



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:39 PM UTC

PDB ID : 7NVG / pdb_00007nvg
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

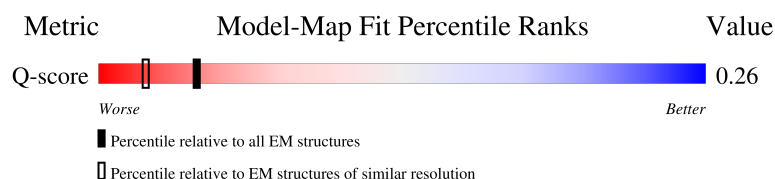
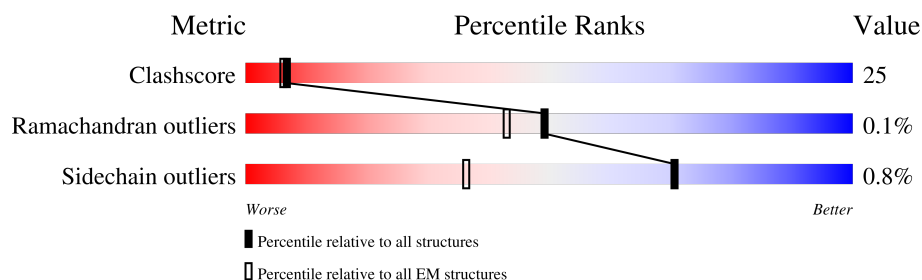
1 Overall quality at a glance i

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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

Mol	Chain	Length	Quality of chain
1	A1	560	12% 19% 8% 73%
1	B1	560	20% 27% 18% 55%
1	C1	560	16% 27% 18% 55%
1	D1	560	12% 17% 10% 73%

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Mol	Chain	Length	Quality of chain
1	E1	560	
1	F1	560	
1	G1	560	
1	H1	560	
1	I1	560	
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	

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Mol	Chain	Length	Quality of chain
1	d1	560	
1	e1	560	
1	f1	560	
1	g1	560	
1	h1	560	
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	

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Mol	Chain	Length	Quality of chain
6	U2	138	
7	V2	134	
7	W2	134	
7	X2	134	
7	Y2	134	
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	

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Mol	Chain	Length	Quality of chain
9	p2	260	
9	q2	260	
9	r2	260	
9	s2	260	
9	t2	260	
9	u2	260	
9	v2	260	
9	w2	260	
9	x2	260	
9	y2	260	
9	z2	260	
10	A3	232	
10	B3	232	
10	C3	232	
10	D3	232	
10	E3	232	
10	F3	232	
10	G3	232	
10	H3	232	
10	I3	232	
10	J3	232	
10	K3	232	
10	L3	232	
10	M3	232	
10	N3	232	

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Mol	Chain	Length	Quality of chain			
10	O3	232	86%	54%	36%	9%
10	P3	232	87%	54%	36%	9%
10	Q3	232	88%	53%	37%	9%
10	R3	232	86%	52%	38%	9%
10	S3	232	88%	53%	37%	9%
10	T3	232	87%	54%	37%	9%
10	U3	232	87%	54%	36%	9%
10	V3	232	87%	55%	36%	9%
10	W3	232	86%	55%	36%	9%
10	X3	232	88%	55%	35%	9%
10	Y3	232	87%	55%	35%	9%
10	Z3	232	84%	53%	37%	9%
11	a3	365	83%	40%	42%	16%
11	b3	365	83%	40%	42%	16%
11	c3	365	84%	40%	42%	16%
11	d3	365	83%	41%	41%	16%
11	e3	365	83%	41%	42%	16%
11	f3	365	84%	40%	42%	16%
11	g3	365	83%	42%	41%	16%
11	h3	365	84%	40%	42%	16%
11	i3	365	83%	40%	42%	16%
11	j3	365	84%	42%	41%	16%
11	k3	365	84%	41%	42%	16%
11	l3	365	84%	41%	42%	16%
11	m3	365	84%	41%	42%	16%

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Mol	Chain	Length	Quality of chain
11	n3	365	83% 41% 42% 16%
11	o3	365	84% 40% 42% 16%
11	p3	365	84% 41% 41% 16%
11	q3	365	84% 40% 42% 16%
11	r3	365	84% 40% 42% 16%
11	s3	365	84% 41% 41% 16%
11	t3	365	84% 40% 42% 16%
11	u3	365	84% 41% 41% 16%
11	v3	365	84% 40% 42% 16%
11	w3	365	84% 41% 41% 16%
11	x3	365	84% 40% 42% 16%
11	y3	365	84% 41% 41% 16%
11	z3	365	83% 41% 42% 16%
12	A4	232	76% 53% 33% 13%
12	B4	232	76% 63% 25% 12%
12	C4	232	79% 56% 30% 14%
12	D4	232	79% 57% 30% 13%
12	E4	232	79% 59% 29% 12%

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		

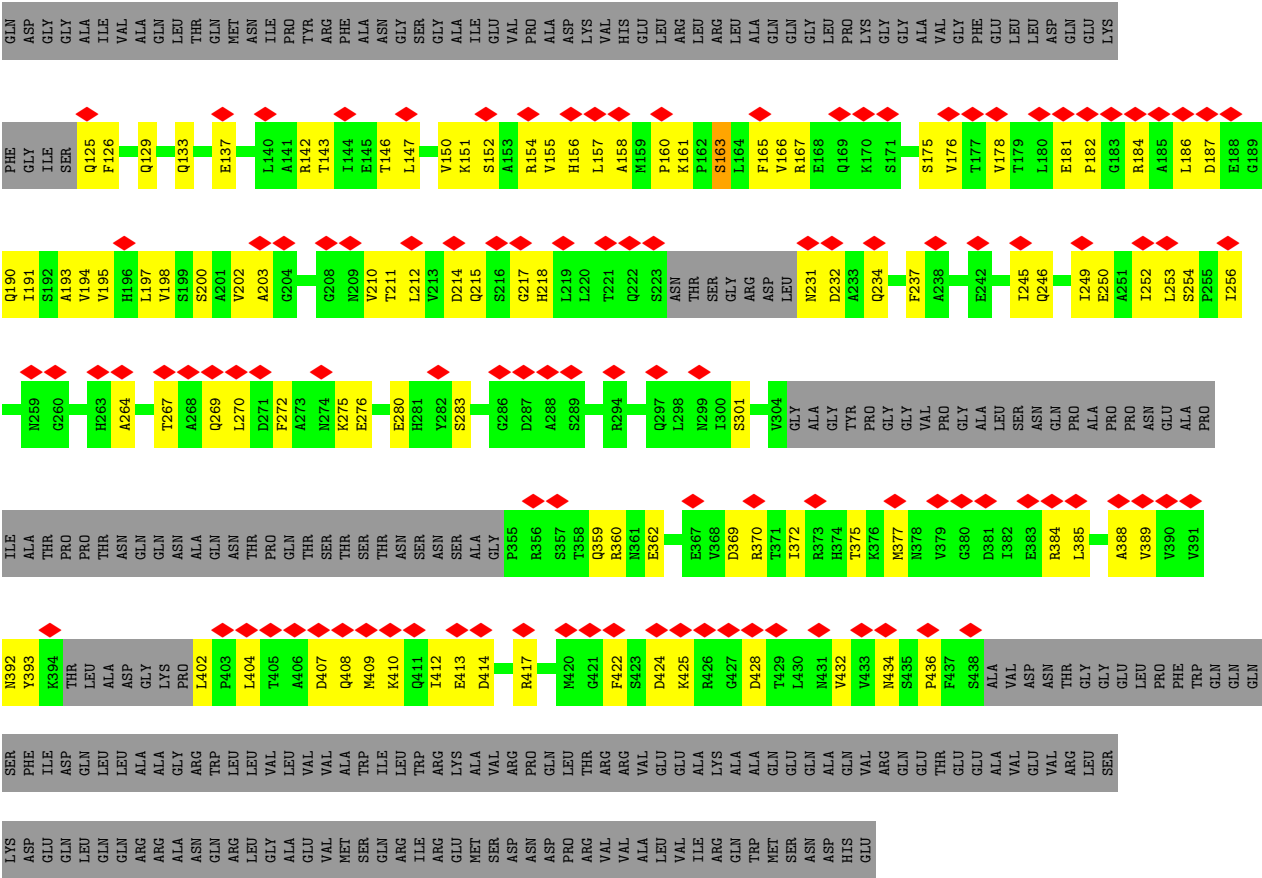
- Molecule 12 is a protein called Basal-body rod modification protein FlgD.

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		

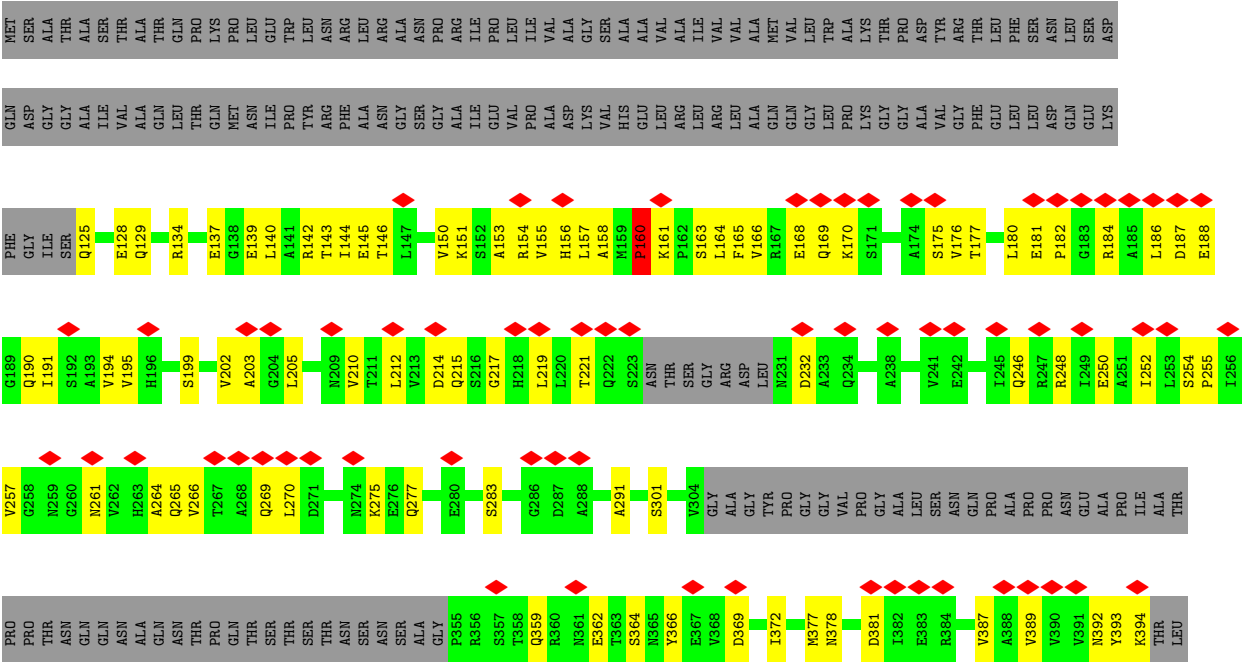
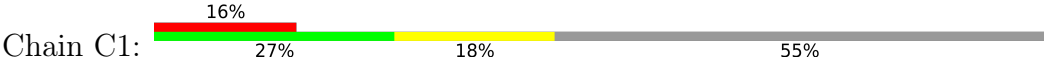
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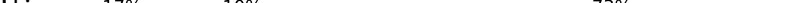
Mol	Chain	Residues	Atoms					AltConf	Trace
12	D4	202	Total	C	N	O	S	0	0
			1482	917	254	310	1		
12	E4	204	Total	C	N	O	S	0	0
			1493	924	256	312	1		

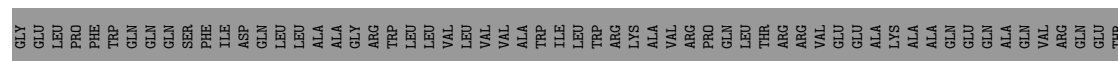
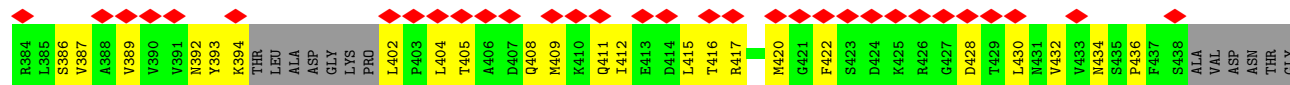
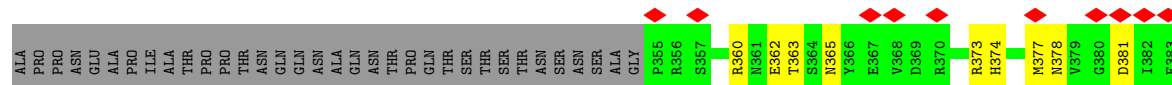
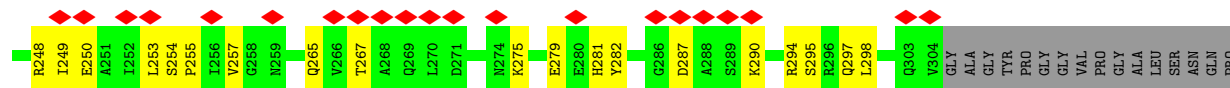
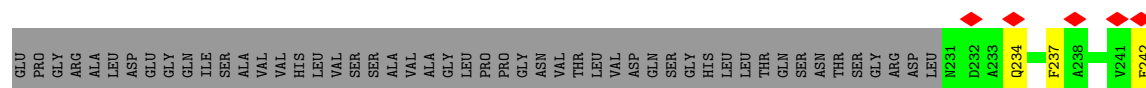


● Molecule 1: Flagellar M-ring protein

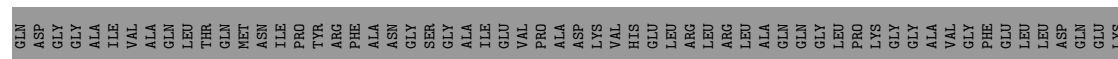
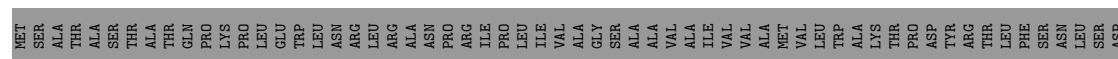




Chain D1: 

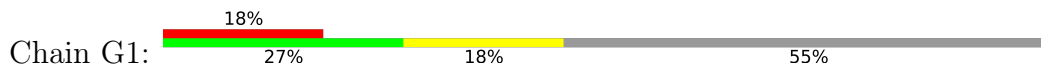
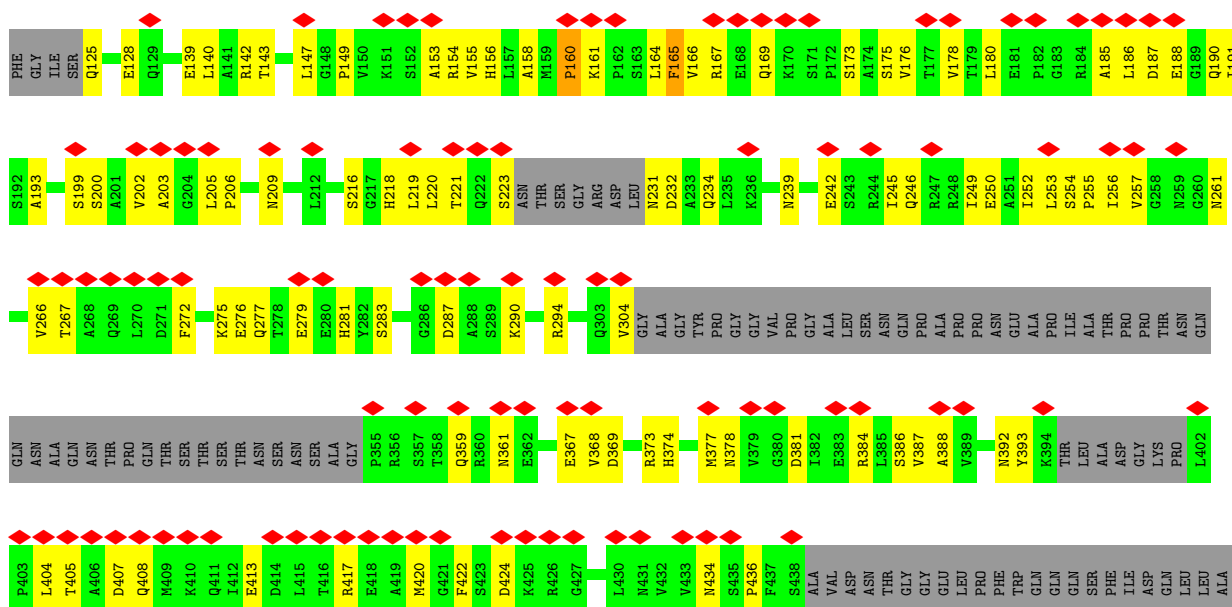


Chain E1: 18% 24% 20% 55%



[illegible]

- Molecule 1: Flagellar M-ring protein

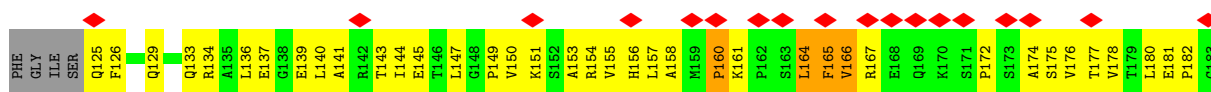
[illegible][illegible]

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



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



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• Molecule 1: Flagellar M-ring protein

Chain J1: 13% 14% 13% 73%

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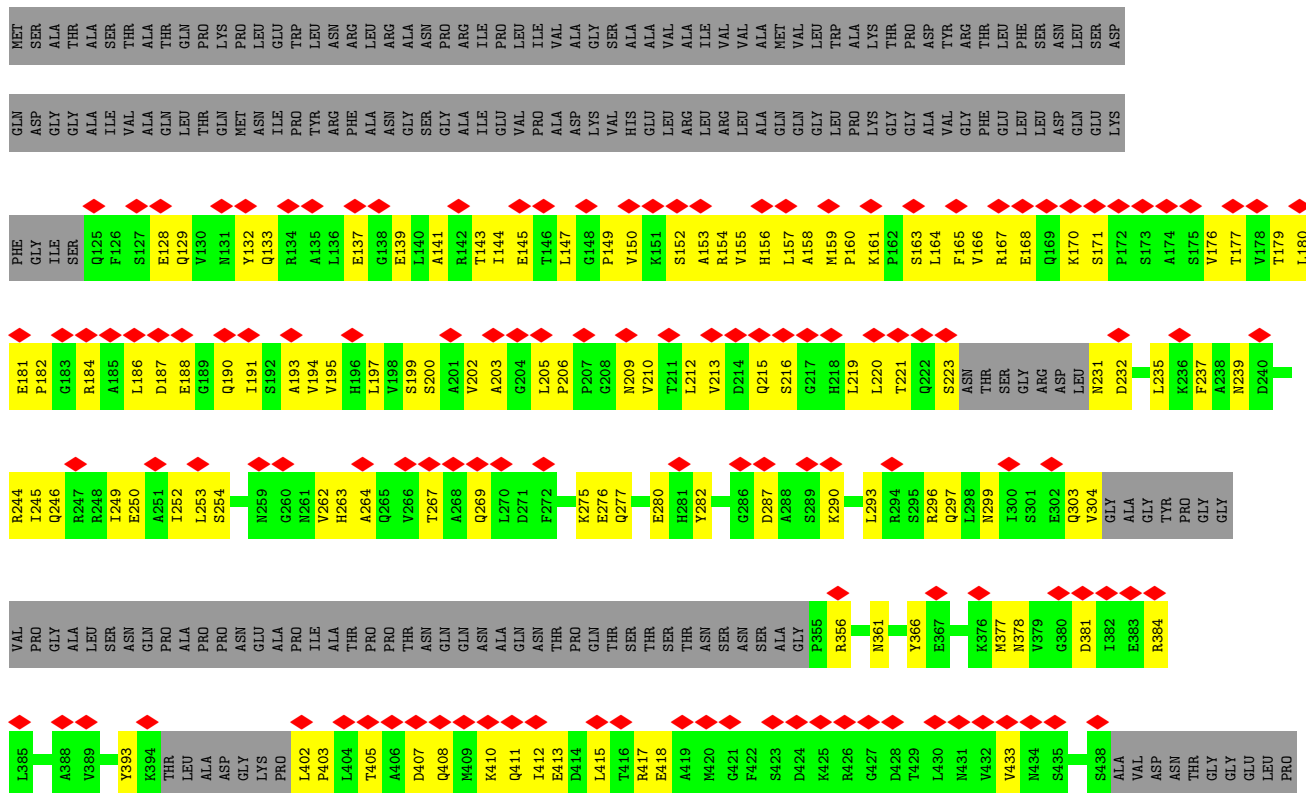
• Molecule 1: Flagellar M-ring protein

Chain K1: 22% 26% 19% 55%

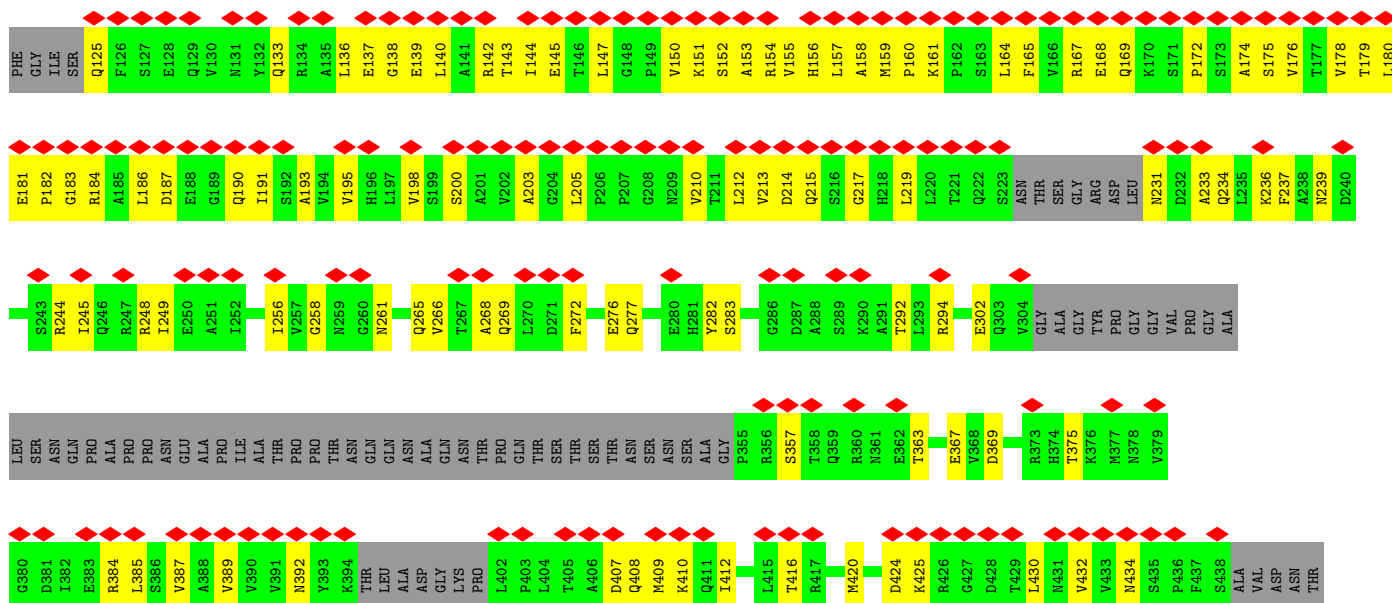
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- Molecule 1: Flagellar M-ring protein



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PRO	GLY	ALA	LEU	SER	ASN	GLN	PRO	PRO	PRO	PRO	ASN	GLU	ALA	ALA	ILE	ALA	THR	PRO	PRO	THR	ASN	GLN	GLN	ASN	ALA	GLN	ASN	THR	PRO	THR	GLN	THR	SER	THR	ASN	SER	ASN	ALA	ALA	GLY	P355	P356	P357	R360	N361	E362	T363	S364	E367	V368	P369	R370	H374	N377
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R378	R379	G380	D381	I382	E383	R384	L385	S386	V387	A388	V389	V390	V391	N392	V393	K394	THR	LEU	ALA	ASP	GLY	LYS	PRO	L402	P403	L404	T405	A406	D407	Q408	M409	K410	Q411	I412	E413	D414	L415	T416	A419	M420	G421	F422	S423	D424	K425	R426	G427	D428	T429	L430	V431	V432	V433	N434	S435	P436	F437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000
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ALA VAL ASP ASN THR GLY GLU PRO PHE TRP GLN GLN SER PHE ILE ASP GLN GLN LEU LEU ALA ALA GLY ARG TRP LEU VAL LEU VAL VAL ALA ALA TRP ILE LEU TRP ARG TRP LYS ALA VAL VAL PRO GLN LEU THR ARG VAL GLU GLU LYS ALA ALA GLN GLN GLN

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

HIS
GLU

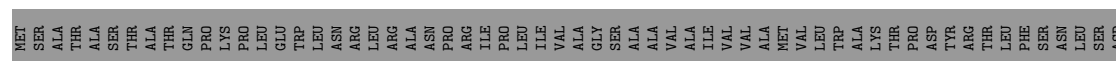
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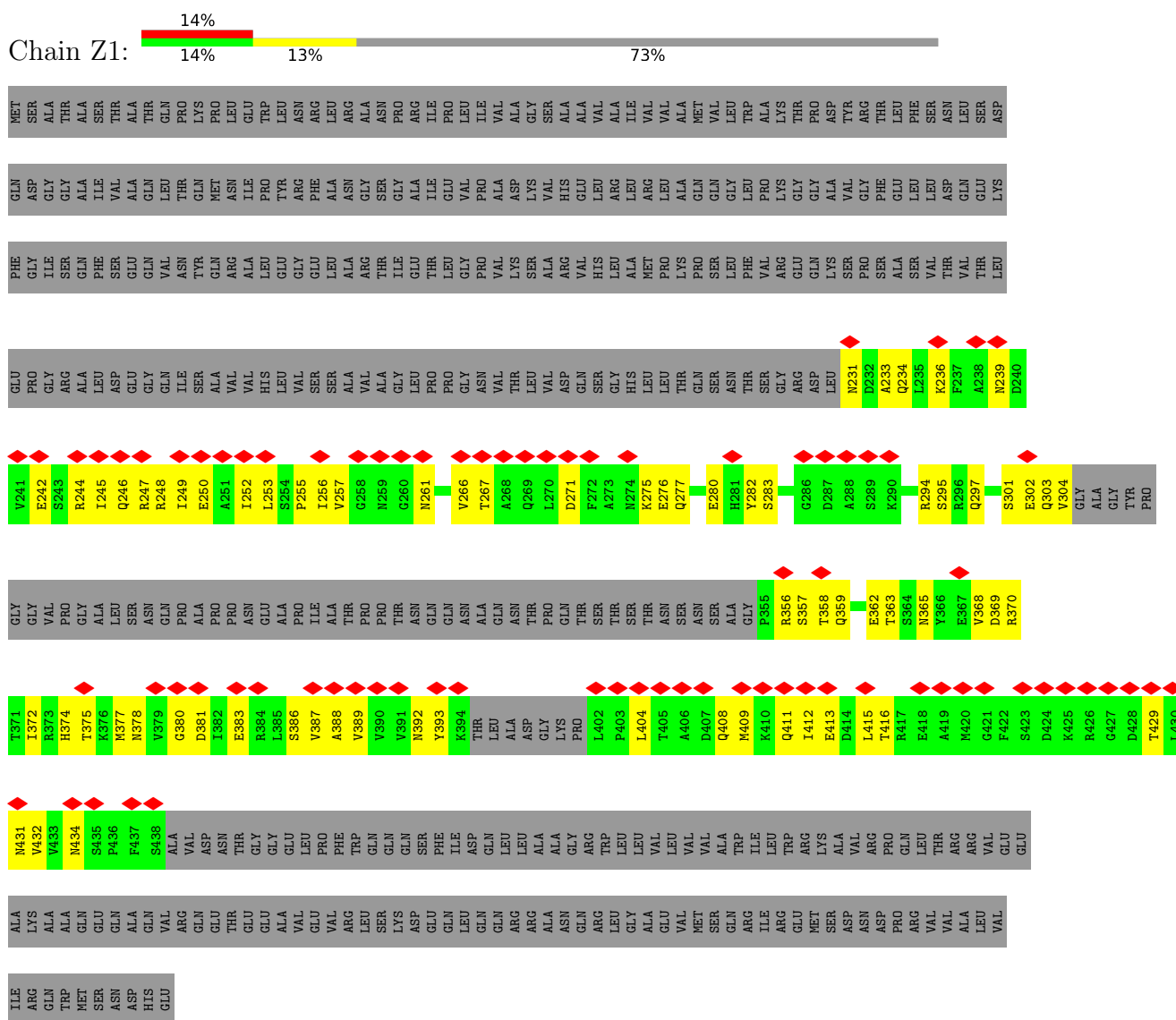


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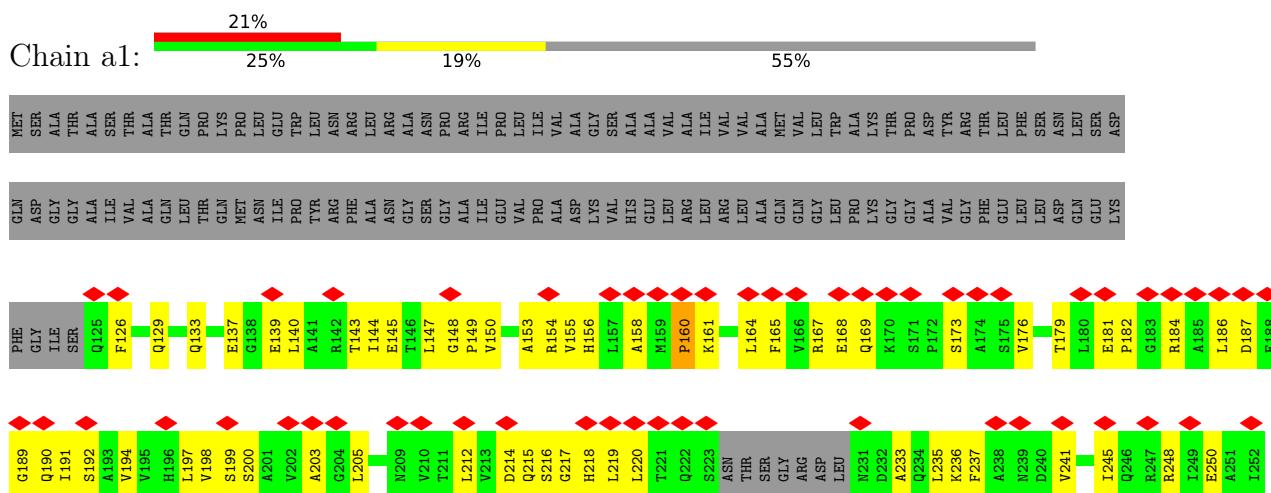
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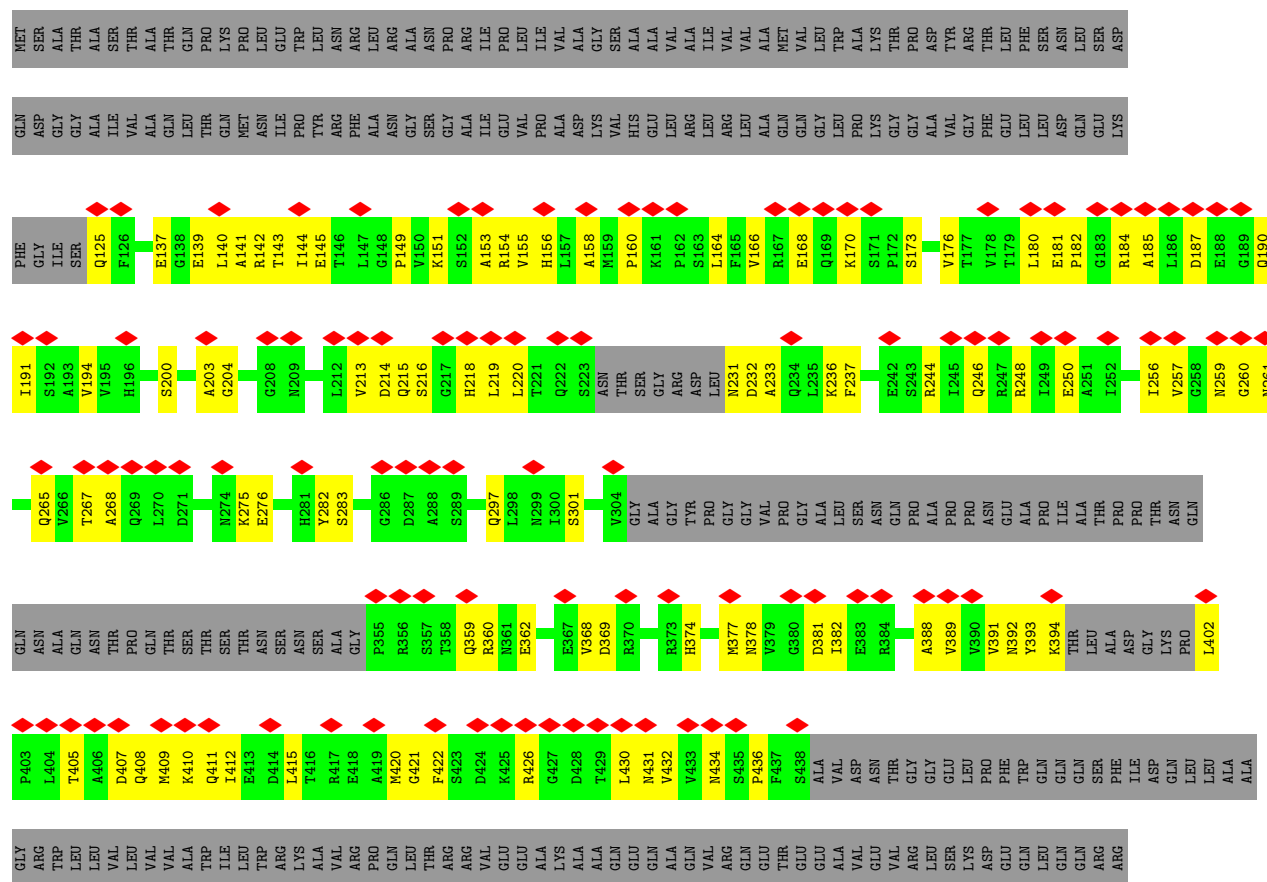




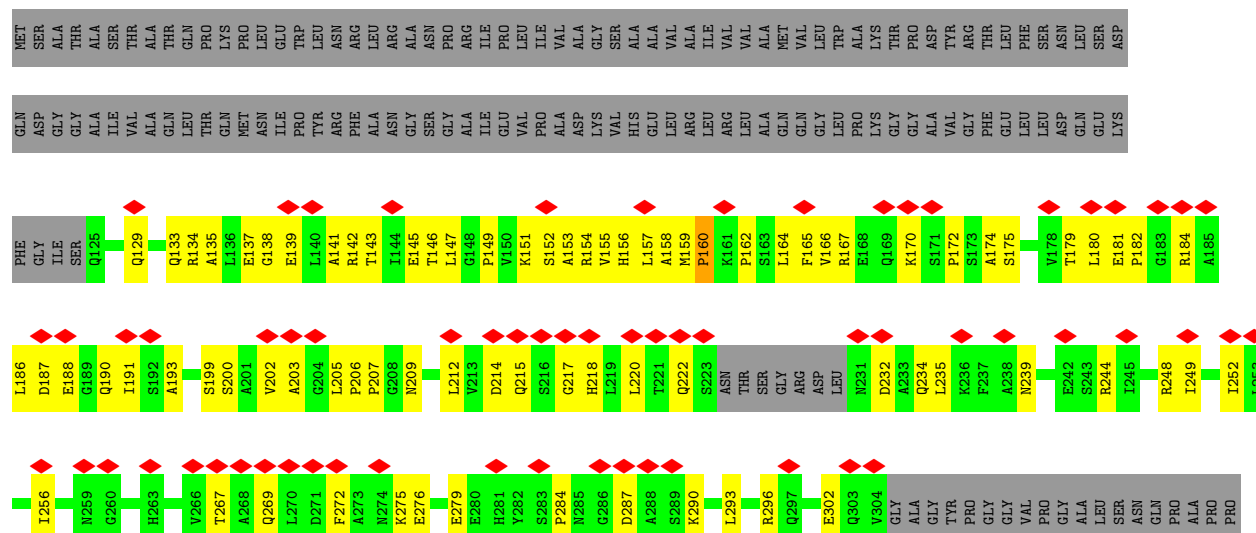
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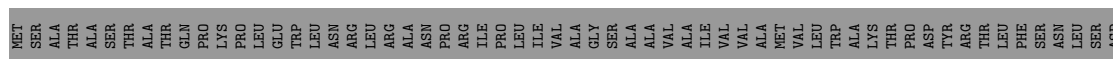


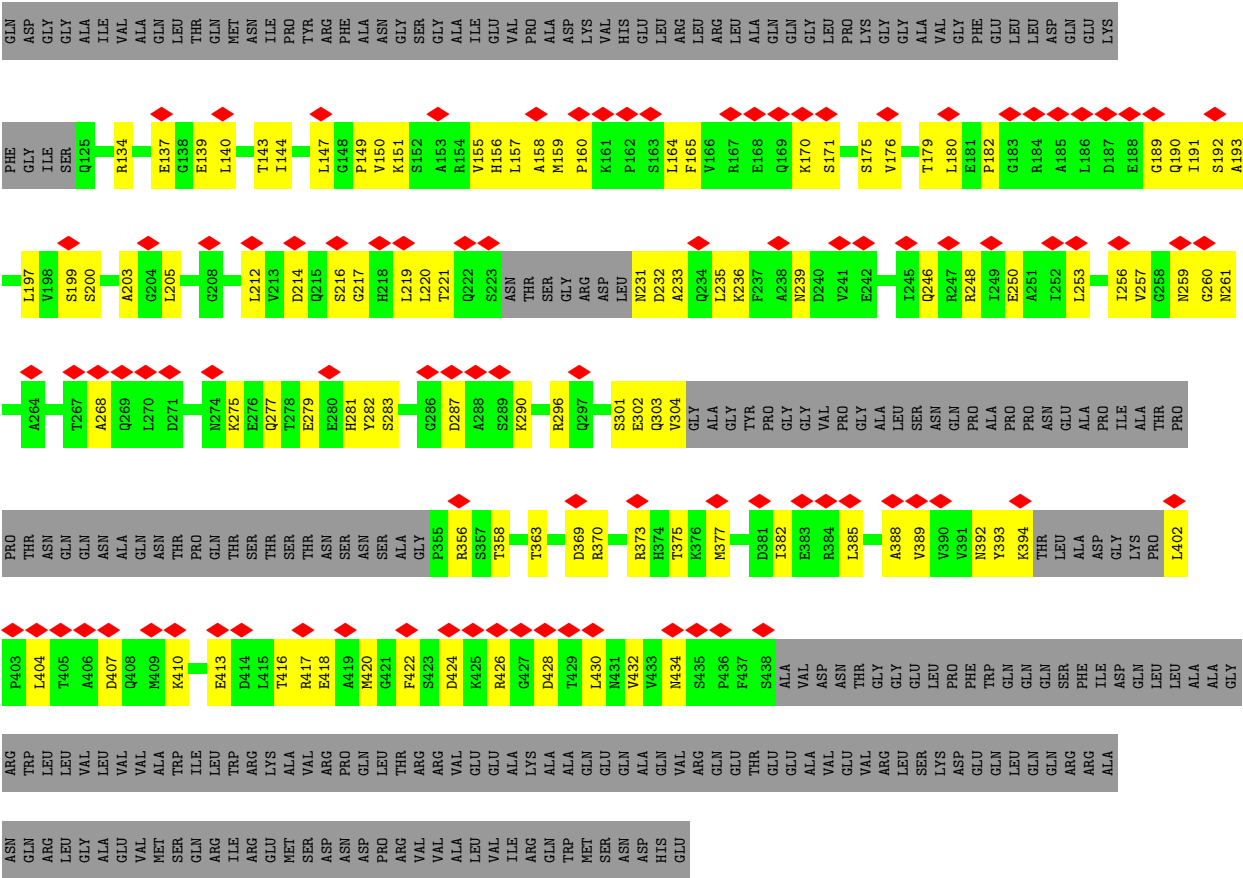


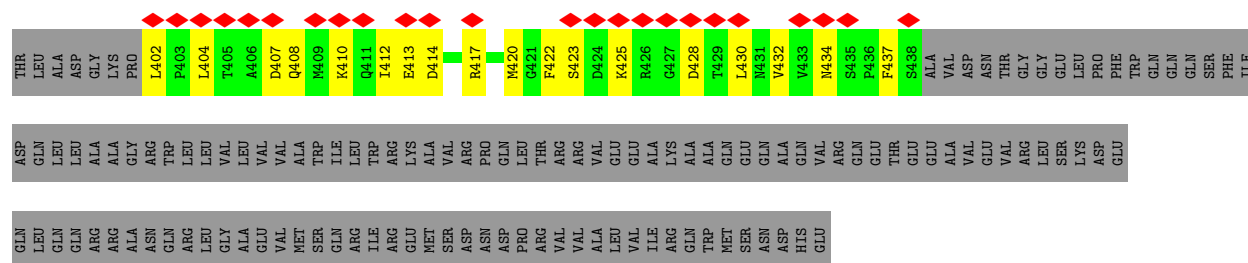


Molecule 1: Flagellar M-ring protein

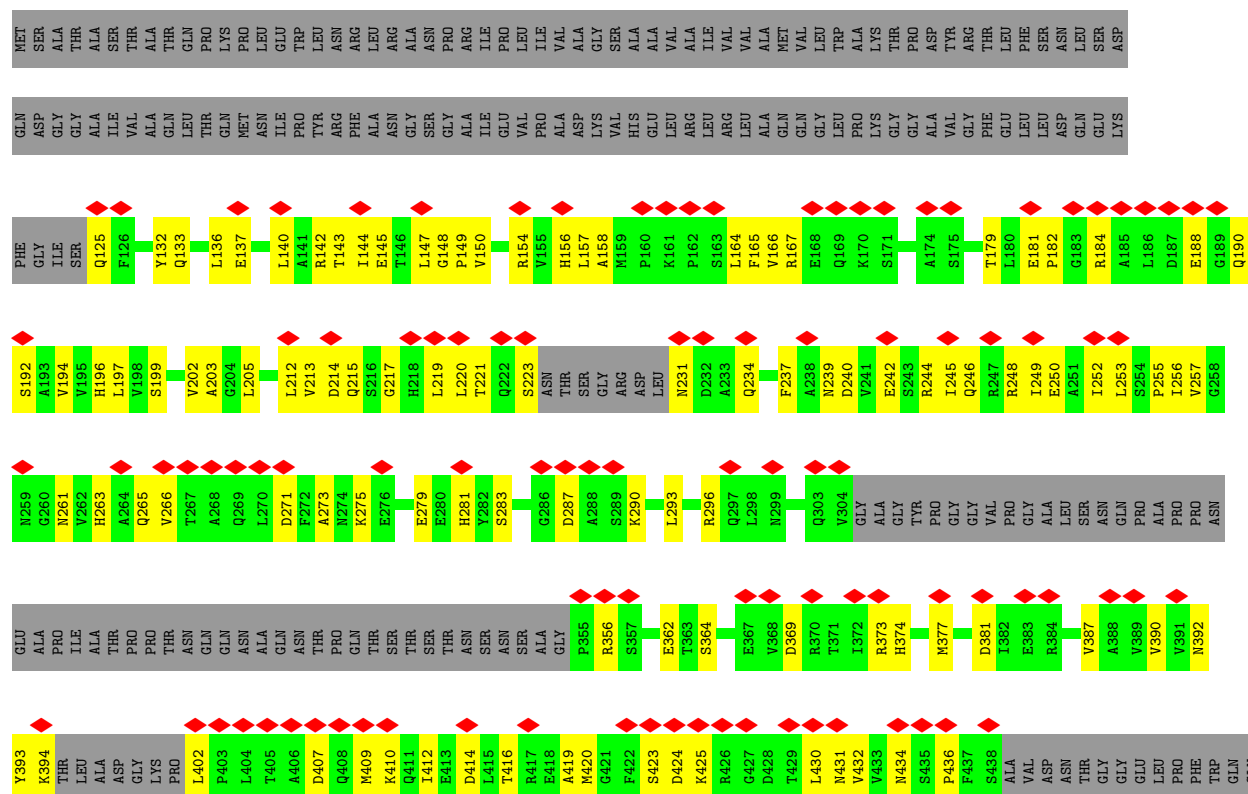
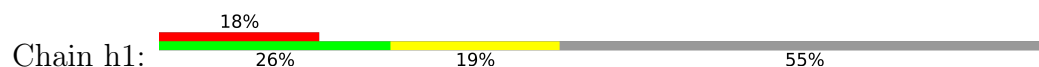




