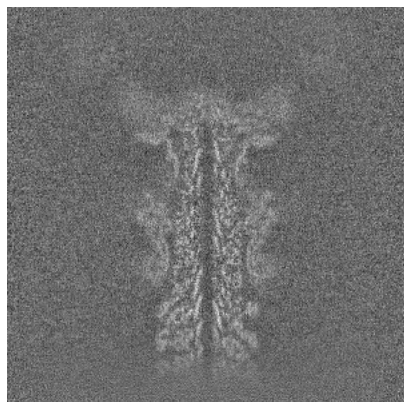


Y Index: 256

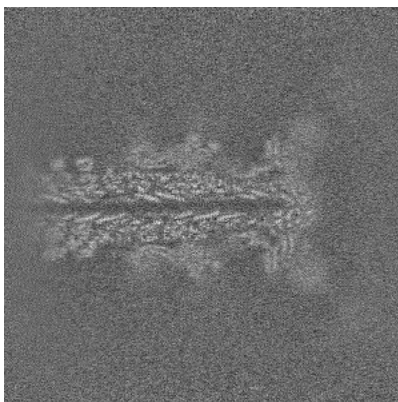


Z Index: 256

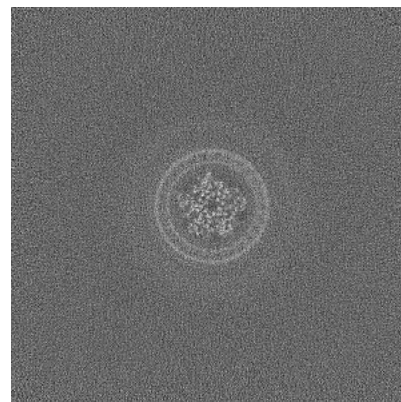
6.2.2 Raw map



X Index: 256



Y Index: 256

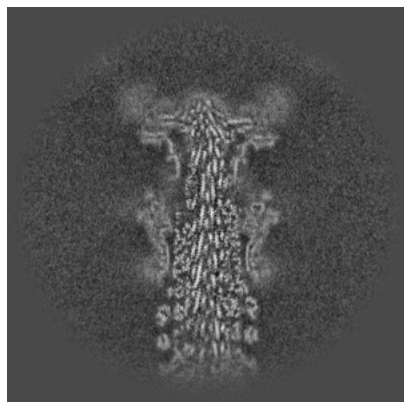


Z Index: 256

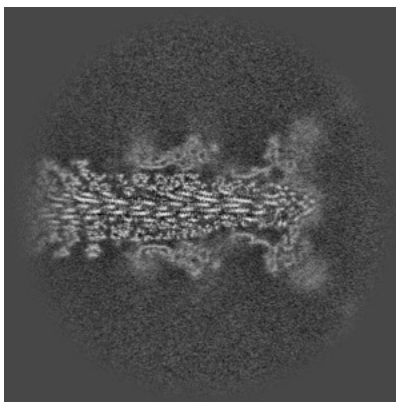
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

