



wwPDB EM Validation Summary Report ⓘ

Aug 27, 2024 – 05:03 PM JST

PDB ID : 8WLQ
EMDB ID : EMD-37628
Title : Cryo-EM structure of the whole rod-export apparatus with hook within the flagellar motor-hook complex in the CCW state.
Authors : Tan, J.X.; Zhang, L.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2023-09-30
Resolution : 3.80 Å(reported)
Based on initial model : .

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.dev112
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.38.2

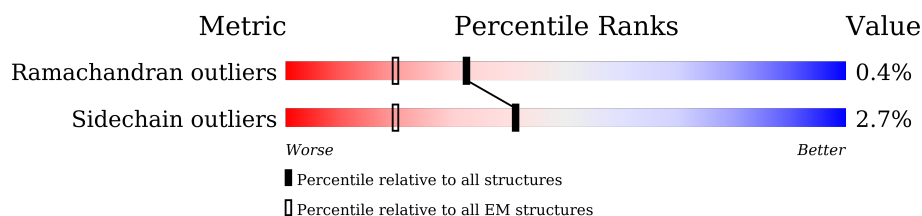
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	0	260	<div> <div>9%</div> <div>92%</div> <div>5%</div> </div>
1	1	260	<div> <div>15%</div> <div>93%</div> <div>5%</div> </div>
1	2	260	<div> <div>12%</div> <div>98%</div> <div>5%</div> </div>
1	3	260	<div> <div>11%</div> <div>98%</div> <div>5%</div> </div>
1	4	260	<div> <div>13%</div> <div>97%</div> <div>5%</div> </div>
1	5	260	<div> <div>12%</div> <div>97%</div> <div>5%</div> </div>
1	6	260	<div> <div>8%</div> <div>97%</div> <div>5%</div> </div>
1	7	260	<div> <div>11%</div> <div>98%</div> <div>5%</div> </div>
1	8	260	<div> <div>8%</div> <div>96%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	9	260	13% 98% .
1	ZA	260	12% 98% .
1	ZB	260	13% 96% .
1	ZC	260	8% 98% .
1	ZD	260	11% 97% .
1	ZE	260	13% 97% .
1	r	260	18% 95% . .
1	s	260	10% 94% . .
1	t	260	11% 93% 5% .
1	u	260	10% 92% 6% .
1	v	260	12% 92% 5% . .
1	w	260	11% 91% . 7%
1	x	260	11% 90% 5% 5%
1	y	260	11% 92% . . 5%
1	z	260	12% 93% . 5%
2	ZF	403	47% 97% .
2	ZG	403	20% 95% .
2	ZH	403	14% 96% .
2	ZI	403	13% 97% .
2	ZJ	403	12% 97% .
2	ZK	403	14% 98% .
2	ZL	403	12% 97% .
2	ZM	403	13% 97% .
2	ZN	403	13% 97% .
2	ZO	403	12% 97% .

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Mol	Chain	Length	Quality of chain
2	ZP	403	12% 95% .
2	ZQ	403	13% 97% .
2	ZR	403	15% 98% .
2	ZS	403	16% 98% .
2	ZT	403	16% 97% .
2	ZU	403	18% 98% .
2	ZV	403	18% 98% .
2	ZW	403	23% 96% .
2	ZX	403	22% 99% .
2	ZY	403	30% 98% .
2	ZZ	403	31% 98% .
2	Za	403	38% 98% .
2	Zb	403	42% 98% .
2	Zc	403	44% 97% .
2	Zd	403	46% 98% .
2	Ze	403	52% 97% .
2	Zf	403	54% 98% .
2	Zg	403	57% 98% .
2	Zh	403	58% 98% .
3	A	89	84% 92% 7% .
3	B	89	58% 98% .
3	C	89	49% 100%
3	D	89	61% 100%
4	E	264	63% 93% . .
5	F	245	46% 82% . 16%

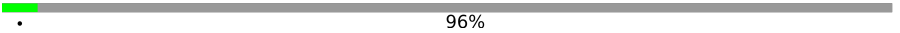
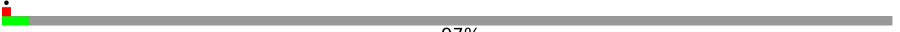
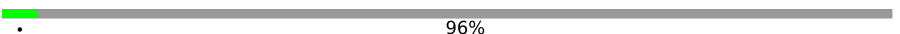
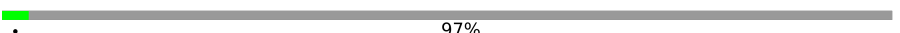
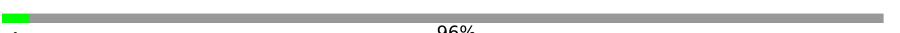
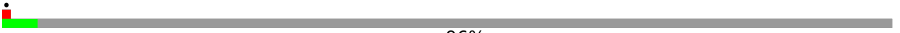





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Mol	Chain	Length	Quality of chain
5	G	245	
5	H	245	
5	I	245	
5	J	245	
6	K	104	
6	L	104	
6	M	104	
6	N	104	
6	O	104	
6	P	104	
7	Q	138	
7	R	138	
7	S	138	
7	T	138	
7	U	138	
8	V	134	
8	W	134	
8	X	134	
8	Y	134	
8	Z	134	
8	a	134	
9	b	560	
9	c	560	
9	d	560	
9	e	560	

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Mol	Chain	Length	Quality of chain
9	f	560	 96%
9	g	560	 97%
9	h	560	 96%
9	i	560	 97%
9	j	560	 96%
9	k	560	 97%
9	l	560	 96%
10	m	251	 23% 97% ..
10	n	251	 13% 96% ...
10	o	251	 9% 98% .
10	p	251	 9% 96% .
10	q	251	 13% 98% ..

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 167758 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	0	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	1	252	Total	C	N	O	S	0	0
			1894	1172	331	385	6		
1	2	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	3	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	4	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	5	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	6	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	7	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	8	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	9	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZA	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZB	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZC	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZD	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZE	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	r	254	Total	C	N	O	S	0	0
			1903	1175	334	389	5		
1	s	255	Total	C	N	O	S	0	0
			1911	1181	335	390	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	t	256	Total	C	N	O	S	0	0
			1919	1186	336	391	6		
1	u	254	Total	C	N	O	S	0	0
			1903	1175	334	389	5		
1	v	255	Total	C	N	O	S	0	0
			1911	1181	335	390	5		
1	w	243	Total	C	N	O	S	0	0
			1823	1127	318	373	5		
1	x	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	y	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	z	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		

- Molecule 2 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	ZF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZH	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZI	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZJ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZK	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZL	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZM	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZN	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZO	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZP	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZQ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	ZR	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZS	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZT	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZU	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZV	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZW	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZX	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZY	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZZ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Za	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zb	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zc	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zd	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Ze	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zf	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zg	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zh	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	B	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	D	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	253	Total	C	N	O	S	0	0
			1945	1305	307	318	15		

- Molecule 5 is a protein called Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	207	Total	C	N	O	S	0	0
			1605	1072	249	272	12		
5	G	209	Total	C	N	O	S	0	0
			1626	1086	252	276	12		
5	H	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
5	I	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
5	J	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 6 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	40	Total	C	N	O	S	0	0
			300	185	52	57	6		
6	L	72	Total	C	N	O	S	0	0
			543	335	99	103	6		
6	M	74	Total	C	N	O	S	0	0
			557	344	101	106	6		
6	N	74	Total	C	N	O	S	0	0
			557	344	101	106	6		
6	O	74	Total	C	N	O	S	0	0
			557	344	101	106	6		
6	P	73	Total	C	N	O	S	0	0
			550	340	100	104	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	119	Total	C	N	O	S	0	0
			922	565	169	183	5		
7	R	108	Total	C	N	O	S	0	0
			848	523	155	165	5		
7	S	108	Total	C	N	O	S	0	0
			848	523	155	165	5		
7	T	110	Total	C	N	O	S	0	0
			863	531	160	167	5		
7	U	106	Total	C	N	O	S	0	0
			832	514	150	163	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
8	W	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
8	X	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
8	Y	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
8	Z	131	Total	C	N	O	S	0	0
			956	595	165	191	5		
8	a	133	Total	C	N	O	S	0	0
			969	604	167	193	5		

- Molecule 9 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	b	13	Total	C	N	O	0	0
			81	50	15	16		
9	c	16	Total	C	N	O	0	0
			103	64	19	20		
9	d	20	Total	C	N	O	0	0
			133	83	23	27		
9	e	16	Total	C	N	O	0	0
			103	64	19	20		
9	f	21	Total	C	N	O	0	0
			140	88	24	28		
9	g	16	Total	C	N	O	0	0
			103	64	19	20		
9	h	21	Total	C	N	O	0	0
			140	88	24	28		

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Mol	Chain	Residues	Atoms				AltConf	Trace
9	i	16	Total	C	N	O	0	0
			103	64	19	20		
9	j	20	Total	C	N	O	0	0
			133	83	23	27		
9	k	16	Total	C	N	O	0	0
			103	64	19	20		
9	l	21	Total	C	N	O	0	0
			140	88	24	28		

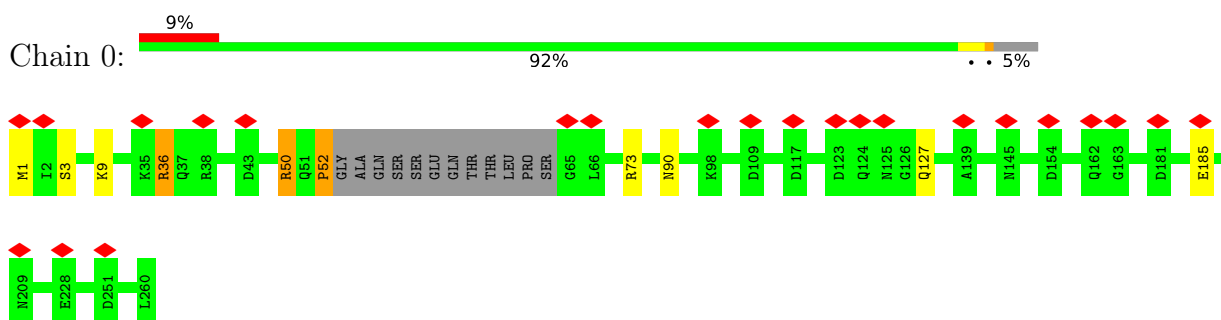
- Molecule 10 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
10	n	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
10	o	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
10	p	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
10	q	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

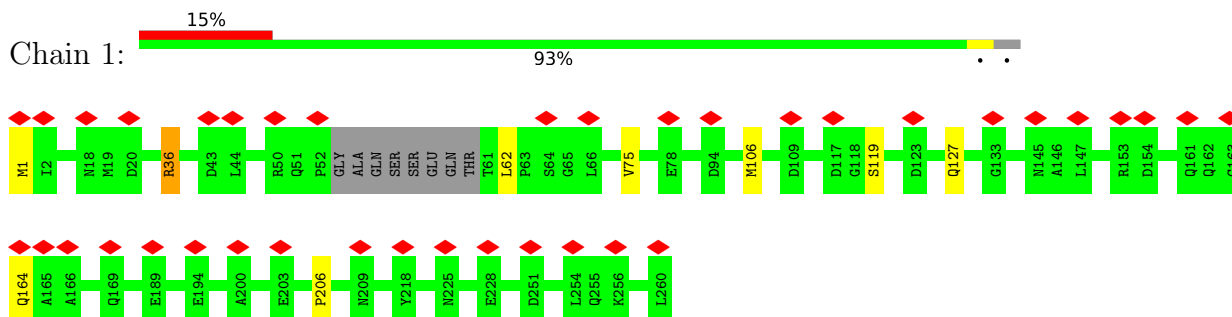
3 Residue-property plots [i](#)

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

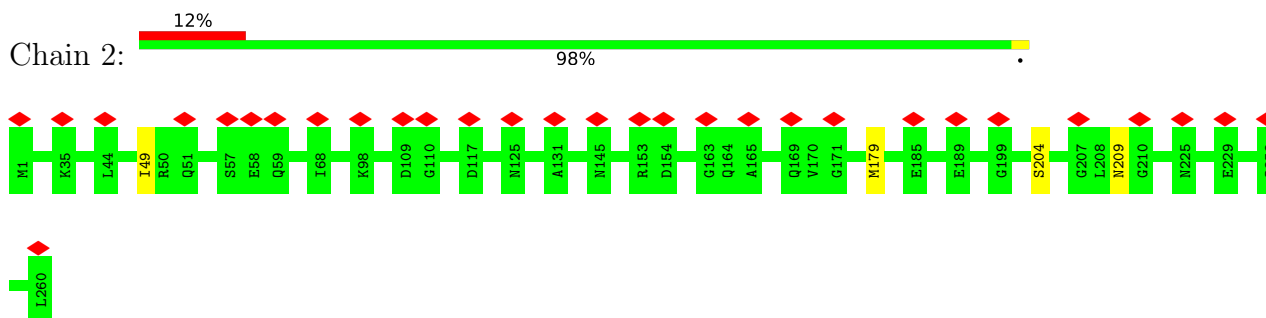
- Molecule 1: Flagellar basal-body rod protein FlgG



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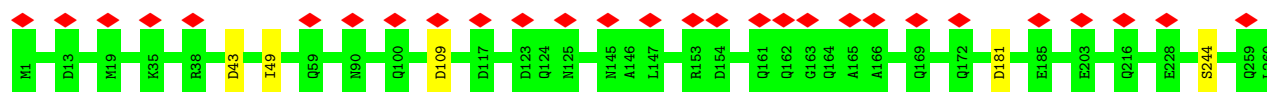


- Molecule 1: Flagellar basal-body rod protein FlgG

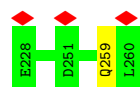
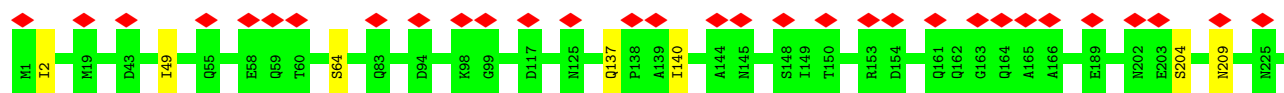


- Molecule 1: Flagellar basal-body rod protein FlgG

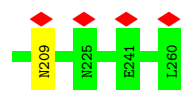
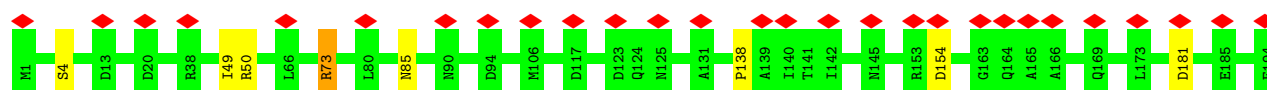




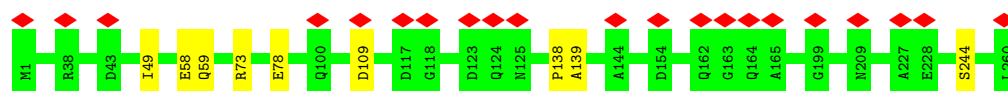
- Molecule 1: Flagellar basal-body rod protein FlgG



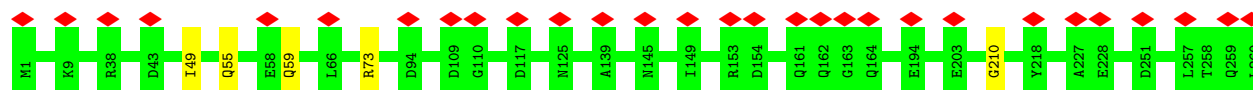
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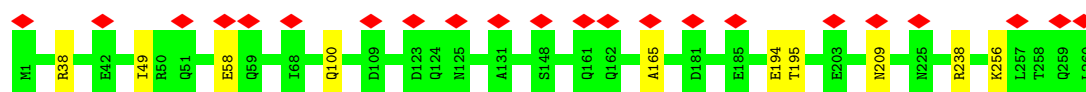
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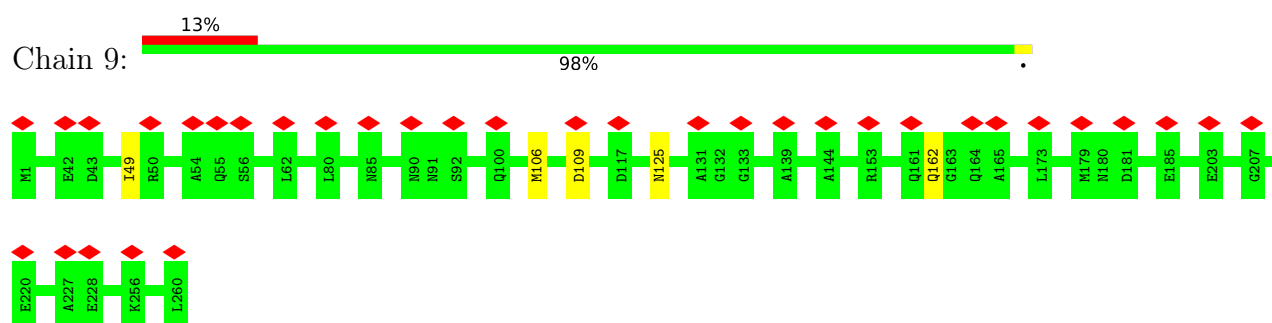
- Molecule 1: Flagellar basal-body rod protein FlgG



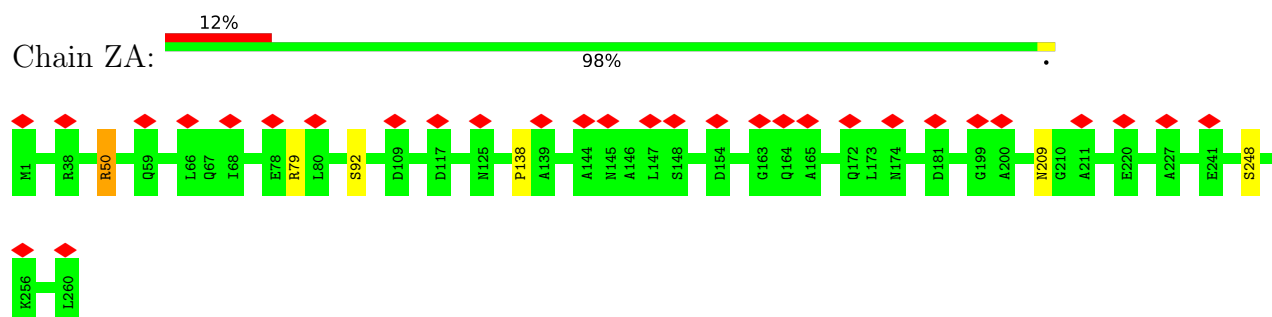
- Molecule 1: Flagellar basal-body rod protein FlgG



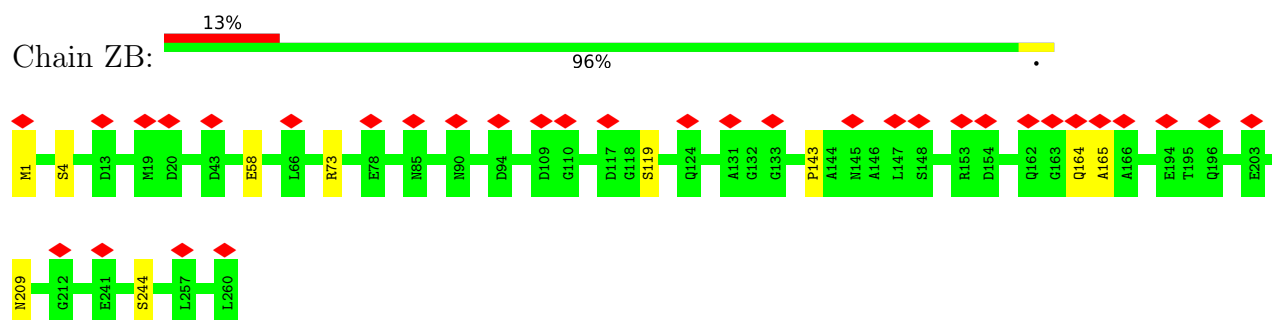
- Molecule 1: Flagellar basal-body rod protein FlgG



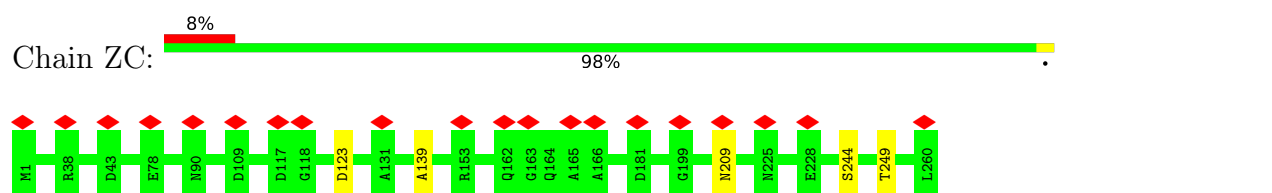
- Molecule 1: Flagellar basal-body rod protein FlgG



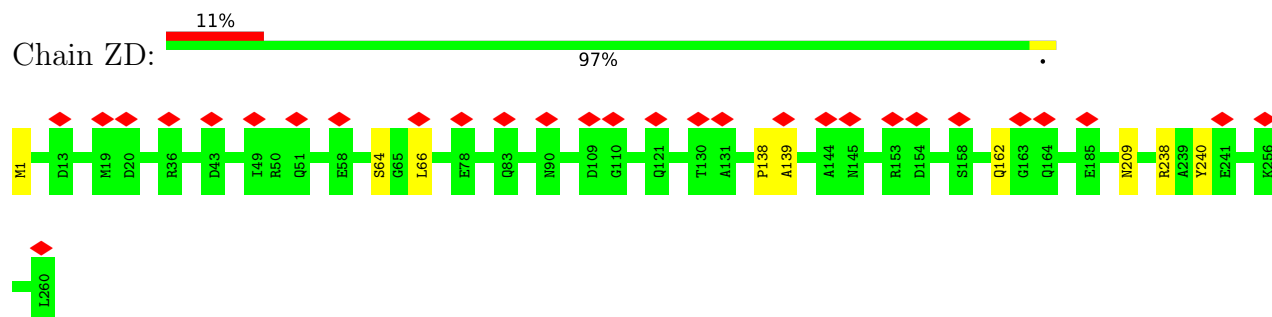
- Molecule 1: Flagellar basal-body rod protein FlgG