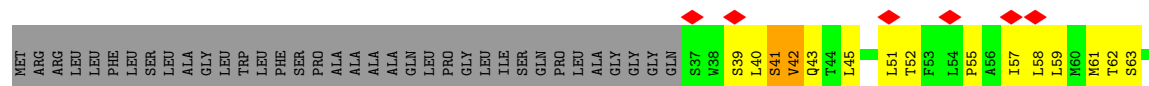
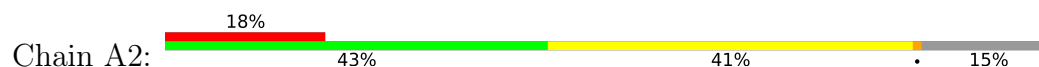


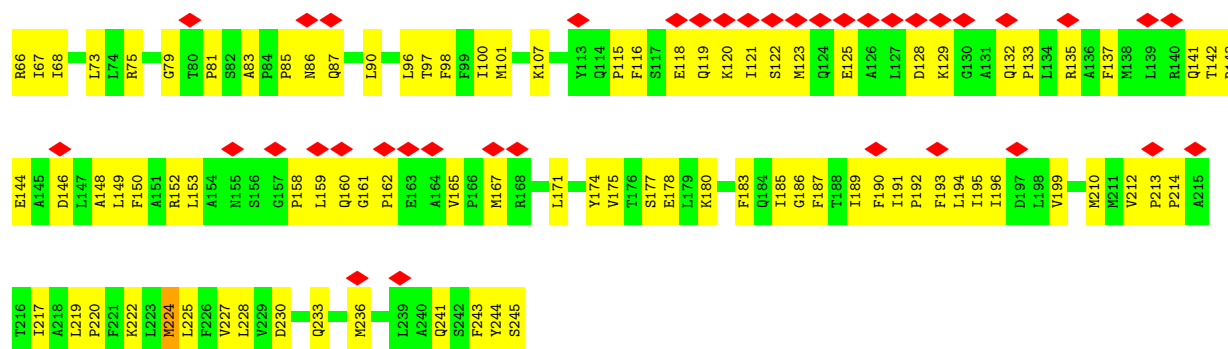


• Molecule 1: Flagellar M-ring protein

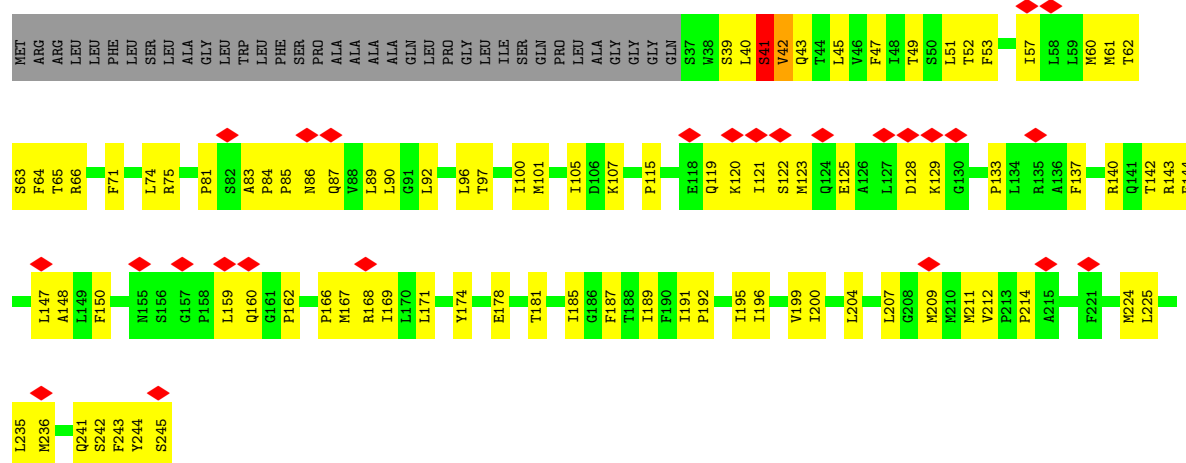


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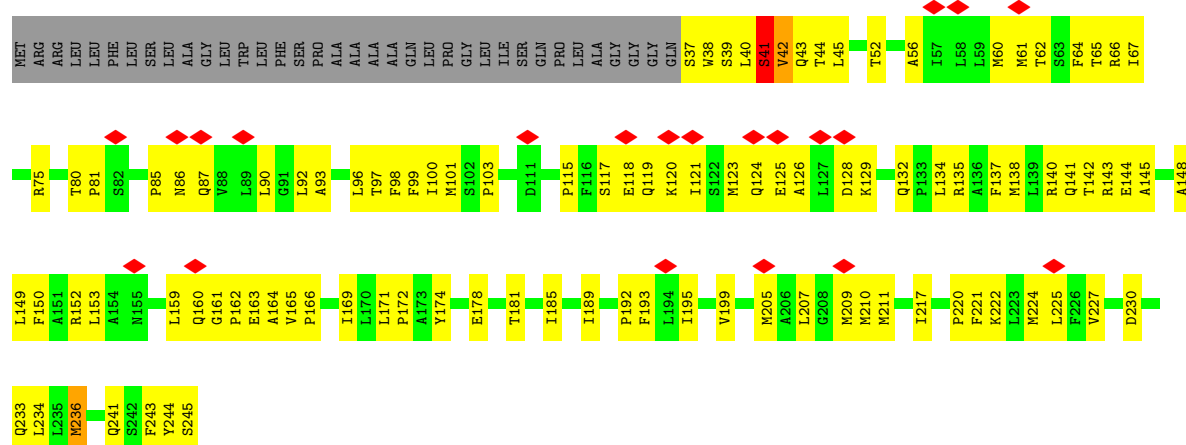




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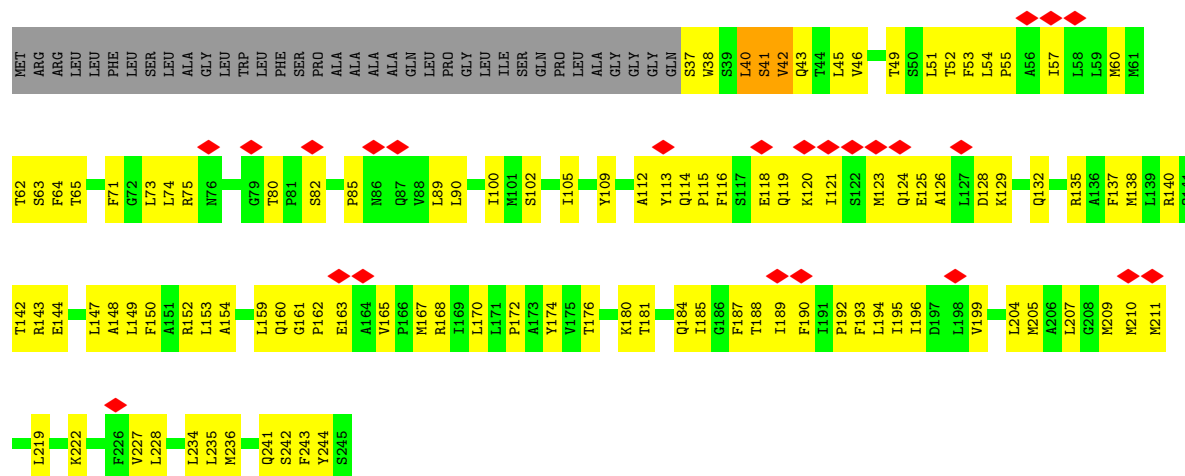


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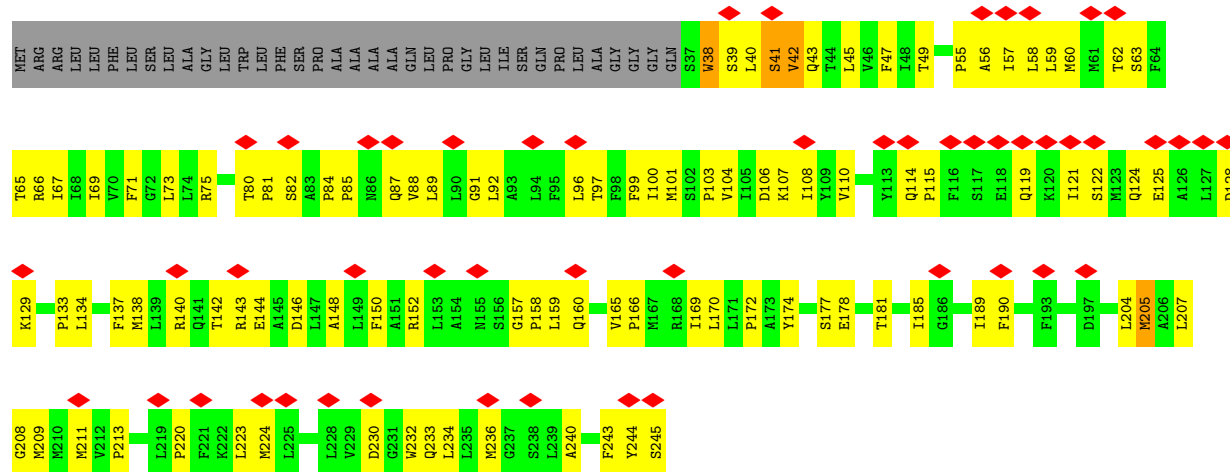
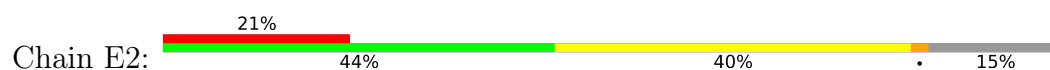


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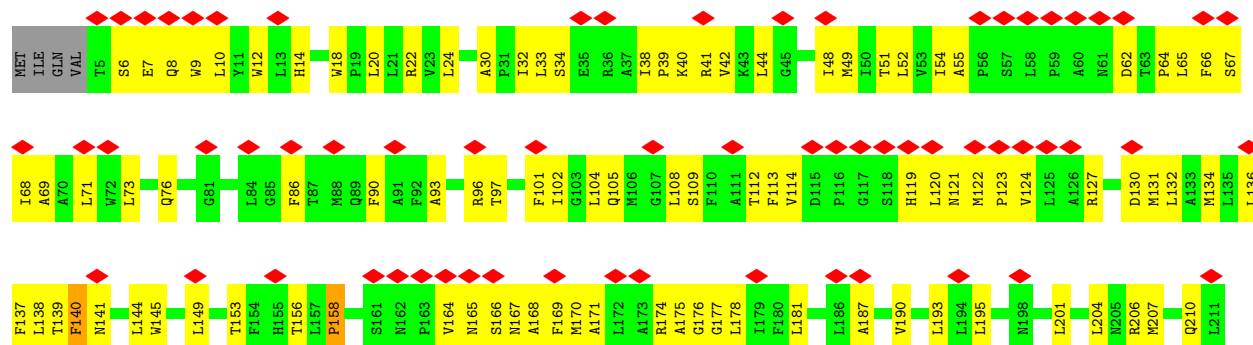


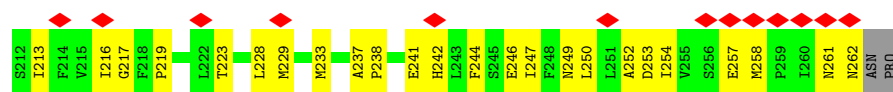


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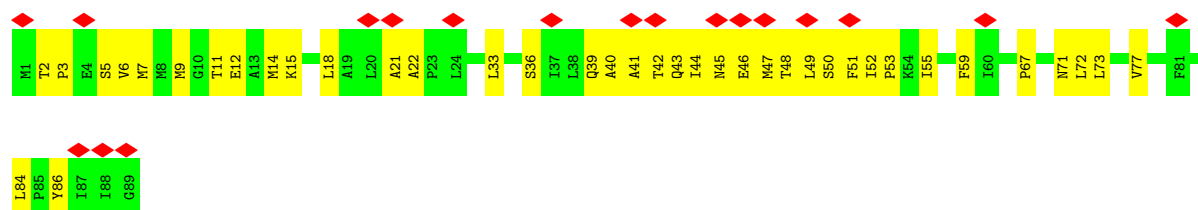


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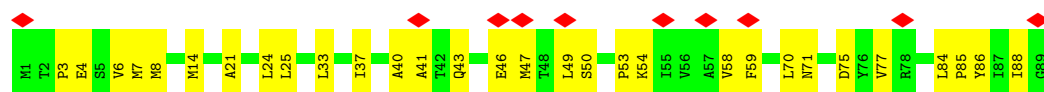




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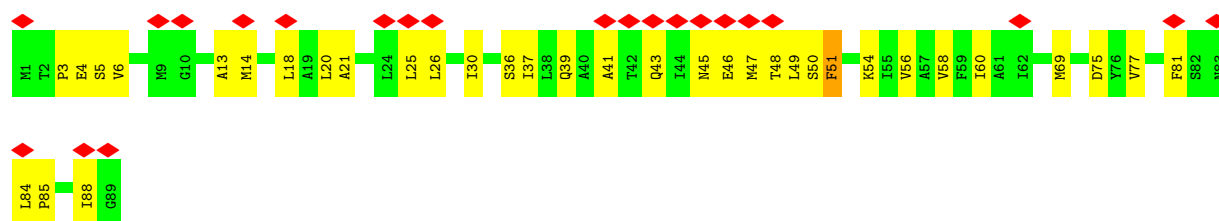
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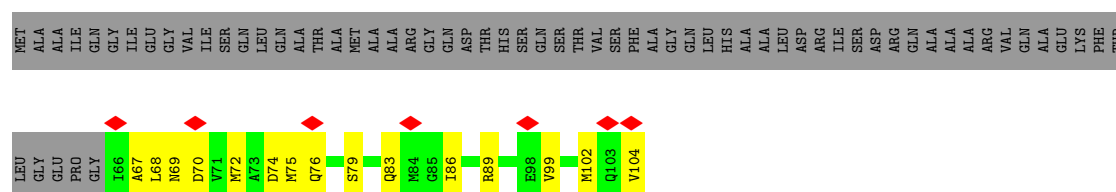
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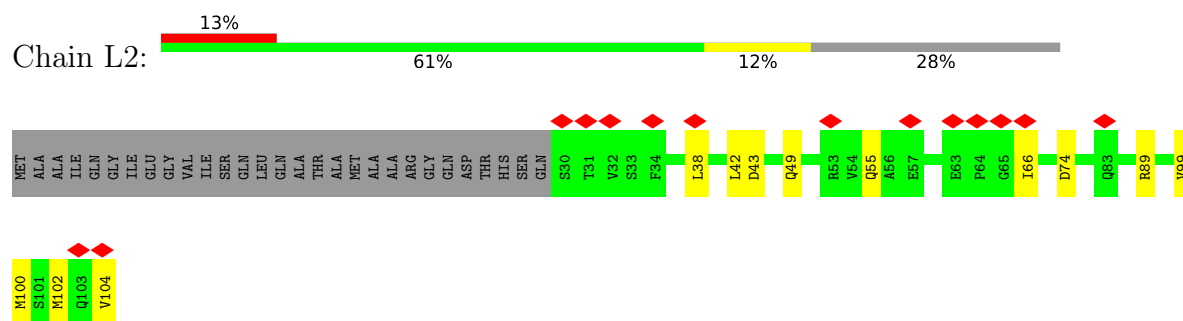
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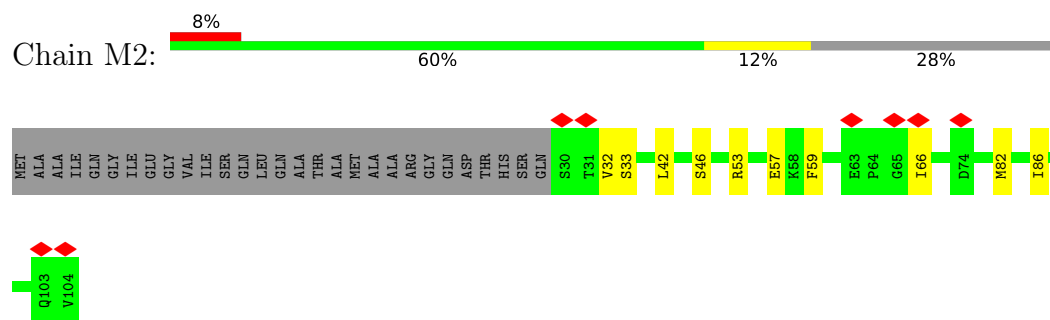
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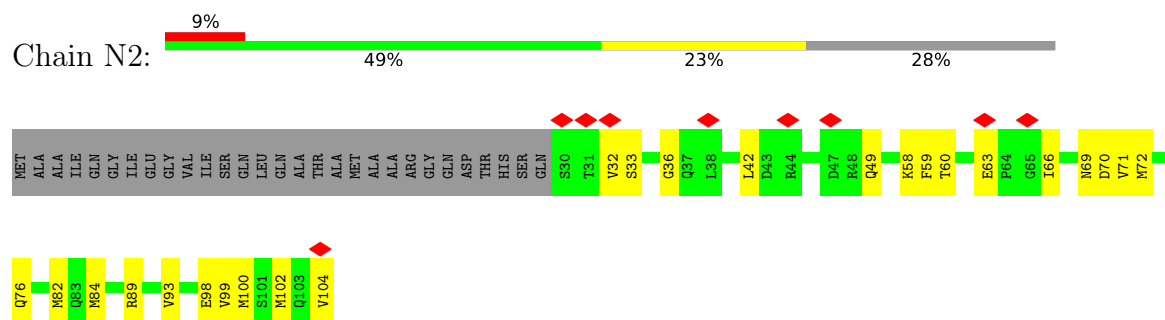
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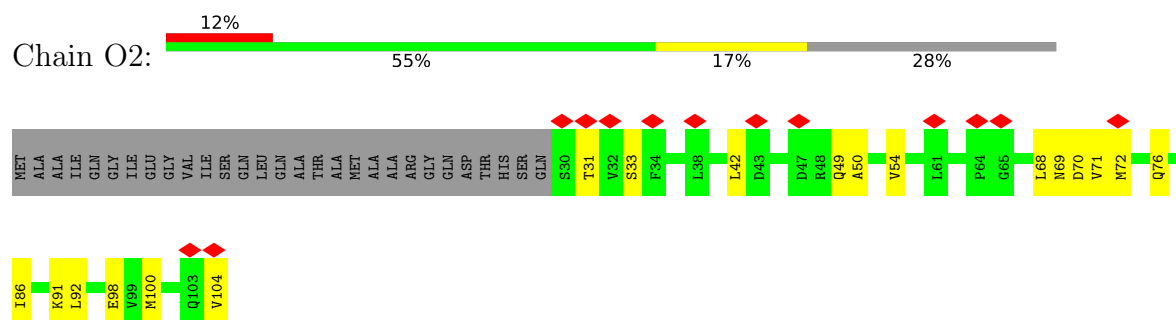
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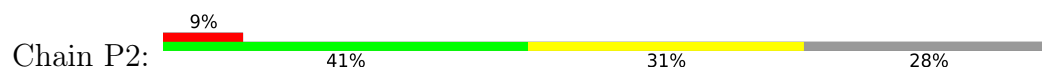
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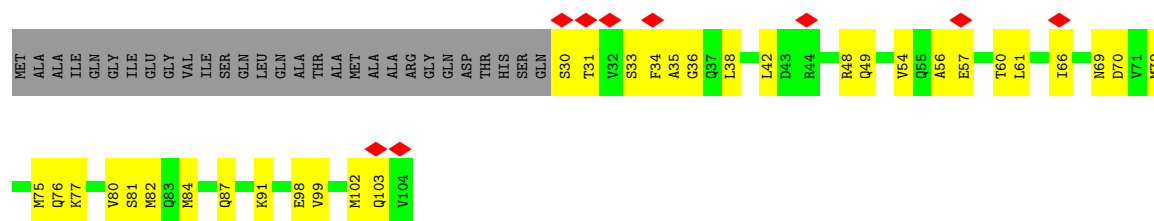


- Molecule 5: Flagellar hook-basal body complex protein FliE

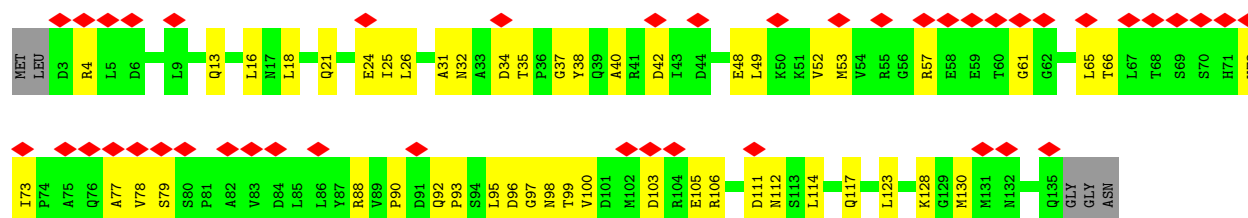


- Molecule 5: Flagellar hook-basal body complex protein FliE

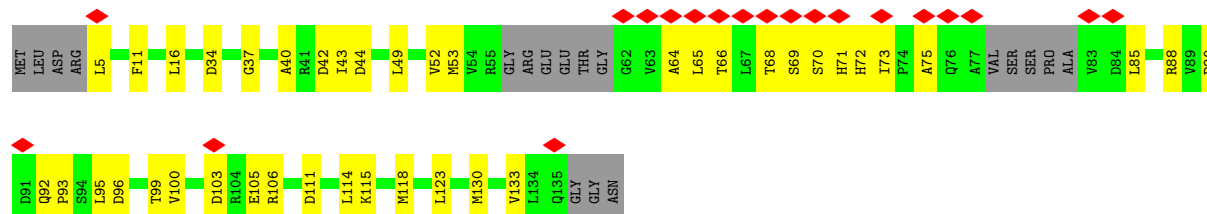




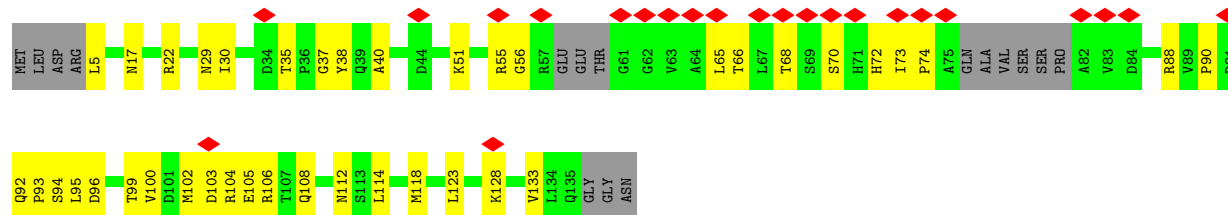
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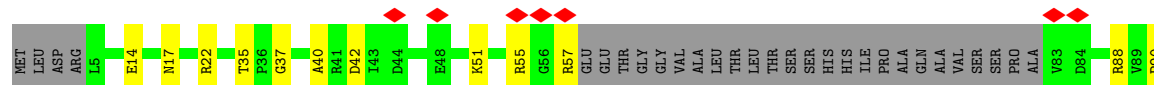
• Molecule 6: Flagellar basal body rod protein FlgB



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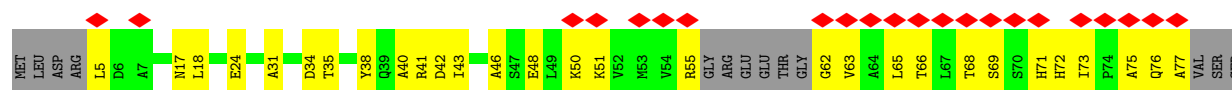


• Molecule 6: Flagellar basal body rod protein FlgB

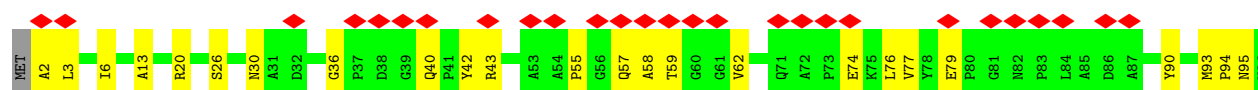
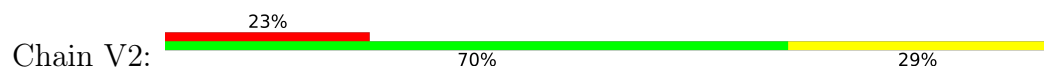




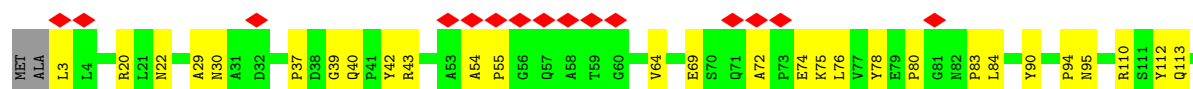
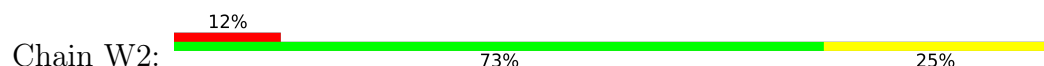
• Molecule 6: Flagellar basal body rod protein FlgB



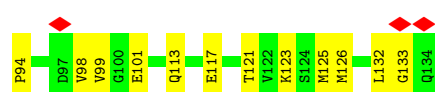
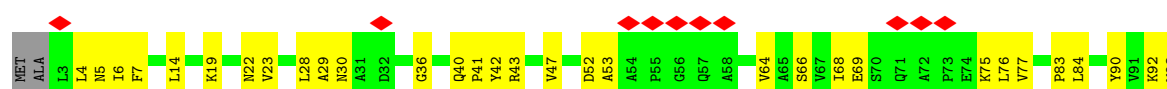
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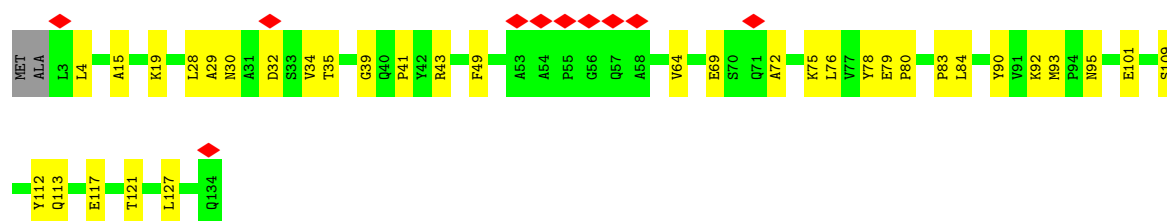
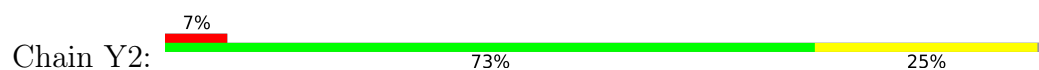
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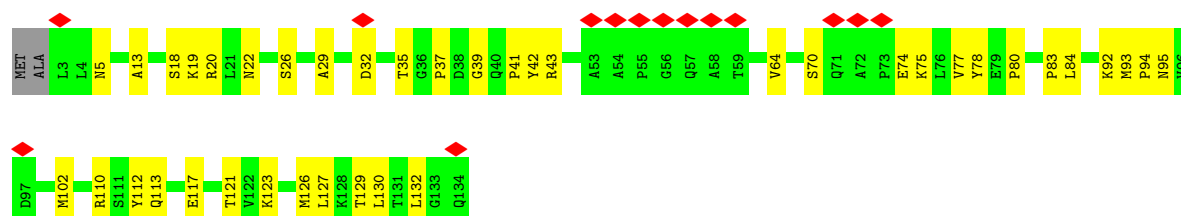
• Molecule 7: Flagellar basal-body rod protein FlgC



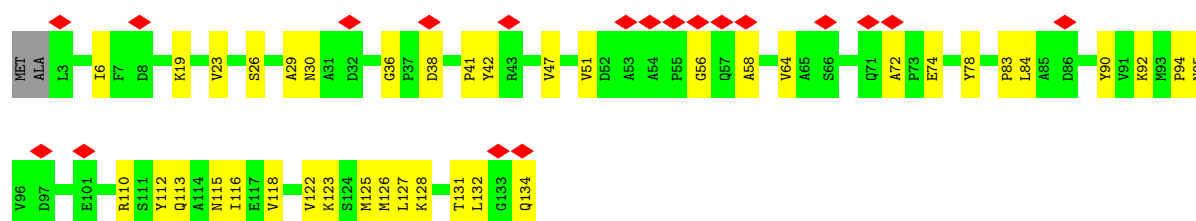
• Molecule 7: Flagellar basal-body rod protein FlgC



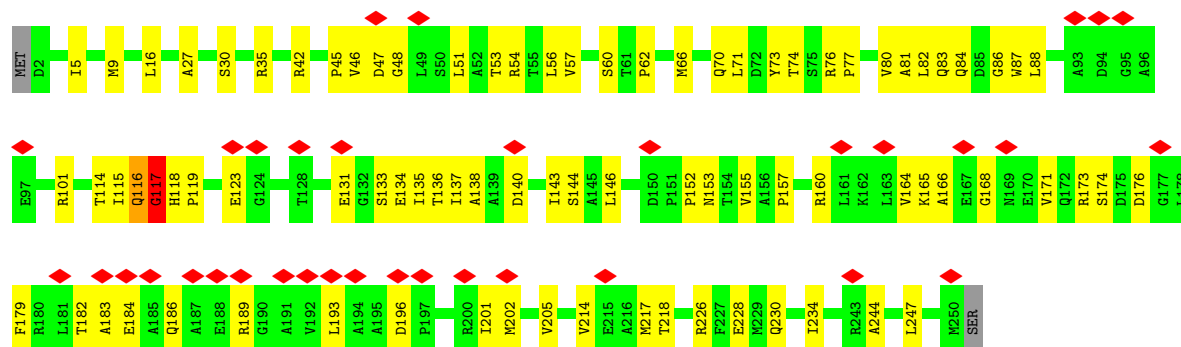
• Molecule 7: Flagellar basal-body rod protein FlgC



• Molecule 7: Flagellar basal-body rod protein FlgC

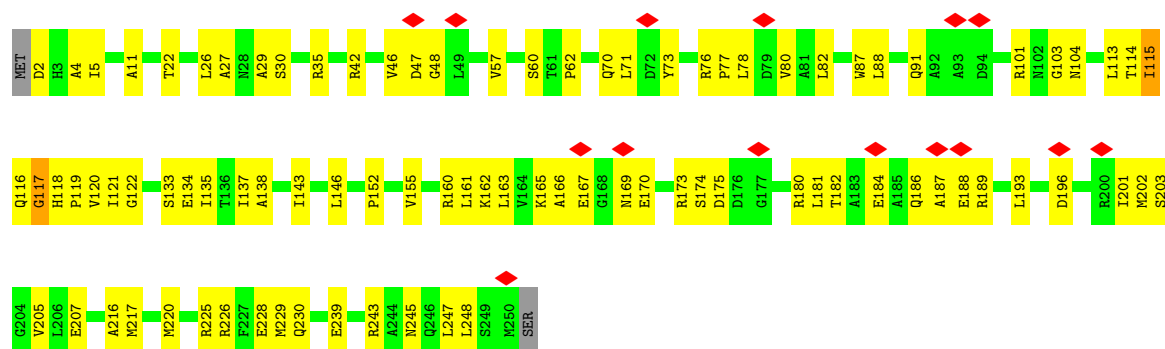


• Molecule 8: Flagellar basal body protein



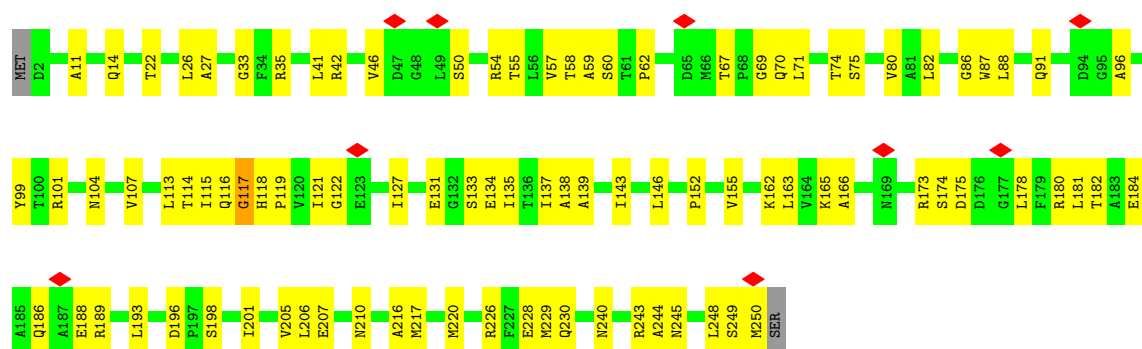
• Molecule 8: Flagellar basal body protein





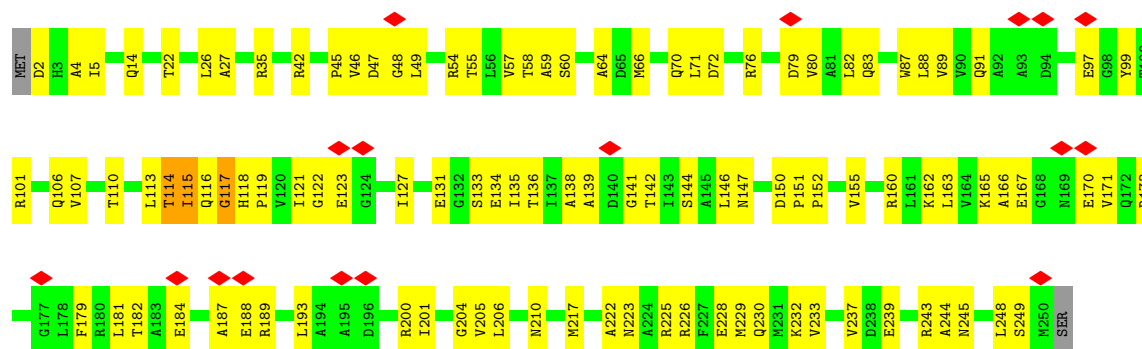
• Molecule 8: Flagellar basal body protein

Chain d2: 62% 37%



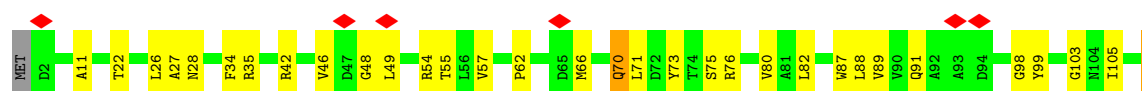
• Molecule 8: Flagellar basal body protein

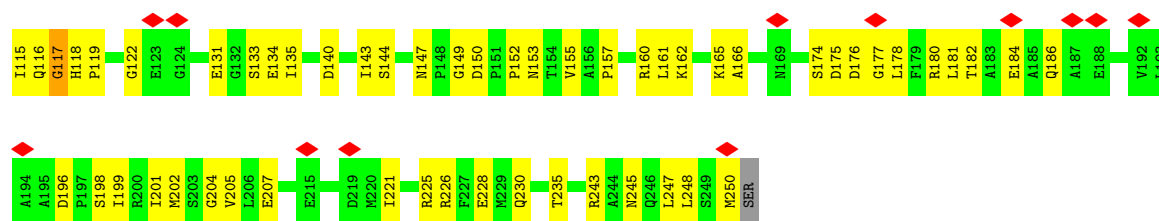
Chain e2: 7% 57% 41%



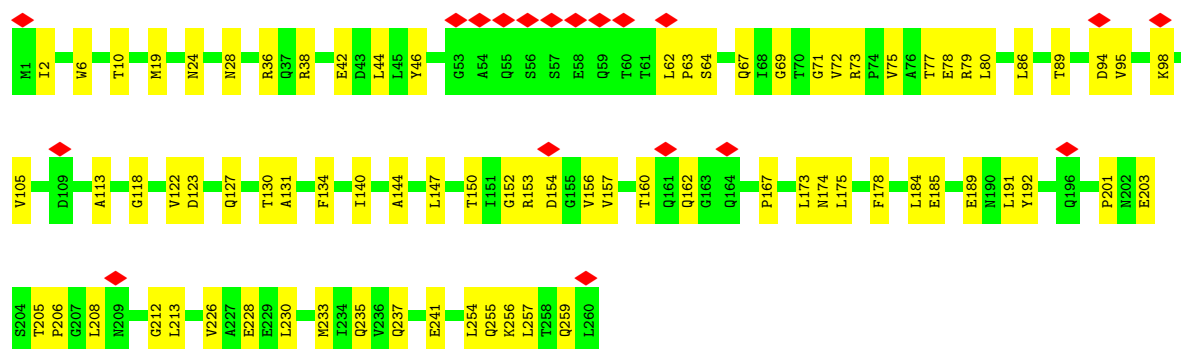
• Molecule 8: Flagellar basal body protein

Chain f2: 7% 65% 33%

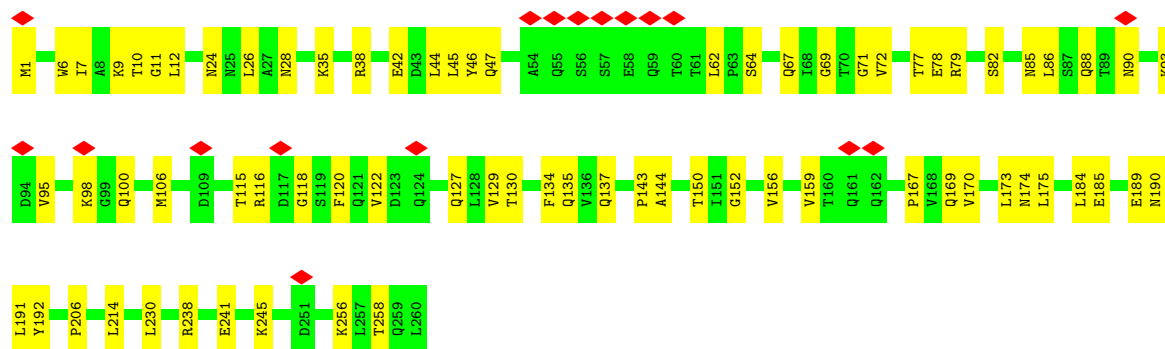
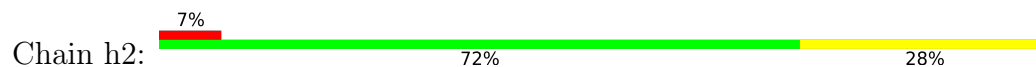




