



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 01:38 AM UTC

PDB ID : 8WIW / pdb_00008wiw
EMDB ID : EMD-37570
Title : Cryo-EM structure of the flagellar C ring in the CW state
Authors : Tan, J.X.; Zhang, L.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2023-09-25
Resolution : 5.60 Å(reported)
Based on initial model : 8XP1

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

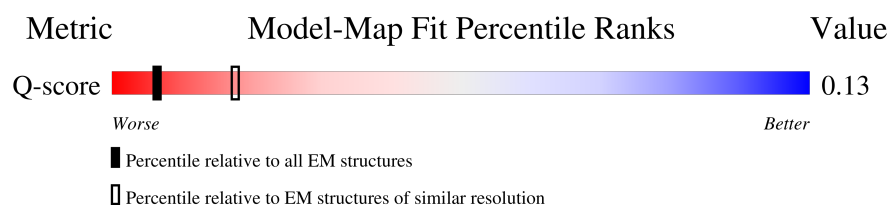
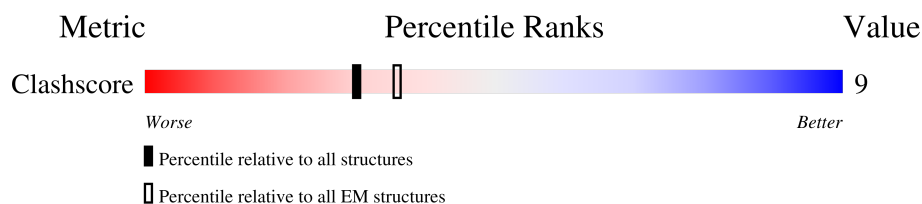
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

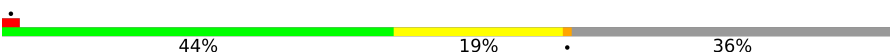
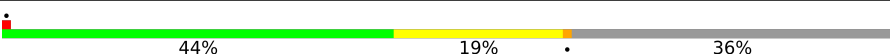
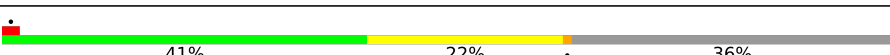
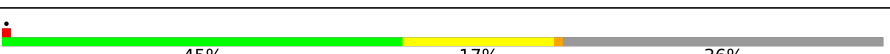
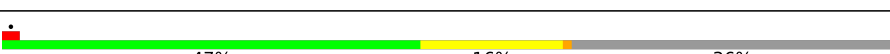
The reported resolution of this entry is 5.60 Å.

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.



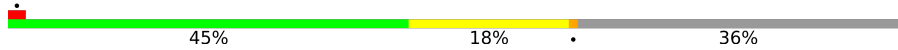
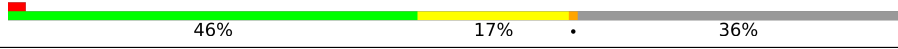
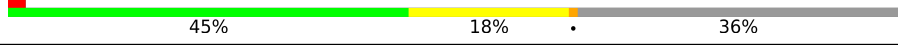
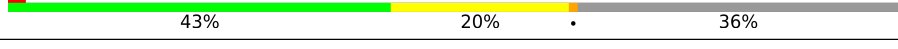
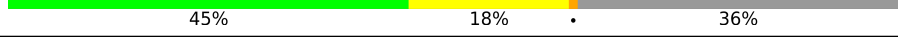
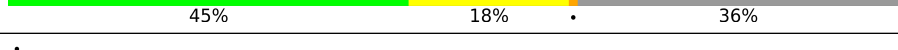
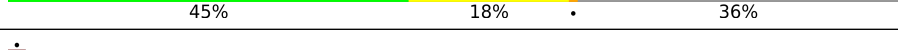
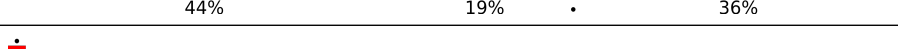
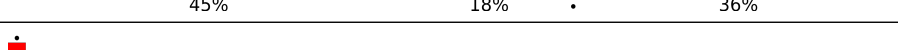
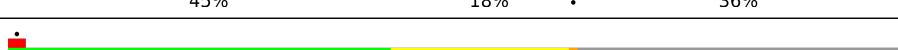
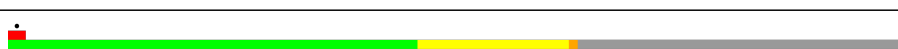
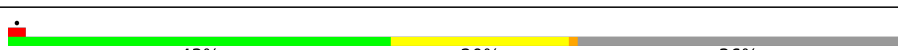
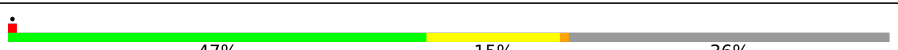
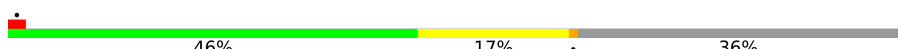
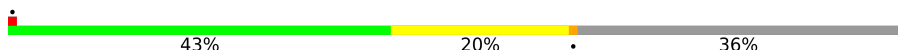
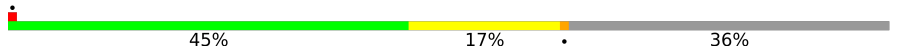
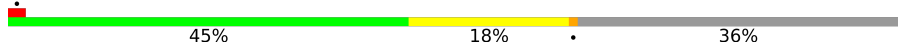
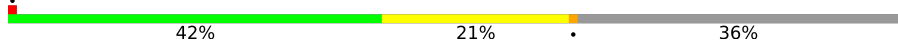
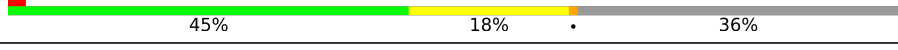
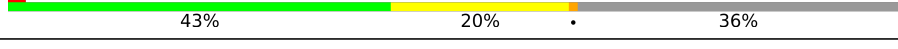
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	513 (5.10 - 6.10)

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	137	 44% 19% . 36%
1	1	137	 44% 19% . 36%
1	2	137	 47% 15% . 36%
1	5	137	 41% 22% . 36%
1	6	137	 45% 17% . 36%
1	A1	137	 47% 16% . 36%

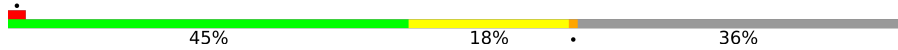
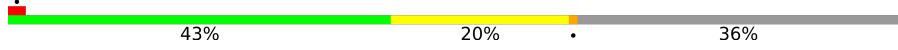
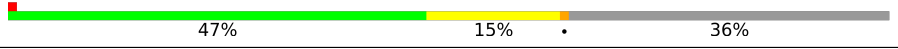
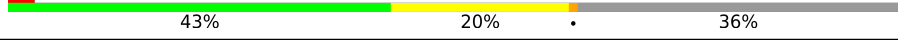
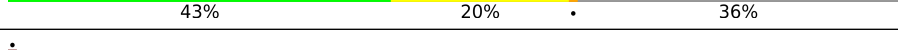
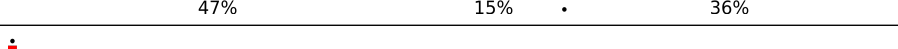
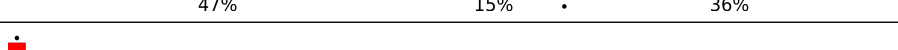
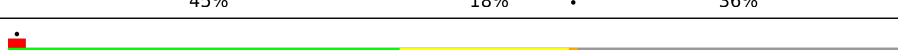
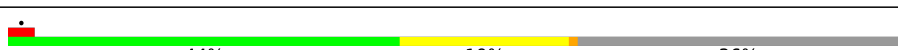
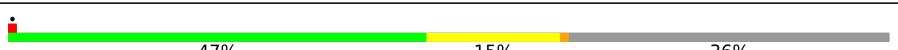
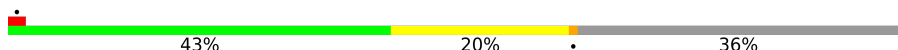
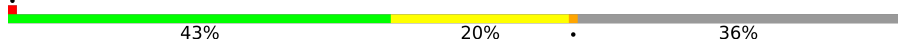
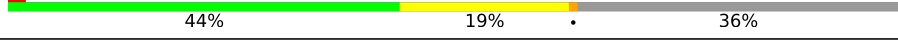
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	A6	137	
1	A7	137	
1	A8	137	
1	AA	137	
1	AB	137	
1	AC	137	
1	AD	137	
1	AE	137	
1	AF	137	
1	AG	137	
1	AH	137	
1	AI	137	
1	AJ	137	
1	AK	137	
1	AO	137	
1	AP	137	
1	AQ	137	
1	AU	137	
1	AV	137	
1	AW	137	
1	Aa	137	
1	Ab	137	
1	Ac	137	
1	Ag	137	
1	Ah	137	

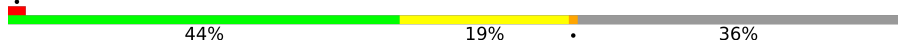
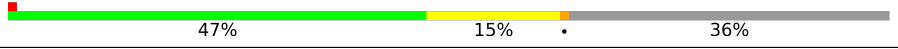
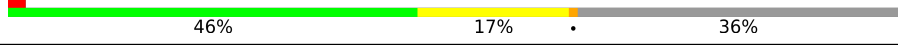
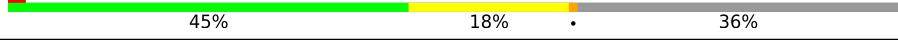
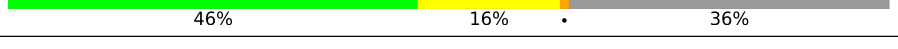
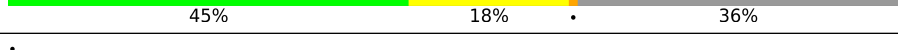
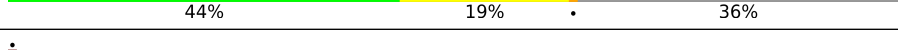
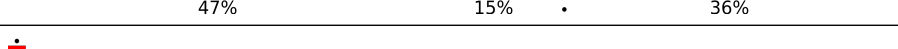
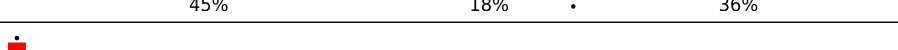
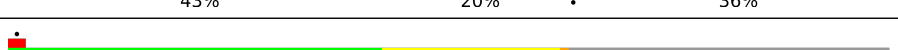
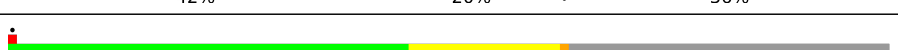
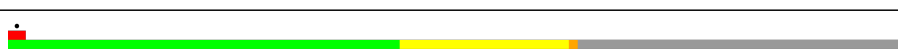
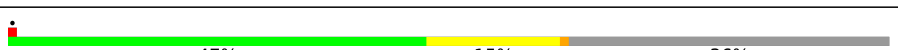
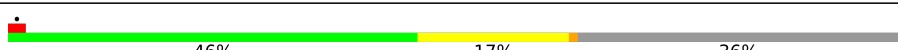
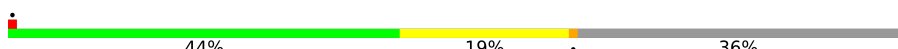
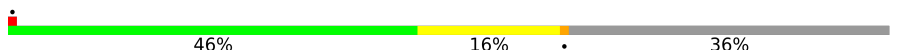
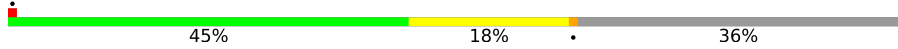
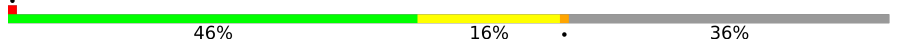
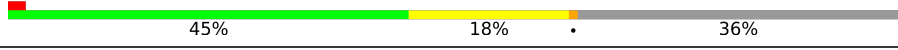
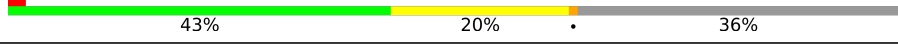
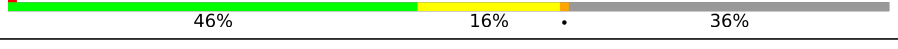
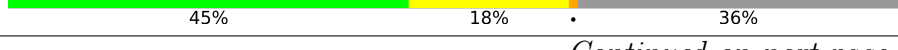
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	Ai	137	
1	Am	137	
1	An	137	
1	Ao	137	
1	As	137	
1	At	137	
1	Au	137	
1	Ay	137	
1	Az	137	
1	B1	137	
1	B2	137	
1	B7	137	
1	B8	137	
1	B9	137	
1	BC	137	
1	BD	137	
1	BE	137	
1	BJ	137	
1	BK	137	
1	BL	137	
1	BQ	137	
1	BR	137	
1	BS	137	
1	BX	137	
1	BY	137	

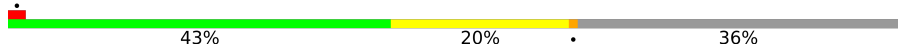
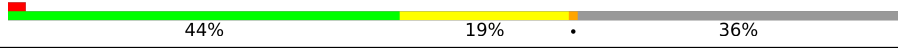
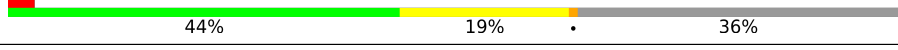
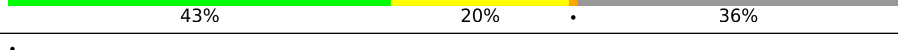
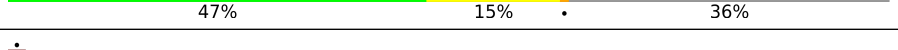
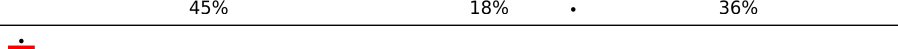
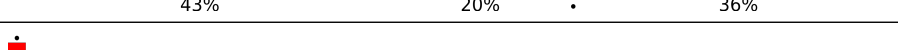
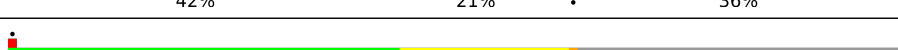
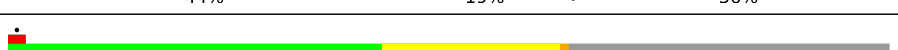
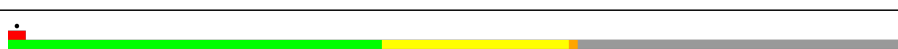
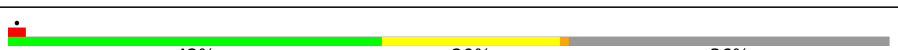
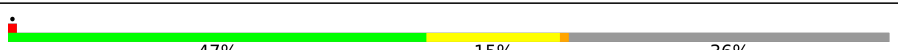
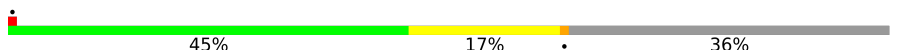
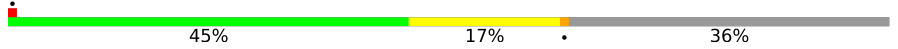
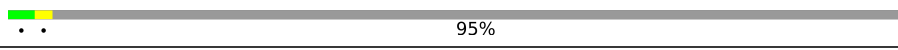
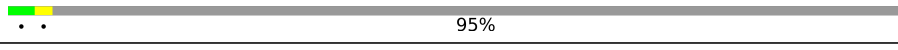
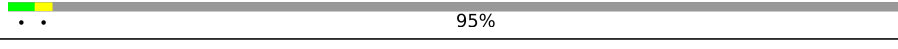
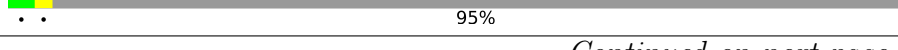
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	BZ	137	
1	Be	137	
1	Bf	137	
1	Bg	137	
1	Bl	137	
1	Bm	137	
1	Bn	137	
1	Bs	137	
1	Bt	137	
1	Bu	137	
1	Bz	137	
1	C1	137	
1	C2	137	
1	CD	137	
1	CE	137	
1	CF	137	
1	CK	137	
1	CL	137	
1	CM	137	
1	CR	137	
1	CS	137	
1	CT	137	
1	CY	137	
1	CZ	137	
1	Ca	137	

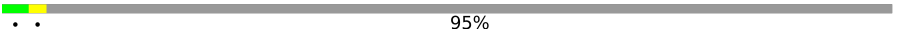
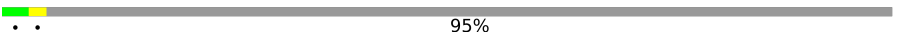
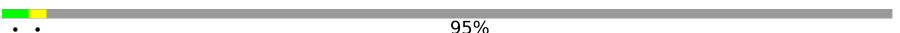
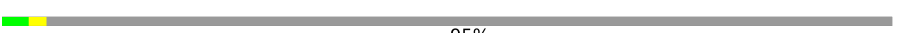
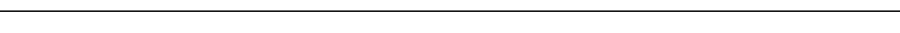
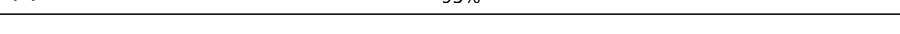
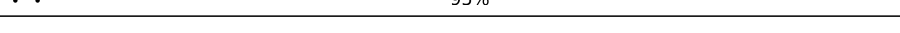
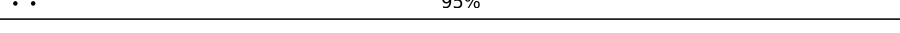
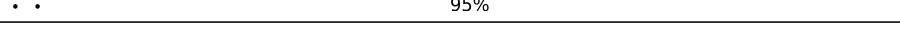
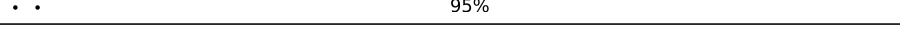
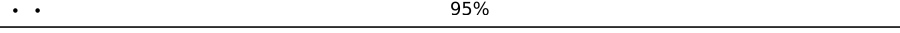
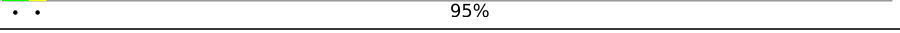
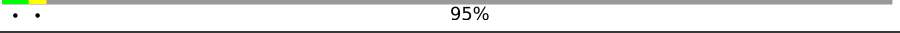
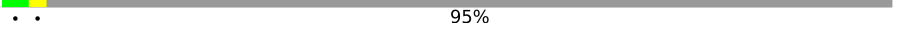
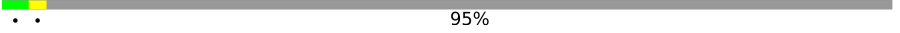
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	Cf	137	
1	Cg	137	
1	Ch	137	
1	Cm	137	
1	Cn	137	
1	Co	137	
1	Ct	137	
1	Cu	137	
1	Cv	137	
1	o	137	
1	p	137	
1	q	137	
1	r	137	
1	s	137	
1	t	137	
1	u	137	
1	v	137	
1	w	137	
1	x	137	
1	y	137	
1	z	137	
2	A2	560	
2	A9	560	
2	B0	560	
2	B3	560	

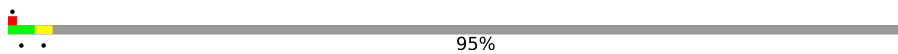
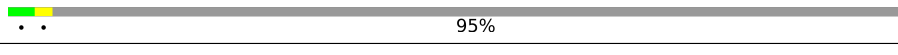
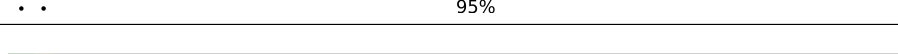
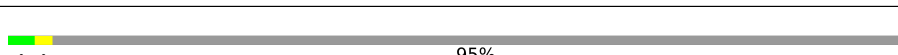
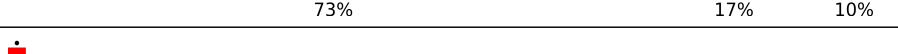
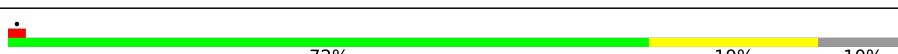
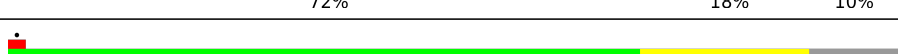
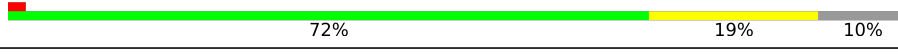
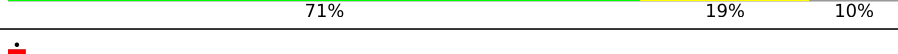
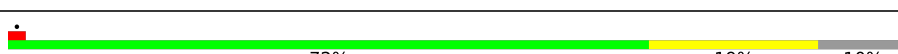
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	BF	560	 95%
2	BM	560	 95%
2	BT	560	 95%
2	Ba	560	 95%
2	Bh	560	 95%
2	Bo	560	 95%
2	Bv	560	 95%
2	C	560	 95%
2	CG	560	 95%
2	CN	560	 95%
2	CU	560	 95%
2	Cb	560	 95%
2	Ci	560	 95%
2	Cp	560	 95%
2	Cw	560	 95%
2	D	560	 95%
2	E	560	 95%
2	F	560	 95%
2	G	560	 95%
2	H	560	 95%
2	I	560	 95%
2	J	560	 95%
2	K	560	 95%
2	L	560	 95%
2	M	560	 95%

