



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:14 AM UTC

PDB ID : 7E80 / pdb_00007e80
EMDB ID : EMD-31006
Title : Cryo-EM structure of the flagellar rod with hook and export apparatus from Salmonella
Authors : Tan, J.X.; Chang, S.H.; Wang, X.F.; Xu, C.H.; Zhou, Y.; Zhang, X.; Zhu, Y.Q.
Deposited on : 2021-02-28
Resolution : 3.67 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

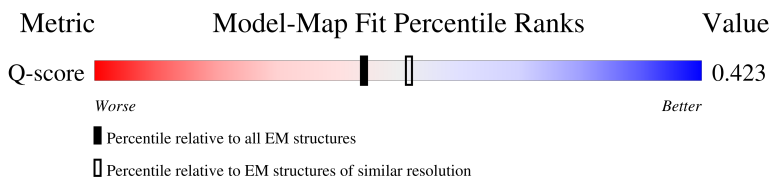
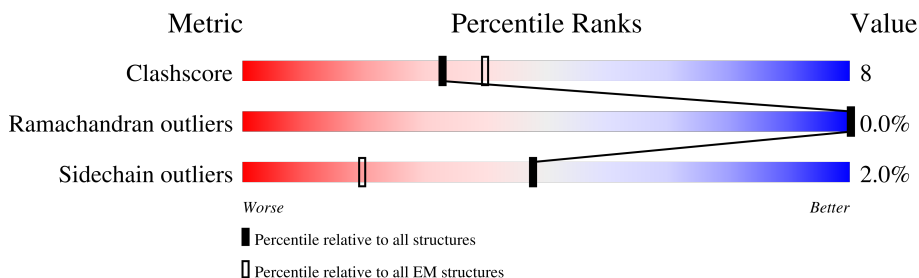
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.67 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.



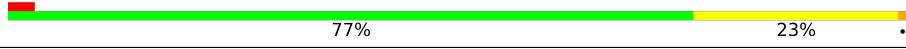
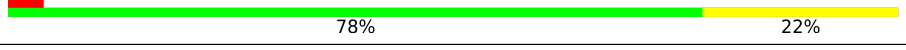
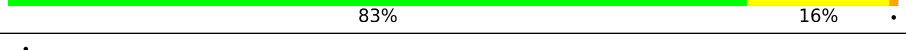
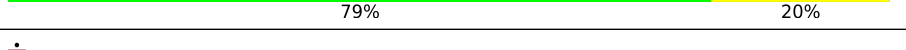
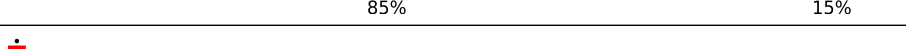
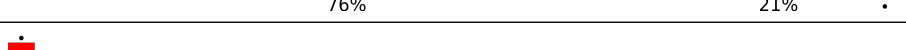
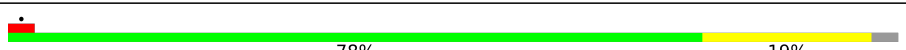
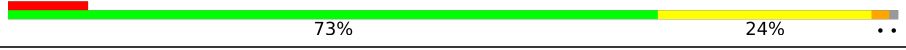
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11424 (3.17 - 4.17)

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

Mol	Chain	Length	Quality of chain
1	A	260	 8% 78% 22%
1	B	260	 8% 75% 25%
1	C	260	 5% 77% 22%
1	D	260	 5% 77% 23%

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Mol	Chain	Length	Quality of chain
1	E	260	 78%21%
1	F	260	 78%22%
1	G	260	 77%23%
1	H	260	 78%22%
1	I	260	 81%19%
1	J	260	 82%17%
1	K	260	 83%16%
1	L	260	 79%20%
1	M	260	 85%15%
1	N	260	 76%21%
1	O	260	 78%18%
1	P	260	 79%17%5%
1	Q	260	 77%17%5%
1	R	260	 77%18%
1	S	260	 78%17%5%
1	T	260	 78%19%
1	U	260	 78%21%
1	V	260	 75%24%
1	W	260	 78%20%
1	X	260	 6%83%17%
2	a	251	 78%21%
2	b	251	 9%73%24%
2	c	251	 77%22%
2	d	251	 79%20%
2	e	251	 6%81%18%

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Mol	Chain	Length	Quality of chain
3	0	15	
3	1	15	
3	2	15	
3	3	15	
3	4	15	
4	5	21	
4	6	21	
4	7	21	
4	8	21	
4	9	21	
5	f	134	
5	g	134	
5	h	134	
5	i	134	
5	j	134	
5	p	134	
6	k	138	
6	l	138	
6	m	138	
6	n	138	
6	o	138	
7	q	104	
7	r	104	
7	s	104	
7	t	104	

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Mol	Chain	Length	Quality of chain
7	u	104	
7	v	104	
8	DA	403	
8	DB	403	
8	DC	403	
8	DD	403	
8	DE	403	
8	DF	403	
8	DG	403	
8	DH	403	
8	DI	403	
8	DJ	403	
8	DK	403	
9	CE	264	
10	CA	89	
10	CB	89	
10	CC	89	
10	CD	89	
11	CF	245	
11	w	245	
11	x	245	
11	y	245	
11	z	245	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 114468 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Flagellar basal-body rod protein FlgG.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

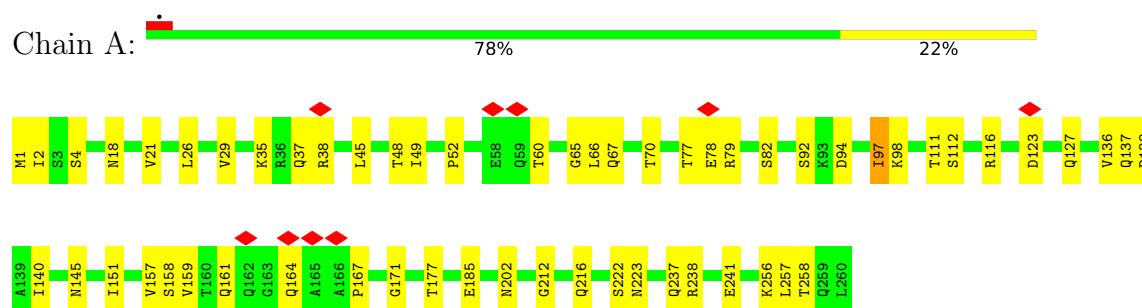
- Molecule 11 is a protein called Flagellar biosynthetic protein FliP.

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

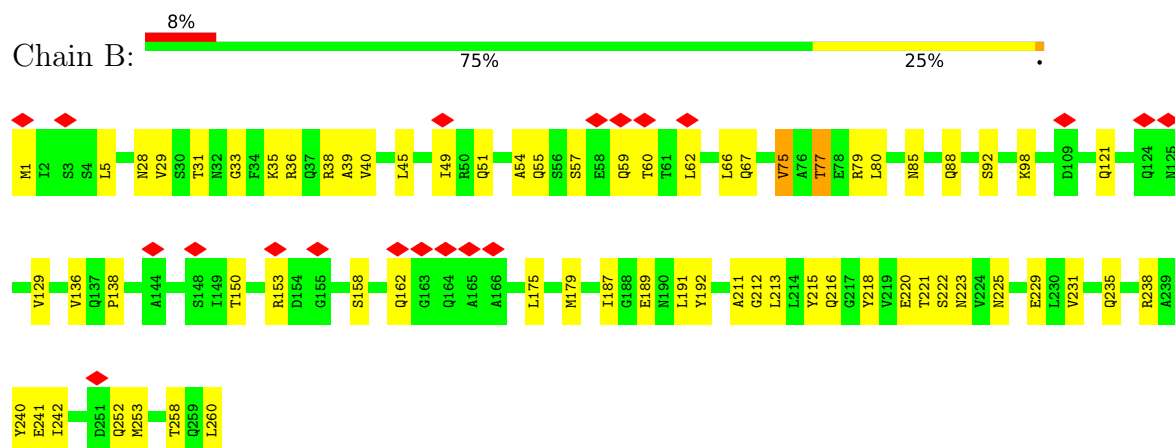
3 Residue-property plots [i](#)

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

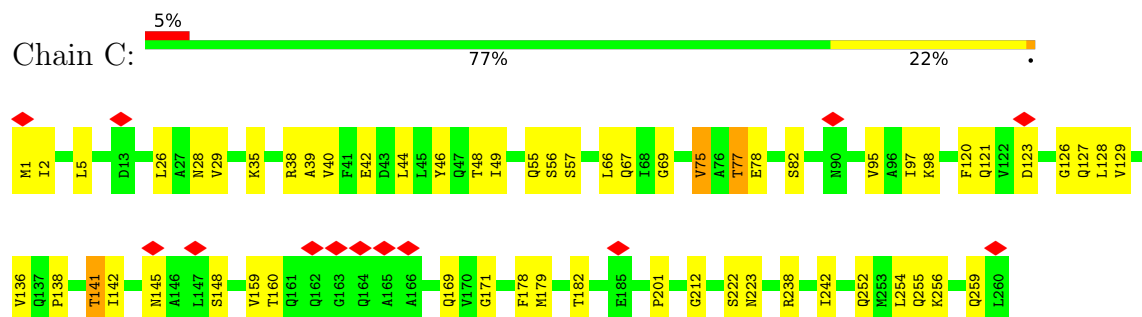
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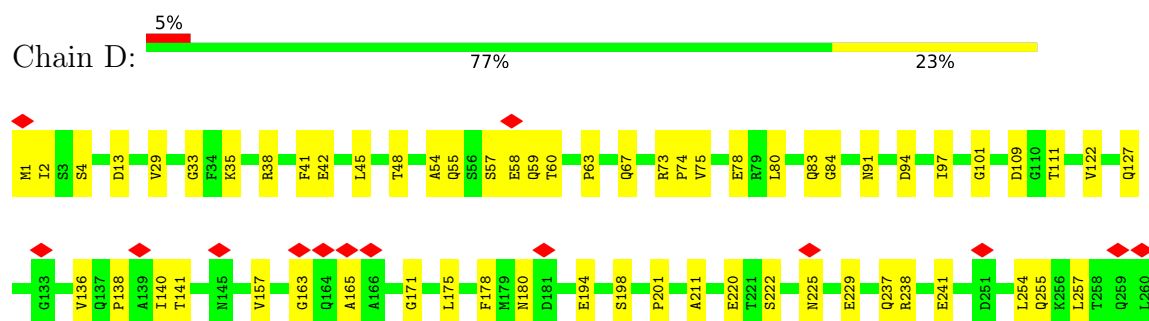
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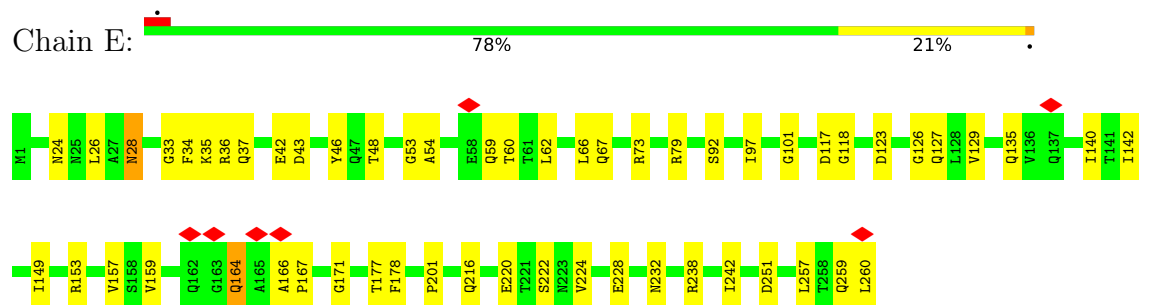
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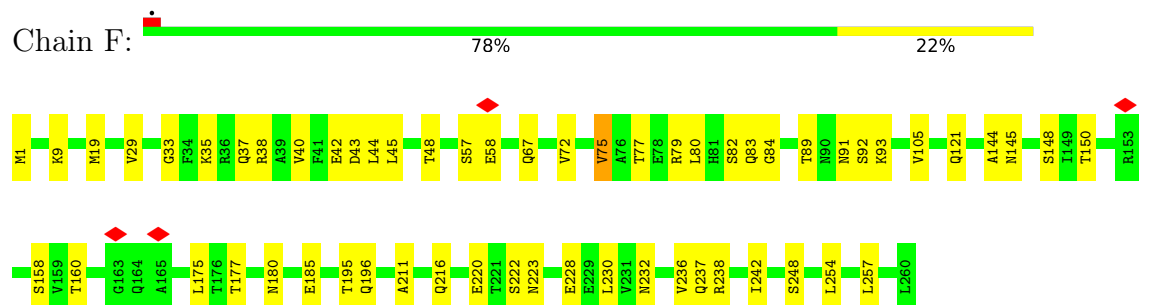
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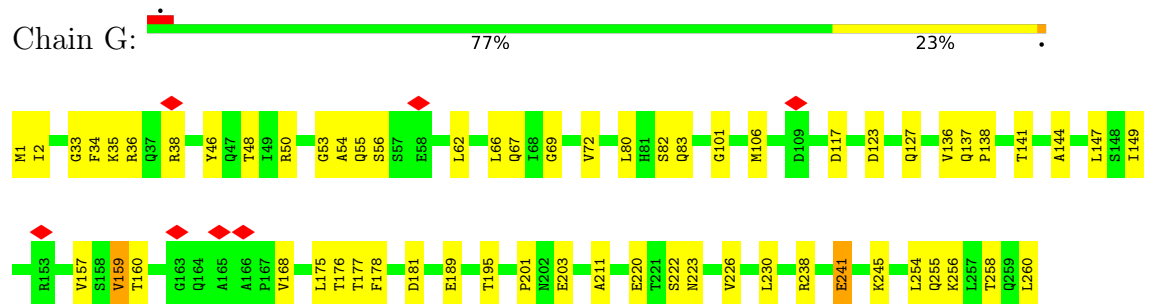
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- Molecule 1: Flagellar basal-body rod protein FlgG

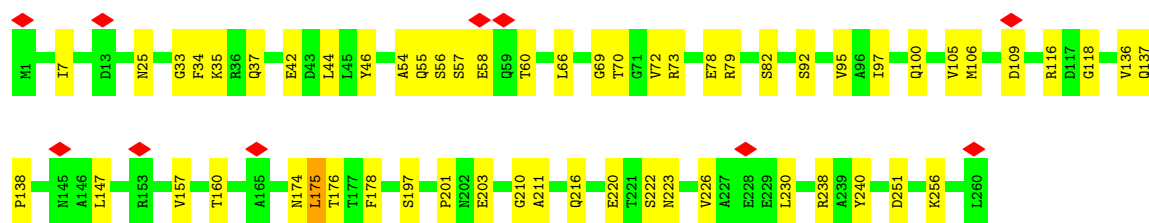


- Molecule 1: Flagellar basal-body rod protein FlgG

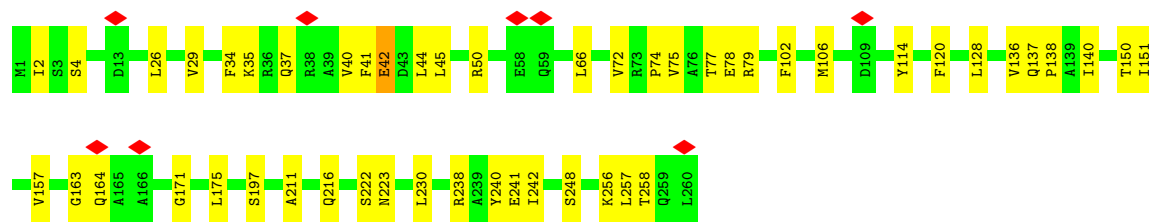
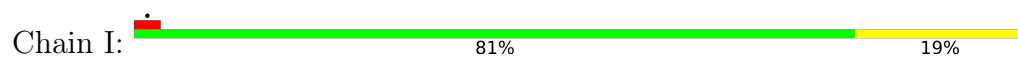


- Molecule 1: Flagellar basal-body rod protein FlgG

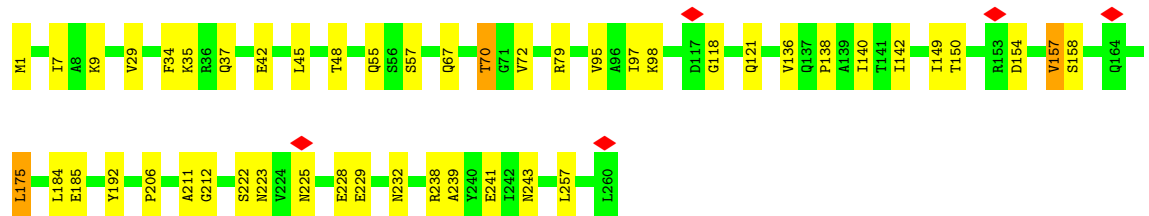
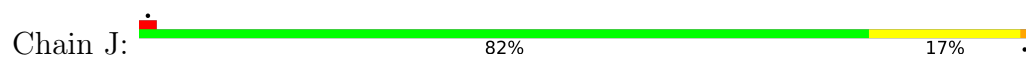




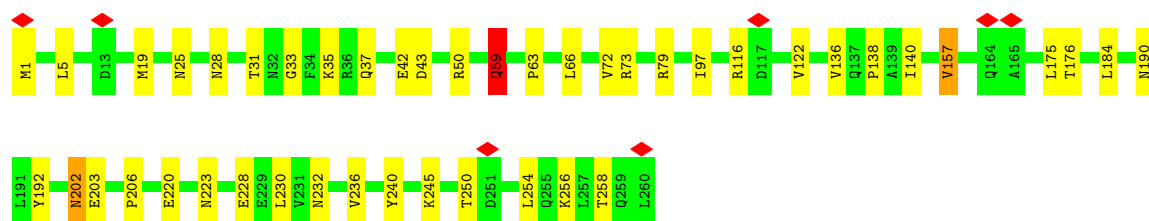
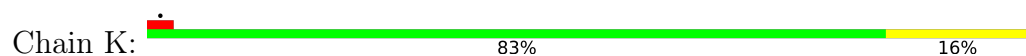
- Molecule 1: Flagellar basal-body rod protein FlgG