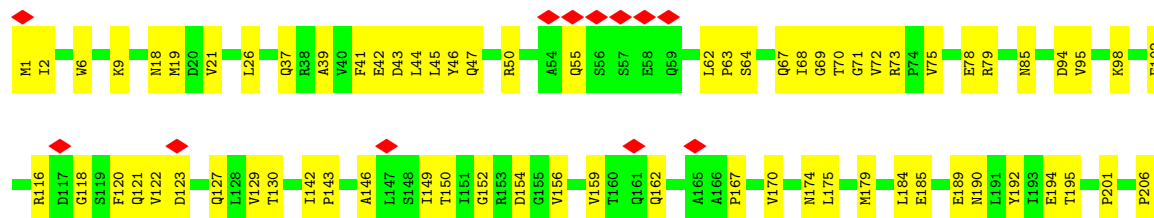
• Molecule 9: Flagellar basal-body rod protein FlgG



• Molecule 9: Flagellar basal-body rod protein FlgG

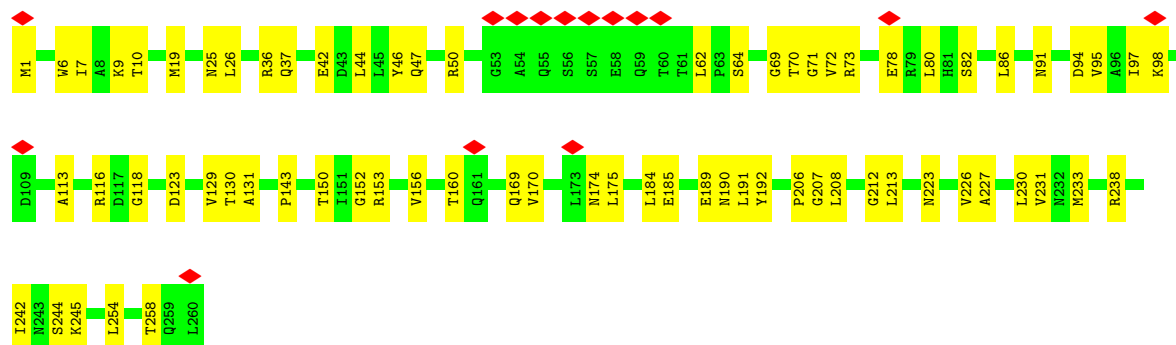
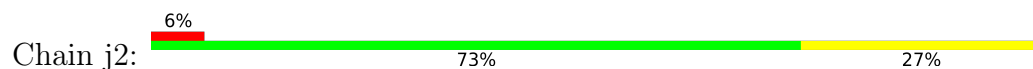


• Molecule 9: Flagellar basal-body rod protein FlgG

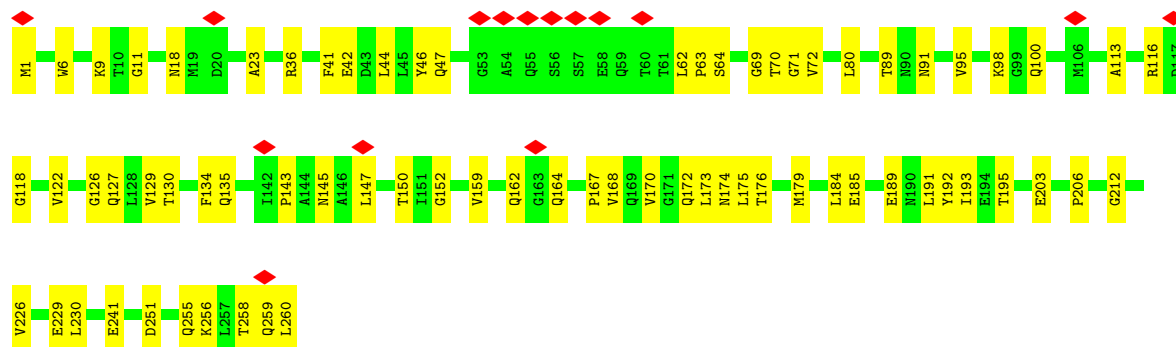
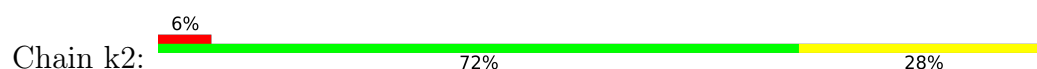




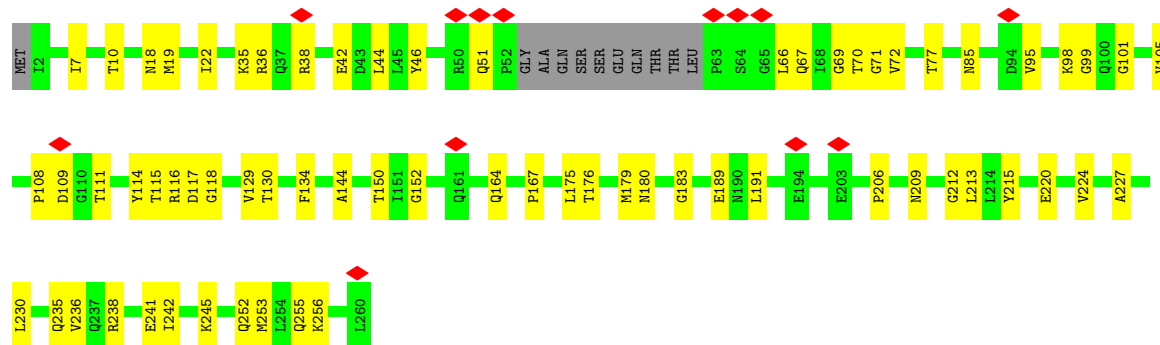
• Molecule 9: Flagellar basal-body rod protein FlgG



• Molecule 9: Flagellar basal-body rod protein FlgG

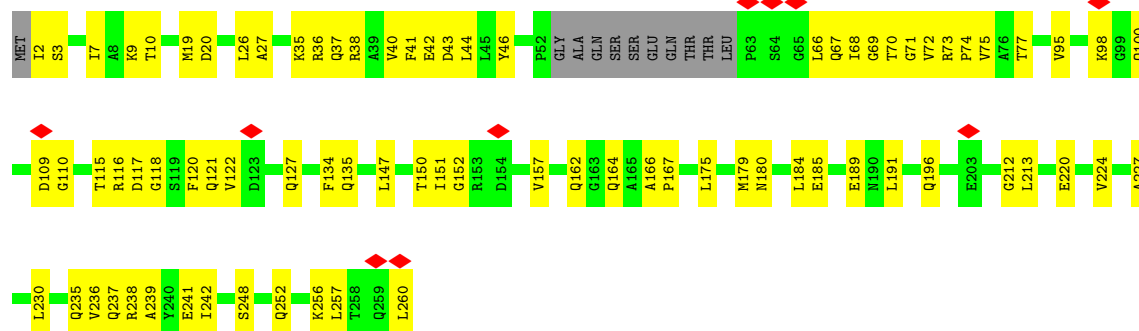


• Molecule 9: Flagellar basal-body rod protein FlgG



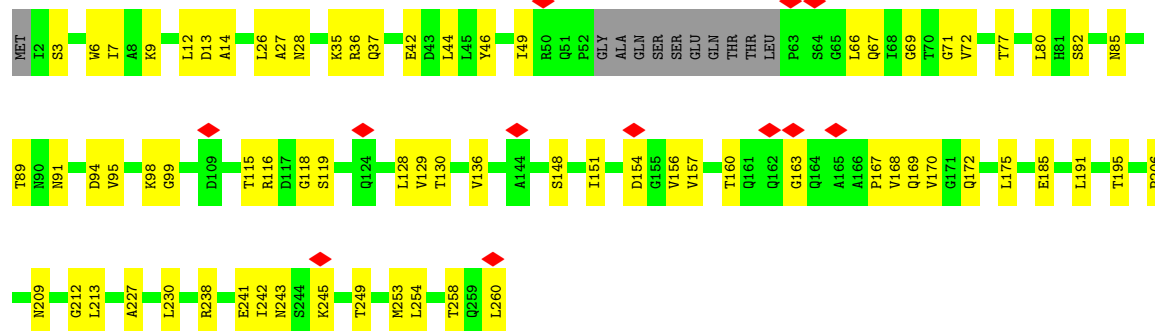
• Molecule 9: Flagellar basal-body rod protein FlgG

Chain m2: 



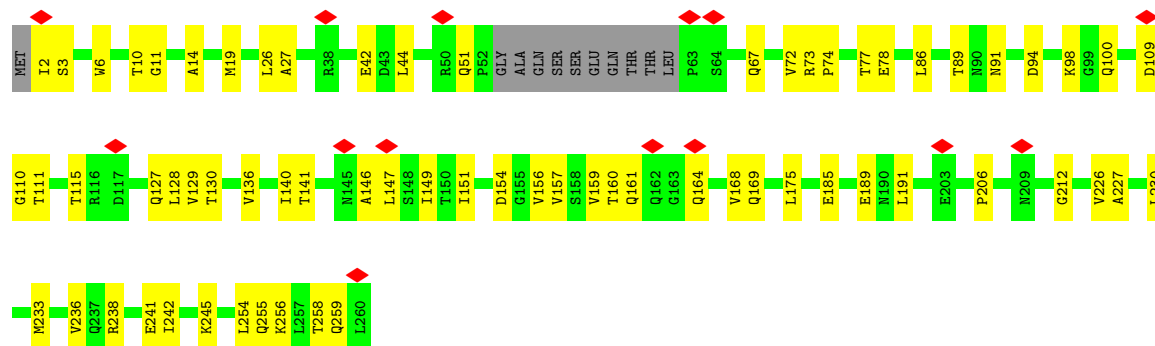
• Molecule 9: Flagellar basal-body rod protein FlgG

Chain n2: 



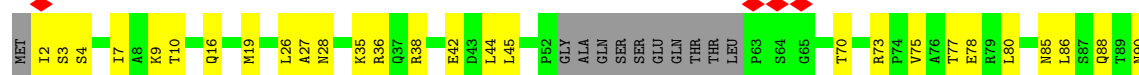
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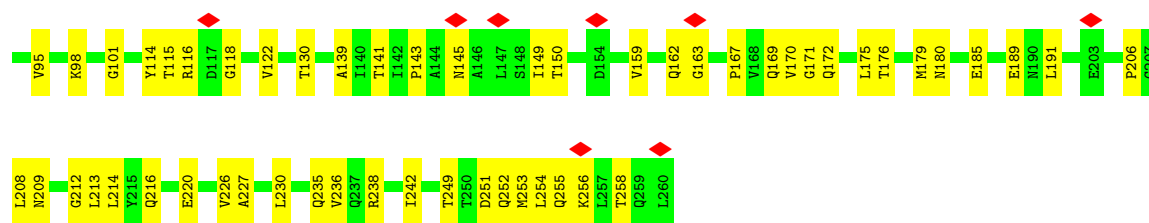
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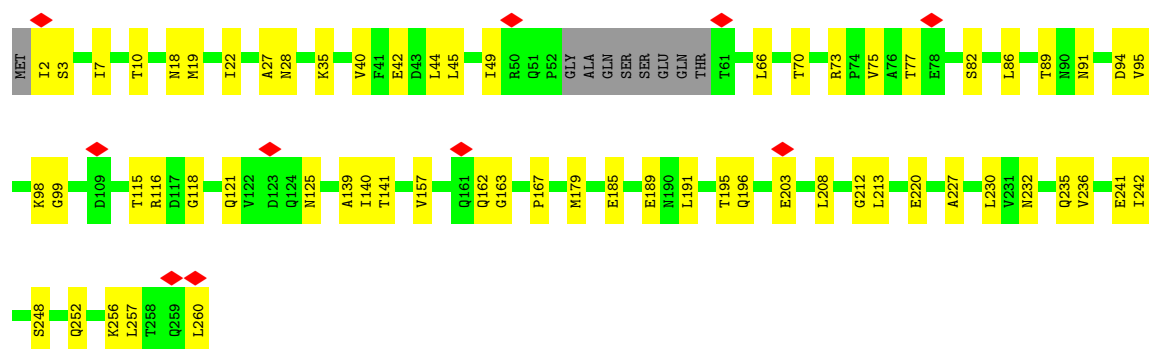
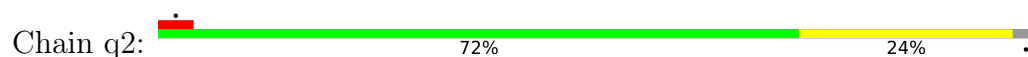
• Molecule 9: Flagellar basal-body rod protein FlgG

Chain p2: 

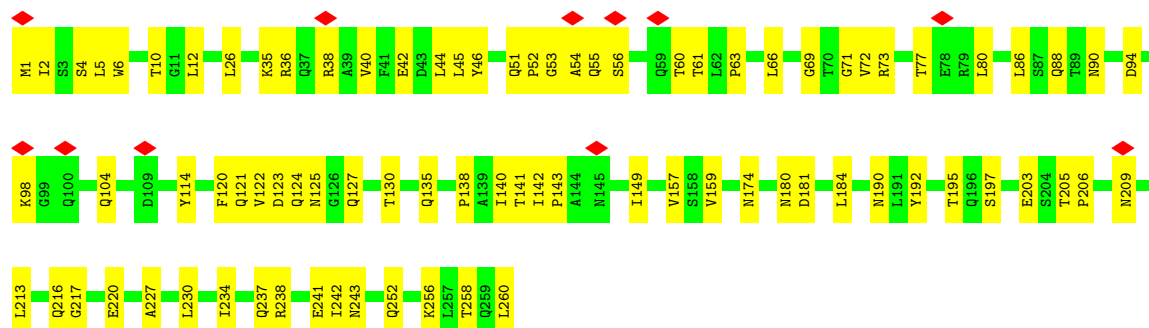




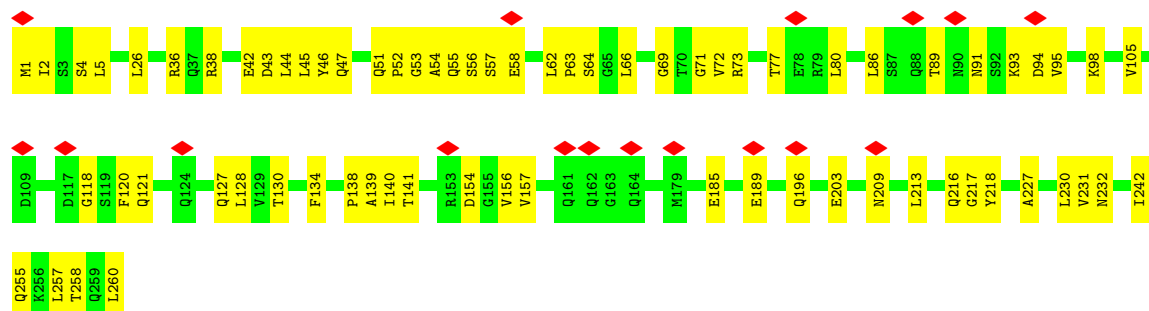
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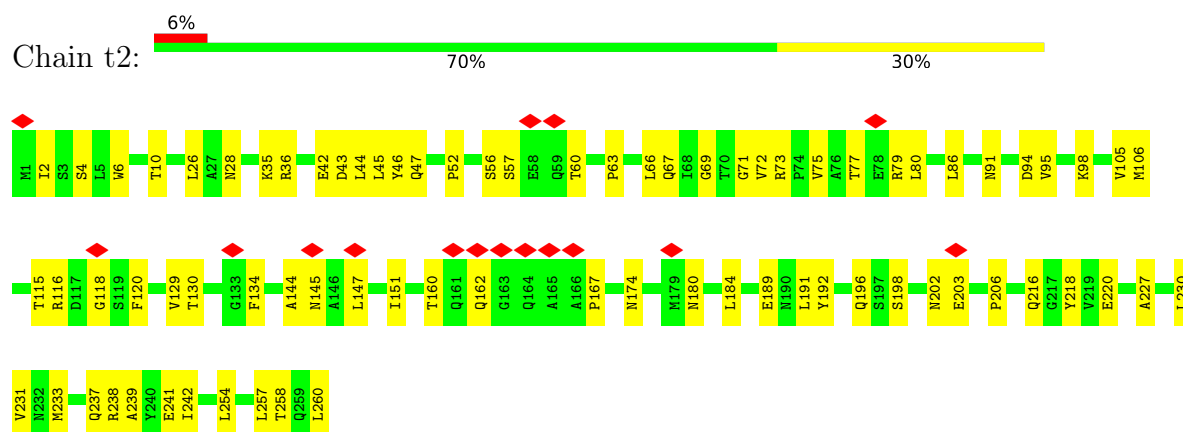
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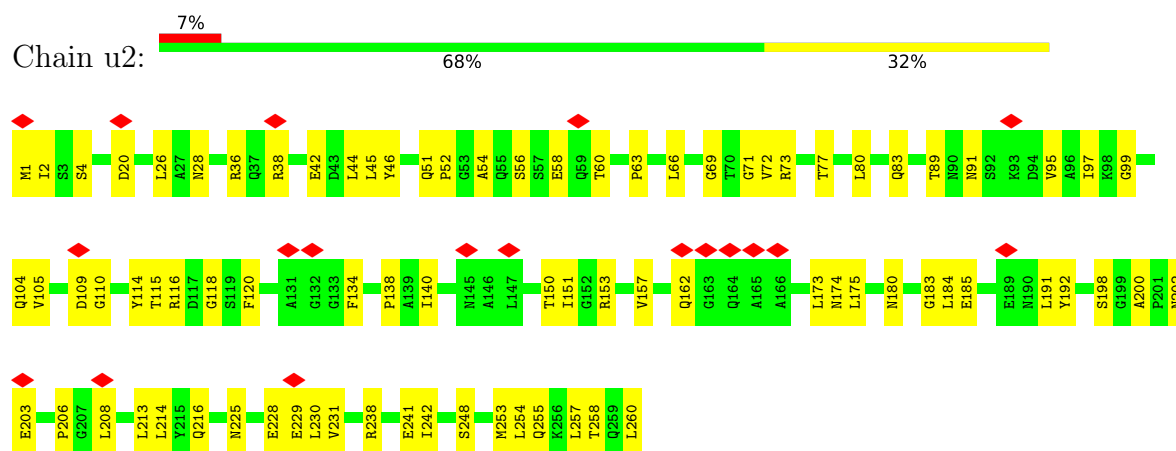
• Molecule 9: Flagellar basal-body rod protein FlgG



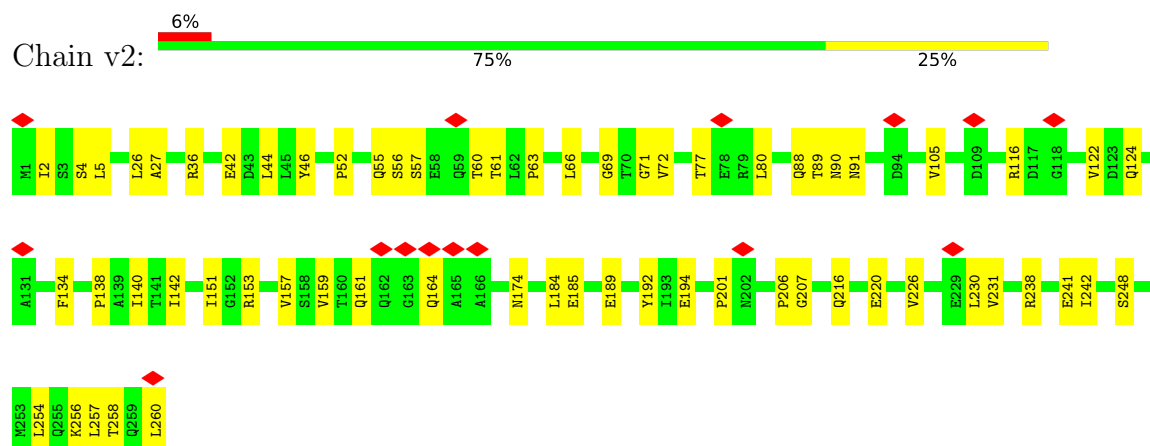
- Molecule 9: Flagellar basal-body rod protein FlgG



- Molecule 9: Flagellar basal-body rod protein FlgG

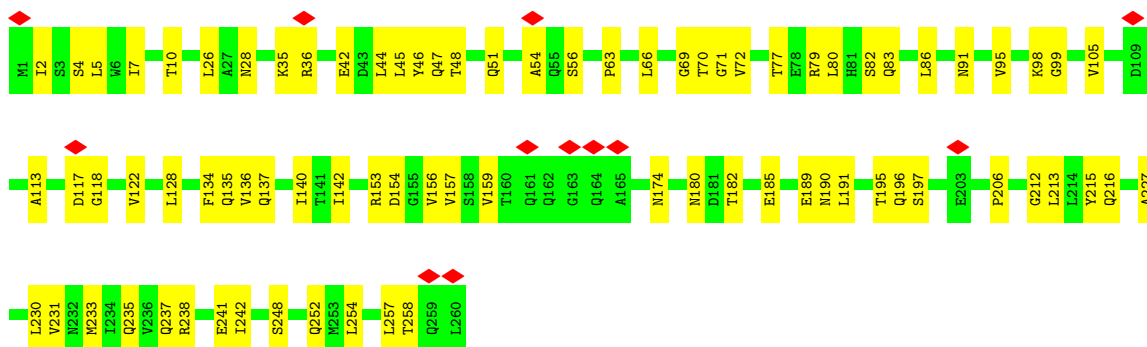


- Molecule 9: Flagellar basal-body rod protein FlgG

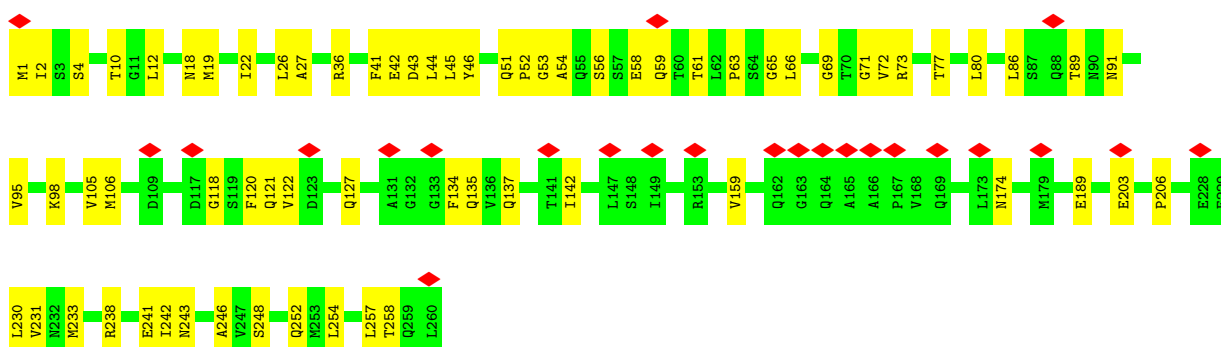
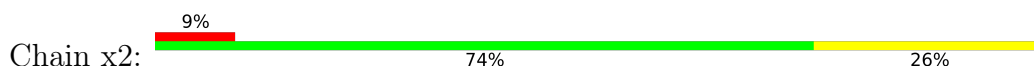


- Molecule 9: Flagellar basal-body rod protein FlgG

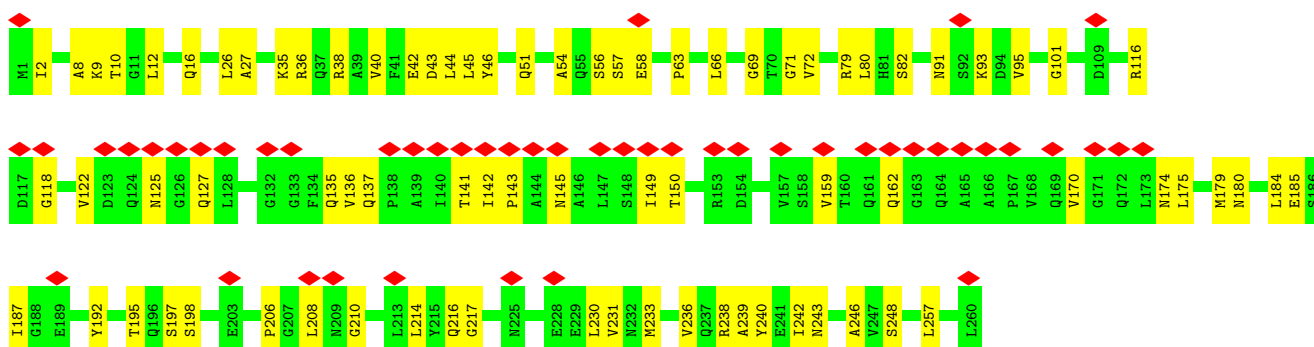




• Molecule 9: Flagellar basal-body rod protein FlgG

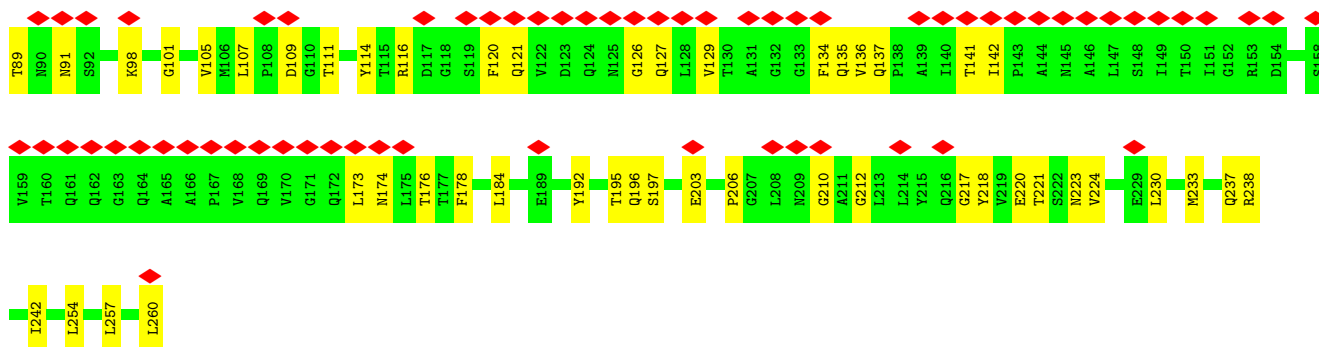


• Molecule 9: Flagellar basal-body rod protein FlgG

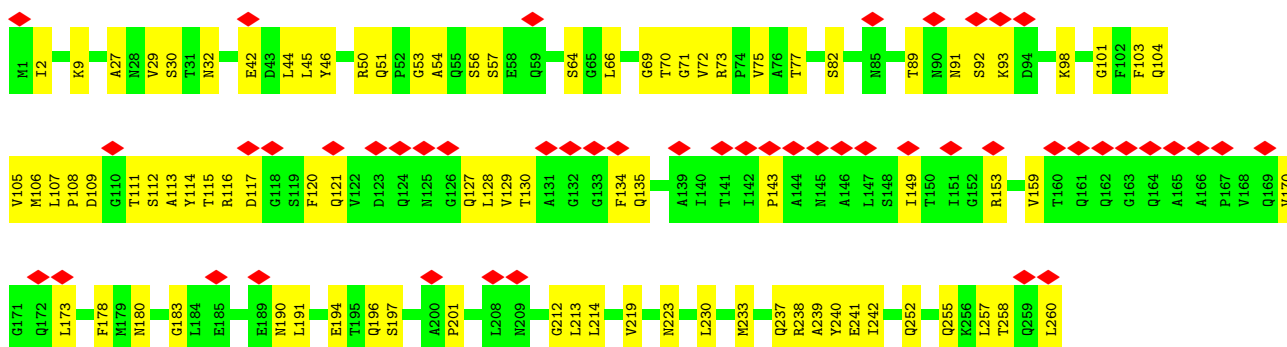


• Molecule 9: Flagellar basal-body rod protein FlgG

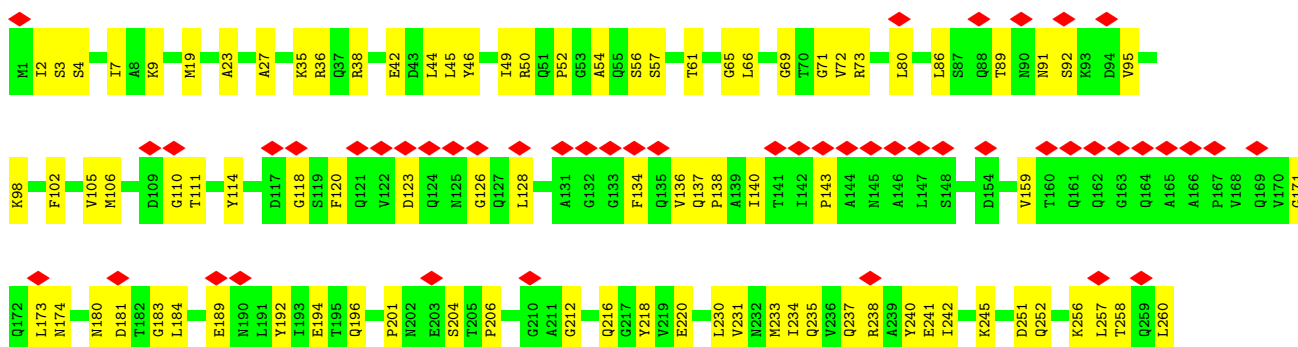




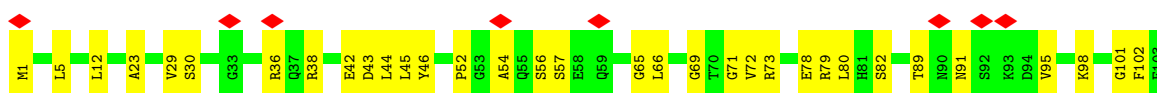
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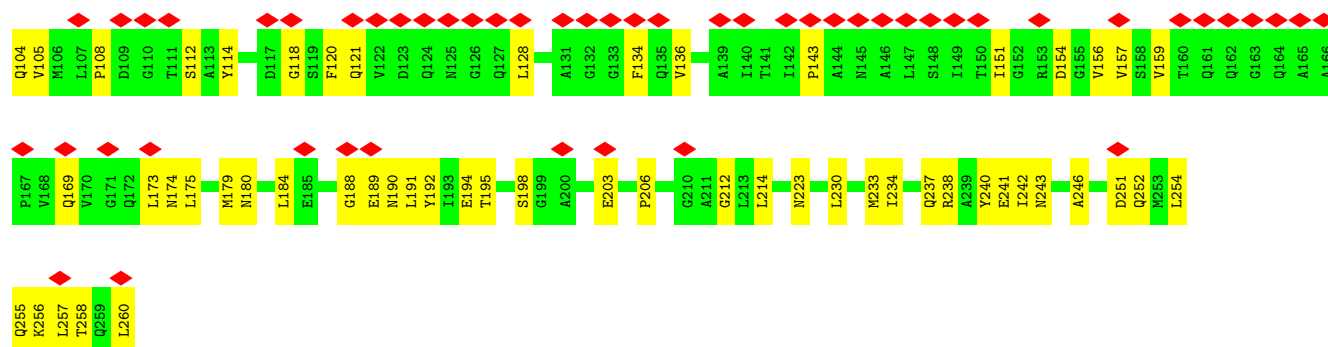


• Molecule 9: Flagellar basal-body rod protein FlgG

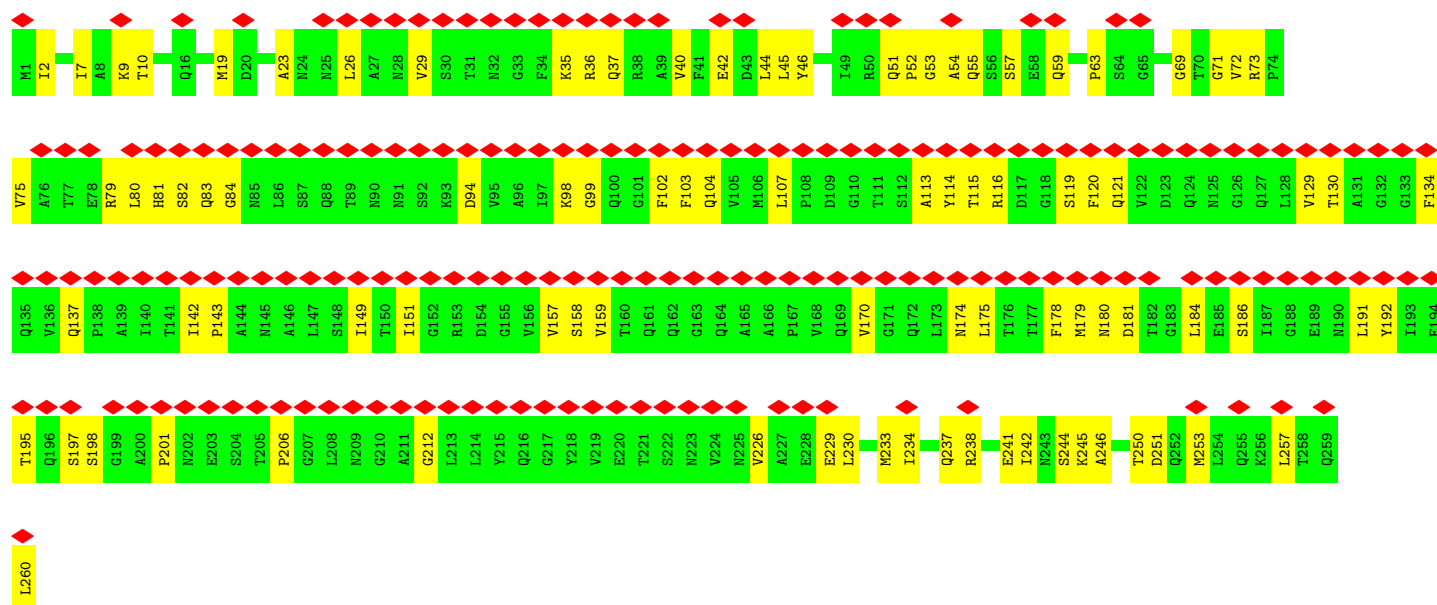
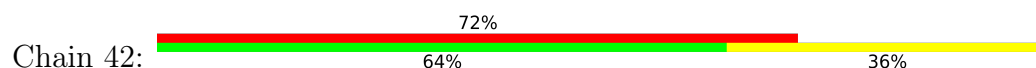


• Molecule 9: Flagellar basal-body rod protein FlgG

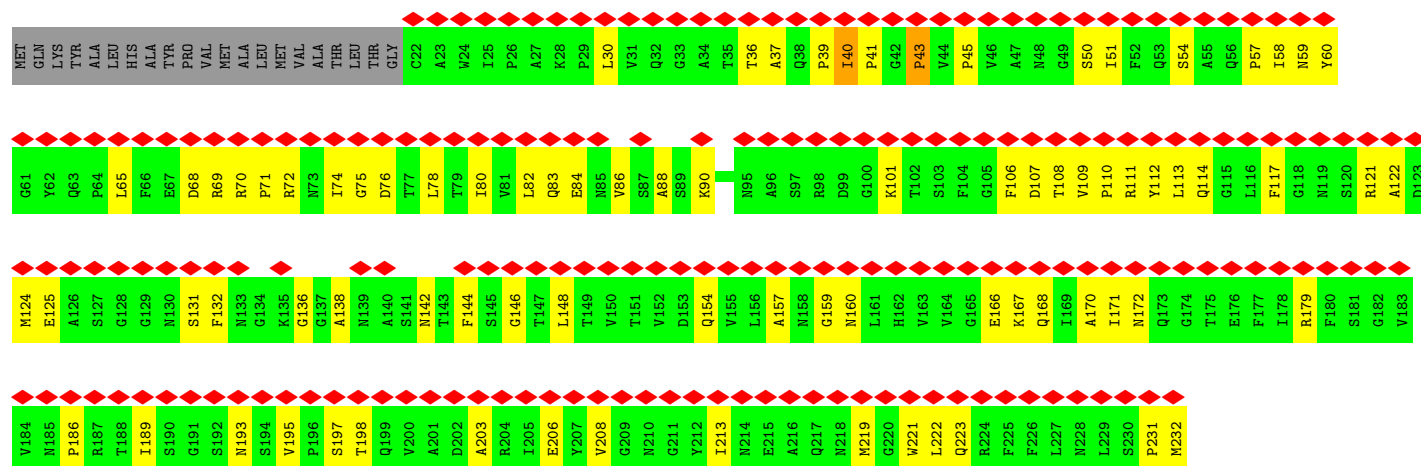
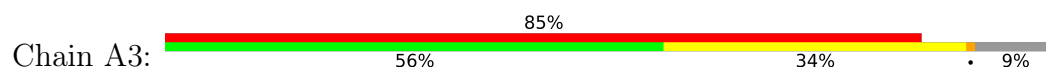




• Molecule 9: Flagellar basal-body rod protein FlgG

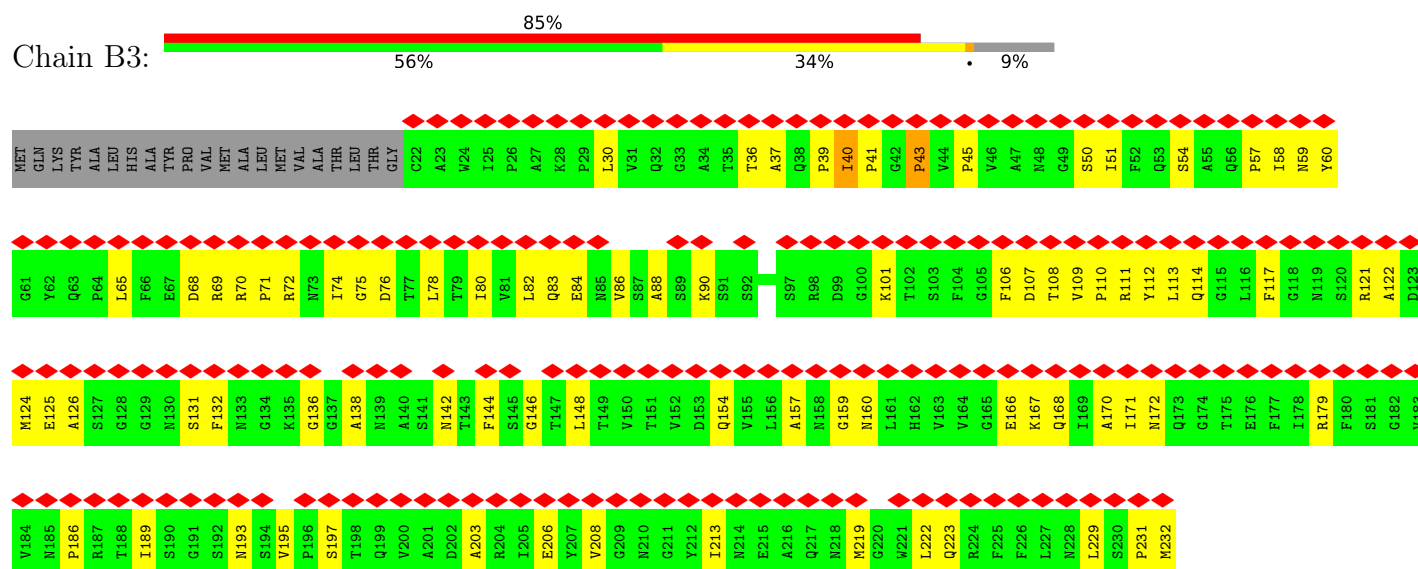


• Molecule 10: Flagellar L-ring protein



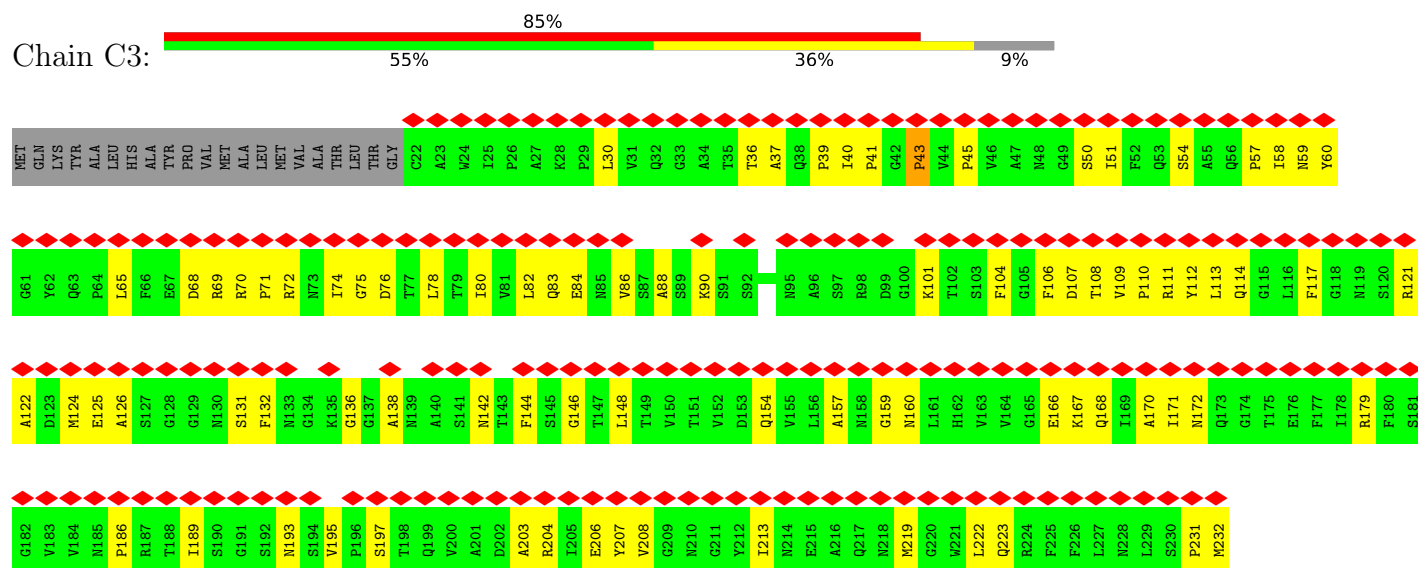
- Molecule 10: Flagellar L-ring protein

Chain B3:



