



## wwPDB EM Validation Summary Report ⓘ

Oct 13, 2024 – 05:33 pm BST

PDB ID : 7NVG  
EMDB ID : EMD-12603  
Title : Salmonella flagellar basal body refined in C1 map  
Authors : Johnson, S.; Furlong, E.; Lea, S.M.  
Deposited on : 2021-03-15  
Resolution : 3.70 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](mailto: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>.

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

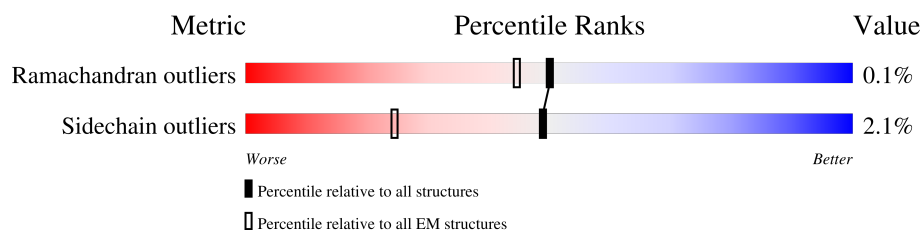
EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

# 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 3.70 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A1	560	<div> <div>12%</div> <div>27%</div> <div>73%</div> </div>
1	B1	560	<div> <div>20%</div> <div>44%</div> <div>55%</div> </div>
1	C1	560	<div> <div>16%</div> <div>44%</div> <div>55%</div> </div>
1	D1	560	<div> <div>12%</div> <div>27%</div> <div>73%</div> </div>
1	E1	560	<div> <div>18%</div> <div>44%</div> <div>55%</div> </div>
1	F1	560	<div> <div>12%</div> <div>27%</div> <div>73%</div> </div>
1	G1	560	<div> <div>18%</div> <div>44%</div> <div>55%</div> </div>
1	H1	560	<div> <div>19%</div> <div>44%</div> <div>55%</div> </div>
1	I1	560	<div> <div>19%</div> <div>44%</div> <div>55%</div> </div>

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Mol	Chain	Length	Quality of chain
1	J1	560	
1	K1	560	
1	L1	560	
1	M1	560	
1	N1	560	
1	O1	560	
1	P1	560	
1	Q1	560	
1	R1	560	
1	S1	560	
1	T1	560	
1	U1	560	
1	V1	560	
1	W1	560	
1	X1	560	
1	Y1	560	
1	Z1	560	
1	a1	560	
1	b1	560	
1	c1	560	
1	d1	560	
1	e1	560	
1	f1	560	
1	g1	560	
1	h1	560	

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Mol	Chain	Length	Quality of chain
2	A2	245	
2	B2	245	
2	C2	245	
2	D2	245	
2	E2	245	
3	F2	264	
4	G2	89	
4	H2	89	
4	I2	89	
4	J2	89	
5	K2	104	
5	L2	104	
5	M2	104	
5	N2	104	
5	O2	104	
5	P2	104	
6	Q2	138	
6	R2	138	
6	S2	138	
6	T2	138	
6	U2	138	
7	V2	134	
7	W2	134	
7	X2	134	
7	Y2	134	

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Mol	Chain	Length	Quality of chain
7	Z2	134	
7	a2	134	
8	b2	251	
8	c2	251	
8	d2	251	
8	e2	251	
8	f2	251	
9	12	260	
9	22	260	
9	32	260	
9	42	260	
9	g2	260	
9	h2	260	
9	i2	260	
9	j2	260	
9	k2	260	
9	l2	260	
9	m2	260	
9	n2	260	
9	o2	260	
9	p2	260	
9	q2	260	
9	r2	260	
9	s2	260	
9	t2	260	

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Mol	Chain	Length	Quality of chain
9	u2	260	<div>7%</div> <div>100%</div>
9	v2	260	<div>6%</div> <div>100%</div>
9	w2	260	<div>5%</div> <div>100%</div>
9	x2	260	<div>9%</div> <div>100%</div>
9	y2	260	<div>19%</div> <div>100%</div>
9	z2	260	<div>27%</div> <div>99%</div>
10	A3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	B3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	C3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	D3	232	<div>86%</div> <div>88%</div> <div>9%</div>
10	E3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	F3	232	<div>84%</div> <div>88%</div> <div>9%</div>
10	G3	232	<div>86%</div> <div>88%</div> <div>9%</div>
10	H3	232	<div>86%</div> <div>88%</div> <div>9%</div>
10	I3	232	<div>87%</div> <div>88%</div> <div>9%</div>
10	J3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	K3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	L3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	M3	232	<div>86%</div> <div>88%</div> <div>9%</div>
10	N3	232	<div>85%</div> <div>88%</div> <div>9%</div>
10	O3	232	<div>86%</div> <div>88%</div> <div>9%</div>
10	P3	232	<div>87%</div> <div>88%</div> <div>9%</div>
10	Q3	232	<div>88%</div> <div>88%</div> <div>9%</div>
10	R3	232	<div>86%</div> <div>88%</div> <div>9%</div>
10	S3	232	<div>88%</div> <div>88%</div> <div>9%</div>

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Mol	Chain	Length	Quality of chain
10	T3	232	87% 88% 9%
10	U3	232	87% 88% 9%
10	V3	232	87% 88% 9%
10	W3	232	86% 88% 9%
10	X3	232	88% 88% 9%
10	Y3	232	87% 88% 9%
10	Z3	232	84% 88% 9%
11	a3	365	83% 80% 16%
11	b3	365	83% 80% 16%
11	c3	365	84% 80% 16%
11	d3	365	83% 80% 16%
11	e3	365	83% 80% 16%
11	f3	365	84% 80% 16%
11	g3	365	83% 80% 16%
11	h3	365	84% 80% 16%
11	i3	365	83% 80% 16%
11	j3	365	84% 80% 16%
11	k3	365	84% 80% 16%
11	l3	365	84% 80% 16%
11	m3	365	84% 80% 16%
11	n3	365	83% 80% 16%
11	o3	365	84% 80% 16%
11	p3	365	84% 80% 16%
11	q3	365	84% 80% 16%
11	r3	365	84% 80% 16%

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Mol	Chain	Length	Quality of chain
11	s3	365	<div>84%</div> <div>80%16%</div>
11	t3	365	<div>84%</div> <div>80%16%</div>
11	u3	365	<div>84%</div> <div>80%16%</div>
11	v3	365	<div>84%</div> <div>80%16%</div>
11	w3	365	<div>84%</div> <div>80%16%</div>
11	x3	365	<div>84%</div> <div>80%16%</div>
11	y3	365	<div>84%</div> <div>80%16%</div>
11	z3	365	<div>83%</div> <div>80%16%</div>
12	A4	232	<div>76%</div> <div>86%13%</div>
12	B4	232	<div>76%</div> <div>88%12%</div>
12	C4	232	<div>79%</div> <div>86%14%</div>
12	D4	232	<div>79%</div> <div>87%13%</div>
12	E4	232	<div>79%</div> <div>88%12%</div>



## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 246311 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	B1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	C1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	D1	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	E1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	F1	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	G1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	H1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	I1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	J1	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	K1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	L1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	M1	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	N1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	O1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0
1	P1	151	Total 1193	C 726	N 223	O 241	S 3	0	0
1	Q1	250	Total 1931	C 1187	N 355	O 385	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	S1	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	T1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	U1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	V1	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	W1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	X1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	Y1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	Z1	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	a1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	b1	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	c1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	d1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	e1	151	Total	C	N	O	S	0	0
			1193	726	223	241	3		
1	f1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	g1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		
1	h1	250	Total	C	N	O	S	0	0
			1931	1187	355	385	4		

- Molecule 2 is a protein called Flagellar biosynthetic protein FlIP.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
2	B2	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
2	D2	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		
2	E2	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 3 is a protein called Flagellar biosynthetic protein FliR.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F2	258	Total	C	N	O	S	0	0
			1986	1329	314	327	16		

- Molecule 4 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G2	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
4	H2	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
4	I2	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
4	J2	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

- Molecule 5 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K2	39	Total	C	N	O	S	0	0
			296	183	51	56	6		
5	L2	75	Total	C	N	O	S	0	0
			563	347	102	108	6		
5	M2	75	Total	C	N	O	S	0	0
			563	347	102	108	6		
5	N2	75	Total	C	N	O	S	0	0
			563	347	102	108	6		
5	O2	75	Total	C	N	O	S	0	0
			563	347	102	108	6		
5	P2	75	Total	C	N	O	S	0	0
			563	347	102	108	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Q2	133	Total	C	N	O	S	0	0
			1023	630	188	200	5		
6	R2	120	Total	C	N	O	S	0	0
			932	578	169	180	5		
6	S2	122	Total	C	N	O	S	0	0
			942	583	173	181	5		
6	T2	106	Total	C	N	O	S	0	0
			835	516	153	161	5		
6	U2	119	Total	C	N	O	S	0	0
			925	573	168	179	5		

- Molecule 7 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	V2	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
7	W2	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
7	X2	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
7	Y2	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
7	Z2	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
7	a2	132	Total	C	N	O	S	0	0
			964	601	166	192	5		

- Molecule 8 is a protein called Flagellar basal body protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	b2	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
8	c2	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
8	d2	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
8	e2	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
8	f2	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

- Molecule 9 is a protein called Flagellar basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	g2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	h2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	i2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	j2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	k2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	l2	249	Total 1871	C 1157	N 328	O 381	S 5	0	0
9	m2	249	Total 1871	C 1157	N 328	O 381	S 5	0	0
9	n2	249	Total 1871	C 1157	N 328	O 381	S 5	0	0
9	o2	249	Total 1871	C 1157	N 328	O 381	S 5	0	0
9	p2	249	Total 1871	C 1157	N 328	O 381	S 5	0	0
9	q2	251	Total 1885	C 1166	N 330	O 384	S 5	0	0
9	r2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	s2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	t2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	u2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	v2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	w2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	x2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	y2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	z2	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	12	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
9	22	260	Total 1949	C 1202	N 341	O 400	S 6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	32	260	Total	C	N	O	S	0	0
			1948	1202	340	400	6		
9	42	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		

- Molecule 10 is a protein called Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	B3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	C3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	D3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	E3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	F3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	G3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	H3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	I3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	J3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	K3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	L3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	M3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	N3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	O3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	P3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	Q3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	R3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	S3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	T3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	U3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	V3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	W3	211	Total	C	N	O	S	0	0
			1580	984	282	310	4		
10	X3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	Y3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		
10	Z3	211	Total	C	N	O	S	0	0
			1581	985	282	310	4		

- Molecule 11 is a protein called Flagellar P-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	b3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	c3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	d3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	e3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	f3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	g3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	h3	306	Total	C	N	O	S	0	0
			2251	1379	408	451	13		
11	i3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	j3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	k3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	l3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	m3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	n3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	o3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	p3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	q3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	r3	306	Total	C	N	O	S	0	0
			2251	1378	409	451	13		
11	s3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	t3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	u3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	v3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	w3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	x3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	y3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		
11	z3	306	Total	C	N	O	S	0	0
			2252	1379	409	451	13		

- Molecule 12 is a protein called Basal-body rod modification protein FlgD.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A4	201	Total	C	N	O	S	0	0
			1475	914	253	307	1		
12	B4	204	Total	C	N	O	S	0	0
			1493	924	256	312	1		
12	C4	199	Total	C	N	O	S	0	0
			1458	903	250	304	1		

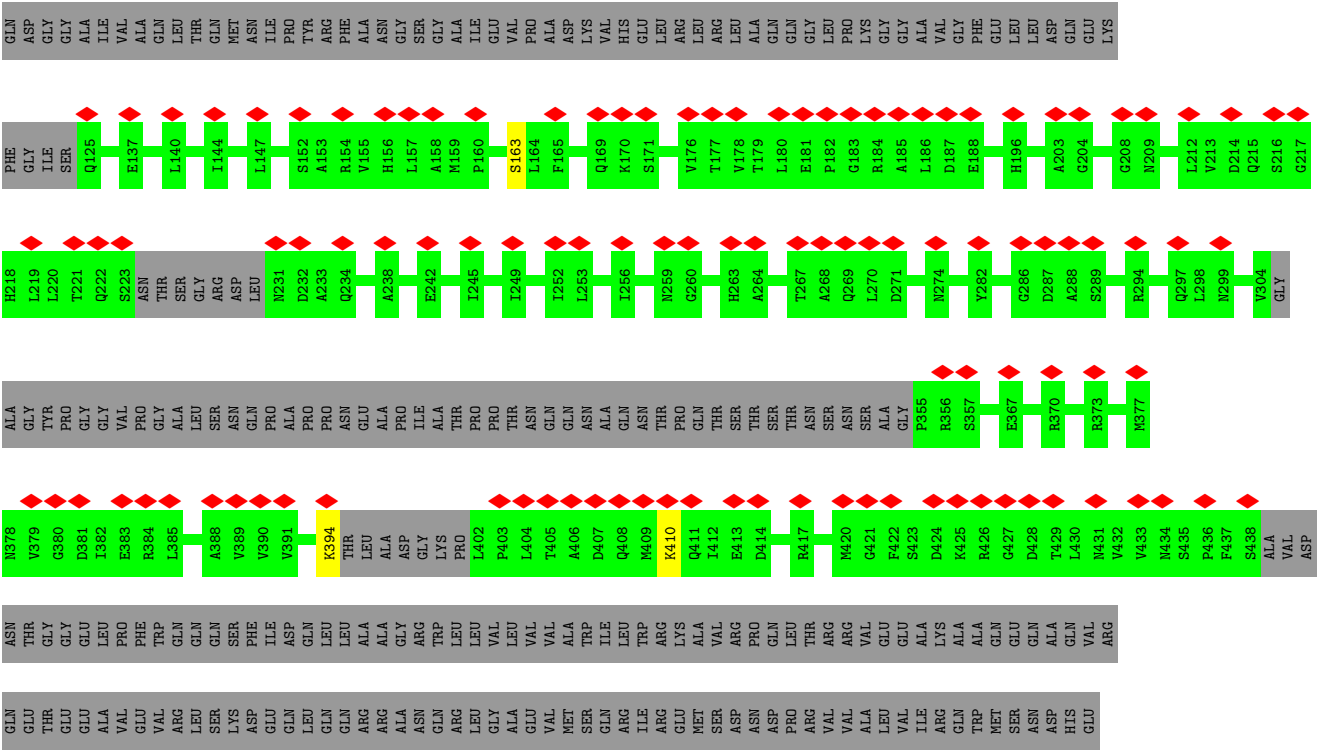
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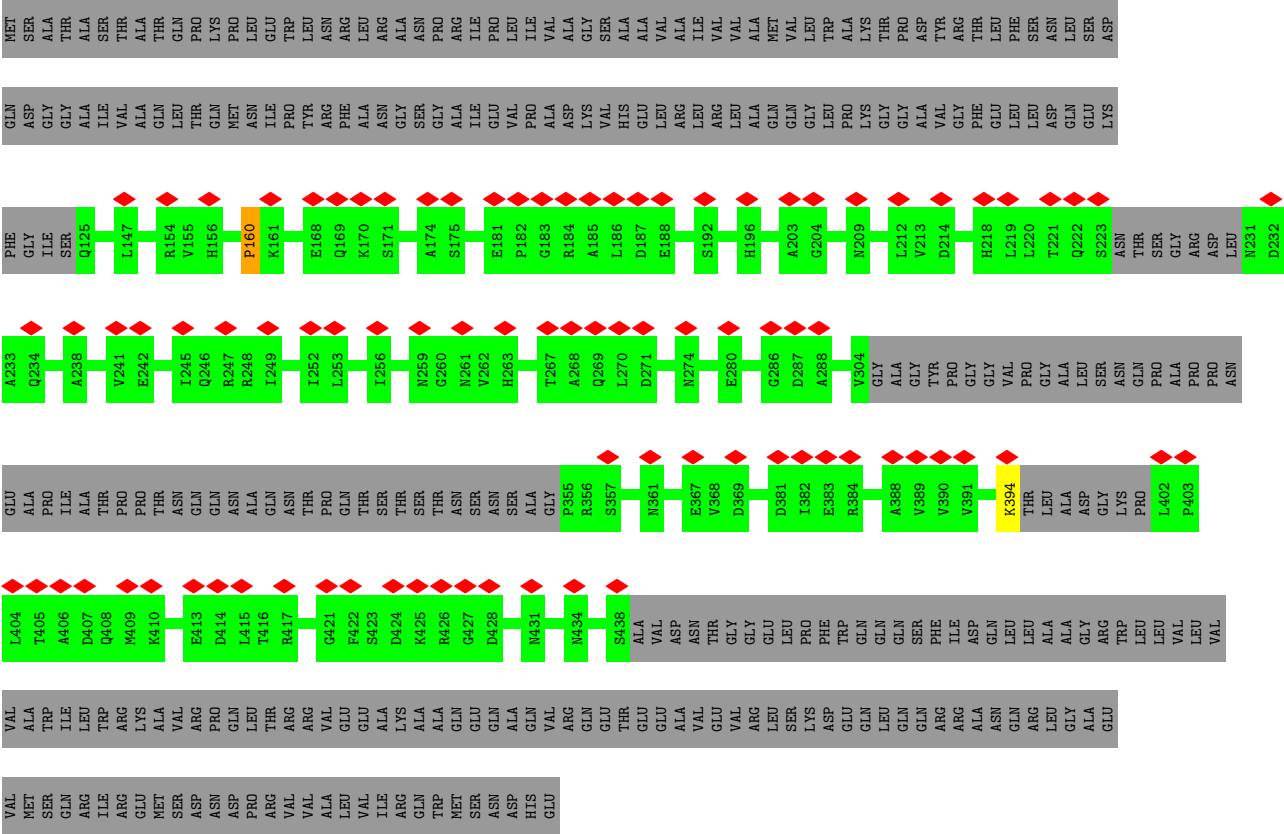
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Mol	Chain	Residues	Atoms					AltConf	Trace
12	D4	202	Total	C	N	O	S	0	0
			1482	917	254	310	1		
12	E4	204	Total	C	N	O	S	0	0
			1493	924	256	312	1		

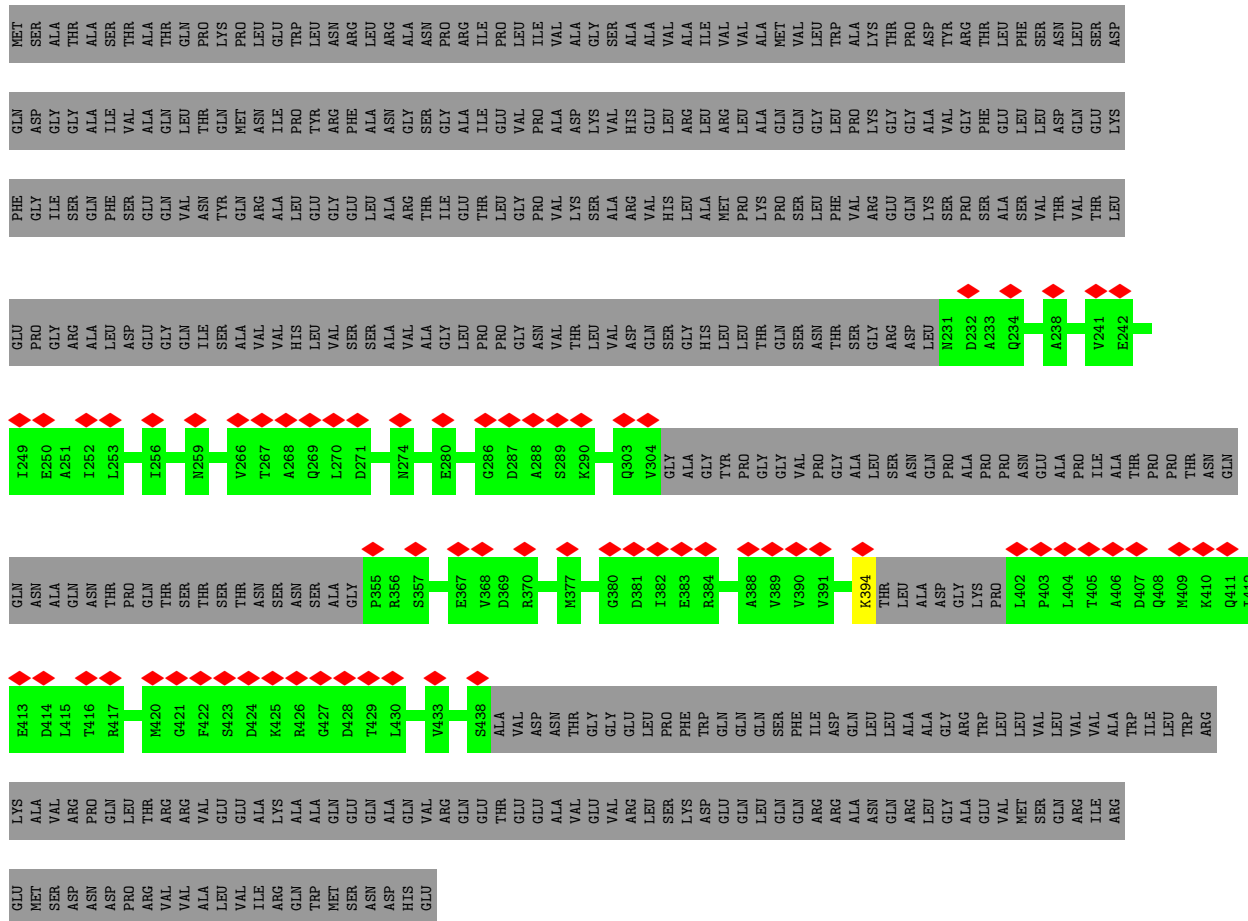




● Molecule 1: Flagellar M-ring protein



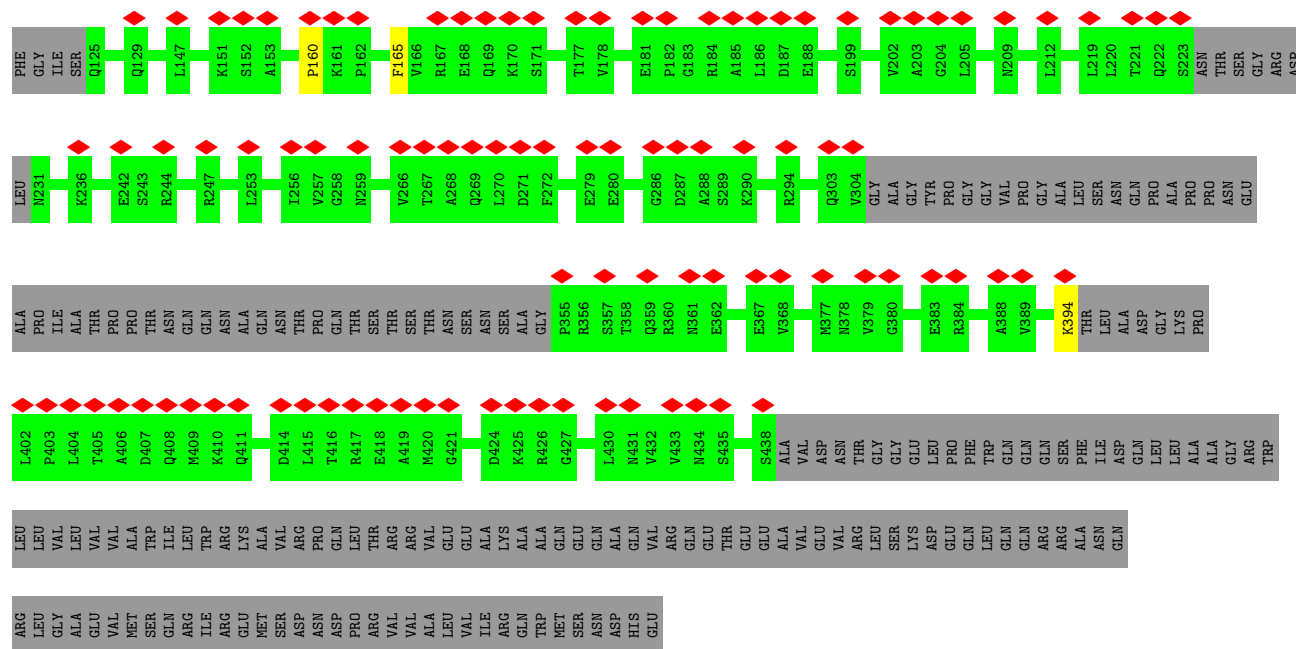
## Chain D1:



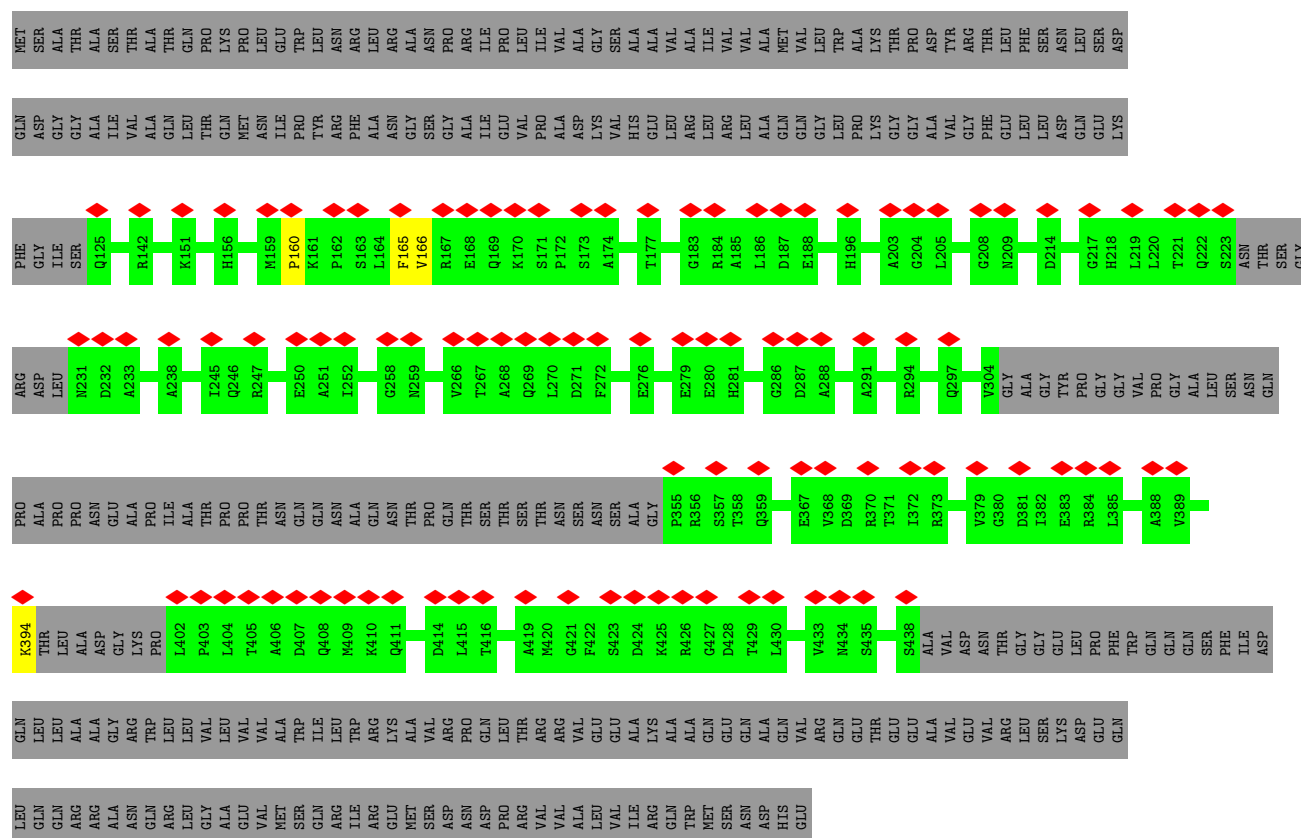
## Chain E1:







• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein

Response	Percentage
U.S. is not a democracy	19%
U.S. is a democracy	44%

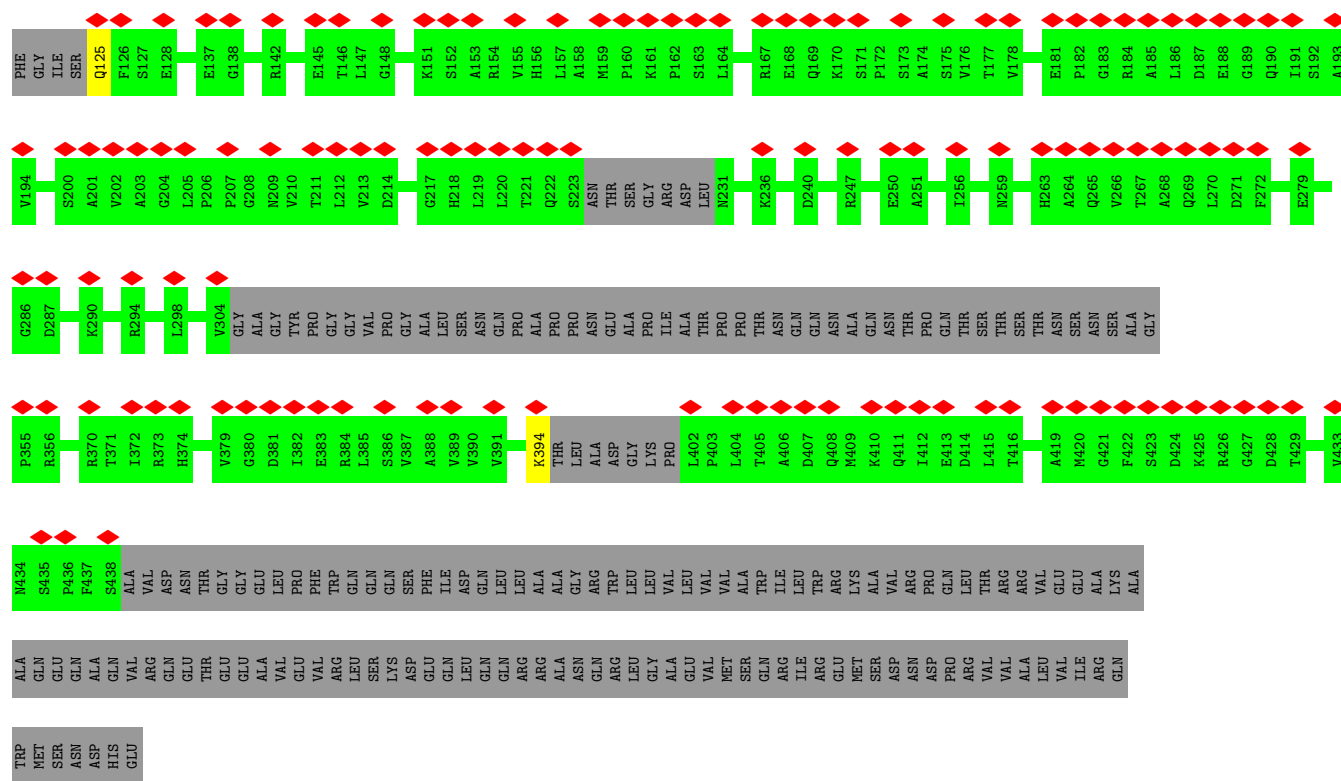


Category	Percentage
Very bad	13%
Bad	26%
Average	0%
Good	73%

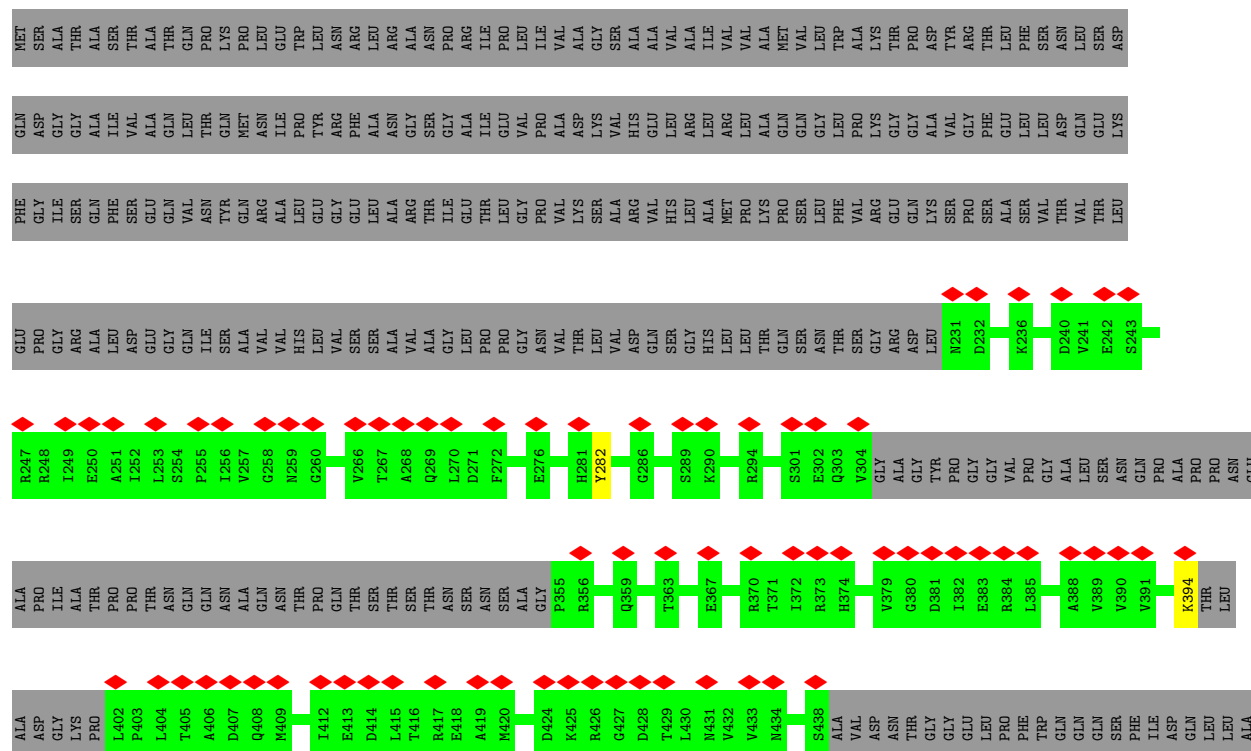


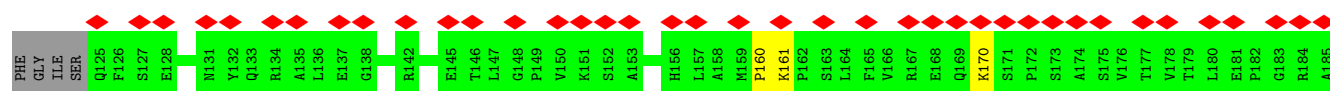


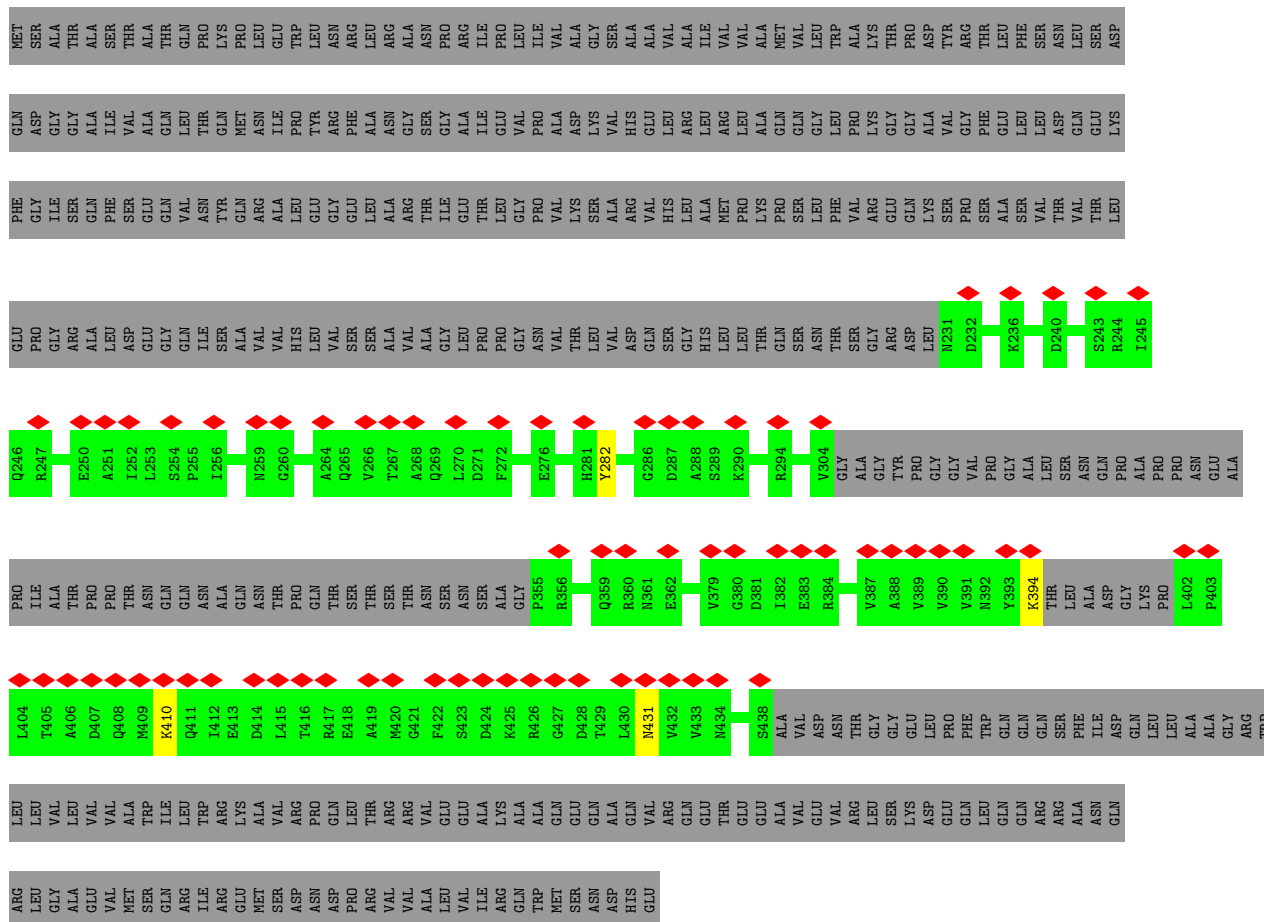




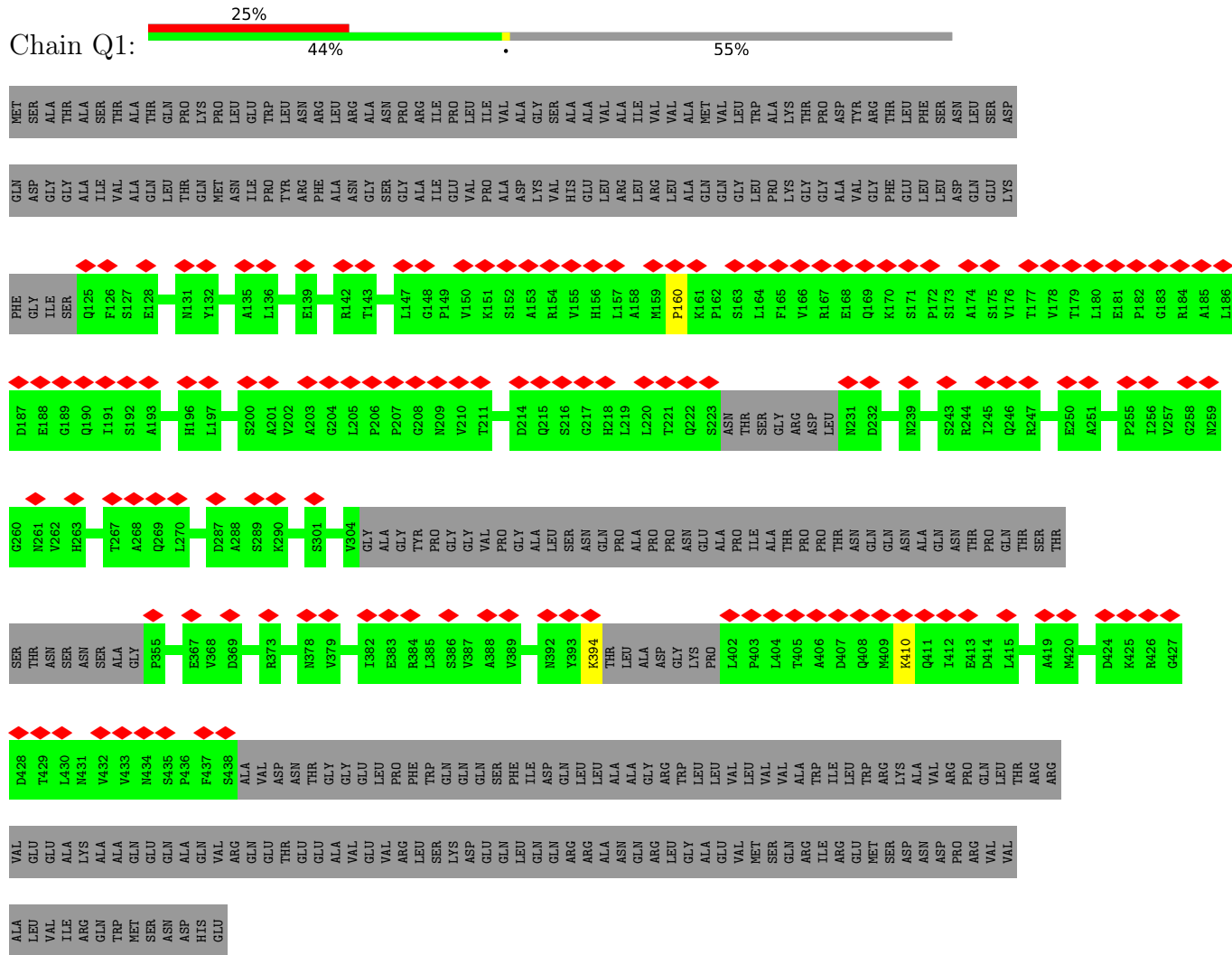
• Molecule 1: Flagellar M-ring protein



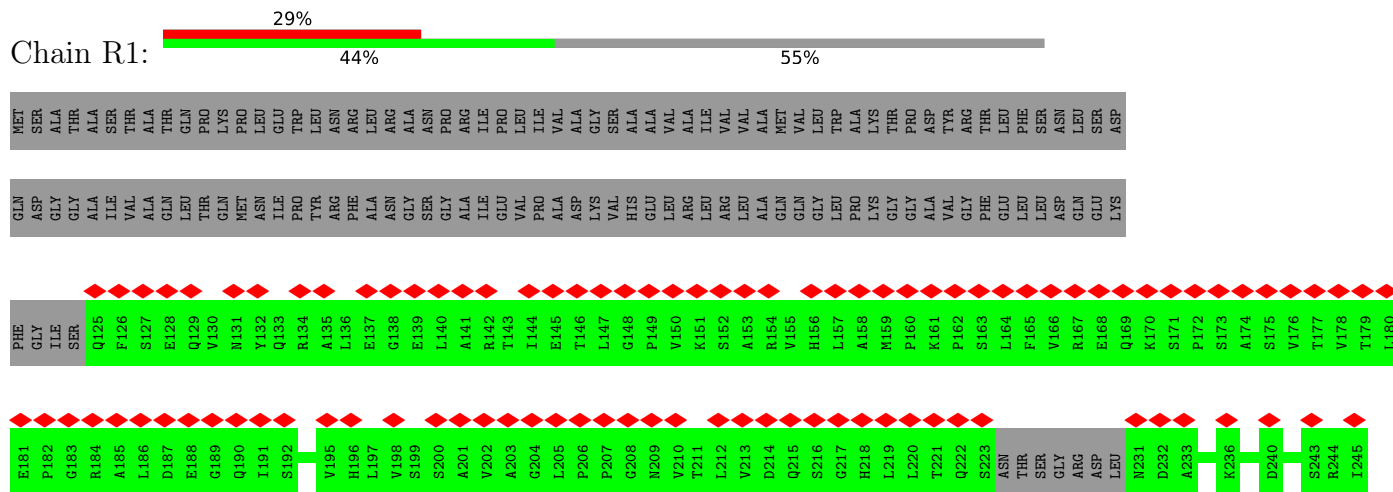




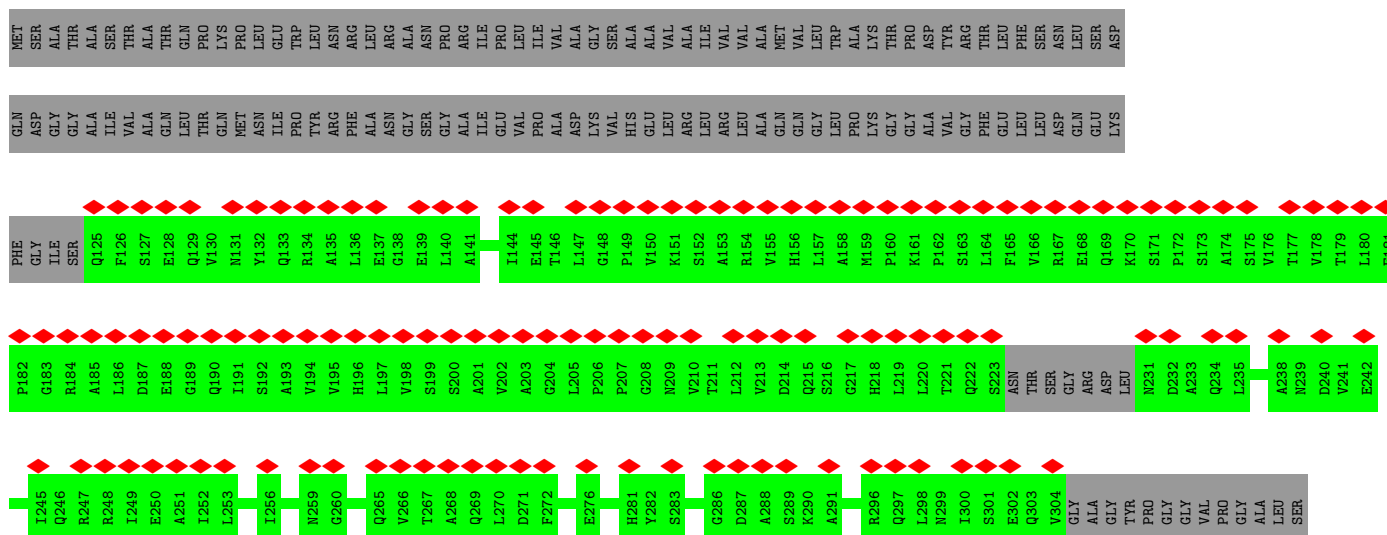
- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein