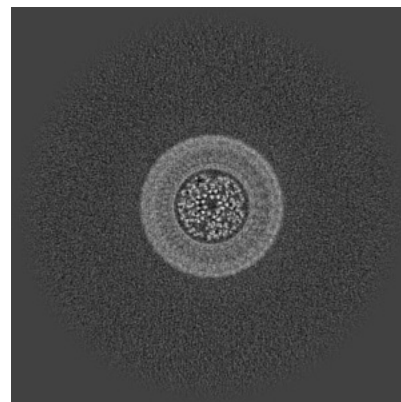
6.3.1 Primary map



X Index: 247

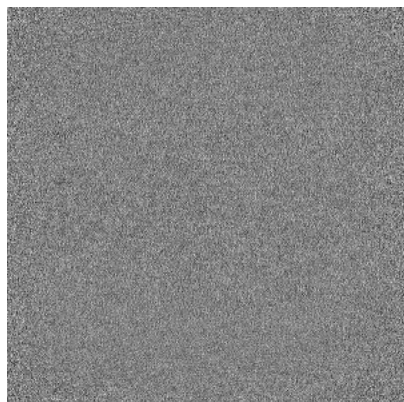


Y Index: 246

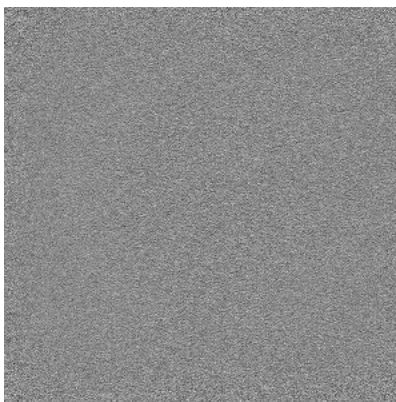


Z Index: 239

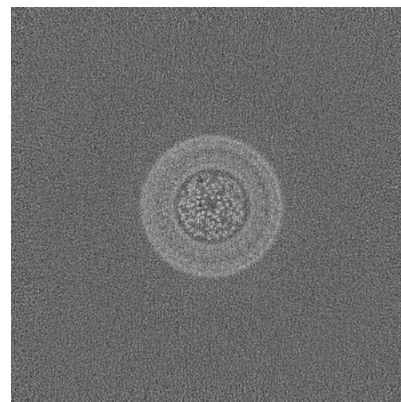
6.3.2 Raw map



X Index: 0



Y Index: 0

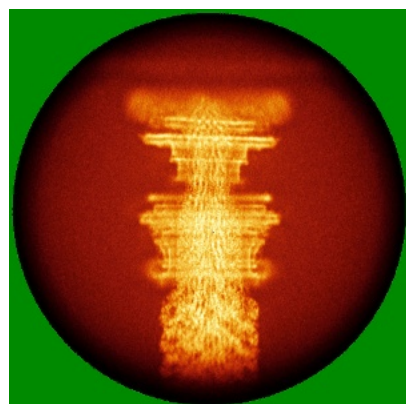


Z Index: 240

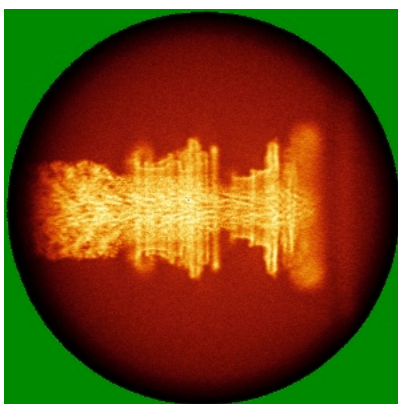
The images above show the largest variance slices of the map in three orthogonal directions.

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

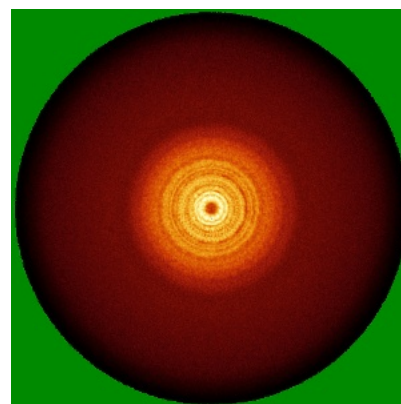
6.4.1 Primary map



X

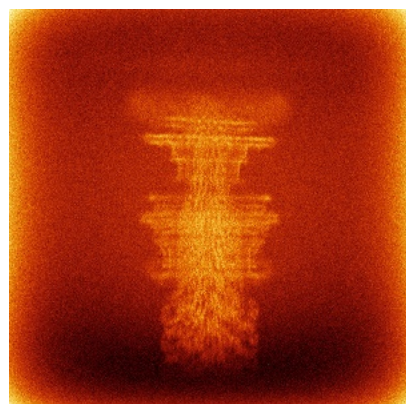


Y

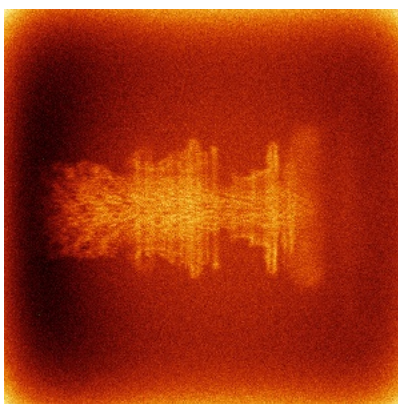


Z

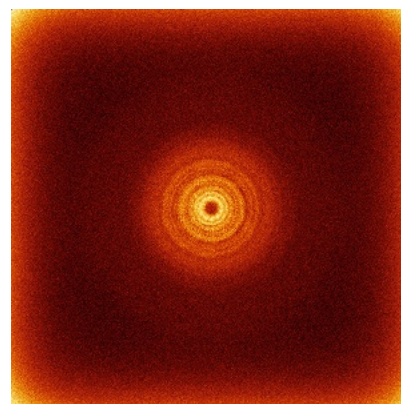
6.4.2 Raw map



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](#)