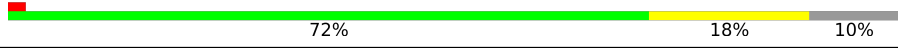
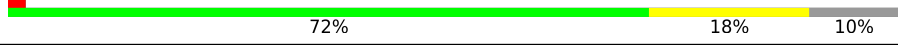
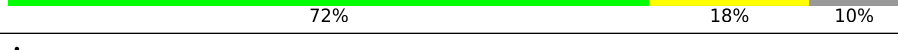
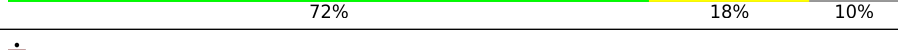
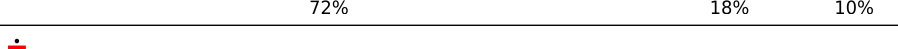
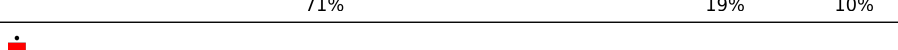
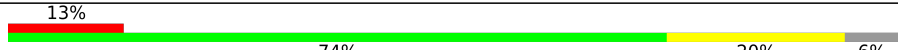
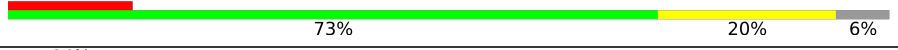
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	N	560	 95%
2	O	560	 95%
2	P	560	 95%
2	Q	560	 95%
2	R	560	 95%
3	7	334	 72% 19% 10%
3	A0	334	 72% 18% 10%
3	A3	334	 72% 18% 10%
3	AL	334	 72% 18% 10%
3	AR	334	 71% 19% 10%
3	AX	334	 72% 18% 10%
3	Ad	334	 73% 17% 10%
3	Aj	334	 72% 18% 10%
3	Ap	334	 72% 19% 10%
3	Av	334	 72% 18% 10%
3	B4	334	 72% 18% 10%
3	BG	334	 72% 18% 10%
3	BN	334	 71% 19% 10%
3	BU	334	 72% 19% 10%
3	Bb	334	 72% 19% 10%
3	Bi	334	 71% 19% 10%
3	Bp	334	 72% 18% 10%
3	Bw	334	 72% 19% 10%
3	CA	334	72% 18% 10%
3	CH	334	72% 18% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	CO	334	
3	CV	334	
3	Cc	334	
3	Cj	334	
3	Cq	334	
3	Cx	334	
3	S	334	
3	T	334	
3	U	334	
3	V	334	
3	W	334	
3	X	334	
3	Y	334	
3	g	334	
4	3	331	
4	8	331	
4	A4	331	
4	AM	331	
4	AS	331	
4	AY	331	
4	Ae	331	
4	Ak	331	
4	Aq	331	
4	Aw	331	
4	B5	331	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	BA	331	
4	BH	331	
4	BO	331	
4	BV	331	
4	Bc	331	
4	Bj	331	
4	Bq	331	
4	Bx	331	
4	CB	331	
4	CI	331	
4	CP	331	
4	CW	331	
4	Cd	331	
4	Ck	331	
4	Cr	331	
4	Cy	331	
4	Z	331	
4	a	331	
4	b	331	
4	c	331	
4	d	331	
4	e	331	
4	f	331	
5	4	129	
5	9	129	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain		
5	A5	129	39%	88%	12%
5	AN	129	40%	87%	13%
5	AT	129	38%	87%	13%
5	AZ	129	41%	88%	12%
5	Af	129	40%	88%	12%
5	Al	129	40%	88%	12%
5	Ar	129	41%	88%	12%
5	Ax	129	39%	88%	12%
5	B6	129	39%	85%	15%
5	BB	129	37%	88%	12%
5	BI	129	36%	87%	13%
5	BP	129	39%	85%	15%
5	BW	129	40%	86%	14%
5	Bd	129	40%	88%	12%
5	Bk	129	40%	86%	14%
5	Br	129	40%	85%	15%
5	By	129	39%	88%	12%
5	CC	129	40%	85%	15%
5	CJ	129	38%	88%	12%
5	CQ	129	41%	85%	15%
5	CX	129	40%	85%	15%
5	Ce	129	40%	88%	12%
5	Cl	129	41%	85%	15%
5	Cs	129	39%	85%	15%
5	Cz	129	39%	87%	13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	h	129	37% 87% 13%
5	i	129	36% 87% 13%
5	j	129	39% 86% 14%
5	k	129	40% 86% 14%
5	l	129	40% 87% 13%
5	m	129	40% 87% 13%
5	n	129	40% 87% 13%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 275366 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 motor switch protein FliN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	o	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	u	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AA	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	p	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	v	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AB	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	q	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	w	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AC	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	r	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	x	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AD	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	s	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	y	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AE	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	t	87	Total 675	C 427	N 118	O 126	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	z	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AF	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	1	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	2	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AG	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	5	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	6	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AH	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AI	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AJ	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AK	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AO	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AP	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AQ	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AU	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AV	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	AW	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Aa	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ab	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ac	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ag	87	Total 675	C 427	N 118	O 126	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ah	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ai	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Am	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	An	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ao	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	As	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	At	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Au	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ay	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Az	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	A1	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	A6	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	A7	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	A8	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BC	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BD	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BE	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BJ	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BK	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BL	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BQ	87	Total 675	C 427	N 118	O 126	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	BR	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BS	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BX	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BY	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	BZ	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Be	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bf	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bg	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bl	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bm	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bn	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bs	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bt	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bu	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Bz	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	B1	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	B2	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	B7	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	B8	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	B9	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CD	87	Total 675	C 427	N 118	O 126	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CE	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CF	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CK	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CL	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CM	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CR	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CS	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CT	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CY	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	CZ	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ca	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Cf	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Cg	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ch	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Cm	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Cn	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Co	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Ct	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Cu	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	Cv	87	Total 675	C 427	N 118	O 126	S 4	0	0
1	C1	87	Total 675	C 427	N 118	O 126	S 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	87	Total	C	N	O	S	0	0
			675	427	118	126	4		

- Molecule 2 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	D	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	E	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	F	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	G	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	H	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	I	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	J	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	K	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	L	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	M	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	N	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	O	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	P	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Q	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	R	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	A2	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	A9	27	Total	C	N	O	S	0	0
			224	135	44	42	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BF	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	BM	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	BT	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Ba	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Bh	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Bo	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Bv	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	B3	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	B0	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	CG	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	CN	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	CU	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Cb	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Ci	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Cp	27	Total	C	N	O	S	0	0
			224	135	44	42	3		
2	Cw	27	Total	C	N	O	S	0	0
			224	135	44	42	3		

- Molecule 3 is a protein called Flagellar motor switch protein FliM.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	T	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	U	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	V	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	W	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	X	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Y	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	g	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	7	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	AL	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	AR	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	AX	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Ad	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Aj	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Ap	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Av	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	A3	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	A0	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	BG	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	BN	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	BU	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Bb	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Bi	301	Total 2431	C 1549	N 437	O 440	S 5	0	0
3	Bp	301	Total 2431	C 1549	N 437	O 440	S 5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Bw	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	B4	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	CA	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	CH	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	CO	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	CV	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	Cc	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	Cj	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	Cq	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		
3	Cx	301	Total	C	N	O	S	0	0
			2431	1549	437	440	5		

- Molecule 4 is a protein called Flagellar motor switch protein FliG.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Z	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	a	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	b	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	c	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	d	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	e	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	f	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	3	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	8	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AM	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	AS	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	AY	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Ae	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Ak	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Aq	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Aw	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	A4	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	BA	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	BH	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	BO	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	BV	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Bc	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Bj	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Bq	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	Bx	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	B5	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	CB	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	CI	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	CP	310	Total 2428	C 1515	N 430	O 474	S 9	0	0
4	CW	310	Total 2428	C 1515	N 430	O 474	S 9	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Cd	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	Ck	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	Cr	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		
4	Cy	310	Total	C	N	O	S	0	0
			2428	1515	430	474	9		

- Molecule 5 is a protein called Chemotaxis protein CheY.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	i	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	j	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	k	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	l	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	m	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	n	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	4	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	9	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	AN	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	AT	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	AZ	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	Af	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	Al	129	Total	C	N	O	S	0	0
			991	634	165	185	7		
5	Ar	129	Total	C	N	O	S	0	0
			991	634	165	185	7		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Ax	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	A5	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	BB	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	BI	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	BP	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	BW	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Bd	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Bk	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Br	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	By	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	B6	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	CC	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	CJ	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	CQ	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	CX	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Ce	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Cl	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Cs	129	Total 991	C 634	N 165	O 185	S 7	0	0
5	Cz	129	Total 991	C 634	N 165	O 185	S 7	0	0

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	13	LYS	ASP	engineered mutation	UNP P0A2D5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
h	106	TRP	TYR	engineered mutation	UNP P0A2D5
i	13	LYS	ASP	engineered mutation	UNP P0A2D5
i	106	TRP	TYR	engineered mutation	UNP P0A2D5
j	13	LYS	ASP	engineered mutation	UNP P0A2D5
j	106	TRP	TYR	engineered mutation	UNP P0A2D5
k	13	LYS	ASP	engineered mutation	UNP P0A2D5
k	106	TRP	TYR	engineered mutation	UNP P0A2D5
l	13	LYS	ASP	engineered mutation	UNP P0A2D5
l	106	TRP	TYR	engineered mutation	UNP P0A2D5
m	13	LYS	ASP	engineered mutation	UNP P0A2D5
m	106	TRP	TYR	engineered mutation	UNP P0A2D5
n	13	LYS	ASP	engineered mutation	UNP P0A2D5
n	106	TRP	TYR	engineered mutation	UNP P0A2D5
4	13	LYS	ASP	engineered mutation	UNP P0A2D5
4	106	TRP	TYR	engineered mutation	UNP P0A2D5
9	13	LYS	ASP	engineered mutation	UNP P0A2D5
9	106	TRP	TYR	engineered mutation	UNP P0A2D5
AN	13	LYS	ASP	engineered mutation	UNP P0A2D5
AN	106	TRP	TYR	engineered mutation	UNP P0A2D5
AT	13	LYS	ASP	engineered mutation	UNP P0A2D5
AT	106	TRP	TYR	engineered mutation	UNP P0A2D5
AZ	13	LYS	ASP	engineered mutation	UNP P0A2D5
AZ	106	TRP	TYR	engineered mutation	UNP P0A2D5
Af	13	LYS	ASP	engineered mutation	UNP P0A2D5
Af	106	TRP	TYR	engineered mutation	UNP P0A2D5
Al	13	LYS	ASP	engineered mutation	UNP P0A2D5
Al	106	TRP	TYR	engineered mutation	UNP P0A2D5
Ar	13	LYS	ASP	engineered mutation	UNP P0A2D5
Ar	106	TRP	TYR	engineered mutation	UNP P0A2D5
Ax	13	LYS	ASP	engineered mutation	UNP P0A2D5
Ax	106	TRP	TYR	engineered mutation	UNP P0A2D5
A5	13	LYS	ASP	engineered mutation	UNP P0A2D5
A5	106	TRP	TYR	engineered mutation	UNP P0A2D5
BB	13	LYS	ASP	engineered mutation	UNP P0A2D5
BB	106	TRP	TYR	engineered mutation	UNP P0A2D5
BI	13	LYS	ASP	engineered mutation	UNP P0A2D5
BI	106	TRP	TYR	engineered mutation	UNP P0A2D5
BP	13	LYS	ASP	engineered mutation	UNP P0A2D5
BP	106	TRP	TYR	engineered mutation	UNP P0A2D5
BW	13	LYS	ASP	engineered mutation	UNP P0A2D5
BW	106	TRP	TYR	engineered mutation	UNP P0A2D5
Bd	13	LYS	ASP	engineered mutation	UNP P0A2D5

Continued on next page...

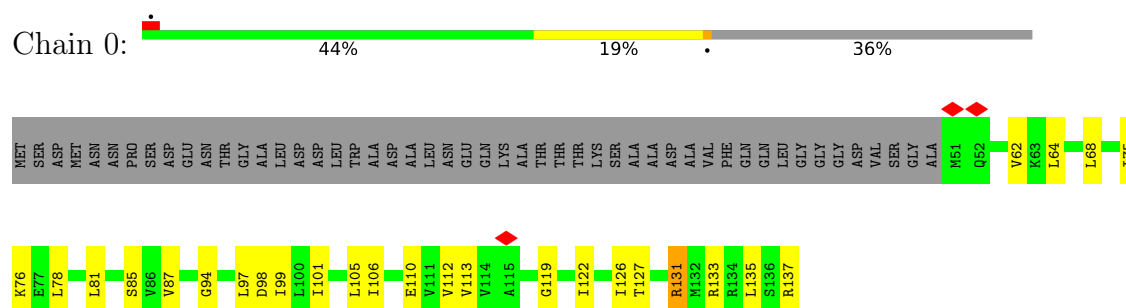
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Bd	106	TRP	TYR	engineered mutation	UNP P0A2D5
Bk	13	LYS	ASP	engineered mutation	UNP P0A2D5
Bk	106	TRP	TYR	engineered mutation	UNP P0A2D5
Br	13	LYS	ASP	engineered mutation	UNP P0A2D5
Br	106	TRP	TYR	engineered mutation	UNP P0A2D5
By	13	LYS	ASP	engineered mutation	UNP P0A2D5
By	106	TRP	TYR	engineered mutation	UNP P0A2D5
B6	13	LYS	ASP	engineered mutation	UNP P0A2D5
B6	106	TRP	TYR	engineered mutation	UNP P0A2D5
CC	13	LYS	ASP	engineered mutation	UNP P0A2D5
CC	106	TRP	TYR	engineered mutation	UNP P0A2D5
CJ	13	LYS	ASP	engineered mutation	UNP P0A2D5
CJ	106	TRP	TYR	engineered mutation	UNP P0A2D5
CQ	13	LYS	ASP	engineered mutation	UNP P0A2D5
CQ	106	TRP	TYR	engineered mutation	UNP P0A2D5
CX	13	LYS	ASP	engineered mutation	UNP P0A2D5
CX	106	TRP	TYR	engineered mutation	UNP P0A2D5
Ce	13	LYS	ASP	engineered mutation	UNP P0A2D5
Ce	106	TRP	TYR	engineered mutation	UNP P0A2D5
Cl	13	LYS	ASP	engineered mutation	UNP P0A2D5
Cl	106	TRP	TYR	engineered mutation	UNP P0A2D5
Cs	13	LYS	ASP	engineered mutation	UNP P0A2D5
Cs	106	TRP	TYR	engineered mutation	UNP P0A2D5
Cz	13	LYS	ASP	engineered mutation	UNP P0A2D5
Cz	106	TRP	TYR	engineered mutation	UNP P0A2D5

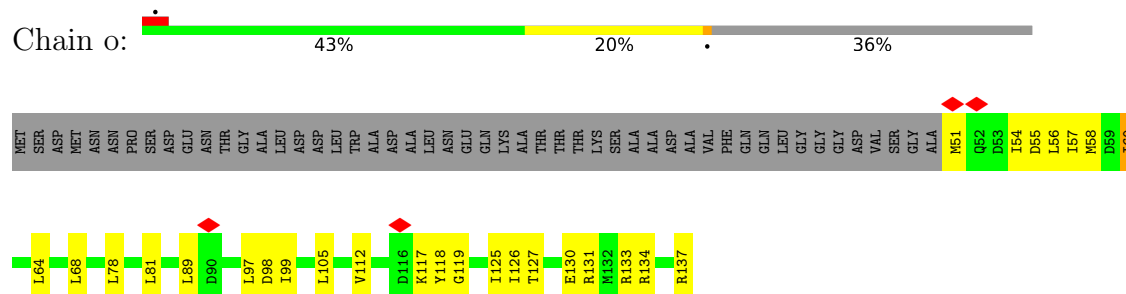
3 Residue-property plots [i](#)

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.

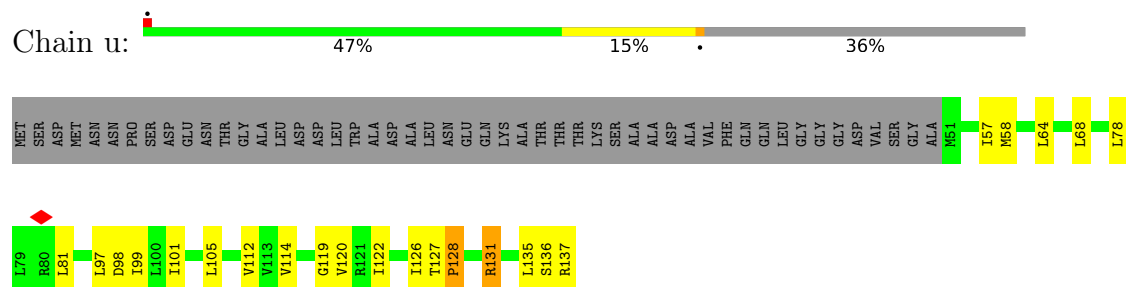
- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN

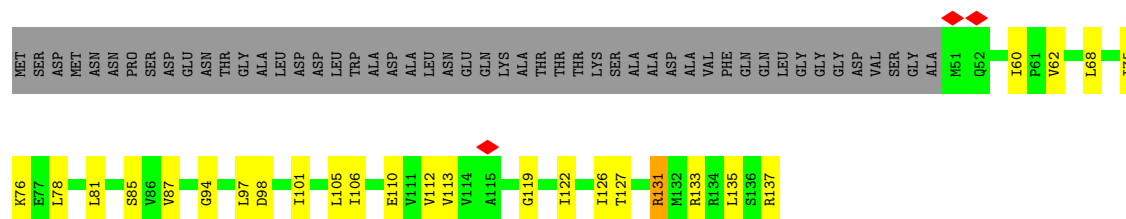


- Molecule 1: Flagellar motor switch protein FliN

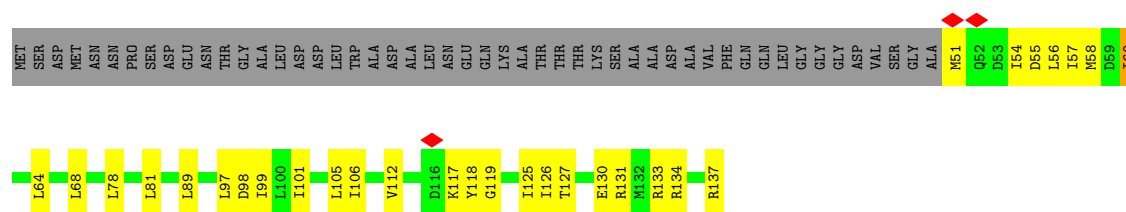


- Molecule 1: Flagellar motor switch protein FliN

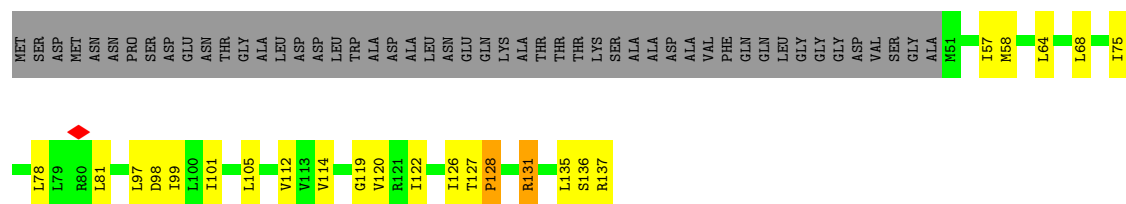




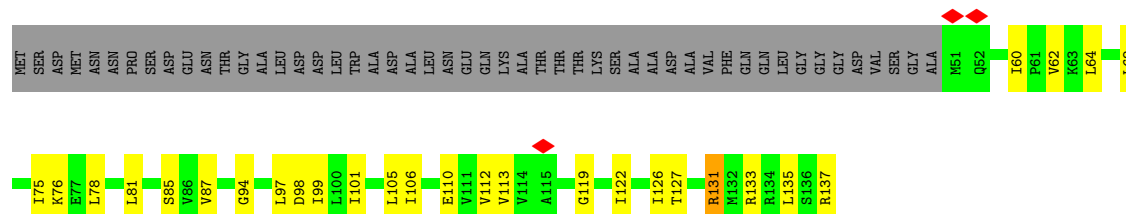
- Molecule 1: Flagellar motor switch protein FliN



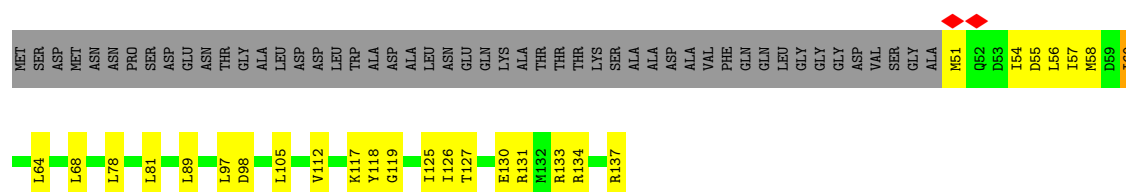
- Molecule 1: Flagellar motor switch protein FliN



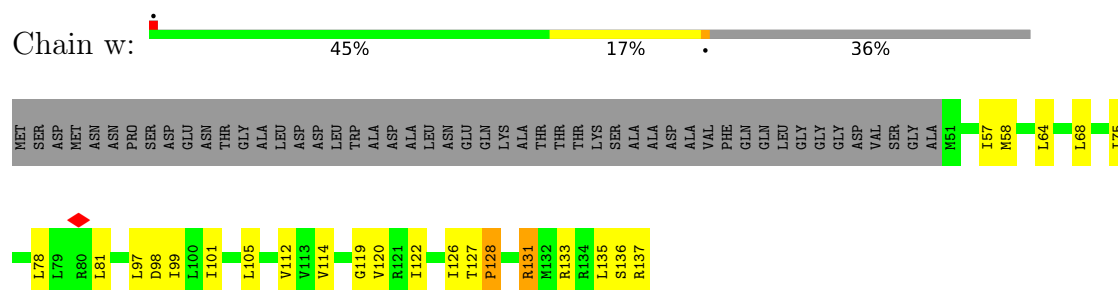
- Molecule 1: Flagellar motor switch protein FliN



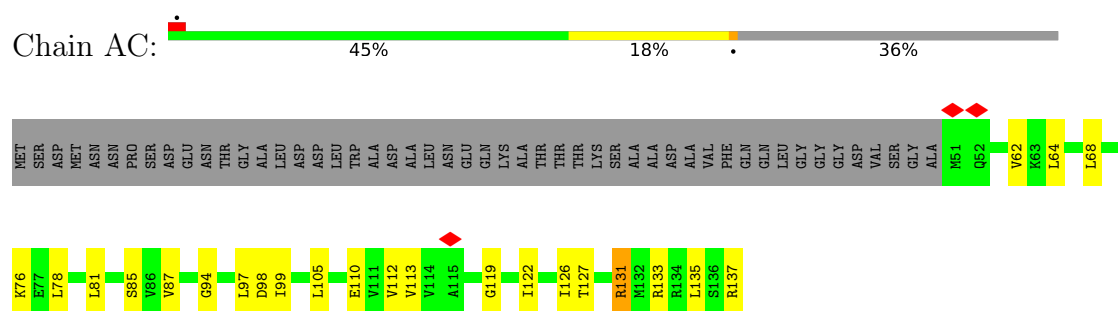
- Molecule 1: Flagellar motor switch protein FliN



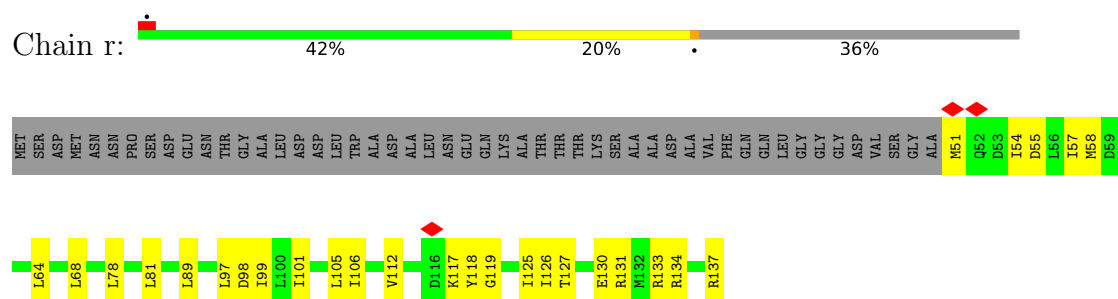
- Molecule 1: Flagellar motor switch protein FlhN



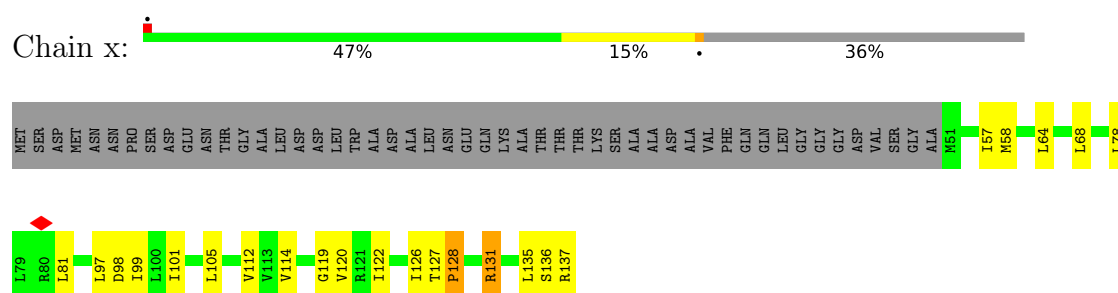
- Molecule 1: Flagellar motor switch protein FlhN



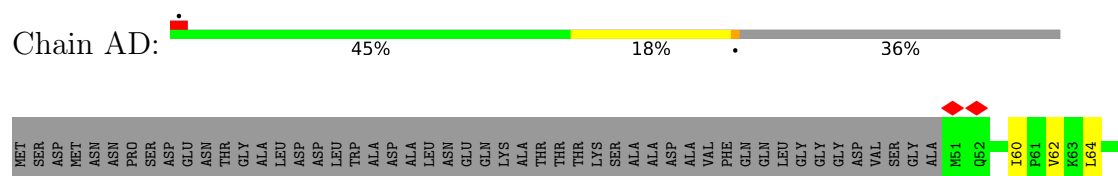
- Molecule 1: Flagellar motor switch protein FlhN

