



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 04:30 AM UTC

PDB ID : 7CGO / pdb_00007cgo
EMDB ID : EMD-30359
Title : Cryo-EM structure of the flagellar motor-hook complex from Salmonella
Authors : Tan, J.X.; Chang, S.H.; Wang, X.F.; Xu, C.H.; Zhou, Y.; Zhang, X.; Zhu, Y.Q.
Deposited on : 2020-07-01
Resolution : 3.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
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

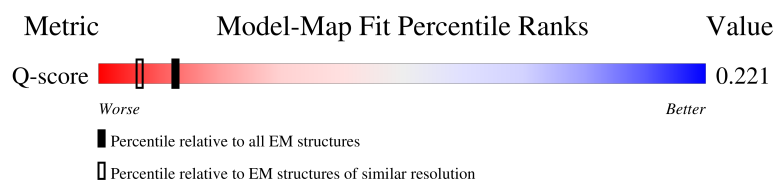
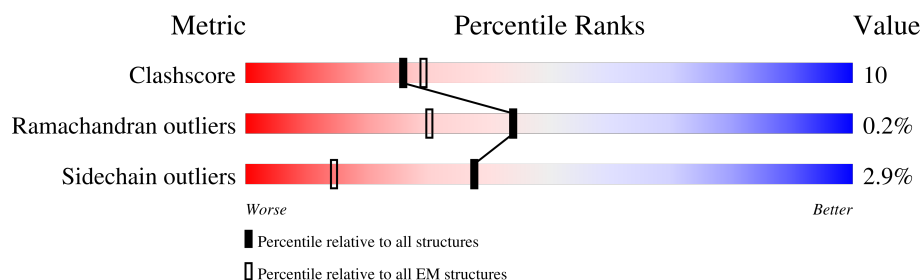
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



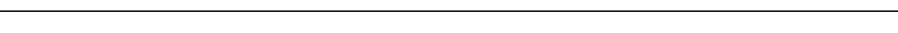
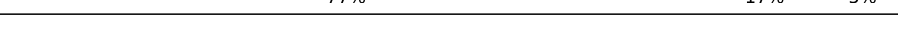
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	260	 78% 22%
1	B	260	 75% 25% .
1	C	260	 77% 22% .
1	D	260	 77% 23%

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Mol	Chain	Length	Quality of chain
1	E	260	 78% 21% .
1	F	260	 78% 22%
1	G	260	 76% 23% .
1	H	260	 78% 22%
1	I	260	 80% 19%
1	J	260	 81% 18% .
1	K	260	 83% 16% .
1	L	260	 79% 20%
1	M	260	 85% 15%
1	N	260	 76% 21% .
1	O	260	 78% 18% . .
1	P	260	 79% 17% 5%
1	Q	260	 77% 17% . 5%
1	R	260	 77% 18% . .
1	S	260	 77% 17% 5%
1	T	260	 78% 20% .
1	U	260	 78% 22%
1	V	260	 73% 25% .
1	W	260	 78% 20% .
1	X	260	 82% 17%
2	a	251	 78% 21% .
2	b	251	 73% 24% . .
2	c	251	 77% 22% .
2	d	251	 79% 20% . .
2	e	251	 81% 18% .

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Mol	Chain	Length	Quality of chain
3	0	15	100%
3	1	15	93% 7%
3	2	15	93% 7%
3	3	15	100%
3	4	15	87% 13%
4	5	21	90% 10%
4	6	21	14% 95% 5%
4	7	21	86% 14%
4	8	21	86% 14%
4	9	21	10% 86% 14%
5	f	134	69% 27% .
5	g	134	74% 21% . .
5	h	134	66% 28% . .
5	i	134	77% 19% .
5	j	134	76% 18% . 5%
5	p	134	78% 18% .
6	k	138	61% 17% 22%
6	l	138	62% 14% . 23%
6	m	138	56% 21% 23%
6	n	138	59% 18% . 22%
6	o	138	64% 15% 21%
7	q	104	59% 10% 32%
7	r	104	57% 11% 33%
7	s	104	65% . 31%
7	t	104	61% 9% 31%

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Mol	Chain	Length	Quality of chain
7	u	104	
7	v	104	
8	DA	403	
8	DB	403	
8	DC	403	
8	DD	403	
8	DE	403	
8	DF	403	
8	DG	403	
8	DH	403	
8	DI	403	
8	DJ	403	
8	DK	403	
8	DL	403	
8	DM	403	
8	DN	403	
8	DO	403	
8	DP	403	
8	DQ	403	
8	DR	403	
8	DS	403	
8	DT	403	
8	DU	403	
8	DV	403	
8	DW	403	

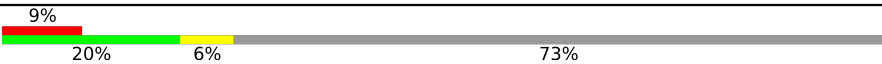
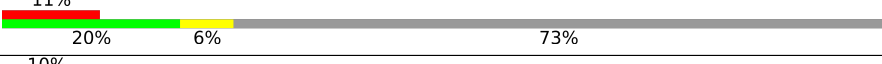
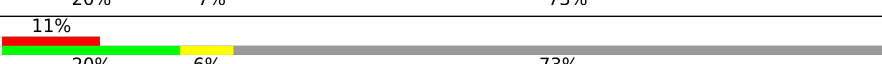
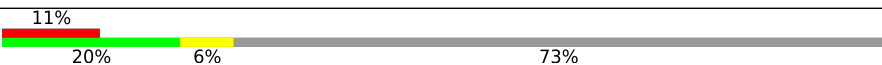
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Mol	Chain	Length	Quality of chain
8	DX	403	75% 67%33%
8	DY	403	75% 70%29%
8	DZ	403	77% 72%28%
8	EA	403	84% 74%26%
8	EB	403	81% 66%34%
8	EC	403	86% 72%27%
8	ED	403	88% 69%31%
8	EE	403	86% 72%27%
8	EF	403	93% 70%30%
8	EG	403	93% 71%28%
9	CE	264	17% 65%33%
10	CA	89	76% 24%
10	CB	89	6% 74%25%
10	CC	89	66% 34%
10	CD	89	20% 80%20%
11	CF	245	64% 21%14%
11	w	245	62% 24%14%
11	x	245	7% 67%17%14%
11	y	245	55% 30%14%
11	z	245	64% 22%14%
12	Ca	560	9% 21%6%73%
12	Cb	560	9% 20%7%73%
12	Cc	560	9% 20%7%73%
12	Cd	560	12% 20%6%73%
12	Ce	560	10% 20%6%73%

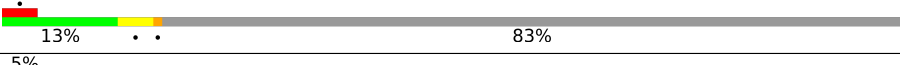
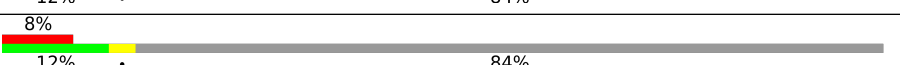
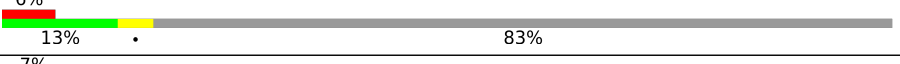
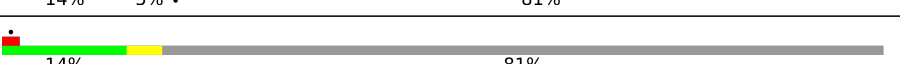
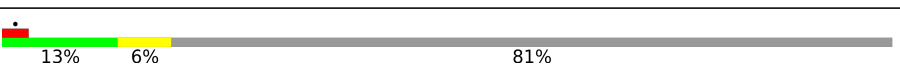
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Mol	Chain	Length	Quality of chain
12	Cf	560	
12	Cg	560	
12	Ch	560	
12	Ci	560	
12	Cj	560	
12	Ck	560	
12	Cl	560	
12	Cm	560	
12	Cn	560	
12	Co	560	
12	Cp	560	
12	Cq	560	
12	Cr	560	
12	Cs	560	
12	Ct	560	
12	Cu	560	
12	Cv	560	
12	Cw	560	
12	Cx	560	
12	Cy	560	
12	Cz	560	
12	Da	560	
12	Db	560	
12	Dc	560	
12	Dd	560	

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Mol	Chain	Length	Quality of chain
12	De	560	 14% 82%
12	Df	560	 13% 83%
12	Dg	560	 5% 12% 84%
12	Dh	560	 6% 12% 84%
12	Di	560	 7% 12% 84%
12	Dj	560	 7% 12% 84%
12	Dk	560	 7% 12% 84%
12	Dl	560	 8% 12% 84%
12	Dm	560	 8% 12% 84%
12	Dn	560	 7% 11% 84%
12	Do	560	 6% 13% 83%
12	Dp	560	 7% 15% 81%
12	Dq	560	 14% 5% 81%
12	Dr	560	 15% 81%
12	Ds	560	 15% 81%
12	Dt	560	 14% 5% 81%
12	Du	560	 14% 81%
12	Dv	560	 13% 6% 81%
12	Dw	560	 15% 81%
12	Ea	560	 8% 20% 7% 73%
12	Eb	560	 8% 21% 6% 73%
12	Ec	560	 7% 20% 6% 73%
12	Ed	560	 7% 20% 6% 73%
12	Ee	560	 6% 20% 6% 73%
12	Ef	560	 7% 20% 6% 73%

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Mol	Chain	Length	Quality of chain
12	Eg	560	
12	Eh	560	
13	GA	12	
13	GB	12	
13	GC	12	
13	GD	12	
13	GE	12	
14	GF	18	
14	GG	18	
14	GH	18	
14	GI	18	
14	GJ	18	
14	GK	18	
15	AA	232	
15	AB	232	
15	AC	232	
15	AD	232	
15	AE	232	
15	AF	232	
15	AG	232	
15	AH	232	
15	AI	232	
15	AJ	232	
15	AK	232	
15	AL	232	

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Mol	Chain	Length	Quality of chain
15	AM	232	
15	AN	232	
15	AO	232	
15	AP	232	
15	AQ	232	
15	AR	232	
15	AS	232	
15	AT	232	
15	AU	232	
15	AV	232	
15	AW	232	
15	AX	232	
15	AY	232	
15	AZ	232	
16	BA	365	
16	BB	365	
16	BC	365	
16	BD	365	
16	BE	365	
16	BF	365	
16	BG	365	
16	BH	365	
16	BI	365	
16	BJ	365	
16	BK	365	

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Mol	Chain	Length	Quality of chain
16	BL	365	
16	BM	365	
16	BN	365	
16	BO	365	
16	BP	365	
16	BQ	365	
16	BR	365	
16	BS	365	
16	BT	365	
16	BU	365	
16	BV	365	
16	BW	365	
16	BX	365	
16	BY	365	
16	BZ	365	

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 335722 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 basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	B	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	C	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	D	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	E	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	F	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	G	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	H	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	I	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	J	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	K	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	L	259	Total 1941	C 1197	N 340	O 399	S 5	0	0
1	M	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
1	N	251	Total 1887	C 1167	N 330	O 384	S 6	0	0
1	O	252	Total 1894	C 1172	N 331	O 385	S 6	0	0
1	P	248	Total 1862	C 1151	N 327	O 379	S 5	0	0
1	Q	247	Total 1858	C 1149	N 326	O 378	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	250	Total	C	N	O	S	0	0
			1875	1159	329	382	5		
1	S	247	Total	C	N	O	S	0	0
			1858	1149	326	378	5		
1	T	253	Total	C	N	O	S	0	0
			1902	1176	333	388	5		
1	U	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		
1	V	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		
1	W	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		
1	X	259	Total	C	N	O	S	0	0
			1941	1197	340	399	5		

- Molecule 2 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
2	b	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
2	c	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
2	d	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
2	e	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

- Molecule 3 is a protein called Flagellar MS ring L2.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	0	15	Total	C	N	O	0	0
			75	45	15	15		
3	1	15	Total	C	N	O	0	0
			75	45	15	15		
3	2	15	Total	C	N	O	0	0
			75	45	15	15		
3	3	15	Total	C	N	O	0	0
			75	45	15	15		
3	4	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 4 is a protein called Flagellar MS ring L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	5	21	Total	C	N	O	0	0
			140	88	24	28		
4	6	21	Total	C	N	O	0	0
			140	88	24	28		
4	7	21	Total	C	N	O	0	0
			140	88	24	28		
4	9	21	Total	C	N	O	0	0
			140	88	24	28		
4	8	21	Total	C	N	O	0	0
			140	88	24	28		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	128	Total	C	N	O	S	0	0
			936	585	160	186	5		
5	g	130	Total	C	N	O	S	0	0
			949	592	163	189	5		
5	h	128	Total	C	N	O	S	0	0
			935	584	160	186	5		
5	j	127	Total	C	N	O	S	0	0
			931	582	159	185	5		
5	p	129	Total	C	N	O	S	0	0
			940	587	161	187	5		
5	i	129	Total	C	N	O	S	0	0
			944	589	162	188	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	l	106	Total	C	N	O	S	0	0
			833	515	150	163	5		
6	m	106	Total	C	N	O	S	0	0
			833	515	150	163	5		
6	o	109	Total	C	N	O	S	0	0
			856	529	156	166	5		
6	k	108	Total	C	N	O	S	0	0
			852	527	155	165	5		
6	n	107	Total	C	N	O	S	0	0
			844	521	154	164	5		

- Molecule 7 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	q	71	Total	C	N	O	S	0	0
			536	330	98	102	6		
7	r	70	Total	C	N	O	S	0	0
			526	323	97	100	6		
7	s	72	Total	C	N	O	S	0	0
			543	335	99	103	6		
7	t	72	Total	C	N	O	S	0	0
			543	335	99	103	6		
7	u	72	Total	C	N	O	S	0	0
			543	335	99	103	6		
7	v	38	Total	C	N	O	S	0	0
			289	178	50	55	6		

- Molecule 8 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	DA	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DB	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DC	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DD	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DE	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DH	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DI	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DJ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DK	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DL	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DM	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DN	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	DO	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DP	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DQ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DR	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DS	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DT	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DU	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DV	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DW	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DX	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DY	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	DZ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	EA	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	EB	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	EC	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	ED	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	EE	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	EF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
8	EG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CE	260	Total	C	N	O	S	0	0
			2002	1339	317	330	16		

- Molecule 10 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CA	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
10	CB	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
10	CC	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
10	CD	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

- Molecule 11 is a protein called Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	w	211	Total	C	N	O	S	0	0
			1636	1091	254	279	12		
11	x	211	Total	C	N	O	S	0	0
			1636	1091	254	279	12		
11	y	211	Total	C	N	O	S	0	0
			1636	1091	254	279	12		
11	z	211	Total	C	N	O	S	0	0
			1636	1091	254	279	12		
11	CF	211	Total	C	N	O	S	0	0
			1636	1091	254	279	12		

- Molecule 12 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Da	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Db	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dc	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dd	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	De	99	Total	C	N	O	S	0	0
			696	432	125	138	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Df	97	Total	C	N	O	S	0	0
			687	427	123	136	1		
12	Dg	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Dh	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Di	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Dj	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Dk	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Dl	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Dm	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Dn	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
12	Do	97	Total	C	N	O	S	0	0
			687	427	123	136	1		
12	Dp	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dq	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dr	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Ds	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dt	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Du	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dv	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Dw	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
12	Ca	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cb	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cc	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Cd	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ce	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cf	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cg	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ch	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ci	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cj	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ck	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cl	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cm	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cn	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Co	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cp	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cq	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cr	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cs	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ct	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cu	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cv	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cw	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cx	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
12	Cy	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Cz	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ea	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Eb	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ec	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ed	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ee	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Ef	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Eg	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
12	Eh	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		

- Molecule 13 is a protein called FlgB-Dc loop.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	GA	11	Total	C	N	O	0	0
			55	33	11	11		
13	GC	11	Total	C	N	O	0	0
			55	33	11	11		
13	GE	12	Total	C	N	O	0	0
			60	36	12	12		
13	GD	10	Total	C	N	O	0	0
			50	30	10	10		
13	GB	5	Total	C	N	O	0	0
			25	15	5	5		

- Molecule 14 is a protein called FliE helix 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	GF	18	Total	C	N	O	0	0
			90	54	18	18		
14	GG	18	Total	C	N	O	0	0
			90	54	18	18		

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Mol	Chain	Residues	Atoms				AltConf	Trace
14	GH	18	Total	C	N	O	0	0
			90	54	18	18		
14	GI	15	Total	C	N	O	0	0
			75	45	15	15		
14	GJ	18	Total	C	N	O	0	0
			90	54	18	18		
14	GK	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 15 is a protein called Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AA	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AB	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AC	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AD	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AE	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AF	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AG	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AH	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AI	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AJ	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AK	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AL	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AM	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AN	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AO	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AQ	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AR	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AS	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AT	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AU	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AV	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AW	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AX	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AY	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		
15	AZ	211	Total	C	N	O	S	0	0
			1589	993	282	310	4		

- Molecule 16 is a protein called Flagellar P-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BA	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BB	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BC	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BD	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BE	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BF	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BG	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
16	BH	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

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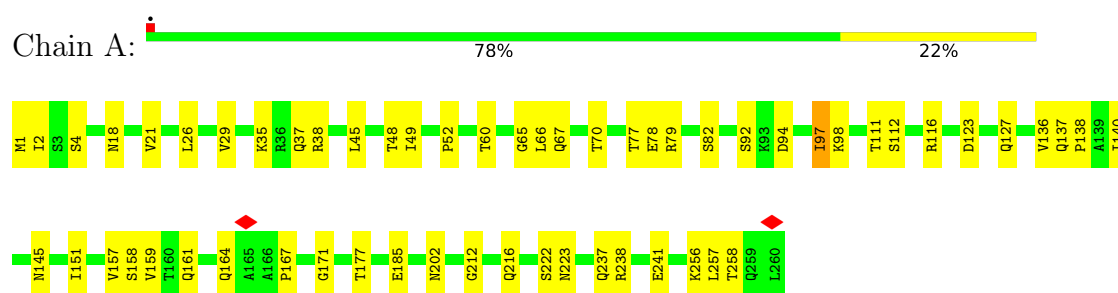
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Mol	Chain	Residues	Atoms					AltConf	Trace
16	BI	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BJ	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BK	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BL	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BM	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BN	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BO	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BP	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BQ	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BR	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BS	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BT	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BU	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BV	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BW	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BX	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BY	303	Total 2228	C 1364	N 405	O 446	S 13	0	0
16	BZ	303	Total 2228	C 1364	N 405	O 446	S 13	0	0

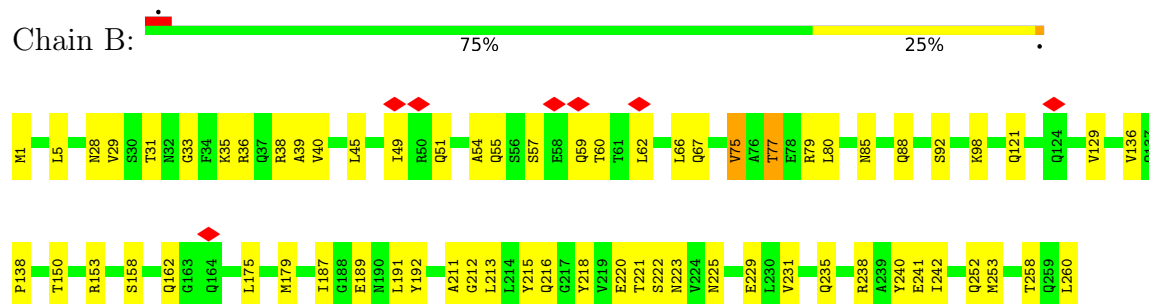
3 Residue-property plots [i](#)

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

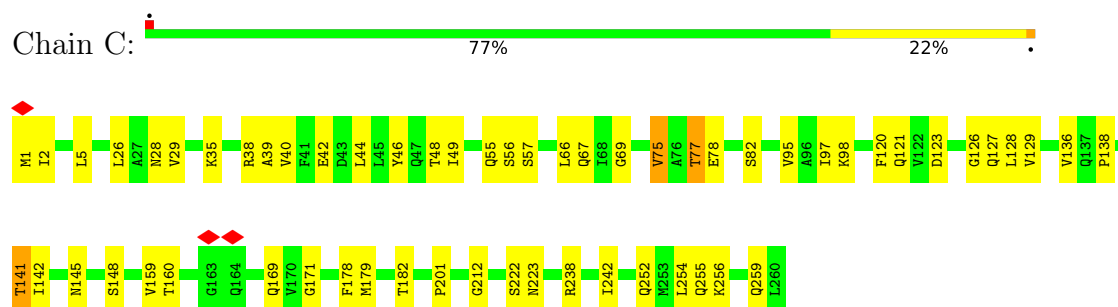
- Molecule 1: Flagellar basal-body rod protein FlgG



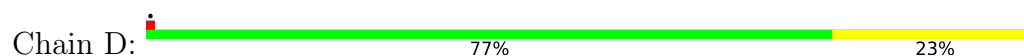
- Molecule 1: Flagellar basal-body rod protein FlgG

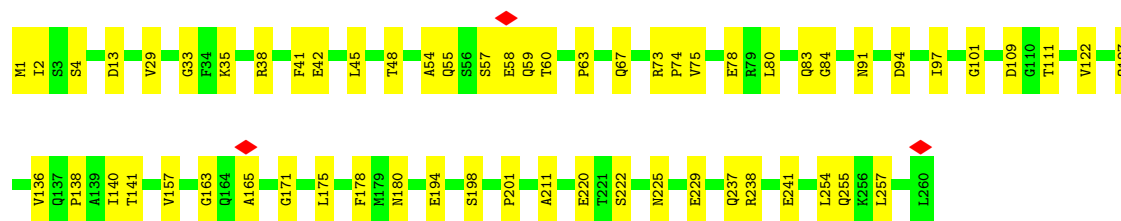


- Molecule 1: Flagellar basal-body rod protein FlgG



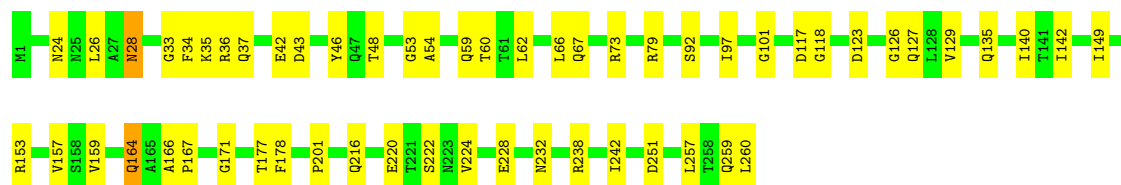
- Molecule 1: Flagellar basal-body rod protein FlgG





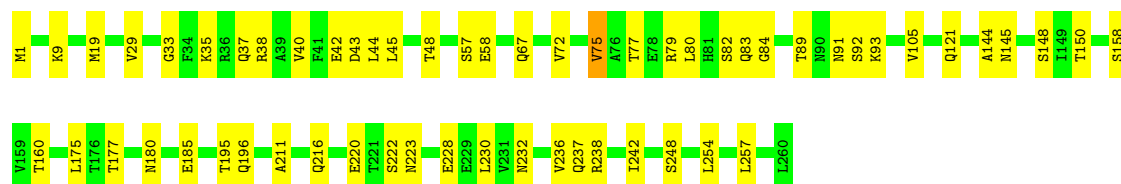
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain E: 78% 21% .



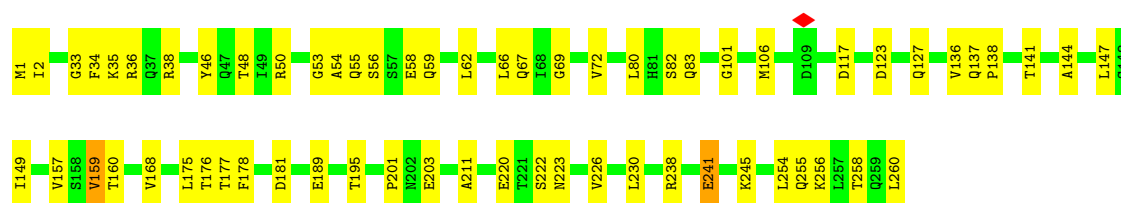
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain F: 78% 22% .



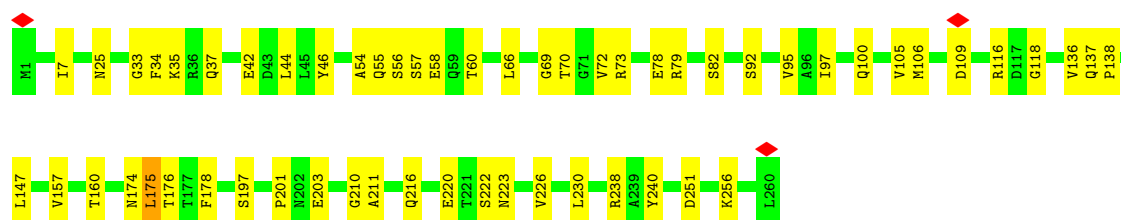
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain G: 76% 23% .



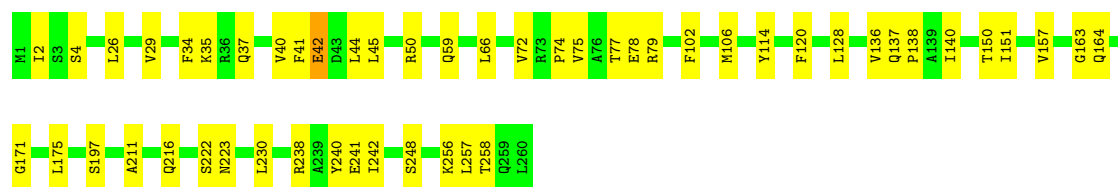
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain H: 78% 22% .



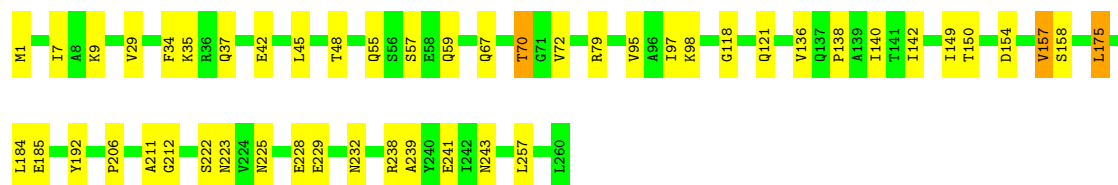
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain I:  80% 19%



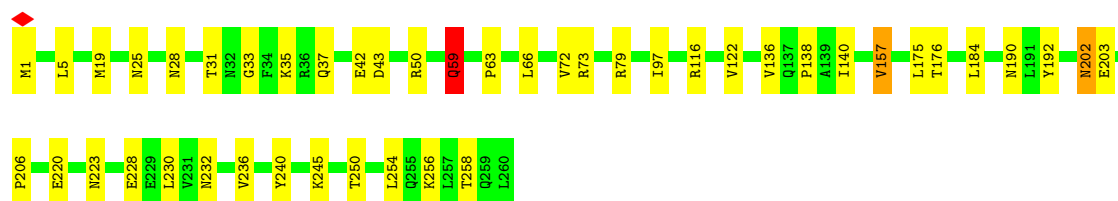
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain J:  81% 18%



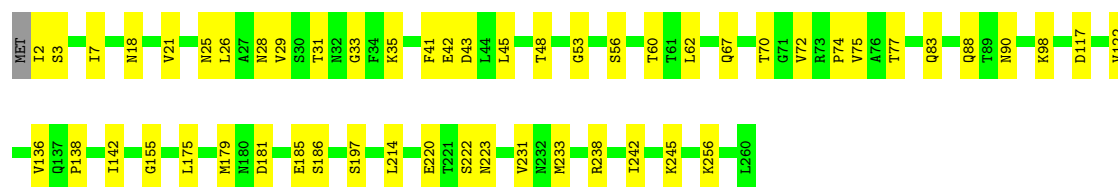
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain K:  83% 16%



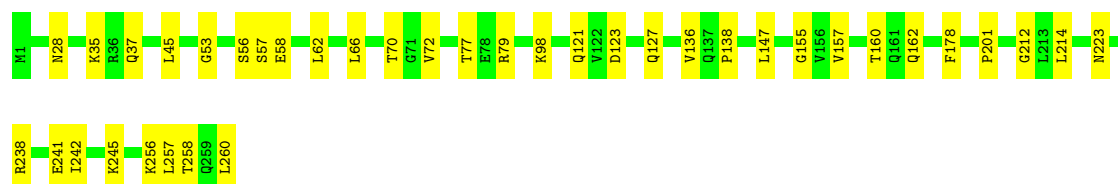
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain L:  79% 20%



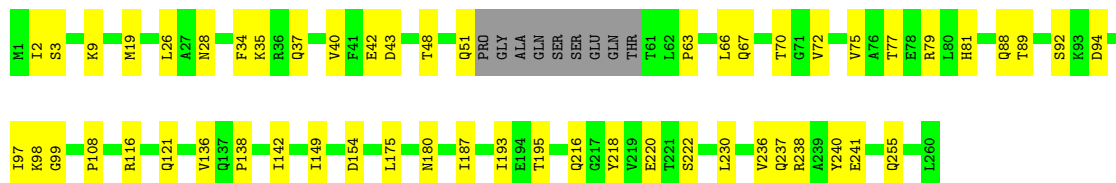
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain M:  85% 15%



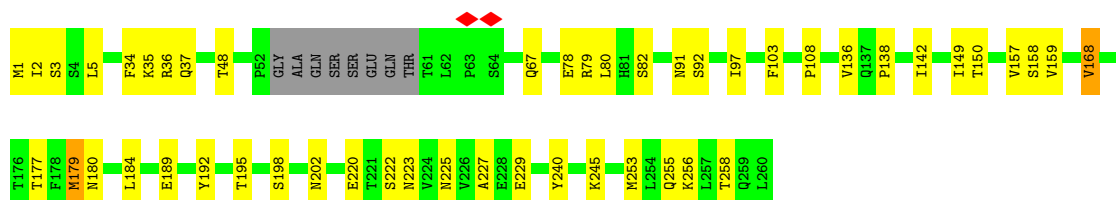
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain N:  76% 21%



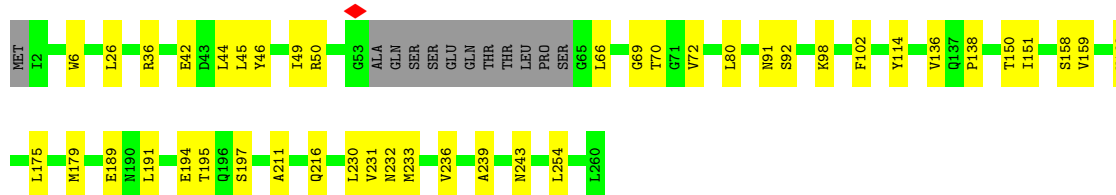
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain O:  78% 18%



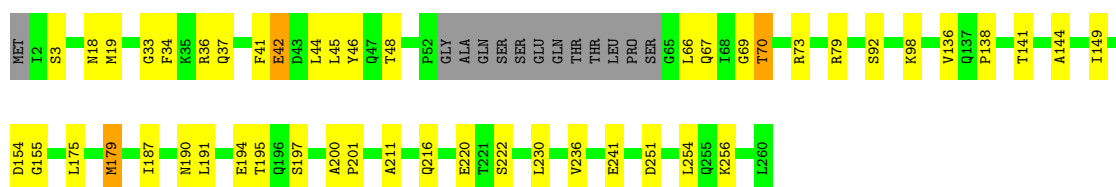
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain P:  79% 17% 5%



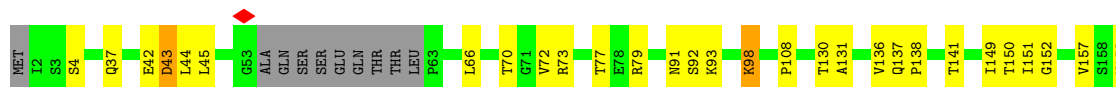
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain Q:  77% 17% 5%



- Molecule 1: Flagellar basal-body rod protein FlgG

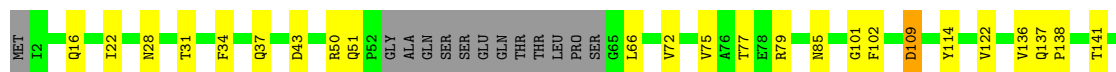
Chain R:  77% 18%





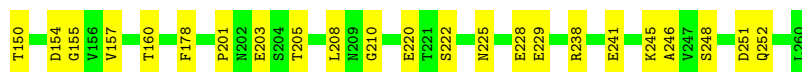
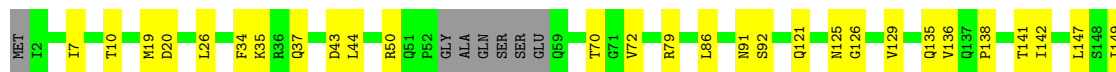
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain S: 77% 17% 5%



- Molecule 1: Flagellar basal-body rod protein FlgG

Chain T: 78% 20% .



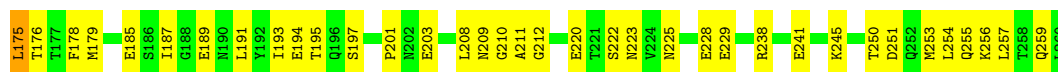
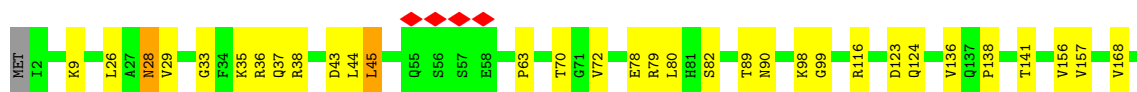
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain U: 78% 22%



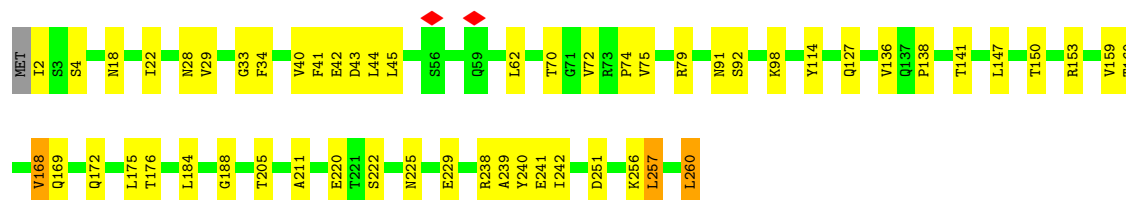
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain V: 73% 25% .

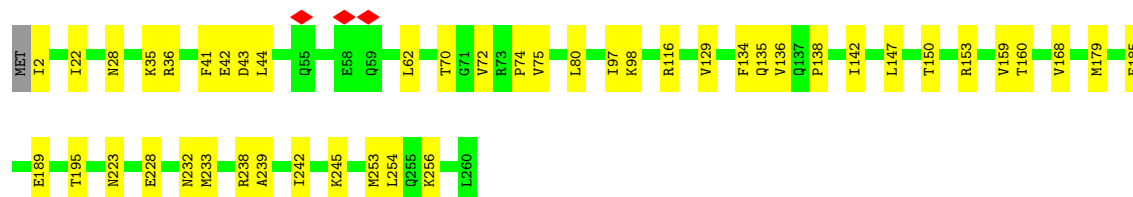
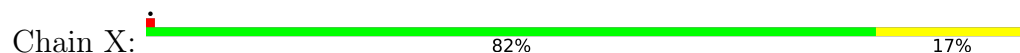


- Molecule 1: Flagellar basal-body rod protein FlgG

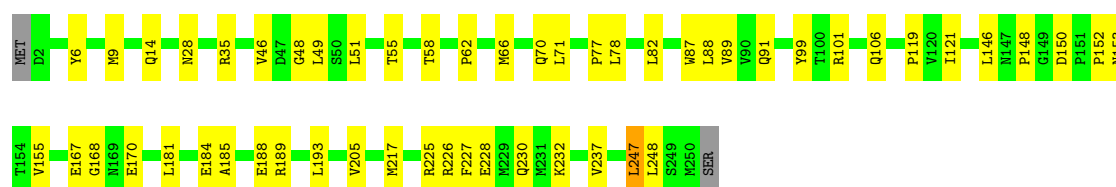
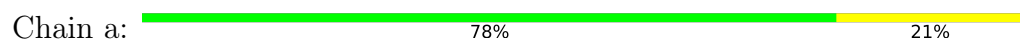
Chain W: 78% 20% .



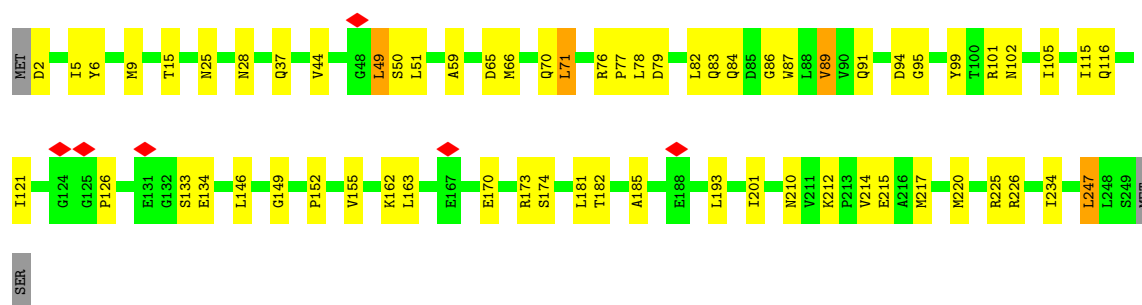
- Molecule 1: Flagellar basal-body rod protein FlgG



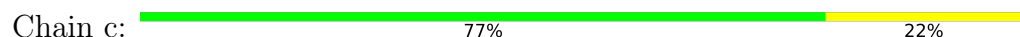
- Molecule 2: Flagellar basal-body rod protein FlgF



- Molecule 2: Flagellar basal-body rod protein FlgF



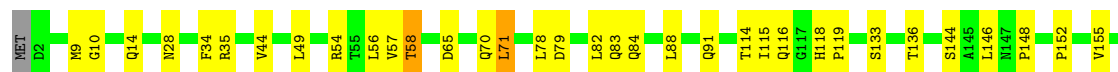
- Molecule 2: Flagellar basal-body rod protein FlgF





- Molecule 2: Flagellar basal-body rod protein FlgF

Chain d: 79% 20% ..



- Molecule 2: Flagellar basal-body rod protein FlgF

Chain e: 81% 18% .



- Molecule 3: Flagellar MS ring L2

Chain 0: 100%

There are no outlier residues recorded for this chain.

- Molecule 3: Flagellar MS ring L2

Chain 1: 93% 7%



- Molecule 3: Flagellar MS ring L2

Chain 2: 93% 7%



- Molecule 3: Flagellar MS ring L2

Chain 3: 100%

There are no outlier residues recorded for this chain.

- Molecule 3: Flagellar MS ring L2

Chain 4:  87% 13%



- Molecule 4: Flagellar MS ring L1

Chain 5:  90% 10%



- Molecule 4: Flagellar MS ring L1

Chain 6:  14% 95% 5%



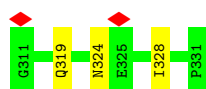
- Molecule 4: Flagellar MS ring L1

Chain 7:  86% 14%



- Molecule 4: Flagellar MS ring L1

Chain 9:  10% 86% 14%



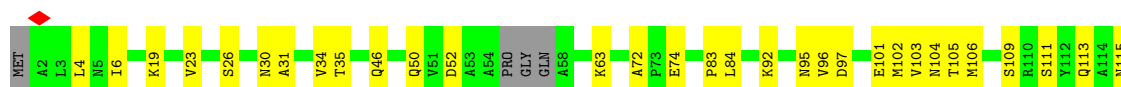
- Molecule 4: Flagellar MS ring L1

Chain 8:  86% 14%



- Molecule 5: Flagellar basal-body rod protein FlgC

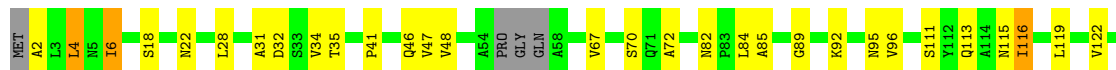
Chain f:  69% 27% .





- Molecule 5: Flagellar basal-body rod protein FlgC

Chain g: 74% 21% . .



- Molecule 5: Flagellar basal-body rod protein FlgC

Chain h: 66% 28% . .



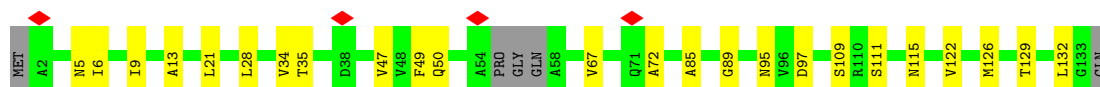
- Molecule 5: Flagellar basal-body rod protein FlgC

Chain j: 76% 18% . 5%



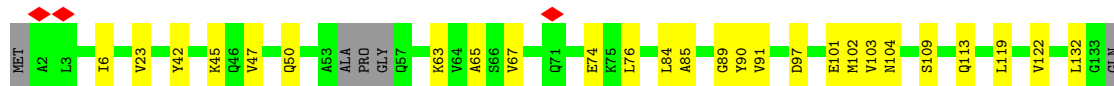
- Molecule 5: Flagellar basal-body rod protein FlgC

Chain p: 78% 18% .



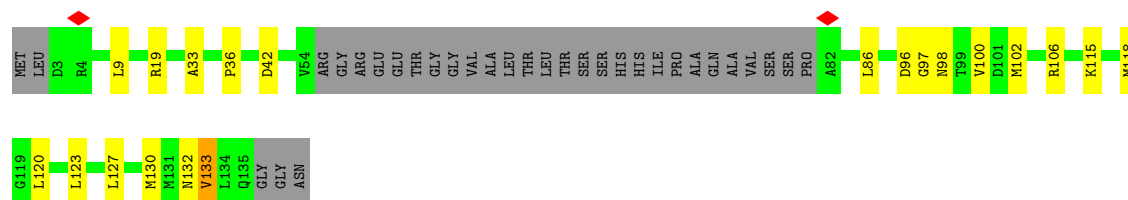
- Molecule 5: Flagellar basal-body rod protein FlgC

Chain i: 77% 19% .

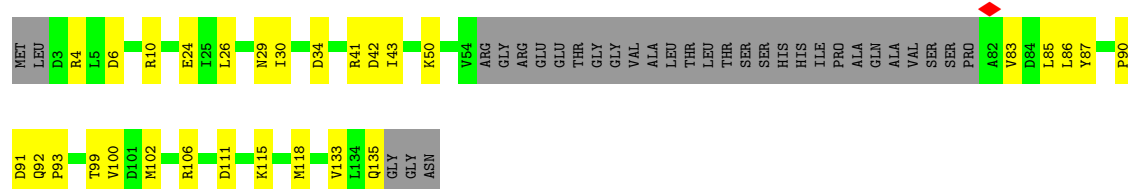


- Molecule 6: Flagellar basal body rod protein FlgB

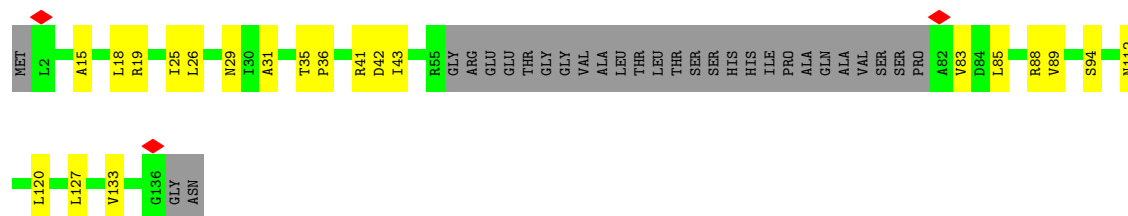
Chain l: 62% 14% . 23%



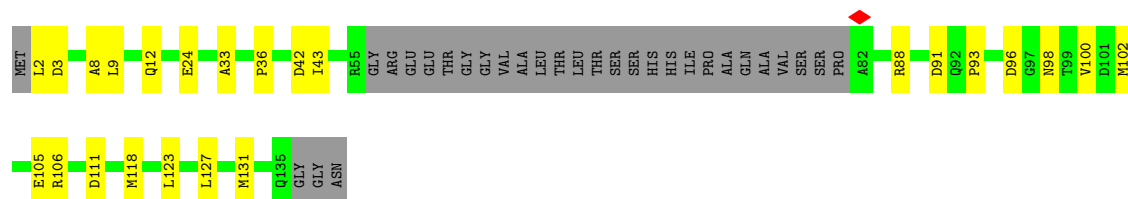
• Molecule 6: Flagellar basal body rod protein FlgB



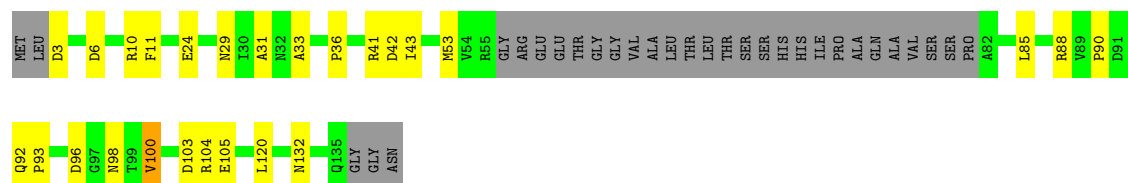
• Molecule 6: Flagellar basal body rod protein FlgB



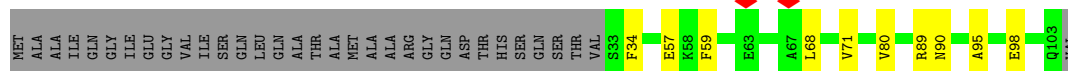
• Molecule 6: Flagellar basal body rod protein FlgB



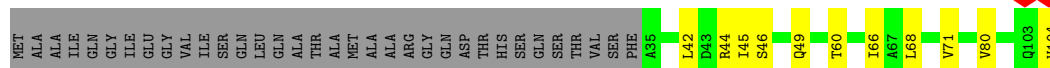
• Molecule 6: Flagellar basal body rod protein FlgB



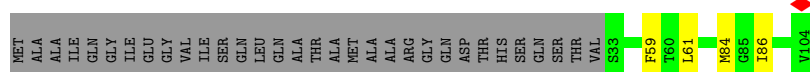
• Molecule 7: Flagellar hook-basal body complex protein FlhE



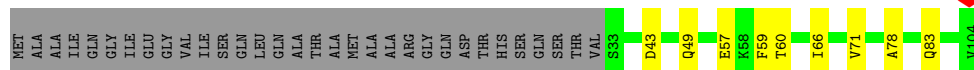
- Molecule 7: Flagellar hook-basal body complex protein FliE



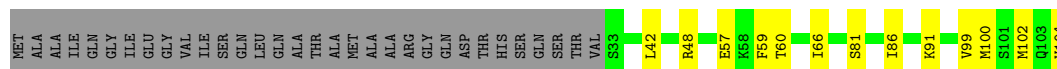
- Molecule 7: Flagellar hook-basal body complex protein FliE



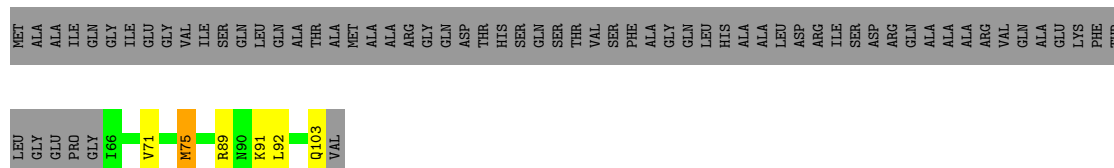
- Molecule 7: Flagellar hook-basal body complex protein FliE



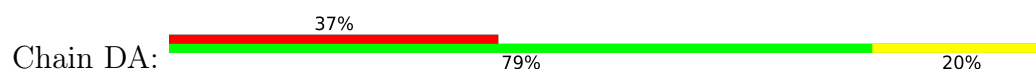
- Molecule 7: Flagellar hook-basal body complex protein FliE

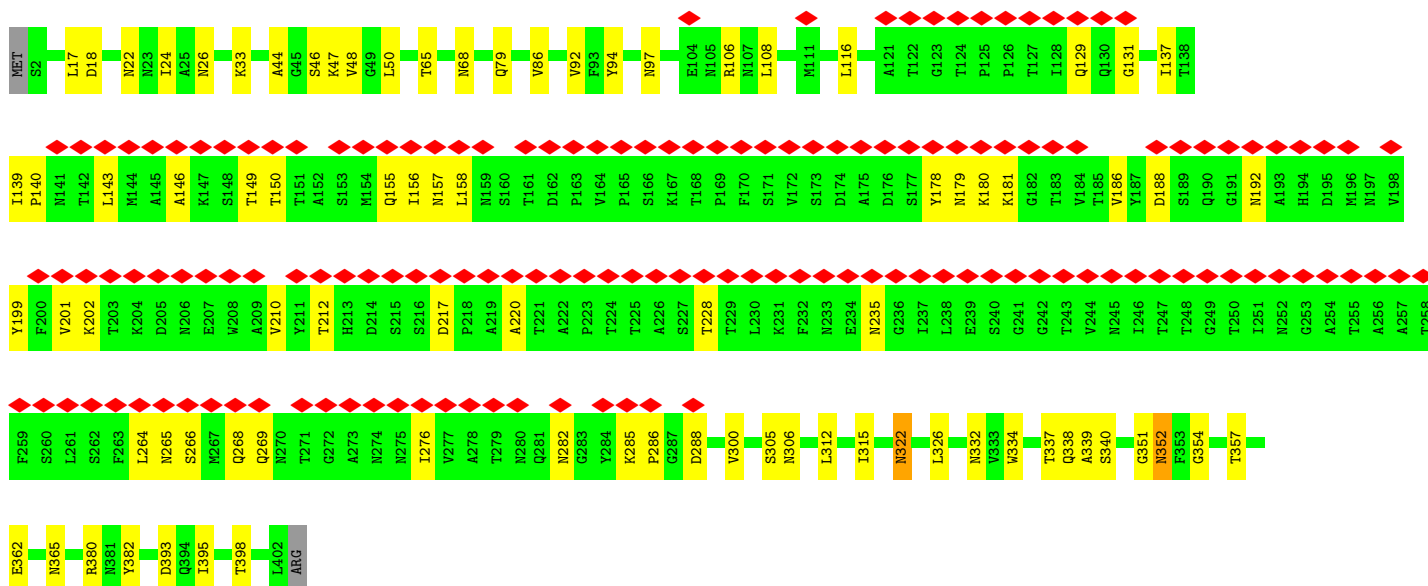


- Molecule 7: Flagellar hook-basal body complex protein FliE

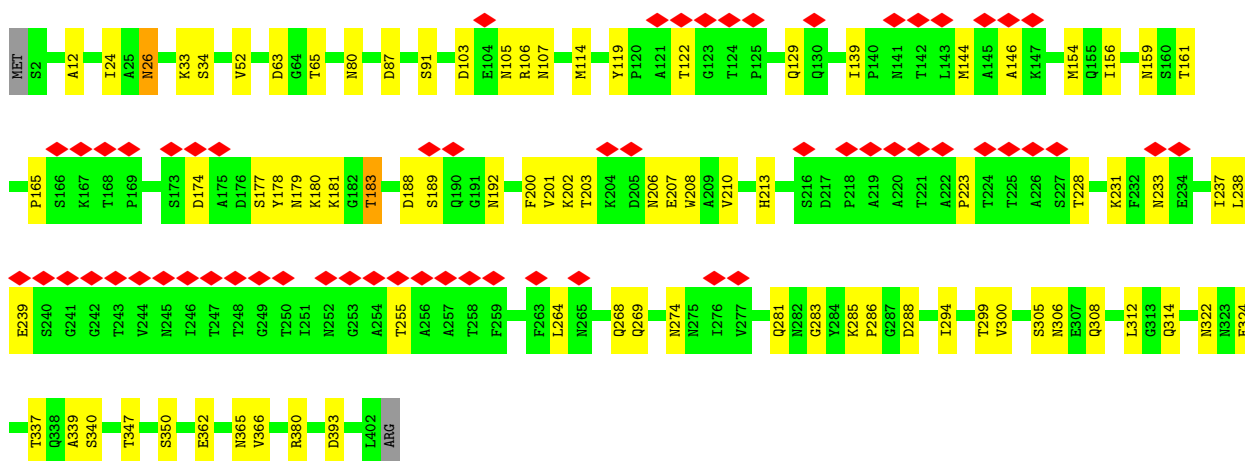
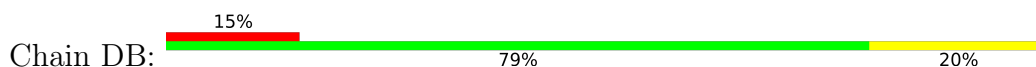


- Molecule 8: Flagellar hook protein FlgE

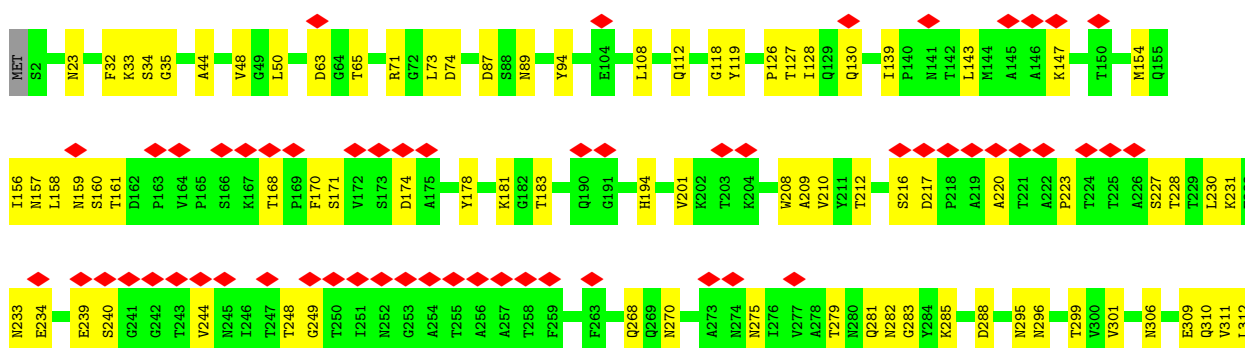
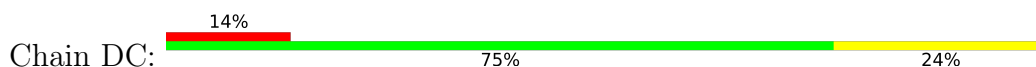