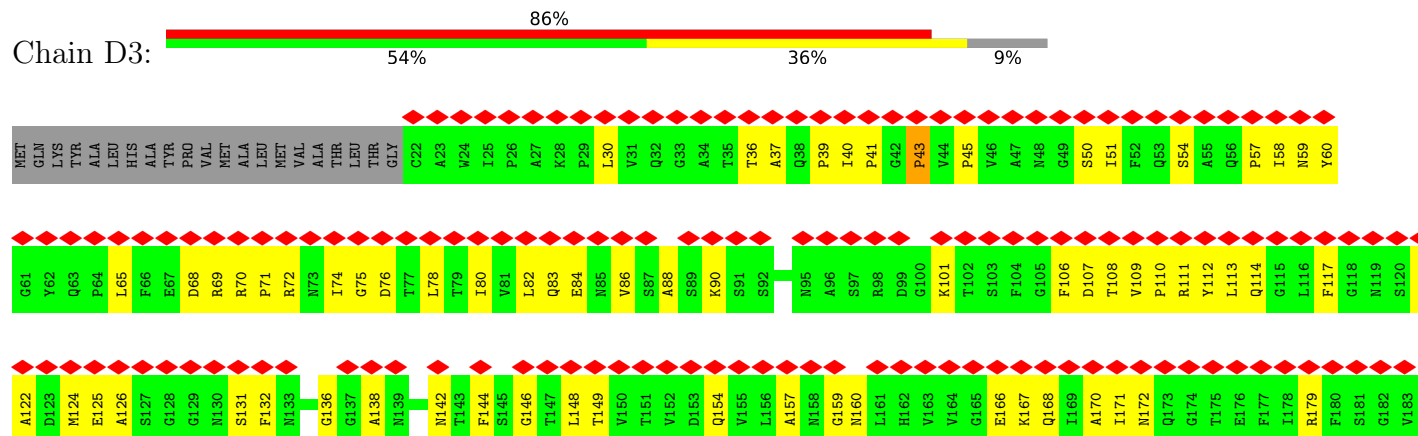
- Molecule 10: Flagellar L-ring protein

Chain C3:



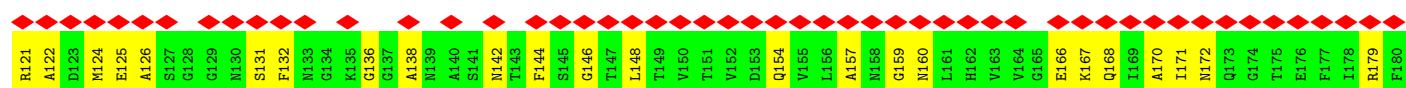
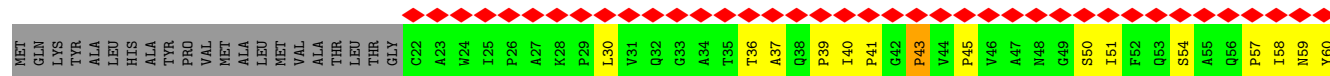
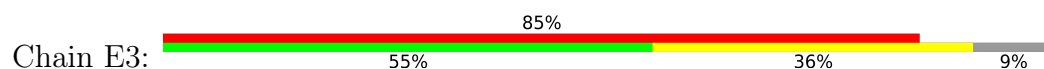
- Molecule 10: Flagellar L-ring protein

Chain D3:

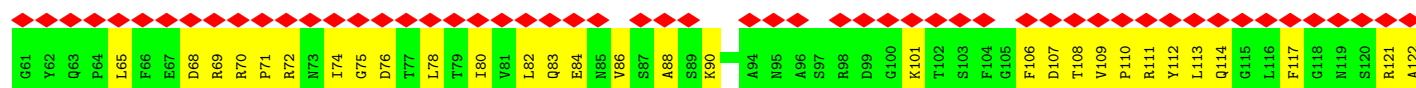
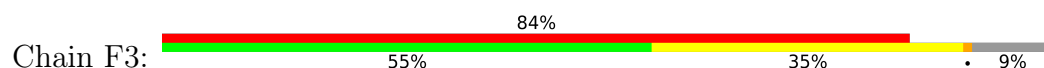




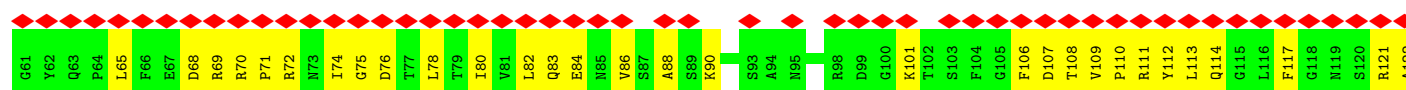
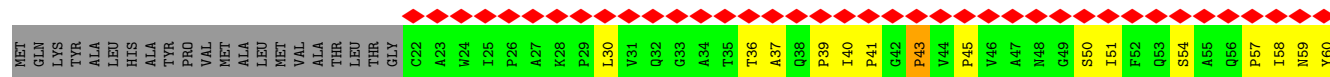
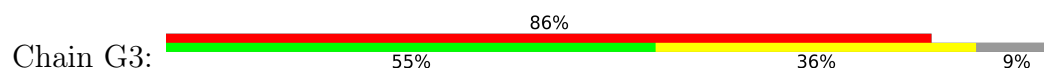
• Molecule 10: Flagellar L-ring protein

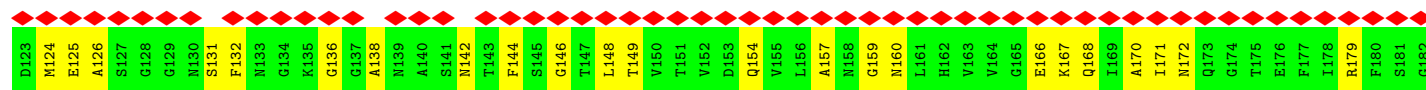


• Molecule 10: Flagellar L-ring protein

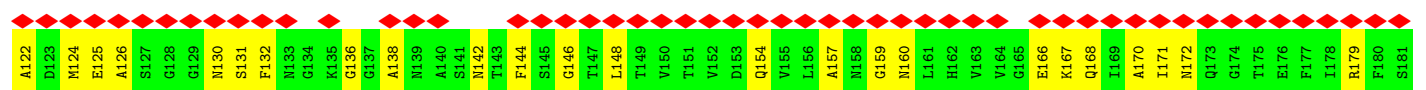
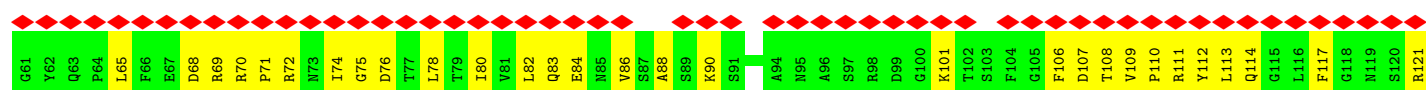
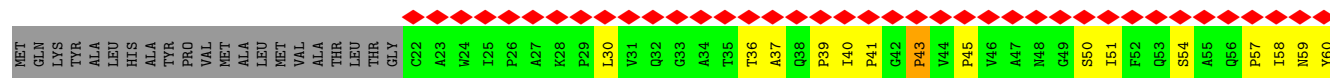


• Molecule 10: Flagellar L-ring protein

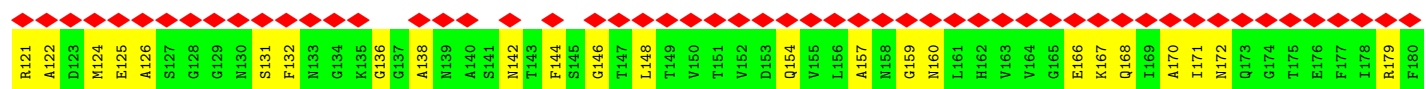
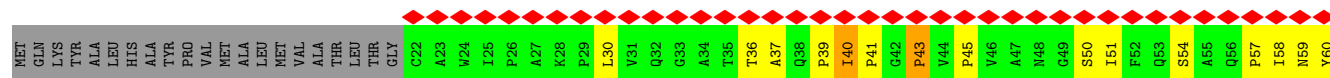
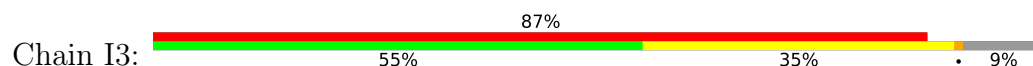




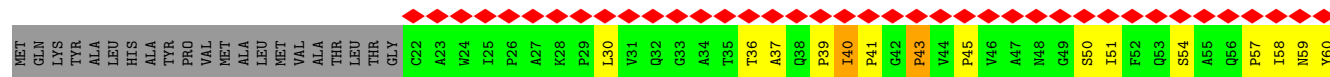
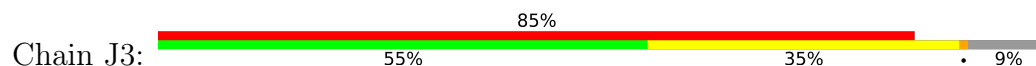
• Molecule 10: Flagellar L-ring protein

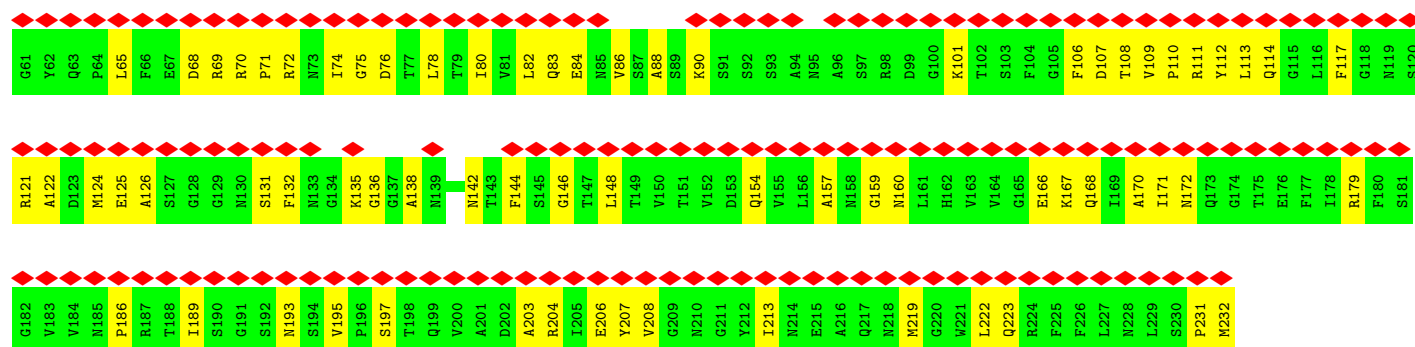


• Molecule 10: Flagellar L-ring protein

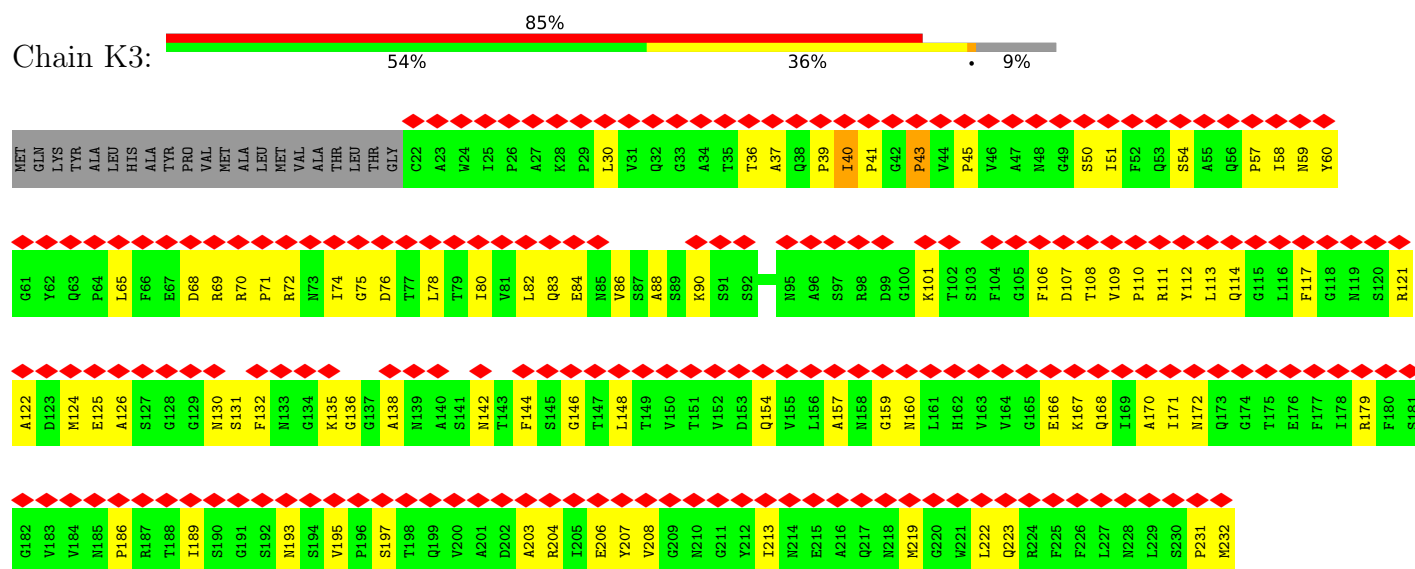


• Molecule 10: Flagellar L-ring protein

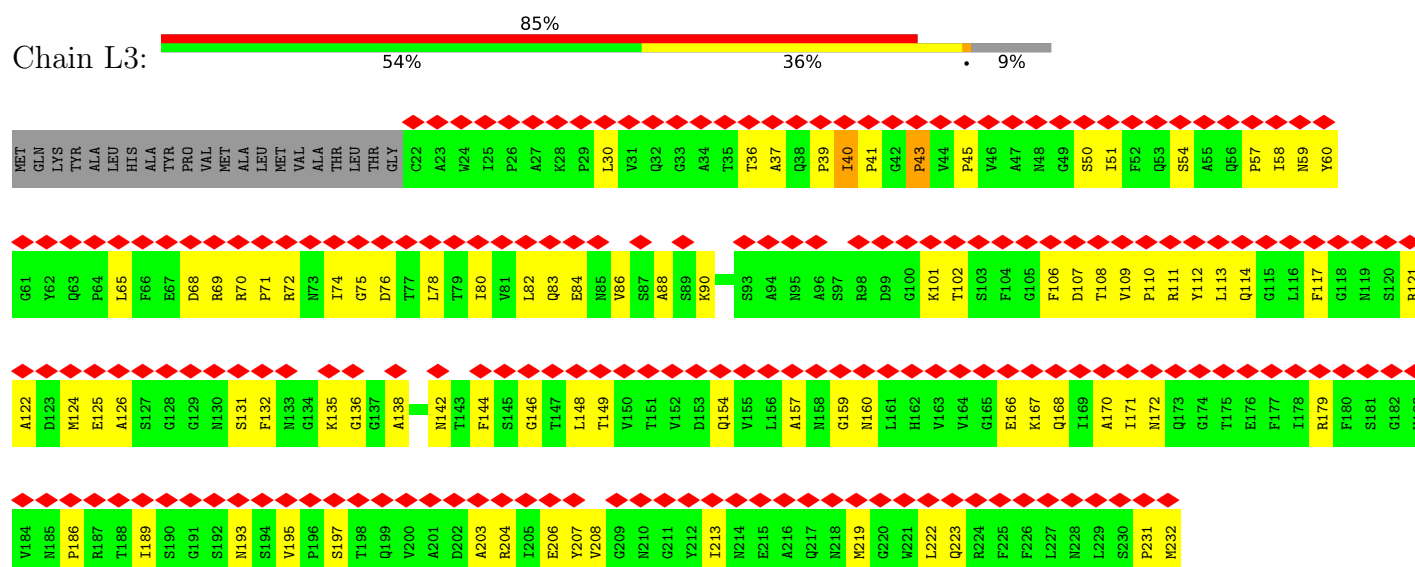




• Molecule 10: Flagellar L-ring protein

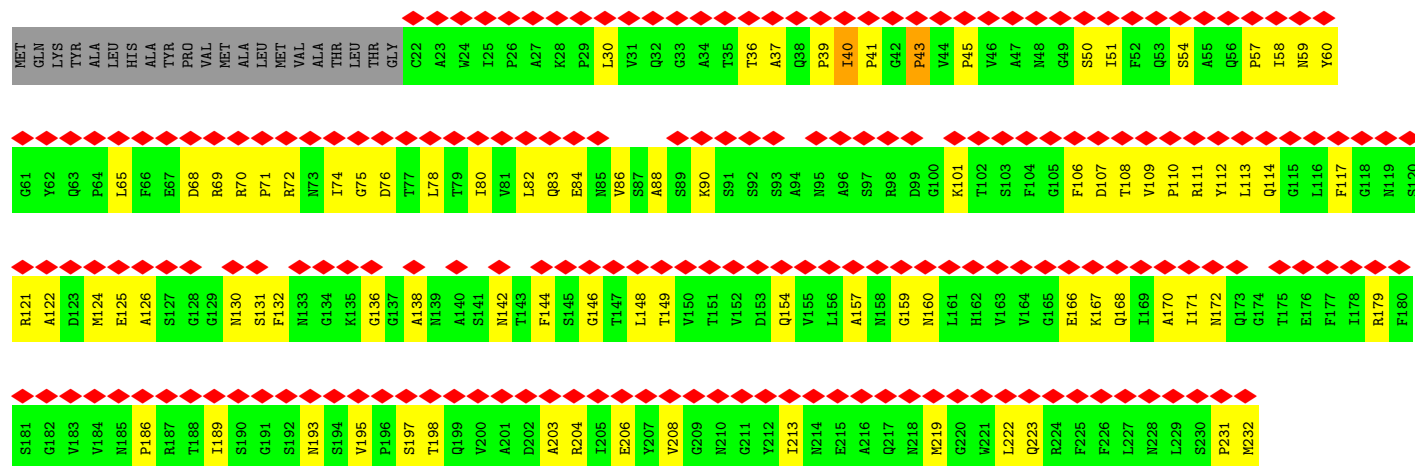


• Molecule 10: Flagellar L-ring protein

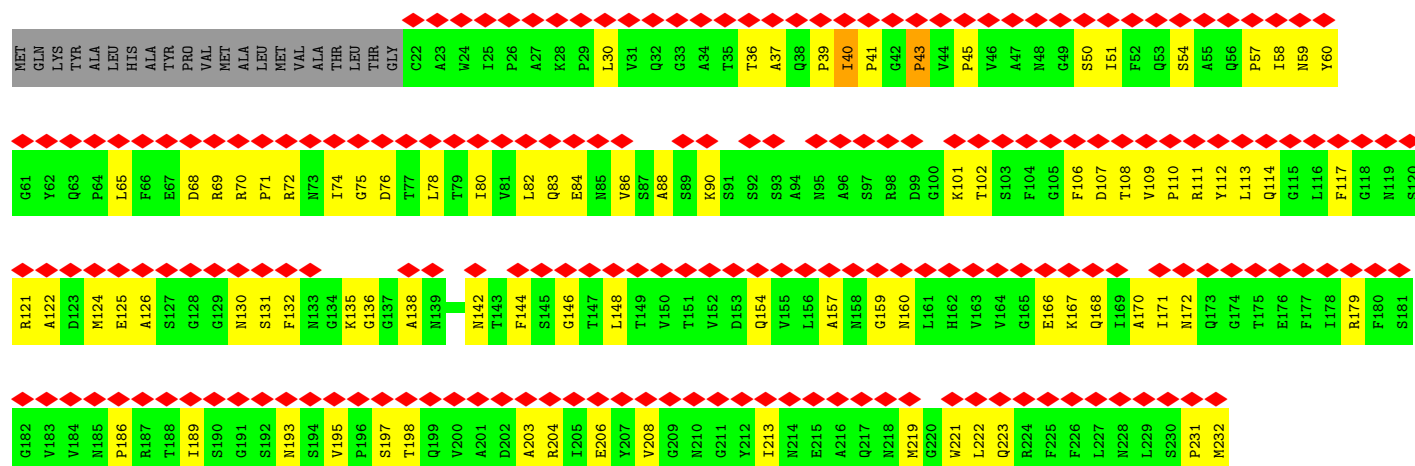
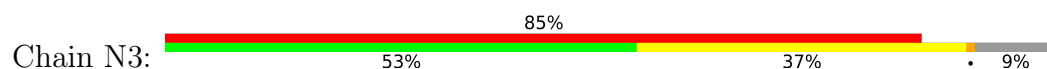


• Molecule 10: Flagellar L-ring protein

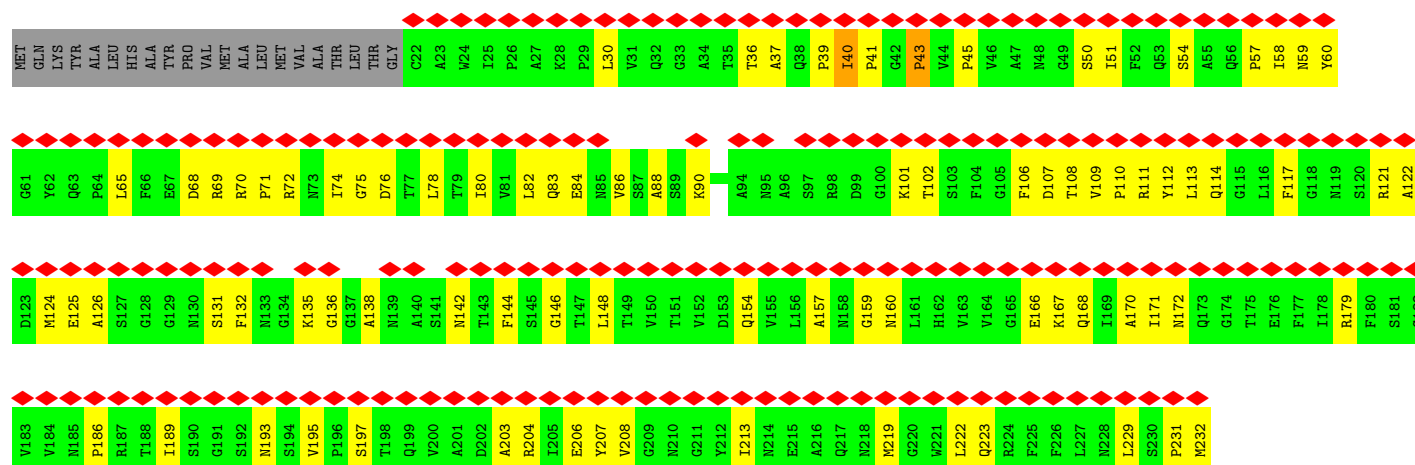
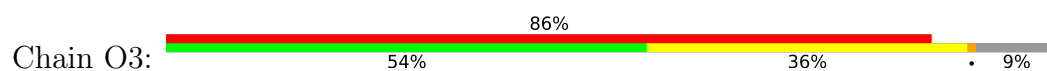




• Molecule 10: Flagellar L-ring protein

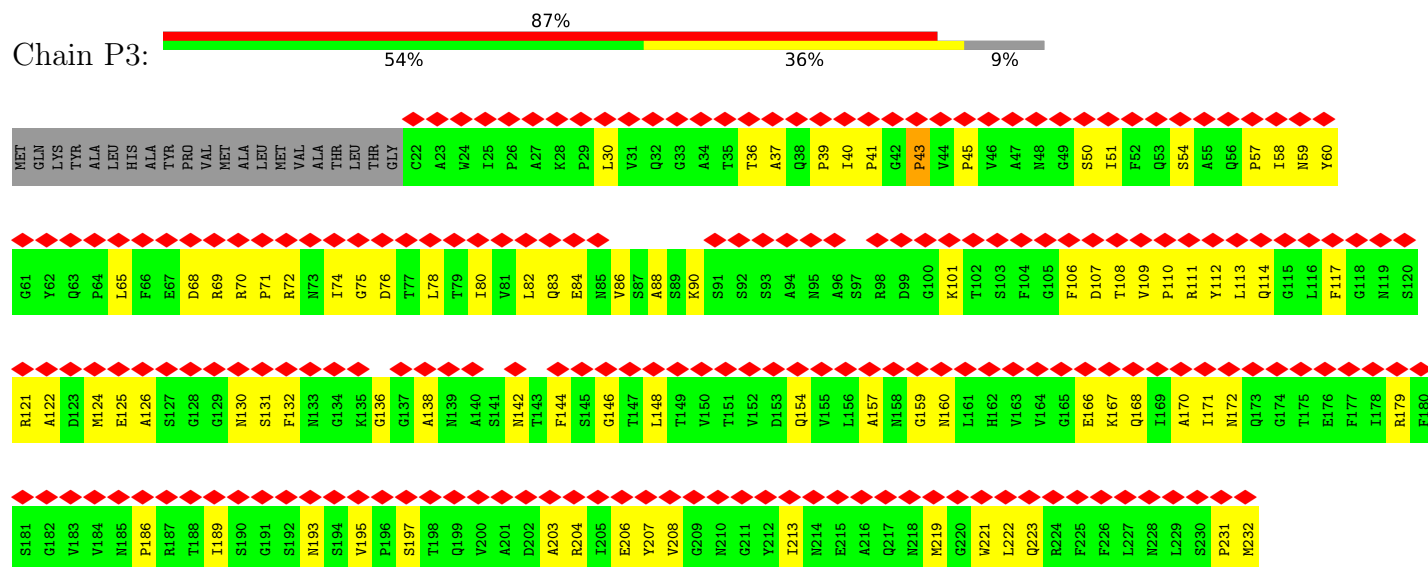


• Molecule 10: Flagellar L-ring protein



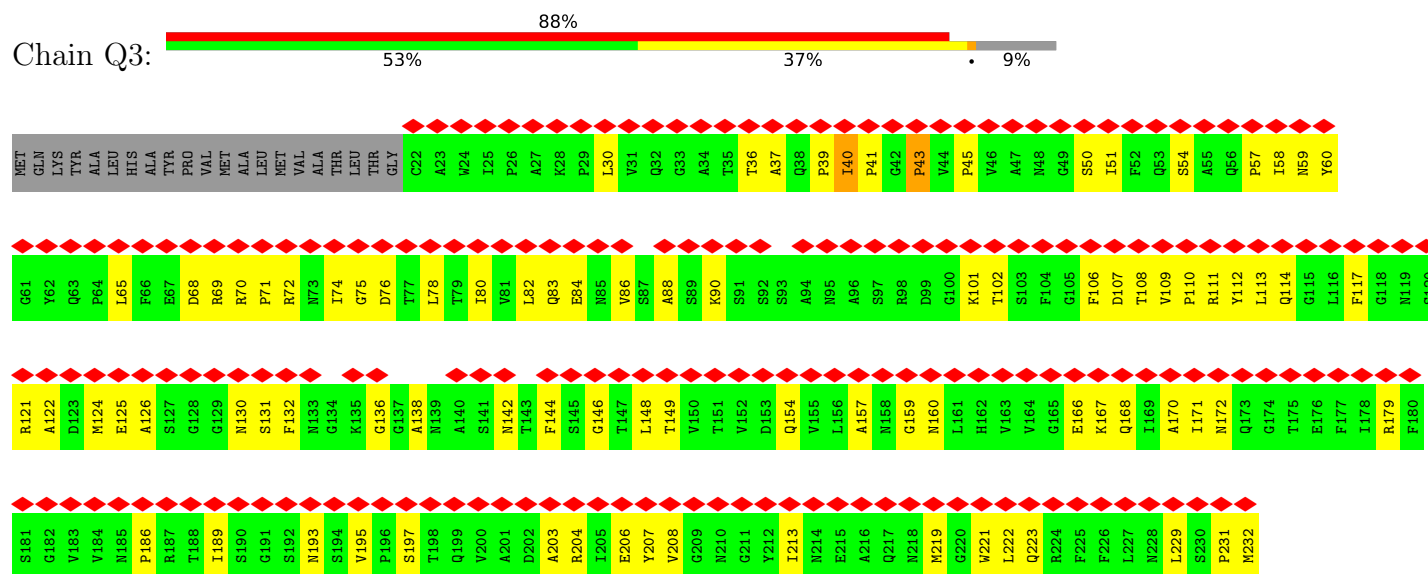
● Molecule 10: Flagellar L-ring protein

Chain P3:



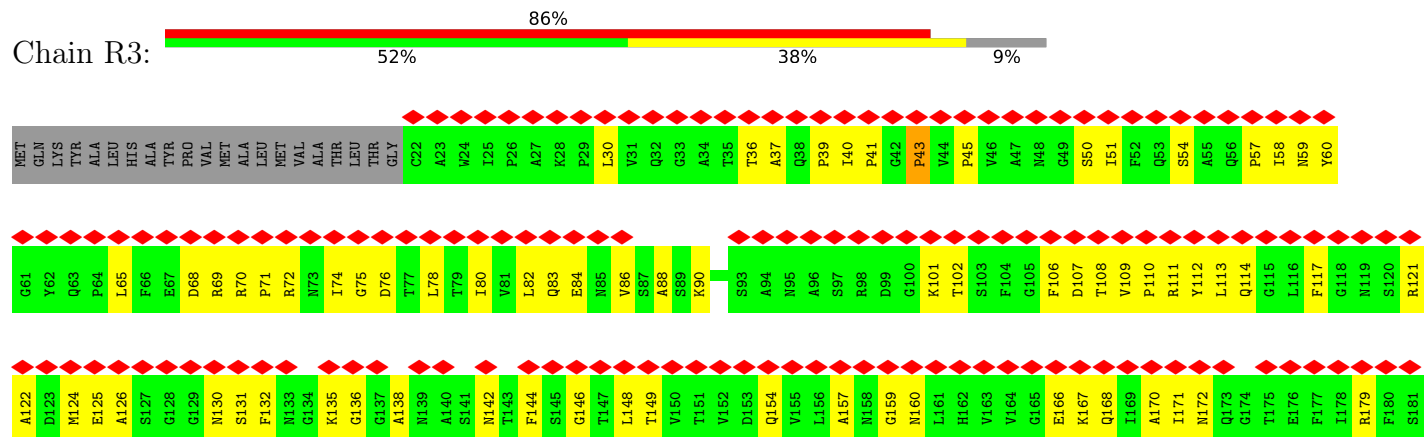
● Molecule 10: Flagellar L-ring protein

Chain Q3:



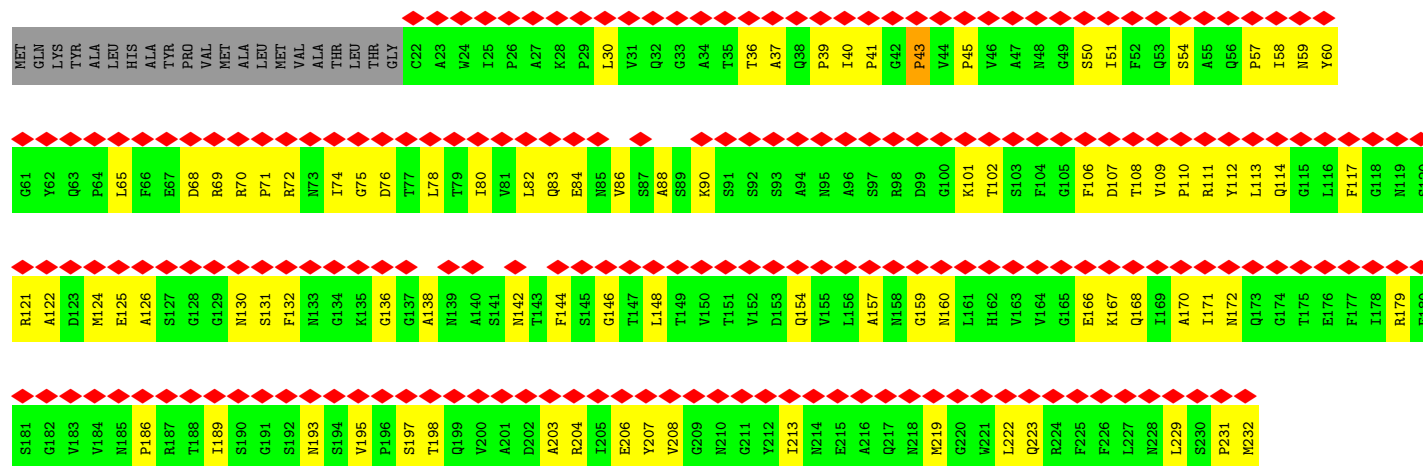
● Molecule 10: Flagellar L-ring protein

Chain R3:

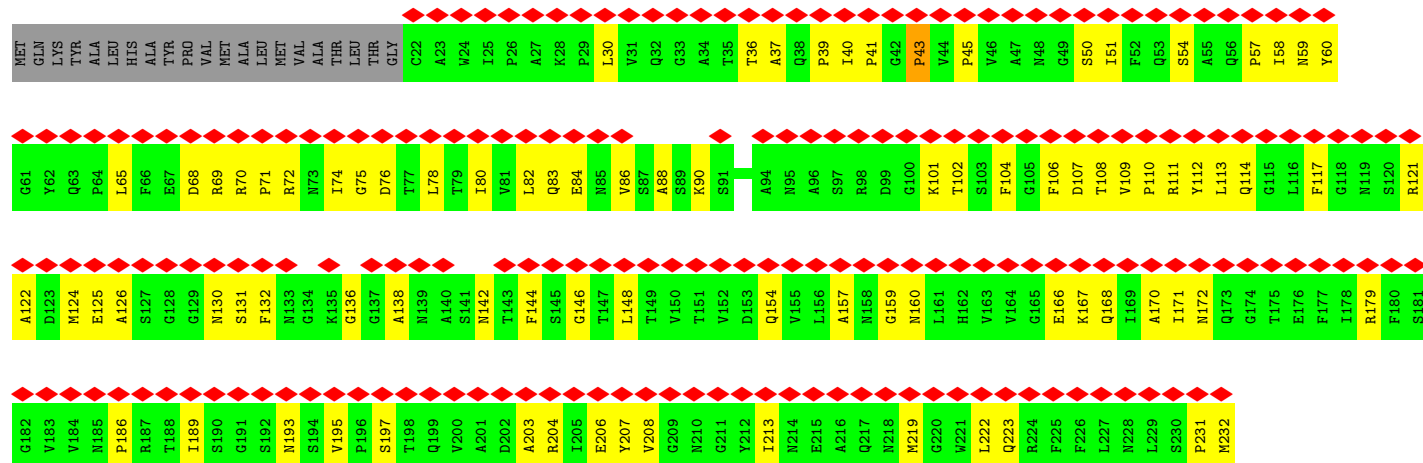
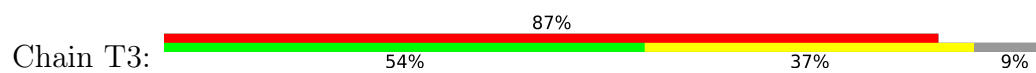




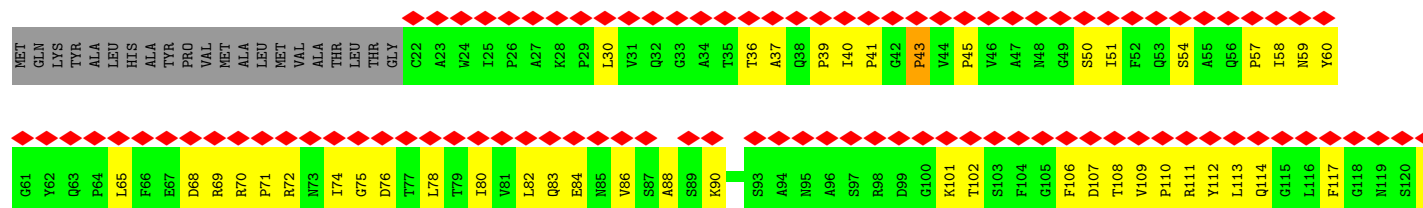
• Molecule 10: Flagellar L-ring protein



• Molecule 10: Flagellar L-ring protein

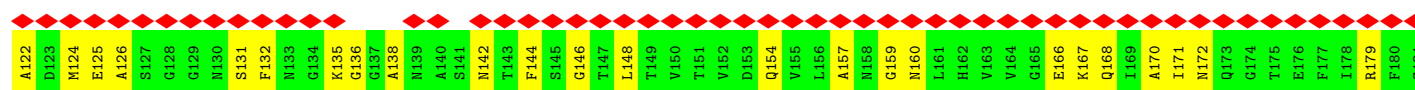
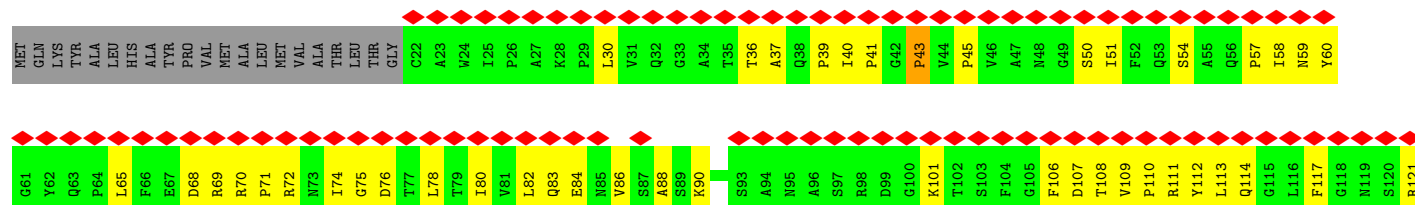
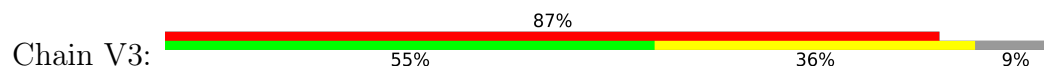


• Molecule 10: Flagellar L-ring protein

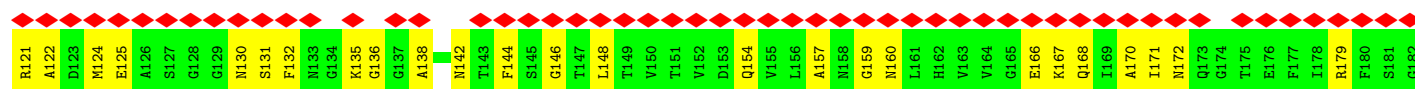
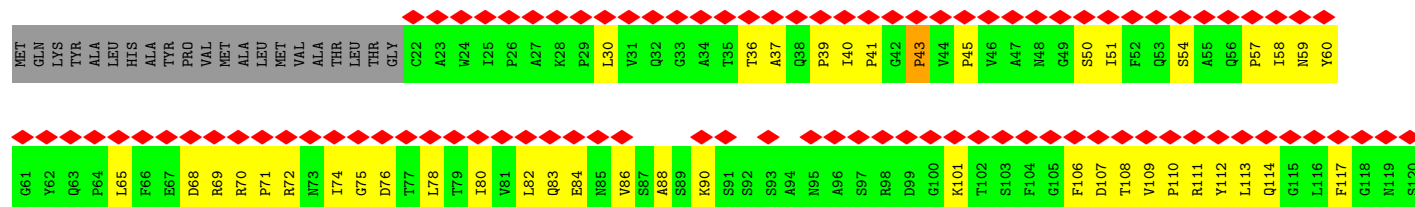




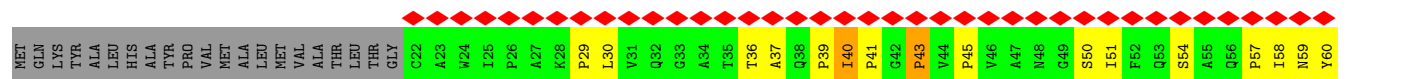
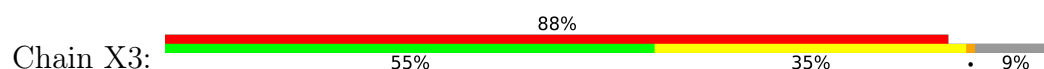
• Molecule 10: Flagellar L-ring protein