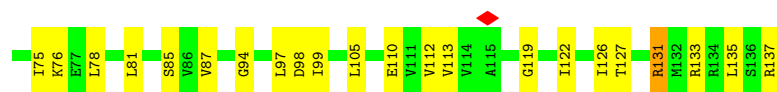


- Molecule 1: Flagellar motor switch protein FlhN

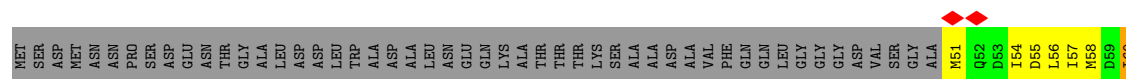


- Molecule 1: Flagellar motor switch protein FlhN

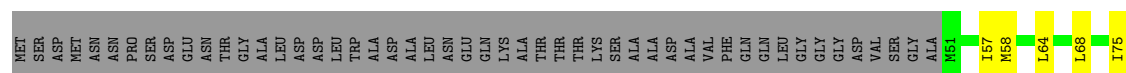




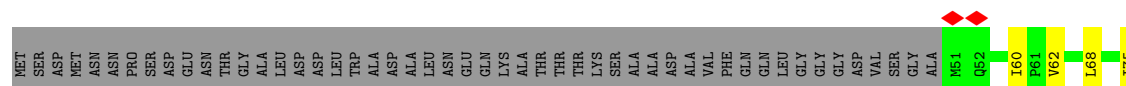
- Molecule 1: Flagellar motor switch protein FliN



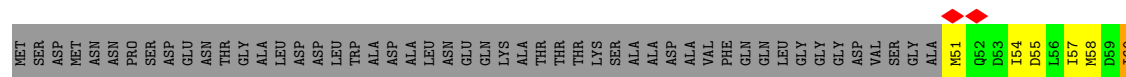
- Molecule 1: Flagellar motor switch protein FliN



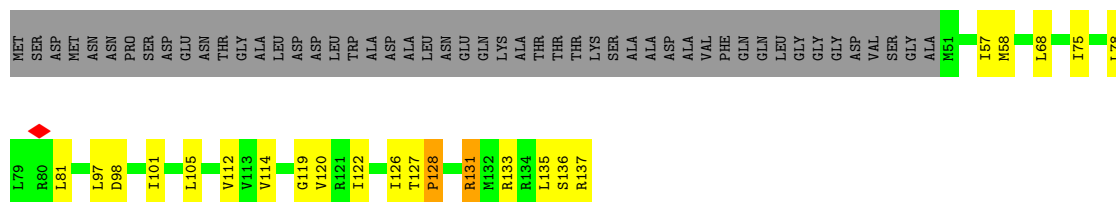
- Molecule 1: Flagellar motor switch protein FliN



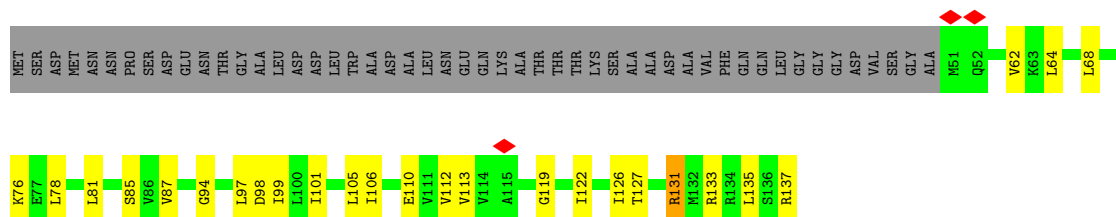
- Molecule 1: Flagellar motor switch protein FliN



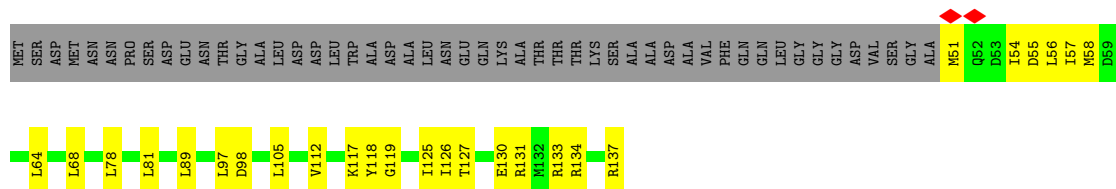
- Molecule 1: Flagellar motor switch protein FliN



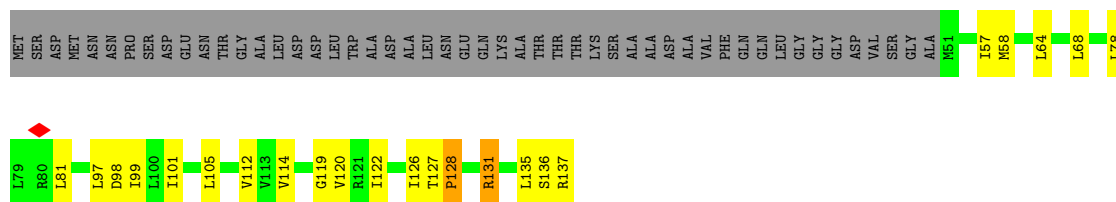
- Molecule 1: Flagellar motor switch protein FliN



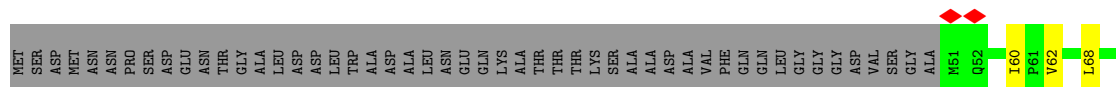
- Molecule 1: Flagellar motor switch protein FliN

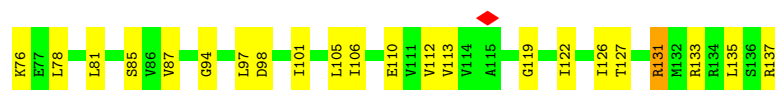


- Molecule 1: Flagellar motor switch protein FliN

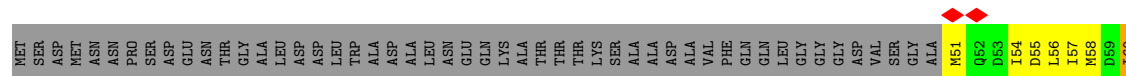


- Molecule 1: Flagellar motor switch protein FliN

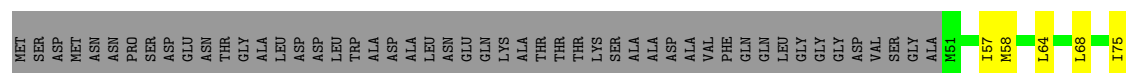




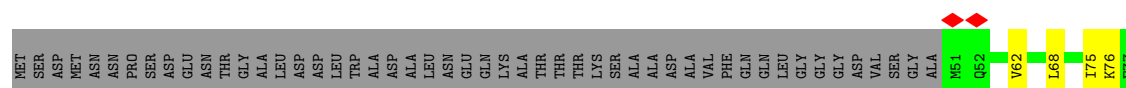
- Molecule 1: Flagellar motor switch protein FliN



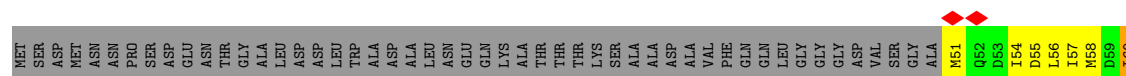
- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN



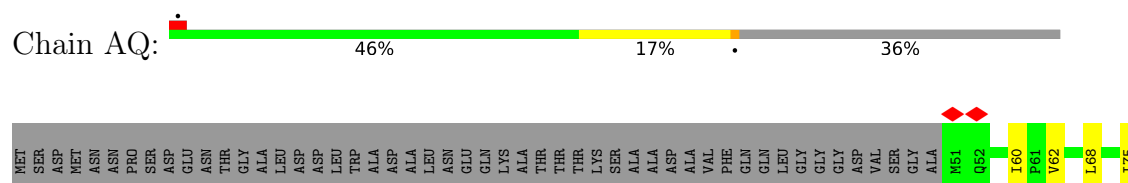
- Molecule 1: Flagellar motor switch protein FliN

- Molecule 1: Flagellar motor switch protein FliN

- Molecule 1: Flagellar motor switch protein FliN

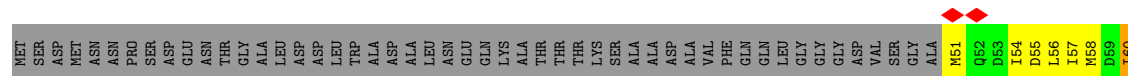
- Molecule 1: Flagellar motor switch protein FliN

- Molecule 1: Flagellar motor switch protein FliN

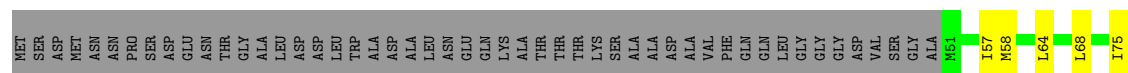




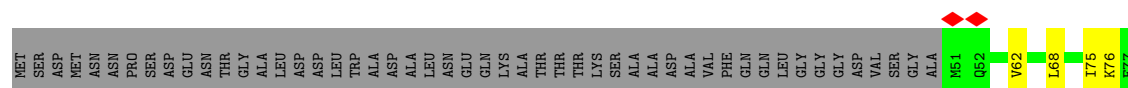
- Molecule 1: Flagellar motor switch protein FliN



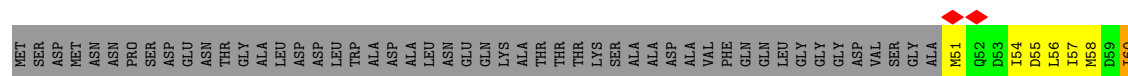
- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN

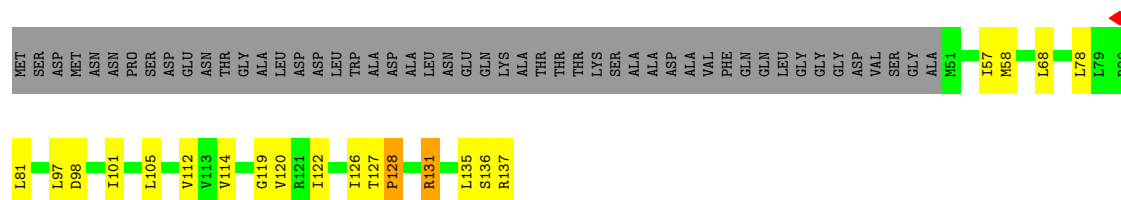


- Molecule 1: Flagellar motor switch protein FliN

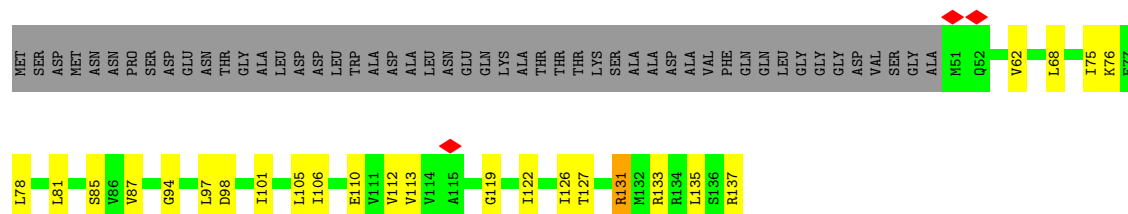


- Molecule 1: Flagellar motor switch protein FliN

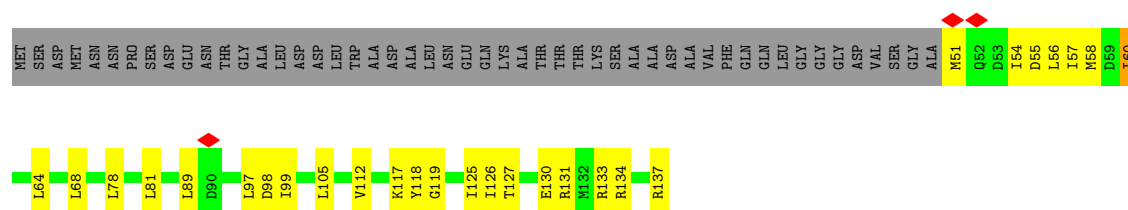




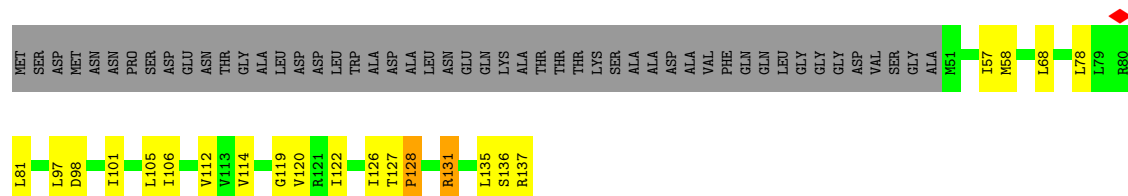
• Molecule 1: Flagellar motor switch protein FliN



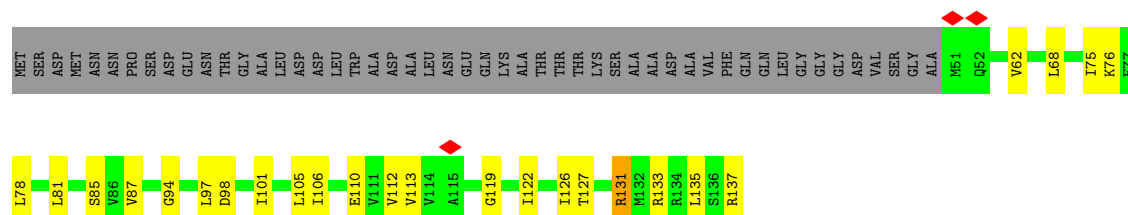
• Molecule 1: Flagellar motor switch protein FliN



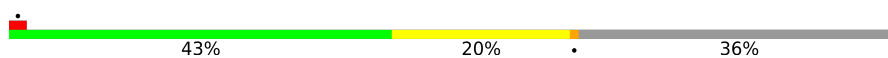
• Molecule 1: Flagellar motor switch protein FliN

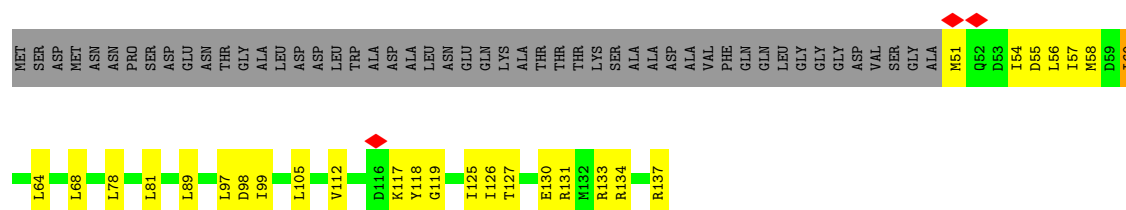


• Molecule 1: Flagellar motor switch protein FliN



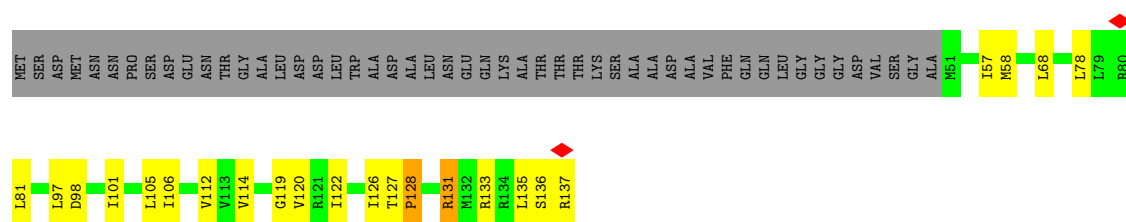
- Molecule 1: Flagellar motor switch protein FliN

Chain Am: 



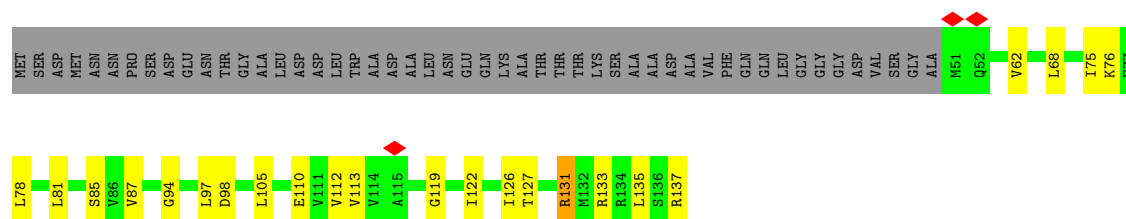
- Molecule 1: Flagellar motor switch protein FliN

Chain An: 

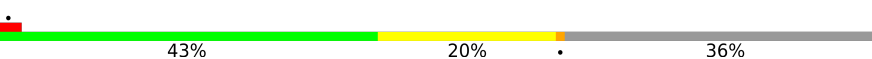


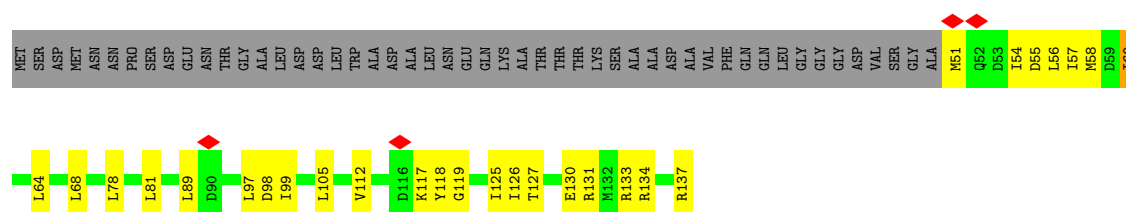
- Molecule 1: Flagellar motor switch protein FliN

Chain Ao: 



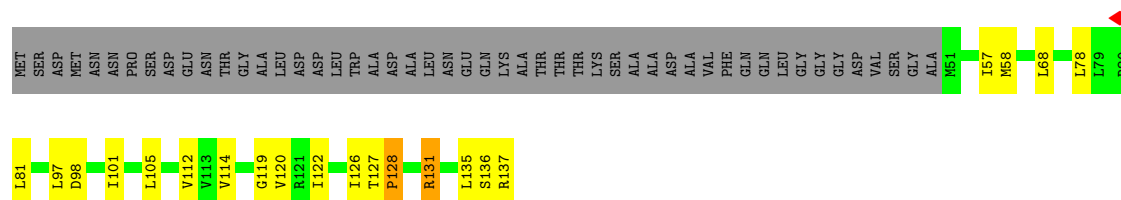
- Molecule 1: Flagellar motor switch protein FliN

Chain As: 

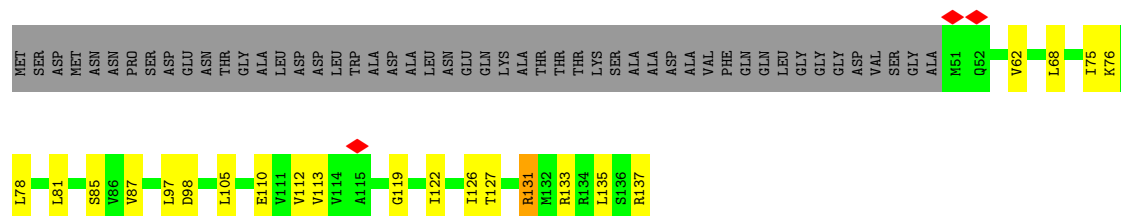


- Molecule 1: Flagellar motor switch protein FliN

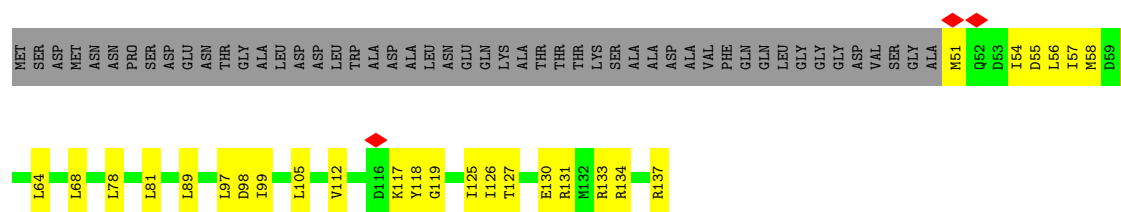
Chain At: 



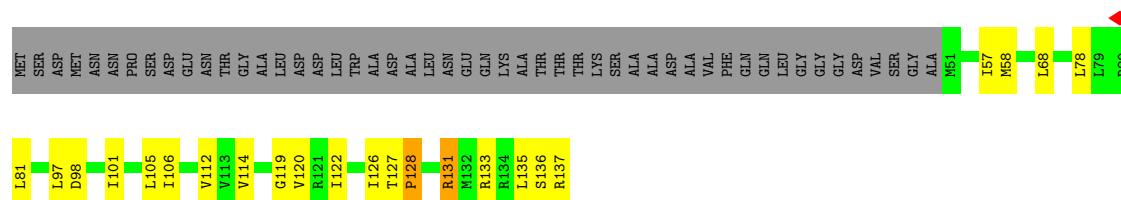
• Molecule 1: Flagellar motor switch protein FliN



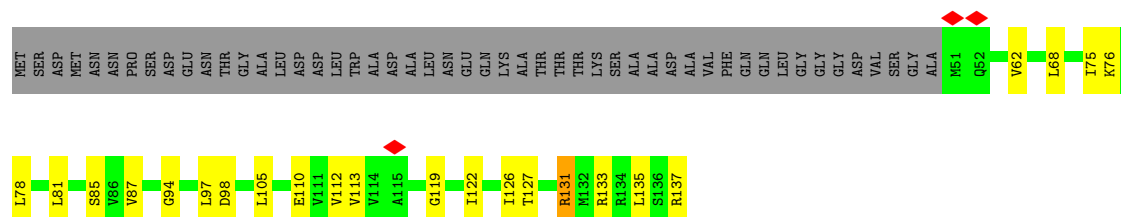
• Molecule 1: Flagellar motor switch protein FliN



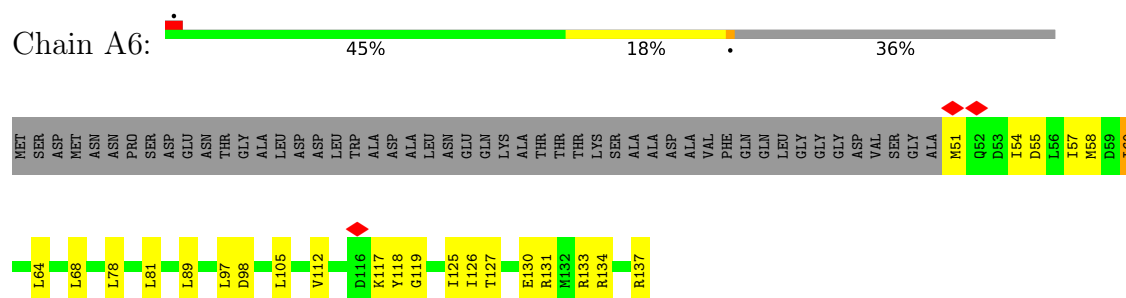
• Molecule 1: Flagellar motor switch protein FliN



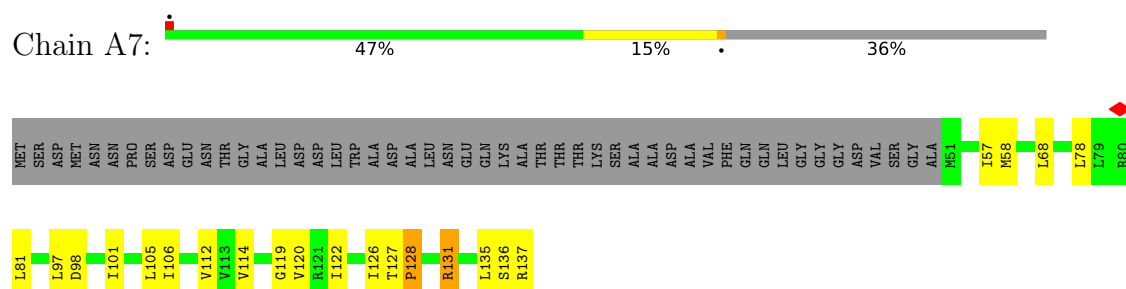
• Molecule 1: Flagellar motor switch protein FliN