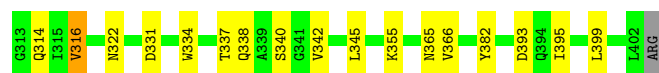


• Molecule 8: Flagellar hook protein FlgE

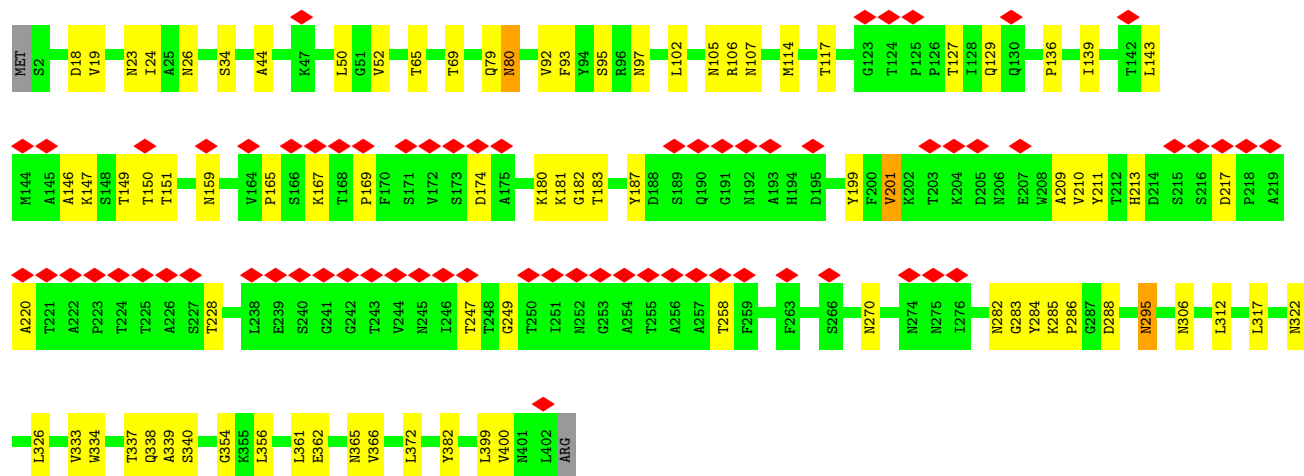
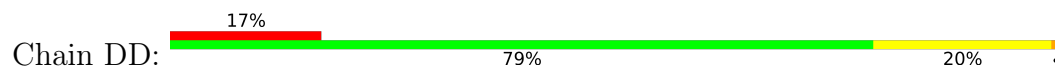


• Molecule 8: Flagellar hook protein FlgE

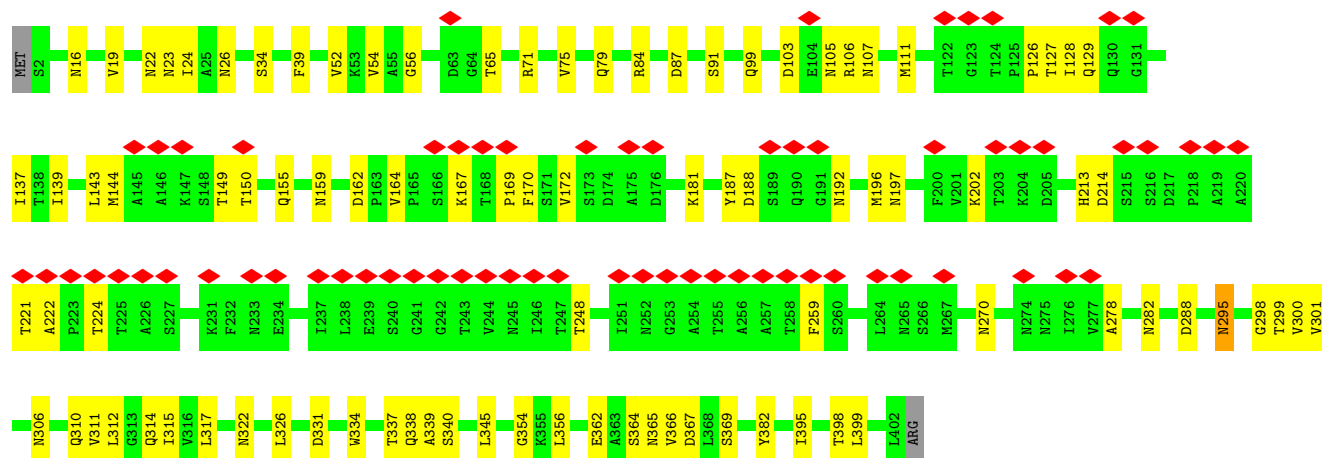
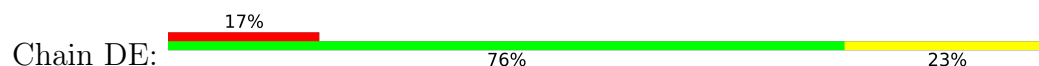




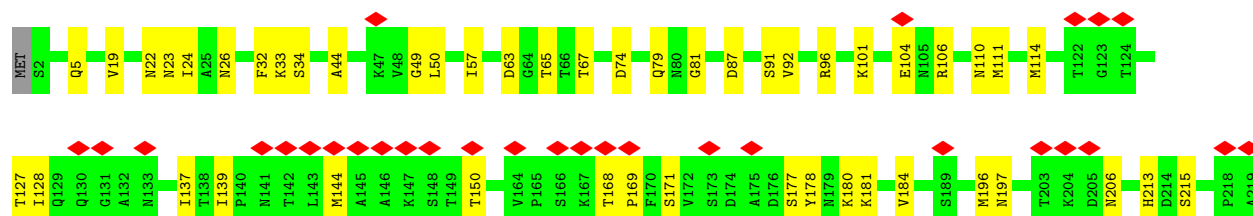
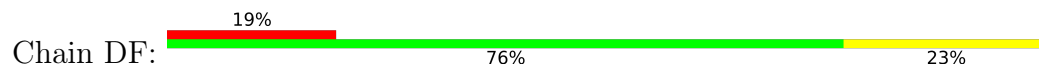
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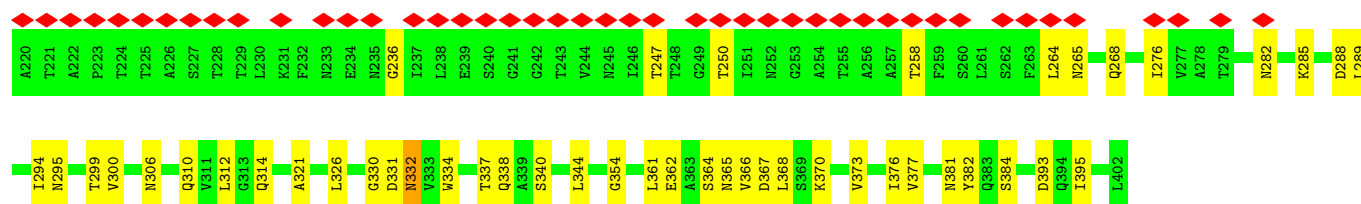


• Molecule 8: Flagellar hook protein FlgE



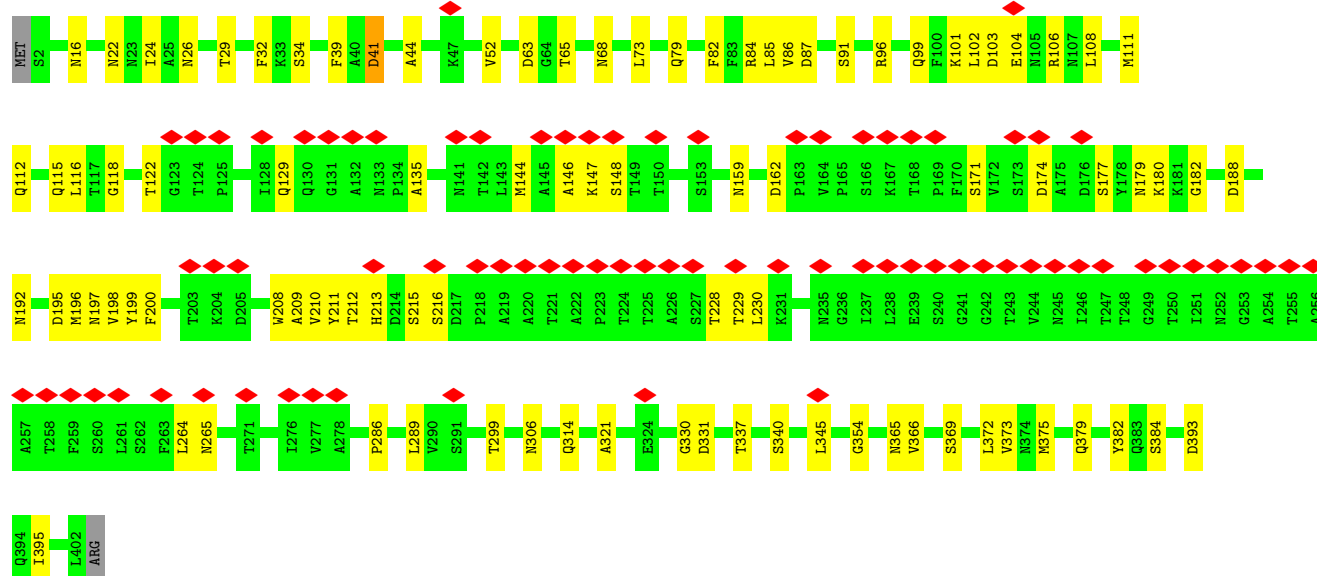
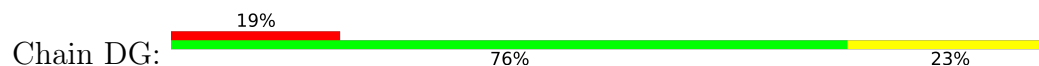
• Molecule 8: Flagellar hook protein FlgE



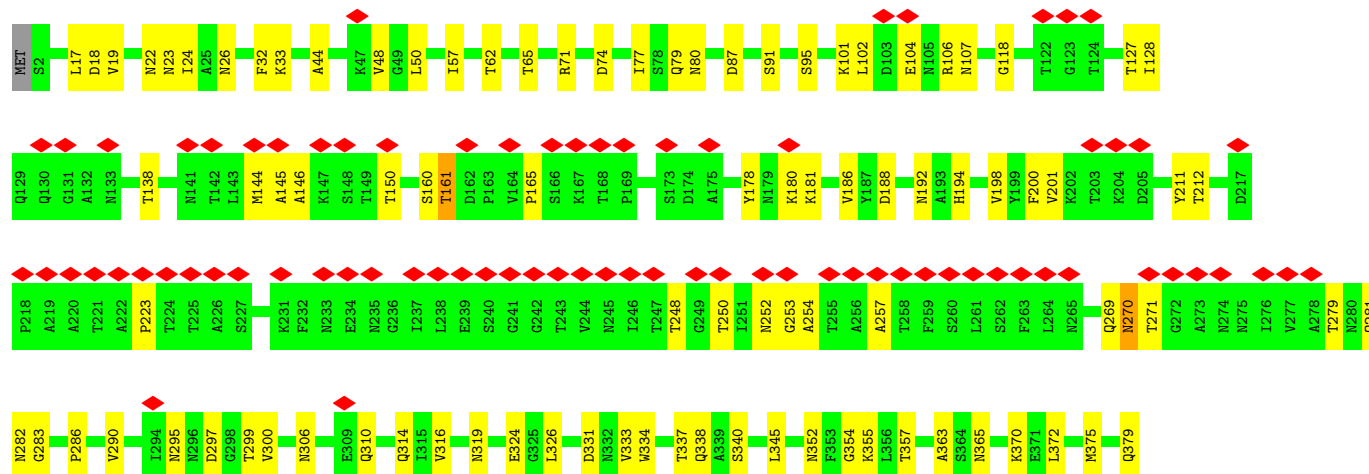
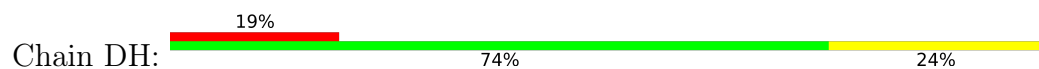


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• Molecule 8: Flagellar hook protein FlgE

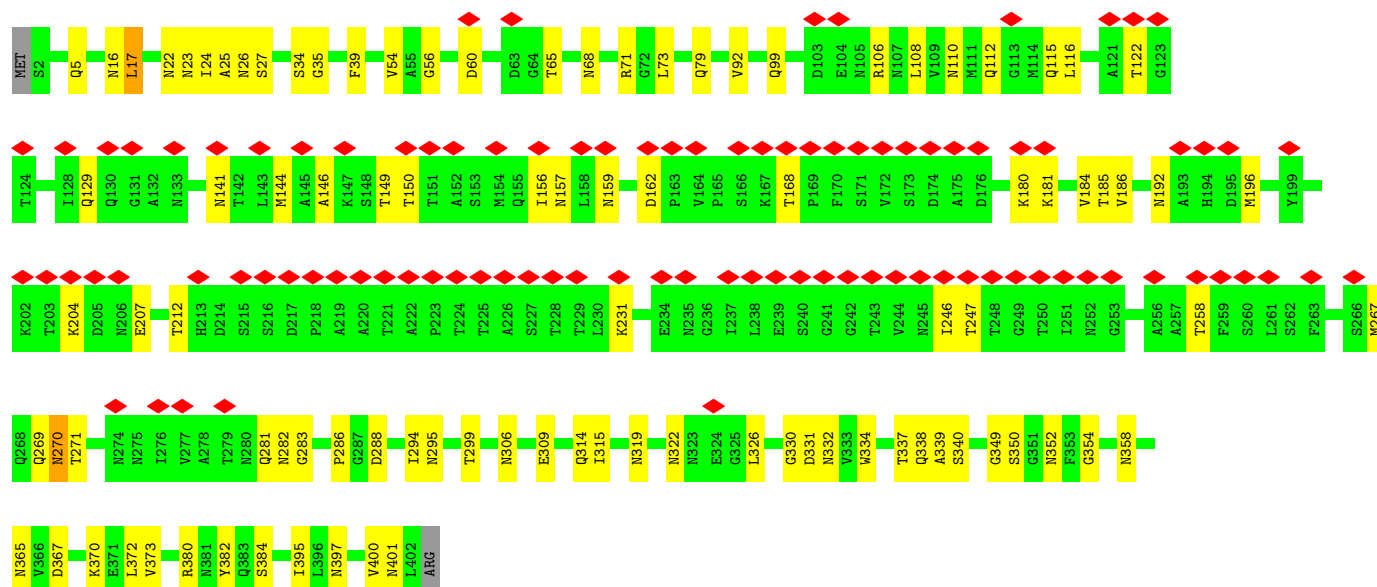
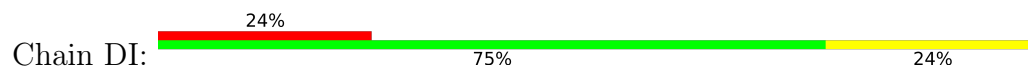


• Molecule 8: Flagellar hook protein FlgE

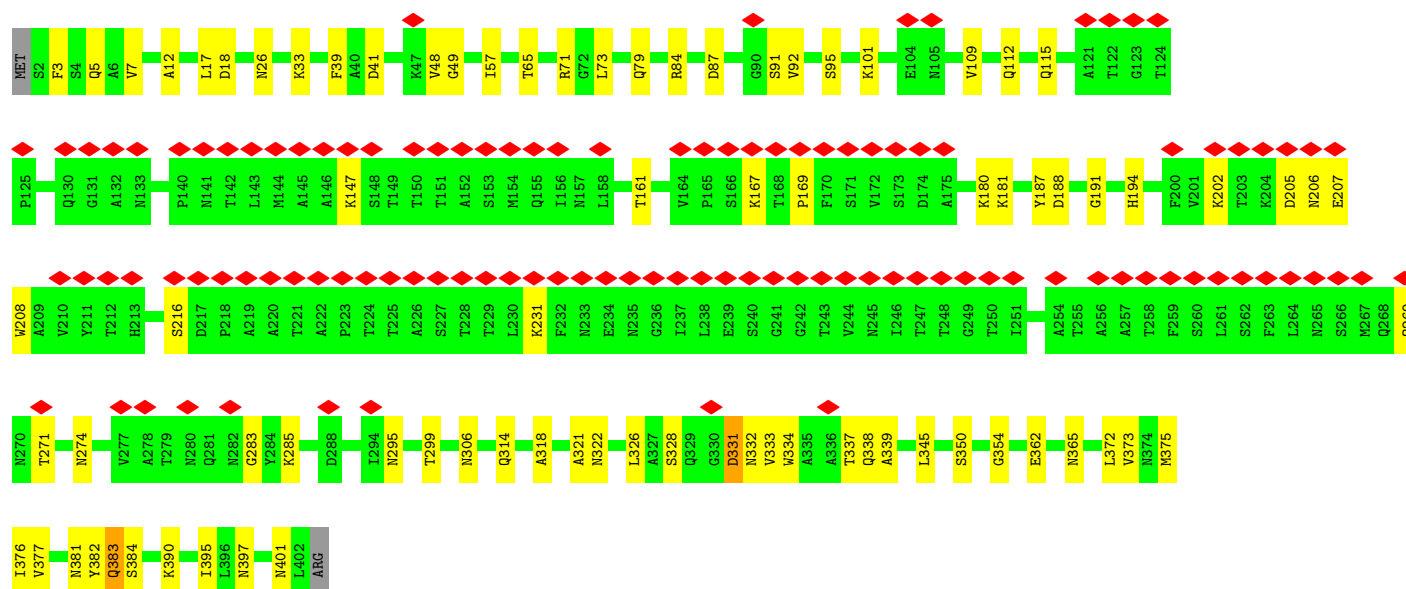
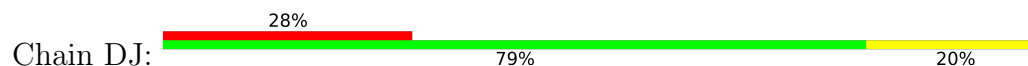




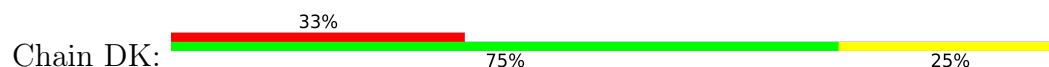
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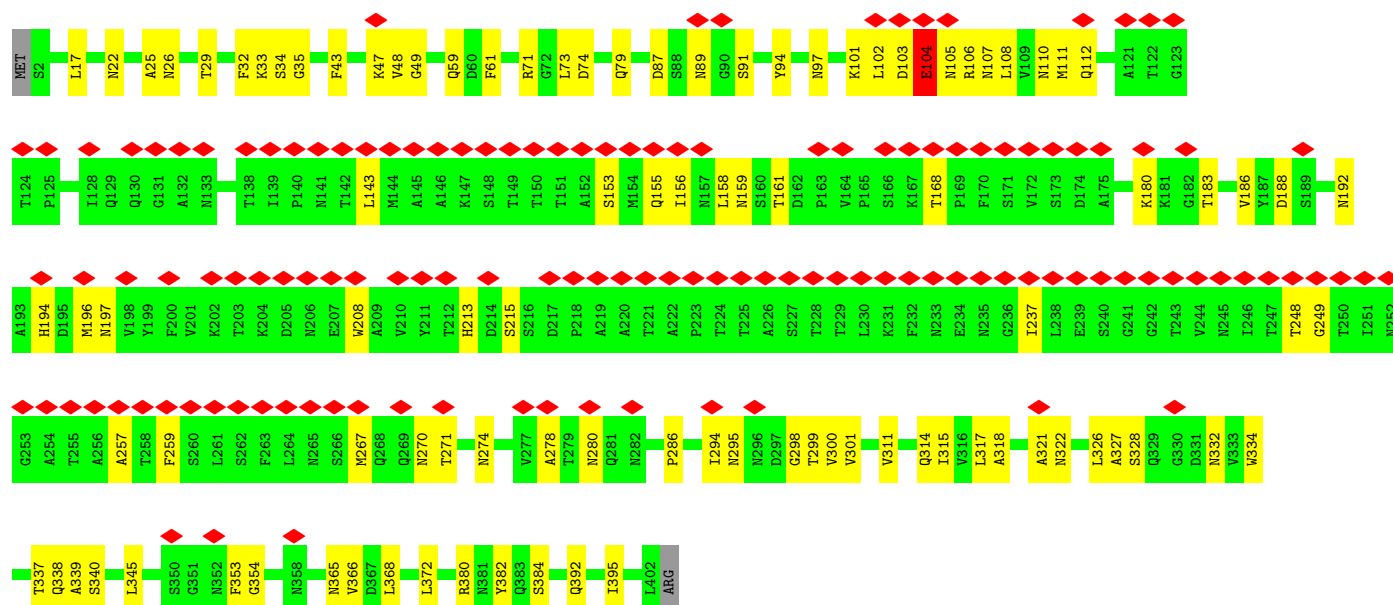


• Molecule 8: Flagellar hook protein FlgE

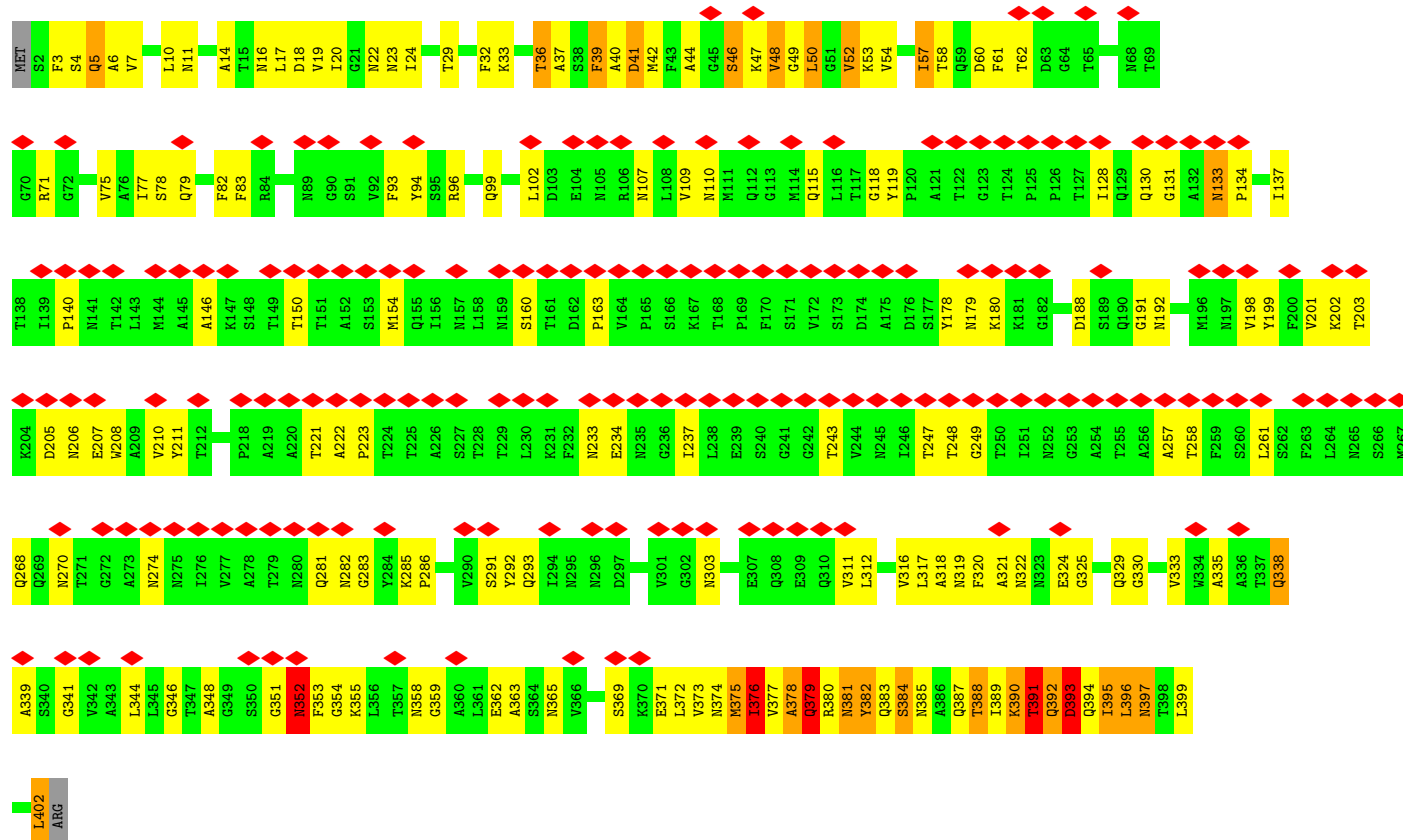


• Molecule 8: Flagellar hook protein FlgE

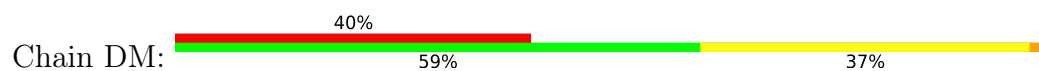


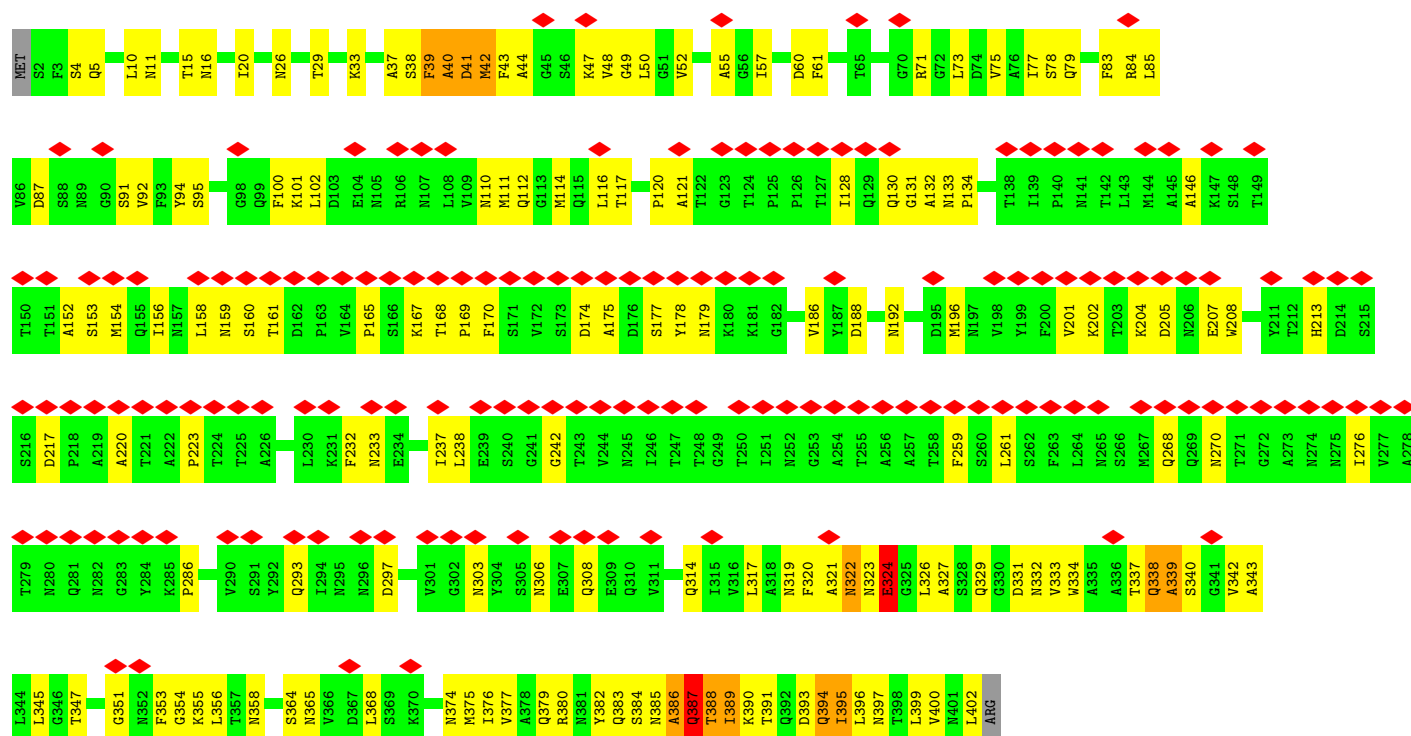


• Molecule 8: Flagellar hook protein FlgE

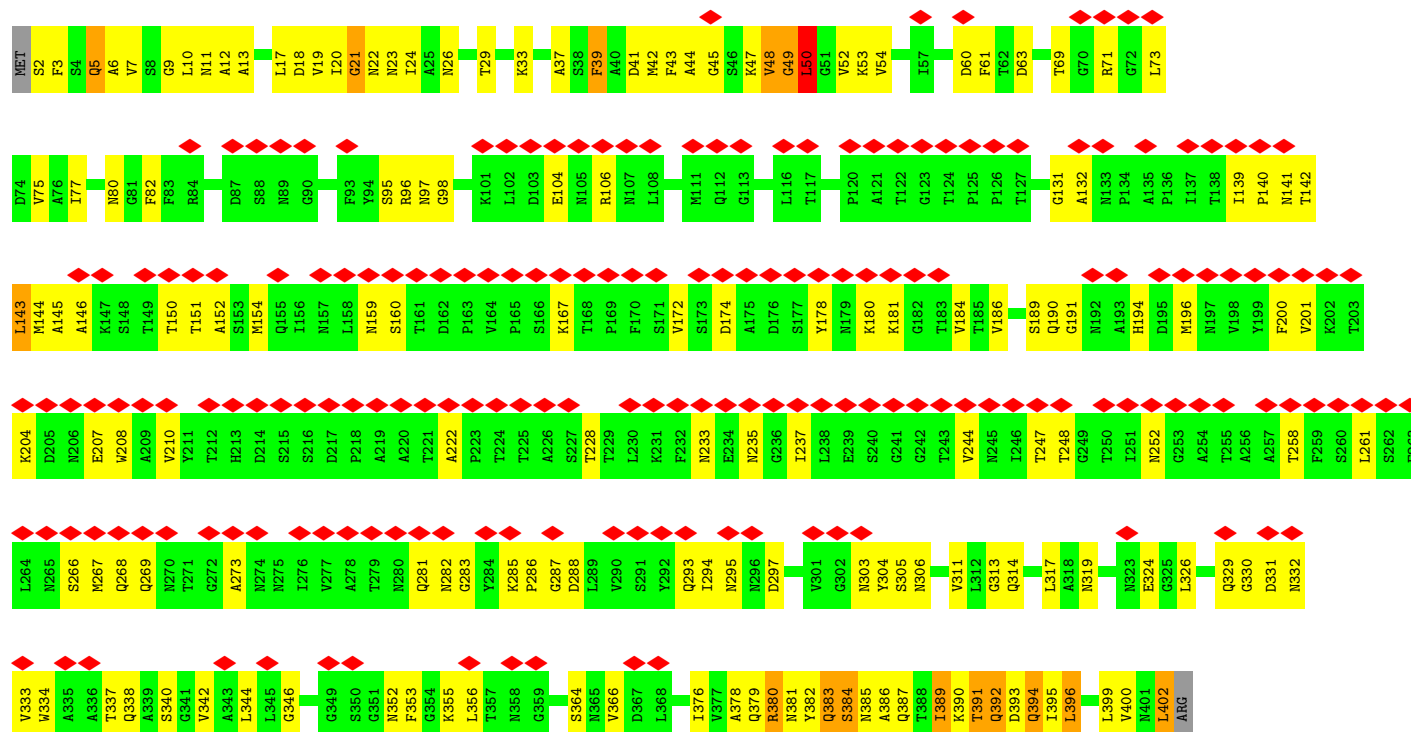


• Molecule 8: Flagellar hook protein FlgE

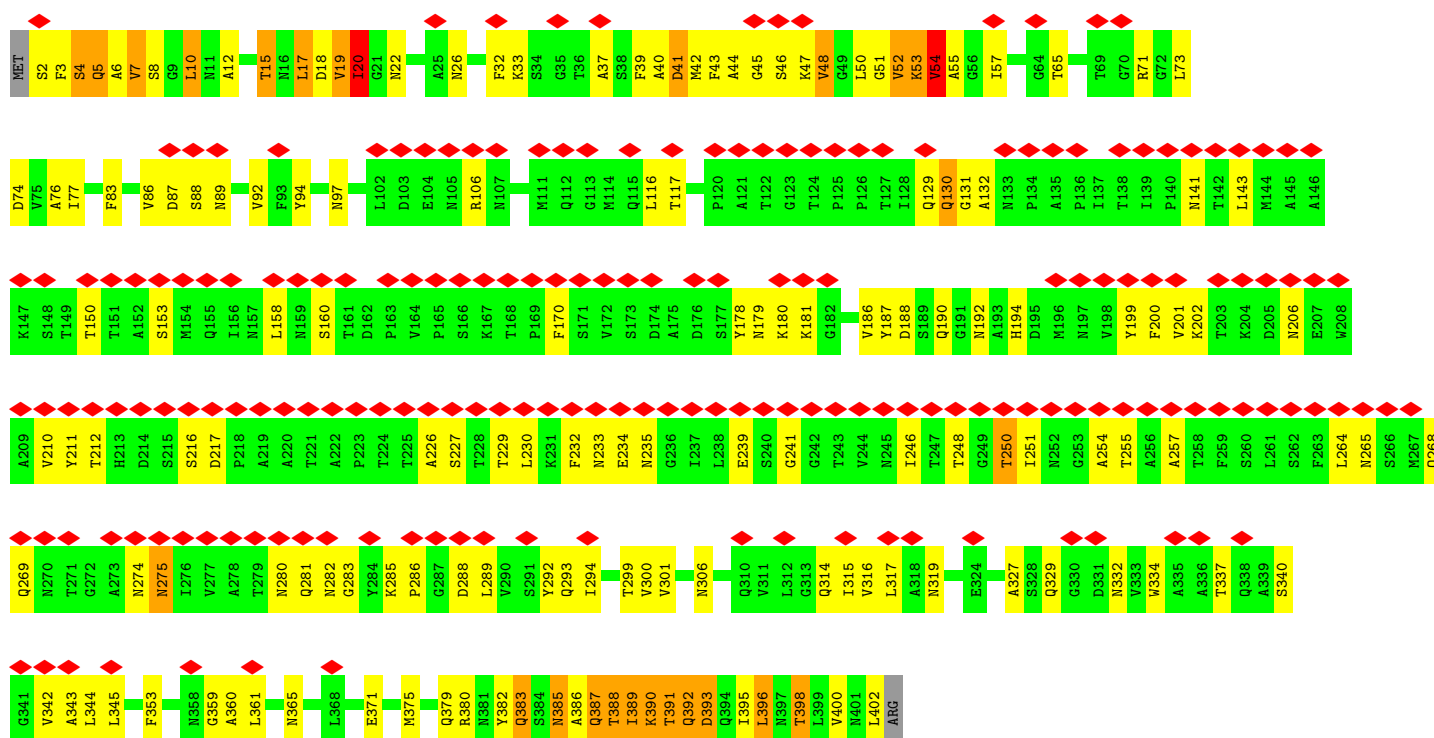




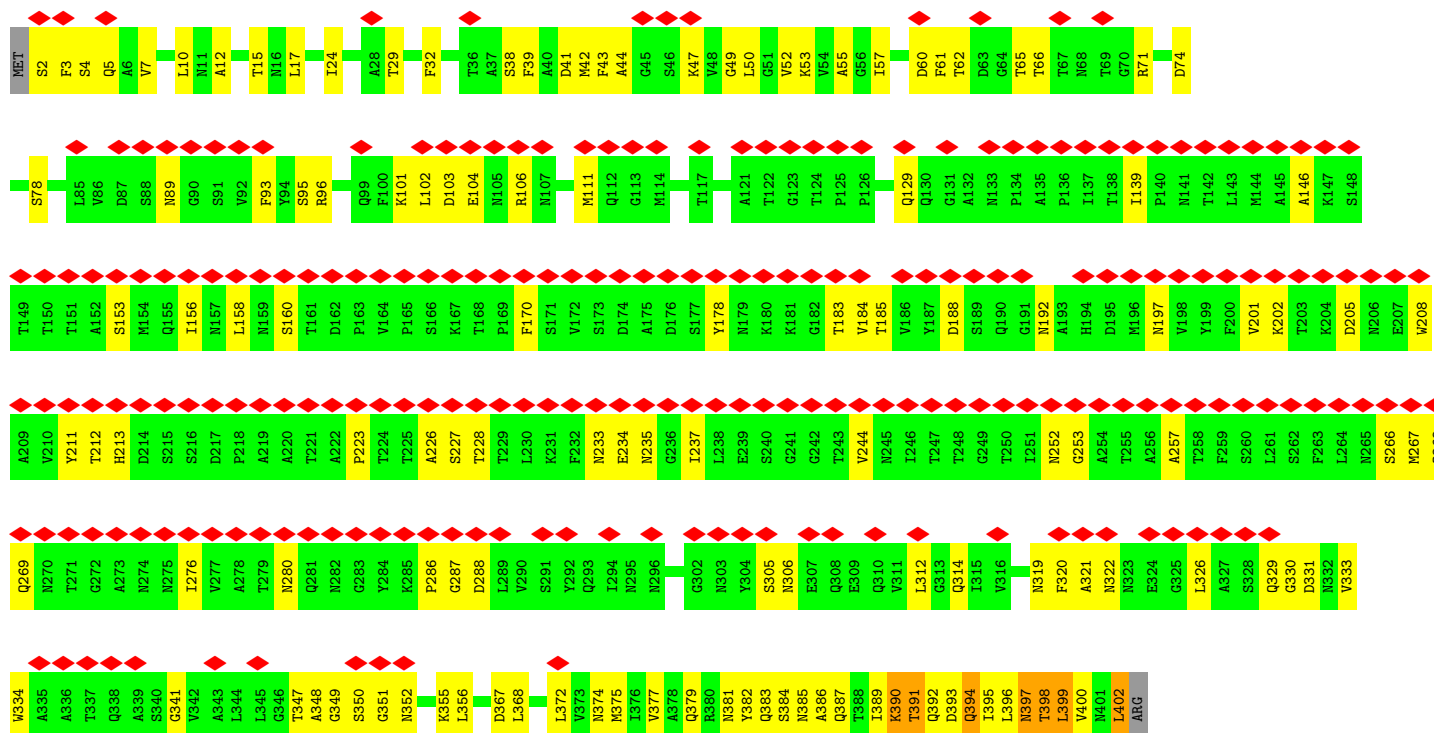
• Molecule 8: Flagellar hook protein FlgE



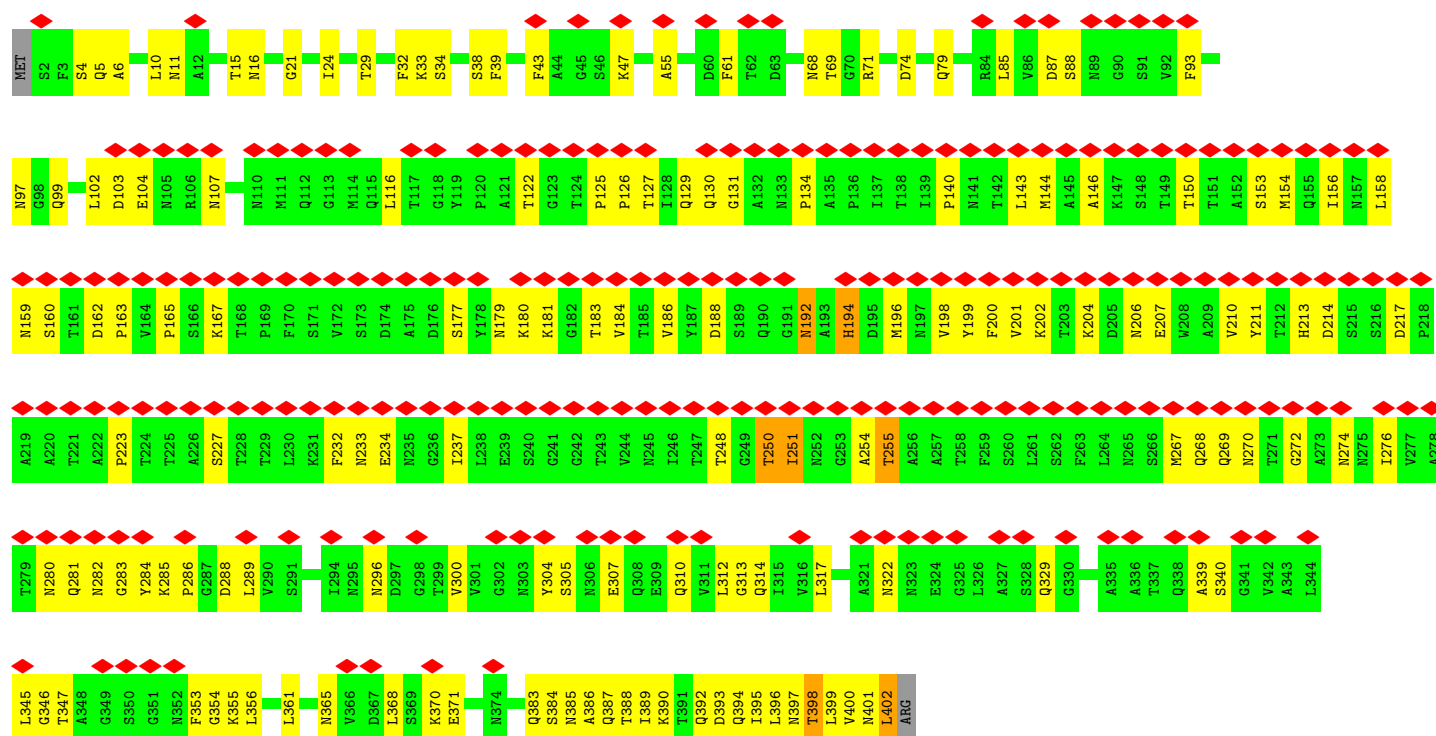
• Molecule 8: Flagellar hook protein FlgE



• Molecule 8: Flagellar hook protein FlgE

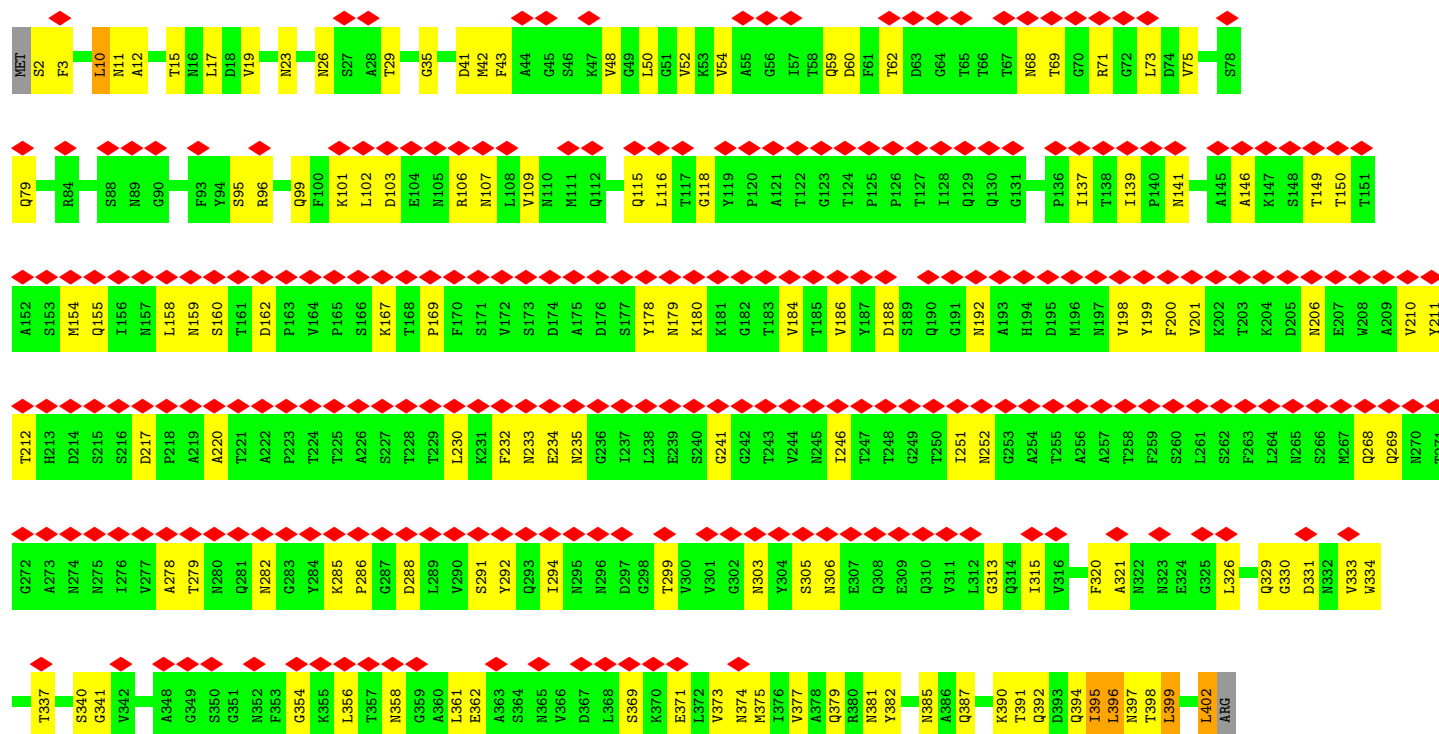


• Molecule 8: Flagellar hook protein FlgE

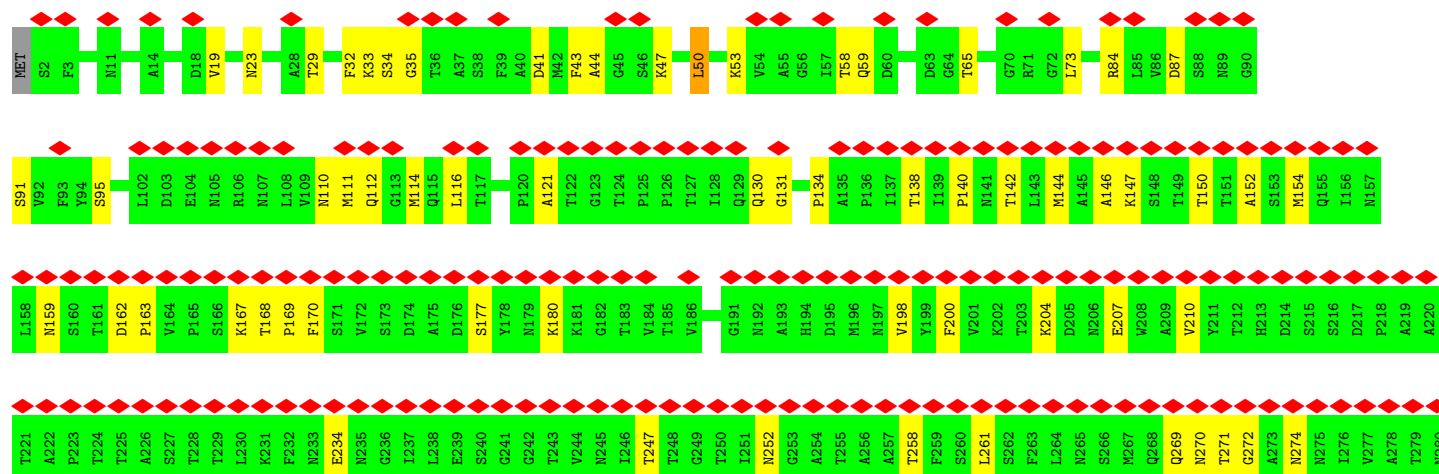
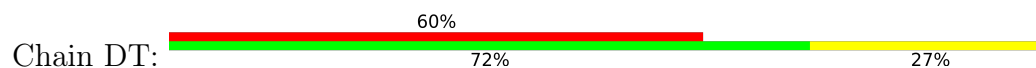


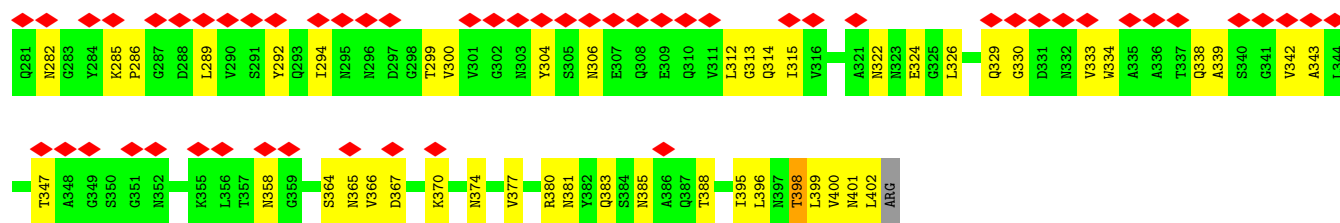


• Molecule 8: Flagellar hook protein FlgE

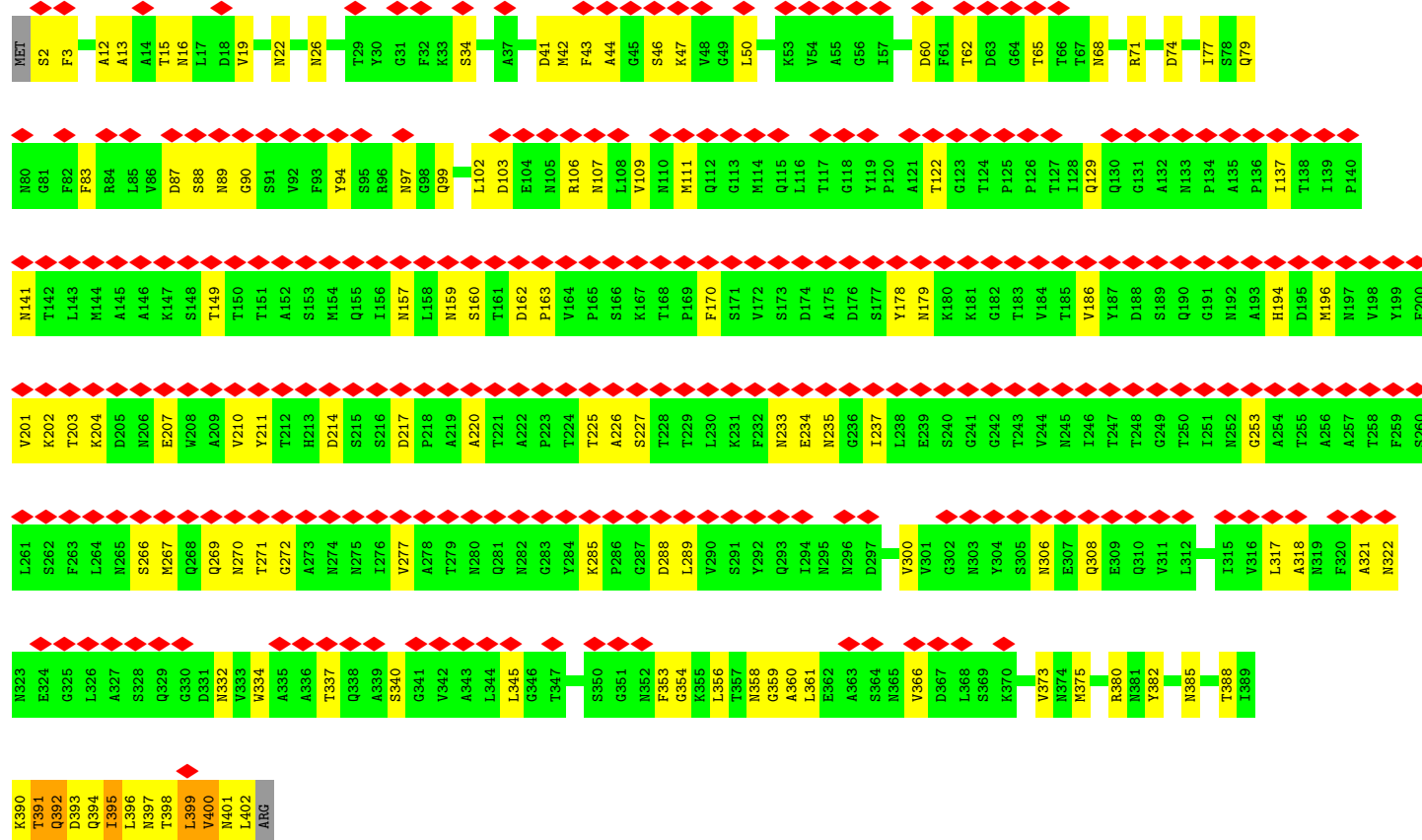
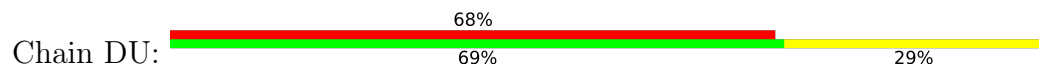