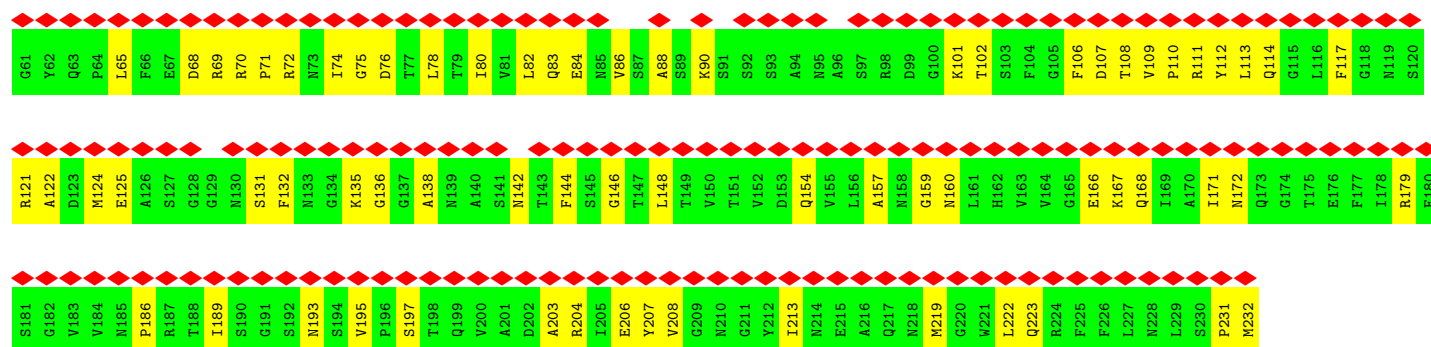


• Molecule 10: Flagellar L-ring protein

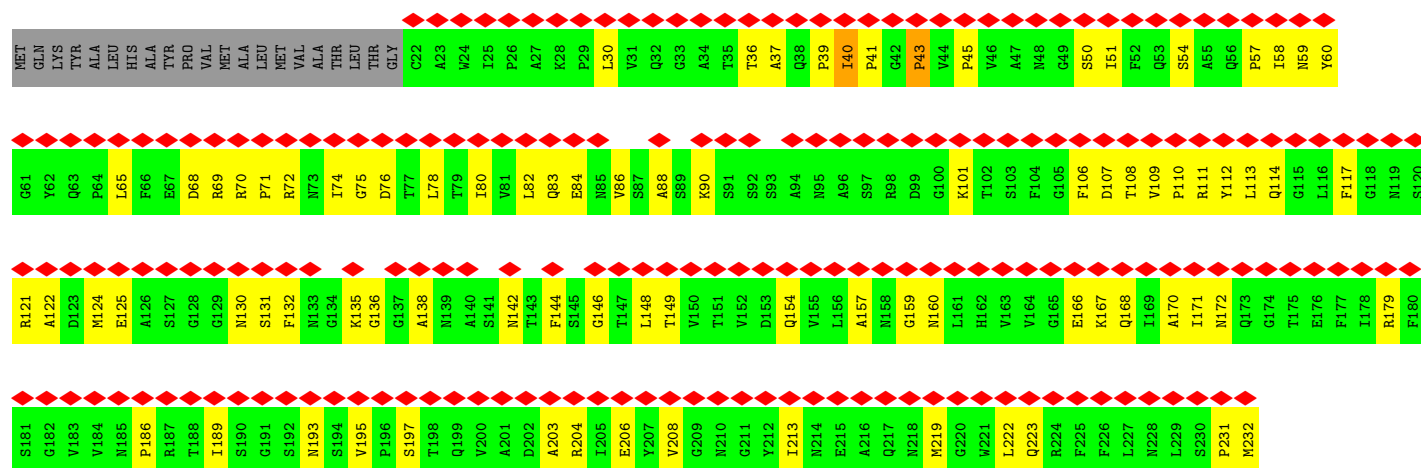


• Molecule 10: Flagellar L-ring protein

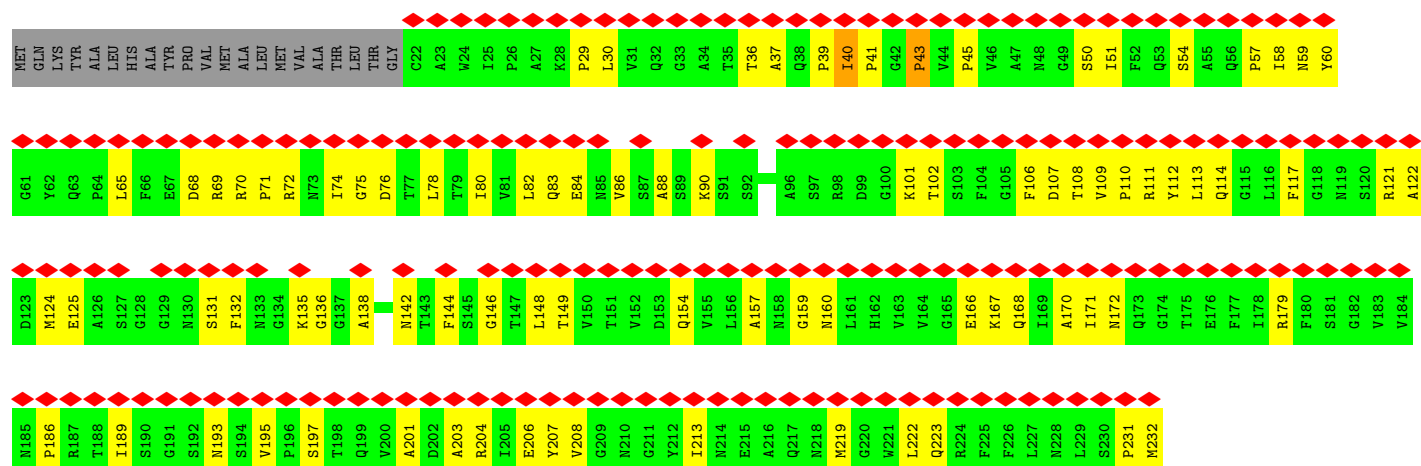
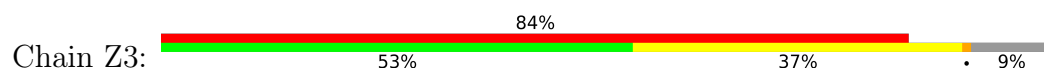




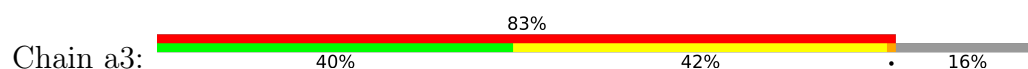
• Molecule 10: Flagellar L-ring protein



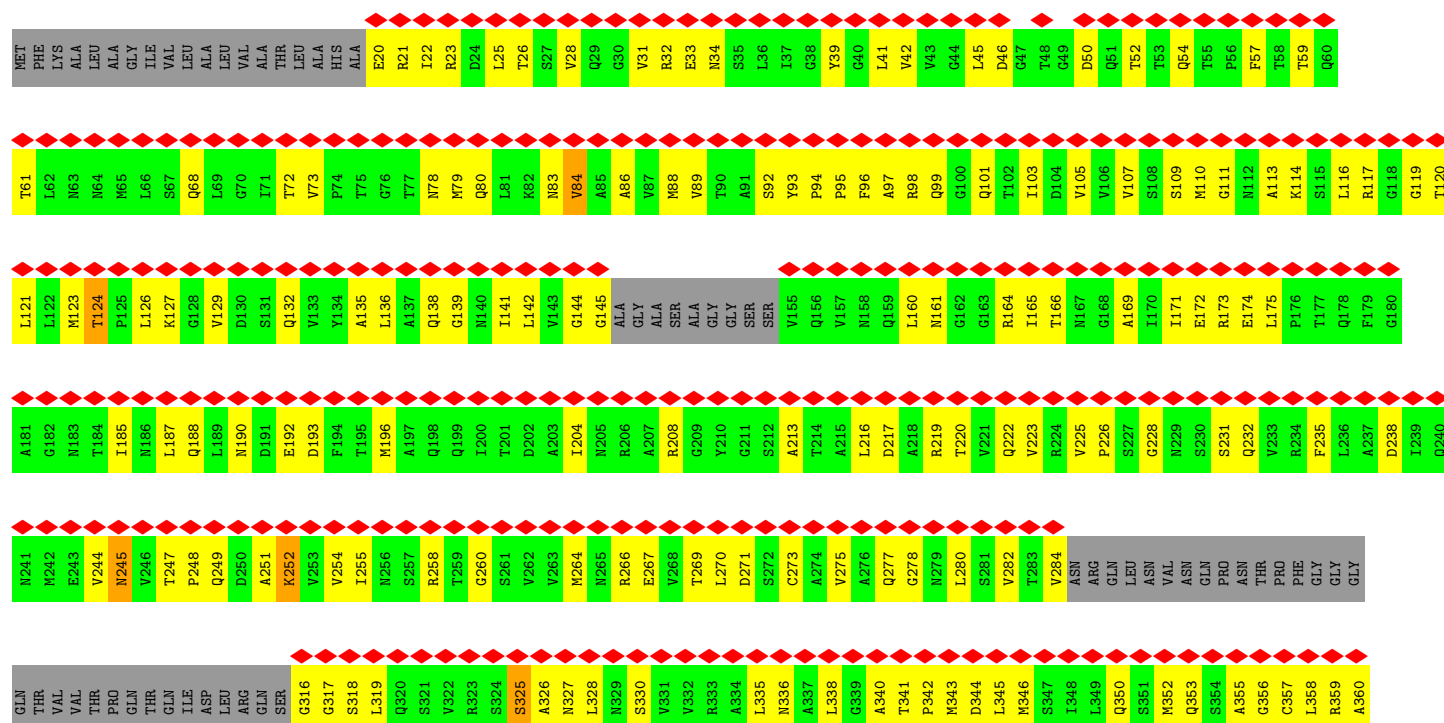
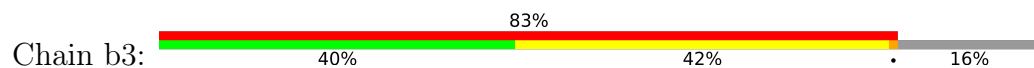
• Molecule 10: Flagellar L-ring protein



• Molecule 11: Flagellar P-ring protein

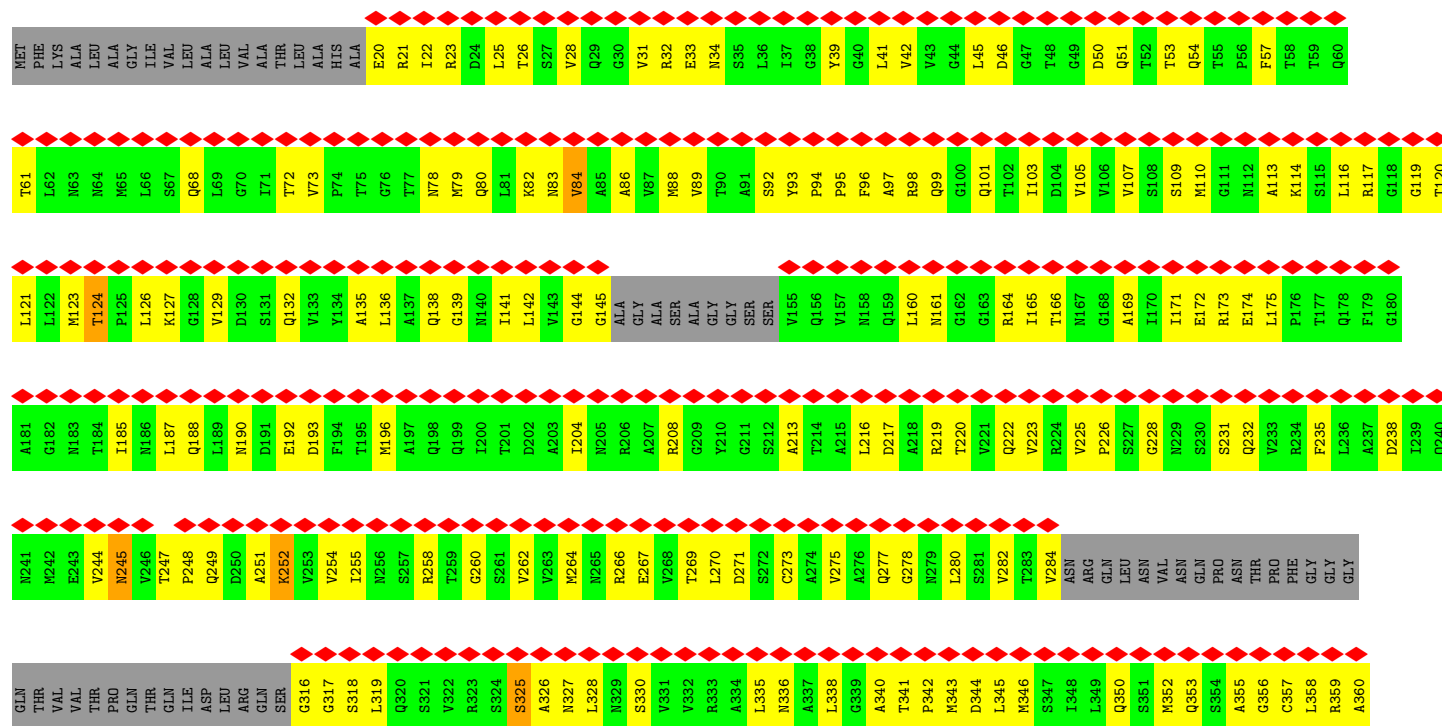
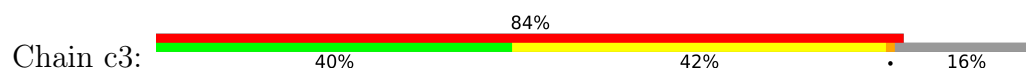


- Molecule 11: Flagellar P-ring protein

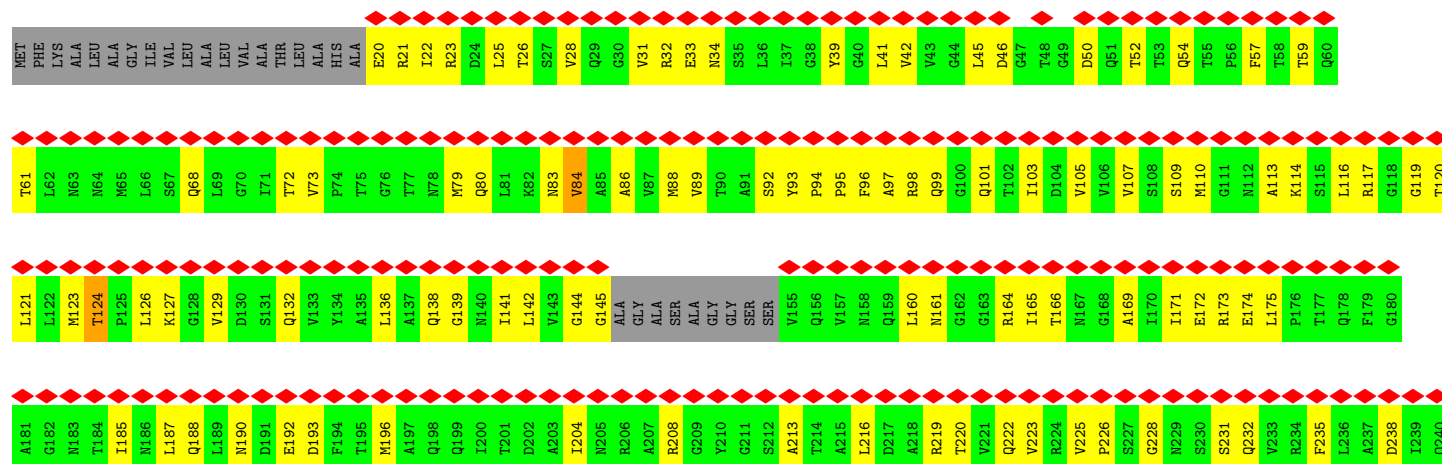
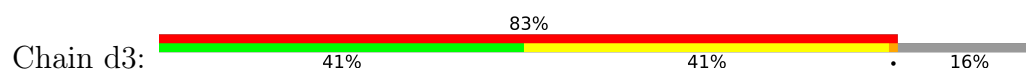




• Molecule 11: Flagellar P-ring protein

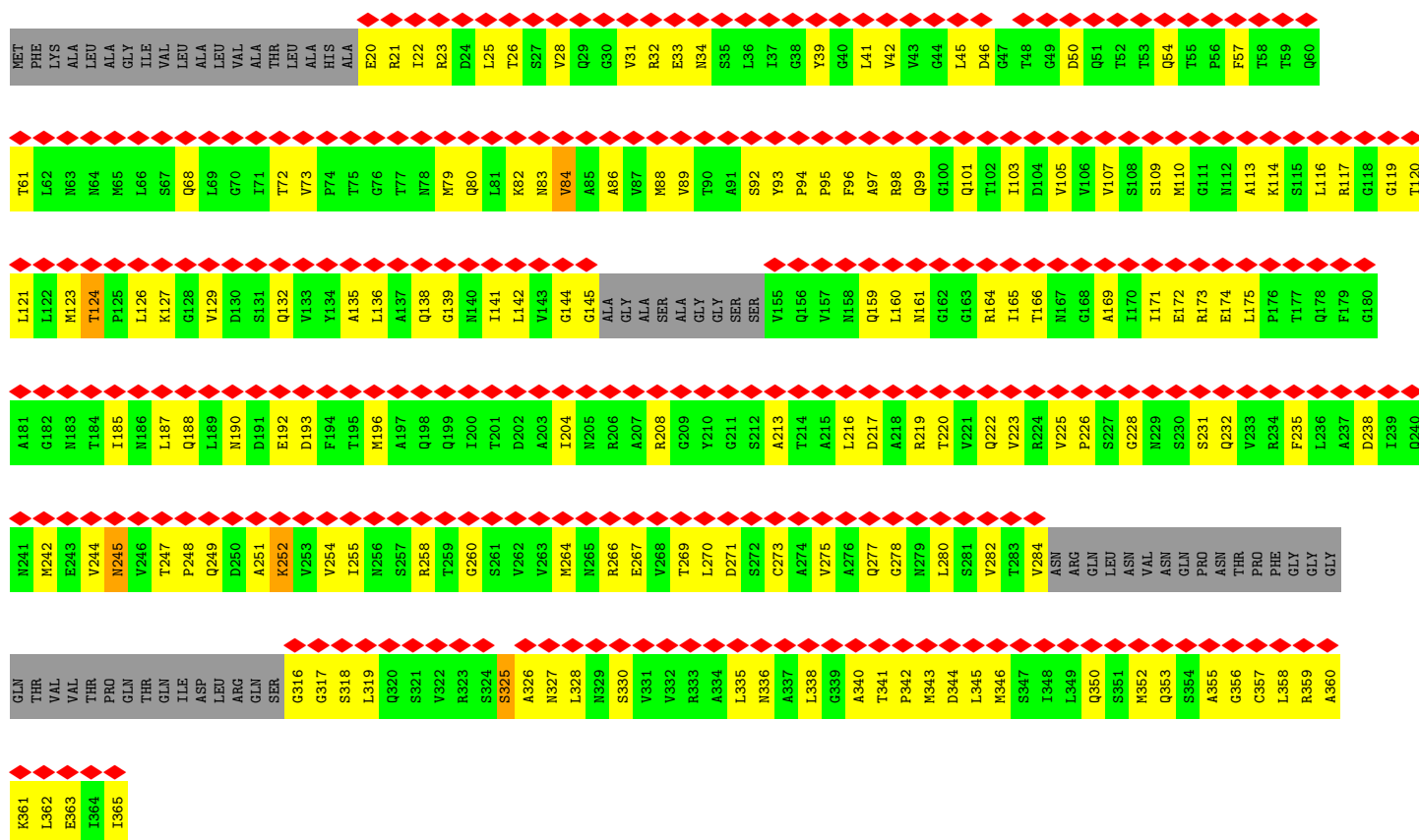
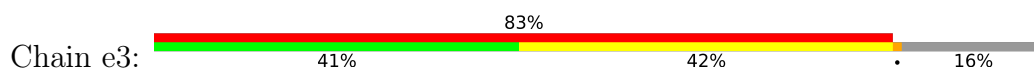


• Molecule 11: Flagellar P-ring protein

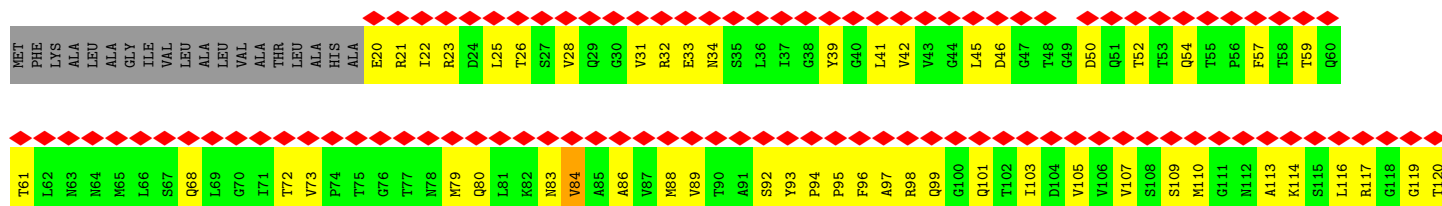
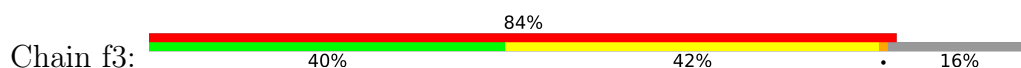


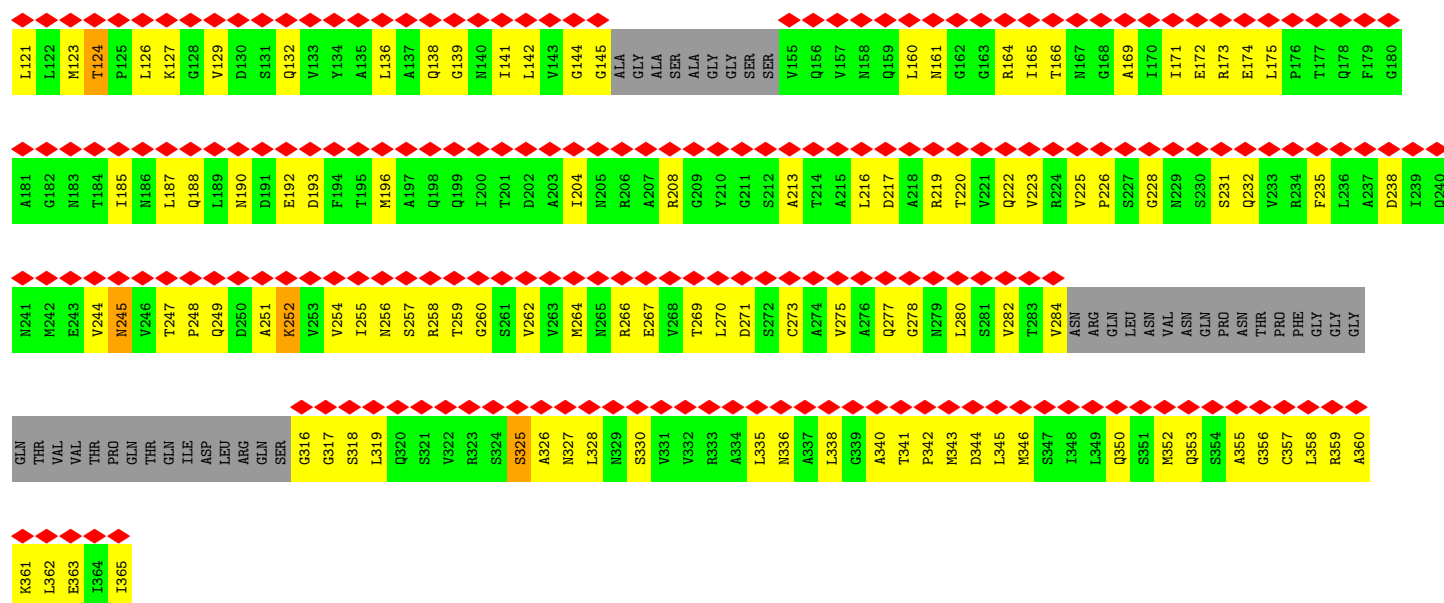


• Molecule 11: Flagellar P-ring protein

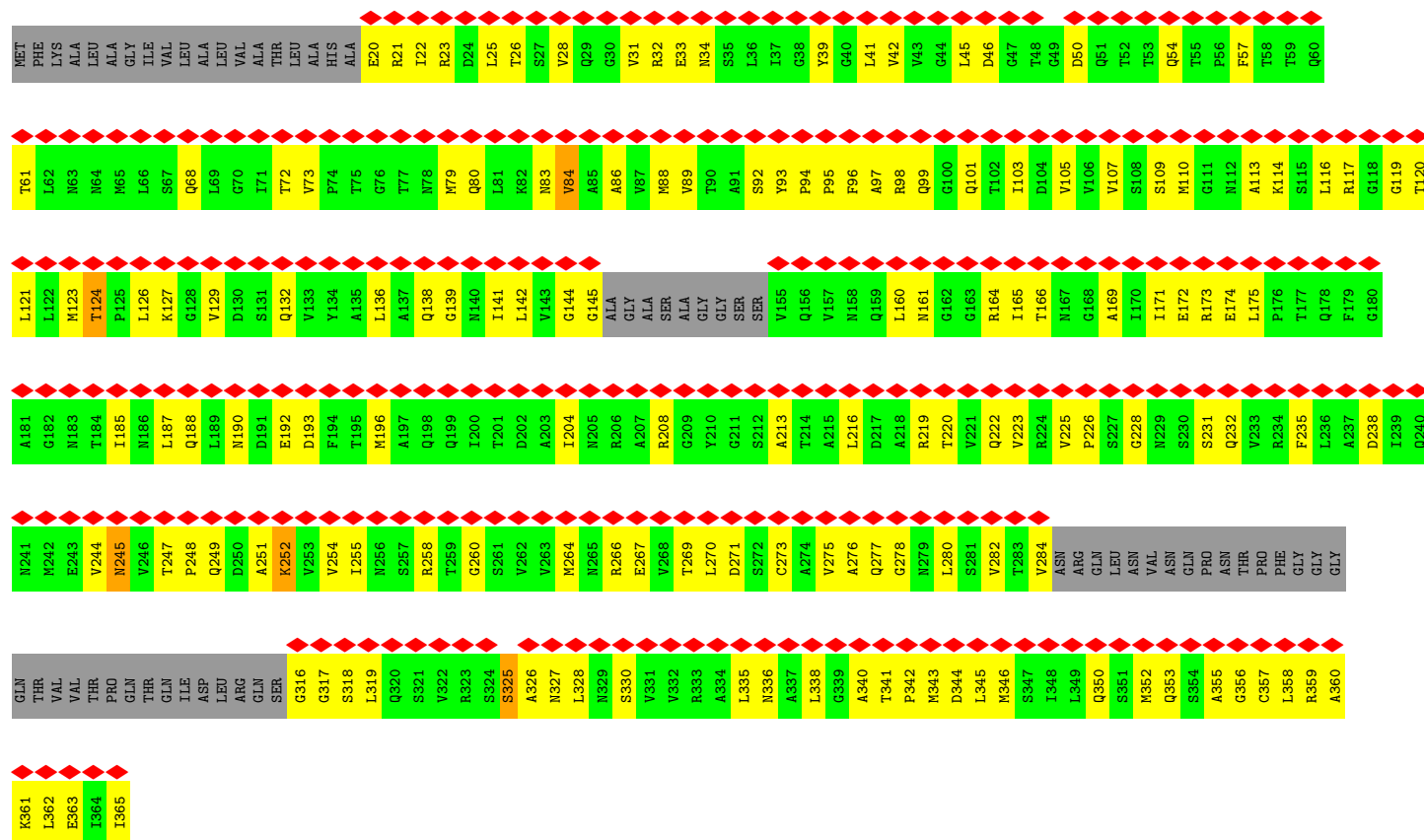
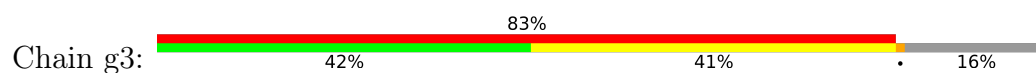


• Molecule 11: Flagellar P-ring protein

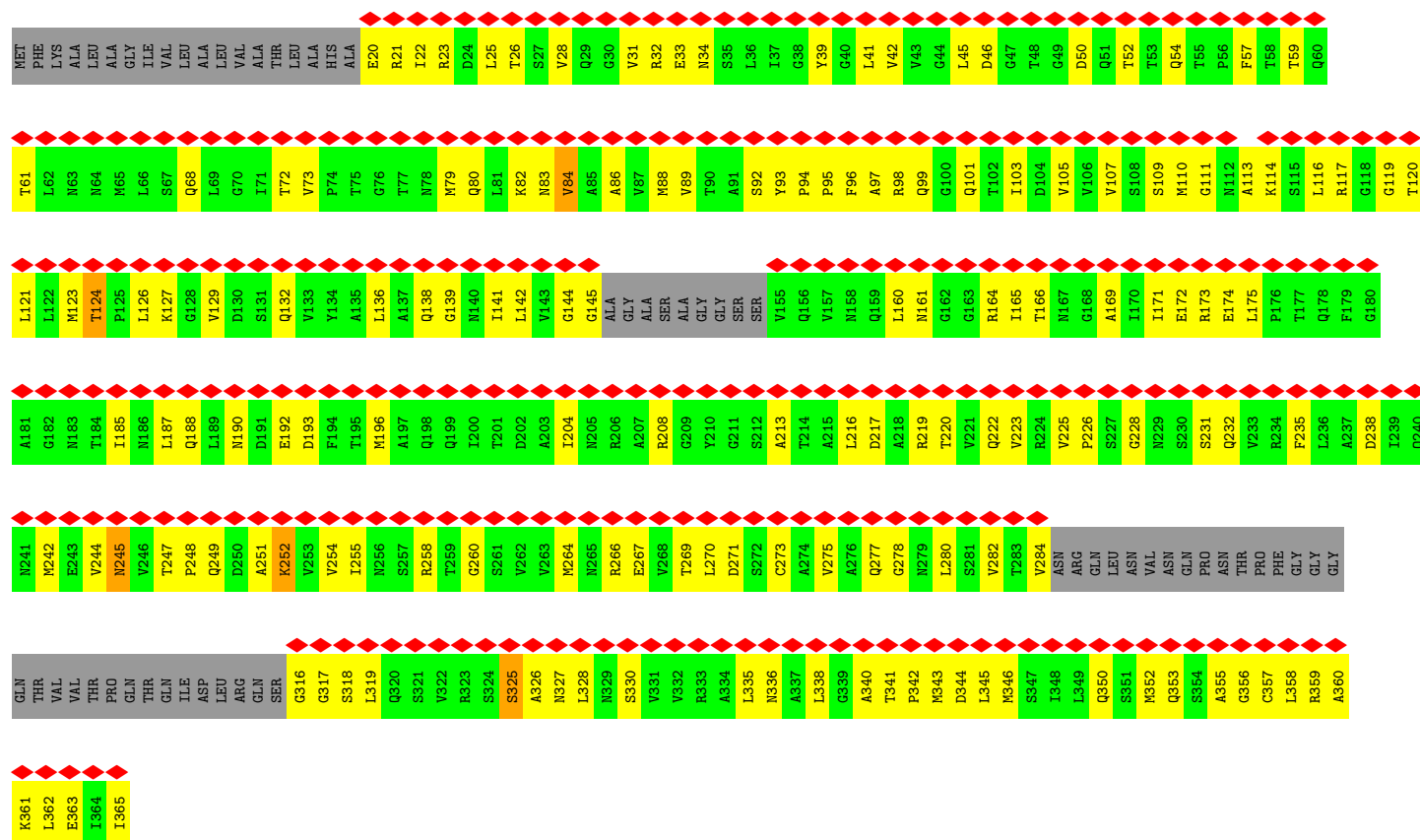
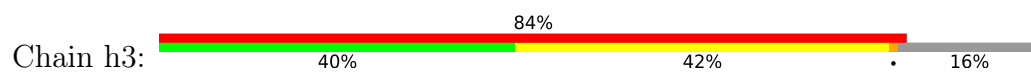




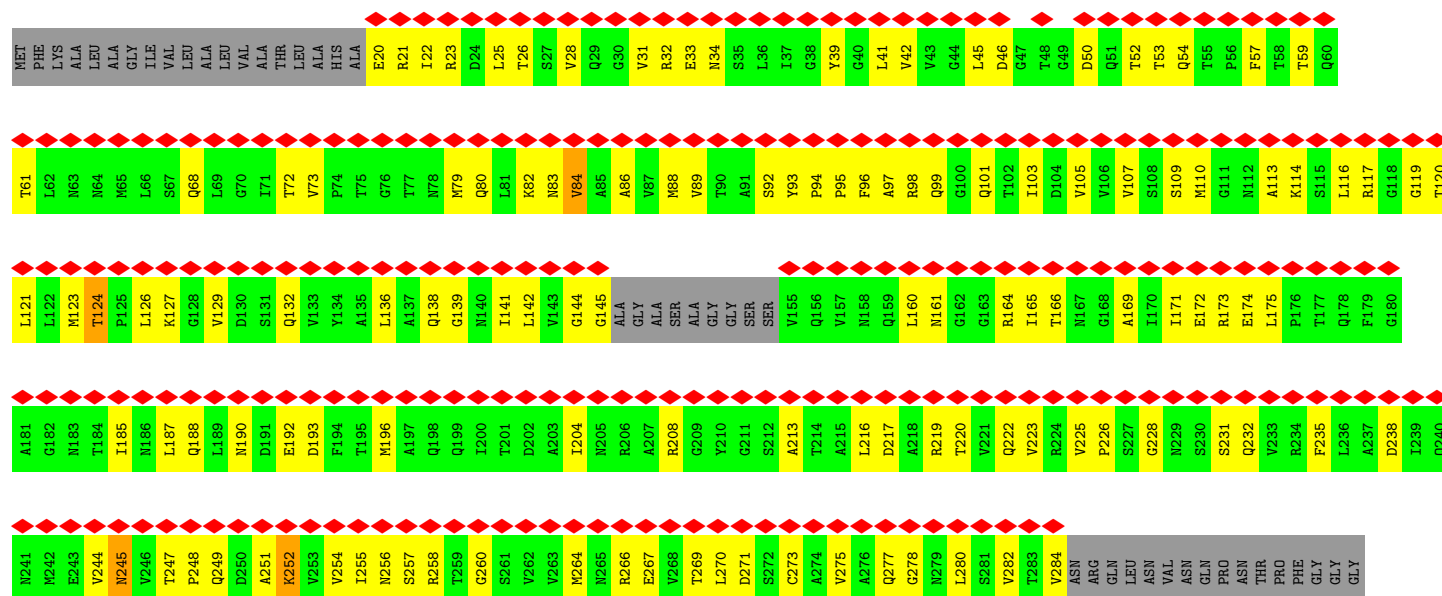
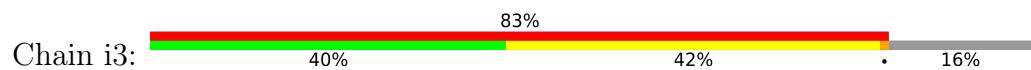
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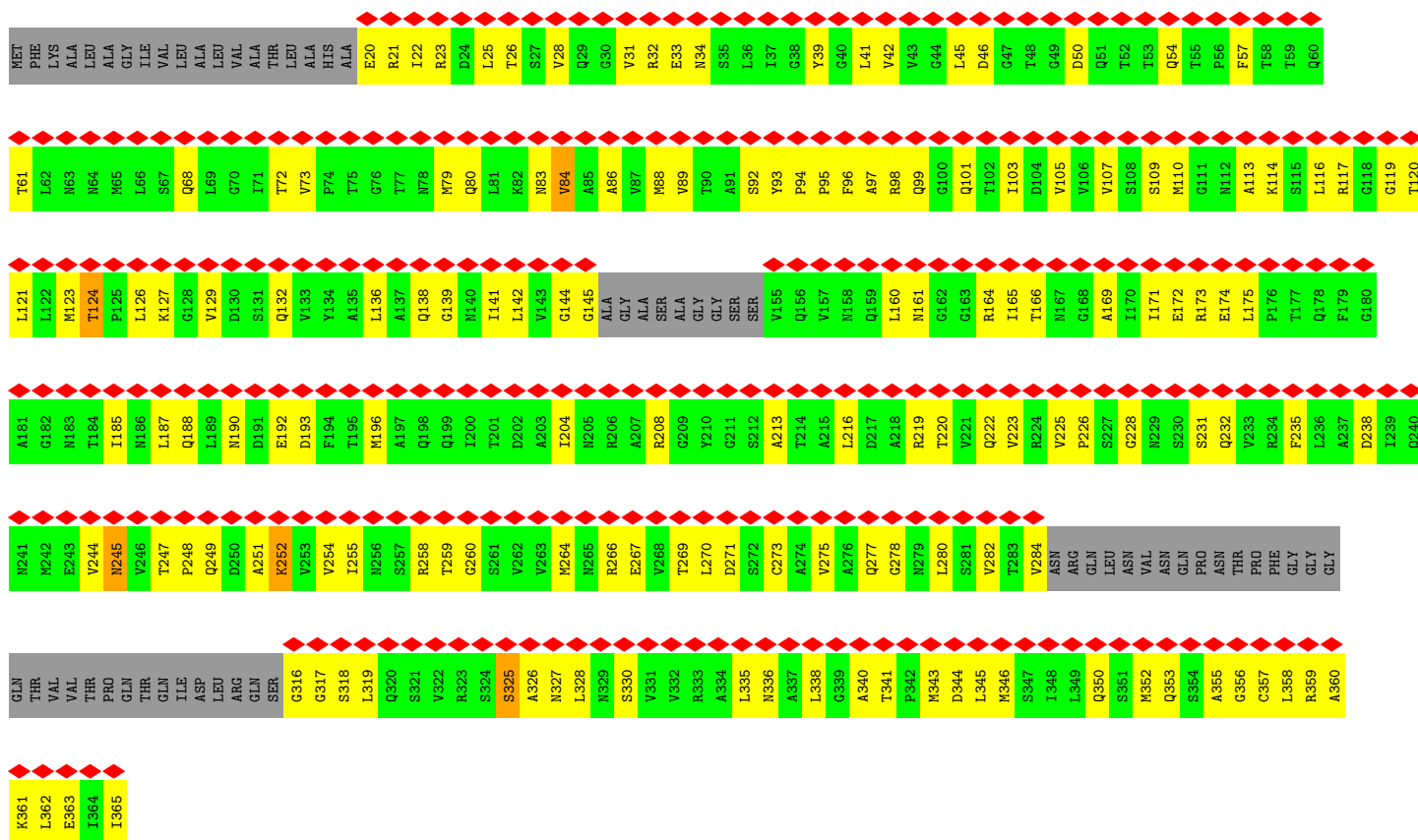
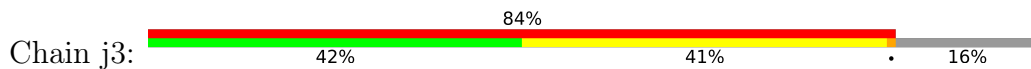
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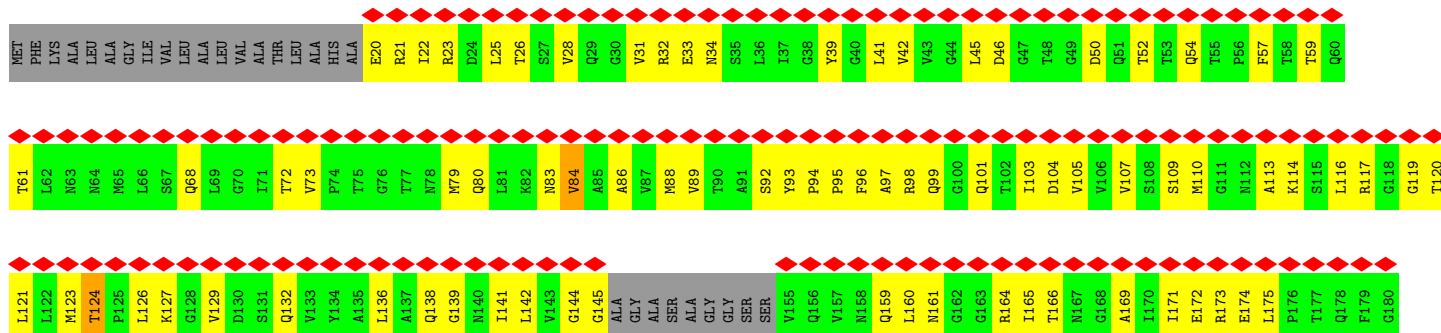
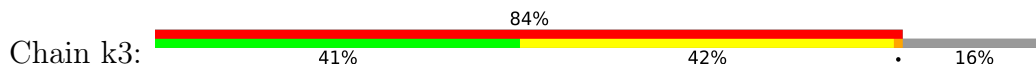
• Molecule 11: Flagellar P-ring protein



- Molecule 11: Flagellar P-ring protein

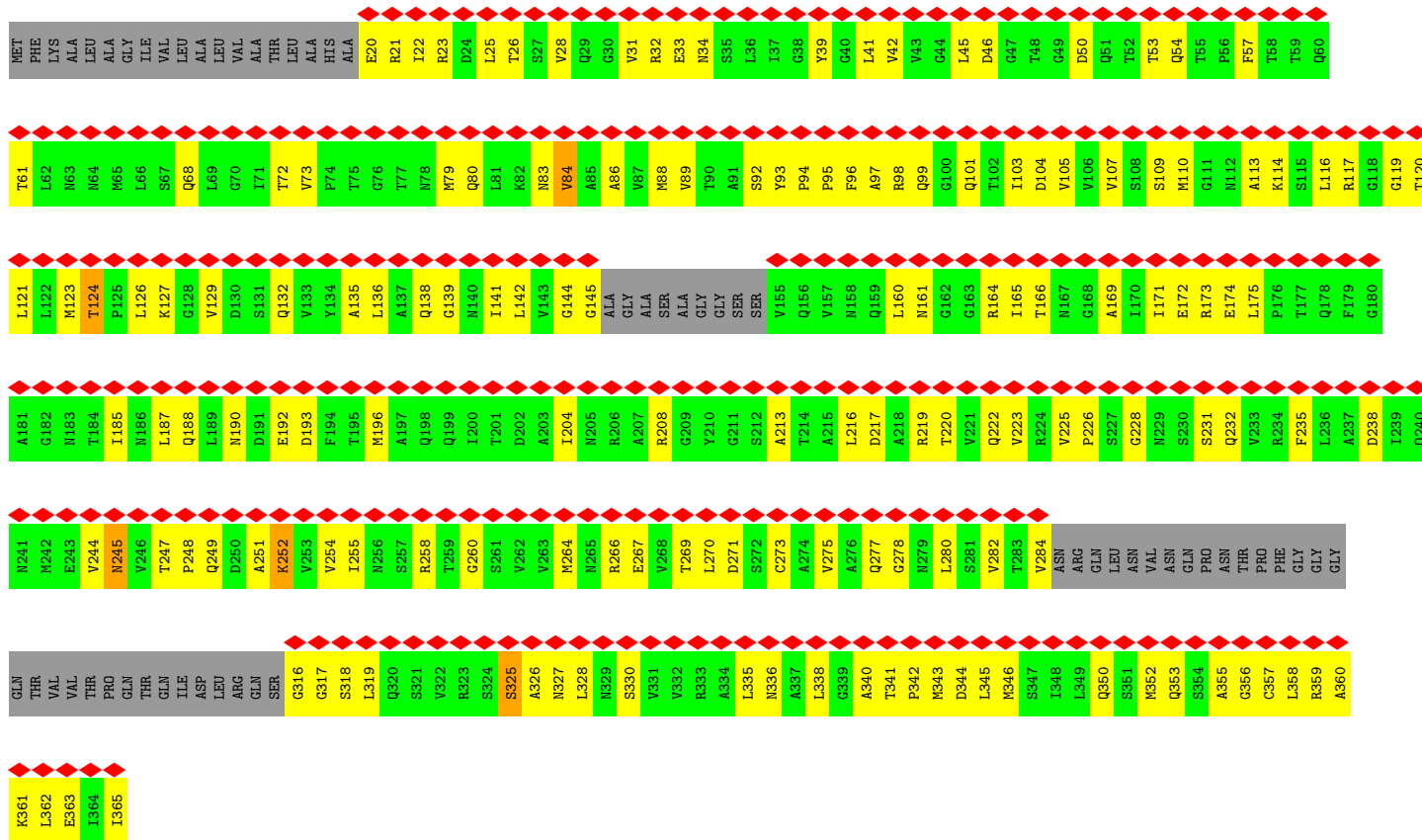
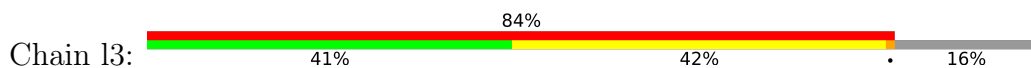