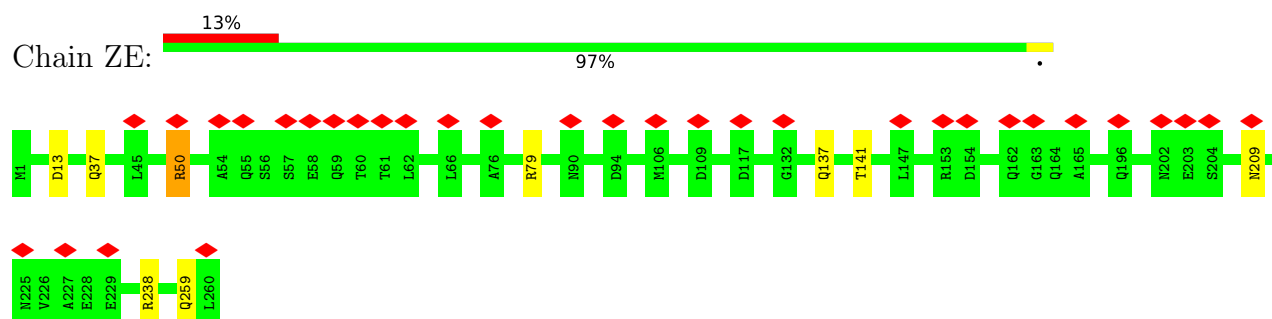
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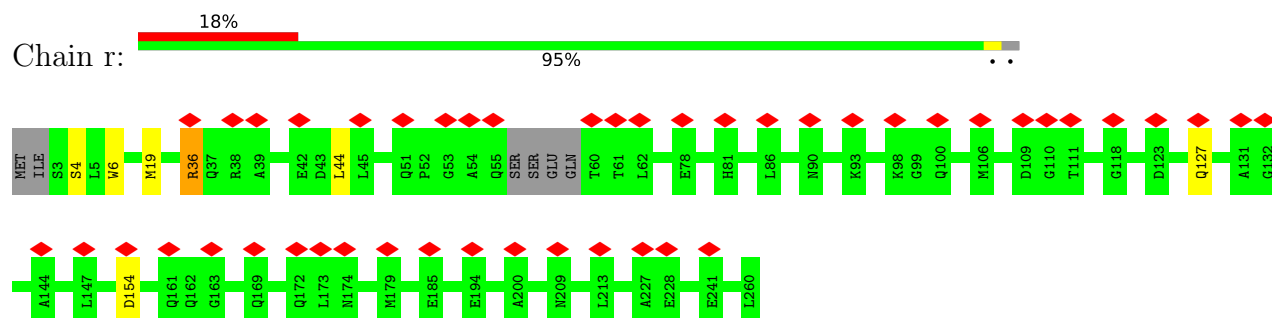
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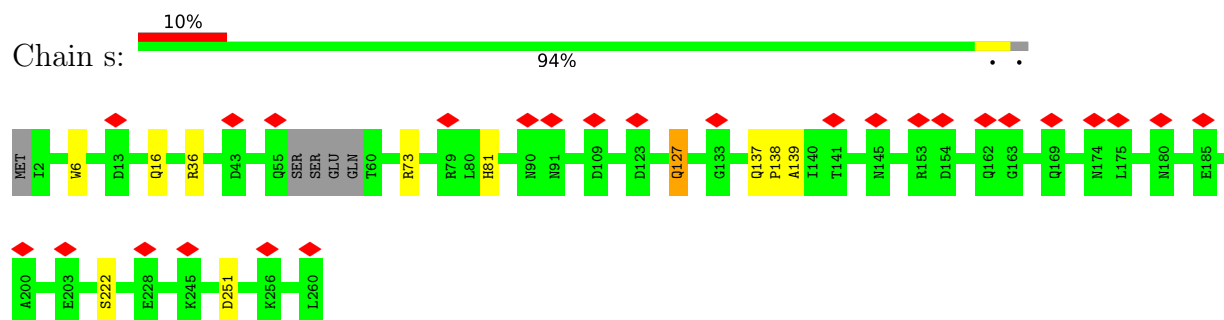
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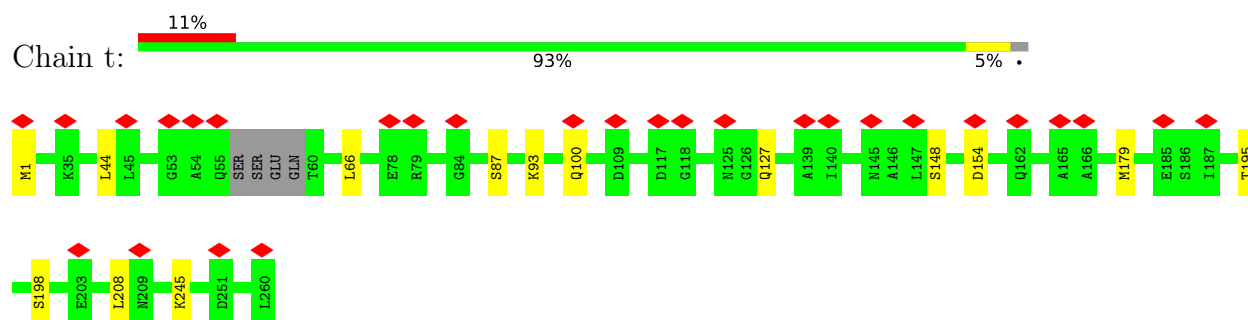
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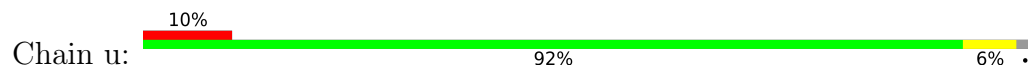
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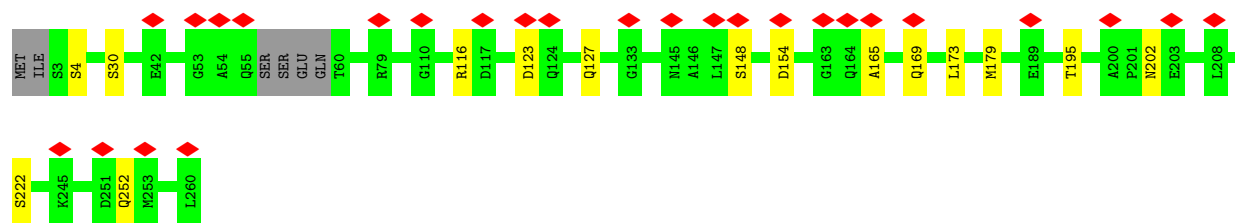


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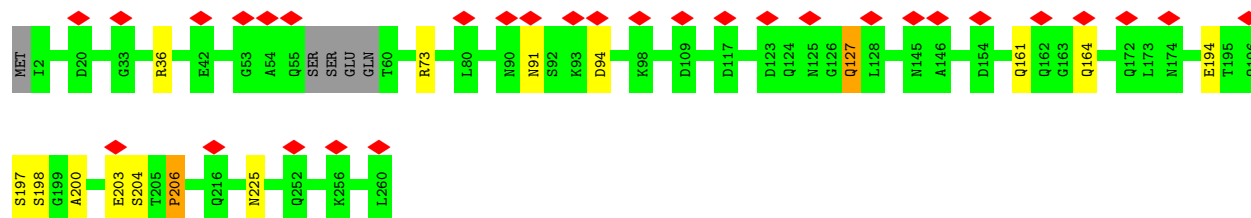
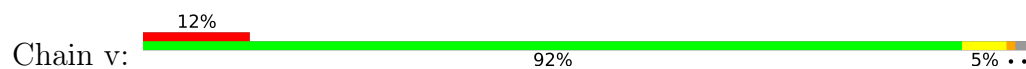


- Molecule 1: Flagellar basal-body rod protein FlgG

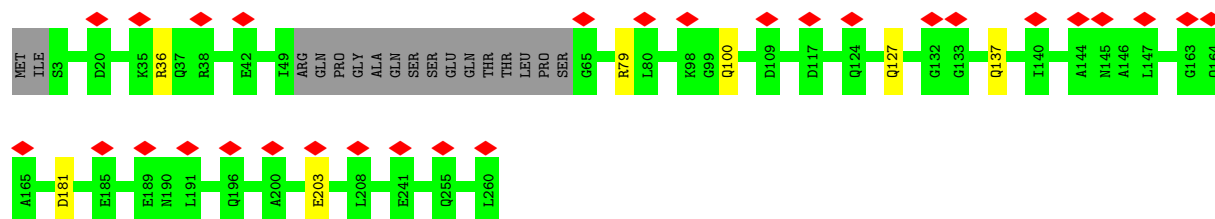
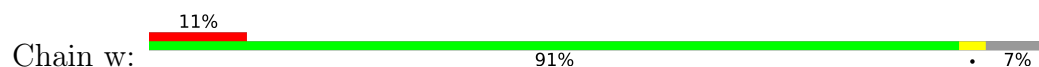




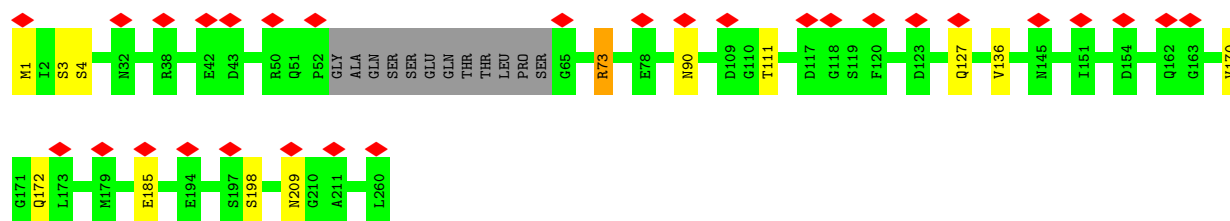
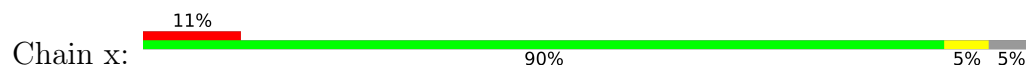
- Molecule 1: Flagellar basal-body rod protein FlgG



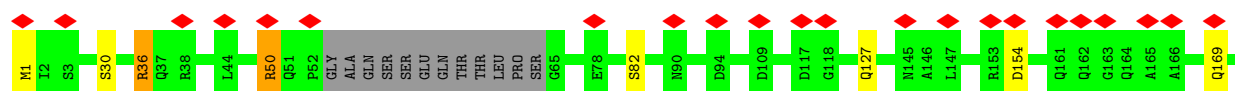
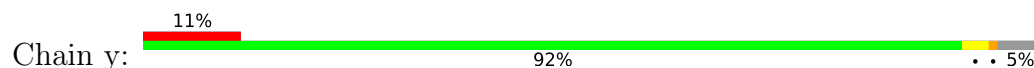
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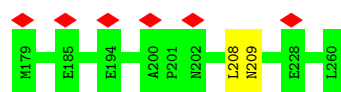


- Molecule 1: Flagellar basal-body rod protein FlgG

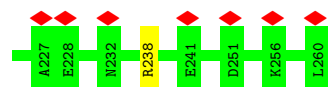
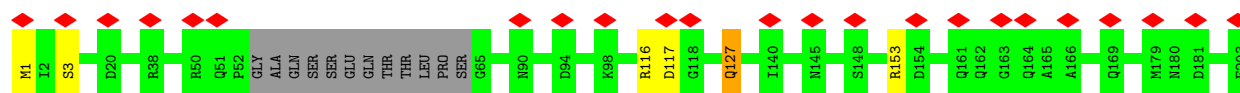


- Molecule 1: Flagellar basal-body rod protein FlgG

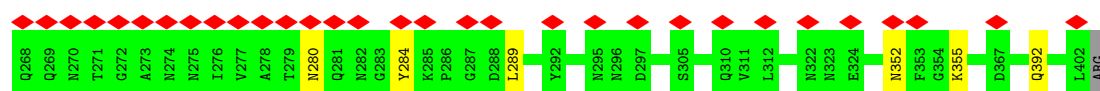
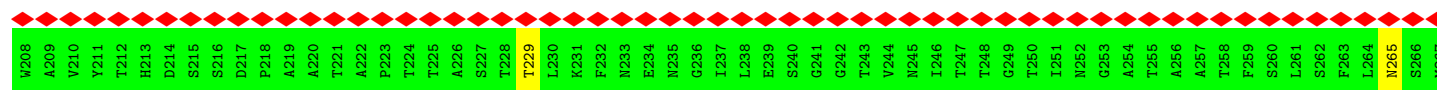
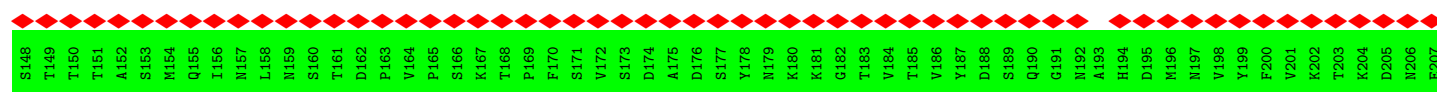
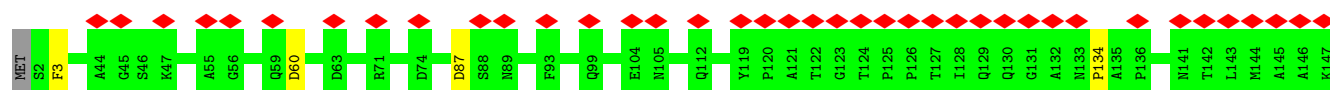




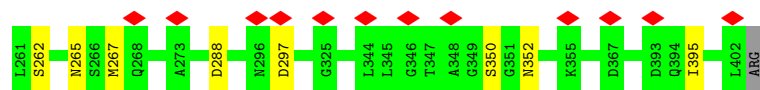
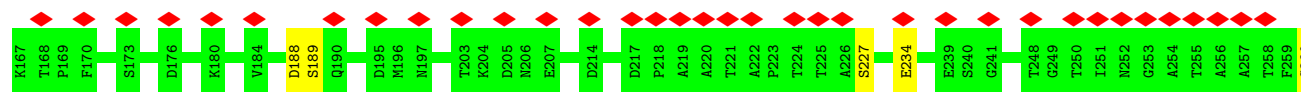
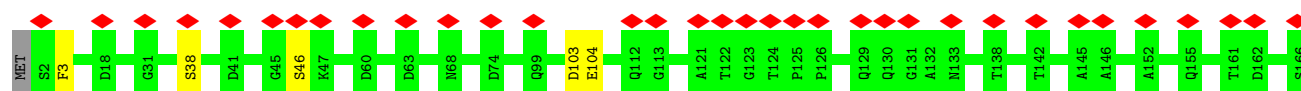
- Molecule 1: Flagellar basal-body rod protein FlgG



- Molecule 2: Flagellar hook protein FlgE

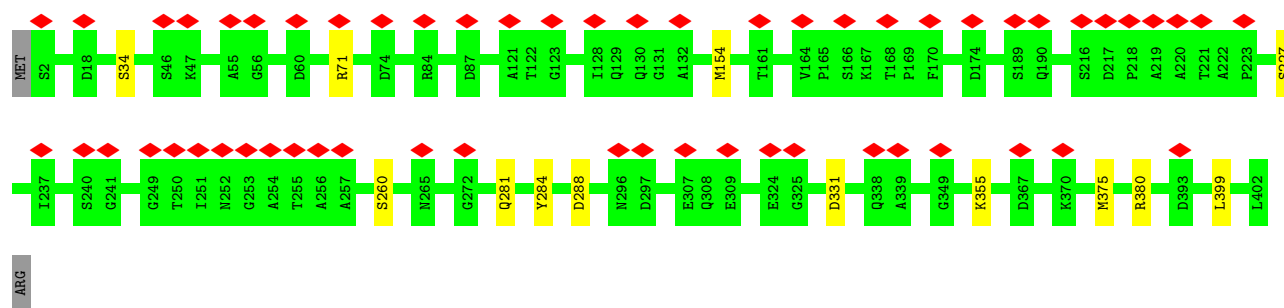


- Molecule 2: Flagellar hook protein FlgE



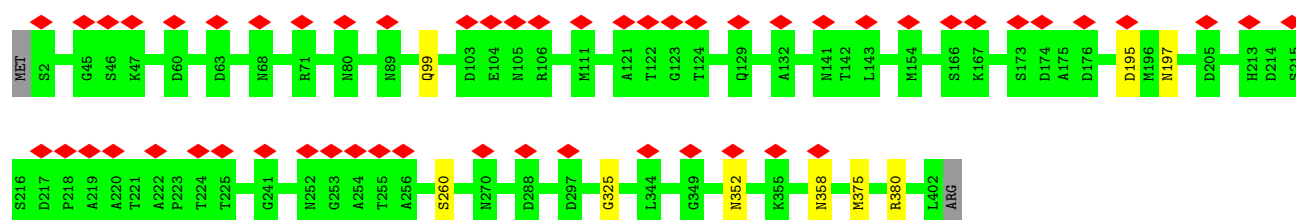
- Molecule 2: Flagellar hook protein FlgE

Chain ZH: 14% 96%



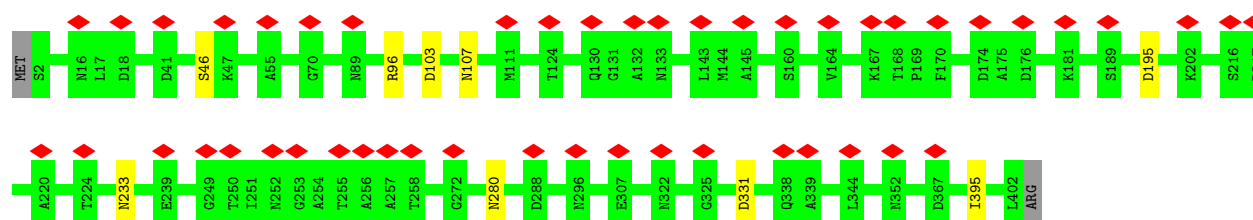
- Molecule 2: Flagellar hook protein FlgE

Chain ZI: 13% 97%



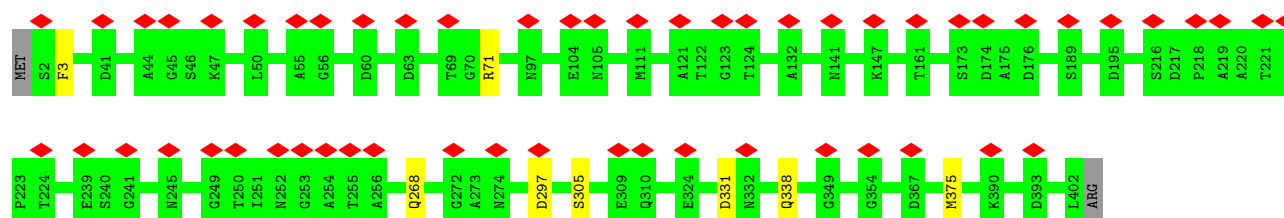
- Molecule 2: Flagellar hook protein FlgE

Chain ZJ: 12% 97%



- Molecule 2: Flagellar hook protein FlgE

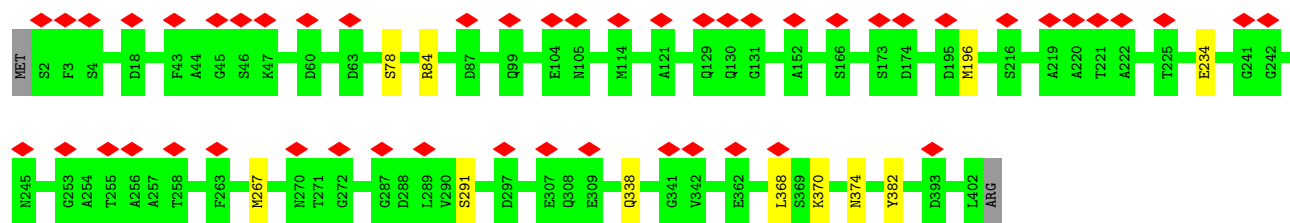
Chain ZK: 14% 98%



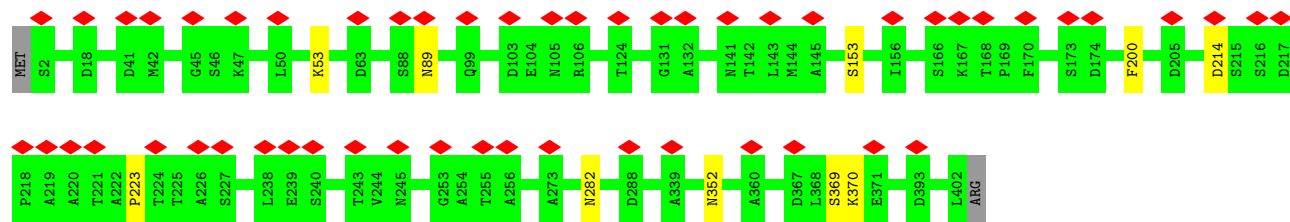
- Molecule 2: Flagellar hook protein FlgE

Chain ZL: 12% 97%

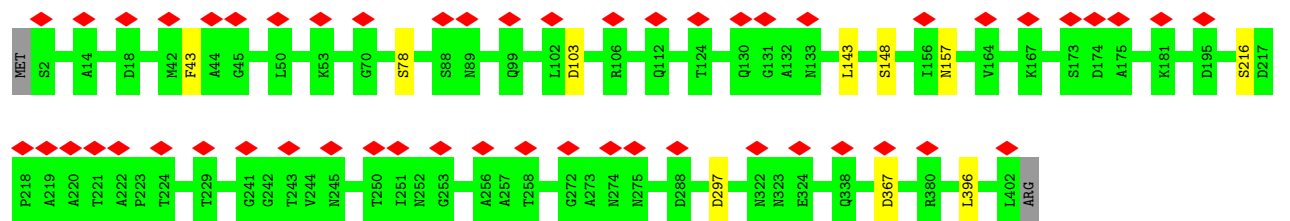




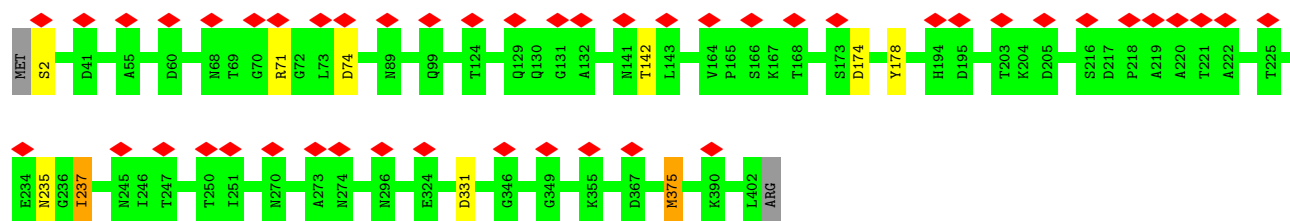
• Molecule 2: Flagellar hook protein FlgE



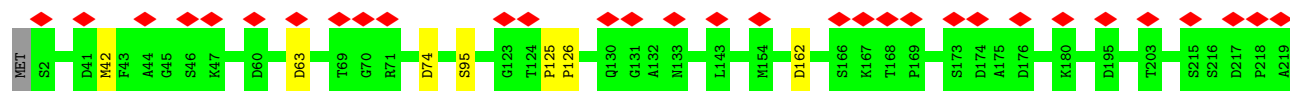
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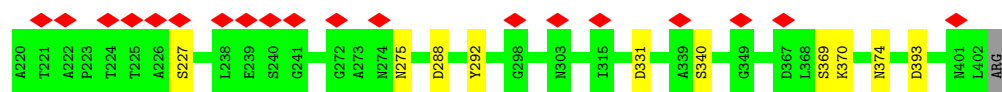


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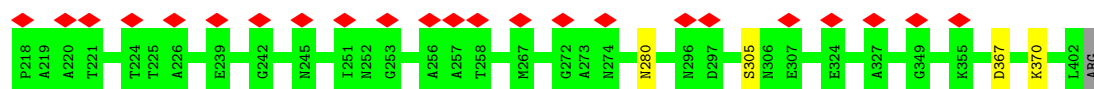
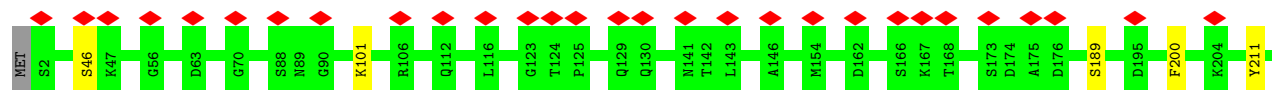


• Molecule 2: Flagellar hook protein FlgE

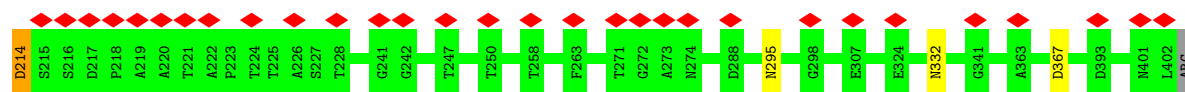
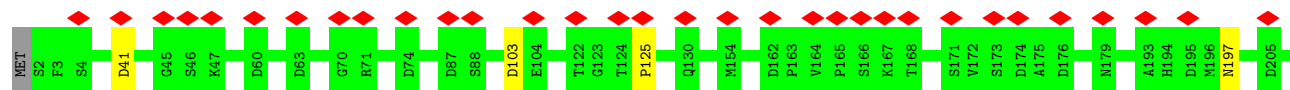




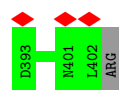
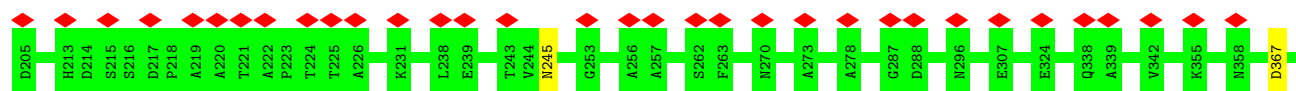
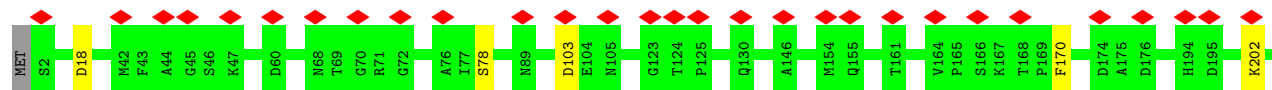
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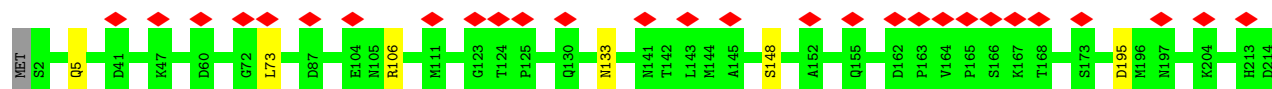
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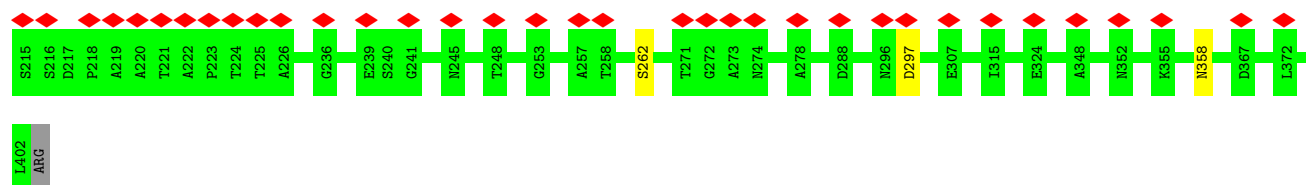