• Molecule 8: Flagellar hook protein FlgE



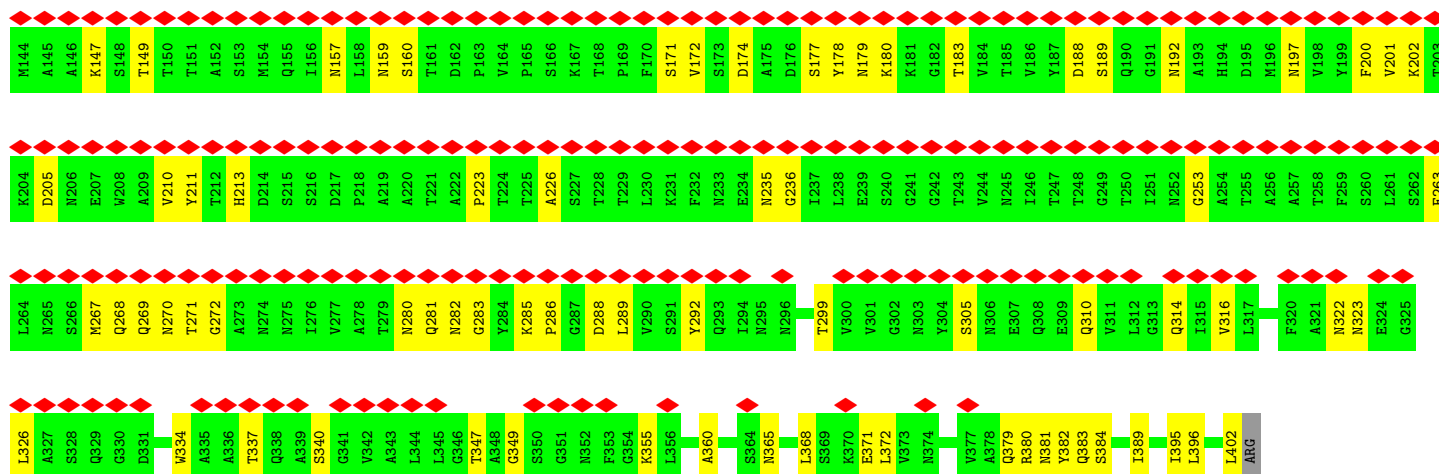


• Molecule 8: Flagellar hook protein FlgE

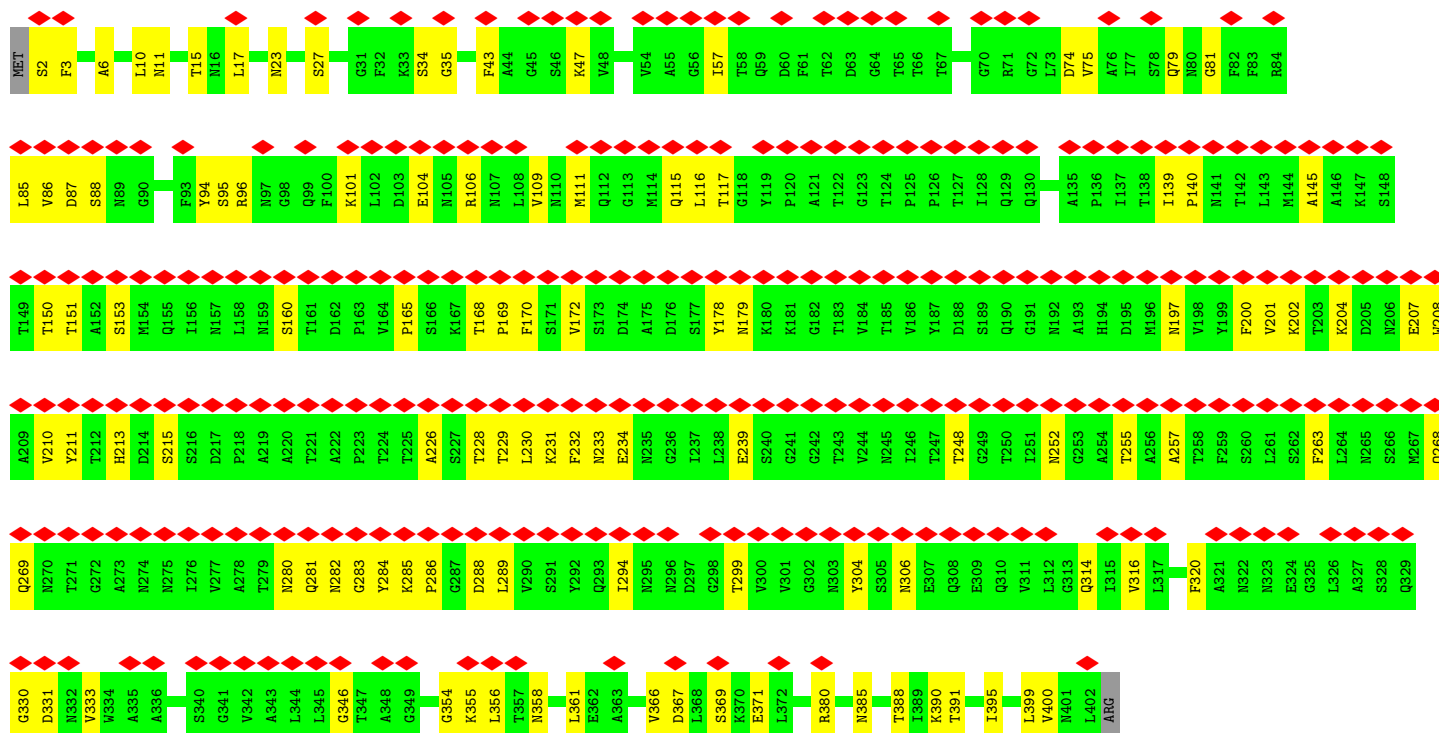
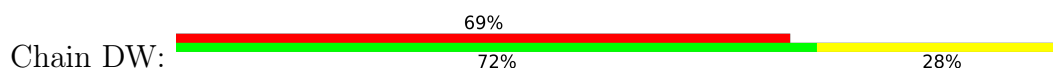


• Molecule 8: Flagellar hook protein FlgE

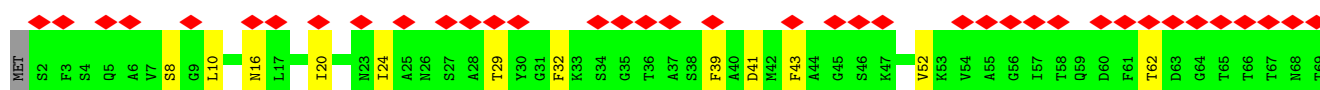
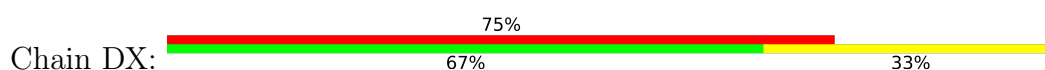


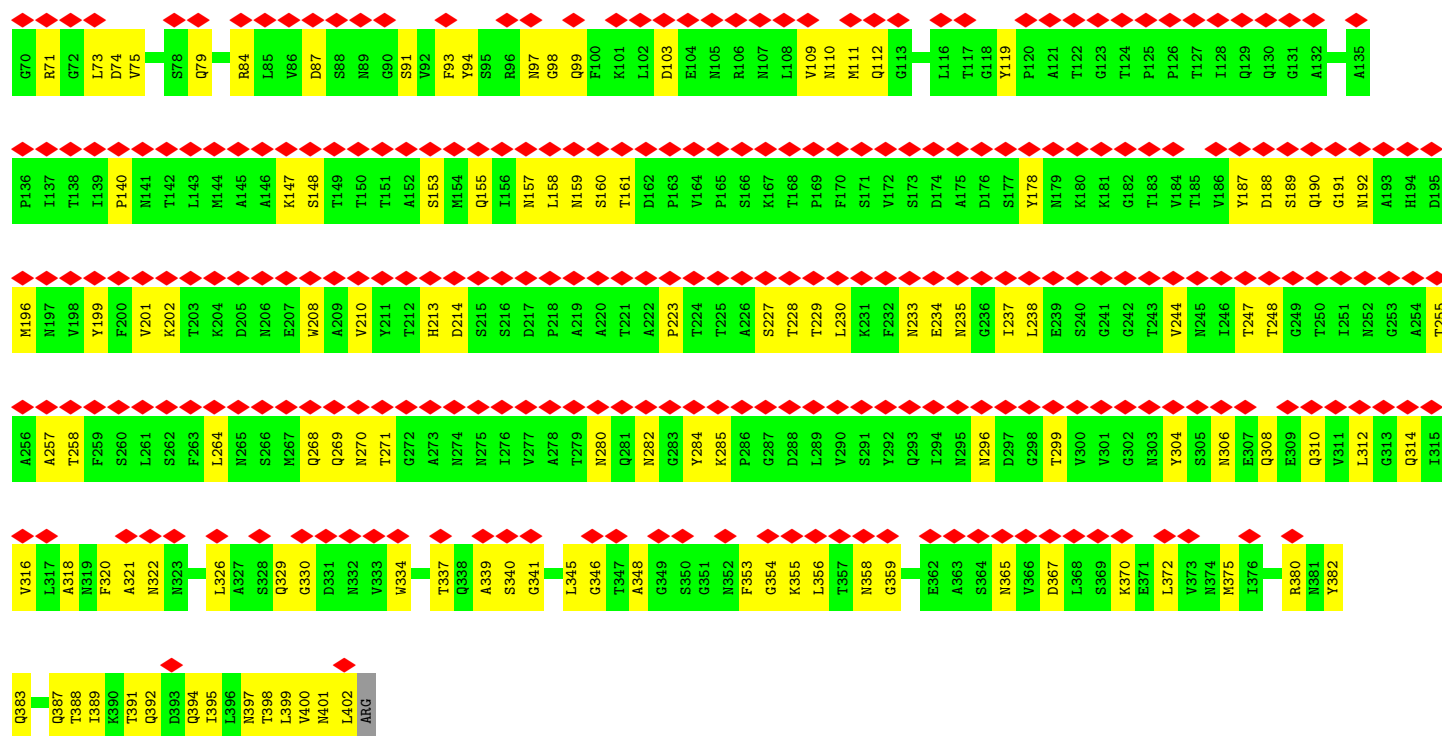


• Molecule 8: Flagellar hook protein FlgE

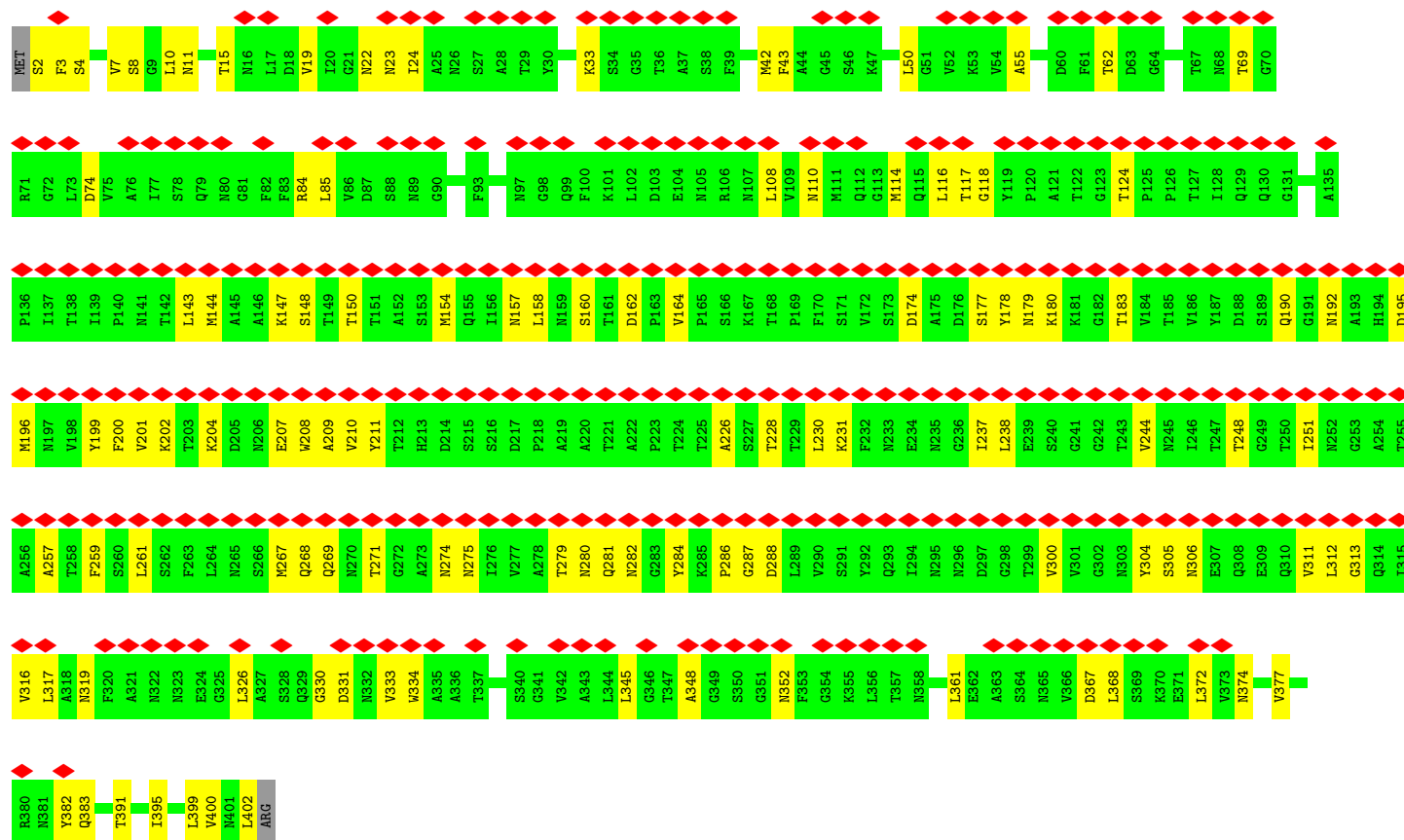
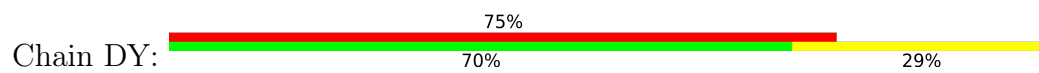


• Molecule 8: Flagellar hook protein FlgE



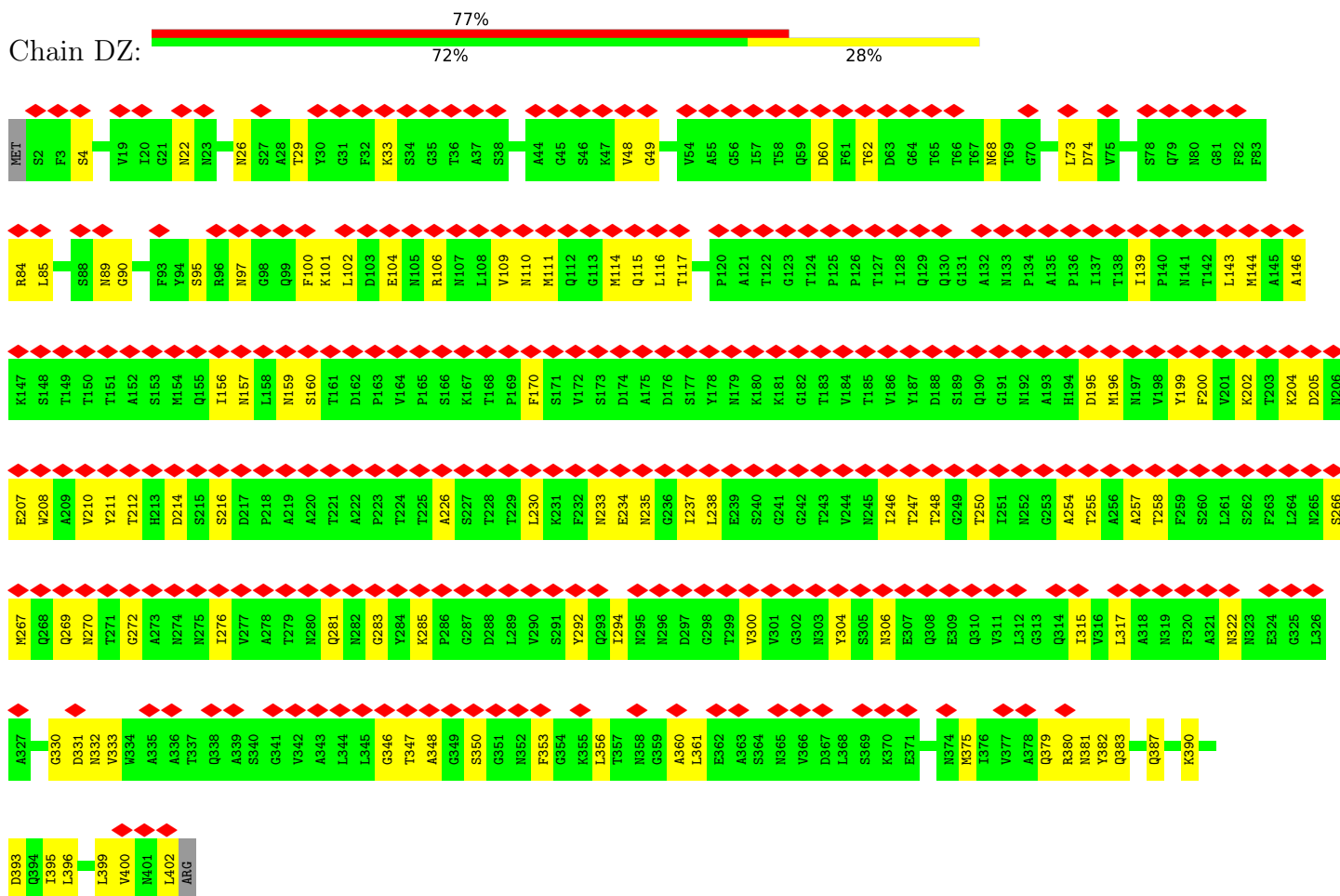


• Molecule 8: Flagellar hook protein FlgE



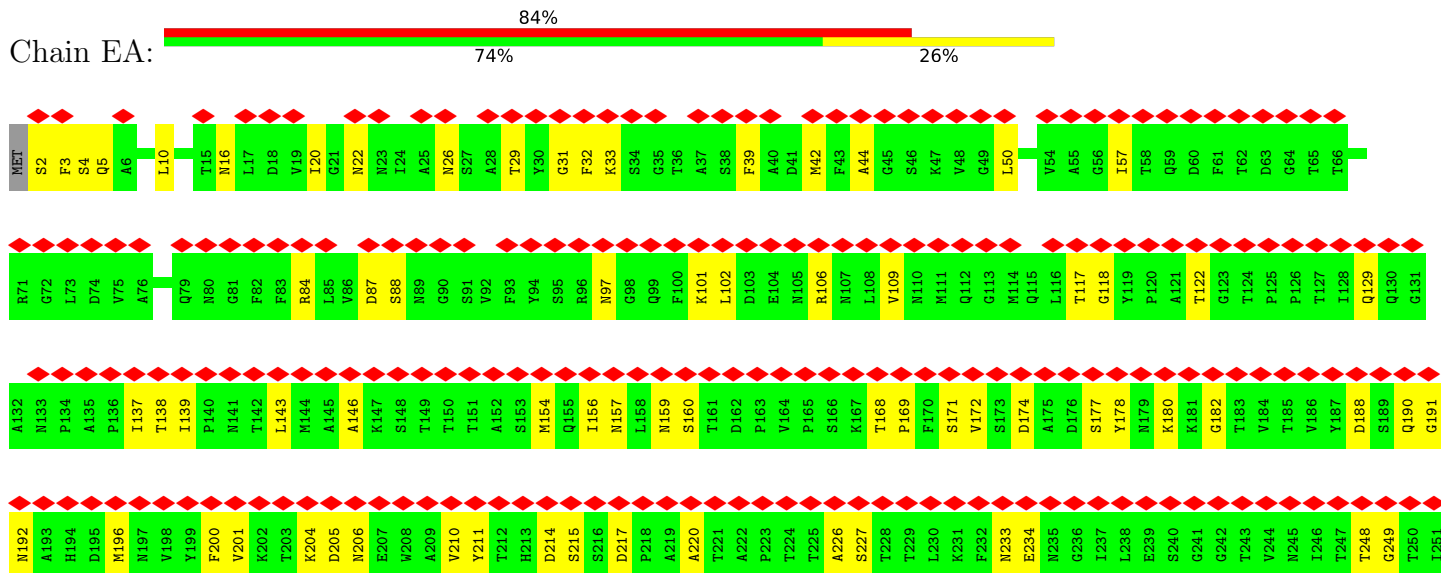
- Molecule 8: Flagellar hook protein FlgE

Chain DZ:



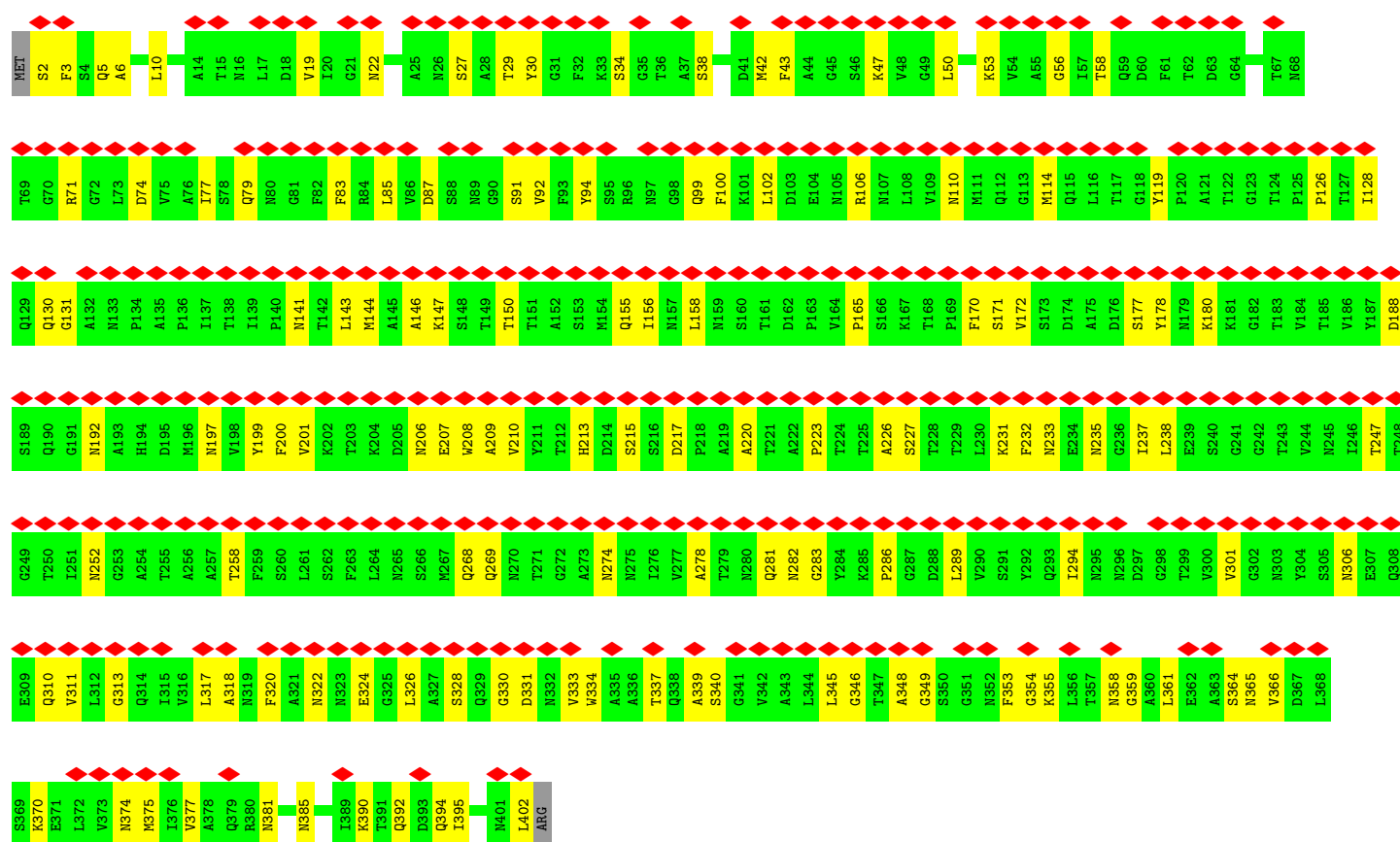
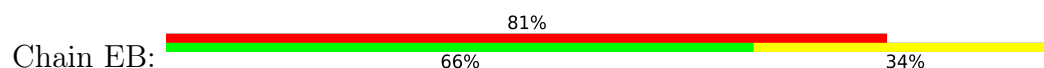
- Molecule 8: Flagellar hook protein FlgE

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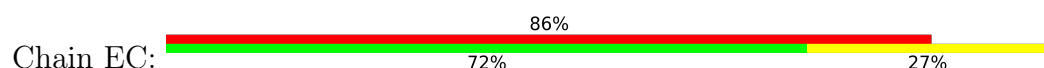


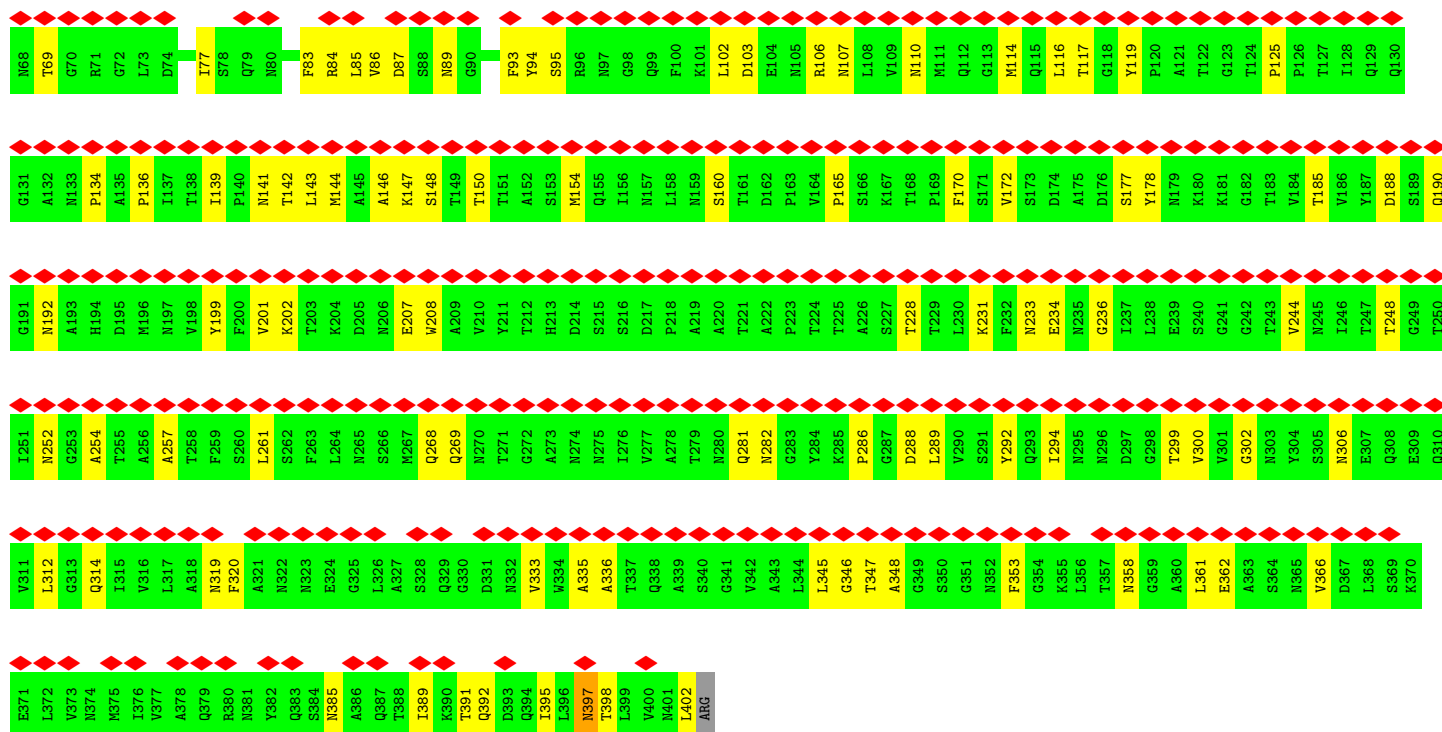


• Molecule 8: Flagellar hook protein FlgE

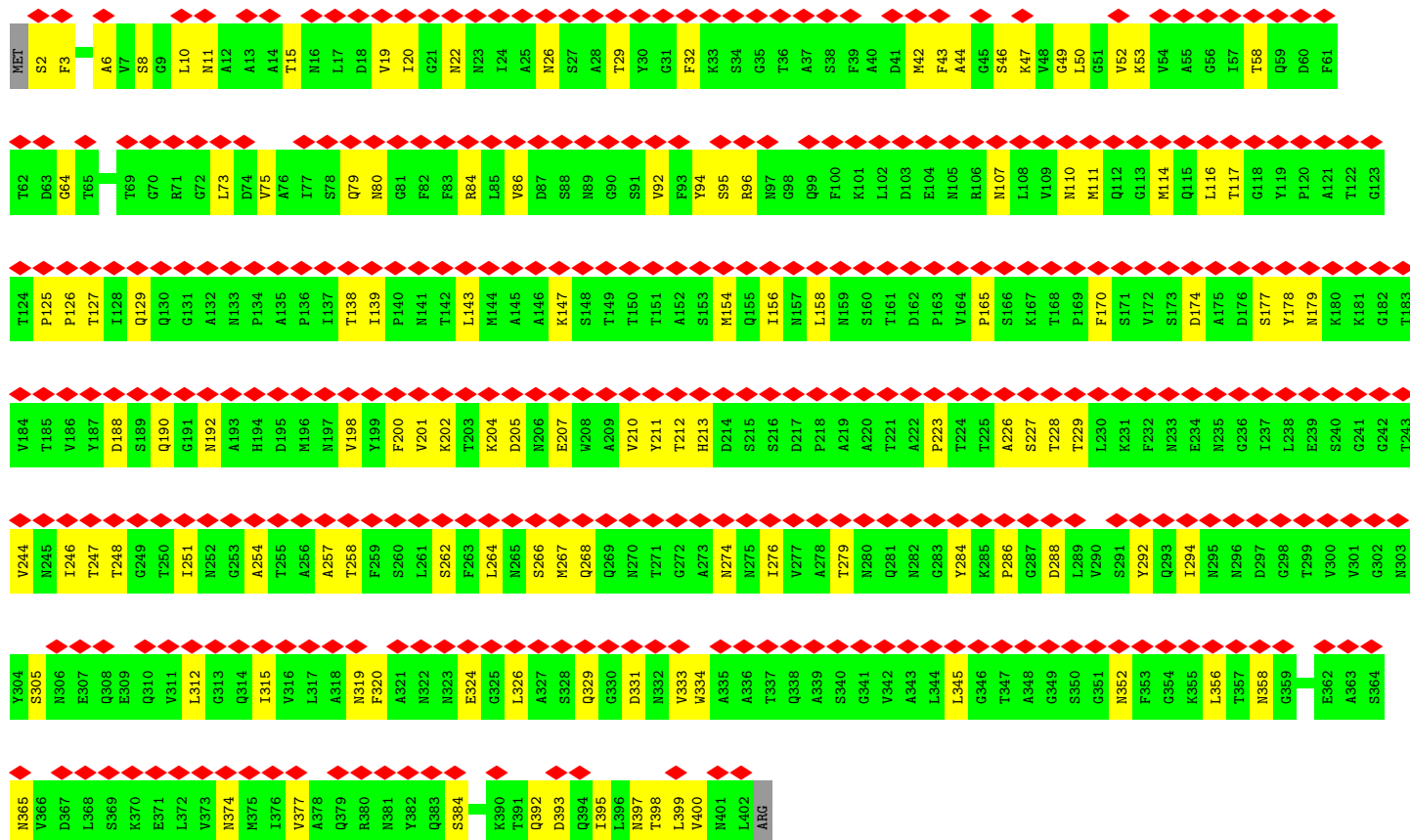
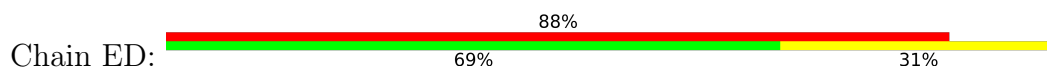


• Molecule 8: Flagellar hook protein FlgE

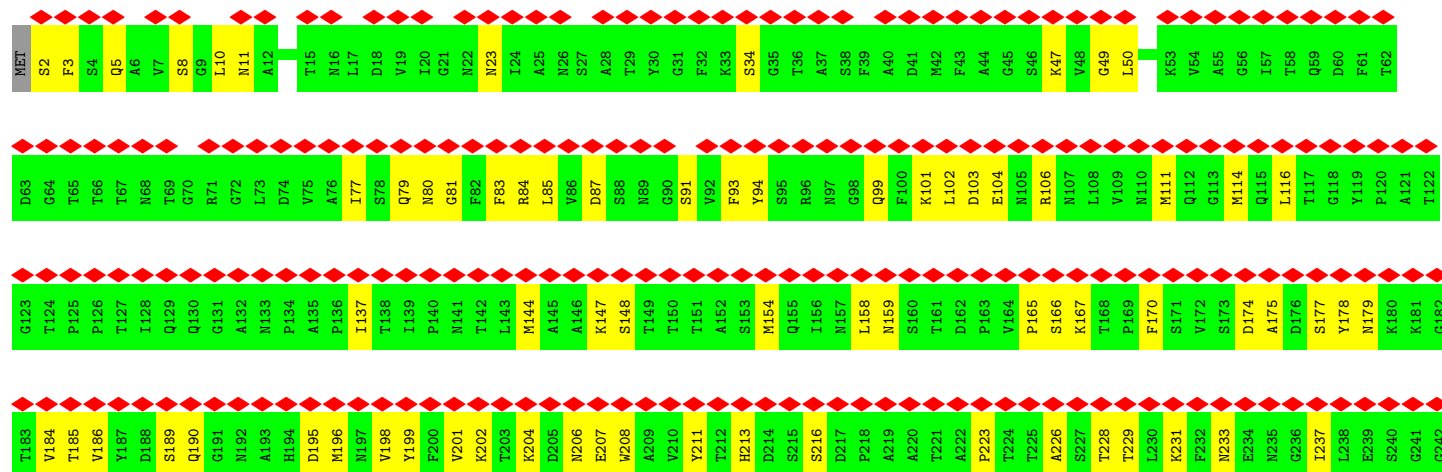
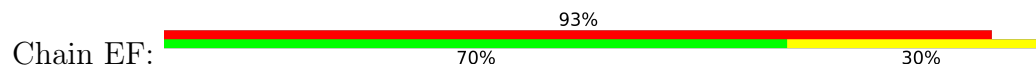


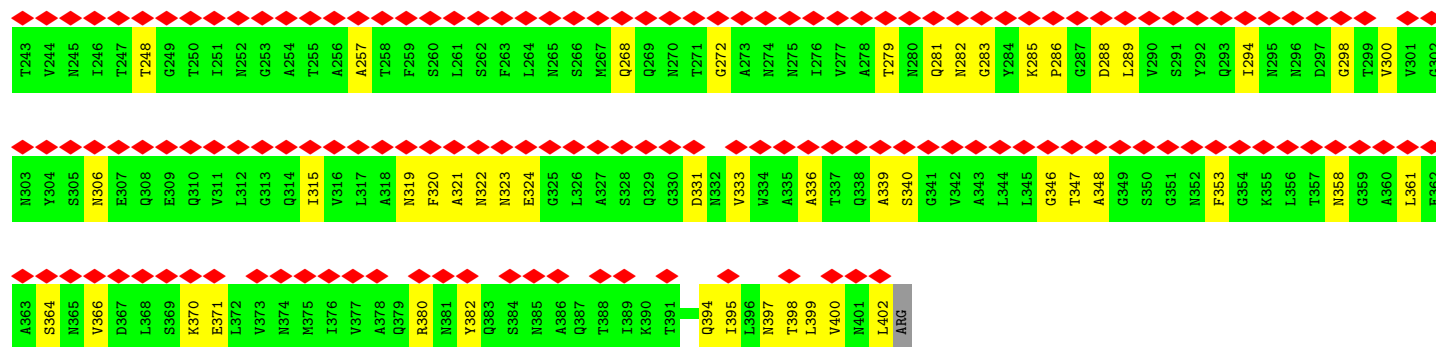


• Molecule 8: Flagellar hook protein FlgE

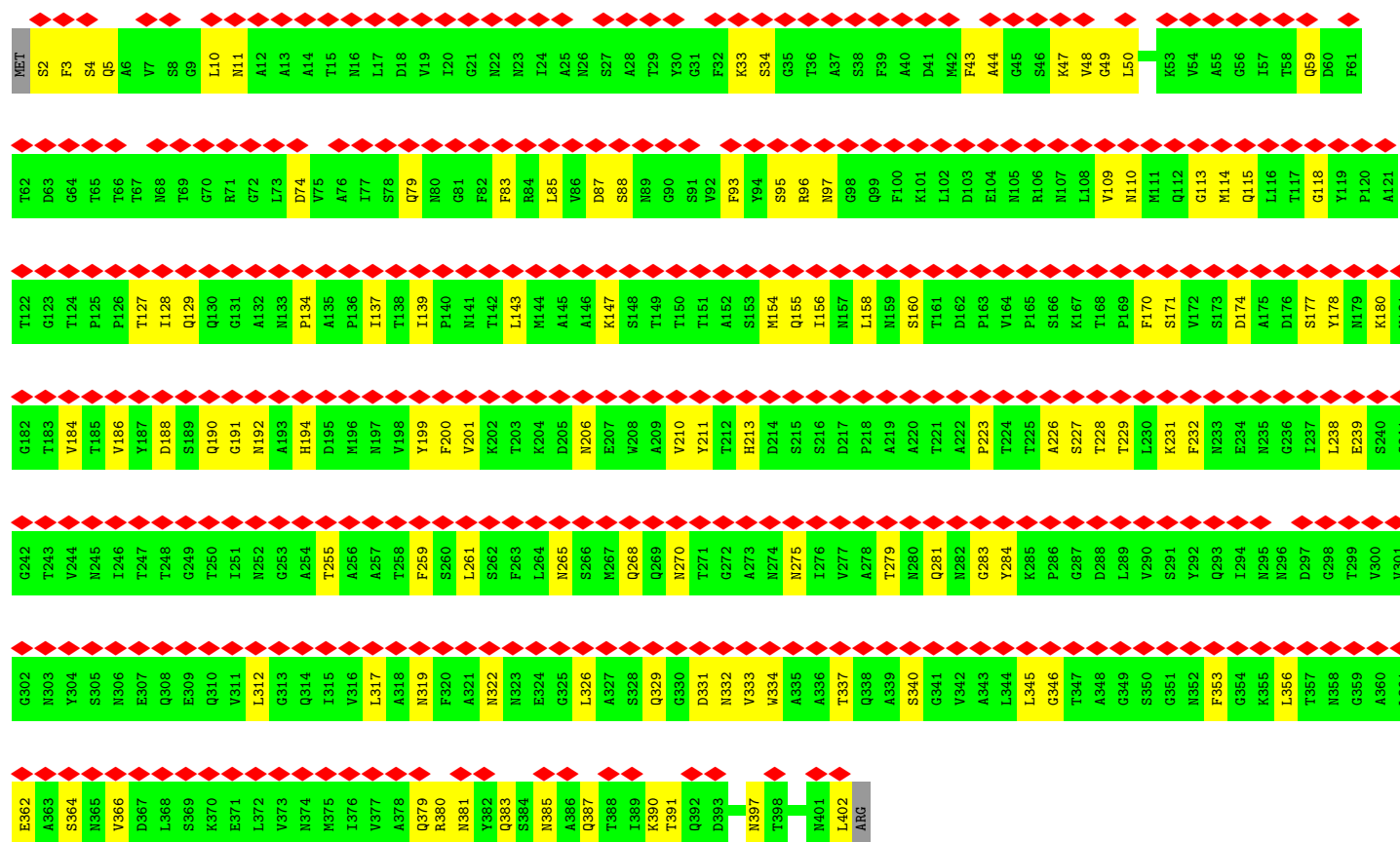
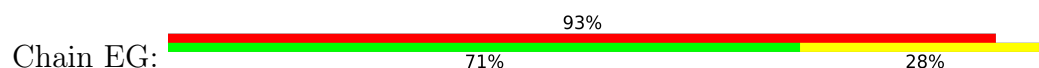


Chain EE: 86% 72% 27%

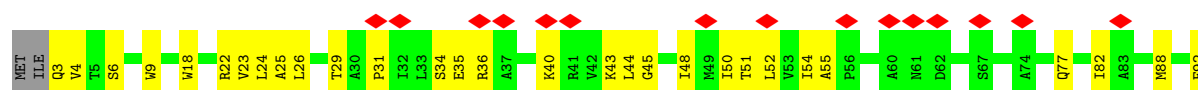


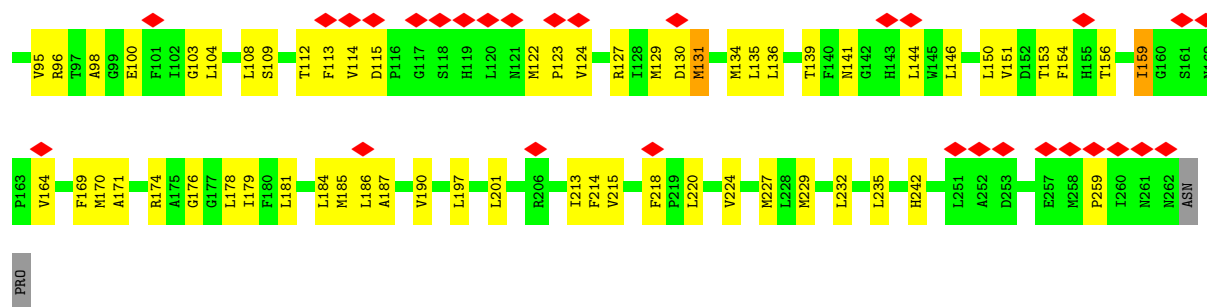


• Molecule 8: Flagellar hook protein FlgE

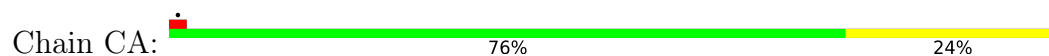


• Molecule 9: Flagellar biosynthetic protein FliR

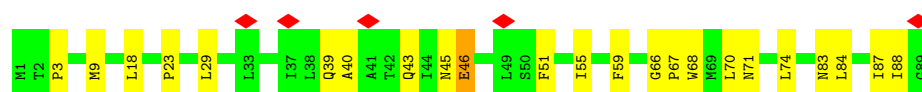
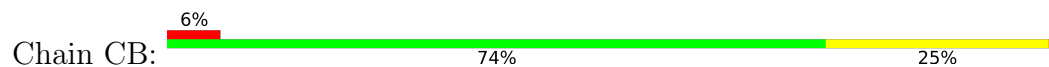




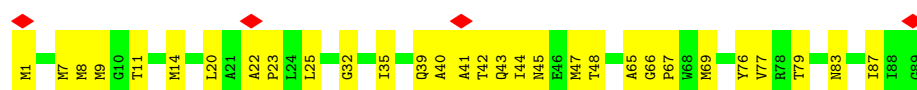
- Molecule 10: Flagellar biosynthetic protein FliQ



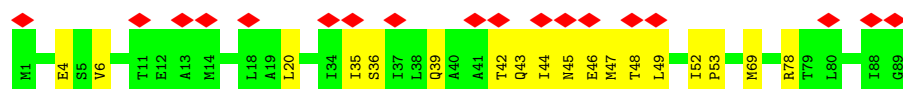
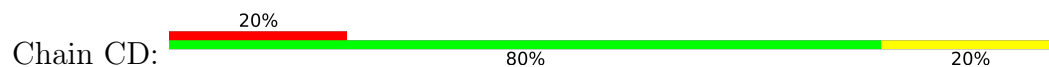
- Molecule 10: Flagellar biosynthetic protein FliQ



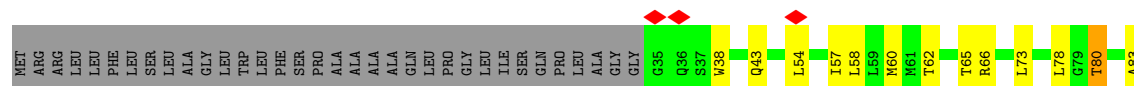
- Molecule 10: Flagellar biosynthetic protein FliQ

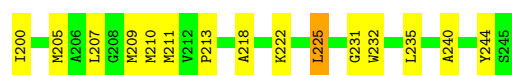


- Molecule 10: Flagellar biosynthetic protein FliQ

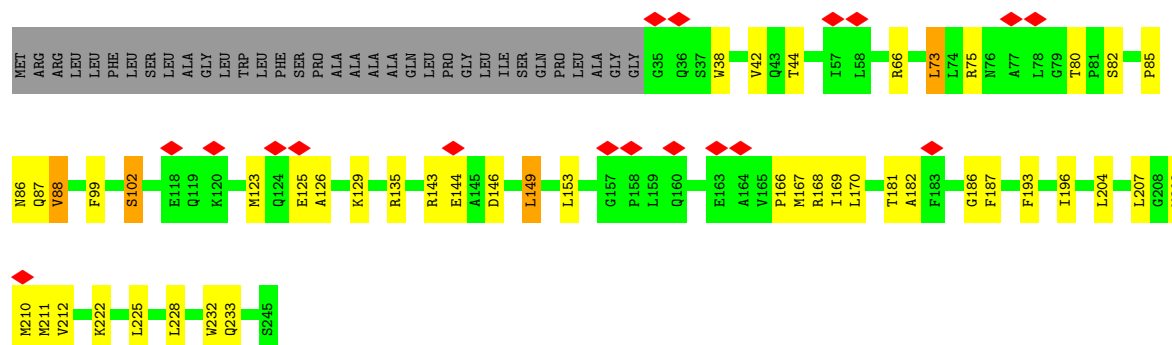


- Molecule 11: Flagellar biosynthetic protein FliP

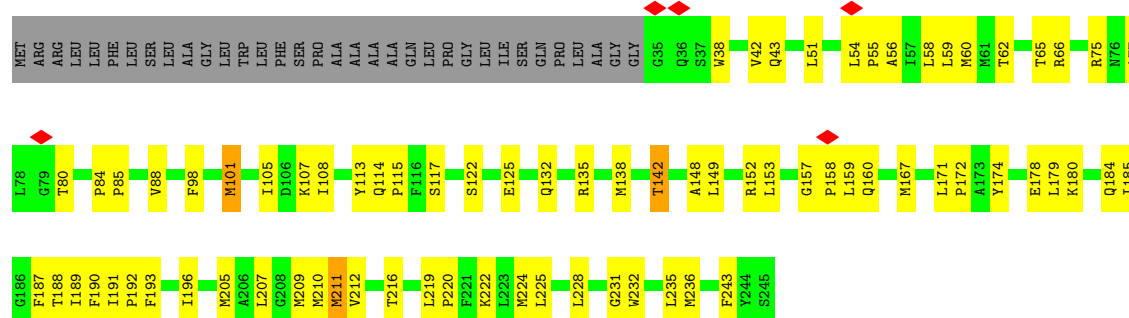




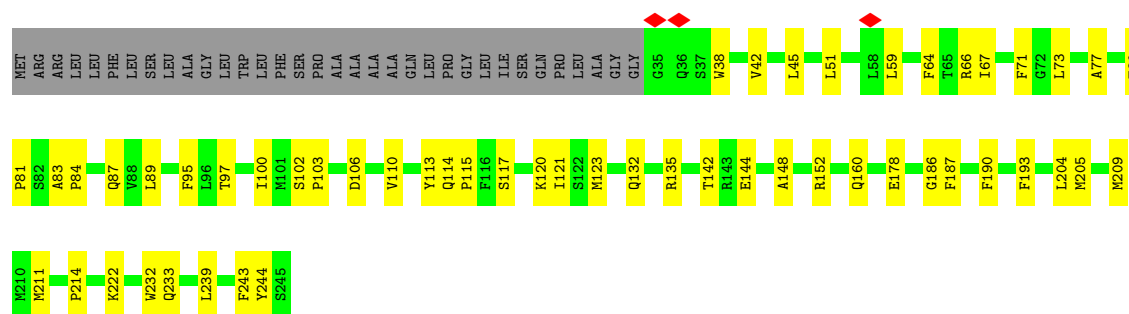
• Molecule 11: Flagellar biosynthetic protein FlhP



• Molecule 11: Flagellar biosynthetic protein FlhP

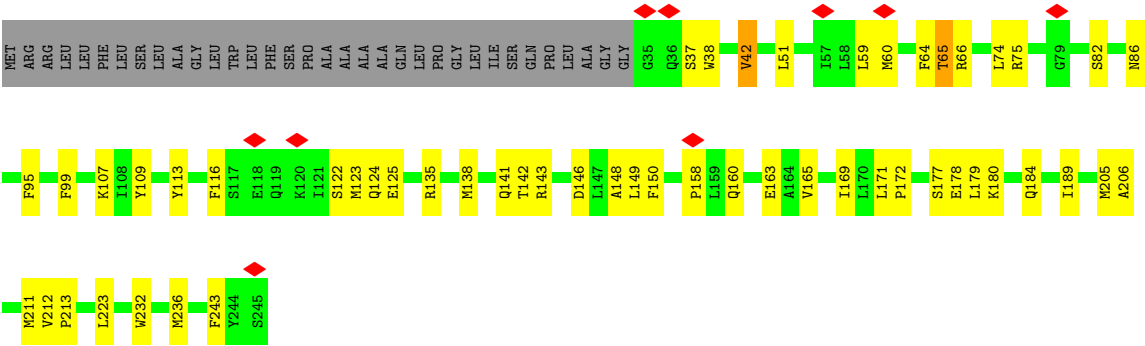


• Molecule 11: Flagellar biosynthetic protein FlhP



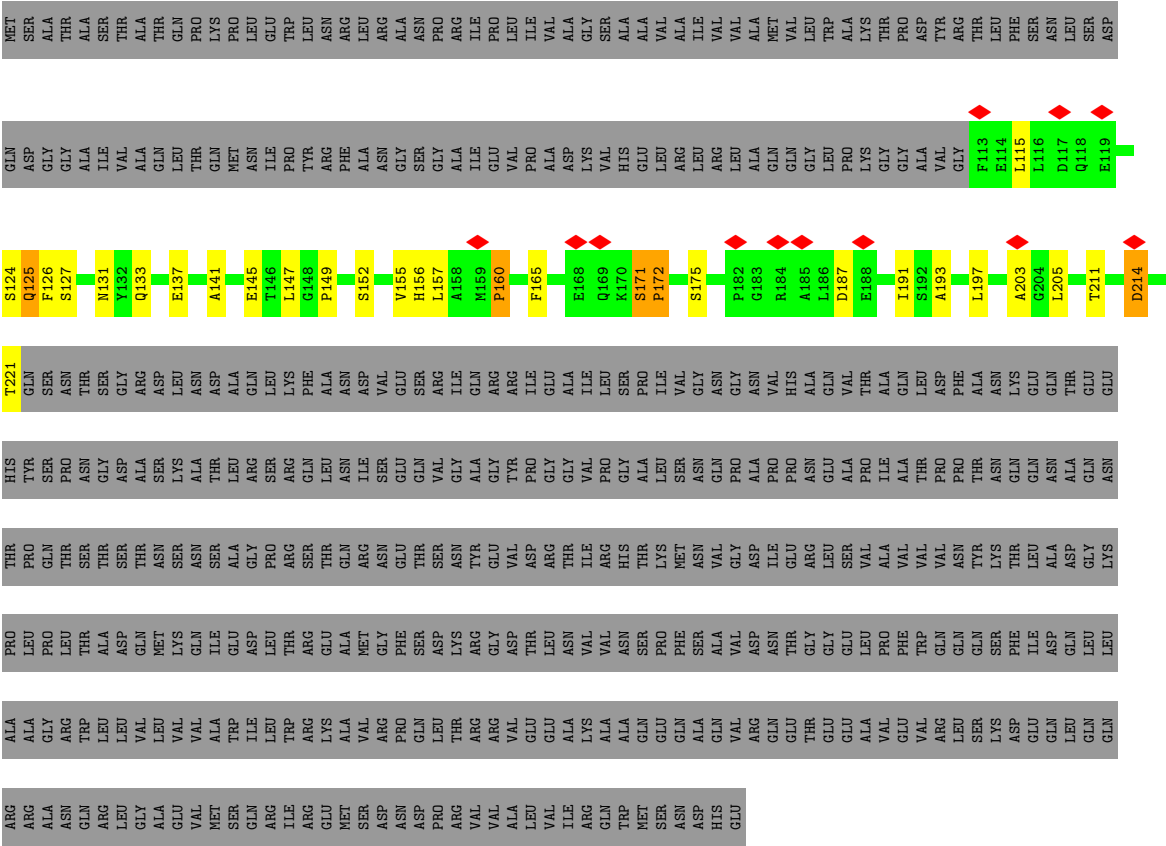
• Molecule 11: Flagellar biosynthetic protein FlhP





