



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:07 PM UTC

PDB ID : 5WK6 / pdb_00005wk6
EMDB ID : EMD-8856
Title : Cryo-EM structure of *P. aeruginosa* flagellar filaments G420A
Authors : Wang, F.; Postel, S.; Sundberg, E.J.; Egelman, E.H.
Deposited on : 2017-07-24
Resolution : 4.30 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

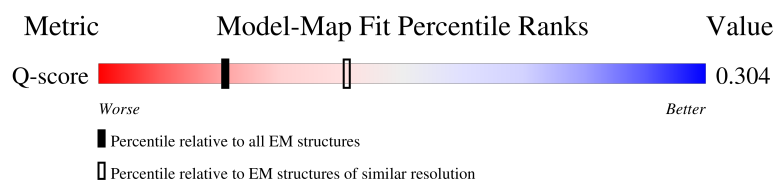
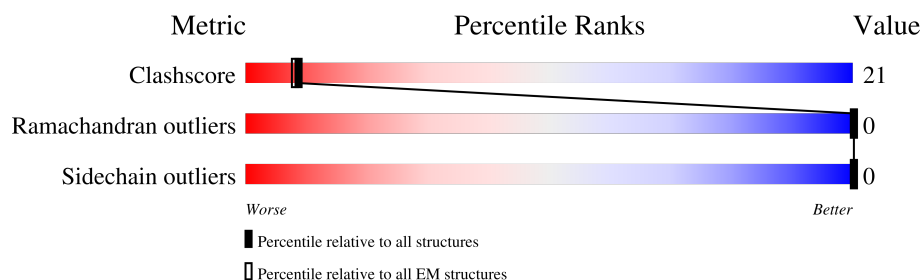
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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	488	22% 39% 16% 45%
1	B	488	23% 39% 16% 45%
1	C	488	22% 39% 16% 45%
1	D	488	23% 39% 15% 45%

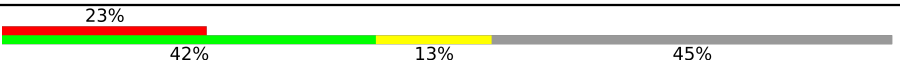
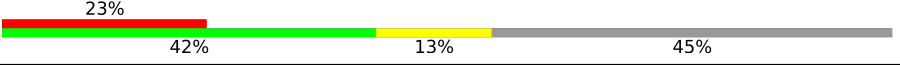
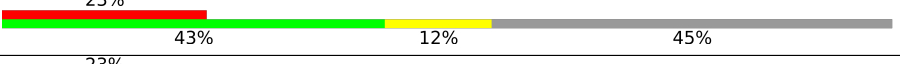
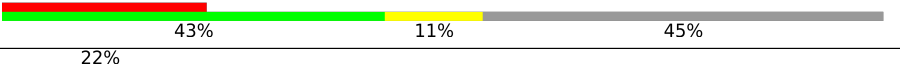
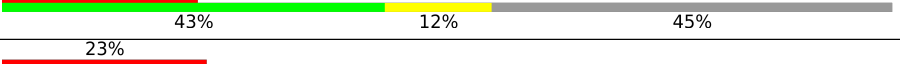
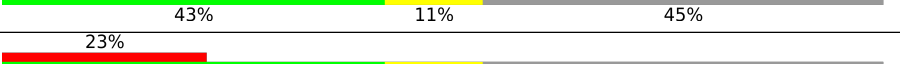
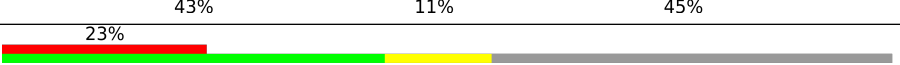
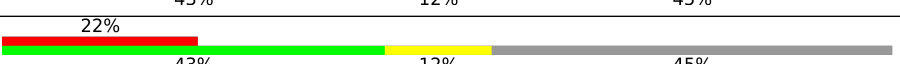
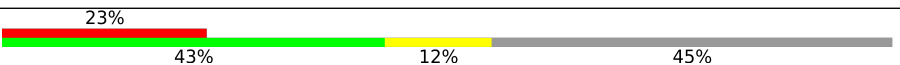
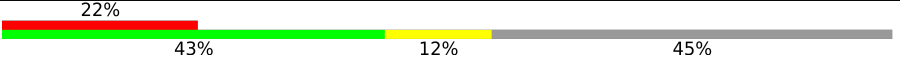
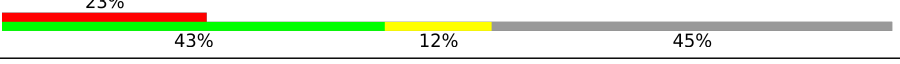
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Mol	Chain	Length	Quality of chain
1	E	488	23% 39% 16% 45%
1	F	488	22% 39% 16% 45%
1	G	488	22% 39% 16% 45%
1	H	488	22% 39% 15% 45%
1	I	488	23% 39% 16% 45%
1	J	488	22% 40% 15% 45%
1	K	488	22% 39% 16% 45%
1	L	488	22% 39% 15% 45%
1	M	488	22% 39% 16% 45%
1	N	488	23% 40% 15% 45%
1	O	488	21% 39% 16% 45%
1	P	488	23% 39% 16% 45%
1	Q	488	22% 39% 16% 45%
1	R	488	23% 39% 15% 45%
1	S	488	22% 39% 16% 45%
1	T	488	23% 41% 14% 45%
1	U	488	22% 41% 14% 45%
1	V	488	23% 41% 14% 45%
1	W	488	23% 41% 14% 45%
1	X	488	24% 41% 14% 45%
1	Y	488	23% 41% 14% 45%
1	Z	488	23% 41% 14% 45%
1	a	488	23% 41% 14% 45%
1	b	488	22% 41% 13% 45%
1	c	488	23% 41% 14% 45%

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Mol	Chain	Length	Quality of chain
1	d	488	
1	e	488	
1	f	488	
1	g	488	
1	h	488	
1	i	488	
1	j	488	
1	k	488	
1	l	488	
1	m	488	
1	n	488	
1	o	488	



2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 161663 atoms, of which 80524 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 B-type flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	B	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	C	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	D	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	E	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	F	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	G	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	H	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	I	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	J	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	K	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	L	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	M	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	N	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	O	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	P	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	Q	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	S	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	T	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	U	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	V	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	W	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	X	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	Y	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	Z	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	a	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	b	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	c	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	d	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	e	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	f	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	g	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	h	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	i	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	j	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	k	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	l	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	n	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0
1	o	269	Total 3943	C 1187	H 1964	N 371	O 421	0	0

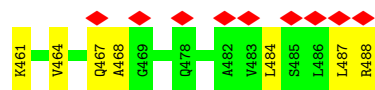
There are 41 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	420	ALA	GLY	engineered mutation	UNP P72151
B	420	ALA	GLY	engineered mutation	UNP P72151
C	420	ALA	GLY	engineered mutation	UNP P72151
D	420	ALA	GLY	engineered mutation	UNP P72151
E	420	ALA	GLY	engineered mutation	UNP P72151
F	420	ALA	GLY	engineered mutation	UNP P72151
G	420	ALA	GLY	engineered mutation	UNP P72151
H	420	ALA	GLY	engineered mutation	UNP P72151
I	420	ALA	GLY	engineered mutation	UNP P72151
J	420	ALA	GLY	engineered mutation	UNP P72151
K	420	ALA	GLY	engineered mutation	UNP P72151
L	420	ALA	GLY	engineered mutation	UNP P72151
M	420	ALA	GLY	engineered mutation	UNP P72151
N	420	ALA	GLY	engineered mutation	UNP P72151
O	420	ALA	GLY	engineered mutation	UNP P72151
P	420	ALA	GLY	engineered mutation	UNP P72151
Q	420	ALA	GLY	engineered mutation	UNP P72151
R	420	ALA	GLY	engineered mutation	UNP P72151
S	420	ALA	GLY	engineered mutation	UNP P72151
T	420	ALA	GLY	engineered mutation	UNP P72151
U	420	ALA	GLY	engineered mutation	UNP P72151
V	420	ALA	GLY	engineered mutation	UNP P72151
W	420	ALA	GLY	engineered mutation	UNP P72151
X	420	ALA	GLY	engineered mutation	UNP P72151
Y	420	ALA	GLY	engineered mutation	UNP P72151
Z	420	ALA	GLY	engineered mutation	UNP P72151
a	420	ALA	GLY	engineered mutation	UNP P72151
b	420	ALA	GLY	engineered mutation	UNP P72151
c	420	ALA	GLY	engineered mutation	UNP P72151
d	420	ALA	GLY	engineered mutation	UNP P72151
e	420	ALA	GLY	engineered mutation	UNP P72151
f	420	ALA	GLY	engineered mutation	UNP P72151

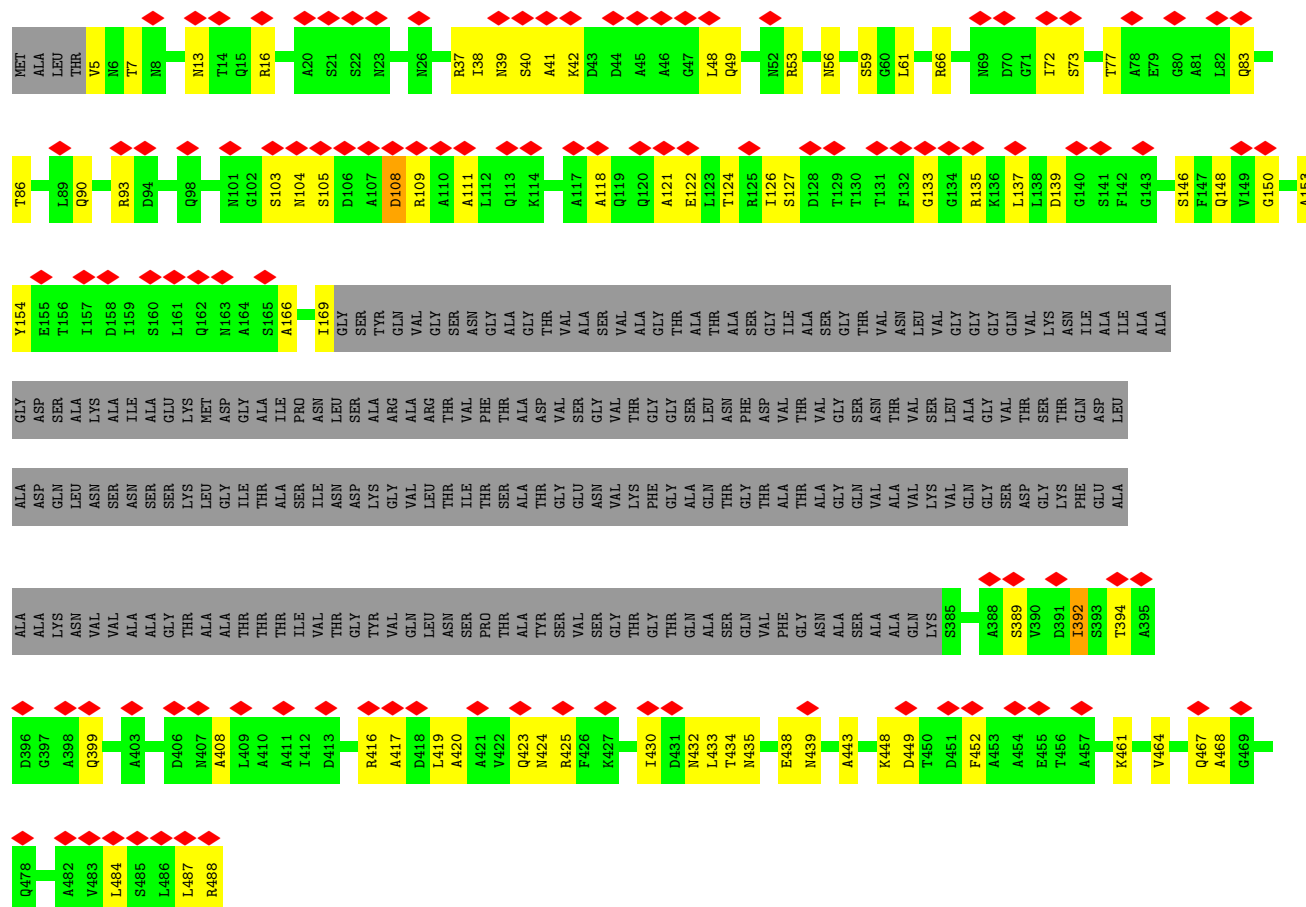
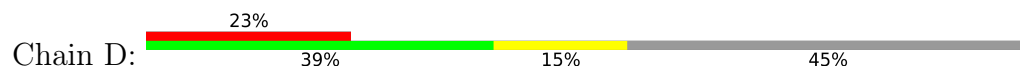
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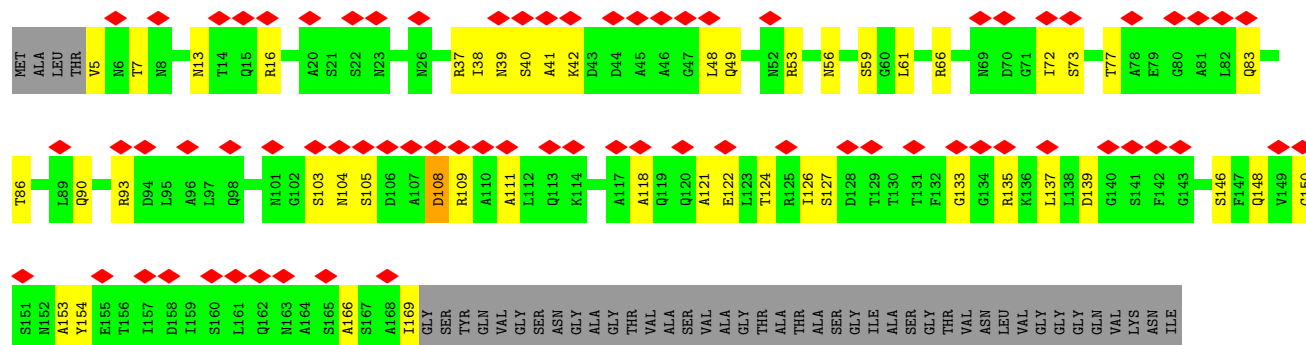
Chain	Residue	Modelled	Actual	Comment	Reference
g	420	ALA	GLY	engineered mutation	UNP P72151
h	420	ALA	GLY	engineered mutation	UNP P72151
i	420	ALA	GLY	engineered mutation	UNP P72151
j	420	ALA	GLY	engineered mutation	UNP P72151
k	420	ALA	GLY	engineered mutation	UNP P72151
l	420	ALA	GLY	engineered mutation	UNP P72151
m	420	ALA	GLY	engineered mutation	UNP P72151
n	420	ALA	GLY	engineered mutation	UNP P72151
o	420	ALA	GLY	engineered mutation	UNP P72151