• Molecule 2: Flagellar hook protein FlgE



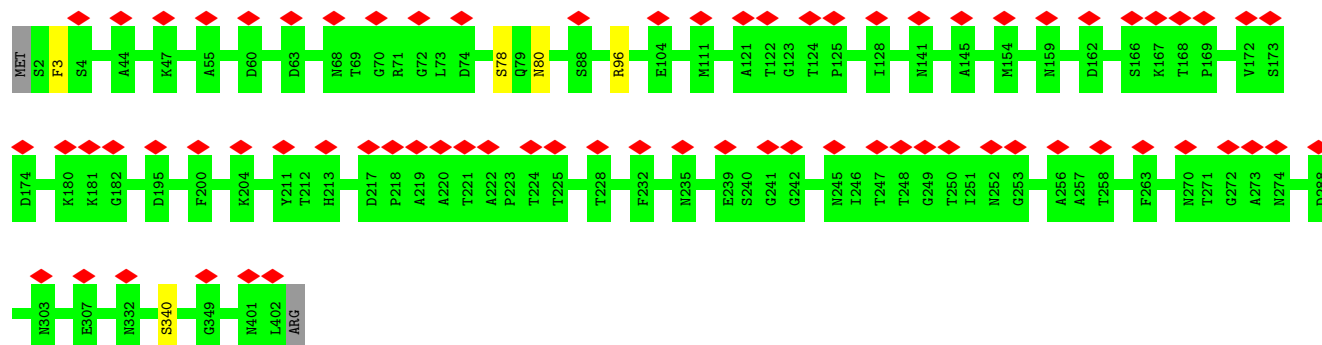
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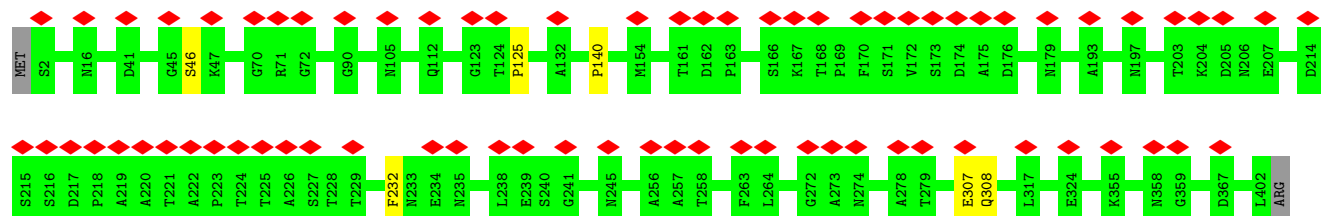
• Molecule 2: Flagellar hook protein FlgE

Chain ZU: 18% 98%



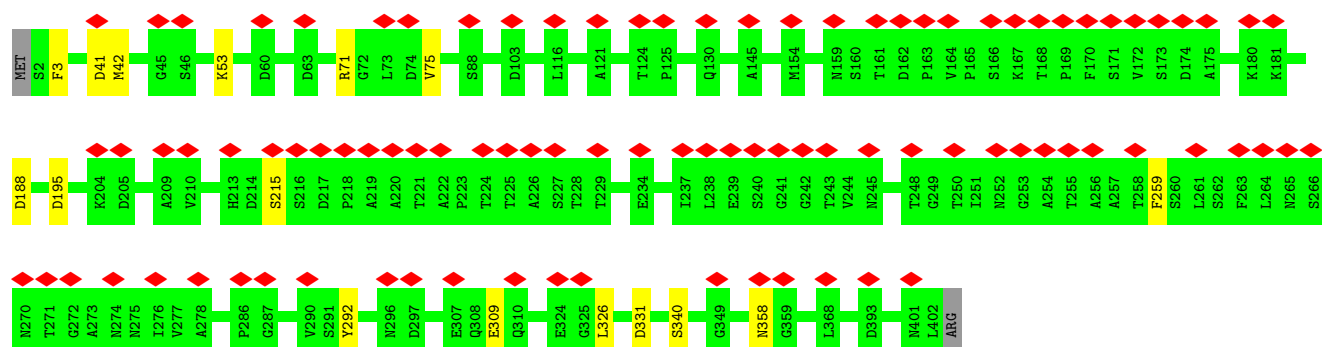
• Molecule 2: Flagellar hook protein FlgE

Chain ZV: 18% 98%



• Molecule 2: Flagellar hook protein FlgE

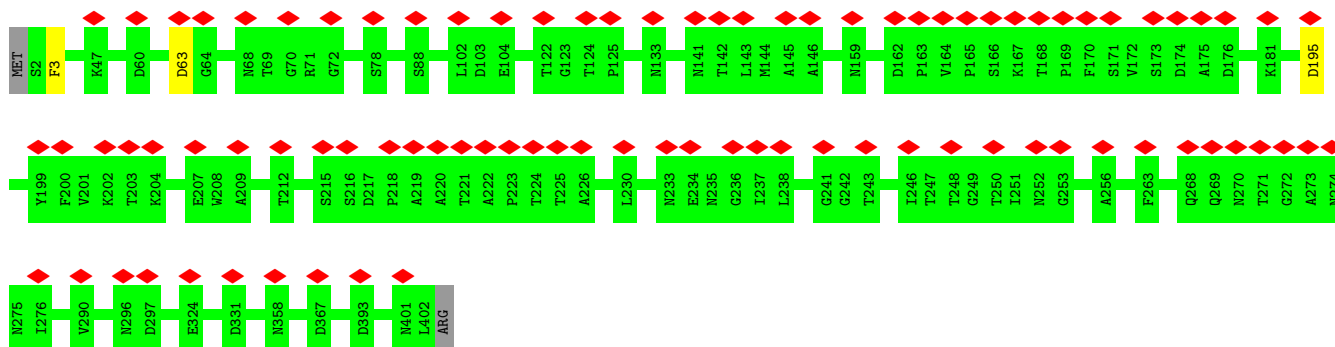
Chain ZW: 23% 96%



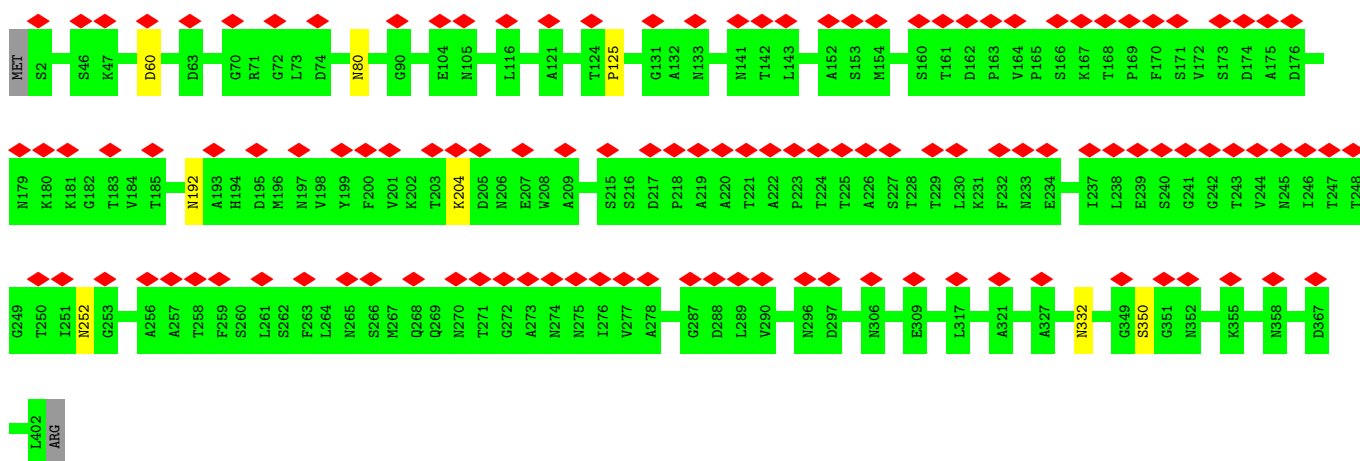
• Molecule 2: Flagellar hook protein FlgE

Chain ZX: 22% 99%

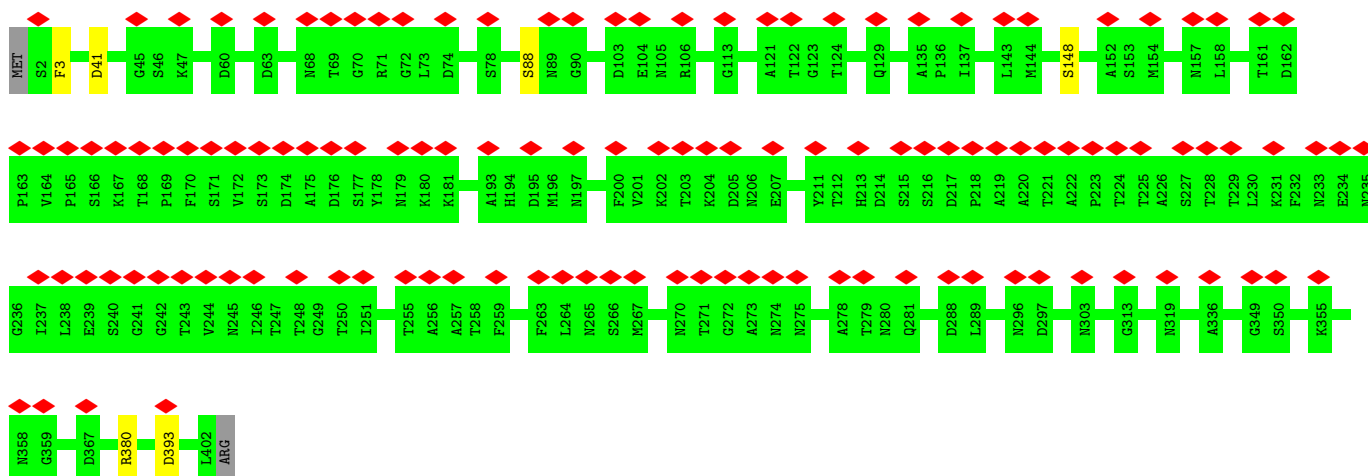




• Molecule 2: Flagellar hook protein FlgE

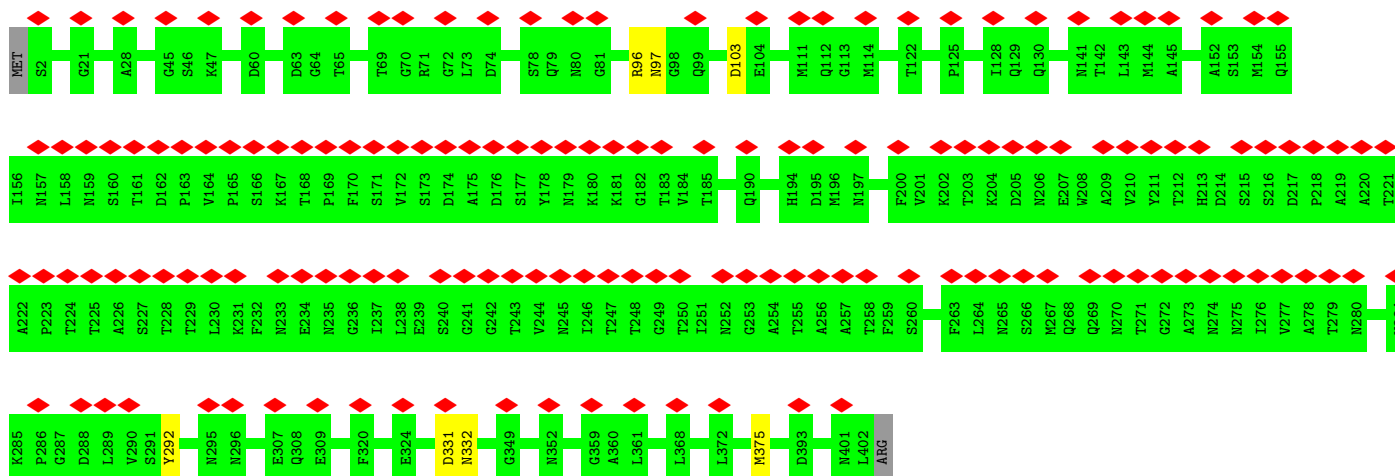


• Molecule 2: Flagellar hook protein FlgE

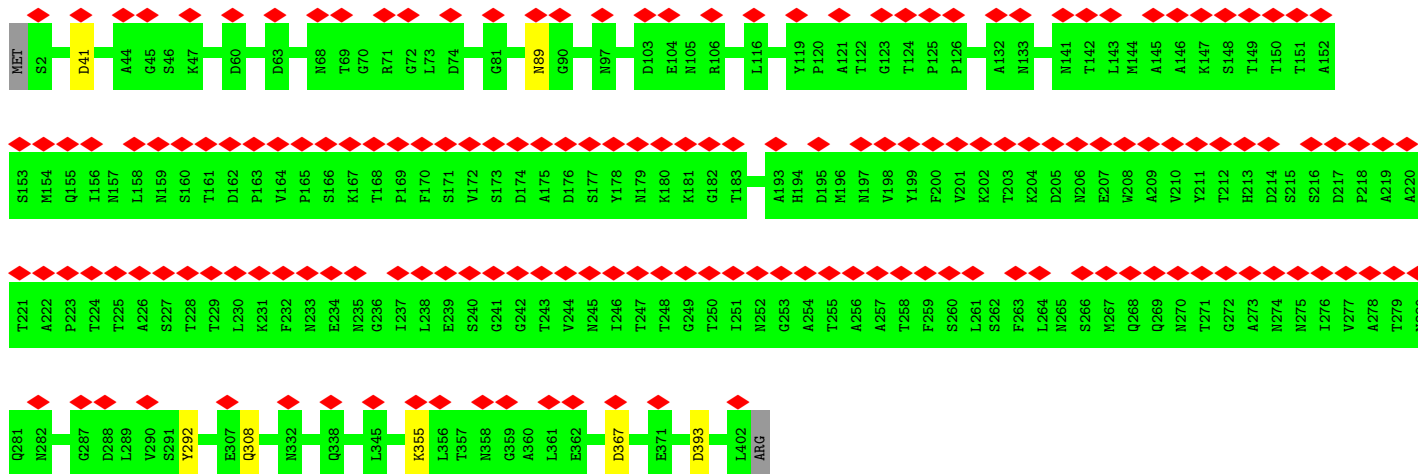
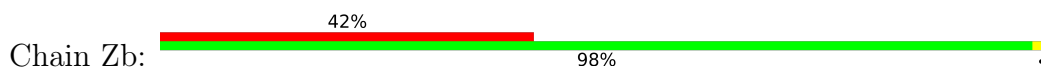


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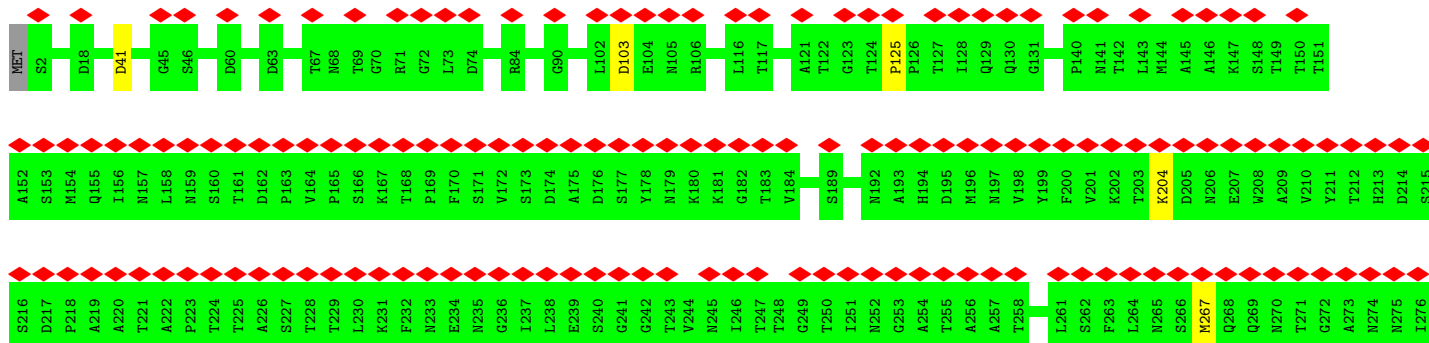
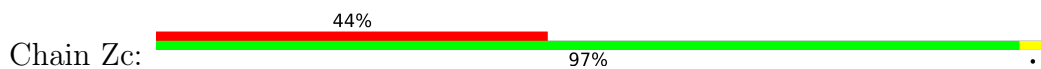


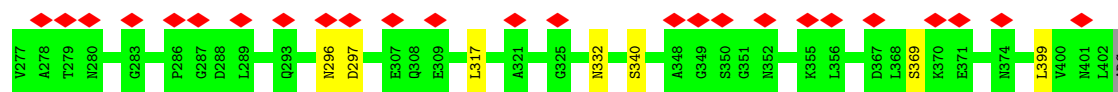


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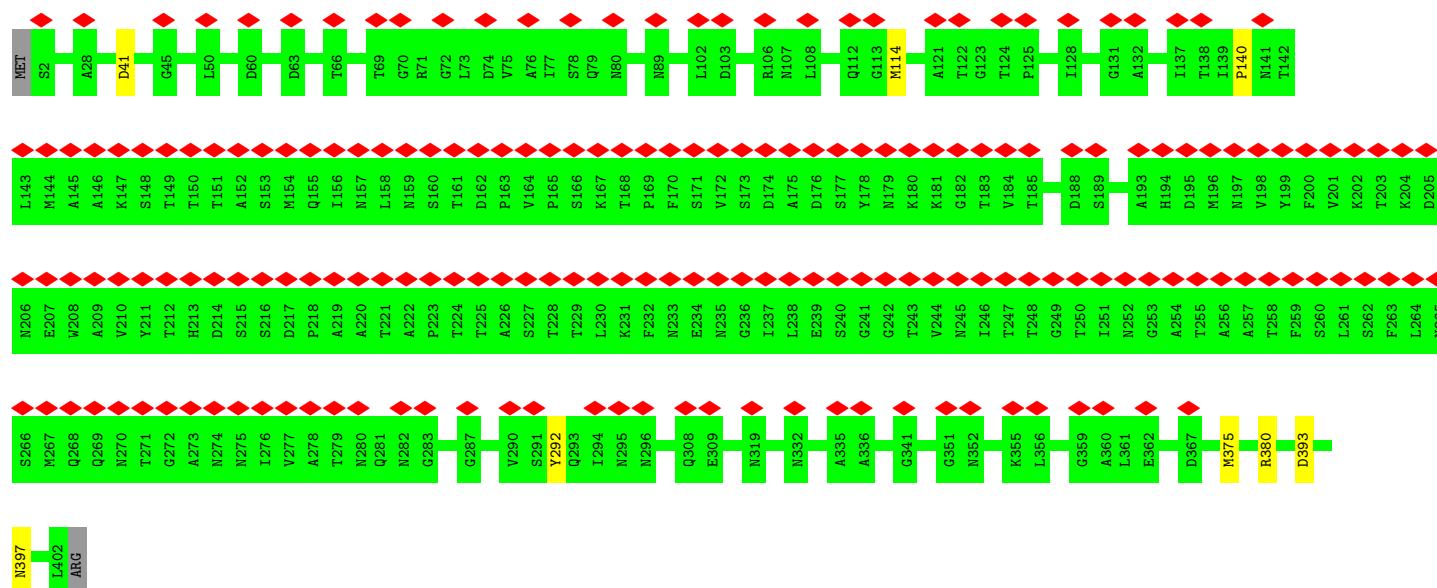


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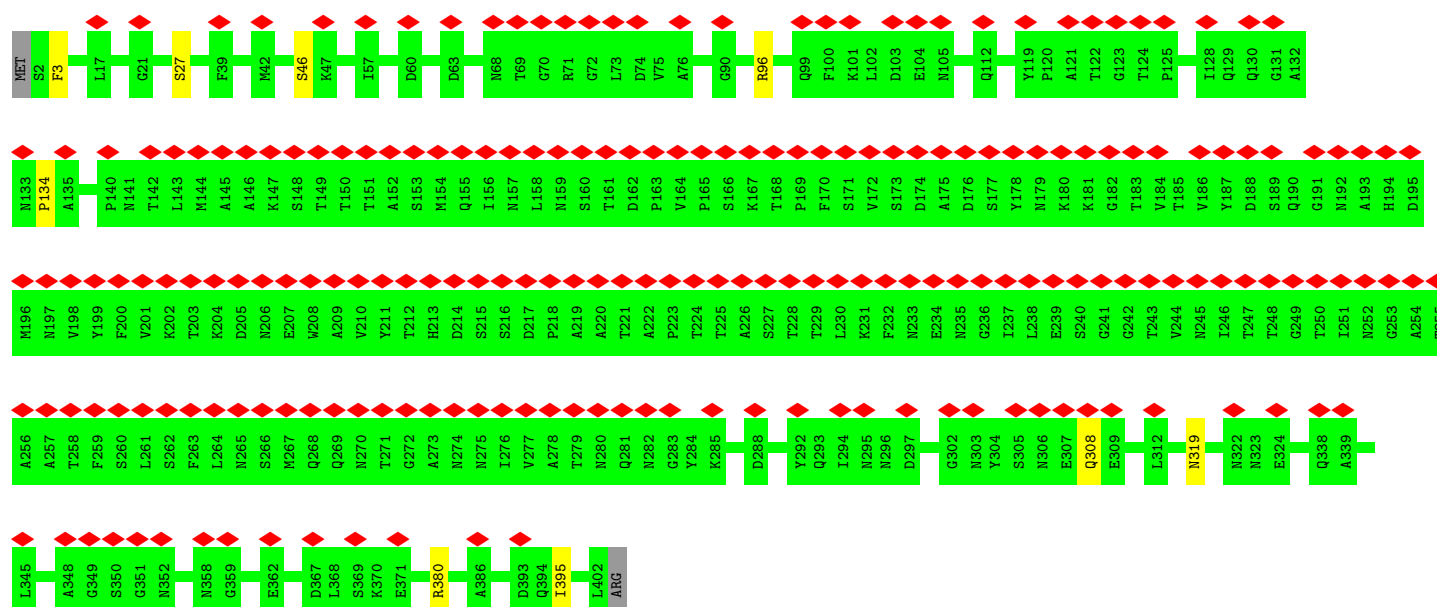