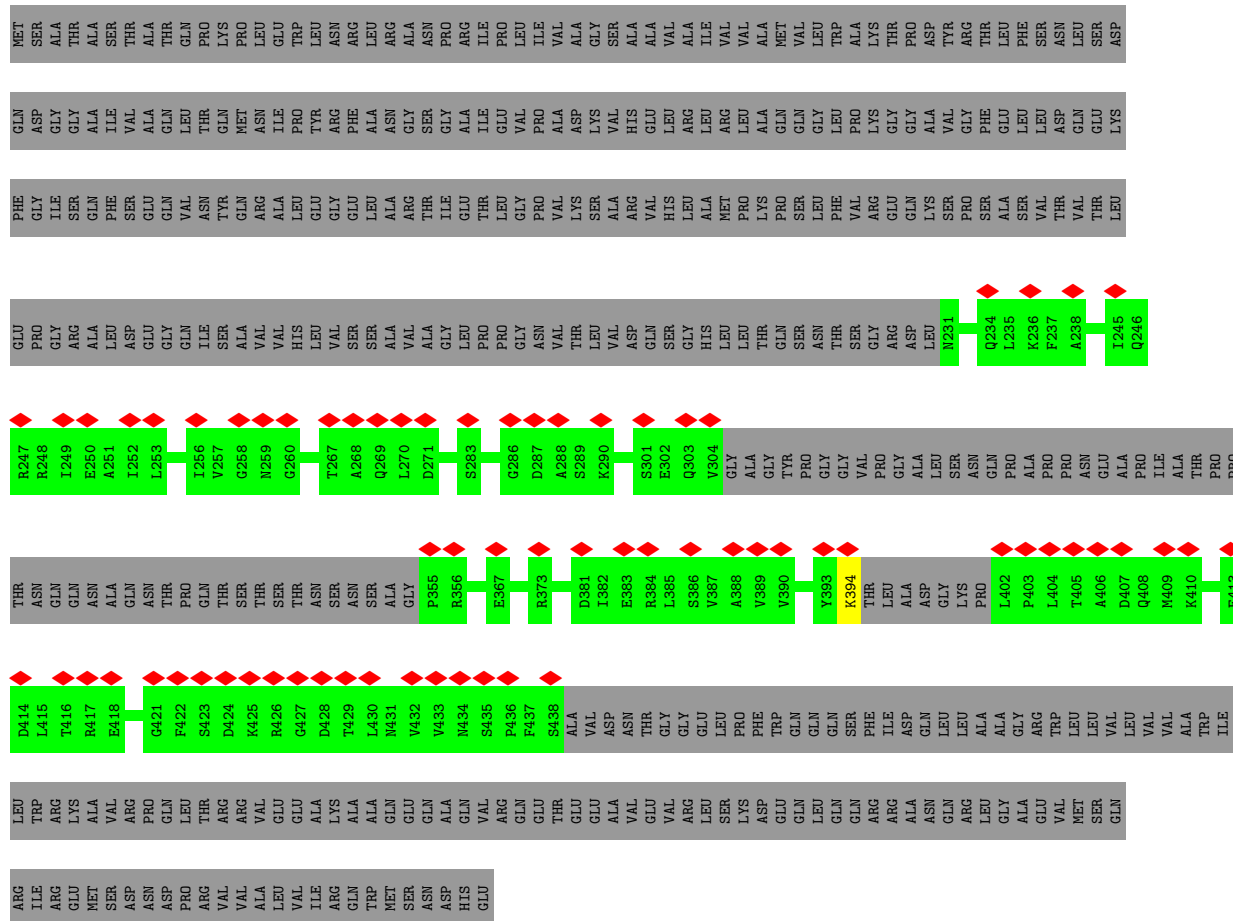




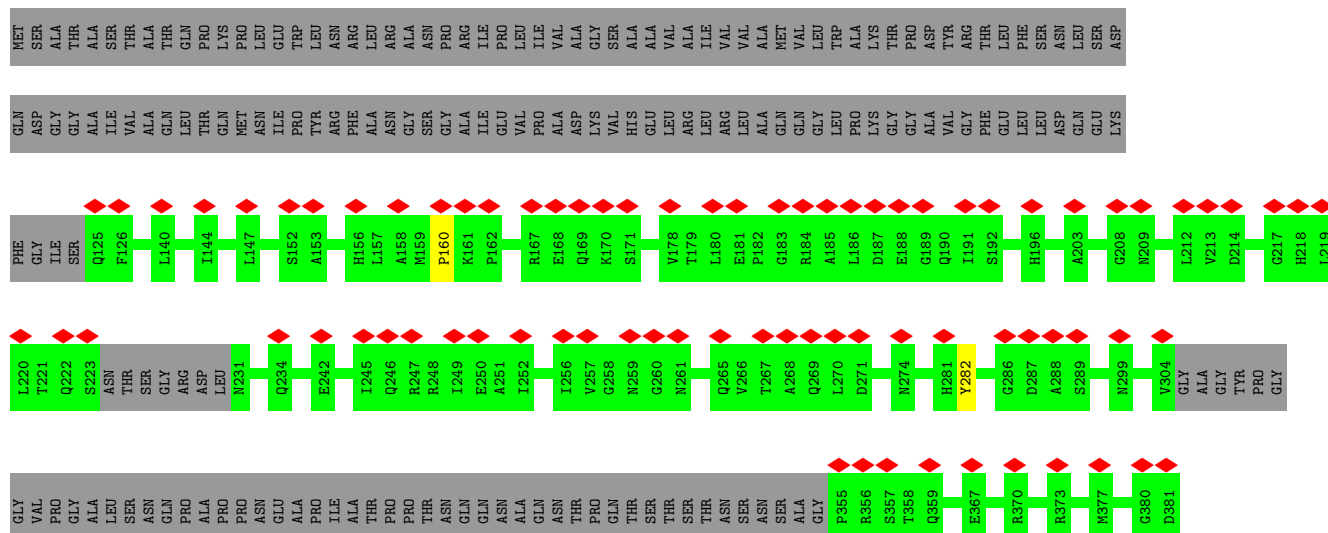
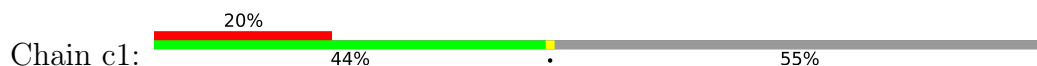




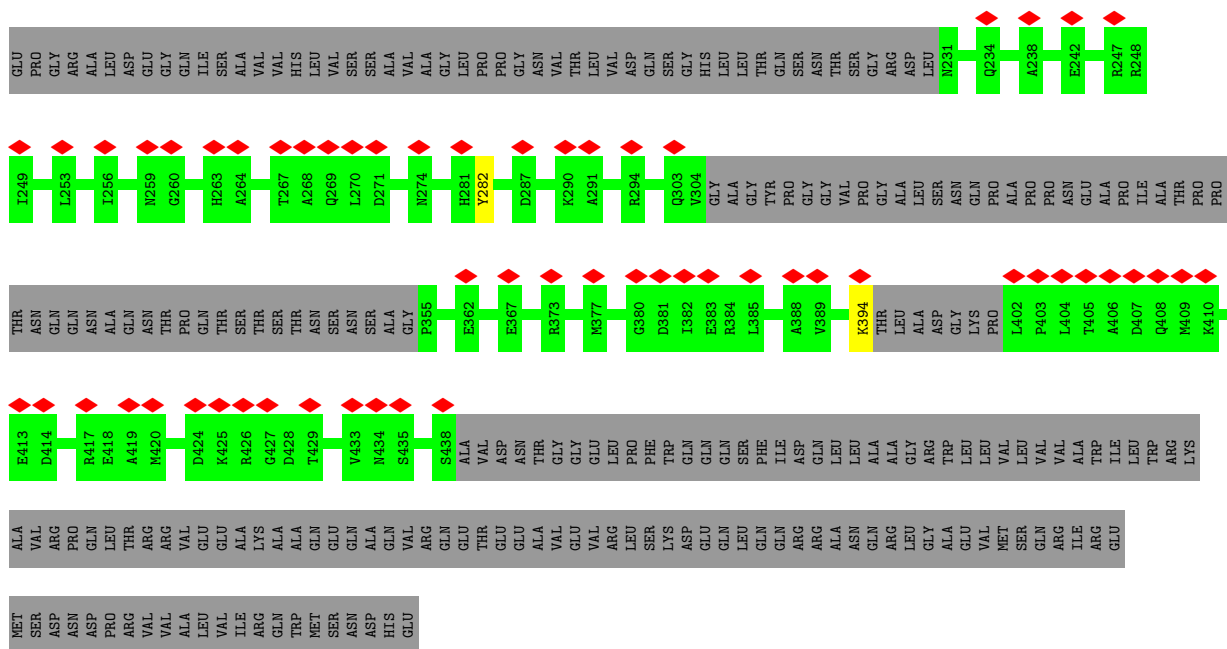
- Molecule 1: Flagellar M-ring protein



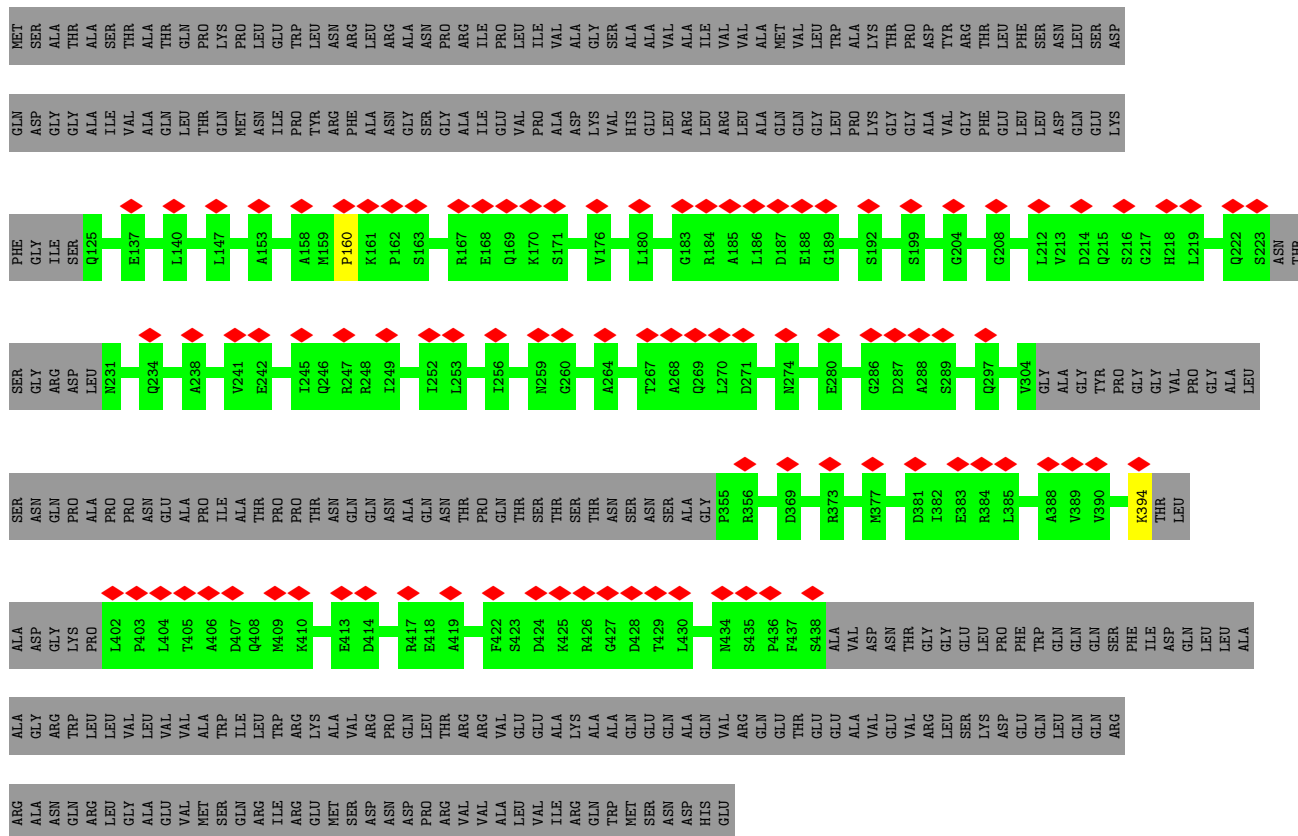
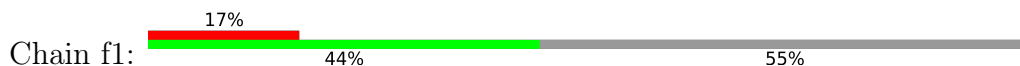
- Molecule 1: Flagellar M-ring protein



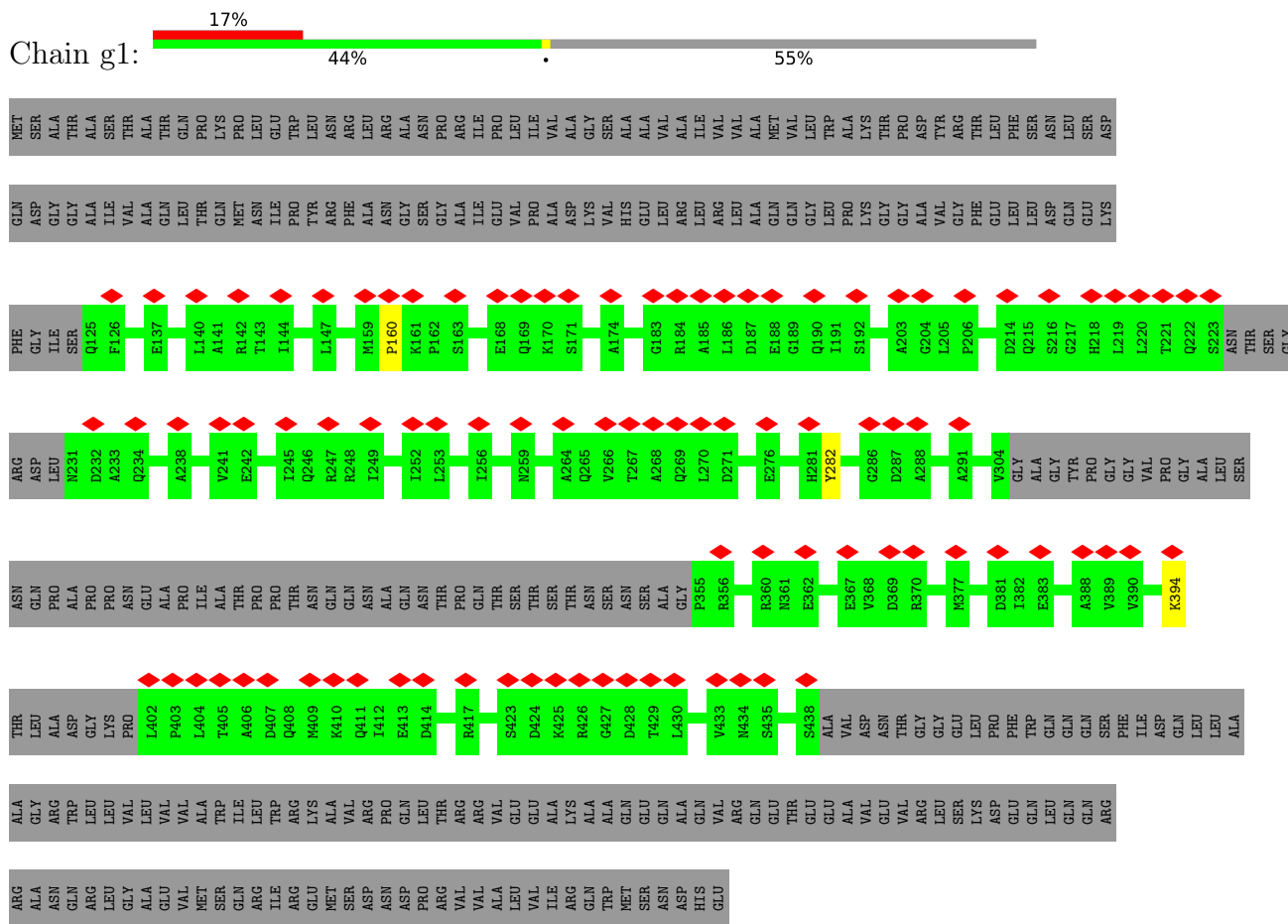




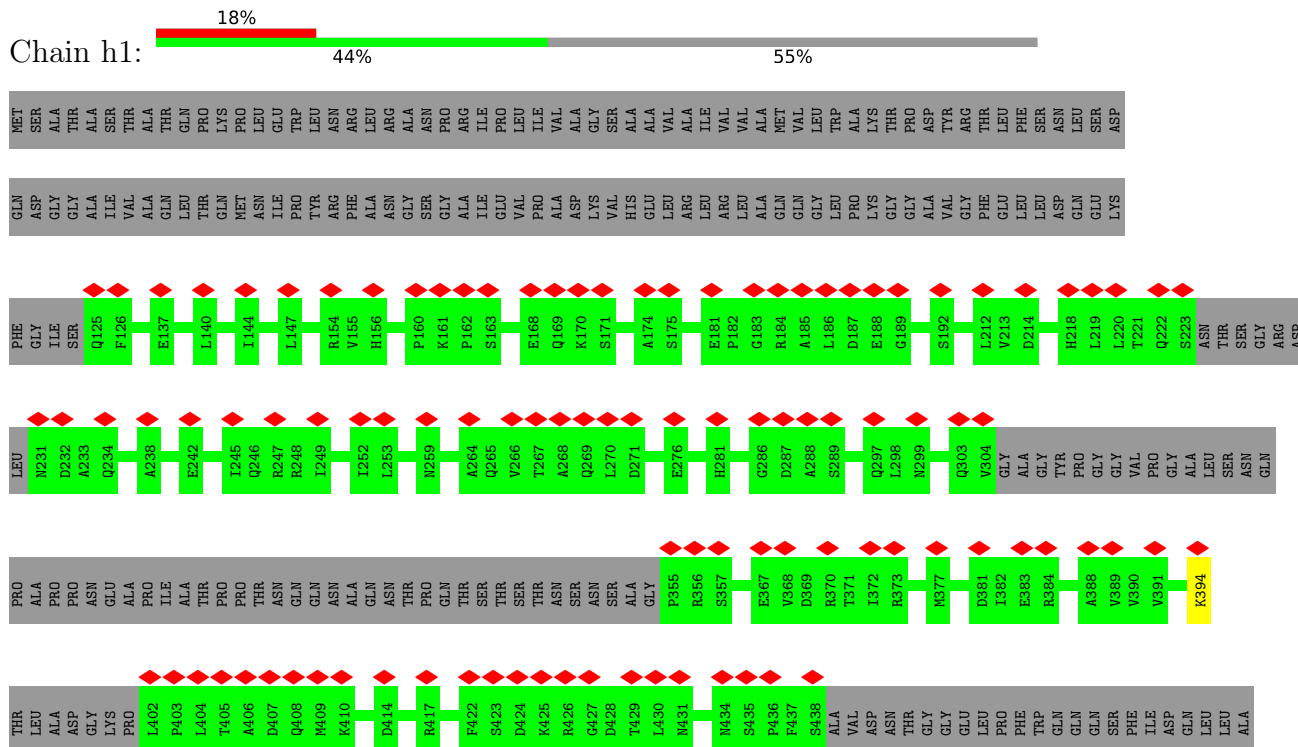
- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein

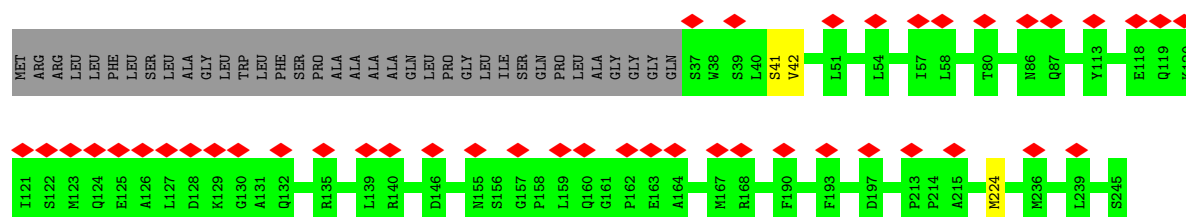
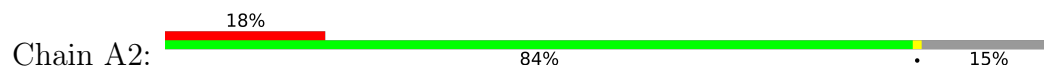


- Molecule 1: Flagellar M-ring protein

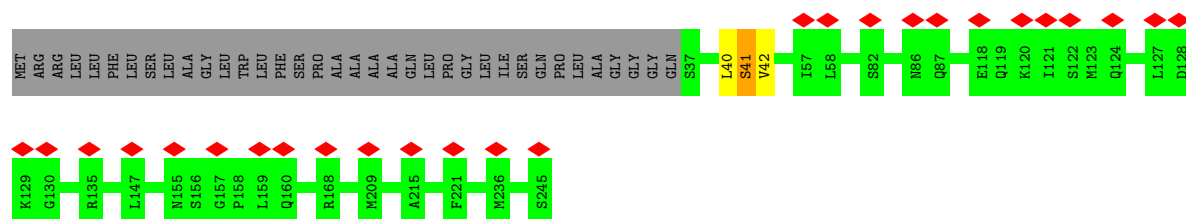
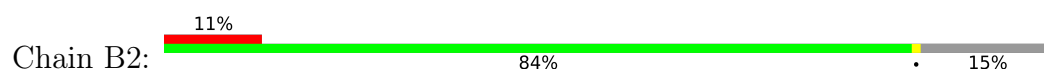


ALA	GLY	TRP	LEU	VAL	LEU	VAL	ALA	TRP	ILE	LEU	TRP	ARG	GLY	LYS	ALA	VAL	ARG	PRO	GLN	THR	ARG	VAL	LEU	GLY	ALA	LYS	ALA	GLY	GLY	GLN	ALA	GLN	VAL	ARG	GLY	TRP	LEU	GLY	GLY	GLN	ASP	HIS	GLU	
ARG	ALA	ASN	ARG	LEU	LEU	PHE	LEU	GLY	VAL	MET	SER	TRP	GLN	ARG	ILE	TRP	PRO	GLY	LYS	MET	SER	ASP	ASN	GLN	ASP	PRO	LEU	THR	ARG	VAL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

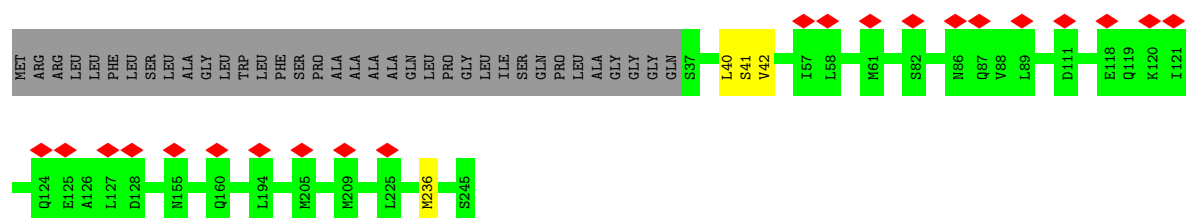
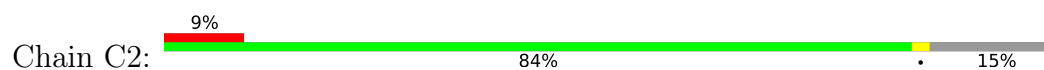
• Molecule 2: Flagellar biosynthetic protein FlhP



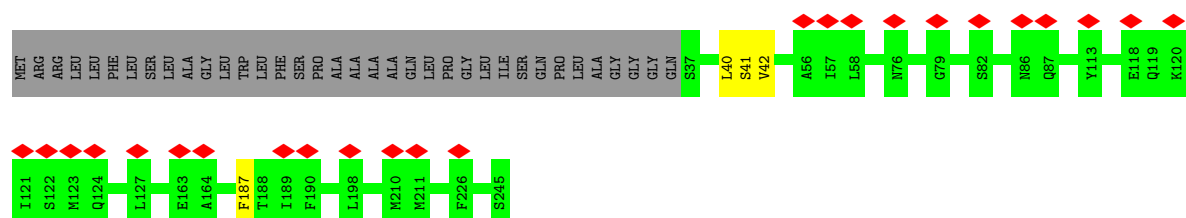
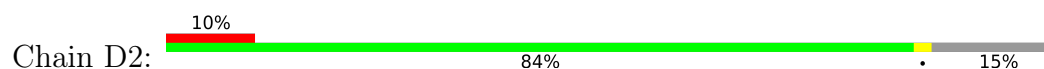
• Molecule 2: Flagellar biosynthetic protein FlhP



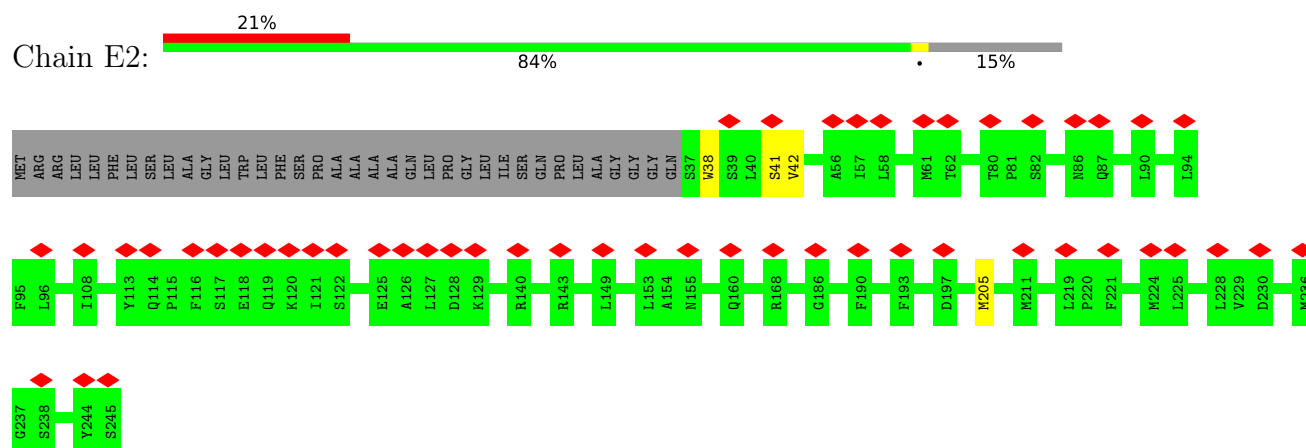
• Molecule 2: Flagellar biosynthetic protein FlhP



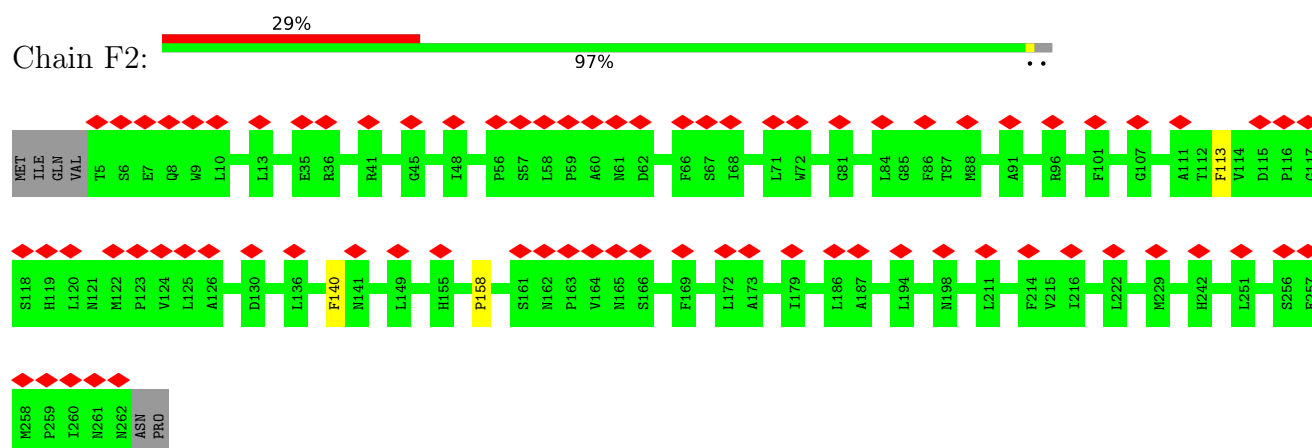
• Molecule 2: Flagellar biosynthetic protein FlhP



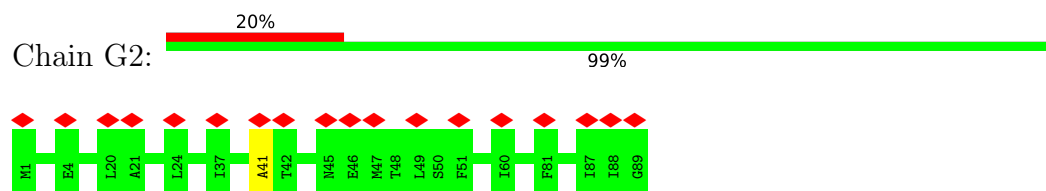
- Molecule 2: Flagellar biosynthetic protein FliP



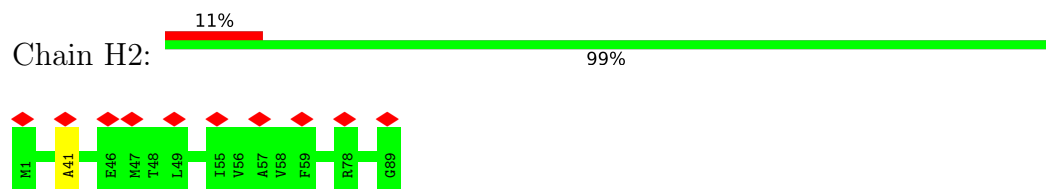
- Molecule 3: Flagellar biosynthetic protein FliR



- Molecule 4: Flagellar biosynthetic protein FliQ



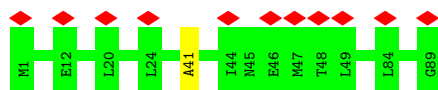
- Molecule 4: Flagellar biosynthetic protein FliQ



- Molecule 4: Flagellar biosynthetic protein FliQ



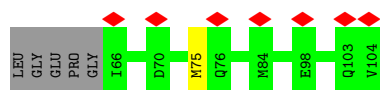
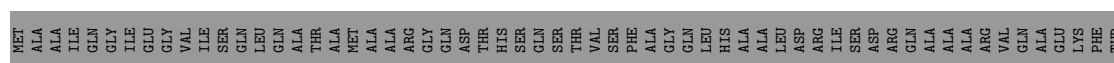




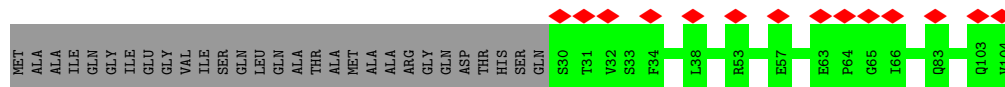
- Molecule 4: Flagellar biosynthetic protein FliQ



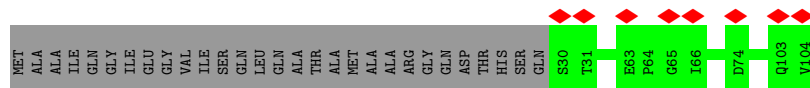
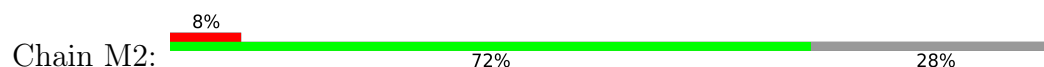
- Molecule 5: Flagellar hook-basal body complex protein FliE



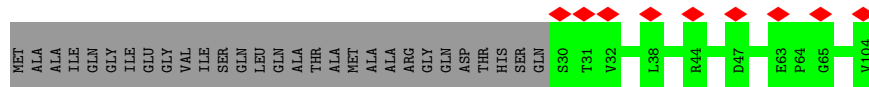
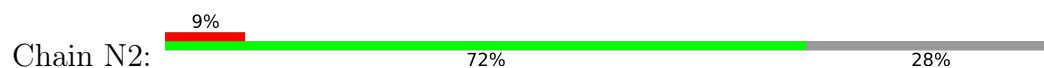
- Molecule 5: Flagellar hook-basal body complex protein FliE



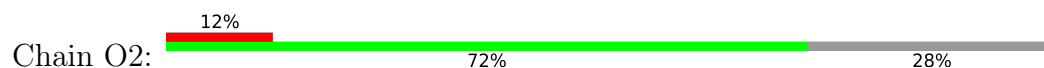
- Molecule 5: Flagellar hook-basal body complex protein FliE

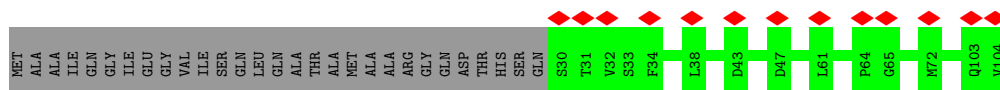


- Molecule 5: Flagellar hook-basal body complex protein FliE

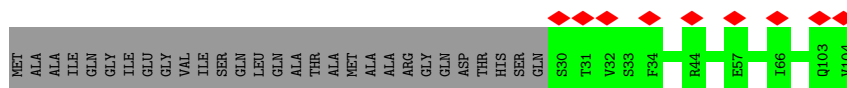
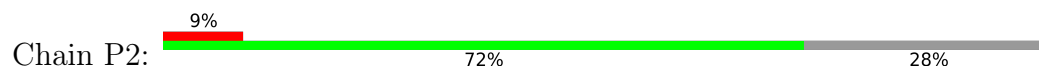


- Molecule 5: Flagellar hook-basal body complex protein FliE

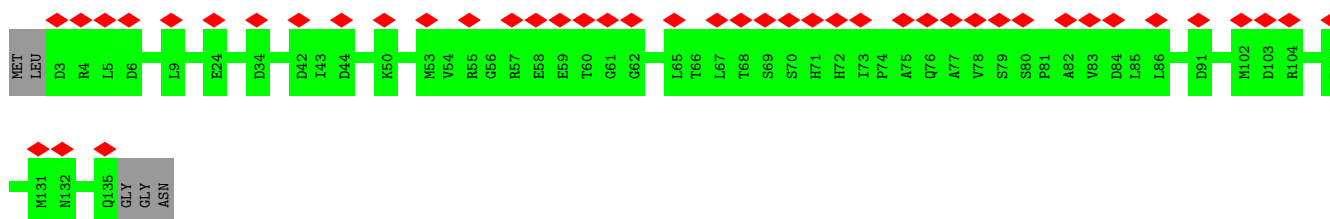




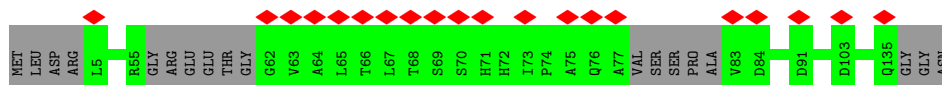
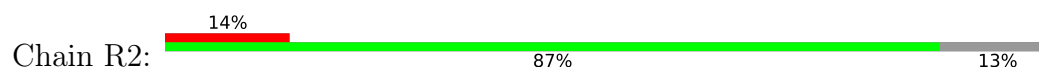
- Molecule 5: Flagellar hook-basal body complex protein FliE



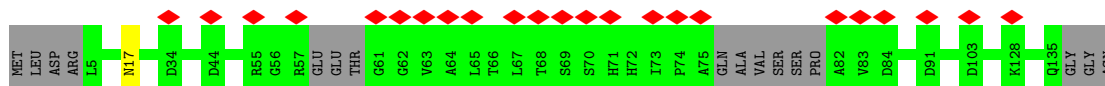
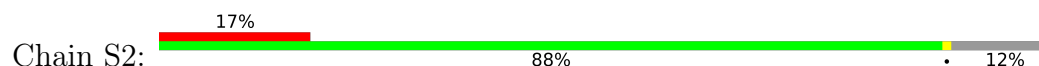
- Molecule 6: Flagellar basal body rod protein FlgB



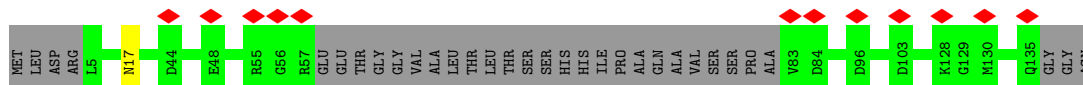
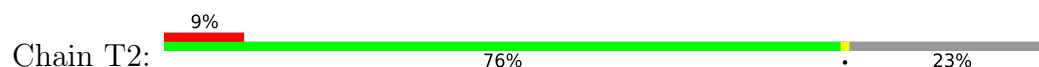
- Molecule 6: Flagellar basal body rod protein FlgB



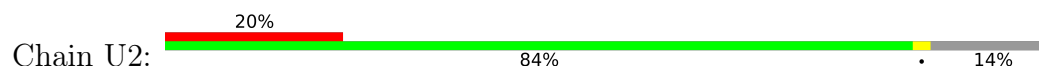
- Molecule 6: Flagellar basal body rod protein FlgB