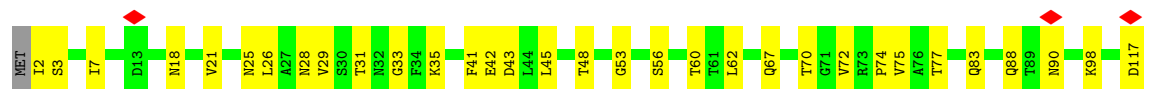
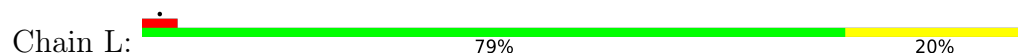
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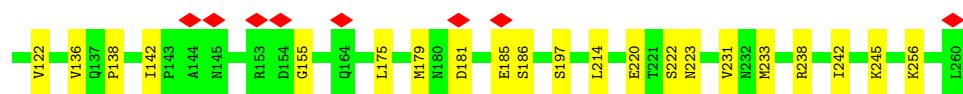


- Molecule 1: Flagellar basal-body rod protein FlgG

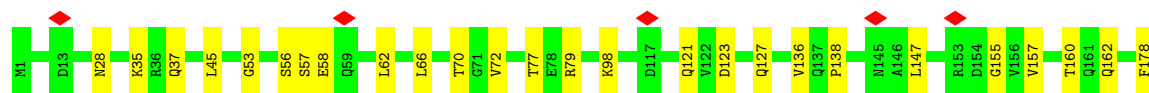
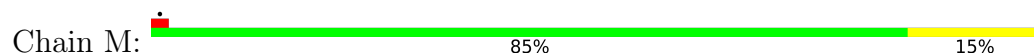


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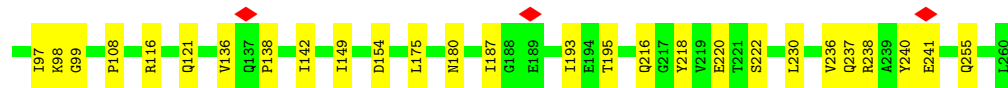
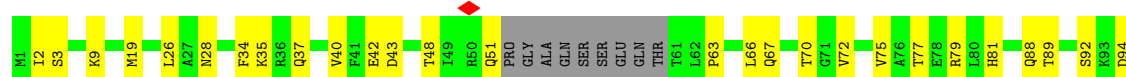
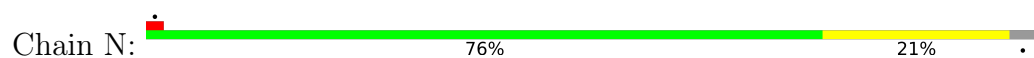




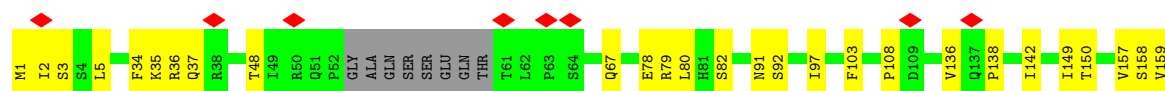
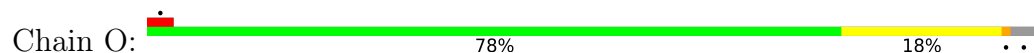
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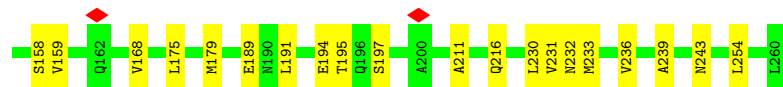
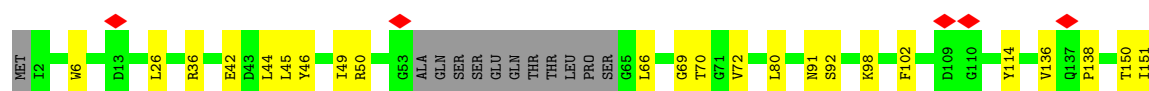
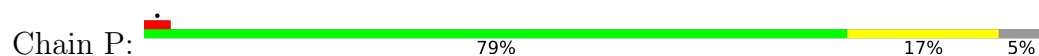
- Molecule 1: Flagellar basal-body rod protein FlgG



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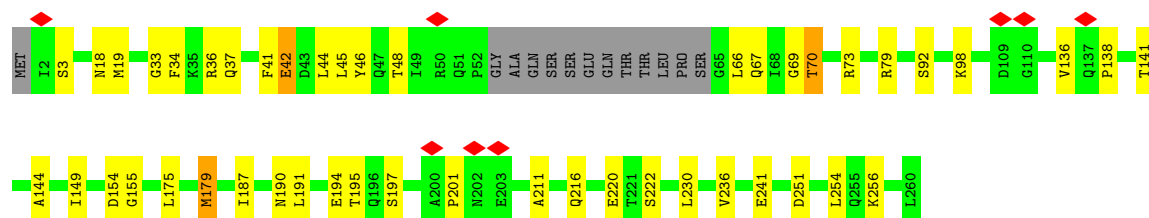


- Molecule 1: Flagellar basal-body rod protein FlgG



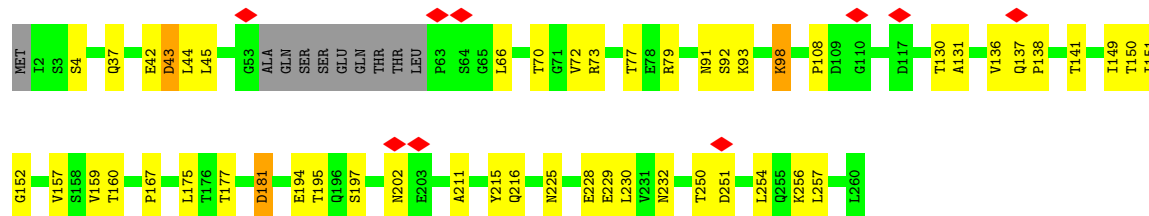
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain Q:  77% 17% 5%



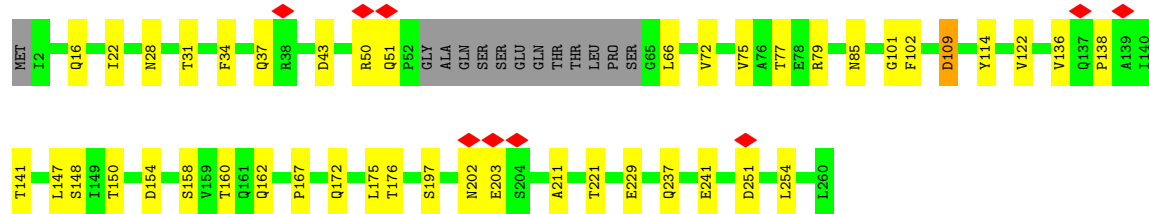
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain R:  77% 18% 5%



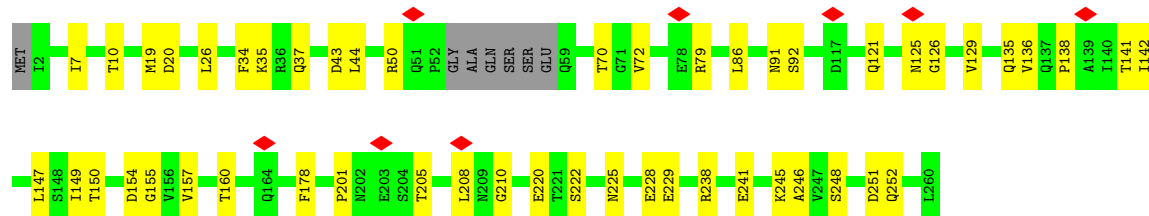
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain S:  78% 17% 5%



- Molecule 1: Flagellar basal-body rod protein FlgG

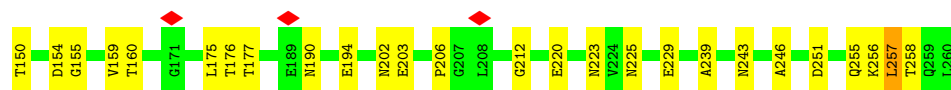
Chain T:  78% 19% 3%



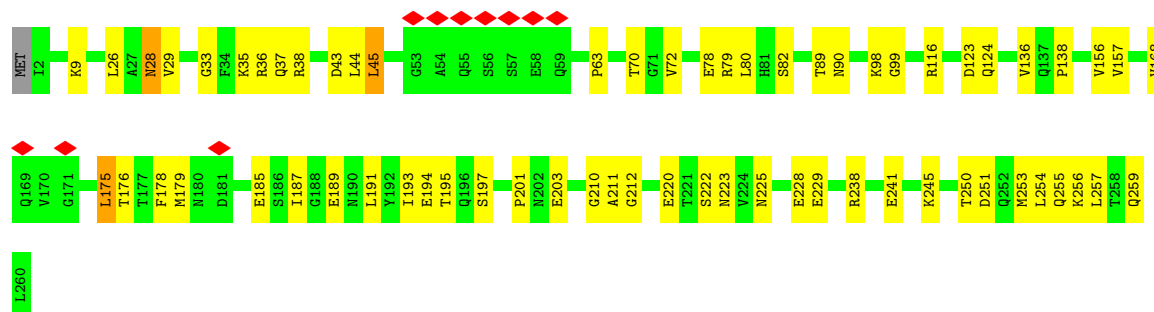
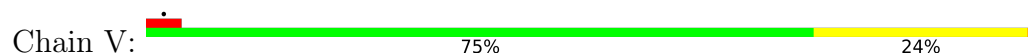
- Molecule 1: Flagellar basal-body rod protein FlgG

Chain U:  78% 21% 1%

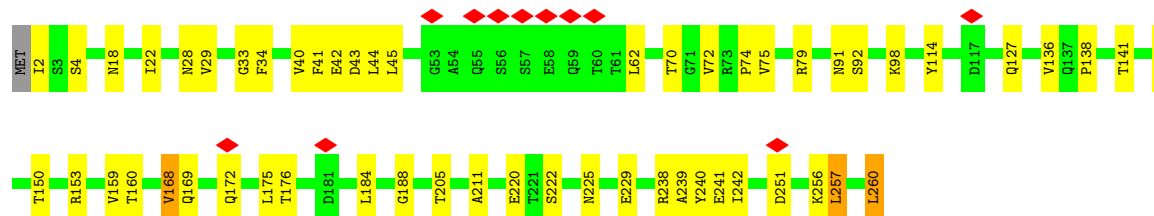
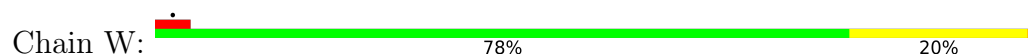




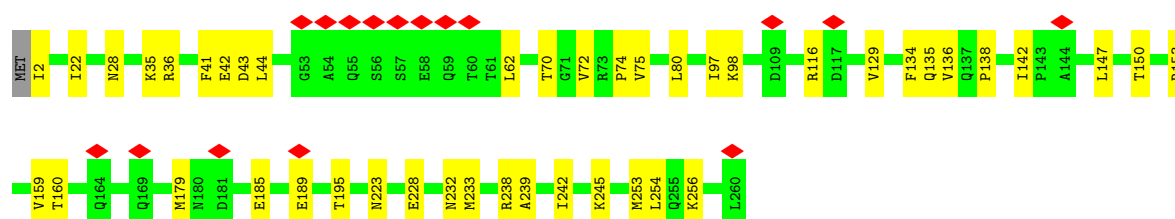
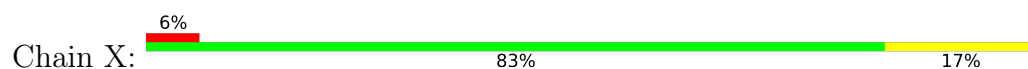
- Molecule 1: Flagellar basal-body rod protein FlgG



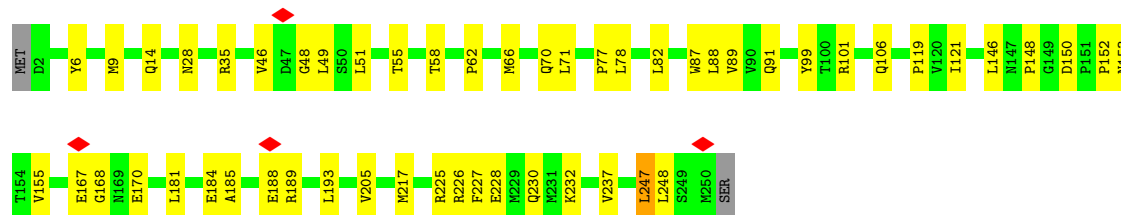
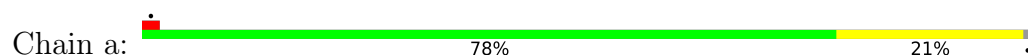
- Molecule 1: Flagellar basal-body rod protein FlgG



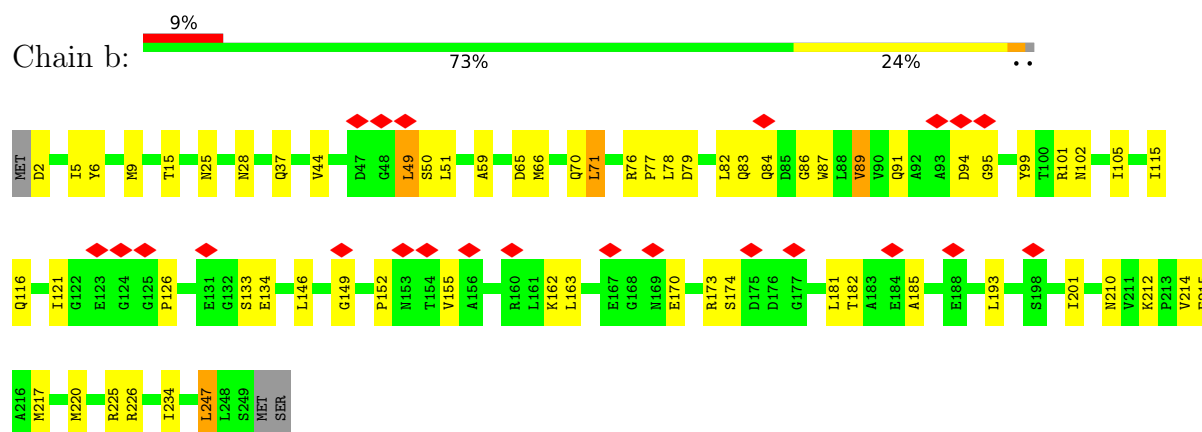
- Molecule 1: Flagellar basal-body rod protein FlgG



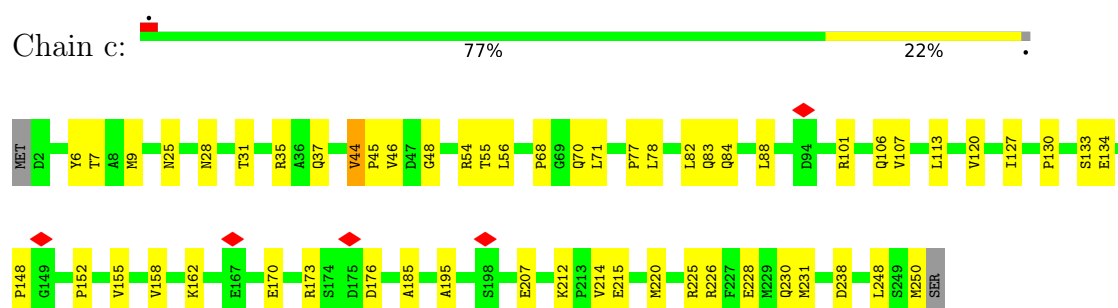
- Molecule 2: Flagellar basal-body rod protein FlgF



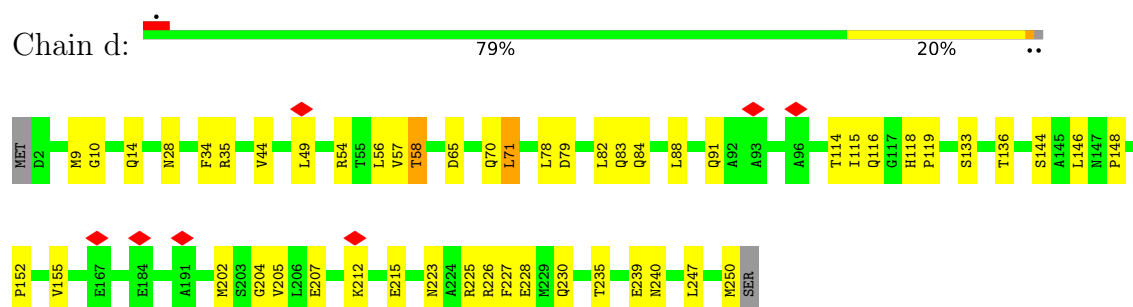
- Molecule 2: Flagellar basal-body rod protein FlgF



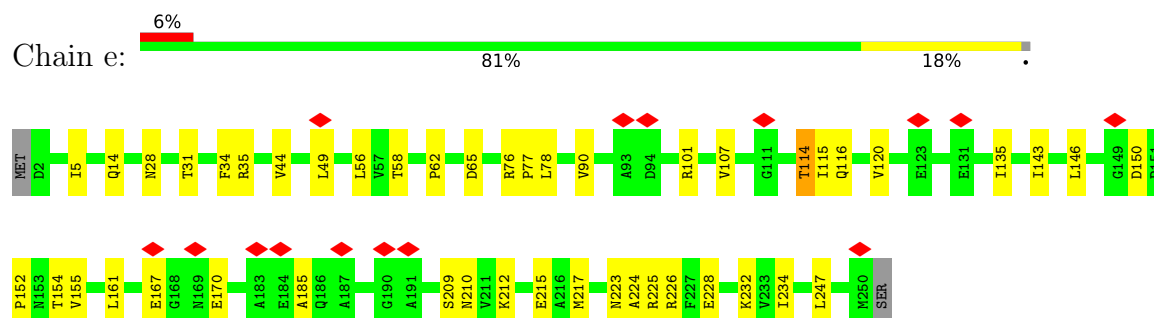
- Molecule 2: Flagellar basal-body rod protein FlgF



- Molecule 2: Flagellar basal-body rod protein FlgF



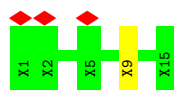
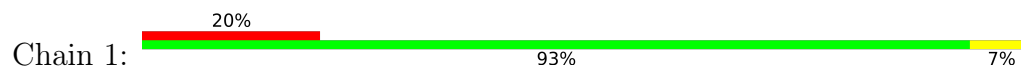
- Molecule 2: Flagellar basal-body rod protein FlgF



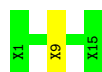
- Molecule 3: Flagellar MS ring L2



- Molecule 3: Flagellar MS ring L2



- Molecule 3: Flagellar MS ring L2

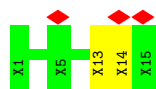
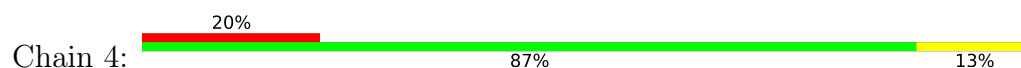


- Molecule 3: Flagellar MS ring L2

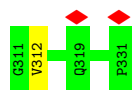


There are no outlier residues recorded for this chain.