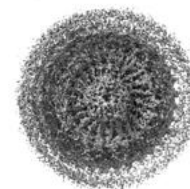
6.5.1 Primary map



X



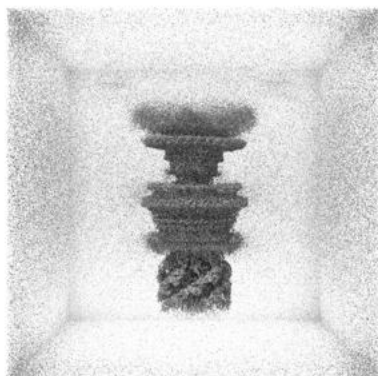
Y



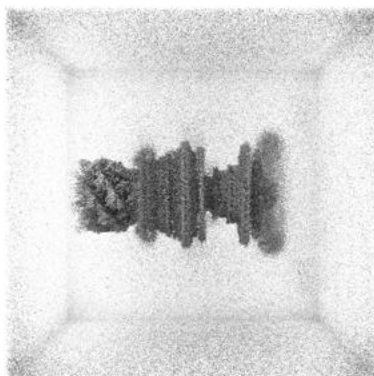
Z

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.

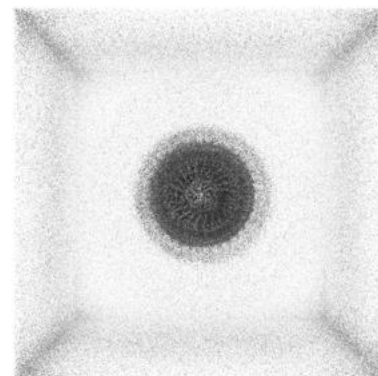
6.5.2 Raw map



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.

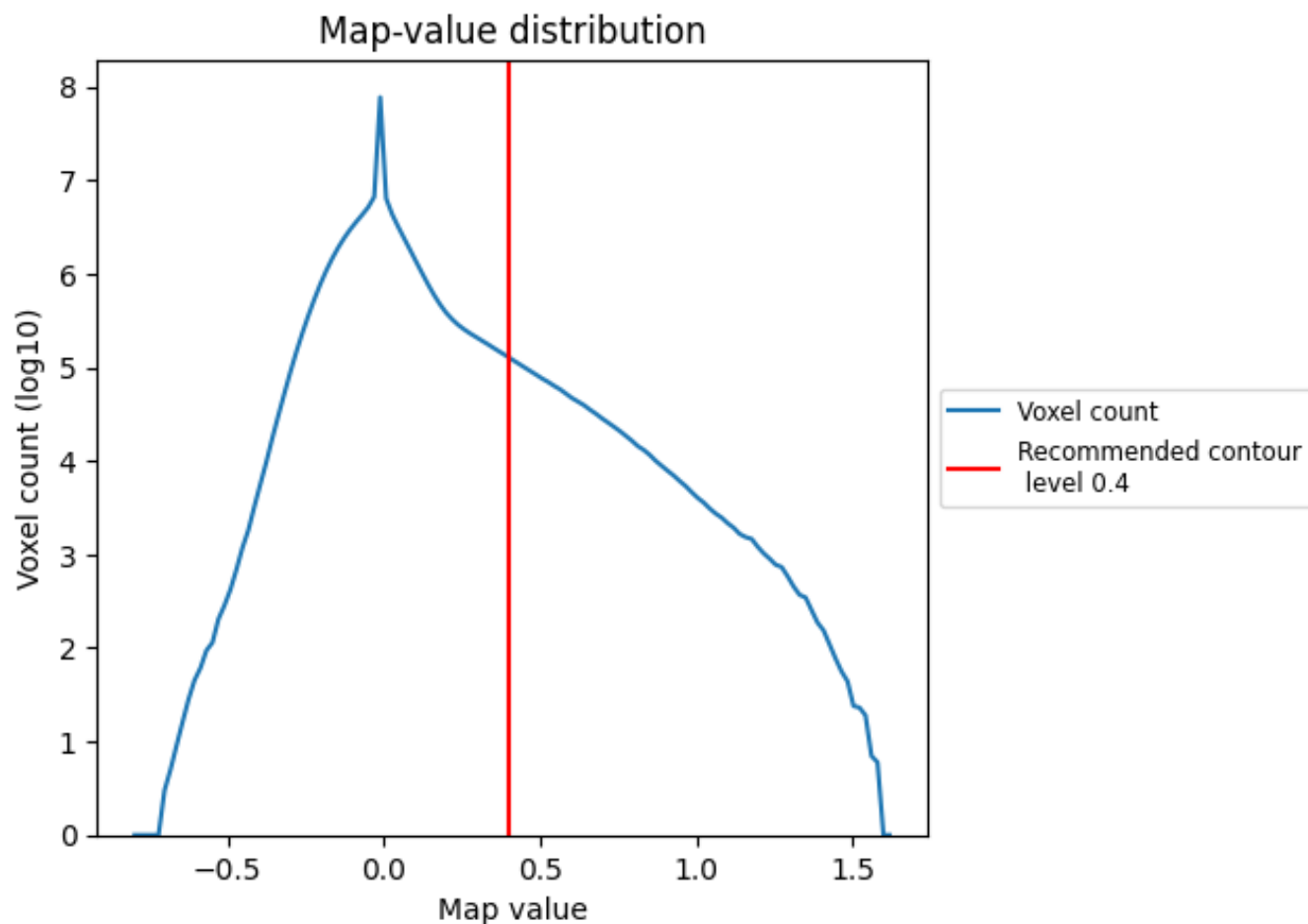
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