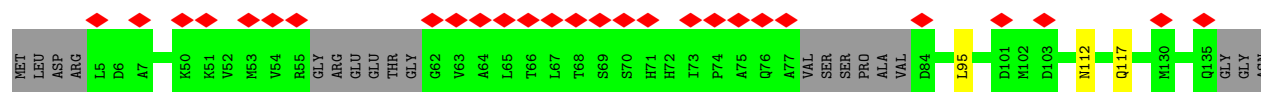


- Molecule 6: Flagellar basal body rod protein FlgB

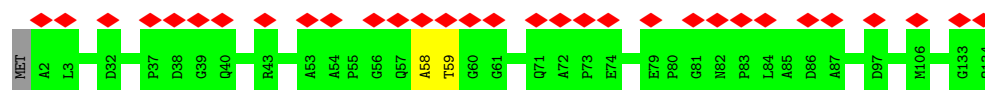


- Molecule 6: Flagellar basal body rod protein FlgB

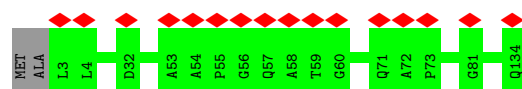




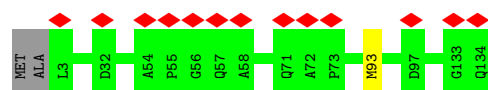
- Molecule 7: Flagellar basal-body rod protein FlgC



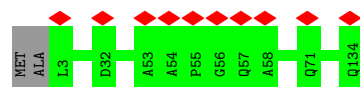
- Molecule 7: Flagellar basal-body rod protein FlgC



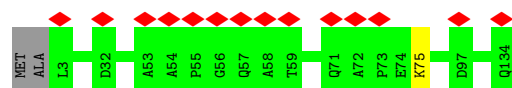
- Molecule 7: Flagellar basal-body rod protein FlgC



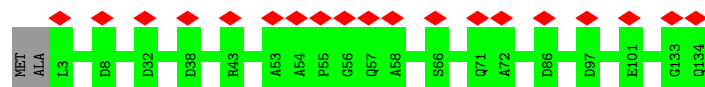
- Molecule 7: Flagellar basal-body rod protein FlgC



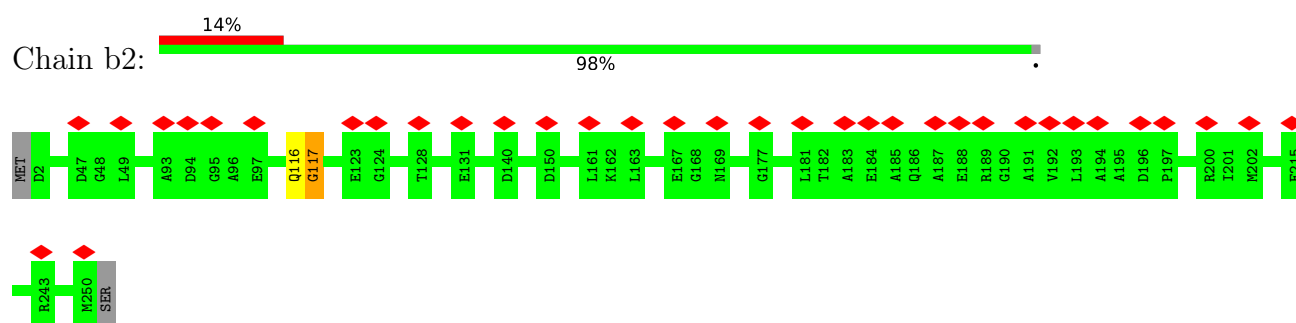
- Molecule 7: Flagellar basal-body rod protein FlgC



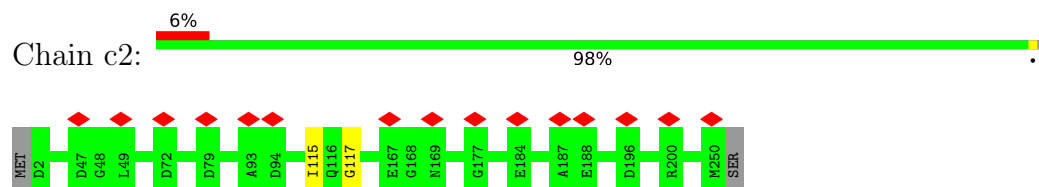
- Molecule 7: Flagellar basal-body rod protein FlgC



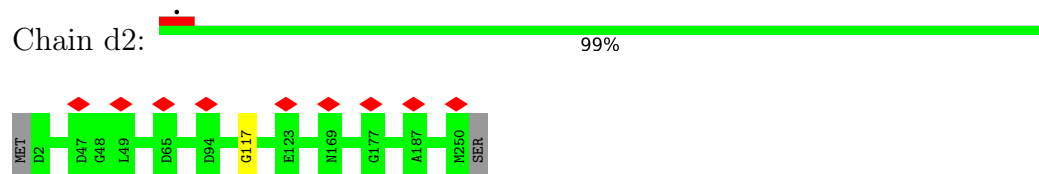
- Molecule 8: Flagellar basal body protein



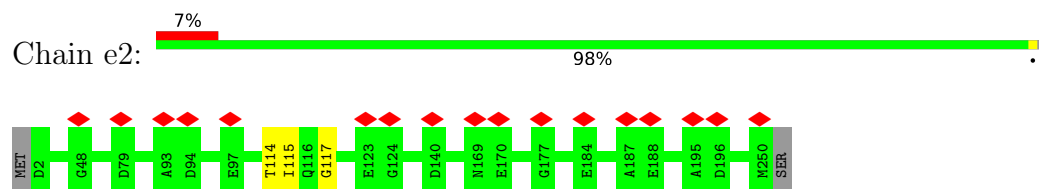
- Molecule 8: Flagellar basal body protein



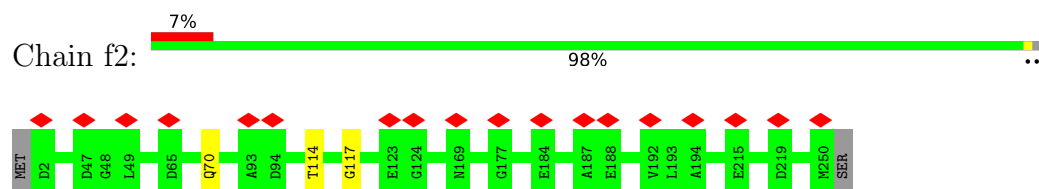
- Molecule 8: Flagellar basal body protein



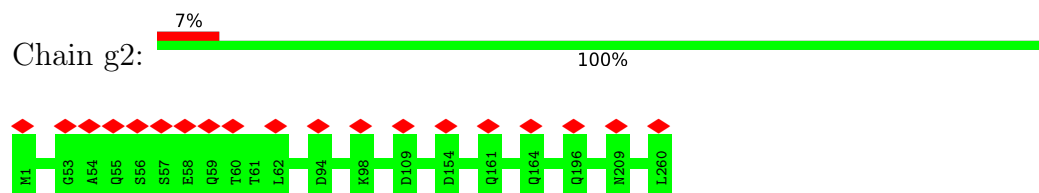
- Molecule 8: Flagellar basal body protein



- Molecule 8: Flagellar basal body protein

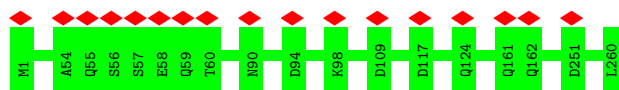


- Molecule 9: Flagellar basal-body rod protein FlgG

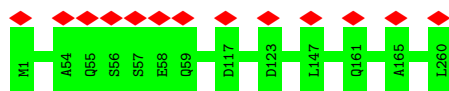


- Molecule 9: Flagellar basal-body rod protein FlgG

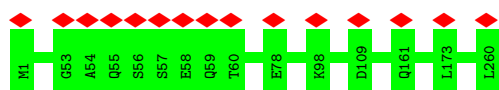




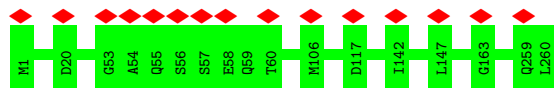
- Molecule 9: Flagellar basal-body rod protein FlgG



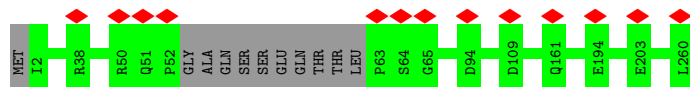
- Molecule 9: Flagellar basal-body rod protein FlgG



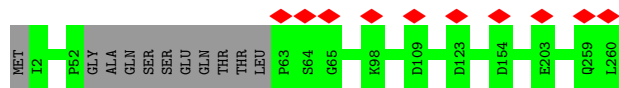
- Molecule 9: Flagellar basal-body rod protein FlgG



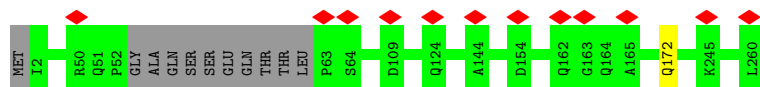
- Molecule 9: Flagellar basal-body rod protein FlgG



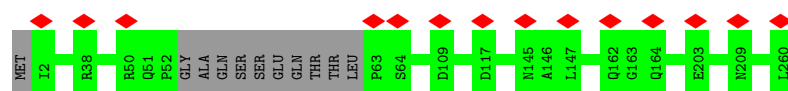
- Molecule 9: Flagellar basal-body rod protein FlgG



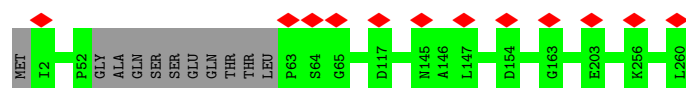
- Molecule 9: Flagellar basal-body rod protein FlgG



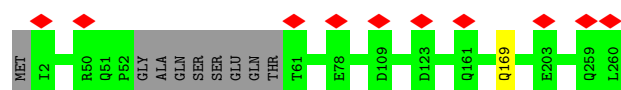
- Molecule 9: Flagellar basal-body rod protein FlgG



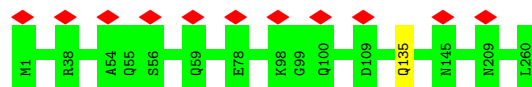
- Molecule 9: Flagellar basal-body rod protein FlgG



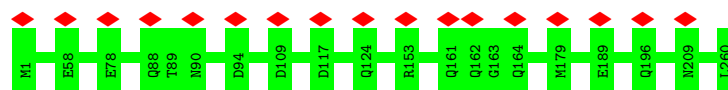
- Molecule 9: Flagellar basal-body rod protein FlgG



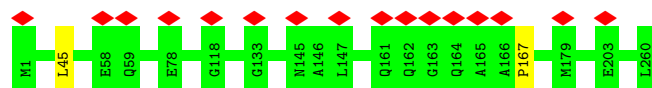
- Molecule 9: Flagellar basal-body rod protein FlgG



- Molecule 9: Flagellar basal-body rod protein FlgG

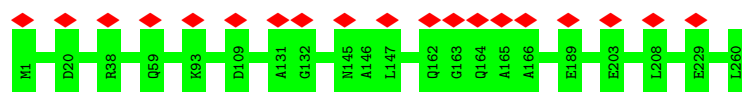


- Molecule 9: Flagellar basal-body rod protein FlgG

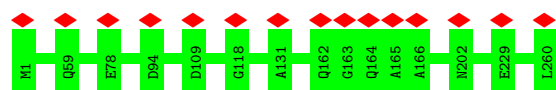


- Molecule 9: Flagellar basal-body rod protein FlgG

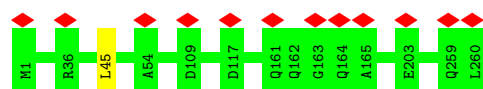




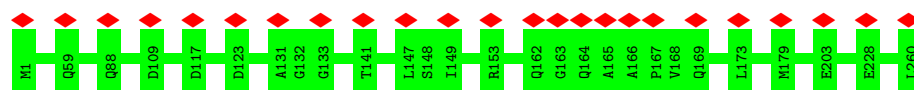
- Molecule 9: Flagellar basal-body rod protein FlgG



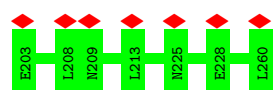
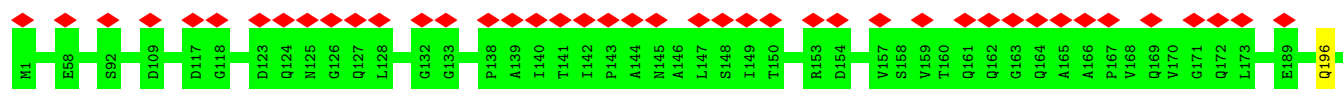
- Molecule 9: Flagellar basal-body rod protein FlgG



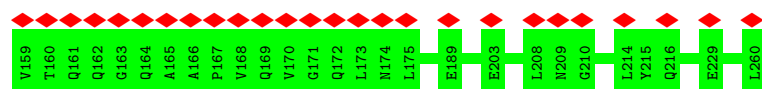
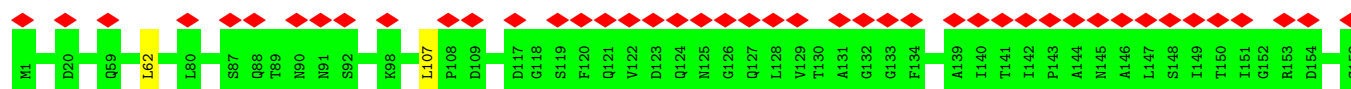
- Molecule 9: Flagellar basal-body rod protein FlgG



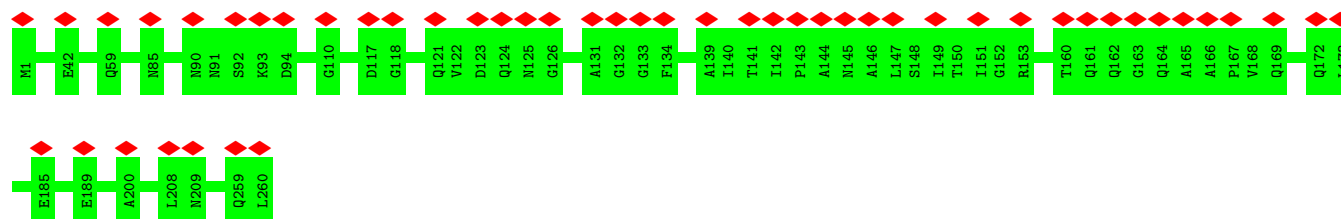
- Molecule 9: Flagellar basal-body rod protein FlgG



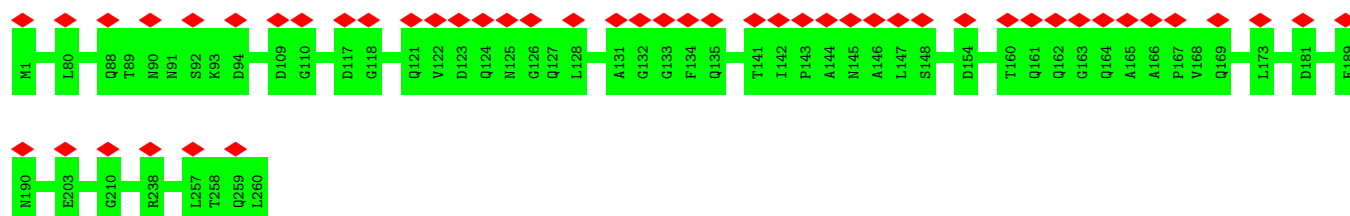
- Molecule 9: Flagellar basal-body rod protein FlgG



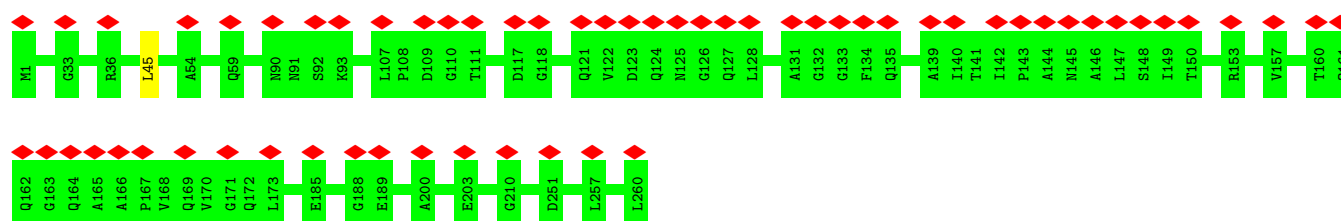
- Molecule 9: Flagellar basal-body rod protein FlgG



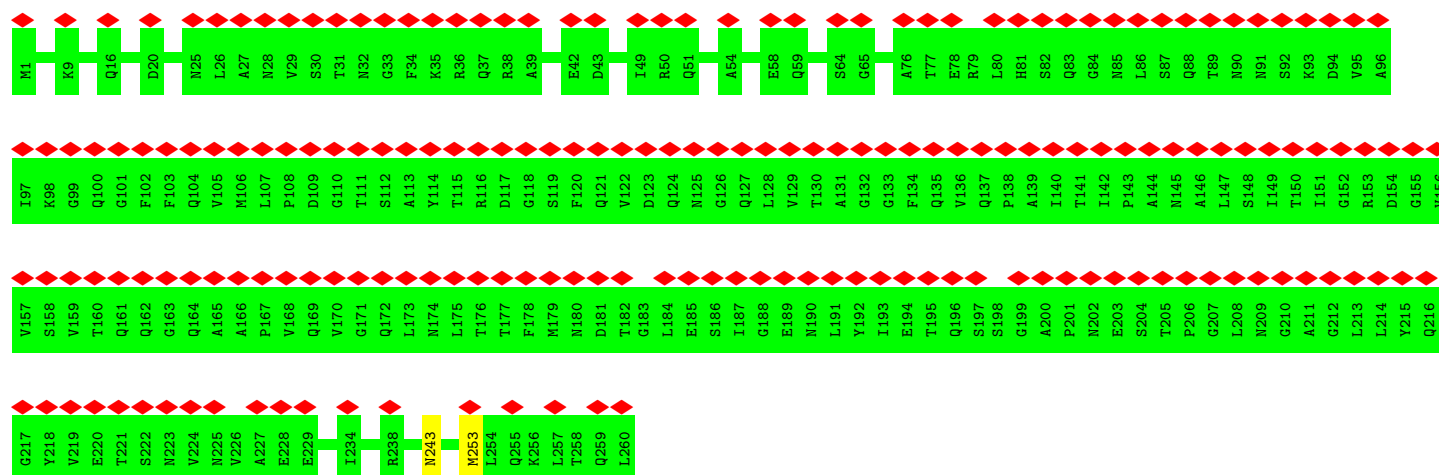
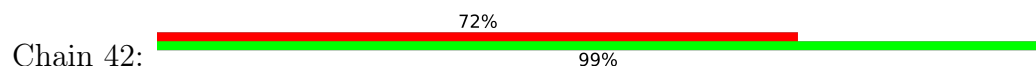
- Molecule 9: Flagellar basal-body rod protein FlgG



- Molecule 9: Flagellar basal-body rod protein FlgG



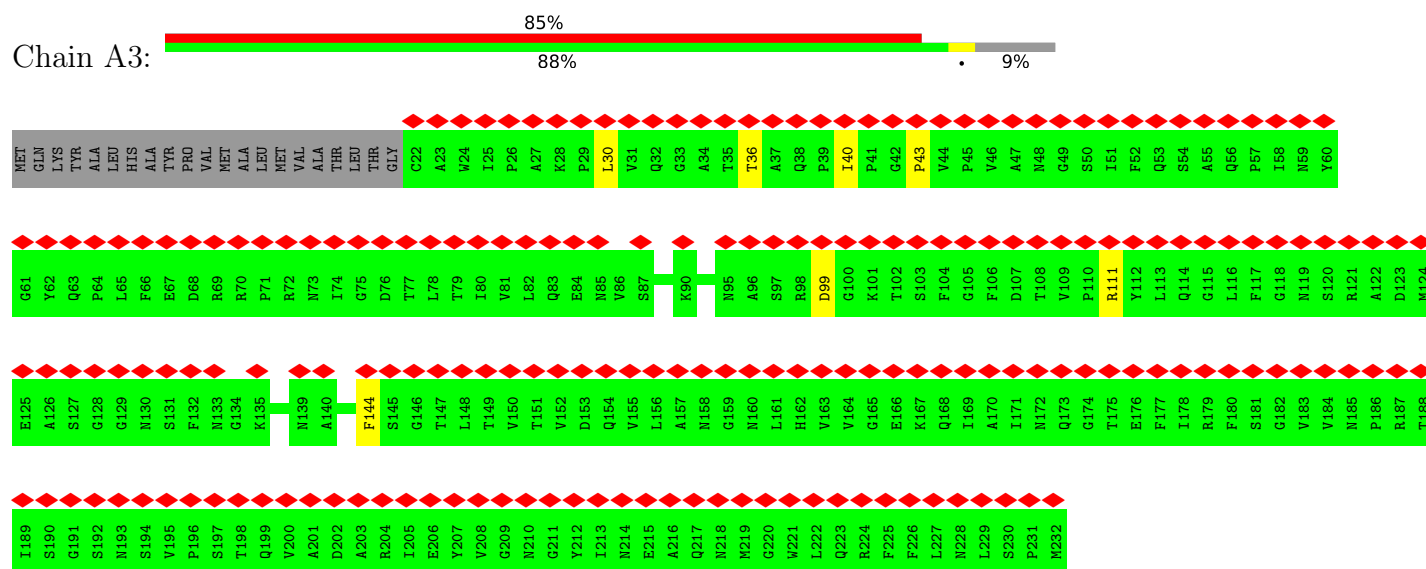
- Molecule 9: Flagellar basal-body rod protein FlgG





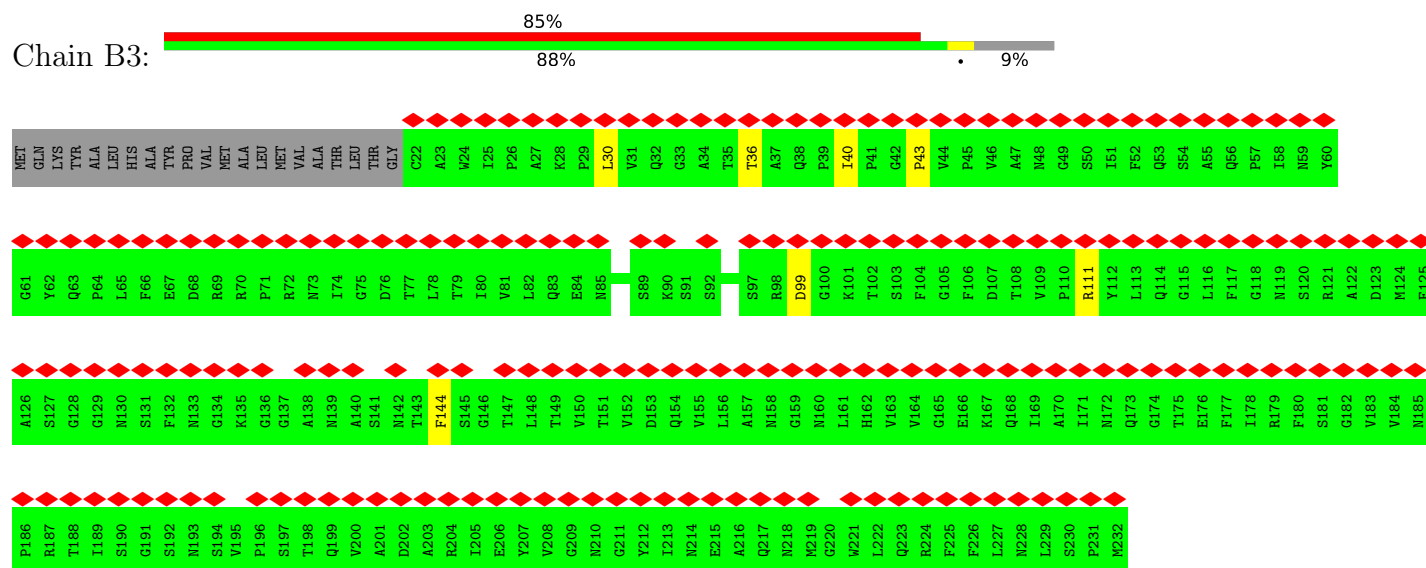
## ● Molecule 10: Flagellar L-ring protein

Chain A3:



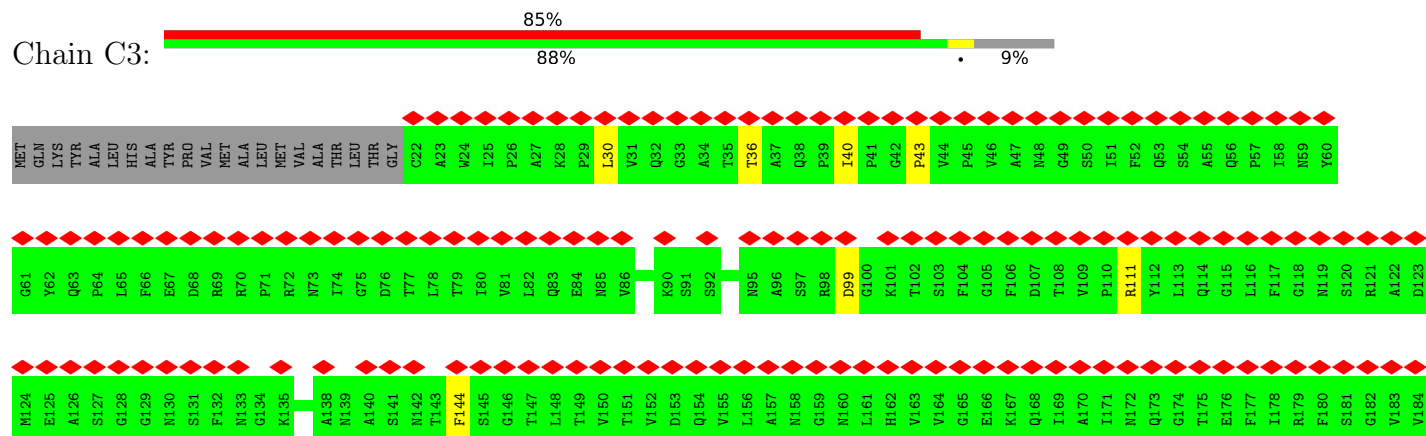
## ● Molecule 10: Flagellar L-ring protein

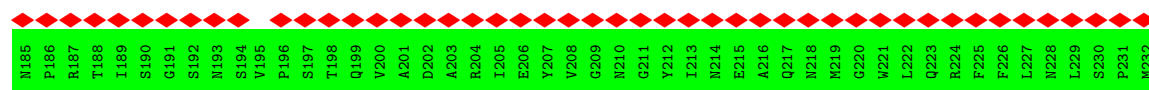
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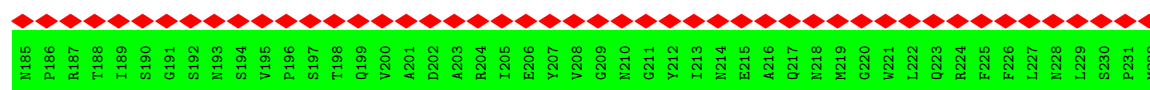
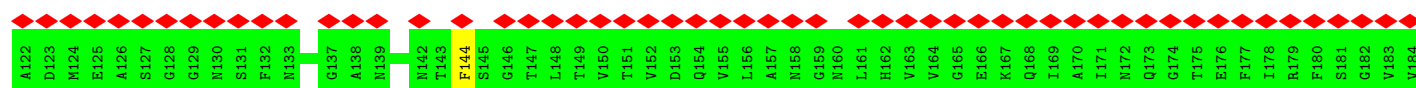
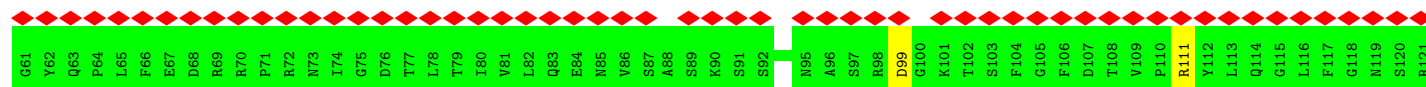
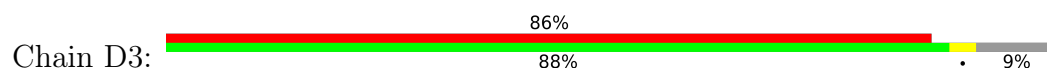
## ● Molecule 10: Flagellar L-ring protein

Chain C3:

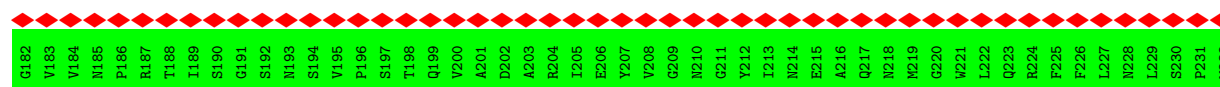
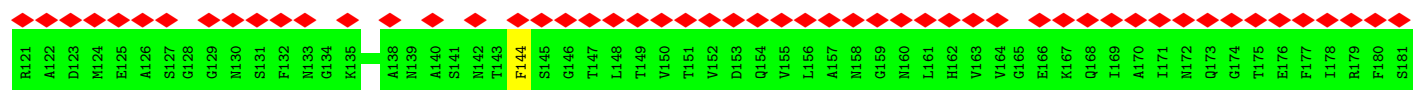
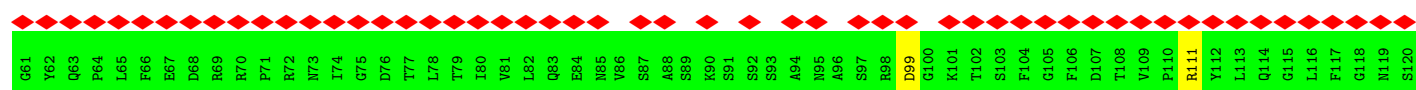
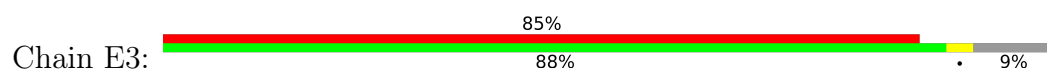




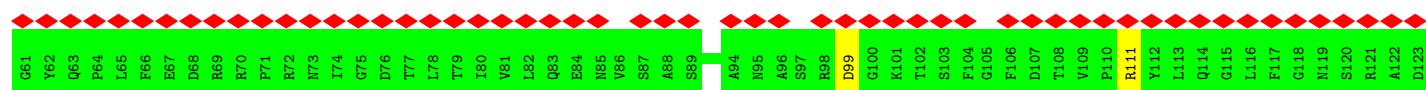
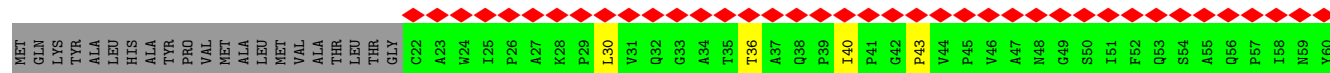
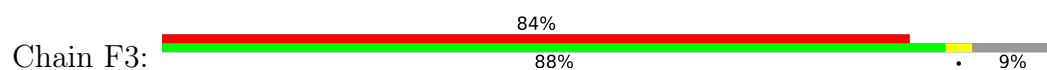
• Molecule 10: Flagellar L-ring protein



• Molecule 10: Flagellar L-ring protein

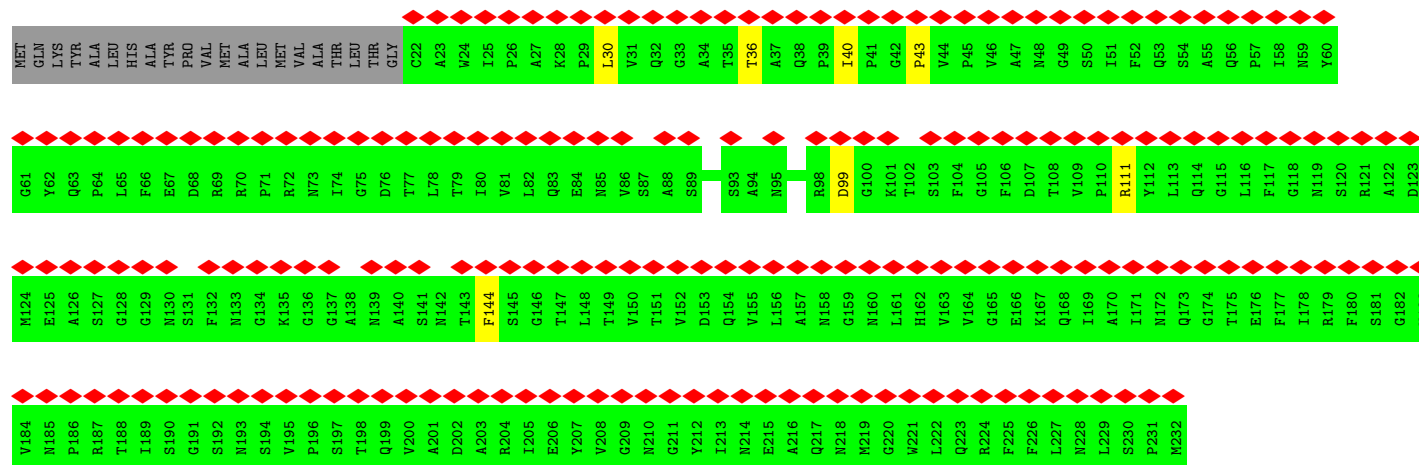
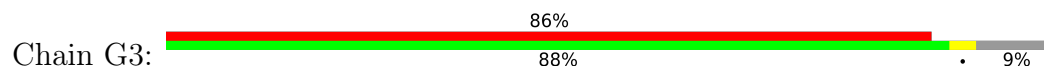


• Molecule 10: Flagellar L-ring protein

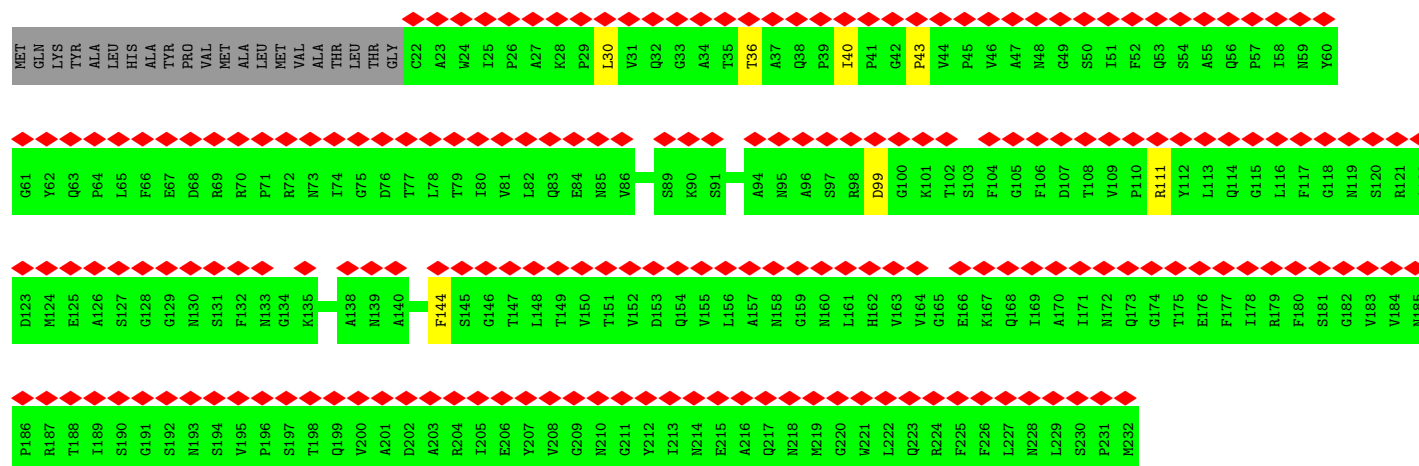
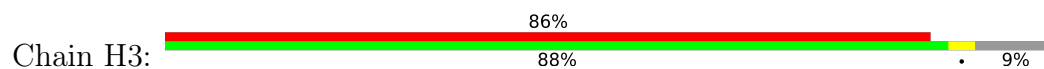




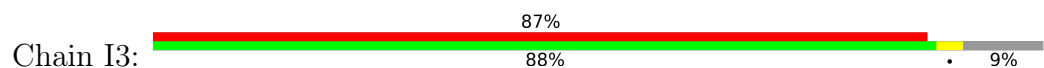
• Molecule 10: Flagellar L-ring protein

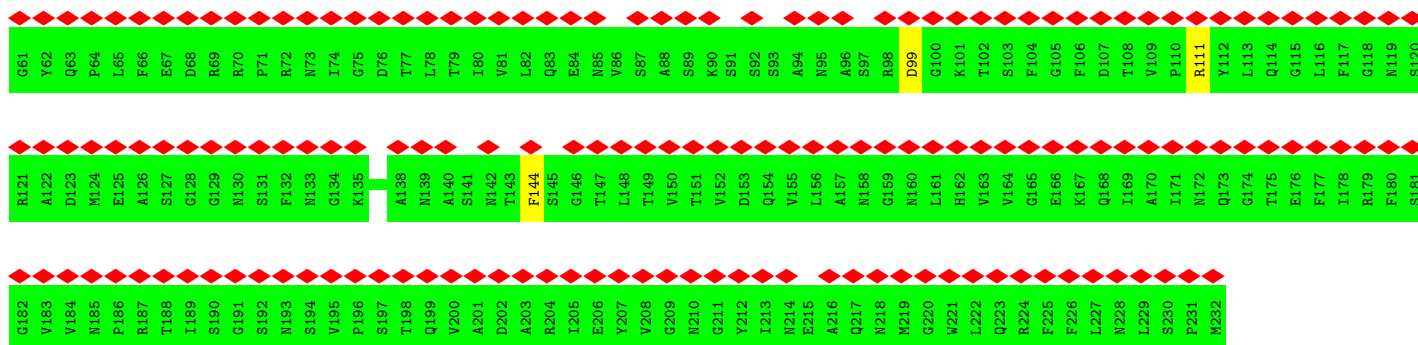


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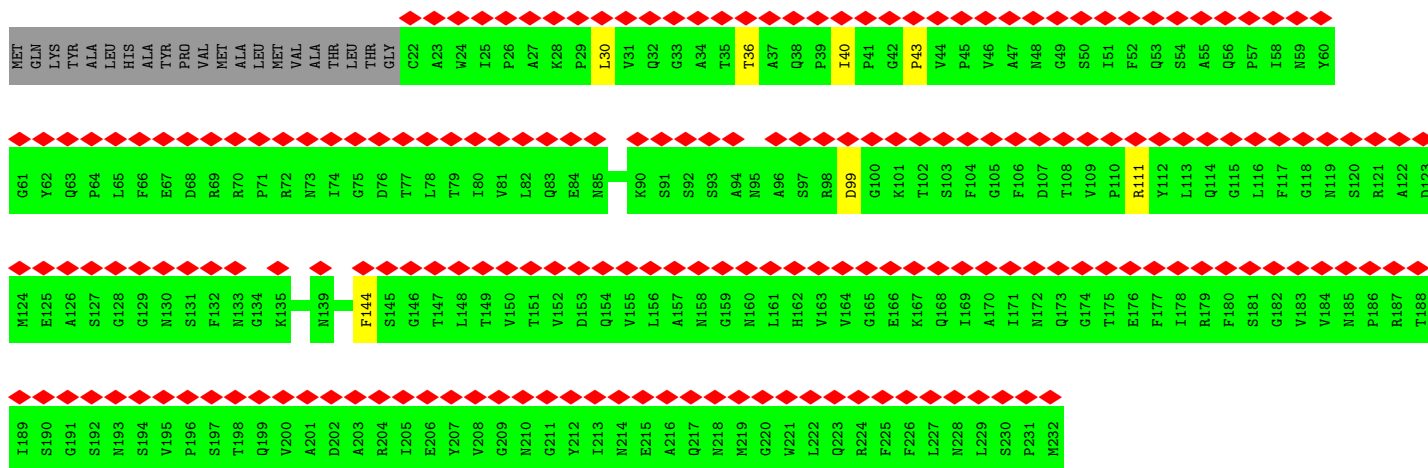
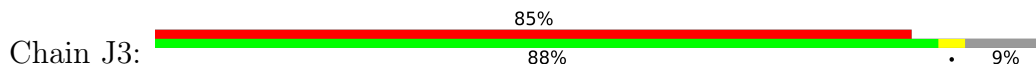


• Molecule 10: Flagellar L-ring protein

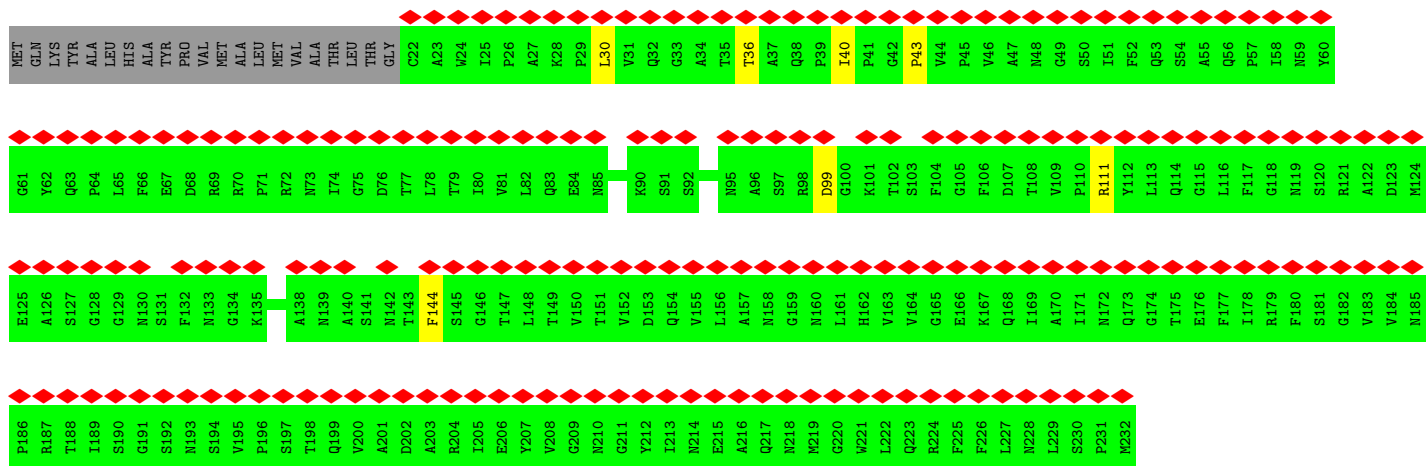
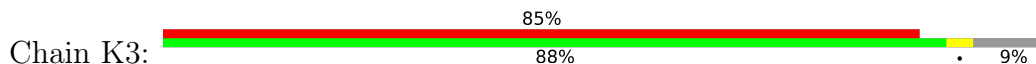