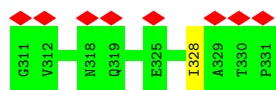
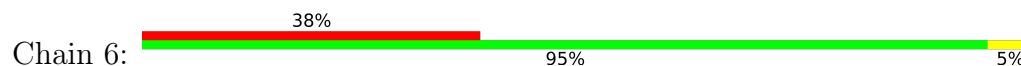
- Molecule 3: Flagellar MS ring L2



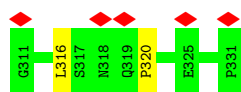
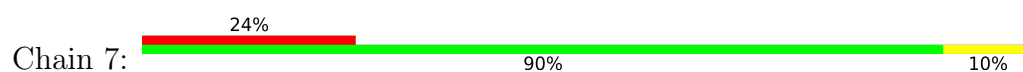
- Molecule 4: Flagellar MS ring L1



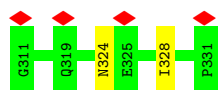
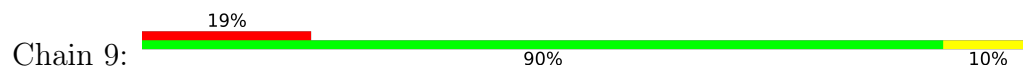
- Molecule 4: Flagellar MS ring L1



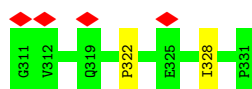
- Molecule 4: Flagellar MS ring L1



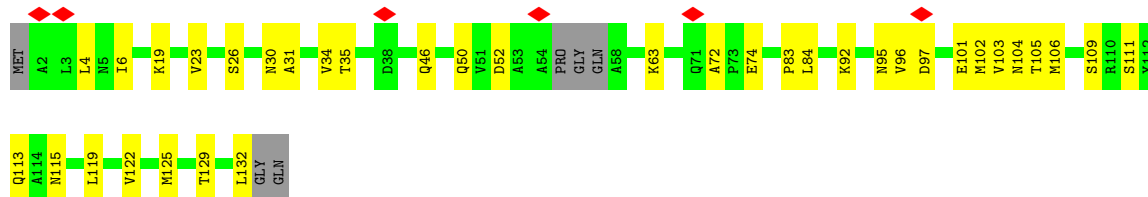
- Molecule 4: Flagellar MS ring L1



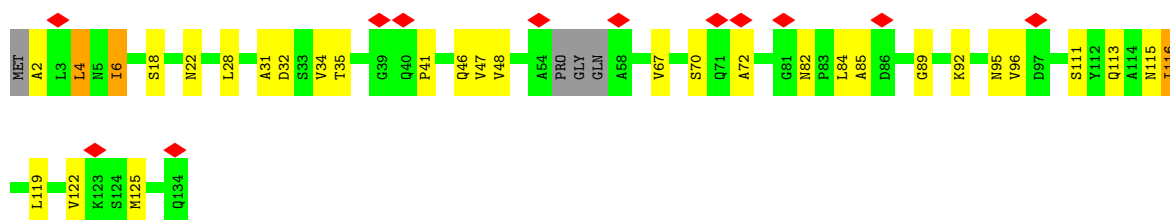
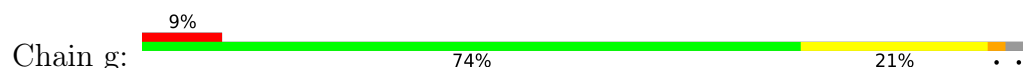
- Molecule 4: Flagellar MS ring L1



- Molecule 5: Flagellar basal-body rod protein FlgC



- Molecule 5: Flagellar basal-body rod protein FlgC



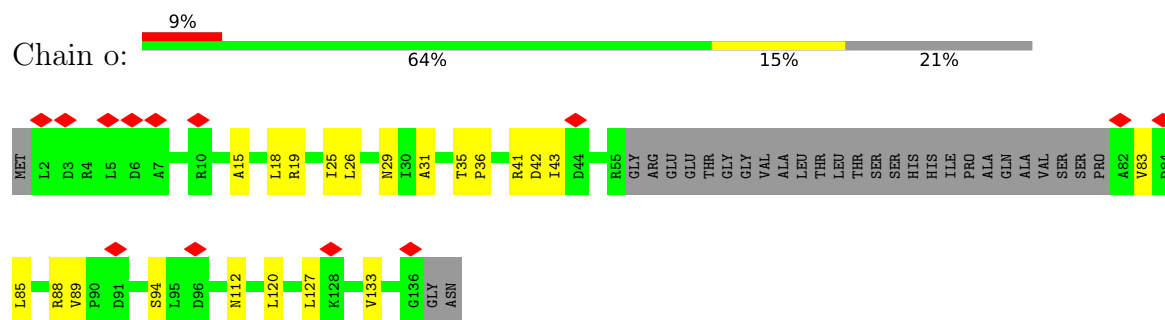
- Molecule 5: Flagellar basal-body rod protein FlgC



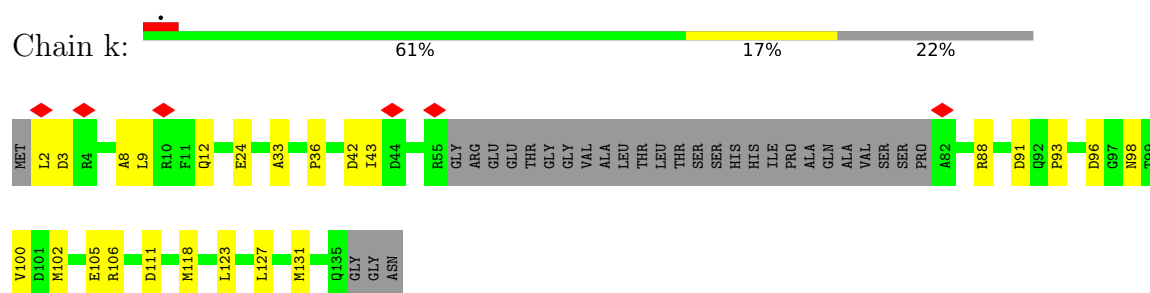




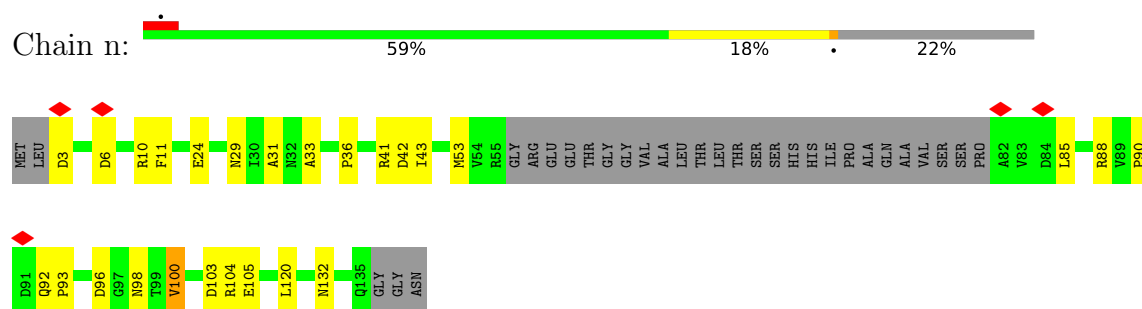
- Molecule 6: Flagellar basal body rod protein FlgB



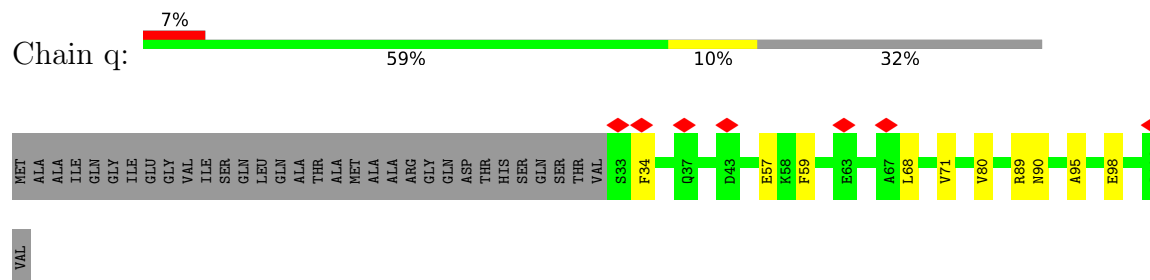
- Molecule 6: Flagellar basal body rod protein FlgB



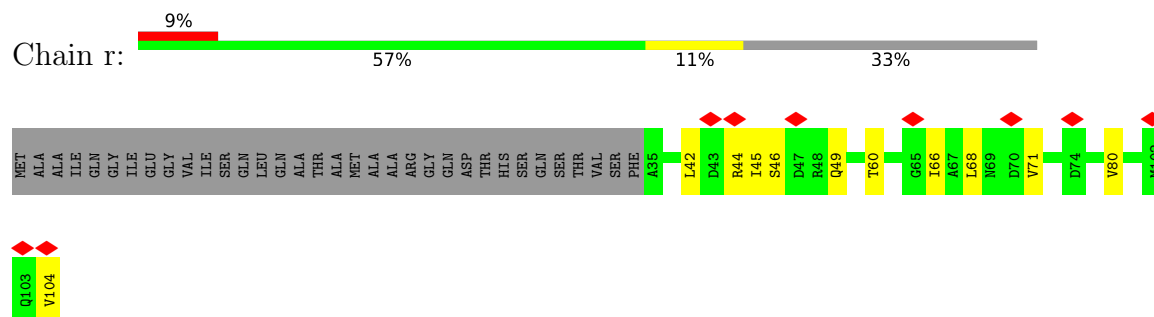
- Molecule 6: Flagellar basal body rod protein FlgB



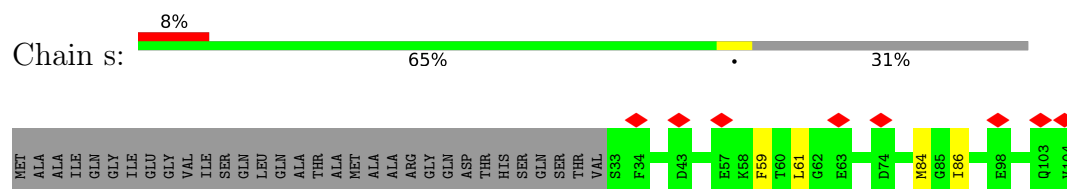
- Molecule 7: Flagellar hook-basal body complex protein FliE



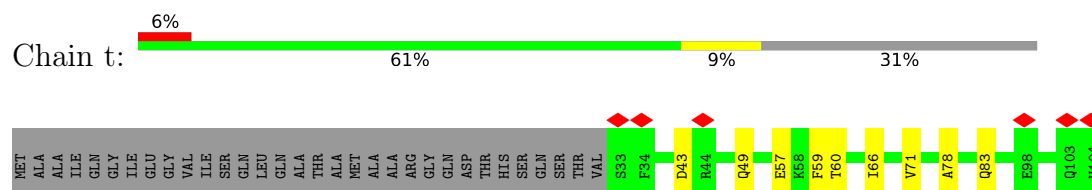
- Molecule 7: Flagellar hook-basal body complex protein FliE



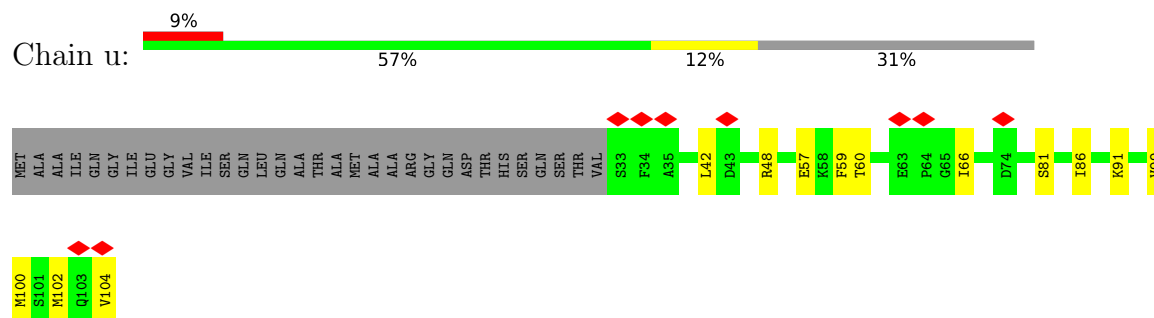
- Molecule 7: Flagellar hook-basal body complex protein FliE



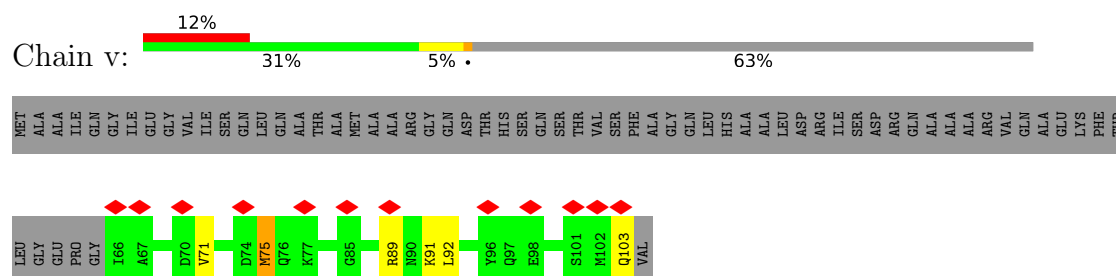
- Molecule 7: Flagellar hook-basal body complex protein FliE



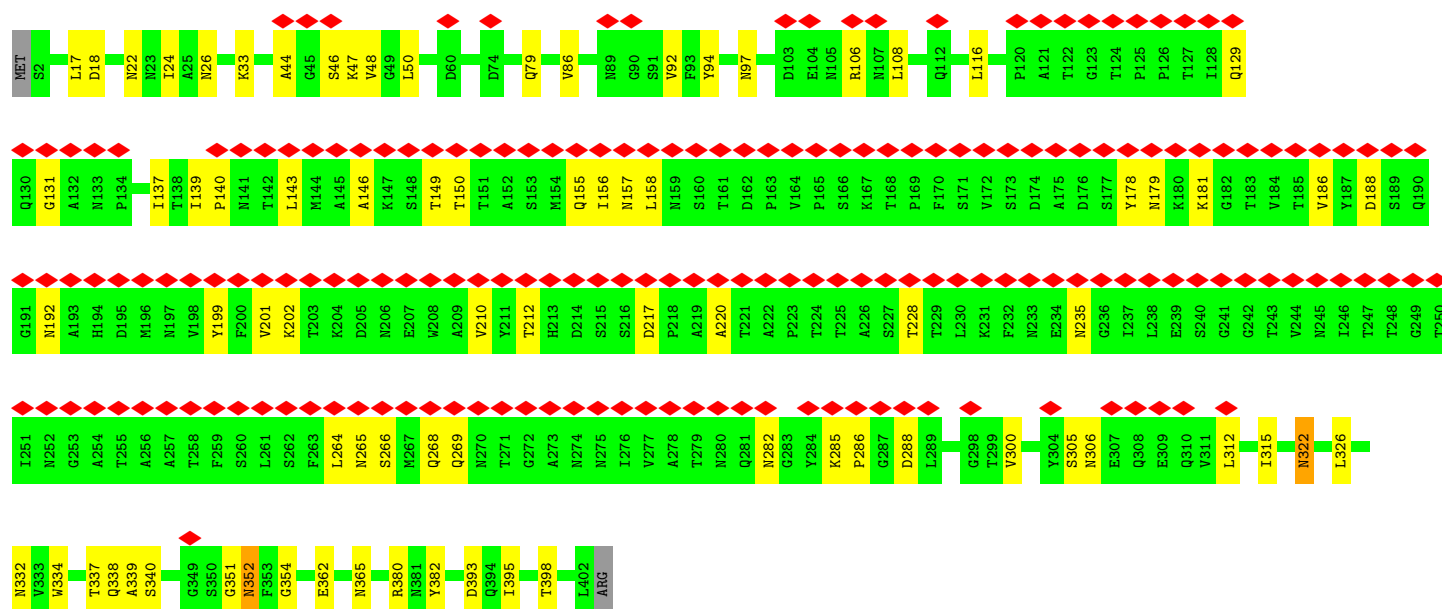
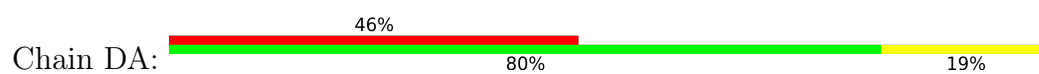
- Molecule 7: Flagellar hook-basal body complex protein FliE