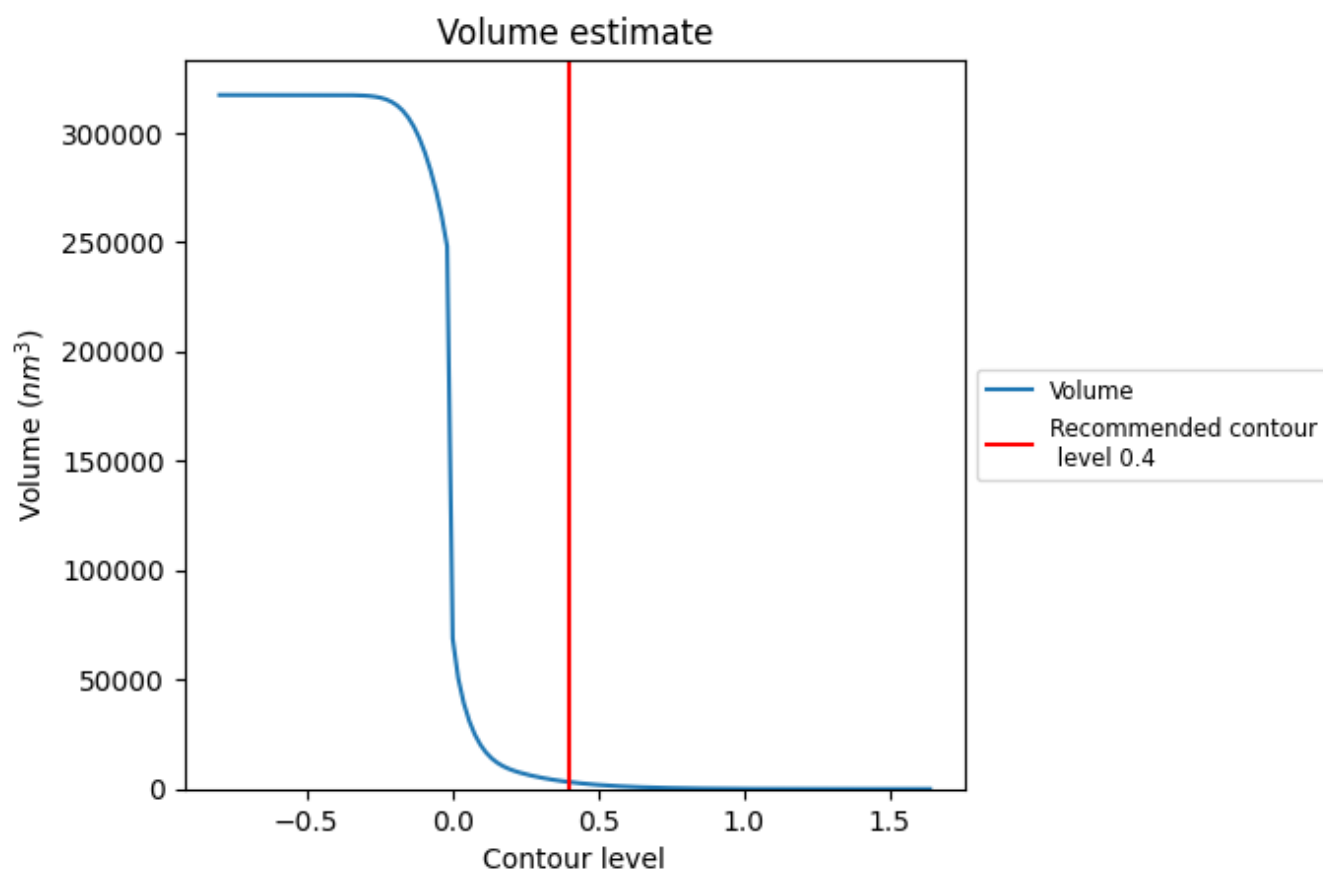
This section contains the results of statistical analysis of the map.