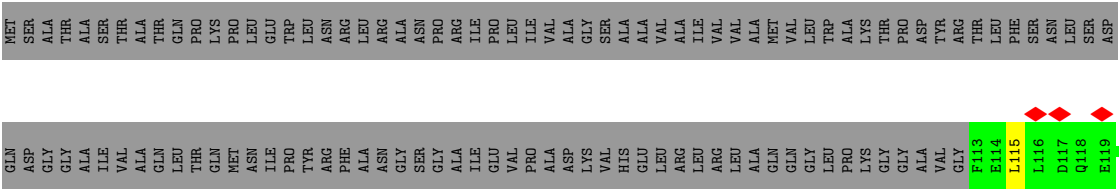
• Molecule 12: Flagellar M-ring protein

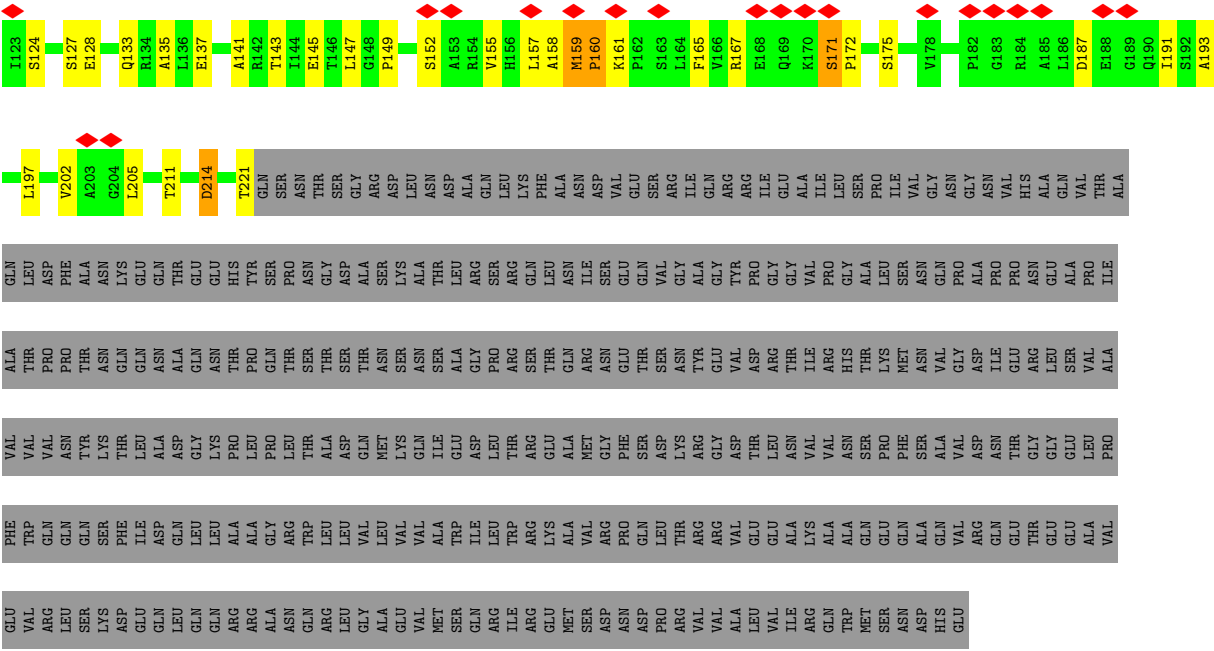
Chain Da: 14% 81%



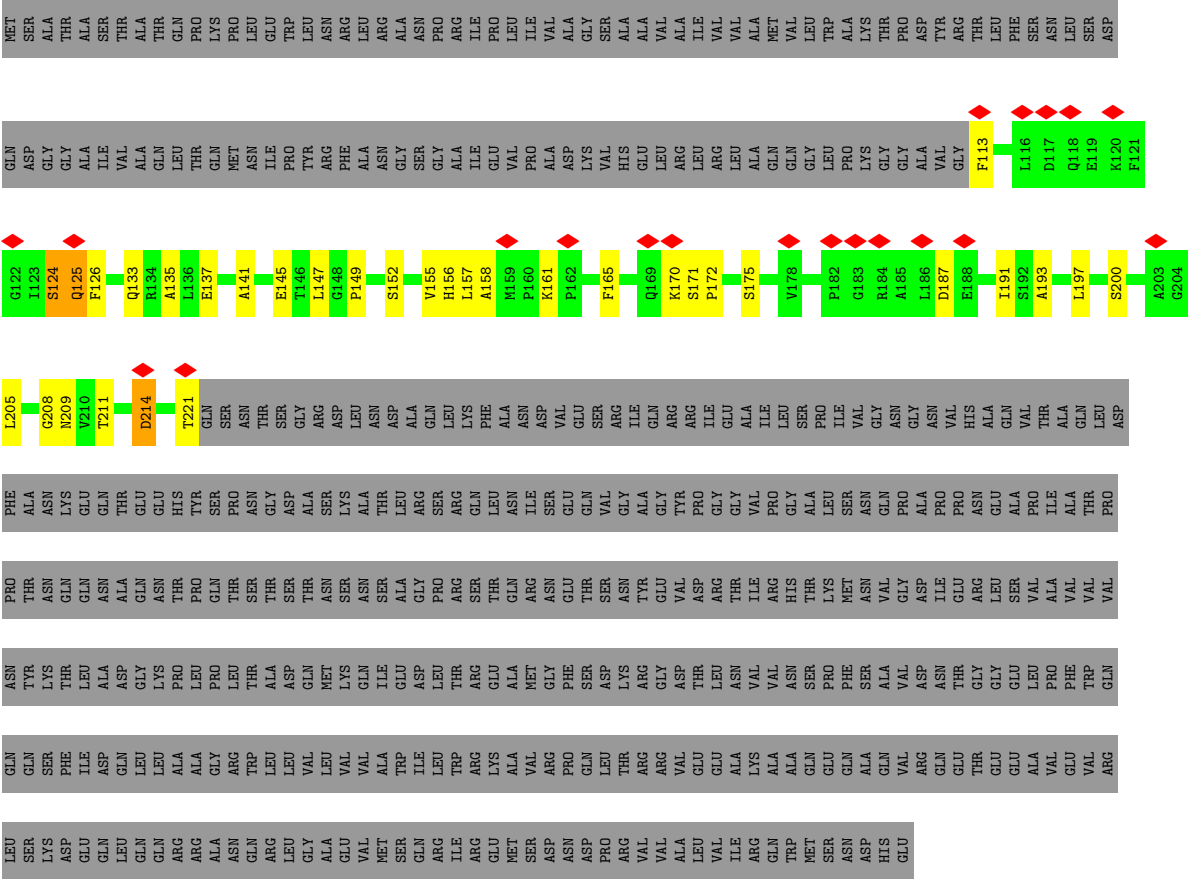
• Molecule 12: Flagellar M-ring protein

Chain Db: 14% 5% 81%

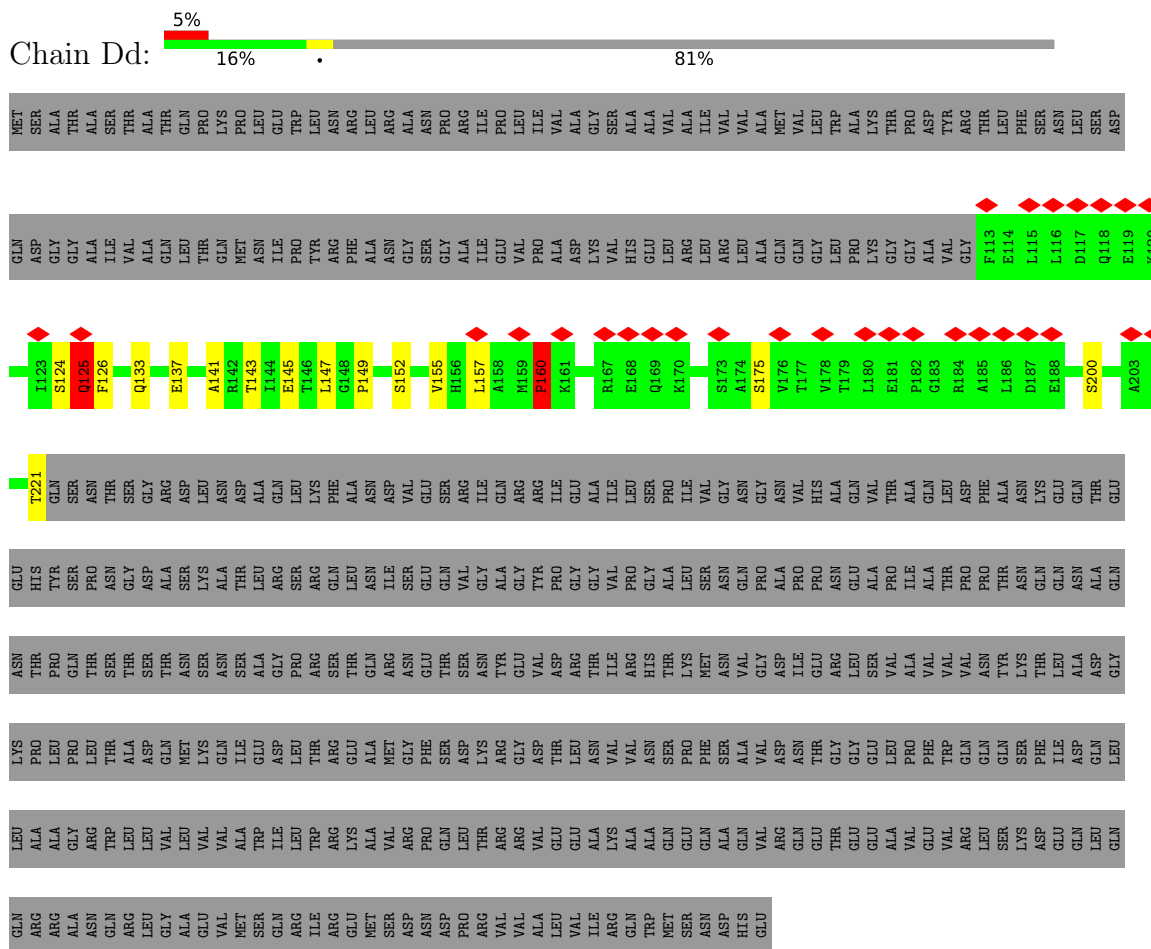




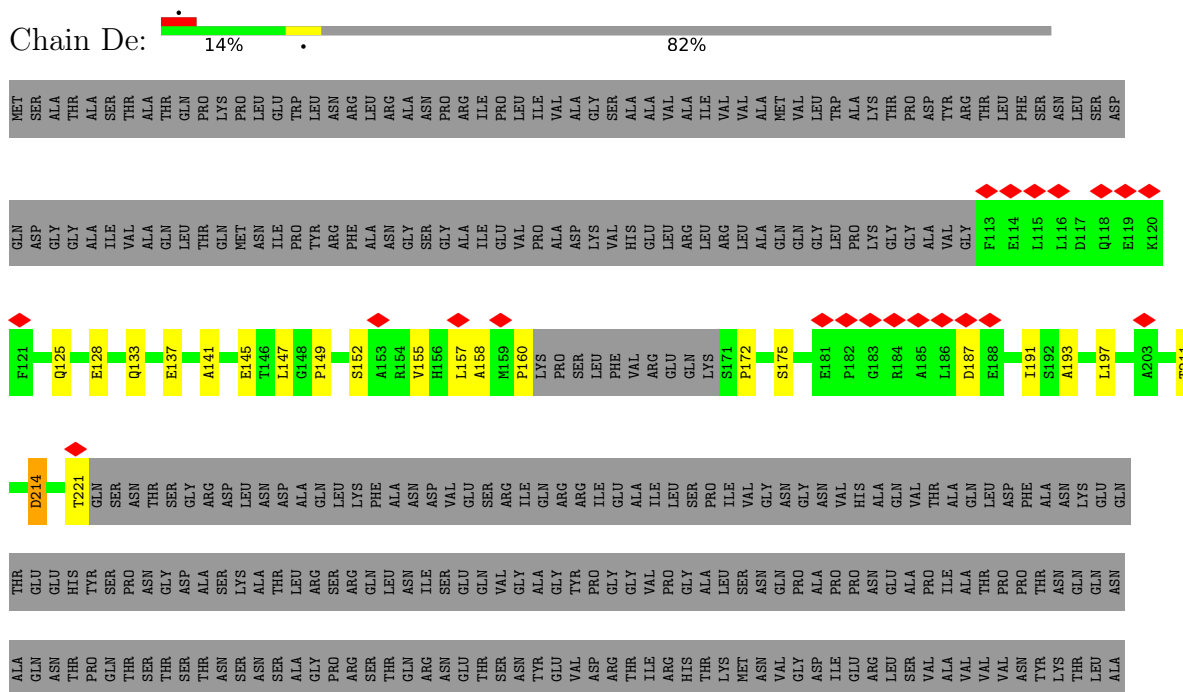
• Molecule 12: Flagellar M-ring protein

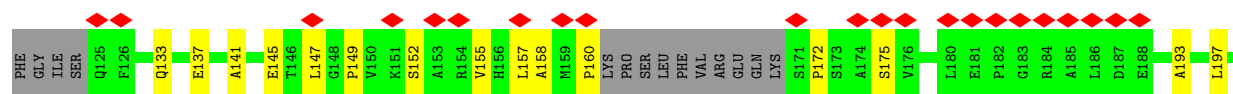


• Molecule 12: Flagellar M-ring protein

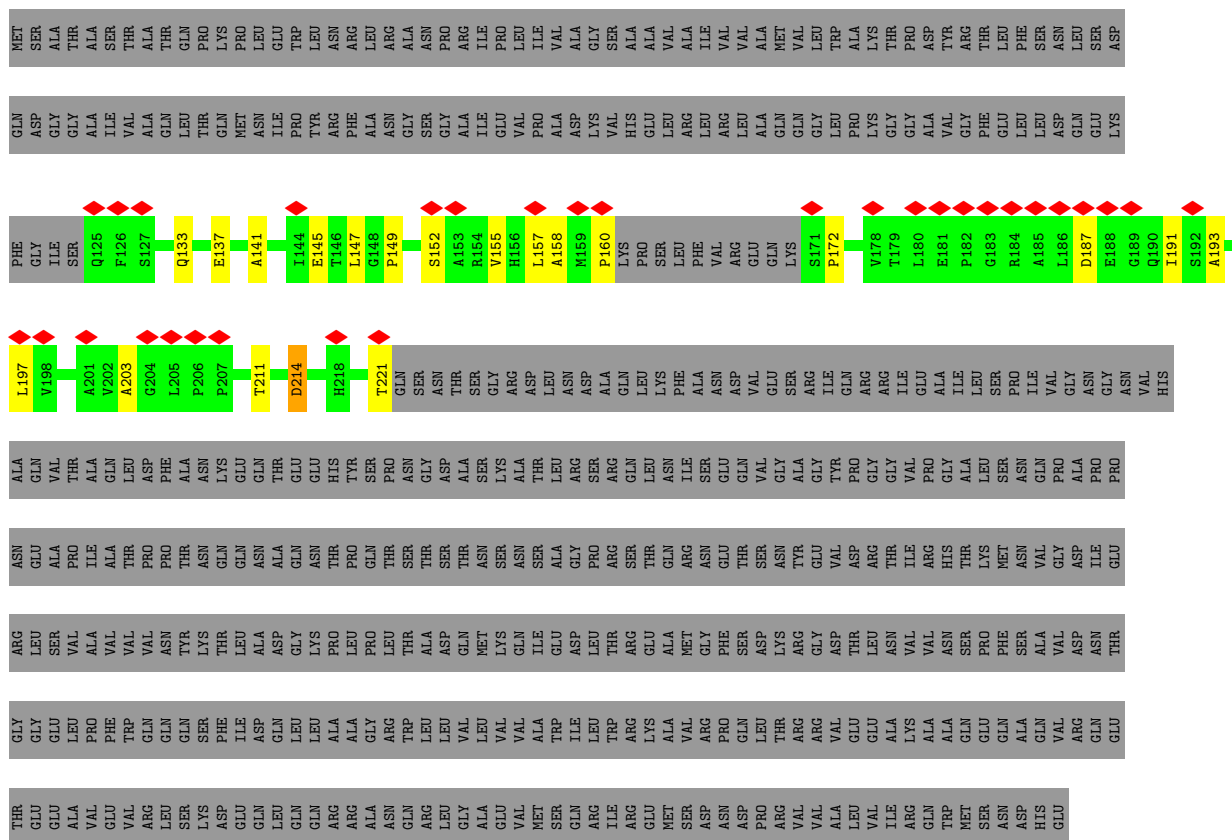


- Molecule 12: Flagellar M-ring protein

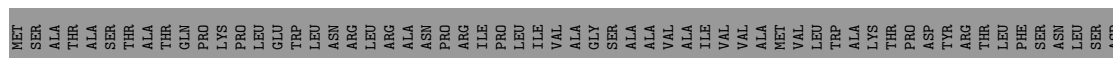


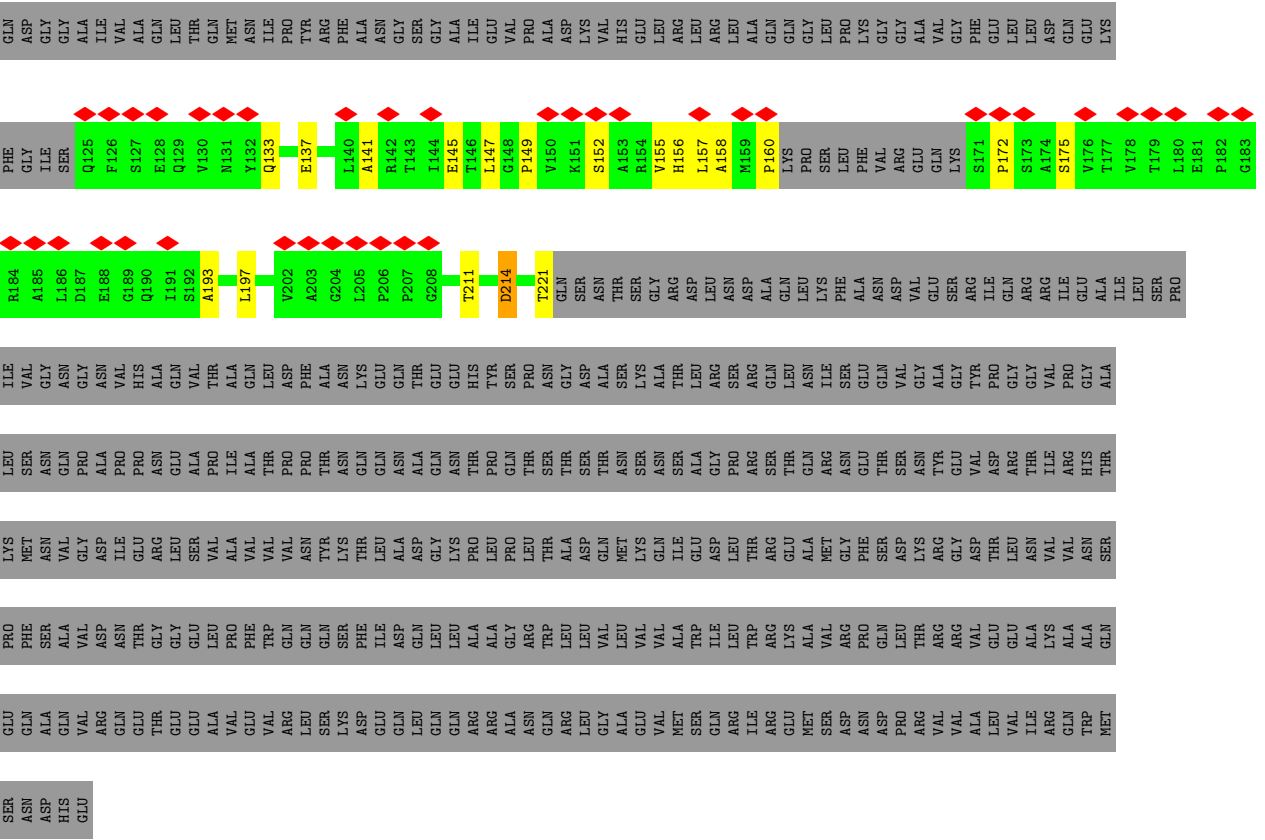


- Molecule 12: Flagellar M-ring protein

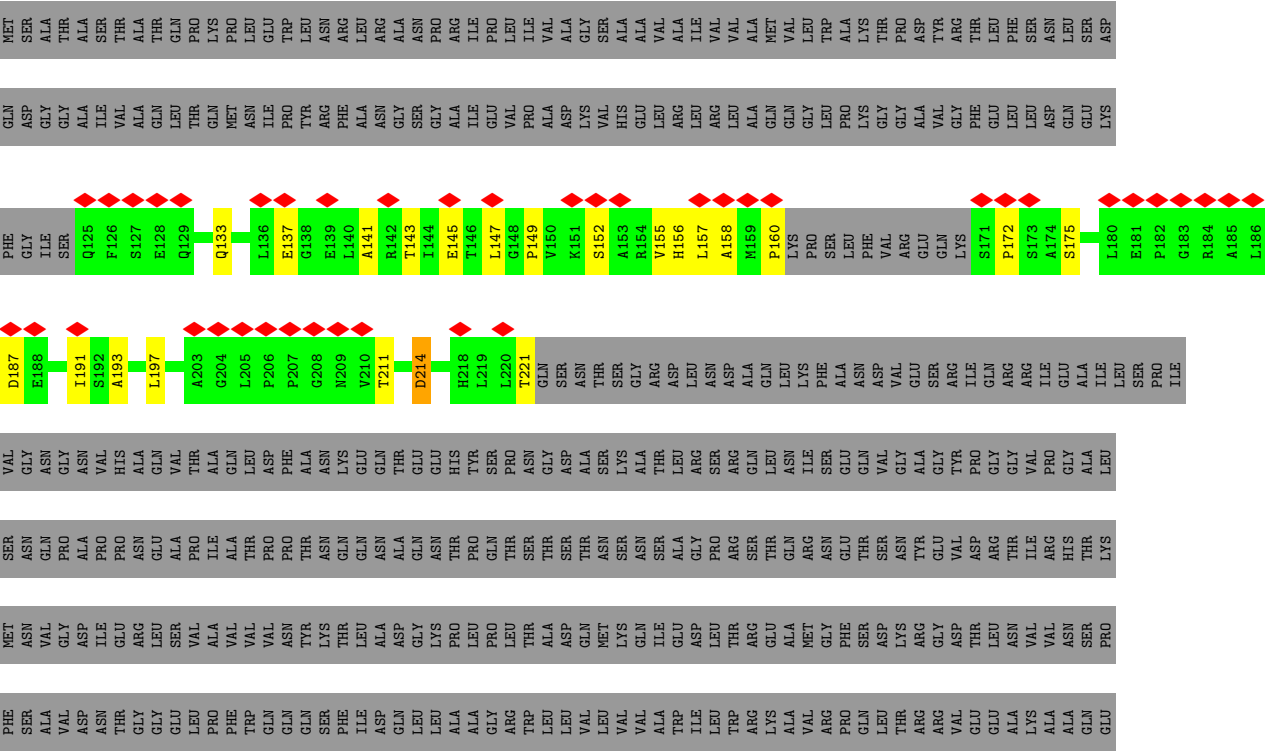


- Molecule 12: Flagellar M-ring protein





• Molecule 12: Flagellar M-ring protein



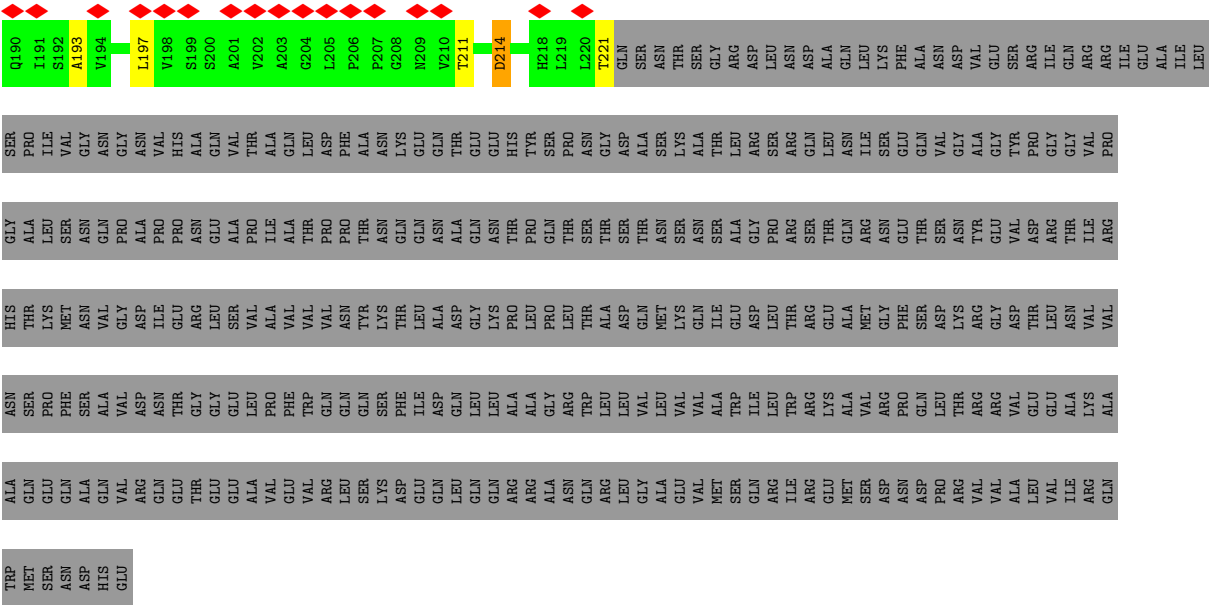
- Molecule 12: Flagellar M-ring protein

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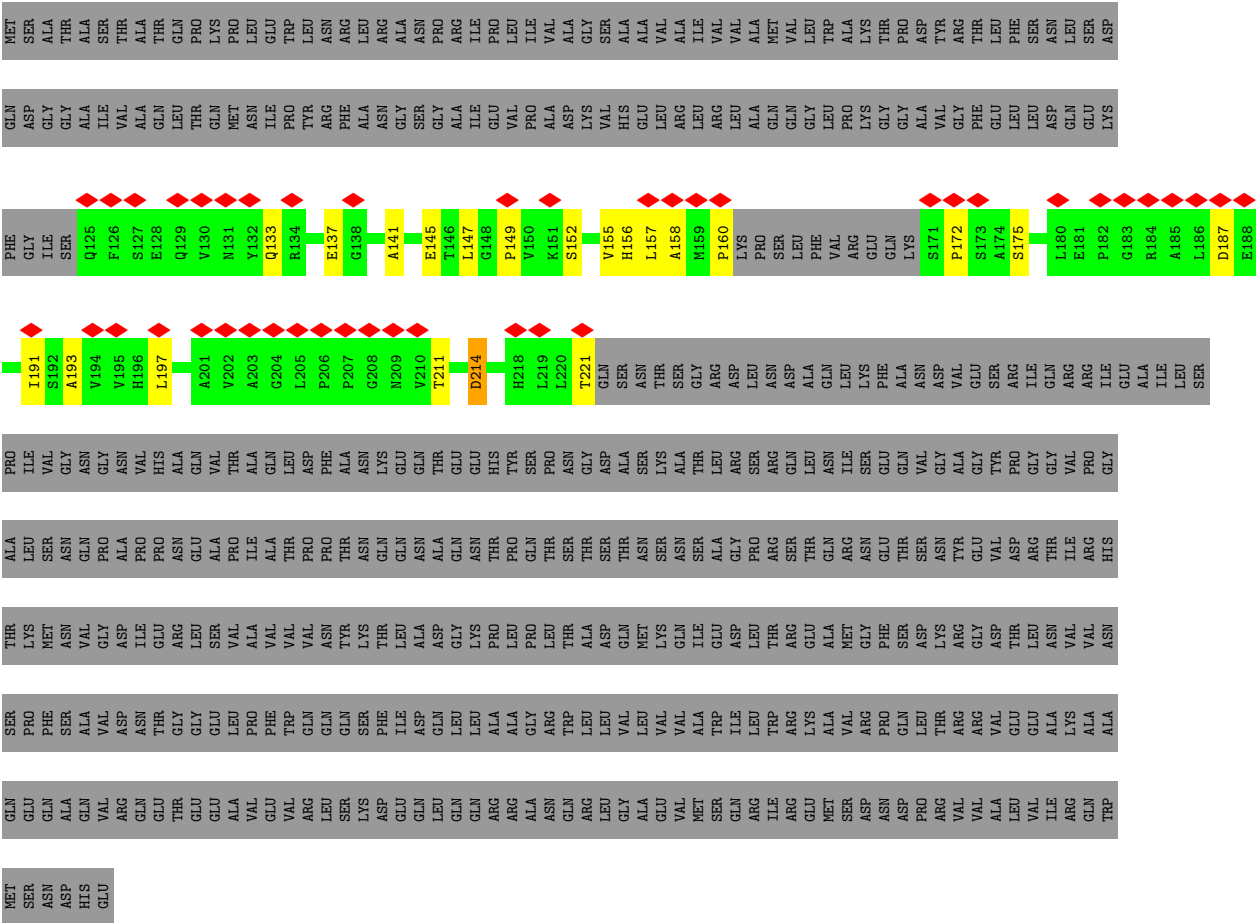
- Molecule 12: Flagellar M-ring protein



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

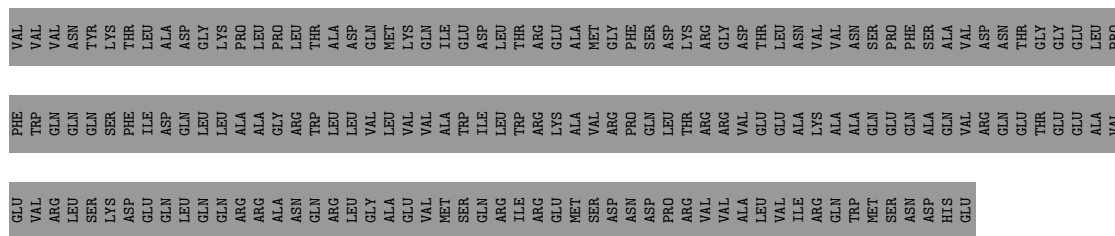


• Molecule 12: Flagellar M-ring protein

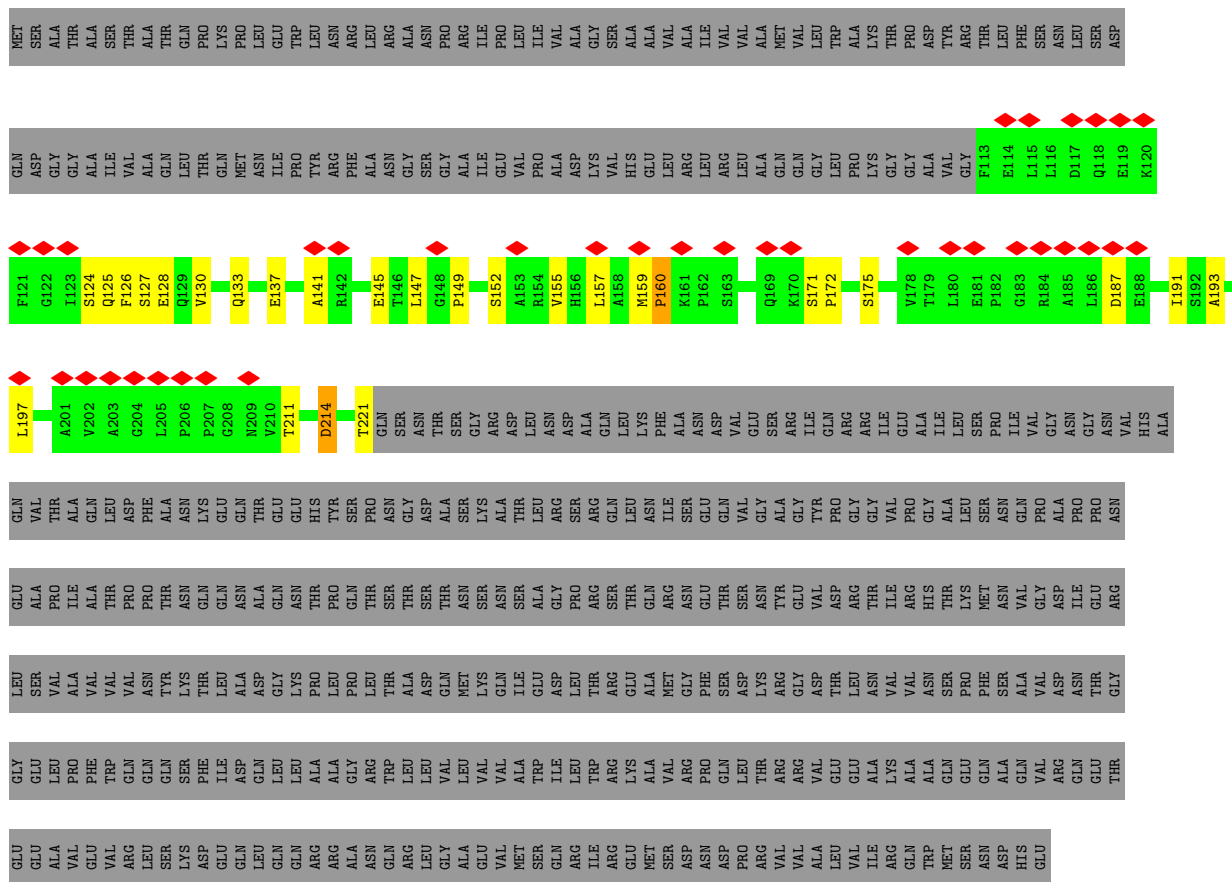


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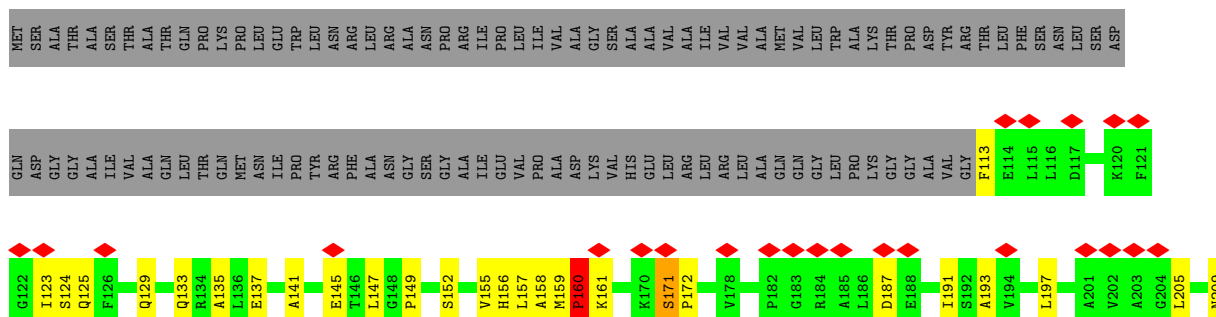




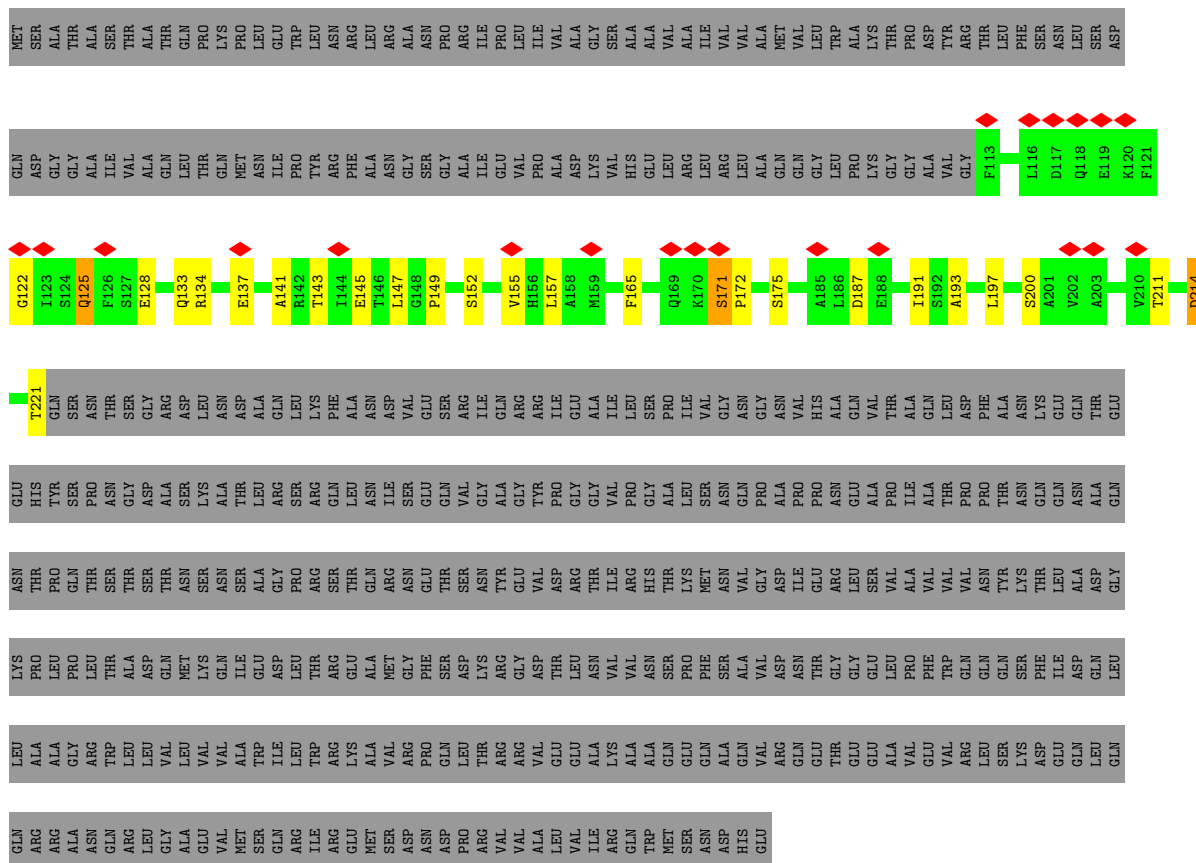
- Molecule 12: Flagellar M-ring protein



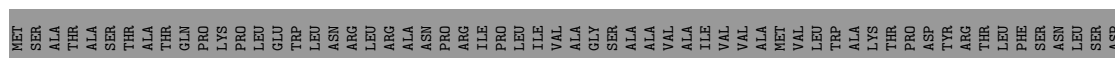
- Molecule 12: Flagellar M-ring protein



- Molecule 12: Flagellar M-ring protein



- Molecule 12: Flagellar M-ring protein



[illegible]

- Molecule 12: Flagellar M-ring protein



MET	SER	ALA	THR	ALA	SER	THR	ALA	THR	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	LEU	ARG	ALA	ALA	ASN	PRO	ARG	ILE	PRO	LEU	ILE	VAL	GLY	GLY	SER	ALA	ALA	VAL	VAL	ALA	ALA	ILE	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	SER	THR	GLN	PRO	LEU	GLU	TRP	LEU	ASN	ARG	LEU	GLN	THR	ALA	SER	THR	ALA	SER	ALA	MET
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GLN	ASP	GLY	GLY	ALA	ILE	VAL	ALA	ALA	GLN	LEU	THR	GLN	MET	ASN	ILE	PRO	TYR	ARG	PHE	ALA	ALA	ASN	GLY	SER	GLY	ALA	ALA	ILE	GLU	VAL	PRO	ALA	ASP	LYS	VAL	HIS	GLU	LEU	ARG	ARG	LEU	ALA	GLN	GLN	GLY	LEU	PRO	LYS	GLY	GLY	ALA	VAL	GLY	F113	E114	L115	L116	D117	K120	L121	L122	L123	L124	L125	L126	L127	L128	L129	L130	L131	L132	L133	L134	L135	L136	L137	L138	L139	L140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582
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Category	Count
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S152	100
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P160	100
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R167	100
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T221
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ASN
THR
SER
GLY
ARG
ASP
LEU
ASN
ASP
ALA
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GLN	THR	GLU	GLU	HIS	TYR	SER	PRO	GLY	ASP	ALA	SER	LYS	ALA	THR	ARG	SER	ARG	GLN	LEU	ASN	ILE	SER	GLU	GLN	VAL	GLY	ALA	GLY	TYR	PRO	GLY	GLY	GLY	VAL	PRO	GLY	GLA	ALA	GLY	LEU	SER	ASN	GLN	PRO	ASN	GLU	ALA	ALA	PRO	THR	THR	ASN	GLN	GLN
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[illegible]

ALA	ASP	GLY	LYS	PRO	LEU	THR	ALA	ASP	GLN	MET	LYS	GLN	ILE	GLU	ASP	LEU	THR	ARG	GLU	ALA	MET	GLY	PHE	SER	ASP	LYS	ARG	GLY	ASP	THR	LEU	ASN	VAL	VAL	ASN	SER	SER	PRO	PHE	SER	ALA	VAL	ASP	ASN	THR	GLY	GLY	GLU	LEU	PRO	PHE	TRP	GLN	GLN	SER	PHE	ILE
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ASP	GILN	LEU	LEU	ALA	ALA	GLY	ARG	TRP	LEU	LEU	VAL	VAL	VAL	ALA	ALA	TRP	IIE	LEU	TRP	LYS	LYS	ALA	VAL	VAL	ARG	ARG	PRO	GILN	LEU	THR	ARG	ARG	VAL	VAL	GIU	GIU	ALA	LYS	ALA	ALA	GILN	GIU	GIU	ALA	ALA	GILN	ALA	GLN	VAL	ARG	ARG	GILN	GIU	THR	GIU	GLU	GLU	ALA	VAL	VAL	VAL	VAL	ARG	SER	LYS	ASP	RUT
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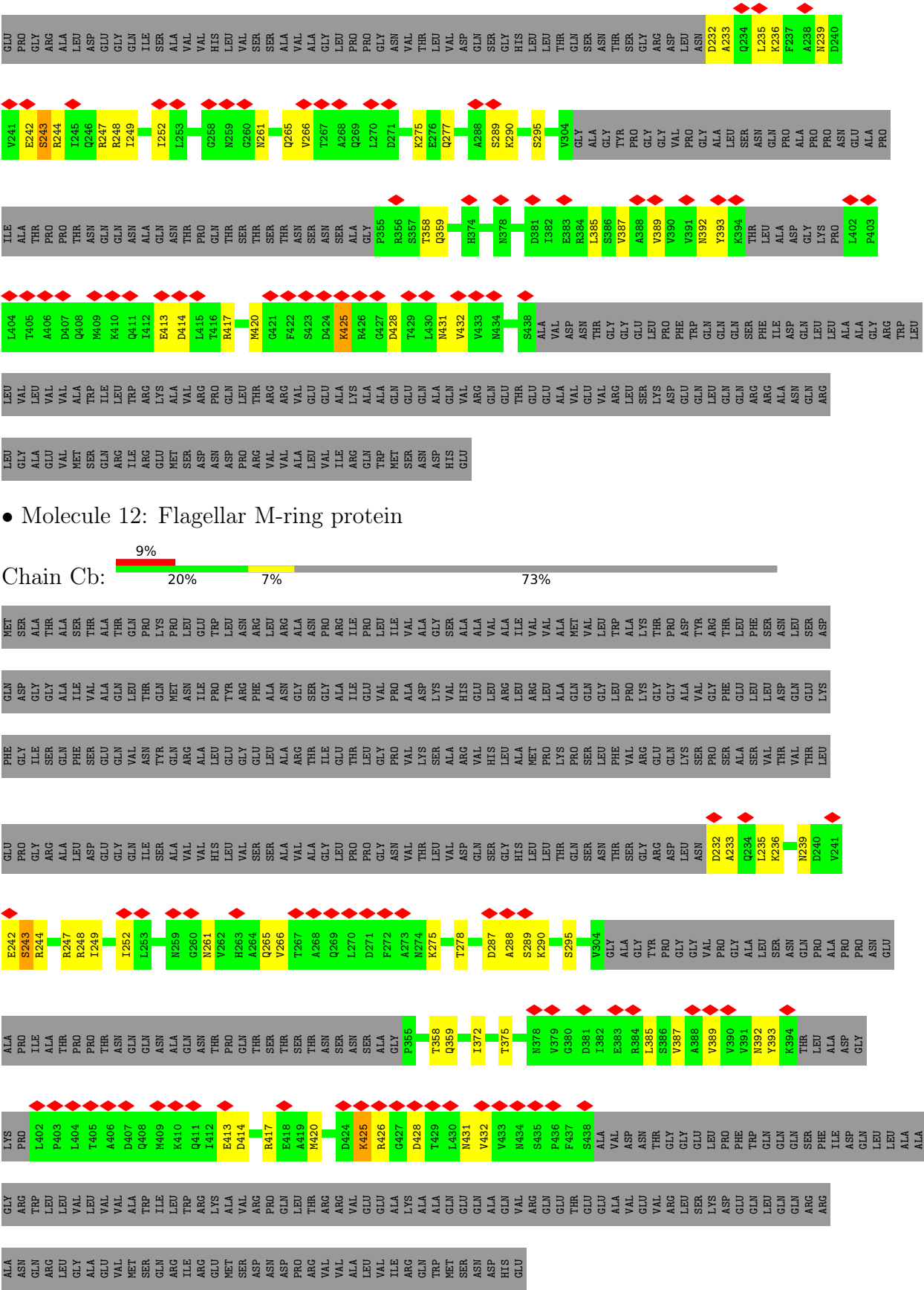
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- Molecule 12: Flagellar M-ring protein

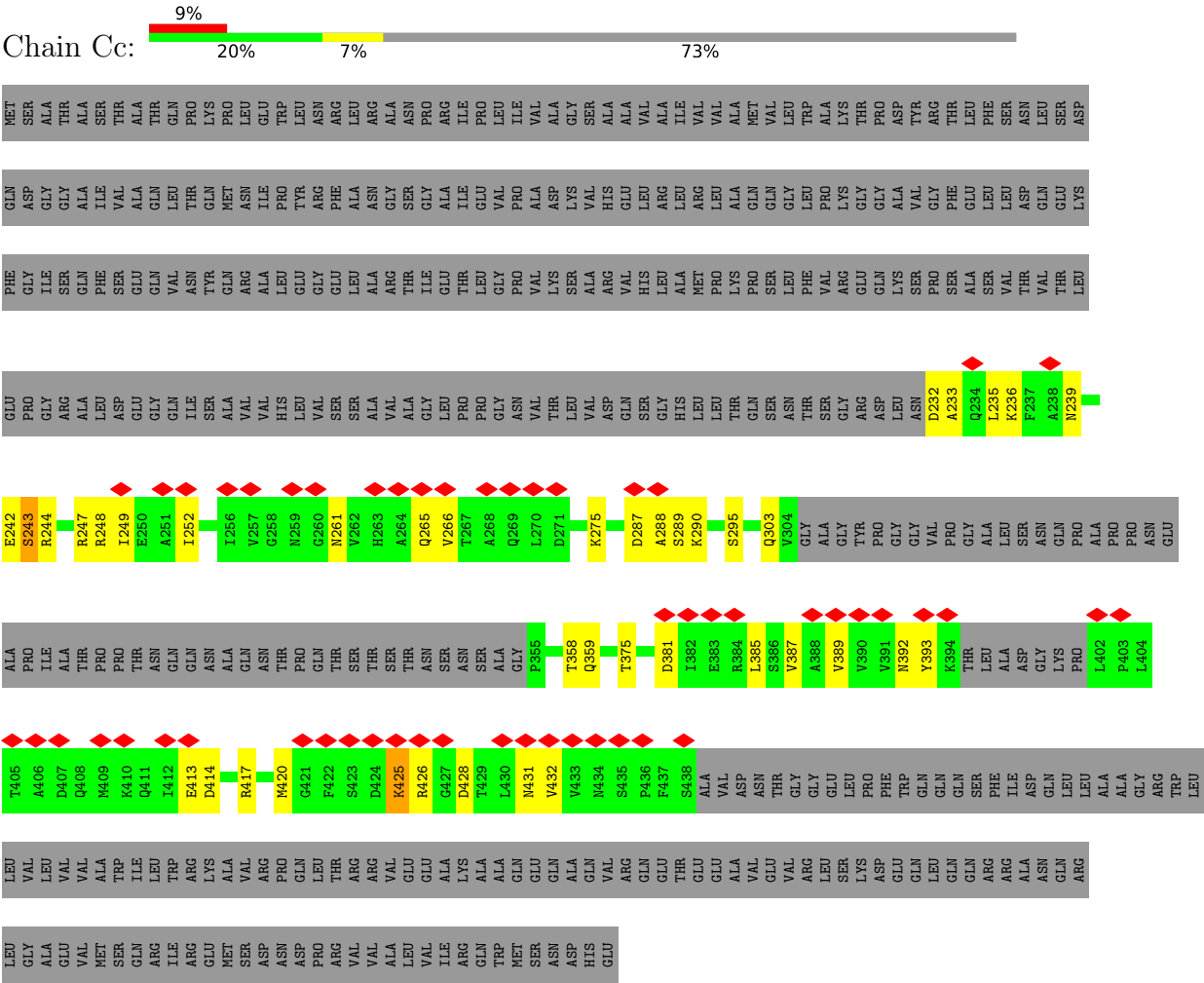
[illegible]

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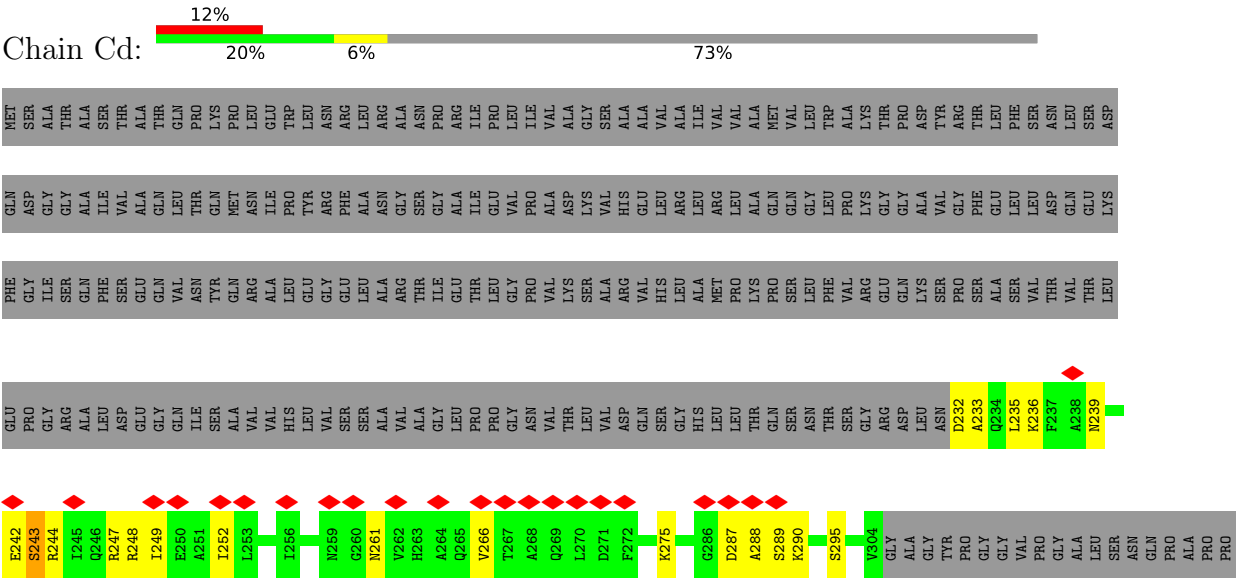
PHE
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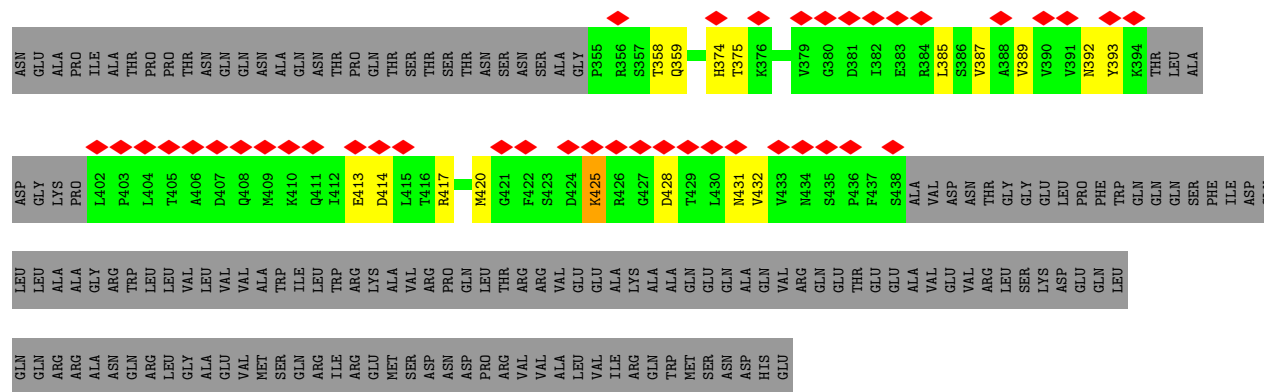