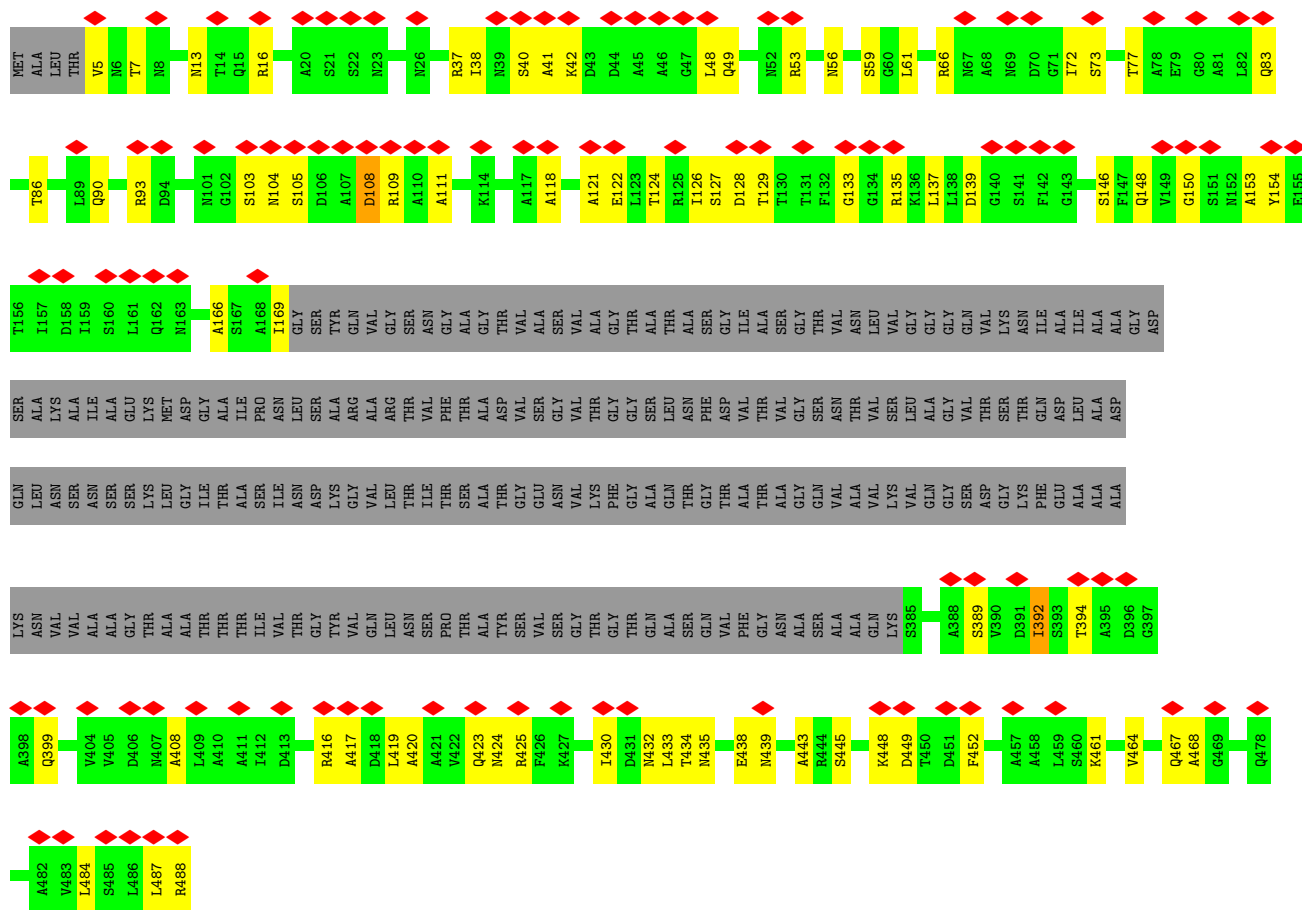


• Molecule 1: B-type flagellin

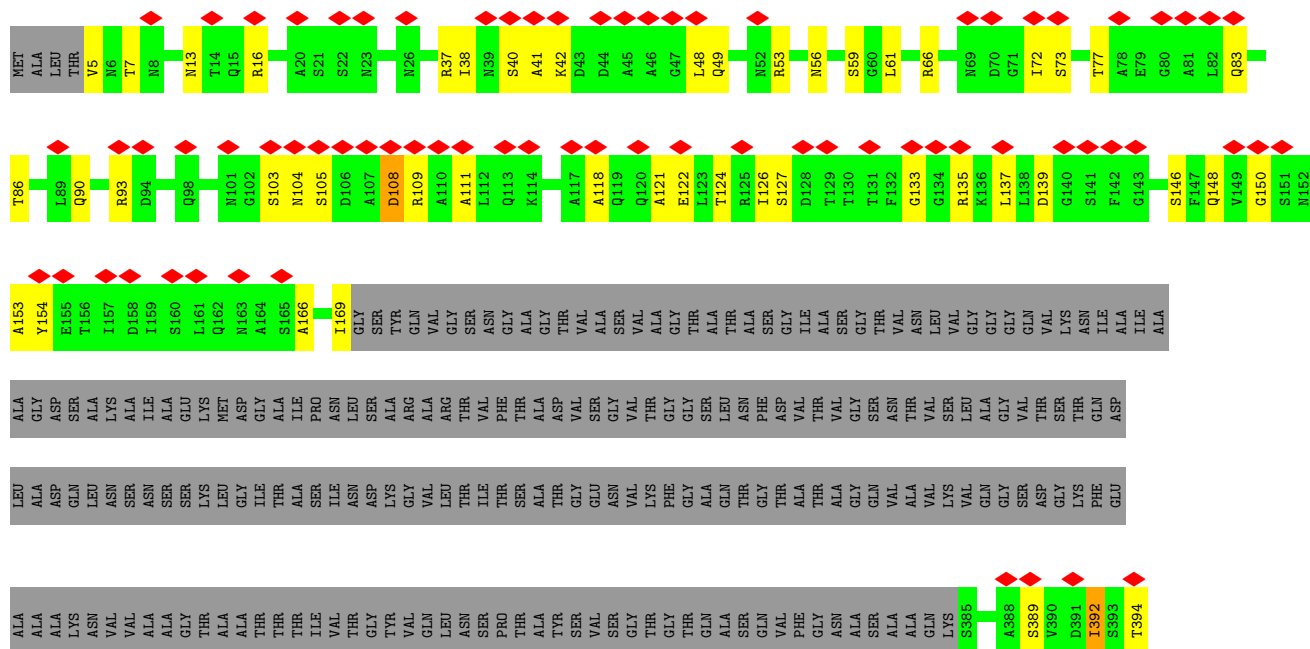
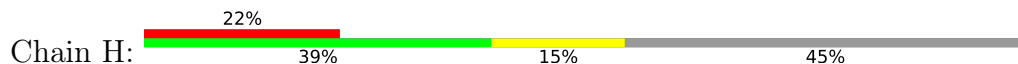


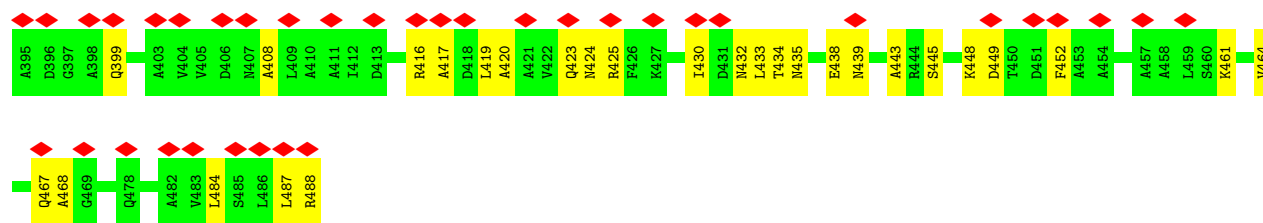
• Molecule 1: B-type flagellin



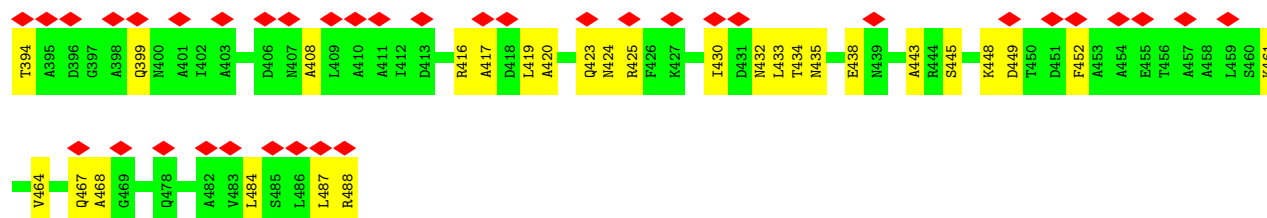
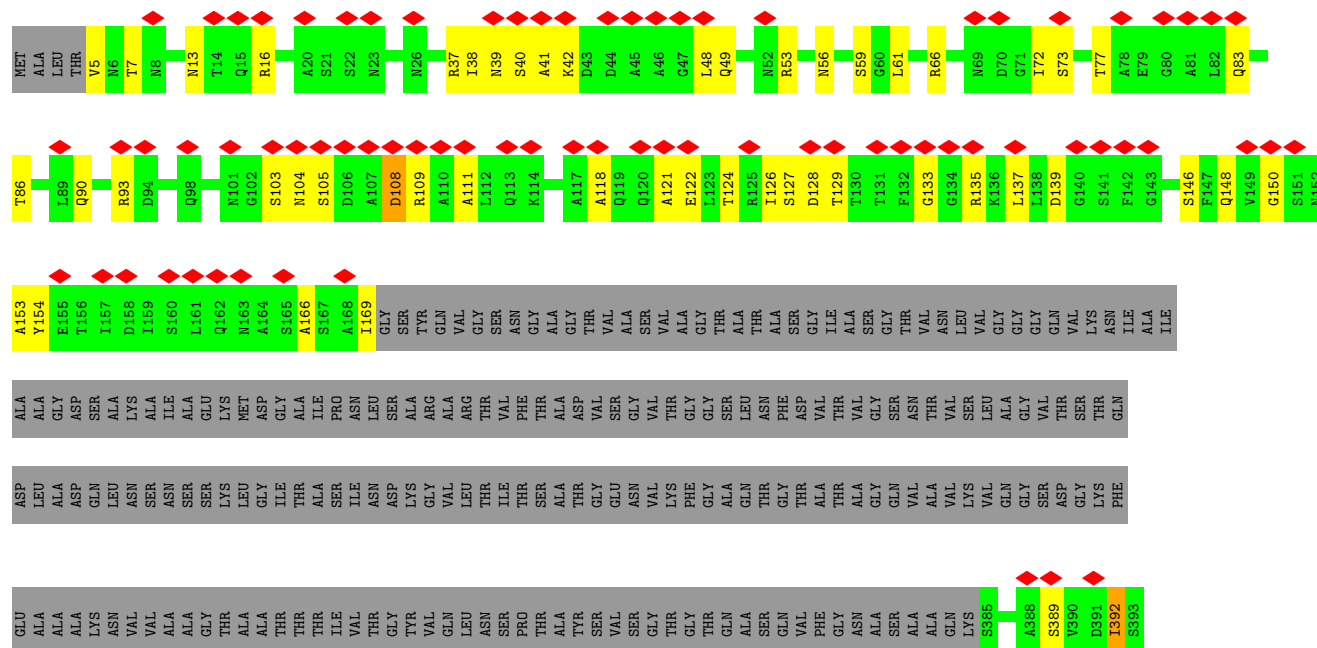
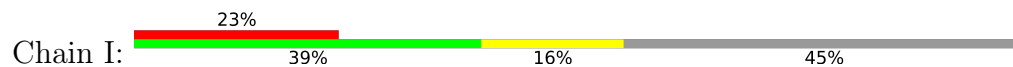


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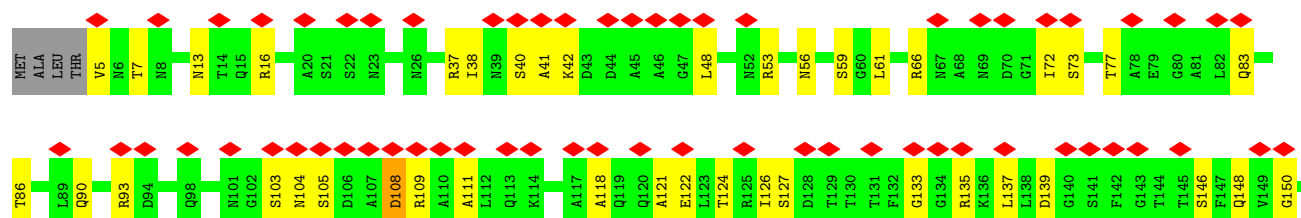


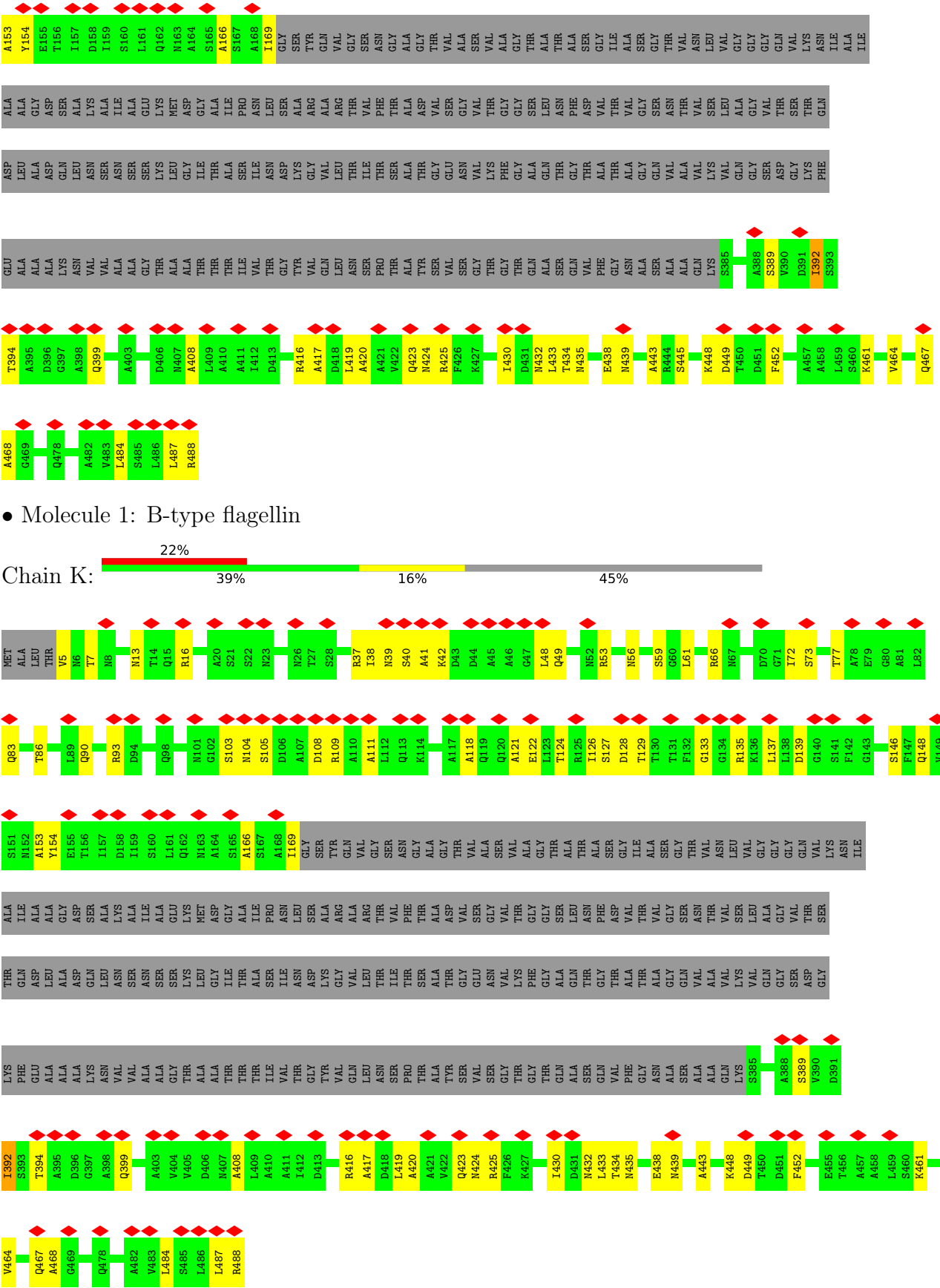


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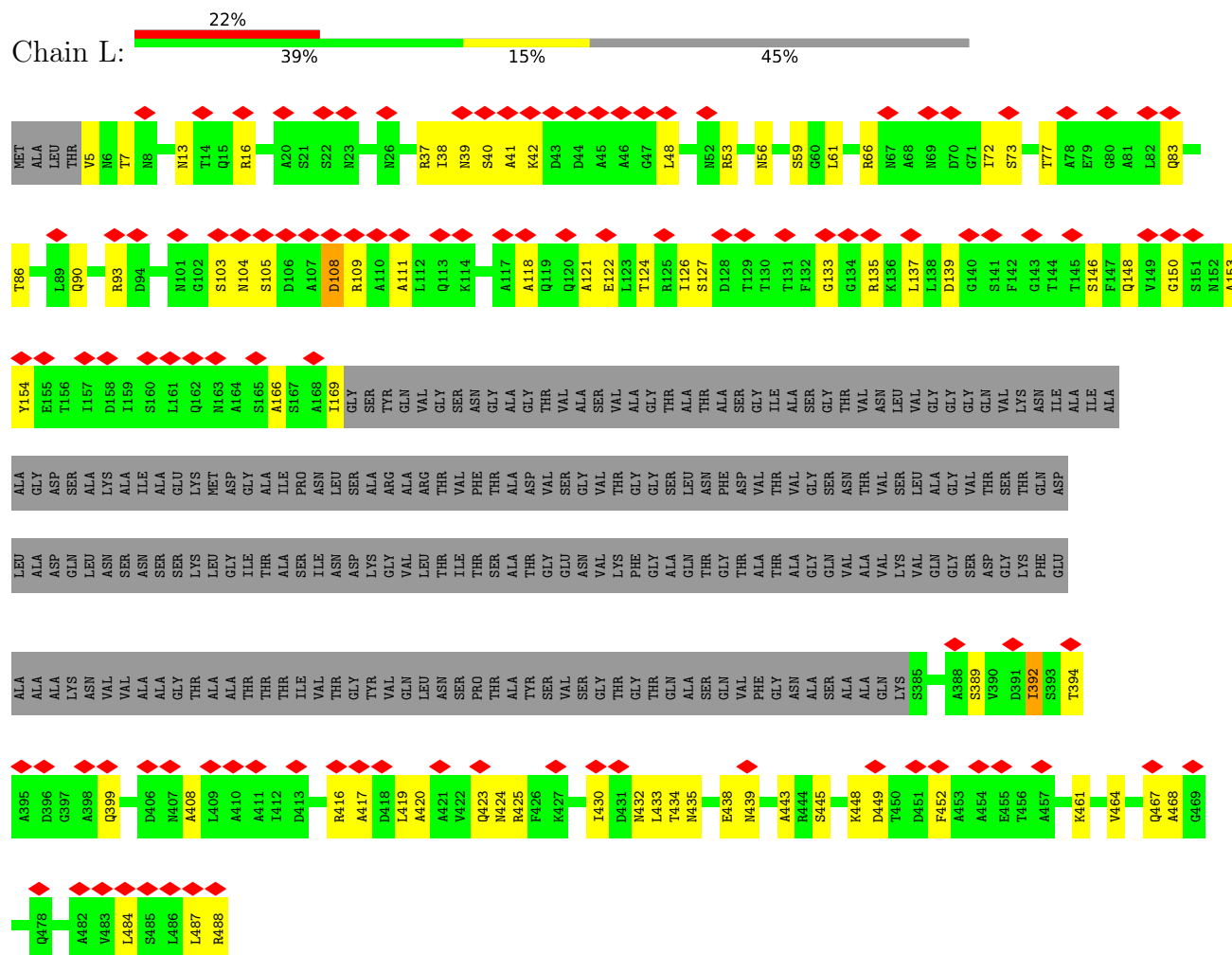