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.

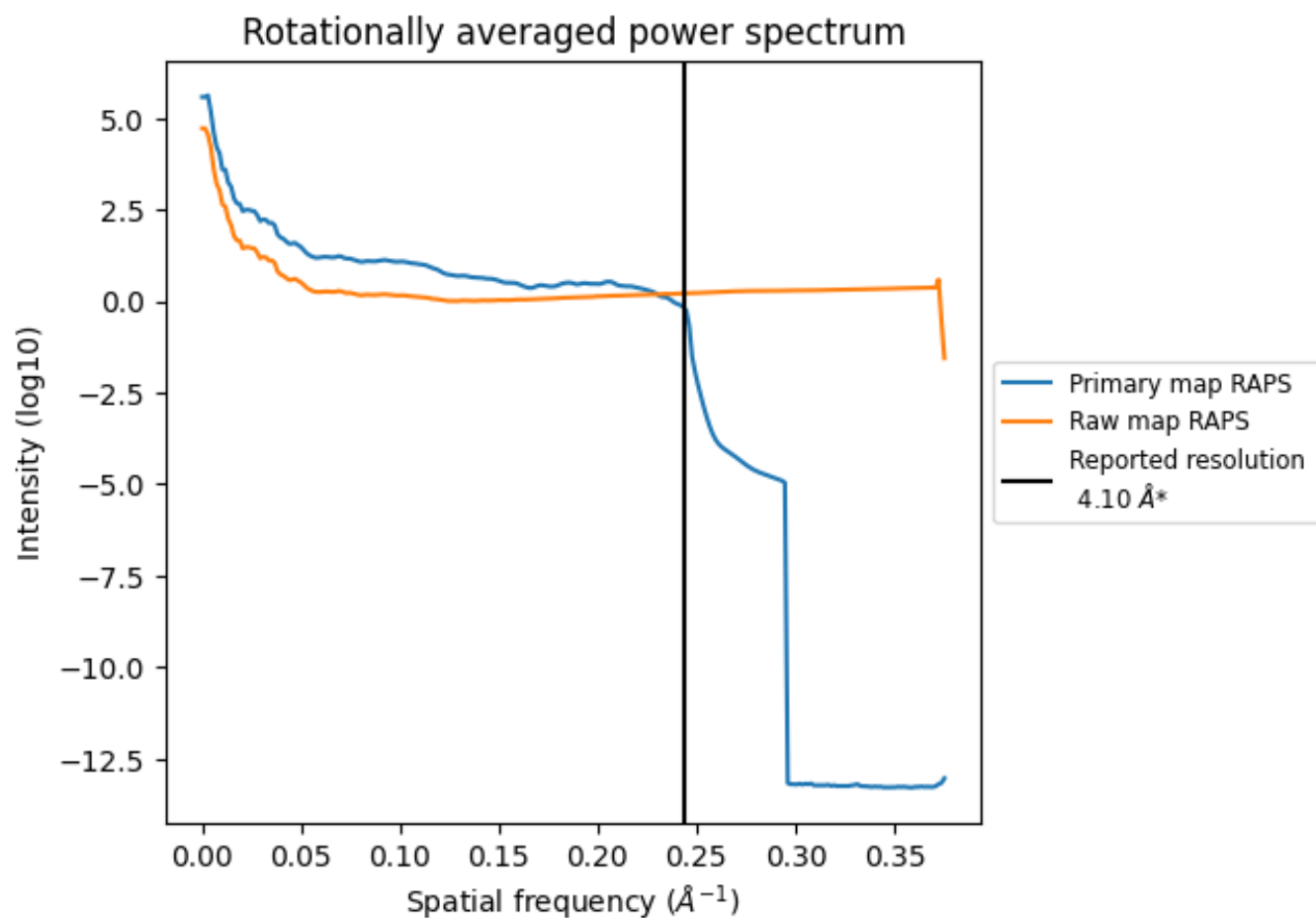
7.2 Volume estimate [i](#)