● Molecule 12: Flagellar M-ring protein

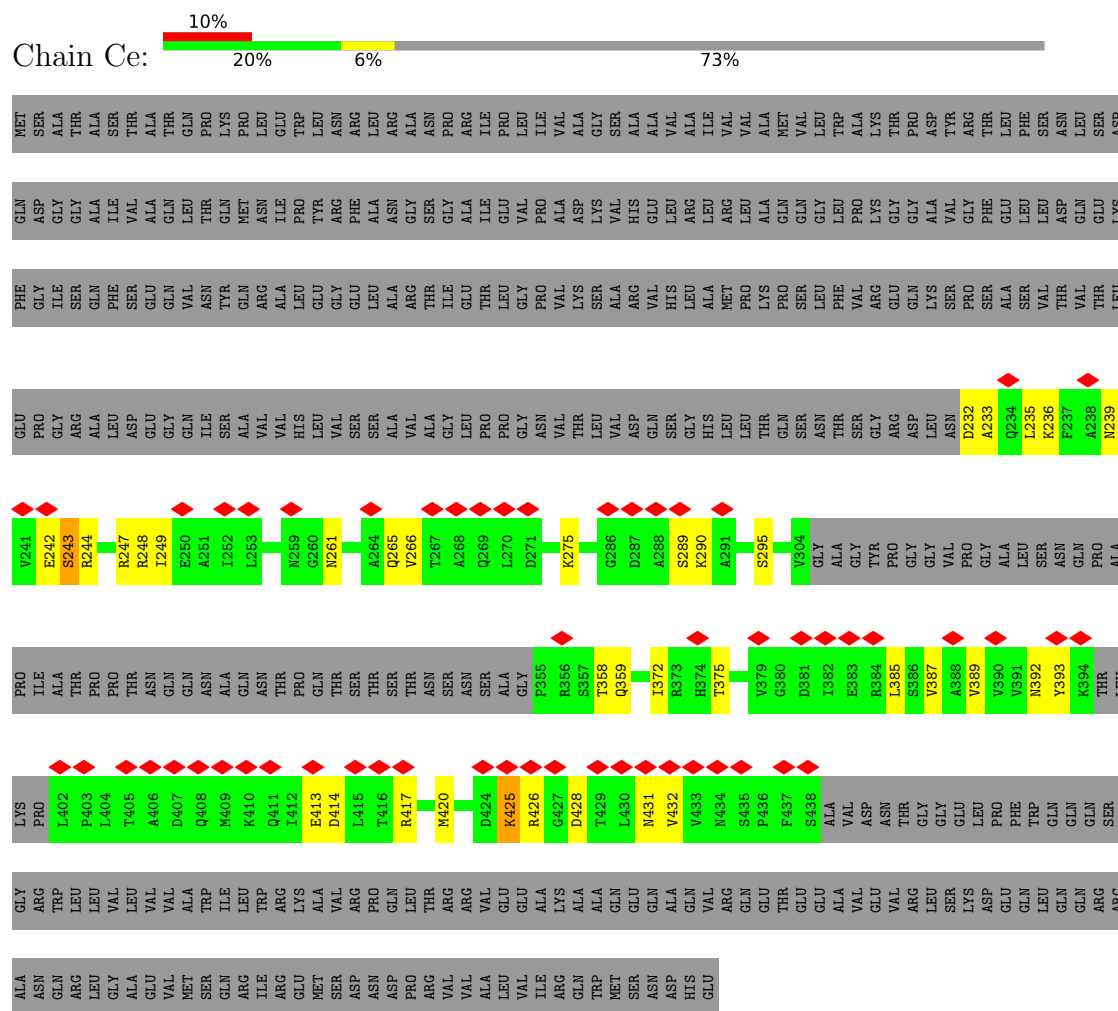


● Molecule 12: Flagellar M-ring protein

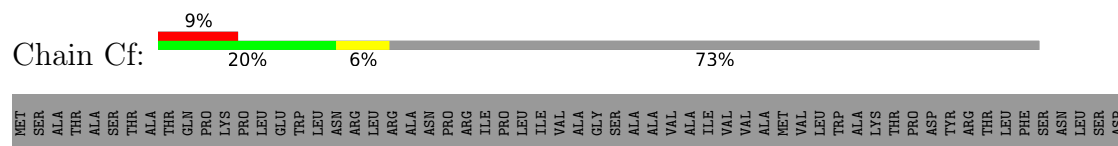


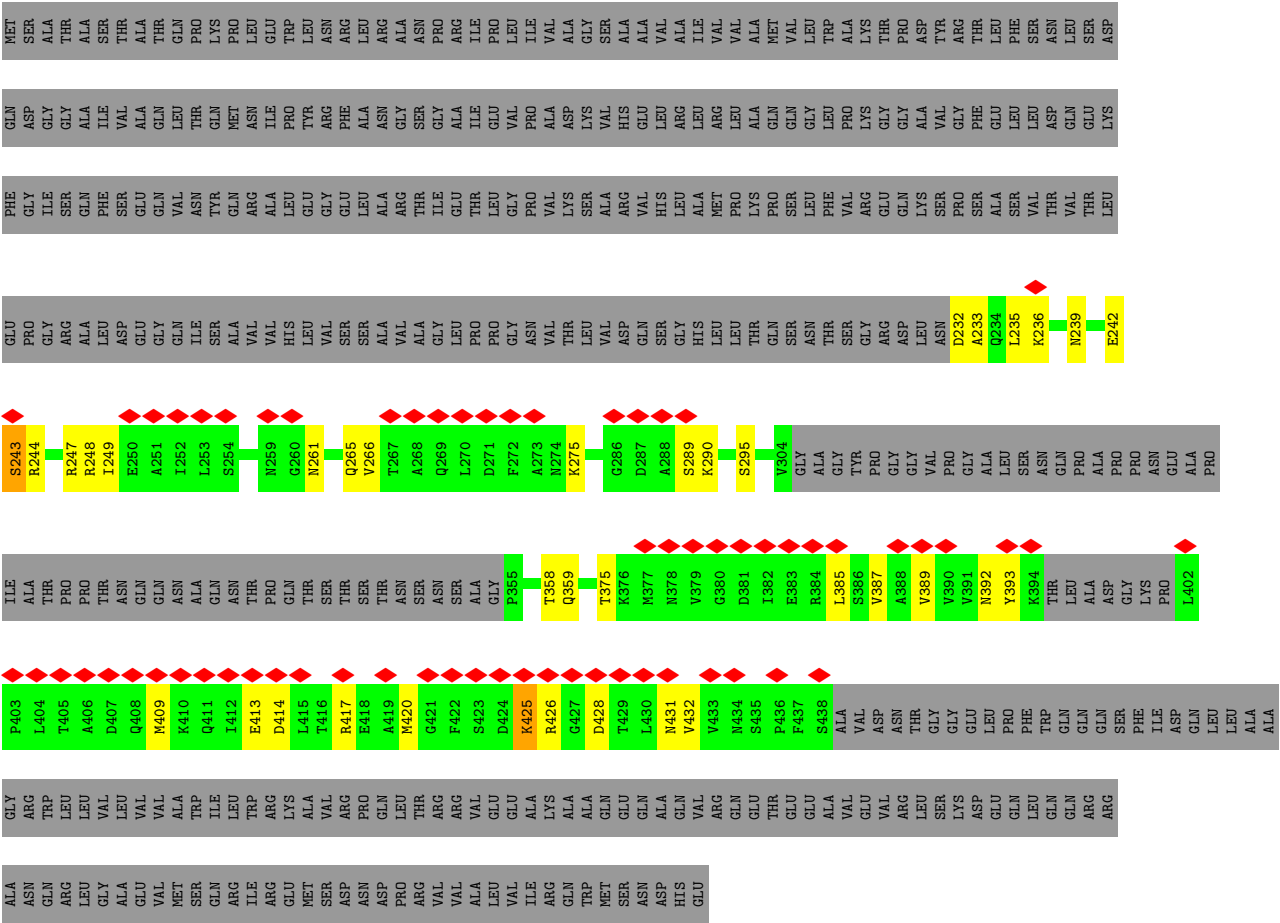


- Molecule 12: Flagellar M-ring protein

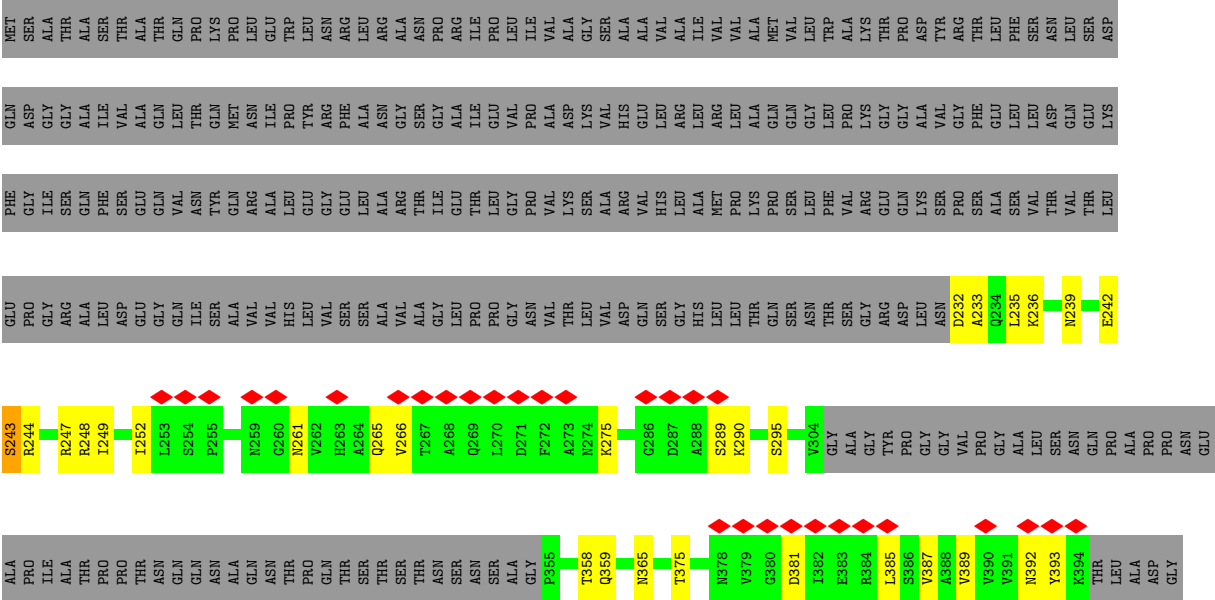


- Molecule 12: Flagellar M-ring protein

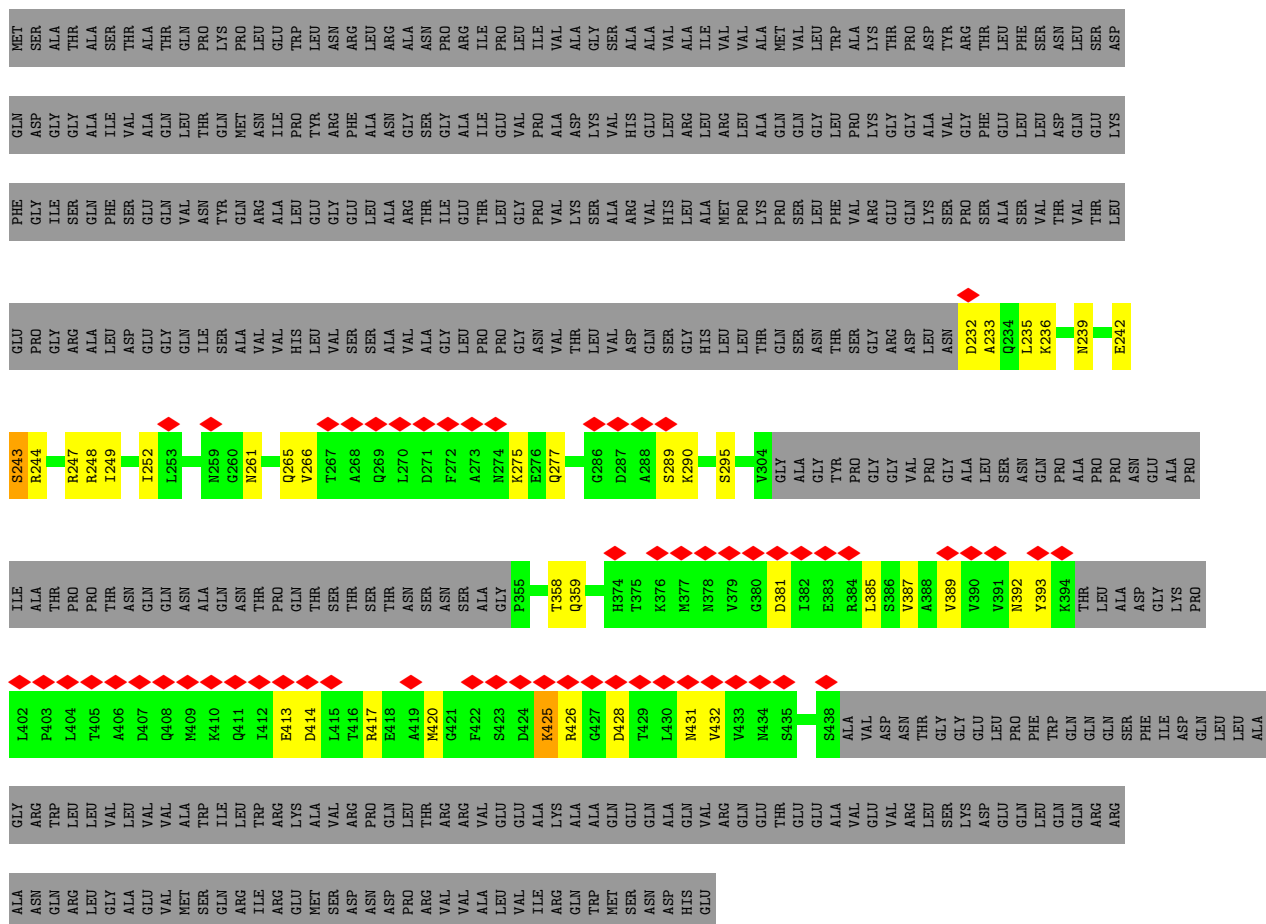




● Molecule 12: Flagellar M-ring protein



- Molecule 12: Flagellar M-ring protein

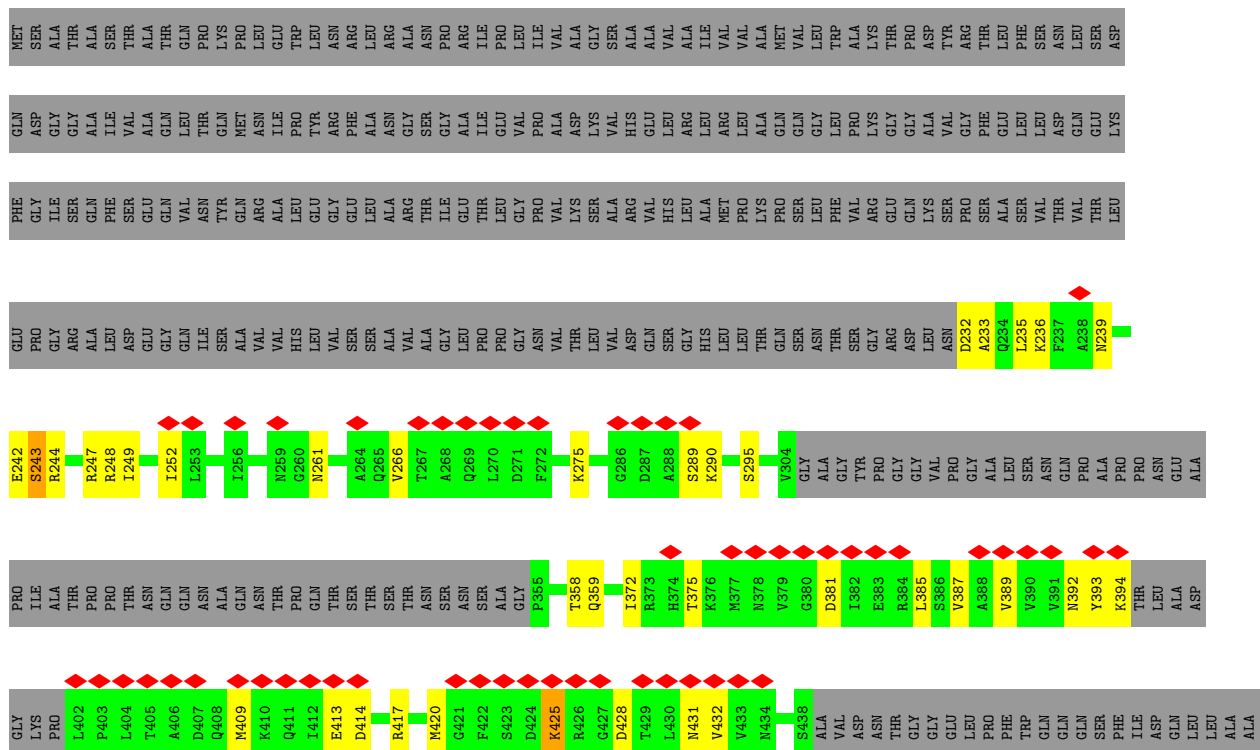


Chain Cp:





- Molecule 12: Flagellar M-ring protein



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

- Molecule 12: Flagellar M-ring protein

[illegible][illegible]

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

GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	GLY	GLN	ASP	GLY	LEU	GLN	SER	ASN	VAL	THR	THR	VAL	ASP	GLN	SER	GLY	HIS	LEU	LEU	THR	THR	GLY	ARG	ASP	LEU	ASN	D232	D233	D234	D235	D236	D239	D240
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S243	R244	R247	R248	I249	I252	I253	N259	G260	N261	Q265	V266	T267	A268	Q269	L270	D271	F272	K275	D287	A288	S289	K290	S295	V304	GLY	ALA	GLY	TYR	PRO	GLY	GLY	VAL	PRO	PRO	GLY	ALA	LEU	SER	ASN	GLN	PRO	ALA	PRO	PRO	PRO	ILE	ALA	THR	PRO
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[illegible]

T405	A406	D407	Q408	M409	K410	Q411	I412	E413	D414			R417	E418	A419	M420	G421	F422	S423	D424	K425	R426	G427	D428	T429	L430	M431	V432	V433	M434	S435		S436	ALA	VAL	ASP	ASN	THR	GLY	GLY	GLU	LEU	PRO	PHE	TRP	GLN	GLN	GLN	SER	PHE	ILE	ASP	GLN	LEU	LEU	ALA	ALA	GLY	ARG	TRP	LEU
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[illegible]

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

- Molecule 12: Flagellar M-ring protein

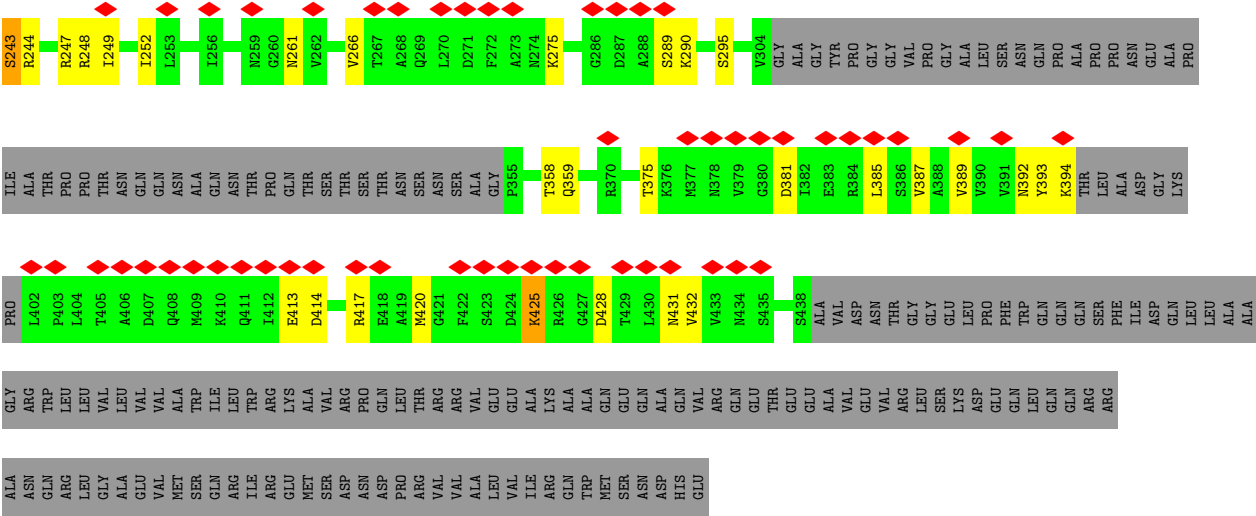


MET	SER	ALA	ALA	ALA	SER	THR	THR	GLN	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	ARG	LEU	ALA	ARG	ALA	ASN	PRO	ARG	ILE	PRO	PRO	ILE	LEU	VAL	ALA	GLY	SER	ALA	ALA	ALA	VAL	VAL	ALA	ALA	ILE	VAL	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ALA	ALA	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	SER
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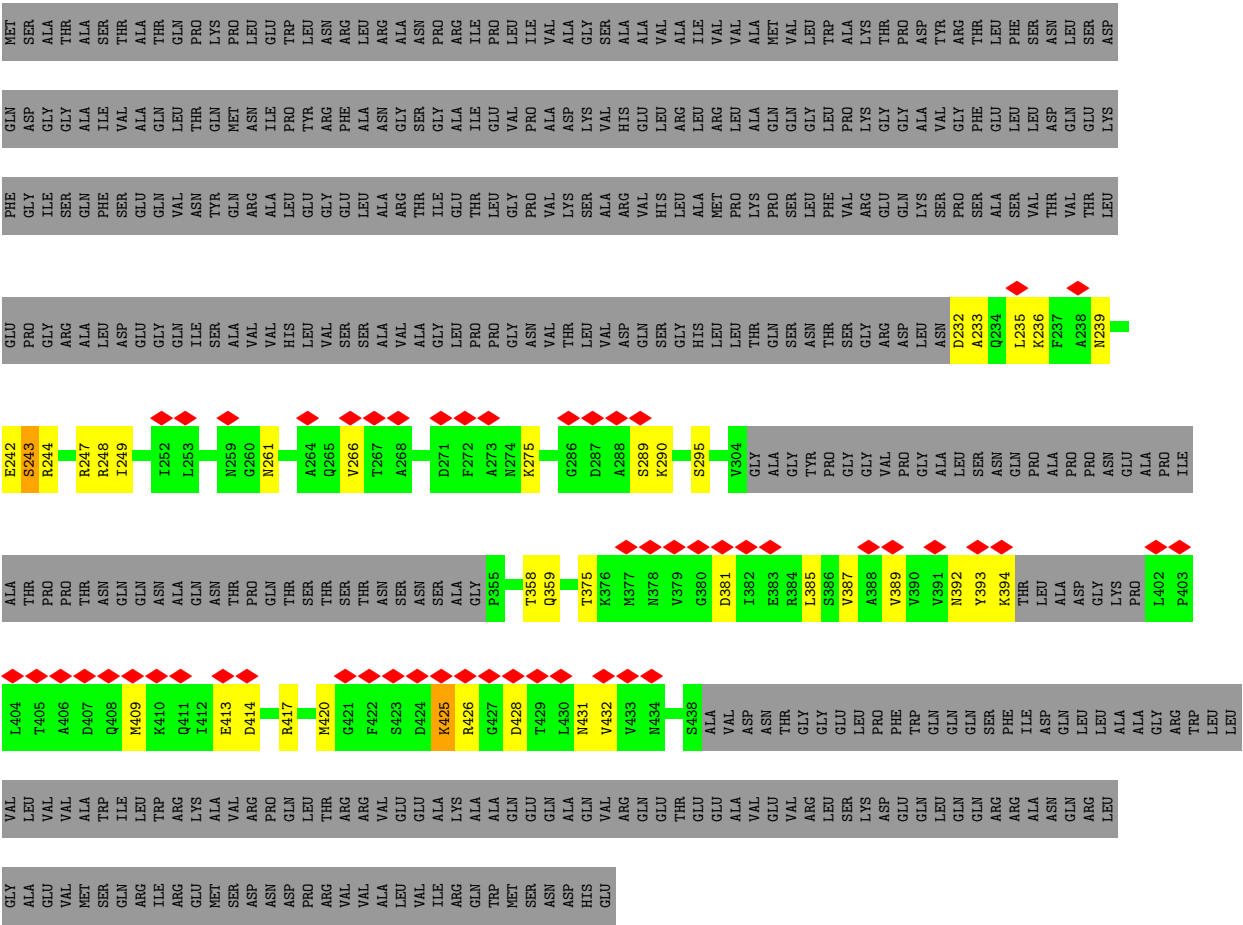
GLN ASP GLY GLY ALA ALA ILE VAL VAL GLN LEU LEU THR MET GLN ASN ILE LEU TYR PRO ARG PHE ALA ALA GLY GLY SER SER GLY GLY ALA ILE GLU VAL VAL PRO PRO ALA ASP LYS VAL VAL HIS HIS LEU LEU ARG ARG ALA ALA GLN GLN GLY GLY LEU LEU PRO PRO LYS LYS GLY GLY VAL VAL GLY GLY PHE PHE GLU GLU LEU LEU ASP ASP GLN GLN 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	VAL	ALA	GLY	LEU	PRO	PRO	GLY	ASN	VAL	THR	THR	VAL	ASP	GLN	SER	GLY	HIS	LEU	LEU	THR	GLN	SER	ASN	THR	SER	GLY	ARG	ASP	LEU	ASN	D232	D233	K236	F237	A238	N239
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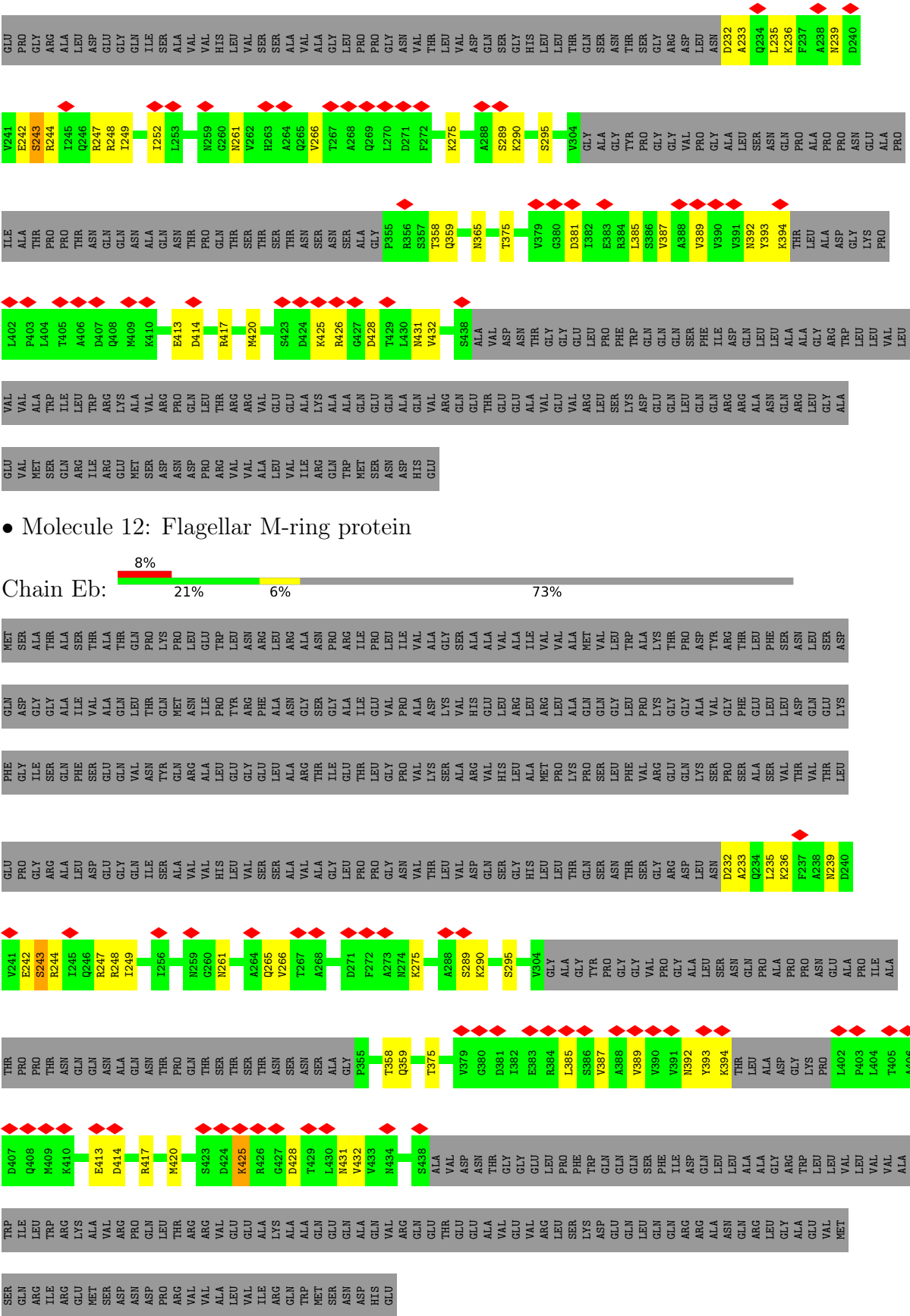
• Molecule 12: Flagellar M-ring protein



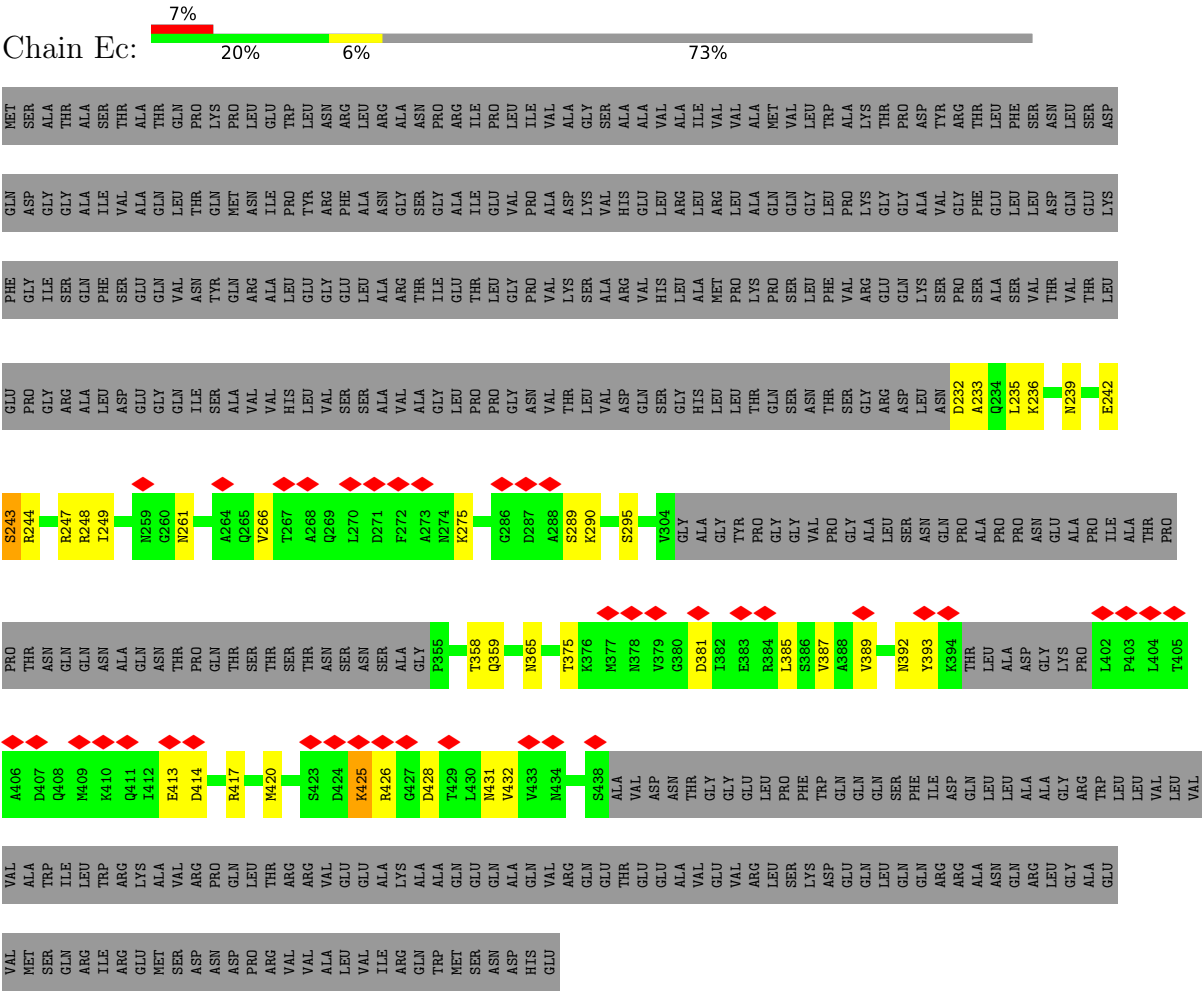
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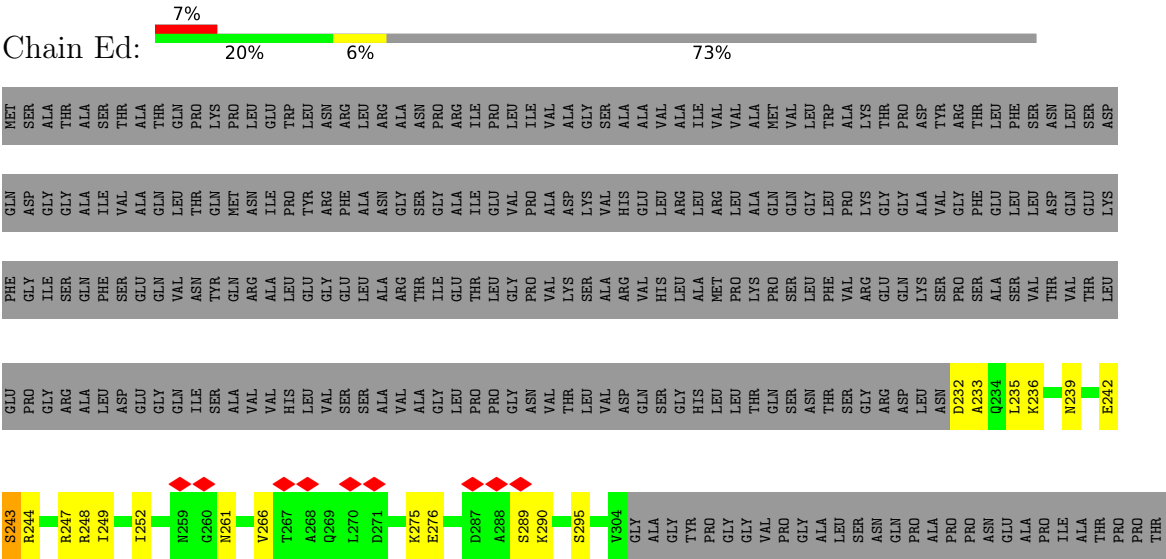


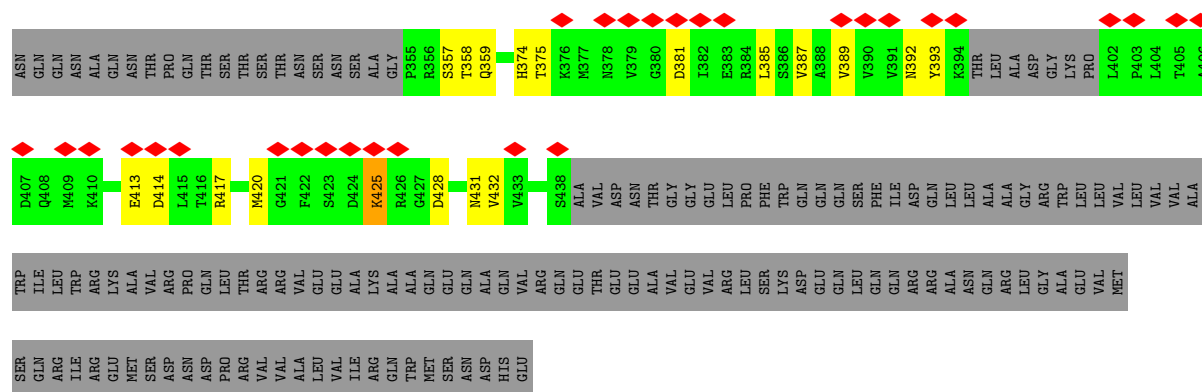


● Molecule 12: Flagellar M-ring protein

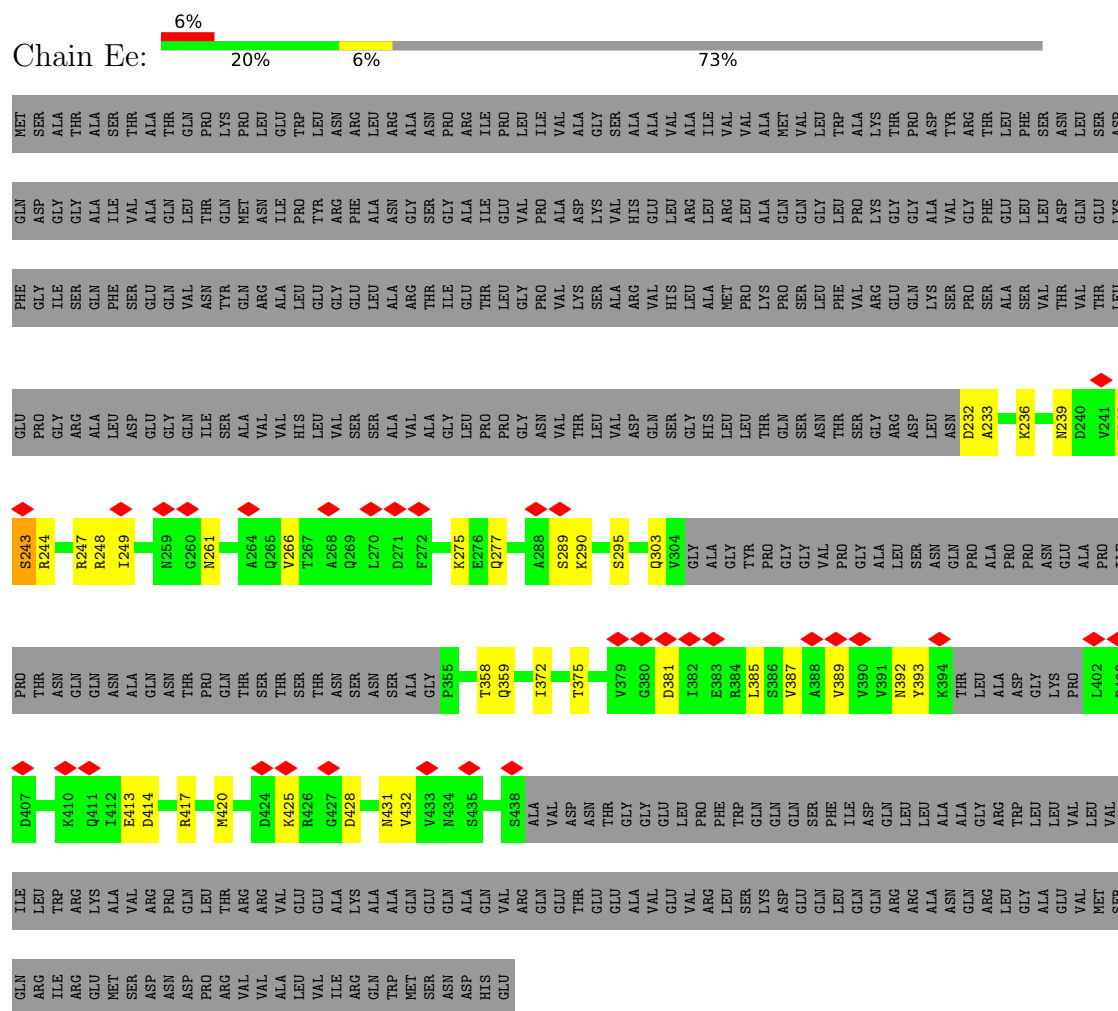


● Molecule 12: Flagellar M-ring protein

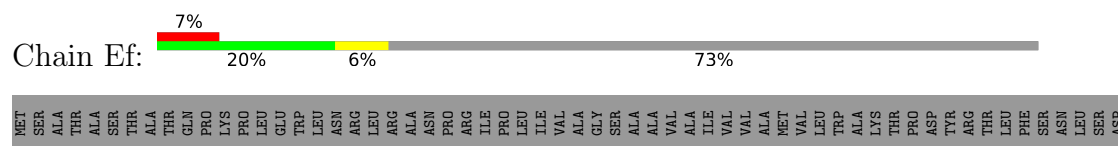


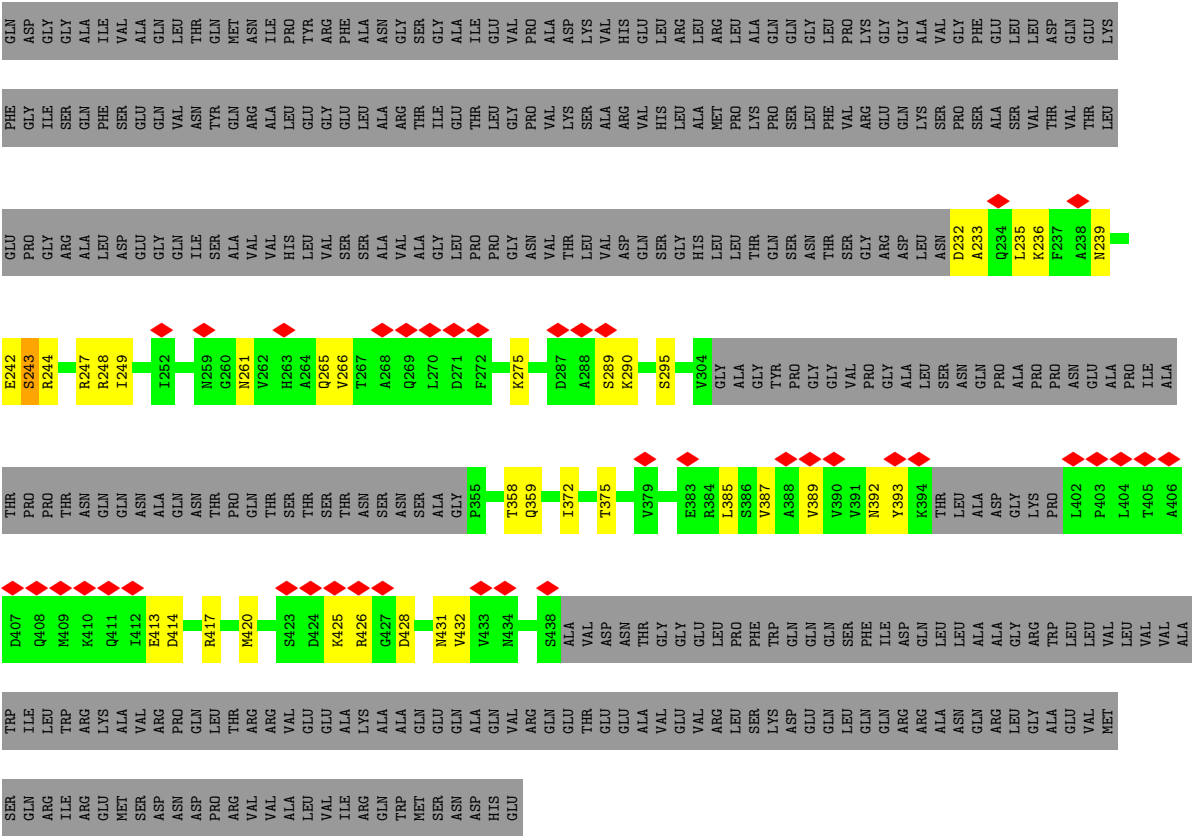


- Molecule 12: Flagellar M-ring protein

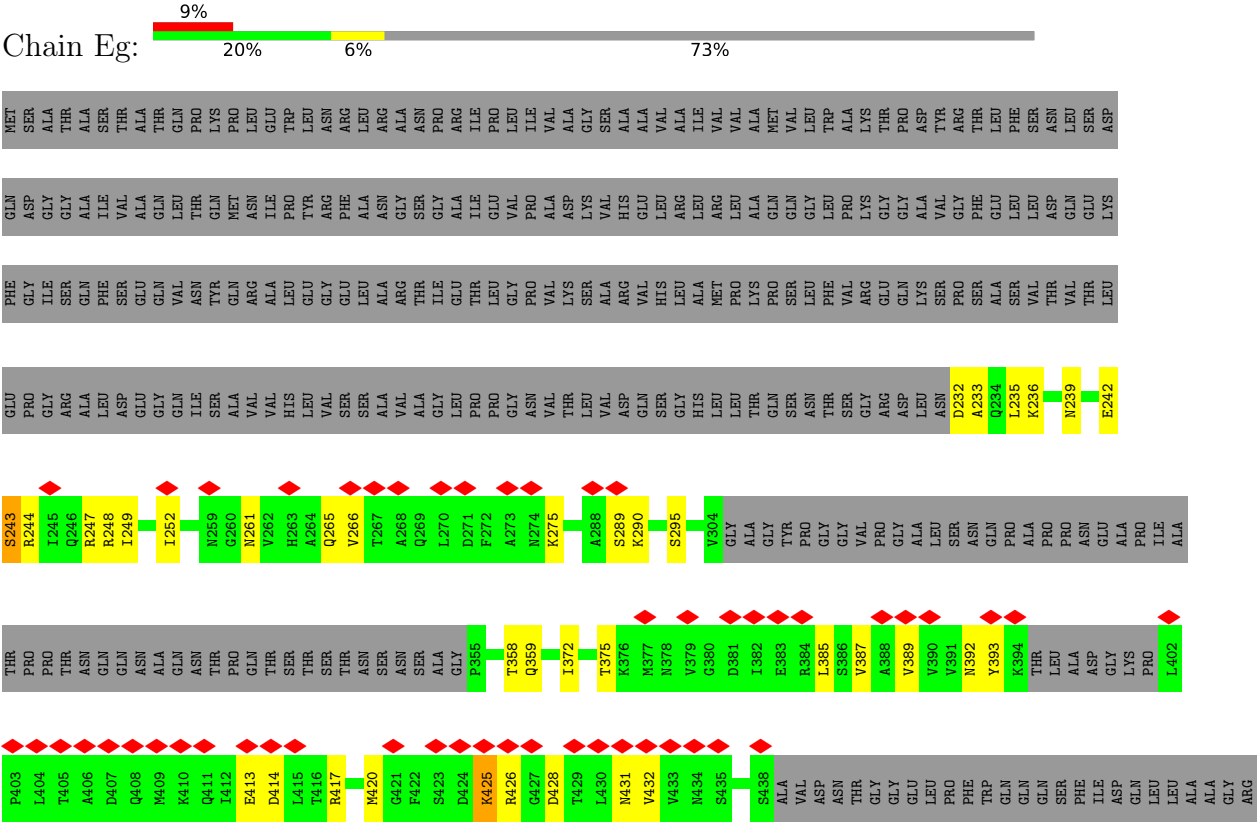


- Molecule 12: Flagellar M-ring protein





• Molecule 12: Flagellar M-ring protein



- Molecule 12: Flagellar M-ring protein



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GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	HIS	HIS	LEU	VAL	SER	SER	ALA	VAL	ALA	GLY	LEU	LEU	VAL	ASP	GLN	SER	GLY	HIS	LEU	LEU	THR	GLN	SER	ASN	THR	SER	GLY	ARG	ASP	LEU	ASN	D232	D233	Q234	L235	L236	N239
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[illegible]

ASN	GLN	GLN	ASN	ALA	GLN	THR	ASN	PRO	GLN	THR	SER	THR	SER	THR	ASN	SER	ASN	SER	SER	ALA	ALA	GLY	P355	R356	P357	T358	Q359	N365	T375	N378	V379	G380	D381	I382	E383	R384	L386	S386	G387	A388	V389	V390	V391	N392	Y393	K394	THR	THR	LEU	ALA	ASP	GLY	LYS	PRO	L402	P403	L404	L405	T406
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D407	Q408	K409	K410	Q411	I412	E413	D414	R417	N420	G421	D424	K425	D426	G427	D428	T429	L430	N431	V432	S435	P436	F437	S438	ALA	VAL	ASP	ASN	THR	GLY	GLY	GLU	LEU	PRO	PHE	TRP	GLN	GLN	GLN	SER	PHE	ILE	ILE	ASP	GLN	LEU	LEU	ALA	ALA	GLY	ARG	TRP	LEU	LEU	VAL	LEU
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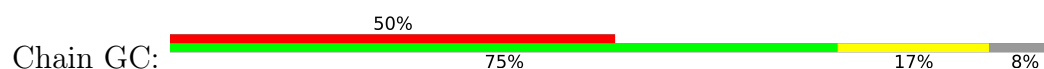
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VAL	MET	SER	GLN	ARG	ILE	ARG	GLU	MET	SER	ASP	ASN	ASP	PRO	ARG	VAL	VAL	ALA	LEU	VAL	ILE	ARG	GLN	TRP	MET	SER	ASN	ASP	HIS	GLU
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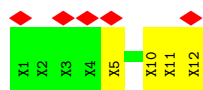
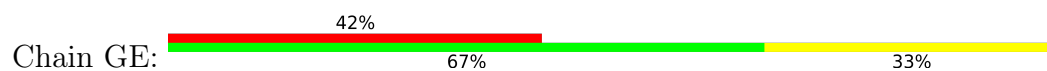
- Molecule 13: FlgB-Dc loop



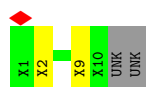
- Molecule 13: FlgB-Dc loop



• Molecule 13: FlgB-Dc loop



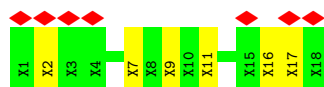
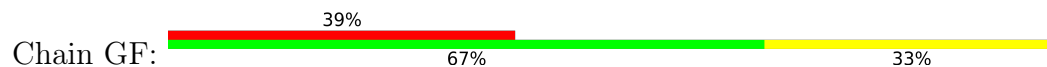
• Molecule 13: FlgB-Dc loop



• Molecule 13: FlgB-Dc loop



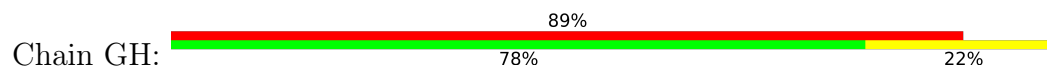
• Molecule 14: FliE helix 1



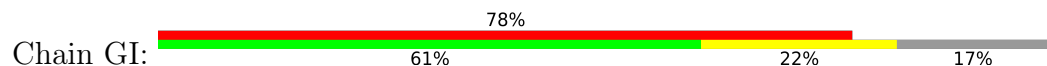
• Molecule 14: FliE helix 1



• Molecule 14: FliE helix 1

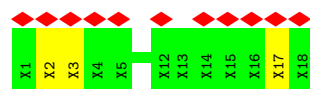
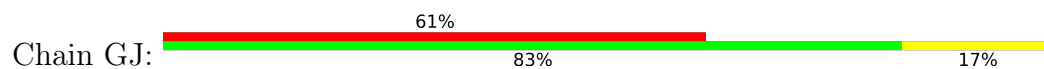


• Molecule 14: FliE helix 1

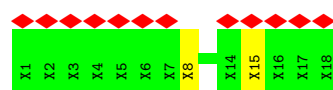




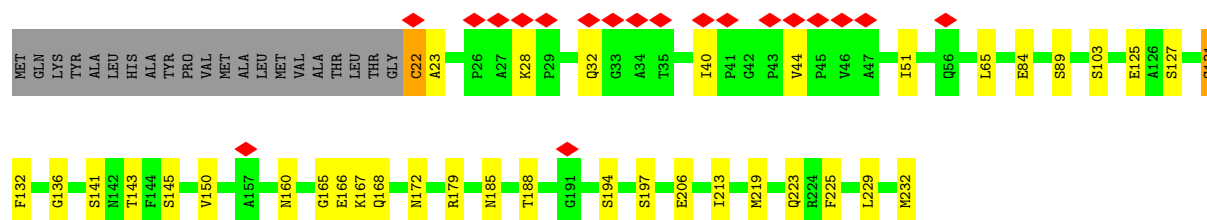
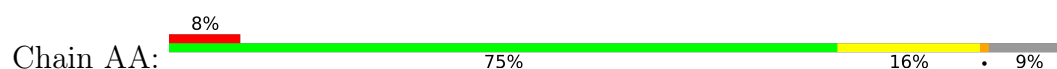
• Molecule 14: FliE helix 1



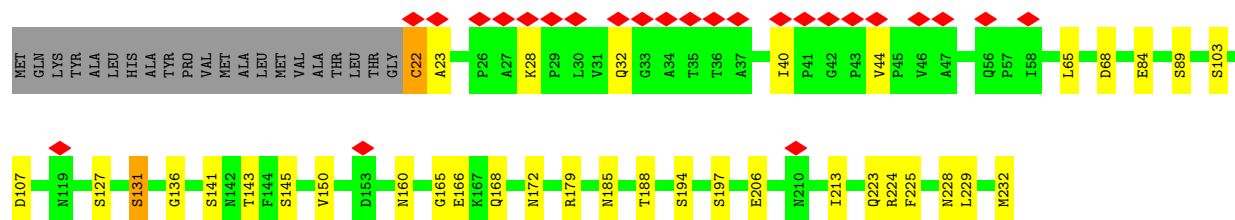
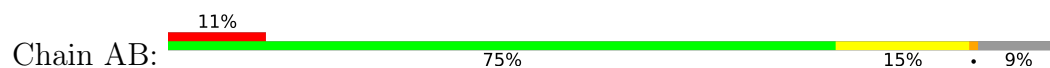
• Molecule 14: FliE helix 1



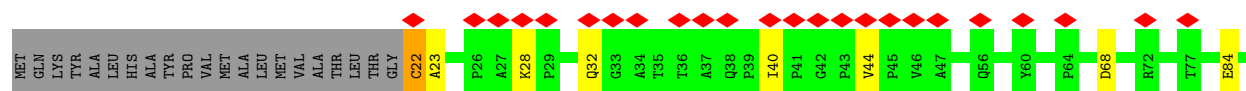
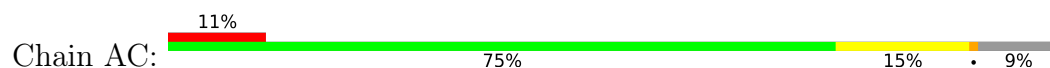
• Molecule 15: Flagellar L-ring protein

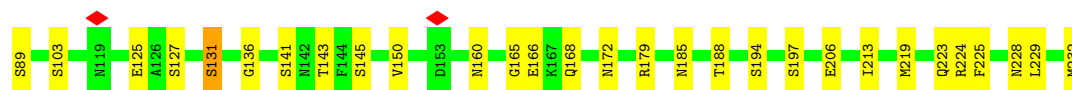


• Molecule 15: Flagellar L-ring protein

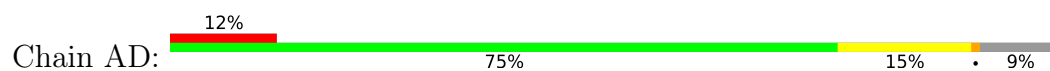


• Molecule 15: Flagellar L-ring protein

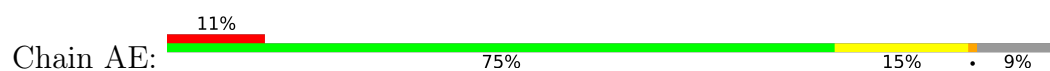




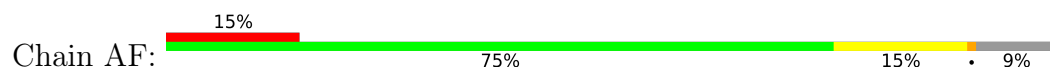
• Molecule 15: Flagellar L-ring protein



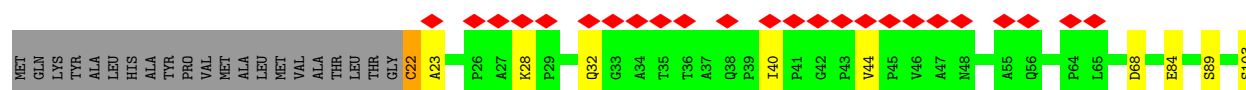
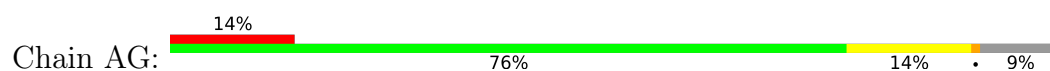
• Molecule 15: Flagellar L-ring protein