- Molecule 11: Flagellar P-ring protein

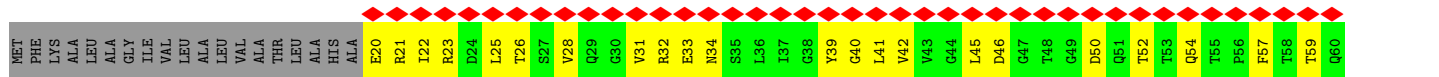
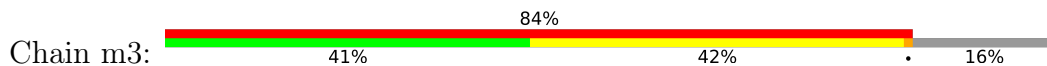


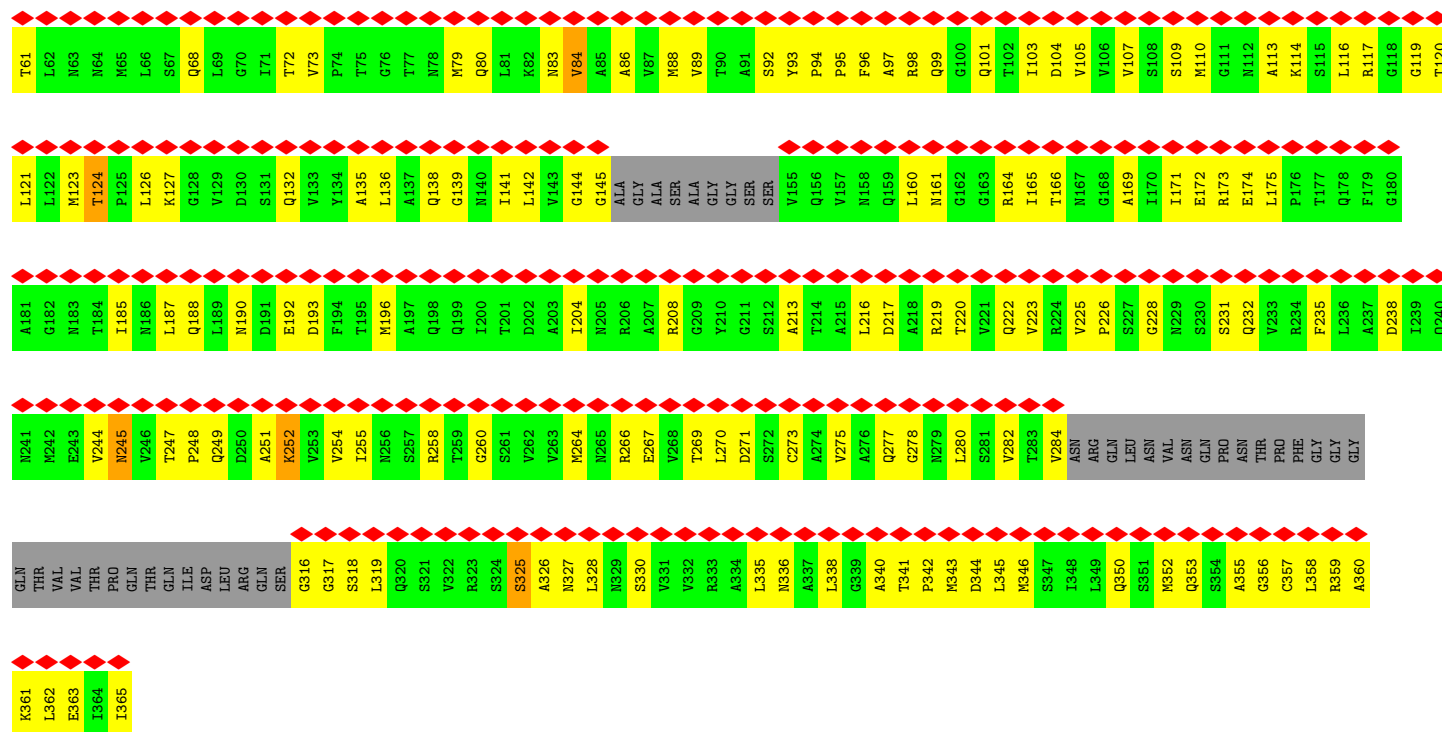


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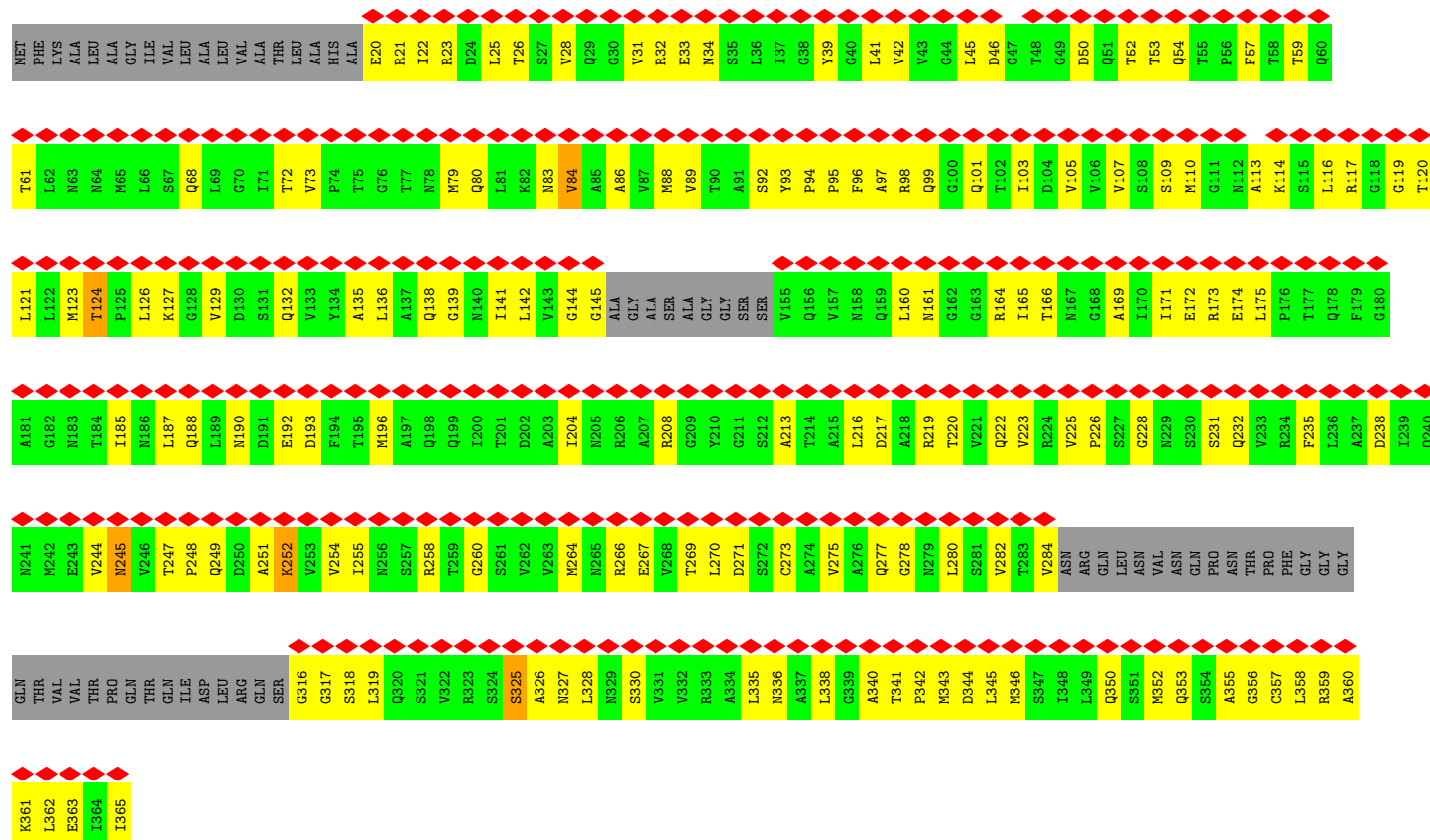
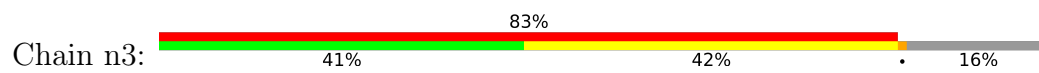


• Molecule 11: Flagellar P-ring protein

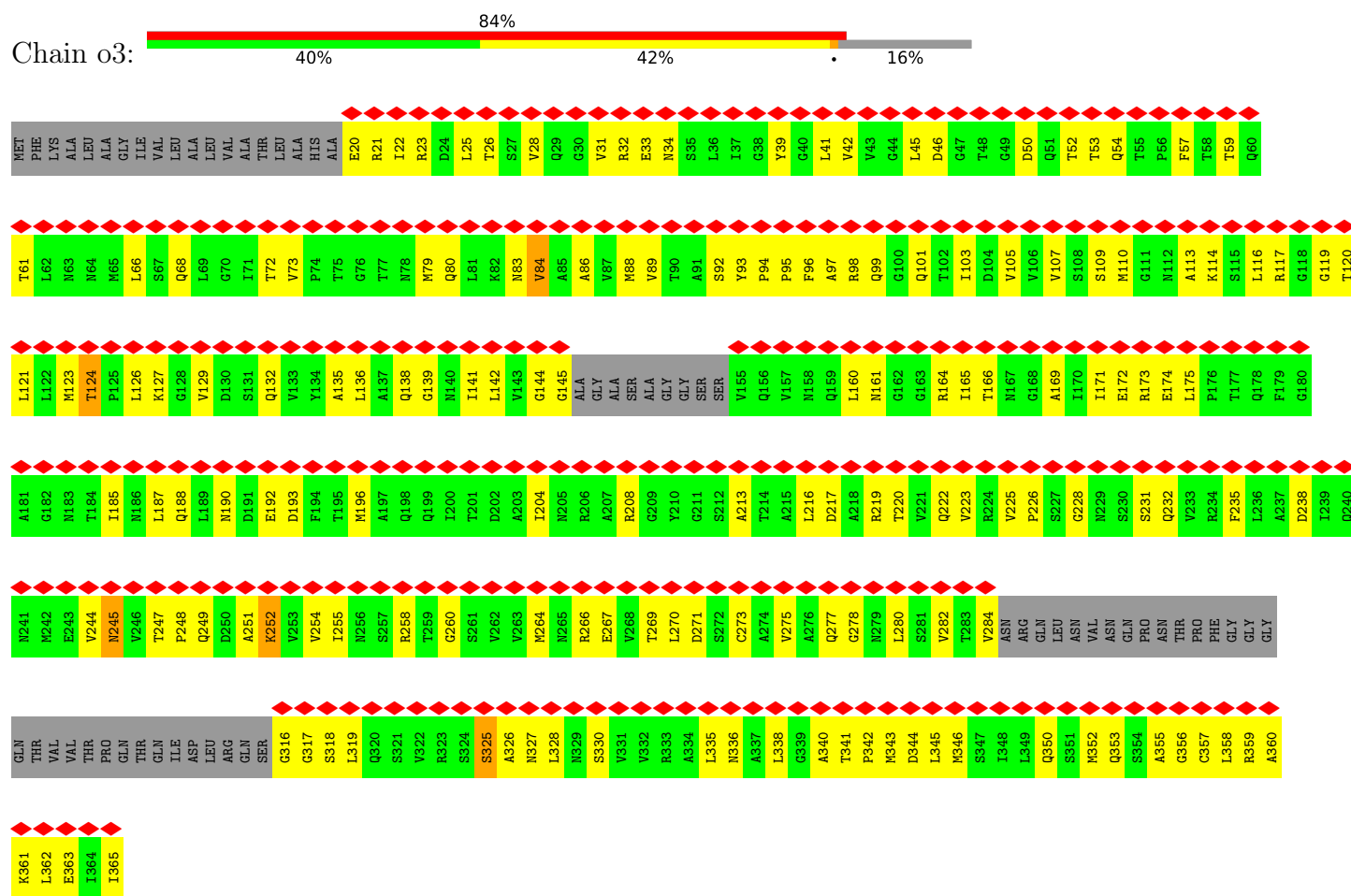




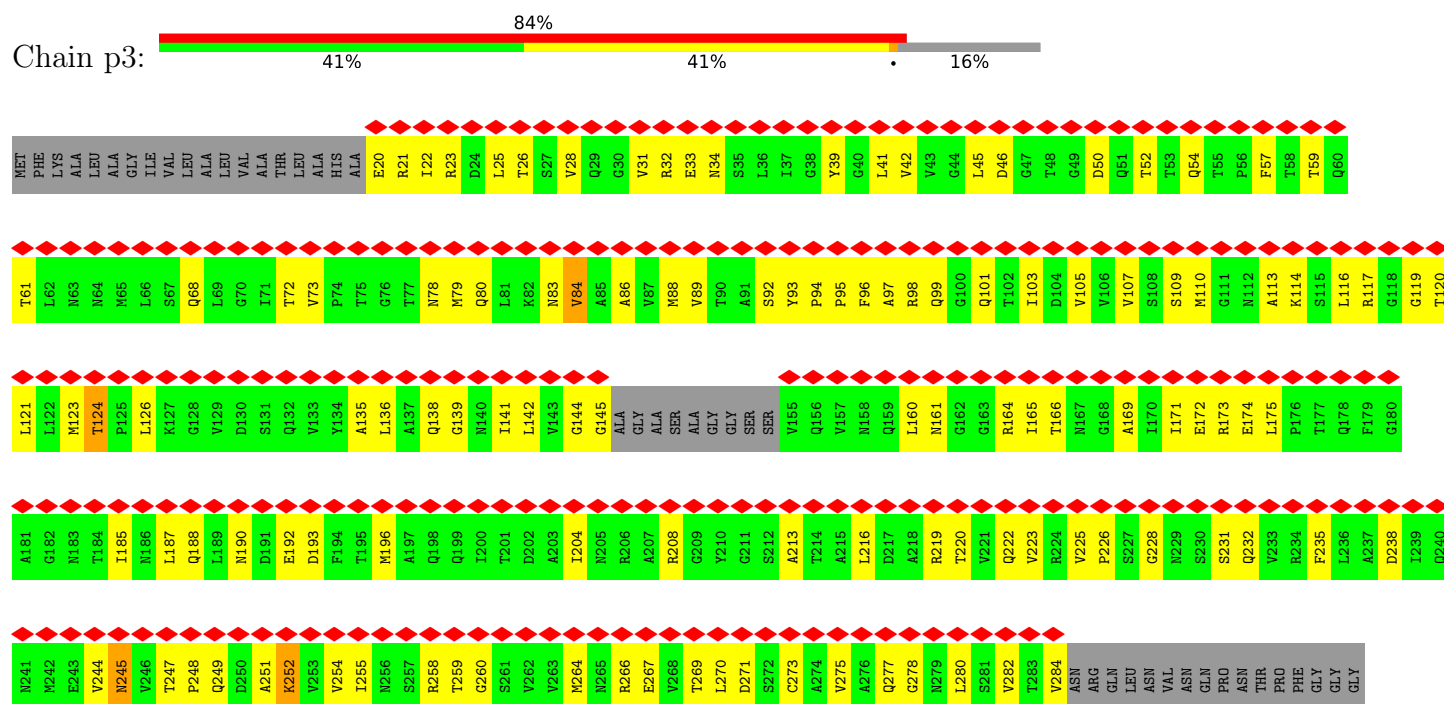
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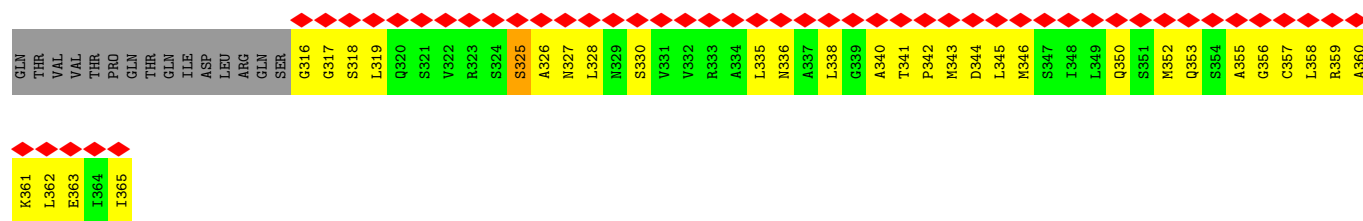


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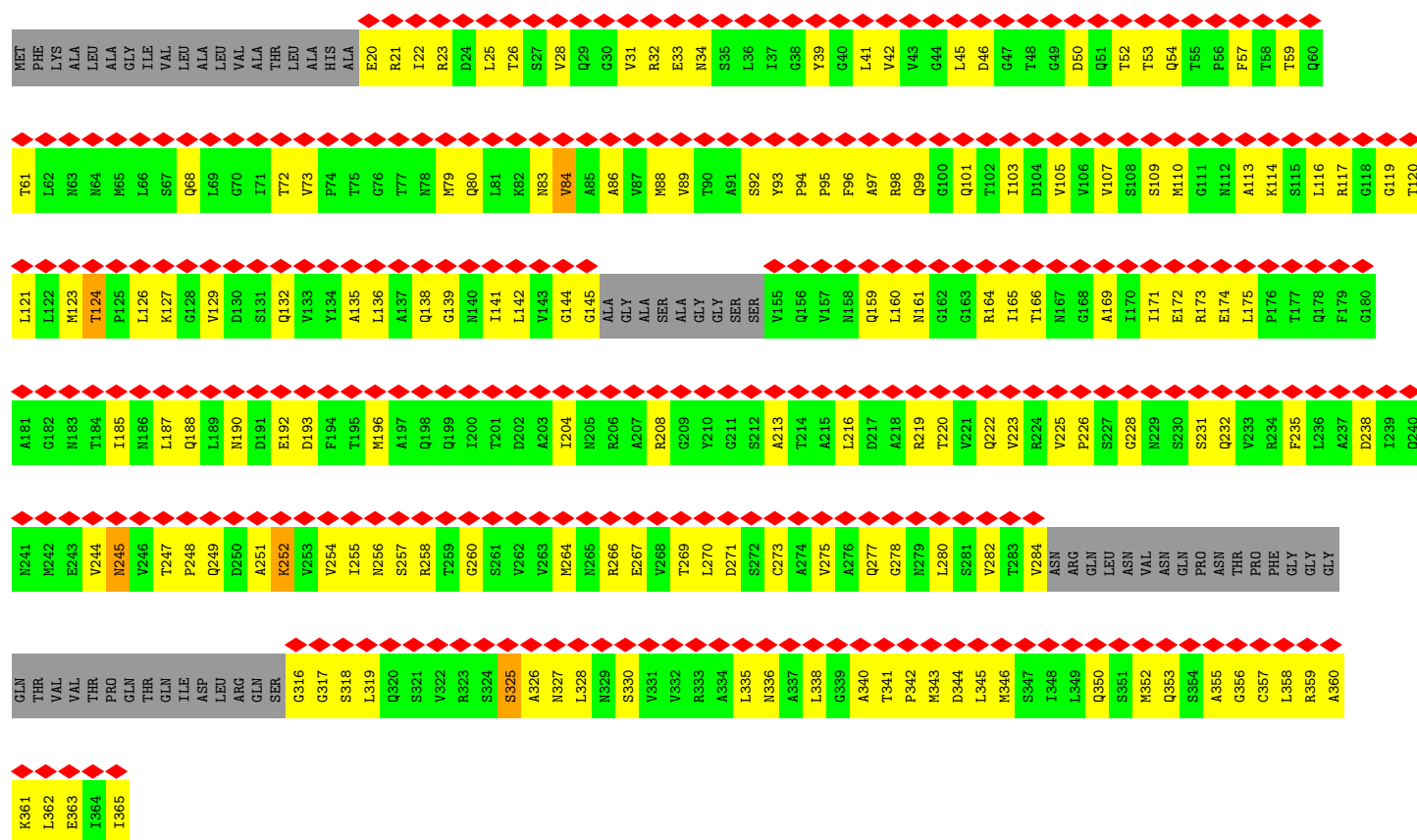
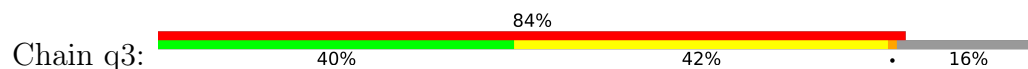


- Molecule 11: Flagellar P-ring protein

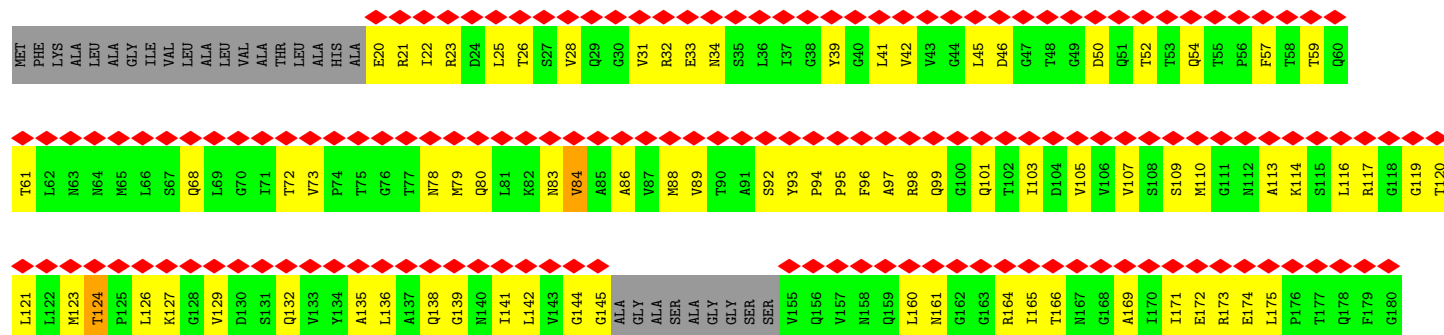
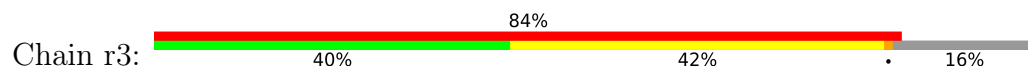


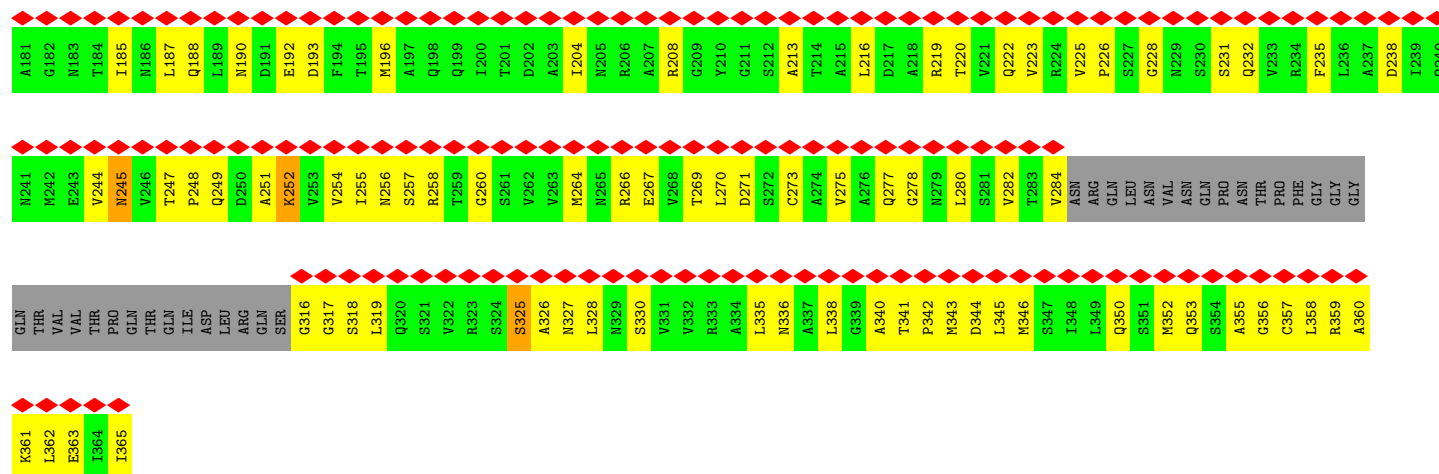


• Molecule 11: Flagellar P-ring protein

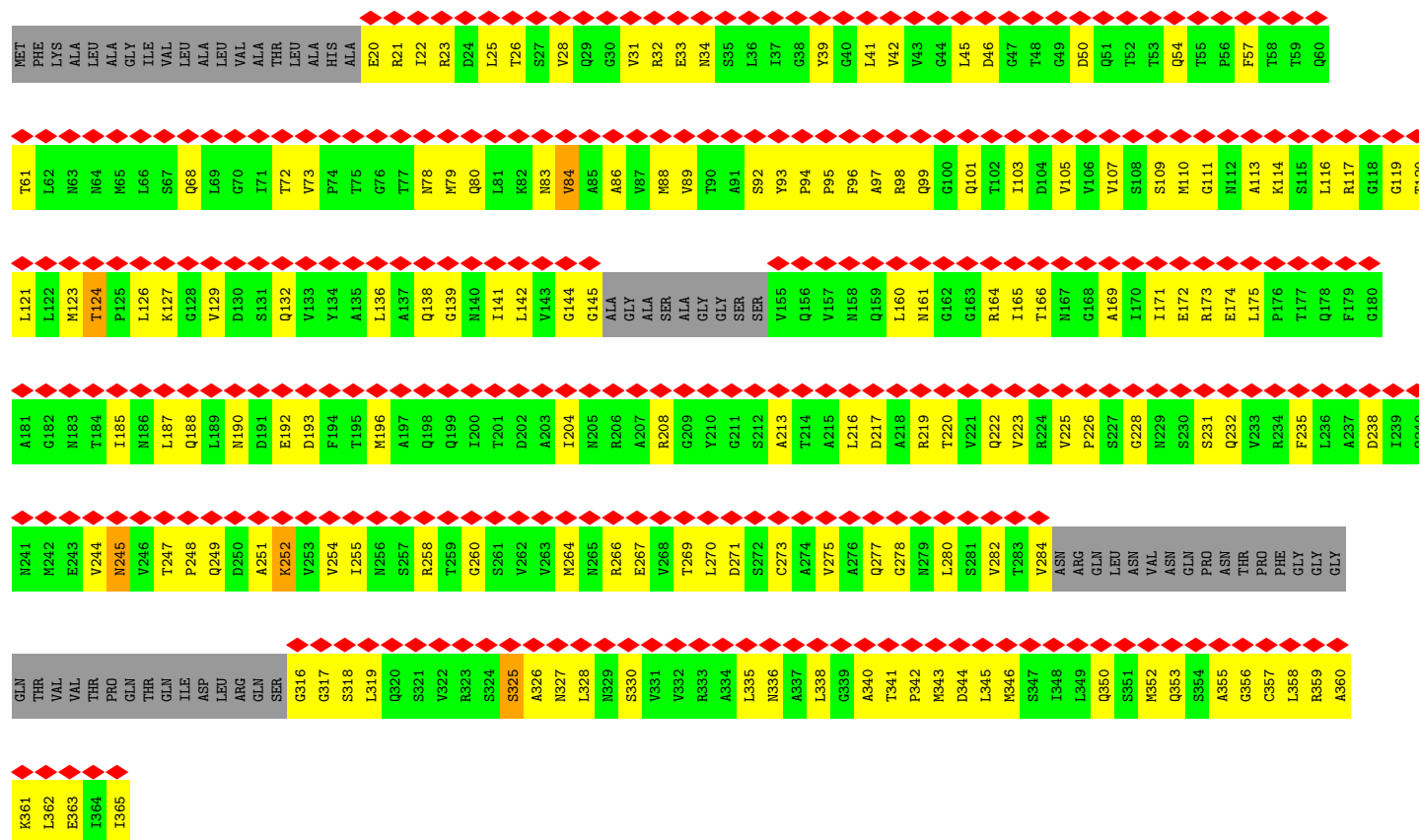
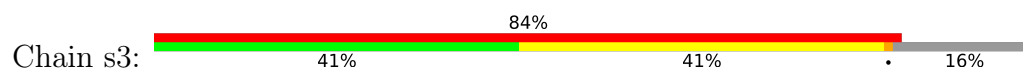


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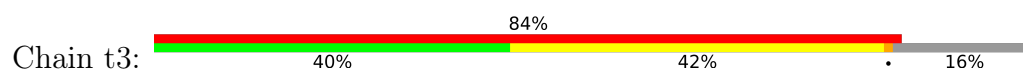


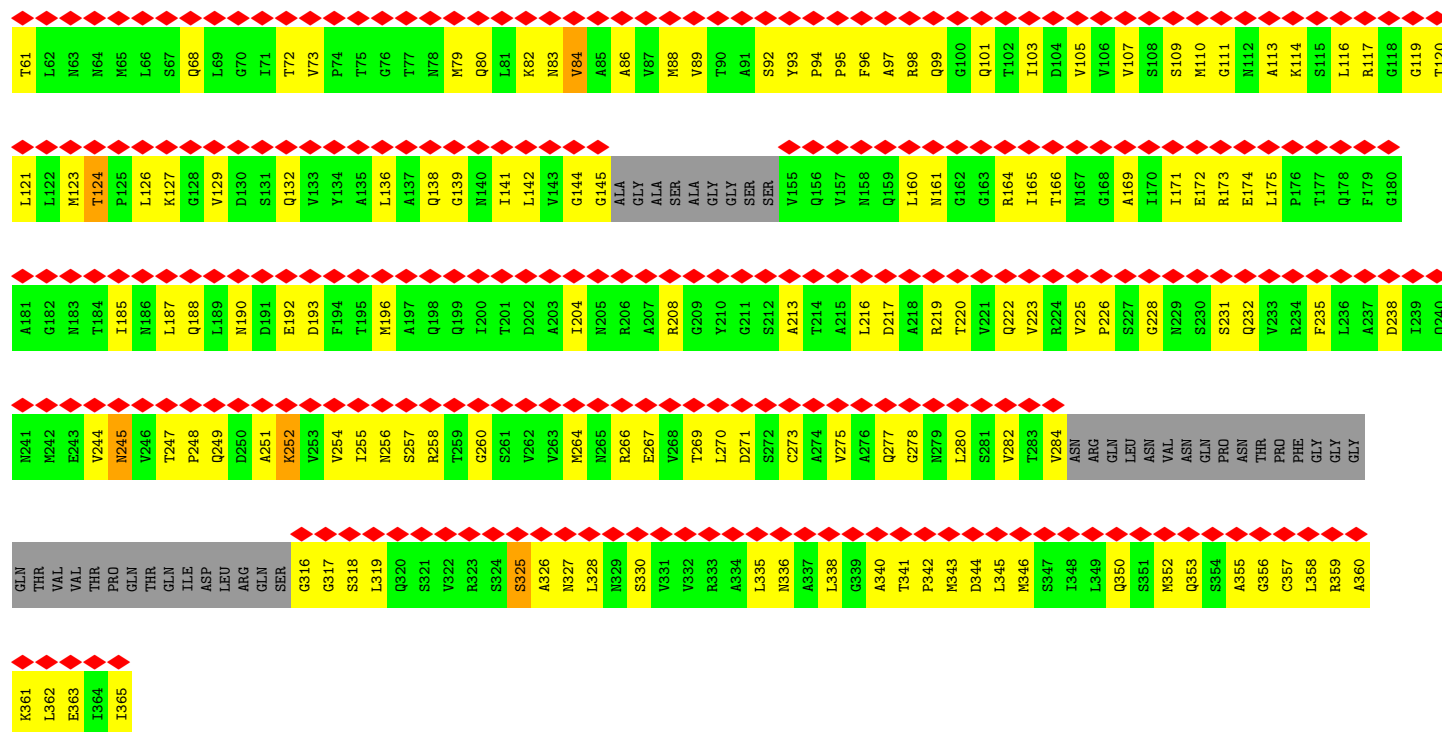


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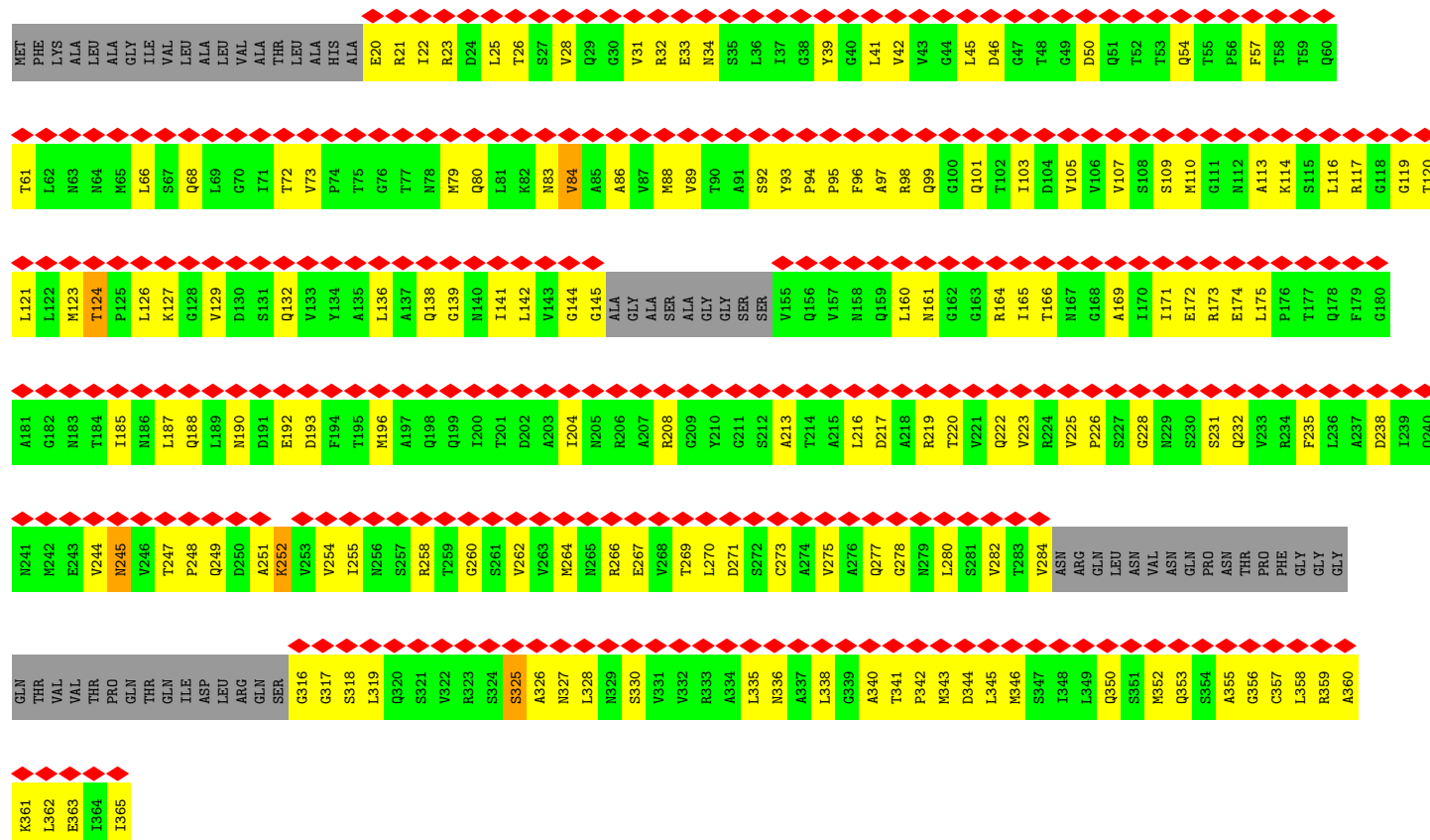
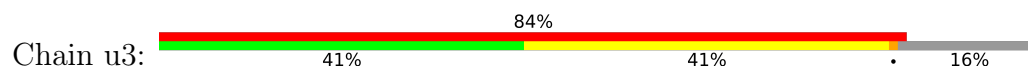


• Molecule 11: Flagellar P-ring protein

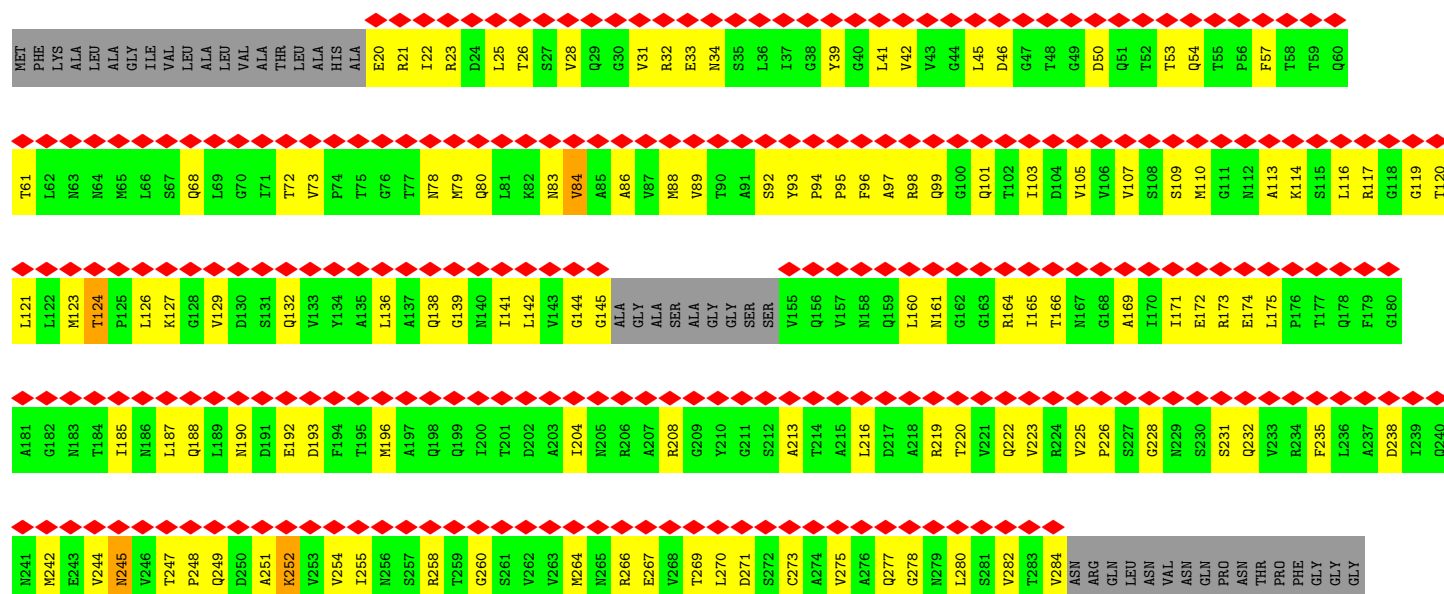
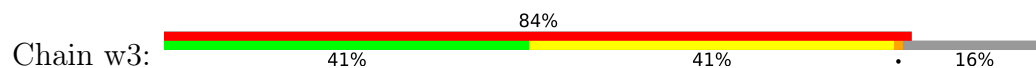