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 ⓘ

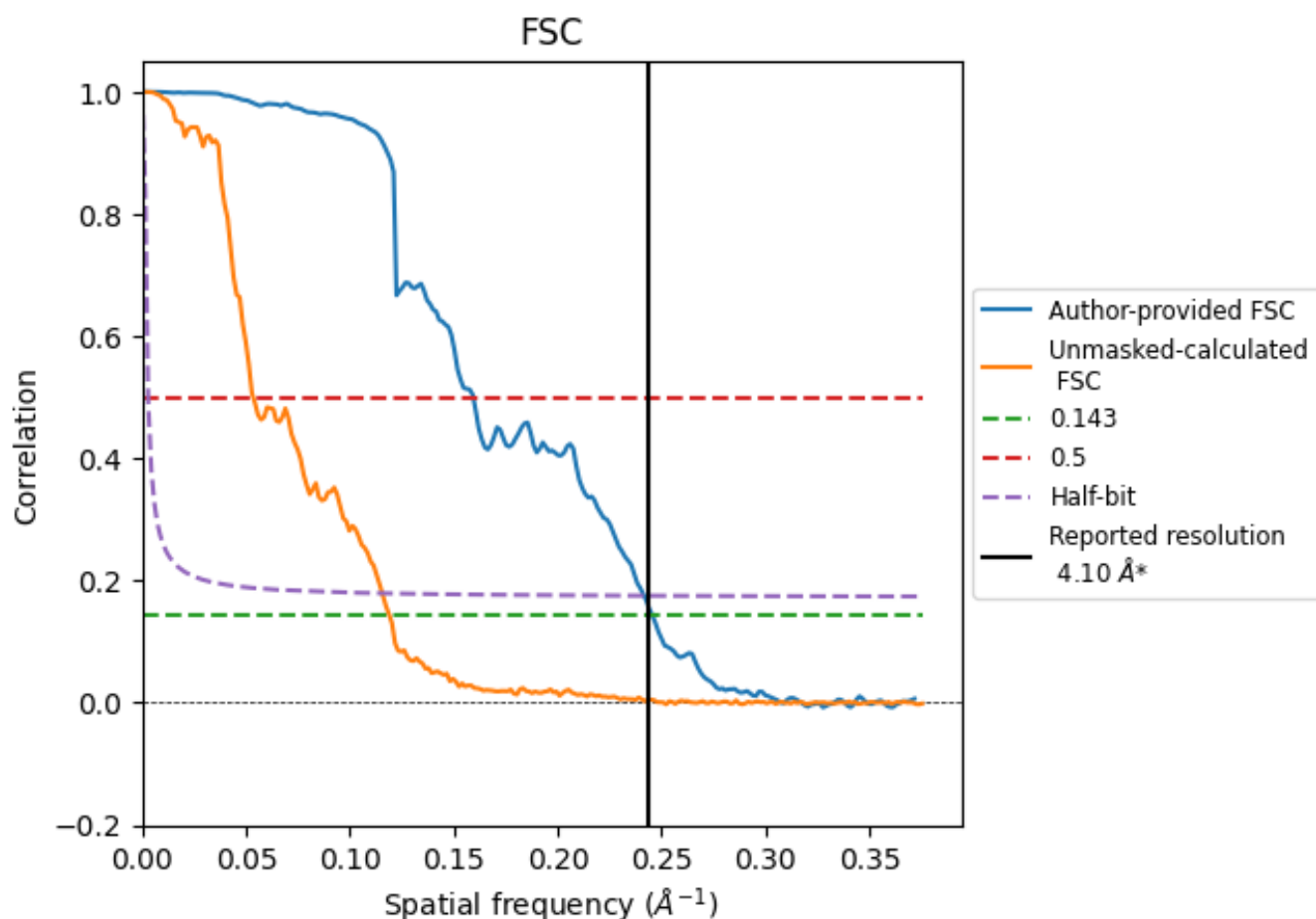


*Reported resolution corresponds to spatial frequency of 0.244 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