• Molecule 15: Flagellar L-ring protein

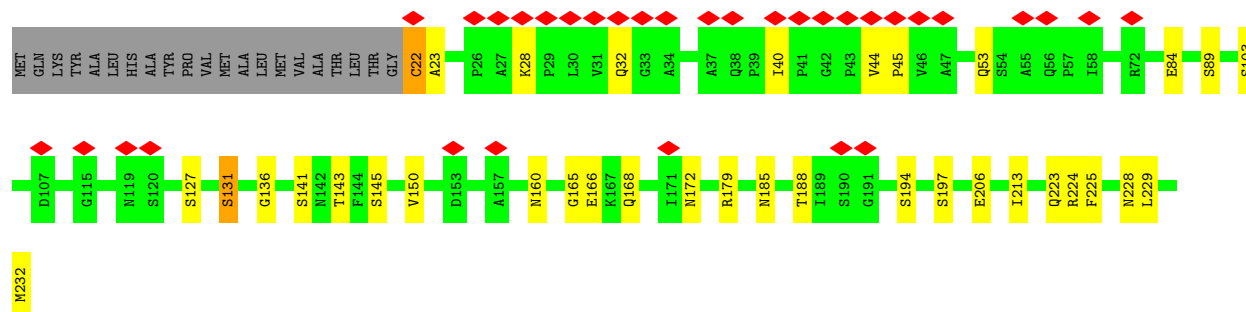
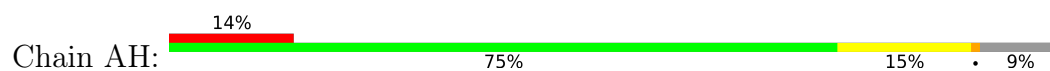


• Molecule 15: Flagellar L-ring protein

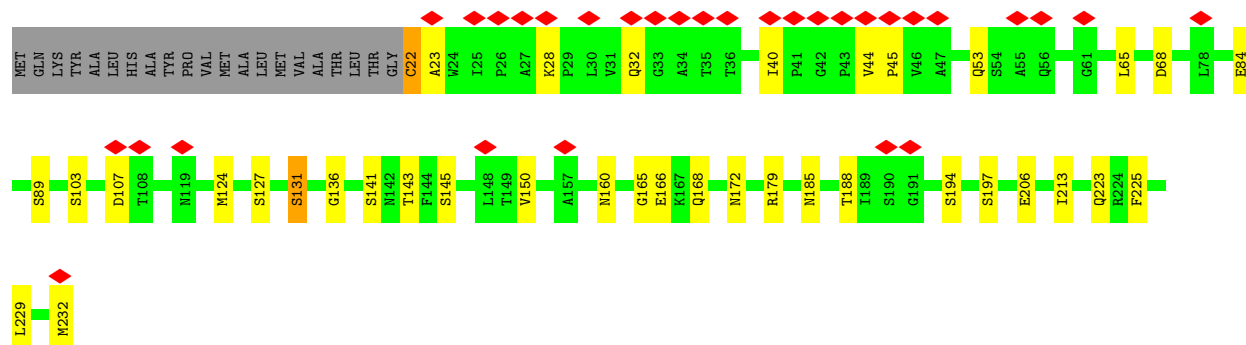
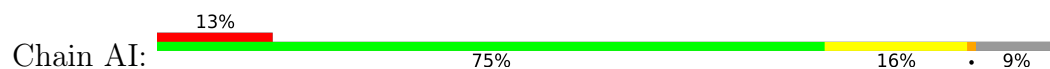




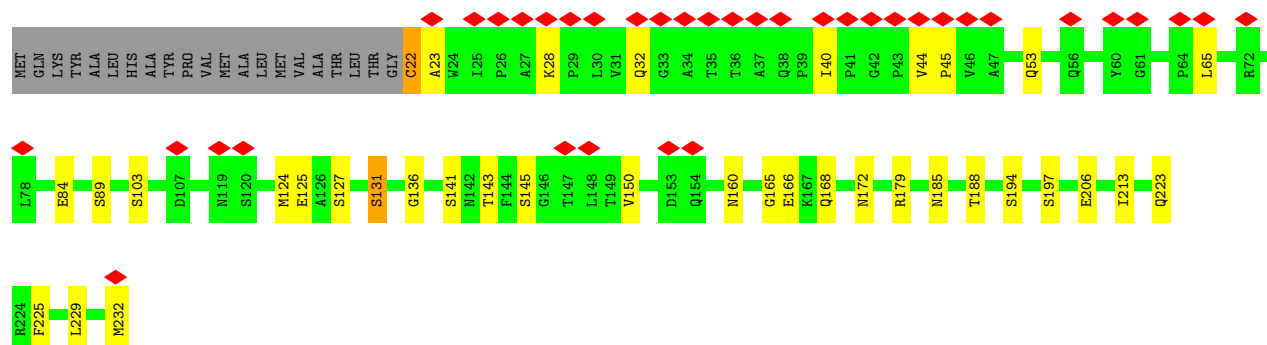
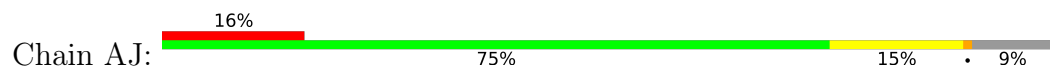
• Molecule 15: Flagellar L-ring protein



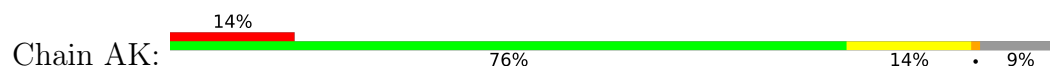
• Molecule 15: Flagellar L-ring protein

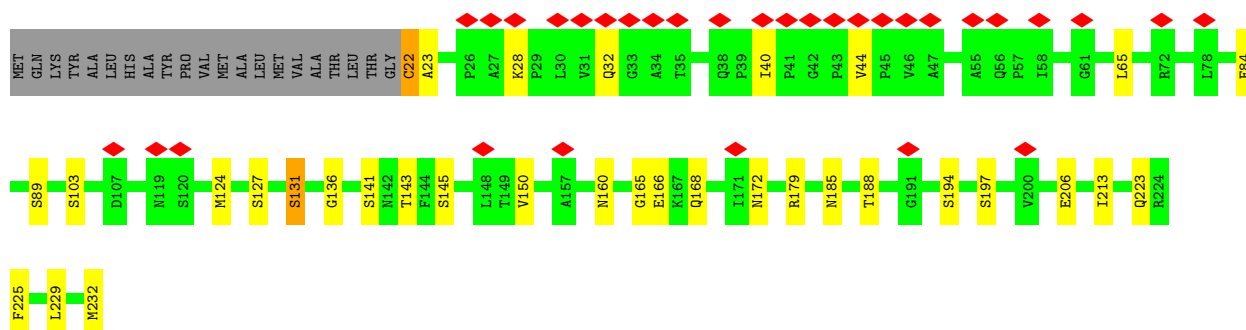


• Molecule 15: Flagellar L-ring protein

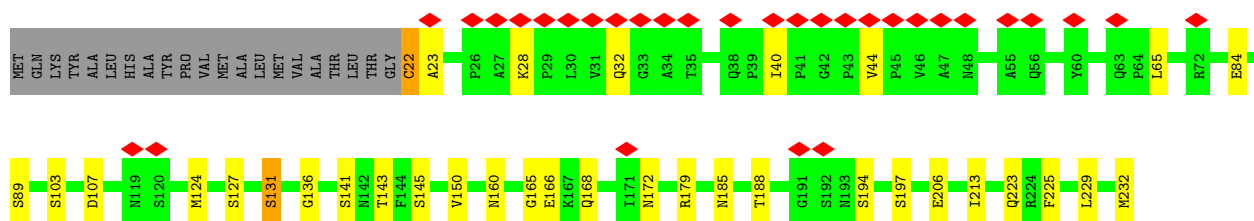
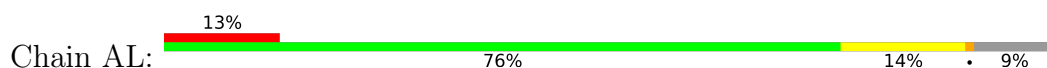


• Molecule 15: Flagellar L-ring protein

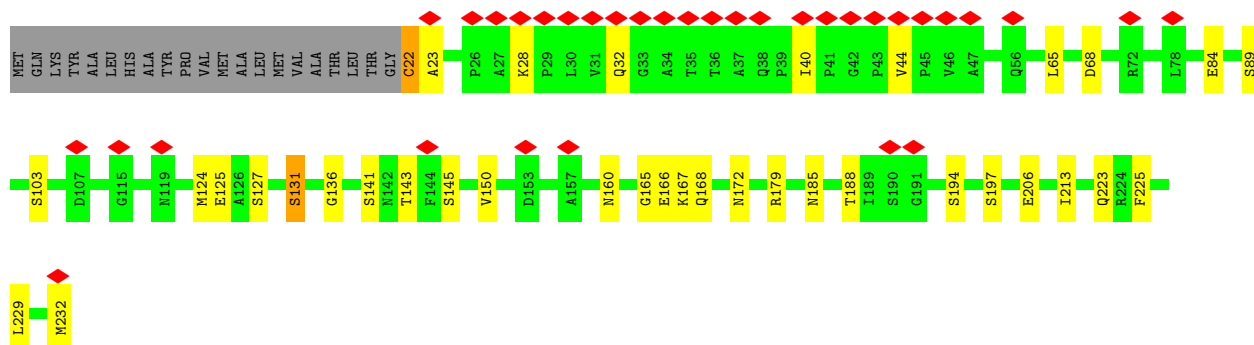
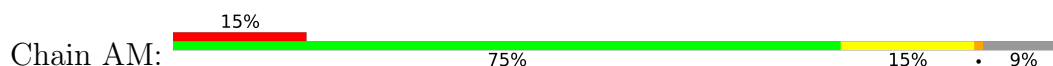




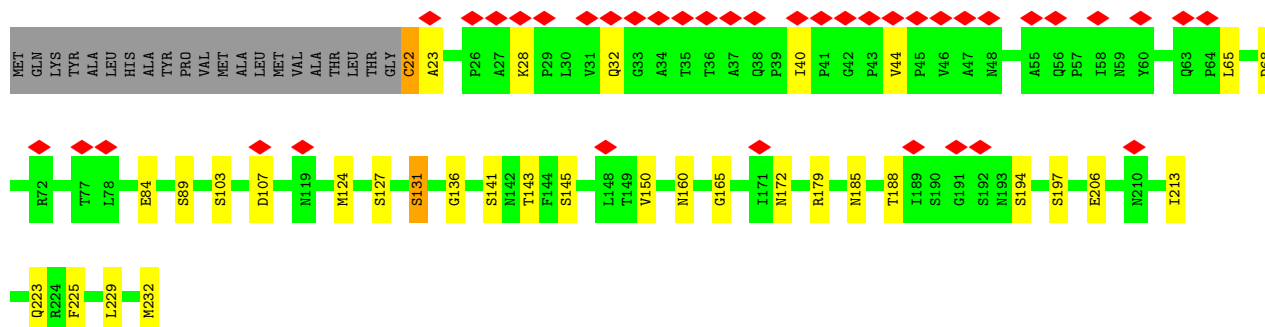
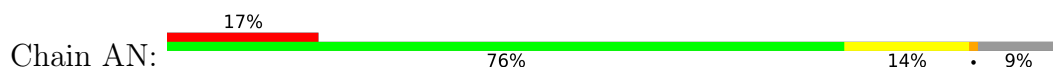
• Molecule 15: Flagellar L-ring protein



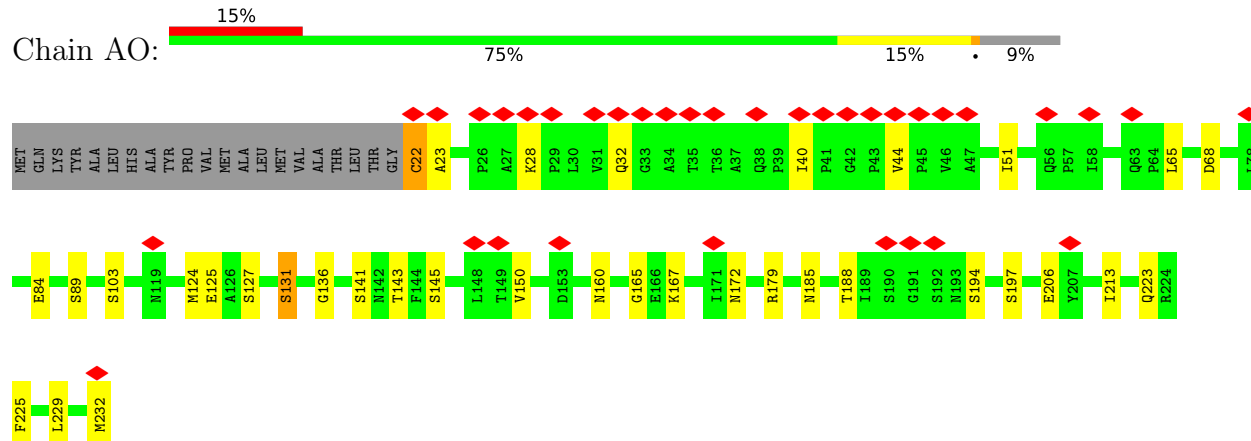
• Molecule 15: Flagellar L-ring protein



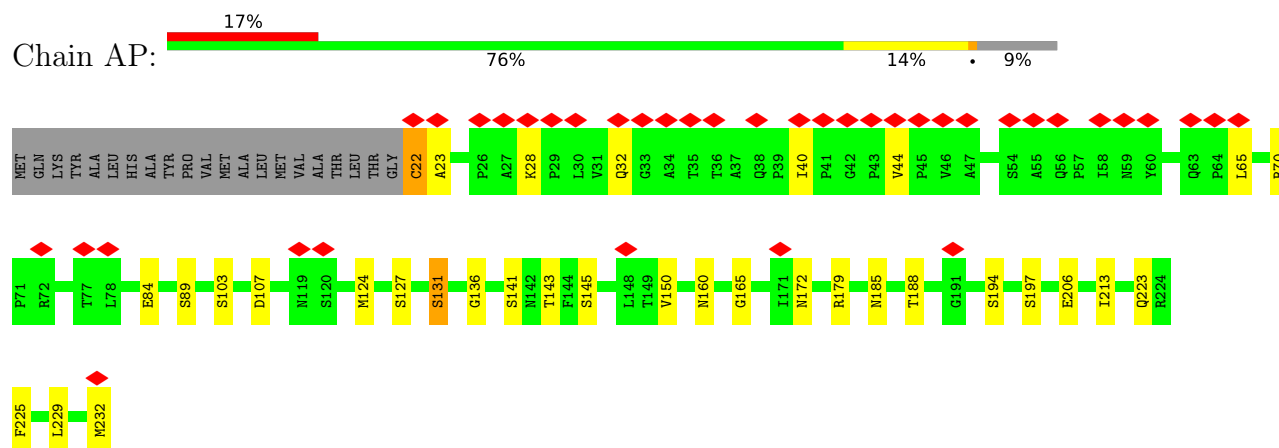
• Molecule 15: Flagellar L-ring protein



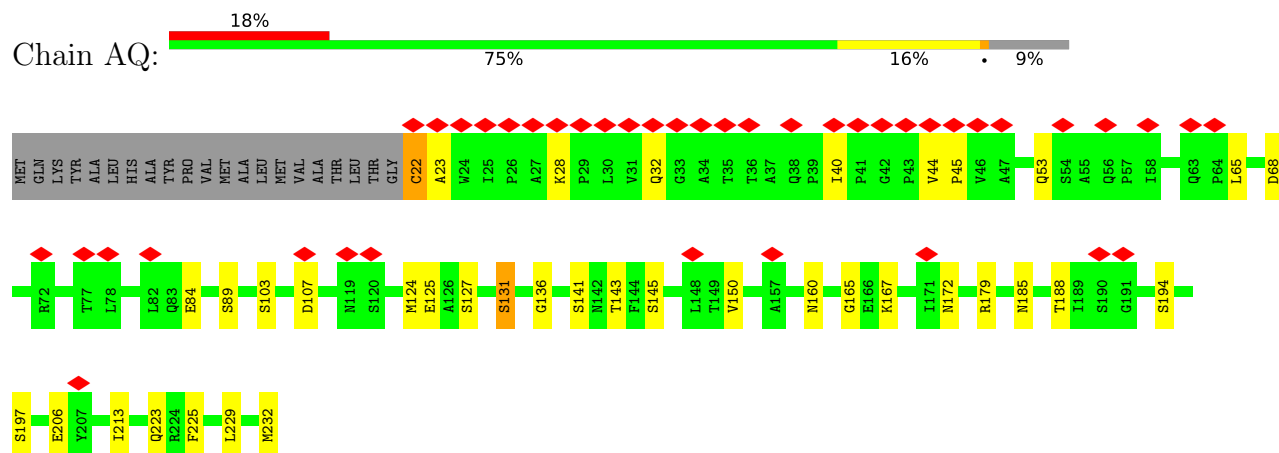
- Molecule 15: Flagellar L-ring protein



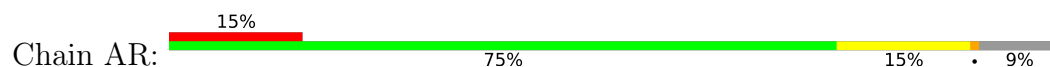
- Molecule 15: Flagellar L-ring protein

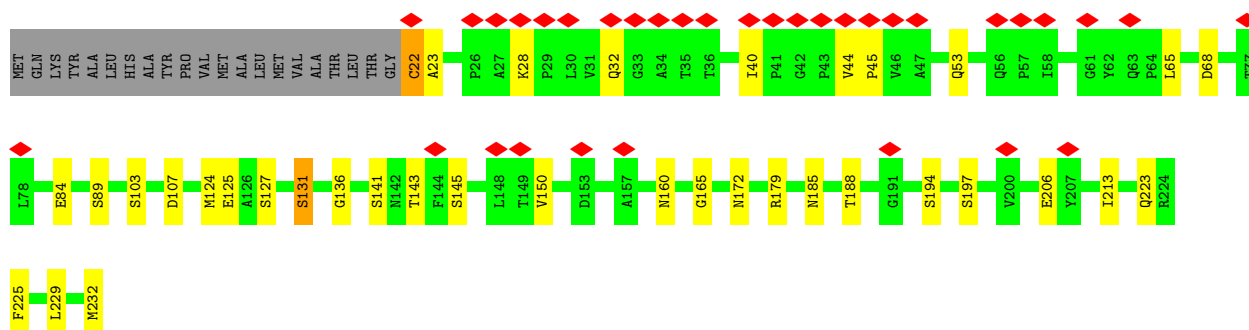


- Molecule 15: Flagellar L-ring protein

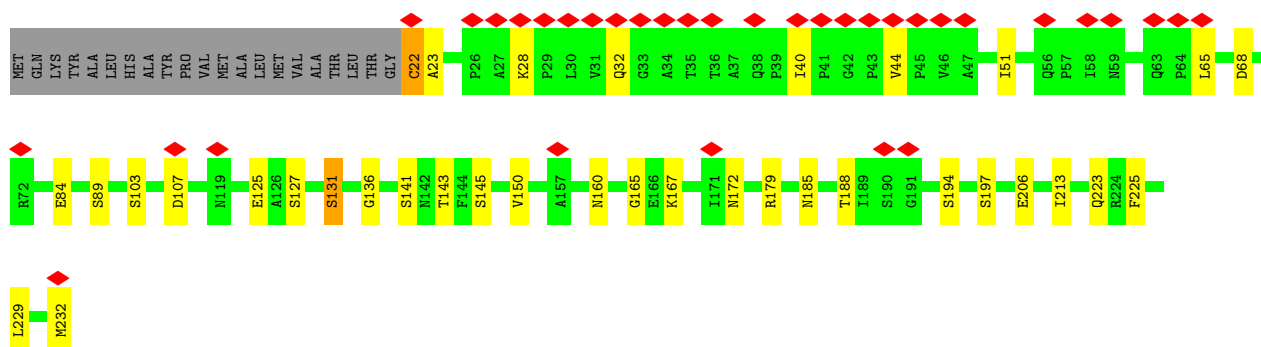
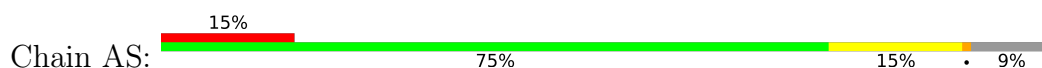


- Molecule 15: Flagellar L-ring protein

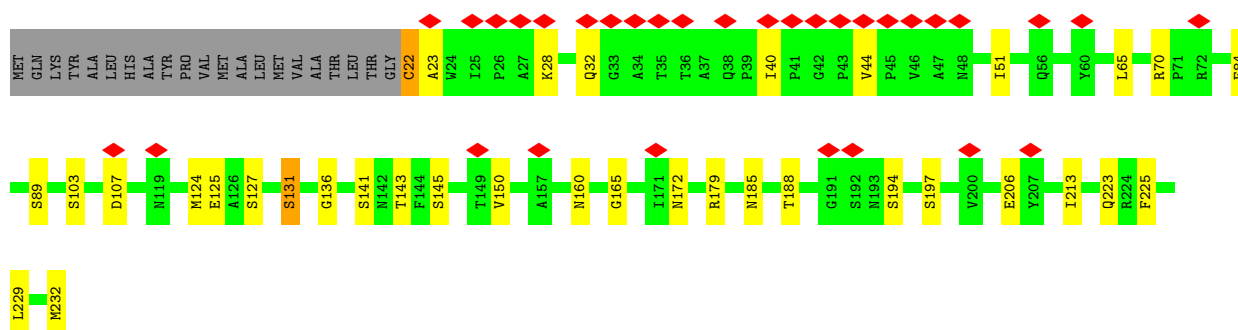
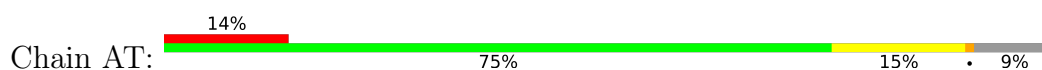




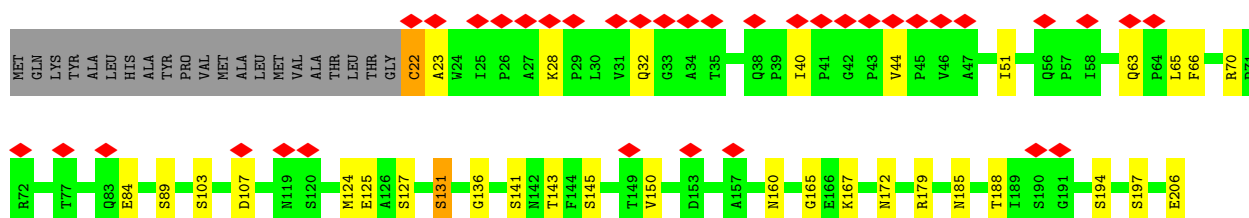
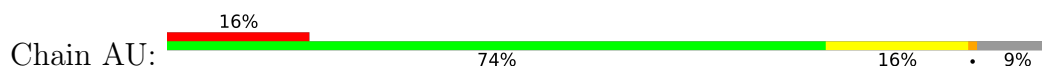
• Molecule 15: Flagellar L-ring protein



• Molecule 15: Flagellar L-ring protein

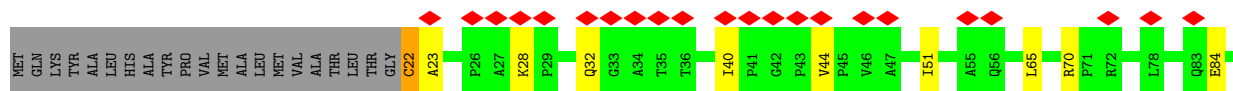
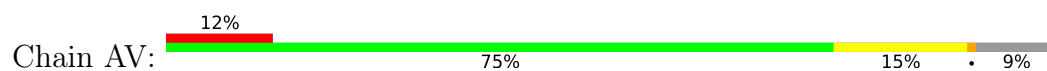


• Molecule 15: Flagellar L-ring protein

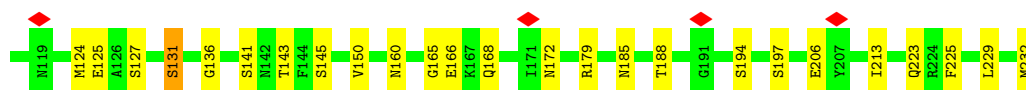
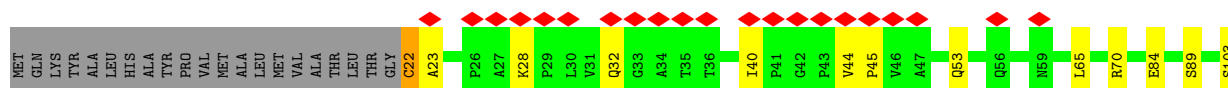
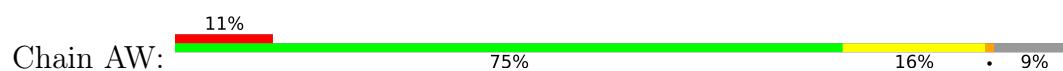




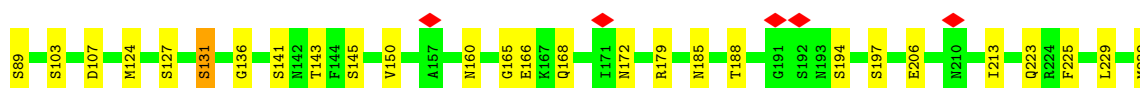
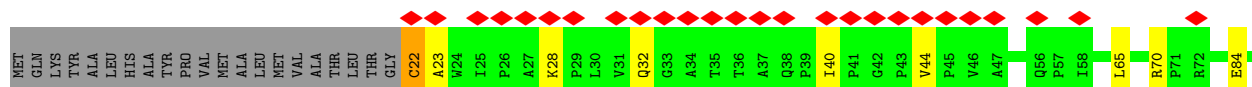
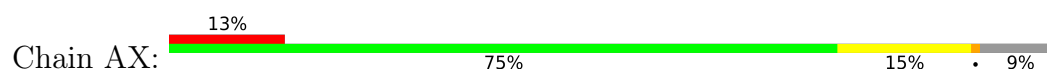
- Molecule 15: Flagellar L-ring protein



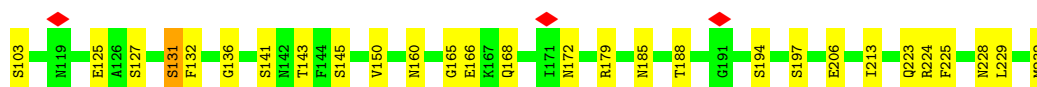
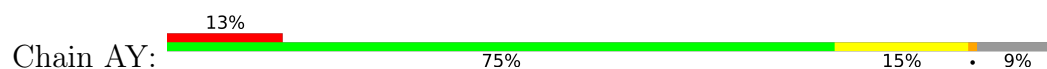
- Molecule 15: Flagellar L-ring protein



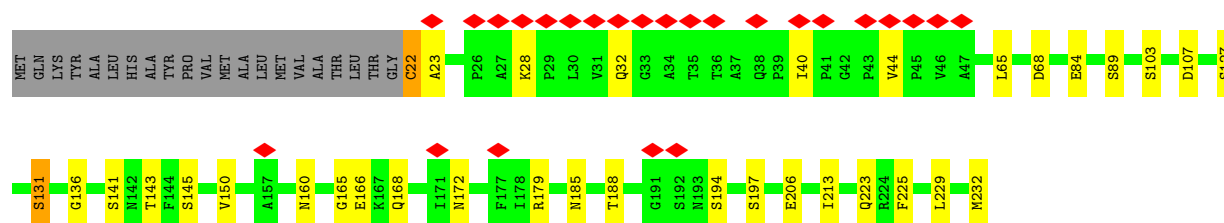
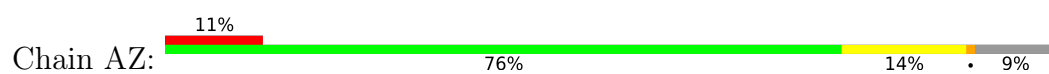
- Molecule 15: Flagellar L-ring protein



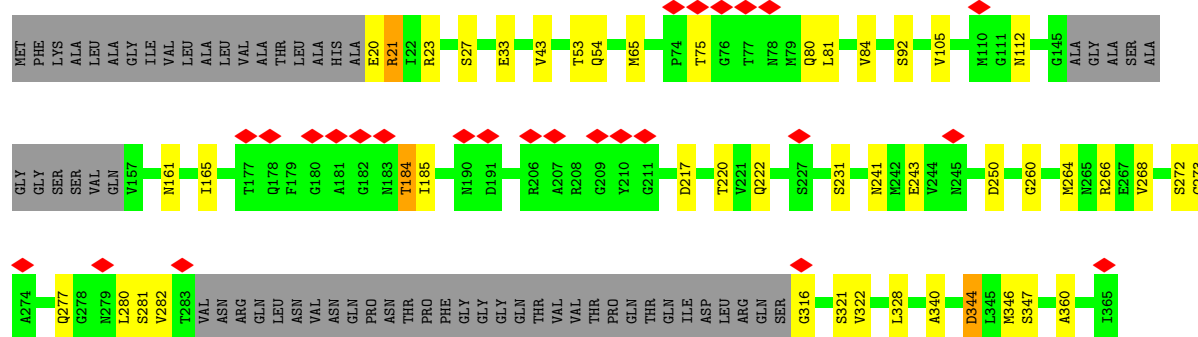
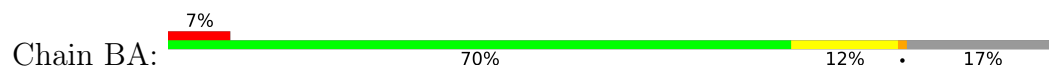
- Molecule 15: Flagellar L-ring protein



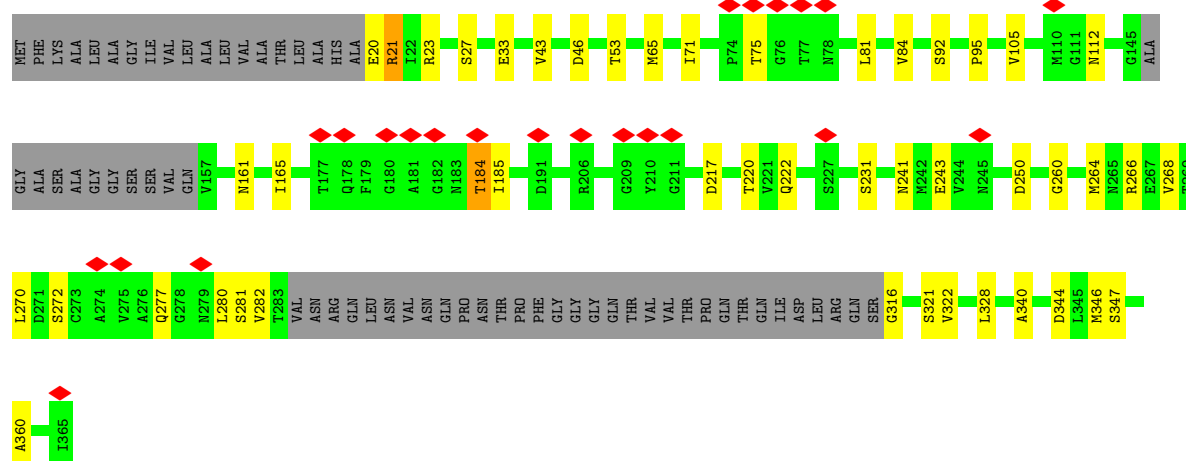
- Molecule 15: Flagellar L-ring protein



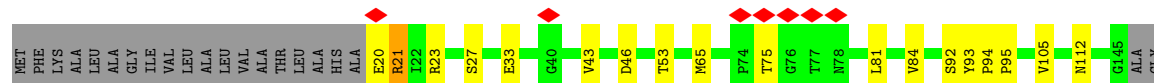
• Molecule 16: Flagellar P-ring protein

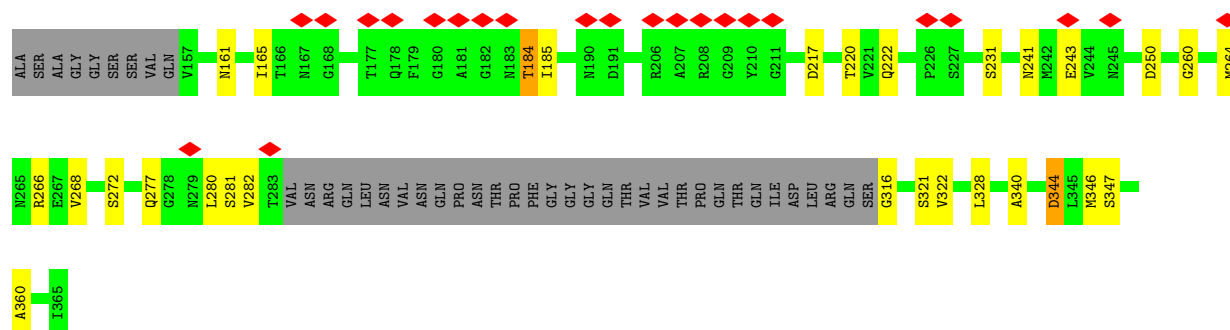


• Molecule 16: Flagellar P-ring protein

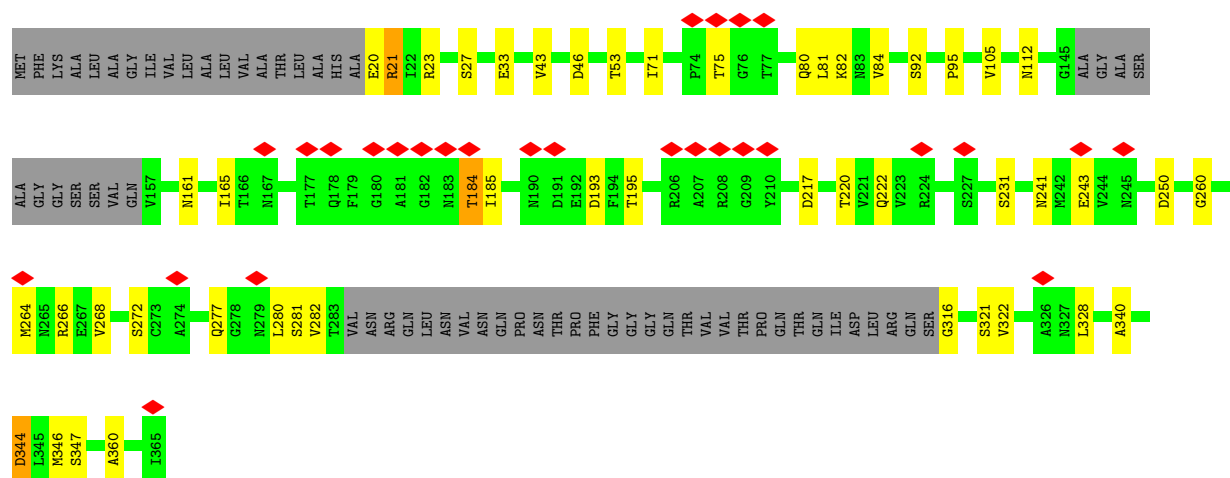
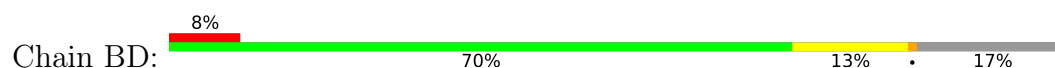


• Molecule 16: Flagellar P-ring protein

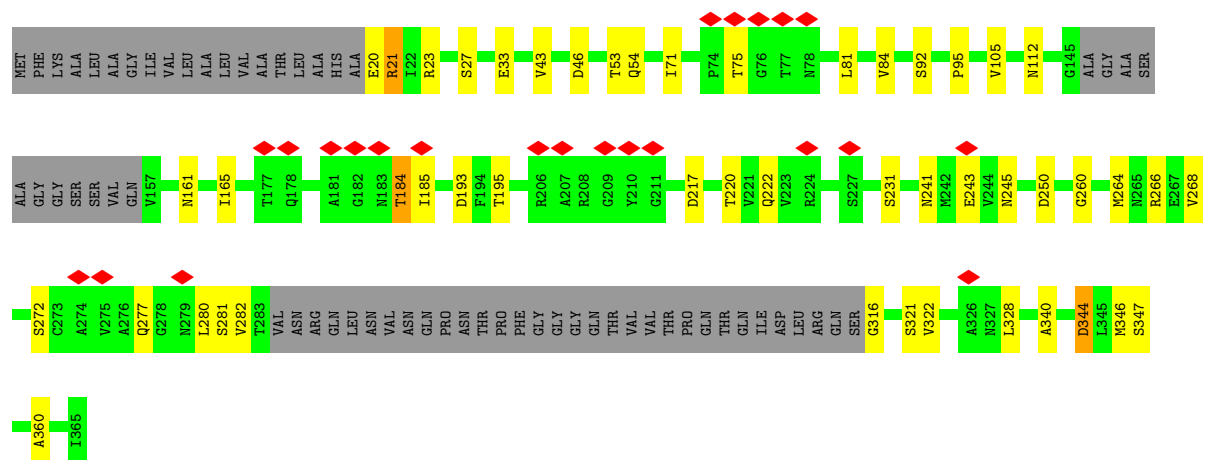




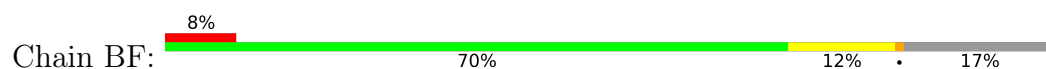
- Molecule 16: Flagellar P-ring protein

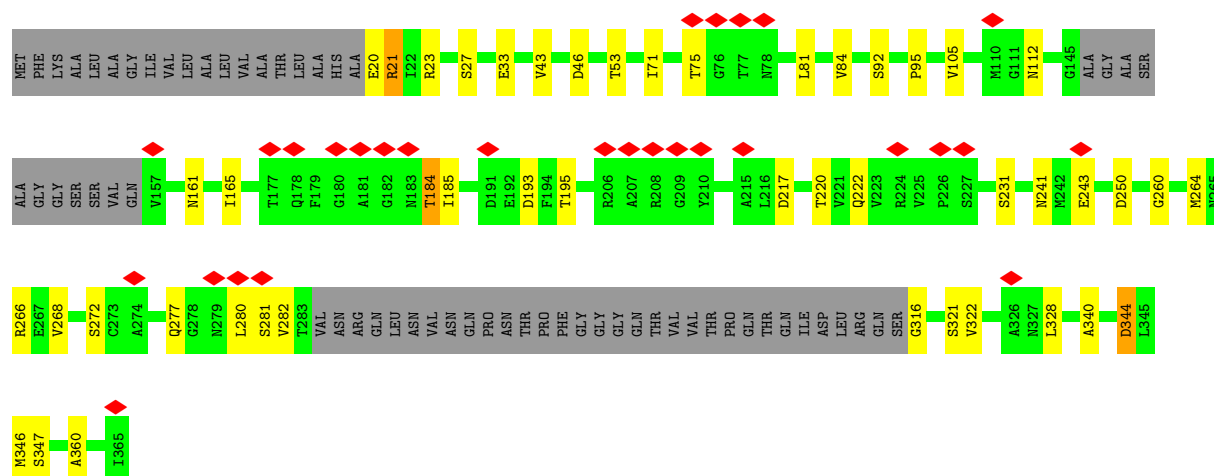


- Molecule 16: Flagellar P-ring protein

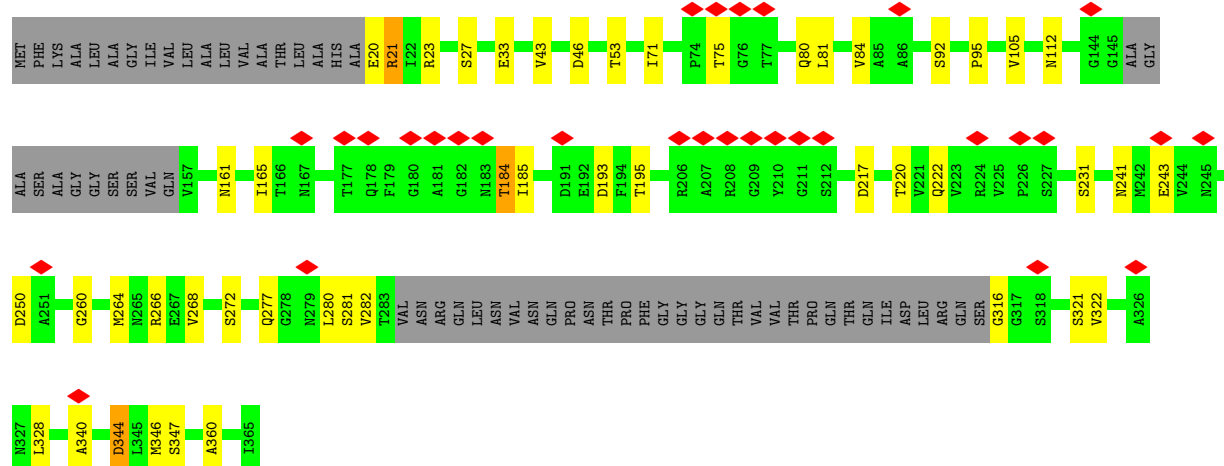
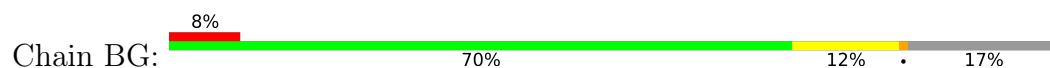


- Molecule 16: Flagellar P-ring protein

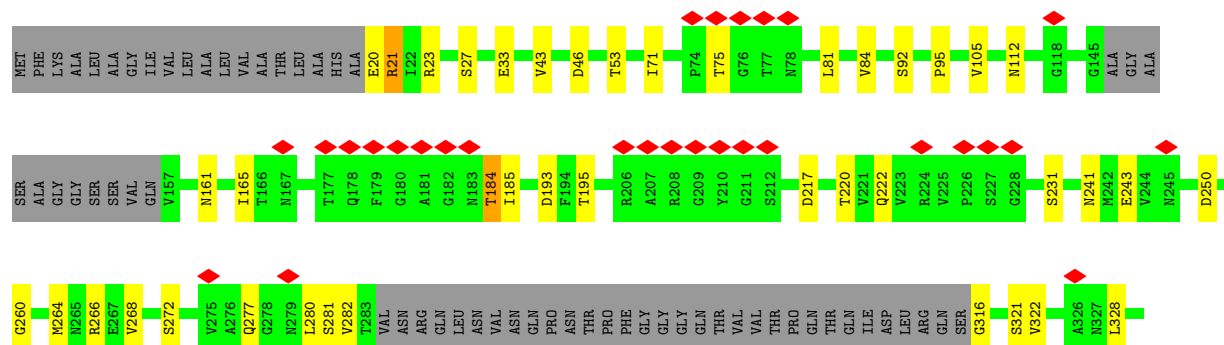
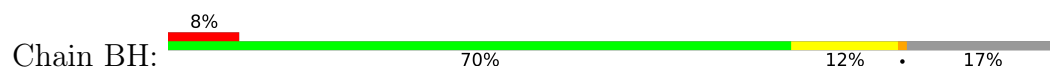


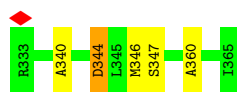


• Molecule 16: Flagellar P-ring protein

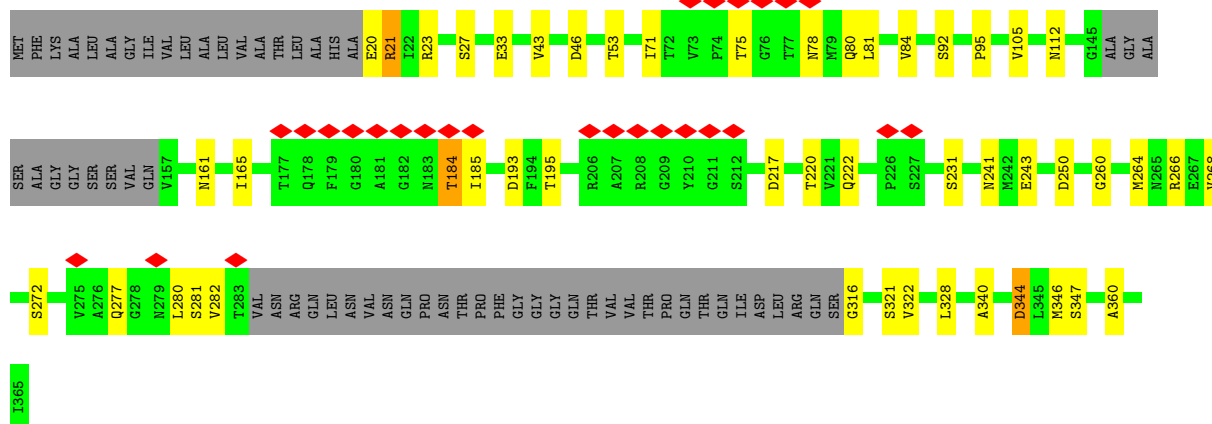


• Molecule 16: Flagellar P-ring protein

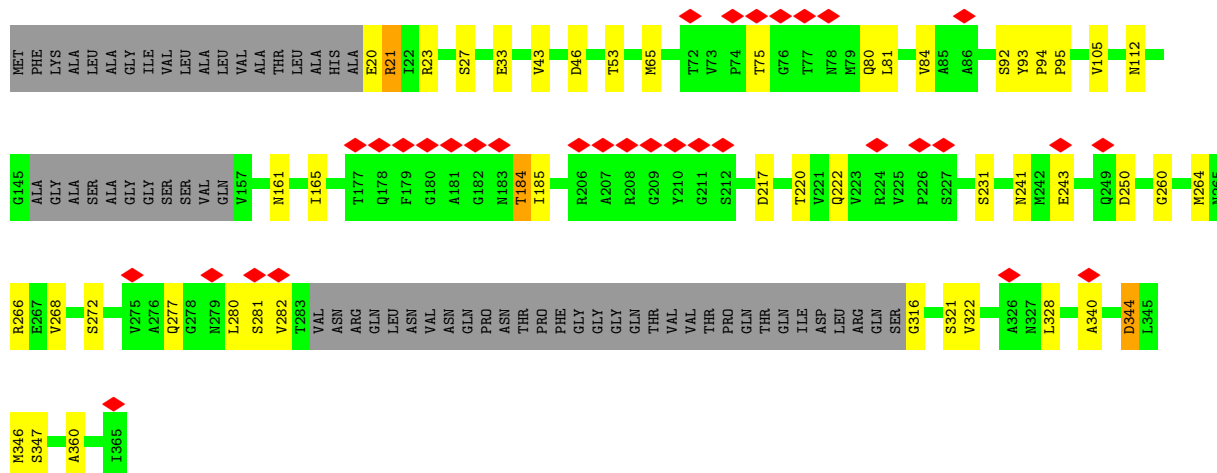




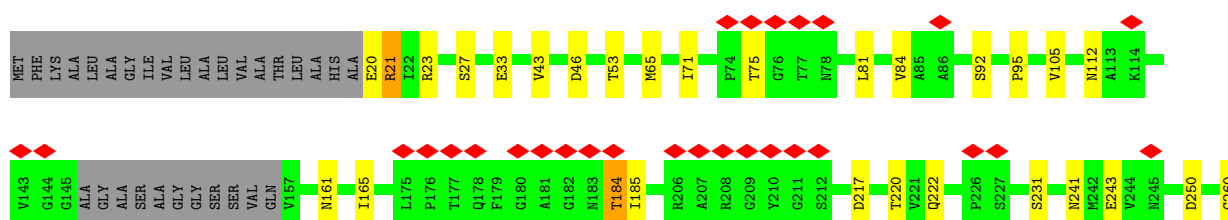
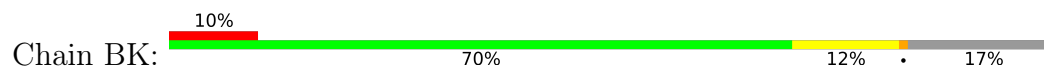
• Molecule 16: Flagellar P-ring protein

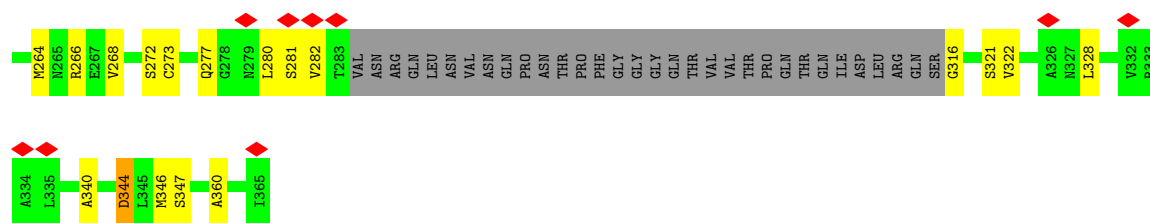


• Molecule 16: Flagellar P-ring protein

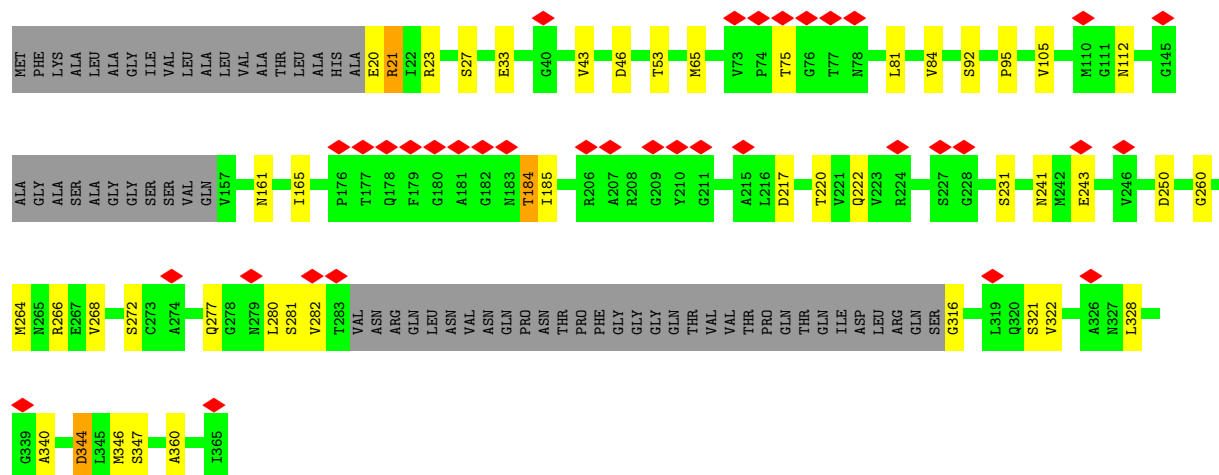
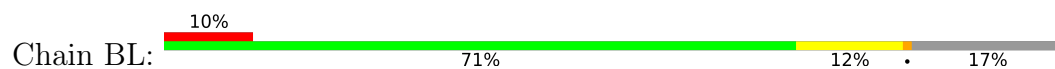


• Molecule 16: Flagellar P-ring protein

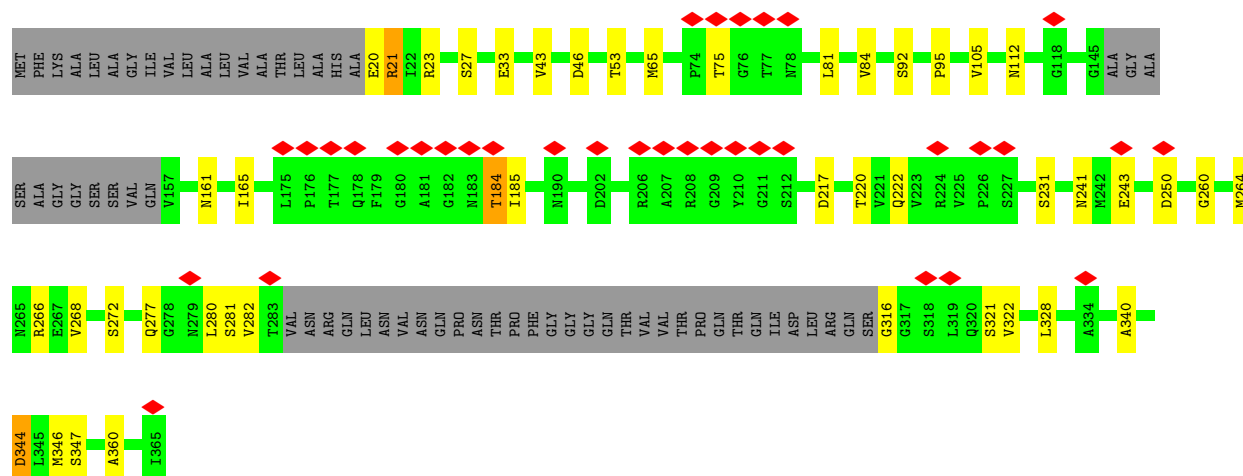
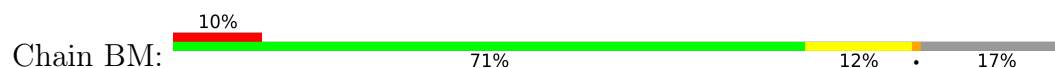