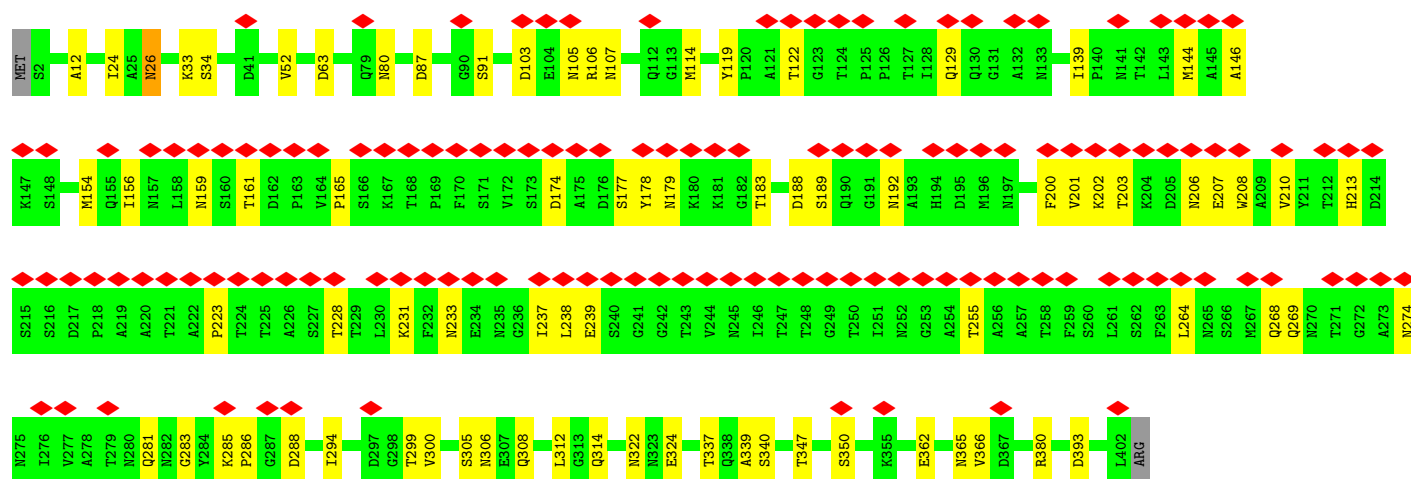
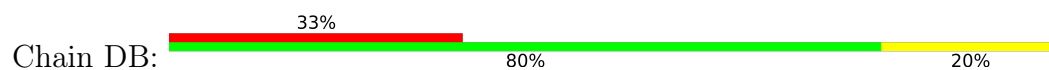
- Molecule 7: Flagellar hook-basal body complex protein FliE



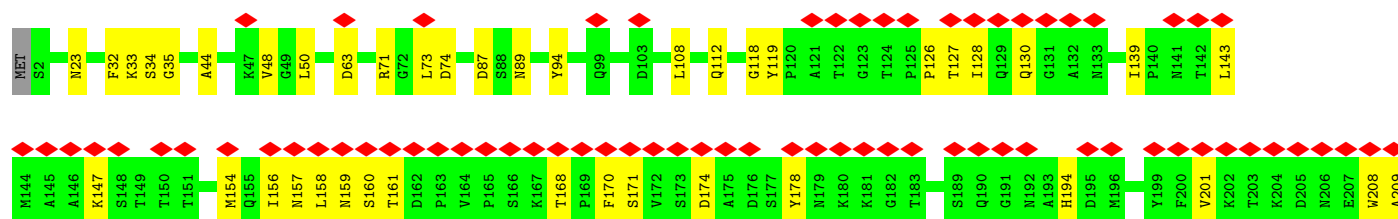
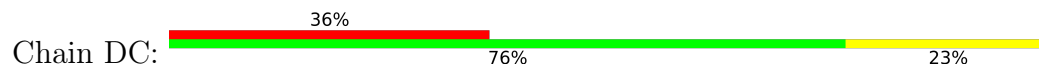
- Molecule 8: Flagellar hook protein FlgE

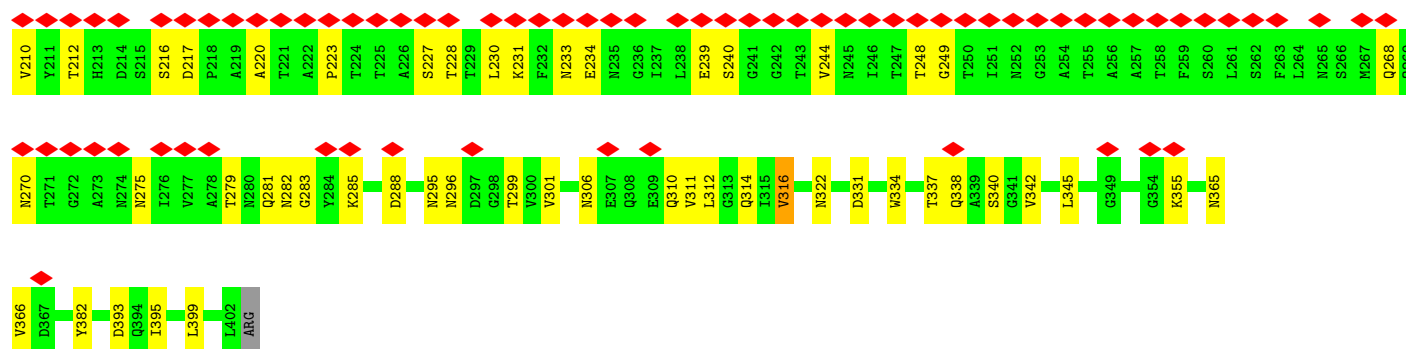


• Molecule 8: Flagellar hook protein FlgE

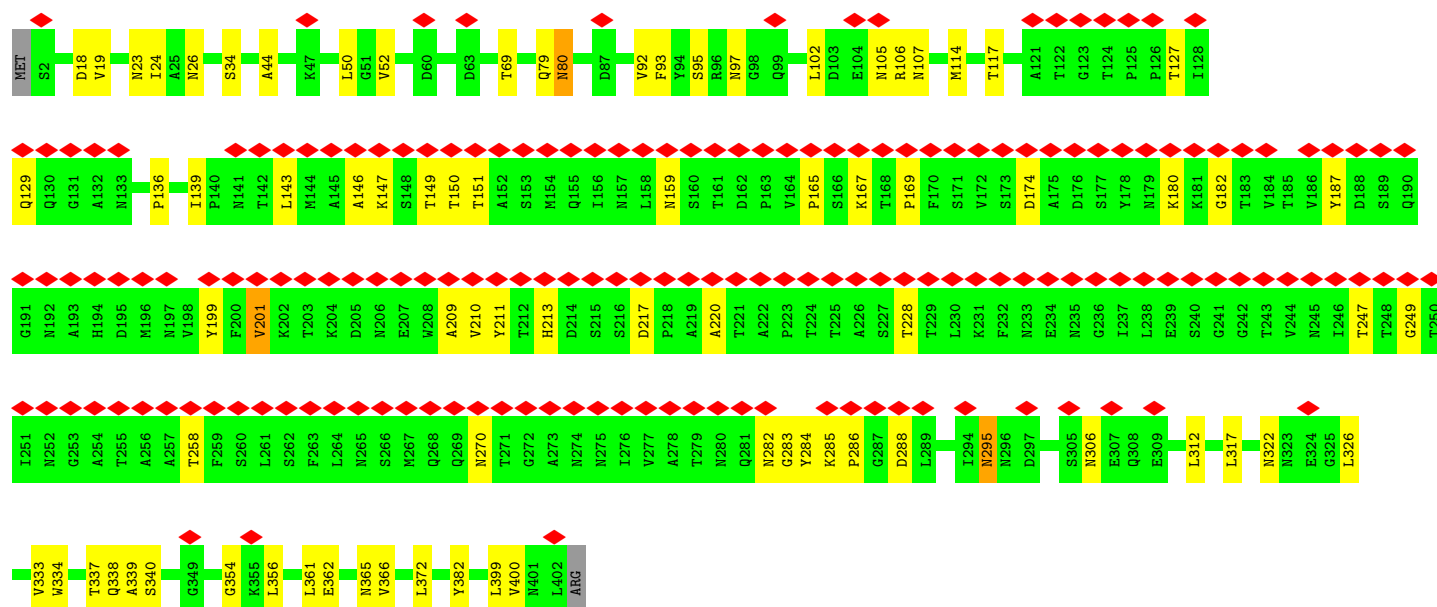
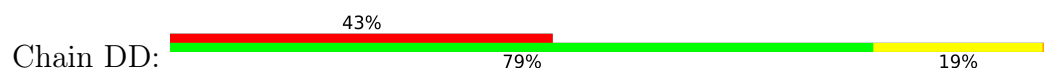


• Molecule 8: Flagellar hook protein FlgE

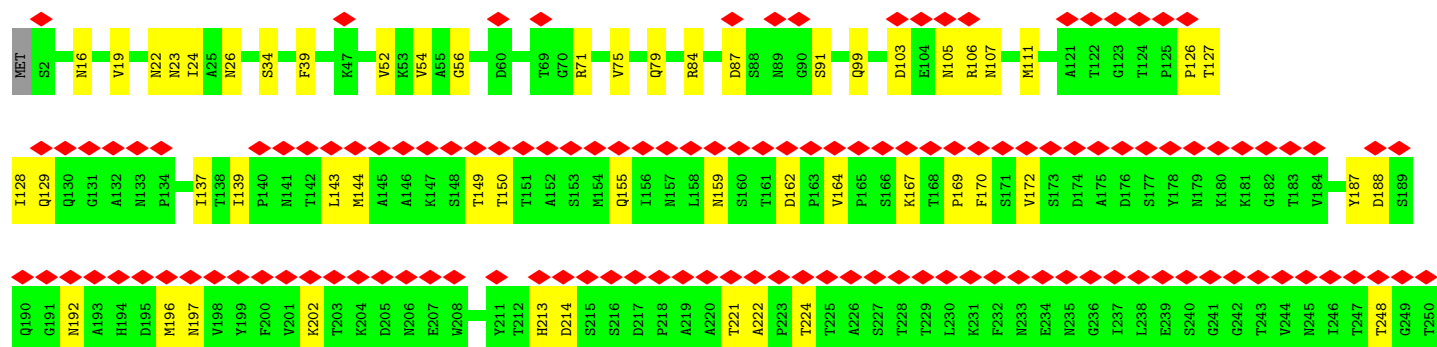
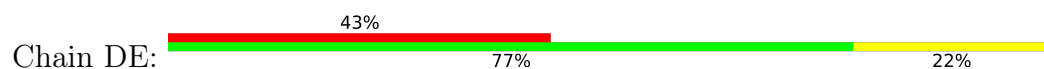


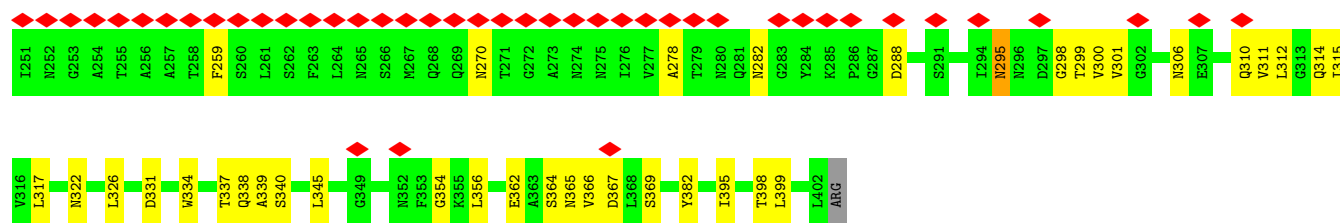


• Molecule 8: Flagellar hook protein FlgE

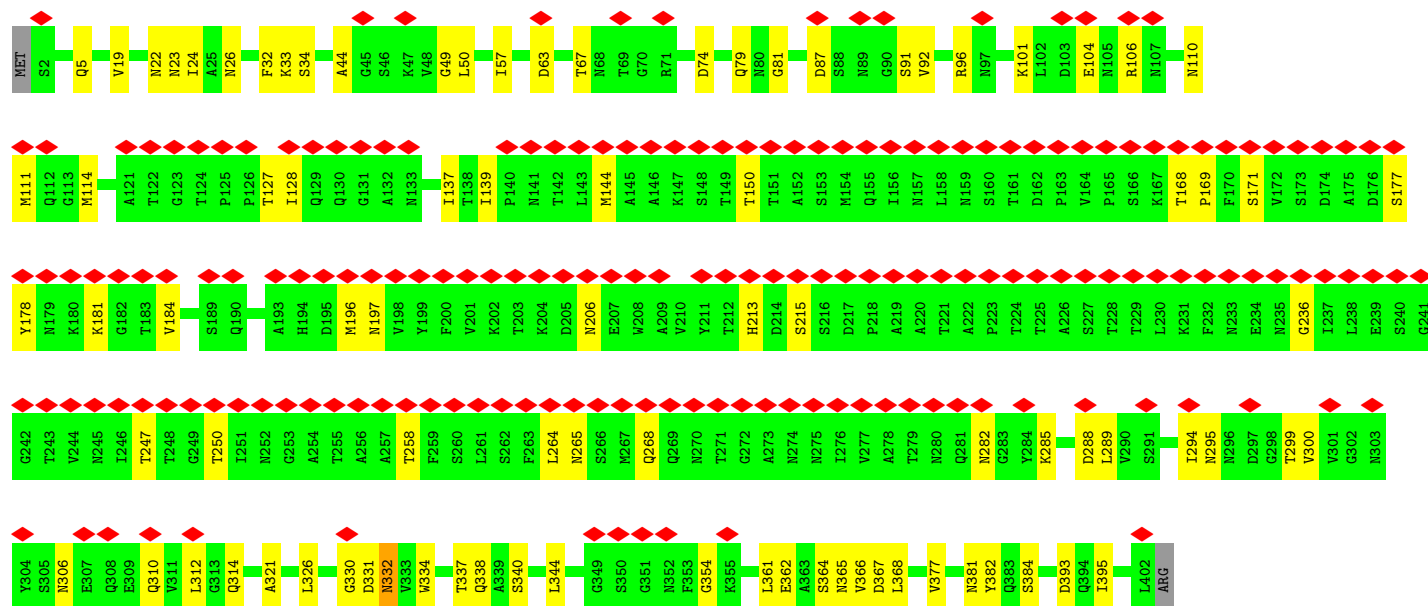
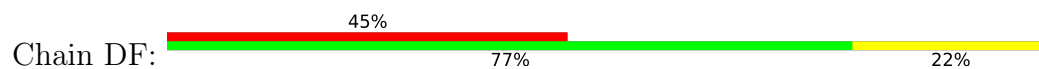


• Molecule 8: Flagellar hook protein FlgE

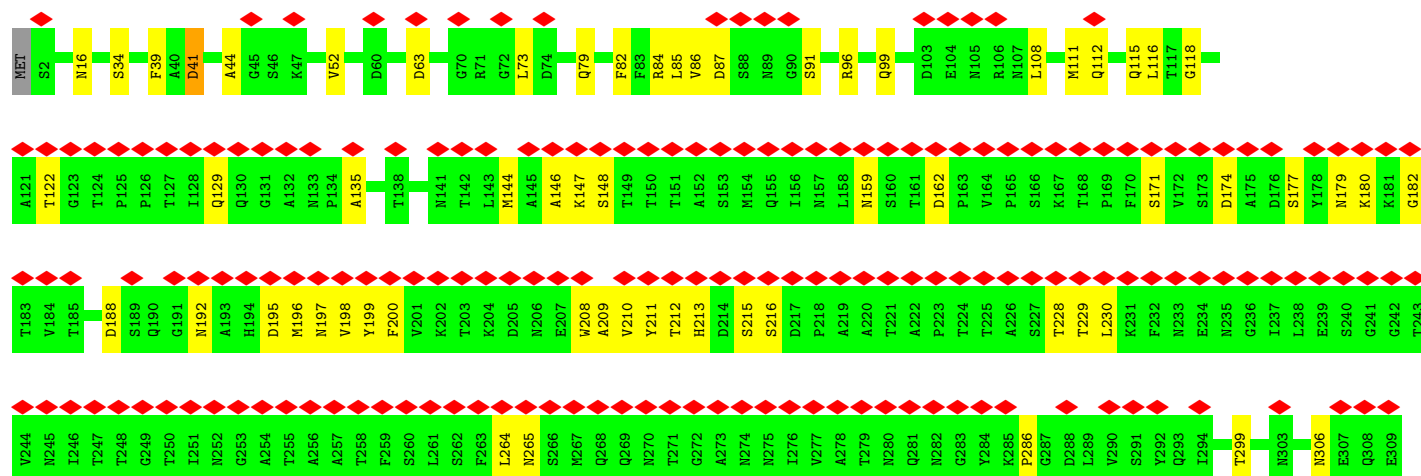
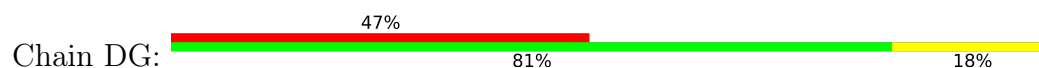