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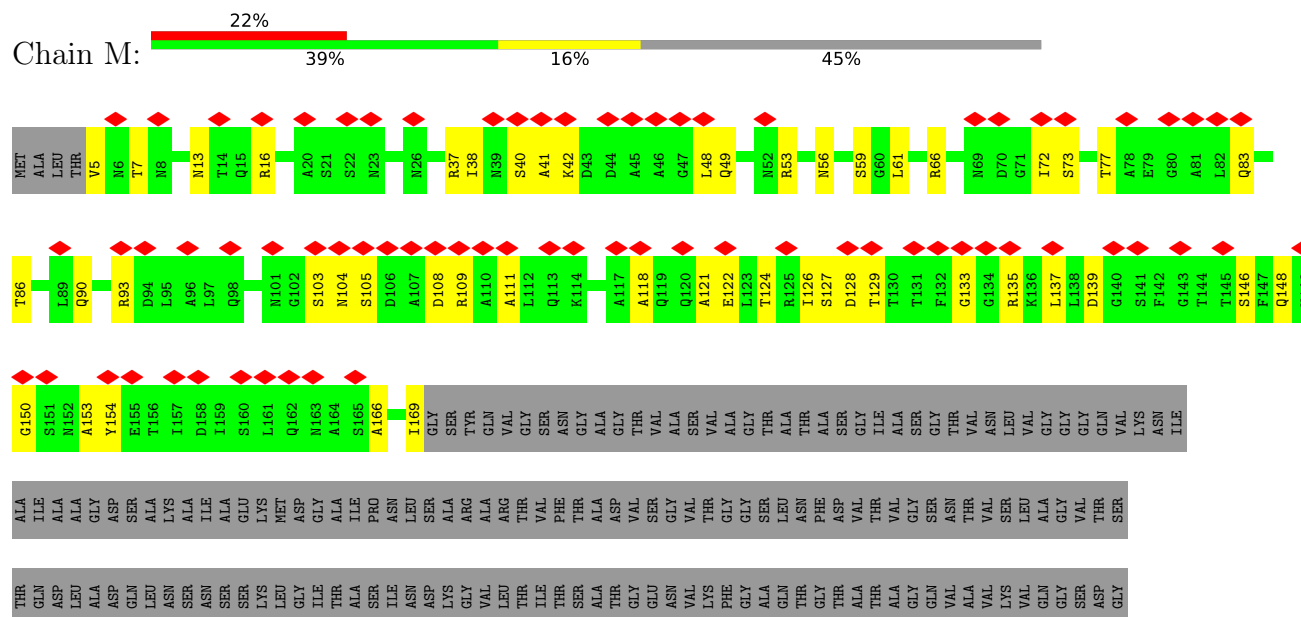


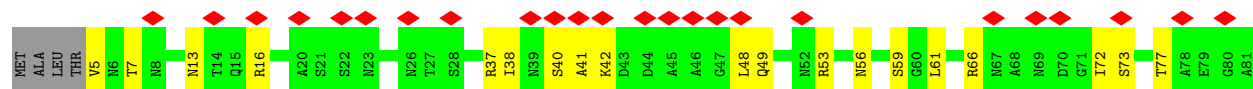


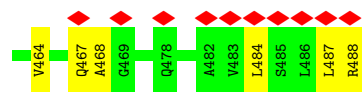
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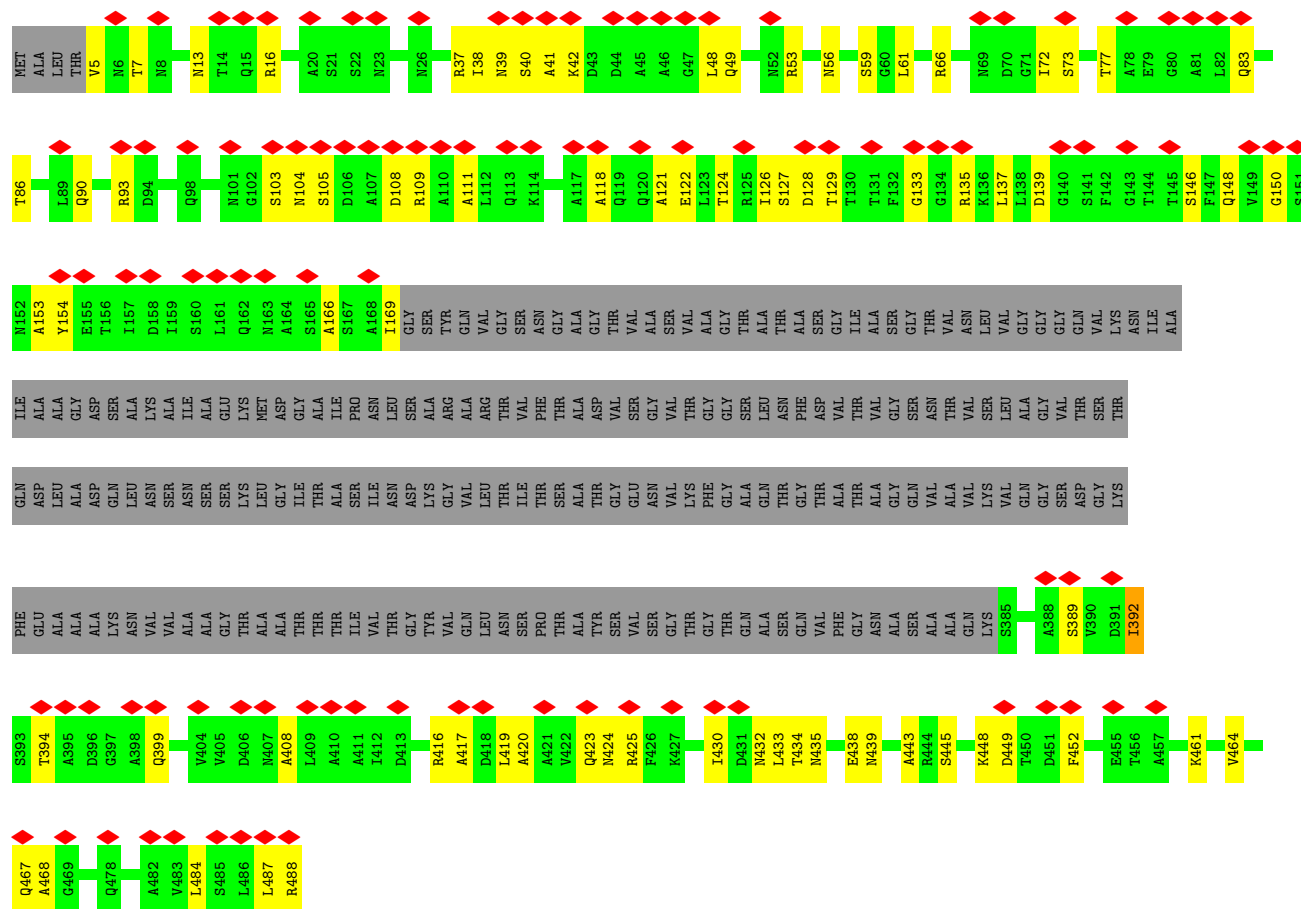
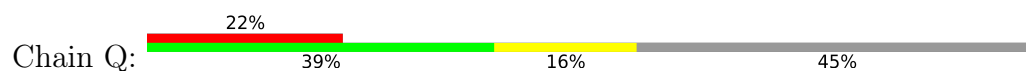
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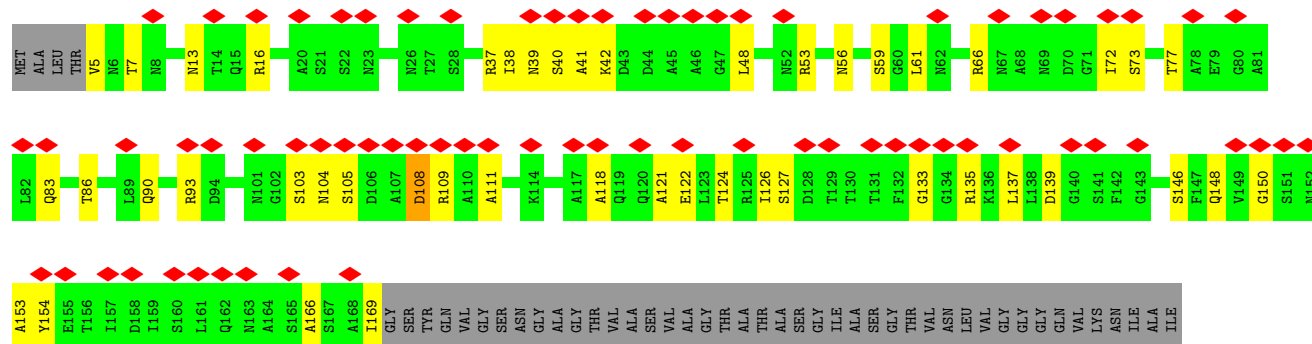
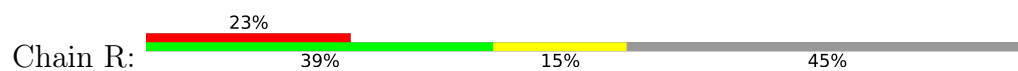




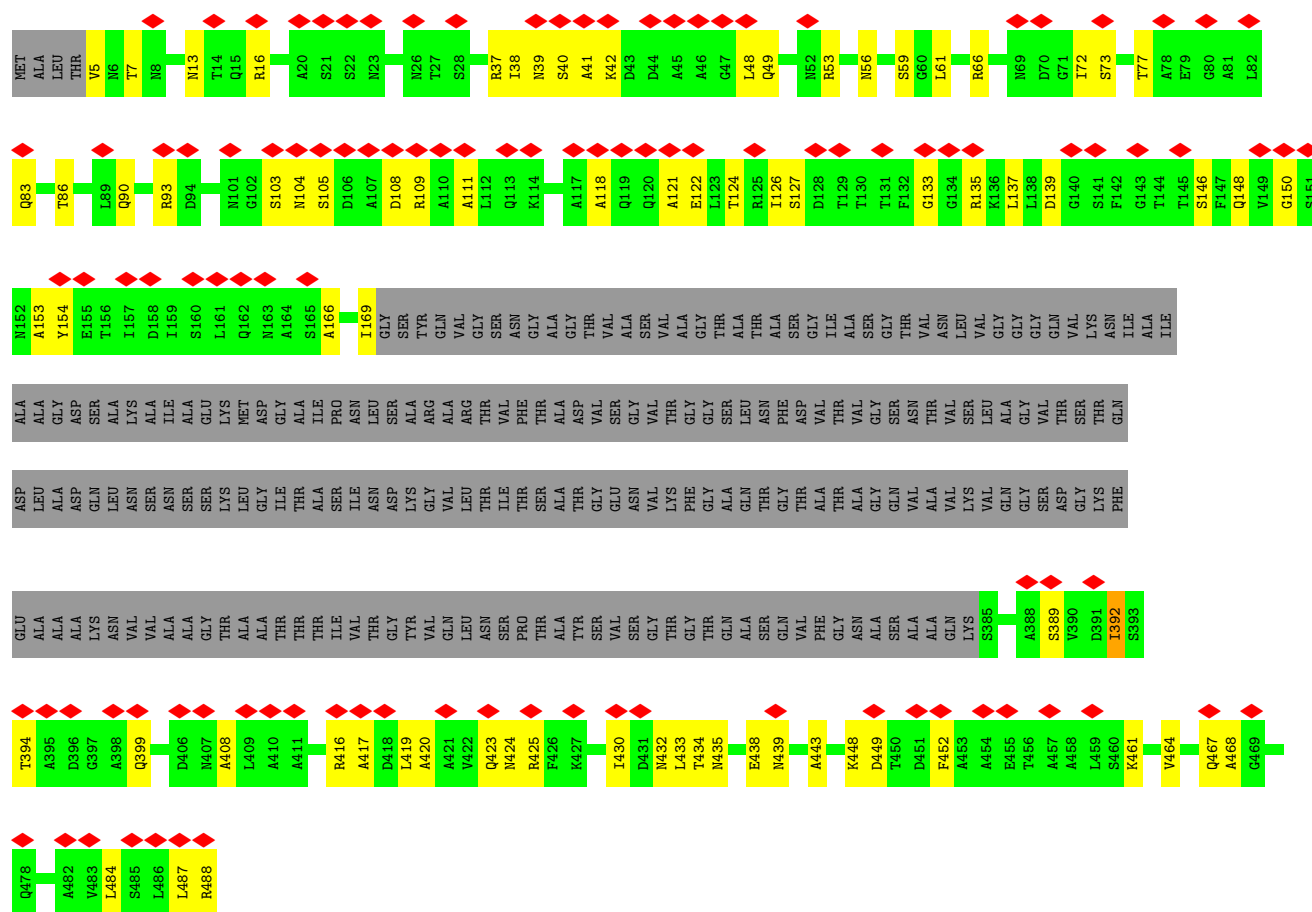
• Molecule 1: B-type flagellin



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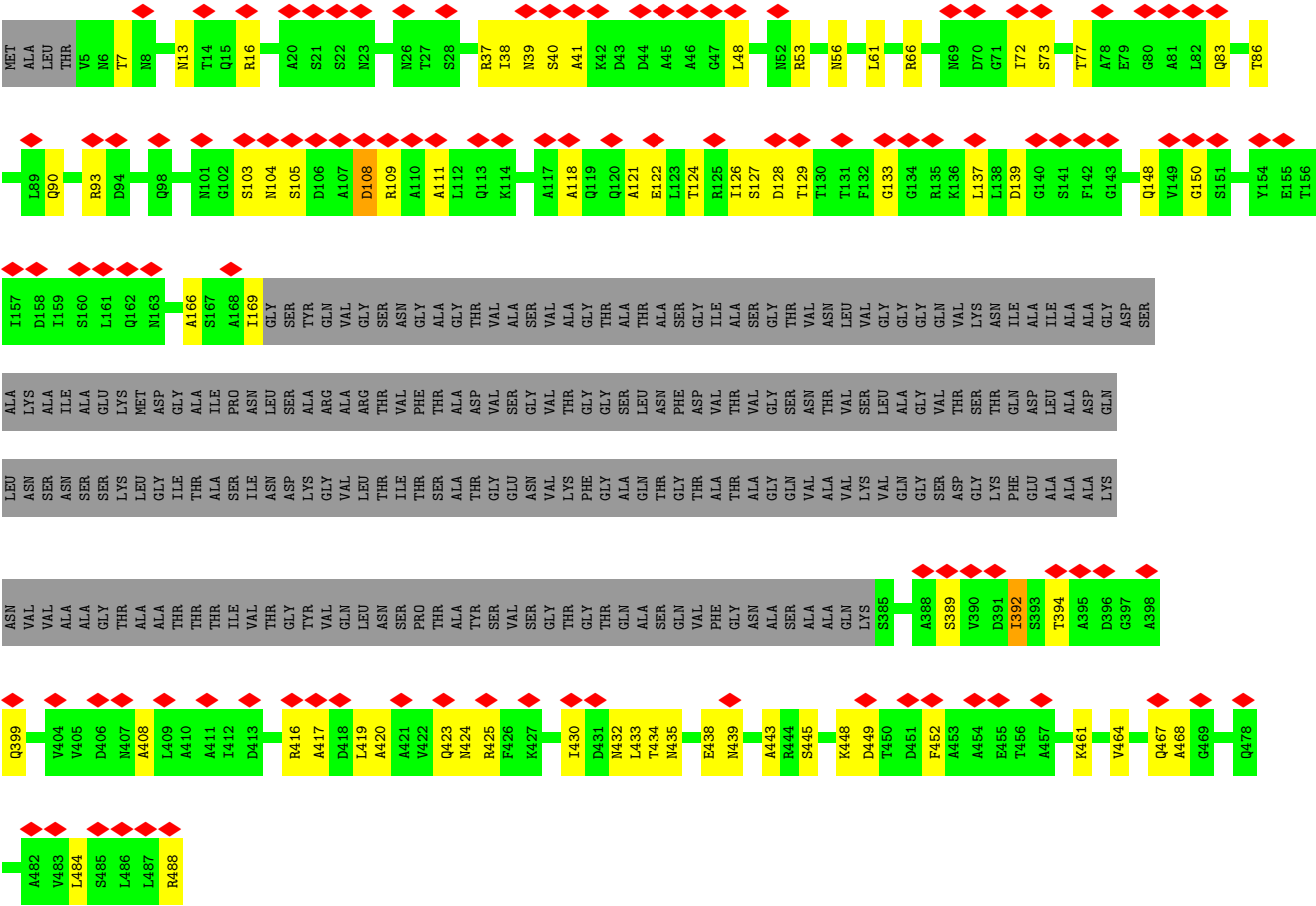