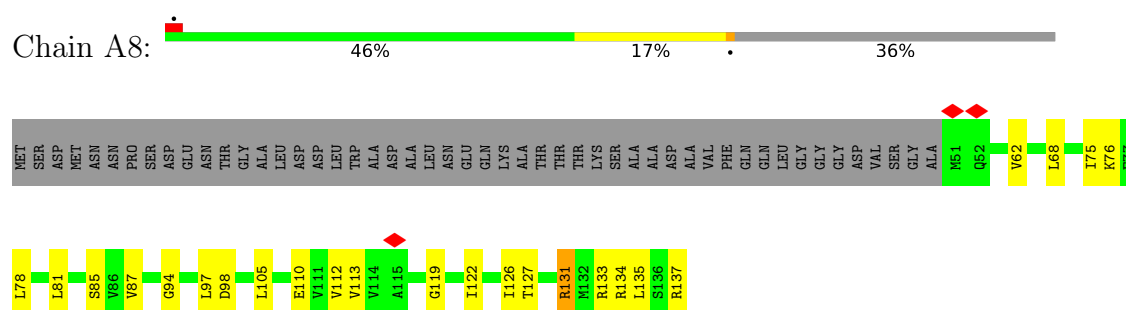
- Molecule 1: Flagellar motor switch protein FliN



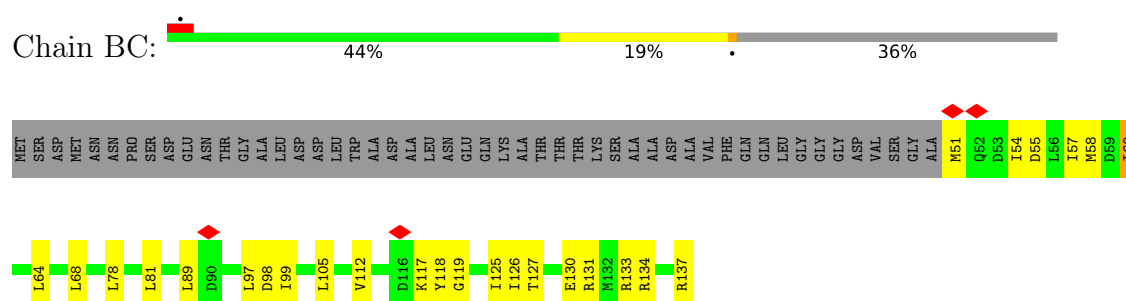
- Molecule 1: Flagellar motor switch protein FliN



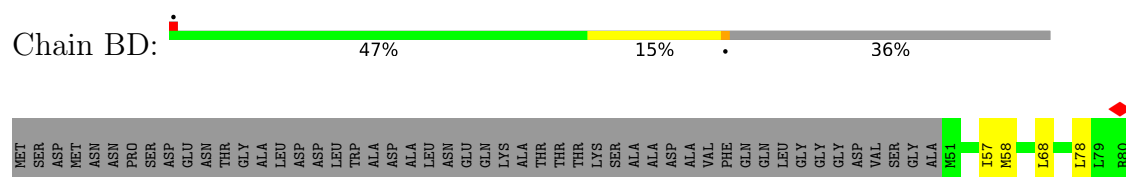
- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN

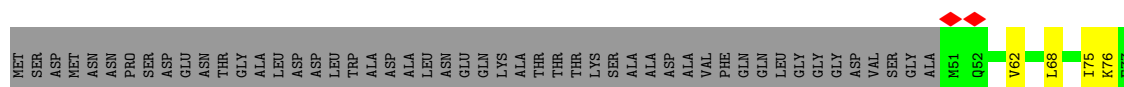


- Molecule 1: Flagellar motor switch protein FliN

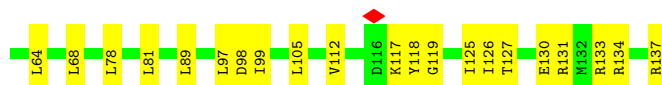
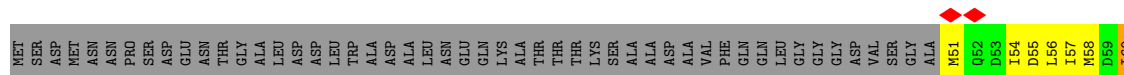




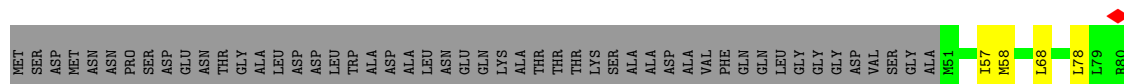
- Molecule 1: Flagellar motor switch protein FliN



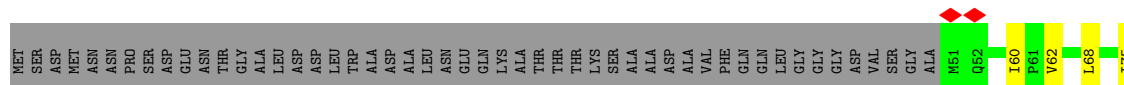
- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN

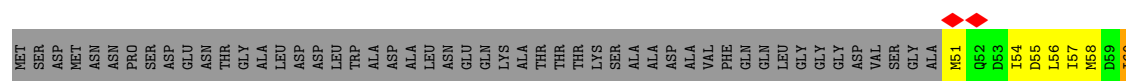


- Molecule 1: Flagellar motor switch protein FliN

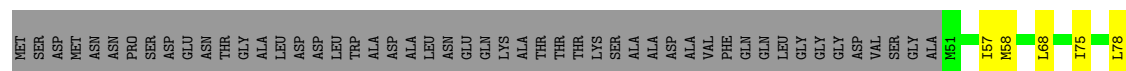


- Molecule 1: Flagellar motor switch protein FliN

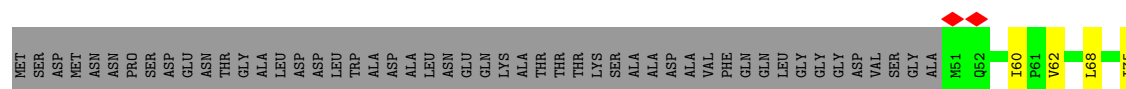




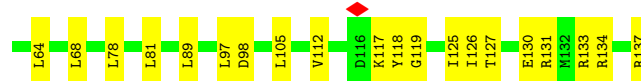
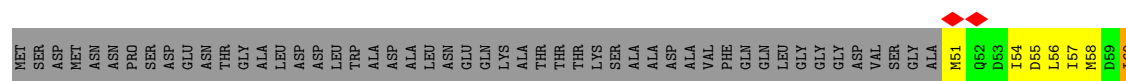
• Molecule 1: Flagellar motor switch protein FliN



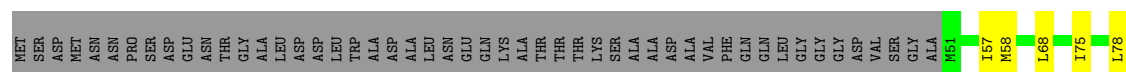
• Molecule 1: Flagellar motor switch protein FliN



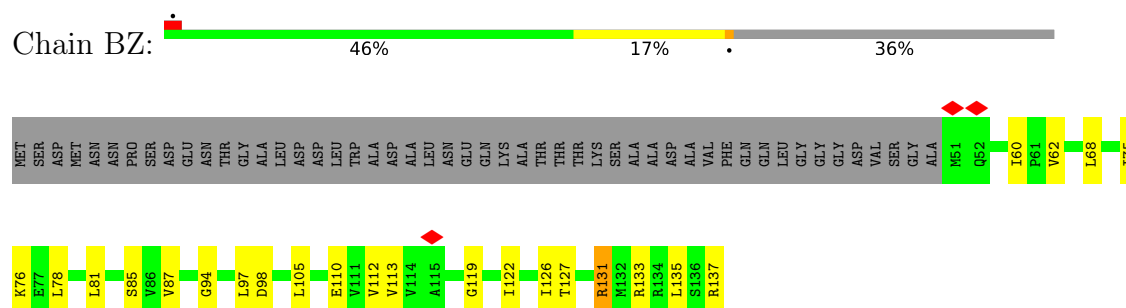
• Molecule 1: Flagellar motor switch protein FliN



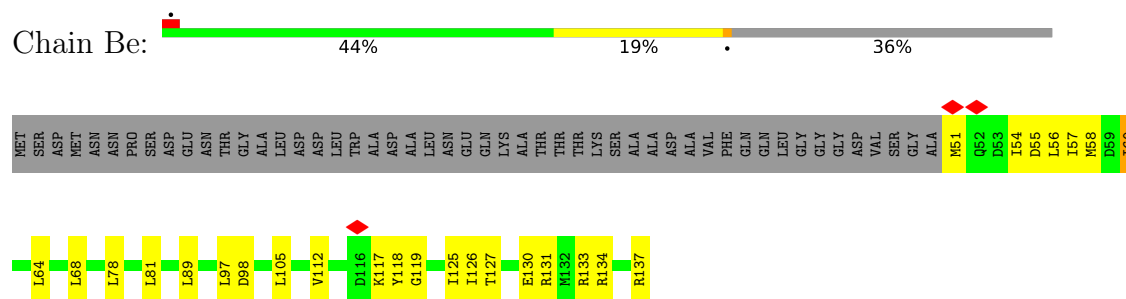
• Molecule 1: Flagellar motor switch protein FliN



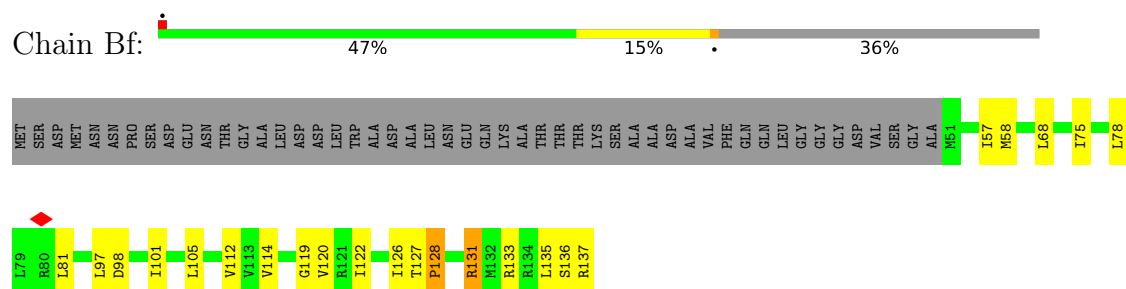
● Molecule 1: Flagellar motor switch protein FliN



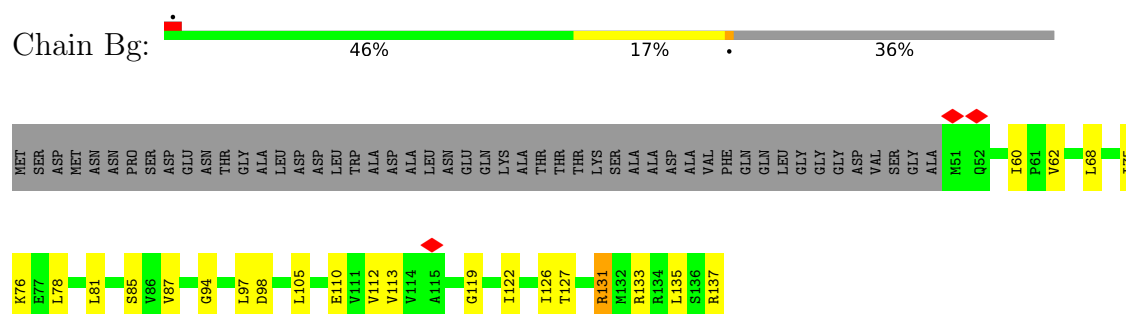
● Molecule 1: Flagellar motor switch protein FliN



● Molecule 1: Flagellar motor switch protein FliN

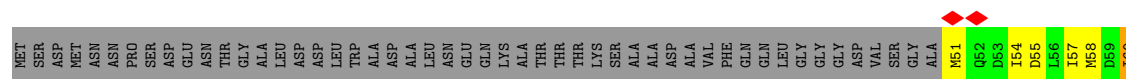


● Molecule 1: Flagellar motor switch protein FliN

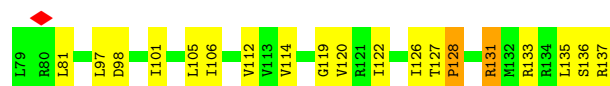
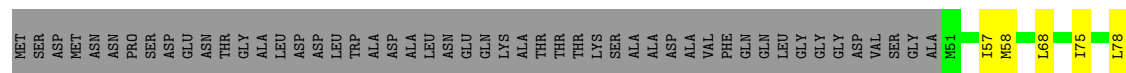


● Molecule 1: Flagellar motor switch protein FliN

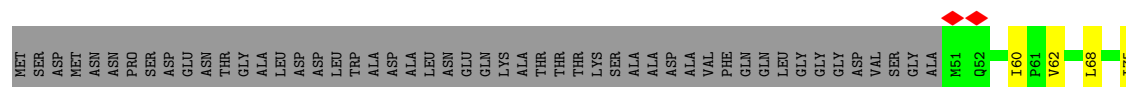




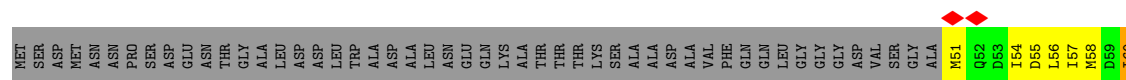
• Molecule 1: Flagellar motor switch protein FliN



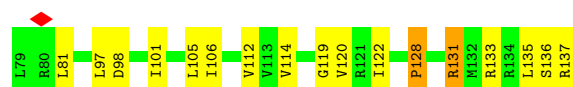
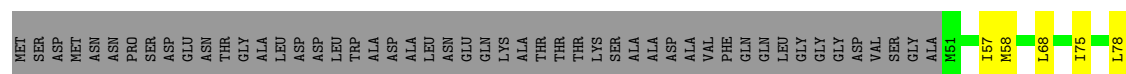
• Molecule 1: Flagellar motor switch protein FliN



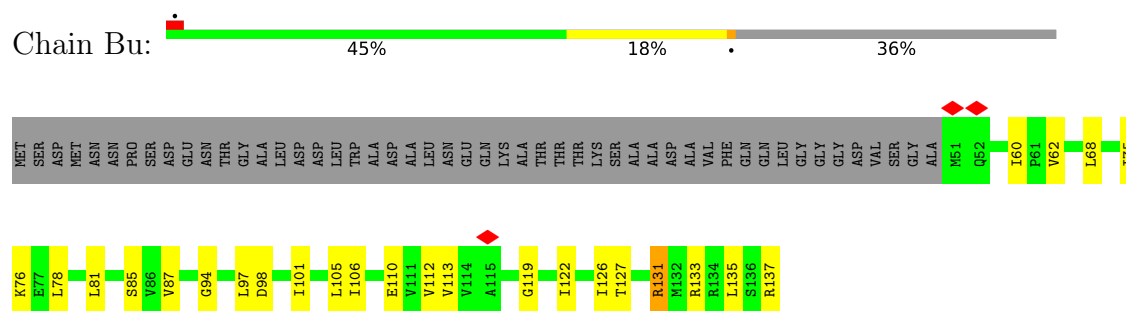
• Molecule 1: Flagellar motor switch protein FliN



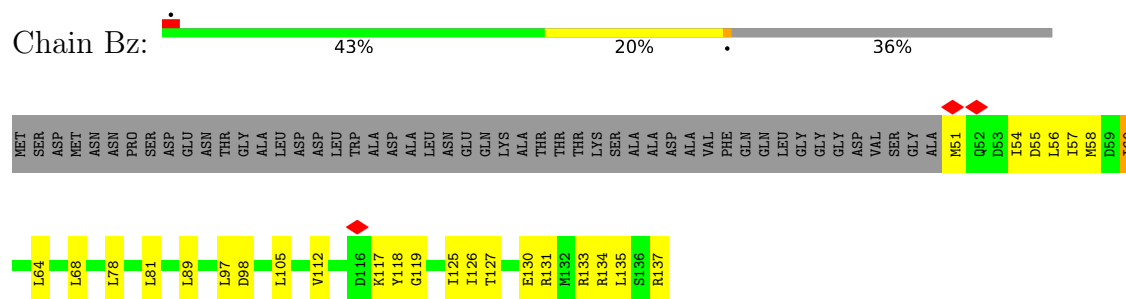
• Molecule 1: Flagellar motor switch protein FliN



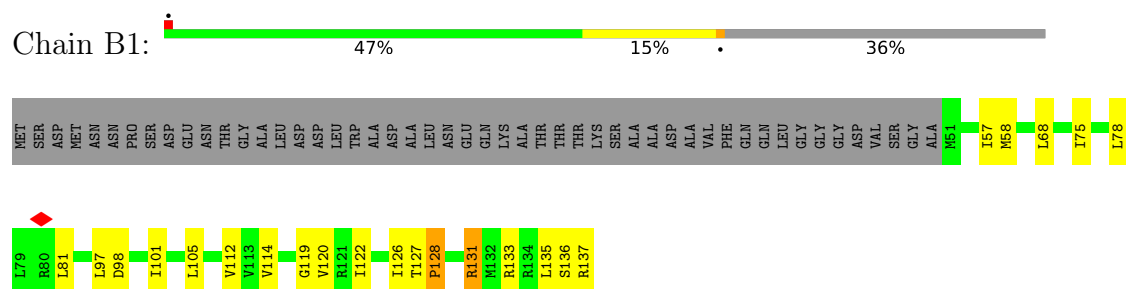
- Molecule 1: Flagellar motor switch protein FliN



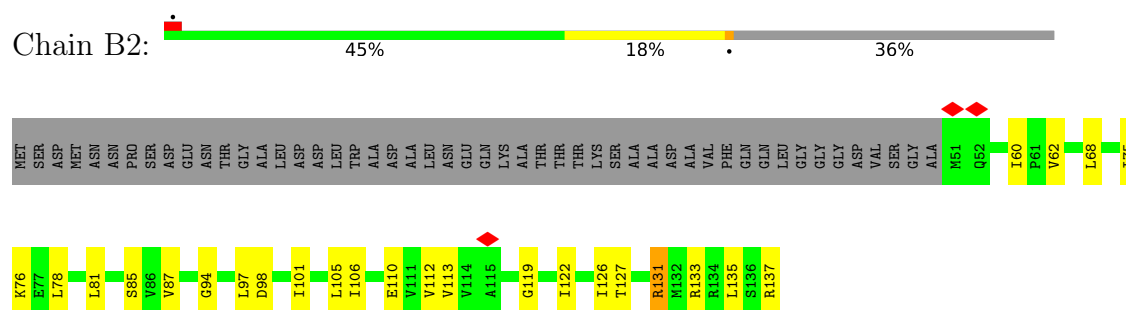
- Molecule 1: Flagellar motor switch protein FliN



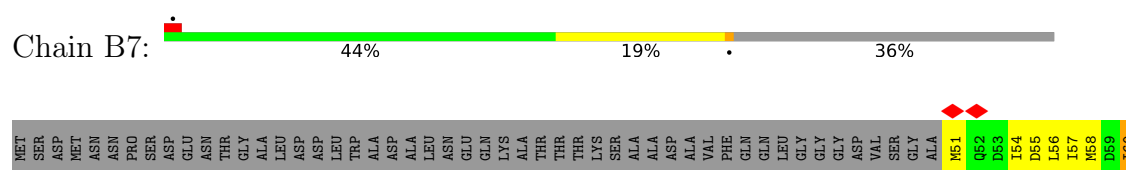
- Molecule 1: Flagellar motor switch protein FliN

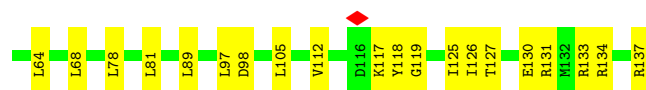


- Molecule 1: Flagellar motor switch protein FliN

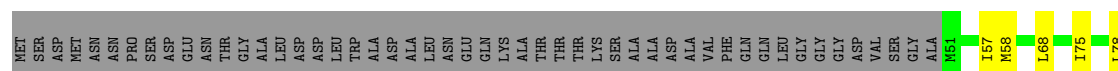


- Molecule 1: Flagellar motor switch protein FliN

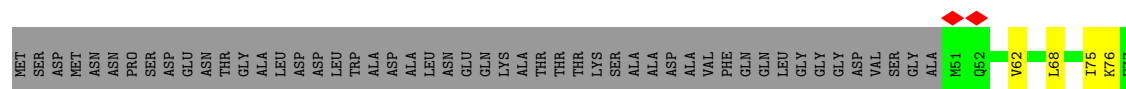




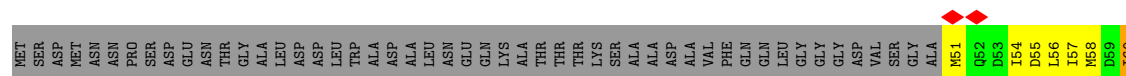
- Molecule 1: Flagellar motor switch protein FliN



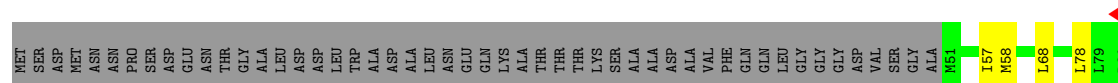
- Molecule 1: Flagellar motor switch protein FliN



- Molecule 1: Flagellar motor switch protein FliN

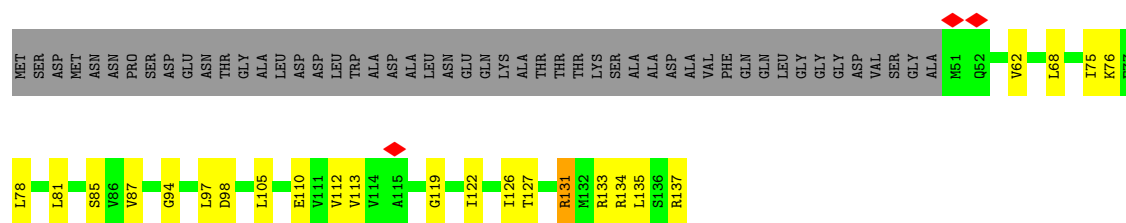


- Molecule 1: Flagellar motor switch protein FliN

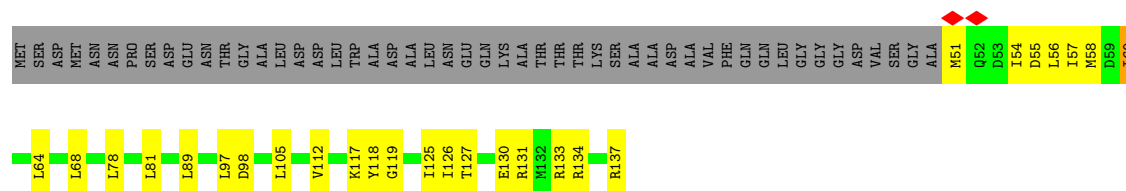


- Molecule 1: Flagellar motor switch protein FliN

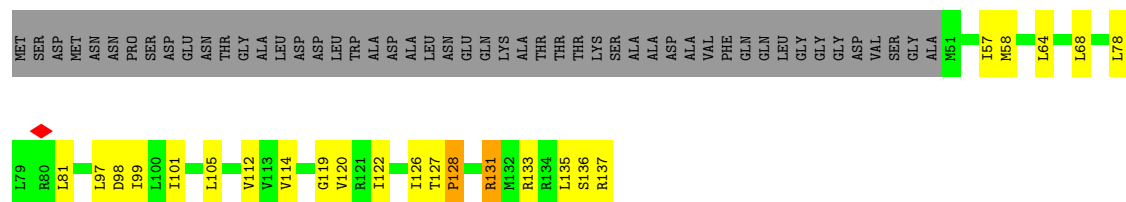




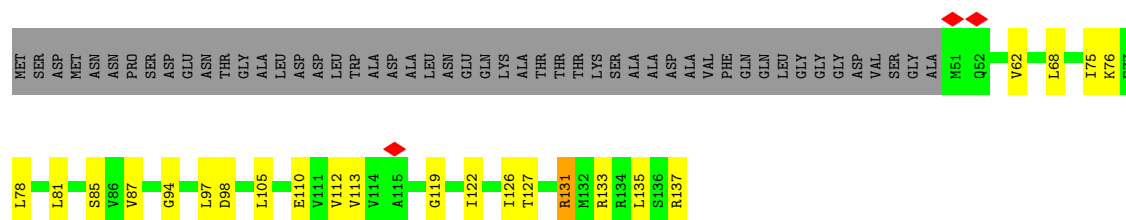
- Molecule 1: Flagellar motor switch protein FliN