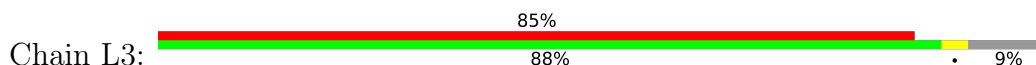
• Molecule 10: Flagellar L-ring protein

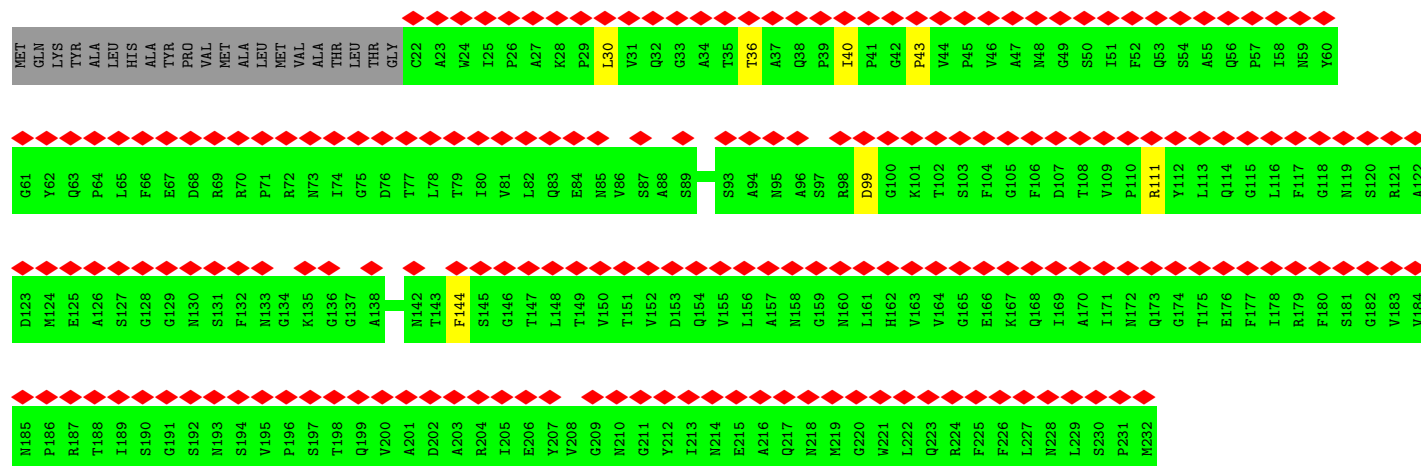


• Molecule 10: Flagellar L-ring protein



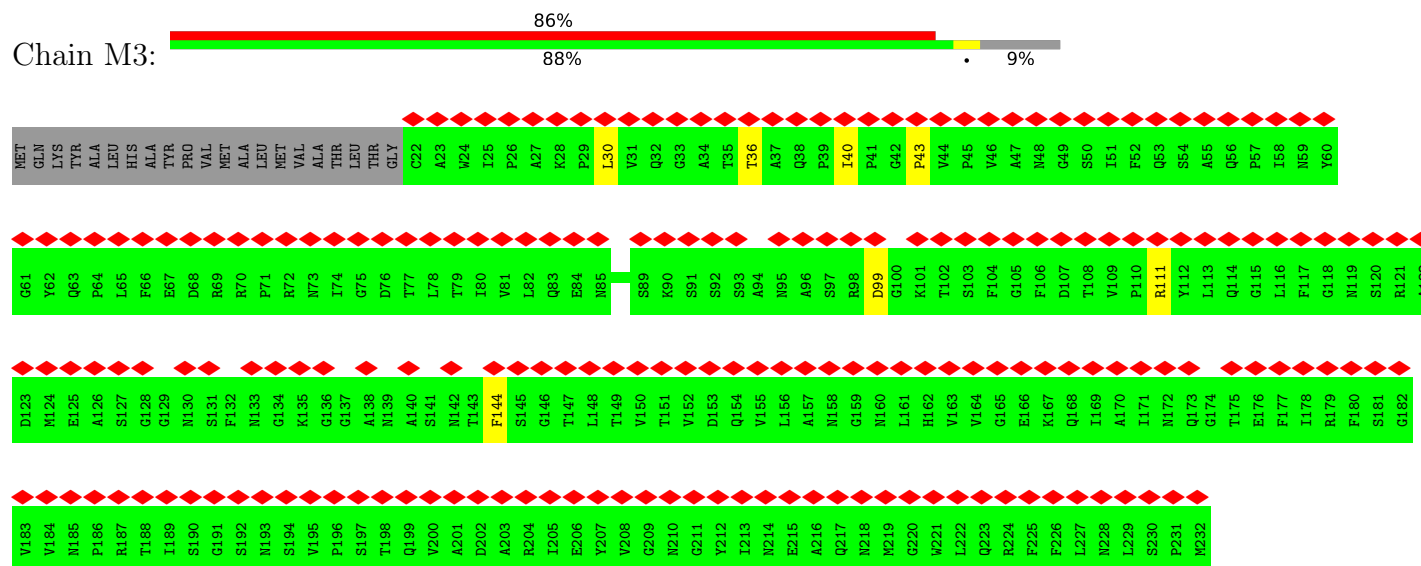
• Molecule 10: Flagellar L-ring protein





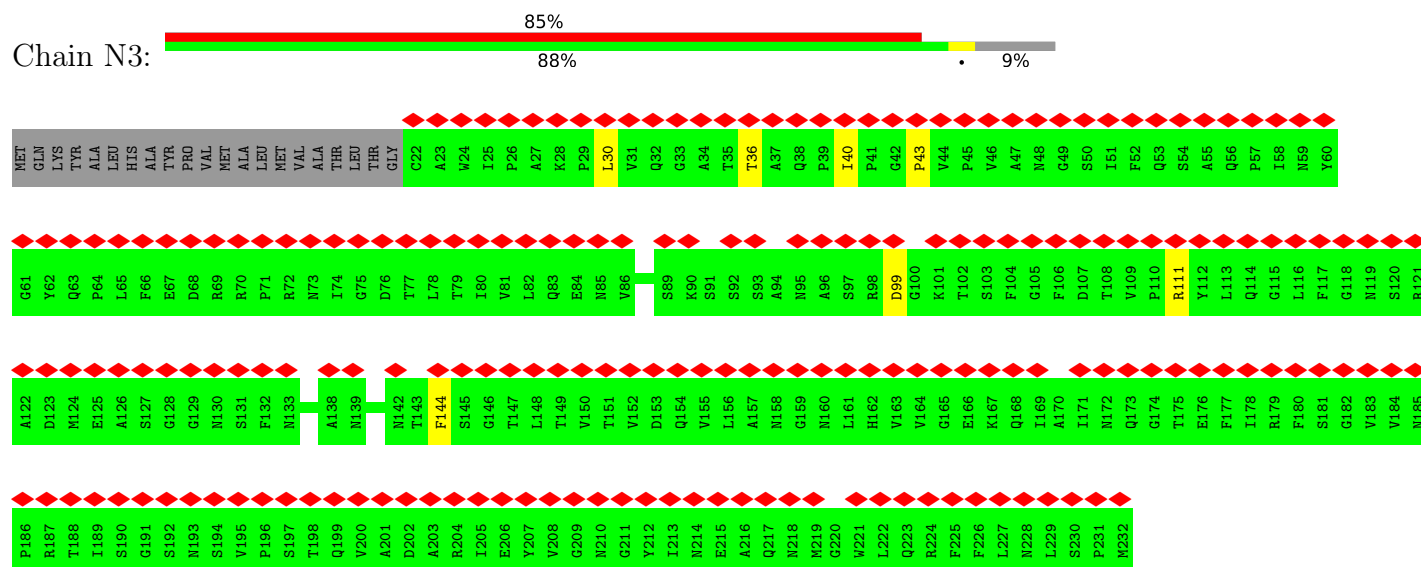
### • Molecule 10: Flagellar L-ring protein

Chain M3:



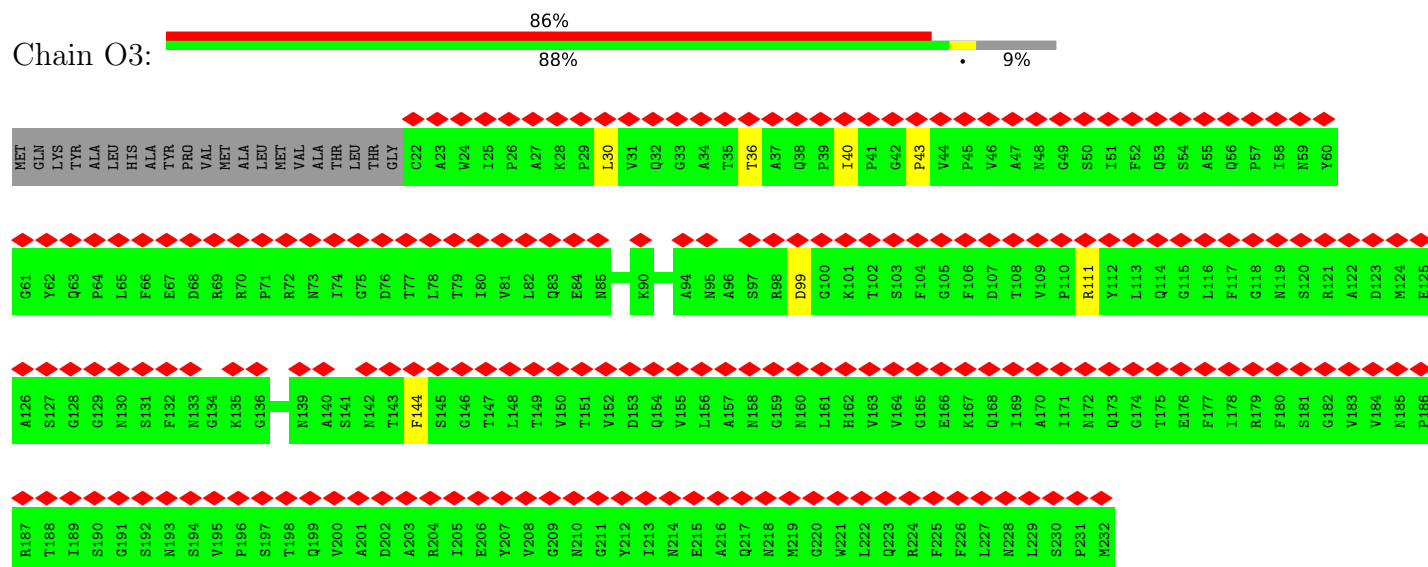
### • Molecule 10: Flagellar L-ring protein

Chain N3:



- Molecule 10: Flagellar L-ring protein

Chain O3:



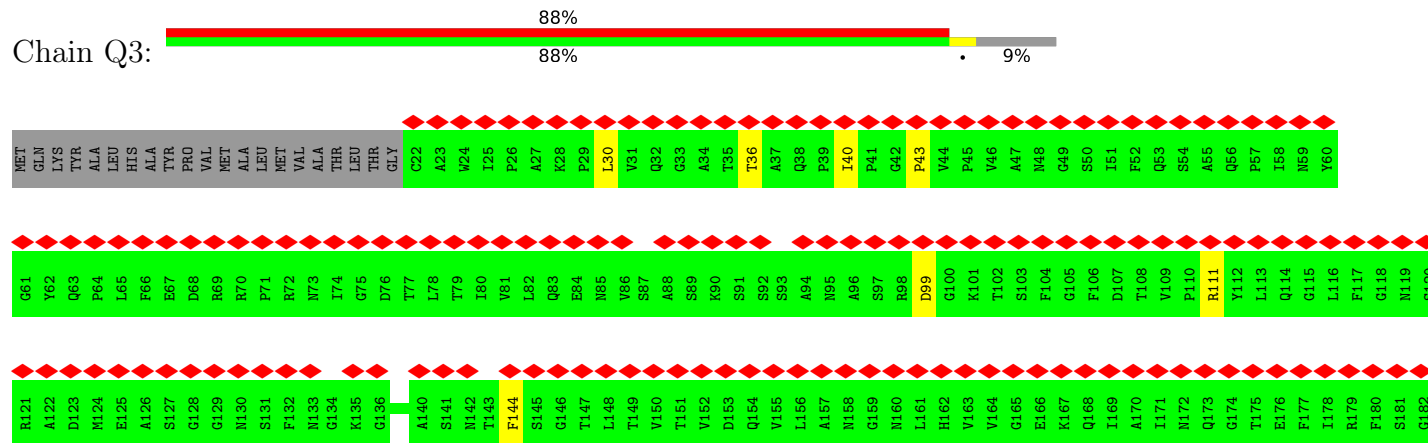
- Molecule 10: Flagellar L-ring protein

Chain P3:



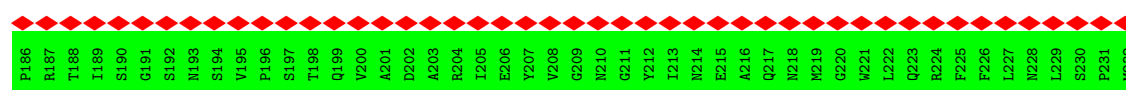
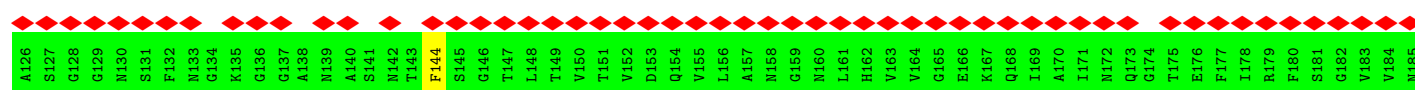
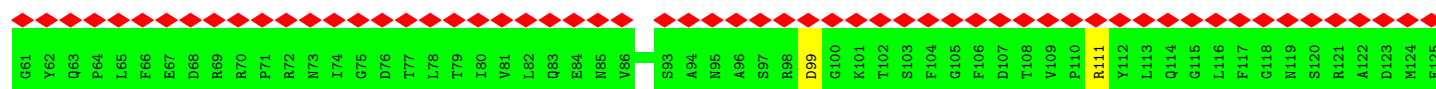
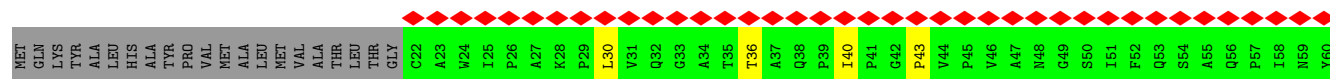
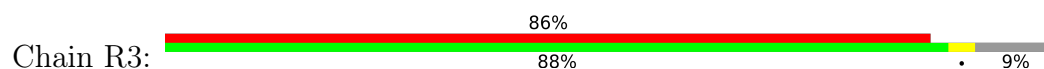
- Molecule 10: Flagellar L-ring protein

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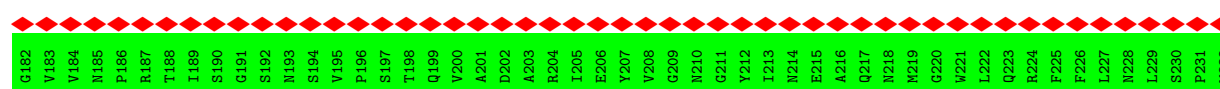
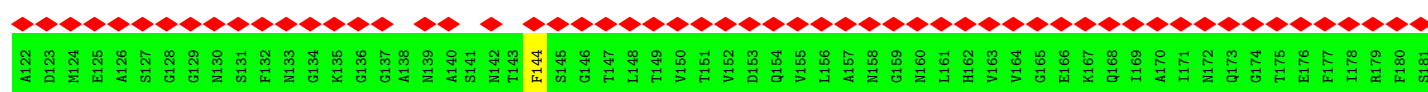
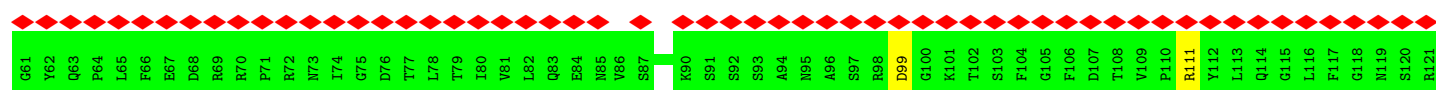
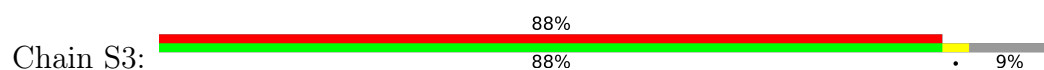




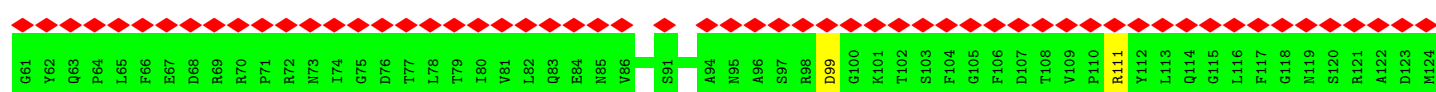
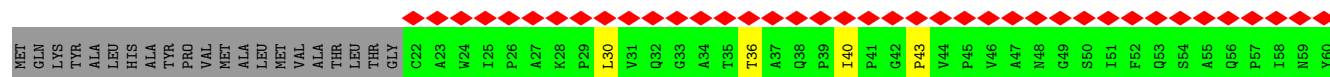
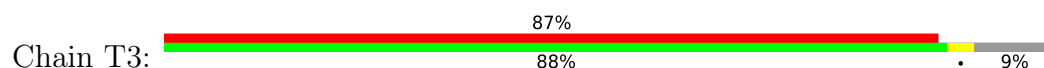
• Molecule 10: Flagellar L-ring protein



• Molecule 10: Flagellar L-ring protein



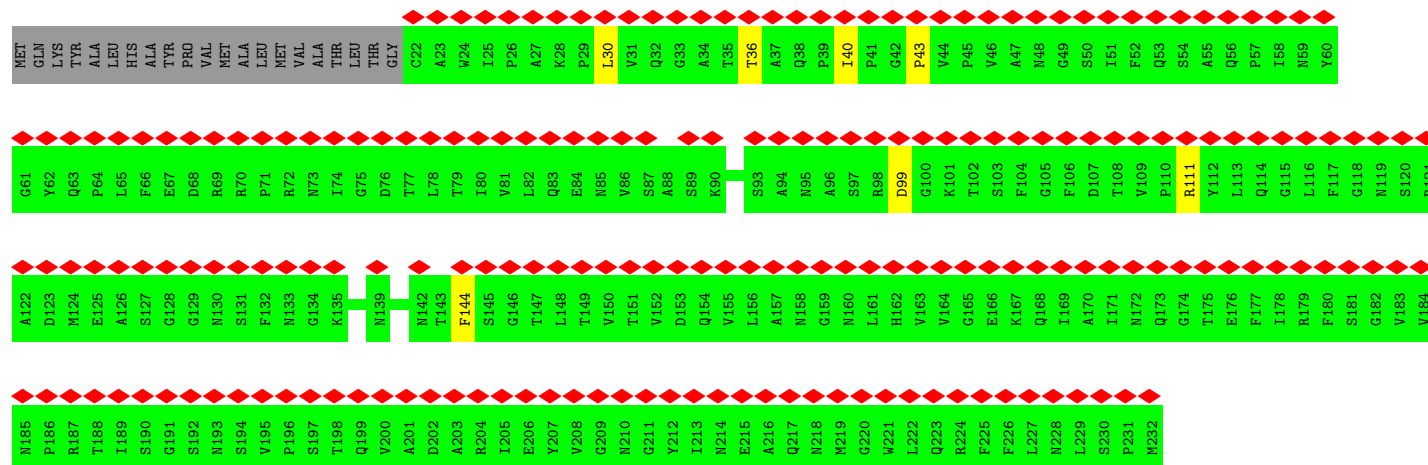
• Molecule 10: Flagellar L-ring protein





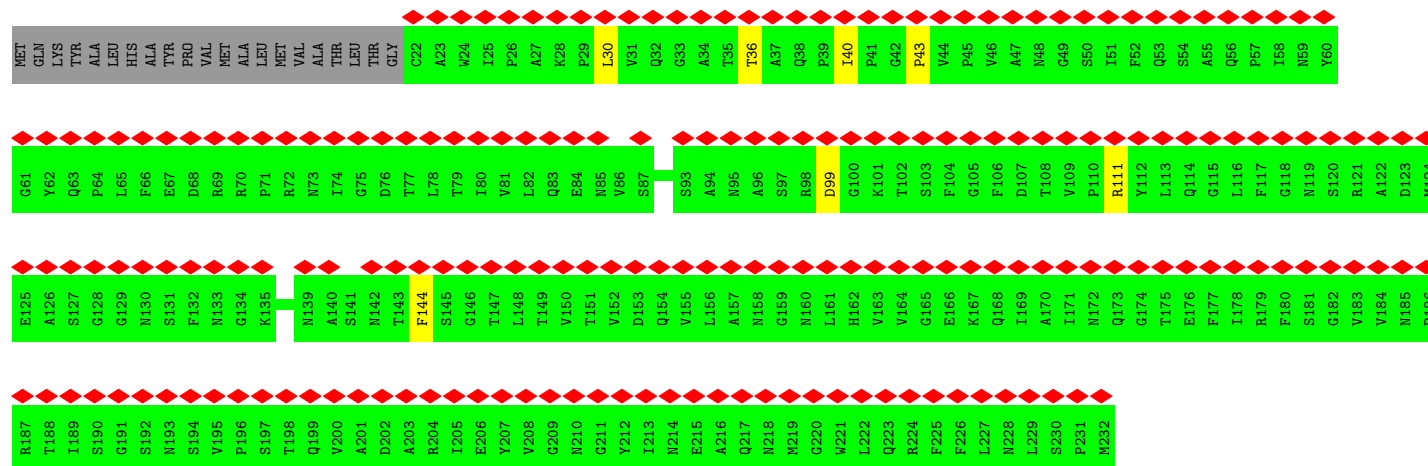
• Molecule 10: Flagellar L-ring protein

Chain U3:



• Molecule 10: Flagellar L-ring protein

Chain V3:

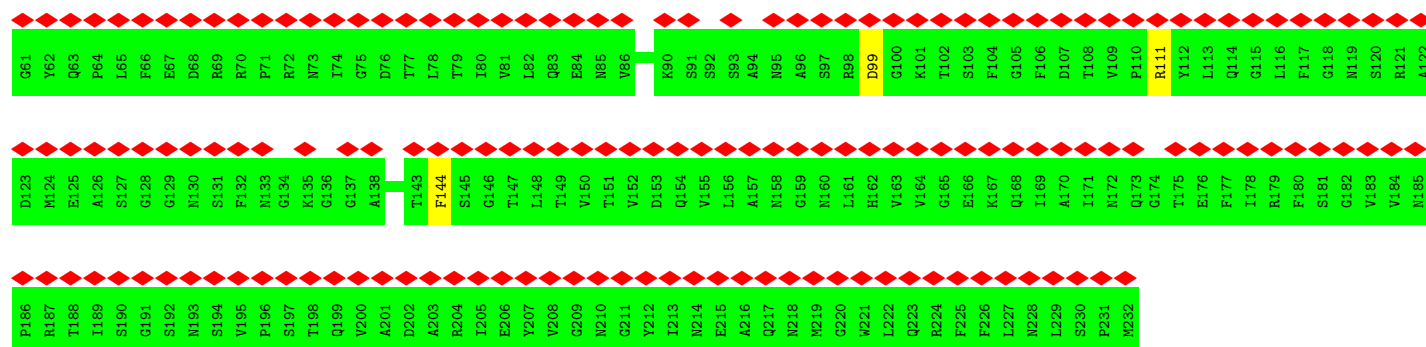


• Molecule 10: Flagellar L-ring protein

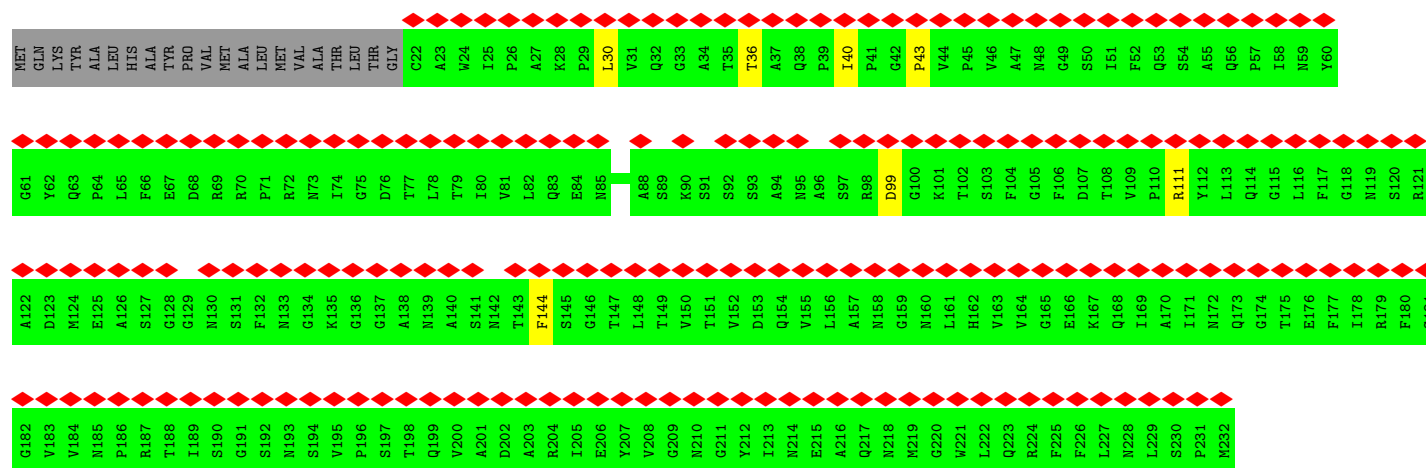
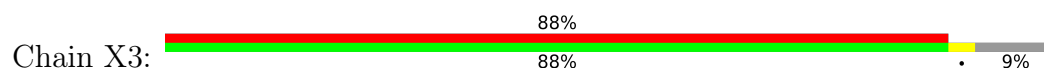
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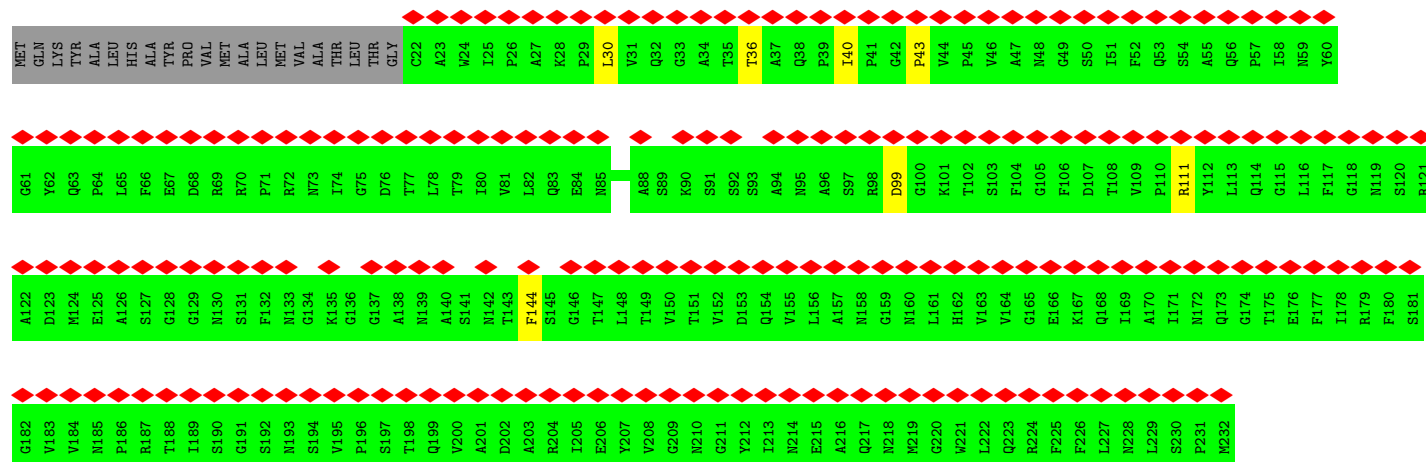
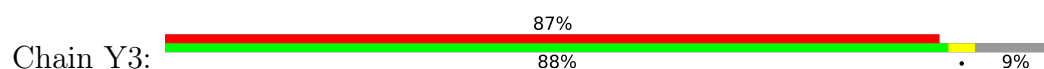




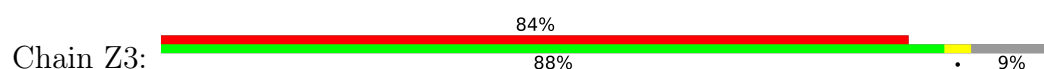
• Molecule 10: Flagellar L-ring protein

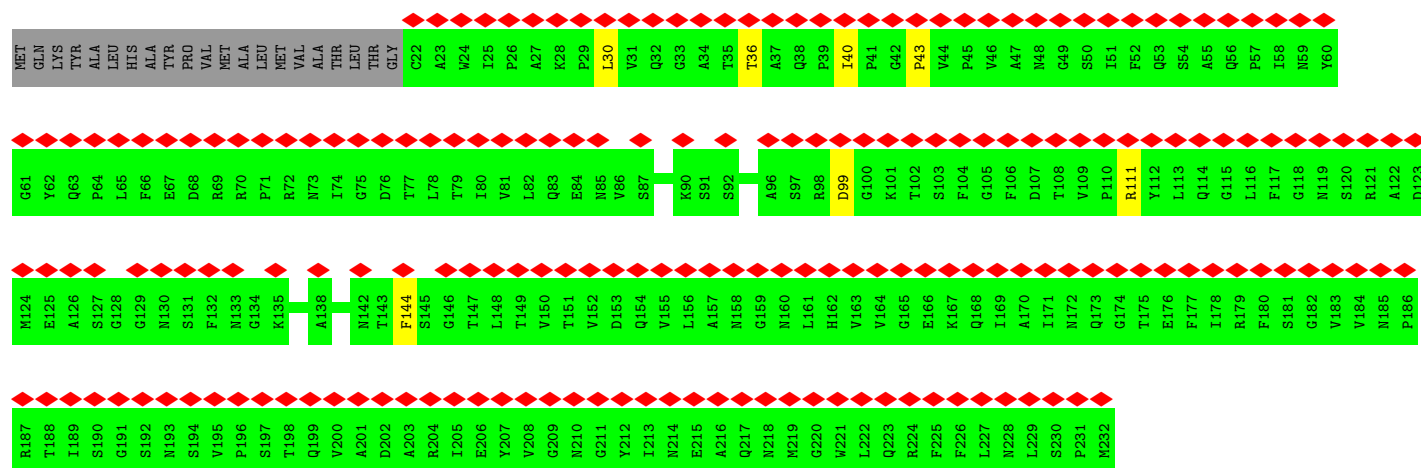


• Molecule 10: Flagellar L-ring protein

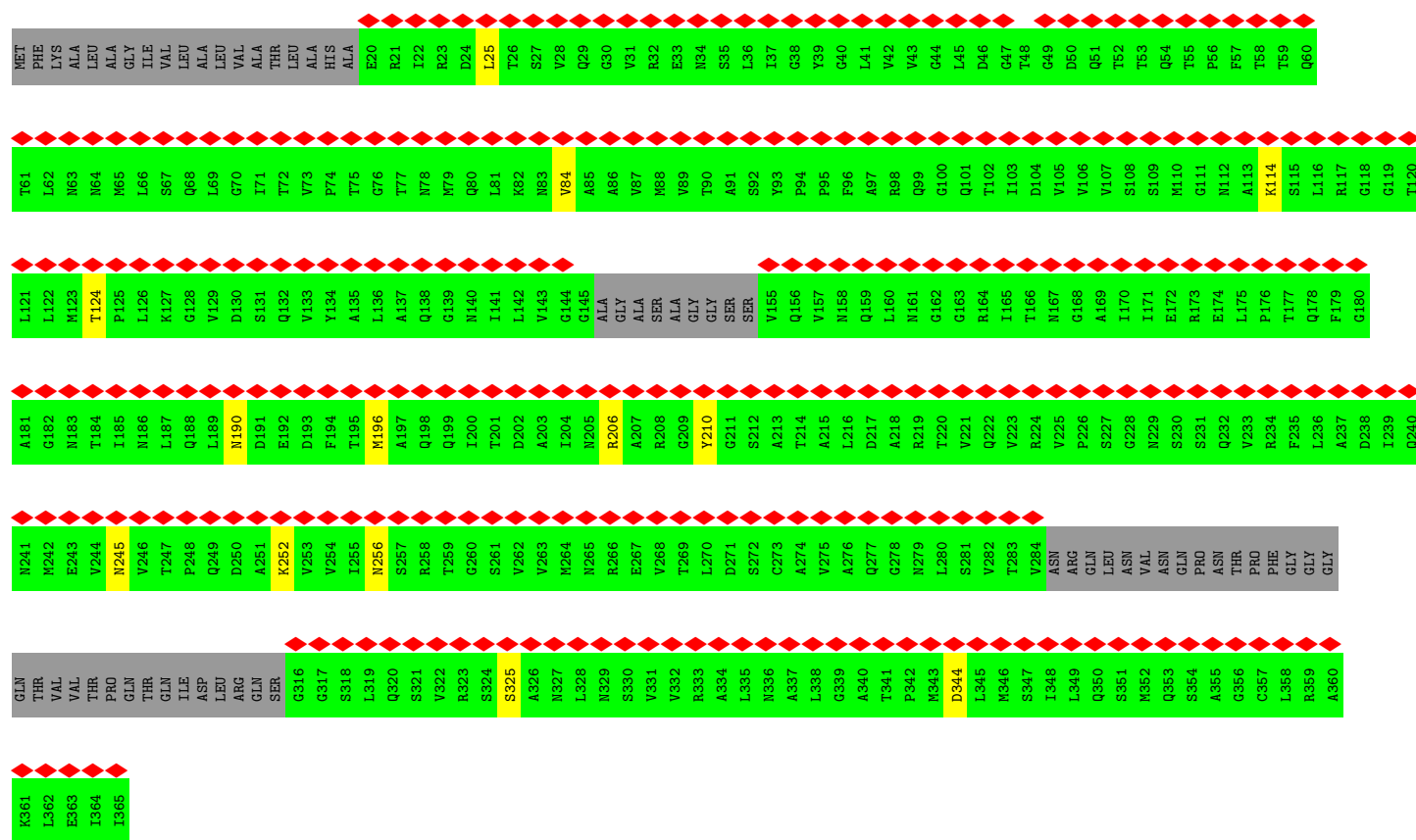
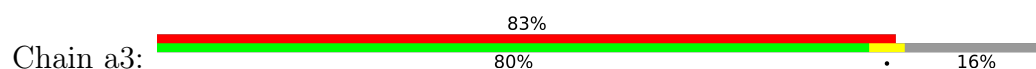


• Molecule 10: Flagellar L-ring protein

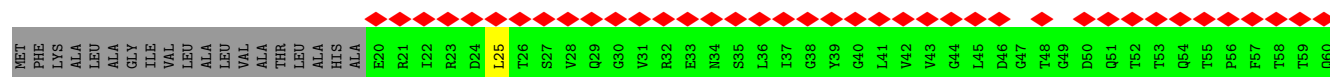
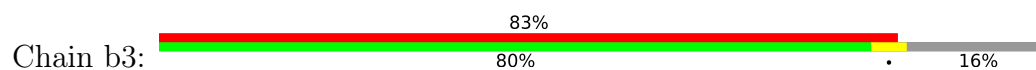