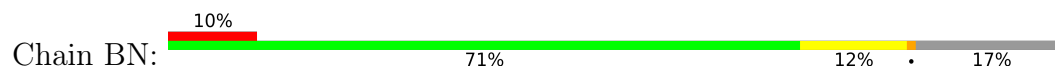
• Molecule 16: Flagellar P-ring protein

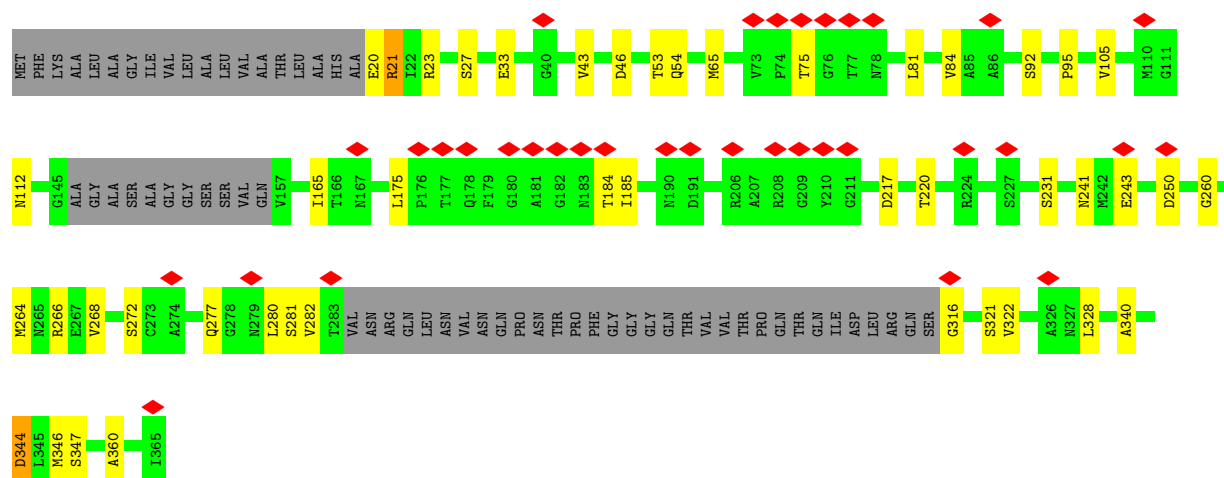


• Molecule 16: Flagellar P-ring protein

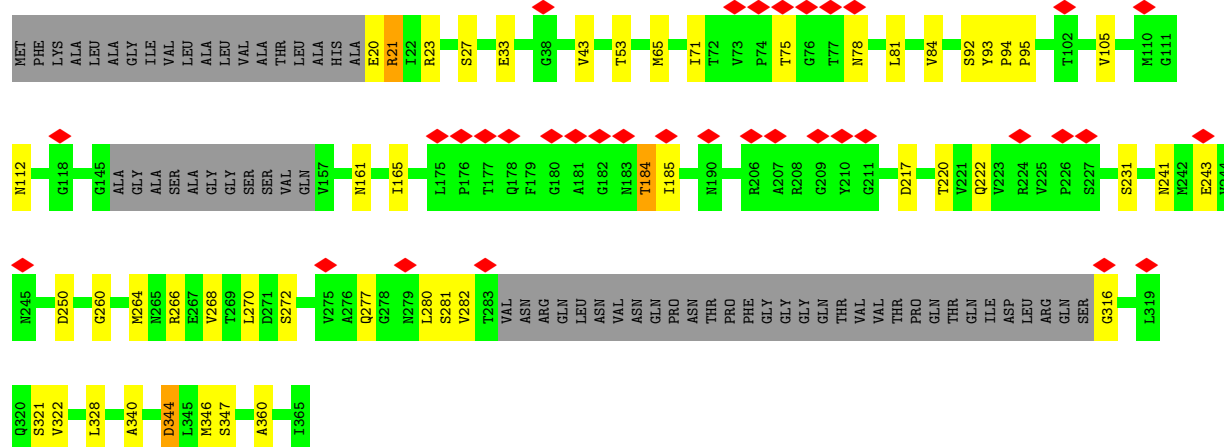


• Molecule 16: Flagellar P-ring protein

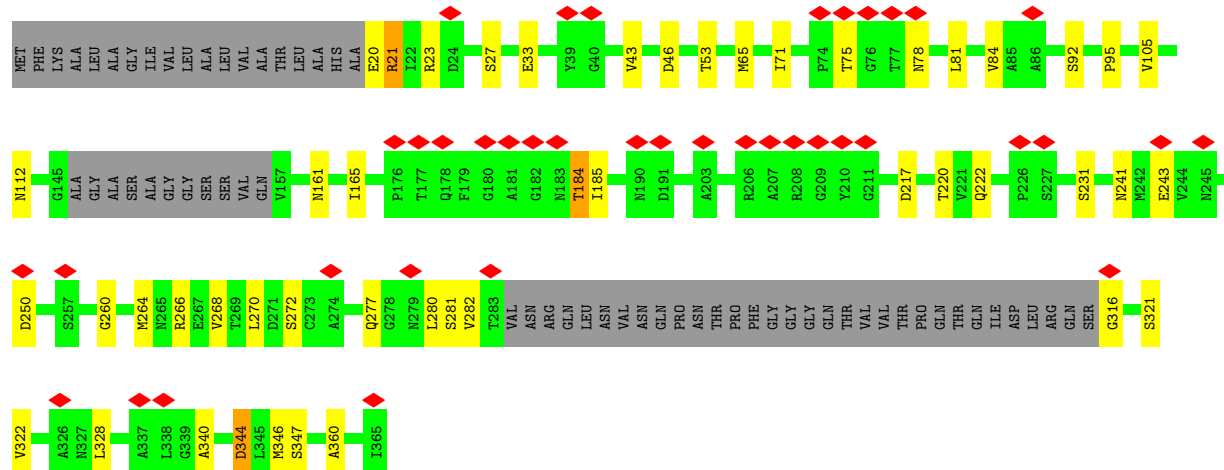
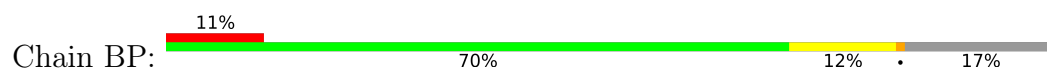




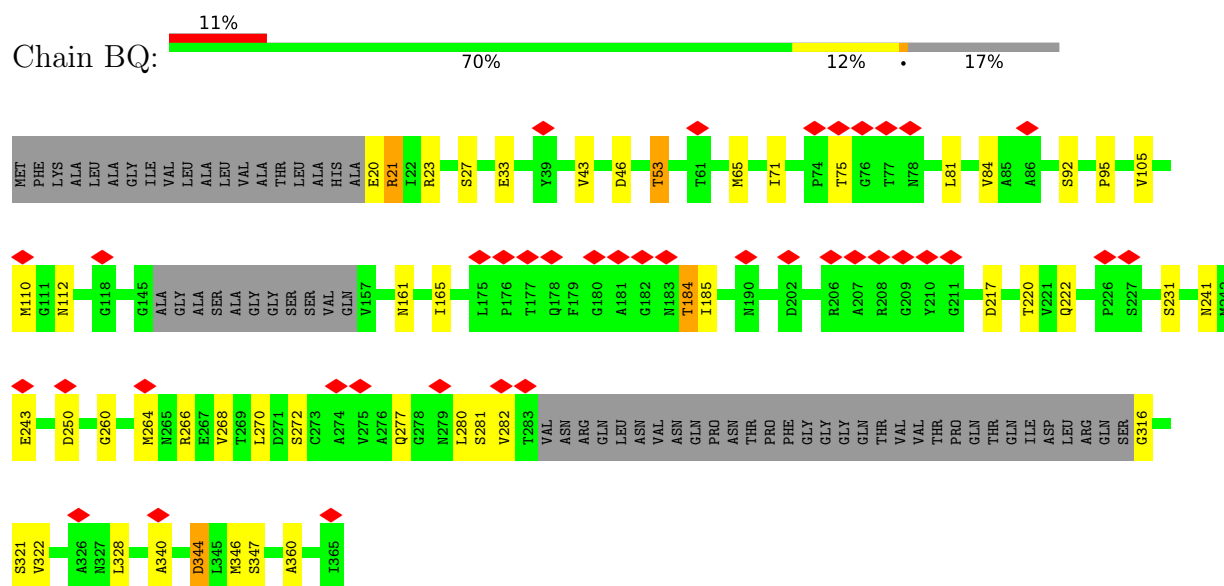
• Molecule 16: Flagellar P-ring protein



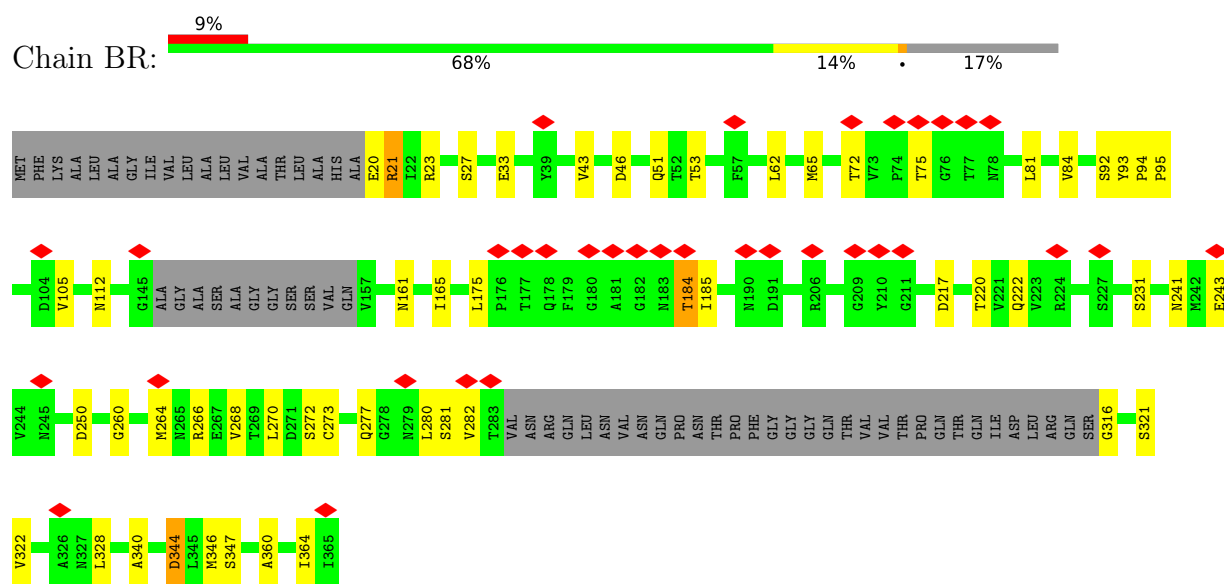
• Molecule 16: Flagellar P-ring protein



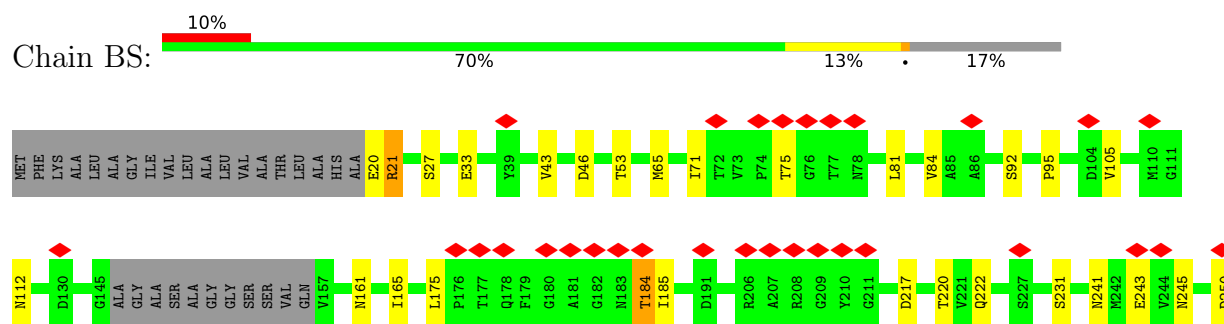
- Molecule 16: Flagellar P-ring protein

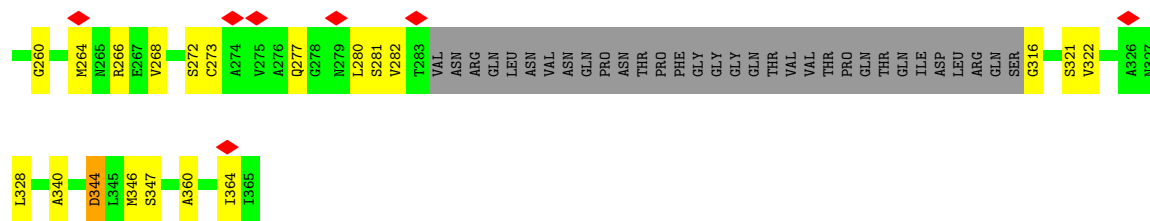


- Molecule 16: Flagellar P-ring protein

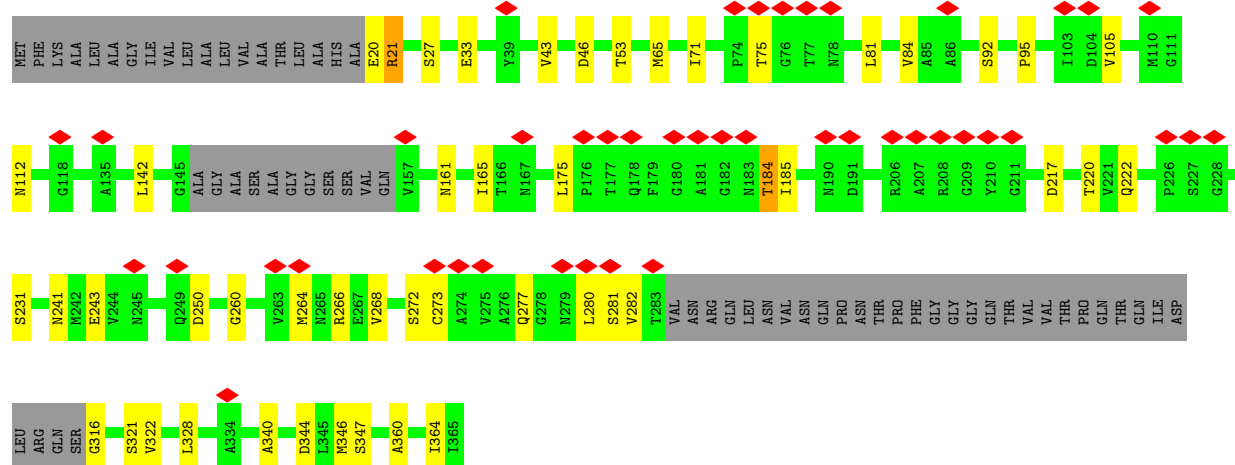
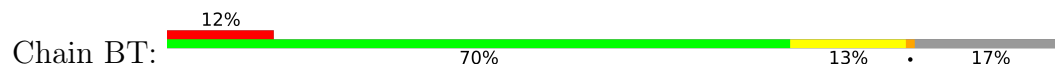


- Molecule 16: Flagellar P-ring protein

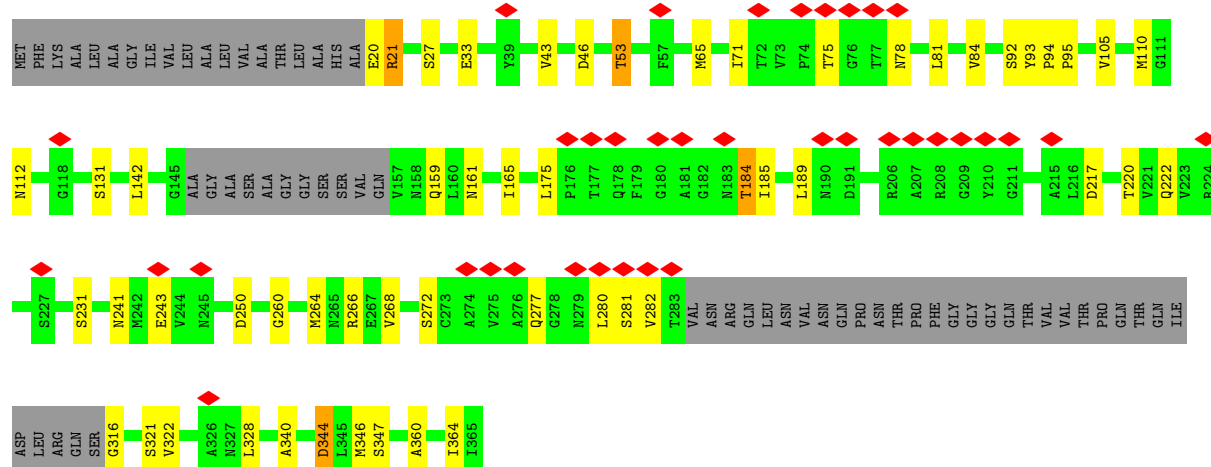




• Molecule 16: Flagellar P-ring protein

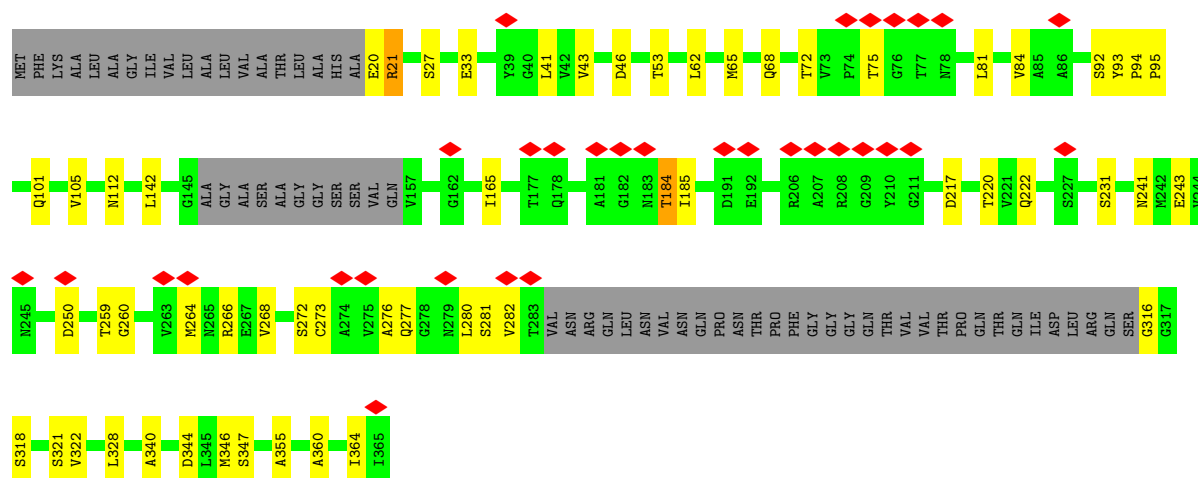


• Molecule 16: Flagellar P-ring protein

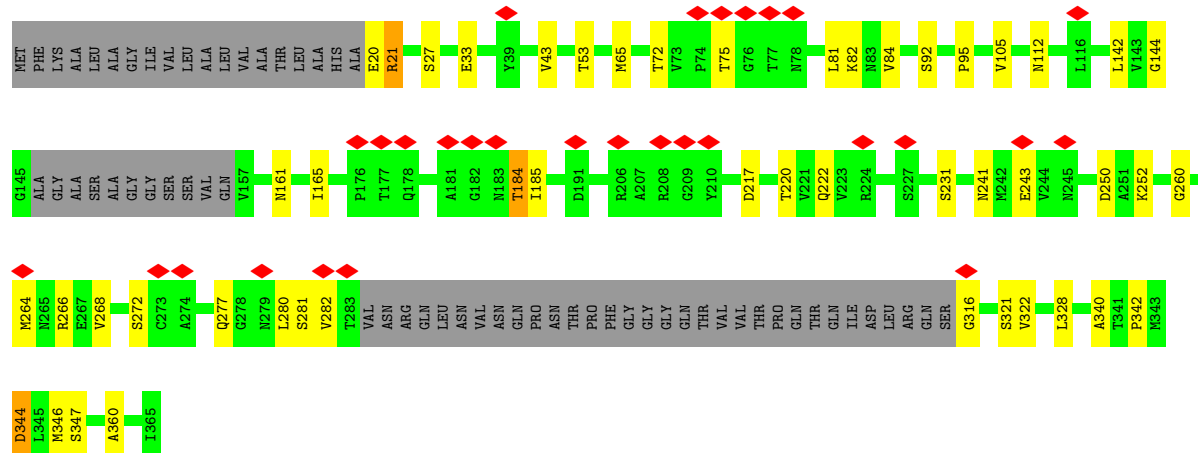
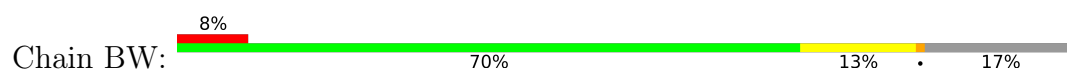


• Molecule 16: Flagellar P-ring protein

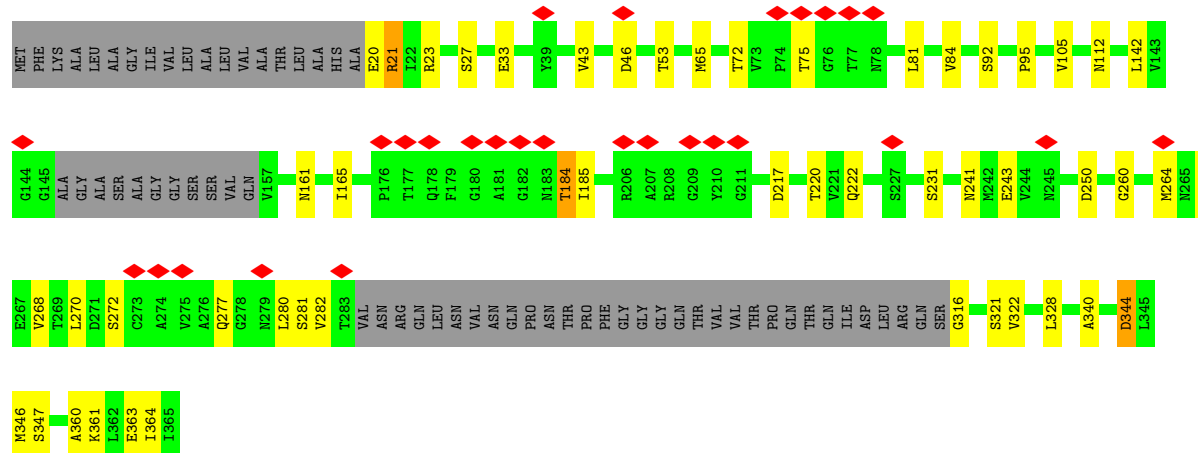




• Molecule 16: Flagellar P-ring protein

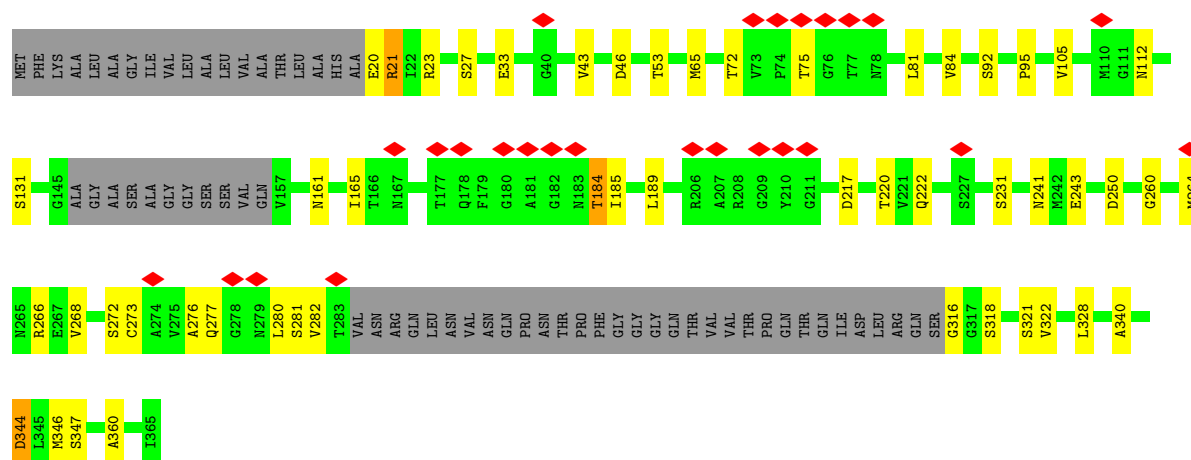


• Molecule 16: Flagellar P-ring protein



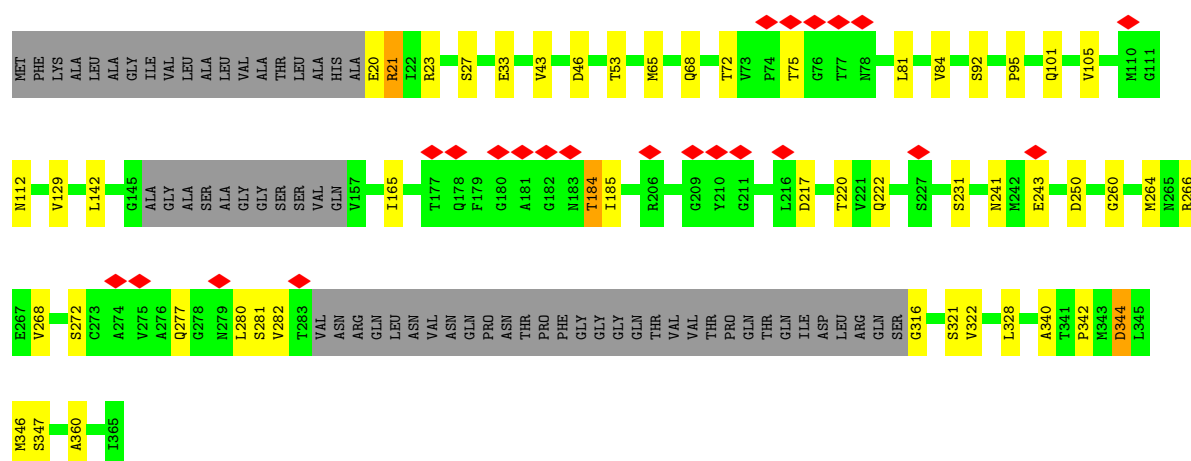
- Molecule 16: Flagellar P-ring protein

Chain BY:  7% 69% 13% 17%



- Molecule 16: Flagellar P-ring protein

Chain BZ:  6% 69% 13% 17%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52714	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 ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.383	Depositor
Minimum map value	-0.418	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.079	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	669.184, 669.184, 669.184	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.307, 1.307, 1.307	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: P1L

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	0.15	0/1973	0.28	0/2682
1	B	0.14	0/1973	0.27	0/2682
1	C	0.15	0/1973	0.26	0/2682
1	D	0.15	0/1973	0.28	0/2682
1	E	0.15	0/1973	0.30	0/2682
1	F	0.16	0/1973	0.28	0/2682
1	G	0.17	0/1973	0.32	0/2682
1	H	0.15	0/1973	0.28	0/2682
1	I	0.16	0/1973	0.31	0/2682
1	J	0.17	0/1973	0.29	0/2682
1	K	0.17	0/1973	0.32	1/2682 (0.0%)
1	L	0.15	0/1965	0.25	0/2672
1	M	0.16	0/1973	0.27	0/2682
1	N	0.15	0/1909	0.26	0/2593
1	O	0.15	0/1917	0.26	0/2605
1	P	0.16	0/1884	0.29	0/2559
1	Q	0.17	0/1880	0.28	0/2554
1	R	0.15	0/1898	0.29	0/2578
1	S	0.21	0/1880	0.36	1/2554 (0.0%)
1	T	0.15	0/1925	0.25	0/2617
1	U	0.15	0/1965	0.27	0/2672
1	V	0.16	0/1965	0.29	0/2672
1	W	0.22	0/1965	0.35	0/2672
1	X	0.15	0/1965	0.32	0/2672
2	a	0.16	0/1836	0.29	0/2502
2	b	0.15	0/1828	0.28	0/2492
2	c	0.14	0/1836	0.25	0/2502
2	d	0.15	0/1836	0.29	0/2502
2	e	0.14	0/1836	0.33	0/2502
4	5	0.14	0/145	0.23	0/203
4	6	0.10	0/145	0.24	0/203
4	7	0.51	0/145	0.86	0/203

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	8	0.13	0/145	0.23	0/203
4	9	0.13	0/145	0.28	0/203
5	f	0.14	0/946	0.24	0/1285
5	g	0.15	0/959	0.29	0/1302
5	h	0.15	0/945	0.26	0/1283
5	i	0.16	0/954	0.28	0/1295
5	j	0.15	0/941	0.27	0/1278
5	p	0.13	0/950	0.25	0/1290
6	k	0.15	0/859	0.28	0/1156
6	l	0.13	0/840	0.25	0/1131
6	m	0.15	0/840	0.26	0/1131
6	n	0.15	0/851	0.25	0/1145
6	o	0.13	0/863	0.28	0/1161
7	q	0.12	0/540	0.24	0/723
7	r	0.16	0/529	0.31	0/709
7	s	0.12	0/547	0.23	0/733
7	t	0.11	0/547	0.28	0/733
7	u	0.11	0/547	0.29	0/733
7	v	0.10	0/289	0.22	0/385
8	DA	0.14	0/2991	0.26	0/4076
8	DB	0.12	0/2991	0.25	0/4076
8	DC	0.12	0/2991	0.25	0/4076
8	DD	0.11	0/2991	0.25	0/4076
8	DE	0.11	0/2991	0.23	0/4076
8	DF	0.11	0/2991	0.23	0/4076
8	DG	0.11	0/2991	0.25	0/4076
8	DH	0.14	0/2991	0.27	0/4076
8	DI	0.15	0/2991	0.32	2/4076 (0.0%)
8	DJ	0.20	0/2991	0.37	2/4076 (0.0%)
8	DK	0.15	0/2991	0.28	1/4076 (0.0%)
8	DL	0.59	8/2991 (0.3%)	0.91	15/4076 (0.4%)
8	DM	0.38	0/2991	0.70	9/4076 (0.2%)
8	DN	0.50	1/2991 (0.0%)	0.80	8/4076 (0.2%)
8	DO	0.47	0/2991	0.87	9/4076 (0.2%)
8	DP	0.26	0/2991	0.56	6/4076 (0.1%)
8	DQ	0.36	1/2991 (0.0%)	0.60	5/4076 (0.1%)
8	DR	0.14	0/2991	0.39	0/4076
8	DS	0.21	0/2991	0.49	1/4076 (0.0%)
8	DT	0.16	0/2991	0.39	1/4076 (0.0%)
8	DU	0.21	0/2991	0.50	4/4076 (0.1%)
8	DV	0.14	0/2991	0.39	0/4076
8	DW	0.15	0/2991	0.43	2/4076 (0.0%)
8	DX	0.14	0/2991	0.35	0/4076

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	DY	0.15	0/2991	0.39	0/4076
8	DZ	0.15	0/2991	0.39	0/4076
8	EA	0.15	0/2991	0.37	0/4076
8	EB	0.14	0/2991	0.36	0/4076
8	EC	0.15	0/2991	0.37	2/4076 (0.0%)
8	ED	0.14	0/2991	0.35	0/4076
8	EE	0.13	0/2991	0.36	0/4076
8	EF	0.15	0/2991	0.37	0/4076
8	EG	0.14	0/2991	0.38	0/4076
9	CE	0.10	0/2052	0.28	0/2803
10	CA	0.10	0/681	0.34	0/930
10	CB	0.10	0/681	0.32	0/930
10	CC	0.10	0/681	0.34	0/930
10	CD	0.09	0/681	0.43	2/930 (0.2%)
11	CF	0.11	0/1675	0.30	0/2280
11	w	0.12	0/1675	0.30	0/2280
11	x	0.12	0/1675	0.30	0/2280
11	y	0.13	0/1675	0.36	0/2280
11	z	0.12	0/1675	0.30	0/2280
12	Ca	0.25	0/1197	0.41	0/1613
12	Cb	0.25	0/1197	0.41	0/1613
12	Cc	0.25	0/1197	0.41	0/1613
12	Cd	0.25	0/1197	0.41	0/1613
12	Ce	0.25	0/1197	0.41	0/1613
12	Cf	0.25	0/1197	0.41	0/1613
12	Cg	0.25	0/1197	0.41	0/1613
12	Ch	0.25	0/1197	0.41	0/1613
12	Ci	0.25	0/1197	0.41	0/1613
12	Cj	0.25	0/1197	0.41	0/1613
12	Ck	0.25	0/1197	0.41	0/1613
12	Cl	0.25	0/1197	0.41	0/1613
12	Cm	0.25	0/1197	0.41	0/1613
12	Cn	0.25	0/1197	0.41	0/1613
12	Co	0.25	0/1197	0.41	0/1613
12	Cp	0.25	0/1197	0.41	0/1613
12	Cq	0.25	0/1197	0.41	0/1613
12	Cr	0.25	0/1197	0.41	0/1613
12	Cs	0.25	0/1197	0.41	0/1613
12	Ct	0.25	0/1197	0.41	0/1613
12	Cu	0.25	0/1197	0.41	0/1613
12	Cv	0.25	0/1197	0.41	0/1613
12	Cw	0.25	0/1197	0.41	0/1613
12	Cx	0.25	0/1197	0.41	0/1613

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
12	Cy	0.25	0/1197	0.41	0/1613
12	Cz	0.25	0/1197	0.41	0/1613
12	Da	0.55	0/756	0.79	0/1036
12	Db	0.91	3/756 (0.4%)	1.26	5/1036 (0.5%)
12	Dc	0.59	0/756	0.76	0/1036
12	Dd	0.58	0/756	0.86	2/1036 (0.2%)
12	De	0.44	0/705	0.57	0/963
12	Df	0.90	3/697 (0.4%)	1.24	5/954 (0.5%)
12	Dg	0.37	0/646	0.50	0/881
12	Dh	0.37	0/646	0.50	0/881
12	Di	0.37	0/646	0.50	0/881
12	Dj	0.37	0/646	0.50	0/881
12	Dk	0.38	0/646	0.50	0/881
12	Dll	0.37	0/646	0.50	0/881
12	Dm	0.37	0/646	0.50	0/881
12	Dn	0.37	0/646	0.50	0/881
12	Do	0.44	0/697	0.59	1/954 (0.1%)
12	Dp	0.56	0/756	0.82	0/1036
12	Dq	0.62	0/756	0.99	4/1036 (0.4%)
12	Dr	0.76	1/756 (0.1%)	1.02	2/1036 (0.2%)
12	Ds	0.77	1/756 (0.1%)	1.15	4/1036 (0.4%)
12	Dt	0.56	0/756	0.80	0/1036
12	Du	0.60	0/756	0.94	5/1036 (0.5%)
12	Dv	0.59	0/756	0.80	0/1036
12	Dw	0.60	0/756	0.88	1/1036 (0.1%)
12	Ea	0.25	0/1197	0.41	0/1613
12	Eb	0.25	0/1197	0.41	0/1613
12	Ec	0.25	0/1197	0.41	0/1613
12	Ed	0.25	0/1197	0.41	0/1613
12	Ee	0.25	0/1197	0.41	0/1613
12	Ef	0.25	0/1197	0.41	0/1613
12	Eg	0.25	0/1197	0.41	0/1613
12	Eh	0.25	0/1197	0.41	0/1613
15	AA	0.28	0/1607	0.35	0/2186
15	AB	0.28	0/1607	0.35	0/2186
15	AC	0.28	0/1607	0.35	0/2186
15	AD	0.28	0/1607	0.35	0/2186
15	AE	0.28	0/1607	0.35	0/2186
15	AF	0.28	0/1607	0.35	0/2186
15	AG	0.28	0/1607	0.35	0/2186
15	AH	0.28	0/1607	0.35	0/2186
15	AI	0.28	0/1607	0.35	0/2186
15	AJ	0.28	0/1607	0.35	0/2186

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	AK	0.27	0/1607	0.35	0/2186
15	AL	0.28	0/1607	0.35	0/2186
15	AM	0.28	0/1607	0.35	0/2186
15	AN	0.28	0/1607	0.35	0/2186
15	AO	0.28	0/1607	0.35	0/2186
15	AP	0.28	0/1607	0.35	0/2186
15	AQ	0.28	0/1607	0.35	0/2186
15	AR	0.28	0/1607	0.35	0/2186
15	AS	0.28	0/1607	0.35	0/2186
15	AT	0.28	0/1607	0.35	0/2186
15	AU	0.28	0/1607	0.35	0/2186
15	AV	0.28	0/1607	0.35	0/2186
15	AW	0.28	0/1607	0.35	0/2186
15	AX	0.28	0/1607	0.35	0/2186
15	AY	0.28	0/1607	0.35	0/2186
15	AZ	0.28	0/1607	0.35	0/2186
16	BA	0.26	0/2243	0.33	0/3041
16	BB	0.26	0/2243	0.34	0/3041
16	BC	0.26	0/2243	0.33	0/3041
16	BD	0.26	0/2243	0.34	0/3041
16	BE	0.26	0/2243	0.33	0/3041
16	BF	0.27	0/2243	0.33	0/3041
16	BG	0.26	0/2243	0.33	0/3041
16	BH	0.26	0/2243	0.33	0/3041
16	BI	0.26	0/2243	0.33	0/3041
16	BJ	0.26	0/2243	0.33	0/3041
16	BK	0.26	0/2243	0.34	0/3041
16	BL	0.26	0/2243	0.33	0/3041
16	BM	0.27	0/2243	0.33	0/3041
16	BN	0.26	0/2243	0.33	0/3041
16	BO	0.26	0/2243	0.33	0/3041
16	BP	0.26	0/2243	0.33	0/3041
16	BQ	0.27	0/2243	0.33	0/3041
16	BR	0.26	0/2243	0.34	0/3041
16	BS	0.26	0/2243	0.33	0/3041
16	BT	0.26	0/2243	0.34	0/3041
16	BU	0.26	0/2243	0.33	0/3041
16	BV	0.26	0/2243	0.34	0/3041
16	BW	0.26	0/2243	0.33	0/3041
16	BX	0.26	0/2243	0.33	0/3041
16	BY	0.26	0/2243	0.33	0/3041
16	BZ	0.26	0/2243	0.33	0/3041
All	All	0.26	18/338629 (0.0%)	0.41	100/460118 (0.0%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	Db	160	PRO	N-CA	17.48	1.69	1.47
12	Df	160	PRO	N-CA	17.46	1.69	1.47
12	Dr	171	SER	C-N	13.99	1.50	1.33
8	DQ	285	LYS	C-N	13.61	1.50	1.33
12	Ds	171	SER	C-N	13.59	1.50	1.33

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	Ds	171	SER	CA-C-N	17.94	138.28	120.52
12	Ds	171	SER	C-N-CA	17.94	138.28	120.52
12	Db	159	MET	CA-C-N	17.44	141.63	119.84
12	Db	159	MET	C-N-CA	17.44	141.63	119.84
12	Df	159	MET	CA-C-N	17.10	141.21	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1949	0	1926	40	0
1	B	1949	0	1926	47	0
1	C	1949	0	1926	38	0
1	D	1949	0	1926	38	0
1	E	1949	0	1926	37	0
1	F	1949	0	1926	43	0
1	G	1949	0	1926	49	0
1	H	1949	0	1926	37	0
1	I	1949	0	1926	39	0
1	J	1949	0	1926	34	0
1	K	1949	0	1926	36	0
1	L	1941	0	1914	39	0
1	M	1949	0	1926	26	0
1	N	1887	0	1871	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	1894	0	1878	34	0
1	P	1862	0	1839	30	0
1	Q	1858	0	1836	40	0
1	R	1875	0	1852	34	0
1	S	1858	0	1836	33	0
1	T	1902	0	1881	42	0
1	U	1941	0	1914	50	0
1	V	1941	0	1914	58	0
1	W	1941	0	1914	49	0
1	X	1941	0	1914	35	0
2	a	1812	0	1800	42	0
2	b	1804	0	1791	48	0
2	c	1812	0	1800	41	0
2	d	1812	0	1800	46	0
2	e	1812	0	1800	35	0
3	0	75	0	18	0	0
3	1	75	0	17	1	0
3	2	75	0	17	1	0
3	3	75	0	18	0	0
3	4	75	0	19	2	0
4	5	140	0	136	7	0
4	6	140	0	136	1	0
4	7	140	0	136	3	0
4	8	140	0	136	7	0
4	9	140	0	136	3	0
5	f	936	0	951	24	0
5	g	949	0	962	20	0
5	h	935	0	949	27	0
5	i	944	0	957	18	0
5	j	931	0	946	19	0
5	p	940	0	954	17	0
6	k	852	0	855	20	0
6	l	833	0	831	15	0
6	m	833	0	831	21	0
6	n	844	0	844	18	0
6	o	856	0	858	17	0
7	q	536	0	541	8	0
7	r	526	0	536	9	0
7	s	543	0	550	4	0
7	t	543	0	550	5	0
7	u	543	0	550	9	0
7	v	289	0	299	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	DA	2947	0	2839	74	0
8	DB	2947	0	2839	66	0
8	DC	2947	0	2839	86	0
8	DD	2947	0	2839	65	0
8	DE	2947	0	2839	68	0
8	DF	2947	0	2839	77	0
8	DG	2947	0	2839	120	0
8	DH	2947	0	2839	136	0
8	DI	2947	0	2839	107	0
8	DJ	2947	0	2839	115	0
8	DK	2947	0	2839	137	0
8	DL	2947	0	2839	237	0
8	DM	2947	0	2839	229	0
8	DN	2947	0	2839	216	0
8	DO	2947	0	2839	191	0
8	DP	2947	0	2839	214	0
8	DQ	2947	0	2839	146	0
8	DR	2947	0	2839	89	0
8	DS	2947	0	2839	119	0
8	DT	2947	0	2839	104	0
8	DU	2947	0	2839	145	0
8	DV	2947	0	2839	97	0
8	DW	2947	0	2839	82	0
8	DX	2947	0	2839	98	0
8	DY	2947	0	2839	94	0
8	DZ	2947	0	2839	83	0
8	EA	2947	0	2839	82	0
8	EB	2947	0	2839	96	0
8	EC	2947	0	2839	77	0
8	ED	2947	0	2839	86	0
8	EE	2947	0	2839	73	0
8	EF	2947	0	2839	85	0
8	EG	2947	0	2839	82	0
9	CE	2002	0	2116	79	0
10	CA	670	0	739	18	0
10	CB	670	0	739	16	0
10	CC	670	0	739	21	0
10	CD	670	0	739	15	0
11	CF	1636	0	1726	48	0
11	w	1636	0	1726	40	0
11	x	1636	0	1726	36	0
11	y	1636	0	1726	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	z	1636	0	1726	50	0
12	Ca	1185	0	1167	28	0
12	Cb	1185	0	1167	30	0
12	Cc	1185	0	1167	34	0
12	Cd	1185	0	1167	30	0
12	Ce	1185	0	1167	31	0
12	Cf	1185	0	1167	34	0
12	Cg	1185	0	1167	28	0
12	Ch	1185	0	1167	28	0
12	Ci	1185	0	1167	27	0
12	Cj	1185	0	1167	25	0
12	Ck	1185	0	1167	28	0
12	Cl	1185	0	1167	31	0
12	Cm	1185	0	1167	35	0
12	Cn	1185	0	1167	35	0
12	Co	1185	0	1167	30	0
12	Cp	1185	0	1167	30	0
12	Cq	1185	0	1167	26	0
12	Cr	1185	0	1167	26	0
12	Cs	1185	0	1167	29	0
12	Ct	1185	0	1167	33	0
12	Cu	1185	0	1167	35	0
12	Cv	1185	0	1167	27	0
12	Cw	1185	0	1167	25	0
12	Cx	1185	0	1167	27	0
12	Cy	1185	0	1167	30	0
12	Cz	1185	0	1167	32	0
12	Da	746	0	689	27	0
12	Db	746	0	689	27	0
12	Dc	746	0	689	36	0
12	Dd	746	0	689	17	0
12	De	696	0	669	13	0
12	Df	687	0	664	30	0
12	Dg	637	0	644	11	0
12	Dh	637	0	644	11	0
12	Di	637	0	644	13	0
12	Dj	637	0	644	18	0
12	Dk	637	0	644	14	0
12	Dl	637	0	644	22	0
12	Dm	637	0	644	13	0
12	Dn	637	0	644	17	0
12	Do	687	0	664	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	Dp	746	0	689	18	0
12	Dq	746	0	689	29	0
12	Dr	746	0	689	17	0
12	Ds	746	0	689	19	0
12	Dt	746	0	689	55	0
12	Du	746	0	689	27	0
12	Dv	746	0	689	30	0
12	Dw	746	0	689	24	0
12	Ea	1185	0	1167	33	0
12	Eb	1185	0	1167	26	0
12	Ec	1185	0	1167	30	0
12	Ed	1185	0	1167	35	0
12	Ee	1185	0	1167	28	0
12	Ef	1185	0	1167	26	0
12	Eg	1185	0	1167	28	0
12	Eh	1185	0	1167	32	0
13	GA	55	0	14	4	0
13	GB	25	0	7	0	0
13	GC	55	0	14	2	0
13	GD	50	0	12	4	0
13	GE	60	0	15	4	0
14	GF	90	0	20	10	0
14	GG	90	0	20	1	0
14	GH	90	0	20	10	0
14	GI	75	0	17	7	0
14	GJ	90	0	20	4	0
14	GK	90	0	20	2	0
15	AA	1589	0	1547	23	0
15	AB	1589	0	1547	21	0
15	AC	1589	0	1547	20	0
15	AD	1589	0	1547	20	0
15	AE	1589	0	1547	20	0
15	AF	1589	0	1547	20	0
15	AG	1589	0	1547	19	0
15	AH	1589	0	1547	18	0
15	AI	1589	0	1547	22	0
15	AJ	1589	0	1547	21	0
15	AK	1589	0	1547	19	0
15	AL	1589	0	1547	21	0
15	AM	1589	0	1547	22	0
15	AN	1589	0	1547	21	0
15	AO	1589	0	1547	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	AP	1589	0	1547	21	0
15	AQ	1589	0	1547	23	0
15	AR	1589	0	1547	23	0
15	AS	1589	0	1547	22	0
15	AT	1589	0	1547	23	0
15	AU	1589	0	1547	26	0
15	AV	1589	0	1547	21	0
15	AW	1589	0	1547	21	0
15	AX	1589	0	1547	21	0
15	AY	1589	0	1547	21	0
15	AZ	1589	0	1547	20	0
16	BA	2228	0	2265	34	0
16	BB	2228	0	2265	27	0
16	BC	2228	0	2265	26	0
16	BD	2228	0	2265	33	0
16	BE	2228	0	2265	29	0
16	BF	2228	0	2265	25	0
16	BG	2228	0	2265	32	0
16	BH	2228	0	2265	25	0
16	BI	2228	0	2265	27	0
16	BJ	2228	0	2265	26	0
16	BK	2228	0	2265	26	0
16	BL	2228	0	2265	25	0
16	BM	2228	0	2265	24	0
16	BN	2228	0	2265	24	0
16	BO	2228	0	2265	28	0
16	BP	2228	0	2265	28	0
16	BQ	2228	0	2265	29	0
16	BR	2228	0	2265	36	0
16	BS	2228	0	2265	29	0
16	BT	2228	0	2265	29	0
16	BU	2228	0	2265	42	0
16	BV	2228	0	2265	38	0
16	BW	2228	0	2265	32	0
16	BX	2228	0	2265	29	0
16	BY	2228	0	2265	31	0
16	BZ	2228	0	2265	32	0
All	All	335722	0	330174	6782	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 10.