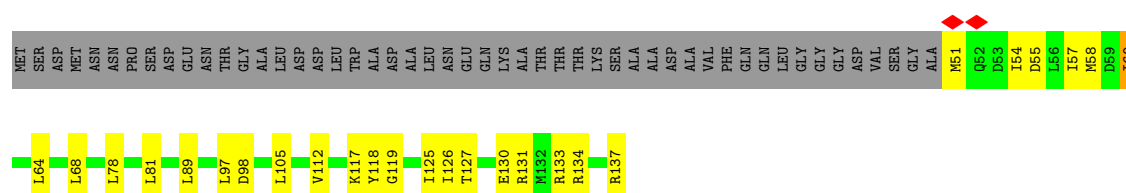
- Molecule 1: Flagellar motor switch protein FliN



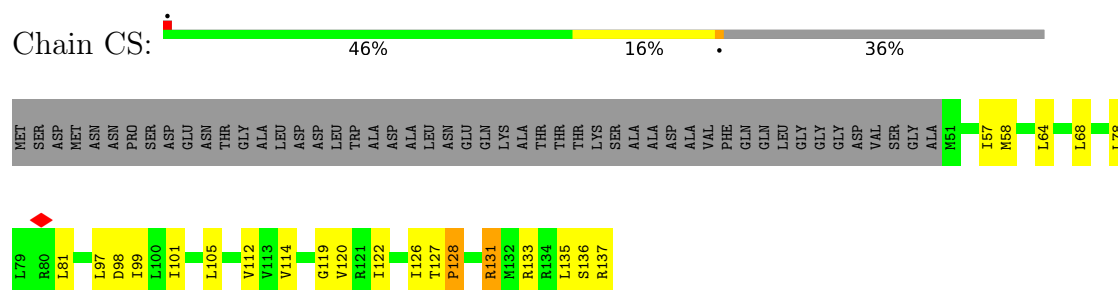
- Molecule 1: Flagellar motor switch protein FliN



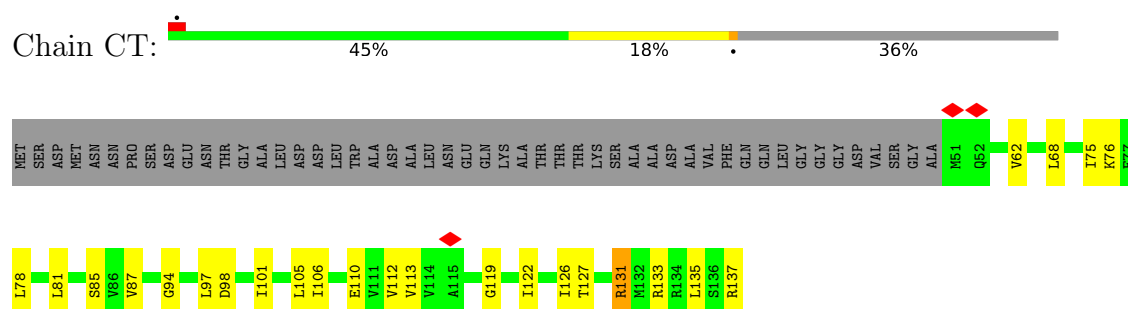
- Molecule 1: Flagellar motor switch protein FliN



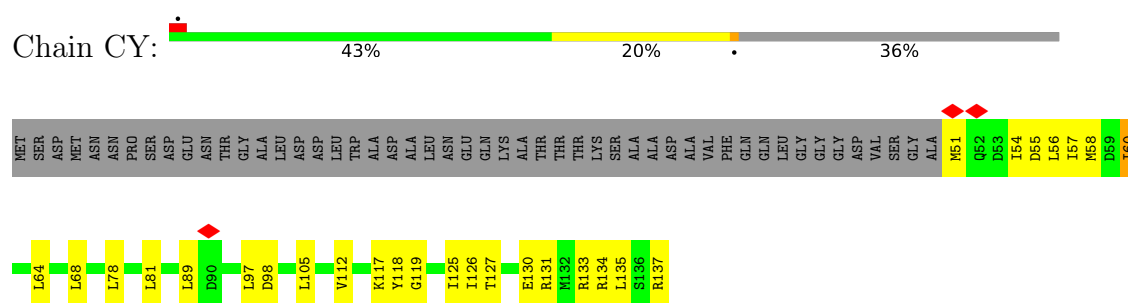
• Molecule 1: Flagellar motor switch protein FliN



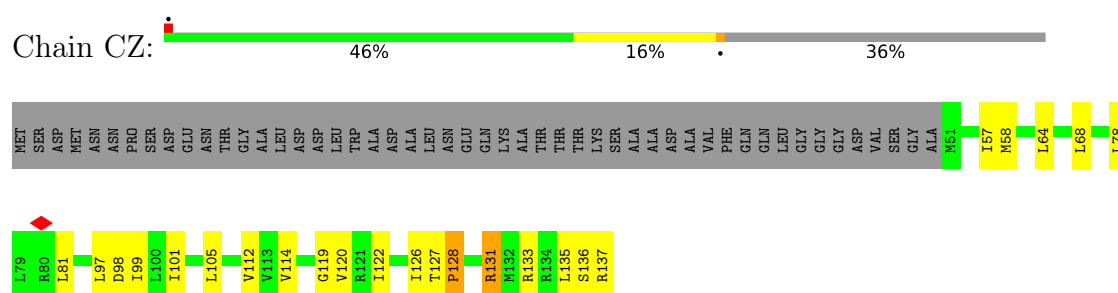
• Molecule 1: Flagellar motor switch protein FliN



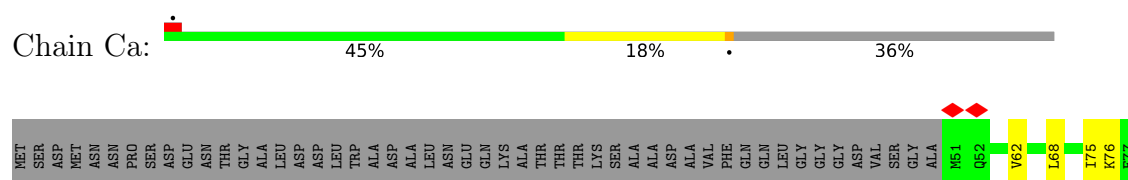
• Molecule 1: Flagellar motor switch protein FliN



• Molecule 1: Flagellar motor switch protein FliN

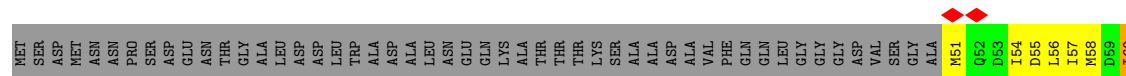


• Molecule 1: Flagellar motor switch protein FliN

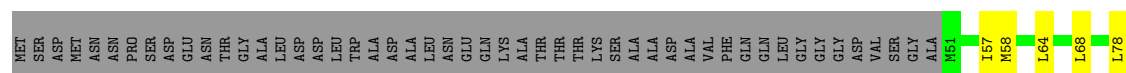




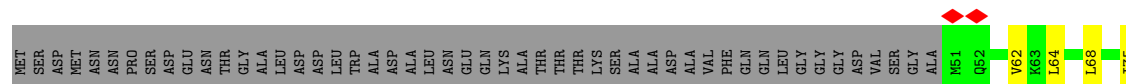
- Molecule 1: Flagellar motor switch protein FliN



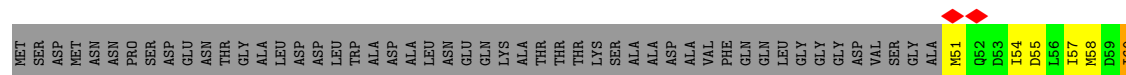
- Molecule 1: Flagellar motor switch protein FliN



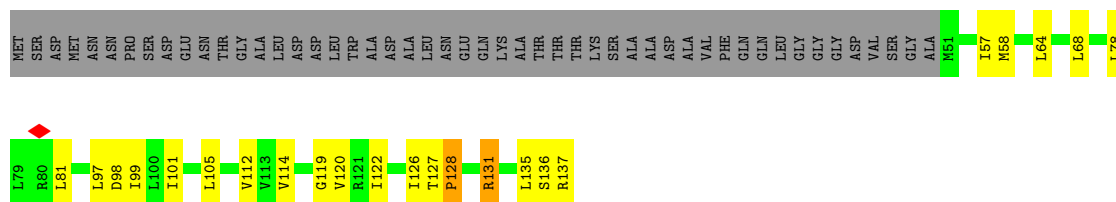
- Molecule 1: Flagellar motor switch protein FliN



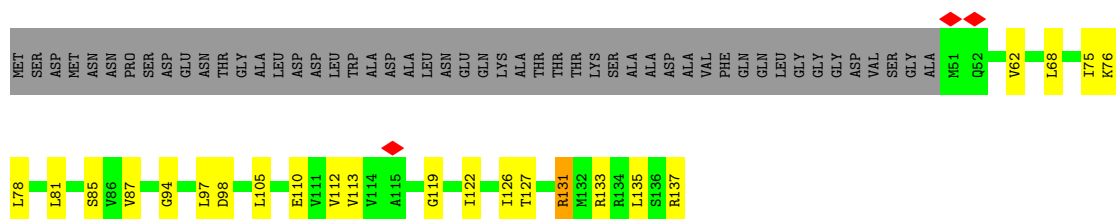
- Molecule 1: Flagellar motor switch protein FliN



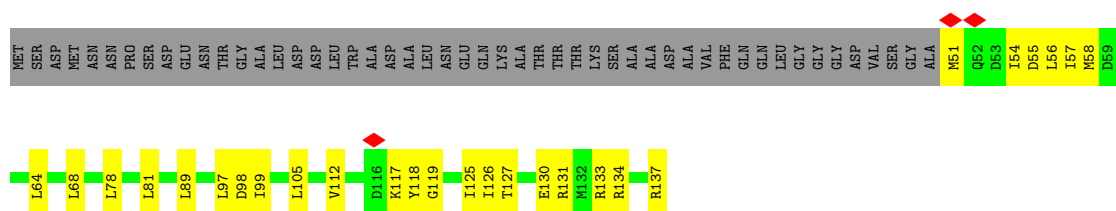
- Molecule 1: Flagellar motor switch protein FliN



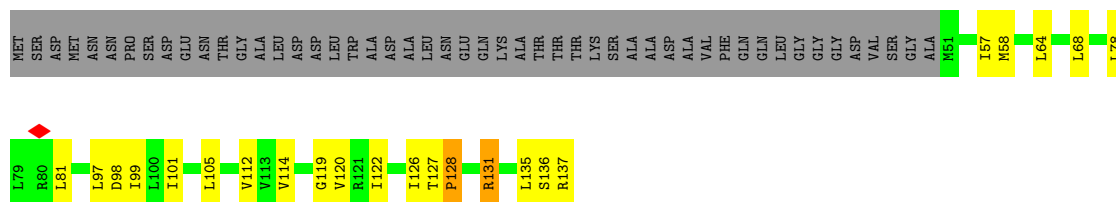
• Molecule 1: Flagellar motor switch protein FliN



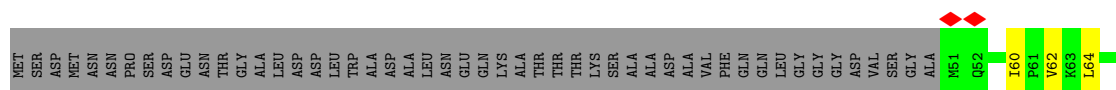
• Molecule 1: Flagellar motor switch protein FliN



• Molecule 1: Flagellar motor switch protein FliN

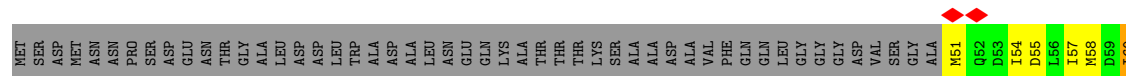


• Molecule 1: Flagellar motor switch protein FliN

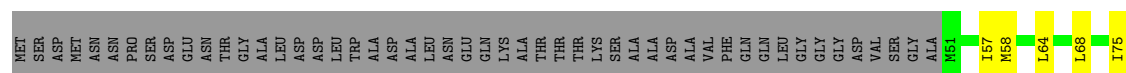




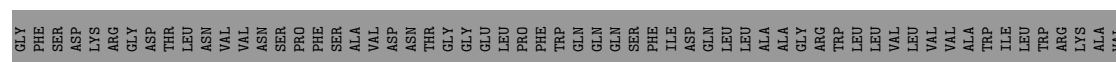
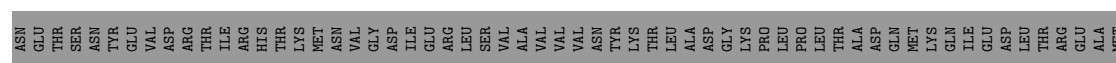
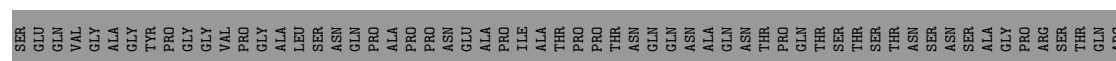
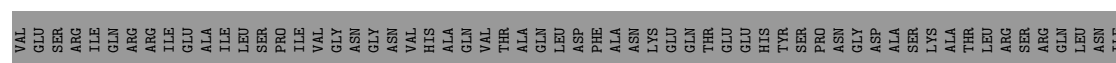
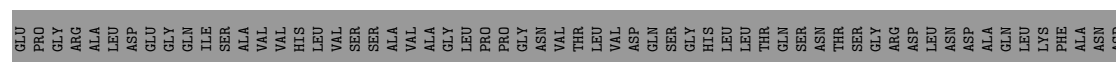
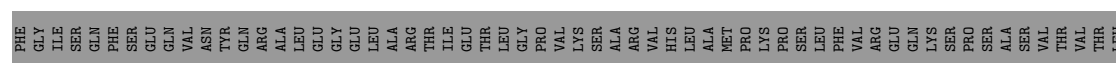
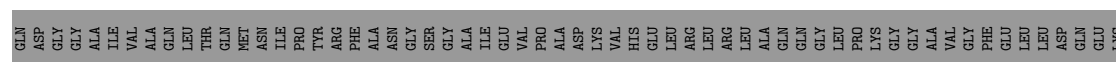
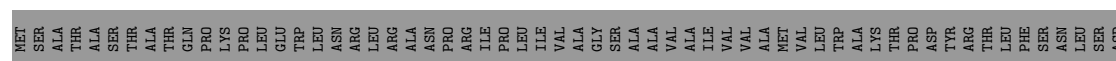
- Molecule 1: Flagellar motor switch protein FlhN