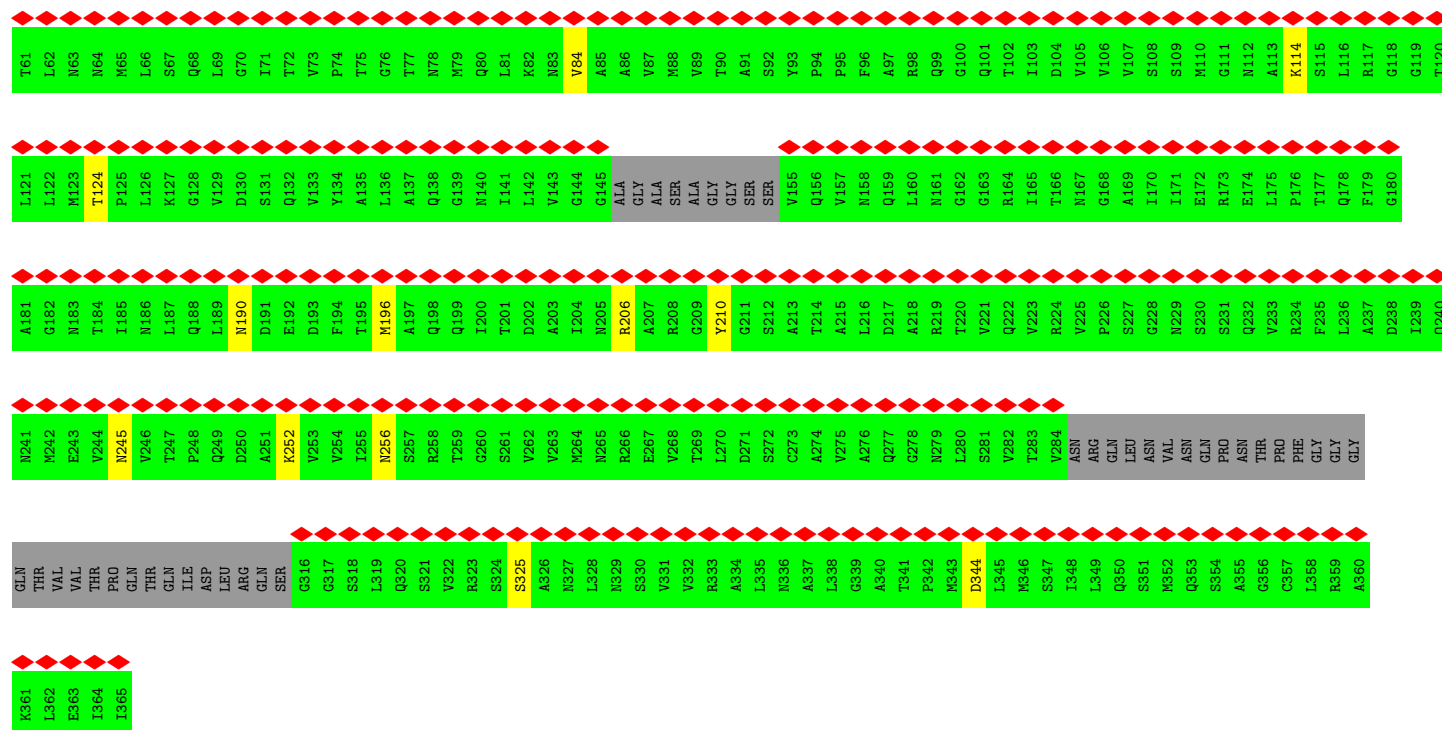


• Molecule 11: Flagellar P-ring protein



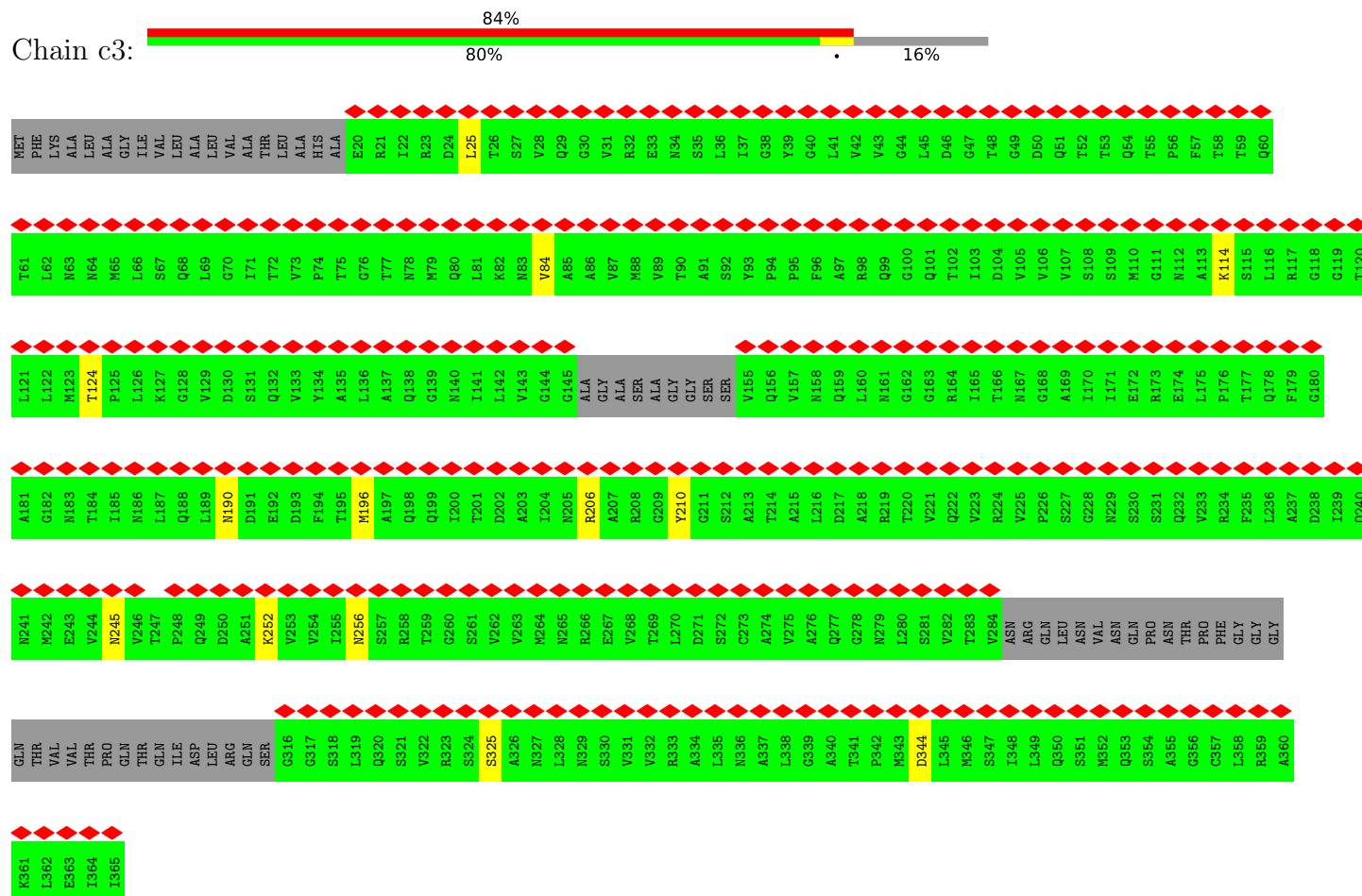
• Molecule 11: Flagellar P-ring protein





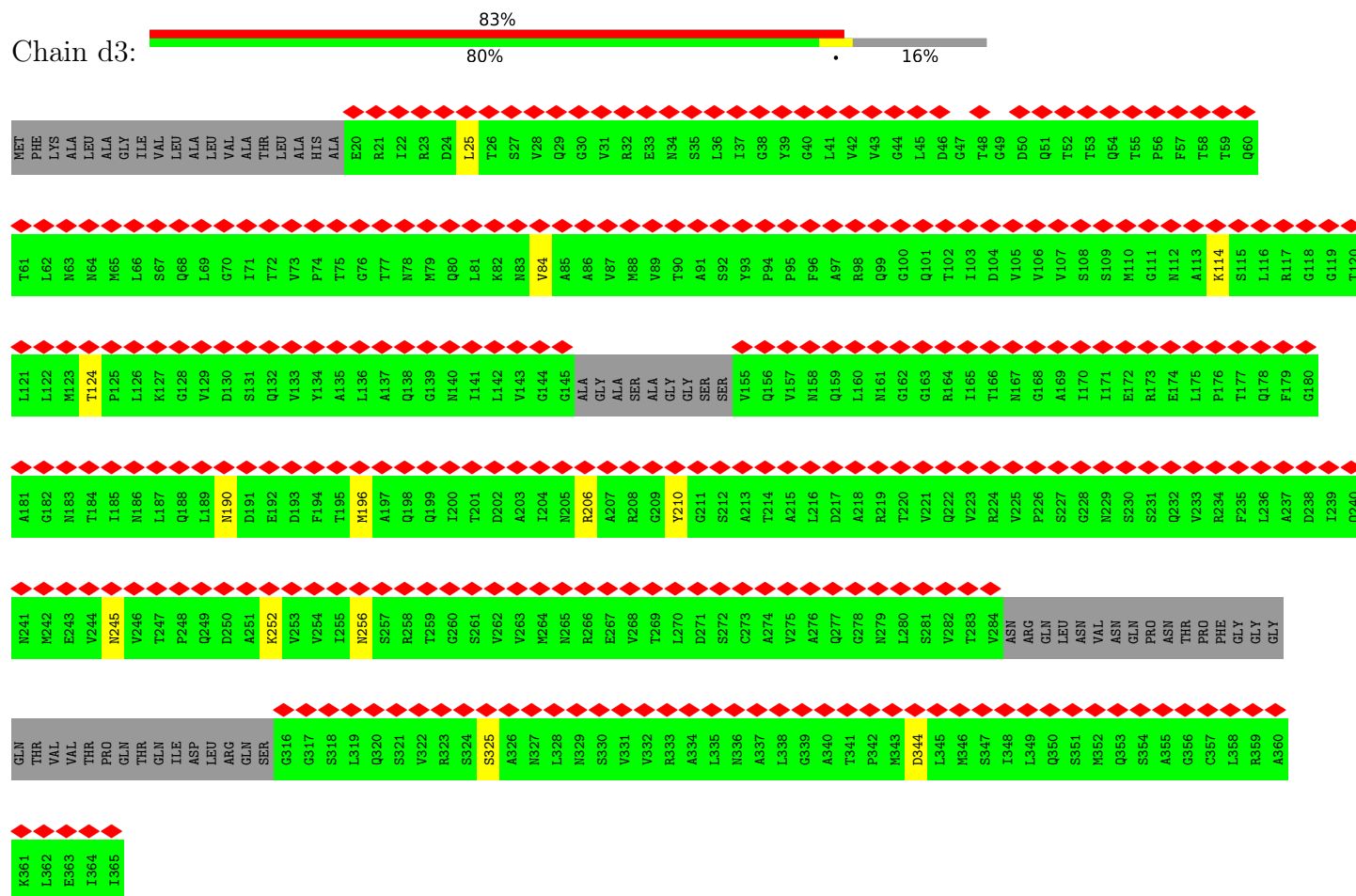
# Molecule 11: Flagellar P-ring protein

Chain c3:



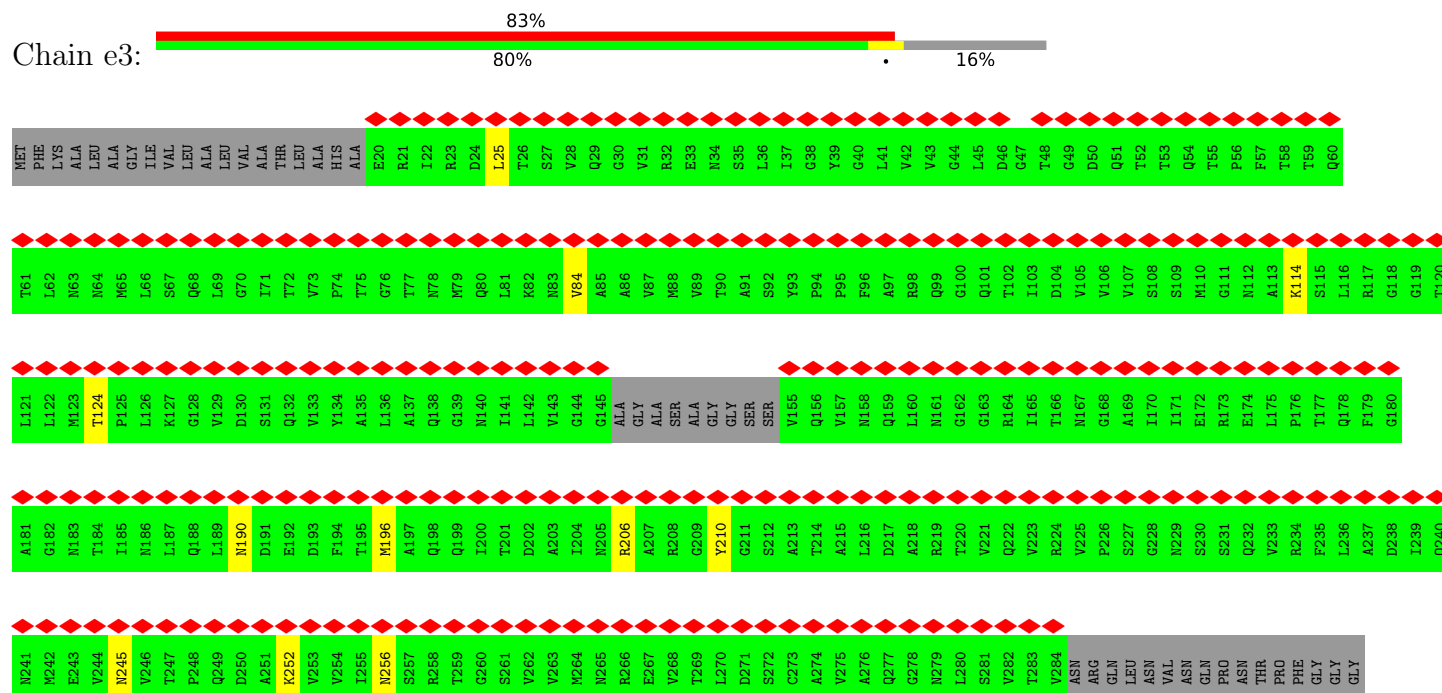
- Molecule 11: Flagellar P-ring protein

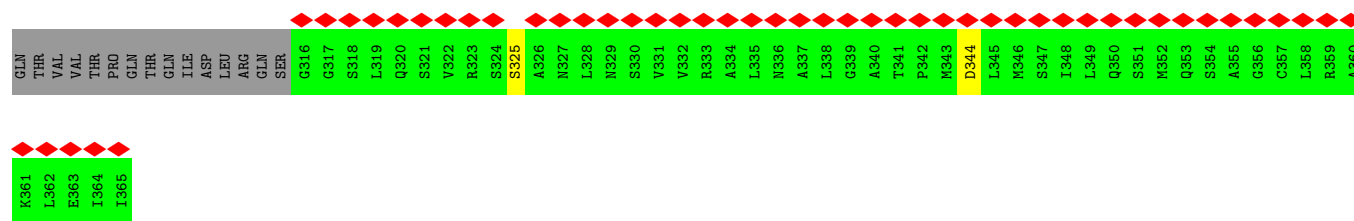
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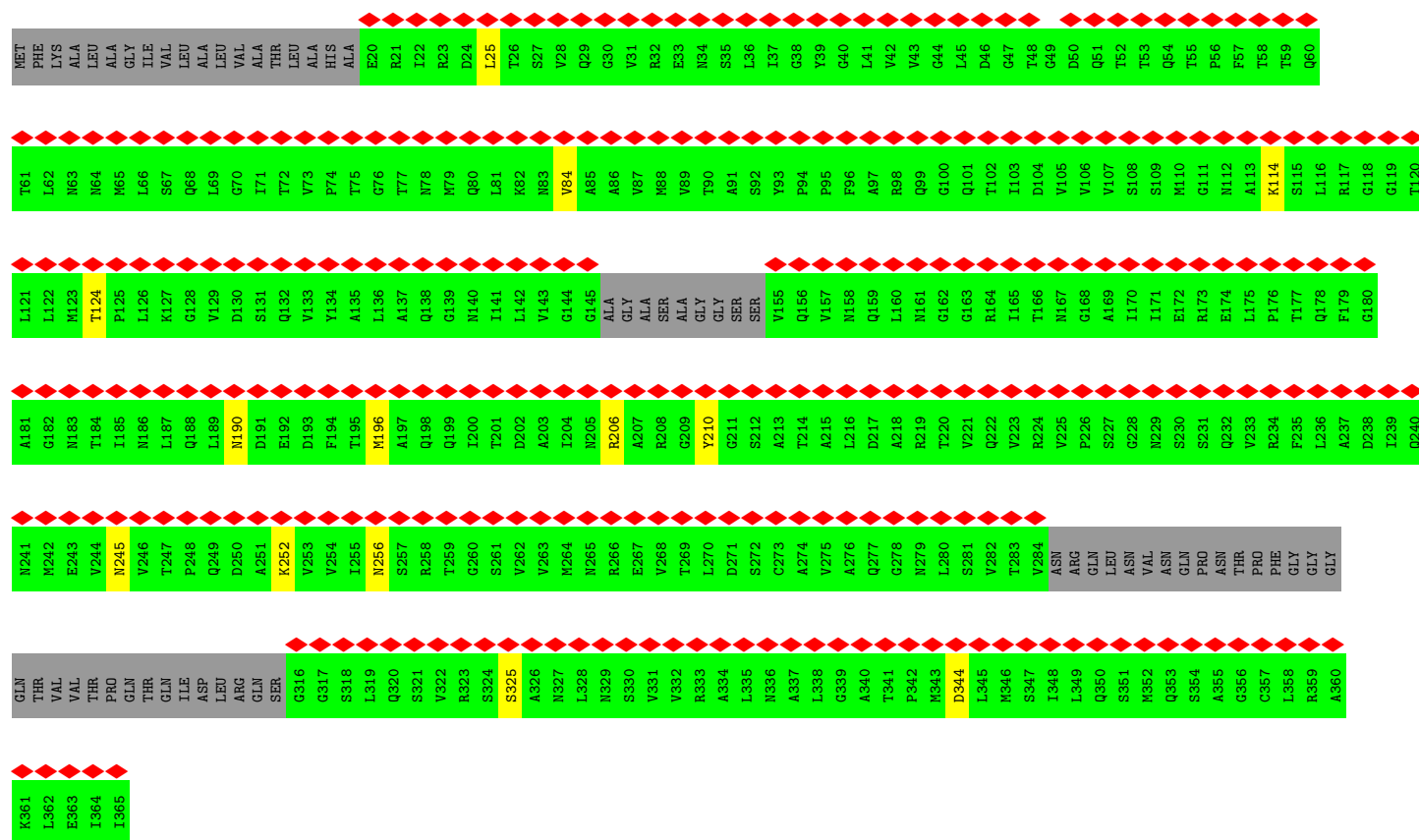
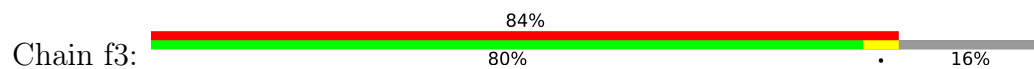
- Molecule 11: Flagellar P-ring protein

Chain e3:

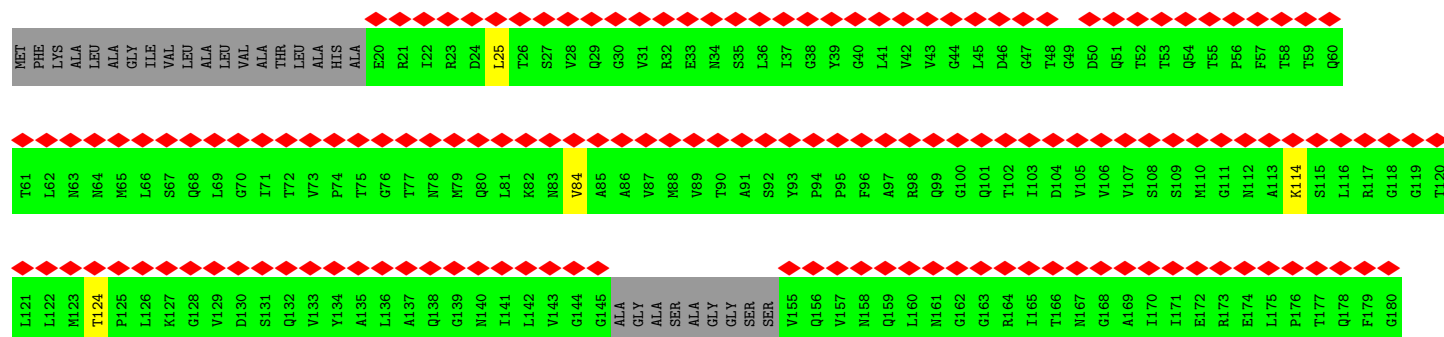
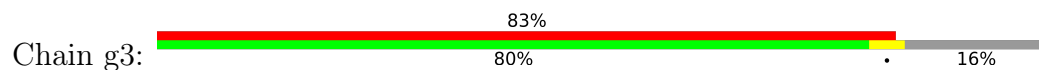


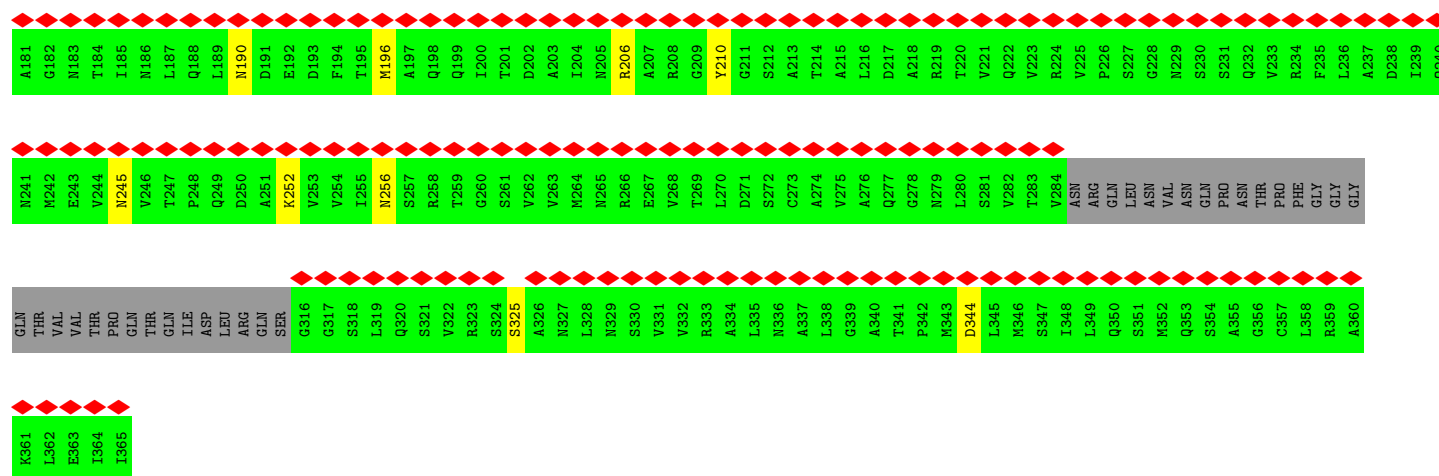


• Molecule 11: Flagellar P-ring protein

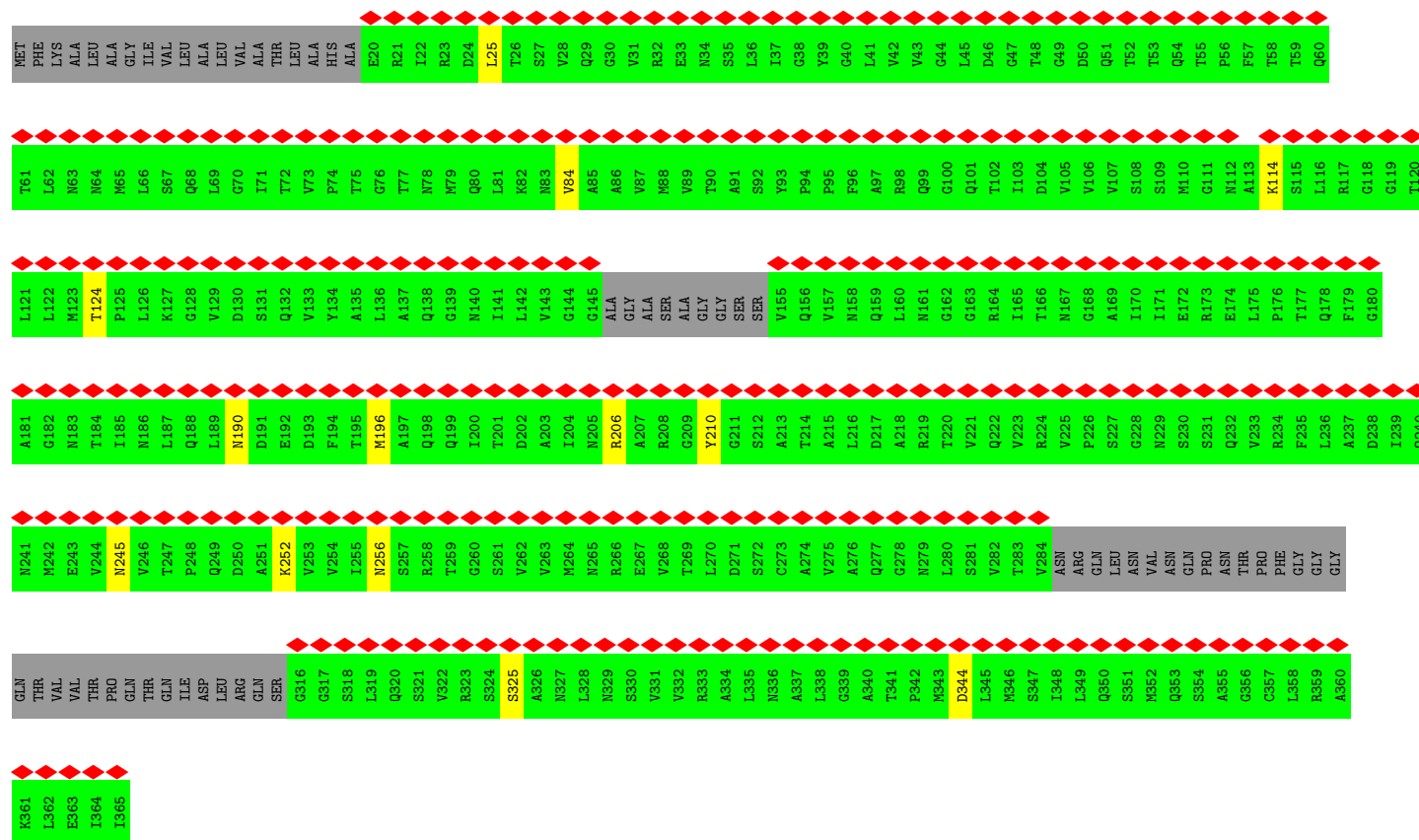
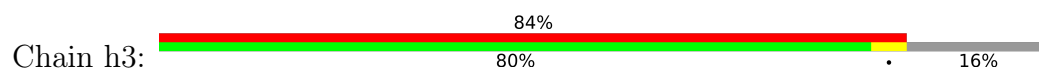


• Molecule 11: Flagellar P-ring protein

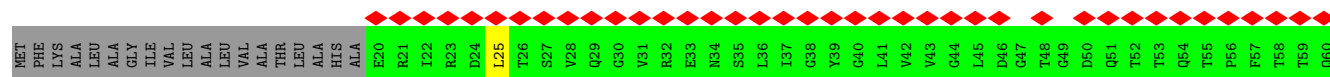
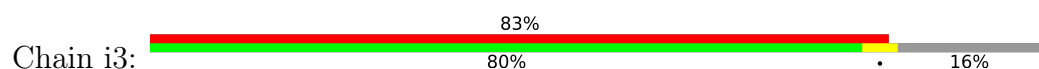


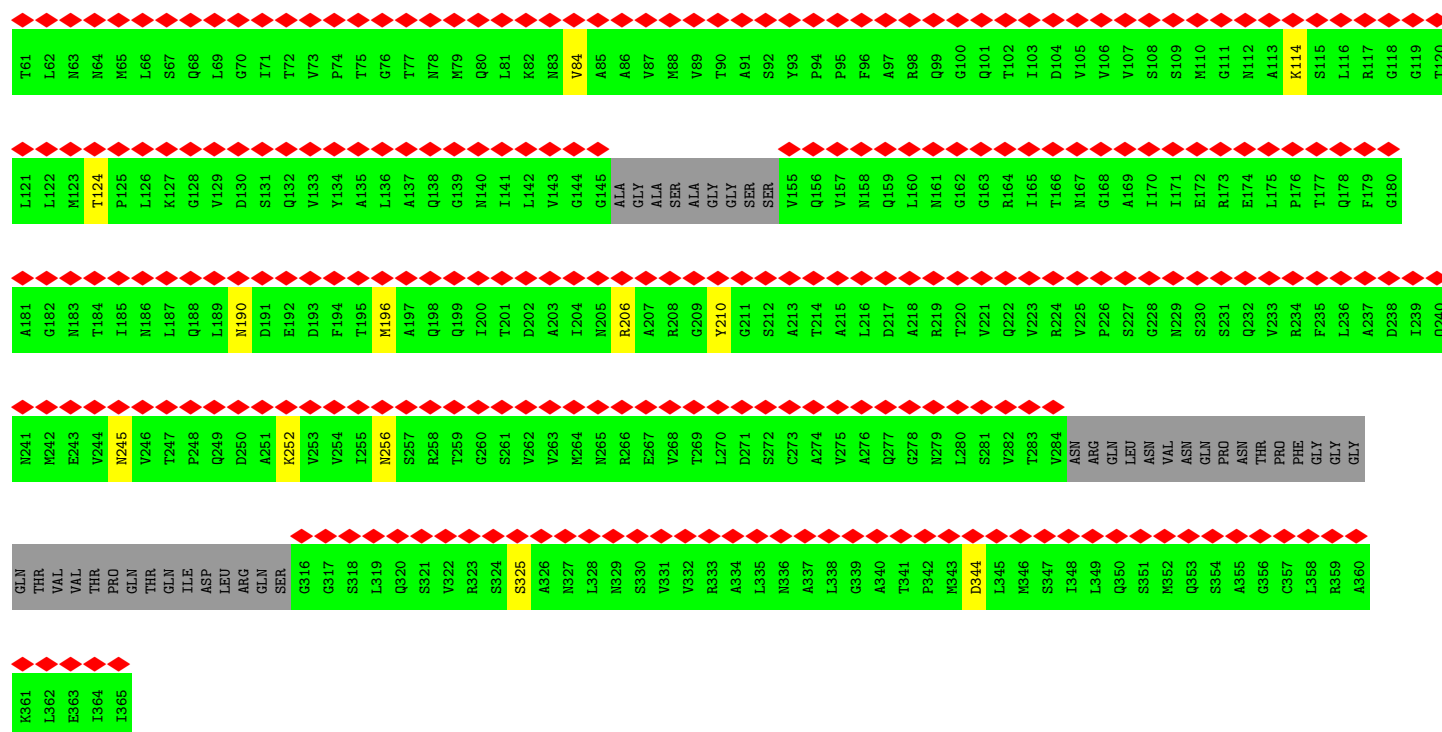


• Molecule 11: Flagellar P-ring protein

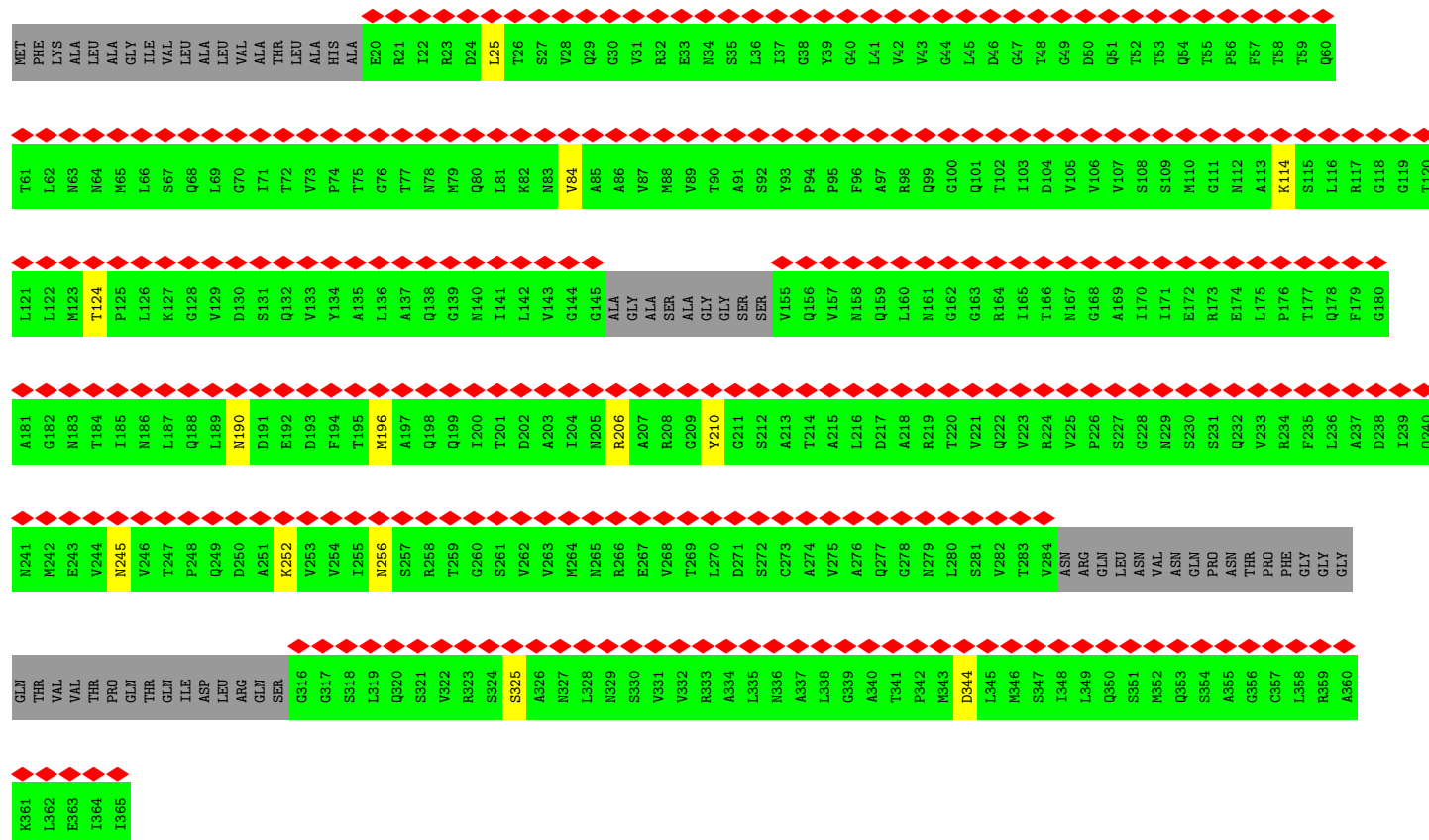
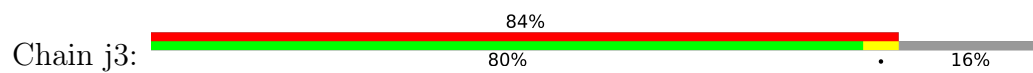


• Molecule 11: Flagellar P-ring protein



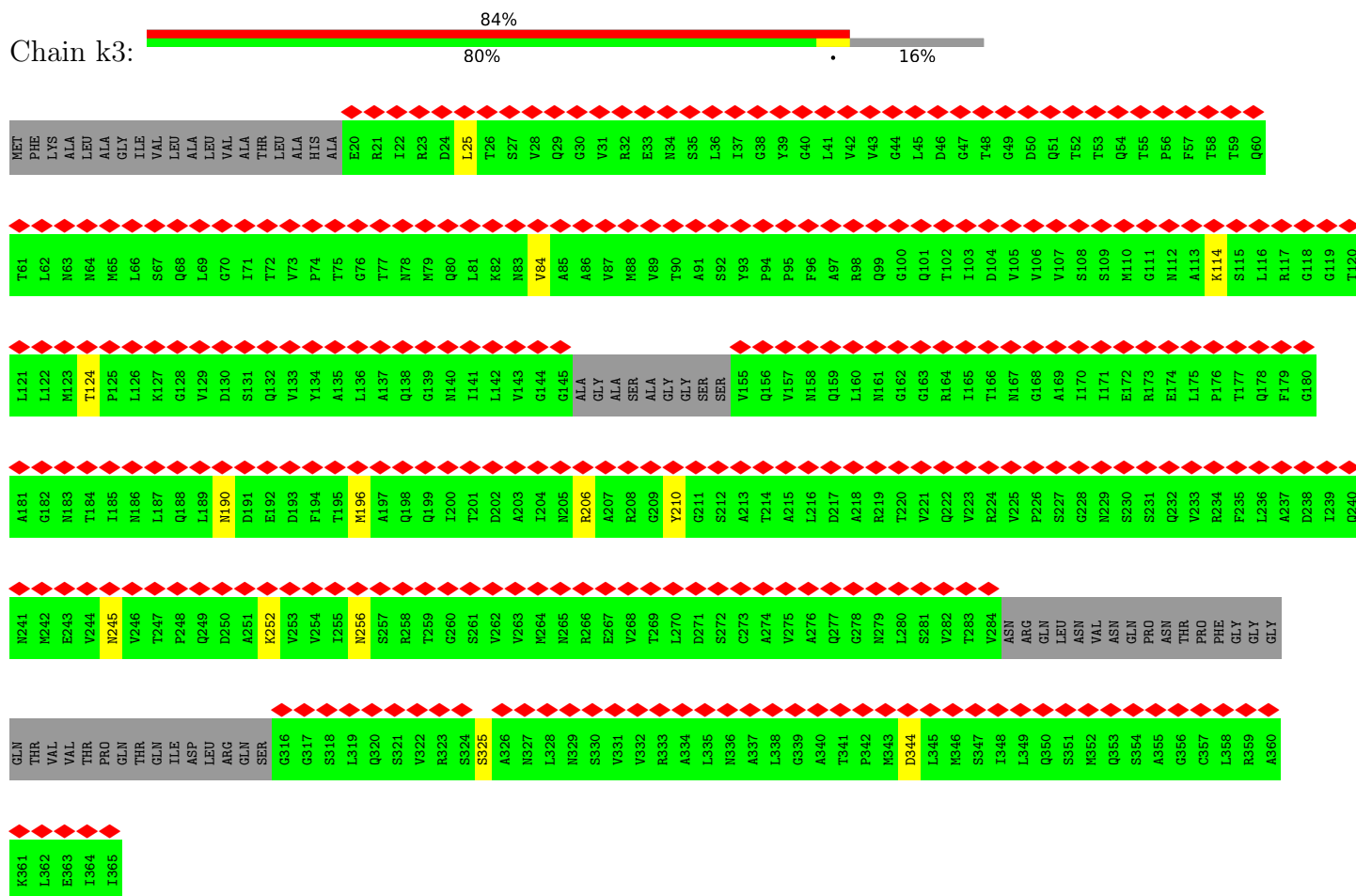


• Molecule 11: Flagellar P-ring protein



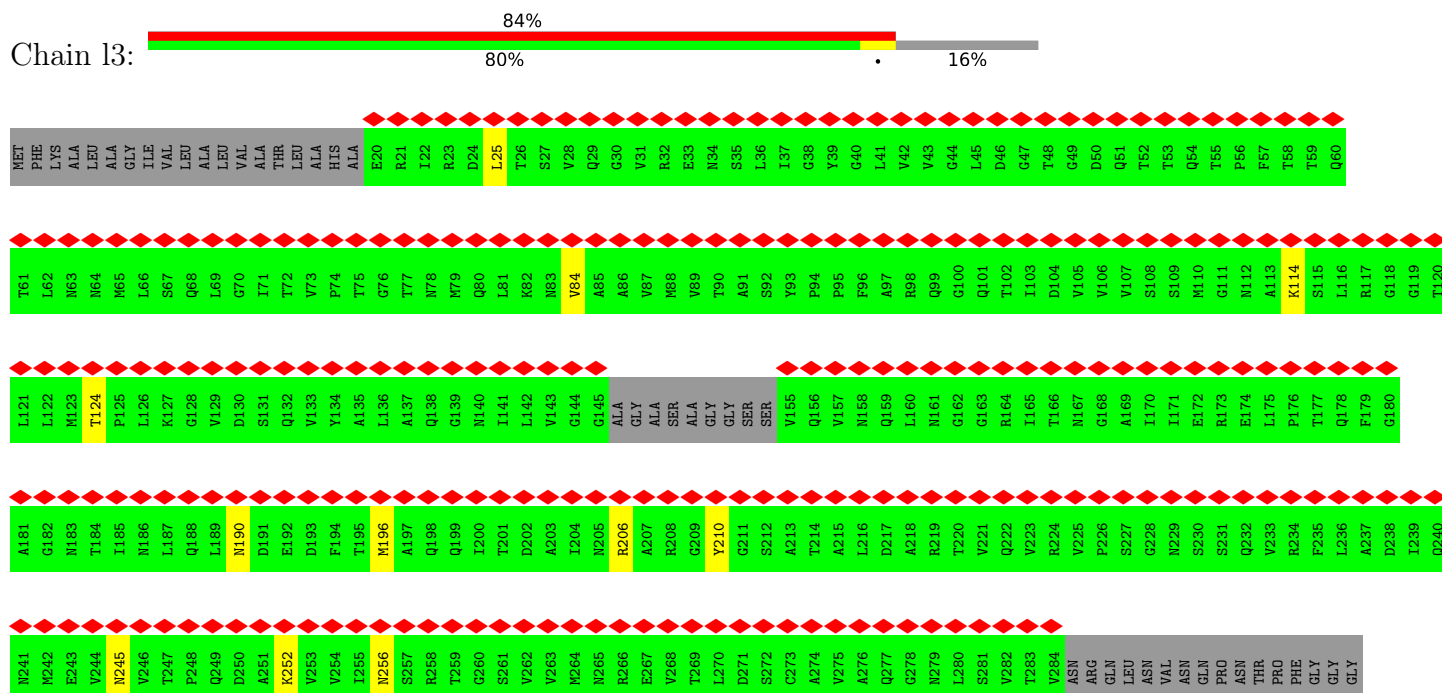
- Molecule 11: Flagellar P-ring protein

Chain k3:

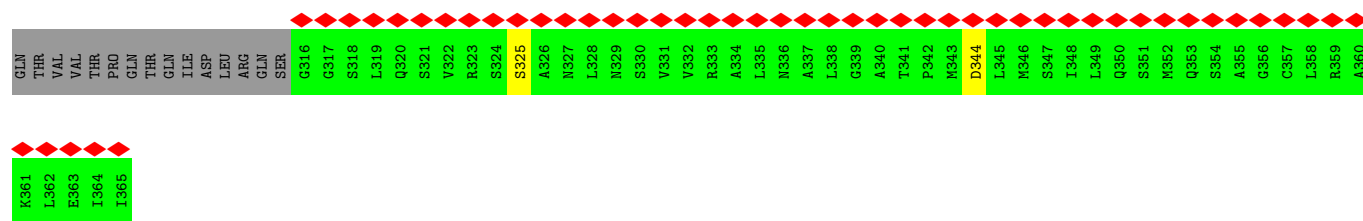


- Molecule 11: Flagellar P-ring protein

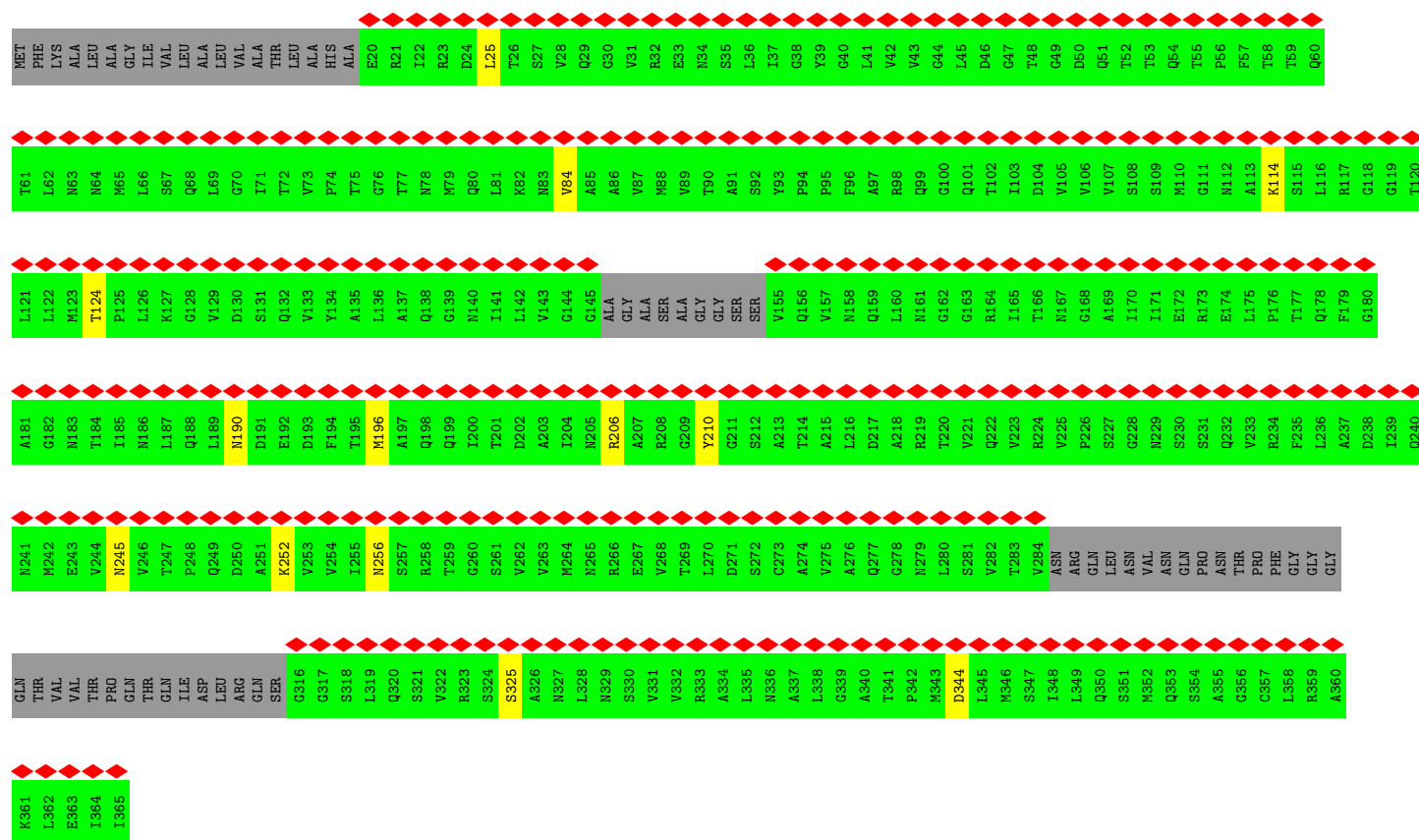
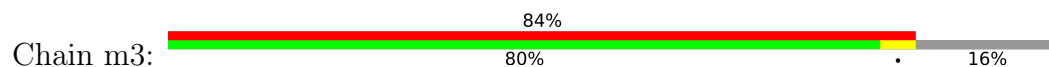
Chain l3:



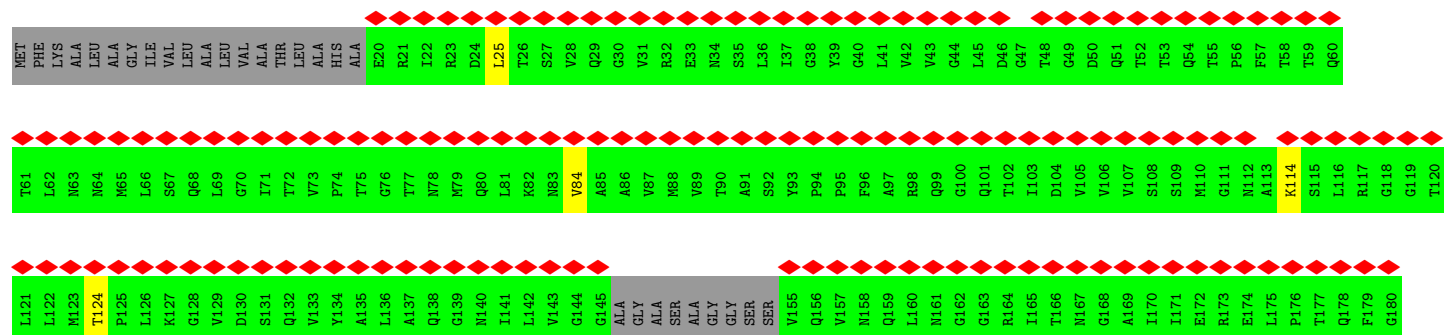
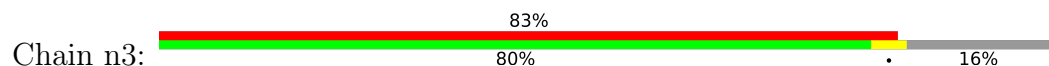


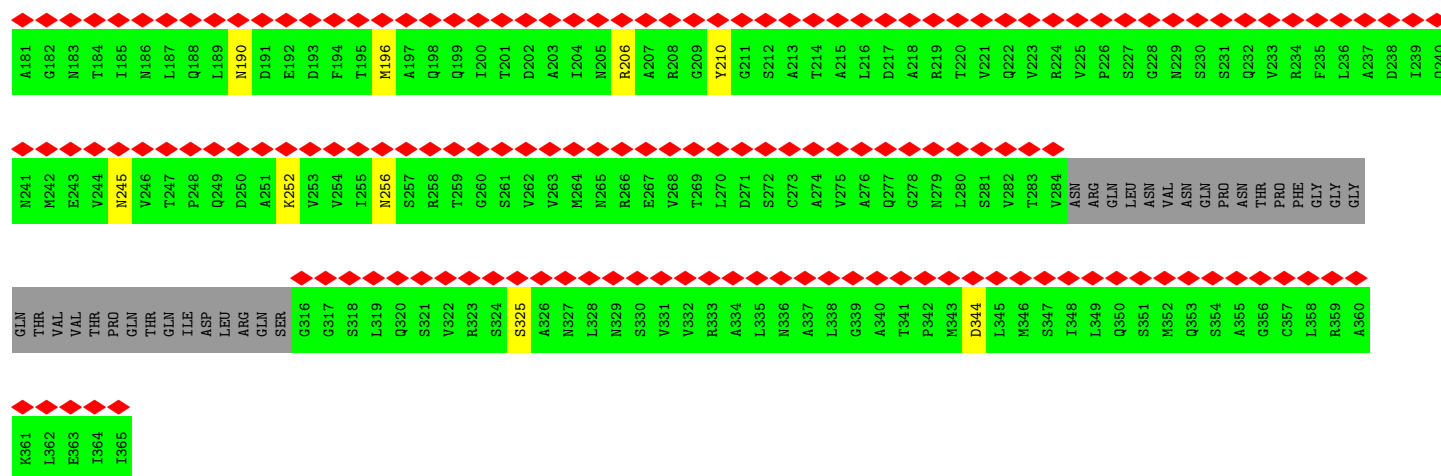


• Molecule 11: Flagellar P-ring protein

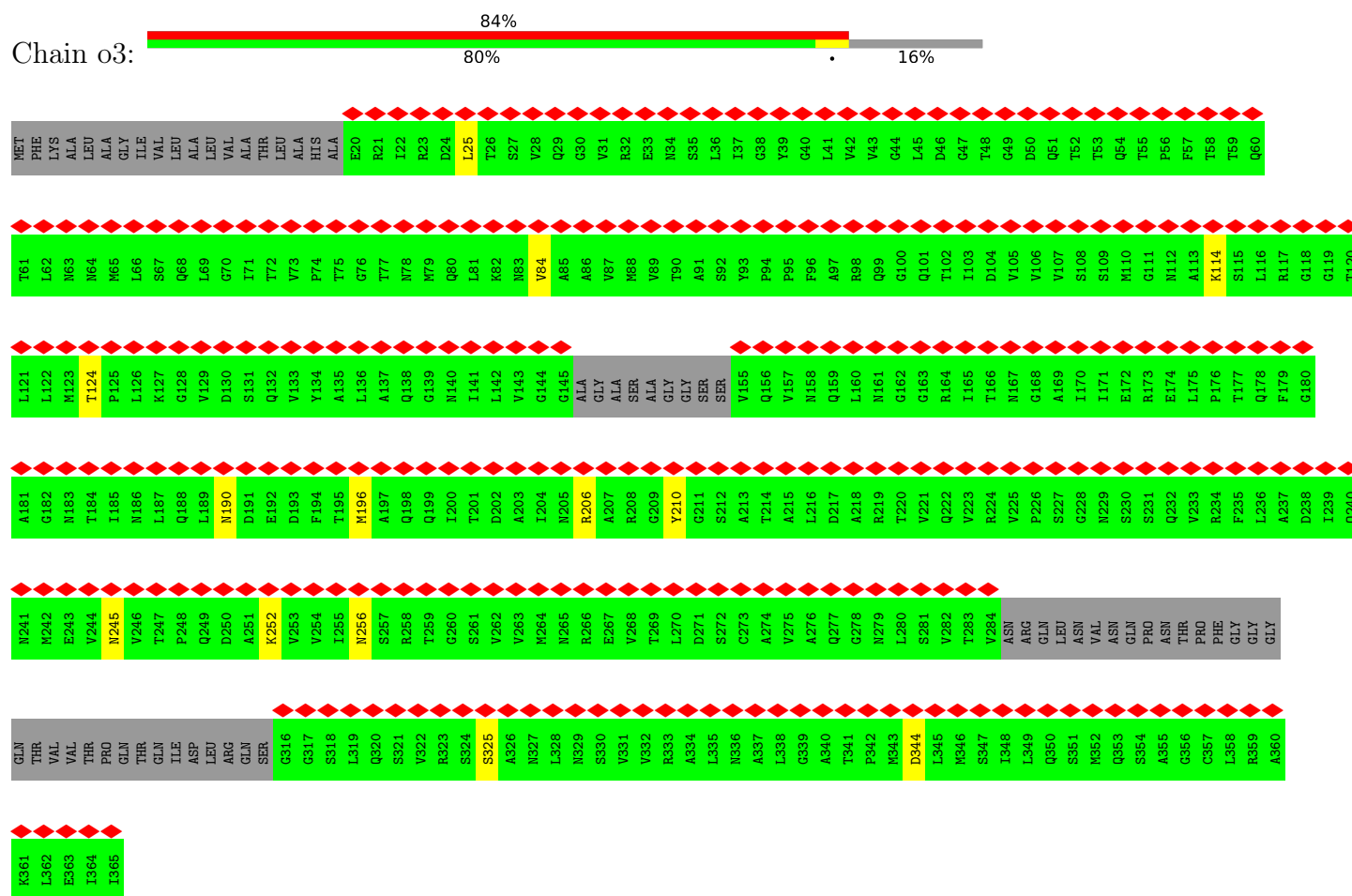


• Molecule 11: Flagellar P-ring protein

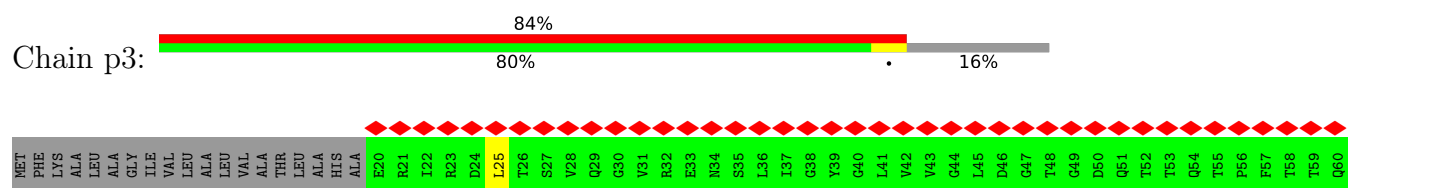




• Molecule 11: Flagellar P-ring protein



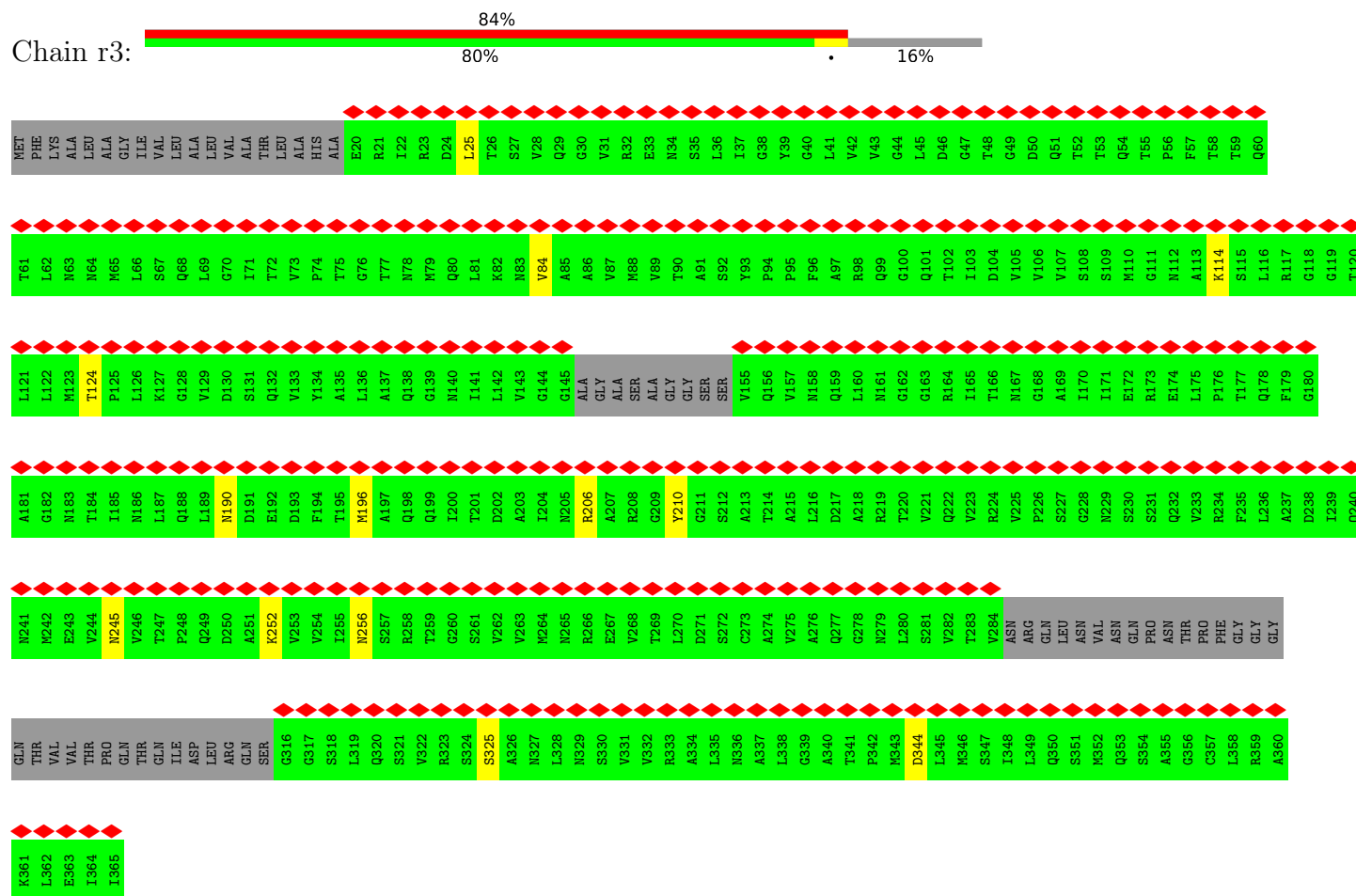
• Molecule 11: Flagellar P-ring protein





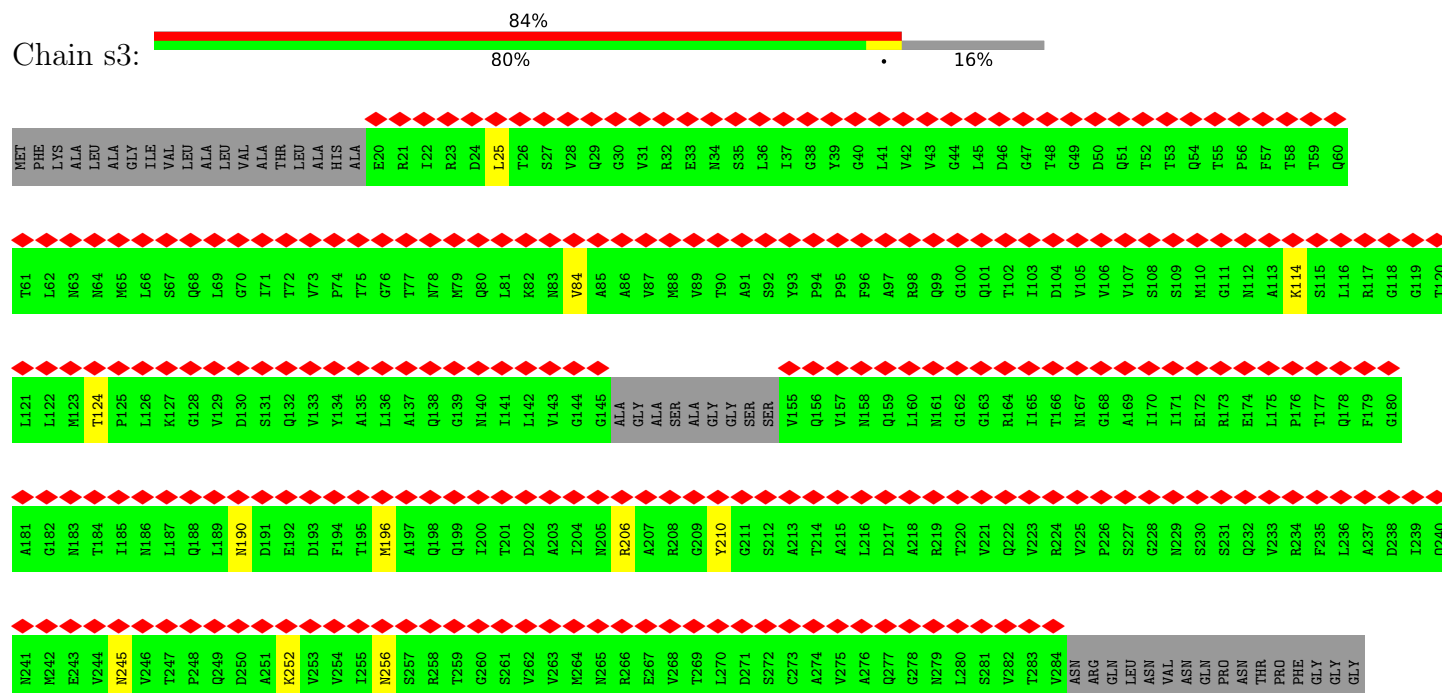
• Molecule 11: Flagellar P-ring protein

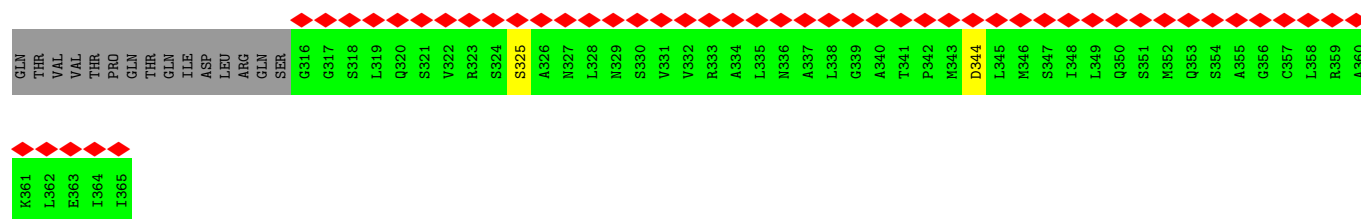
Chain r3:



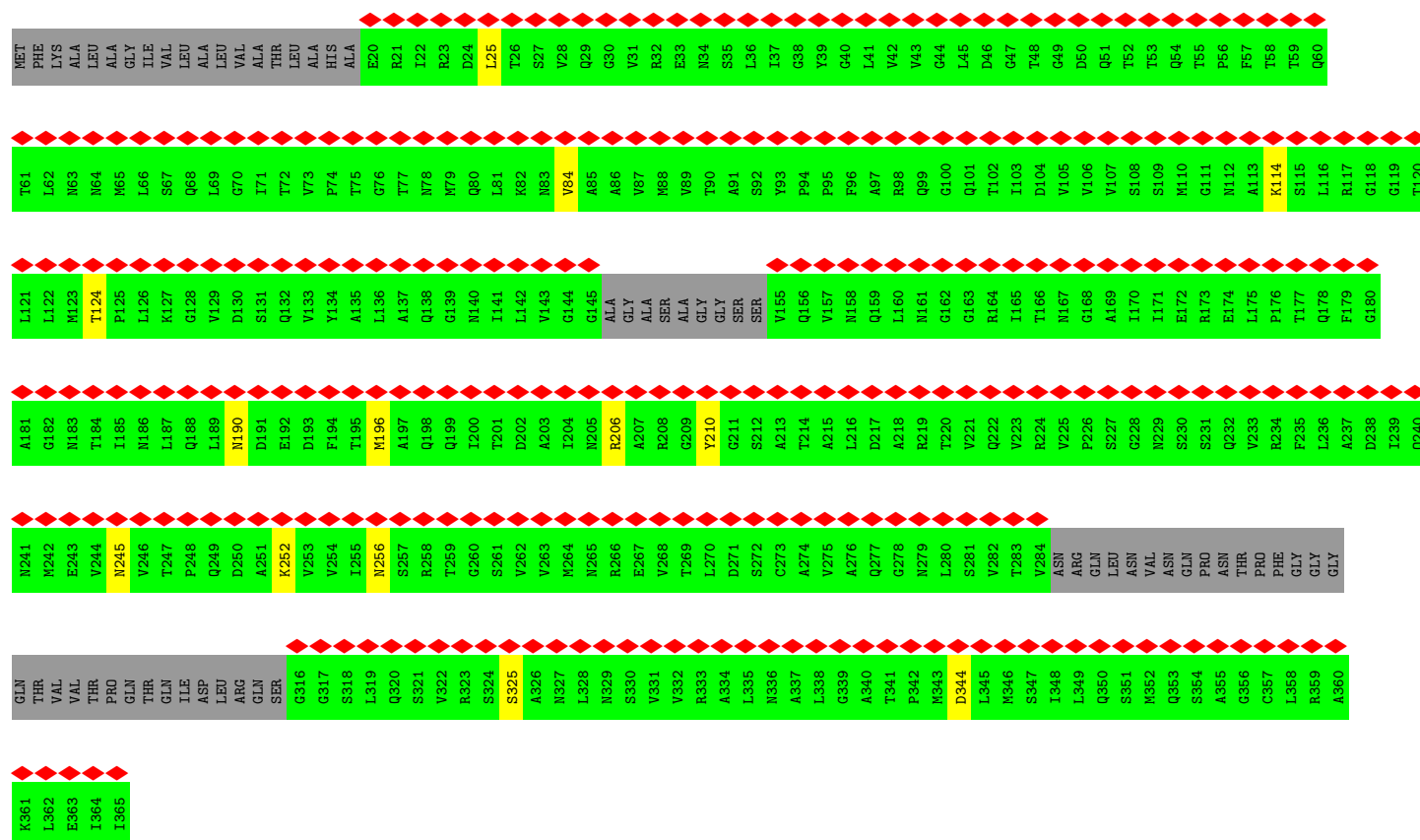
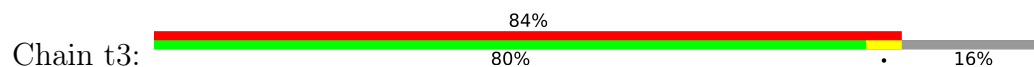
• Molecule 11: Flagellar P-ring protein

Chain s3:

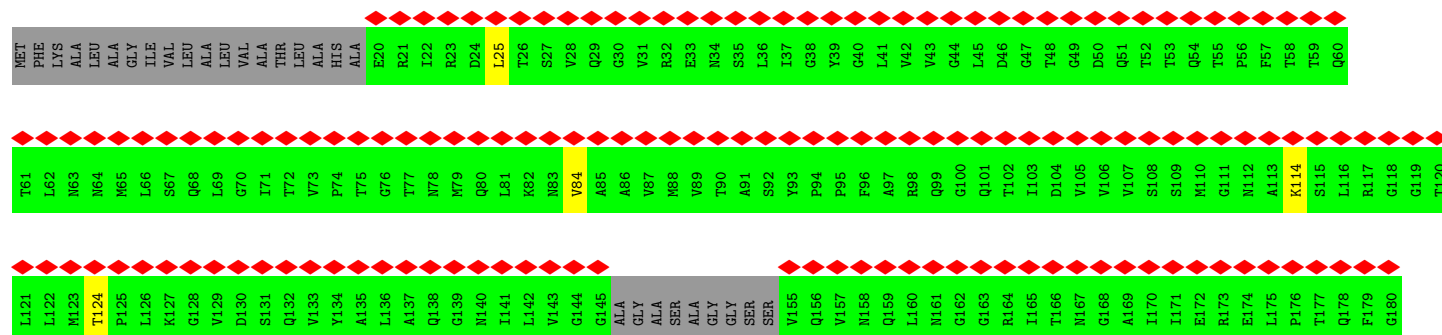
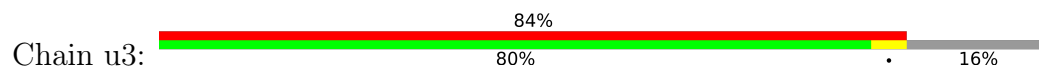


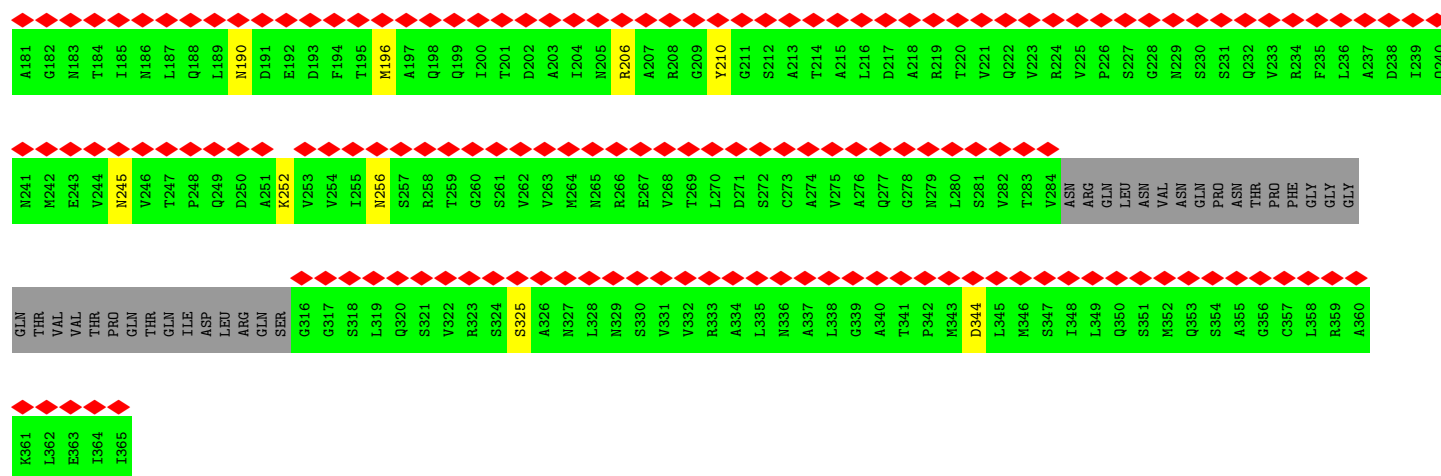


• Molecule 11: Flagellar P-ring protein

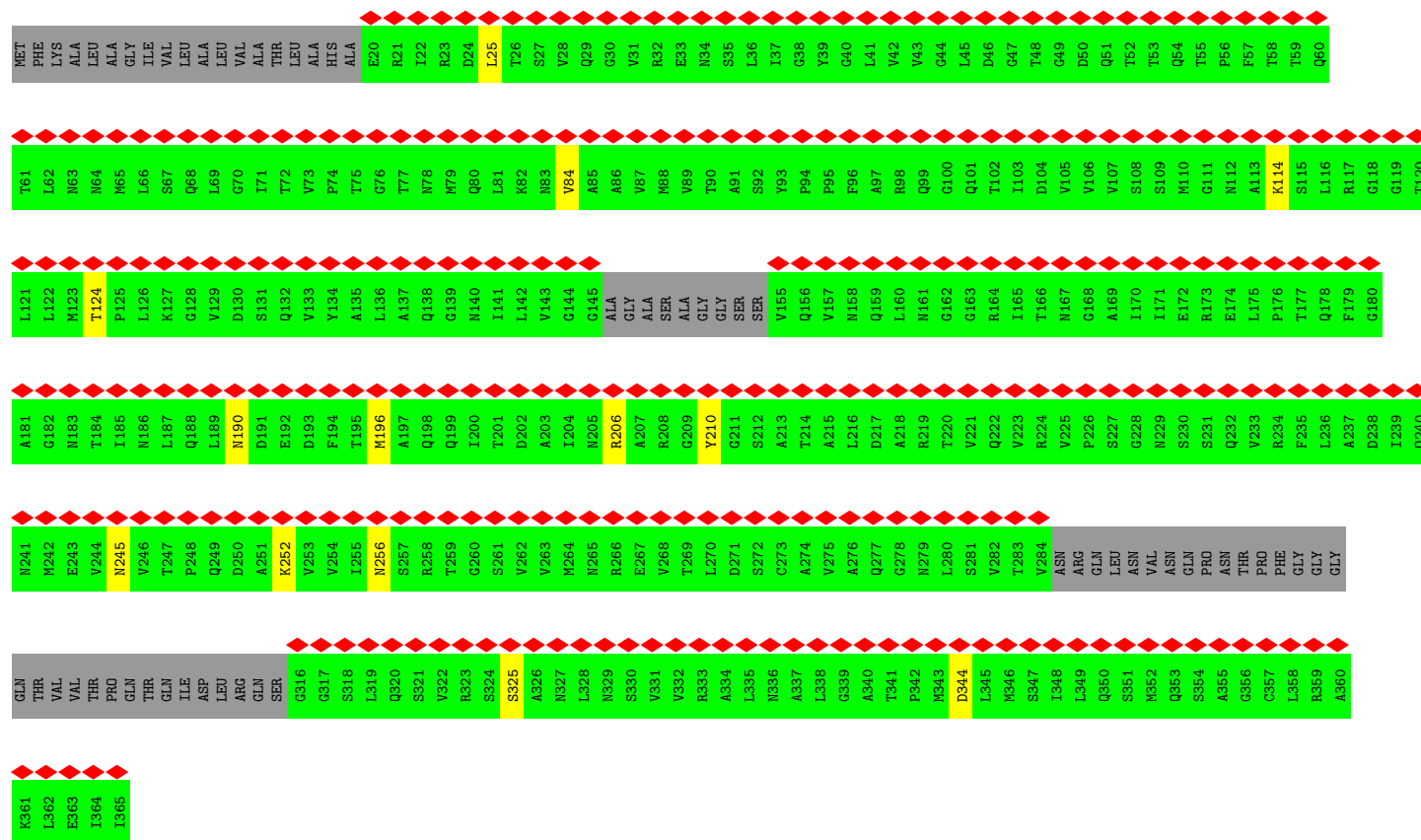
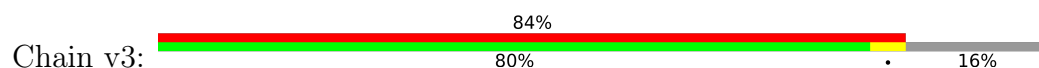


• Molecule 11: Flagellar P-ring protein

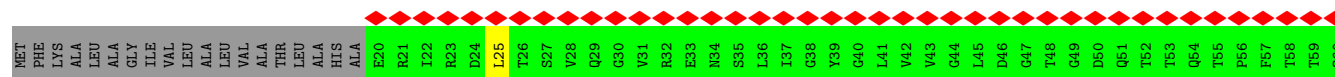
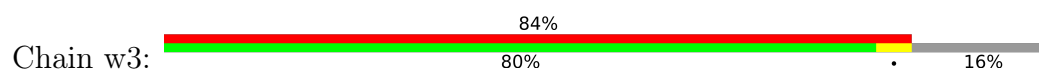




• Molecule 11: Flagellar P-ring protein



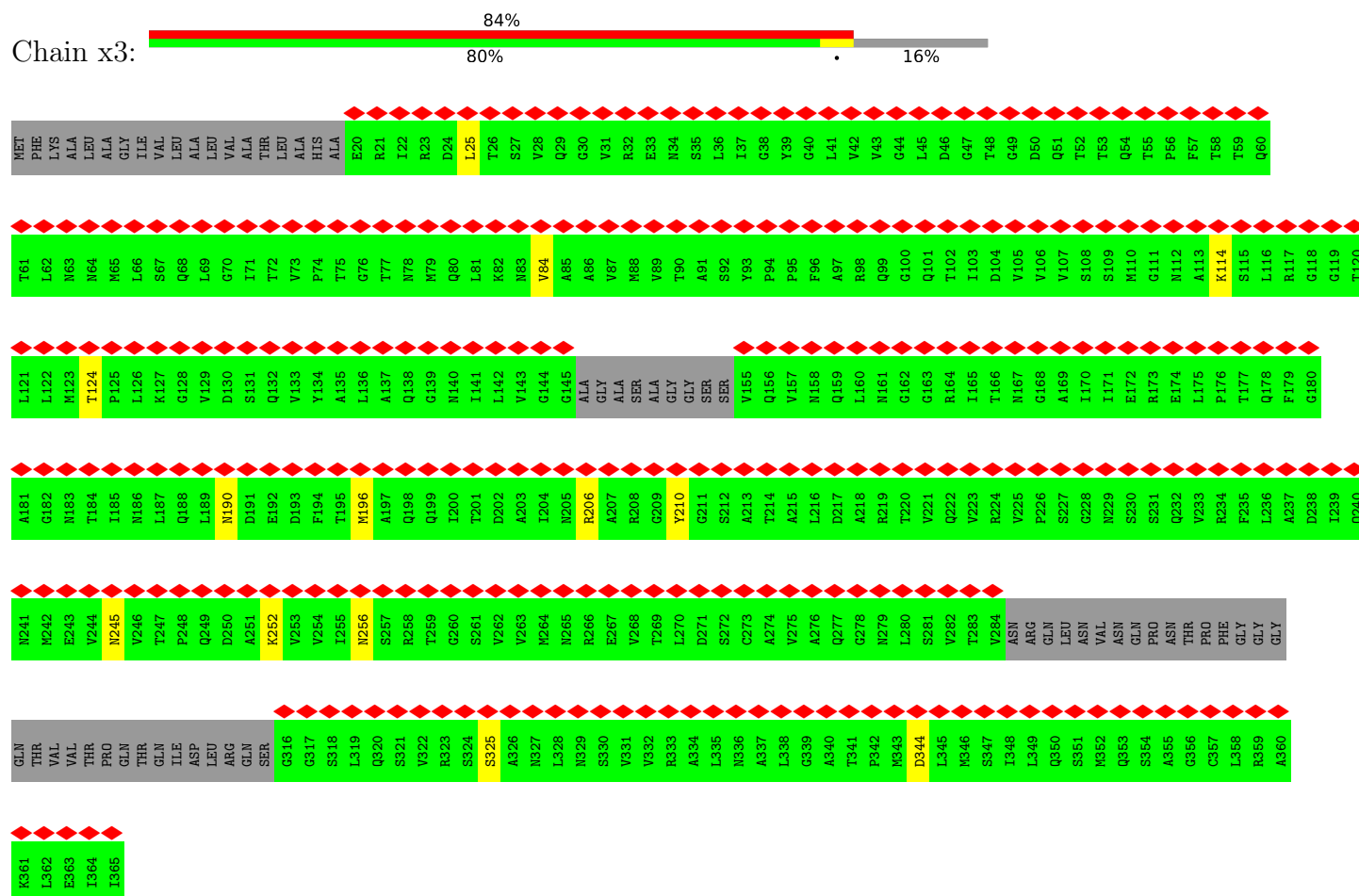
• Molecule 11: Flagellar P-ring protein





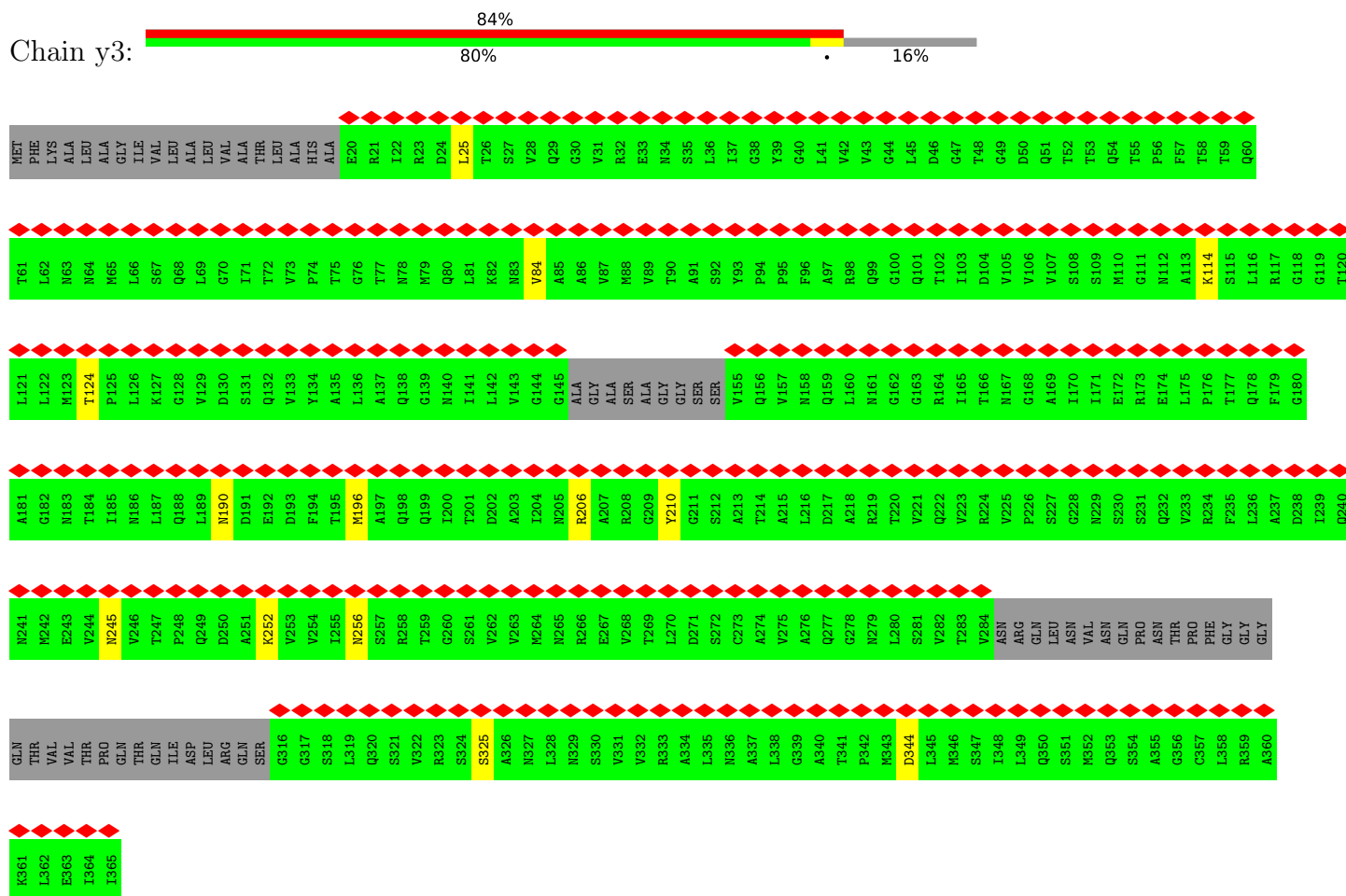
# Molecule 11: Flagellar P-ring protein

Chain x3:



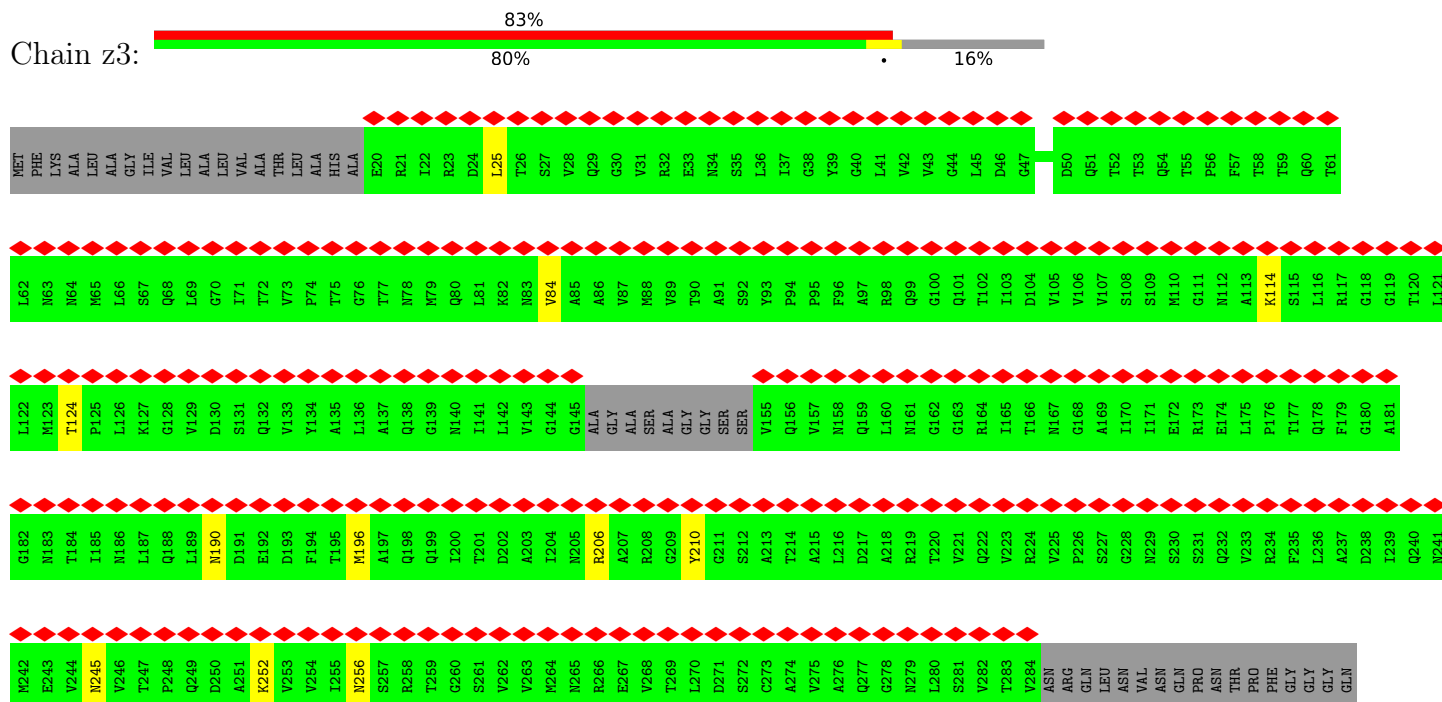
## ● Molecule 11: Flagellar P-ring protein

Chain y3:

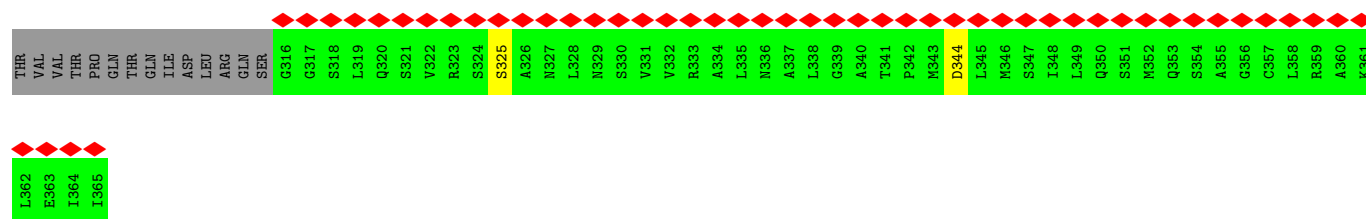


## ● Molecule 11: Flagellar P-ring protein

Chain z3:

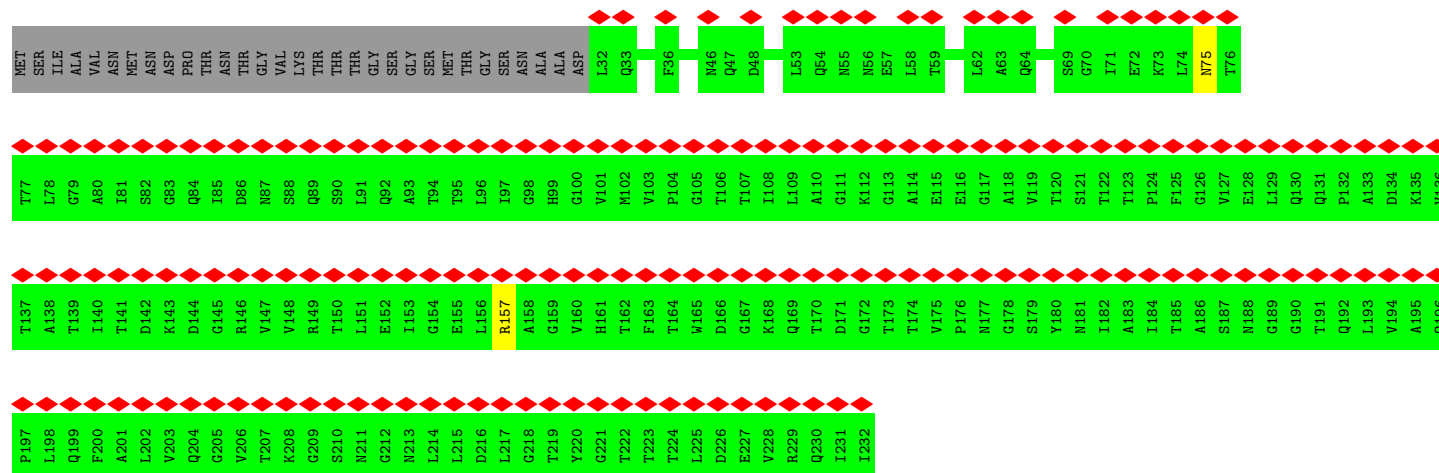






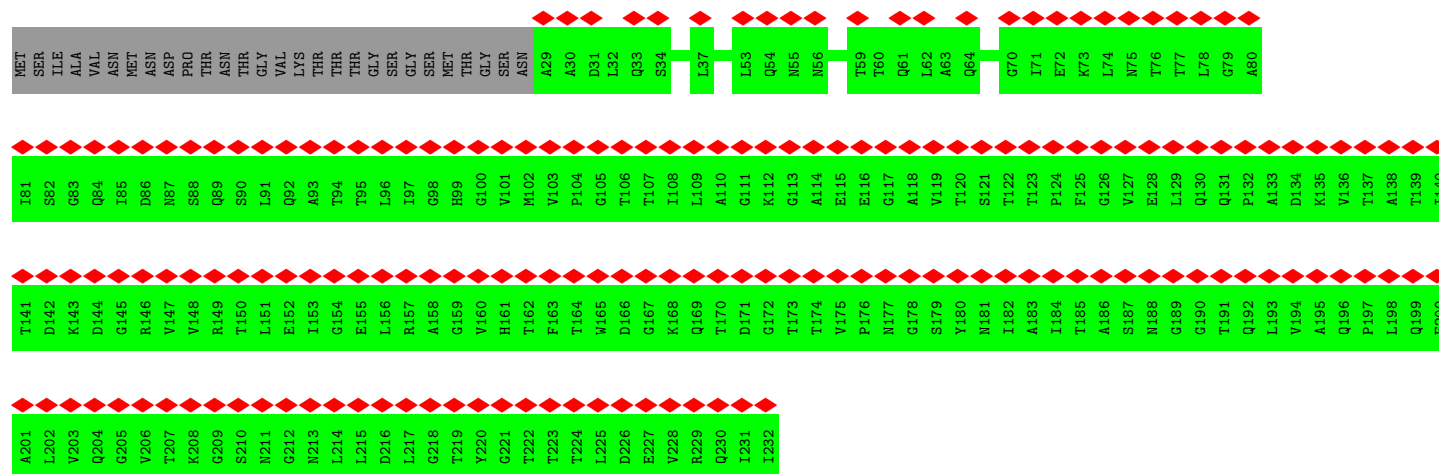
• Molecule 12: Basal-body rod modification protein FlgD

Chain A4: 76% 86% 13%



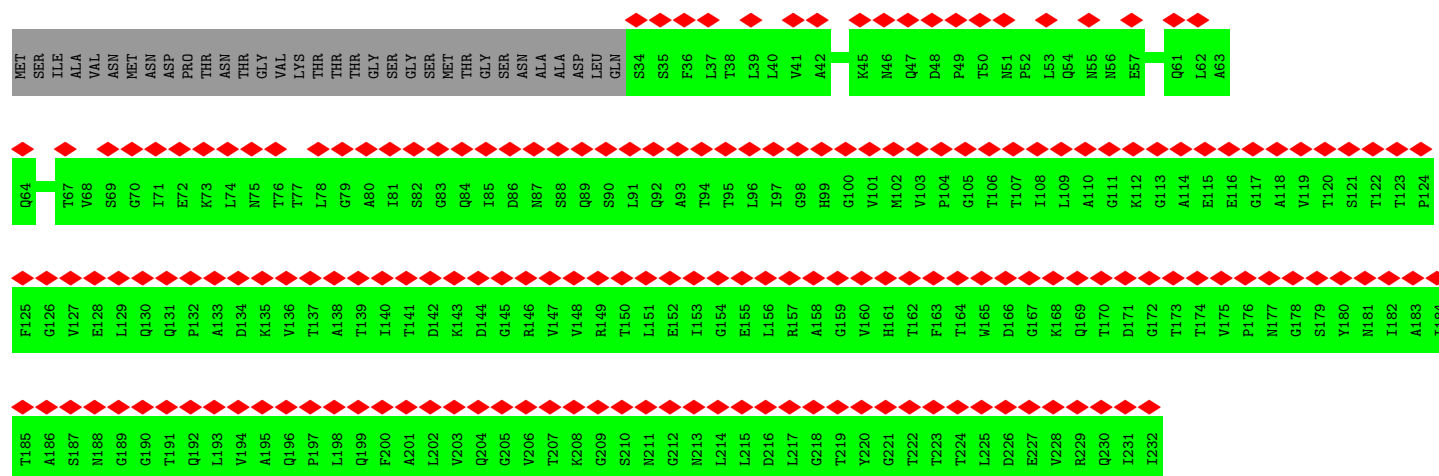
• Molecule 12: Basal-body rod modification protein FlgD

Chain B4: 76% 88% 12%

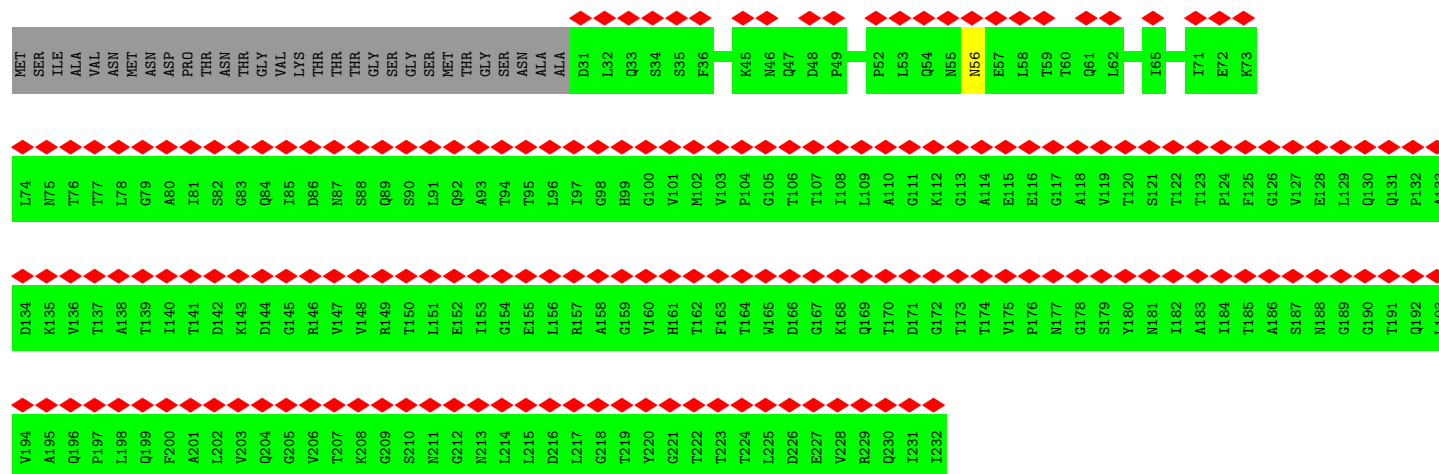
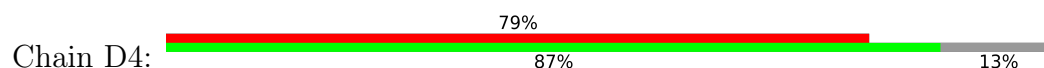


• Molecule 12: Basal-body rod modification protein FlgD

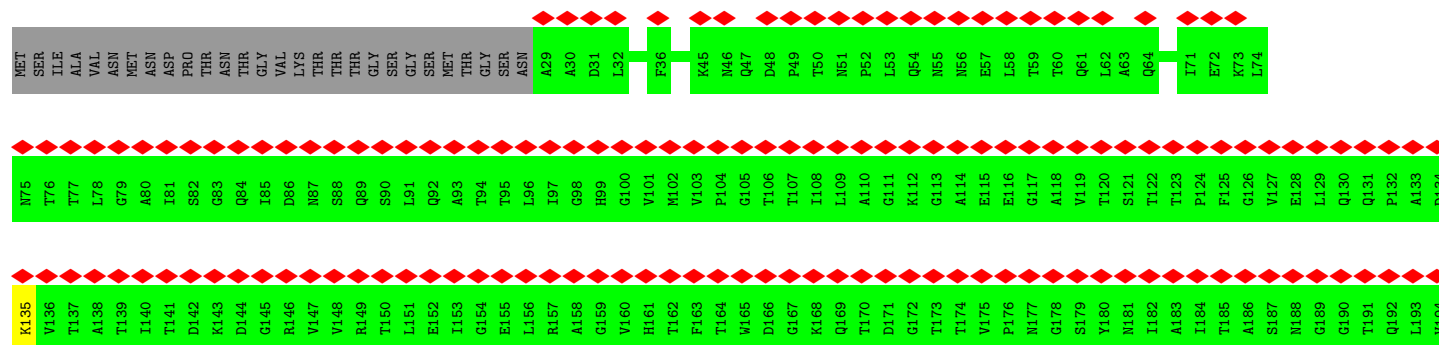
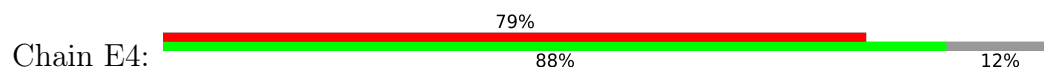
Chain C4: 79% 86% 14%



• Molecule 12: Basal-body rod modification protein FlgD



• Molecule 12: Basal-body rod modification protein FlgD



A195	Q196	P197	L198	Q199	F200	A201	L202	V203	Q204	G205	V206	T207	K208	G209	S210	N211	G212	N213	L214	L215	D216	L217	G218	T219	Y220	G221	T222	T223	T224	L225	D226	E227	V228	R229	Q230	I231	I232
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60497	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 ( $e^-/\text{\AA}^2$ )	59	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.023	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0075	Depositor
Map size ( $\text{\AA}$ )	638.976, 638.976, 638.976	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.832, 0.832, 0.832	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A1	0.39	0/1205	0.52	0/1624
1	B1	0.38	0/1955	0.55	0/2645
1	C1	0.39	0/1955	0.54	1/2645 (0.0%)
1	D1	0.40	0/1205	0.53	0/1624
1	E1	0.38	0/1955	0.55	1/2645 (0.0%)
1	F1	0.39	0/1205	0.57	1/1624 (0.1%)
1	G1	0.37	0/1955	0.54	0/2645
1	H1	0.38	0/1955	0.56	0/2645
1	I1	0.37	0/1955	0.53	0/2645
1	J1	0.42	0/1205	0.53	1/1624 (0.1%)
1	K1	0.36	0/1955	0.52	0/2645
1	L1	0.36	0/1955	0.54	0/2645
1	M1	0.40	0/1205	0.55	1/1624 (0.1%)
1	N1	0.36	0/1955	0.55	0/2645
1	O1	0.35	0/1955	0.53	1/2645 (0.0%)
1	P1	0.37	0/1205	0.52	1/1624 (0.1%)
1	Q1	0.35	0/1955	0.52	0/2645
1	R1	0.35	0/1955	0.51	1/2645 (0.0%)
1	S1	0.38	0/1205	0.50	1/1624 (0.1%)
1	T1	0.35	0/1955	0.52	0/2645
1	U1	0.36	0/1955	0.56	0/2645
1	V1	0.38	0/1205	0.52	0/1624
1	W1	0.35	0/1955	0.52	1/2645 (0.0%)
1	X1	0.35	0/1955	0.52	1/2645 (0.0%)
1	Y1	0.34	0/1955	0.53	0/2645
1	Z1	0.41	0/1205	0.54	0/1624
1	a1	0.36	0/1955	0.53	0/2645
1	b1	0.39	0/1205	0.51	0/1624
1	c1	0.37	0/1955	0.53	1/2645 (0.0%)
1	d1	0.37	0/1955	0.54	0/2645
1	e1	0.39	0/1205	0.52	1/1624 (0.1%)
1	f1	0.37	0/1955	0.53	0/2645
1	g1	0.37	0/1955	0.54	1/2645 (0.0%)
1	h1	0.37	0/1955	0.51	0/2645

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	A2	0.39	0/1662	0.62	1/2263 (0.0%)
2	B2	0.41	0/1662	0.61	0/2263
2	C2	0.40	0/1662	0.61	0/2263
2	D2	0.43	1/1662 (0.1%)	0.58	0/2263
2	E2	0.61	1/1662 (0.1%)	0.71	1/2263 (0.0%)
3	F2	0.35	0/2035	0.58	0/2777
4	G2	0.34	0/681	0.61	0/930
4	H2	0.34	0/681	0.55	0/930
4	I2	0.37	0/681	0.53	0/930
4	J2	2.82	6/681 (0.9%)	0.65	0/930
5	K2	0.35	0/296	0.60	1/395 (0.3%)
5	L2	0.33	0/567	0.44	0/761
5	M2	0.36	0/567	0.45	0/761
5	N2	0.36	0/567	0.46	0/761
5	O2	0.34	0/567	0.47	0/761
5	P2	0.36	0/567	0.47	0/761
6	Q2	0.39	0/1035	0.52	0/1399
6	R2	0.37	0/941	0.53	0/1269
6	S2	0.40	0/951	0.51	0/1281
6	T2	0.40	0/842	0.53	0/1132
6	U2	0.37	0/934	0.50	0/1259
7	V2	0.44	0/981	0.65	0/1334
7	W2	0.44	0/976	0.57	0/1327
7	X2	0.48	0/976	0.56	0/1327
7	Y2	0.46	0/976	0.56	0/1327
7	Z2	0.46	0/976	0.55	0/1327
7	a2	0.42	0/976	0.57	0/1327
8	b2	0.39	0/1836	0.59	0/2502
8	c2	0.42	0/1836	0.59	0/2502
8	d2	0.44	0/1836	0.58	0/2502
8	e2	0.43	0/1836	0.56	0/2502
8	f2	0.40	0/1836	0.56	0/2502
9	l2	0.38	0/1973	0.55	0/2682
9	22	0.37	0/1973	0.54	0/2682
9	32	0.36	0/1971	0.55	1/2677 (0.0%)
9	42	0.31	0/1973	0.56	1/2682 (0.0%)
9	g2	0.41	0/1973	0.52	0/2682
9	h2	0.43	0/1973	0.51	0/2682
9	i2	0.43	0/1973	0.53	0/2682
9	j2	0.44	0/1973	0.52	0/2682
9	k2	0.43	0/1973	0.54	0/2682
9	l2	0.43	0/1894	0.51	0/2573
9	m2	0.46	0/1894	0.54	0/2573

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
9	n2	0.43	0/1894	0.51	0/2573
9	o2	0.44	0/1894	0.53	0/2573
9	p2	0.44	0/1894	0.52	0/2573
9	q2	0.43	0/1907	0.52	0/2590
9	r2	0.42	0/1973	0.56	0/2682
9	s2	0.43	0/1973	0.56	0/2682
9	t2	0.42	0/1973	0.58	2/2682 (0.1%)
9	u2	0.42	0/1973	0.56	0/2682
9	v2	0.43	0/1973	0.54	0/2682
9	w2	0.42	0/1973	0.57	1/2682 (0.0%)
9	x2	0.39	0/1973	0.54	0/2682
9	y2	0.36	0/1973	0.53	0/2682
9	z2	0.35	0/1973	0.54	2/2682 (0.1%)
10	A3	0.26	0/1614	0.52	1/2194 (0.0%)
10	B3	0.27	0/1614	0.52	1/2194 (0.0%)
10	C3	0.26	0/1614	0.52	1/2194 (0.0%)
10	D3	0.26	0/1614	0.52	1/2194 (0.0%)
10	E3	0.26	0/1614	0.52	1/2194 (0.0%)
10	F3	0.26	0/1614	0.52	1/2194 (0.0%)
10	G3	0.26	0/1614	0.52	1/2194 (0.0%)
10	H3	0.26	0/1614	0.52	1/2194 (0.0%)
10	I3	0.26	0/1614	0.52	1/2194 (0.0%)
10	J3	0.26	0/1614	0.52	1/2194 (0.0%)
10	K3	0.26	0/1614	0.52	1/2194 (0.0%)
10	L3	0.26	0/1614	0.52	1/2194 (0.0%)
10	M3	0.26	0/1614	0.52	1/2194 (0.0%)
10	N3	0.26	0/1614	0.52	1/2194 (0.0%)
10	O3	0.26	0/1614	0.52	1/2194 (0.0%)
10	P3	0.26	0/1614	0.52	1/2194 (0.0%)
10	Q3	0.26	0/1614	0.52	1/2194 (0.0%)
10	R3	0.26	0/1614	0.52	1/2194 (0.0%)
10	S3	0.27	0/1614	0.52	1/2194 (0.0%)
10	T3	0.26	0/1614	0.52	1/2194 (0.0%)
10	U3	0.26	0/1614	0.52	1/2194 (0.0%)
10	V3	0.26	0/1614	0.52	1/2194 (0.0%)
10	W3	0.26	0/1611	0.52	1/2188 (0.0%)
10	X3	0.26	0/1614	0.52	1/2194 (0.0%)
10	Y3	0.26	0/1614	0.52	1/2194 (0.0%)
10	Z3	0.26	0/1614	0.52	1/2194 (0.0%)
11	a3	0.24	0/2267	0.50	0/3073
11	b3	0.24	0/2267	0.50	0/3073
11	c3	0.24	0/2267	0.50	0/3073
11	d3	0.24	0/2267	0.50	0/3073

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
11	e3	0.24	0/2267	0.50	0/3073
11	f3	0.24	0/2267	0.50	0/3073
11	g3	0.24	0/2267	0.50	0/3073
11	h3	0.24	0/2266	0.50	0/3071
11	i3	0.24	0/2267	0.50	0/3073
11	j3	0.24	0/2267	0.50	0/3073
11	k3	0.24	0/2267	0.50	0/3073
11	l3	0.24	0/2267	0.50	0/3073
11	m3	0.24	0/2267	0.50	0/3073
11	n3	0.24	0/2267	0.50	0/3073
11	o3	0.24	0/2267	0.50	0/3073
11	p3	0.24	0/2267	0.50	0/3073
11	q3	0.24	0/2267	0.50	0/3073
11	r3	0.24	0/2264	0.50	0/3066
11	s3	0.24	0/2267	0.50	0/3073
11	t3	0.24	0/2267	0.50	0/3073
11	u3	0.24	0/2267	0.50	0/3073
11	v3	0.24	0/2267	0.50	0/3073
11	w3	0.24	0/2267	0.50	0/3073
11	x3	0.24	0/2267	0.50	0/3073
11	y3	0.24	0/2267	0.50	0/3073
11	z3	0.24	0/2267	0.50	0/3073
12	A4	0.25	0/1491	0.47	0/2033
12	B4	0.25	0/1509	0.48	0/2058
12	C4	0.25	0/1474	0.48	0/2010
12	D4	0.25	0/1496	0.49	0/2040
12	E4	0.25	0/1509	0.48	0/2058
All	All	0.37	8/249431 (0.0%)	0.53	50/338382 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B1	0	1
1	E1	0	1
1	G1	0	1
1	H1	0	1
1	L1	0	1
1	N1	0	1
2	B2	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	C2	0	2
2	D2	0	2
2	E2	0	1
3	F2	0	2
4	G2	0	1
4	H2	0	1
4	I2	0	1
4	J2	0	1
6	U2	0	1
8	b2	0	2
8	c2	0	2
8	d2	0	1
8	e2	0	3
8	f2	0	3
All	All	0	31

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	J2	51	PHE	CE2-CZ	34.87	2.03	1.37
4	J2	51	PHE	CE1-CZ	33.72	2.01	1.37
4	J2	51	PHE	CD1-CE1	32.60	2.04	1.39
4	J2	51	PHE	CD2-CE2	31.33	2.02	1.39
4	J2	51	PHE	CG-CD1	21.84	1.71	1.38

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E2	205	MET	CG-SD-CE	20.16	132.46	100.20
9	t2	167	PRO	CA-N-CD	-8.46	99.66	111.50
1	E1	282	TYR	C-N-CA	-6.66	105.04	121.70
1	g1	282	TYR	C-N-CA	-6.65	105.07	121.70
10	Z3	43	PRO	CA-N-CD	-6.36	102.59	111.50

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B1	163	SER	Peptide
1	E1	162	PRO	Peptide
1	G1	165	PHE	Peptide

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Mol	Chain	Res	Type	Group
1	H1	165	PHE	Peptide
1	L1	125	GLN	Peptide

## 5.2 Too-close contacts [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	145/560 (26%)	143 (99%)	2 (1%)	0	100	100
1	B1	242/560 (43%)	227 (94%)	15 (6%)	0	100	100
1	C1	242/560 (43%)	230 (95%)	11 (4%)	1 (0%)	30	62
1	D1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100
1	E1	242/560 (43%)	226 (93%)	16 (7%)	0	100	100
1	F1	145/560 (26%)	141 (97%)	4 (3%)	0	100	100
1	G1	242/560 (43%)	225 (93%)	16 (7%)	1 (0%)	30	62
1	H1	242/560 (43%)	221 (91%)	19 (8%)	2 (1%)	16	49
1	I1	242/560 (43%)	229 (95%)	12 (5%)	1 (0%)	30	62
1	J1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100
1	K1	242/560 (43%)	230 (95%)	11 (4%)	1 (0%)	30	62
1	L1	242/560 (43%)	224 (93%)	18 (7%)	0	100	100
1	M1	145/560 (26%)	141 (97%)	4 (3%)	0	100	100
1	N1	242/560 (43%)	223 (92%)	19 (8%)	0	100	100
1	O1	242/560 (43%)	231 (96%)	10 (4%)	1 (0%)	30	62
1	P1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100
1	Q1	242/560 (43%)	224 (93%)	17 (7%)	1 (0%)	30	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R1	242/560 (43%)	229 (95%)	13 (5%)	0	100	100
1	S1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100
1	T1	242/560 (43%)	230 (95%)	12 (5%)	0	100	100
1	U1	242/560 (43%)	231 (96%)	11 (4%)	0	100	100
1	V1	145/560 (26%)	141 (97%)	4 (3%)	0	100	100
1	W1	242/560 (43%)	227 (94%)	14 (6%)	1 (0%)	30	62
1	X1	242/560 (43%)	225 (93%)	17 (7%)	0	100	100
1	Y1	242/560 (43%)	228 (94%)	14 (6%)	0	100	100
1	Z1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100
1	a1	242/560 (43%)	227 (94%)	14 (6%)	1 (0%)	30	62
1	b1	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	c1	242/560 (43%)	225 (93%)	16 (7%)	1 (0%)	30	62
1	d1	242/560 (43%)	225 (93%)	16 (7%)	1 (0%)	30	62
1	e1	145/560 (26%)	144 (99%)	1 (1%)	0	100	100
1	f1	242/560 (43%)	229 (95%)	12 (5%)	1 (0%)	30	62
1	g1	242/560 (43%)	226 (93%)	15 (6%)	1 (0%)	30	62
1	h1	242/560 (43%)	232 (96%)	10 (4%)	0	100	100
2	A2	207/245 (84%)	182 (88%)	23 (11%)	2 (1%)	13	44
2	B2	207/245 (84%)	183 (88%)	22 (11%)	2 (1%)	13	44
2	C2	207/245 (84%)	177 (86%)	29 (14%)	1 (0%)	25	57
2	D2	207/245 (84%)	181 (87%)	25 (12%)	1 (0%)	25	57
2	E2	207/245 (84%)	183 (88%)	22 (11%)	2 (1%)	13	44
3	F2	254/264 (96%)	223 (88%)	30 (12%)	1 (0%)	30	62
4	G2	87/89 (98%)	75 (86%)	12 (14%)	0	100	100
4	H2	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
4	I2	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
4	J2	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
5	K2	37/104 (36%)	37 (100%)	0	0	100	100
5	L2	73/104 (70%)	68 (93%)	5 (7%)	0	100	100
5	M2	73/104 (70%)	68 (93%)	5 (7%)	0	100	100
5	N2	73/104 (70%)	69 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	O2	73/104 (70%)	69 (94%)	4 (6%)	0	100	100
5	P2	73/104 (70%)	68 (93%)	5 (7%)	0	100	100
6	Q2	131/138 (95%)	115 (88%)	16 (12%)	0	100	100
6	R2	114/138 (83%)	98 (86%)	16 (14%)	0	100	100
6	S2	116/138 (84%)	104 (90%)	12 (10%)	0	100	100
6	T2	102/138 (74%)	95 (93%)	7 (7%)	0	100	100
6	U2	113/138 (82%)	102 (90%)	11 (10%)	0	100	100
7	V2	131/134 (98%)	112 (86%)	18 (14%)	1 (1%)	16	49
7	W2	130/134 (97%)	108 (83%)	22 (17%)	0	100	100
7	X2	130/134 (97%)	107 (82%)	22 (17%)	1 (1%)	16	49
7	Y2	130/134 (97%)	109 (84%)	21 (16%)	0	100	100
7	Z2	130/134 (97%)	113 (87%)	17 (13%)	0	100	100
7	a2	130/134 (97%)	109 (84%)	21 (16%)	0	100	100
8	b2	247/251 (98%)	217 (88%)	29 (12%)	1 (0%)	30	62
8	c2	247/251 (98%)	212 (86%)	35 (14%)	0	100	100
8	d2	247/251 (98%)	215 (87%)	32 (13%)	0	100	100
8	e2	247/251 (98%)	212 (86%)	35 (14%)	0	100	100
8	f2	247/251 (98%)	210 (85%)	37 (15%)	0	100	100
9	12	258/260 (99%)	231 (90%)	27 (10%)	0	100	100
9	22	258/260 (99%)	231 (90%)	27 (10%)	0	100	100
9	32	256/260 (98%)	230 (90%)	26 (10%)	0	100	100
9	42	258/260 (99%)	239 (93%)	19 (7%)	0	100	100
9	g2	258/260 (99%)	240 (93%)	18 (7%)	0	100	100
9	h2	258/260 (99%)	239 (93%)	19 (7%)	0	100	100
9	i2	258/260 (99%)	240 (93%)	18 (7%)	0	100	100
9	j2	258/260 (99%)	240 (93%)	18 (7%)	0	100	100
9	k2	258/260 (99%)	242 (94%)	16 (6%)	0	100	100
9	l2	245/260 (94%)	229 (94%)	16 (6%)	0	100	100
9	m2	245/260 (94%)	230 (94%)	15 (6%)	0	100	100
9	n2	245/260 (94%)	232 (95%)	13 (5%)	0	100	100
9	o2	245/260 (94%)	230 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	p2	245/260 (94%)	232 (95%)	13 (5%)	0	100	100
9	q2	247/260 (95%)	233 (94%)	14 (6%)	0	100	100
9	r2	258/260 (99%)	233 (90%)	25 (10%)	0	100	100
9	s2	258/260 (99%)	230 (89%)	28 (11%)	0	100	100
9	t2	258/260 (99%)	236 (92%)	22 (8%)	0	100	100
9	u2	258/260 (99%)	234 (91%)	24 (9%)	0	100	100
9	v2	258/260 (99%)	233 (90%)	25 (10%)	0	100	100
9	w2	258/260 (99%)	232 (90%)	26 (10%)	0	100	100
9	x2	258/260 (99%)	236 (92%)	22 (8%)	0	100	100
9	y2	258/260 (99%)	238 (92%)	20 (8%)	0	100	100
9	z2	258/260 (99%)	240 (93%)	18 (7%)	0	100	100
10	A3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	B3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	C3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	D3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	E3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	F3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100
10	G3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100
10	H3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	I3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100
10	J3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	K3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100
10	L3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	M3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	N3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	O3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	P3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	Q3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	R3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	S3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	T3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	U3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100
10	V3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	W3	208/232 (90%)	192 (92%)	16 (8%)	0	100	100
10	X3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	Y3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
10	Z3	209/232 (90%)	193 (92%)	16 (8%)	0	100	100
11	a3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	b3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	c3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	d3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	e3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	f3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	g3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	h3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	i3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	j3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	k3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	l3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	m3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	n3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	o3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	p3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	q3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	r3	299/365 (82%)	288 (96%)	11 (4%)	0	100	100
11	s3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	t3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	u3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	v3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	w3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	x3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
11	y3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	z3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
12	A4	199/232 (86%)	194 (98%)	5 (2%)	0	100	100
12	B4	202/232 (87%)	200 (99%)	2 (1%)	0	100	100
12	C4	197/232 (85%)	185 (94%)	12 (6%)	0	100	100
12	D4	200/232 (86%)	194 (97%)	6 (3%)	0	100	100
12	E4	202/232 (87%)	197 (98%)	5 (2%)	0	100	100
All	All	32138/47180 (68%)	29936 (93%)	2176 (7%)	26 (0%)	50	78

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B2	42	VAL
2	C2	42	VAL
2	D2	42	VAL
2	A2	42	VAL
2	E2	42	VAL

### 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	A1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	B1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	C1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	D1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	E1	217/467 (46%)	217 (100%)	0	100	100
1	F1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	G1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	H1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	I1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	J1	134/467 (29%)	132 (98%)	2 (2%)	60	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	L1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	M1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	N1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	O1	217/467 (46%)	213 (98%)	4 (2%)	54	71
1	P1	134/467 (29%)	131 (98%)	3 (2%)	47	65
1	Q1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	R1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	S1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	T1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	U1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	V1	134/467 (29%)	132 (98%)	2 (2%)	60	75
1	W1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	X1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	Y1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	Z1	134/467 (29%)	132 (98%)	2 (2%)	60	75
1	a1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	b1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	c1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	d1	217/467 (46%)	215 (99%)	2 (1%)	75	84
1	e1	134/467 (29%)	133 (99%)	1 (1%)	81	88
1	f1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	g1	217/467 (46%)	216 (100%)	1 (0%)	86	92
1	h1	217/467 (46%)	216 (100%)	1 (0%)	86	92
2	A2	179/204 (88%)	179 (100%)	0	100	100
2	B2	179/204 (88%)	179 (100%)	0	100	100
2	C2	179/204 (88%)	178 (99%)	1 (1%)	84	90
2	D2	179/204 (88%)	179 (100%)	0	100	100
2	E2	179/204 (88%)	179 (100%)	0	100	100
3	F2	215/221 (97%)	215 (100%)	0	100	100
4	G2	74/74 (100%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H2	74/74 (100%)	74 (100%)	0	100	100
4	I2	74/74 (100%)	74 (100%)	0	100	100
4	J2	74/74 (100%)	74 (100%)	0	100	100
5	K2	33/79 (42%)	33 (100%)	0	100	100
5	L2	59/79 (75%)	59 (100%)	0	100	100
5	M2	59/79 (75%)	59 (100%)	0	100	100
5	N2	59/79 (75%)	59 (100%)	0	100	100
5	O2	59/79 (75%)	59 (100%)	0	100	100
5	P2	59/79 (75%)	59 (100%)	0	100	100
6	Q2	109/113 (96%)	109 (100%)	0	100	100
6	R2	100/113 (88%)	100 (100%)	0	100	100
6	S2	100/113 (88%)	99 (99%)	1 (1%)	73	82
6	T2	89/113 (79%)	88 (99%)	1 (1%)	70	80
6	U2	99/113 (88%)	97 (98%)	2 (2%)	50	68
7	V2	104/105 (99%)	103 (99%)	1 (1%)	73	82
7	W2	104/105 (99%)	104 (100%)	0	100	100
7	X2	104/105 (99%)	104 (100%)	0	100	100
7	Y2	104/105 (99%)	104 (100%)	0	100	100
7	Z2	104/105 (99%)	103 (99%)	1 (1%)	73	82
7	a2	104/105 (99%)	104 (100%)	0	100	100
8	b2	191/193 (99%)	191 (100%)	0	100	100
8	c2	191/193 (99%)	191 (100%)	0	100	100
8	d2	191/193 (99%)	191 (100%)	0	100	100
8	e2	191/193 (99%)	191 (100%)	0	100	100
8	f2	191/193 (99%)	191 (100%)	0	100	100
9	12	215/215 (100%)	215 (100%)	0	100	100
9	22	215/215 (100%)	215 (100%)	0	100	100
9	32	214/215 (100%)	214 (100%)	0	100	100
9	42	215/215 (100%)	214 (100%)	1 (0%)	86	92
9	g2	215/215 (100%)	215 (100%)	0	100	100
9	h2	215/215 (100%)	215 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	i2	215/215 (100%)	215 (100%)	0	100	100
9	j2	215/215 (100%)	215 (100%)	0	100	100
9	k2	215/215 (100%)	215 (100%)	0	100	100
9	l2	206/215 (96%)	206 (100%)	0	100	100
9	m2	206/215 (96%)	206 (100%)	0	100	100
9	n2	206/215 (96%)	205 (100%)	1 (0%)	86	92
9	o2	206/215 (96%)	206 (100%)	0	100	100
9	p2	206/215 (96%)	206 (100%)	0	100	100
9	q2	207/215 (96%)	206 (100%)	1 (0%)	86	92
9	r2	215/215 (100%)	214 (100%)	1 (0%)	86	92
9	s2	215/215 (100%)	215 (100%)	0	100	100
9	t2	215/215 (100%)	215 (100%)	0	100	100
9	u2	215/215 (100%)	215 (100%)	0	100	100
9	v2	215/215 (100%)	215 (100%)	0	100	100
9	w2	215/215 (100%)	215 (100%)	0	100	100
9	x2	215/215 (100%)	215 (100%)	0	100	100
9	y2	215/215 (100%)	214 (100%)	1 (0%)	86	92
9	z2	215/215 (100%)	215 (100%)	0	100	100
10	A3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	B3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	C3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	D3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	E3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	F3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	G3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	H3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	I3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	J3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	K3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	L3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	M3	170/186 (91%)	164 (96%)	6 (4%)	31	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	N3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	O3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	P3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	Q3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	R3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	S3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	T3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	U3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	V3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	W3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	X3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	Y3	170/186 (91%)	164 (96%)	6 (4%)	31	56
10	Z3	170/186 (91%)	164 (96%)	6 (4%)	31	56
11	a3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	b3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	c3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	d3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	e3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	f3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	g3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	h3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	i3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	j3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	k3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	l3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	m3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	n3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	o3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	p3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	q3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	r3	250/294 (85%)	237 (95%)	13 (5%)	19	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	s3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	t3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	u3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	v3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	w3	251/294 (85%)	237 (94%)	14 (6%)	17	45
11	x3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	y3	251/294 (85%)	238 (95%)	13 (5%)	19	46
11	z3	251/294 (85%)	238 (95%)	13 (5%)	19	46
12	A4	164/188 (87%)	162 (99%)	2 (1%)	67	79
12	B4	165/188 (88%)	165 (100%)	0	100	100
12	C4	162/188 (86%)	162 (100%)	0	100	100
12	D4	164/188 (87%)	163 (99%)	1 (1%)	84	90
12	E4	165/188 (88%)	164 (99%)	1 (1%)	84	90
All	All	27146/38629 (70%)	26584 (98%)	562 (2%)	49	67

5 of 562 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	s3	256	ASN
11	t3	256	ASN
11	s3	252	LYS
11	x3	84	VAL
10	V3	144	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 200 such sidechains are listed below:

Mol	Chain	Res	Type
11	e3	161	ASN
11	m3	161	ASN
12	E4	54	GLN
11	f3	350	GLN
11	j3	161	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	F2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F2	115:ASP	C	116:PRO	N	5.09

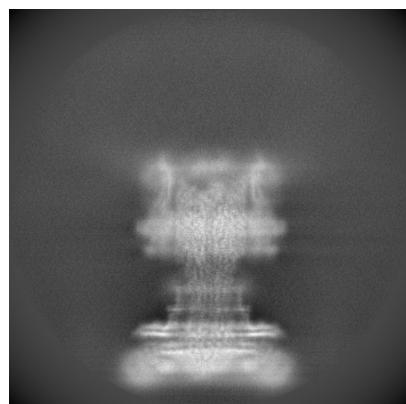
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12603. These allow visual inspection of the internal detail of the map and identification of artifacts.