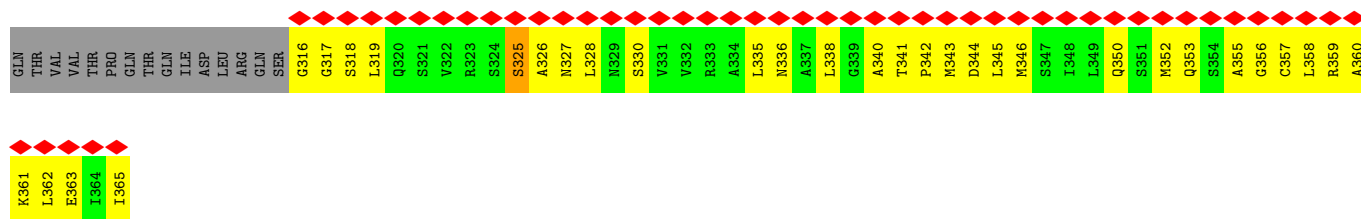


• Molecule 11: Flagellar P-ring protein

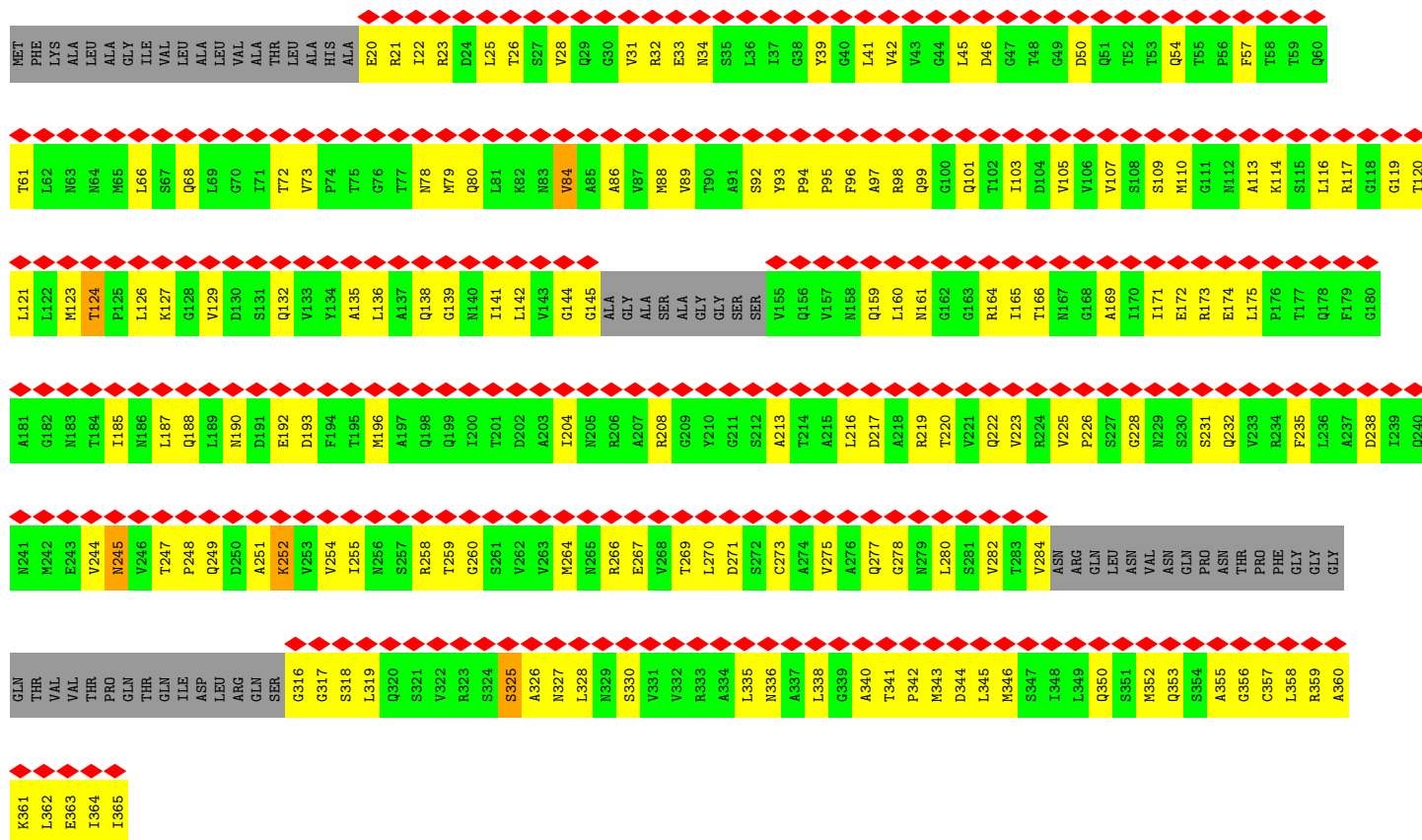
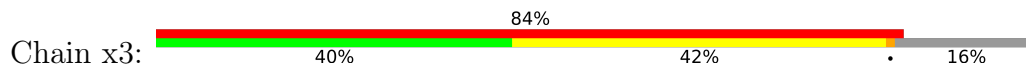


Chain v3: 84% 40% 42% 16%

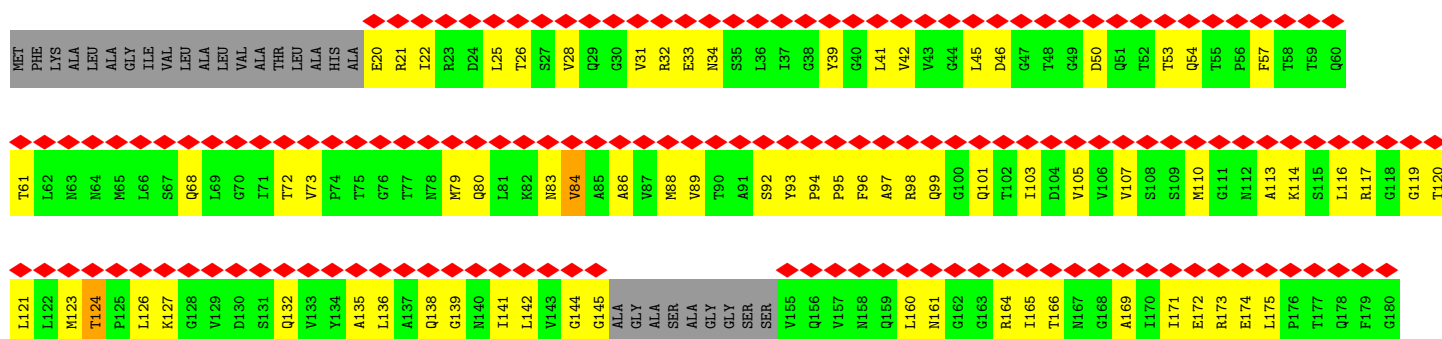
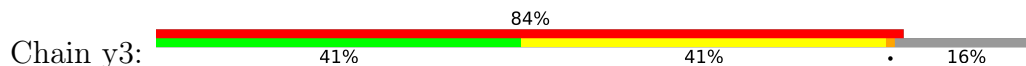




• Molecule 11: Flagellar P-ring protein

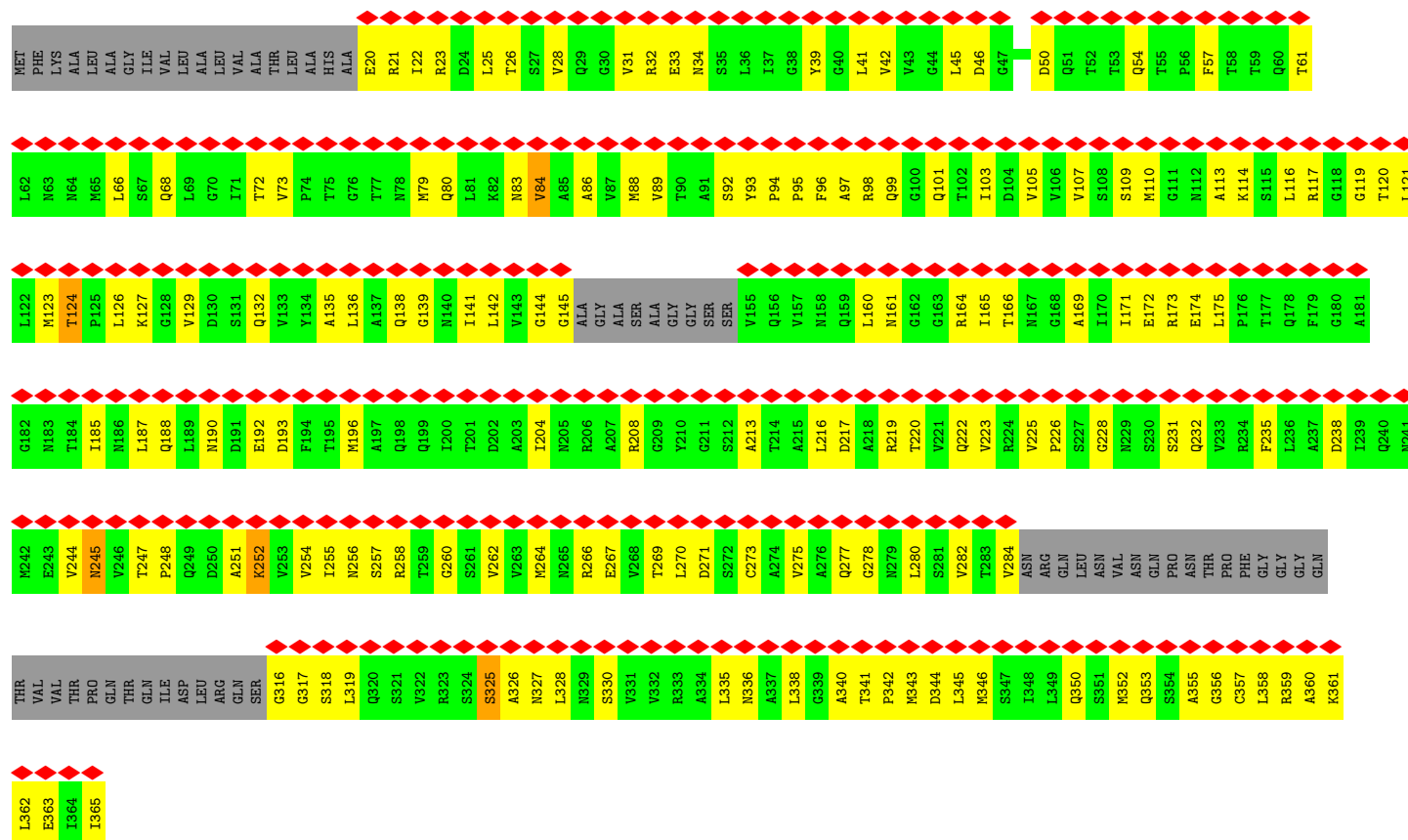
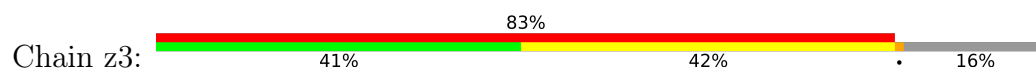


• Molecule 11: Flagellar P-ring protein

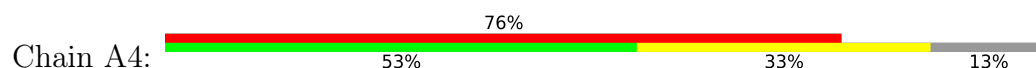


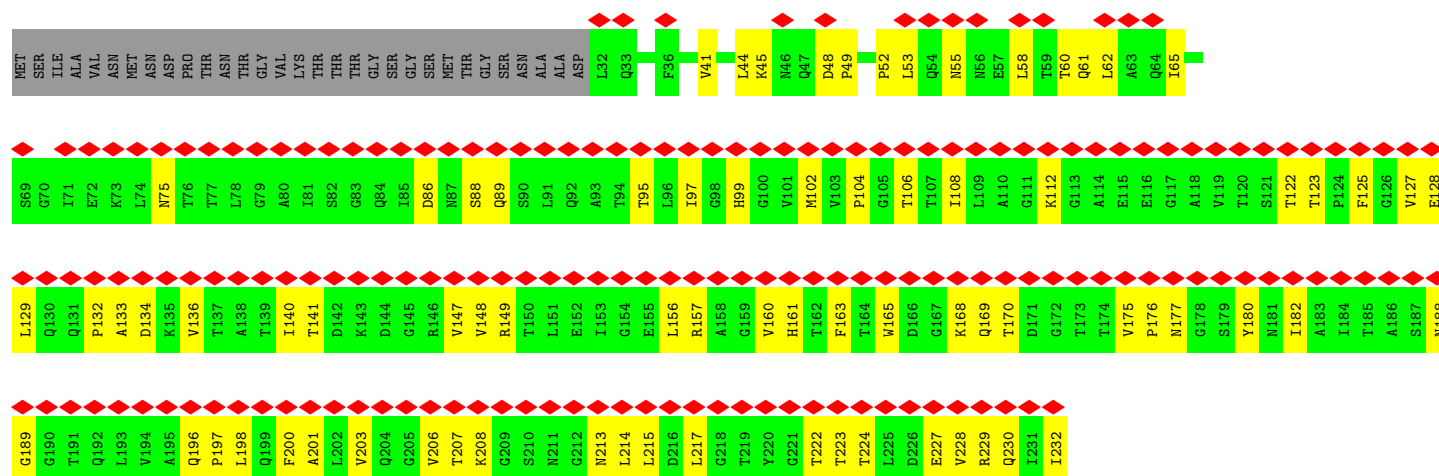


• Molecule 11: Flagellar P-ring protein

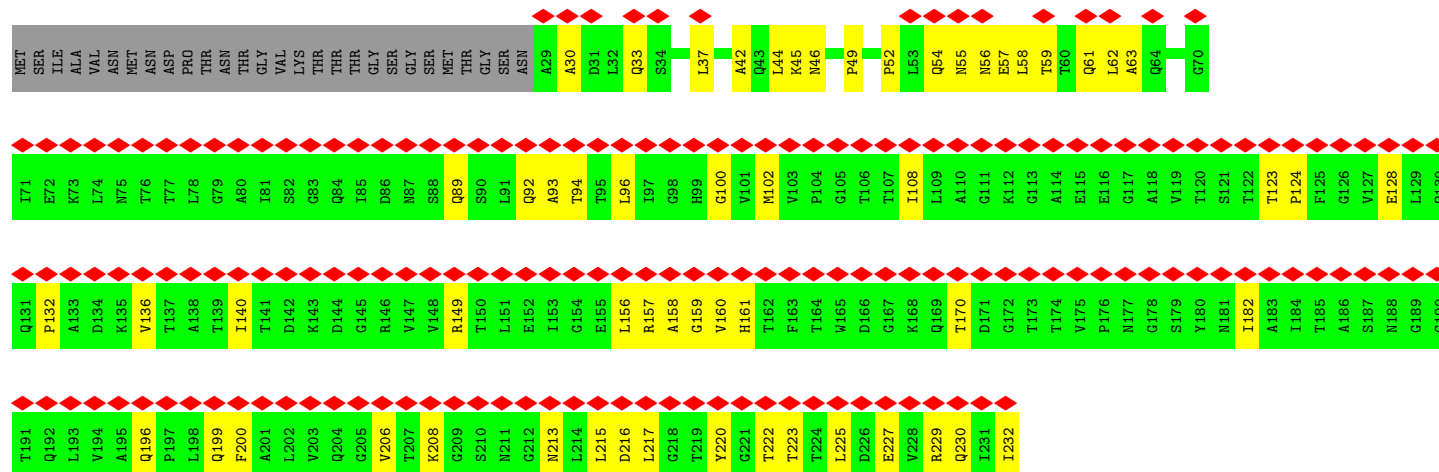
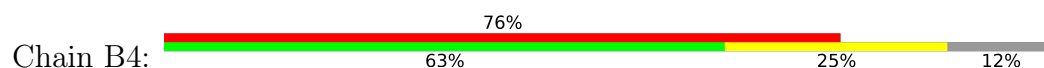


• Molecule 12: Basal-body rod modification protein FlgD

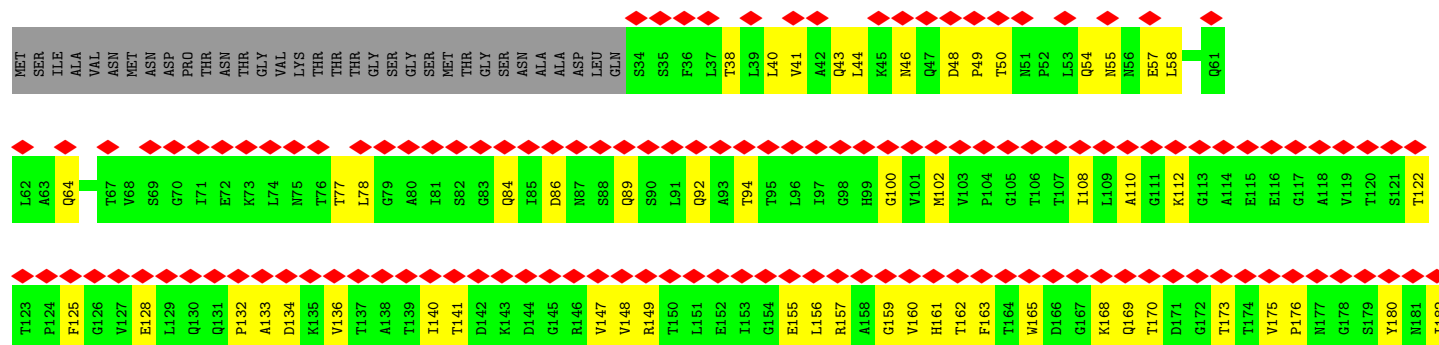
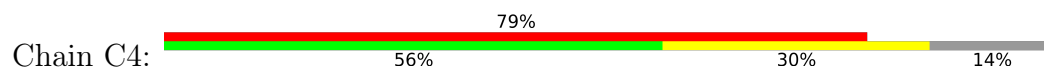


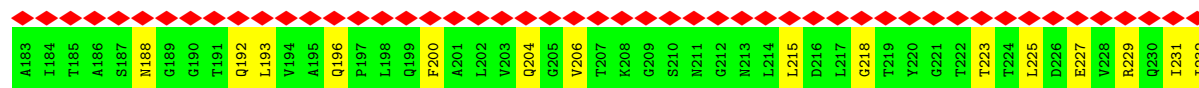


• Molecule 12: Basal-body rod modification protein FlgD

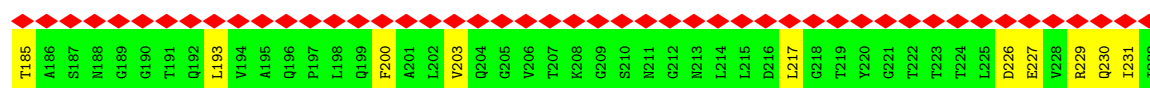
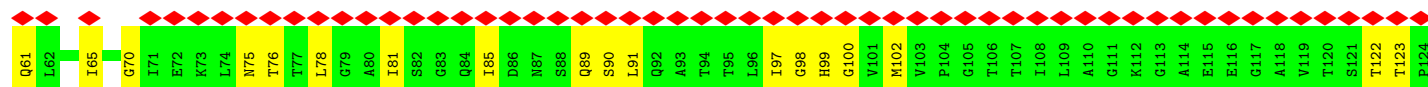
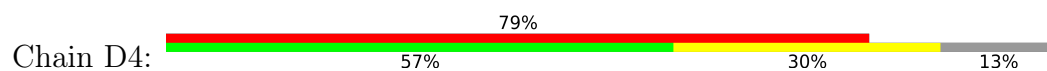


• Molecule 12: Basal-body rod modification protein FlgD

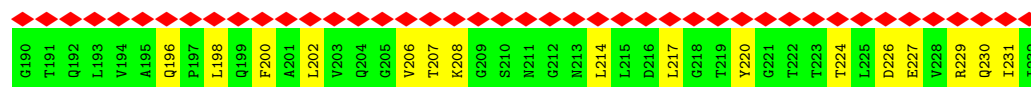
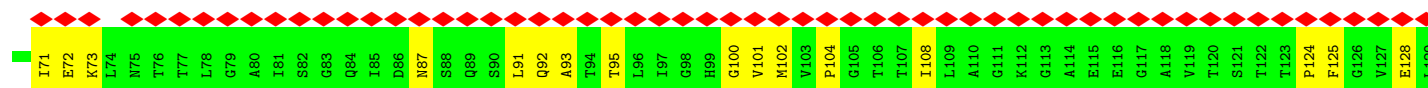
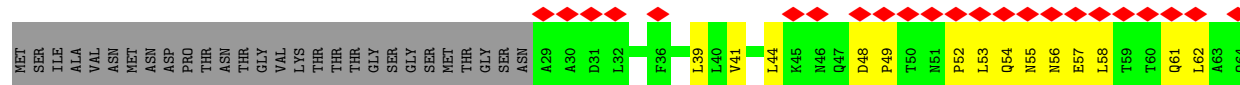
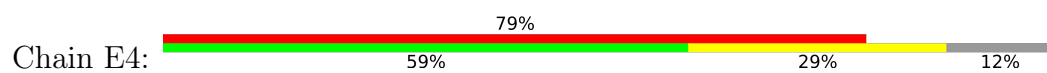




• Molecule 12: Basal-body rod modification protein FlgD



• Molecule 12: Basal-body rod modification protein FlgD



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 (Å)	638.976, 638.976, 638.976	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.35	0/1205	0.48	0/1624
1	B1	0.33	0/1955	0.53	0/2645
1	C1	0.34	0/1955	0.52	2/2645 (0.1%)
1	D1	0.36	0/1205	0.50	0/1624
1	E1	0.33	0/1955	0.53	0/2645
1	F1	0.35	0/1205	0.51	0/1624
1	G1	0.33	0/1955	0.50	0/2645
1	H1	0.34	0/1955	0.56	2/2645 (0.1%)
1	I1	0.33	0/1955	0.48	0/2645
1	J1	0.36	0/1205	0.50	0/1624
1	K1	0.31	0/1955	0.53	2/2645 (0.1%)
1	L1	0.32	0/1955	0.51	1/2645 (0.0%)
1	M1	0.35	0/1205	0.52	0/1624
1	N1	0.31	0/1955	0.54	1/2645 (0.0%)
1	O1	0.30	0/1955	0.49	0/2645
1	P1	0.32	0/1205	0.49	0/1624
1	Q1	0.30	0/1955	0.48	0/2645
1	R1	0.29	0/1955	0.47	0/2645
1	S1	0.33	0/1205	0.47	0/1624
1	T1	0.29	0/1955	0.50	0/2645
1	U1	0.30	0/1955	0.56	2/2645 (0.1%)
1	V1	0.33	0/1205	0.50	0/1624
1	W1	0.29	0/1955	0.50	0/2645
1	X1	0.30	0/1955	0.50	0/2645
1	Y1	0.29	0/1955	0.49	0/2645
1	Z1	0.35	0/1205	0.54	0/1624
1	a1	0.30	0/1955	0.50	0/2645
1	b1	0.35	0/1205	0.50	0/1624
1	c1	0.31	0/1955	0.49	0/2645
1	d1	0.32	0/1955	0.50	0/2645
1	e1	0.35	0/1205	0.48	0/1624
1	f1	0.32	0/1955	0.49	0/2645
1	g1	0.32	0/1955	0.50	0/2645
1	h1	0.32	0/1955	0.46	0/2645

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	A2	0.34	0/1662	0.63	2/2263 (0.1%)
2	B2	0.35	0/1662	0.62	0/2263
2	C2	0.36	0/1662	0.64	1/2263 (0.0%)
2	D2	0.36	0/1662	0.62	2/2263 (0.1%)
2	E2	1.11	1/1662 (0.1%)	0.64	2/2263 (0.1%)
3	F2	0.31	0/2035	0.60	2/2777 (0.1%)
4	G2	0.28	0/681	0.60	0/930
4	H2	0.29	0/681	0.56	0/930
4	I2	0.31	0/681	0.51	0/930
4	J2	1.86	6/681 (0.9%)	0.56	0/930
5	K2	0.31	0/296	0.53	0/395
5	L2	0.28	0/567	0.39	0/761
5	M2	0.31	0/567	0.45	0/761
5	N2	0.30	0/567	0.42	0/761
5	O2	0.29	0/567	0.44	0/761
5	P2	0.30	0/567	0.43	0/761
6	Q2	0.34	0/1035	0.52	0/1399
6	R2	0.34	0/941	0.49	0/1269
6	S2	0.38	0/951	0.52	0/1281
6	T2	0.37	0/842	0.48	0/1132
6	U2	0.33	0/934	0.46	0/1259
7	V2	0.40	0/981	0.66	0/1334
7	W2	0.37	0/976	0.56	0/1327
7	X2	0.40	0/976	0.56	0/1327
7	Y2	0.38	0/976	0.54	0/1327
7	Z2	0.37	0/976	0.54	0/1327
7	a2	0.36	0/976	0.56	0/1327
8	b2	0.35	0/1836	0.57	0/2502
8	c2	0.39	0/1836	0.58	0/2502
8	d2	0.40	0/1836	0.58	0/2502
8	e2	0.38	0/1836	0.55	0/2502
8	f2	0.36	0/1836	0.54	0/2502
9	l2	0.31	0/1973	0.48	0/2682
9	22	0.30	0/1973	0.47	0/2682
9	32	0.29	0/1971	0.47	0/2677
9	42	0.23	0/1973	0.47	0/2682
9	g2	0.34	0/1973	0.46	0/2682
9	h2	0.37	0/1973	0.46	0/2682
9	i2	0.37	0/1973	0.47	0/2682
9	j2	0.38	0/1973	0.47	0/2682
9	k2	0.37	0/1973	0.47	0/2682
9	l2	0.37	0/1894	0.45	0/2573
9	m2	0.39	0/1894	0.47	0/2573

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	n2	0.37	0/1894	0.45	0/2573
9	o2	0.38	0/1894	0.46	0/2573
9	p2	0.38	0/1894	0.47	0/2573
9	q2	0.37	0/1907	0.45	0/2590
9	r2	0.37	0/1973	0.50	0/2682
9	s2	0.37	0/1973	0.53	0/2682
9	t2	0.37	0/1973	0.52	1/2682 (0.0%)
9	u2	0.36	0/1973	0.50	0/2682
9	v2	0.38	0/1973	0.49	0/2682
9	w2	0.37	0/1973	0.50	0/2682
9	x2	0.33	0/1973	0.47	0/2682
9	y2	0.30	0/1973	0.45	0/2682
9	z2	0.29	0/1973	0.44	0/2682
10	A3	0.12	0/1614	0.29	1/2194 (0.0%)
10	B3	0.12	0/1614	0.29	1/2194 (0.0%)
10	C3	0.12	0/1614	0.29	1/2194 (0.0%)
10	D3	0.12	0/1614	0.29	1/2194 (0.0%)
10	E3	0.12	0/1614	0.29	1/2194 (0.0%)
10	F3	0.12	0/1614	0.29	1/2194 (0.0%)
10	G3	0.12	0/1614	0.29	1/2194 (0.0%)
10	H3	0.12	0/1614	0.29	1/2194 (0.0%)
10	I3	0.12	0/1614	0.29	1/2194 (0.0%)
10	J3	0.12	0/1614	0.29	1/2194 (0.0%)
10	K3	0.12	0/1614	0.29	1/2194 (0.0%)
10	L3	0.12	0/1614	0.29	1/2194 (0.0%)
10	M3	0.12	0/1614	0.29	1/2194 (0.0%)
10	N3	0.12	0/1614	0.29	1/2194 (0.0%)
10	O3	0.12	0/1614	0.29	1/2194 (0.0%)
10	P3	0.12	0/1614	0.29	1/2194 (0.0%)
10	Q3	0.12	0/1614	0.29	1/2194 (0.0%)
10	R3	0.12	0/1614	0.29	1/2194 (0.0%)
10	S3	0.12	0/1614	0.29	1/2194 (0.0%)
10	T3	0.12	0/1614	0.29	1/2194 (0.0%)
10	U3	0.12	0/1614	0.29	1/2194 (0.0%)
10	V3	0.12	0/1614	0.29	1/2194 (0.0%)
10	W3	0.12	0/1611	0.29	1/2188 (0.0%)
10	X3	0.12	0/1614	0.29	1/2194 (0.0%)
10	Y3	0.12	0/1614	0.29	1/2194 (0.0%)
10	Z3	0.12	0/1614	0.29	1/2194 (0.0%)
11	a3	0.07	0/2267	0.21	0/3073
11	b3	0.08	0/2267	0.21	0/3073
11	c3	0.08	0/2267	0.22	0/3073
11	d3	0.08	0/2267	0.21	0/3073

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	e3	0.08	0/2267	0.21	0/3073
11	f3	0.07	0/2267	0.21	0/3073
11	g3	0.07	0/2267	0.22	0/3073
11	h3	0.08	0/2266	0.21	0/3071
11	i3	0.07	0/2267	0.21	0/3073
11	j3	0.08	0/2267	0.22	0/3073
11	k3	0.07	0/2267	0.21	0/3073
11	l3	0.08	0/2267	0.22	0/3073
11	m3	0.07	0/2267	0.21	0/3073
11	n3	0.08	0/2267	0.22	0/3073
11	o3	0.07	0/2267	0.22	0/3073
11	p3	0.08	0/2267	0.21	0/3073
11	q3	0.07	0/2267	0.22	0/3073
11	r3	0.08	0/2264	0.22	0/3066
11	s3	0.07	0/2267	0.21	0/3073
11	t3	0.07	0/2267	0.21	0/3073
11	u3	0.08	0/2267	0.21	0/3073
11	v3	0.07	0/2267	0.22	0/3073
11	w3	0.08	0/2267	0.21	0/3073
11	x3	0.08	0/2267	0.21	0/3073
11	y3	0.08	0/2267	0.22	0/3073
11	z3	0.08	0/2267	0.22	0/3073
12	A4	0.13	0/1491	0.25	0/2033
12	B4	0.14	0/1509	0.27	0/2058
12	C4	0.13	0/1474	0.27	0/2010
12	D4	0.14	0/1496	0.35	0/2040
12	E4	0.14	0/1509	0.28	0/2058
All	All	0.29	7/249431 (0.0%)	0.42	46/338382 (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 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E2	205	MET	SD-CE	43.51	2.88	1.79
4	J2	51	PHE	CD1-CE1	21.93	2.04	1.38
4	J2	51	PHE	CE2-CZ	21.65	2.03	1.38
4	J2	51	PHE	CD2-CE2	21.09	2.02	1.38
4	J2	51	PHE	CE1-CZ	20.92	2.01	1.38

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E2	205	MET	CG-SD-CE	14.35	132.46	100.90
9	t2	167	PRO	CA-N-CD	-8.81	99.66	112.00
1	K1	282	TYR	CA-C-N	-7.46	111.24	121.61
1	K1	282	TYR	C-N-CA	-7.46	111.24	121.61
10	Z3	43	PRO	CA-N-CD	-6.72	102.59	112.00

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	1193	0	1173	46	0
1	B1	1931	0	1922	130	0
1	C1	1931	0	1921	112	0
1	D1	1193	0	1173	62	0
1	E1	1931	0	1922	159	0
1	F1	1193	0	1173	64	0
1	G1	1931	0	1919	121	0
1	H1	1931	0	1925	124	0
1	I1	1931	0	1919	100	0
1	J1	1193	0	1173	56	0
1	K1	1931	0	1921	107	0
1	L1	1931	0	1924	121	0
1	M1	1193	0	1173	89	0
1	N1	1931	0	1924	149	0
1	O1	1931	0	1921	110	0
1	P1	1193	0	1173	50	0
1	Q1	1931	0	1921	135	0
1	R1	1931	0	1921	134	0
1	S1	1193	0	1173	55	0
1	T1	1931	0	1922	199	0
1	U1	1931	0	1925	135	0
1	V1	1193	0	1173	59	0
1	W1	1931	0	1922	134	0
1	X1	1931	0	1922	116	0
1	Y1	1931	0	1918	134	0
1	Z1	1193	0	1171	85	0
1	a1	1931	0	1924	121	0
1	b1	1193	0	1173	52	0
1	c1	1931	0	1923	96	0
1	d1	1931	0	1923	135	0
1	e1	1193	0	1173	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	f1	1931	0	1918	102	0
1	g1	1931	0	1921	114	0
1	h1	1931	0	1923	132	0
2	A2	1623	0	1706	141	0
2	B2	1623	0	1707	161	0
2	C2	1623	0	1707	197	0
2	D2	1623	0	1708	172	0
2	E2	1623	0	1709	246	0
3	F2	1986	0	2098	230	0
4	G2	670	0	739	40	0
4	H2	670	0	739	47	0
4	I2	670	0	737	48	0
4	J2	670	0	738	67	0
5	K2	296	0	308	18	0
5	L2	563	0	571	11	0
5	M2	563	0	571	13	0
5	N2	563	0	571	24	0
5	O2	563	0	571	20	0
5	P2	563	0	571	39	0
6	Q2	1023	0	1020	71	0
6	R2	932	0	931	67	0
6	S2	942	0	943	73	0
6	T2	835	0	838	34	0
6	U2	925	0	923	101	0
7	V2	969	0	979	45	0
7	W2	964	0	976	32	0
7	X2	964	0	976	47	0
7	Y2	964	0	976	35	0
7	Z2	964	0	976	44	0
7	a2	964	0	976	41	0
8	b2	1812	0	1800	80	0
8	c2	1812	0	1800	89	0
8	d2	1812	0	1800	98	0
8	e2	1812	0	1800	91	0
8	f2	1812	0	1800	82	0
9	12	1949	0	1925	94	0
9	22	1949	0	1924	108	0
9	32	1948	0	1922	121	0
9	42	1949	0	1925	107	0
9	g2	1949	0	1926	71	0
9	h2	1949	0	1926	83	0
9	i2	1949	0	1926	86	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	j2	1949	0	1925	76	0
9	k2	1949	0	1926	76	0
9	l2	1871	0	1849	65	0
9	m2	1871	0	1849	91	0
9	n2	1871	0	1849	94	0
9	o2	1871	0	1849	92	0
9	p2	1871	0	1849	101	0
9	q2	1885	0	1862	66	0
9	r2	1949	0	1926	101	0
9	s2	1949	0	1924	95	0
9	t2	1949	0	1926	89	0
9	u2	1949	0	1926	107	0
9	v2	1949	0	1926	55	0
9	w2	1949	0	1926	95	0
9	x2	1949	0	1926	65	0
9	y2	1949	0	1926	88	0
9	z2	1949	0	1926	91	0
10	A3	1581	0	1534	92	0
10	B3	1581	0	1534	92	0
10	C3	1581	0	1534	95	0
10	D3	1581	0	1534	94	0
10	E3	1581	0	1534	95	0
10	F3	1581	0	1534	93	0
10	G3	1581	0	1534	94	0
10	H3	1581	0	1534	94	0
10	I3	1581	0	1534	96	0
10	J3	1581	0	1534	95	0
10	K3	1581	0	1534	96	0
10	L3	1581	0	1534	95	0
10	M3	1581	0	1534	95	0
10	N3	1581	0	1534	99	0
10	O3	1581	0	1534	98	0
10	P3	1581	0	1534	93	0
10	Q3	1581	0	1534	100	0
10	R3	1581	0	1534	100	0
10	S3	1581	0	1534	98	0
10	T3	1581	0	1534	95	0
10	U3	1581	0	1534	93	0
10	V3	1581	0	1534	91	0
10	W3	1580	0	1529	94	0
10	X3	1581	0	1534	95	0
10	Y3	1581	0	1534	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	Z3	1581	0	1534	101	0
11	a3	2252	0	2292	193	0
11	b3	2252	0	2293	194	0
11	c3	2252	0	2292	205	0
11	d3	2252	0	2293	188	0
11	e3	2252	0	2293	189	0
11	f3	2252	0	2293	197	0
11	g3	2252	0	2293	192	0
11	h3	2251	0	2291	190	0
11	i3	2252	0	2291	189	0
11	j3	2252	0	2293	187	0
11	k3	2252	0	2293	185	0
11	l3	2252	0	2291	197	0
11	m3	2252	0	2293	193	0
11	n3	2252	0	2293	185	0
11	o3	2252	0	2291	193	0
11	p3	2252	0	2293	188	0
11	q3	2252	0	2293	195	0
11	r3	2251	0	2287	192	0
11	s3	2252	0	2293	198	0
11	t3	2252	0	2293	198	0
11	u3	2252	0	2293	187	0
11	v3	2252	0	2293	199	0
11	w3	2252	0	2293	190	0
11	x3	2252	0	2293	198	0
11	y3	2252	0	2291	198	0
11	z3	2252	0	2293	205	0
12	A4	1475	0	1488	85	0
12	B4	1493	0	1501	86	0
12	C4	1458	0	1468	73	0
12	D4	1482	0	1487	89	0
12	E4	1493	0	1502	63	0
All	All	246311	0	246056	12078	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

The worst 5 of 12078 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B2:96:LEU:HD22	2:B2:236:MET:CE	1.21	1.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T1:167:ARG:CZ	2:E2:107:LYS:CD	1.74	1.64
1:R1:125:GLN:CG	2:E2:230:ASP:HB3	1.32	1.58
1:a1:167:ARG:HD3	2:D2:244:TYR:CD2	1.36	1.58
1:W1:164:LEU:HD11	2:E2:143:ARG:CA	1.11	1.57

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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	60
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	60
1	H1	242/560 (43%)	221 (91%)	19 (8%)	2 (1%)	16	48
1	I1	242/560 (43%)	229 (95%)	12 (5%)	1 (0%)	30	60
1	J1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100
1	K1	242/560 (43%)	230 (95%)	11 (4%)	1 (0%)	30	60
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	60
1	P1	145/560 (26%)	142 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q1	242/560 (43%)	224 (93%)	17 (7%)	1 (0%)	30	60
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	60
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	60
1	b1	145/560 (26%)	140 (97%)	5 (3%)	0	100	100
1	c1	242/560 (43%)	225 (93%)	16 (7%)	1 (0%)	30	60
1	d1	242/560 (43%)	225 (93%)	16 (7%)	1 (0%)	30	60
1	e1	145/560 (26%)	144 (99%)	1 (1%)	0	100	100
1	f1	242/560 (43%)	229 (95%)	12 (5%)	1 (0%)	30	60
1	g1	242/560 (43%)	226 (93%)	15 (6%)	1 (0%)	30	60
1	h1	242/560 (43%)	232 (96%)	10 (4%)	0	100	100
2	A2	207/245 (84%)	182 (88%)	23 (11%)	2 (1%)	12	43
2	B2	207/245 (84%)	183 (88%)	22 (11%)	2 (1%)	12	43
2	C2	207/245 (84%)	177 (86%)	29 (14%)	1 (0%)	24	56
2	D2	207/245 (84%)	181 (87%)	25 (12%)	1 (0%)	24	56
2	E2	207/245 (84%)	183 (88%)	22 (11%)	2 (1%)	12	43
3	F2	254/264 (96%)	223 (88%)	30 (12%)	1 (0%)	30	60
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	N2	73/104 (70%)	69 (94%)	4 (6%)	0	100	100
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	48
7	W2	130/134 (97%)	108 (83%)	22 (17%)	0	100	100
7	X2	130/134 (97%)	107 (82%)	22 (17%)	1 (1%)	16	48
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	60
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	o2	245/260 (94%)	230 (94%)	15 (6%)	0	100	100
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	T3	209/232 (90%)	192 (92%)	17 (8%)	0	100	100
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	y3	300/365 (82%)	288 (96%)	12 (4%)	0	100	100
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%)	49	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%)	134 (100%)	0	100	100
1	B1	217/467 (46%)	217 (100%)	0	100	100
1	C1	217/467 (46%)	217 (100%)	0	100	100
1	D1	134/467 (29%)	134 (100%)	0	100	100
1	E1	217/467 (46%)	217 (100%)	0	100	100
1	F1	134/467 (29%)	134 (100%)	0	100	100
1	G1	217/467 (46%)	217 (100%)	0	100	100
1	H1	217/467 (46%)	217 (100%)	0	100	100
1	I1	217/467 (46%)	217 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J1	134/467 (29%)	134 (100%)	0	100	100
1	K1	217/467 (46%)	217 (100%)	0	100	100
1	L1	217/467 (46%)	217 (100%)	0	100	100
1	M1	134/467 (29%)	134 (100%)	0	100	100
1	N1	217/467 (46%)	217 (100%)	0	100	100
1	O1	217/467 (46%)	217 (100%)	0	100	100
1	P1	134/467 (29%)	134 (100%)	0	100	100
1	Q1	217/467 (46%)	217 (100%)	0	100	100
1	R1	217/467 (46%)	217 (100%)	0	100	100
1	S1	134/467 (29%)	134 (100%)	0	100	100
1	T1	217/467 (46%)	217 (100%)	0	100	100
1	U1	217/467 (46%)	217 (100%)	0	100	100
1	V1	134/467 (29%)	134 (100%)	0	100	100
1	W1	217/467 (46%)	217 (100%)	0	100	100
1	X1	217/467 (46%)	217 (100%)	0	100	100
1	Y1	217/467 (46%)	217 (100%)	0	100	100
1	Z1	134/467 (29%)	134 (100%)	0	100	100
1	a1	217/467 (46%)	217 (100%)	0	100	100
1	b1	134/467 (29%)	134 (100%)	0	100	100
1	c1	217/467 (46%)	217 (100%)	0	100	100
1	d1	217/467 (46%)	217 (100%)	0	100	100
1	e1	134/467 (29%)	134 (100%)	0	100	100
1	f1	217/467 (46%)	217 (100%)	0	100	100
1	g1	217/467 (46%)	217 (100%)	0	100	100
1	h1	217/467 (46%)	217 (100%)	0	100	100
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%)	78	79
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	G2	74/74 (100%)	74 (100%)	0	100	100
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%)	100 (100%)	0	100	100
6	T2	89/113 (79%)	89 (100%)	0	100	100
6	U2	99/113 (88%)	98 (99%)	1 (1%)	68	74
7	V2	104/105 (99%)	103 (99%)	1 (1%)	68	74
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%)	104 (100%)	0	100	100
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%)	215 (100%)	0	100	100
9	g2	215/215 (100%)	215 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	h2	215/215 (100%)	215 (100%)	0	100	100
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%)	81	80
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%)	207 (100%)	0	100	100
9	r2	215/215 (100%)	215 (100%)	0	100	100
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%)	215 (100%)	0	100	100
9	z2	215/215 (100%)	215 (100%)	0	100	100
10	A3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	B3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	C3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	D3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	E3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	F3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	G3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	H3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	I3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	J3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	K3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	L3	170/186 (91%)	168 (99%)	2 (1%)	63	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	M3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	N3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	O3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	P3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	Q3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	R3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	S3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	T3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	U3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	V3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	W3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	X3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	Y3	170/186 (91%)	168 (99%)	2 (1%)	63	72
10	Z3	170/186 (91%)	168 (99%)	2 (1%)	63	72
11	a3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	b3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	c3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	d3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	e3	251/294 (85%)	244 (97%)	7 (3%)	38	58
11	f3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	g3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	h3	251/294 (85%)	244 (97%)	7 (3%)	38	58
11	i3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	j3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	k3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	l3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	m3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	n3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	o3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	p3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	q3	251/294 (85%)	245 (98%)	6 (2%)	43	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	r3	250/294 (85%)	244 (98%)	6 (2%)	43	61
11	s3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	t3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	u3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	v3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	w3	251/294 (85%)	243 (97%)	8 (3%)	34	56
11	x3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	y3	251/294 (85%)	245 (98%)	6 (2%)	43	61
11	z3	251/294 (85%)	245 (98%)	6 (2%)	43	61
12	A4	164/188 (87%)	164 (100%)	0	100	100
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%)	164 (100%)	0	100	100
12	E4	165/188 (88%)	165 (100%)	0	100	100
All	All	27146/38629 (70%)	26930 (99%)	216 (1%)	70	76

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	j3	245	ASN
11	o3	124	THR
11	x3	124	THR
11	k3	124	THR
11	m3	84	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 514 such sidechains are listed below:

Mol	Chain	Res	Type
11	v3	161	ASN
11	x3	99	GLN
11	v3	159	GLN
9	r2	15	GLN
9	p2	137	GLN

5.3.3 RNA [i](#)

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

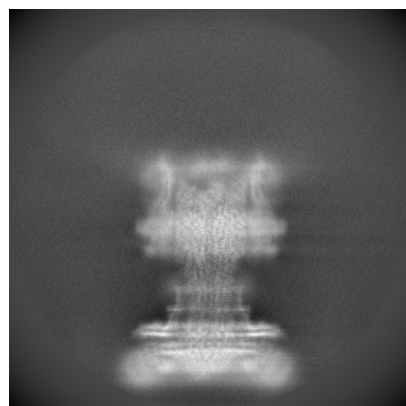
6 Map visualisation [i](#)

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.