- Molecule 1: Flagellar motor switch protein FlhN



- Molecule 2: Flagellar M-ring protein





Chain D: 95%

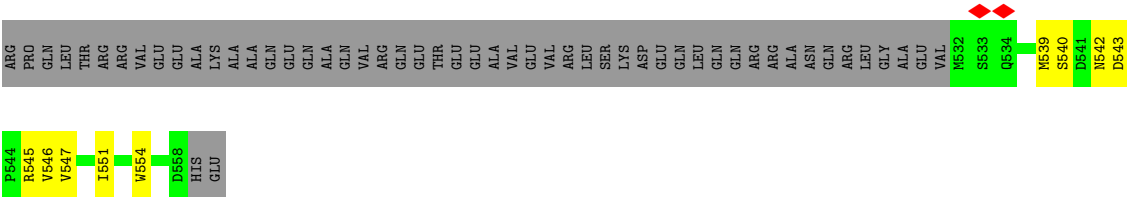


Chain E: 95%



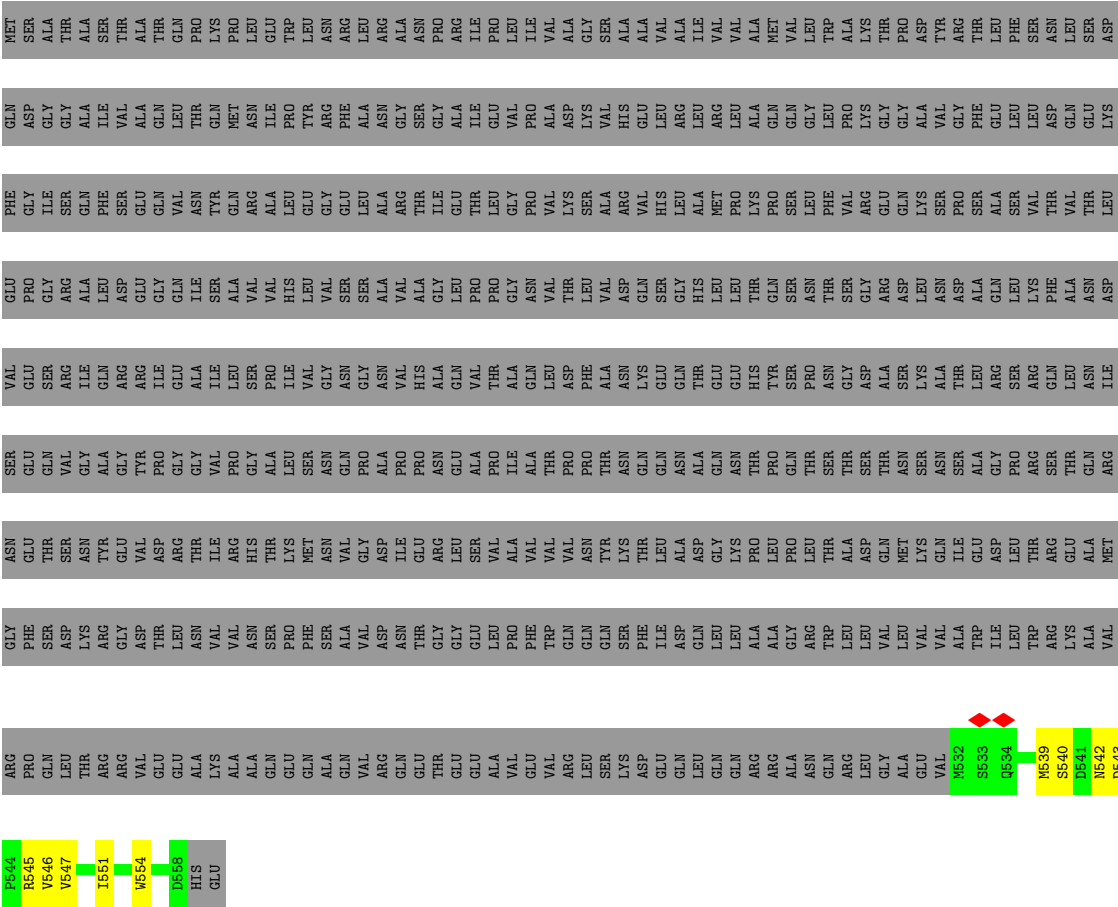






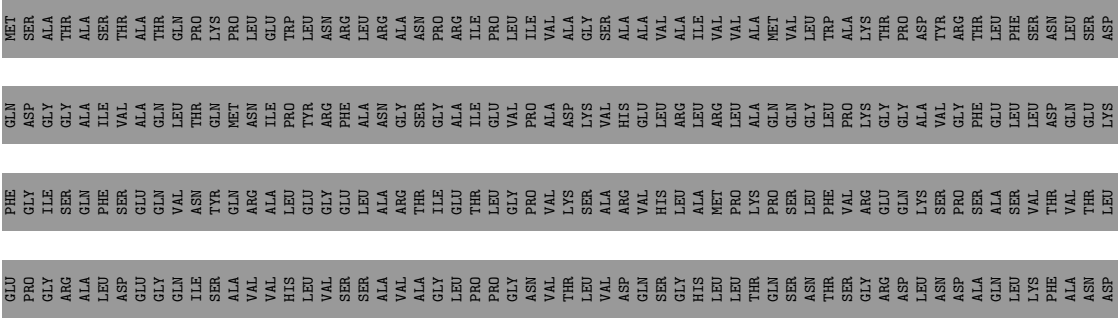
• Molecule 2: Flagellar M-ring protein

Chain I: . . 95%



• Molecule 2: Flagellar M-ring protein

Chain J: . . 95%





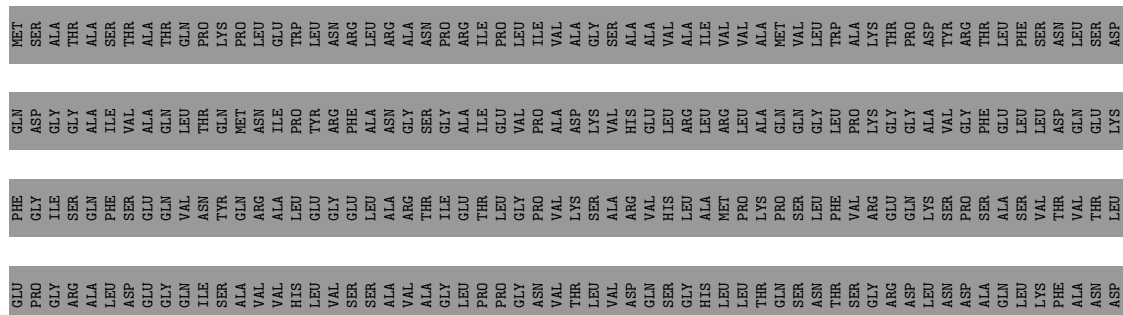




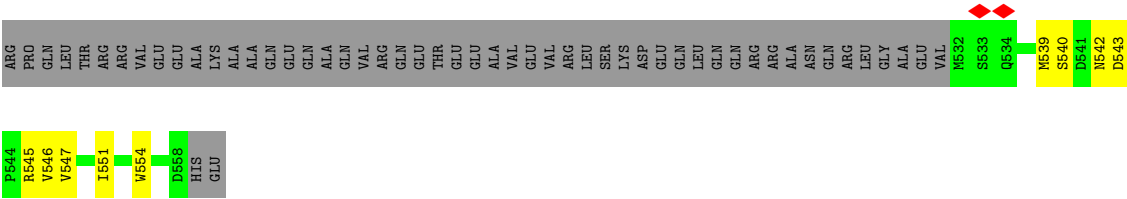
Chain N: 95%



Chain 0: 95%

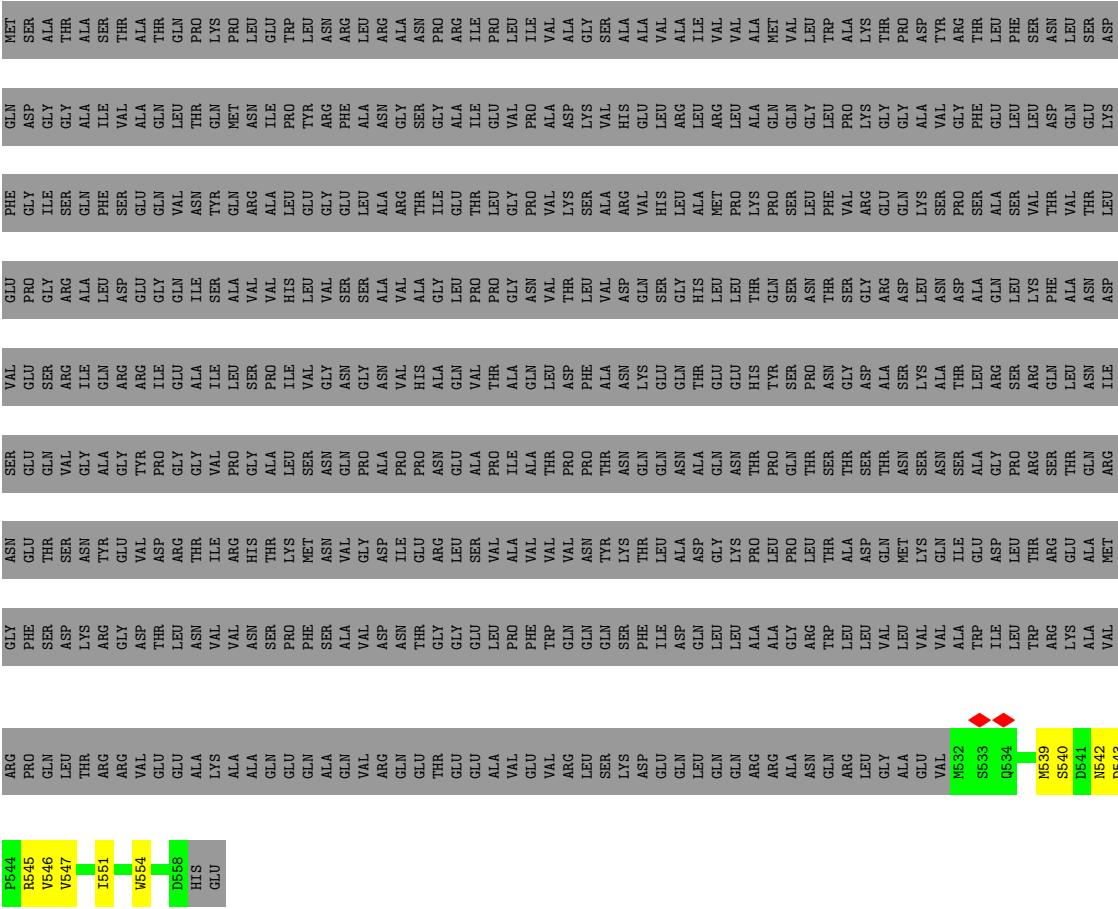






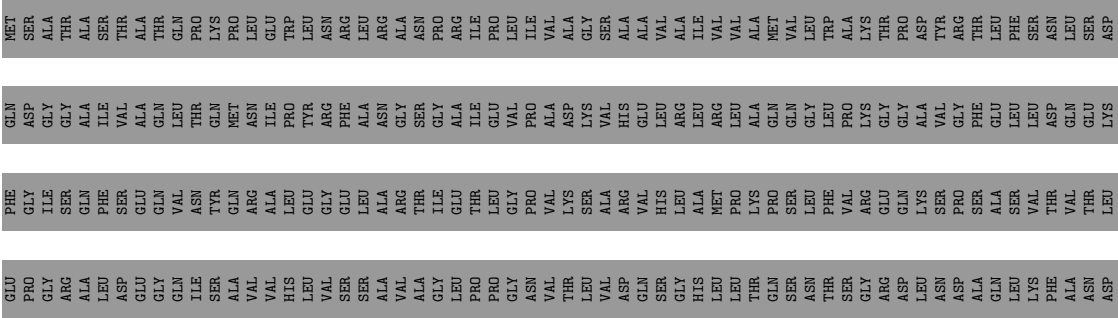
• Molecule 2: Flagellar M-ring protein

Chain A2: 95%



• Molecule 2: Flagellar M-ring protein

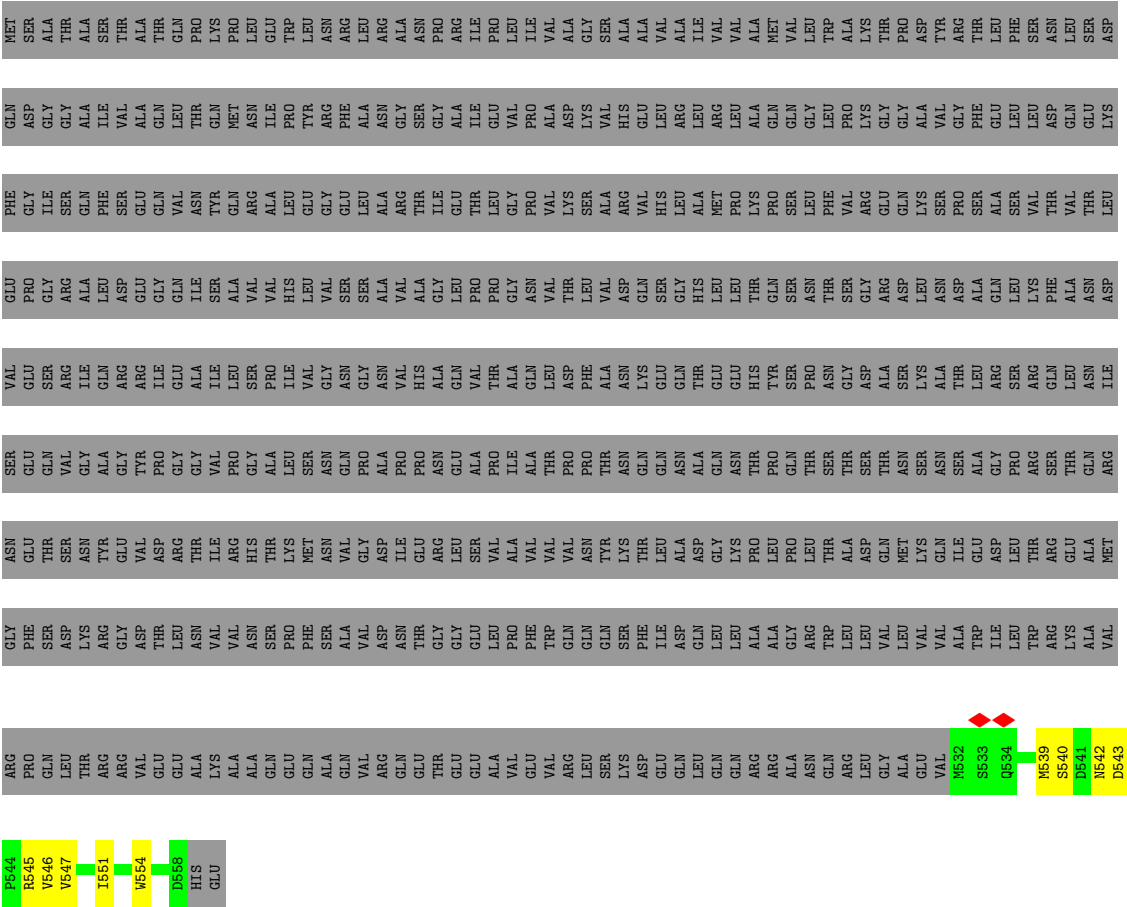
Chain A9: 95%





● Molecule 2: Flagellar M-ring protein

Chain BF: . . 95%



● Molecule 2: Flagellar M-ring protein

Chain BM: . . 95%





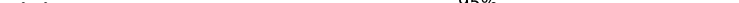
Chain Ba: 95%

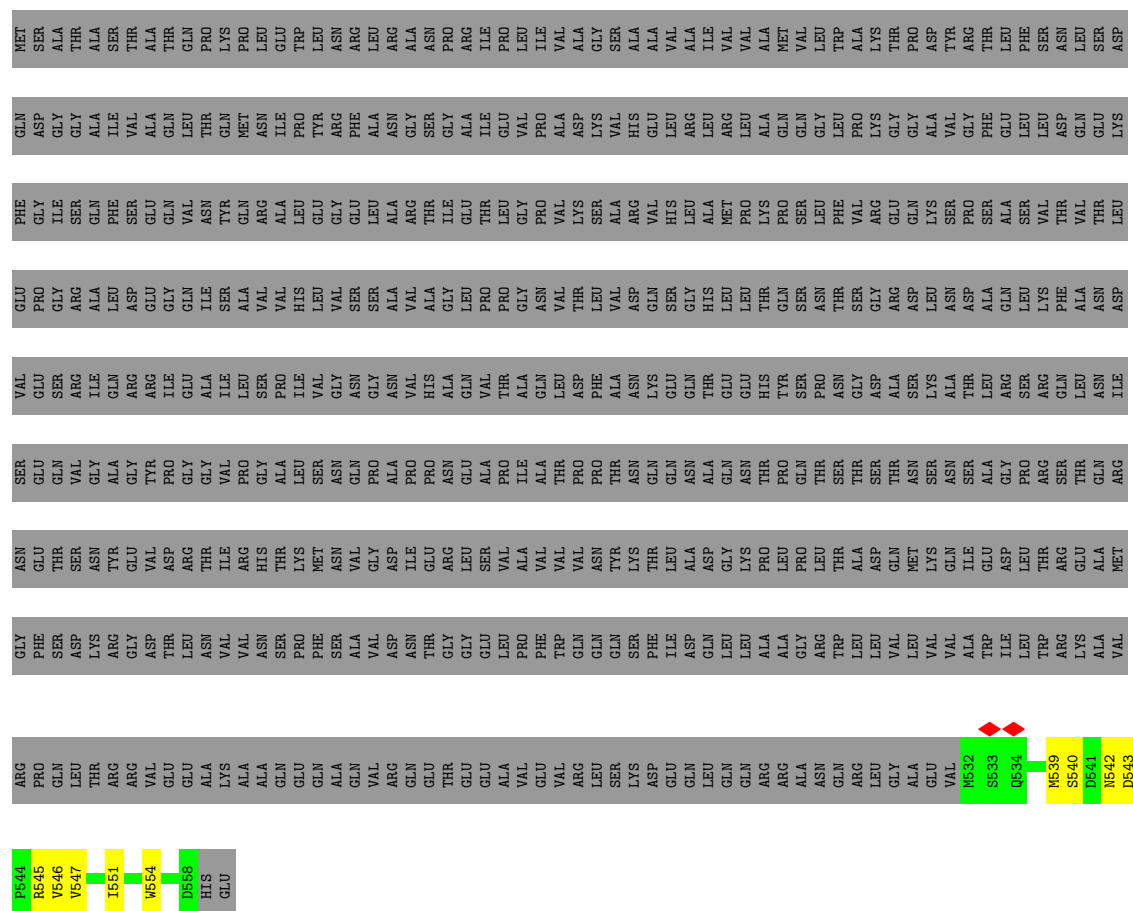


Chain Bh: 95%



- Molecule 2: Flagellar M-ring protein

Chain Bo:  95%



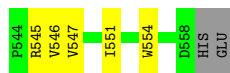
- Molecule 2: Flagellar M-ring protein

Chain Bv: 95%

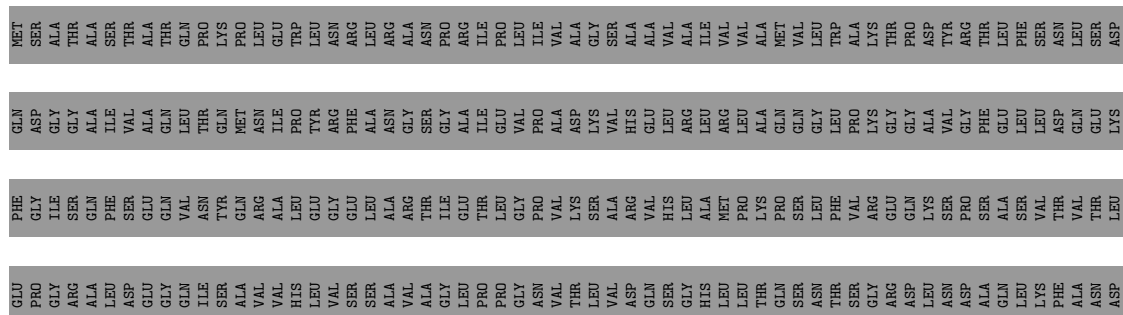




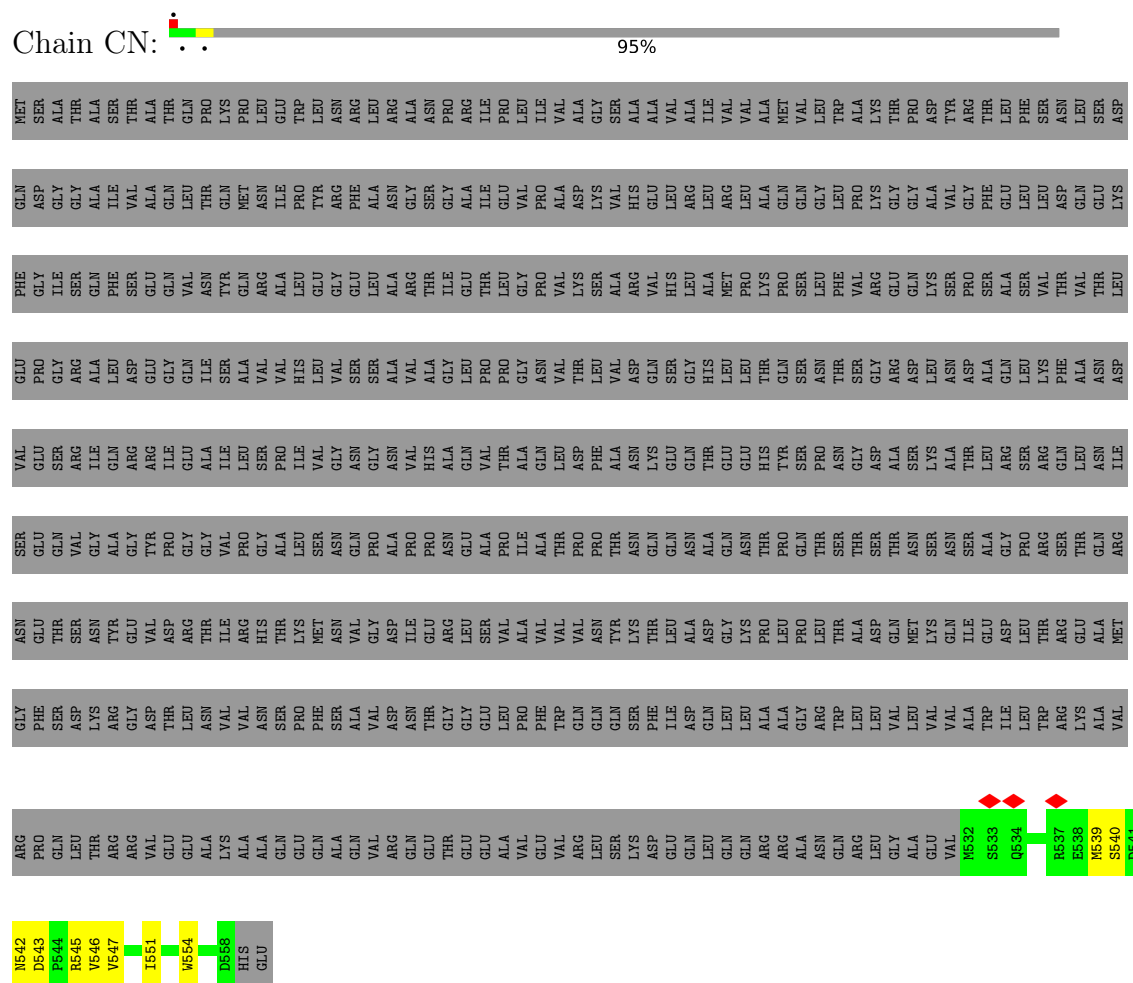
Chain B0: 95%



Chain CG: 95%



- Molecule 2: Flagellar M-ring protein



- Molecule 2: Flagellar M-ring protein





ARG	PRO	GLN	LEU	THR	ARG	ARG	VAL	GLU	GLU	ALA	LYS	LYS	ALA	ALA	GLN	GLU	GLN	ALA	ASN	GLN	ARG	GLY	ALA	GLU	VAL	M532	S533	Q534	M539	S540	D541	N542	D543
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------

P544	R545	V546	V547	I551	W554	D558	HIS	GLU
------	------	------	------	------	------	------	-----	-----

● Molecule 2: Flagellar M-ring protein

Chain Ci: . . 95%

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

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

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

GLU	PRO	GLY	ARG	VAL	ALA	LYS	LEU	ASP	GLY	THR	ALA	GLN	ILE	GLY	VAL	THR	GLY	GLY	LEU	ALA	ASN	ARG	GLY	THR	PRO	GLU	GLY	ASN	VAL	VAL	VAL	THR	GLY	THR	PRO	GLU	GLY	THR	PRO	LEU	VAL	GLY	THR	THR	LEU	GLN	ASP	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

VAL	GLU	SER	ARG	ILE	GLN	ARG	GLY	THR	ILE	GLY	GLU	VAL	ILE	ALA	ILE	SER	VAL	GLY	ASN	GLY	SER	LEU	ALA	ASN	THR	VAL	THR	GLY	ASN	VAL	VAL	THR	GLY	THR	PRO	GLU	GLY	THR	PRO	LEU	VAL	GLY	THR	THR	LEU	GLN	ASP	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

SER	GLU	GLN	VAL	GLY	ALA	GLY	TYR	GLU	VAL	ASP	PRO	GLY	ALA	GLN	VAL	THR	GLY	GLY	ASN	GLN	PRO	ALA	ASP	THR	THR	GLN	ASN	LYS	THR	GLN	VAL	THR	GLY	THR	THR	ASN	GLY	THR	THR	GLN	VAL	GLY	THR	THR	LEU	GLN	ASP	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ASN	GLU	THR	SER	ASP	TYR	GLU	VAL	VAL	ASP	THR	GLY	VAL	GLY	ASN	VAL	VAL	VAL	VAL	ASN	GLY	PRO	ALA	ASP	THR	TYR	ASN	GLN	LYS	THR	GLN	VAL	THR	GLY	THR	THR	ASN	GLY	THR	THR	GLN	VAL	GLY	THR	THR	LEU	GLN	ASP	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLY	PHE	SER	ASP	LYS	ARG	GLY	ASP	THR	LEU	ASN	VAL	VAL	ASN	VAL	ASN	THR	GLY	GLY	SER	ALA	VAL	ASP	VAL	GLY	LEU	VAL	GLN	LYS	THR	GLN	VAL	THR	GLY	THR	THR	ASN	GLY	THR	THR	GLN	VAL	GLY	THR	THR	LEU	GLN	ASP	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ARG	PRO	GLN	LEU	THR	ARG	ARG	VAL	GLU	GLU	ALA	LYS	ALA	ALA	ALA	GLN	GLN	ALA	GLU	GLU	GLN	VAL	ARG	GLU	GLU	ALA	VAL	VAL	VAL	VAL	VAL	VAL	THR	GLY	SER	LYS	VAL	GLY	THR	THR	GLN	ARG	GLY	THR	THR	LEU	GLN	ASP	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

P544	R545	V546	V547	I551	W554	D558	HIS	GLU
------	------	------	------	------	------	------	-----	-----

● Molecule 2: Flagellar M-ring protein

Chain Cp: . . 95%

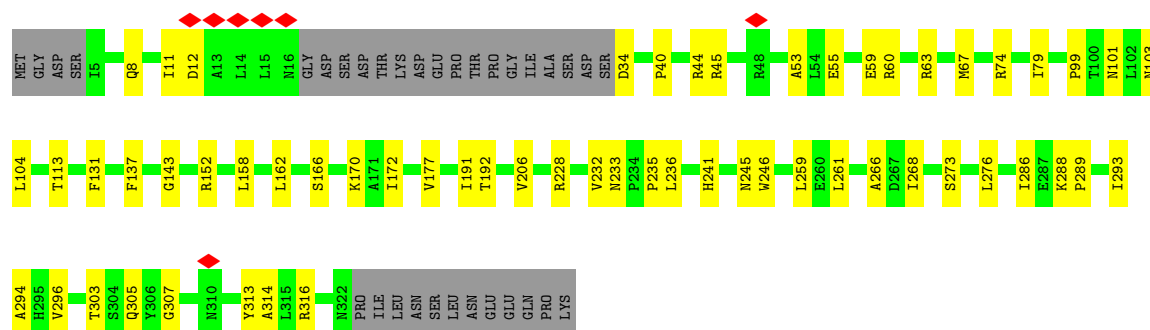
MET	SER	ALA	THR	THR	SER	THR	ALA	GLN	LYS	PRO	PRO	LEU	LEU	GLU	TRP	LEU	ASN	ARG	LEU	ALA	ASN	ARG	GLY	ILE	PRO	PRO	ILE	VAL	GLU	LEU	VAL	GLN	ARG	GLY	THR	THR	LEU	PHE	ASN	LEU	SER	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----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

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

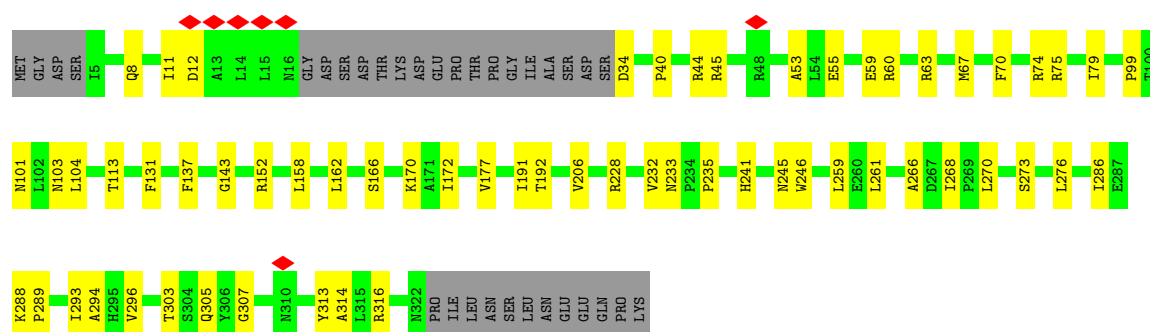
PHE	GLY	ILE	SER	GLN	GLN	VAL	VAL	ASN	THR	GLN	VAL	ARG	ALA	GLN	THR	GLY	GLY	LEU	ALA	ASN	ARG	GLY	THR	LEU	PRO	GLU	GLY	ASN	VAL	VAL	THR	GLY	THR	PRO	GLY	THR	THR	ASN	GLY	THR	THR	LEU	VAL	GLY	THR	THR	LEU	GLN	ASP	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----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

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

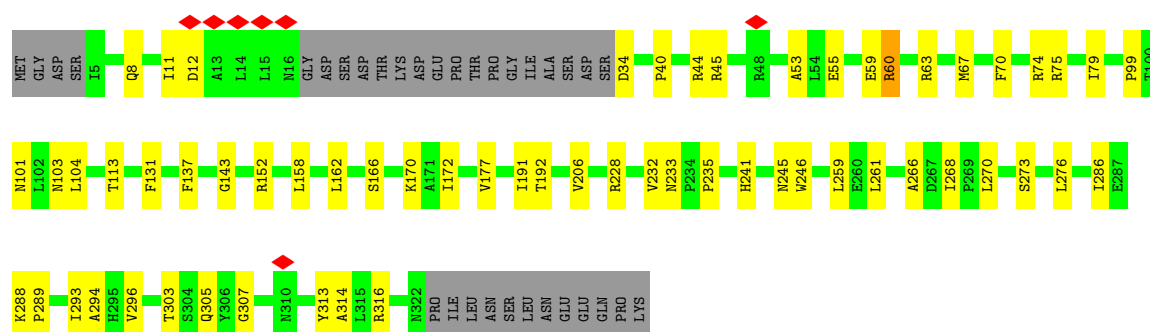




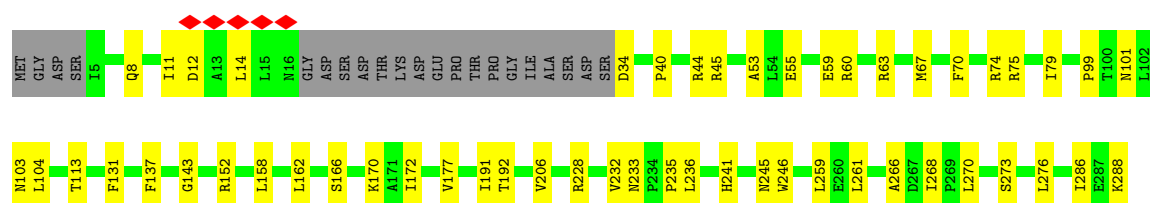
• Molecule 3: Flagellar motor switch protein FlIM

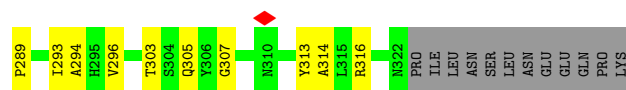


• Molecule 3: Flagellar motor switch protein FlIM



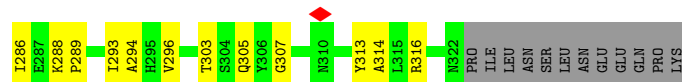
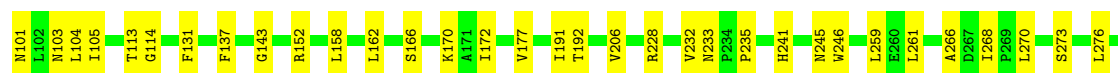
• Molecule 3: Flagellar motor switch protein FlIM