• Molecule 2: Flagellar hook protein FlgE

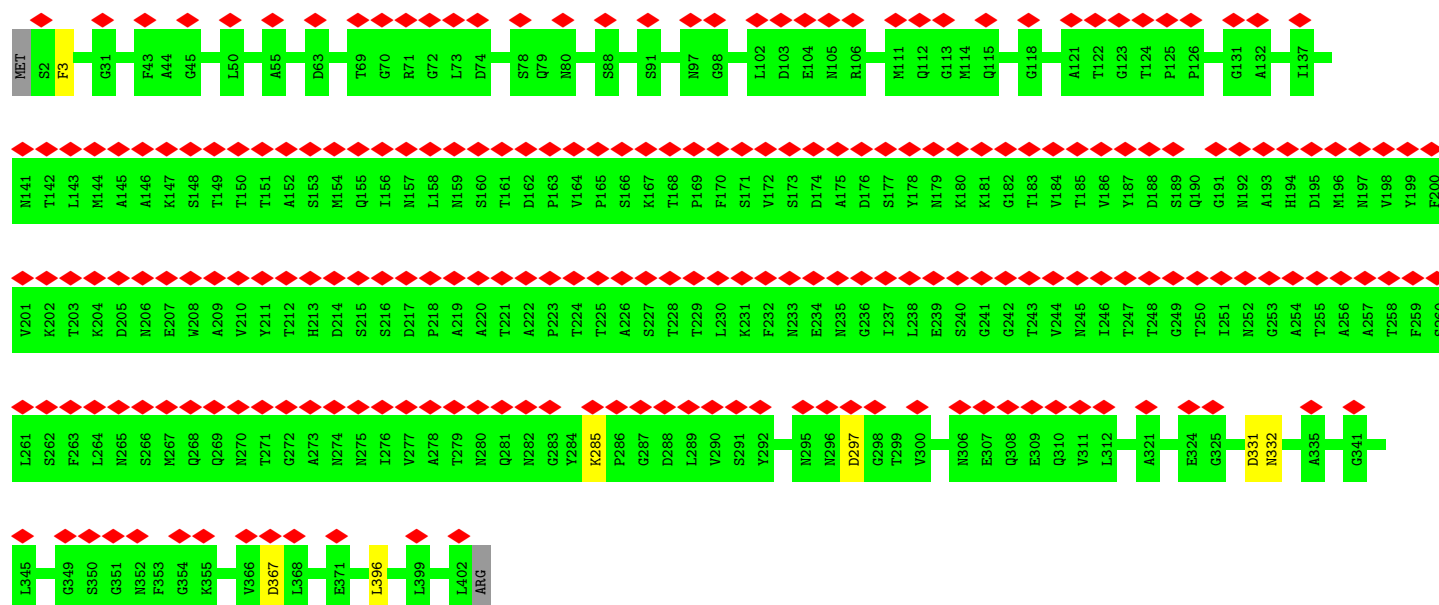


• Molecule 2: Flagellar hook protein FlgE

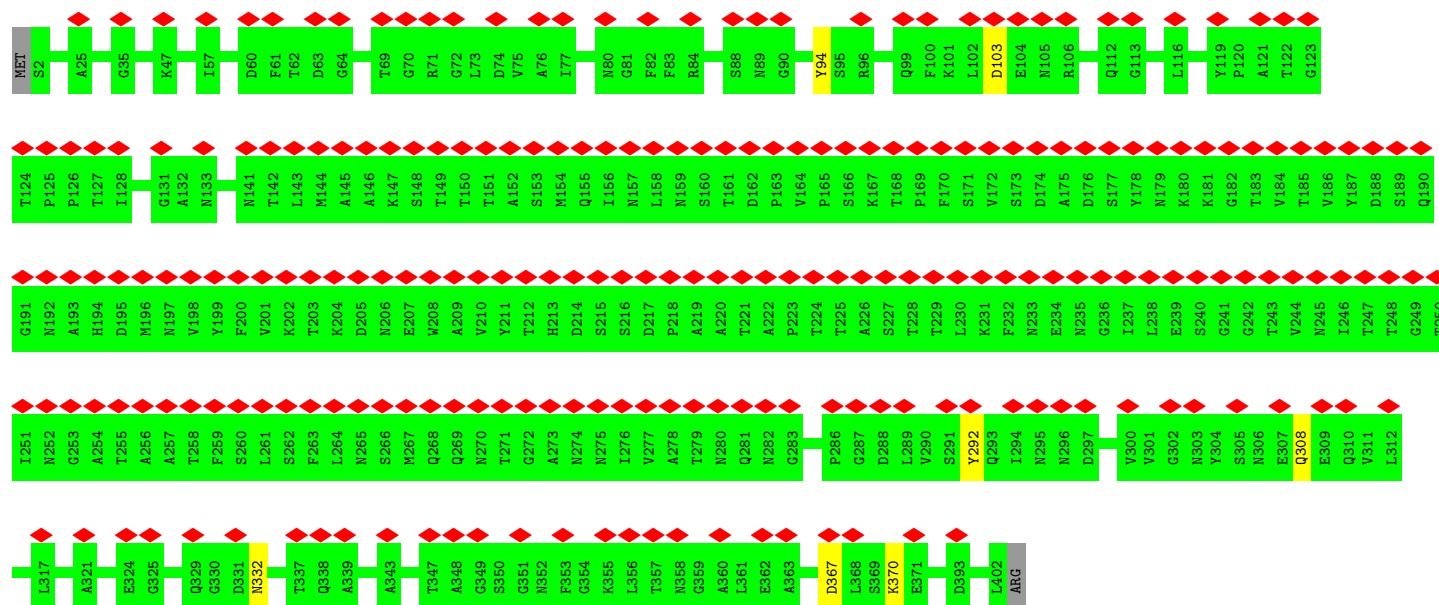


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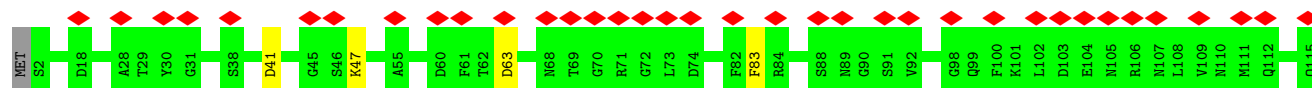


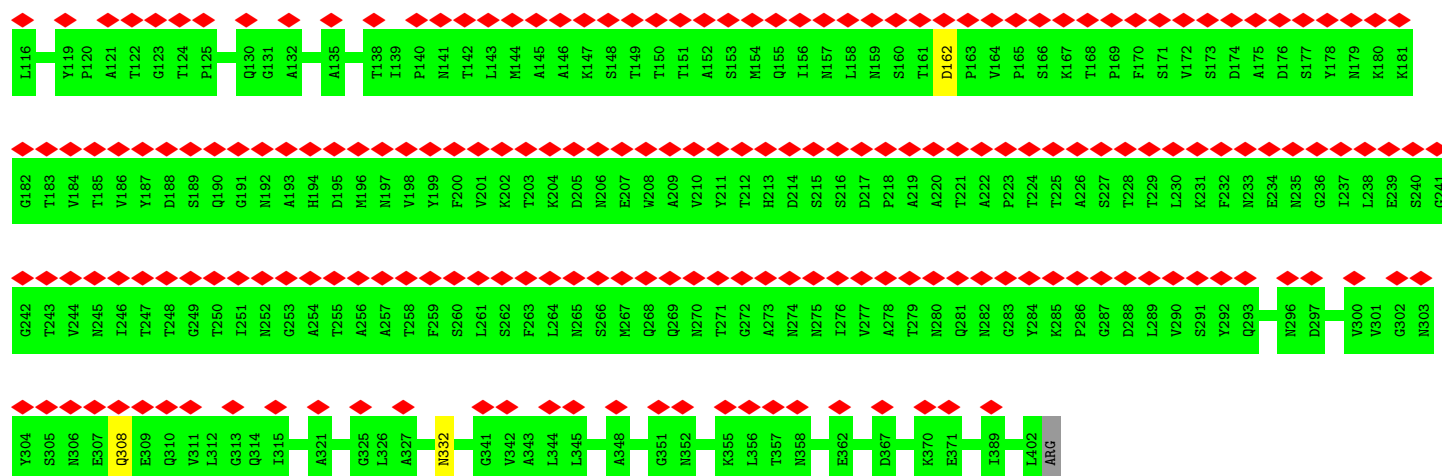


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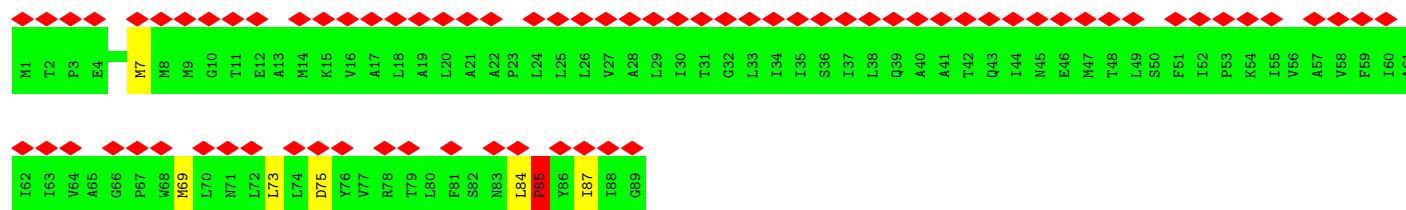
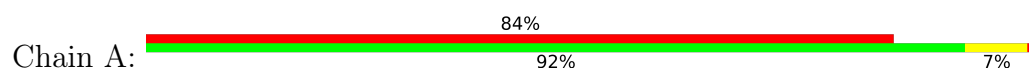


• Molecule 2: Flagellar hook protein FlgE

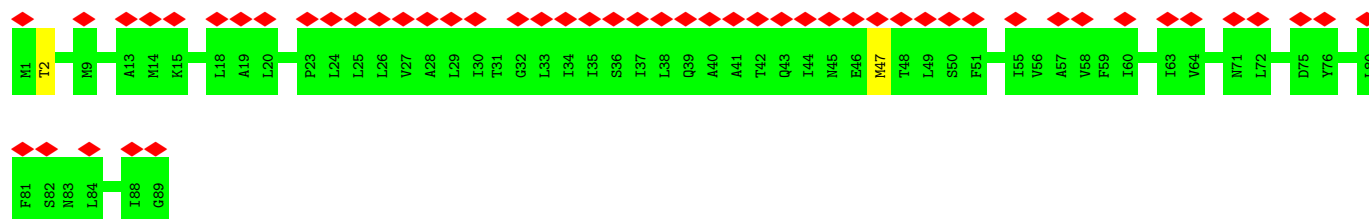




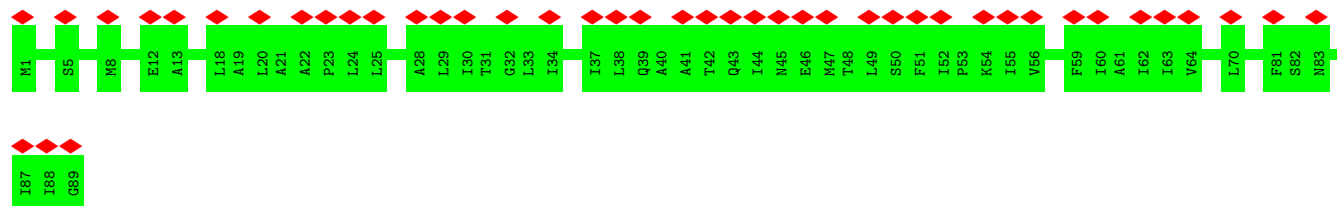
• Molecule 3: Flagellar biosynthetic protein FliQ



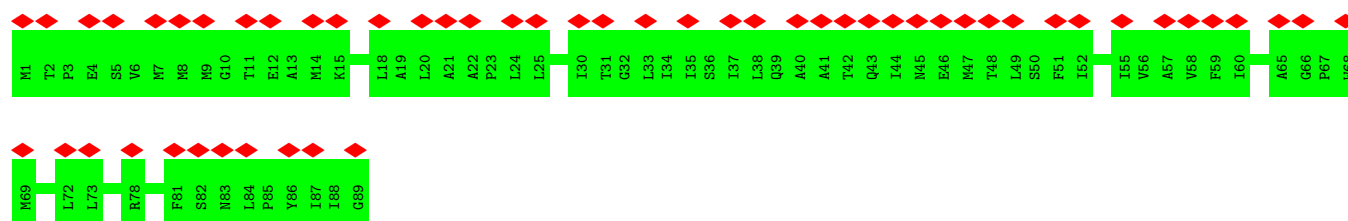
• Molecule 3: Flagellar biosynthetic protein FliQ



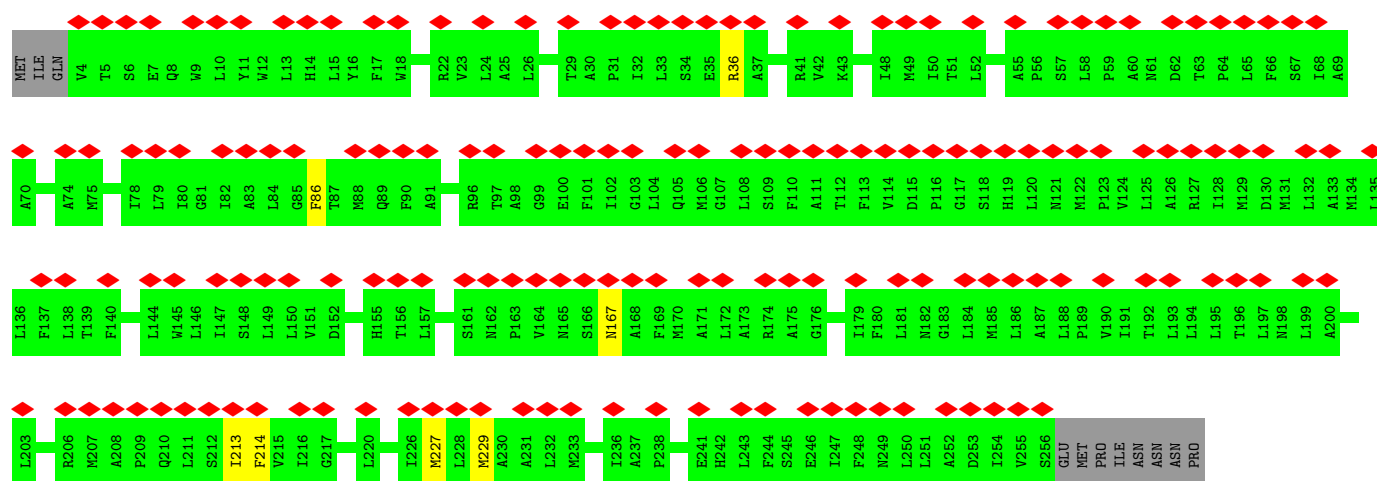
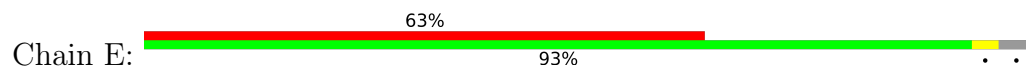
• Molecule 3: Flagellar biosynthetic protein FliQ



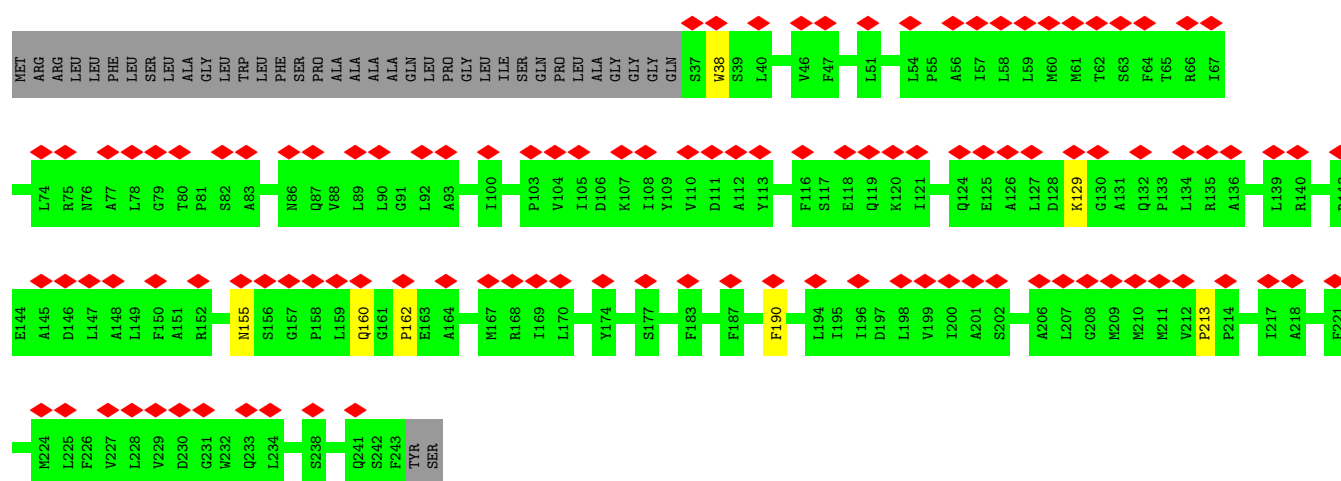
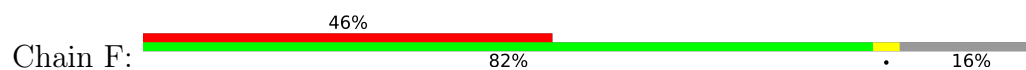
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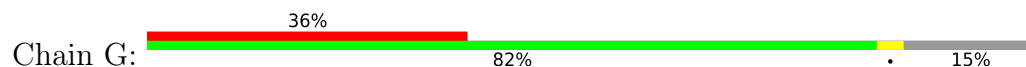
• Molecule 4: Flagellar biosynthetic protein FliR

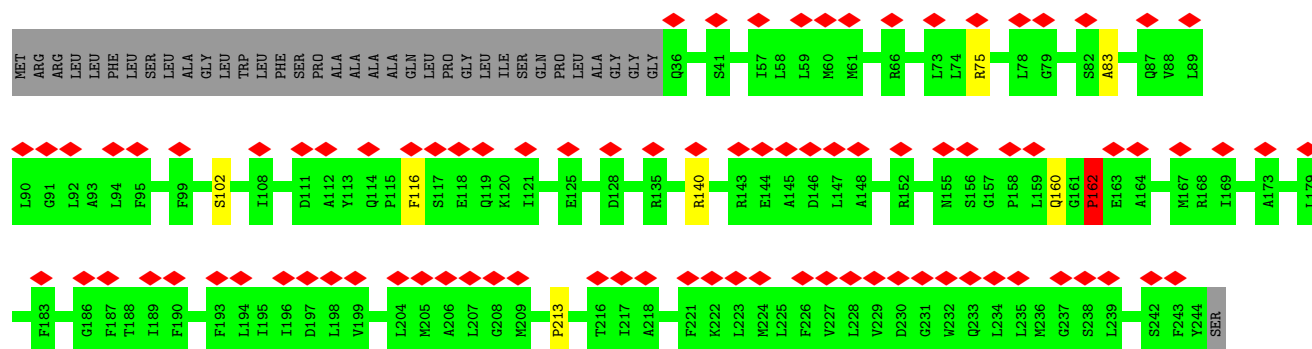


• Molecule 5: Flagellar biosynthetic protein FliP

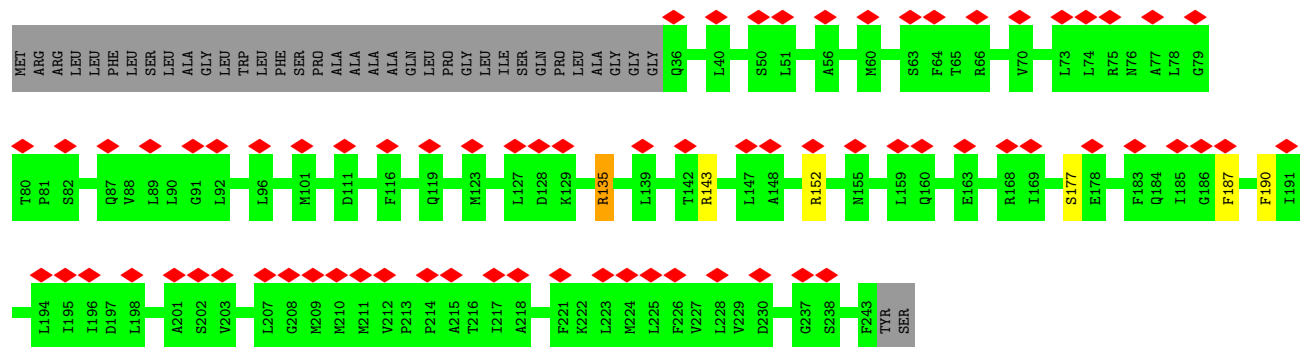
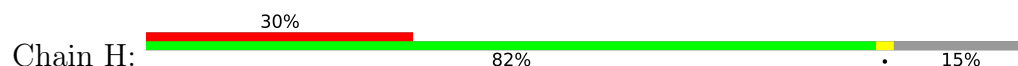


• Molecule 5: Flagellar biosynthetic protein FliP

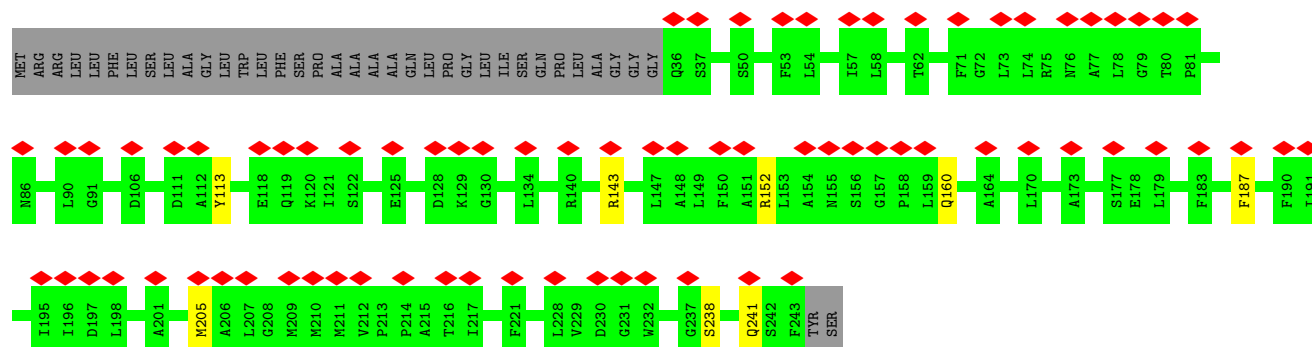
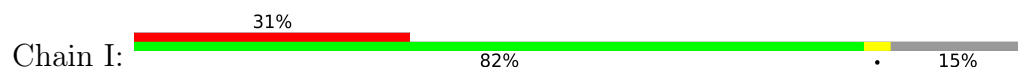




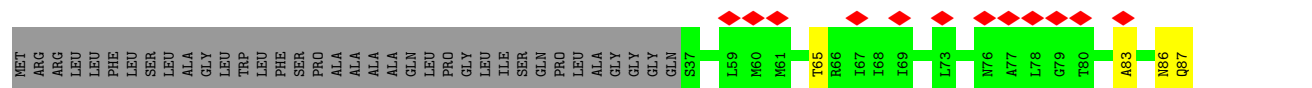
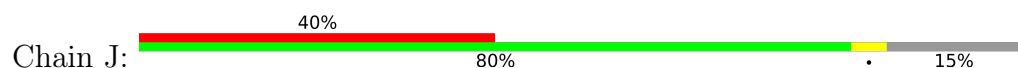
• Molecule 5: Flagellar biosynthetic protein FlpP

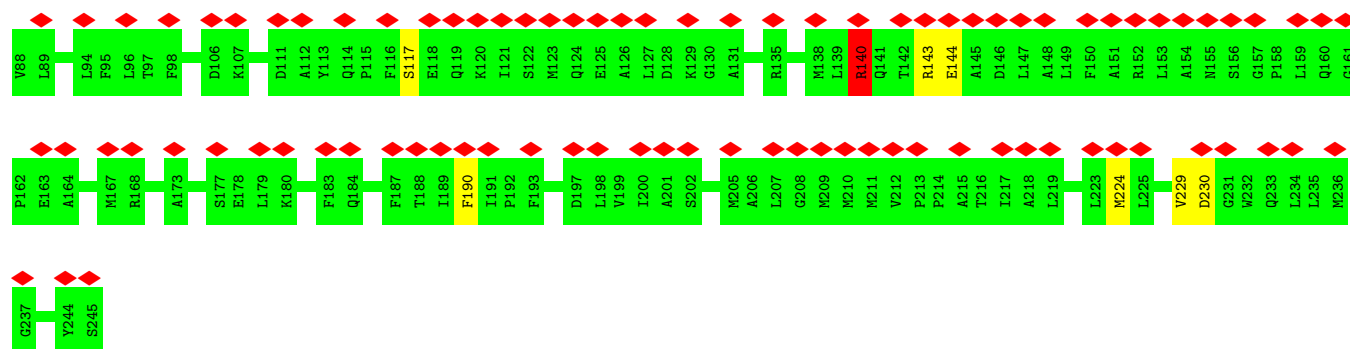


• Molecule 5: Flagellar biosynthetic protein FlpP

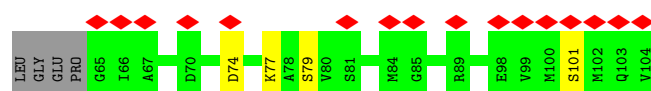
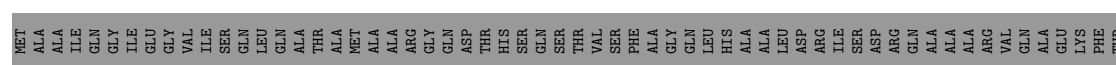