- Molecule 1: B-type flagellin

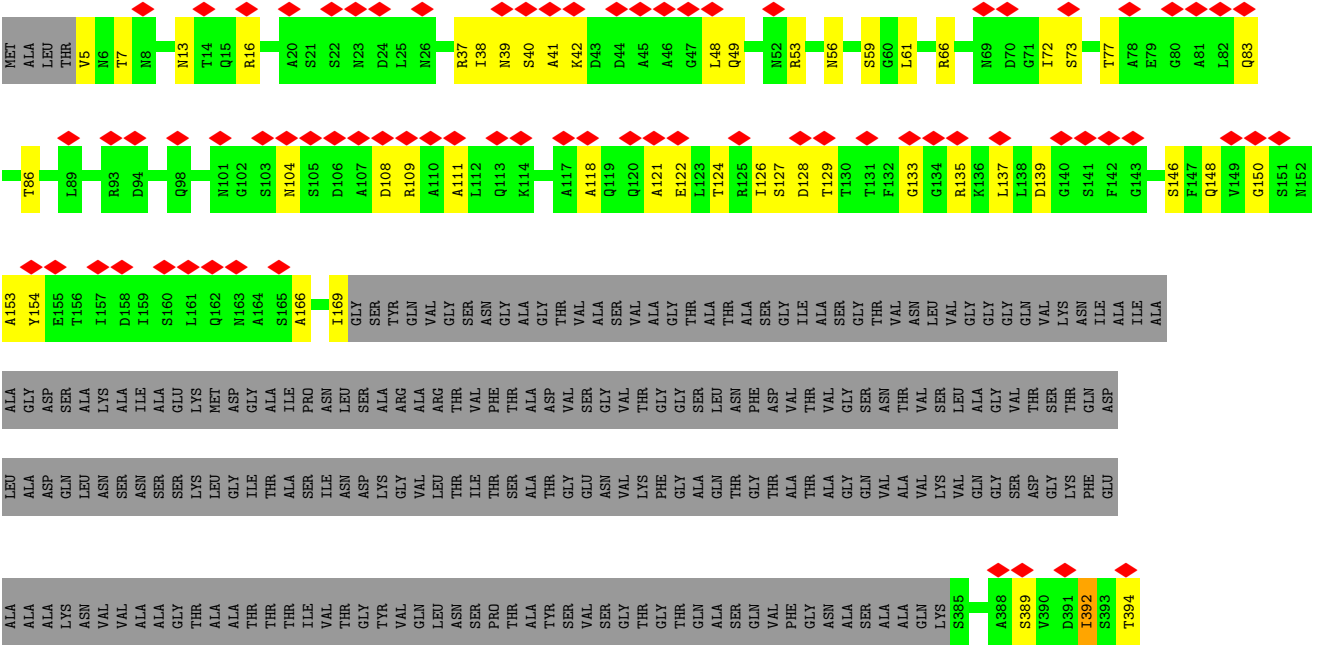


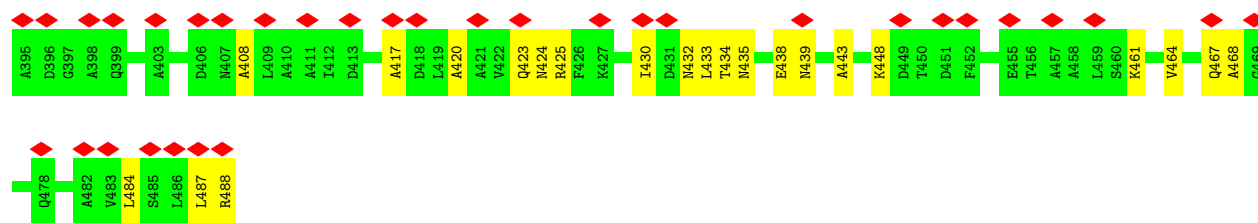
- Molecule 1: B-type flagellin



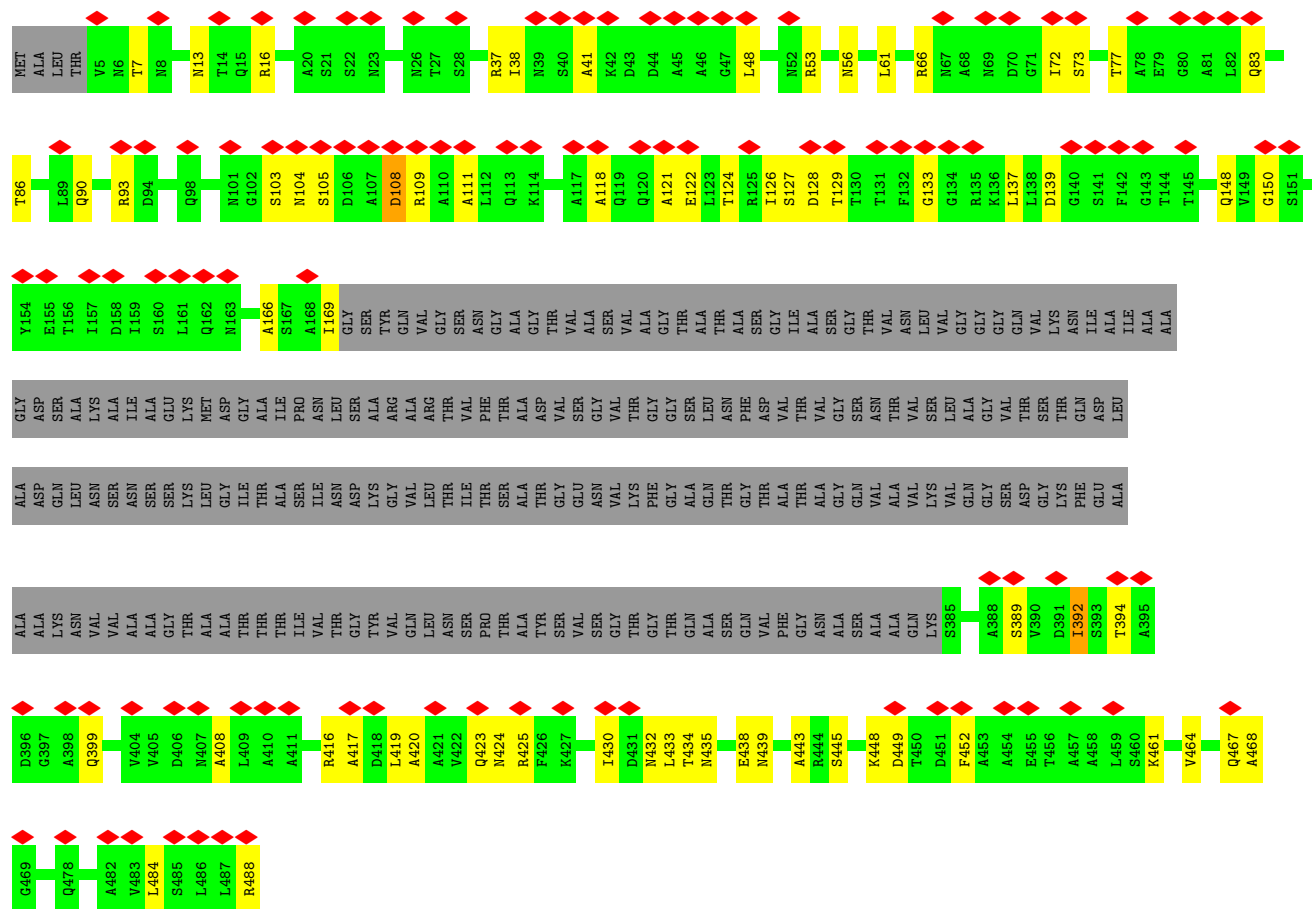
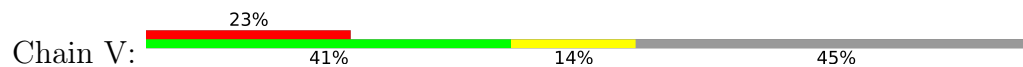


● Molecule 1: B-type flagellin

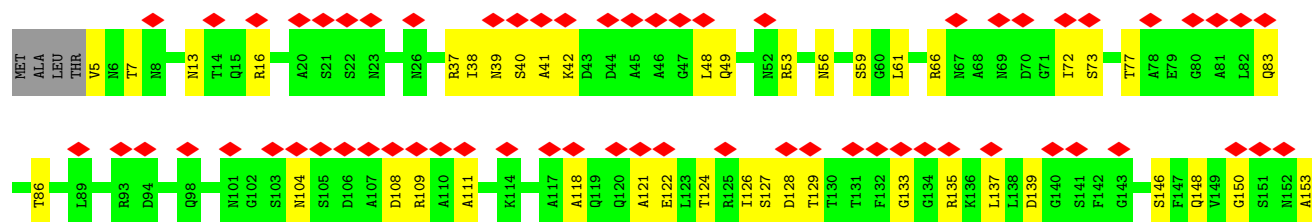
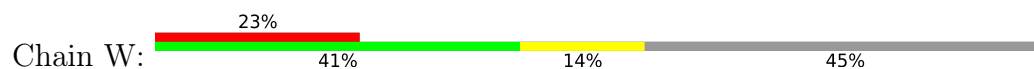