The worst 5 of 6782 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)
8:DG:382:TYR:CE2	8:DL:395:ILE:HG23	1.39	1.54
8:DC:181:LYS:CD	8:DN:131:GLY:HA3	1.36	1.50
8:DJ:377:VAL:HG22	8:DP:3:PHE:CD2	1.44	1.49
11:y:152:ARG:NH1	12:Dt:164:LEU:HA	1.17	1.45
8:DK:382:TYR:CE2	8:DP:395:ILE:HG23	1.50	1.45

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	A	258/260 (99%)	249 (96%)	9 (4%)	0	100	100
1	B	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	C	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	D	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	E	258/260 (99%)	246 (95%)	12 (5%)	0	100	100
1	F	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	G	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	H	258/260 (99%)	245 (95%)	13 (5%)	0	100	100
1	I	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	J	258/260 (99%)	251 (97%)	7 (3%)	0	100	100
1	K	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	L	257/260 (99%)	250 (97%)	7 (3%)	0	100	100
1	M	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	N	247/260 (95%)	240 (97%)	7 (3%)	0	100	100
1	O	248/260 (95%)	240 (97%)	8 (3%)	0	100	100
1	P	244/260 (94%)	236 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	243/260 (94%)	237 (98%)	6 (2%)	0	100	100
1	R	246/260 (95%)	238 (97%)	8 (3%)	0	100	100
1	S	243/260 (94%)	235 (97%)	8 (3%)	0	100	100
1	T	249/260 (96%)	241 (97%)	8 (3%)	0	100	100
1	U	257/260 (99%)	243 (95%)	14 (5%)	0	100	100
1	V	257/260 (99%)	249 (97%)	8 (3%)	0	100	100
1	W	257/260 (99%)	242 (94%)	15 (6%)	0	100	100
1	X	257/260 (99%)	244 (95%)	13 (5%)	0	100	100
2	a	247/251 (98%)	235 (95%)	12 (5%)	0	100	100
2	b	246/251 (98%)	236 (96%)	10 (4%)	0	100	100
2	c	247/251 (98%)	237 (96%)	10 (4%)	0	100	100
2	d	247/251 (98%)	232 (94%)	15 (6%)	0	100	100
2	e	247/251 (98%)	231 (94%)	16 (6%)	0	100	100
4	5	19/21 (90%)	19 (100%)	0	0	100	100
4	6	19/21 (90%)	19 (100%)	0	0	100	100
4	7	19/21 (90%)	19 (100%)	0	0	100	100
4	8	19/21 (90%)	18 (95%)	1 (5%)	0	100	100
4	9	19/21 (90%)	19 (100%)	0	0	100	100
5	f	124/134 (92%)	121 (98%)	3 (2%)	0	100	100
5	g	126/134 (94%)	121 (96%)	5 (4%)	0	100	100
5	h	124/134 (92%)	120 (97%)	4 (3%)	0	100	100
5	i	125/134 (93%)	121 (97%)	4 (3%)	0	100	100
5	j	123/134 (92%)	119 (97%)	4 (3%)	0	100	100
5	p	125/134 (93%)	120 (96%)	5 (4%)	0	100	100
6	k	104/138 (75%)	99 (95%)	5 (5%)	0	100	100
6	l	102/138 (74%)	101 (99%)	1 (1%)	0	100	100
6	m	102/138 (74%)	99 (97%)	3 (3%)	0	100	100
6	n	103/138 (75%)	99 (96%)	4 (4%)	0	100	100
6	o	105/138 (76%)	103 (98%)	2 (2%)	0	100	100
7	q	69/104 (66%)	68 (99%)	1 (1%)	0	100	100
7	r	68/104 (65%)	64 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	s	70/104 (67%)	70 (100%)	0	0	100	100
7	t	70/104 (67%)	69 (99%)	1 (1%)	0	100	100
7	u	70/104 (67%)	70 (100%)	0	0	100	100
7	v	36/104 (35%)	36 (100%)	0	0	100	100
8	DA	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
8	DB	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
8	DC	399/403 (99%)	375 (94%)	24 (6%)	0	100	100
8	DD	399/403 (99%)	378 (95%)	21 (5%)	0	100	100
8	DE	399/403 (99%)	380 (95%)	19 (5%)	0	100	100
8	DF	399/403 (99%)	376 (94%)	23 (6%)	0	100	100
8	DG	399/403 (99%)	382 (96%)	17 (4%)	0	100	100
8	DH	399/403 (99%)	378 (95%)	19 (5%)	2 (0%)	24	59
8	DI	399/403 (99%)	381 (96%)	18 (4%)	0	100	100
8	DJ	399/403 (99%)	375 (94%)	23 (6%)	1 (0%)	36	69
8	DK	399/403 (99%)	386 (97%)	13 (3%)	0	100	100
8	DL	399/403 (99%)	369 (92%)	27 (7%)	3 (1%)	16	50
8	DM	399/403 (99%)	383 (96%)	14 (4%)	2 (0%)	24	59
8	DN	399/403 (99%)	366 (92%)	31 (8%)	2 (0%)	24	59
8	DO	399/403 (99%)	373 (94%)	23 (6%)	3 (1%)	16	50
8	DP	399/403 (99%)	375 (94%)	24 (6%)	0	100	100
8	DQ	399/403 (99%)	379 (95%)	20 (5%)	0	100	100
8	DR	399/403 (99%)	382 (96%)	17 (4%)	0	100	100
8	DS	399/403 (99%)	381 (96%)	18 (4%)	0	100	100
8	DT	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
8	DU	399/403 (99%)	381 (96%)	18 (4%)	0	100	100
8	DV	399/403 (99%)	374 (94%)	23 (6%)	2 (0%)	24	59
8	DW	399/403 (99%)	381 (96%)	18 (4%)	0	100	100
8	DX	399/403 (99%)	380 (95%)	19 (5%)	0	100	100
8	DY	399/403 (99%)	378 (95%)	21 (5%)	0	100	100
8	DZ	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
8	EA	399/403 (99%)	378 (95%)	21 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	EB	399/403 (99%)	373 (94%)	26 (6%)	0	100	100
8	EC	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
8	ED	399/403 (99%)	380 (95%)	19 (5%)	0	100	100
8	EE	399/403 (99%)	379 (95%)	20 (5%)	0	100	100
8	EF	399/403 (99%)	379 (95%)	20 (5%)	0	100	100
8	EG	399/403 (99%)	376 (94%)	23 (6%)	0	100	100
9	CE	258/264 (98%)	239 (93%)	18 (7%)	1 (0%)	30	64
10	CA	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
10	CB	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
10	CC	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
10	CD	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
11	CF	209/245 (85%)	203 (97%)	6 (3%)	0	100	100
11	w	209/245 (85%)	203 (97%)	6 (3%)	0	100	100
11	x	209/245 (85%)	197 (94%)	12 (6%)	0	100	100
11	y	209/245 (85%)	201 (96%)	8 (4%)	0	100	100
11	z	209/245 (85%)	204 (98%)	5 (2%)	0	100	100
12	Ca	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cb	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cc	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cd	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ce	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cf	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cg	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ch	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ci	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cj	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ck	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cl	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cm	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cn	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Co	144/560 (26%)	136 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Cp	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cq	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cr	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cs	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ct	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cu	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cv	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cw	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cx	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cy	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Cz	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Da	107/560 (19%)	94 (88%)	10 (9%)	3 (3%)	4	27
12	Db	107/560 (19%)	95 (89%)	10 (9%)	2 (2%)	6	33
12	Dc	107/560 (19%)	93 (87%)	10 (9%)	4 (4%)	2	22
12	Dd	107/560 (19%)	93 (87%)	12 (11%)	2 (2%)	6	33
12	De	95/560 (17%)	86 (90%)	8 (8%)	1 (1%)	11	43
12	Df	95/560 (17%)	83 (87%)	12 (13%)	0	100	100
12	Dg	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Dh	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Di	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Dj	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Dk	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Di	83/560 (15%)	76 (92%)	6 (7%)	1 (1%)	10	41
12	Dm	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Dn	83/560 (15%)	75 (90%)	7 (8%)	1 (1%)	10	41
12	Do	95/560 (17%)	86 (90%)	7 (7%)	2 (2%)	5	31
12	Dp	107/560 (19%)	94 (88%)	12 (11%)	1 (1%)	14	47
12	Dq	107/560 (19%)	96 (90%)	8 (8%)	3 (3%)	4	27
12	Dr	107/560 (19%)	96 (90%)	10 (9%)	1 (1%)	14	47
12	Ds	107/560 (19%)	93 (87%)	11 (10%)	3 (3%)	4	27
12	Dt	107/560 (19%)	93 (87%)	11 (10%)	3 (3%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Du	107/560 (19%)	94 (88%)	11 (10%)	2 (2%)	6	33
12	Dv	107/560 (19%)	96 (90%)	8 (8%)	3 (3%)	4	27
12	Dw	107/560 (19%)	90 (84%)	13 (12%)	4 (4%)	2	22
12	Ea	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Eb	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ec	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ed	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ee	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Ef	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Eg	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
12	Eh	144/560 (26%)	136 (94%)	8 (6%)	0	100	100
15	AA	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AB	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AC	209/232 (90%)	198 (95%)	11 (5%)	0	100	100
15	AD	209/232 (90%)	198 (95%)	11 (5%)	0	100	100
15	AE	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AF	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AG	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AH	209/232 (90%)	198 (95%)	11 (5%)	0	100	100
15	AI	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AJ	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AK	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AL	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AM	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AN	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AO	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AP	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AQ	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AR	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AS	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AT	209/232 (90%)	199 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	AU	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AV	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AW	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AX	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
15	AY	209/232 (90%)	198 (95%)	11 (5%)	0	100	100
15	AZ	209/232 (90%)	199 (95%)	10 (5%)	0	100	100
16	BA	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BB	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BC	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BD	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BE	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BF	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BG	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BH	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BI	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BJ	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BK	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BL	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BM	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BN	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BO	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BP	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BQ	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BR	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BS	297/365 (81%)	290 (98%)	6 (2%)	1 (0%)	36	69
16	BT	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BU	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BV	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BW	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BX	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
16	BY	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	BZ	297/365 (81%)	291 (98%)	5 (2%)	1 (0%)	36	69
All	All	44179/72304 (61%)	42089 (95%)	2006 (4%)	84 (0%)	44	74

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	DJ	332	ASN
12	Dc	124	SER
12	Dc	125	GLN
12	Dd	160	PRO
12	Dq	124	SER

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	215/215 (100%)	212 (99%)	3 (1%)	59	71
1	B	215/215 (100%)	212 (99%)	3 (1%)	59	71
1	C	215/215 (100%)	209 (97%)	6 (3%)	38	59
1	D	215/215 (100%)	213 (99%)	2 (1%)	70	75
1	E	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	F	215/215 (100%)	212 (99%)	3 (1%)	59	71
1	G	215/215 (100%)	207 (96%)	8 (4%)	30	53
1	H	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	I	215/215 (100%)	211 (98%)	4 (2%)	50	66
1	J	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	K	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	L	214/215 (100%)	211 (99%)	3 (1%)	59	71
1	M	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	N	208/215 (97%)	208 (100%)	0	100	100
1	O	209/215 (97%)	206 (99%)	3 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	204/215 (95%)	201 (98%)	3 (2%)	57	70
1	Q	204/215 (95%)	199 (98%)	5 (2%)	42	62
1	R	206/215 (96%)	199 (97%)	7 (3%)	32	55
1	S	204/215 (95%)	202 (99%)	2 (1%)	68	75
1	T	210/215 (98%)	208 (99%)	2 (1%)	68	75
1	U	214/215 (100%)	210 (98%)	4 (2%)	50	66
1	V	214/215 (100%)	207 (97%)	7 (3%)	33	56
1	W	214/215 (100%)	211 (99%)	3 (1%)	59	71
1	X	214/215 (100%)	209 (98%)	5 (2%)	44	63
2	a	191/193 (99%)	184 (96%)	7 (4%)	30	53
2	b	190/193 (98%)	184 (97%)	6 (3%)	34	56
2	c	191/193 (99%)	183 (96%)	8 (4%)	26	50
2	d	191/193 (99%)	187 (98%)	4 (2%)	47	65
2	e	191/193 (99%)	187 (98%)	4 (2%)	47	65
4	5	15/15 (100%)	14 (93%)	1 (7%)	15	41
4	6	15/15 (100%)	15 (100%)	0	100	100
4	7	15/15 (100%)	15 (100%)	0	100	100
4	8	15/15 (100%)	15 (100%)	0	100	100
4	9	15/15 (100%)	15 (100%)	0	100	100
5	f	101/105 (96%)	98 (97%)	3 (3%)	36	57
5	g	102/105 (97%)	98 (96%)	4 (4%)	28	52
5	h	101/105 (96%)	99 (98%)	2 (2%)	48	65
5	i	102/105 (97%)	98 (96%)	4 (4%)	28	52
5	j	101/105 (96%)	100 (99%)	1 (1%)	68	75
5	p	101/105 (96%)	101 (100%)	0	100	100
6	k	91/113 (80%)	90 (99%)	1 (1%)	65	74
6	l	89/113 (79%)	86 (97%)	3 (3%)	32	55
6	m	89/113 (79%)	86 (97%)	3 (3%)	32	55
6	n	90/113 (80%)	87 (97%)	3 (3%)	33	56
6	o	91/113 (80%)	87 (96%)	4 (4%)	25	49
7	q	55/79 (70%)	54 (98%)	1 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	r	54/79 (68%)	53 (98%)	1 (2%)	50	66
7	s	56/79 (71%)	56 (100%)	0	100	100
7	t	56/79 (71%)	55 (98%)	1 (2%)	51	67
7	u	56/79 (71%)	56 (100%)	0	100	100
7	v	32/79 (40%)	30 (94%)	2 (6%)	16	42
8	DA	321/323 (99%)	315 (98%)	6 (2%)	50	66
8	DB	321/323 (99%)	316 (98%)	5 (2%)	55	69
8	DC	321/323 (99%)	317 (99%)	4 (1%)	63	72
8	DD	321/323 (99%)	314 (98%)	7 (2%)	45	64
8	DE	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	DF	321/323 (99%)	315 (98%)	6 (2%)	50	66
8	DG	321/323 (99%)	318 (99%)	3 (1%)	70	75
8	DH	321/323 (99%)	314 (98%)	7 (2%)	45	64
8	DI	321/323 (99%)	315 (98%)	6 (2%)	50	66
8	DJ	321/323 (99%)	316 (98%)	5 (2%)	55	69
8	DK	321/323 (99%)	318 (99%)	3 (1%)	70	75
8	DL	321/323 (99%)	300 (94%)	21 (6%)	15	42
8	DM	321/323 (99%)	304 (95%)	17 (5%)	20	46
8	DN	321/323 (99%)	305 (95%)	16 (5%)	22	47
8	DO	321/323 (99%)	294 (92%)	27 (8%)	10	33
8	DP	321/323 (99%)	315 (98%)	6 (2%)	50	66
8	DQ	321/323 (99%)	315 (98%)	6 (2%)	50	66
8	DR	321/323 (99%)	321 (100%)	0	100	100
8	DS	321/323 (99%)	314 (98%)	7 (2%)	45	64
8	DT	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	DU	321/323 (99%)	315 (98%)	6 (2%)	50	66
8	DV	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	DW	321/323 (99%)	321 (100%)	0	100	100
8	DX	321/323 (99%)	321 (100%)	0	100	100
8	DY	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	DZ	321/323 (99%)	321 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	EA	321/323 (99%)	321 (100%)	0	100	100
8	EB	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	EC	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	ED	321/323 (99%)	321 (100%)	0	100	100
8	EE	321/323 (99%)	321 (100%)	0	100	100
8	EF	321/323 (99%)	320 (100%)	1 (0%)	86	85
8	EG	321/323 (99%)	320 (100%)	1 (0%)	86	85
9	CE	217/221 (98%)	212 (98%)	5 (2%)	44	63
10	CA	74/74 (100%)	74 (100%)	0	100	100
10	CB	74/74 (100%)	71 (96%)	3 (4%)	27	51
10	CC	74/74 (100%)	74 (100%)	0	100	100
10	CD	74/74 (100%)	74 (100%)	0	100	100
11	CF	180/204 (88%)	178 (99%)	2 (1%)	65	74
11	w	180/204 (88%)	176 (98%)	4 (2%)	45	64
11	x	180/204 (88%)	175 (97%)	5 (3%)	38	59
11	y	180/204 (88%)	170 (94%)	10 (6%)	19	45
11	z	180/204 (88%)	178 (99%)	2 (1%)	65	74
12	Ca	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cb	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cc	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cd	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ce	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cf	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cg	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ch	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ci	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cj	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ck	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cl	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cm	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cn	133/467 (28%)	130 (98%)	3 (2%)	44	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Co	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cp	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cq	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cr	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cs	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ct	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cu	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cv	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cw	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cx	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cy	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Cz	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Da	71/467 (15%)	69 (97%)	2 (3%)	38	59
12	Db	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dc	71/467 (15%)	69 (97%)	2 (3%)	38	59
12	Dd	71/467 (15%)	68 (96%)	3 (4%)	26	50
12	De	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Df	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dg	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dh	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Di	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dj	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dk	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dl	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dm	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dn	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Do	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dp	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dq	71/467 (15%)	69 (97%)	2 (3%)	38	59
12	Dr	71/467 (15%)	69 (97%)	2 (3%)	38	59
12	Ds	71/467 (15%)	70 (99%)	1 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	Dt	71/467 (15%)	69 (97%)	2 (3%)	38	59
12	Du	71/467 (15%)	70 (99%)	1 (1%)	59	71
12	Dv	71/467 (15%)	68 (96%)	3 (4%)	26	50
12	Dw	71/467 (15%)	68 (96%)	3 (4%)	26	50
12	Ea	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Eb	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ec	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ed	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ee	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Ef	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Eg	133/467 (28%)	130 (98%)	3 (2%)	44	63
12	Eh	133/467 (28%)	130 (98%)	3 (2%)	44	63
15	AA	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AB	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AC	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AD	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AE	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AF	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AG	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AH	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AI	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AJ	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AK	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AL	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AM	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AN	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AO	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AP	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AQ	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AR	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AS	169/185 (91%)	159 (94%)	10 (6%)	18	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	AT	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AU	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AV	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AW	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AX	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AY	169/185 (91%)	159 (94%)	10 (6%)	18	44
15	AZ	169/185 (91%)	159 (94%)	10 (6%)	18	44
16	BA	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BB	248/294 (84%)	237 (96%)	11 (4%)	25	49
16	BC	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BD	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BE	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BF	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BG	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BH	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BI	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BJ	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BK	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BL	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BM	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BN	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BO	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BP	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BQ	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BR	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BS	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BT	248/294 (84%)	237 (96%)	11 (4%)	25	49
16	BU	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BV	248/294 (84%)	237 (96%)	11 (4%)	25	49
16	BW	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BX	248/294 (84%)	236 (95%)	12 (5%)	23	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	BY	248/294 (84%)	236 (95%)	12 (5%)	23	48
16	BZ	248/294 (84%)	236 (95%)	12 (5%)	23	48
All	All	36494/59138 (62%)	35431 (97%)	1063 (3%)	38	58

5 of 1063 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	BY	21	ARG
8	DL	46	SER
16	BX	344	ASP
8	DQ	398	THR
15	AA	143	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 859 such sidechains are listed below:

Mol	Chain	Res	Type
15	AY	139	ASN
16	BM	159	GLN
8	DX	387	GLN
16	BA	188	GLN
15	AY	133	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

26 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	P1L	AR	22	15	13,14,23	0.89	0	11,15,25	1.85	3 (27%)
15	P1L	AB	22	15	13,14,23	0.89	0	11,15,25	1.89	3 (27%)
15	P1L	AM	22	15	13,14,23	0.88	0	11,15,25	1.87	3 (27%)
15	P1L	AF	22	15	13,14,23	0.90	0	11,15,25	1.86	3 (27%)
15	P1L	AJ	22	15	13,14,23	0.87	0	11,15,25	1.88	3 (27%)
15	P1L	AK	22	15	13,14,23	0.89	0	11,15,25	1.85	3 (27%)
15	P1L	AV	22	15	13,14,23	0.89	0	11,15,25	1.85	3 (27%)
15	P1L	AC	22	15	13,14,23	0.87	0	11,15,25	1.88	3 (27%)
15	P1L	AZ	22	15	13,14,23	0.89	0	11,15,25	1.86	3 (27%)
15	P1L	AS	22	15	13,14,23	0.89	0	11,15,25	1.88	3 (27%)
15	P1L	AW	22	15	13,14,23	0.90	0	11,15,25	1.88	3 (27%)
15	P1L	AY	22	15	13,14,23	0.88	0	11,15,25	1.87	3 (27%)
15	P1L	AE	22	15	13,14,23	0.89	0	11,15,25	1.86	3 (27%)
15	P1L	AH	22	15	13,14,23	0.89	0	11,15,25	1.88	3 (27%)
15	P1L	AP	22	15	13,14,23	0.89	0	11,15,25	1.87	3 (27%)
15	P1L	AO	22	15	13,14,23	0.90	0	11,15,25	1.83	3 (27%)
15	P1L	AI	22	15	13,14,23	0.91	0	11,15,25	1.86	3 (27%)
15	P1L	AT	22	15	13,14,23	0.88	0	11,15,25	1.86	3 (27%)
15	P1L	AX	22	15	13,14,23	0.87	0	11,15,25	1.90	3 (27%)
15	P1L	AQ	22	15	13,14,23	0.86	0	11,15,25	1.86	3 (27%)
15	P1L	AU	22	15	13,14,23	0.87	0	11,15,25	1.89	3 (27%)
15	P1L	AL	22	15	13,14,23	0.90	0	11,15,25	1.85	3 (27%)
15	P1L	AA	22	15	13,14,23	0.90	0	11,15,25	1.87	3 (27%)
15	P1L	AN	22	15	13,14,23	0.91	0	11,15,25	1.88	3 (27%)
15	P1L	AG	22	15	13,14,23	0.90	0	11,15,25	1.86	3 (27%)
15	P1L	AD	22	15	13,14,23	0.87	0	11,15,25	1.86	3 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	P1L	AR	22	15	-	7/12/14/24	-
15	P1L	AB	22	15	-	7/12/14/24	-
15	P1L	AM	22	15	-	7/12/14/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	P1L	AF	22	15	-	7/12/14/24	-
15	P1L	AJ	22	15	-	7/12/14/24	-
15	P1L	AK	22	15	-	7/12/14/24	-
15	P1L	AV	22	15	-	7/12/14/24	-
15	P1L	AC	22	15	-	7/12/14/24	-
15	P1L	AZ	22	15	-	7/12/14/24	-
15	P1L	AS	22	15	-	7/12/14/24	-
15	P1L	AW	22	15	-	7/12/14/24	-
15	P1L	AY	22	15	-	7/12/14/24	-
15	P1L	AE	22	15	-	7/12/14/24	-
15	P1L	AH	22	15	-	7/12/14/24	-
15	P1L	AP	22	15	-	7/12/14/24	-
15	P1L	AO	22	15	-	7/12/14/24	-
15	P1L	AI	22	15	-	7/12/14/24	-
15	P1L	AT	22	15	-	7/12/14/24	-
15	P1L	AX	22	15	-	7/12/14/24	-
15	P1L	AQ	22	15	-	7/12/14/24	-
15	P1L	AU	22	15	-	7/12/14/24	-
15	P1L	AL	22	15	-	7/12/14/24	-
15	P1L	AA	22	15	-	7/12/14/24	-
15	P1L	AN	22	15	-	7/12/14/24	-
15	P1L	AG	22	15	-	7/12/14/24	-
15	P1L	AD	22	15	-	7/12/14/24	-

There are no bond length outliers.

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AU	22	P1L	C8-C7-SG	-4.14	108.46	113.40
15	AX	22	P1L	C8-C7-SG	-4.11	108.50	113.40
15	AJ	22	P1L	C8-C7-SG	-4.09	108.53	113.40
15	AC	22	P1L	C8-C7-SG	-4.08	108.54	113.40
15	AB	22	P1L	C8-C7-SG	-4.06	108.56	113.40

There are no chirality outliers.

5 of 182 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
15	AA	22	P1L	O7-C7-SG-CB
15	AA	22	P1L	C8-C7-SG-CB
15	AB	22	P1L	O7-C7-SG-CB
15	AB	22	P1L	C8-C7-SG-CB
15	AC	22	P1L	O7-C7-SG-CB

There are no ring outliers.

26 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	AR	22	P1L	2	0
15	AB	22	P1L	2	0
15	AM	22	P1L	2	0
15	AF	22	P1L	2	0
15	AJ	22	P1L	2	0
15	AK	22	P1L	2	0
15	AV	22	P1L	1	0
15	AC	22	P1L	1	0
15	AZ	22	P1L	1	0
15	AS	22	P1L	2	0
15	AW	22	P1L	1	0
15	AY	22	P1L	2	0
15	AE	22	P1L	1	0
15	AH	22	P1L	1	0
15	AP	22	P1L	2	0
15	AO	22	P1L	2	0
15	AI	22	P1L	2	0
15	AT	22	P1L	2	0
15	AX	22	P1L	2	0
15	AQ	22	P1L	2	0
15	AU	22	P1L	2	0
15	AL	22	P1L	2	0
15	AA	22	P1L	2	0
15	AN	22	P1L	2	0
15	AG	22	P1L	2	0
15	AD	22	P1L	2	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

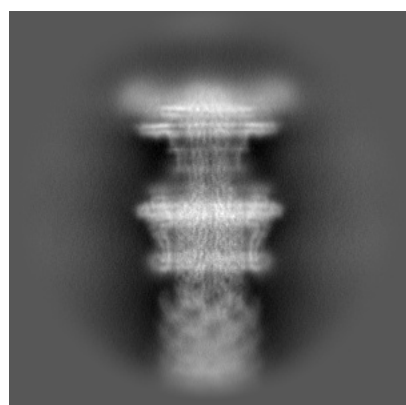
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30359. These allow visual inspection of the internal detail of the map and identification of artifacts.

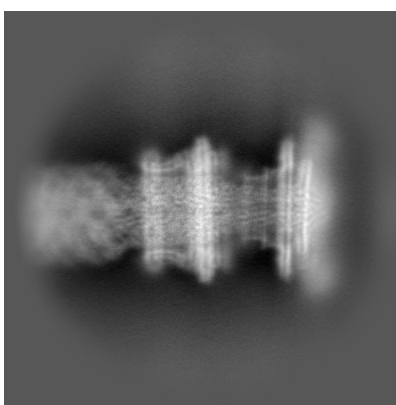
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

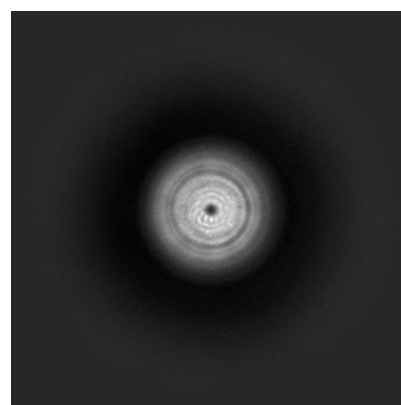
6.1.1 Primary map



X



Y

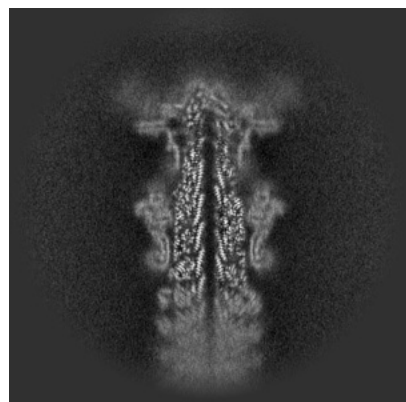


Z

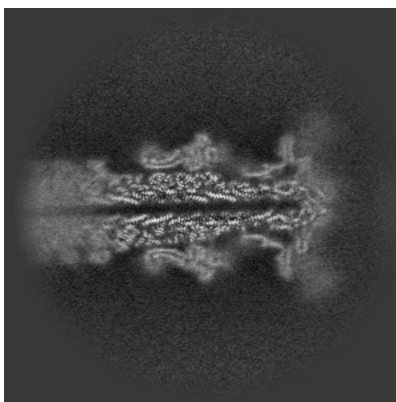
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

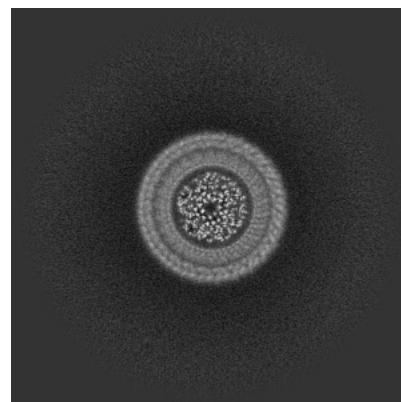
6.2.1 Primary map



X Index: 256



Y Index: 256

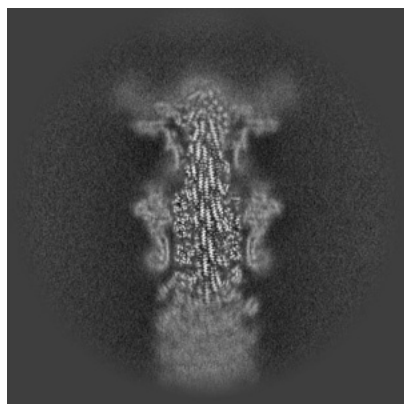


Z Index: 256

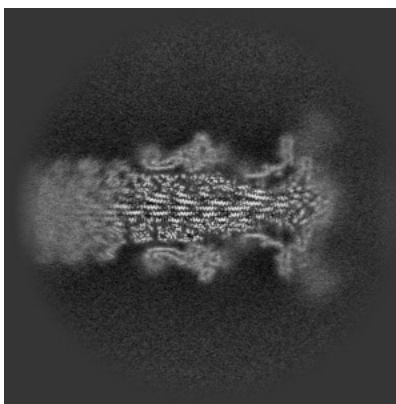
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

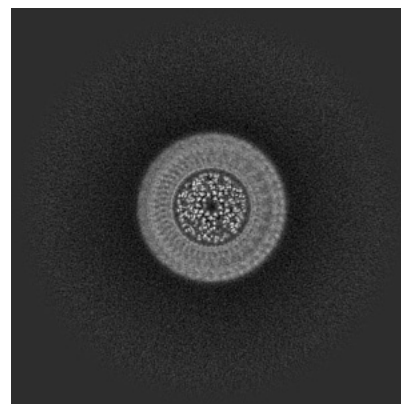
6.3.1 Primary map



X Index: 269



Y Index: 244

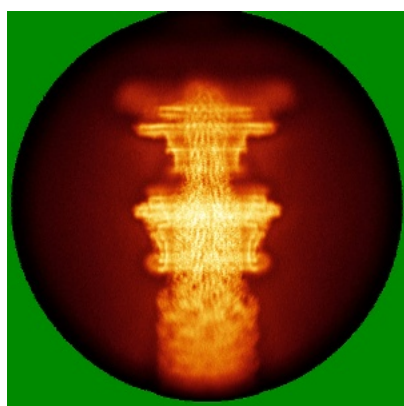


Z Index: 251

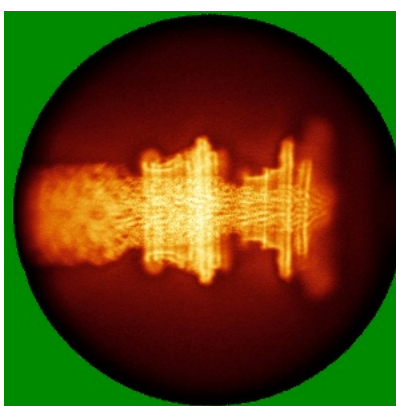
The images above show the largest variance slices of the map in three orthogonal directions.

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

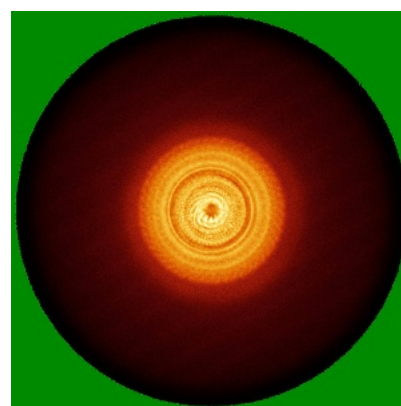
6.4.1 Primary map



X



Y

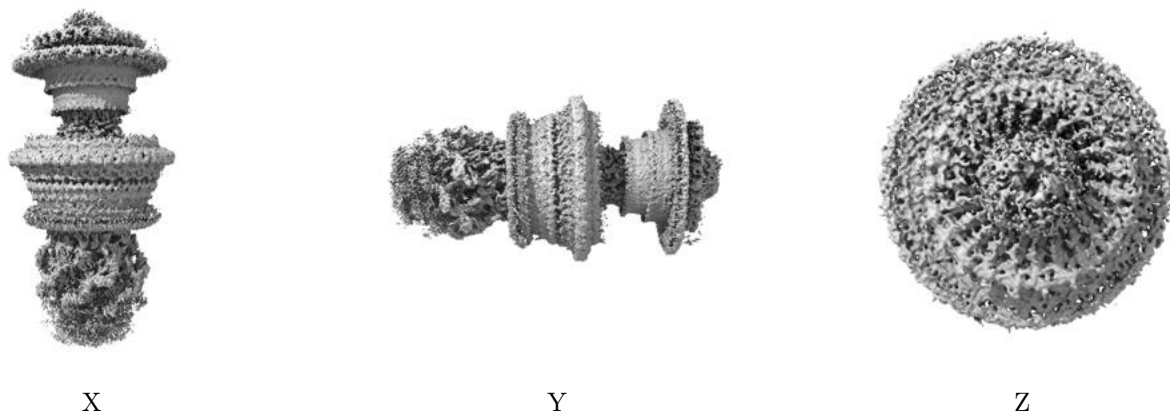


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

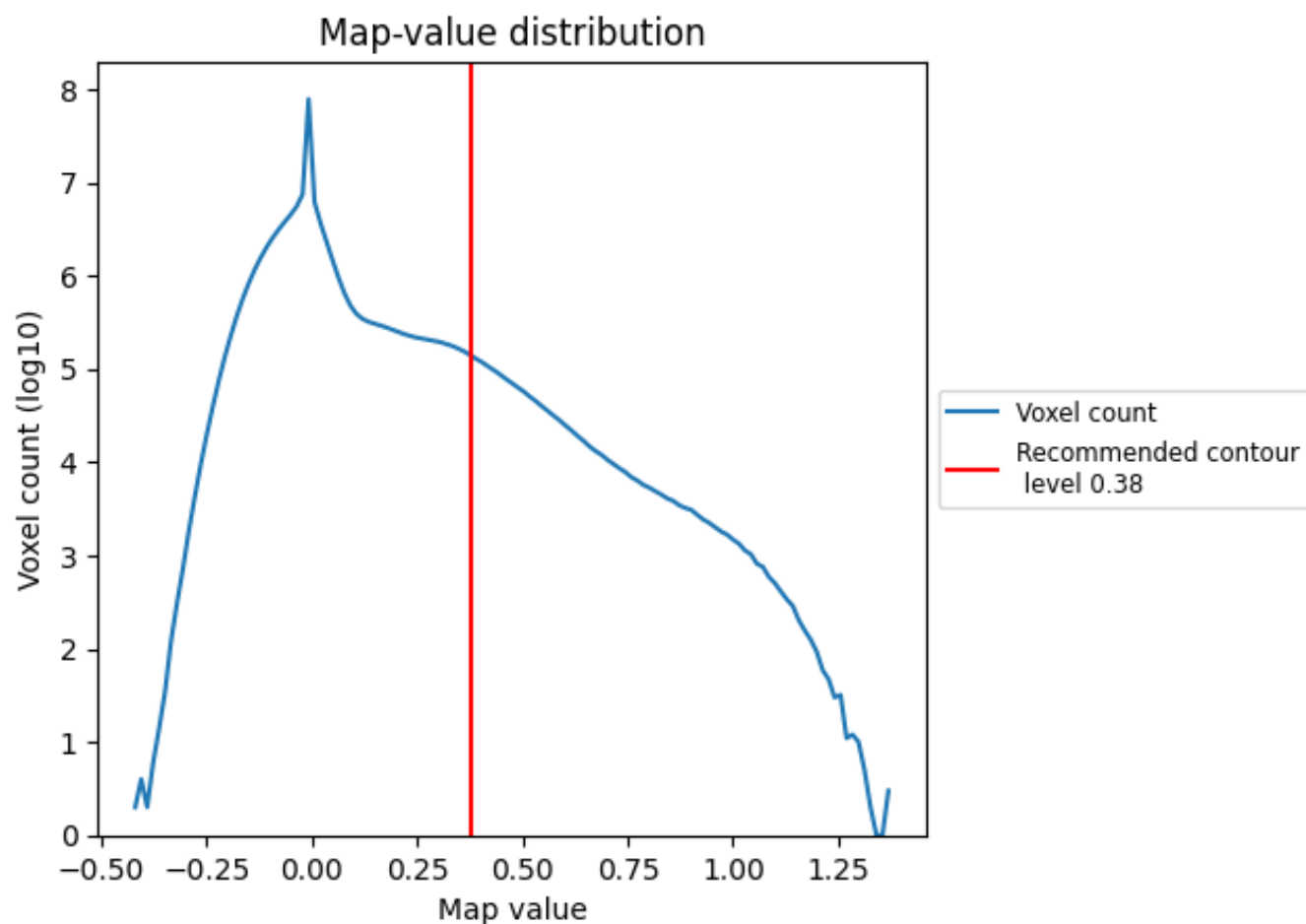
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

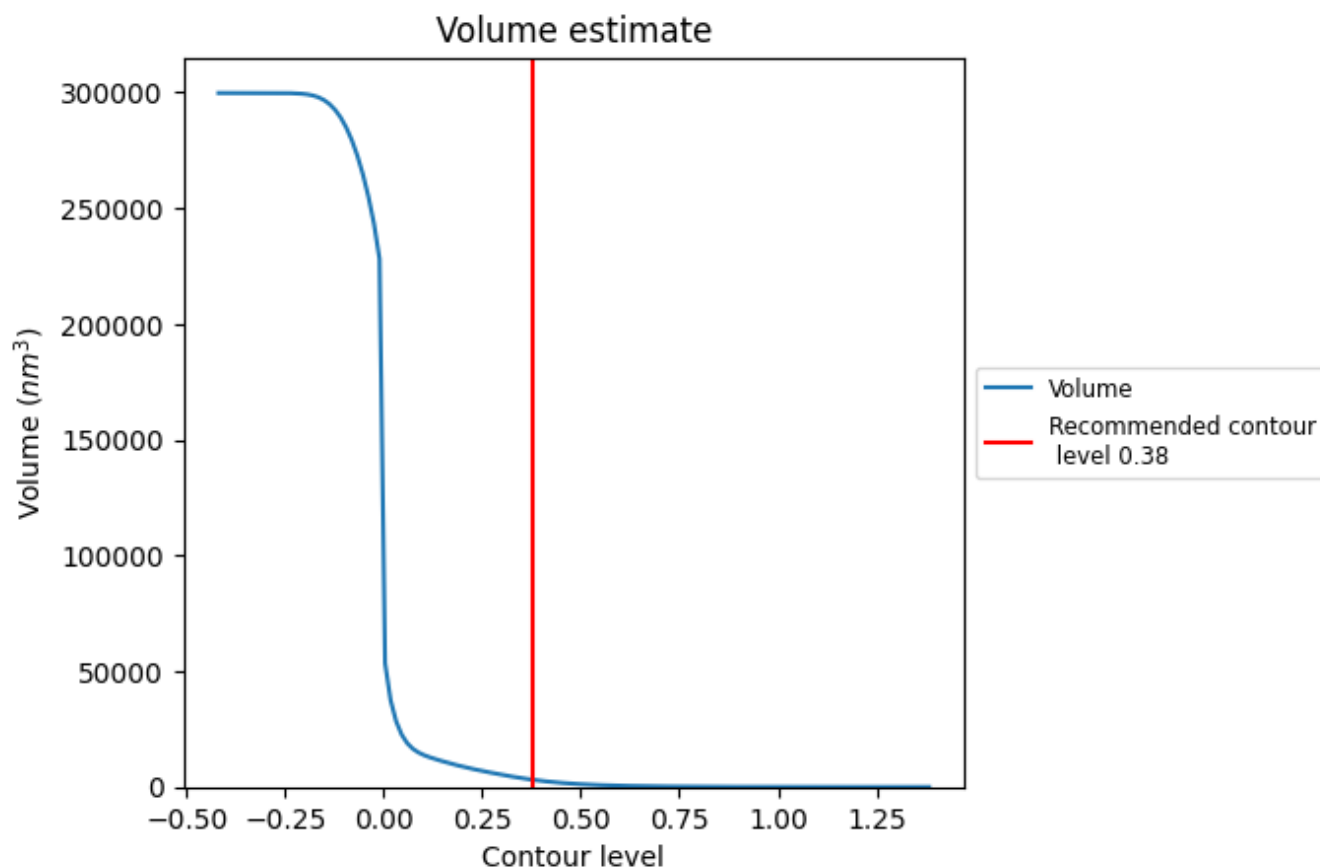
This section contains the results of statistical analysis of the map.

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.

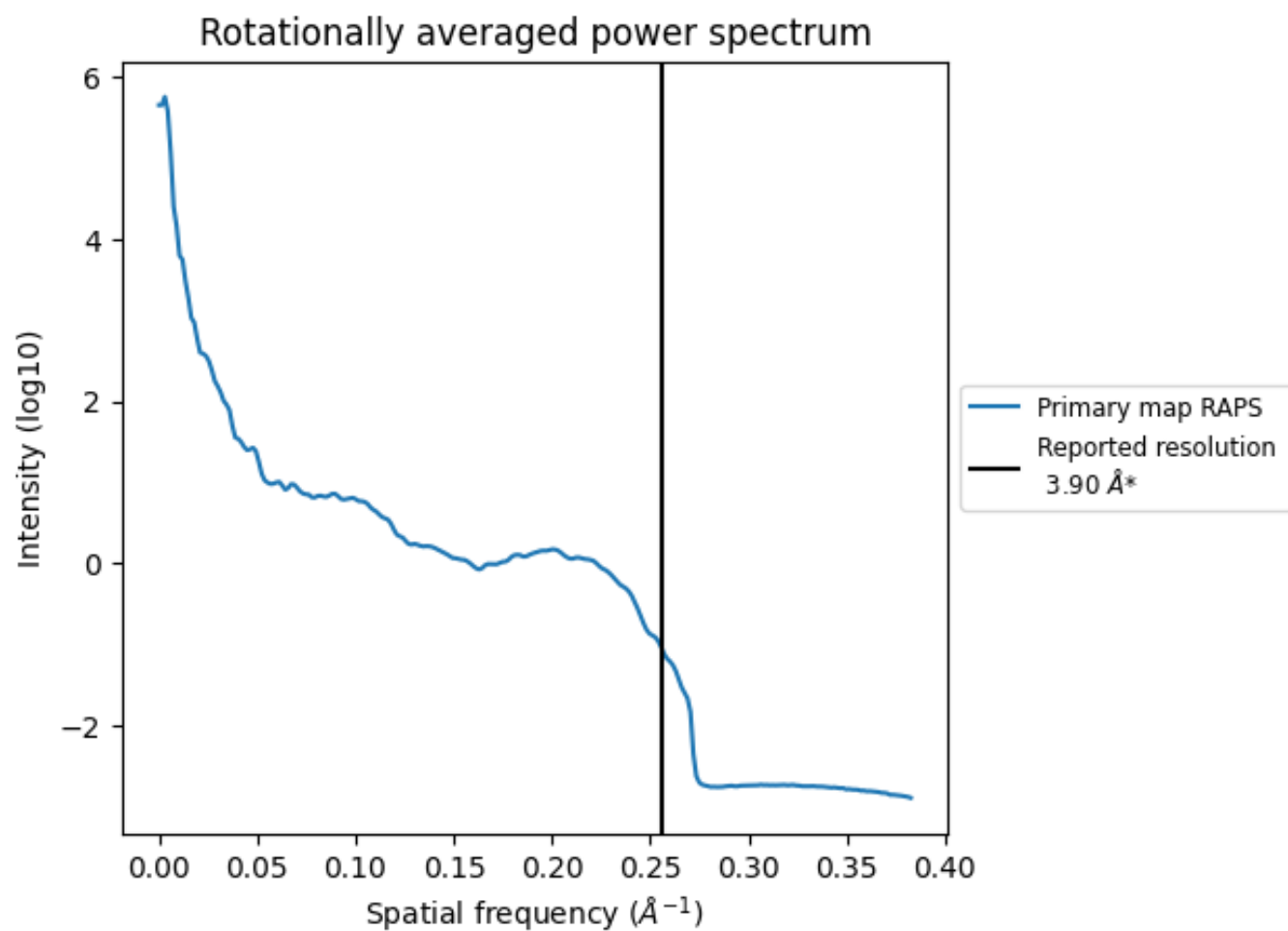
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3068 nm³; this corresponds to an approximate mass of 2771 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 0.256 Å⁻¹

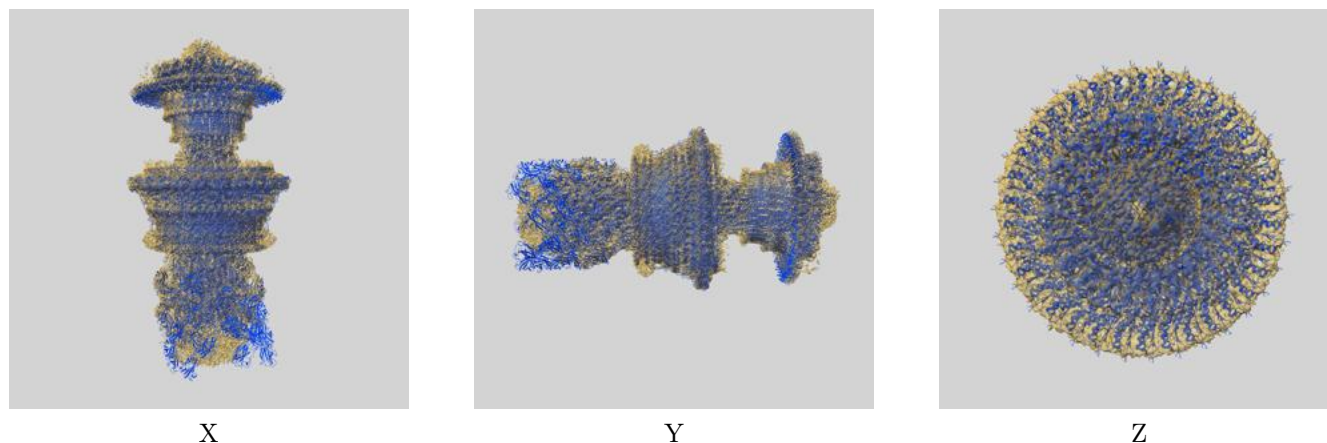
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

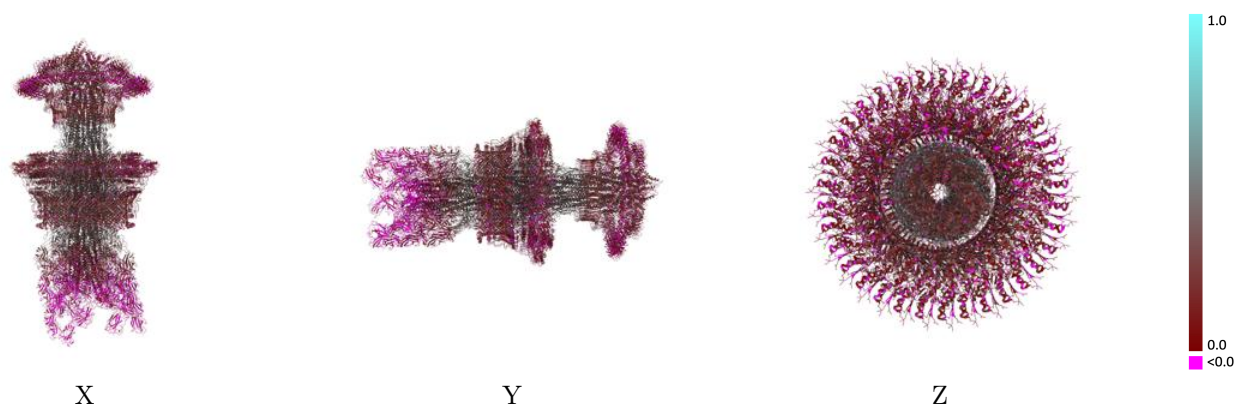
This section contains information regarding the fit between EMDB map EMD-30359 and PDB model 7CGO. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



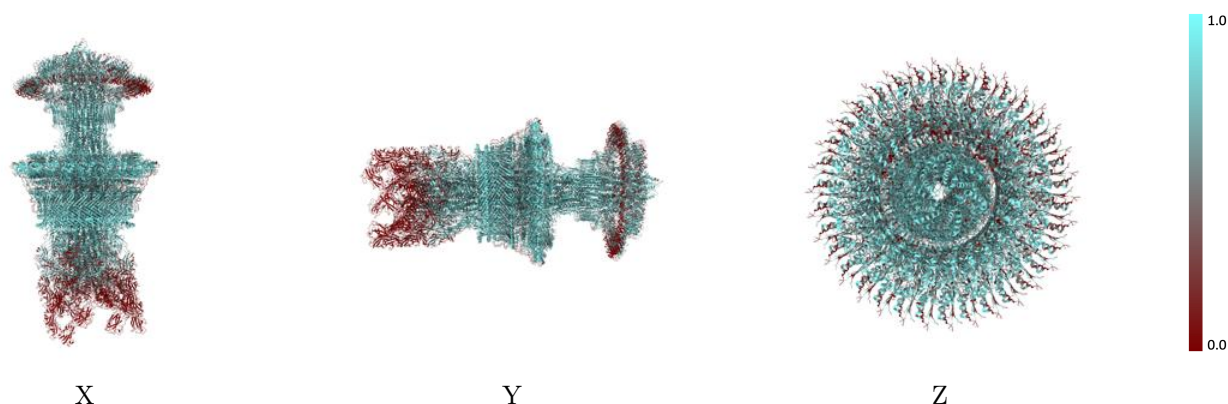
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



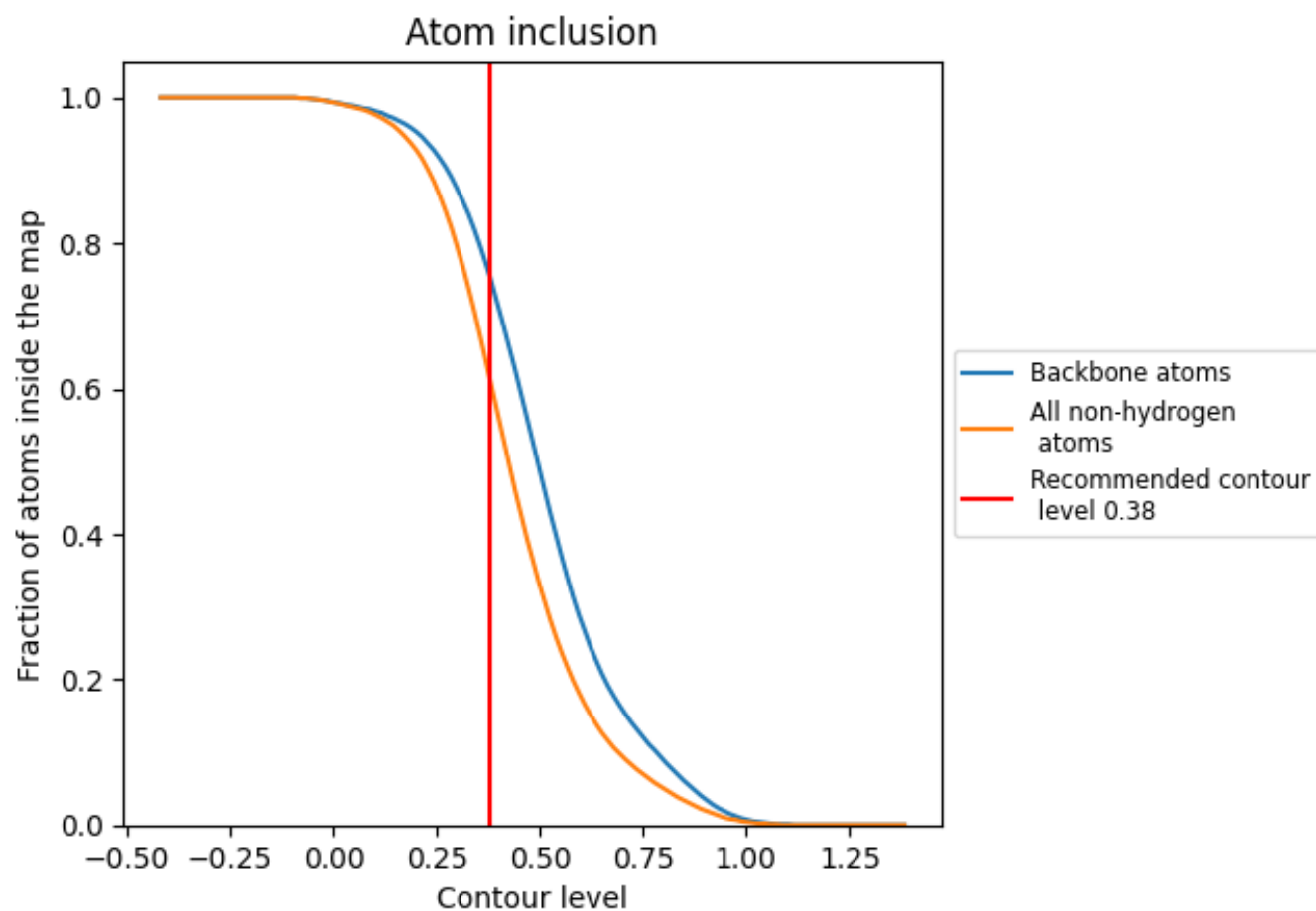
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.38).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 61% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6110	 0.2210
0	 0.8930	 0.4500
1	 0.9070	 0.4270
2	 0.9470	 0.4930
3	 0.8800	 0.4400
4	 0.9070	 0.4600
5	 0.8500	 0.4640
6	 0.6710	 0.4240
7	 0.8430	 0.4520
8	 0.8360	 0.4430
9	 0.7790	 0.4420
A	 0.8060	 0.4250
AA	 0.7250	 0.2400
AB	 0.7370	 0.2460
AC	 0.7250	 0.2380
AD	 0.7050	 0.2210
AE	 0.7160	 0.2310
AF	 0.7060	 0.2190
AG	 0.6930	 0.2240
AH	 0.6950	 0.2120
AI	 0.6800	 0.1990
AJ	 0.6700	 0.1870
AK	 0.6920	 0.1890
AL	 0.6770	 0.1720
AM	 0.6600	 0.1770
AN	 0.6500	 0.1490
AO	 0.6650	 0.1540
AP	 0.6580	 0.1350
AQ	 0.6620	 0.1360
AR	 0.6750	 0.1550
AS	 0.6750	 0.1610
AT	 0.6690	 0.1560
AU	 0.6770	 0.1750
AV	 0.7060	 0.2050
AW	 0.7130	 0.2040



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Chain	Atom inclusion	Q-score
AX	 0.7150	 0.2290
AY	 0.7160	 0.2250
AZ	 0.7220	 0.2230
B	 0.7740	 0.4090
BA	 0.7860	 0.2310
BB	 0.7710	 0.2260
BC	 0.7680	 0.2300
BD	 0.7700	 0.2210
BE	 0.7750	 0.2290
BF	 0.7640	 0.2150
BG	 0.7690	 0.2040
BH	 0.7640	 0.1980
BI	 0.7720	 0.1930
BJ	 0.7580	 0.1830
BK	 0.7580	 0.1780
BL	 0.7350	 0.1660
BM	 0.7320	 0.1510
BN	 0.7410	 0.1320
BO	 0.7290	 0.1340
BP	 0.7180	 0.1220
BQ	 0.7080	 0.1270
BR	 0.7270	 0.1310
BS	 0.7380	 0.1460
BT	 0.7320	 0.1390
BU	 0.7440	 0.1520
BV	 0.7600	 0.1690
BW	 0.7740	 0.1900
BX	 0.7690	 0.2040
BY	 0.7830	 0.2250
BZ	 0.7850	 0.2240
C	 0.8110	 0.4230
CA	 0.7230	 0.2260
CB	 0.7290	 0.2420
CC	 0.6840	 0.2410
CD	 0.6140	 0.2210
CE	 0.6420	 0.2360
CF	 0.7260	 0.2860
Ca	 0.5340	 0.1090
Cb	 0.5340	 0.1260
Cc	 0.5090	 0.1180
Cd	 0.4790	 0.1030
Ce	 0.5060	 0.1160

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Chain	Atom inclusion	Q-score
Cf	0.5020	0.1070
Cg	0.4830	0.0970
Ch	0.4930	0.1200
Ci	0.4830	0.1190
Cj	0.4800	0.1320
Ck	0.4660	0.1320
Cl	0.4920	0.1390
Cm	0.4740	0.1490
Cn	0.4560	0.1390
Co	0.4720	0.1570
Cp	0.4670	0.1430
Cq	0.4660	0.1300
Cr	0.4710	0.1280
Cs	0.5010	0.1350
Ct	0.5300	0.1630
Cu	0.5200	0.1290
Cv	0.5220	0.1370
Cw	0.5250	0.1430
Cx	0.5220	0.1370
Cy	0.5470	0.1620
Cz	0.5420	0.1400
D	0.8060	0.4220
DA	0.5190	0.3360
DB	0.6960	0.3470
DC	0.6990	0.3310
DD	0.6760	0.3100
DE	0.6800	0.3230
DF	0.6560	0.3150
DG	0.6630	0.3140
DH	0.6610	0.3080
DI	0.6180	0.2800
DJ	0.5790	0.2670
DK	0.5320	0.2560
DL	0.4750	0.1410
DM	0.4900	0.1570
DN	0.4540	0.1470
DO	0.4430	0.1660
DP	0.3490	0.0950
DQ	0.3590	0.1350
DR	0.3420	0.0940
DS	0.3010	0.0620
DT	0.3400	0.1240

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Chain	Atom inclusion	Q-score
DU	 0.2570	 0.0660
DV	 0.2390	 0.0520
DW	 0.2520	 0.0960
DX	 0.2110	 0.0180
DY	 0.2050	 0.0410
DZ	 0.1940	 0.0600
Da	 0.7030	 0.2190
Db	 0.6490	 0.1990
Dc	 0.6540	 0.1900
Dd	 0.6380	 0.1770
De	 0.6100	 0.1800
Df	 0.6060	 0.1740
Dg	 0.5560	 0.1100
Dh	 0.5060	 0.1350
Di	 0.4540	 0.1110
Dj	 0.4310	 0.1280
Dk	 0.4510	 0.1440
Di	 0.4140	 0.1010
Dm	 0.4240	 0.1170
Dn	 0.4590	 0.1250
Do	 0.5000	 0.1580
Dp	 0.5780	 0.1810
Dq	 0.6360	 0.1880
Dr	 0.6280	 0.1980
Ds	 0.6320	 0.2160
Dt	 0.6590	 0.2010
Du	 0.7020	 0.2200
Dv	 0.6770	 0.2320
Dw	 0.6570	 0.2050
E	 0.8200	 0.4270
EA	 0.1370	 0.0090
EB	 0.1620	 0.0480
EC	 0.1270	 0.0050
ED	 0.1040	 -0.0140
EE	 0.1200	 0.0400
EF	 0.0810	 0.0100
EG	 0.0760	 0.0240
Ea	 0.5680	 0.1500
Eb	 0.5590	 0.1460
Ec	 0.5710	 0.1320
Ed	 0.5820	 0.1580
Ee	 0.5950	 0.1340

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Chain	Atom inclusion	Q-score
Ef	 0.5800	 0.1450
Eg	 0.5330	 0.1300
Eh	 0.5560	 0.1230
F	 0.8110	 0.4240
G	 0.8110	 0.4290
GA	 0.6360	 0.2900
GB	 0.6400	 0.2500
GC	 0.4730	 0.2790
GD	 0.7200	 0.3160
GE	 0.6670	 0.2860
GF	 0.5330	 0.2750
GG	 0.4330	 0.3040
GH	 0.2220	 0.2370
GI	 0.1330	 0.1770
GJ	 0.4000	 0.2520
GK	 0.3330	 0.2420
H	 0.8130	 0.4320
I	 0.8190	 0.4330
J	 0.8120	 0.4360
K	 0.8040	 0.4360
L	 0.8070	 0.4340
M	 0.8140	 0.4340
N	 0.7950	 0.4370
O	 0.8110	 0.4320
P	 0.8100	 0.4310
Q	 0.8120	 0.4300
R	 0.8060	 0.4290
S	 0.8120	 0.4270
T	 0.8140	 0.4330
U	 0.8240	 0.4380
V	 0.8180	 0.4300
W	 0.8200	 0.4360
X	 0.8070	 0.4230
a	 0.8490	 0.4350
b	 0.8160	 0.4130
c	 0.8470	 0.4370
d	 0.8320	 0.4260
e	 0.8100	 0.4220
f	 0.8210	 0.4150
g	 0.8060	 0.3760
h	 0.8240	 0.4170
i	 0.8280	 0.4180

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Chain	Atom inclusion	Q-score
j	 0.8070	 0.4120
k	 0.8160	 0.3950
l	 0.7790	 0.3840
m	 0.8260	 0.4000
n	 0.8150	 0.3870
o	 0.7960	 0.3830
p	 0.8000	 0.3950
q	 0.7720	 0.3570
r	 0.7580	 0.3120
s	 0.7530	 0.3550
t	 0.7810	 0.3660
u	 0.7550	 0.3500
v	 0.6850	 0.3130
w	 0.7330	 0.3110
x	 0.6670	 0.2840
y	 0.7330	 0.3080
z	 0.7340	 0.3040