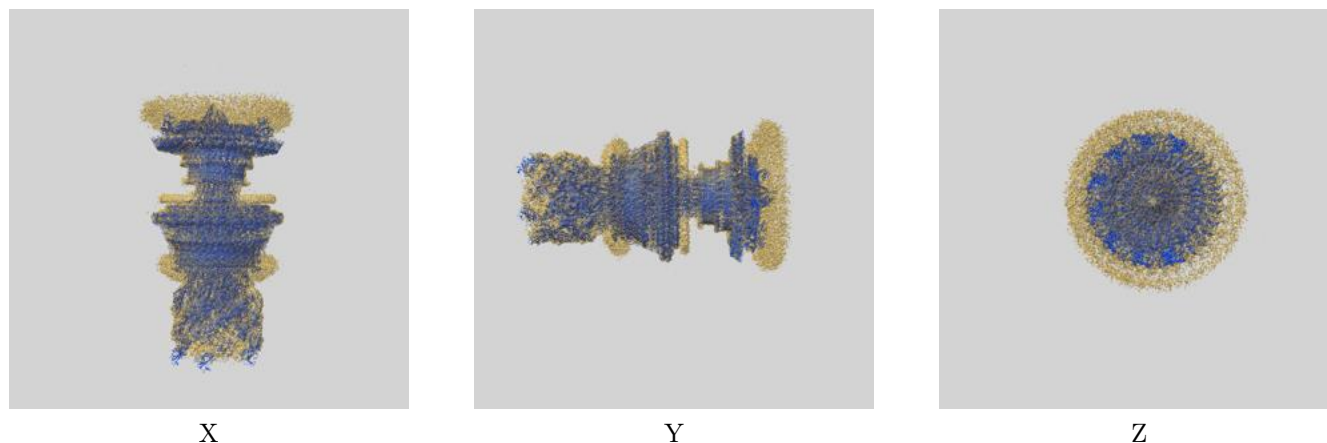
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.07	6.28	4.14
Unmasked-calculated*	8.41	18.73	8.66

*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](#)

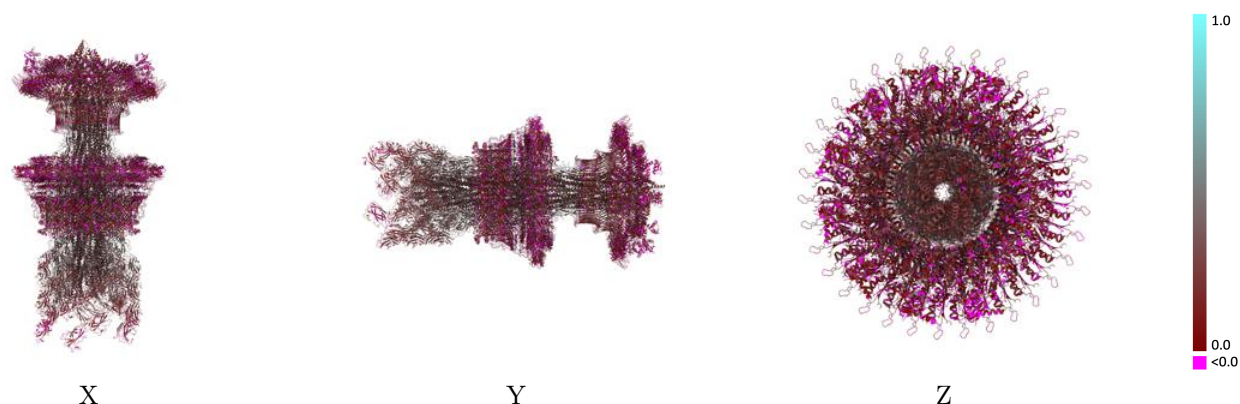
This section contains information regarding the fit between EMDB map EMD-37630 and PDB model 8WLT. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



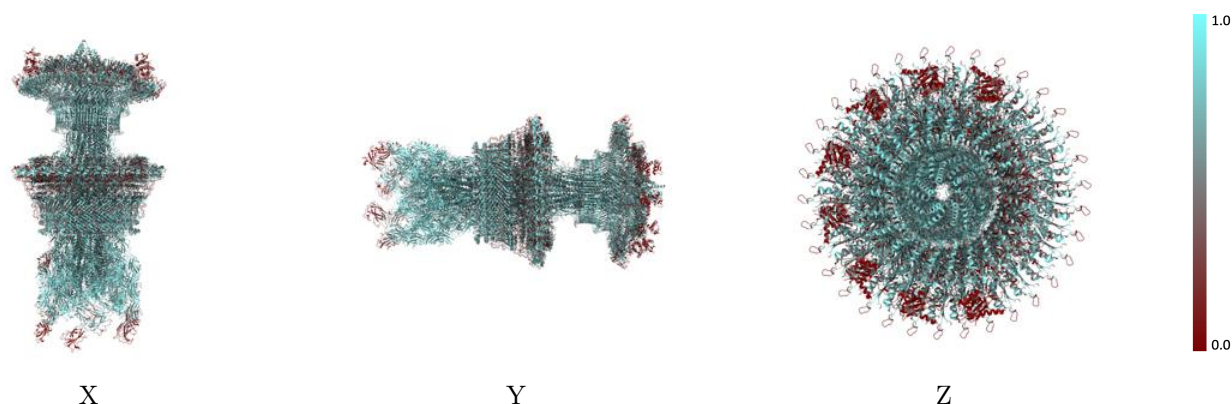
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