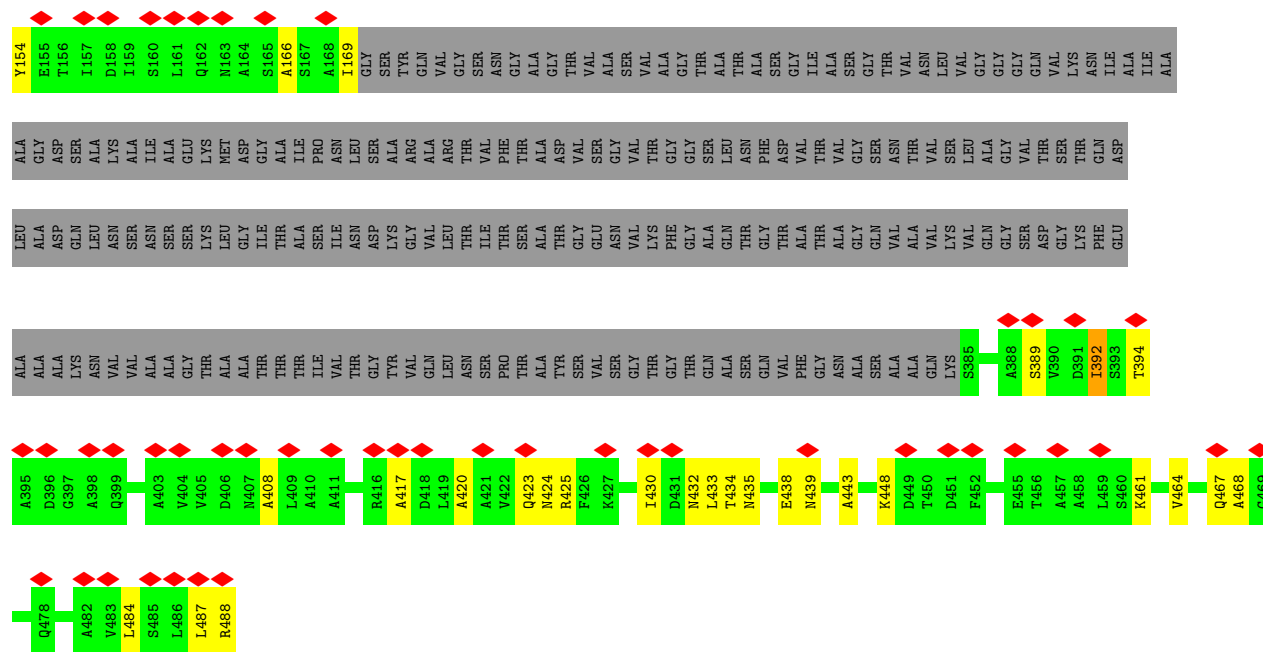


• Molecule 1: B-type flagellin

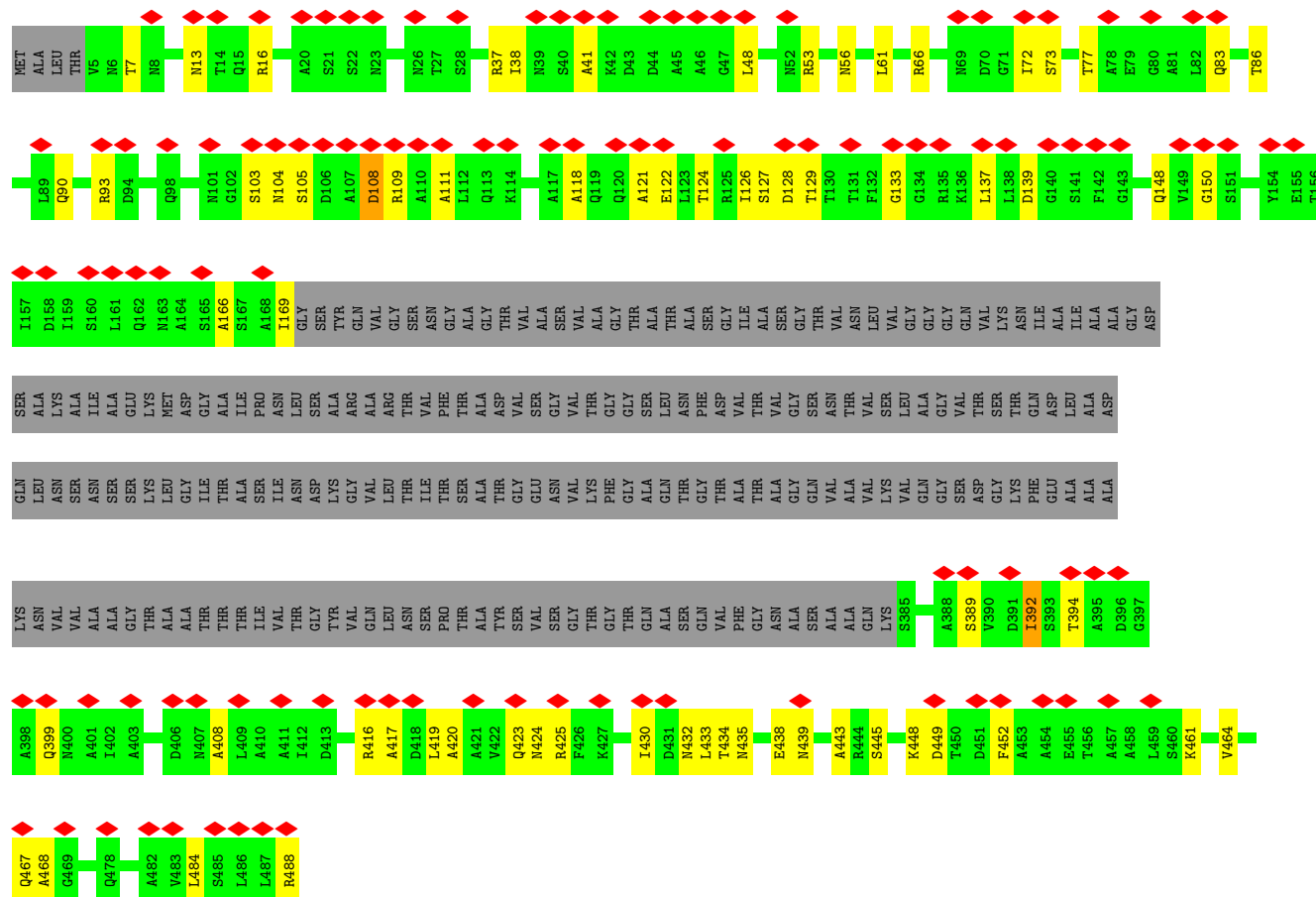


• Molecule 1: B-type flagellin





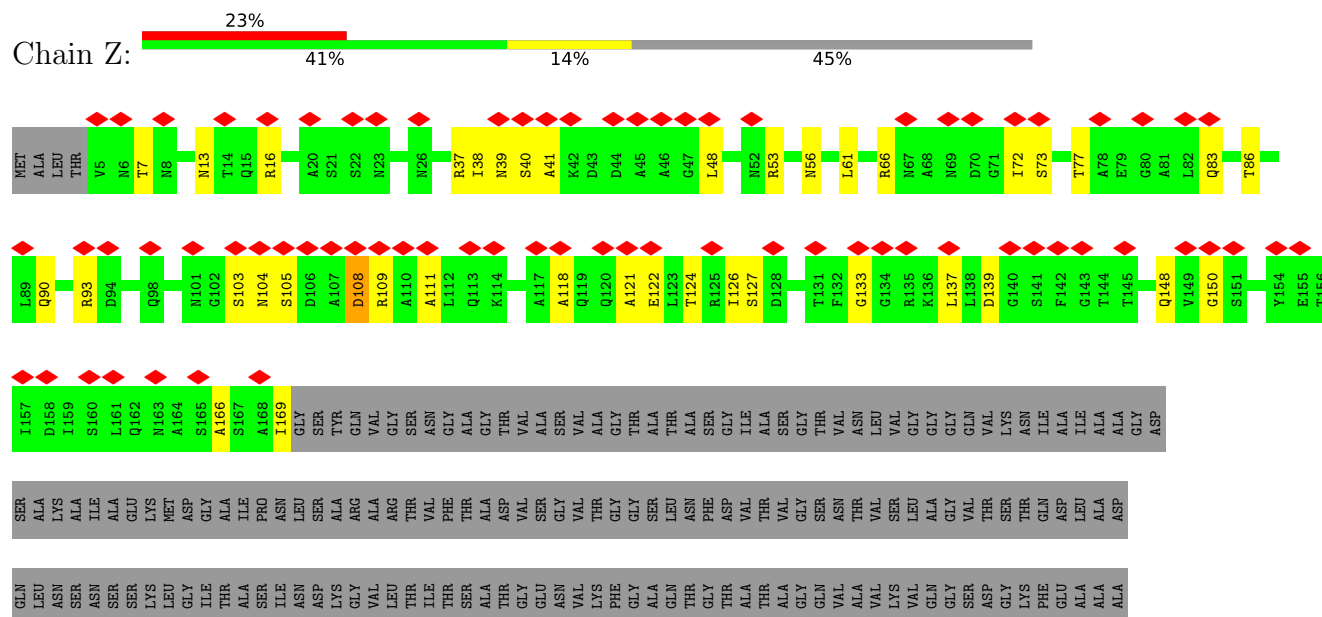
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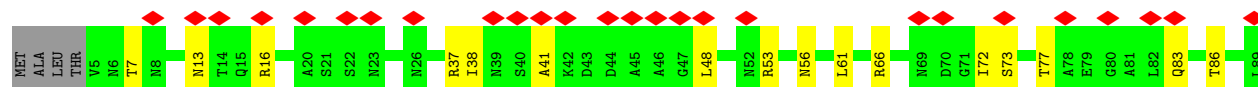


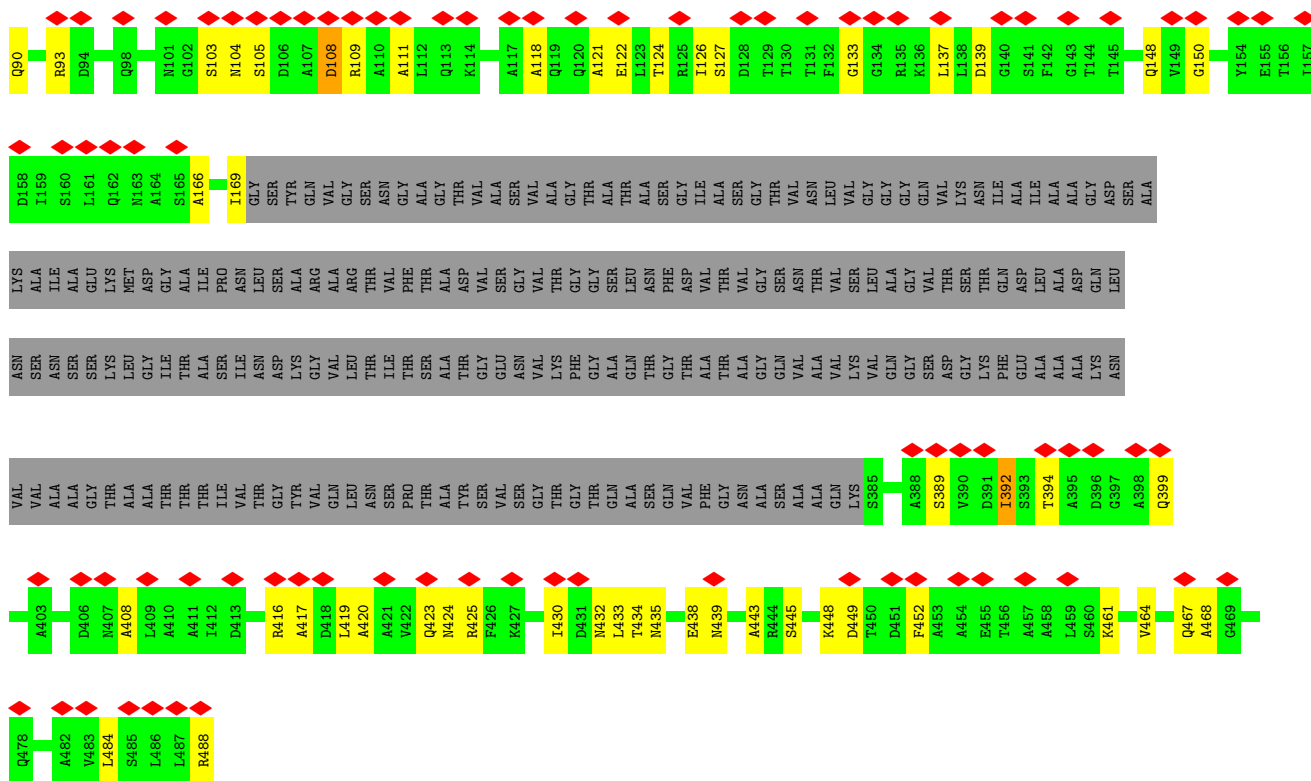
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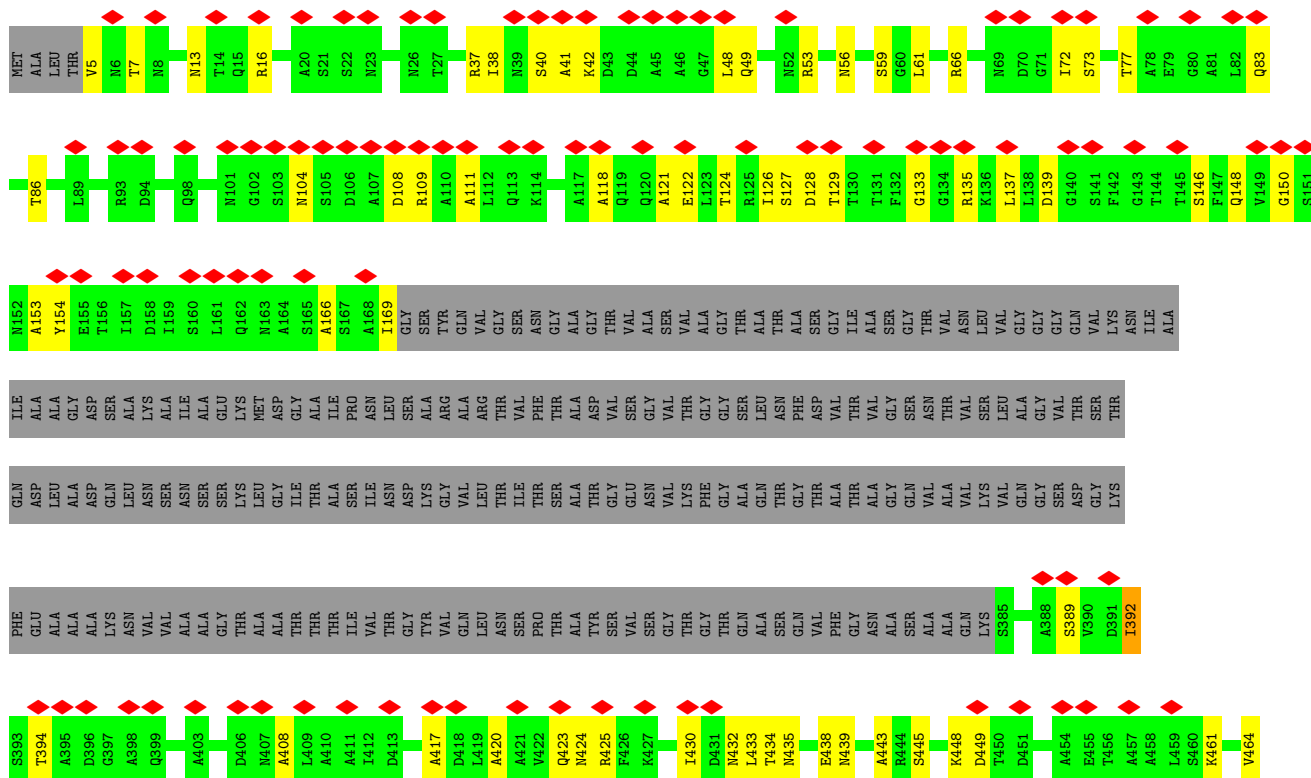
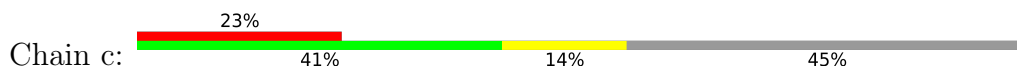
Chain Z:

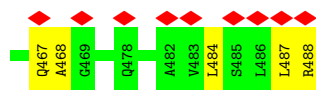




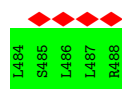
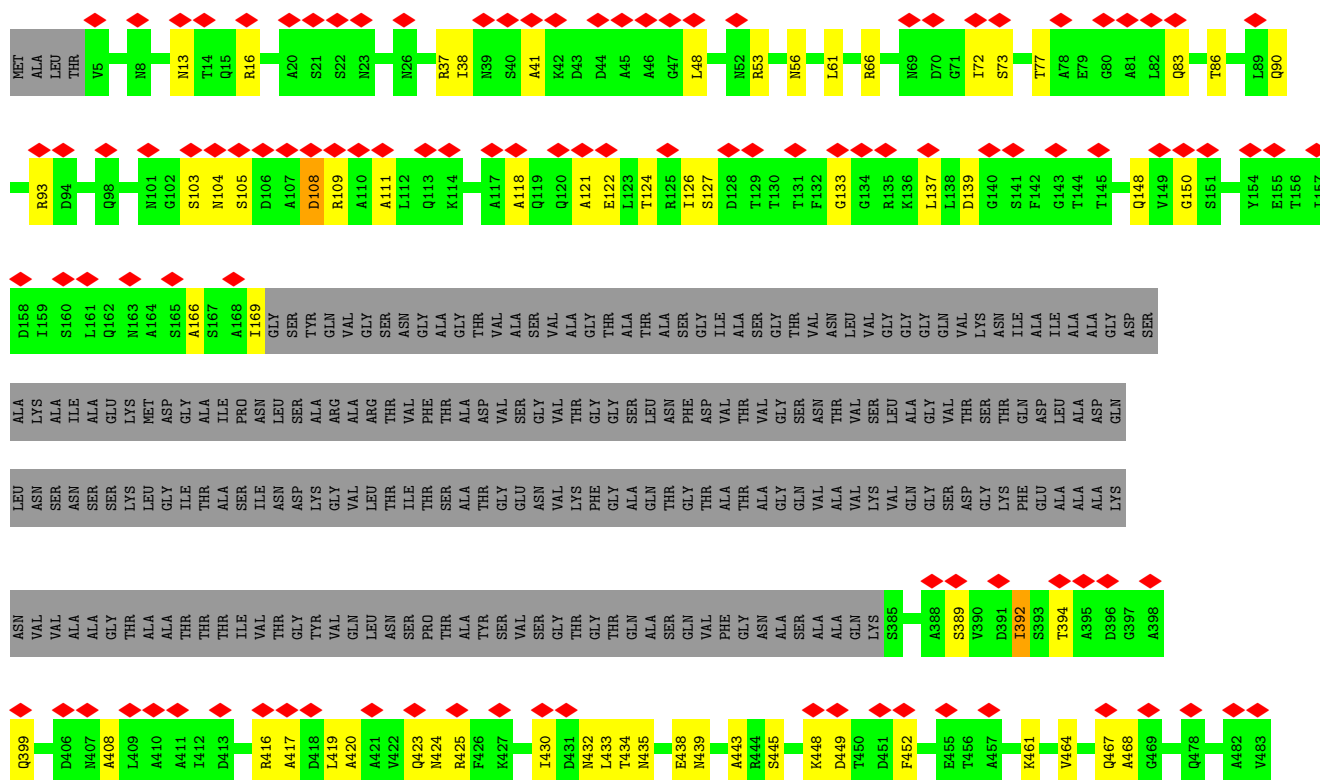
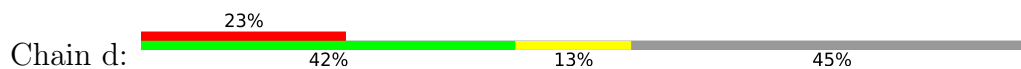


- Molecule 1: B-type flagellin

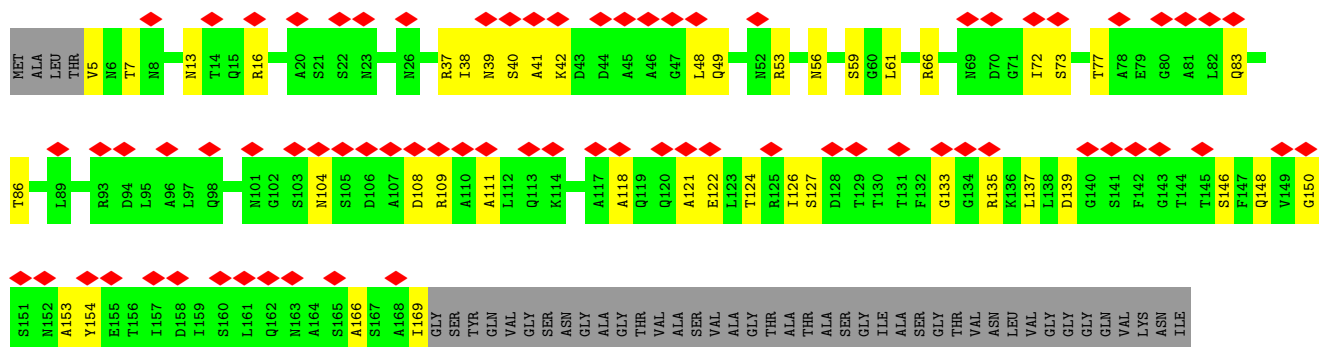




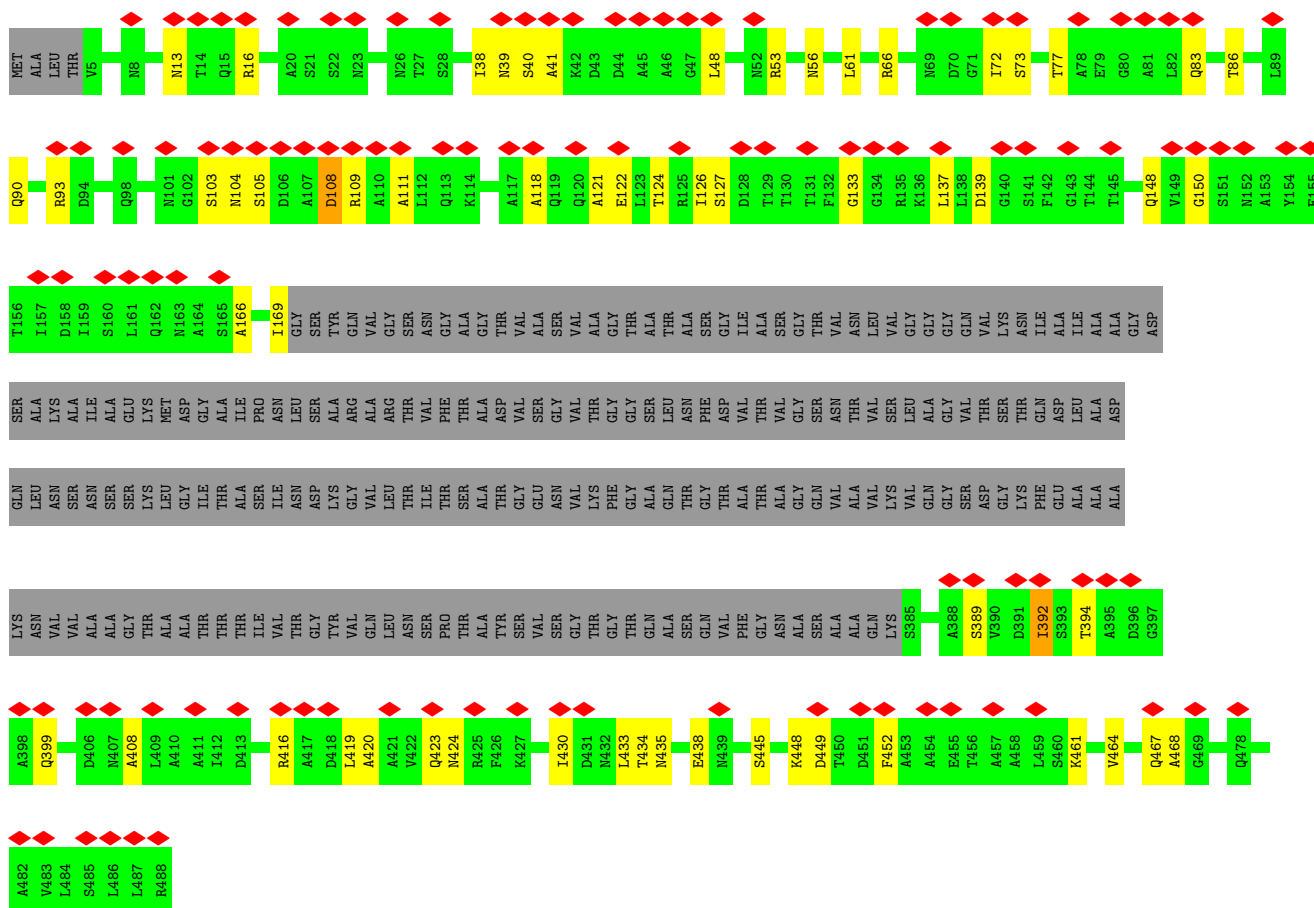
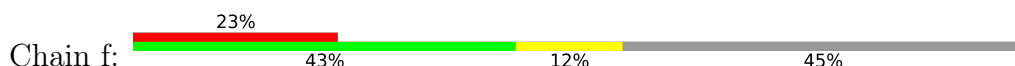
• Molecule 1: B-type flagellin