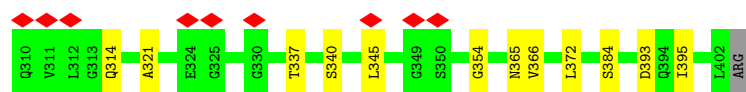


• Molecule 8: Flagellar hook protein FlgE

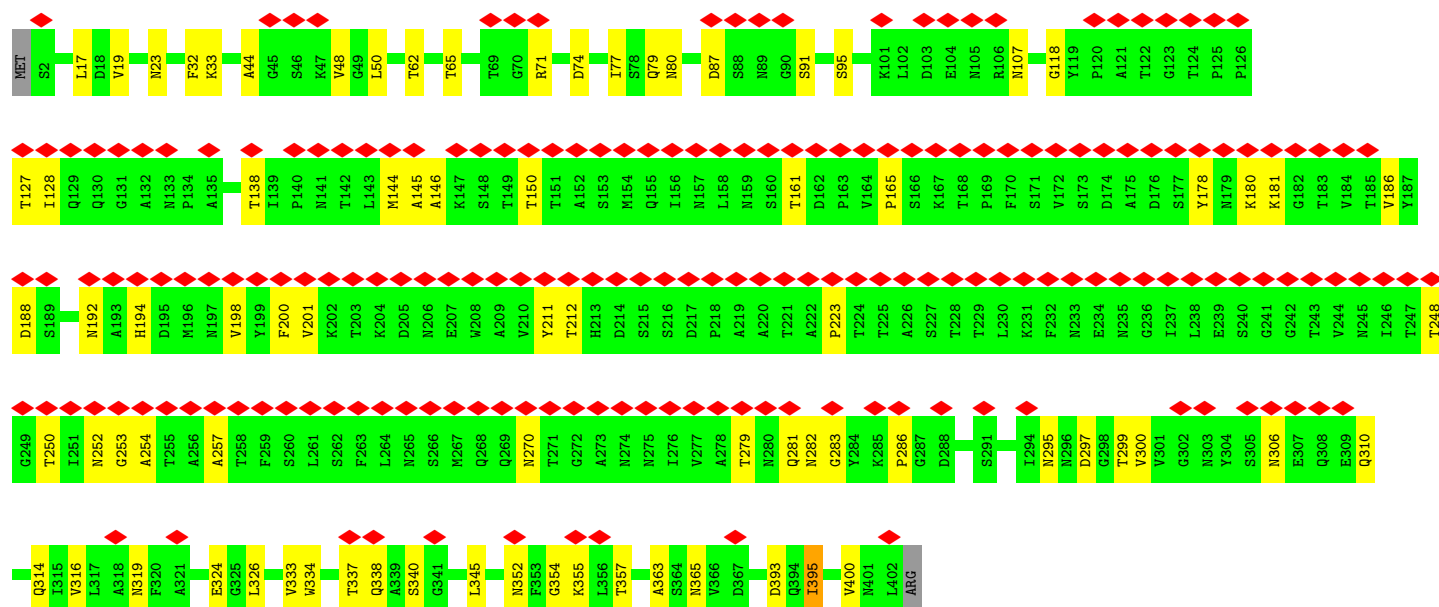
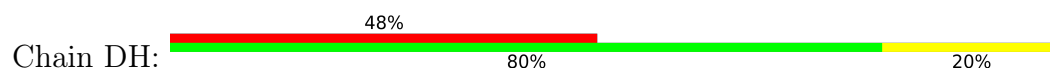


• Molecule 8: Flagellar hook protein FlgE

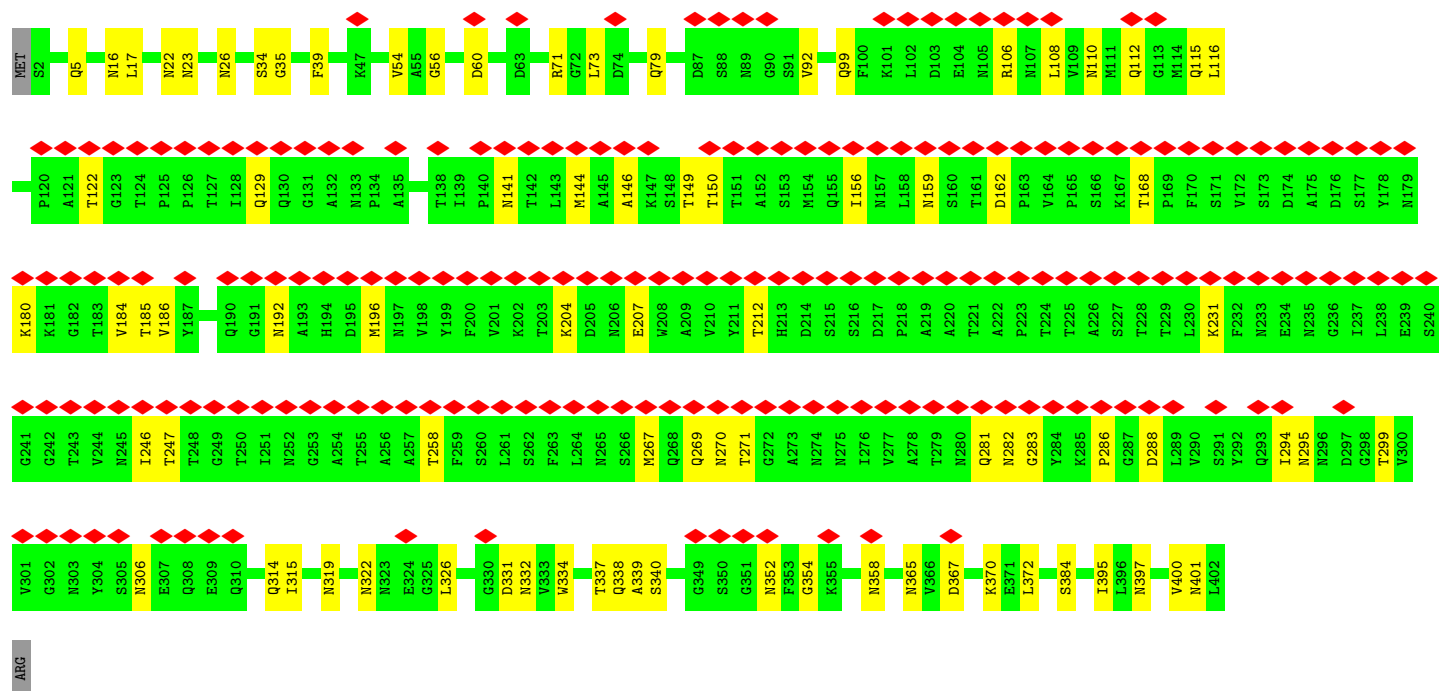
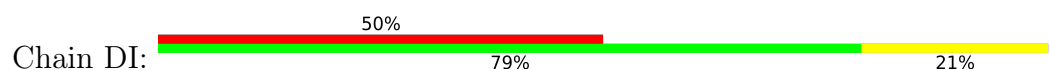




• Molecule 8: Flagellar hook protein FlgE

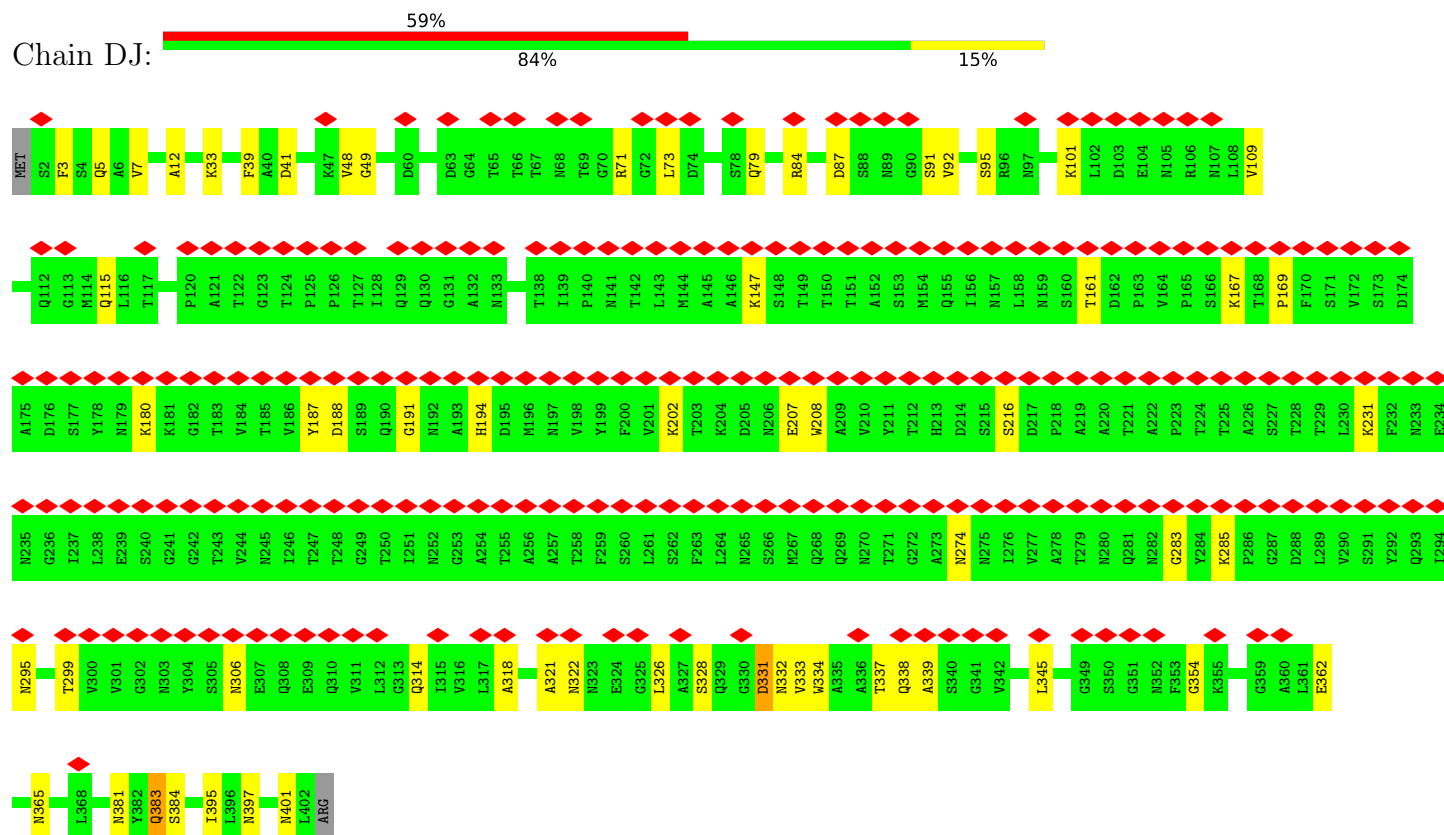


• Molecule 8: Flagellar hook protein FlgE



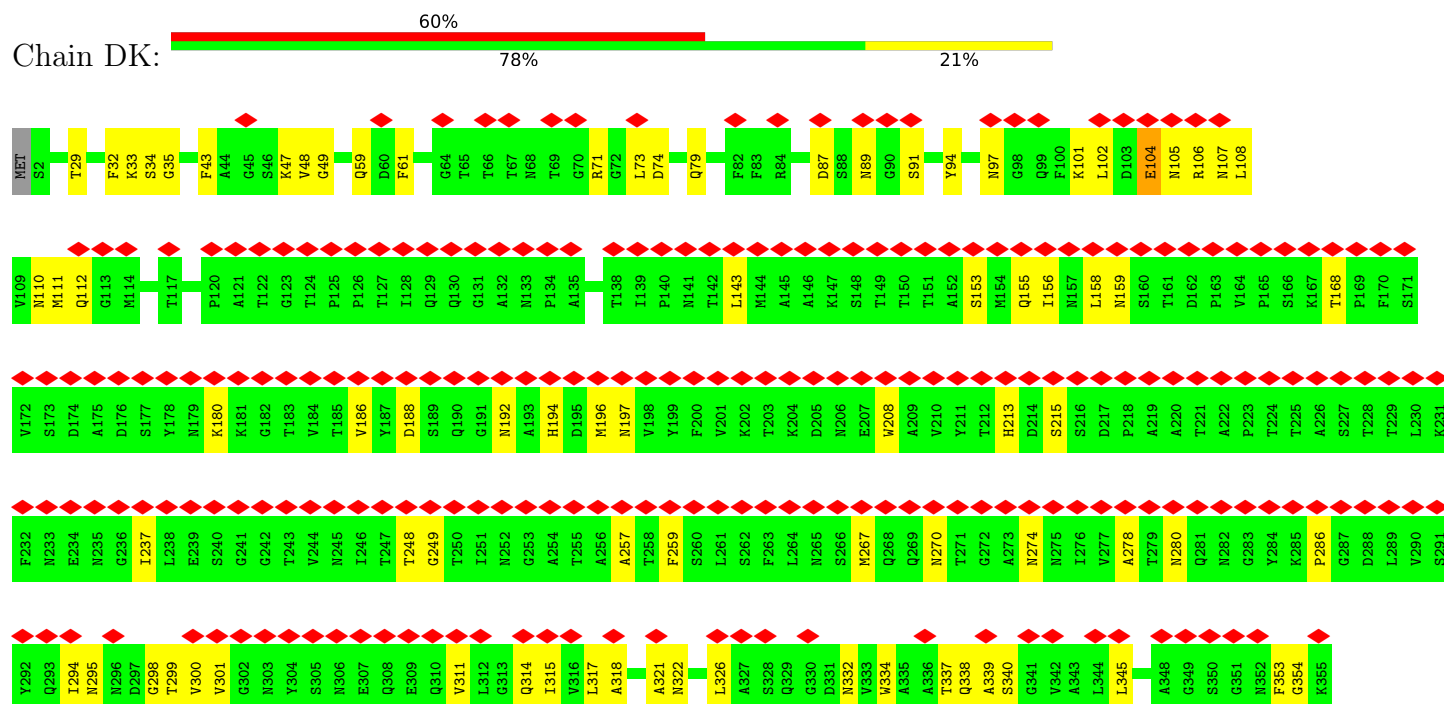
- Molecule 8: Flagellar hook protein FlgE

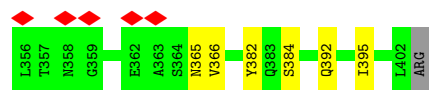
Chain DJ:



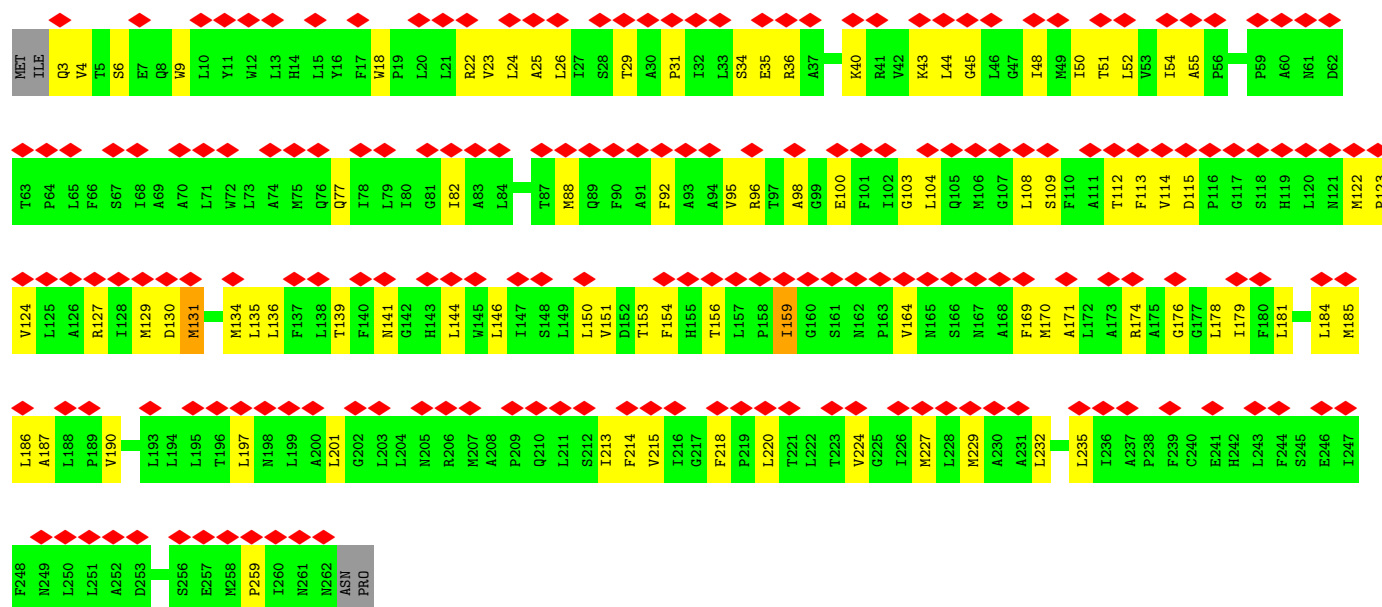
- Molecule 8: Flagellar hook protein FlgE

Chain DK:

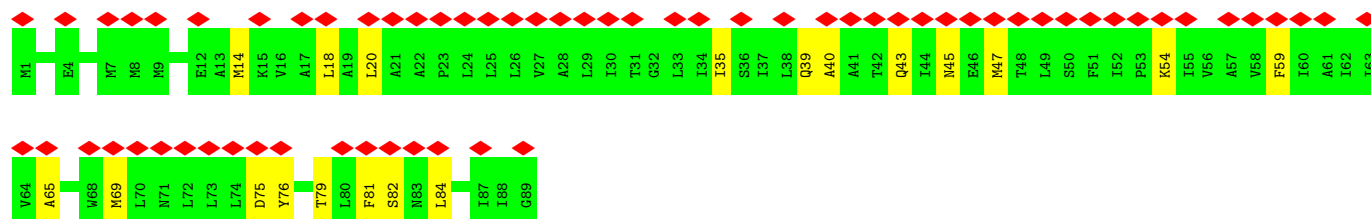
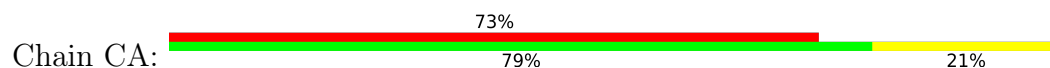




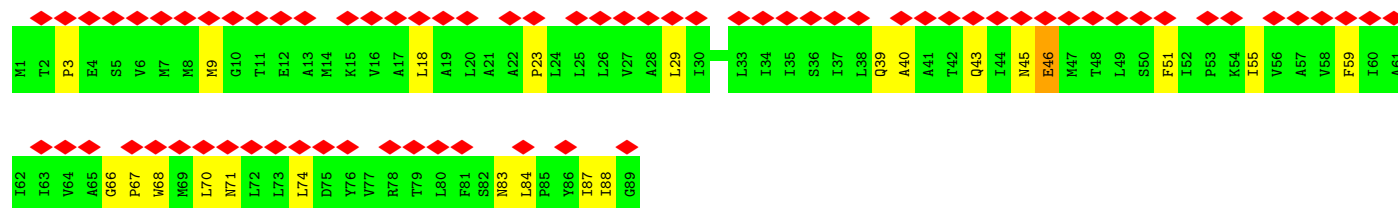
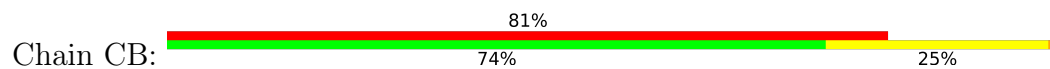
• Molecule 9: Flagellar biosynthetic protein FliR