• Molecule 5: Flagellar biosynthetic protein FlpP

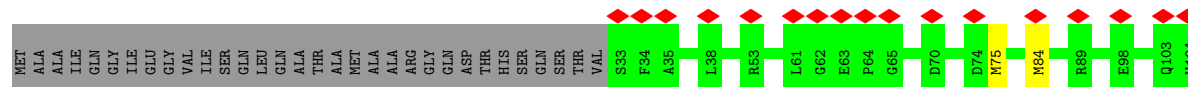




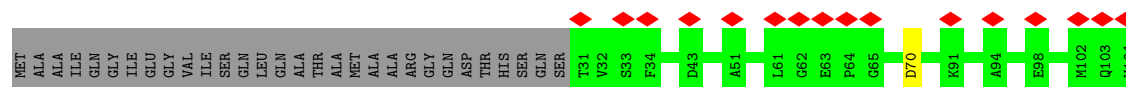
- Molecule 6: Flagellar hook-basal body complex protein FliE



- Molecule 6: Flagellar hook-basal body complex protein FliE



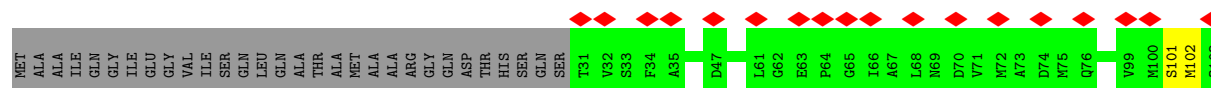
- Molecule 6: Flagellar hook-basal body complex protein FliE



- Molecule 6: Flagellar hook-basal body complex protein FliE

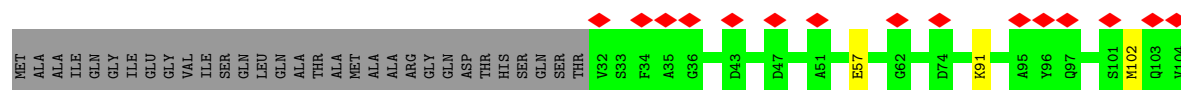


- Molecule 6: Flagellar hook-basal body complex protein FliE

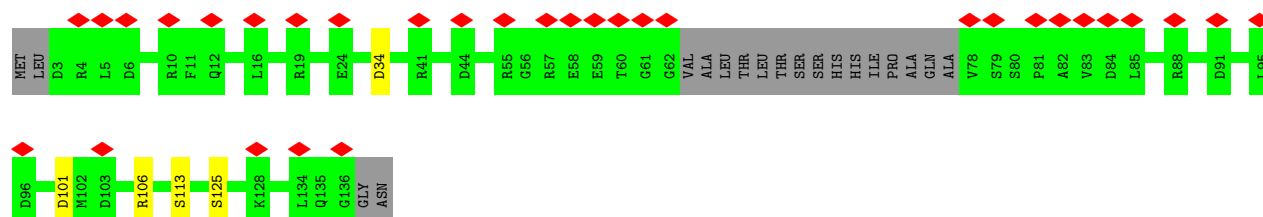
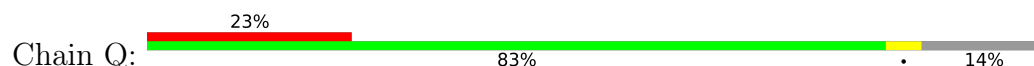




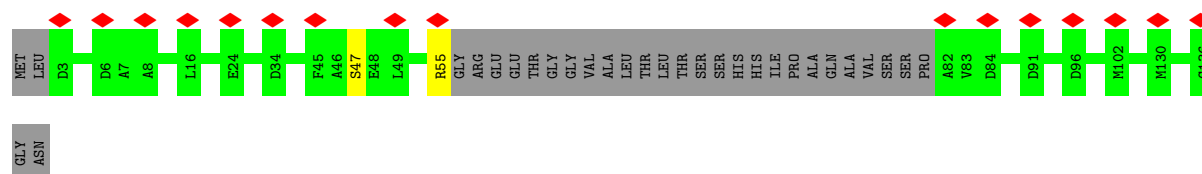
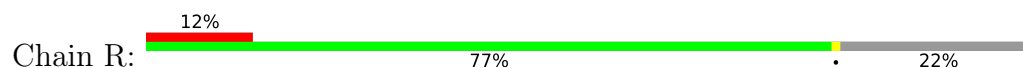
- Molecule 6: Flagellar hook-basal body complex protein FliE



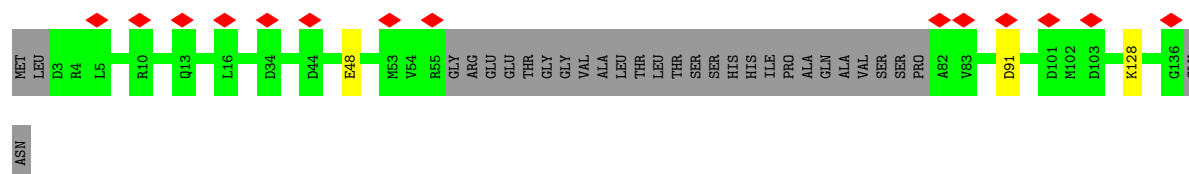
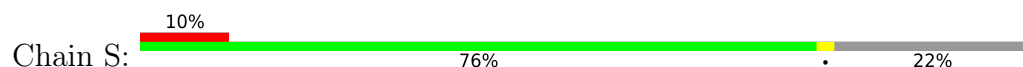
- Molecule 7: Flagellar basal body rod protein FlgB



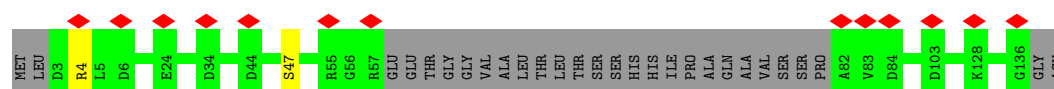
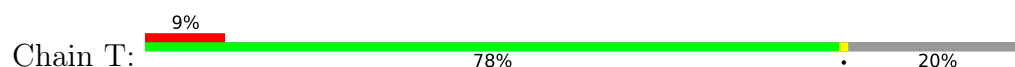
- Molecule 7: Flagellar basal body rod protein FlgB



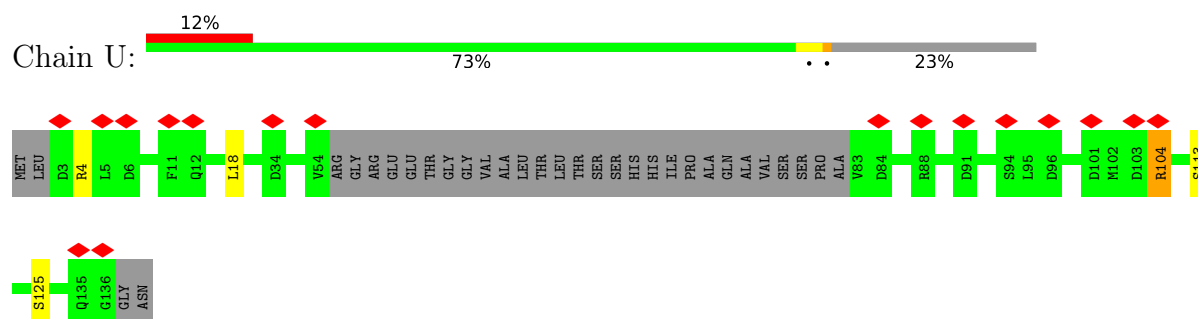
- Molecule 7: Flagellar basal body rod protein FlgB



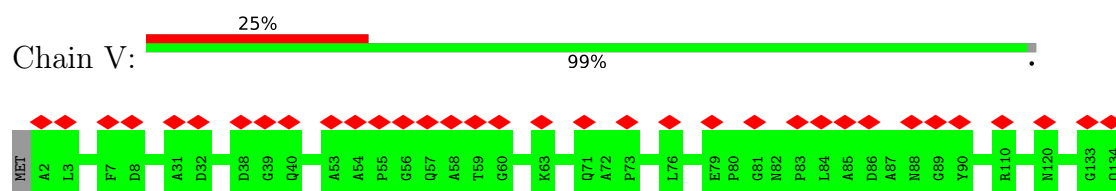
- Molecule 7: Flagellar basal body rod protein FlgB



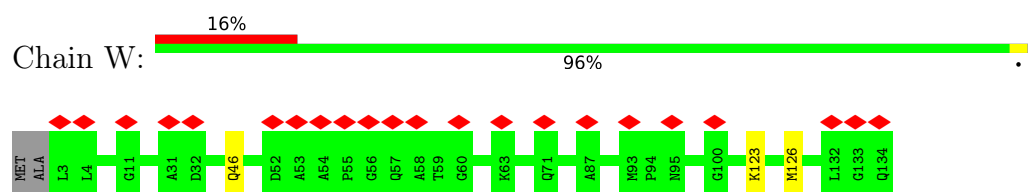
- Molecule 7: Flagellar basal body rod protein FlgB



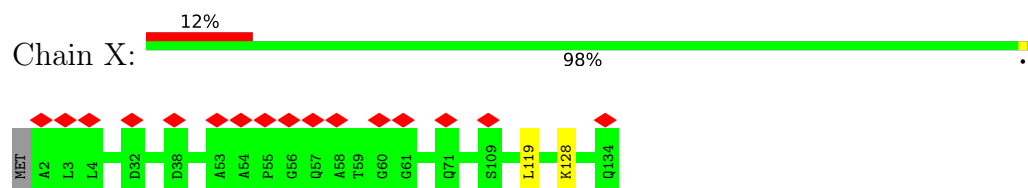
- Molecule 8: Flagellar basal-body rod protein FlgC



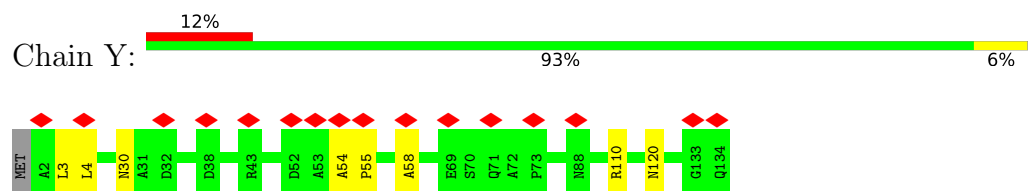
- Molecule 8: Flagellar basal-body rod protein FlgC



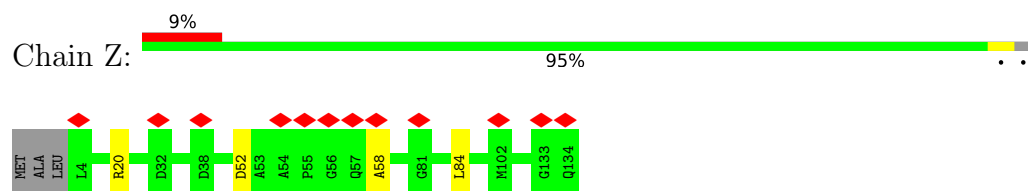
- Molecule 8: Flagellar basal-body rod protein FlgC



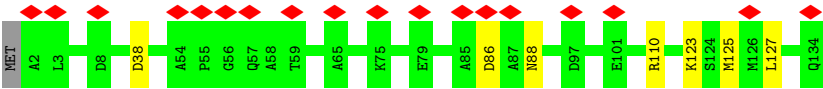
- Molecule 8: Flagellar basal-body rod protein FlgC



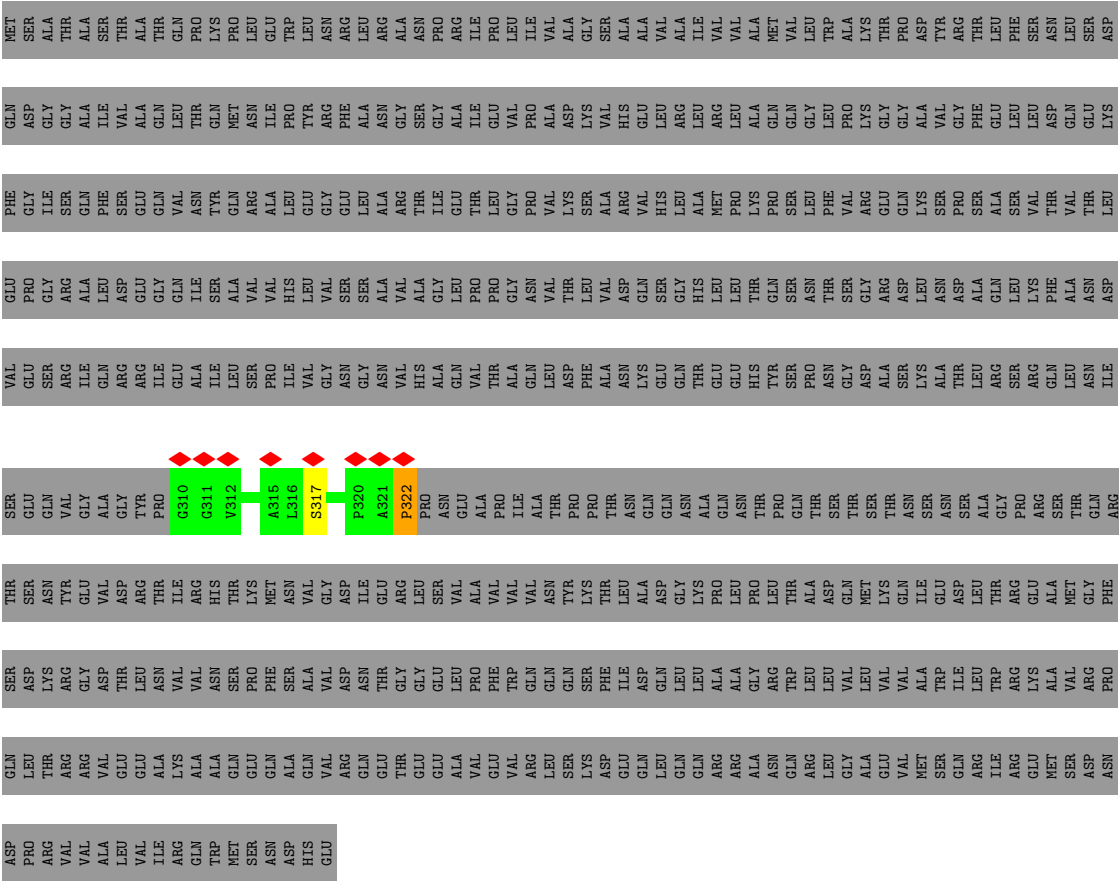
- Molecule 8: Flagellar basal-body rod protein FlgC



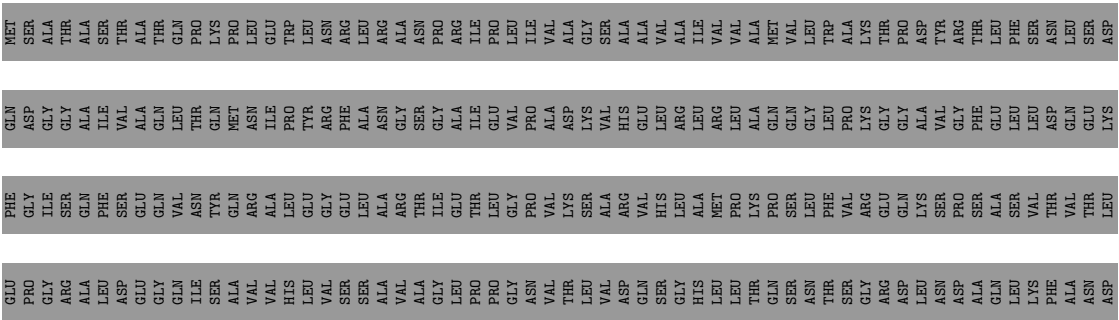
- Molecule 8: Flagellar basal-body rod protein FlgC

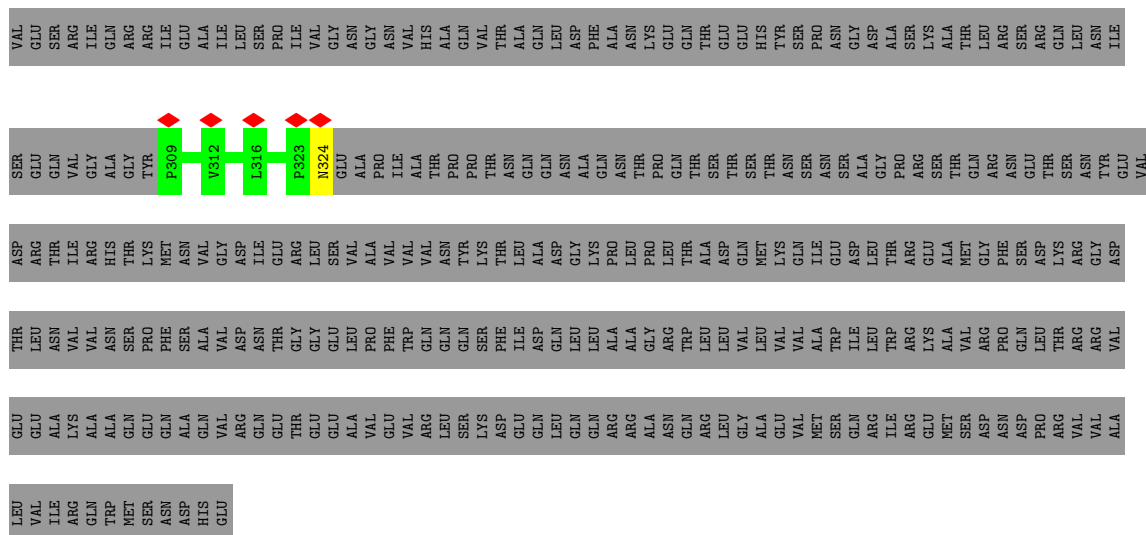


• Molecule 9: Flagellar M-ring protein

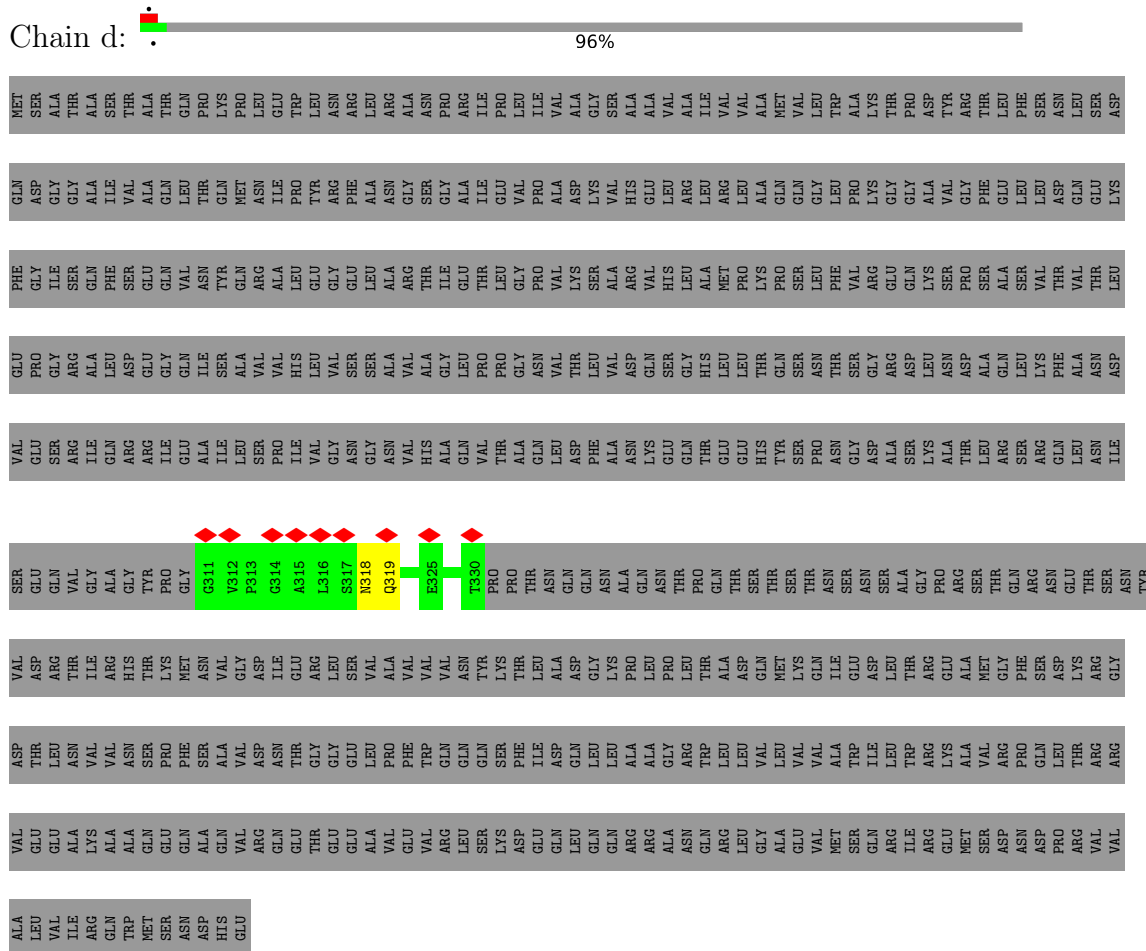


• Molecule 9: Flagellar M-ring protein





- Molecule 9: Flagellar M-ring protein



- Molecule 9: Flagellar M-ring protein

ASN	GLN
ASP	ALA
HIS	ARG
GLU	VAL

- Molecule 9: Flagellar M-ring protein

Chain g:  97%

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

GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	VAL	LEU	HIS	LEU	VAL	SER	SER	ALA	ALA	VAL	VAL	GLY	ASN	VAL	THR	THR	THR	GLN	SER	ASN	HIS	LEU	LEU	LEU	ASP	ARG	ALA	GLN	ALA	ASP	ASN	LYS	PHE	ASN	ASP
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VAL	GLU	SER	SER	ARG	ILE	GLN	ARG	ARG	ILE	ALA	ILE	LEU	SER	PRO	ILE	VAL	GLY	ASN	GLY	ASN	VAL	THR	VAL	ALA	ALA	ALA	GLN	LEU	ASP	PHE	ALA	ASN	LYS	GLN	GLN	THR	GLU	GLY	TYR	SER	PRO	ASN	GLY	ASP	ALA	SER	LYS	THR	LEU	ARG	SER	ARG	GLN	LEU	ASN	ILE
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 P309
 L516
 P323
 N324
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 ALA
 PRO
 ILE
 ALA
 THR
 PRO
 PRO
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 ALA
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 PRO
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 SER
 ASN
 TYR
 GLU
 VAL
 ASP

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

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

- Molecule 9: Flagellar M-ring protein

Chain h: 96%

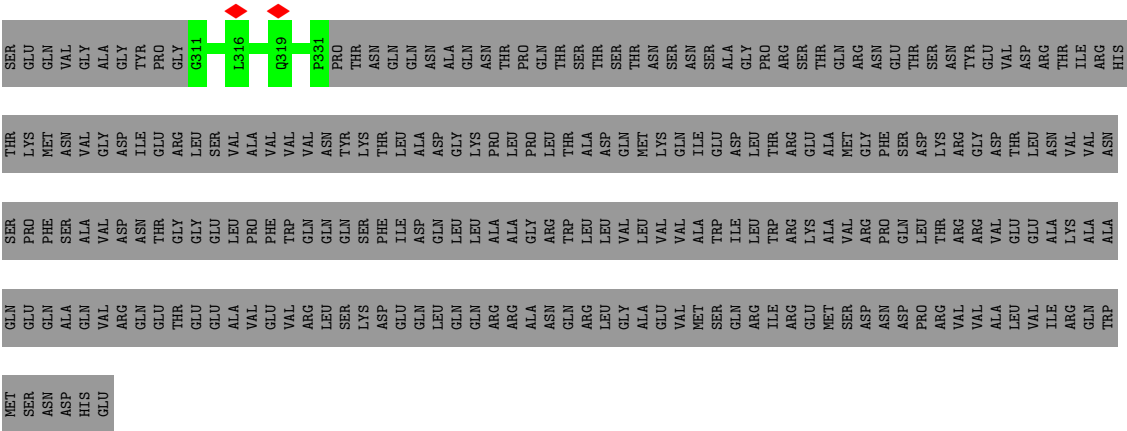
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[illegible]