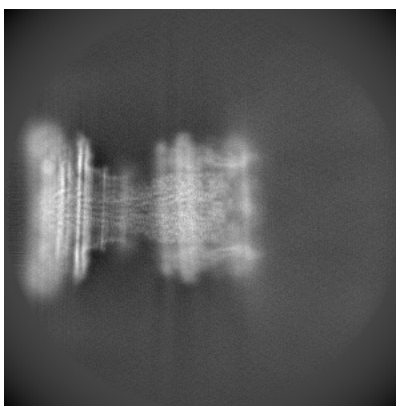
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

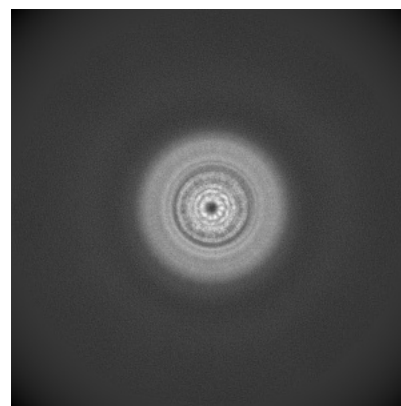
6.1.1 Primary map



X

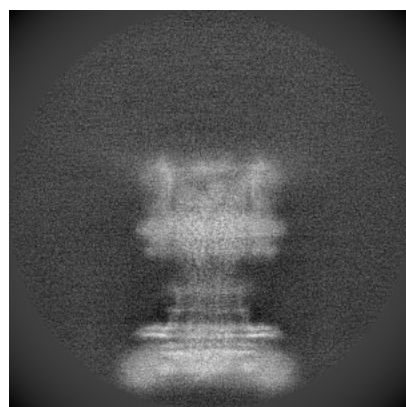


Y

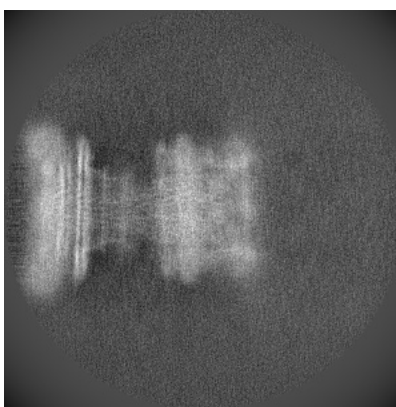


Z

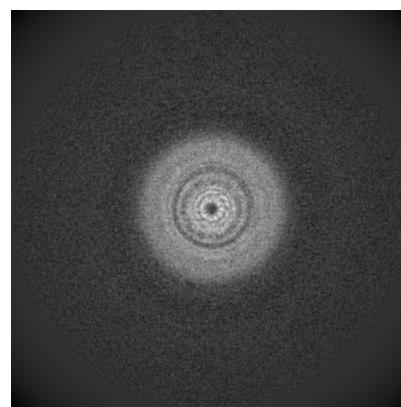
6.1.2 Raw map



X



Y

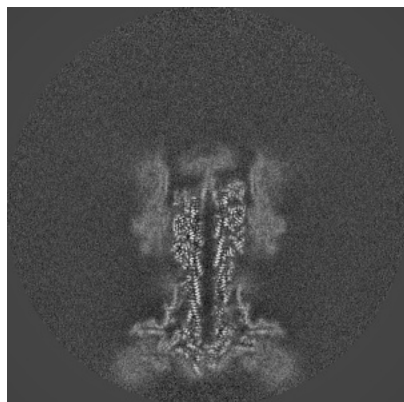


Z

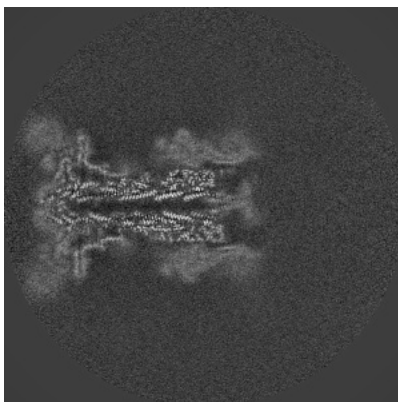
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

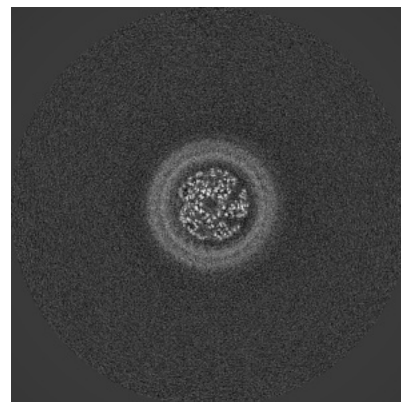
6.2.1 Primary map



X Index: 384

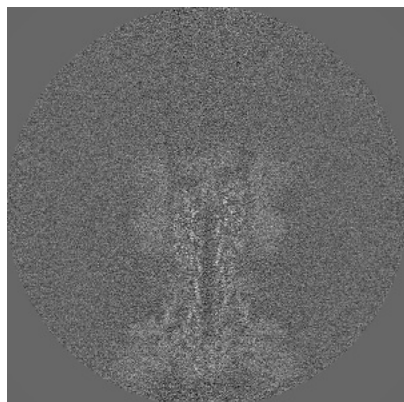


Y Index: 384

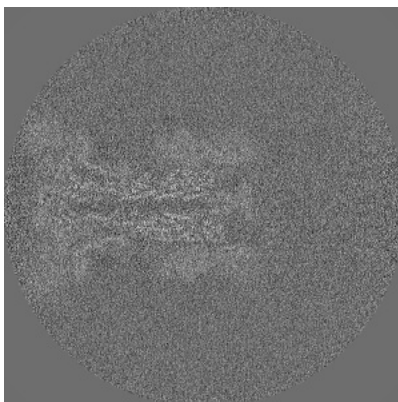


Z Index: 384

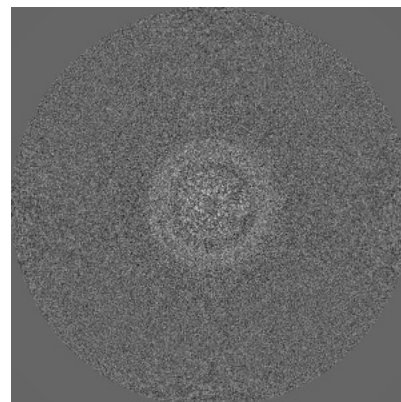
6.2.2 Raw map



X Index: 384



Y Index: 384

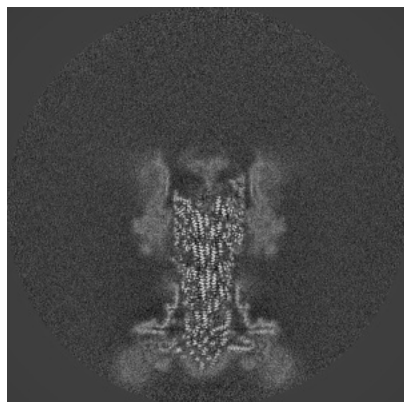


Z Index: 384

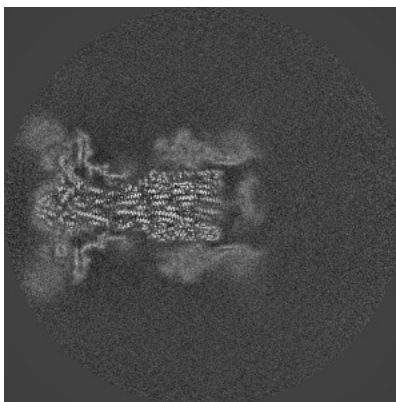
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

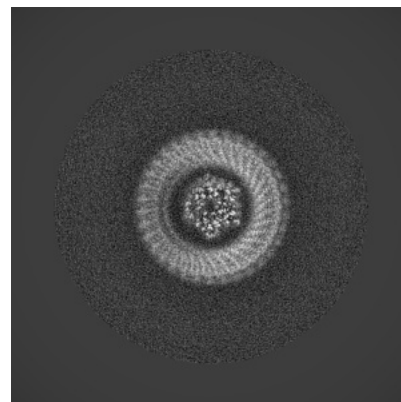
6.3.1 Primary map



X Index: 402

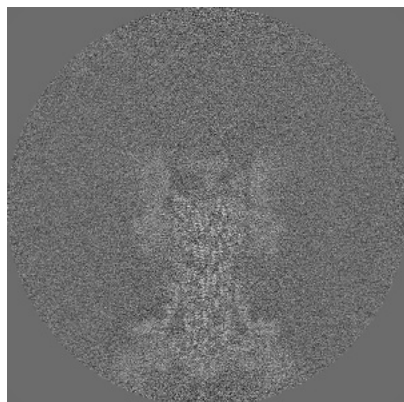


Y Index: 371

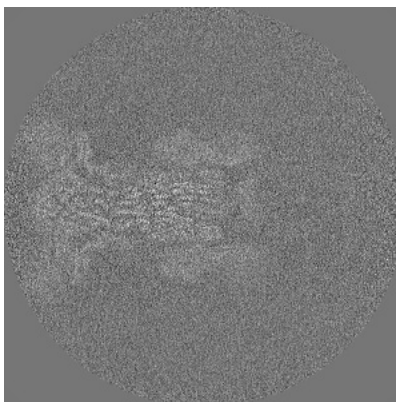


Z Index: 144

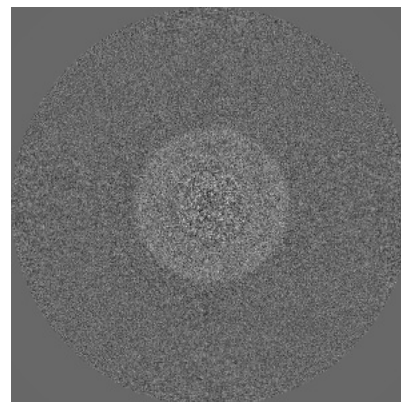
6.3.2 Raw map



X Index: 402



Y Index: 371

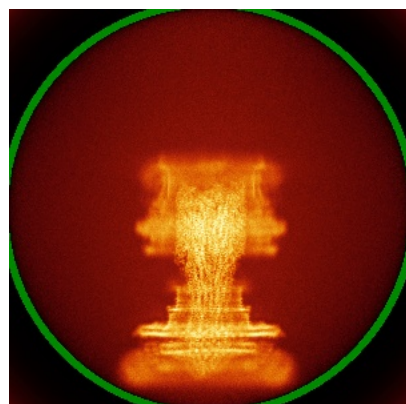


Z Index: 350

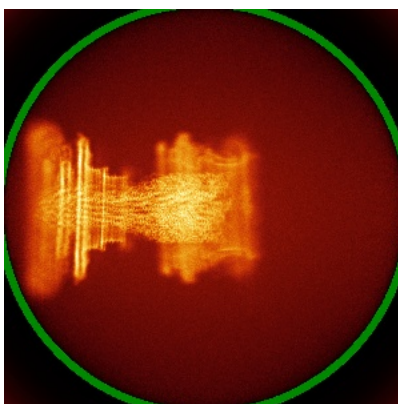
The images above show the largest variance slices of the map in three orthogonal directions.

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

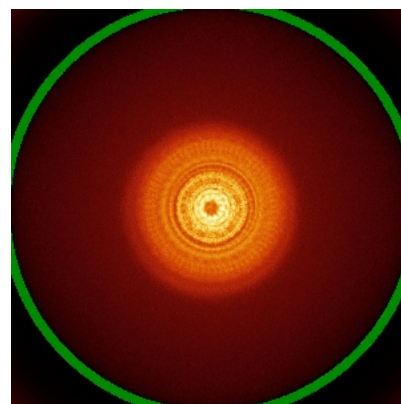
6.4.1 Primary map



X

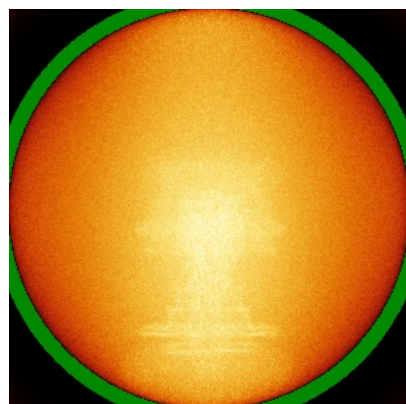


Y

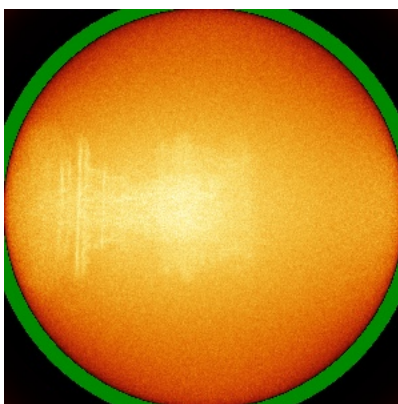


Z

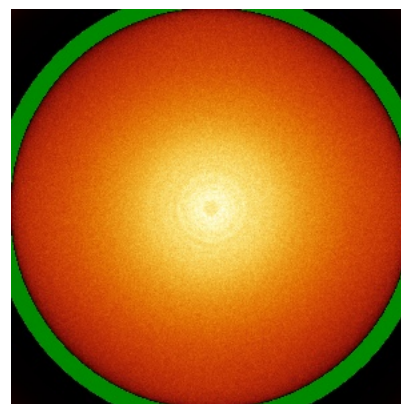
6.4.2 Raw map



X



Y

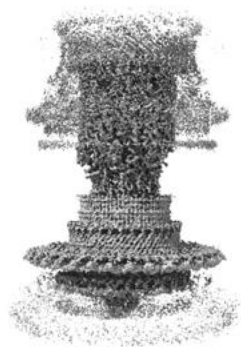


Z

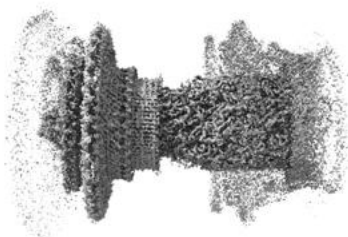
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

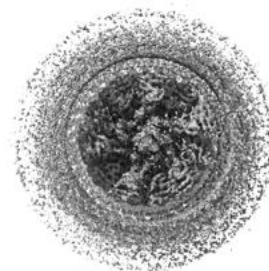
6.5.1 Primary map



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.

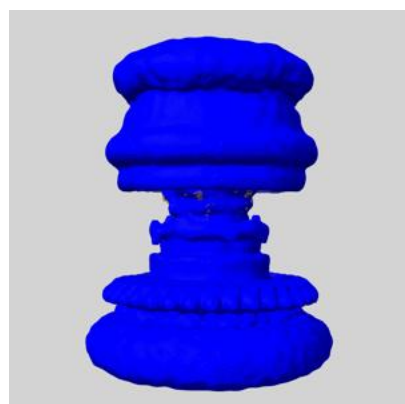
6.6 Mask visualisation [i](#)

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

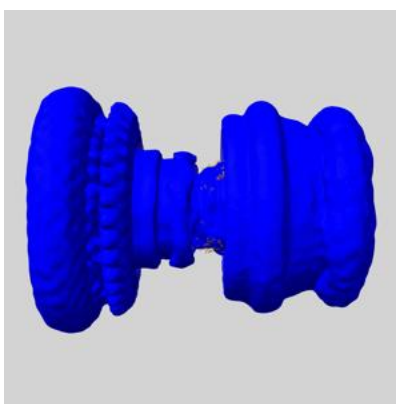
A mask typically either:

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

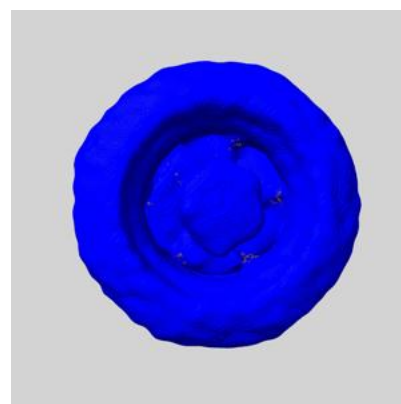
6.6.1 emd_12603_msk_1.map [i](#)



X



Y

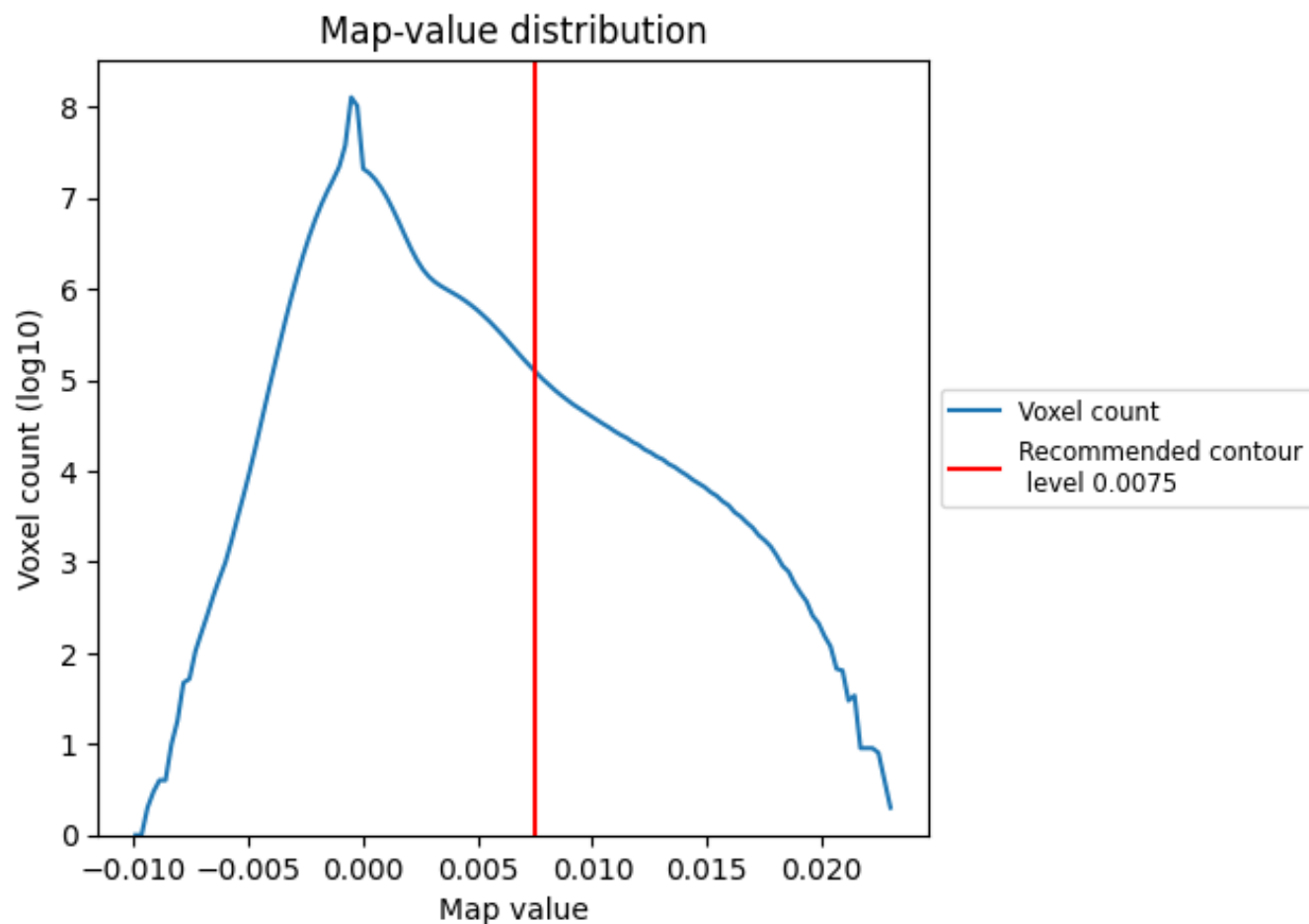


Z

7 Map analysis [i](#)

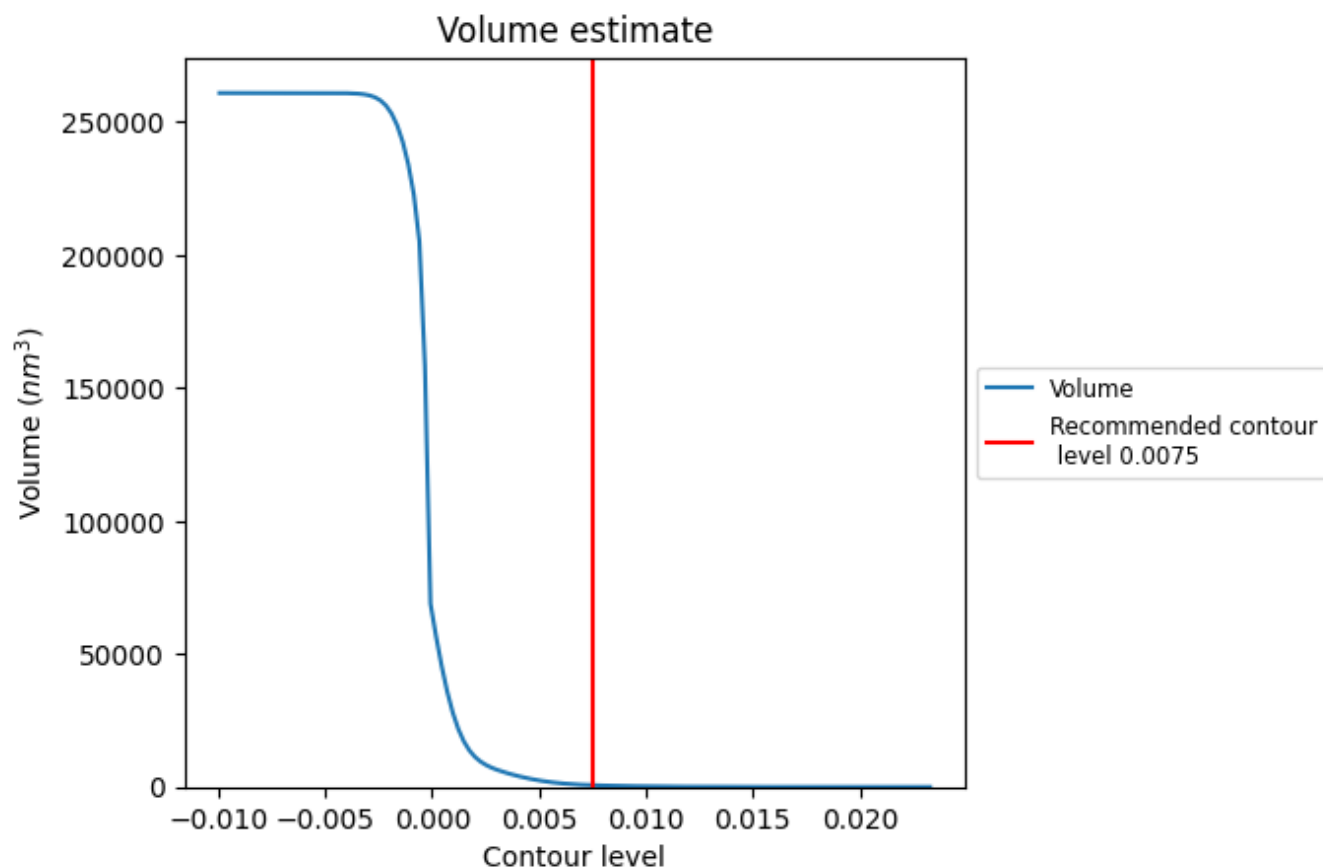
This section contains the results of statistical analysis of the map.

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.

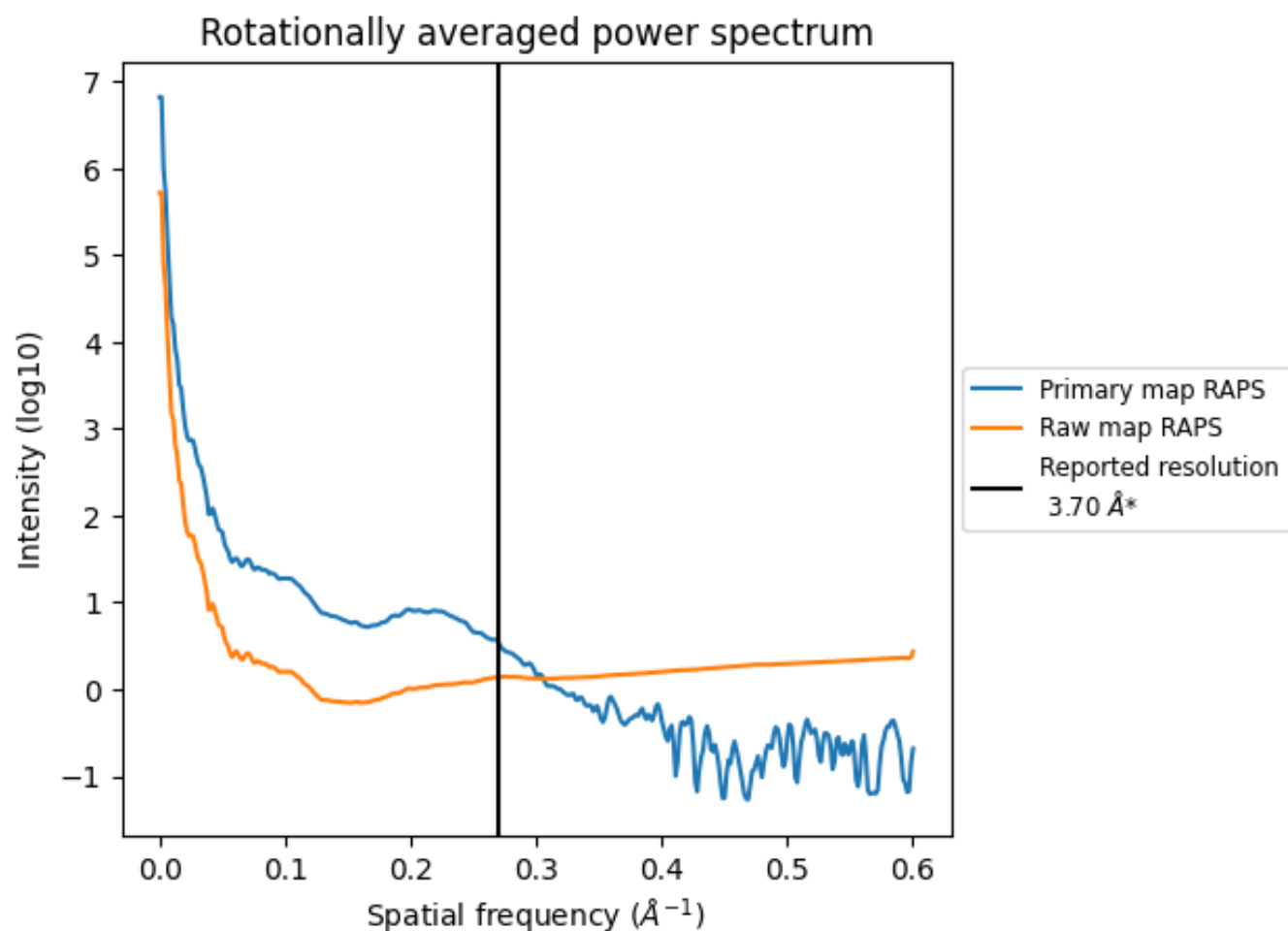
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 648 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 ⓘ

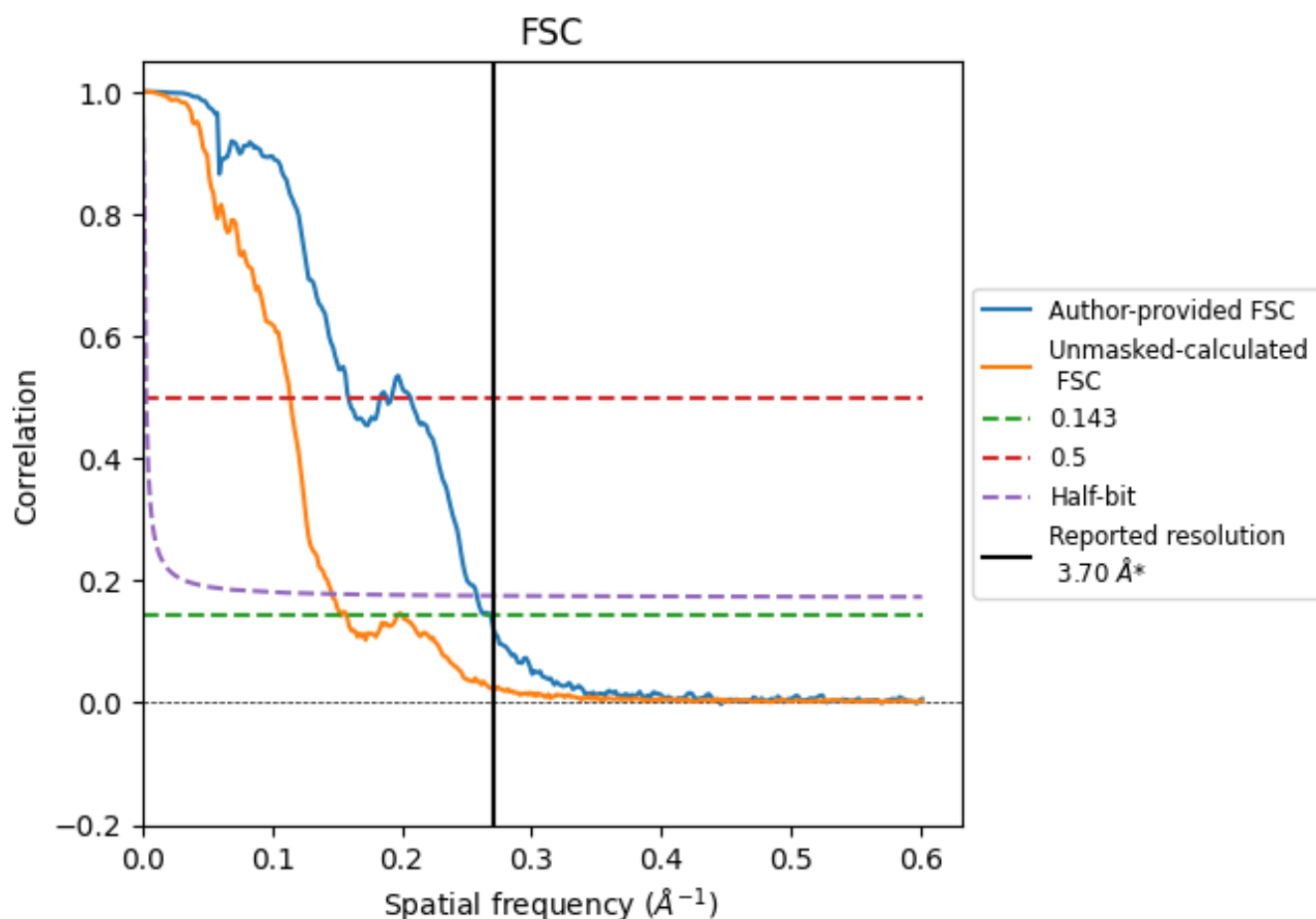


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

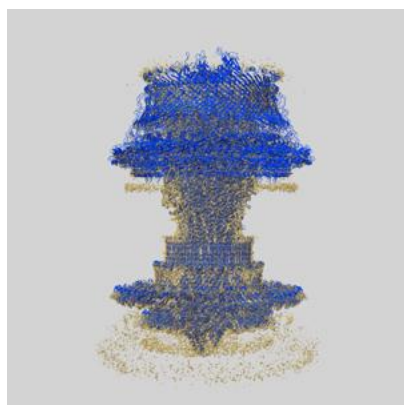
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.73	6.30	3.88
Unmasked-calculated*	6.53	8.78	6.84

*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 %

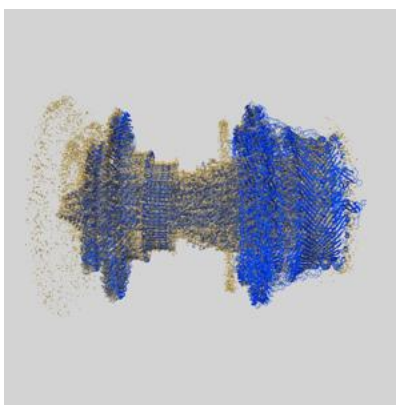
9 Map-model fit [i](#)

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](#).

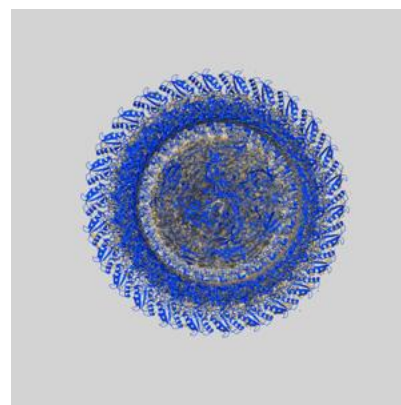
9.1 Map-model overlay [i](#)



X



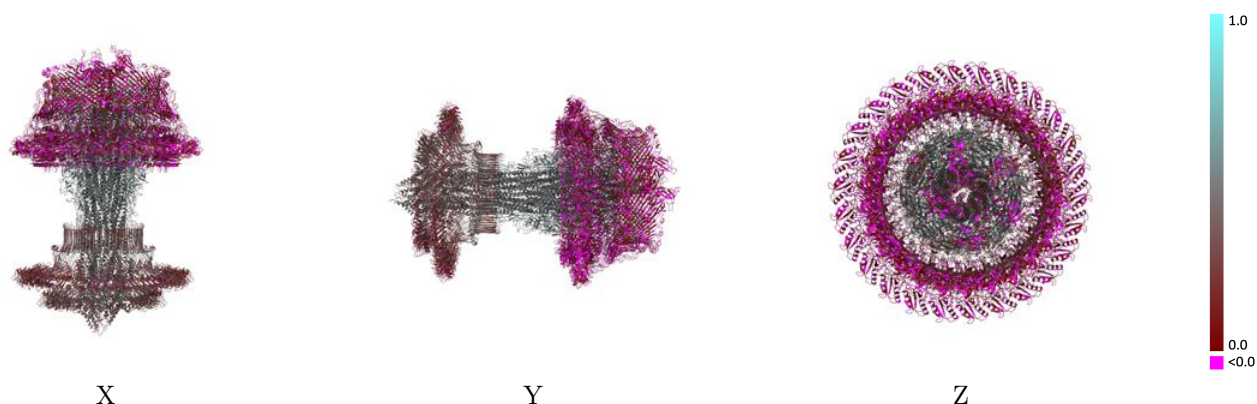
Y



Z

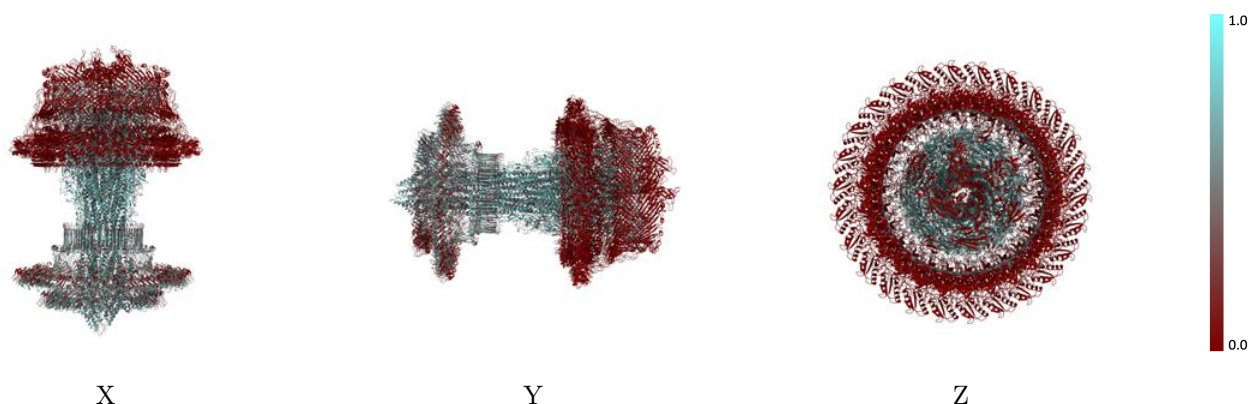
The images above show the 3D surface view of the map at the recommended contour level 0.0075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



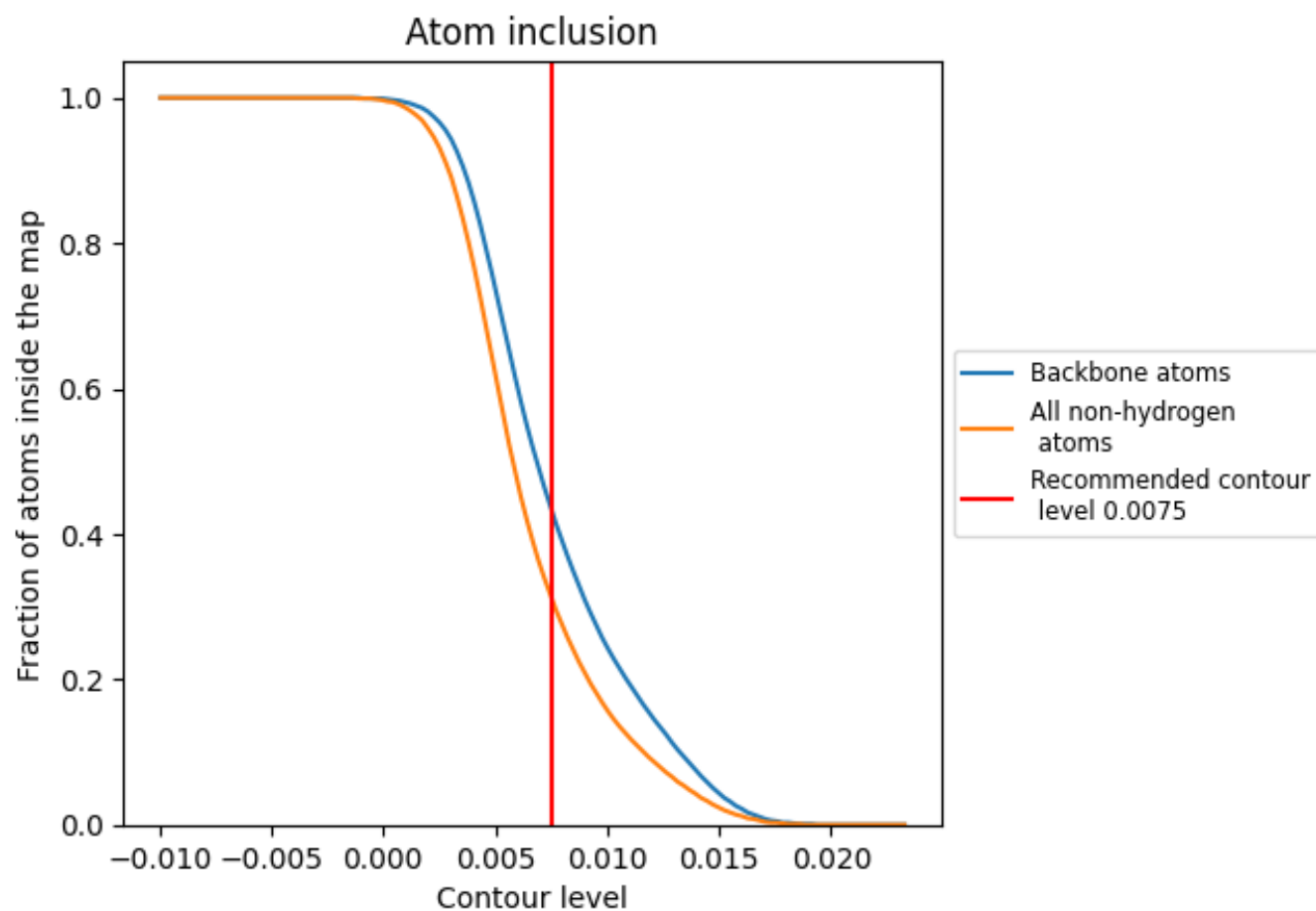
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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