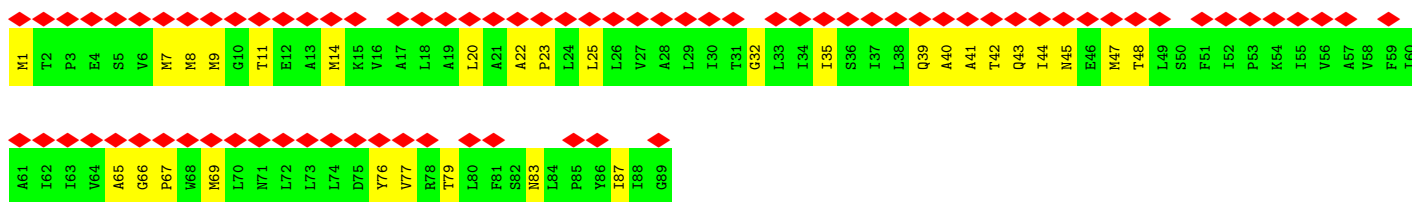
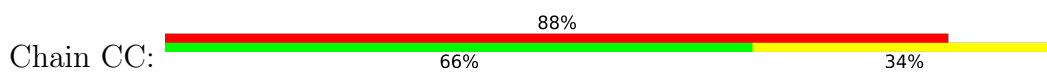
• Molecule 10: Flagellar biosynthetic protein FliQ



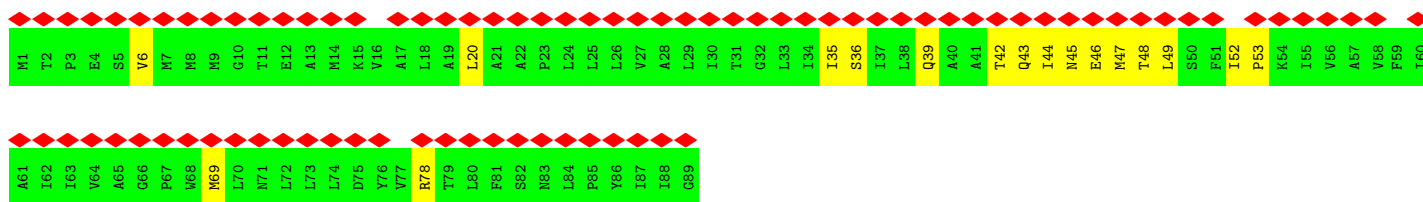
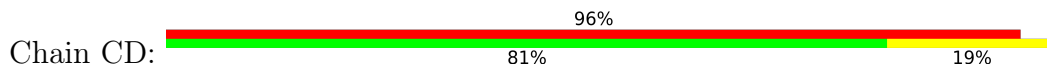
• Molecule 10: Flagellar biosynthetic protein FliQ



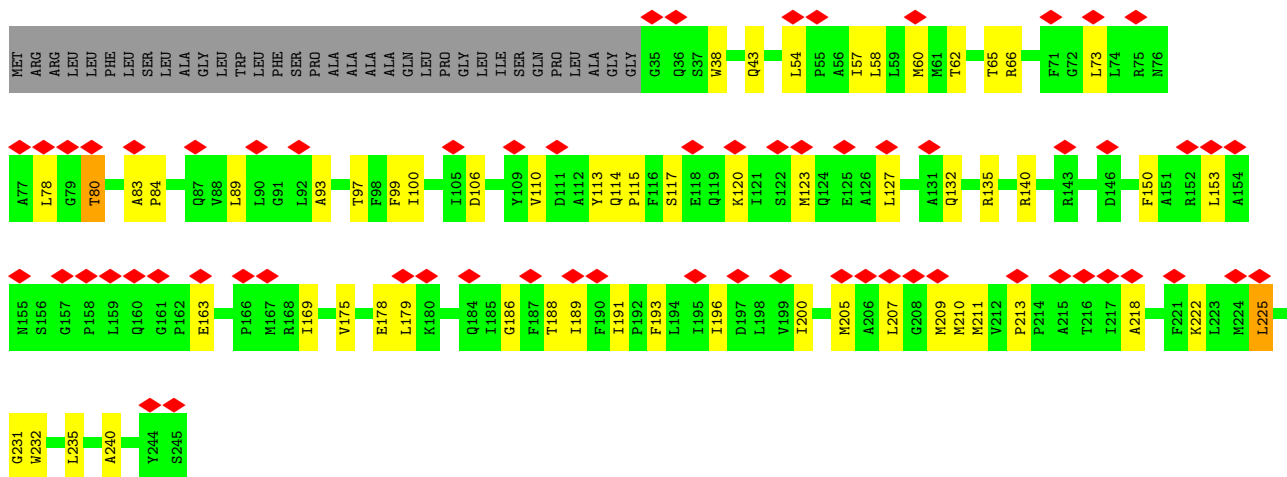
• Molecule 10: Flagellar biosynthetic protein FliQ



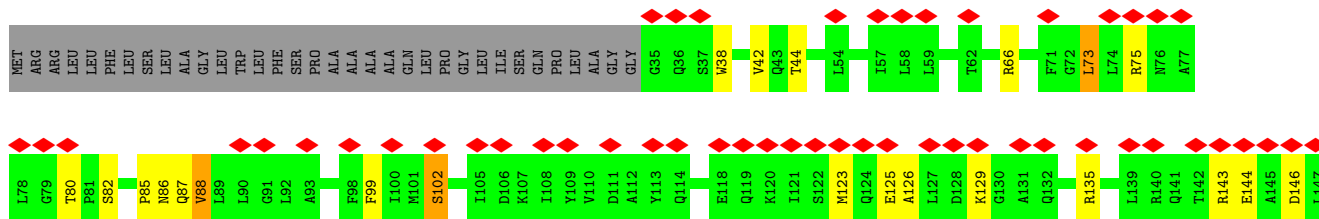
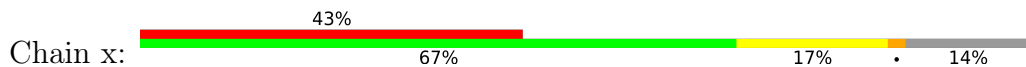
• Molecule 10: Flagellar biosynthetic protein FliQ

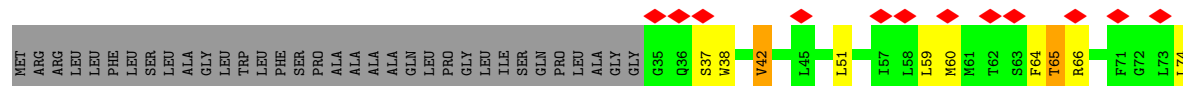


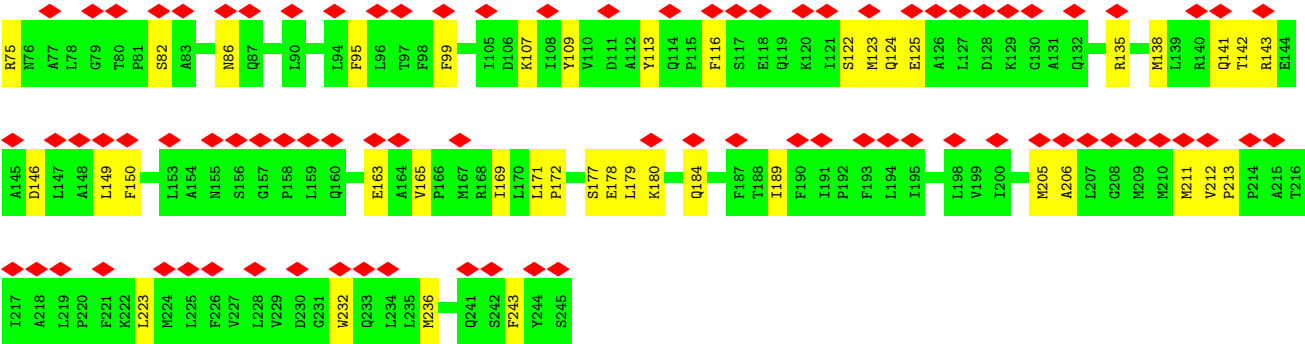
• Molecule 11: Flagellar biosynthetic protein FliP



• Molecule 11: Flagellar biosynthetic protein FliP







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52714	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.440	Depositor
Minimum map value	-1.067	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	669.184, 669.184, 669.184	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.307, 1.307, 1.307	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.15	0/1973	0.28	0/2682
1	B	0.14	0/1973	0.27	0/2682
1	C	0.15	0/1973	0.26	0/2682
1	D	0.15	0/1973	0.28	0/2682
1	E	0.15	0/1973	0.30	0/2682
1	F	0.16	0/1973	0.28	0/2682
1	G	0.17	0/1973	0.32	0/2682
1	H	0.15	0/1973	0.28	0/2682
1	I	0.16	0/1973	0.31	0/2682
1	J	0.17	0/1973	0.29	0/2682
1	K	0.17	0/1973	0.32	1/2682 (0.0%)
1	L	0.15	0/1965	0.25	0/2672
1	M	0.16	0/1973	0.27	0/2682
1	N	0.15	0/1909	0.26	0/2593
1	O	0.15	0/1917	0.26	0/2605
1	P	0.16	0/1884	0.29	0/2559
1	Q	0.17	0/1880	0.28	0/2554
1	R	0.15	0/1898	0.29	0/2578
1	S	0.21	0/1880	0.36	1/2554 (0.0%)
1	T	0.15	0/1925	0.25	0/2617
1	U	0.15	0/1965	0.27	0/2672
1	V	0.16	0/1965	0.29	0/2672
1	W	0.22	0/1965	0.35	0/2672
1	X	0.15	0/1965	0.32	0/2672
2	a	0.16	0/1836	0.29	0/2502
2	b	0.15	0/1828	0.28	0/2492
2	c	0.14	0/1836	0.25	0/2502
2	d	0.15	0/1836	0.29	0/2502
2	e	0.14	0/1836	0.33	0/2502
4	5	0.14	0/145	0.23	0/203
4	6	0.10	0/145	0.24	0/203
4	7	0.51	0/145	0.86	0/203
4	8	0.13	0/145	0.23	0/203
4	9	0.13	0/145	0.28	0/203

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	f	0.14	0/946	0.24	0/1285
5	g	0.15	0/959	0.29	0/1302
5	h	0.15	0/945	0.26	0/1283
5	i	0.16	0/954	0.28	0/1295
5	j	0.15	0/941	0.27	0/1278
5	p	0.13	0/950	0.25	0/1290
6	k	0.15	0/859	0.28	0/1156
6	l	0.13	0/840	0.25	0/1131
6	m	0.15	0/840	0.26	0/1131
6	n	0.15	0/851	0.25	0/1145
6	o	0.13	0/863	0.28	0/1161
7	q	0.12	0/540	0.24	0/723
7	r	0.16	0/529	0.31	0/709
7	s	0.12	0/547	0.23	0/733
7	t	0.11	0/547	0.28	0/733
7	u	0.11	0/547	0.29	0/733
7	v	0.10	0/289	0.22	0/385
8	DA	0.14	0/2991	0.26	0/4076
8	DB	0.12	0/2991	0.25	0/4076
8	DC	0.12	0/2991	0.25	0/4076
8	DD	0.11	0/2991	0.25	0/4076
8	DE	0.11	0/2991	0.23	0/4076
8	DF	0.11	0/2991	0.23	0/4076
8	DG	0.11	0/2991	0.25	0/4076
8	DH	0.14	0/2991	0.27	0/4076
8	DI	0.15	0/2991	0.32	2/4076 (0.0%)
8	DJ	0.20	0/2991	0.37	2/4076 (0.0%)
8	DK	0.15	0/2991	0.28	1/4076 (0.0%)
9	CE	0.10	0/2052	0.28	0/2803
10	CA	0.10	0/681	0.34	0/930
10	CB	0.10	0/681	0.32	0/930
10	CC	0.10	0/681	0.34	0/930
10	CD	0.09	0/681	0.43	2/930 (0.2%)
11	CF	0.11	0/1675	0.30	0/2280
11	w	0.12	0/1675	0.30	0/2280
11	x	0.12	0/1675	0.30	0/2280
11	y	0.13	0/1675	0.36	0/2280
11	z	0.12	0/1675	0.30	0/2280
All	All	0.15	0/115690	0.29	9/157351 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	DJ	383	GLN	CB-CA-C	-7.49	99.12	110.88
1	S	202	ASN	CA-CB-CG	-6.86	105.74	112.60
10	CD	42	THR	CA-C-N	6.47	133.90	121.54
10	CD	42	THR	C-N-CA	6.47	133.90	121.54
8	DI	270	ASN	CA-C-N	-6.41	110.41	122.27

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1949	0	1926	40	0
1	B	1949	0	1926	47	0
1	C	1949	0	1926	38	0
1	D	1949	0	1926	38	0
1	E	1949	0	1926	37	0
1	F	1949	0	1926	43	0
1	G	1949	0	1926	47	0
1	H	1949	0	1926	37	0
1	I	1949	0	1926	36	0
1	J	1949	0	1926	33	0
1	K	1949	0	1926	36	0
1	L	1941	0	1914	39	0
1	M	1949	0	1926	26	0
1	N	1887	0	1871	41	0
1	O	1894	0	1878	34	0
1	P	1862	0	1839	30	0
1	Q	1858	0	1836	33	0
1	R	1875	0	1852	34	0
1	S	1858	0	1836	30	0
1	T	1902	0	1881	33	0
1	U	1941	0	1914	40	0
1	V	1941	0	1914	47	0
1	W	1941	0	1914	48	0
1	X	1941	0	1914	33	0
2	a	1812	0	1800	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	b	1804	0	1791	48	0
2	c	1812	0	1800	41	0
2	d	1812	0	1800	46	0
2	e	1812	0	1800	35	0
3	0	75	0	18	0	0
3	1	75	0	17	1	0
3	2	75	0	17	1	0
3	3	75	0	18	0	0
3	4	75	0	19	2	0
4	5	140	0	136	0	0
4	6	140	0	136	1	0
4	7	140	0	136	2	0
4	8	140	0	136	2	0
4	9	140	0	136	2	0
5	f	936	0	951	24	0
5	g	949	0	962	20	0
5	h	935	0	949	27	0
5	i	944	0	957	18	0
5	j	931	0	946	19	0
5	p	940	0	954	17	0
6	k	852	0	855	20	0
6	l	833	0	831	15	0
6	m	833	0	831	21	0
6	n	844	0	844	18	0
6	o	856	0	858	17	0
7	q	536	0	541	8	0
7	r	526	0	536	9	0
7	s	543	0	550	4	0
7	t	543	0	550	5	0
7	u	543	0	550	9	0
7	v	289	0	299	6	0
8	DA	2947	0	2839	47	0
8	DB	2947	0	2839	49	0
8	DC	2947	0	2839	61	0
8	DD	2947	0	2839	52	0
8	DE	2947	0	2839	59	0
8	DF	2947	0	2839	61	0
8	DG	2947	0	2839	46	0
8	DH	2947	0	2839	47	0
8	DI	2947	0	2839	51	0
8	DJ	2947	0	2839	35	0
8	DK	2947	0	2839	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	CE	2002	0	2116	66	0
10	CA	670	0	739	15	0
10	CB	670	0	739	16	0
10	CC	670	0	739	21	0
10	CD	670	0	739	13	0
11	CF	1636	0	1726	41	0
11	w	1636	0	1726	38	0
11	x	1636	0	1726	36	0
11	y	1636	0	1726	47	0
11	z	1636	0	1726	35	0
All	All	114468	0	113330	1903	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 8.