• Molecule 1: B-type flagellin

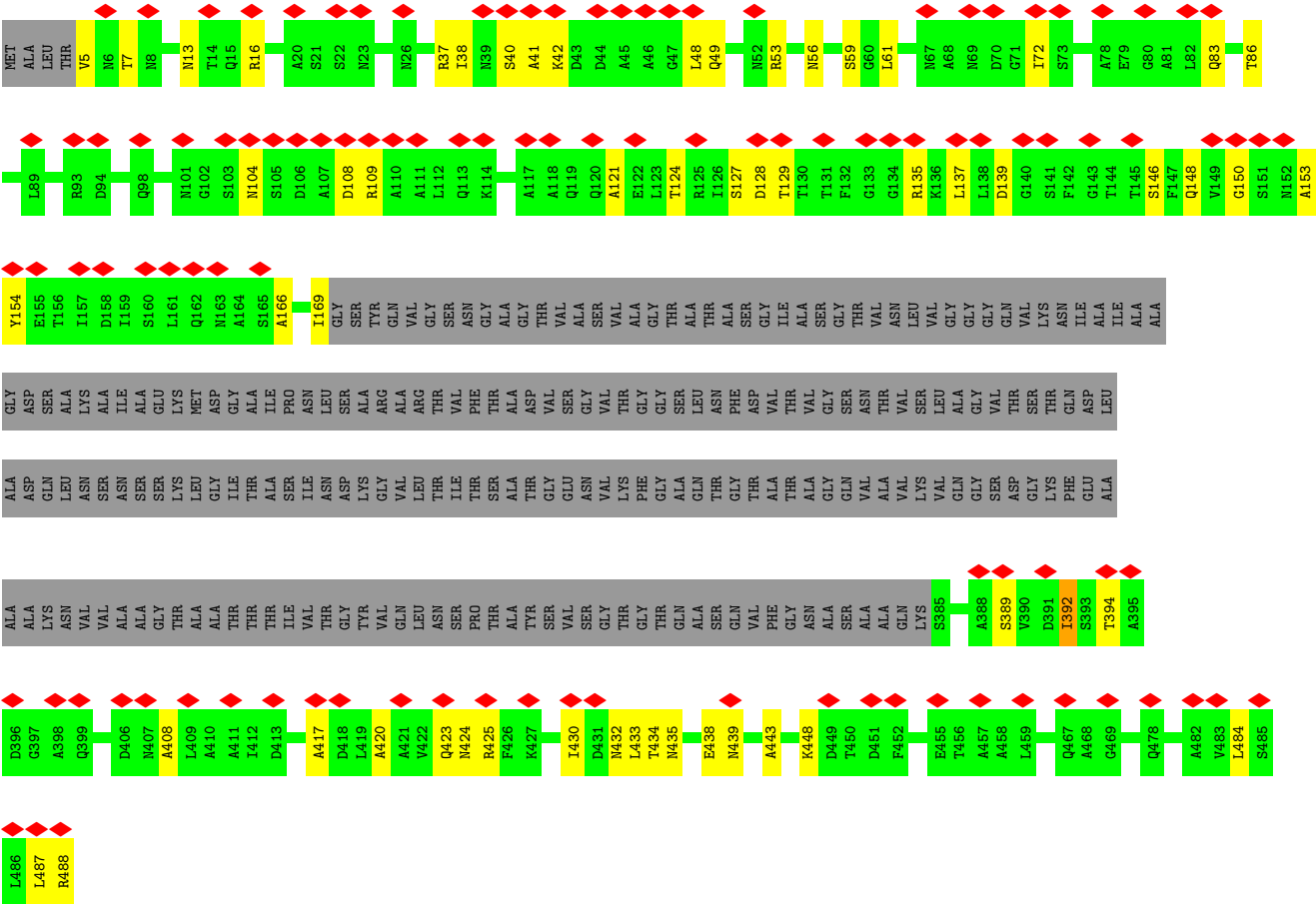


- Molecule 1: B-type flagellin

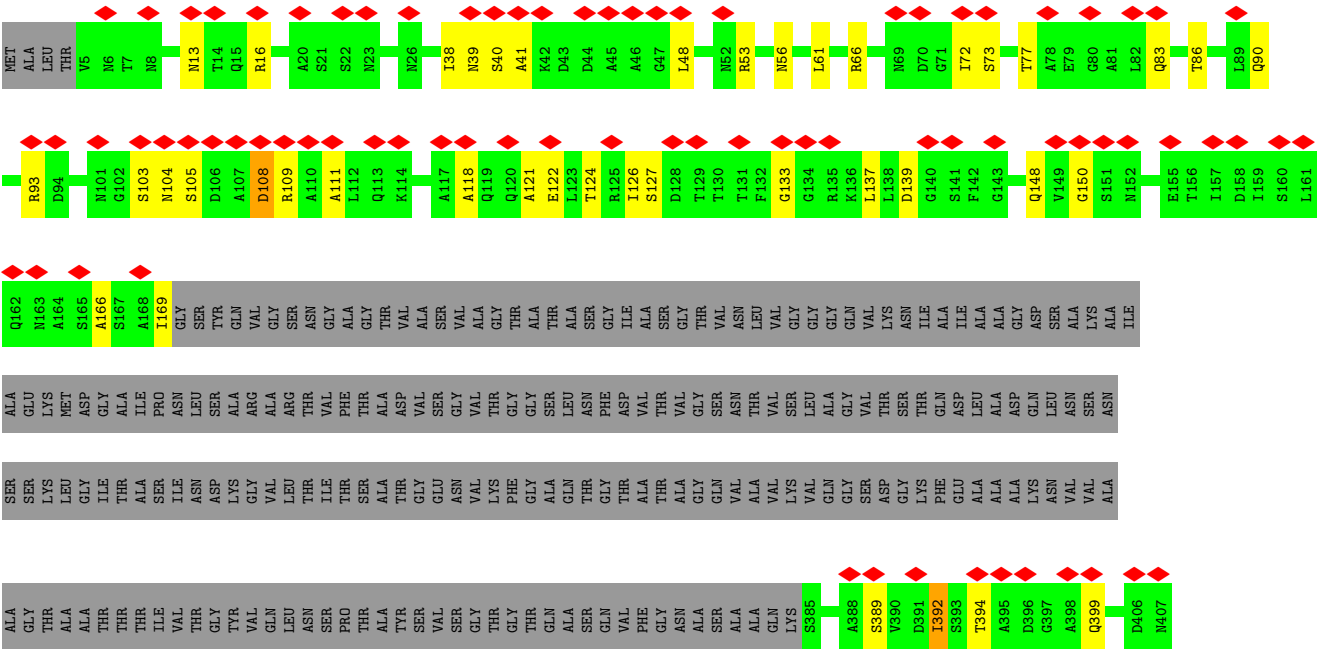


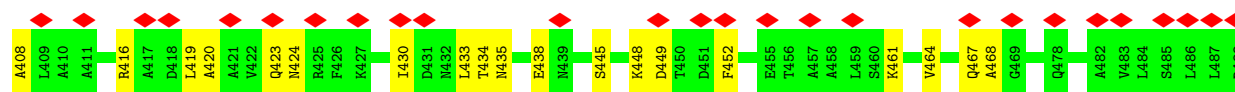
- Molecule 1: B-type flagellin



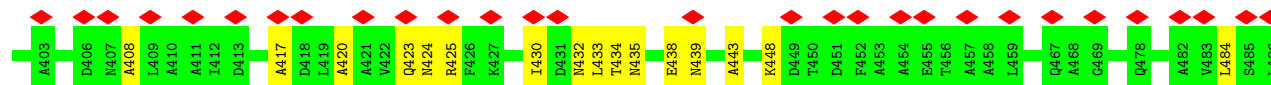
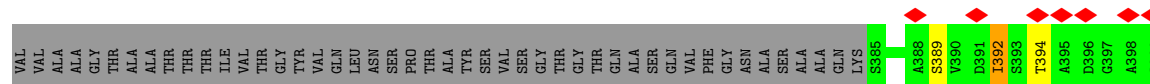
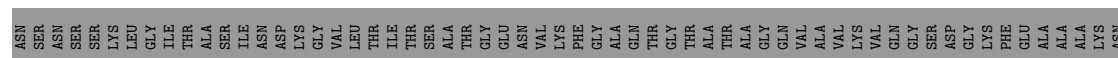
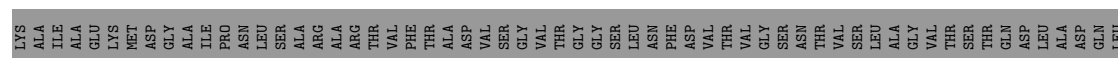
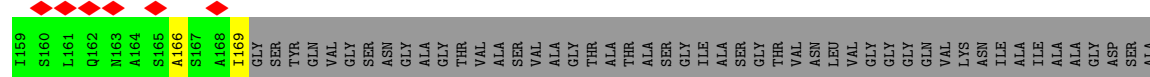
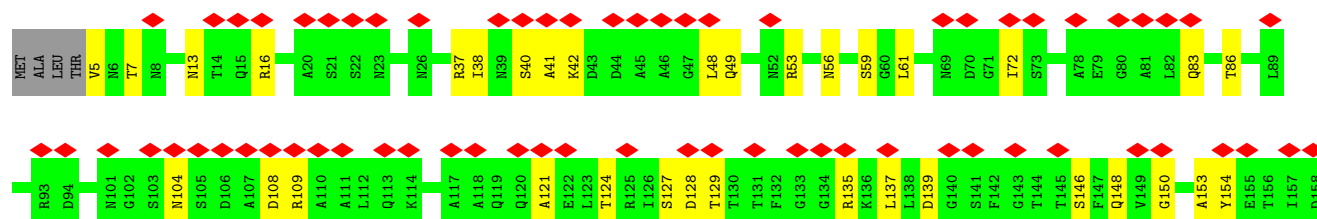
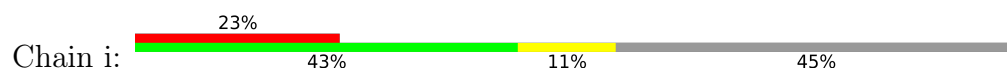


● Molecule 1: B-type flagellin

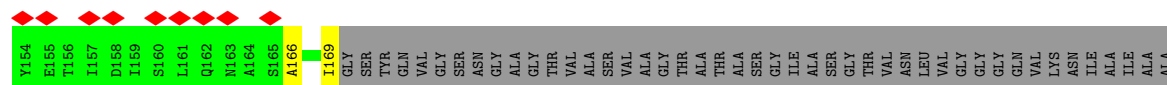
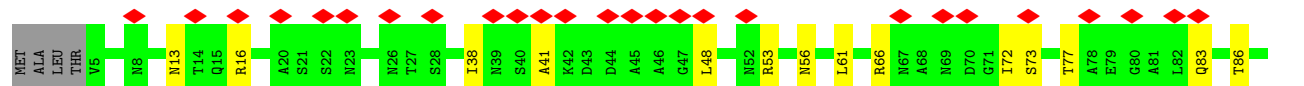