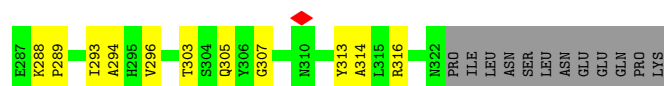
• Molecule 3: Flagellar motor switch protein FliM

Chain W: 71% 19% 10%



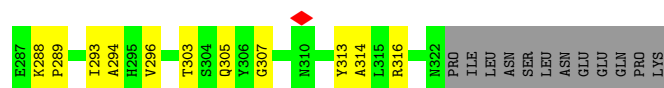
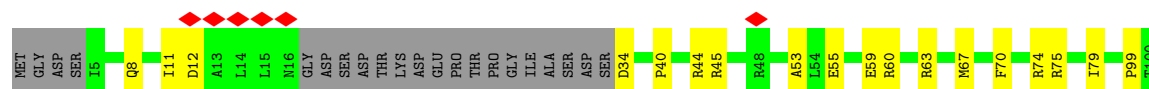
• Molecule 3: Flagellar motor switch protein FliM

Chain X: 72% 19% 10%



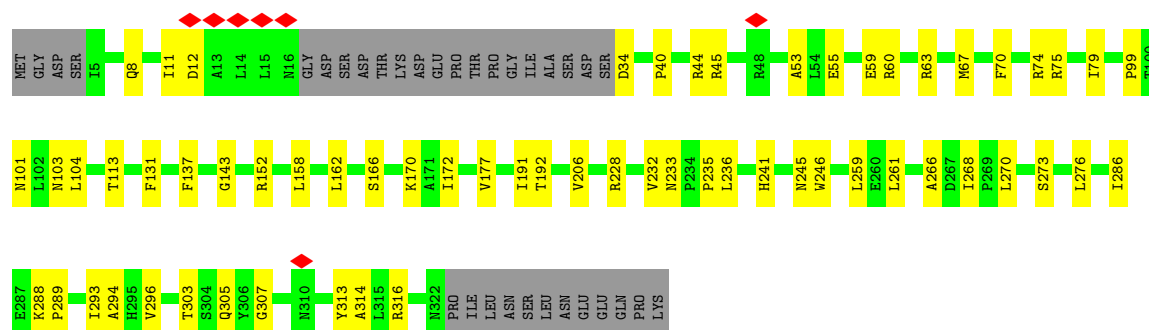
• Molecule 3: Flagellar motor switch protein FliM

Chain Y: 72% 19% 10%

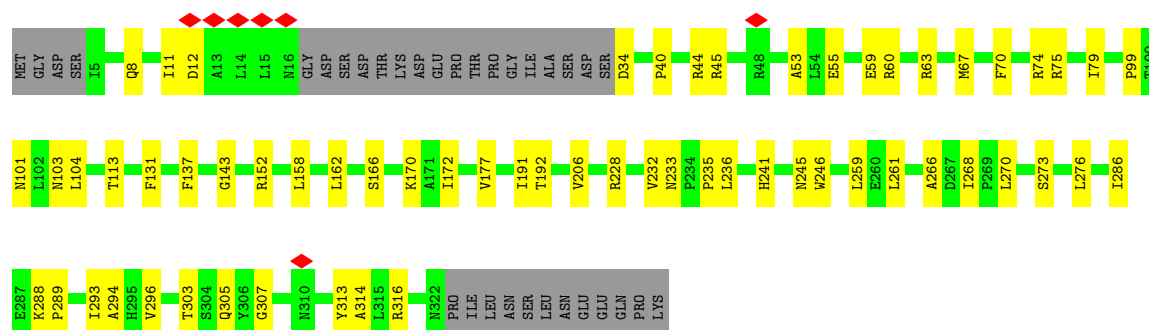


• Molecule 3: Flagellar motor switch protein FliM

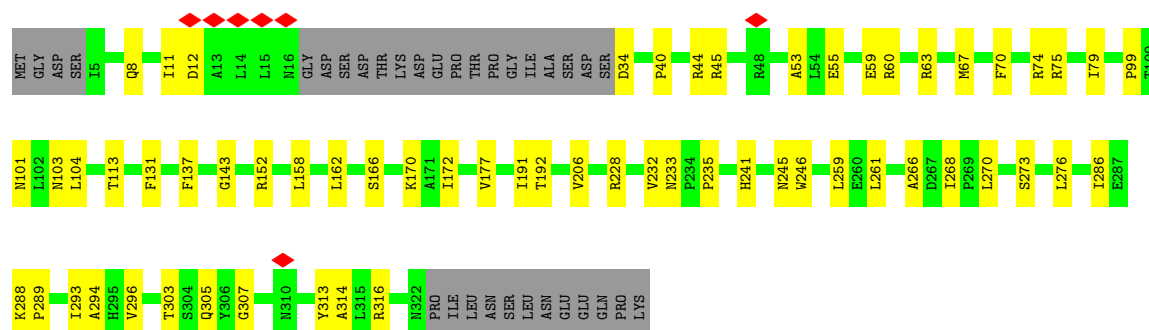
Chain g: 72% 19% 10%



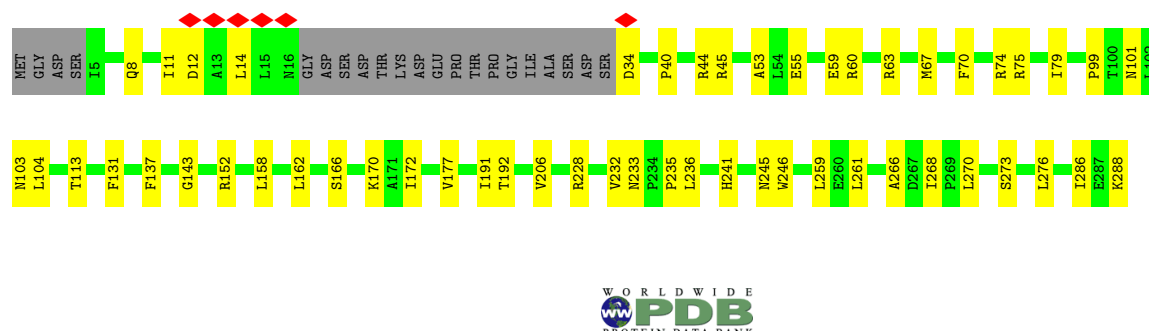
• Molecule 3: Flagellar motor switch protein FlIM

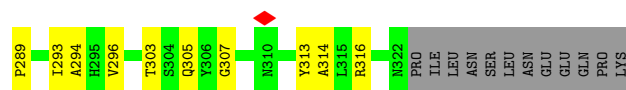


• Molecule 3: Flagellar motor switch protein FlIM



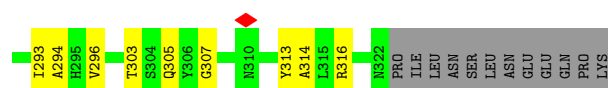
• Molecule 3: Flagellar motor switch protein FlIM





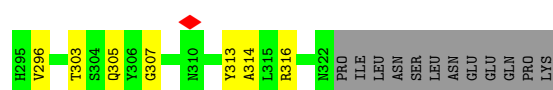
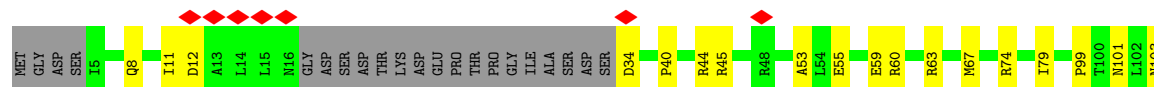
• Molecule 3: Flagellar motor switch protein FlIM

Chain AX: 72% 18% 10%



• Molecule 3: Flagellar motor switch protein FlIM

Chain Ad: 73% 17% 10%



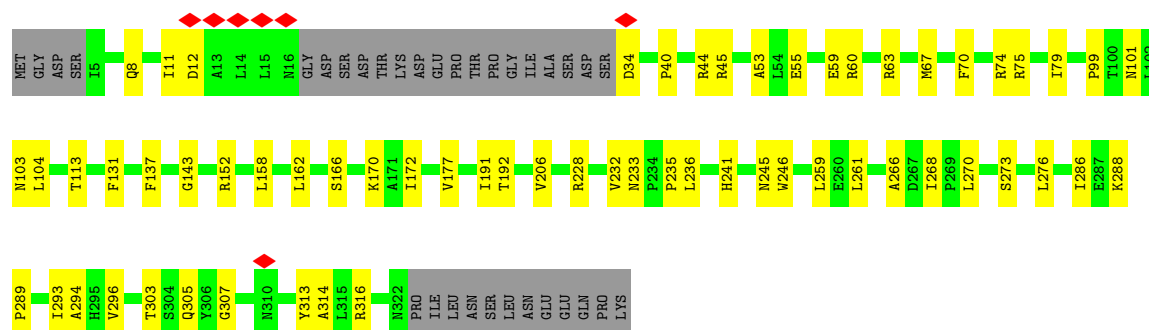
• Molecule 3: Flagellar motor switch protein FlIM

Chain Aj: 72% 18% 10%

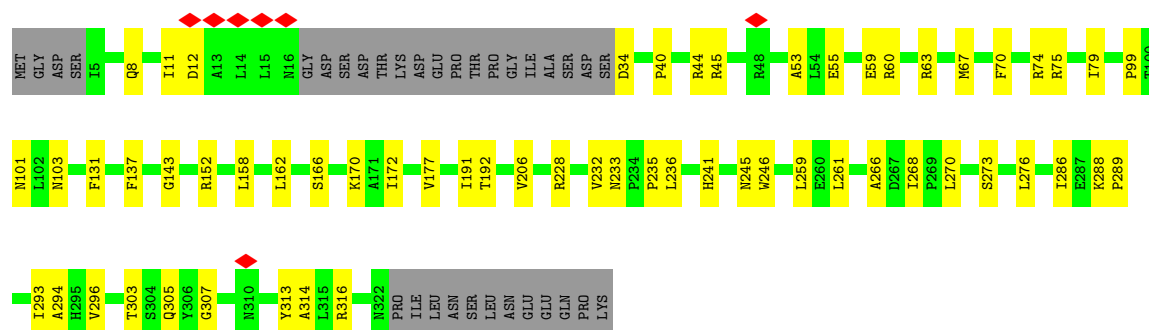


• Molecule 3: Flagellar motor switch protein FlIM

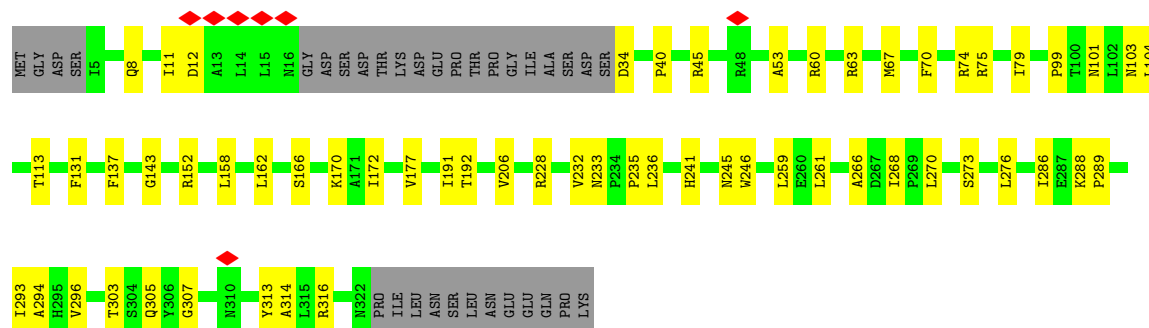
Chain Ap: 72% 19% 10%



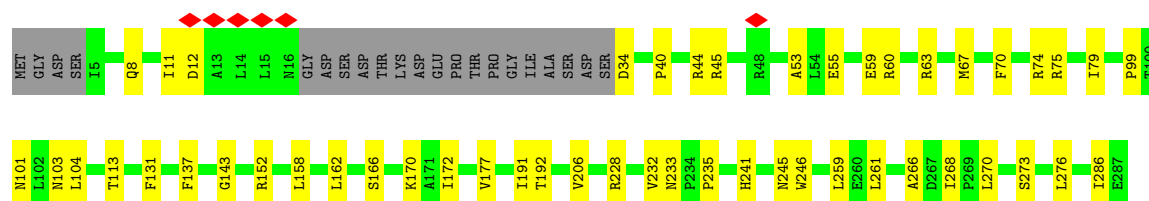
• Molecule 3: Flagellar motor switch protein FlIM



• Molecule 3: Flagellar motor switch protein FlIM



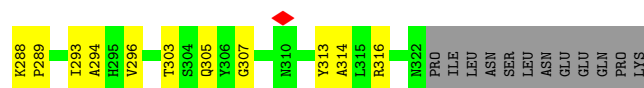
• Molecule 3: Flagellar motor switch protein FlIM





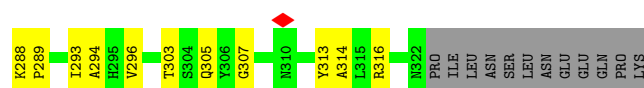
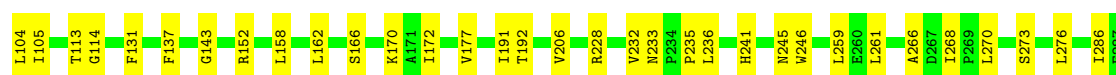
• Molecule 3: Flagellar motor switch protein FlIM

Chain BG: 72% 18% 10%



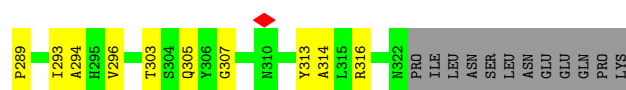
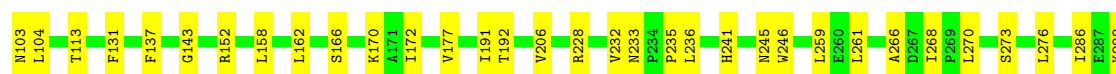
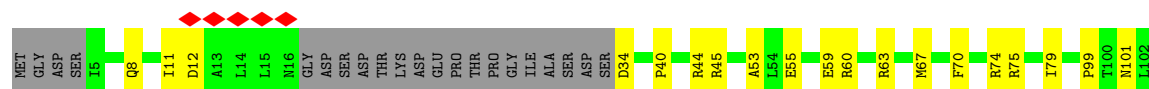
• Molecule 3: Flagellar motor switch protein FlIM

Chain BN: 71% 19% 10%



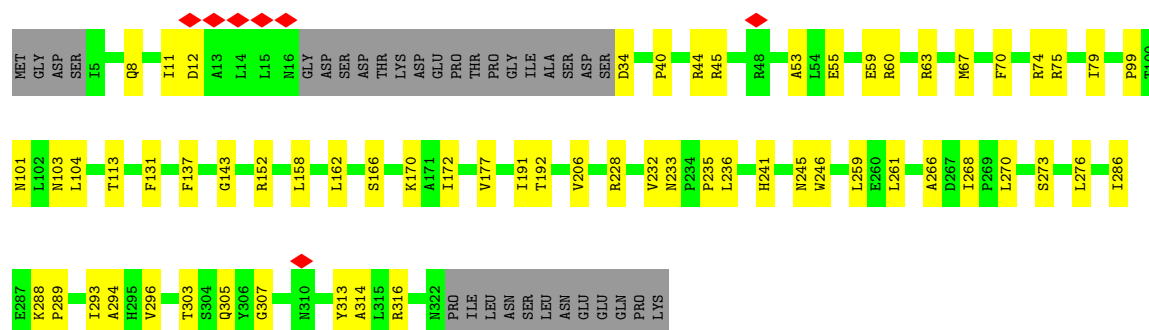
• Molecule 3: Flagellar motor switch protein FlIM

Chain BU: 72% 19% 10%

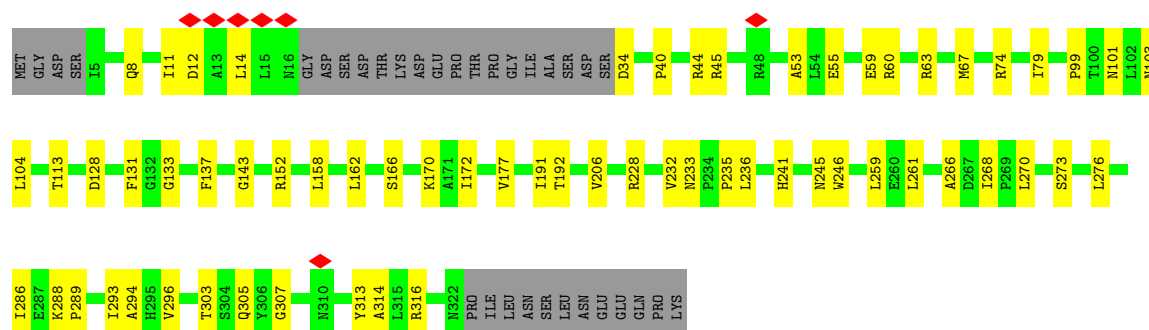


• Molecule 3: Flagellar motor switch protein FlIM

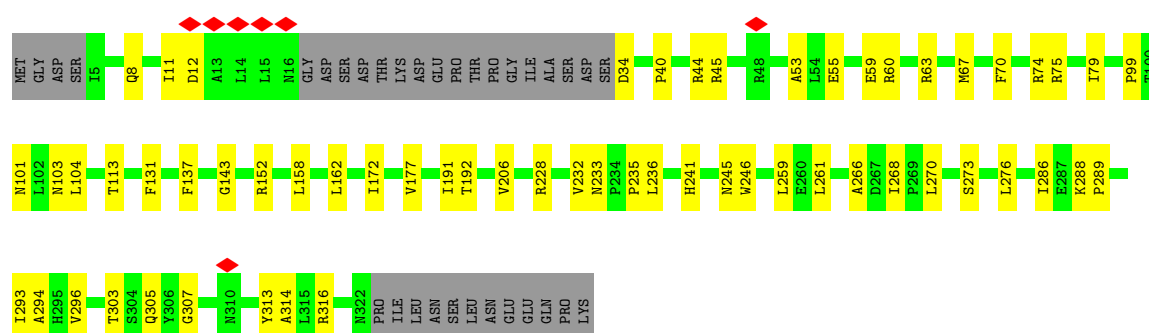
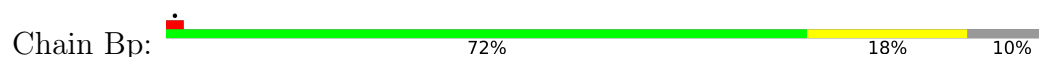
Chain Bb: 72% 19% 10%



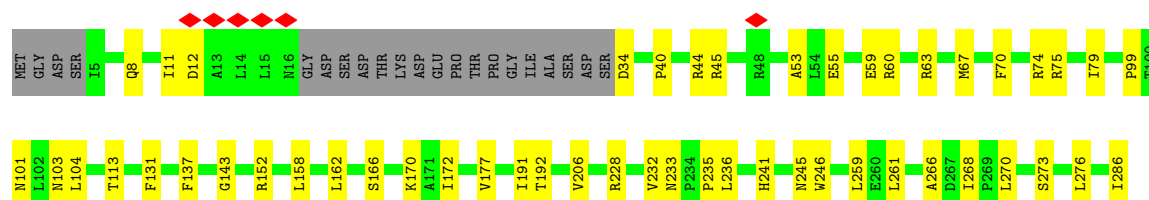
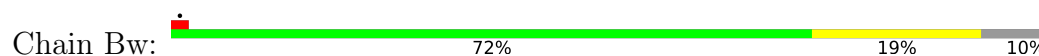
• Molecule 3: Flagellar motor switch protein FlIM

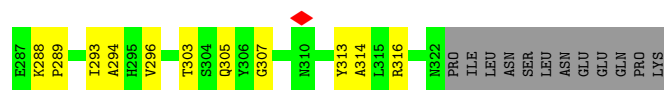


• Molecule 3: Flagellar motor switch protein FlIM

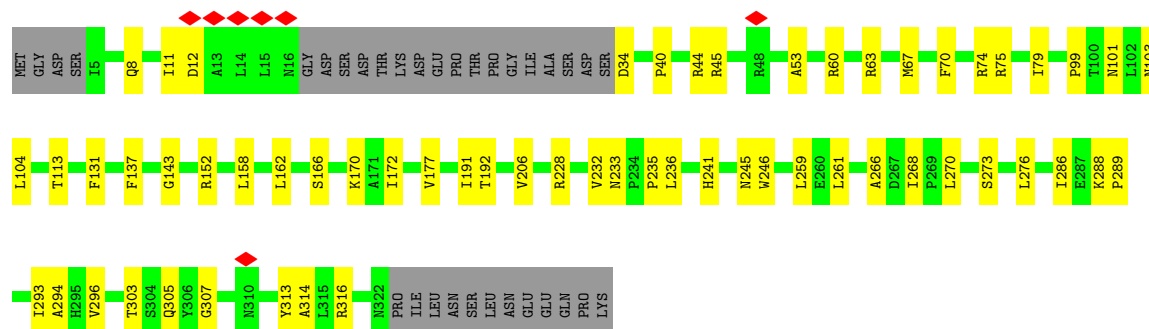
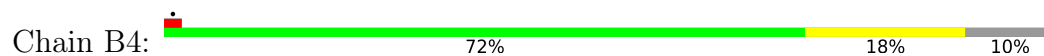


• Molecule 3: Flagellar motor switch protein FlIM

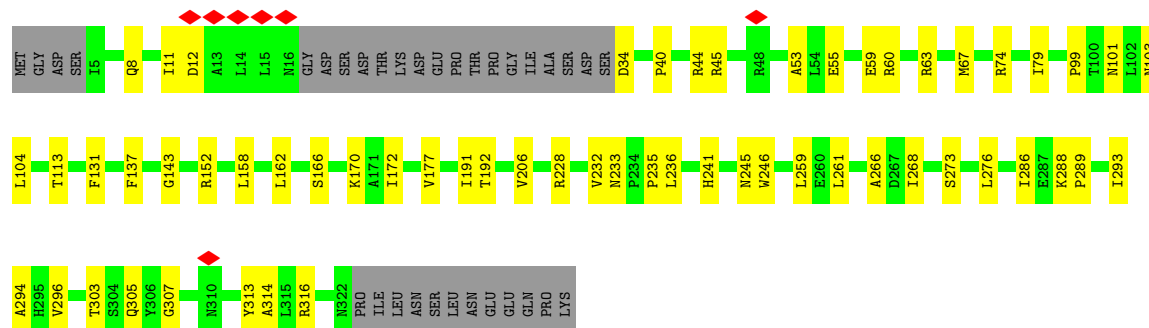
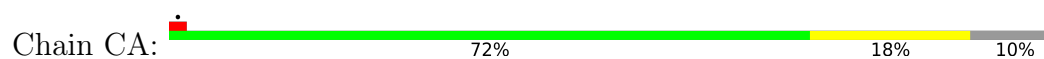




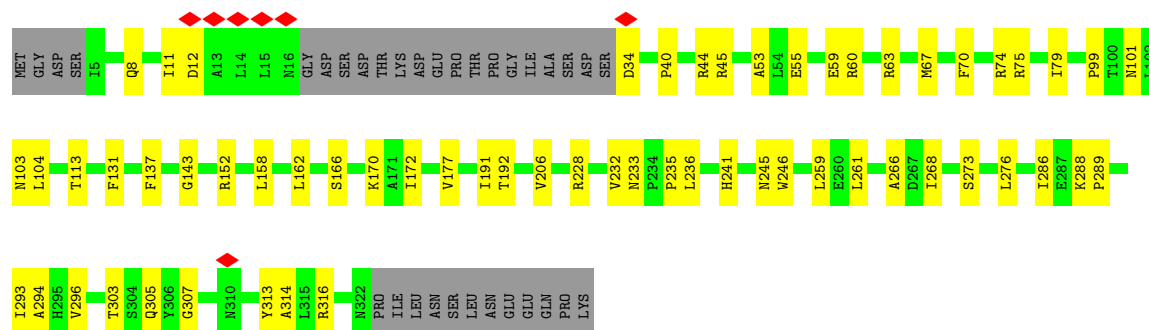
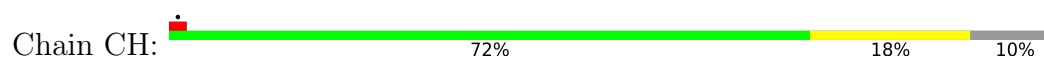
• Molecule 3: Flagellar motor switch protein FlIM