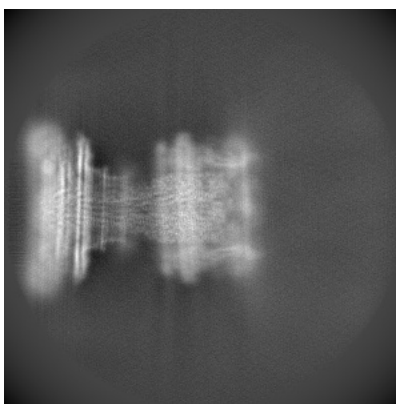
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

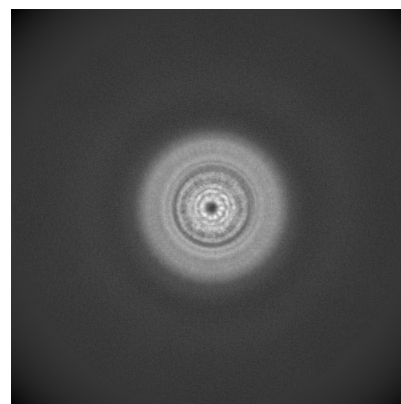
#### 6.1.1 Primary map



X

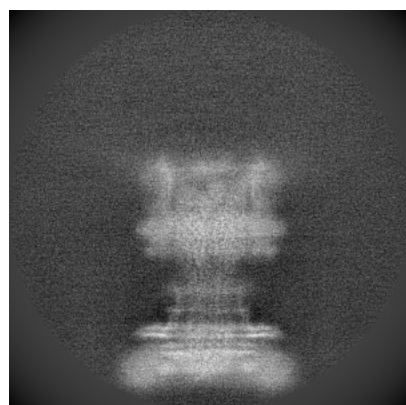


Y

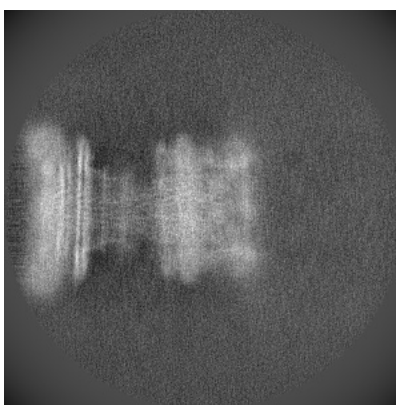


Z

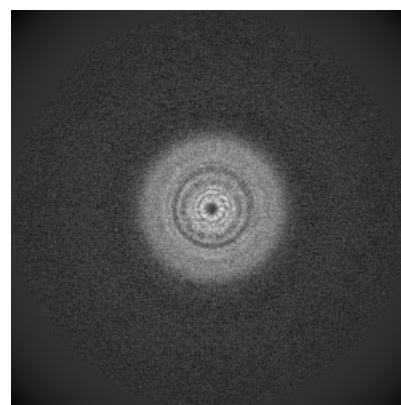
#### 6.1.2 Raw map



X



Y



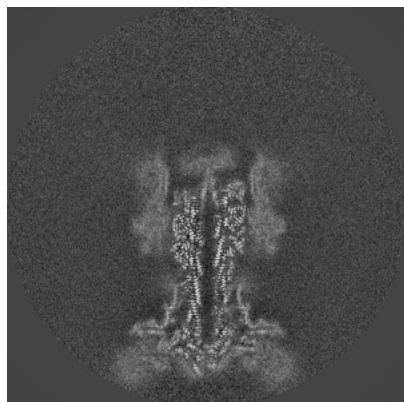
Z

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

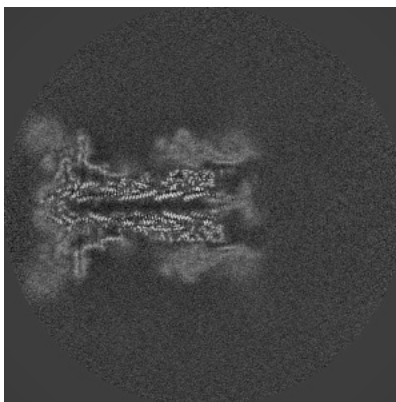


## 6.2 Central slices [i](#)

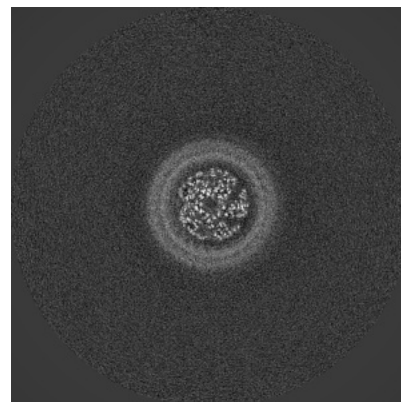
### 6.2.1 Primary map



X Index: 384

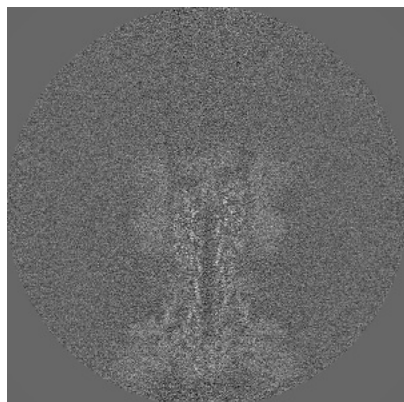


Y Index: 384

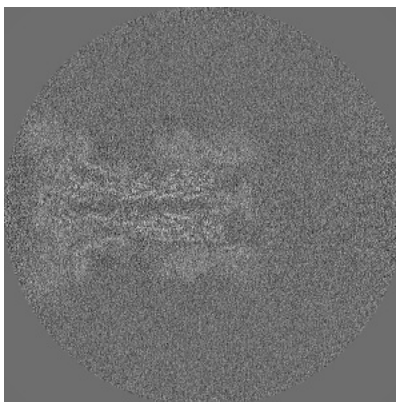


Z Index: 384

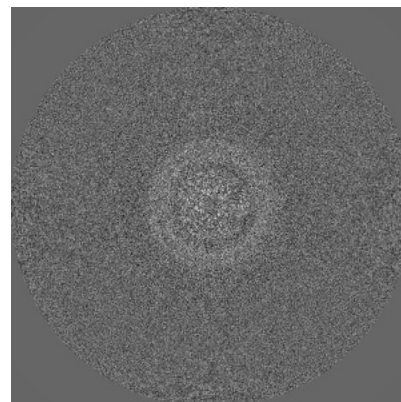
### 6.2.2 Raw map



X Index: 384



Y Index: 384

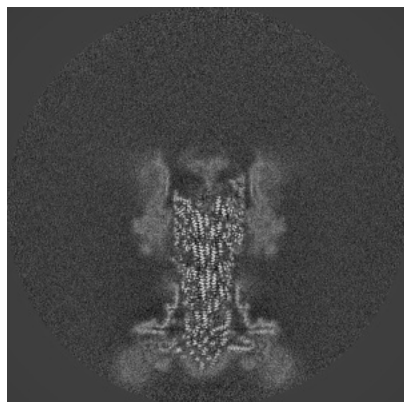


Z Index: 384

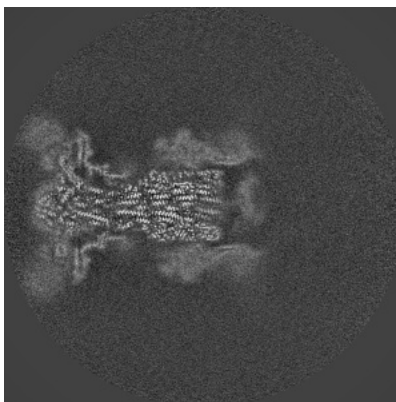
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

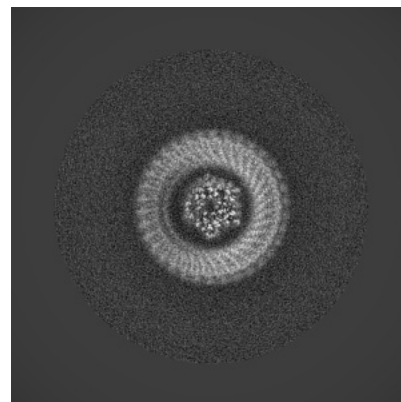
### 6.3.1 Primary map



X Index: 402

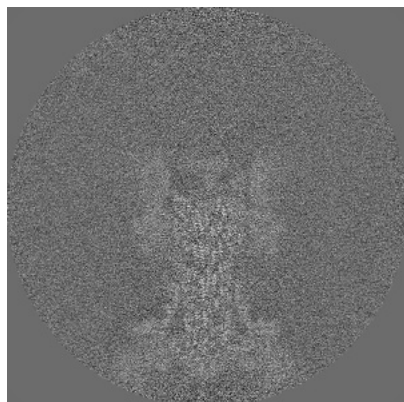


Y Index: 371

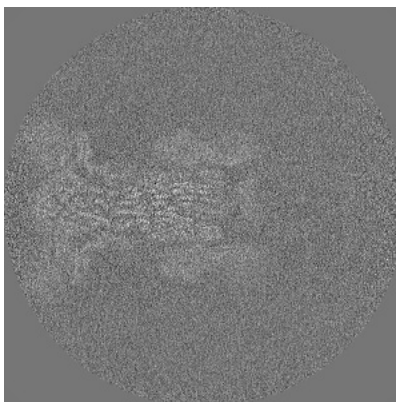


Z Index: 144

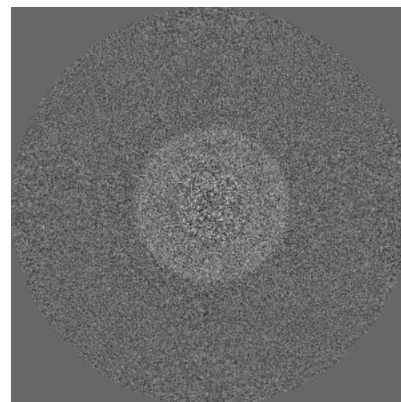
### 6.3.2 Raw map



X Index: 402



Y Index: 371



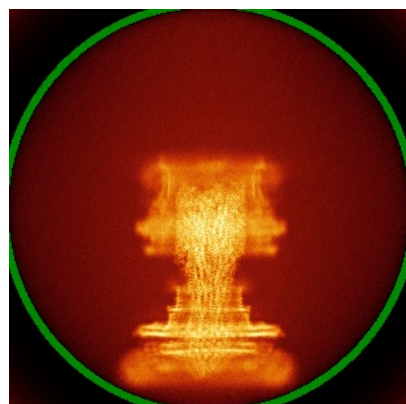
Z Index: 350

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

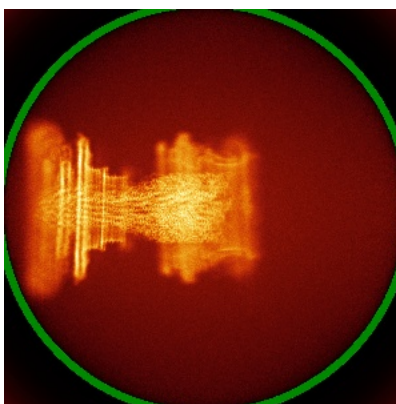


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

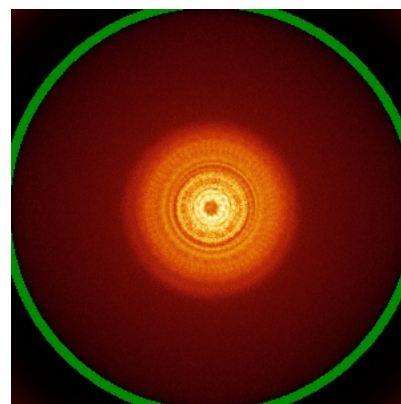
### 6.4.1 Primary map



X

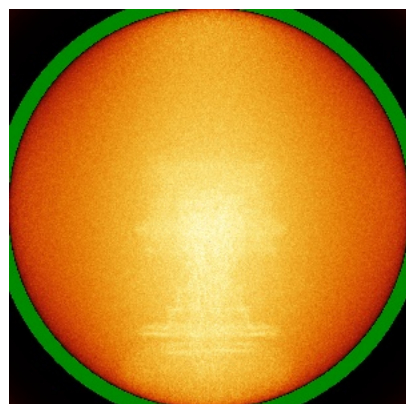


Y

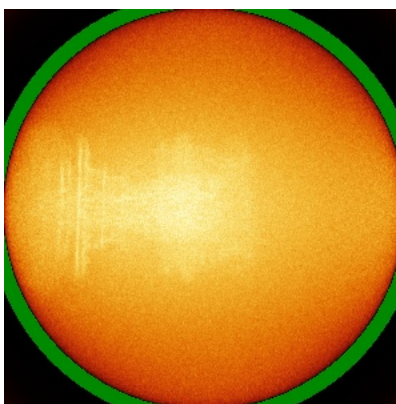


Z

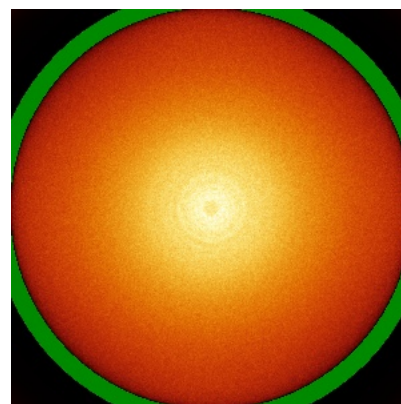
### 6.4.2 Raw map



X



Y

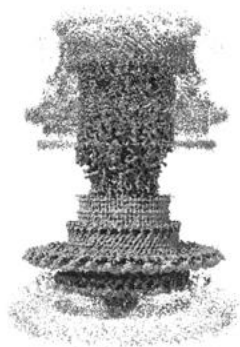


Z

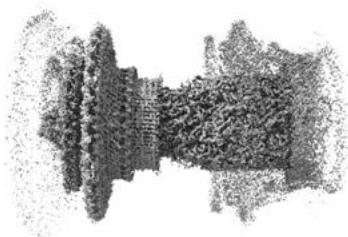
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

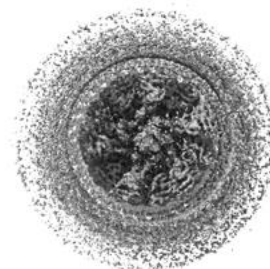
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

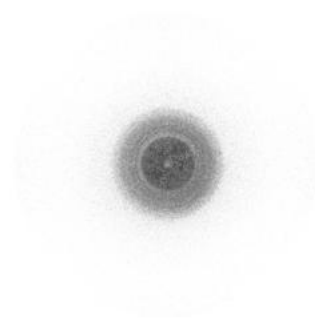
### 6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

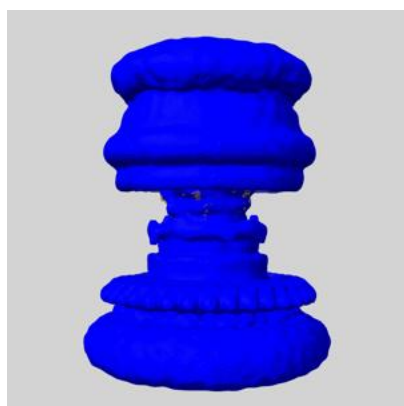
## 6.6 Mask visualisation [i](#)

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

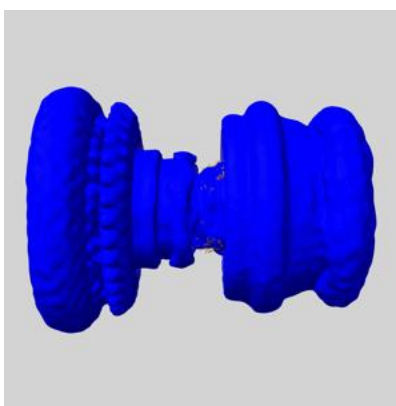
A mask typically either:

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

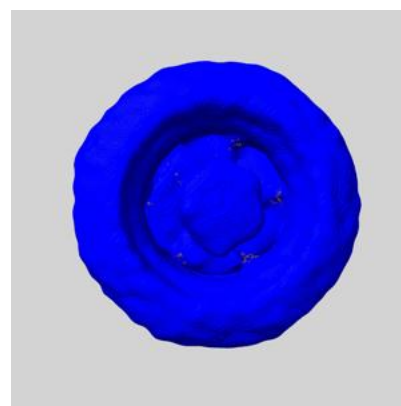
### 6.6.1 emd\_12603\_msk\_1.map [i](#)



X



Y

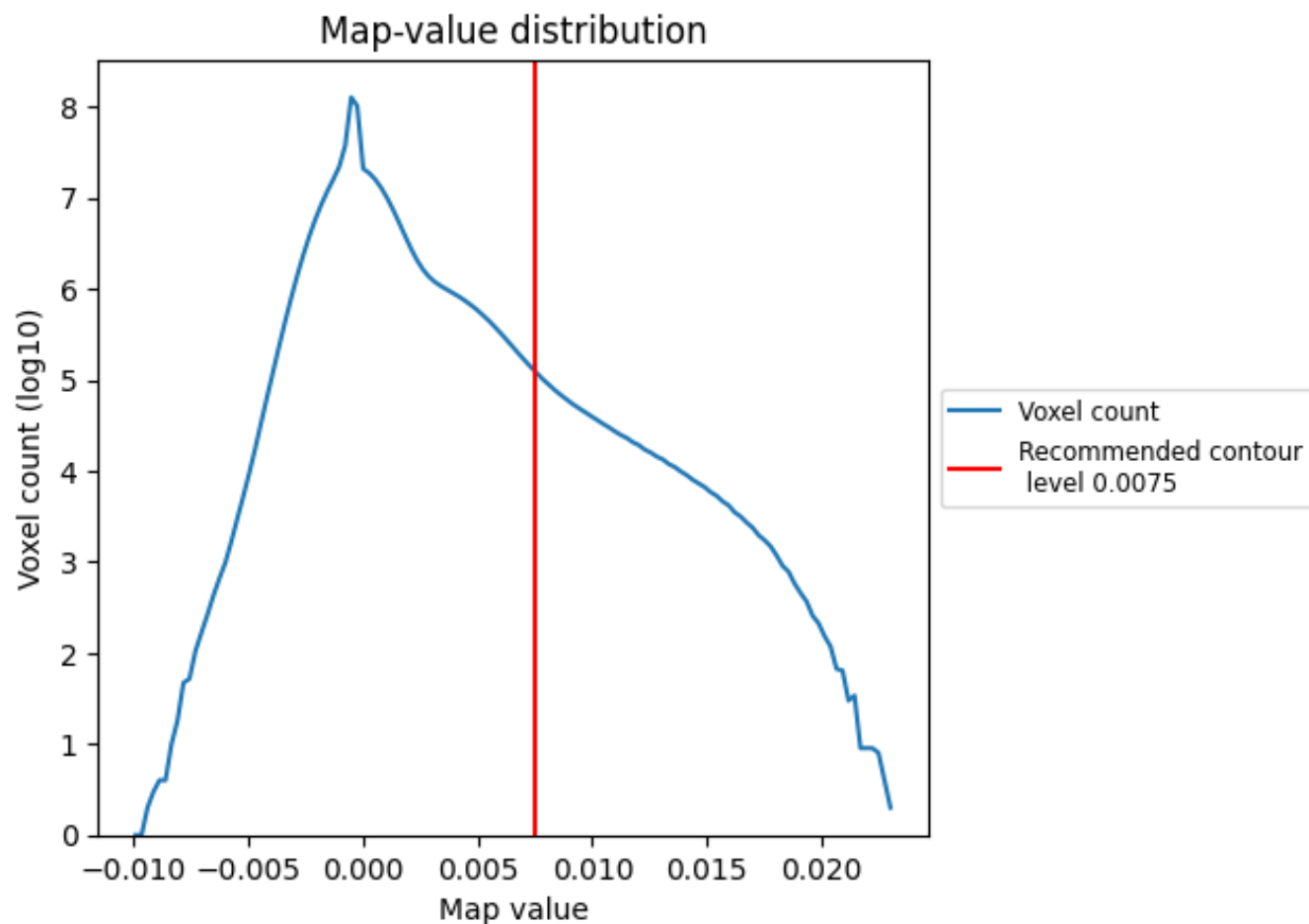


Z

## 7 Map analysis [i](#)

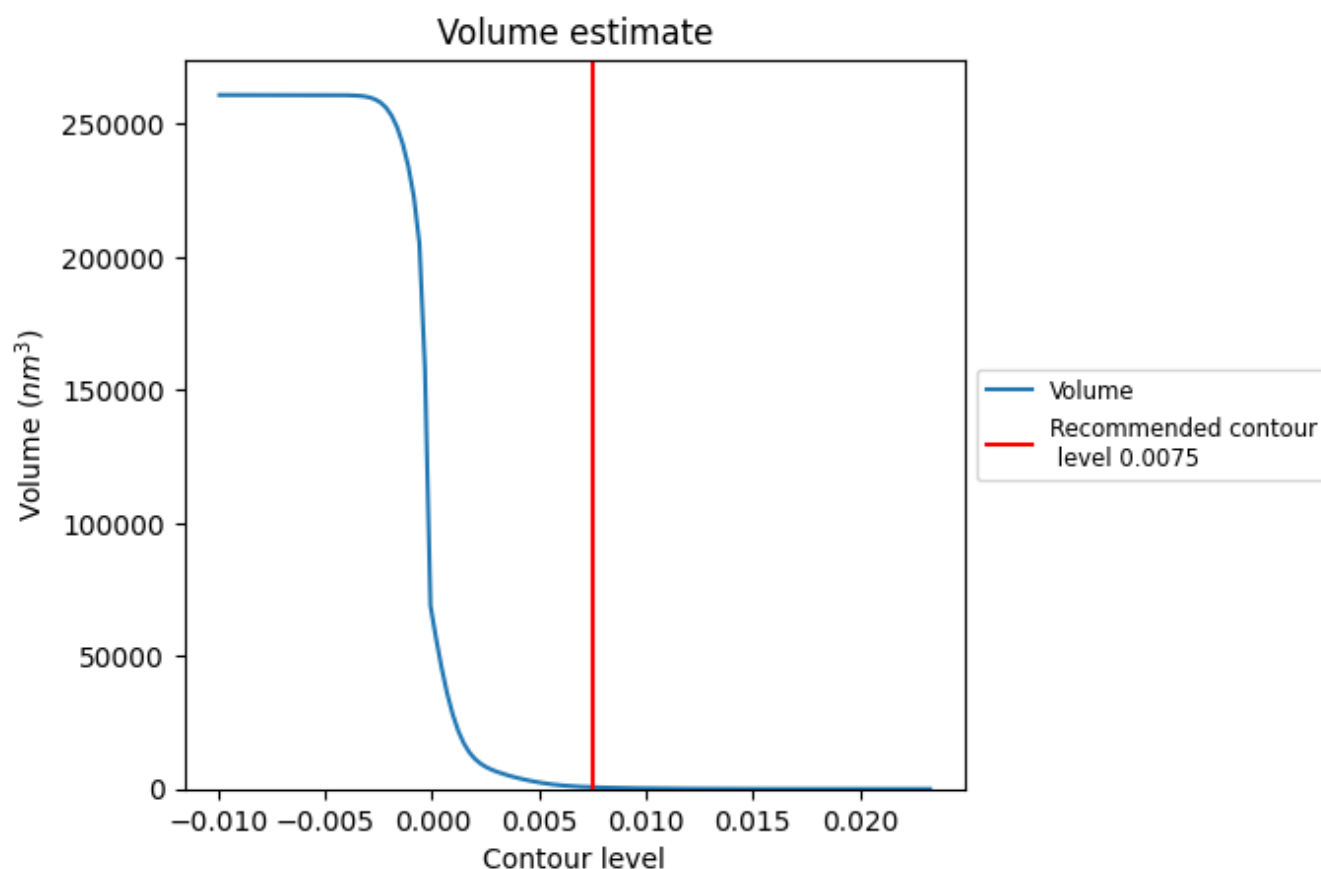
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

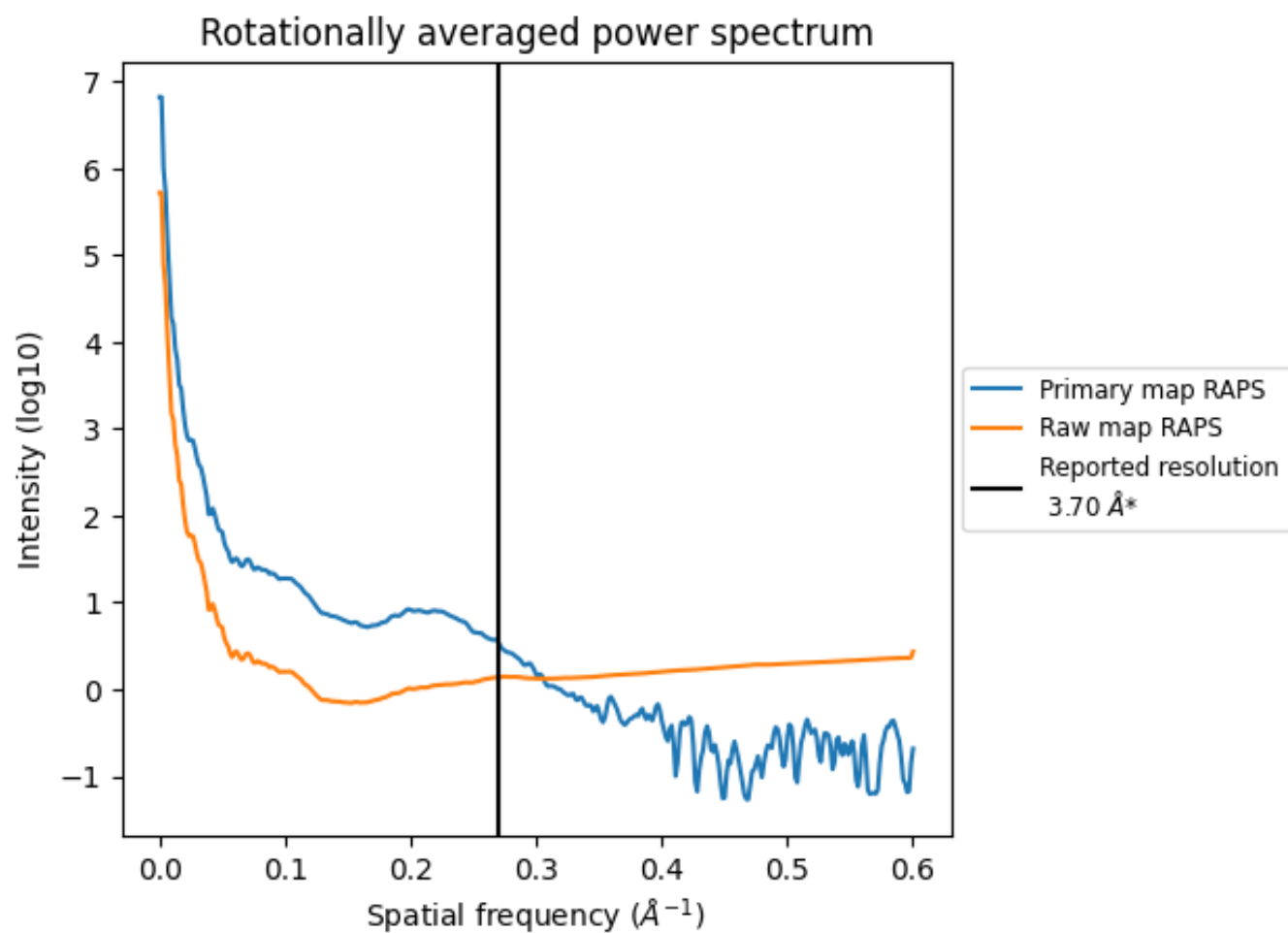
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 648  $\text{nm}^3$ ; this corresponds to an approximate mass of 586 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 ⓘ

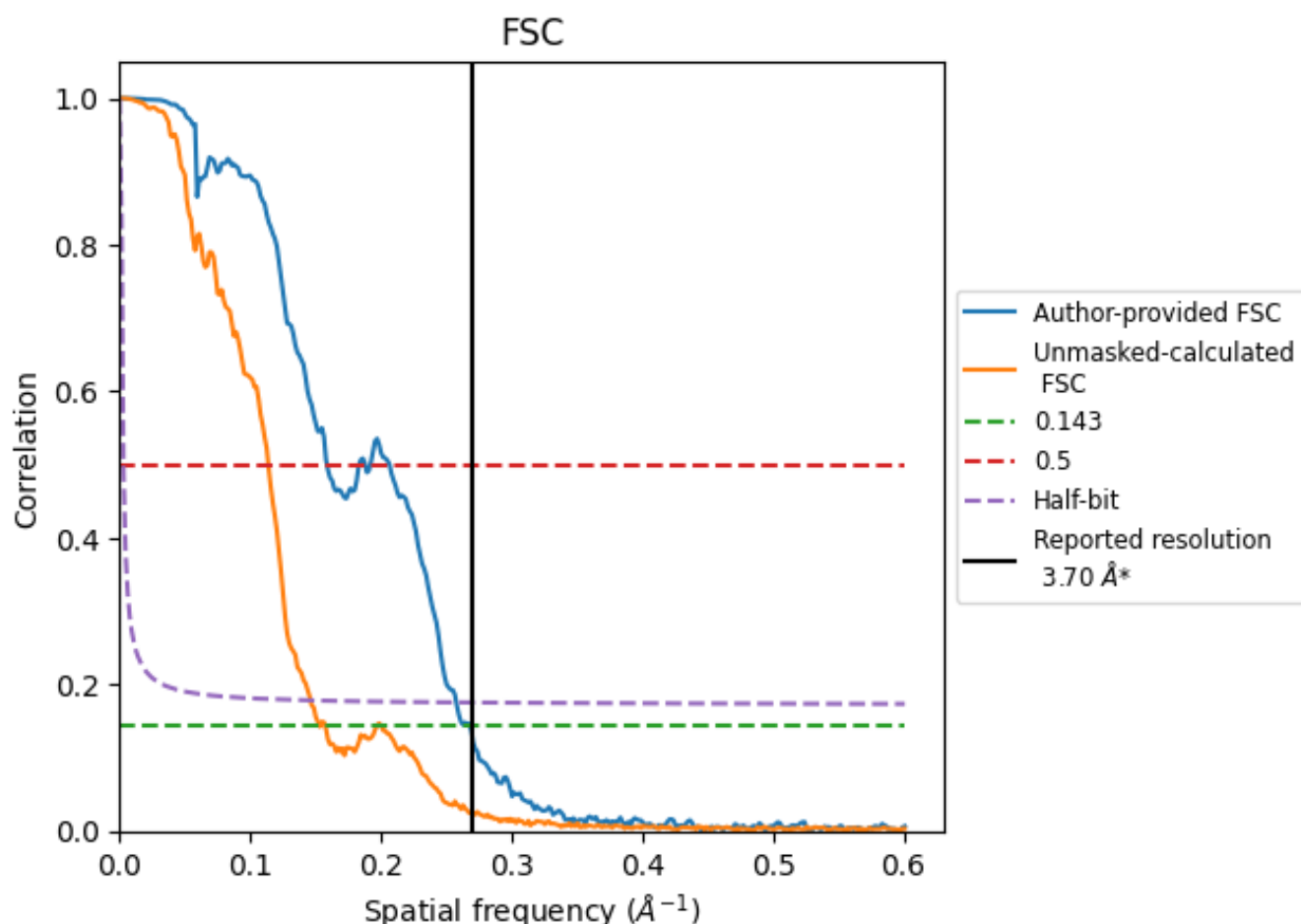


\*Reported resolution corresponds to spatial frequency of 0.270 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.270 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	6.30	3.88
Unmasked-calculated*	6.53	8.78	6.84

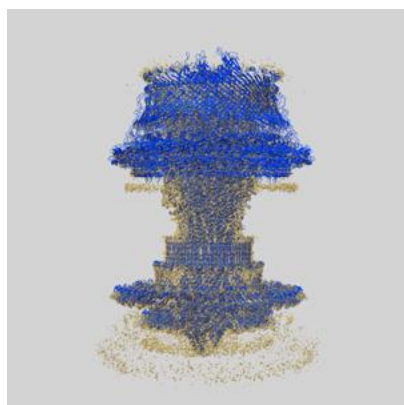
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.53 differs from the reported value 3.7 by more than 10 %



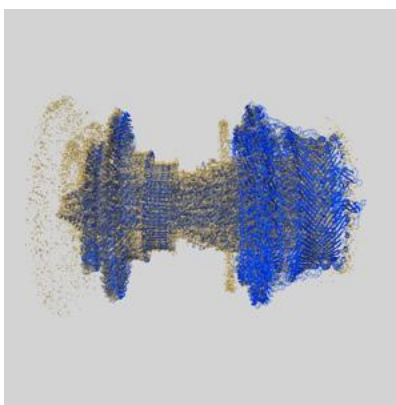
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12603 and PDB model 7NVG. Per-residue inclusion information can be found in section [3](#) on page [18](#).

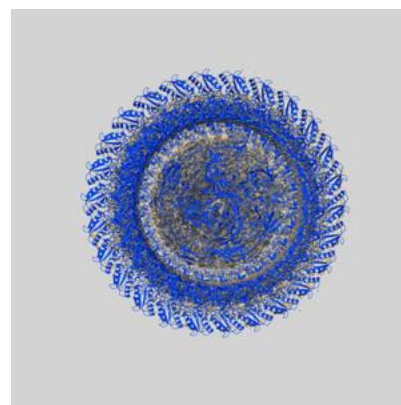
### 9.1 Map-model overlay [i](#)



X



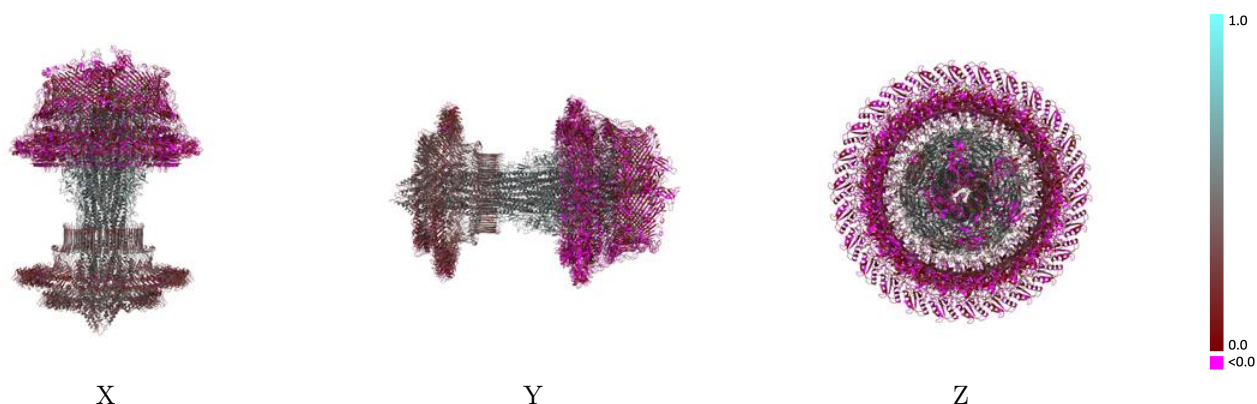
Y



Z

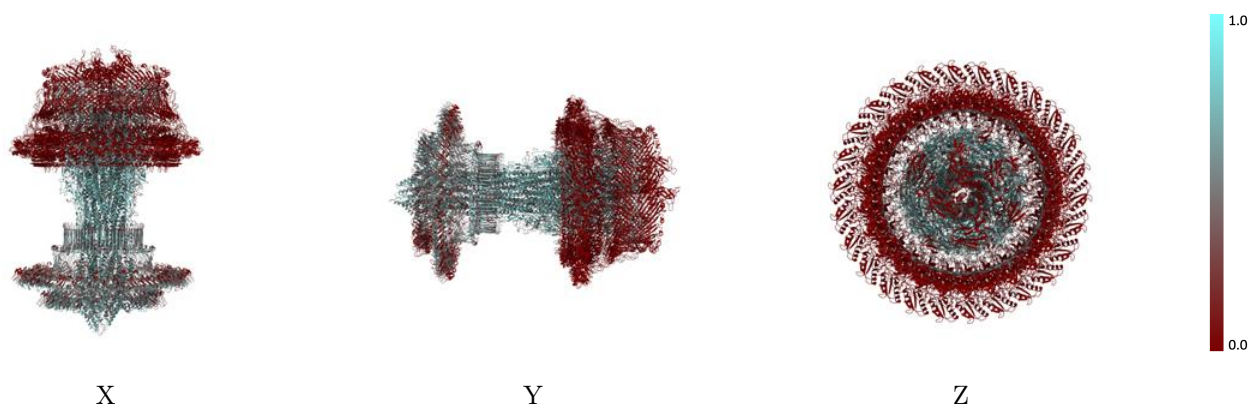
The images above show the 3D surface view of the map at the recommended contour level 0.0075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



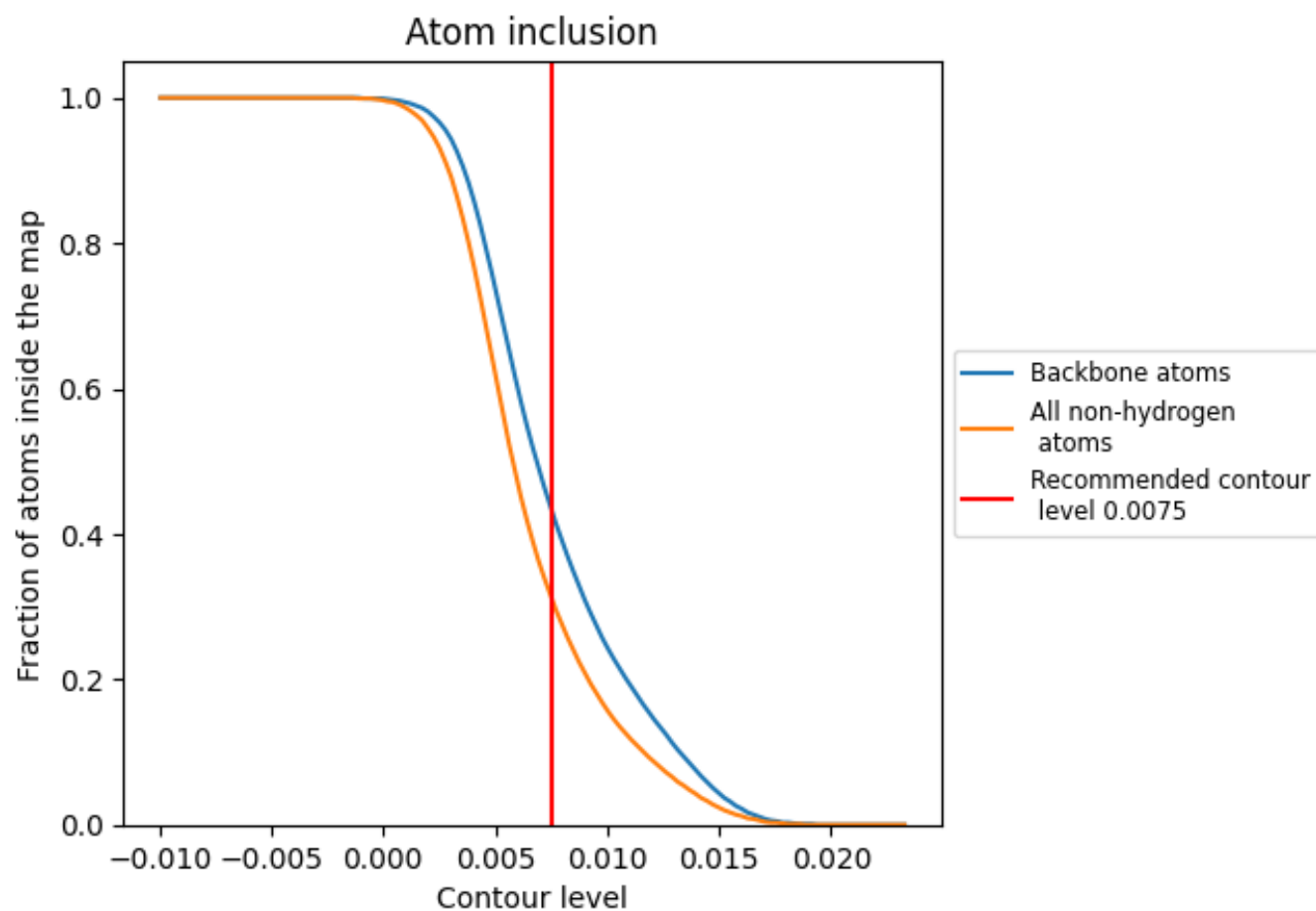
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0075).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 44% of all backbone atoms, 31% 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 (0.0075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3140	 0.2600
12	 0.5820	 0.4540
22	 0.5740	 0.4590
32	 0.5370	 0.4490
42	 0.2200	 0.3100
A1	 0.4300	 0.2750
A2	 0.5380	 0.4390
A3	 0.0690	 0.0910
A4	 0.0850	 0.1010
B1	 0.4340	 0.3030
B2	 0.5800	 0.4430
B3	 0.0710	 0.1080
B4	 0.1010	 0.0920
C1	 0.4640	 0.3060
C2	 0.6100	 0.4410
C3	 0.0720	 0.1010
C4	 0.0760	 0.1210
D1	 0.4240	 0.2850
D2	 0.5880	 0.4330
D3	 0.0710	 0.0870
D4	 0.0690	 0.0820
E1	 0.4420	 0.3140
E2	 0.5410	 0.4190
E3	 0.0840	 0.1060
E4	 0.0870	 0.1120
F1	 0.4230	 0.3020
F2	 0.4960	 0.4070
F3	 0.0740	 0.1080
G1	 0.4420	 0.3180
G2	 0.5370	 0.3880
G3	 0.0820	 0.1110
H1	 0.4500	 0.3230
H2	 0.6050	 0.4120
H3	 0.0790	 0.1110
I1	 0.4290	 0.3090























































































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Chain	Atom inclusion	Q-score
I2	 0.5700	 0.4000
I3	 0.0710	 0.1020
J1	 0.4160	 0.2950
J2	 0.4990	 0.3730
J3	 0.0770	 0.1060
K1	 0.4060	 0.2910
K2	 0.5490	 0.4530
K3	 0.0600	 0.0850
L1	 0.3980	 0.3000
L2	 0.5450	 0.4600
L3	 0.0660	 0.0880
M1	 0.4170	 0.2860
M2	 0.5960	 0.4700
M3	 0.0580	 0.0840
N1	 0.3840	 0.2760
N2	 0.6070	 0.4750
N3	 0.0690	 0.0920
O1	 0.3940	 0.2840
O2	 0.5720	 0.4610
O3	 0.0650	 0.0800
P1	 0.4130	 0.2780
P2	 0.5520	 0.4700
P3	 0.0530	 0.0860
Q1	 0.3510	 0.2740
Q2	 0.5120	 0.4850
Q3	 0.0510	 0.1000
R1	 0.3270	 0.2640
R2	 0.6080	 0.4760
R3	 0.0490	 0.0760
S1	 0.3950	 0.2700
S2	 0.6050	 0.4750
S3	 0.0430	 0.0760
T1	 0.2860	 0.2480
T2	 0.6450	 0.4990
T3	 0.0480	 0.0960
U1	 0.2810	 0.2090
U2	 0.5750	 0.4800
U3	 0.0520	 0.0880
V1	 0.3510	 0.2380
V2	 0.5560	 0.4590
V3	 0.0550	 0.0850
W1	 0.2980	 0.2380



























































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Chain	Atom inclusion	Q-score
W2	 0.6130	 0.4770
W3	 0.0580	 0.0740
X1	 0.3350	 0.2480
X2	 0.6340	 0.4930
X3	 0.0430	 0.0870
Y1	 0.3600	 0.2720
Y2	 0.6360	 0.4890
Y3	 0.0570	 0.0980
Z1	 0.3890	 0.2530
Z2	 0.6360	 0.4810
Z3	 0.0700	 0.1080
a1	 0.4160	 0.2790
a2	 0.6140	 0.4580
a3	 0.0180	 0.0990
b1	 0.4100	 0.2630
b2	 0.6010	 0.5010
b3	 0.0240	 0.0990
c1	 0.4270	 0.2960
c2	 0.6670	 0.5000
c3	 0.0260	 0.0820
d1	 0.4540	 0.2960
d2	 0.6980	 0.5070
d3	 0.0270	 0.1050
e1	 0.4590	 0.2880
e2	 0.6820	 0.5060
e3	 0.0210	 0.0810
f1	 0.4580	 0.3080
f2	 0.6650	 0.5050
f3	 0.0300	 0.1040
g1	 0.4720	 0.3040
g2	 0.6390	 0.4990
g3	 0.0280	 0.0810
h1	 0.4570	 0.3010
h2	 0.6560	 0.5060
h3	 0.0230	 0.0980
i2	 0.6690	 0.5130
i3	 0.0300	 0.0890
j2	 0.6560	 0.5050
j3	 0.0150	 0.0810
k2	 0.6640	 0.5070
k3	 0.0160	 0.0840
l2	 0.6570	 0.5090

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Chain	Atom inclusion	Q-score
l3	 0.0110	 0.0710
m2	 0.6610	 0.5130
m3	 0.0060	 0.0480
n2	 0.6630	 0.5160
n3	 0.0120	 0.0500
o2	 0.6640	 0.5040
o3	 0.0140	 0.0610
p2	 0.6600	 0.5020
p3	 0.0070	 0.0430
q2	 0.6710	 0.5110
q3	 0.0050	 0.0530
r2	 0.6620	 0.5030
r3	 0.0060	 0.0570
s2	 0.6590	 0.5030
s3	 0.0060	 0.0580
t2	 0.6570	 0.4970
t3	 0.0110	 0.0570
u2	 0.6580	 0.4910
u3	 0.0080	 0.0530
v2	 0.6700	 0.4960
v3	 0.0060	 0.0640
w2	 0.6740	 0.4930
w3	 0.0110	 0.0690
x2	 0.6430	 0.4870
x3	 0.0160	 0.0790
y2	 0.5760	 0.4470
y3	 0.0170	 0.0750
z2	 0.5250	 0.4040
z3	 0.0170	 0.0910