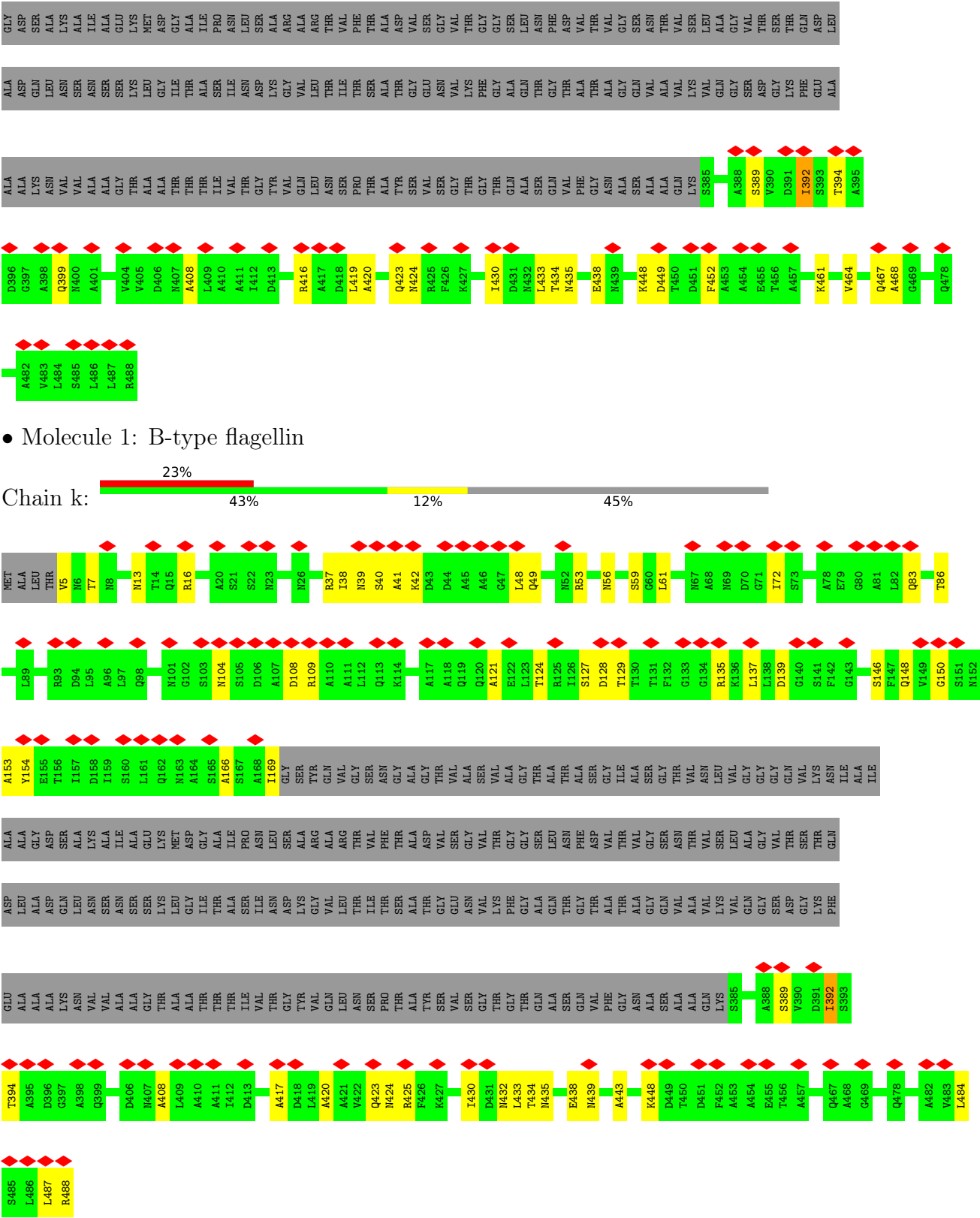


• Molecule 1: B-type flagellin



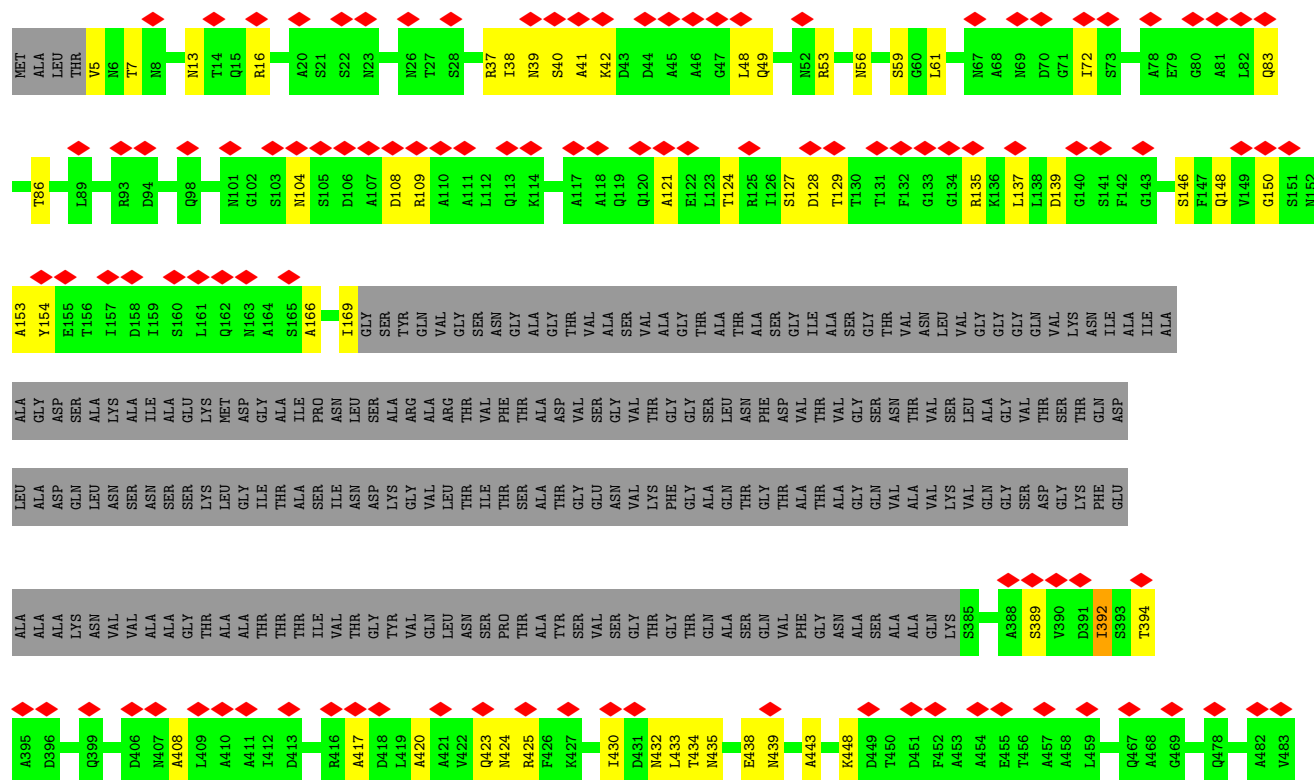
• Molecule 1: B-type flagellin





• Molecule 1: B-type flagellin







4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=65.27°, rise=4.73 Å, axial sym=C1	Depositor
Number of segments used	17450	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	4.550	Depositor
Minimum map value	-3.185	Depositor
Average map value	0.099	Depositor
Map value standard deviation	0.695	Depositor
Recommended contour level	1.7	Depositor
Map size (Å)	230.99998, 230.99998, 1050.0	wwPDB
Map dimensions	220, 220, 1000	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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	0.58	0/1985	0.76	2/2692 (0.1%)
1	B	0.58	0/1985	0.76	2/2692 (0.1%)
1	C	0.58	0/1985	0.76	2/2692 (0.1%)
1	D	0.58	0/1985	0.76	2/2692 (0.1%)
1	E	0.58	0/1985	0.76	2/2692 (0.1%)
1	F	0.58	0/1985	0.77	2/2692 (0.1%)
1	G	0.58	0/1985	0.76	2/2692 (0.1%)
1	H	0.58	0/1985	0.76	2/2692 (0.1%)
1	I	0.58	0/1985	0.76	2/2692 (0.1%)
1	J	0.58	0/1985	0.76	2/2692 (0.1%)
1	K	0.58	0/1985	0.76	2/2692 (0.1%)
1	L	0.58	0/1985	0.76	2/2692 (0.1%)
1	M	0.58	0/1985	0.76	2/2692 (0.1%)
1	N	0.58	0/1985	0.76	2/2692 (0.1%)
1	O	0.58	0/1985	0.76	2/2692 (0.1%)
1	P	0.58	0/1985	0.76	2/2692 (0.1%)
1	Q	0.58	0/1985	0.76	2/2692 (0.1%)
1	R	0.58	0/1985	0.76	2/2692 (0.1%)
1	S	0.58	0/1985	0.76	2/2692 (0.1%)
1	T	0.58	0/1985	0.76	2/2692 (0.1%)
1	U	0.58	0/1985	0.76	2/2692 (0.1%)
1	V	0.58	0/1985	0.76	2/2692 (0.1%)
1	W	0.58	0/1985	0.76	2/2692 (0.1%)
1	X	0.58	0/1985	0.76	2/2692 (0.1%)
1	Y	0.58	0/1985	0.76	2/2692 (0.1%)
1	Z	0.58	0/1985	0.76	2/2692 (0.1%)
1	a	0.58	0/1985	0.76	2/2692 (0.1%)
1	b	0.58	0/1985	0.76	2/2692 (0.1%)
1	c	0.58	0/1985	0.76	2/2692 (0.1%)
1	d	0.58	0/1985	0.76	2/2692 (0.1%)
1	e	0.58	0/1985	0.76	2/2692 (0.1%)
1	f	0.58	0/1985	0.76	2/2692 (0.1%)
1	g	0.58	0/1985	0.76	2/2692 (0.1%)
1	h	0.58	0/1985	0.76	2/2692 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	i	0.58	0/1985	0.76	2/2692 (0.1%)
1	j	0.58	0/1985	0.76	2/2692 (0.1%)
1	k	0.58	0/1985	0.76	2/2692 (0.1%)
1	l	0.58	0/1985	0.76	2/2692 (0.1%)
1	m	0.58	0/1985	0.76	2/2692 (0.1%)
1	n	0.58	0/1985	0.77	2/2692 (0.1%)
1	o	0.58	0/1985	0.76	2/2692 (0.1%)
All	All	0.58	0/81385	0.76	82/110372 (0.1%)

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	A	0	4
1	B	0	4
1	C	0	4
1	D	0	4
1	E	0	4
1	F	0	4
1	G	0	4
1	H	0	4
1	I	0	4
1	J	0	4
1	K	0	4
1	L	0	4
1	M	0	4
1	N	0	4
1	O	0	4
1	P	0	4
1	Q	0	4
1	R	0	4
1	S	0	4
1	T	0	4
1	U	0	4
1	V	0	4
1	W	0	4
1	X	0	4
1	Y	0	4
1	Z	0	4
1	a	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	b	0	4
1	c	0	4
1	d	0	4
1	e	0	4
1	f	0	4
1	g	0	4
1	h	0	4
1	i	0	4
1	j	0	4
1	k	0	4
1	l	0	4
1	m	0	4
1	n	0	4
1	o	0	4
All	All	0	164

There are no bond length outliers.

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	41	ALA	CA-C-N	5.16	127.92	120.38
1	P	41	ALA	C-N-CA	5.16	127.92	120.38
1	c	41	ALA	CA-C-N	5.16	127.91	120.38
1	c	41	ALA	C-N-CA	5.16	127.91	120.38
1	k	41	ALA	CA-C-N	5.16	127.91	120.38

There are no chirality outliers.

5 of 164 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	ASP	Peptide
1	A	137	LEU	Peptide
1	A	389	SER	Peptide
1	A	392	ILE	Peptide
1	B	108	ASP	Peptide

5.2 Too-close contacts [i](#)

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	1979	1964	1964	147	0
1	B	1979	1964	1964	154	0
1	C	1979	1964	1964	151	0
1	D	1979	1964	1964	148	0
1	E	1979	1964	1964	151	0
1	F	1979	1964	1964	157	0
1	G	1979	1964	1964	149	0
1	H	1979	1964	1964	152	0
1	I	1979	1964	1964	152	0
1	J	1979	1964	1964	149	0
1	K	1979	1964	1964	150	0
1	L	1979	1964	1964	150	0
1	M	1979	1964	1964	145	0
1	N	1979	1964	1964	147	0
1	O	1979	1964	1964	151	0
1	P	1979	1964	1964	145	0
1	Q	1979	1964	1964	151	0
1	R	1979	1964	1964	149	0
1	S	1979	1964	1964	149	0
1	T	1979	1964	1964	118	0
1	U	1979	1964	1964	120	0
1	V	1979	1964	1964	116	0
1	W	1979	1964	1964	116	0
1	X	1979	1964	1964	118	0
1	Y	1979	1964	1964	119	0
1	Z	1979	1964	1964	114	0
1	a	1979	1964	1964	115	0
1	b	1979	1964	1964	118	0
1	c	1979	1964	1964	117	0
1	d	1979	1964	1964	113	0
1	e	1979	1964	1964	111	0
1	f	1979	1964	1964	96	0
1	g	1979	1964	1964	95	0
1	h	1979	1964	1964	99	0
1	i	1979	1964	1964	95	0
1	j	1979	1964	1964	93	0
1	k	1979	1964	1964	97	0
1	l	1979	1964	1964	96	0
1	m	1979	1964	1964	96	0
1	n	1979	1964	1964	97	0
1	o	1979	1964	1964	100	0
All	All	81139	80524	80524	3414	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 21.

The worst 5 of 3414 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:R:38:ILE:HD11	1:R:48:LEU:HB2	1.36	1.08
1:k:38:ILE:HD11	1:k:48:LEU:HB2	1.36	1.07
1:m:38:ILE:HD11	1:m:48:LEU:HB2	1.36	1.07
1:n:38:ILE:HD11	1:n:48:LEU:HB2	1.36	1.07
1:E:38:ILE:HD11	1:E:48:LEU:HB2	1.36	1.07

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	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	B	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	C	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	D	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	E	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	F	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	G	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	H	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	I	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	J	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	K	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	L	265/488 (54%)	246 (93%)	19 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	N	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	O	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	P	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	Q	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	R	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	S	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	T	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	U	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	V	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	W	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	X	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	Y	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	Z	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	a	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	b	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	c	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	d	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	e	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	f	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	g	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	h	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	i	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	j	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	k	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	l	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	m	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	n	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
1	o	265/488 (54%)	246 (93%)	19 (7%)	0	100	100
All	All	10865/20008 (54%)	10086 (93%)	779 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	211/363 (58%)	211 (100%)	0	100	100
1	B	211/363 (58%)	211 (100%)	0	100	100
1	C	211/363 (58%)	211 (100%)	0	100	100
1	D	211/363 (58%)	211 (100%)	0	100	100
1	E	211/363 (58%)	211 (100%)	0	100	100
1	F	211/363 (58%)	211 (100%)	0	100	100
1	G	211/363 (58%)	211 (100%)	0	100	100
1	H	211/363 (58%)	211 (100%)	0	100	100
1	I	211/363 (58%)	211 (100%)	0	100	100
1	J	211/363 (58%)	211 (100%)	0	100	100
1	K	211/363 (58%)	211 (100%)	0	100	100
1	L	211/363 (58%)	211 (100%)	0	100	100
1	M	211/363 (58%)	211 (100%)	0	100	100
1	N	211/363 (58%)	211 (100%)	0	100	100
1	O	211/363 (58%)	211 (100%)	0	100	100
1	P	211/363 (58%)	211 (100%)	0	100	100
1	Q	211/363 (58%)	211 (100%)	0	100	100
1	R	211/363 (58%)	211 (100%)	0	100	100
1	S	211/363 (58%)	211 (100%)	0	100	100
1	T	211/363 (58%)	211 (100%)	0	100	100
1	U	211/363 (58%)	211 (100%)	0	100	100
1	V	211/363 (58%)	211 (100%)	0	100	100
1	W	211/363 (58%)	211 (100%)	0	100	100
1	X	211/363 (58%)	211 (100%)	0	100	100
1	Y	211/363 (58%)	211 (100%)	0	100	100
1	Z	211/363 (58%)	211 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	a	211/363 (58%)	211 (100%)	0	100	100
1	b	211/363 (58%)	211 (100%)	0	100	100
1	c	211/363 (58%)	211 (100%)	0	100	100
1	d	211/363 (58%)	211 (100%)	0	100	100
1	e	211/363 (58%)	211 (100%)	0	100	100
1	f	211/363 (58%)	211 (100%)	0	100	100
1	g	211/363 (58%)	211 (100%)	0	100	100
1	h	211/363 (58%)	211 (100%)	0	100	100
1	i	211/363 (58%)	211 (100%)	0	100	100
1	j	211/363 (58%)	211 (100%)	0	100	100
1	k	211/363 (58%)	211 (100%)	0	100	100
1	l	211/363 (58%)	211 (100%)	0	100	100
1	m	211/363 (58%)	211 (100%)	0	100	100
1	n	211/363 (58%)	211 (100%)	0	100	100
1	o	211/363 (58%)	211 (100%)	0	100	100
All	All	8651/14883 (58%)	8651 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	a	30	GLN
1	g	162	GLN
1	b	30	GLN
1	d	162	GLN
1	i	8	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 [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.

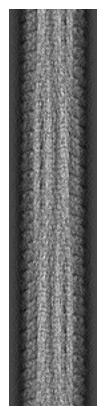
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8856. These allow visual inspection of the internal detail of the map and identification of artifacts.

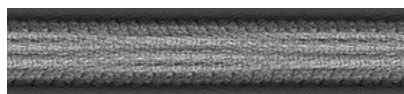
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

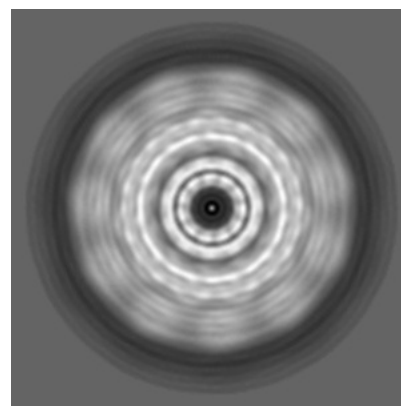
6.1.1 Primary map



X



Y

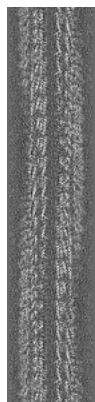


Z

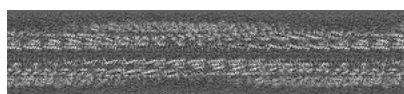
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

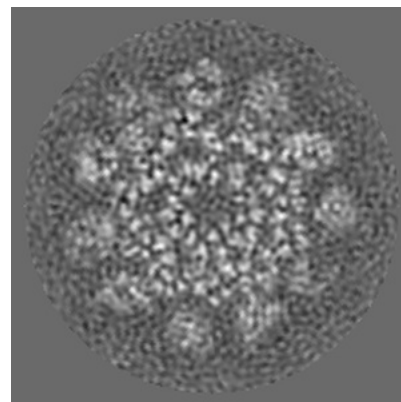
6.2.1 Primary map



X
Index:
110



Y Index: 110

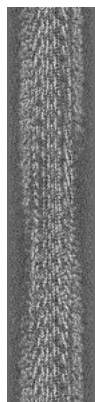


Z Index: 500

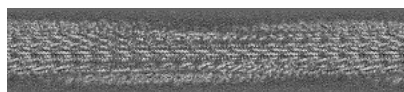
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

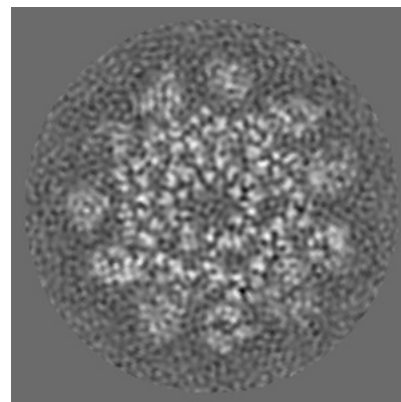
6.3.1 Primary map



X
Index:
124



Y Index: 127

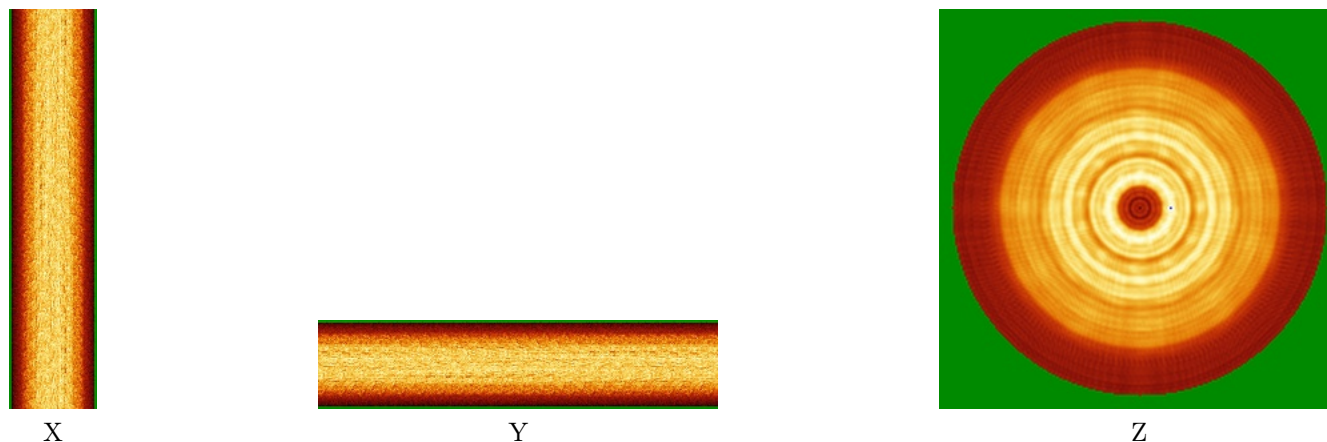


Z Index: 40

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



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](#)

This section was not generated.