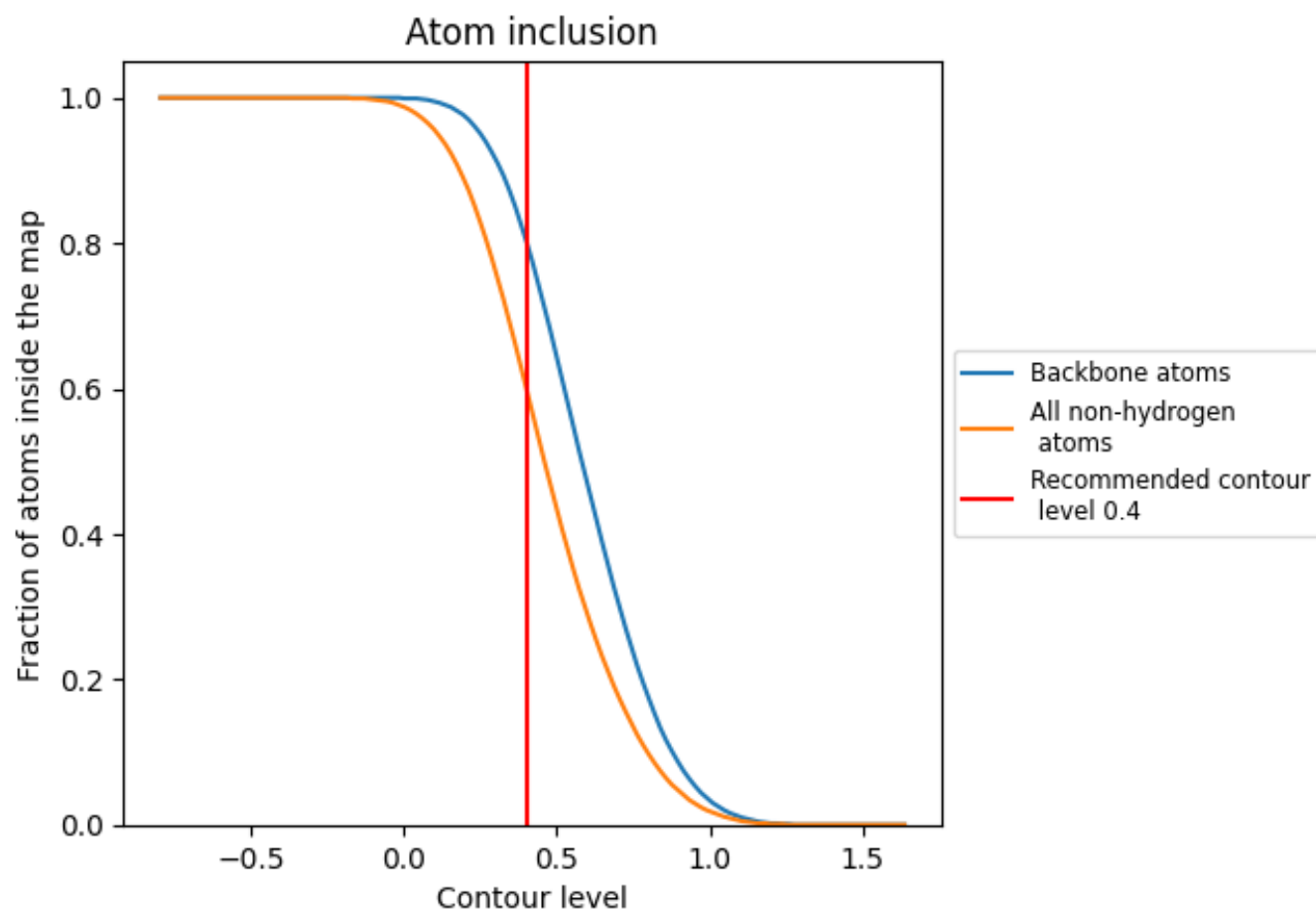
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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