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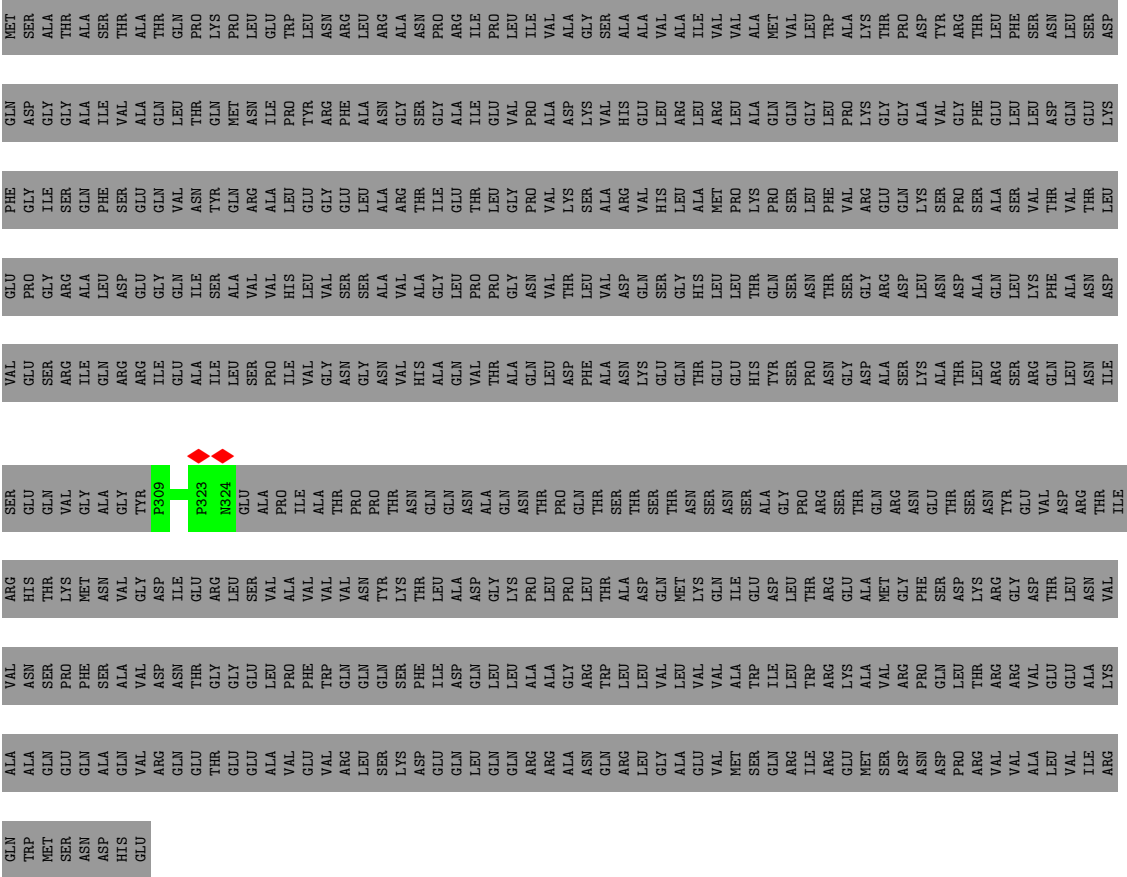
GLU PRO GLY ARG LEU ASP GLU GLY ILE SER ALA VAL VAL HIS VAL VAL VAL ALA GLY LEU PRO PRO GLY ASN VAL THR LEU LEU HIS LEU THR GLN SER SER THR THR GLY ARG ASP LEU ASN ASP ALA GLN LEU PHE LYS ALA ASN ASP

[illegible]



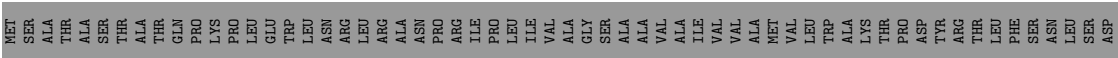
● Molecule 9: Flagellar M-ring protein

Chain i:  97%



● Molecule 9: Flagellar M-ring protein

Chain j:  96%



[illegible]

VAL VAL
VAL ALA
LEU LEU
VAL ALA
TLE ARG
GLN TRP
MET MET
SER ASP
ASN ASP
HIS HIS
GLU GLU

• Molecule 9: Flagellar M-ring protein

Chain l:  96%

MET SER
THR ALA
GLY THR
SER THR
SER THR
TLE THR
GLN THR
PRO THR
LYS THR
PRO THR
LEU THR

GLN ASP
GLY THR
SER THR
GLN THR
TLE THR
VAL THR
GLN THR
LEU THR
GLY THR
ASN THR
MET THR
ASN THR
LEU THR

PHE GLY
TLE THR
SER THR
GLN THR
PHE THR
SER THR
GLN THR
VAL THR
GLN THR
ASN THR
TLE THR
ARG THR

GLU PRO
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VAL GLU
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ASN THR
GLY THR

SER GLU
GLN THR
VAL THR
GLY THR
ALA THR
GLY THR
TLE THR
GLY THR
G311
L316
S317
N318
E325
A329
T330
P331

THR TLE
HIS THR
SER THR
MET THR
LYS THR
ASN THR
VAL THR
GLY THR
ILE THR
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LEU THR
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ASN VAL
VAL THR
ASN THR
SER THR
PRO THR
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ALA THR
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GLY THR
GLU THR
LEU THR

ALA LYS
ALA THR
GLN THR
GLN THR
GLN THR
VAL THR
ARG THR
GLN THR
THR THR
GLU THR
GLU THR
ALA THR

TLE ARG
GLN THR
TRP THR
MET THR
SER THR
ASN THR
HIS THR
GLU THR

• Molecule 10: Flagellar basal-body rod protein FlgF

Chain m:  23% 97%

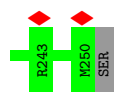
MET D2
G19
L38
L49
S50
L51
A52
D72
Y73
T74
S75
R76
L82
D85
L88
Q91
A92
A93
D94
G95
A96
E97
G111
Q116
E123
G124
E131
G132
S133
E134
A138
A139
D140
F148
G149
D150
R160
L161
K162
L163
V164
K165
A166
E167

G168
M169
E170
D175
D176
G177
L178
L181
T182
A183
E184
A185
E188
R189
G190
A191
D192
L193
A194
A195
D196
P197
S198
I199
R200
E207
E241
G242
R243
Q246
L247
L248
S249
MET
SER

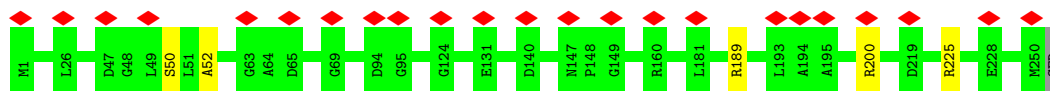
• Molecule 10: Flagellar basal-body rod protein FlgF

Chain n:  13% 96%

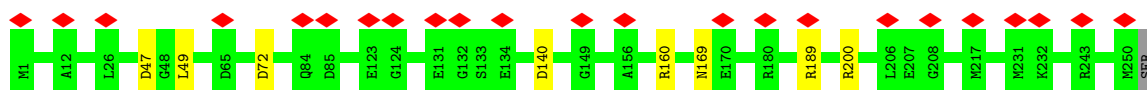
MET D2
L26
G48
L49
A52
T53
R54
Q70
L71
D72
Y73
A92
A93
D94
G95
A96
E97
G122
E123
G124
E131
G132
S133
E134
S144
G149
M153
R160
E167
G168
D175
D176
E188
L193
D196
D219
R225
E228
D238



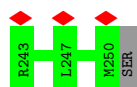
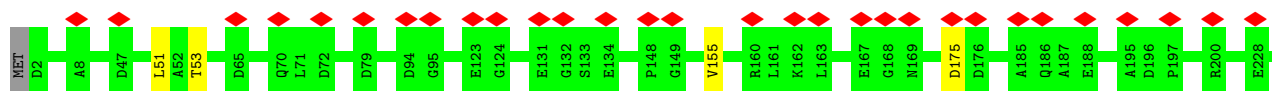
- Molecule 10: Flagellar basal-body rod protein FlgF



- Molecule 10: Flagellar basal-body rod protein FlgF



- Molecule 10: Flagellar basal-body rod protein FlgF



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11858	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.384	Depositor
Minimum map value	-1.313	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.124	Depositor
Recommended contour level	0.65	Depositor
Map size (Å)	681.984, 681.984, 681.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.332, 1.332, 1.332	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.33	0/1888	0.54	1/2564 (0.0%)
1	1	0.31	0/1917	0.51	0/2605
1	2	0.29	0/1973	0.51	0/2682
1	3	0.28	0/1973	0.52	0/2682
1	4	0.28	0/1973	0.51	0/2682
1	5	0.33	0/1973	0.52	0/2682
1	6	0.32	0/1973	0.54	0/2682
1	7	0.32	0/1973	0.53	0/2682
1	8	0.33	0/1973	0.56	0/2682
1	9	0.30	0/1973	0.53	1/2682 (0.0%)
1	ZA	0.31	0/1973	0.53	0/2682
1	ZB	0.29	0/1973	0.49	0/2682
1	ZC	0.34	0/1973	0.54	0/2682
1	ZD	0.31	0/1973	0.52	0/2682
1	ZE	0.30	0/1973	0.51	1/2682 (0.0%)
1	r	0.34	0/1926	0.53	0/2618
1	s	0.38	0/1934	0.59	0/2629
1	t	0.39	0/1942	0.56	0/2639
1	u	0.35	0/1926	0.58	1/2618 (0.0%)
1	v	0.35	0/1934	0.54	0/2629
1	w	0.34	0/1844	0.51	0/2505
1	x	0.33	0/1888	0.52	0/2564
1	y	0.33	0/1888	0.56	1/2564 (0.0%)
1	z	0.31	0/1888	0.51	0/2564
2	ZF	0.28	0/2991	0.49	0/4076
2	ZG	0.34	0/2991	0.52	1/4076 (0.0%)
2	ZH	0.29	0/2991	0.50	0/4076
2	ZI	0.30	0/2991	0.51	0/4076
2	ZJ	0.31	0/2991	0.49	0/4076
2	ZK	0.29	0/2991	0.50	0/4076
2	ZL	0.29	0/2991	0.49	0/4076
2	ZM	0.29	0/2991	0.53	1/4076 (0.0%)
2	ZN	0.28	0/2991	0.51	0/4076
2	ZO	0.30	0/2991	0.50	0/4076

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	ZP	0.28	0/2991	0.50	1/4076 (0.0%)
2	ZQ	0.29	0/2991	0.51	0/4076
2	ZR	0.30	1/2991 (0.0%)	0.55	3/4076 (0.1%)
2	ZS	0.29	0/2991	0.52	1/4076 (0.0%)
2	ZT	0.29	0/2991	0.48	0/4076
2	ZU	0.29	0/2991	0.50	0/4076
2	ZV	0.50	4/2991 (0.1%)	0.67	6/4076 (0.1%)
2	ZW	0.27	0/2991	0.49	0/4076
2	ZX	0.28	0/2991	0.48	0/4076
2	ZY	0.30	1/2991 (0.0%)	0.54	2/4076 (0.0%)
2	ZZ	0.26	0/2991	0.46	0/4076
2	Za	0.28	0/2991	0.49	0/4076
2	Zb	0.30	0/2991	0.49	0/4076
2	Zc	0.29	0/2991	0.52	2/4076 (0.0%)
2	Zd	0.30	0/2991	0.51	0/4076
2	Ze	0.28	0/2991	0.48	0/4076
2	Zf	0.27	0/2991	0.48	0/4076
2	Zg	0.28	0/2991	0.49	0/4076
2	Zh	0.28	0/2991	0.48	0/4076
3	A	0.45	0/681	0.67	1/930 (0.1%)
3	B	0.33	0/681	0.53	0/930
3	C	0.28	0/681	0.50	0/930
3	D	0.26	0/681	0.48	0/930
4	E	0.31	0/1994	0.52	0/2724
5	F	0.36	0/1643	0.62	2/2237 (0.1%)
5	G	0.30	0/1665	0.49	1/2267 (0.0%)
5	H	0.29	0/1652	0.50	0/2249
5	I	0.29	0/1652	0.47	0/2249
5	J	0.33	0/1662	0.52	0/2263
6	K	0.28	0/300	0.52	0/400
6	L	0.25	0/547	0.44	0/733
6	M	0.26	0/561	0.44	0/753
6	N	0.25	0/561	0.46	0/753
6	O	0.27	0/561	0.49	0/753
6	P	0.31	0/554	0.48	0/743
7	Q	0.29	0/930	0.56	0/1251
7	R	0.26	0/855	0.49	0/1150
7	S	0.28	0/855	0.53	0/1150
7	T	0.26	0/870	0.49	0/1169
7	U	0.26	0/839	0.47	0/1129
8	V	0.30	0/981	0.47	0/1334
8	W	0.29	0/976	0.50	0/1327
8	X	0.34	0/981	0.50	0/1334

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	Y	0.33	0/981	0.62	0/1334
8	Z	0.29	0/968	0.48	0/1316
8	a	0.36	0/981	0.52	0/1334
9	b	0.46	0/83	0.86	1/114 (0.9%)
9	c	0.27	0/107	0.38	0/148
9	d	0.31	0/137	0.49	0/191
9	e	0.28	0/107	0.57	0/148
9	f	0.39	0/145	0.55	0/203
9	g	0.33	0/107	0.51	0/148
9	h	0.26	0/145	0.43	0/203
9	i	0.29	0/107	0.38	0/148
9	j	0.33	0/137	0.70	0/191
9	k	0.30	0/107	0.37	0/148
9	l	0.29	0/145	0.45	0/203
10	m	0.32	0/1828	0.56	0/2492
10	n	0.33	0/1836	0.56	2/2502 (0.1%)
10	o	0.37	0/1844	0.57	0/2512
10	p	0.33	0/1844	0.57	0/2512
10	q	0.33	0/1836	0.58	0/2502
All	All	0.31	6/170171 (0.0%)	0.52	29/231606 (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	0	0	2
1	1	0	1
1	5	0	2
1	7	0	1
1	8	0	2
1	ZA	0	2
1	ZD	0	1
1	ZE	0	3
1	r	0	1
1	u	0	1
1	w	0	1
1	x	0	1
1	y	0	2
1	z	0	3
2	ZI	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	ZK	0	1
2	ZO	0	1
2	ZT	0	1
2	ZU	0	1
2	ZW	0	1
2	ZZ	0	1
2	Zd	0	1
2	Ze	0	1
5	H	0	2
5	J	0	2
7	Q	0	1
7	R	0	1
7	T	0	1
7	U	0	1
8	Y	0	1
8	a	0	1
10	m	0	1
10	n	0	2
10	p	0	1
All	All	0	46

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	ZV	140	PRO	CG-CD	-16.12	0.97	1.50
2	ZV	125	PRO	CG-CD	-10.14	1.17	1.50
2	ZV	140	PRO	N-CD	8.29	1.59	1.47
2	ZV	125	PRO	N-CD	6.59	1.57	1.47
2	ZY	125	PRO	CG-CD	-5.45	1.32	1.50

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	ZV	140	PRO	N-CD-CG	-17.34	77.19	103.20
2	ZR	125	PRO	CA-N-CD	-13.94	91.98	111.50
2	ZY	125	PRO	CA-N-CD	-13.33	92.84	111.50
2	ZV	125	PRO	CA-N-CD	-13.25	92.95	111.50
5	F	162	PRO	CA-N-CD	-11.93	94.80	111.50

There are no chirality outliers.

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	36	ARG	Sidechain
1	0	50	ARG	Sidechain
1	1	36	ARG	Sidechain
1	5	50	ARG	Sidechain
1	5	73	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	244/260 (94%)	236 (97%)	5 (2%)	3 (1%)	11	40
1	1	248/260 (95%)	238 (96%)	9 (4%)	1 (0%)	30	63
1	2	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	49
1	3	258/260 (99%)	247 (96%)	9 (4%)	2 (1%)	16	49
1	4	258/260 (99%)	245 (95%)	11 (4%)	2 (1%)	16	49
1	5	258/260 (99%)	240 (93%)	15 (6%)	3 (1%)	11	40
1	6	258/260 (99%)	244 (95%)	10 (4%)	4 (2%)	8	36
1	7	258/260 (99%)	244 (95%)	11 (4%)	3 (1%)	11	40
1	8	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	11	40
1	9	258/260 (99%)	244 (95%)	13 (5%)	1 (0%)	30	63
1	ZA	258/260 (99%)	242 (94%)	13 (5%)	3 (1%)	11	40
1	ZB	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	11	40
1	ZC	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	49
1	ZD	258/260 (99%)	237 (92%)	18 (7%)	3 (1%)	11	40
1	ZE	258/260 (99%)	242 (94%)	15 (6%)	1 (0%)	30	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	r	250/260 (96%)	238 (95%)	11 (4%)	1 (0%)	30	63
1	s	251/260 (96%)	234 (93%)	14 (6%)	3 (1%)	11	40
1	t	252/260 (97%)	234 (93%)	16 (6%)	2 (1%)	16	49
1	u	250/260 (96%)	239 (96%)	9 (4%)	2 (1%)	16	49
1	v	251/260 (96%)	235 (94%)	10 (4%)	6 (2%)	5	29
1	w	239/260 (92%)	231 (97%)	7 (3%)	1 (0%)	30	63
1	x	244/260 (94%)	229 (94%)	10 (4%)	5 (2%)	6	32
1	y	244/260 (94%)	234 (96%)	9 (4%)	1 (0%)	30	63
1	z	244/260 (94%)	239 (98%)	4 (2%)	1 (0%)	30	63
2	ZF	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
2	ZG	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	37	69
2	ZH	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
2	ZI	399/403 (99%)	387 (97%)	10 (2%)	2 (0%)	25	58
2	ZJ	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
2	ZK	399/403 (99%)	387 (97%)	11 (3%)	1 (0%)	37	69
2	ZL	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	37	69
2	ZM	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
2	ZN	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
2	ZO	399/403 (99%)	381 (96%)	15 (4%)	3 (1%)	16	49
2	ZP	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	37	69
2	ZQ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
2	ZR	399/403 (99%)	391 (98%)	8 (2%)	0	100	100
2	ZS	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
2	ZT	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
2	ZU	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
2	ZV	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
2	ZW	399/403 (99%)	380 (95%)	18 (4%)	1 (0%)	37	69
2	ZX	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
2	ZY	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
2	ZZ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
2	Za	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	37	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Zb	399/403 (99%)	392 (98%)	7 (2%)	0	100	100
2	Zc	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
2	Zd	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
2	Ze	399/403 (99%)	385 (96%)	13 (3%)	1 (0%)	37	69
2	Zf	399/403 (99%)	386 (97%)	13 (3%)	0	100	100
2	Zg	399/403 (99%)	383 (96%)	16 (4%)	0	100	100
2	Zh	399/403 (99%)	391 (98%)	8 (2%)	0	100	100
3	A	87/89 (98%)	81 (93%)	4 (5%)	2 (2%)	5	30
3	B	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
3	C	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
3	D	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
4	E	251/264 (95%)	234 (93%)	15 (6%)	2 (1%)	16	49
5	F	205/245 (84%)	197 (96%)	8 (4%)	0	100	100
5	G	207/245 (84%)	199 (96%)	6 (3%)	2 (1%)	13	44
5	H	206/245 (84%)	201 (98%)	5 (2%)	0	100	100
5	I	206/245 (84%)	199 (97%)	6 (3%)	1 (0%)	25	58
5	J	207/245 (84%)	192 (93%)	10 (5%)	5 (2%)	5	29
6	K	38/104 (36%)	35 (92%)	3 (8%)	0	100	100
6	L	70/104 (67%)	70 (100%)	0	0	100	100
6	M	72/104 (69%)	70 (97%)	2 (3%)	0	100	100
6	N	72/104 (69%)	72 (100%)	0	0	100	100
6	O	72/104 (69%)	72 (100%)	0	0	100	100
6	P	71/104 (68%)	71 (100%)	0	0	100	100
7	Q	115/138 (83%)	114 (99%)	1 (1%)	0	100	100
7	R	104/138 (75%)	103 (99%)	1 (1%)	0	100	100
7	S	104/138 (75%)	103 (99%)	1 (1%)	0	100	100
7	T	106/138 (77%)	104 (98%)	2 (2%)	0	100	100
7	U	102/138 (74%)	101 (99%)	1 (1%)	0	100	100
8	V	131/134 (98%)	122 (93%)	9 (7%)	0	100	100
8	W	130/134 (97%)	123 (95%)	7 (5%)	0	100	100
8	X	131/134 (98%)	124 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	Y	131/134 (98%)	121 (92%)	7 (5%)	3 (2%)	5	30
8	Z	129/134 (96%)	123 (95%)	5 (4%)	1 (1%)	16	49
8	a	131/134 (98%)	124 (95%)	7 (5%)	0	100	100
9	b	11/560 (2%)	9 (82%)	2 (18%)	0	100	100
9	c	14/560 (2%)	12 (86%)	2 (14%)	0	100	100
9	d	18/560 (3%)	18 (100%)	0	0	100	100
9	e	14/560 (2%)	14 (100%)	0	0	100	100
9	f	19/560 (3%)	18 (95%)	1 (5%)	0	100	100
9	g	14/560 (2%)	13 (93%)	1 (7%)	0	100	100
9	h	19/560 (3%)	19 (100%)	0	0	100	100
9	i	14/560 (2%)	14 (100%)	0	0	100	100
9	j	18/560 (3%)	18 (100%)	0	0	100	100
9	k	14/560 (2%)	14 (100%)	0	0	100	100
9	l	19/560 (3%)	19 (100%)	0	0	100	100
10	m	246/251 (98%)	238 (97%)	7 (3%)	1 (0%)	30	63
10	n	247/251 (98%)	242 (98%)	4 (2%)	1 (0%)	30	63
10	o	248/251 (99%)	233 (94%)	13 (5%)	2 (1%)	16	49
10	p	248/251 (99%)	235 (95%)	13 (5%)	0	100	100
10	q	247/251 (98%)	236 (96%)	9 (4%)	2 (1%)	16	49
All	All	22391/29305 (76%)	21536 (96%)	763 (3%)	92 (0%)	32	63