The worst 5 of 1903 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)
1:K:59:GLN:O	1:K:59:GLN:NE2	2.07	0.87
1:C:256:LYS:HD3	1:G:241:GLU:HG2	1.59	0.84
8:DG:199:TYR:HB2	8:DG:211:TYR:HB2	1.61	0.82
1:B:98:LYS:O	1:B:212:GLY:HA3	1.80	0.81
1:V:136:VAL:HG12	1:V:138:PRO:HD2	1.62	0.81

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	258/260 (99%)	249 (96%)	9 (4%)	0	100	100
1	B	258/260 (99%)	247 (96%)	11 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	D	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	E	258/260 (99%)	246 (95%)	12 (5%)	0	100	100
1	F	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	G	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	H	258/260 (99%)	245 (95%)	13 (5%)	0	100	100
1	I	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	J	258/260 (99%)	251 (97%)	7 (3%)	0	100	100
1	K	258/260 (99%)	248 (96%)	10 (4%)	0	100	100
1	L	257/260 (99%)	250 (97%)	7 (3%)	0	100	100
1	M	258/260 (99%)	247 (96%)	11 (4%)	0	100	100
1	N	247/260 (95%)	240 (97%)	7 (3%)	0	100	100
1	O	248/260 (95%)	240 (97%)	8 (3%)	0	100	100
1	P	244/260 (94%)	236 (97%)	8 (3%)	0	100	100
1	Q	243/260 (94%)	237 (98%)	6 (2%)	0	100	100
1	R	246/260 (95%)	238 (97%)	8 (3%)	0	100	100
1	S	243/260 (94%)	235 (97%)	8 (3%)	0	100	100
1	T	249/260 (96%)	241 (97%)	8 (3%)	0	100	100
1	U	257/260 (99%)	243 (95%)	14 (5%)	0	100	100
1	V	257/260 (99%)	249 (97%)	8 (3%)	0	100	100
1	W	257/260 (99%)	242 (94%)	15 (6%)	0	100	100
1	X	257/260 (99%)	244 (95%)	13 (5%)	0	100	100
2	a	247/251 (98%)	235 (95%)	12 (5%)	0	100	100
2	b	246/251 (98%)	236 (96%)	10 (4%)	0	100	100
2	c	247/251 (98%)	237 (96%)	10 (4%)	0	100	100
2	d	247/251 (98%)	232 (94%)	15 (6%)	0	100	100
2	e	247/251 (98%)	231 (94%)	16 (6%)	0	100	100
4	5	19/21 (90%)	19 (100%)	0	0	100	100
4	6	19/21 (90%)	19 (100%)	0	0	100	100
4	7	19/21 (90%)	19 (100%)	0	0	100	100
4	8	19/21 (90%)	18 (95%)	1 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	9	19/21 (90%)	19 (100%)	0	0	100	100
5	f	124/134 (92%)	121 (98%)	3 (2%)	0	100	100
5	g	126/134 (94%)	121 (96%)	5 (4%)	0	100	100
5	h	124/134 (92%)	120 (97%)	4 (3%)	0	100	100
5	i	125/134 (93%)	121 (97%)	4 (3%)	0	100	100
5	j	123/134 (92%)	119 (97%)	4 (3%)	0	100	100
5	p	125/134 (93%)	120 (96%)	5 (4%)	0	100	100
6	k	104/138 (75%)	99 (95%)	5 (5%)	0	100	100
6	l	102/138 (74%)	101 (99%)	1 (1%)	0	100	100
6	m	102/138 (74%)	99 (97%)	3 (3%)	0	100	100
6	n	103/138 (75%)	99 (96%)	4 (4%)	0	100	100
6	o	105/138 (76%)	103 (98%)	2 (2%)	0	100	100
7	q	69/104 (66%)	68 (99%)	1 (1%)	0	100	100
7	r	68/104 (65%)	64 (94%)	4 (6%)	0	100	100
7	s	70/104 (67%)	70 (100%)	0	0	100	100
7	t	70/104 (67%)	69 (99%)	1 (1%)	0	100	100
7	u	70/104 (67%)	70 (100%)	0	0	100	100
7	v	36/104 (35%)	36 (100%)	0	0	100	100
8	DA	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
8	DB	399/403 (99%)	377 (94%)	22 (6%)	0	100	100
8	DC	399/403 (99%)	375 (94%)	24 (6%)	0	100	100
8	DD	399/403 (99%)	378 (95%)	21 (5%)	0	100	100
8	DE	399/403 (99%)	380 (95%)	19 (5%)	0	100	100
8	DF	399/403 (99%)	376 (94%)	23 (6%)	0	100	100
8	DG	399/403 (99%)	382 (96%)	17 (4%)	0	100	100
8	DH	399/403 (99%)	378 (95%)	19 (5%)	2 (0%)	24	56
8	DI	399/403 (99%)	381 (96%)	18 (4%)	0	100	100
8	DJ	399/403 (99%)	375 (94%)	23 (6%)	1 (0%)	36	65
8	DK	399/403 (99%)	386 (97%)	13 (3%)	0	100	100
9	CE	258/264 (98%)	239 (93%)	18 (7%)	1 (0%)	30	60
10	CA	87/89 (98%)	77 (88%)	10 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	CB	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
10	CC	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
10	CD	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
11	CF	209/245 (85%)	203 (97%)	6 (3%)	0	100	100
11	w	209/245 (85%)	203 (97%)	6 (3%)	0	100	100
11	x	209/245 (85%)	197 (94%)	12 (6%)	0	100	100
11	y	209/245 (85%)	201 (96%)	8 (4%)	0	100	100
11	z	209/245 (85%)	204 (98%)	5 (2%)	0	100	100
All	All	15116/15996 (94%)	14452 (96%)	660 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	DJ	332	ASN
8	DH	270	ASN
9	CE	159	ILE
8	DH	71	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	215/215 (100%)	212 (99%)	3 (1%)	59	70
1	B	215/215 (100%)	212 (99%)	3 (1%)	59	70
1	C	215/215 (100%)	209 (97%)	6 (3%)	38	58
1	D	215/215 (100%)	213 (99%)	2 (1%)	70	75
1	E	215/215 (100%)	210 (98%)	5 (2%)	44	62
1	F	215/215 (100%)	212 (99%)	3 (1%)	59	70
1	G	215/215 (100%)	207 (96%)	8 (4%)	30	53
1	H	215/215 (100%)	210 (98%)	5 (2%)	44	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	215/215 (100%)	211 (98%)	4 (2%)	50	65
1	J	215/215 (100%)	210 (98%)	5 (2%)	44	62
1	K	215/215 (100%)	210 (98%)	5 (2%)	44	62
1	L	214/215 (100%)	211 (99%)	3 (1%)	59	70
1	M	215/215 (100%)	210 (98%)	5 (2%)	44	62
1	N	208/215 (97%)	208 (100%)	0	100	100
1	O	209/215 (97%)	206 (99%)	3 (1%)	59	70
1	P	204/215 (95%)	201 (98%)	3 (2%)	57	68
1	Q	204/215 (95%)	199 (98%)	5 (2%)	42	60
1	R	206/215 (96%)	199 (97%)	7 (3%)	32	54
1	S	204/215 (95%)	202 (99%)	2 (1%)	68	74
1	T	210/215 (98%)	208 (99%)	2 (1%)	68	74
1	U	214/215 (100%)	210 (98%)	4 (2%)	50	65
1	V	214/215 (100%)	207 (97%)	7 (3%)	33	55
1	W	214/215 (100%)	211 (99%)	3 (1%)	59	70
1	X	214/215 (100%)	209 (98%)	5 (2%)	44	62
2	a	191/193 (99%)	184 (96%)	7 (4%)	30	53
2	b	190/193 (98%)	184 (97%)	6 (3%)	34	55
2	c	191/193 (99%)	183 (96%)	8 (4%)	26	50
2	d	191/193 (99%)	187 (98%)	4 (2%)	47	63
2	e	191/193 (99%)	187 (98%)	4 (2%)	47	63
4	5	15/15 (100%)	14 (93%)	1 (7%)	15	42
4	6	15/15 (100%)	15 (100%)	0	100	100
4	7	15/15 (100%)	15 (100%)	0	100	100
4	8	15/15 (100%)	15 (100%)	0	100	100
4	9	15/15 (100%)	15 (100%)	0	100	100
5	f	101/105 (96%)	98 (97%)	3 (3%)	36	57
5	g	102/105 (97%)	98 (96%)	4 (4%)	28	52
5	h	101/105 (96%)	99 (98%)	2 (2%)	48	64
5	i	102/105 (97%)	98 (96%)	4 (4%)	28	52
5	j	101/105 (96%)	100 (99%)	1 (1%)	68	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	p	101/105 (96%)	101 (100%)	0	100	100
6	k	91/113 (80%)	90 (99%)	1 (1%)	65	72
6	l	89/113 (79%)	86 (97%)	3 (3%)	32	54
6	m	89/113 (79%)	86 (97%)	3 (3%)	32	54
6	n	90/113 (80%)	87 (97%)	3 (3%)	33	55
6	o	91/113 (80%)	87 (96%)	4 (4%)	25	49
7	q	55/79 (70%)	54 (98%)	1 (2%)	51	66
7	r	54/79 (68%)	53 (98%)	1 (2%)	50	65
7	s	56/79 (71%)	56 (100%)	0	100	100
7	t	56/79 (71%)	55 (98%)	1 (2%)	51	66
7	u	56/79 (71%)	56 (100%)	0	100	100
7	v	32/79 (40%)	30 (94%)	2 (6%)	16	43
8	DA	321/323 (99%)	315 (98%)	6 (2%)	50	65
8	DB	321/323 (99%)	316 (98%)	5 (2%)	55	67
8	DC	321/323 (99%)	317 (99%)	4 (1%)	63	71
8	DD	321/323 (99%)	314 (98%)	7 (2%)	45	62
8	DE	321/323 (99%)	320 (100%)	1 (0%)	86	83
8	DF	321/323 (99%)	315 (98%)	6 (2%)	50	65
8	DG	321/323 (99%)	318 (99%)	3 (1%)	70	75
8	DH	321/323 (99%)	314 (98%)	7 (2%)	45	62
8	DI	321/323 (99%)	315 (98%)	6 (2%)	50	65
8	DJ	321/323 (99%)	316 (98%)	5 (2%)	55	67
8	DK	321/323 (99%)	318 (99%)	3 (1%)	70	75
9	CE	217/221 (98%)	212 (98%)	5 (2%)	44	62
10	CA	74/74 (100%)	74 (100%)	0	100	100
10	CB	74/74 (100%)	71 (96%)	3 (4%)	27	51
10	CC	74/74 (100%)	74 (100%)	0	100	100
10	CD	74/74 (100%)	74 (100%)	0	100	100
11	CF	180/204 (88%)	178 (99%)	2 (1%)	65	72
11	w	180/204 (88%)	176 (98%)	4 (2%)	45	62
11	x	180/204 (88%)	175 (97%)	5 (3%)	38	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	y	180/204 (88%)	170 (94%)	10 (6%)	19	45
11	z	180/204 (88%)	178 (99%)	2 (1%)	65	72
All	All	12435/12959 (96%)	12190 (98%)	245 (2%)	48	64

5 of 245 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	f	132	LEU
10	CB	88	ILE
1	V	90	ASN
10	CB	29	LEU
11	y	149	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 179 such sidechains are listed below:

Mol	Chain	Res	Type
8	DC	296	ASN
8	DH	179	ASN
8	DD	22	ASN
8	DF	22	ASN
8	DI	133	ASN

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](#)

There are no chain breaks in this entry.

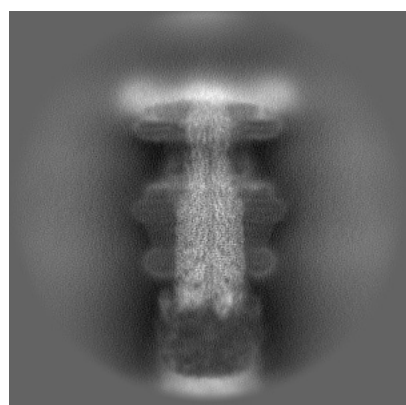
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31006. These allow visual inspection of the internal detail of the map and identification of artifacts.

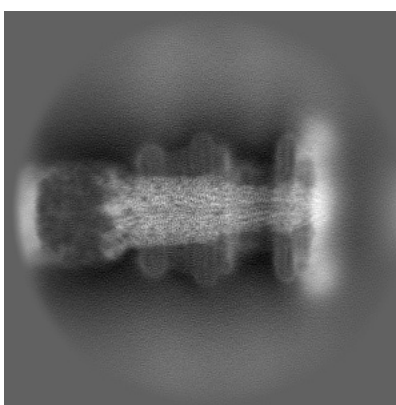
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

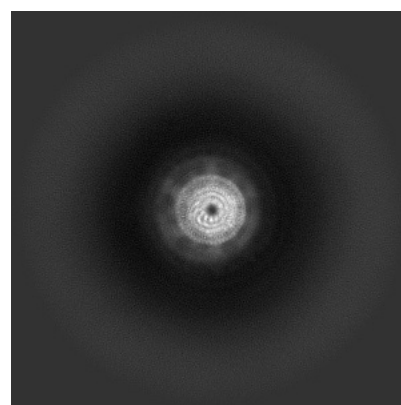
6.1.1 Primary map



X



Y

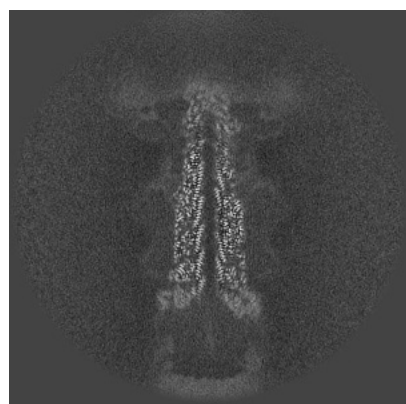


Z

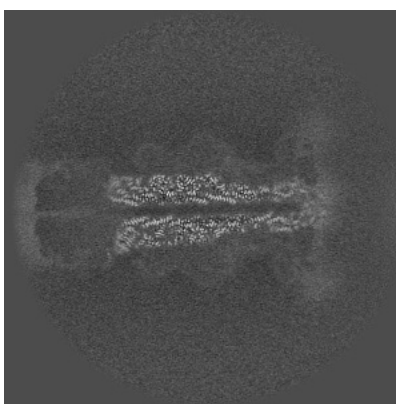
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

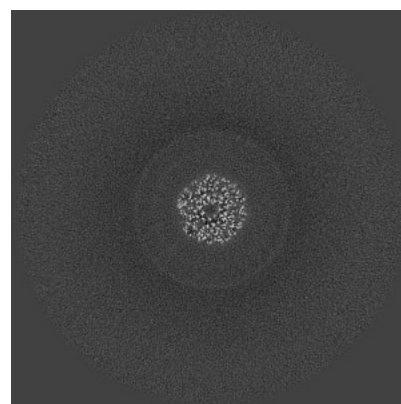
6.2.1 Primary map



X Index: 256



Y Index: 256

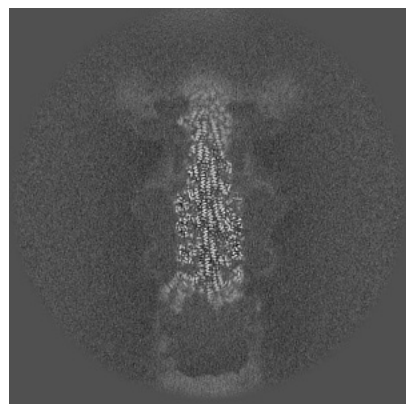


Z Index: 256

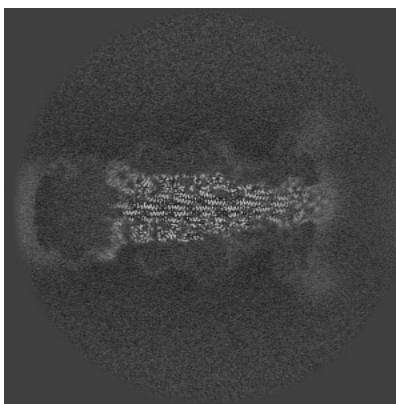
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

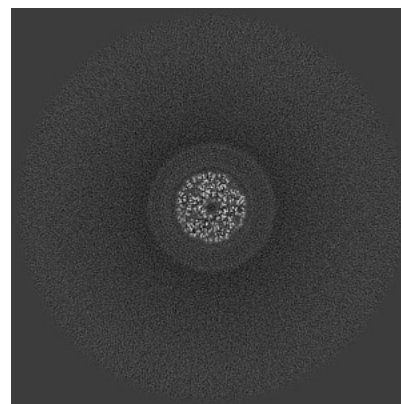
6.3.1 Primary map



X Index: 269



Y Index: 243

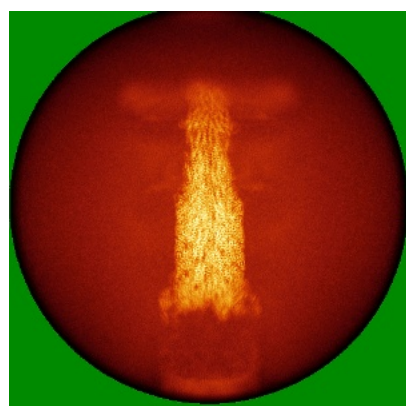


Z Index: 228

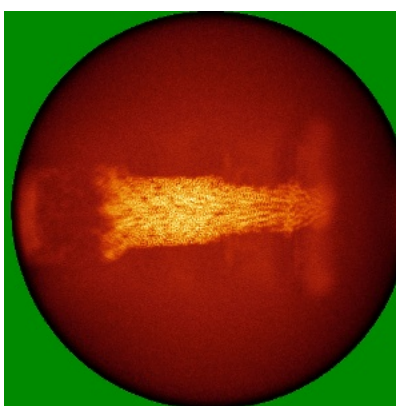
The images above show the largest variance slices of the map in three orthogonal directions.