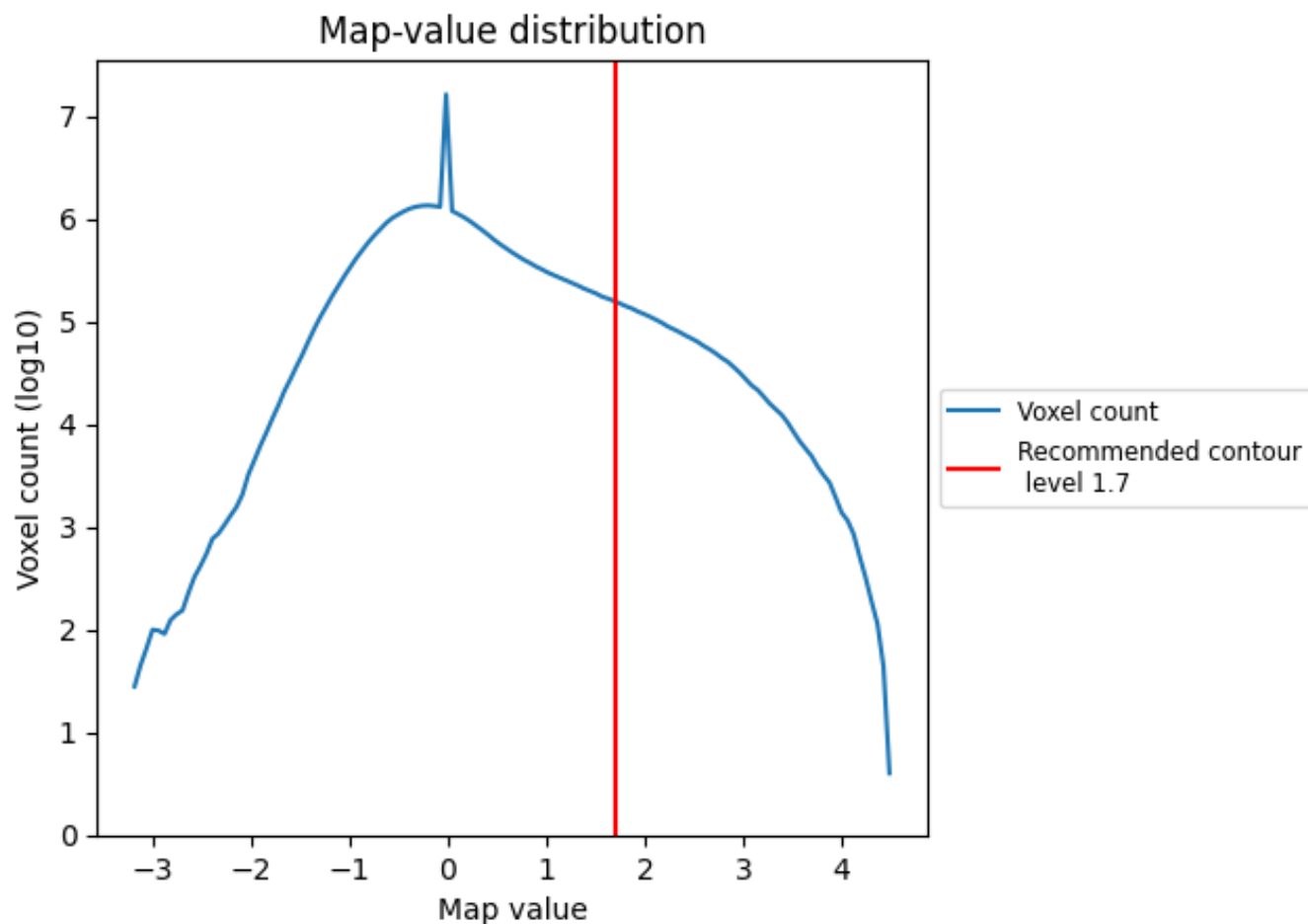
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

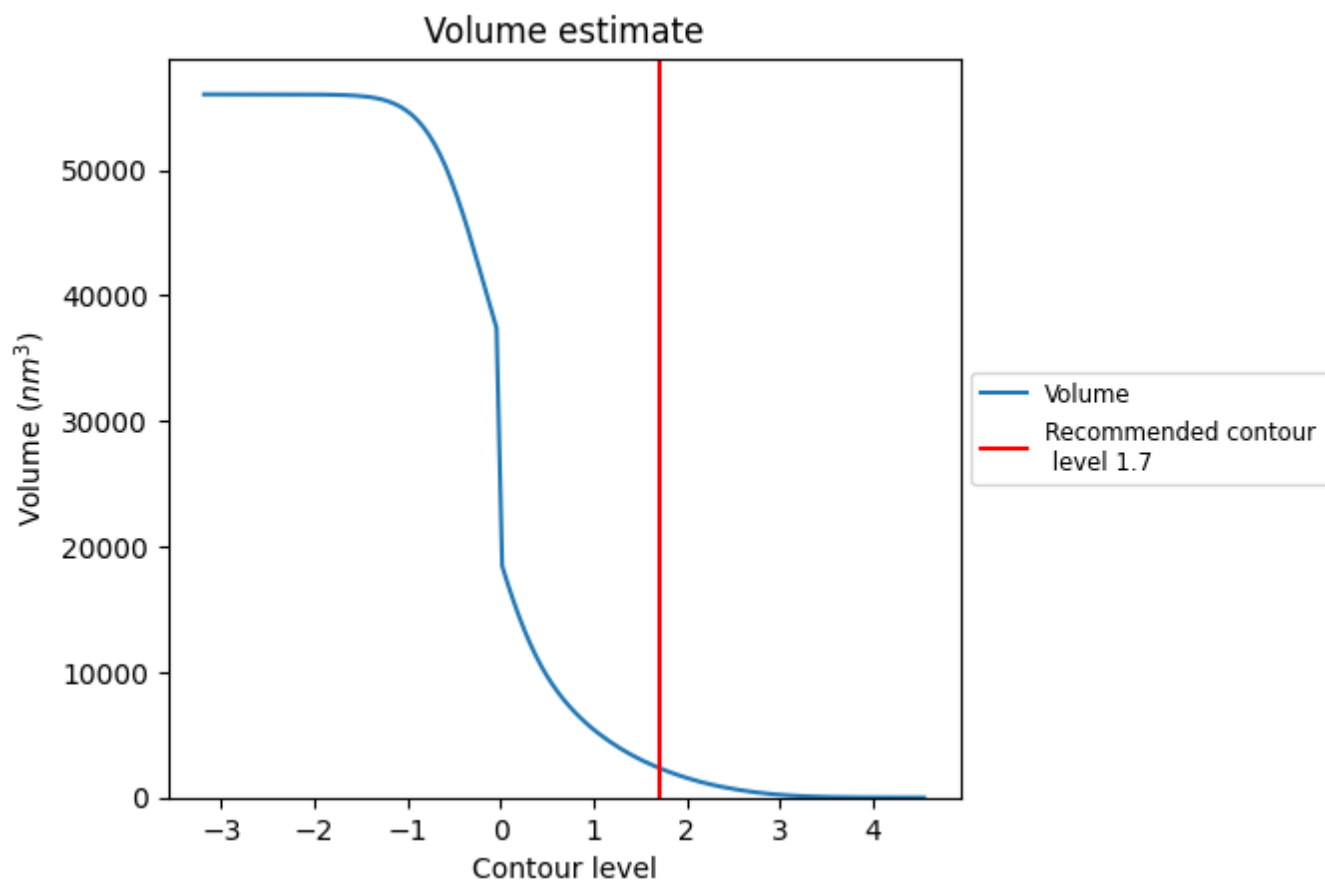
This section contains the results of statistical analysis of the map.

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 2370 nm³; this corresponds to an approximate mass of 2141 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

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

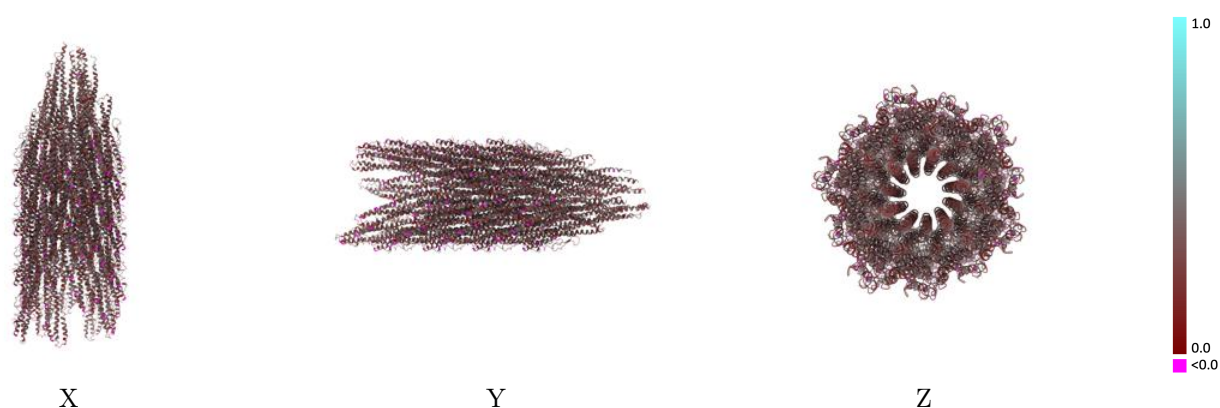
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8856 and PDB model 5WK6. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

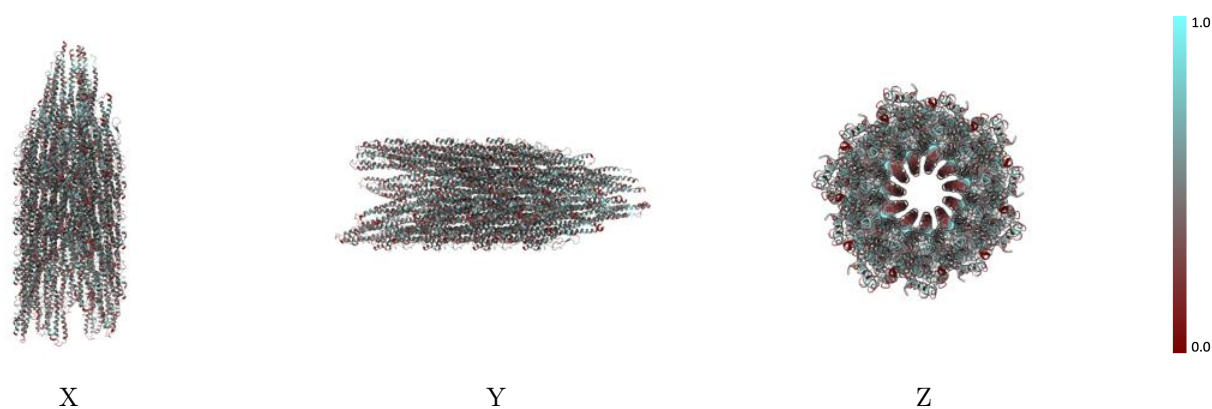
This section was not generated.

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



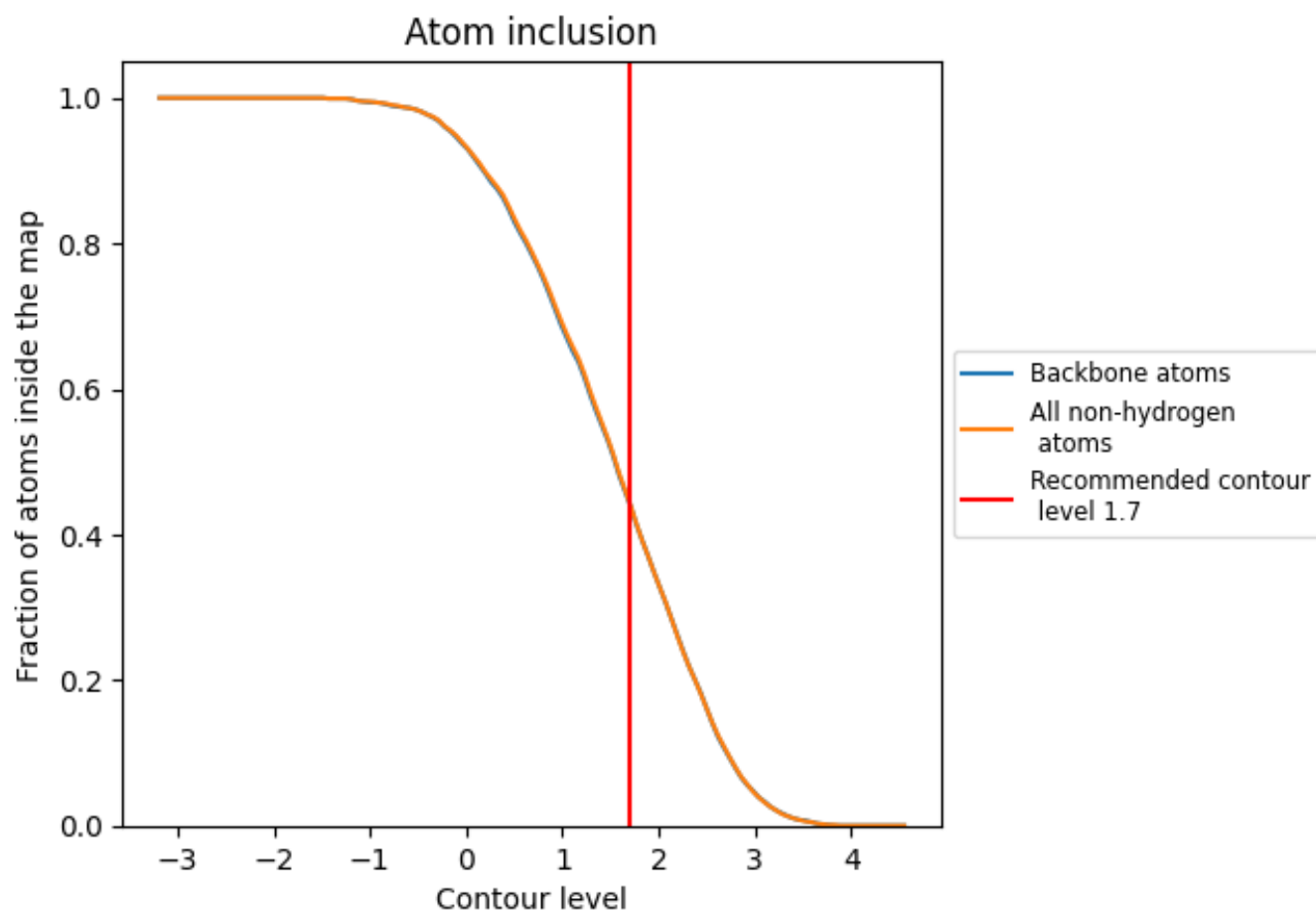
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 44% of all backbone atoms, 44% 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 (1.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4420	0.3040
A	0.4460	0.3040
B	0.4520	0.3030
C	0.4500	0.3050
D	0.4510	0.3020
E	0.4520	0.3060
F	0.4520	0.3050
G	0.4480	0.3020
H	0.4500	0.3050
I	0.4530	0.3010
J	0.4490	0.3040
K	0.4520	0.3040
L	0.4490	0.3040
M	0.4500	0.3040
N	0.4500	0.3000
O	0.4570	0.3040
P	0.4470	0.3040
Q	0.4460	0.3040
R	0.4450	0.3060
S	0.4480	0.3030
T	0.4520	0.3060
U	0.4500	0.3030
V	0.4480	0.3030
W	0.4490	0.3000
X	0.4480	0.3010
Y	0.4530	0.3040
Z	0.4490	0.3030
a	0.4500	0.3050
b	0.4560	0.3050
c	0.4500	0.3020
d	0.4470	0.3040
e	0.4500	0.3020
f	0.4440	0.3050
g	0.4560	0.3040
h	0.4540	0.3040



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Chain	Atom inclusion	Q-score
i	 0.4460	 0.3030
j	 0.4510	 0.3010
k	 0.4520	 0.3050
l	 0.4500	 0.3030
m	 0.4480	 0.3040
n	 0.4540	 0.3050
o	 0.4510	 0.3040