5 of 92 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2	209	ASN
1	4	140	ILE
1	5	209	ASN
1	6	139	ALA
1	8	209	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	205/215 (95%)	198 (97%)	7 (3%)	32	55
1	1	209/215 (97%)	201 (96%)	8 (4%)	28	52
1	2	215/215 (100%)	213 (99%)	2 (1%)	75	82
1	3	215/215 (100%)	212 (99%)	3 (1%)	62	75
1	4	215/215 (100%)	209 (97%)	6 (3%)	38	59
1	5	215/215 (100%)	210 (98%)	5 (2%)	45	63
1	6	215/215 (100%)	210 (98%)	5 (2%)	45	63
1	7	215/215 (100%)	214 (100%)	1 (0%)	86	90
1	8	215/215 (100%)	210 (98%)	5 (2%)	45	63
1	9	215/215 (100%)	212 (99%)	3 (1%)	62	75
1	ZA	215/215 (100%)	213 (99%)	2 (1%)	75	82
1	ZB	215/215 (100%)	208 (97%)	7 (3%)	33	56
1	ZC	215/215 (100%)	212 (99%)	3 (1%)	62	75
1	ZD	215/215 (100%)	210 (98%)	5 (2%)	45	63
1	ZE	215/215 (100%)	210 (98%)	5 (2%)	45	63
1	r	209/215 (97%)	203 (97%)	6 (3%)	37	58
1	s	210/215 (98%)	201 (96%)	9 (4%)	25	49
1	t	211/215 (98%)	199 (94%)	12 (6%)	17	43
1	u	209/215 (97%)	198 (95%)	11 (5%)	19	44
1	v	210/215 (98%)	199 (95%)	11 (5%)	19	44
1	w	200/215 (93%)	195 (98%)	5 (2%)	42	62
1	x	205/215 (95%)	197 (96%)	8 (4%)	27	51
1	y	205/215 (95%)	197 (96%)	8 (4%)	27	51
1	z	205/215 (95%)	201 (98%)	4 (2%)	50	68
2	ZF	321/323 (99%)	309 (96%)	12 (4%)	29	53
2	ZG	321/323 (99%)	305 (95%)	16 (5%)	20	45
2	ZH	321/323 (99%)	308 (96%)	13 (4%)	27	50
2	ZI	321/323 (99%)	315 (98%)	6 (2%)	52	69
2	ZJ	321/323 (99%)	312 (97%)	9 (3%)	38	59
2	ZK	321/323 (99%)	315 (98%)	6 (2%)	52	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	ZL	321/323 (99%)	311 (97%)	10 (3%)	35	56
2	ZM	321/323 (99%)	312 (97%)	9 (3%)	38	59
2	ZN	321/323 (99%)	311 (97%)	10 (3%)	35	56
2	ZO	321/323 (99%)	313 (98%)	8 (2%)	42	62
2	ZP	321/323 (99%)	306 (95%)	15 (5%)	22	46
2	ZQ	321/323 (99%)	312 (97%)	9 (3%)	38	59
2	ZR	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	ZS	321/323 (99%)	315 (98%)	6 (2%)	52	69
2	ZT	321/323 (99%)	313 (98%)	8 (2%)	42	62
2	ZU	321/323 (99%)	317 (99%)	4 (1%)	67	77
2	ZV	321/323 (99%)	317 (99%)	4 (1%)	67	77
2	ZW	321/323 (99%)	307 (96%)	14 (4%)	24	48
2	ZX	321/323 (99%)	318 (99%)	3 (1%)	75	82
2	ZY	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	ZZ	321/323 (99%)	316 (98%)	5 (2%)	58	73
2	Za	321/323 (99%)	315 (98%)	6 (2%)	52	69
2	Zb	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	Zc	321/323 (99%)	310 (97%)	11 (3%)	32	55
2	Zd	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	Ze	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	Zf	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	Zg	321/323 (99%)	314 (98%)	7 (2%)	47	64
2	Zh	321/323 (99%)	314 (98%)	7 (2%)	47	64
3	A	74/74 (100%)	68 (92%)	6 (8%)	9	32
3	B	74/74 (100%)	72 (97%)	2 (3%)	40	60
3	C	74/74 (100%)	74 (100%)	0	100	100
3	D	74/74 (100%)	74 (100%)	0	100	100
4	E	210/221 (95%)	205 (98%)	5 (2%)	44	62
5	F	177/204 (87%)	171 (97%)	6 (3%)	32	55
5	G	179/204 (88%)	172 (96%)	7 (4%)	27	51
5	H	178/204 (87%)	173 (97%)	5 (3%)	38	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	I	178/204 (87%)	171 (96%)	7 (4%)	27	51
5	J	179/204 (88%)	172 (96%)	7 (4%)	27	51
6	K	33/79 (42%)	29 (88%)	4 (12%)	4	19
6	L	56/79 (71%)	54 (96%)	2 (4%)	30	54
6	M	58/79 (73%)	57 (98%)	1 (2%)	56	72
6	N	58/79 (73%)	56 (97%)	2 (3%)	32	55
6	O	58/79 (73%)	56 (97%)	2 (3%)	32	55
6	P	57/79 (72%)	54 (95%)	3 (5%)	19	44
7	Q	98/113 (87%)	94 (96%)	4 (4%)	26	50
7	R	90/113 (80%)	89 (99%)	1 (1%)	70	79
7	S	90/113 (80%)	87 (97%)	3 (3%)	33	56
7	T	91/113 (80%)	90 (99%)	1 (1%)	70	79
7	U	89/113 (79%)	84 (94%)	5 (6%)	17	43
8	V	104/105 (99%)	104 (100%)	0	100	100
8	W	104/105 (99%)	101 (97%)	3 (3%)	37	58
8	X	104/105 (99%)	102 (98%)	2 (2%)	52	69
8	Y	104/105 (99%)	100 (96%)	4 (4%)	28	52
8	Z	103/105 (98%)	100 (97%)	3 (3%)	37	58
8	a	104/105 (99%)	98 (94%)	6 (6%)	17	42
9	b	8/467 (2%)	6 (75%)	2 (25%)	0	3
9	c	11/467 (2%)	10 (91%)	1 (9%)	7	28
9	d	14/467 (3%)	12 (86%)	2 (14%)	2	16
9	e	11/467 (2%)	11 (100%)	0	100	100
9	f	15/467 (3%)	15 (100%)	0	100	100
9	g	11/467 (2%)	11 (100%)	0	100	100
9	h	15/467 (3%)	15 (100%)	0	100	100
9	i	11/467 (2%)	11 (100%)	0	100	100
9	j	14/467 (3%)	13 (93%)	1 (7%)	12	36
9	k	11/467 (2%)	11 (100%)	0	100	100
9	l	15/467 (3%)	14 (93%)	1 (7%)	13	38
10	m	190/193 (98%)	188 (99%)	2 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	n	191/193 (99%)	186 (97%)	5 (3%)	41	61
10	o	192/193 (100%)	189 (98%)	3 (2%)	58	73
10	p	192/193 (100%)	185 (96%)	7 (4%)	30	54
10	q	191/193 (99%)	189 (99%)	2 (1%)	73	80
All	All	18272/23835 (77%)	17774 (97%)	498 (3%)	41	60

5 of 498 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	ZW	340	SER
7	Q	125	SER
2	Zf	3	PHE
6	P	91	LYS
9	b	322	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 487 such sidechains are listed below:

Mol	Chain	Res	Type
2	ZU	133	ASN
8	X	50	GLN
2	Za	190	GLN
8	V	30	ASN
10	p	28	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

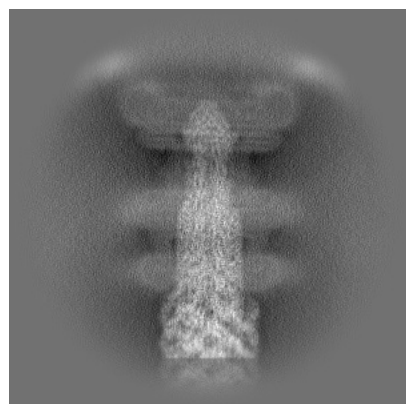
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37628. These allow visual inspection of the internal detail of the map and identification of artifacts.

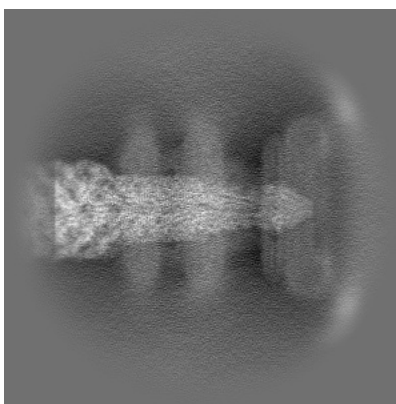
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

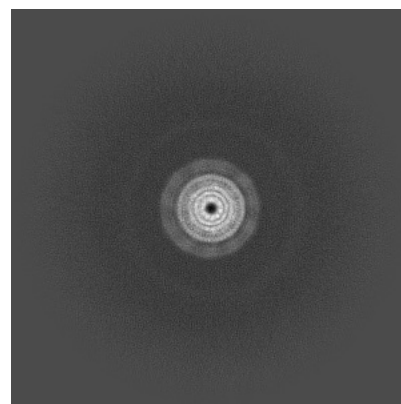
6.1.1 Primary map



X

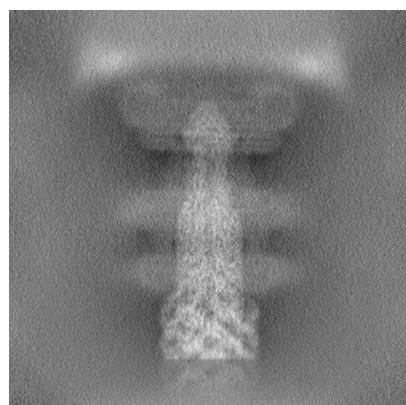


Y

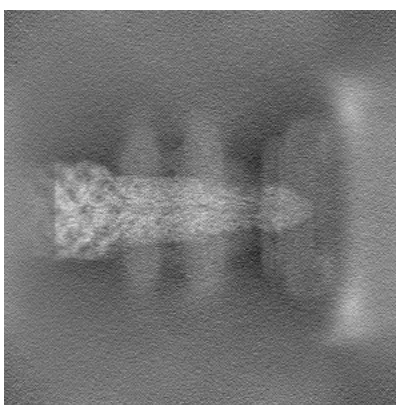


Z

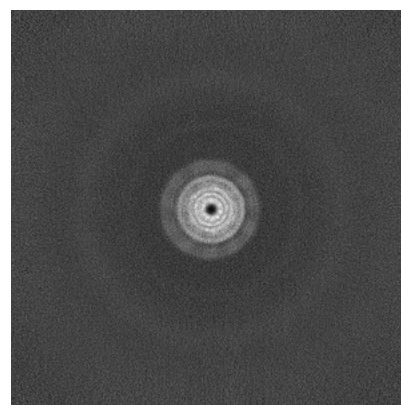
6.1.2 Raw map



X



Y

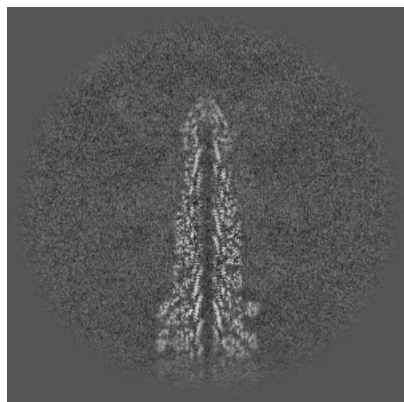


Z

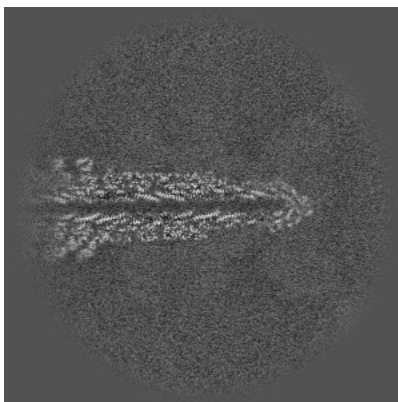
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

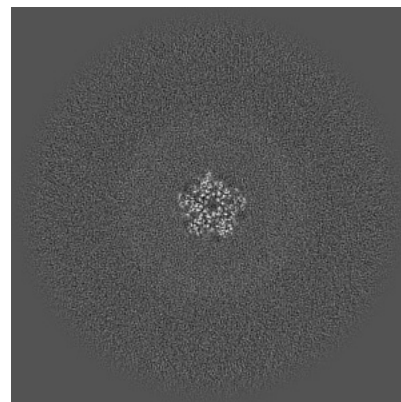
6.2.1 Primary map



X Index: 256

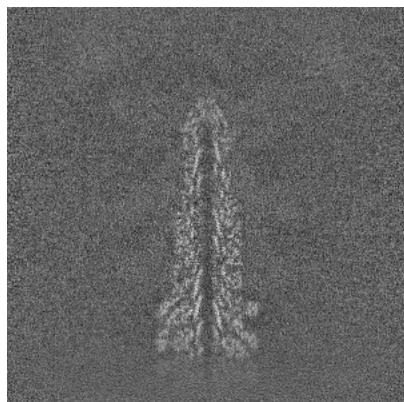


Y Index: 256

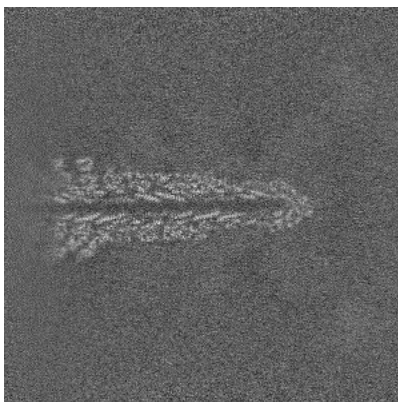


Z Index: 256

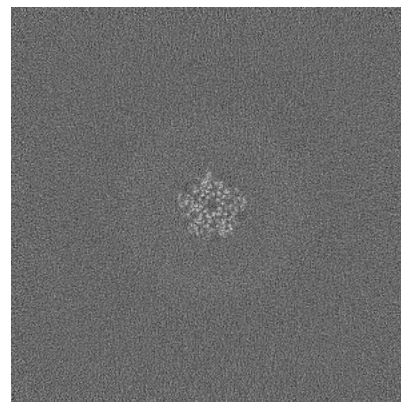
6.2.2 Raw map



X Index: 256



Y Index: 256

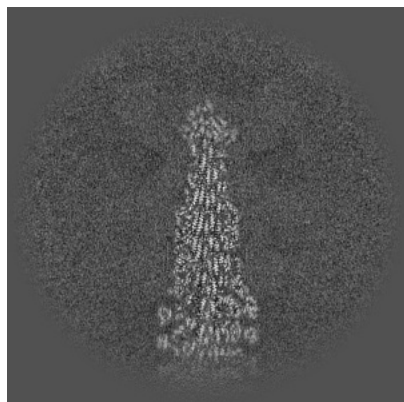


Z Index: 256

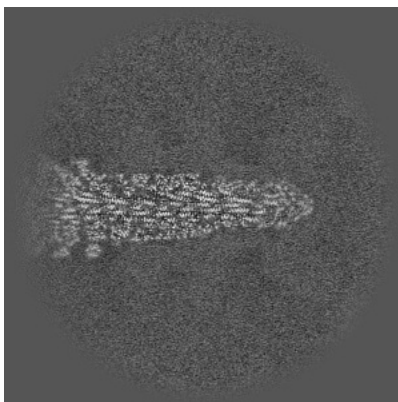
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

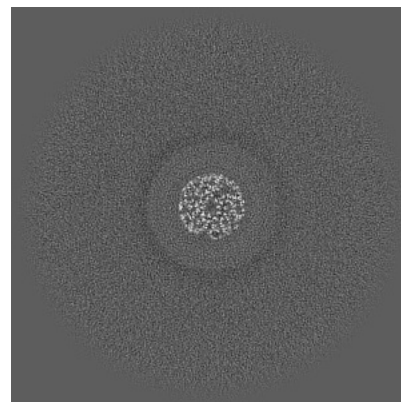
6.3.1 Primary map



X Index: 245

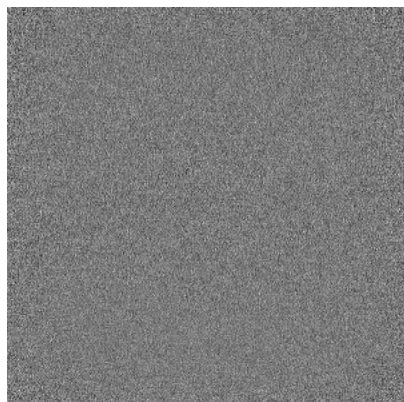


Y Index: 246

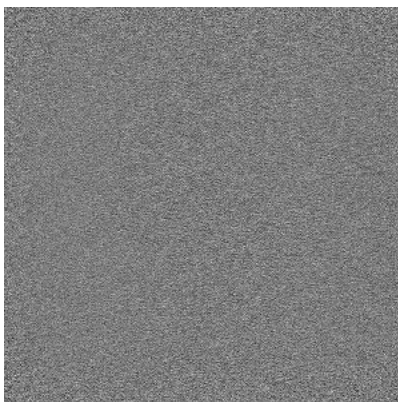


Z Index: 229

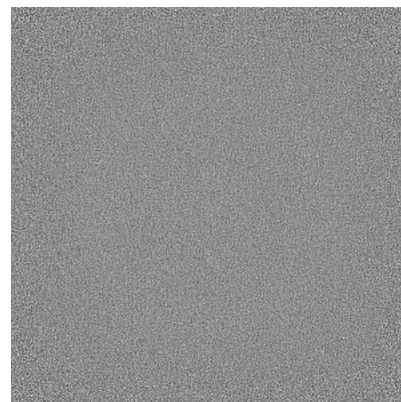
6.3.2 Raw map



X Index: 0



Y Index: 0

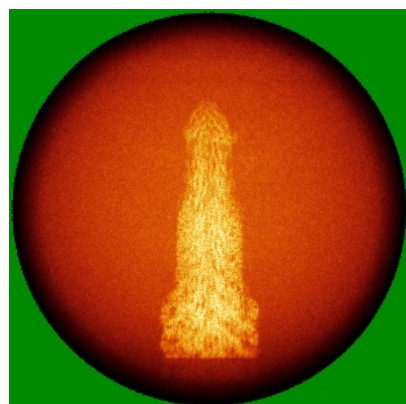


Z Index: 511

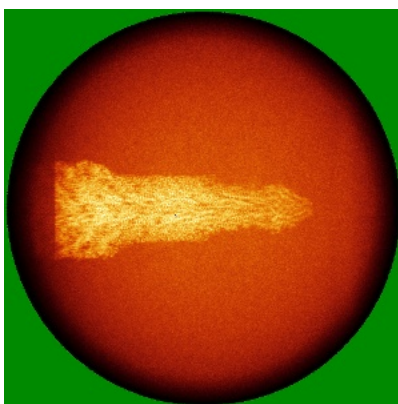
The images above show the largest variance slices of the map in three orthogonal directions.

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

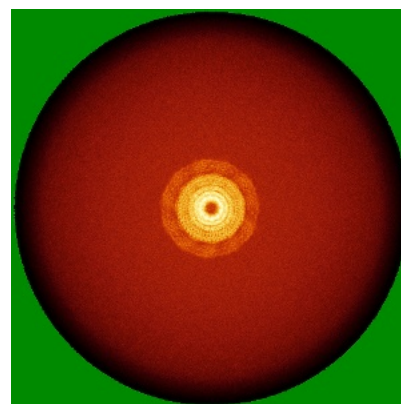
6.4.1 Primary map



X

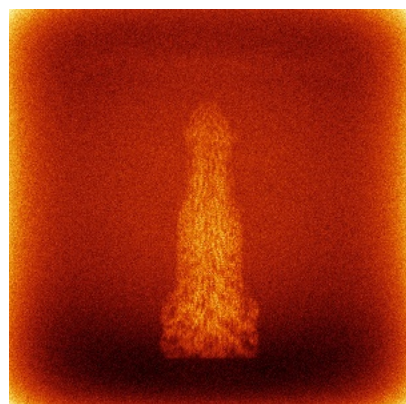


Y

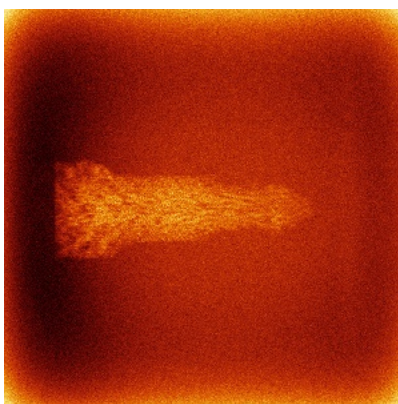


Z

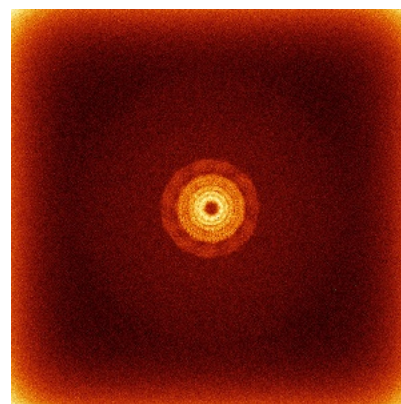
6.4.2 Raw map



X



Y

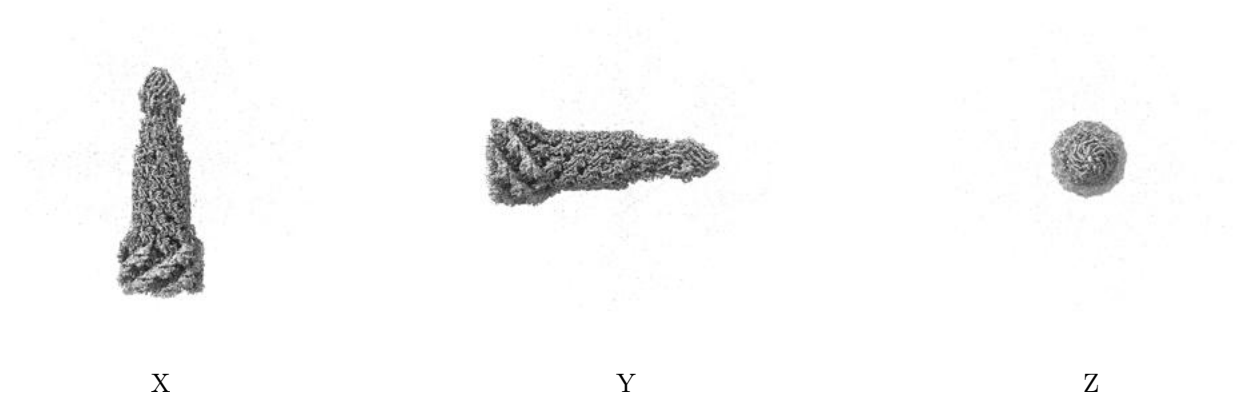


Z

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.

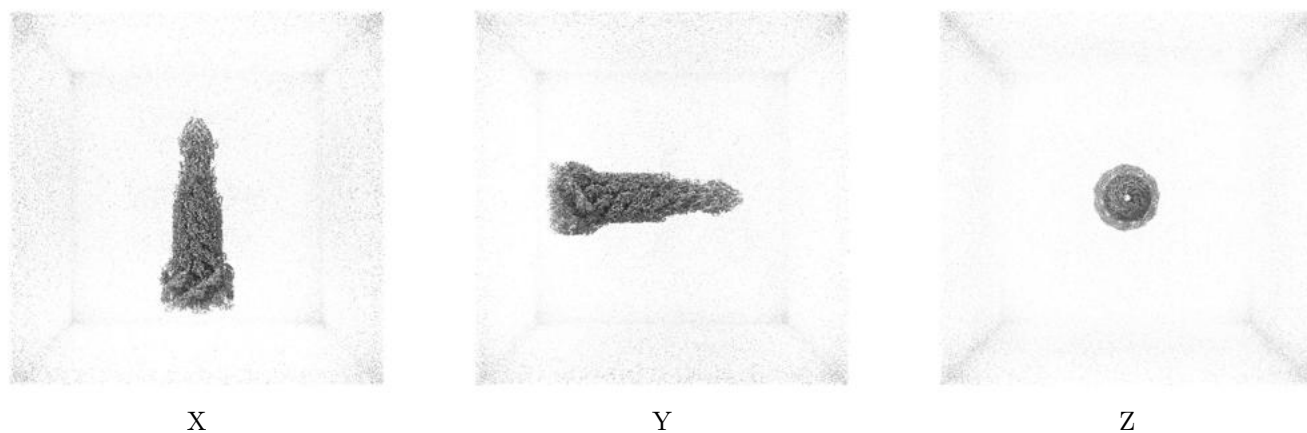
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.65. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

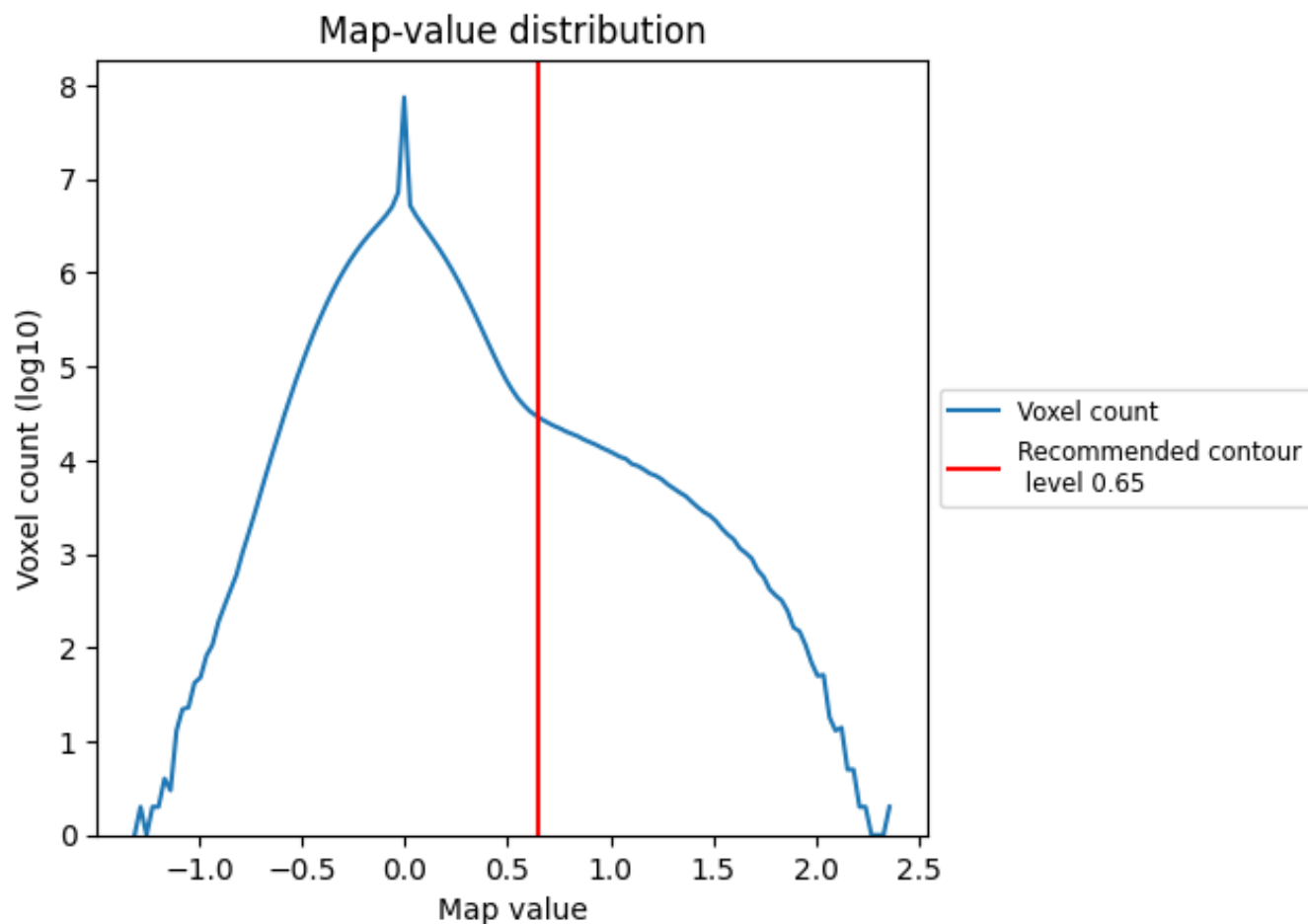
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