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

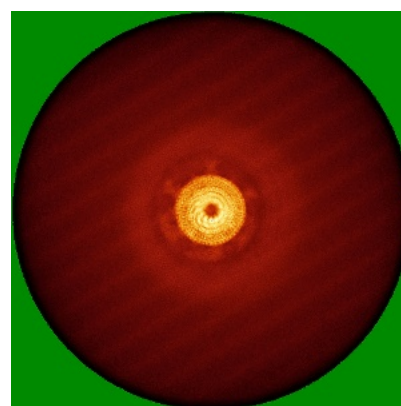
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

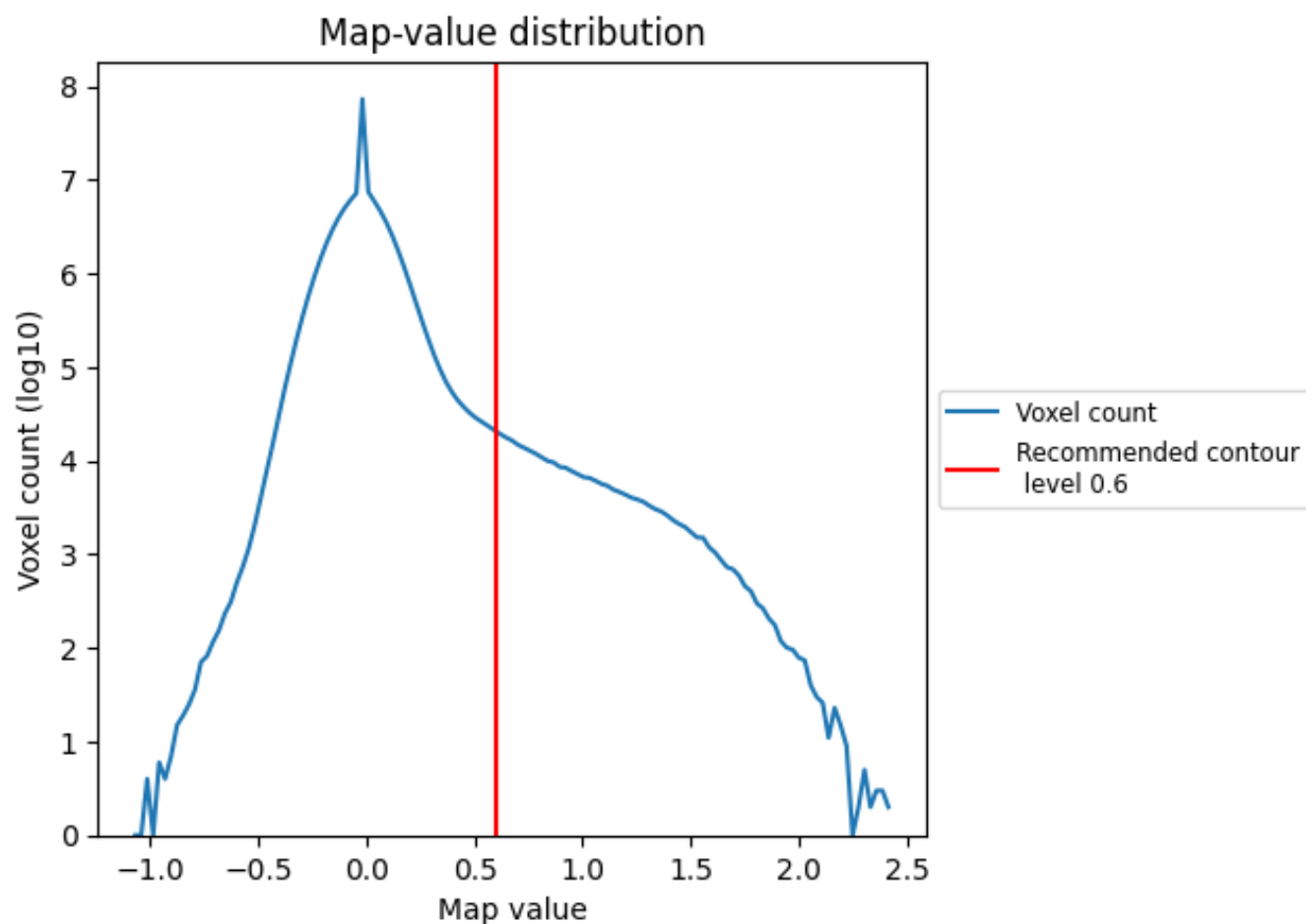
6.6 Mask visualisation

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

7 Map analysis [i](#)

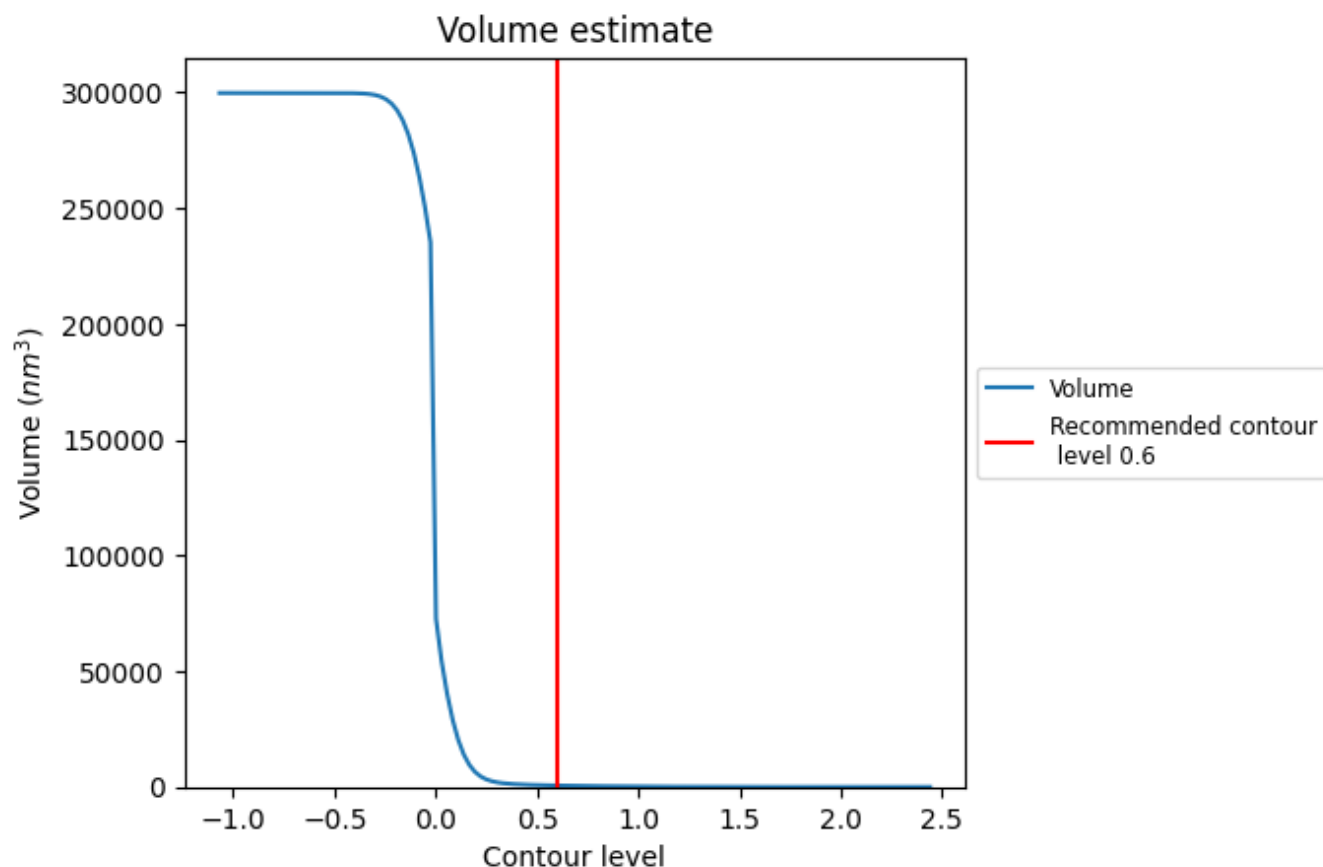
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

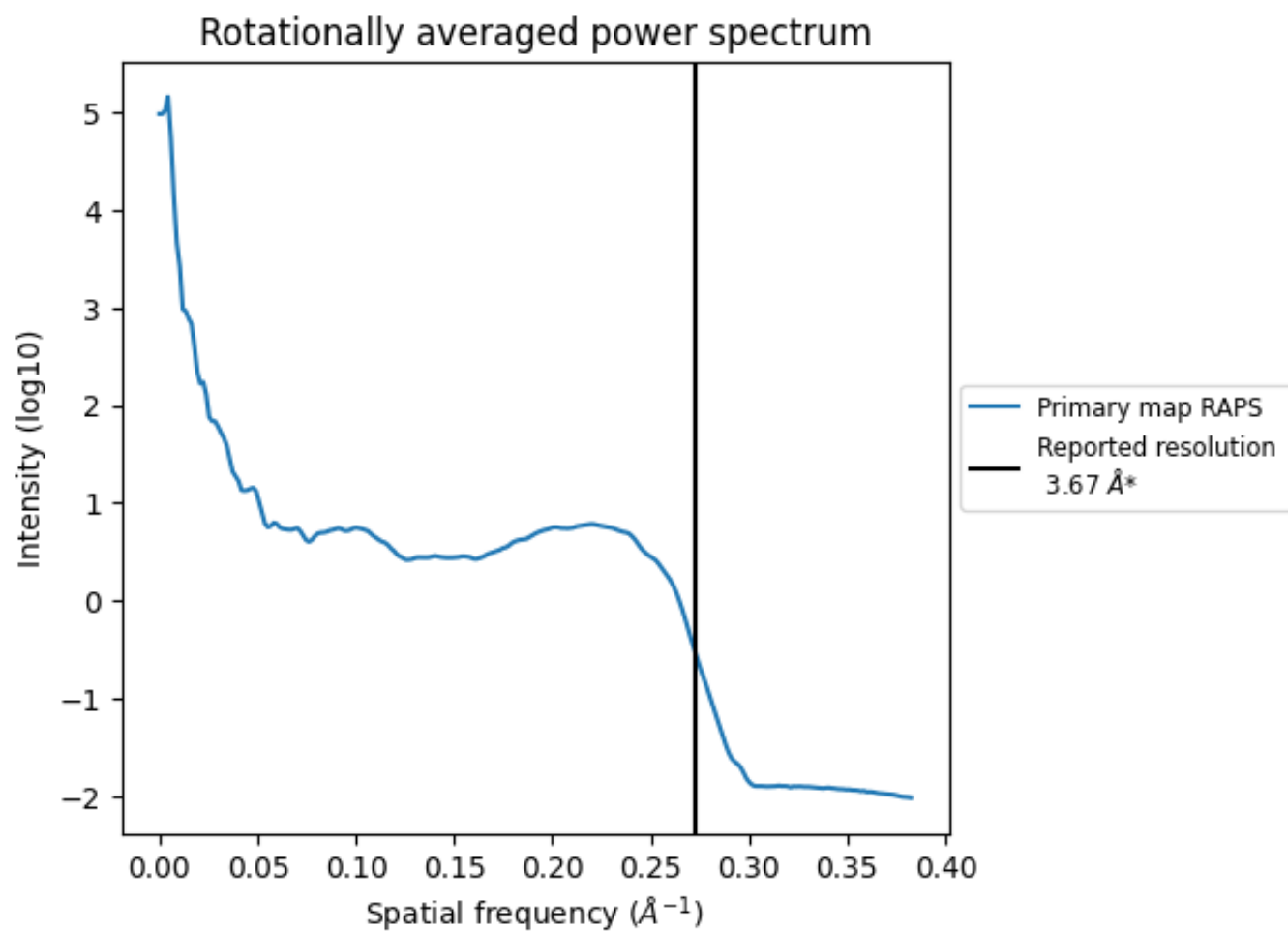
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 603 nm³; this corresponds to an approximate mass of 545 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 0.272 Å⁻¹

8 Fourier-Shell correlation

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

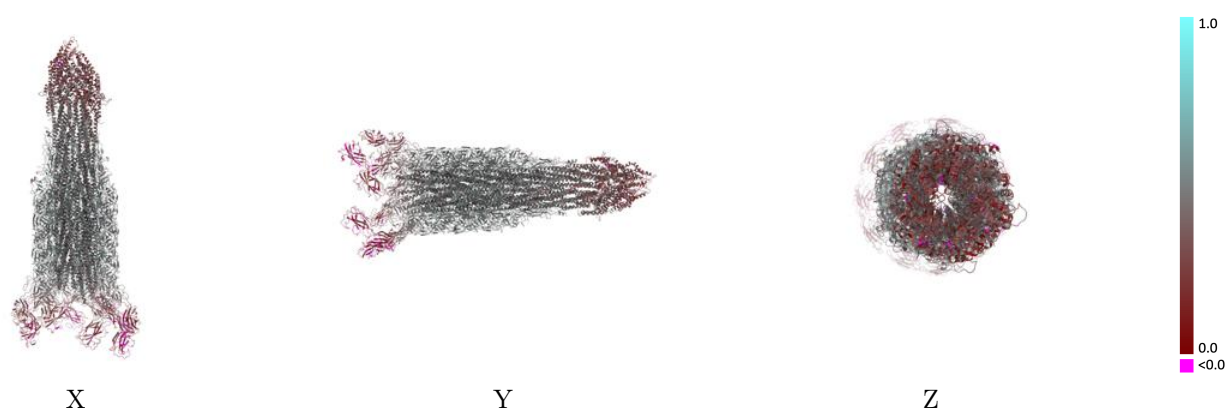
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31006 and PDB model 7E80. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

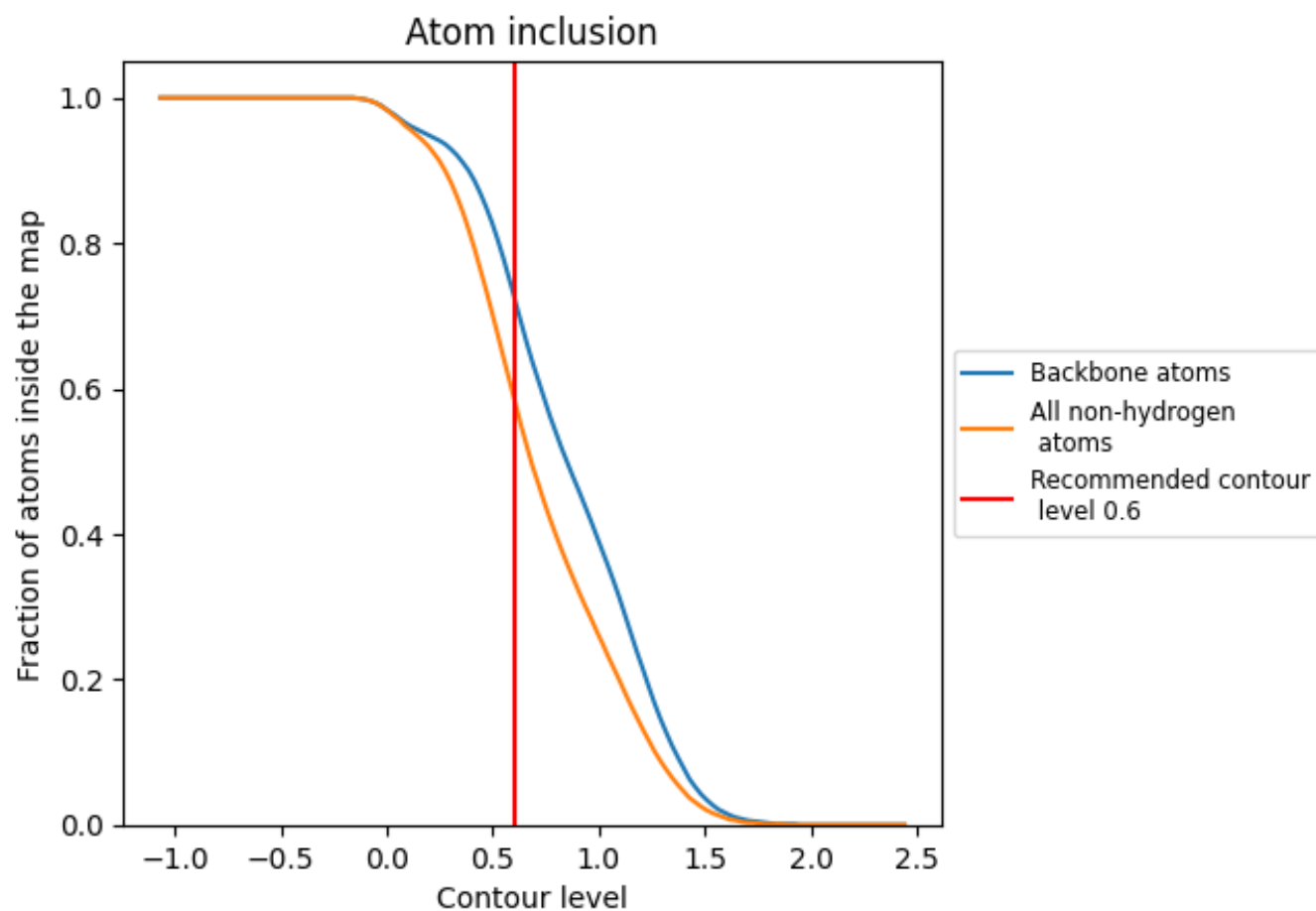


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 59% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5860	 0.4230
0	 0.7330	 0.4950
1	 0.7330	 0.4700
2	 0.8670	 0.5240
3	 0.8130	 0.4680
4	 0.6930	 0.4640
5	 0.7070	 0.4870
6	 0.4930	 0.4500
7	 0.6640	 0.4700
8	 0.6360	 0.4830
9	 0.5290	 0.4590
A	 0.6970	 0.4820
B	 0.6480	 0.4640
C	 0.7030	 0.4790
CA	 0.2990	 0.2650
CB	 0.2360	 0.2680
CC	 0.2100	 0.2600
CD	 0.1080	 0.2520
CE	 0.2840	 0.2720
CF	 0.4310	 0.3320
D	 0.7140	 0.4810
DA	 0.4060	 0.3830
DB	 0.4970	 0.3960
DC	 0.4970	 0.3830
DD	 0.4360	 0.3500
DE	 0.4270	 0.3560
DF	 0.4120	 0.3580
DG	 0.4100	 0.3500
DH	 0.3960	 0.3480
DI	 0.3790	 0.3100
DJ	 0.3150	 0.3040
DK	 0.2870	 0.2850
E	 0.7260	 0.4810
F	 0.7200	 0.4810
G	 0.7180	 0.4820



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Chain	Atom inclusion	Q-score
H	 0.7160	 0.4900
I	 0.7230	 0.4880
J	 0.7160	 0.4900
K	 0.7190	 0.4890
L	 0.7140	 0.4890
M	 0.7120	 0.4900
N	 0.7300	 0.4960
O	 0.7130	 0.4890
P	 0.7150	 0.4870
Q	 0.7130	 0.4880
R	 0.7120	 0.4830
S	 0.7110	 0.4870
T	 0.7110	 0.4870
U	 0.7030	 0.4900
V	 0.7200	 0.4820
W	 0.7160	 0.4880
X	 0.6880	 0.4780
a	 0.7420	 0.4850
b	 0.6800	 0.4740
c	 0.7360	 0.4860
d	 0.7430	 0.4800
e	 0.6950	 0.4720
f	 0.7280	 0.4770
g	 0.6700	 0.4390
h	 0.7270	 0.4790
i	 0.7200	 0.4790
j	 0.7310	 0.4770
k	 0.7320	 0.4580
l	 0.6740	 0.4500
m	 0.7240	 0.4600
n	 0.7360	 0.4630
o	 0.6830	 0.4460
p	 0.6740	 0.4580
q	 0.6510	 0.4310
r	 0.6170	 0.3770
s	 0.6650	 0.4380
t	 0.6440	 0.4320
u	 0.6200	 0.4200
v	 0.5100	 0.3790
w	 0.5070	 0.3620
x	 0.4070	 0.3360
y	 0.5140	 0.3650

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Chain	Atom inclusion	Q-score
z	 0.4910	 0.3630