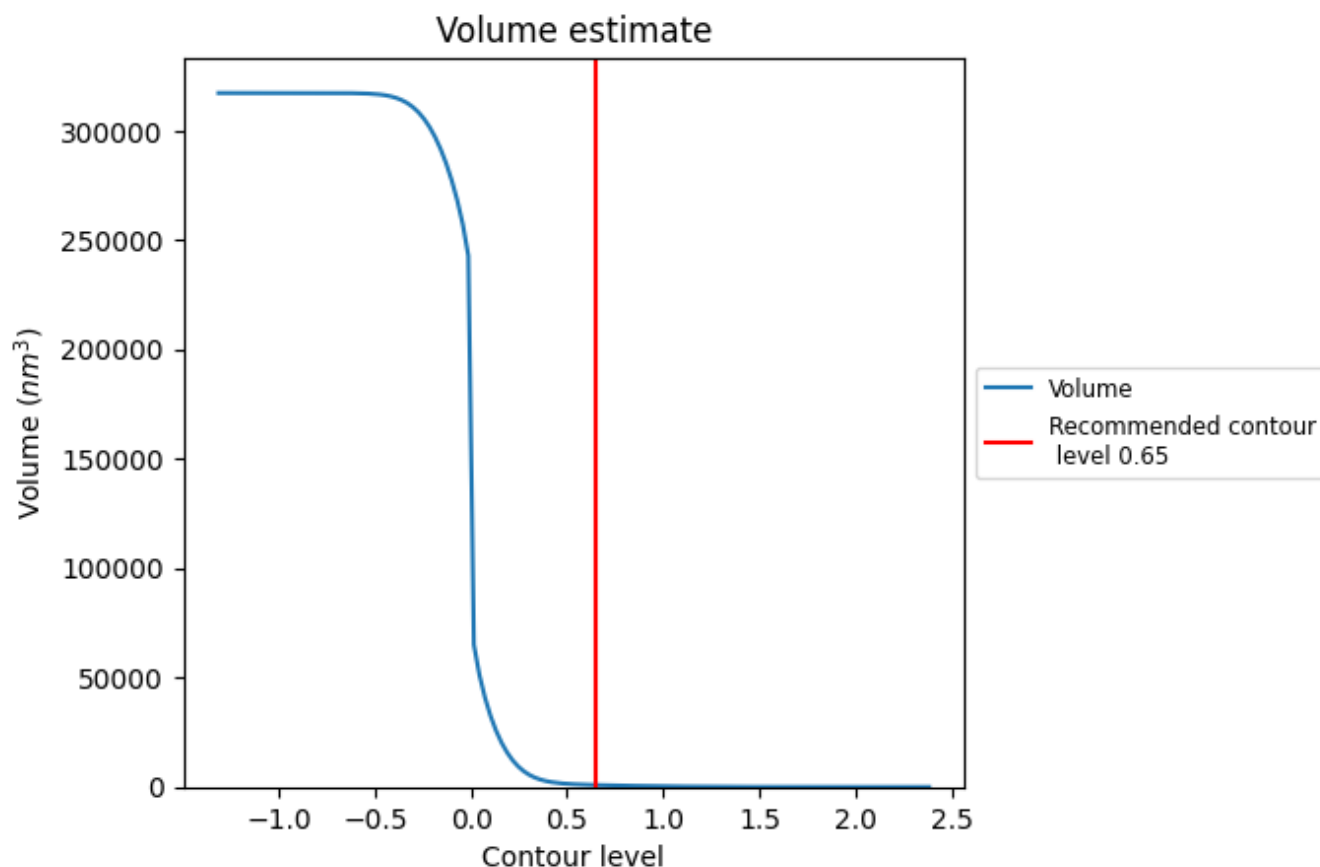
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

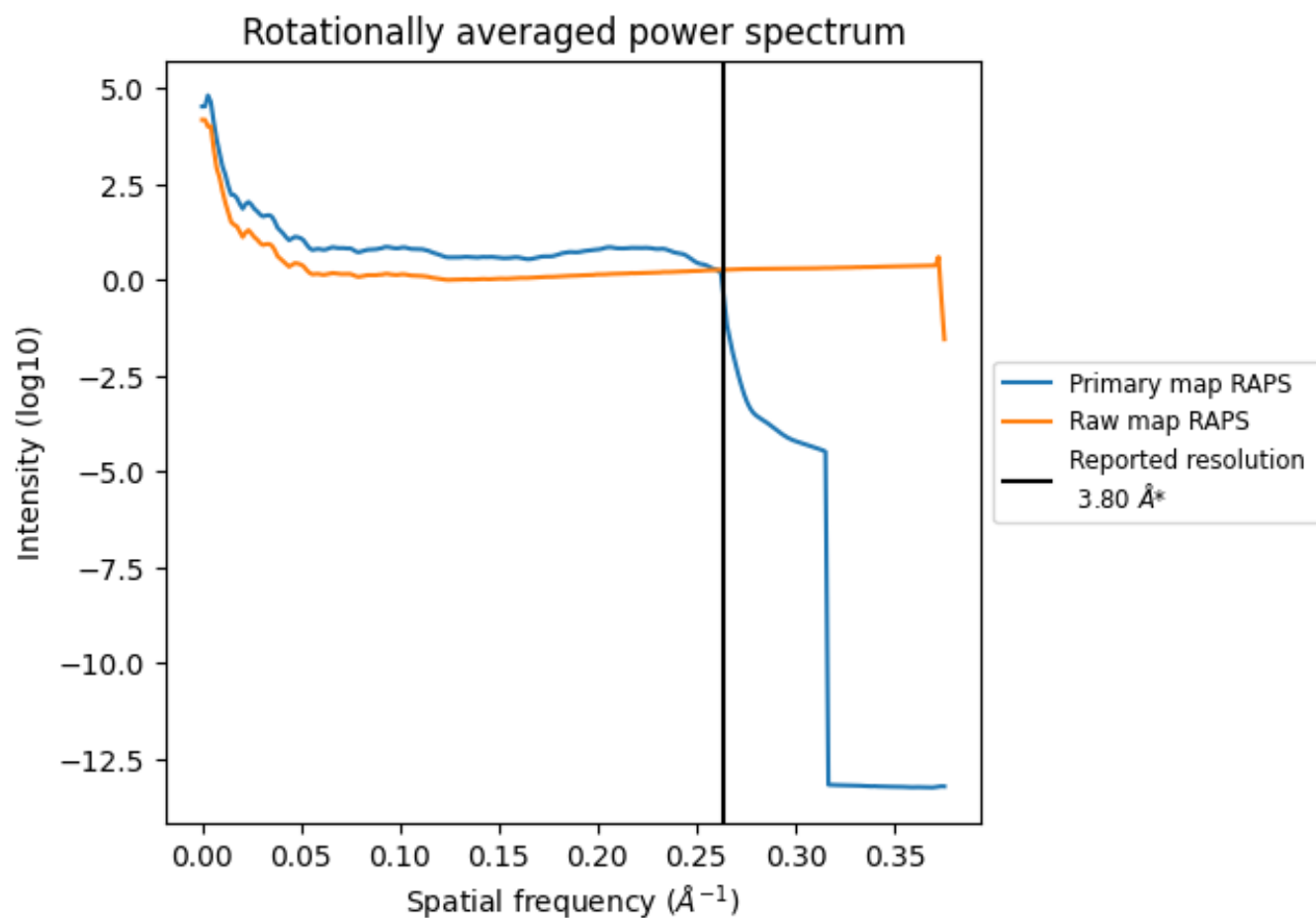
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm³; this corresponds to an approximate mass of 787 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 ⓘ

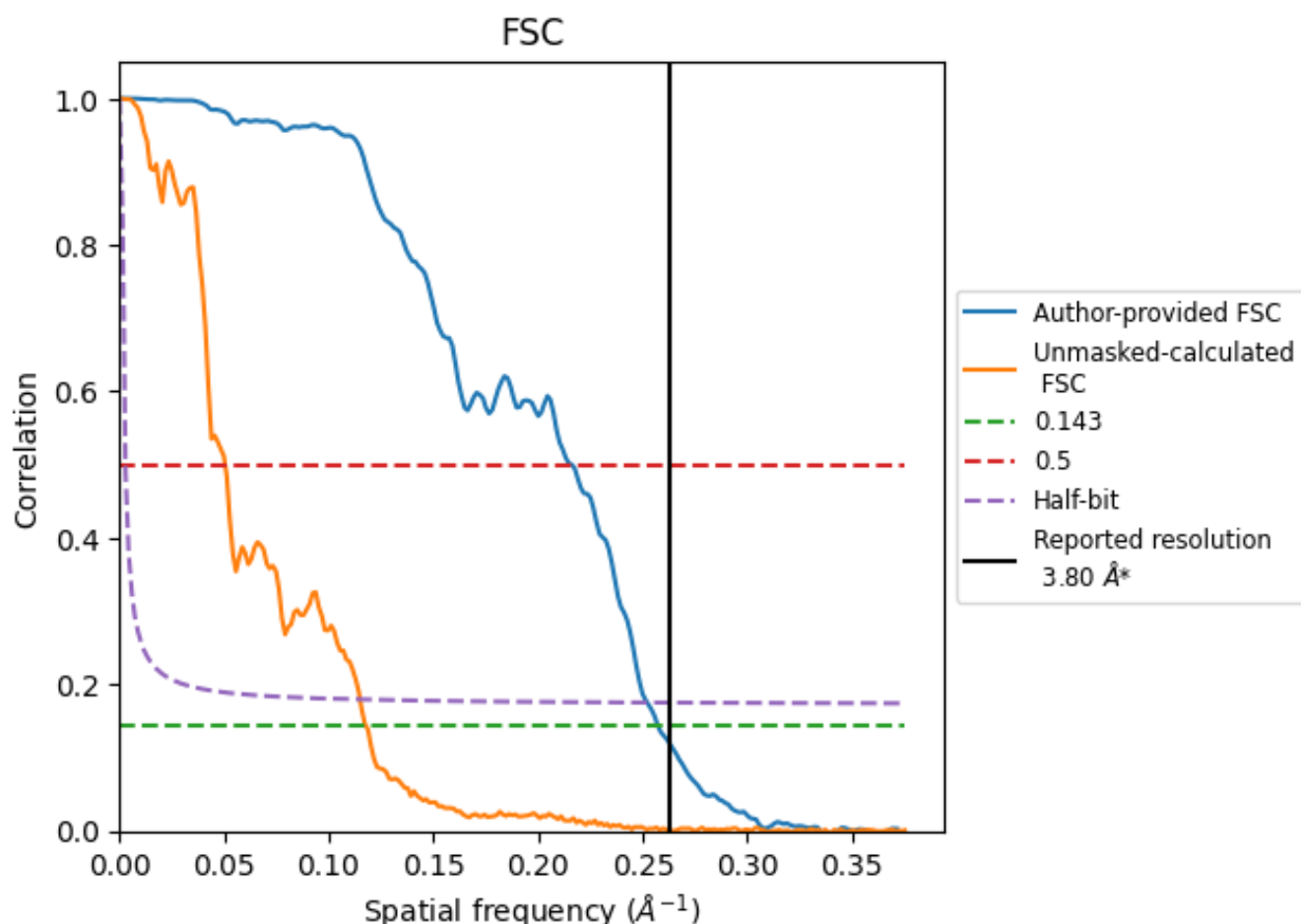


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

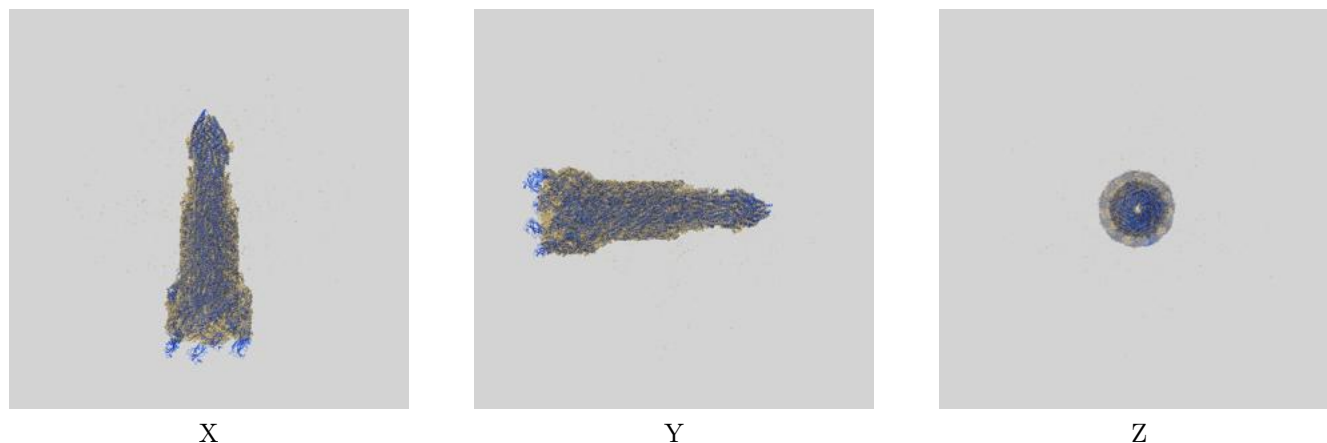
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.89	4.63	3.97
Unmasked-calculated*	8.49	19.80	8.70

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.49 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

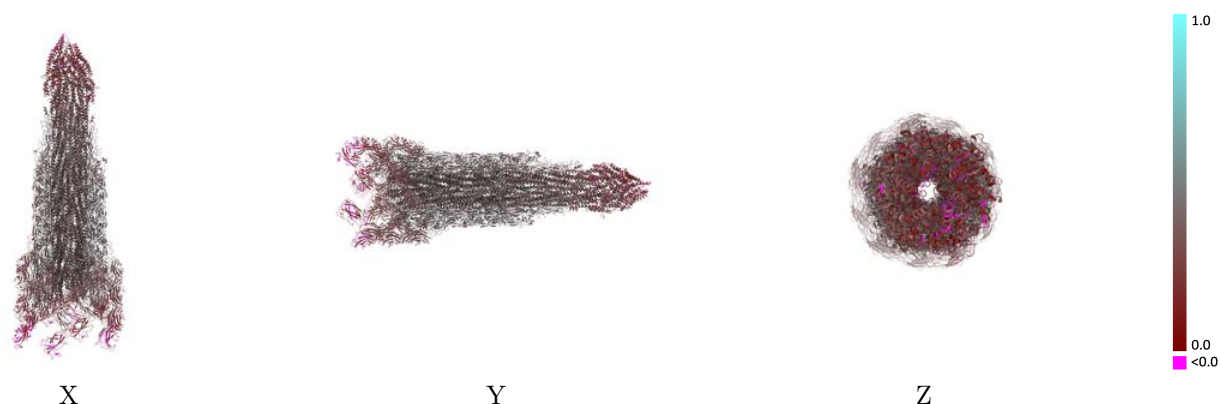
This section contains information regarding the fit between EMDB map EMD-37628 and PDB model 8WLQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



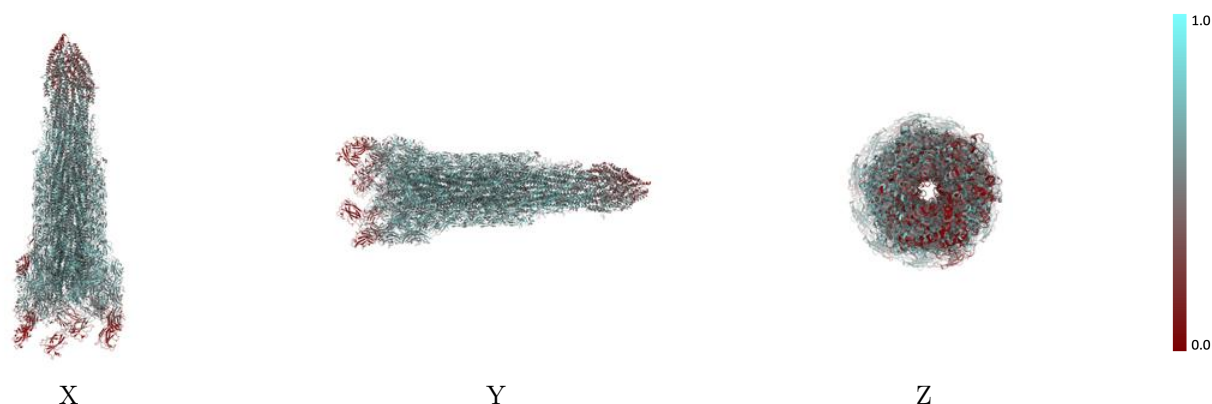
The images above show the 3D surface view of the map at the recommended contour level 0.65 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



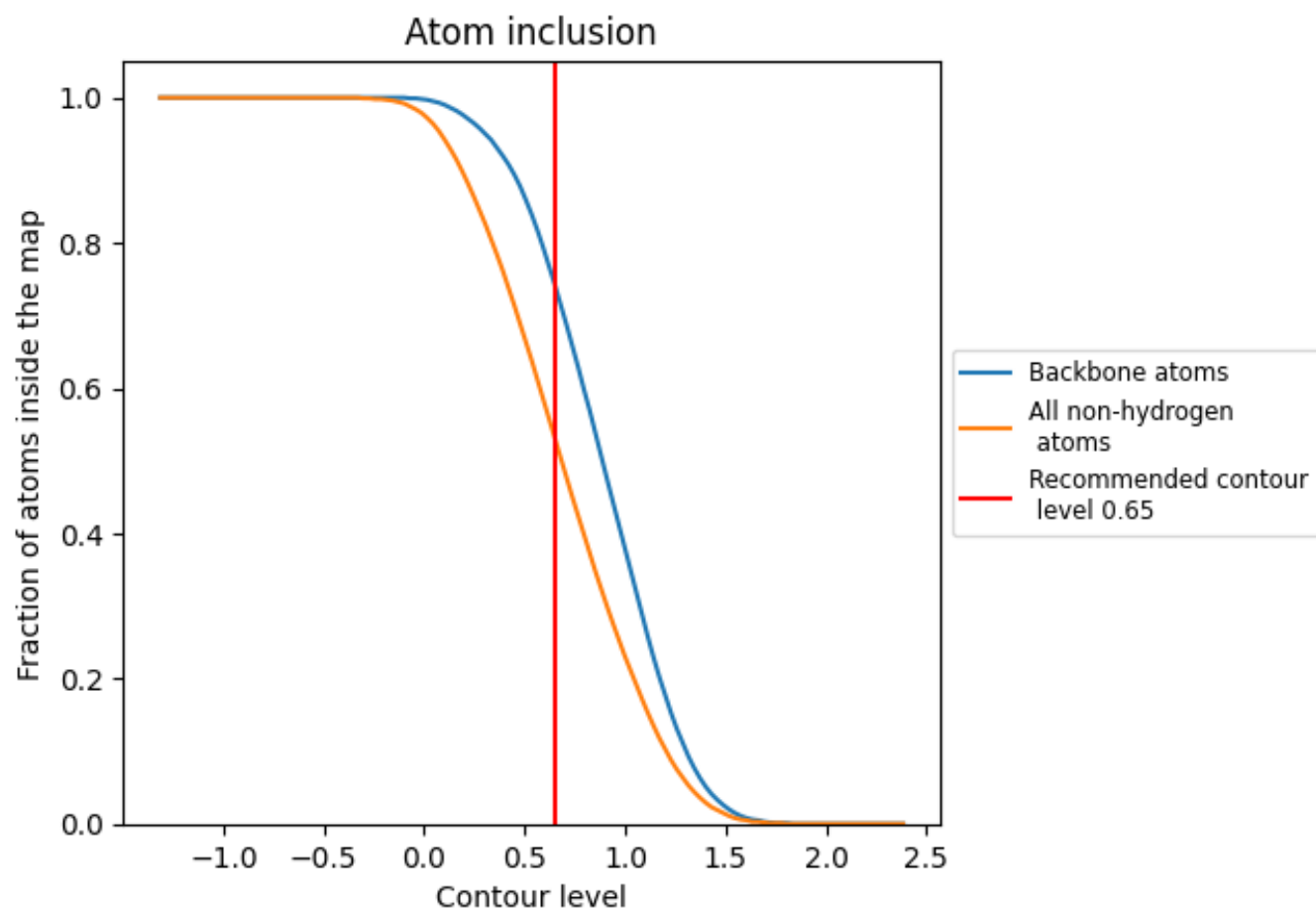
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.65).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 53% 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 (0.65) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5300	 0.3500
0	 0.6070	 0.4090
1	 0.5800	 0.4020
2	 0.5900	 0.4060
3	 0.5980	 0.3990
4	 0.6000	 0.3950
5	 0.5870	 0.4010
6	 0.6040	 0.4060
7	 0.5970	 0.4070
8	 0.5940	 0.4040
9	 0.5740	 0.3940
A	 0.1730	 0.1850
B	 0.3560	 0.2400
C	 0.3900	 0.2320
D	 0.3590	 0.1900
E	 0.3230	 0.2250
F	 0.3730	 0.2390
G	 0.4440	 0.2750
H	 0.4670	 0.2980
I	 0.4650	 0.2870
J	 0.4240	 0.2890
K	 0.4440	 0.2800
L	 0.5070	 0.3100
M	 0.5330	 0.3380
N	 0.5530	 0.3390
O	 0.5200	 0.3260
P	 0.5320	 0.3370
Q	 0.4940	 0.3360
R	 0.5870	 0.3710
S	 0.5930	 0.3730
T	 0.6070	 0.3750
U	 0.5700	 0.3680
V	 0.5200	 0.3610
W	 0.5610	 0.3730
X	 0.5850	 0.4010











































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Chain	Atom inclusion	Q-score
Y	 0.5810	 0.4000
Z	 0.6090	 0.3980
ZA	 0.5780	 0.3920
ZB	 0.5910	 0.3970
ZC	 0.6080	 0.4120
ZD	 0.5910	 0.4090
ZE	 0.5700	 0.3960
ZF	 0.3840	 0.3220
ZG	 0.5490	 0.3670
ZH	 0.5850	 0.3690
ZI	 0.6000	 0.3760
ZJ	 0.6020	 0.3740
ZK	 0.5880	 0.3660
ZL	 0.5930	 0.3710
ZM	 0.5910	 0.3750
ZN	 0.6010	 0.3710
ZO	 0.6000	 0.3650
ZP	 0.6030	 0.3630
ZQ	 0.5830	 0.3570
ZR	 0.5800	 0.3520
ZS	 0.5890	 0.3550
ZT	 0.5660	 0.3490
ZU	 0.5590	 0.3420
ZV	 0.5520	 0.3350
ZW	 0.5380	 0.3290
ZX	 0.5310	 0.3240
ZY	 0.5000	 0.3190
ZZ	 0.4900	 0.3060
Za	 0.4610	 0.3080
Zb	 0.4190	 0.2820
Zc	 0.4030	 0.2900
Zd	 0.3780	 0.2790
Ze	 0.3450	 0.2630
Zf	 0.3370	 0.2470
Zg	 0.3130	 0.2380
Zh	 0.2950	 0.2350
a	 0.5650	 0.3790
b	 0.3210	 0.3210
c	 0.4470	 0.3630
d	 0.3990	 0.3370
e	 0.6210	 0.4010
f	 0.5500	 0.3570

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Chain	Atom inclusion	Q-score
g	 0.5240	 0.3350
h	 0.6000	 0.4050
i	 0.5530	 0.3420
j	 0.5870	 0.3990
k	 0.4560	 0.2680
l	 0.4860	 0.3280
m	 0.5430	 0.3860
n	 0.6180	 0.4010
o	 0.6160	 0.4150
p	 0.6110	 0.4030
q	 0.5920	 0.3880
r	 0.5490	 0.3830
s	 0.5910	 0.4050
t	 0.6130	 0.4110
u	 0.5920	 0.4070
v	 0.5820	 0.4080
w	 0.5950	 0.4020
x	 0.5890	 0.3990
y	 0.5950	 0.4080
z	 0.5810	 0.3980