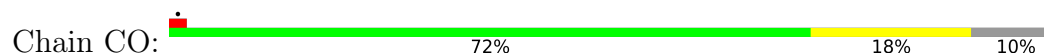
• Molecule 3: Flagellar motor switch protein FlIM

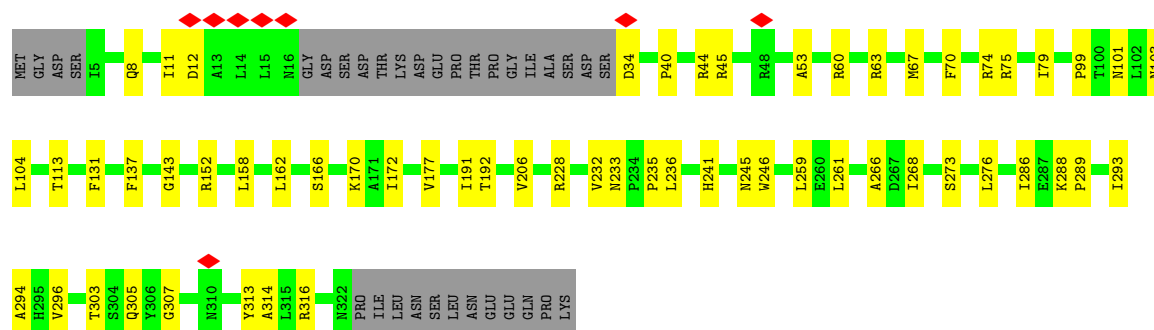


• Molecule 3: Flagellar motor switch protein FlIM

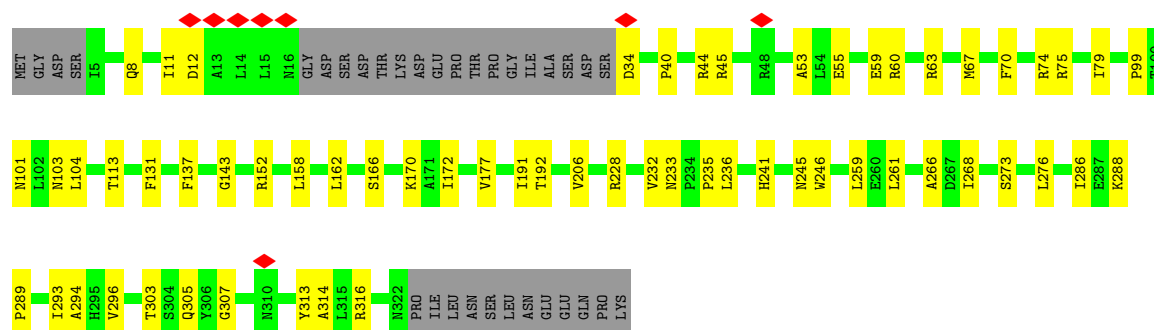
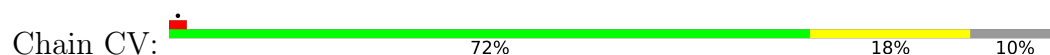


• Molecule 3: Flagellar motor switch protein FlIM





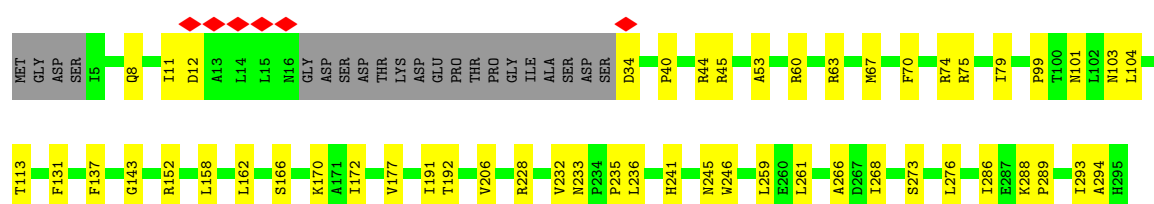
• Molecule 3: Flagellar motor switch protein FlIM



• Molecule 3: Flagellar motor switch protein FlIM

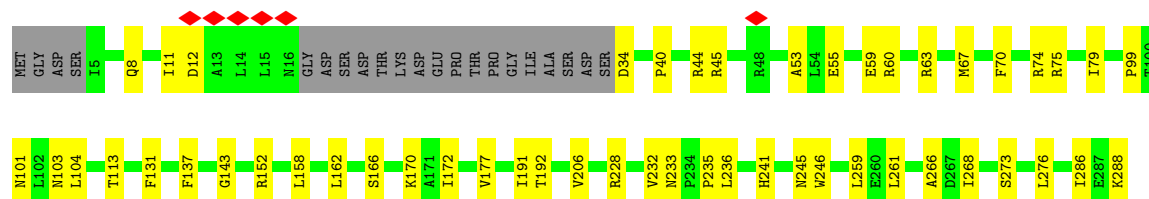
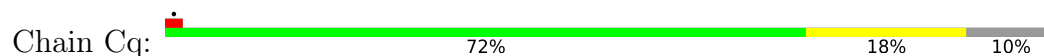


• Molecule 3: Flagellar motor switch protein FlIM

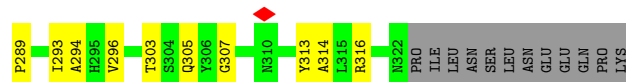
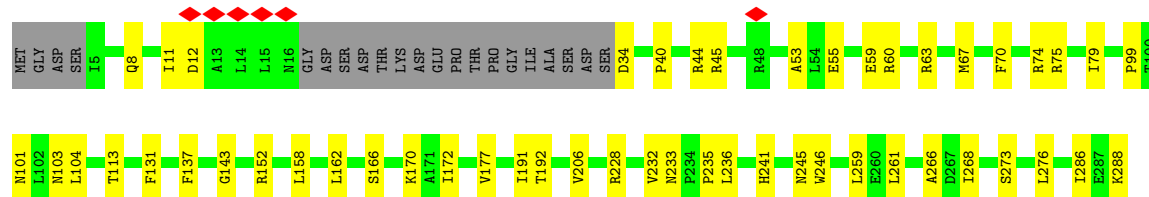
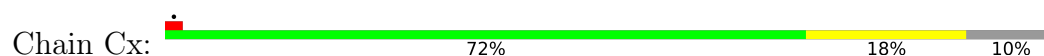




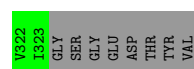
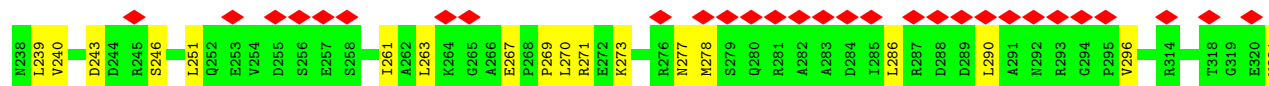
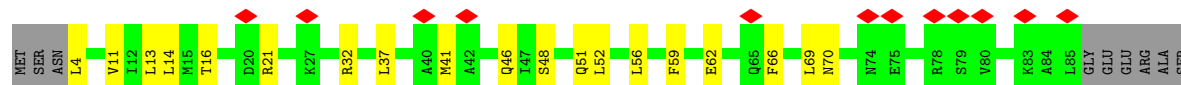
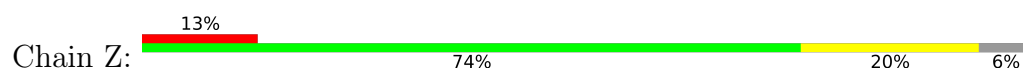
• Molecule 3: Flagellar motor switch protein FlIM



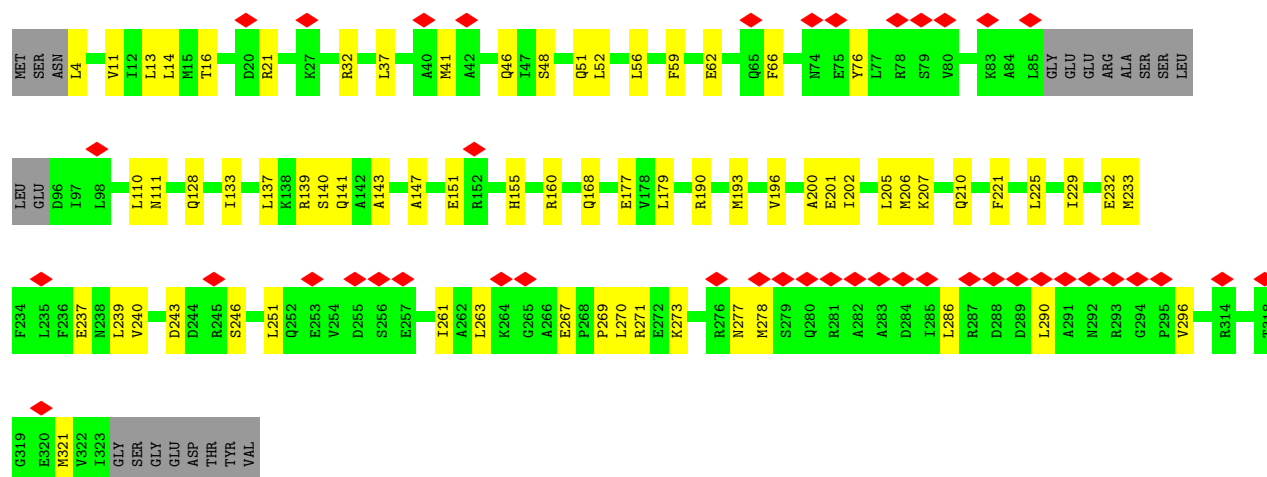
• Molecule 3: Flagellar motor switch protein FlIM



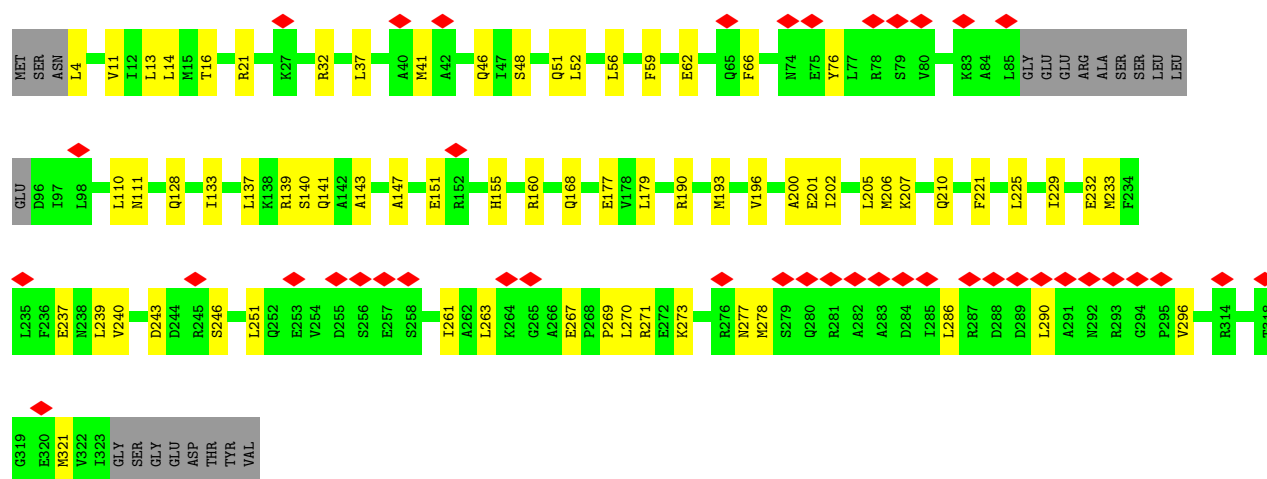
• Molecule 4: Flagellar motor switch protein FlIG



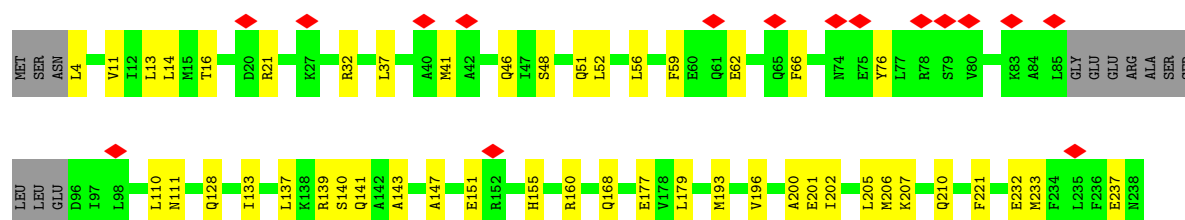
Chain a:

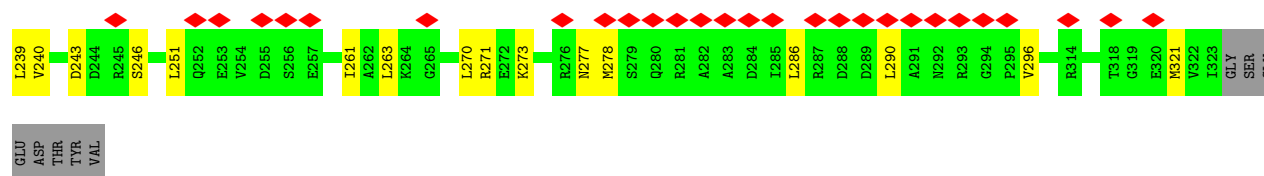


Chain b:

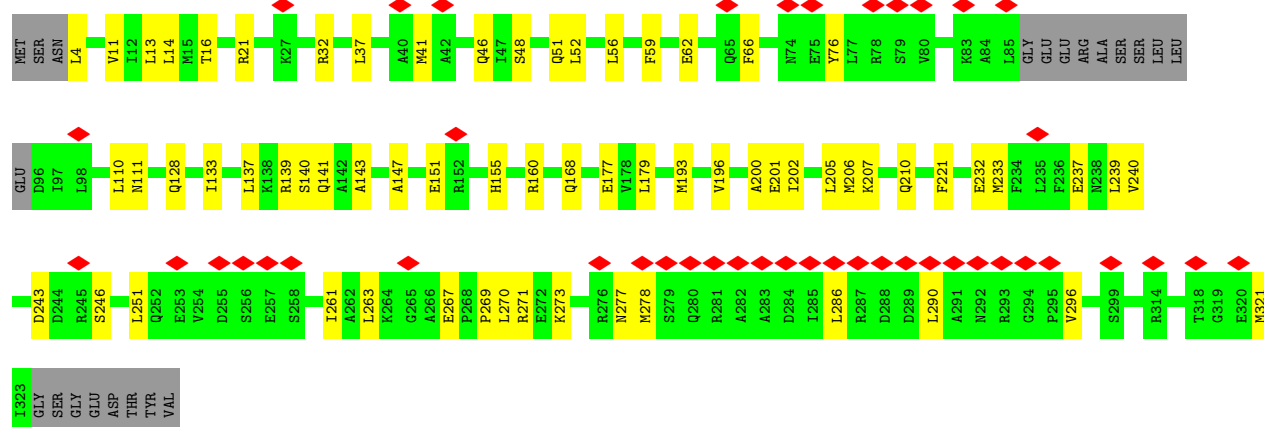
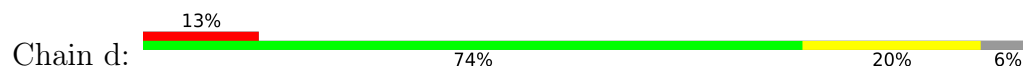


Chain c:

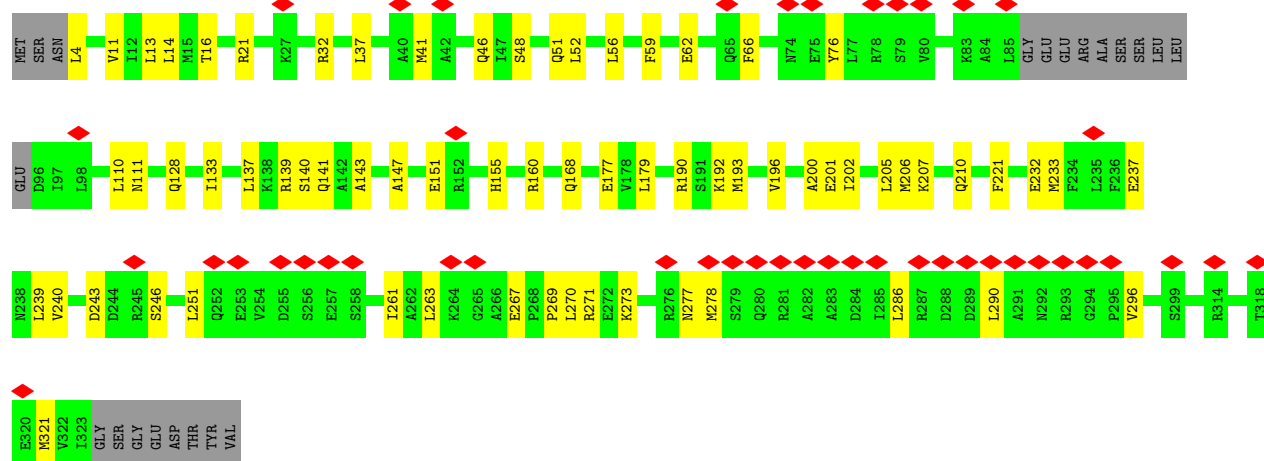
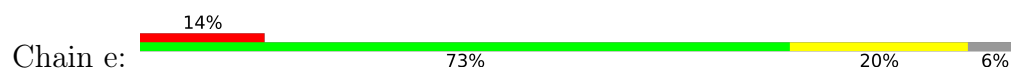




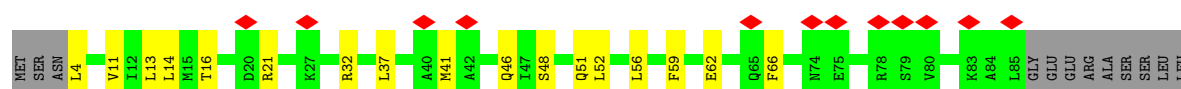
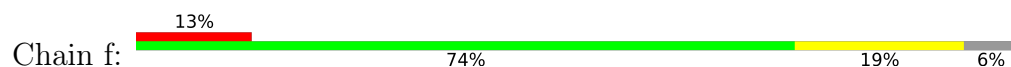
• Molecule 4: Flagellar motor switch protein Flig

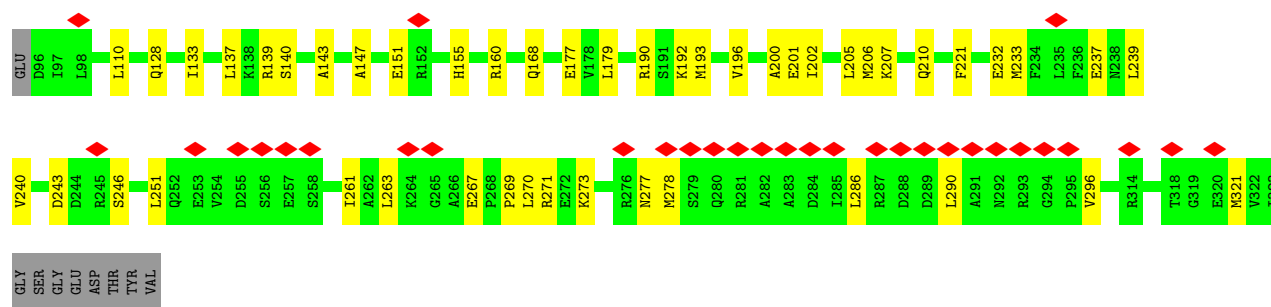


• Molecule 4: Flagellar motor switch protein Flig

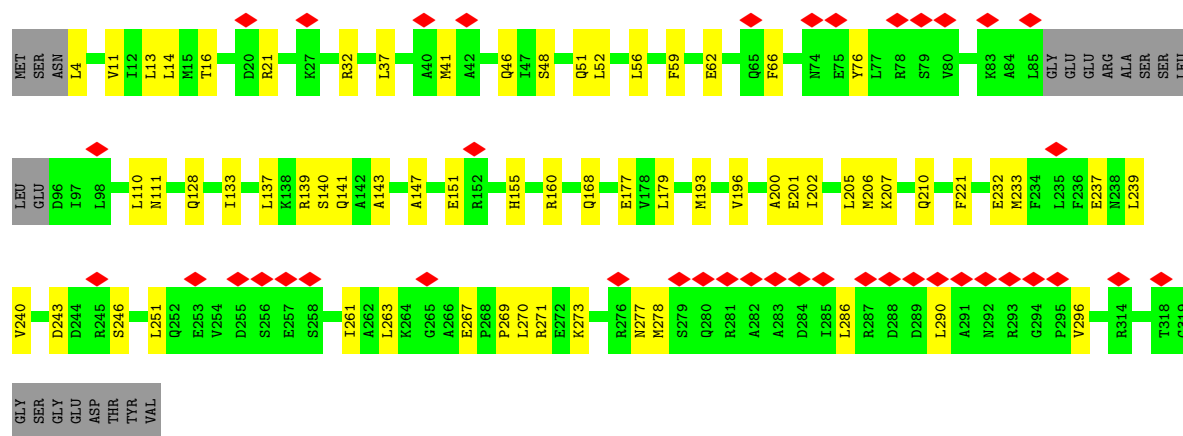
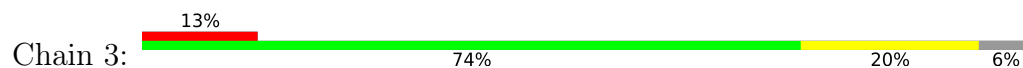


• Molecule 4: Flagellar motor switch protein Flig

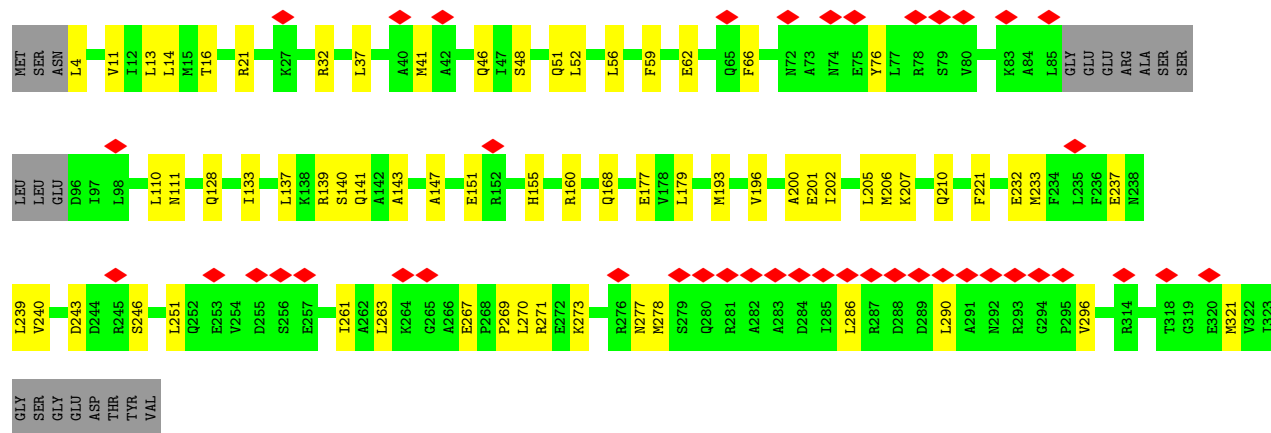
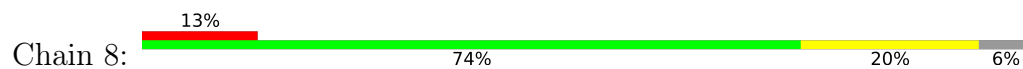




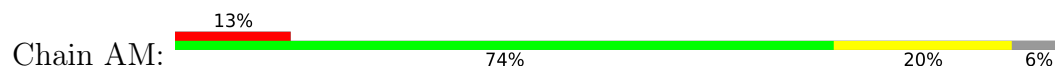
• Molecule 4: Flagellar motor switch protein FlgG

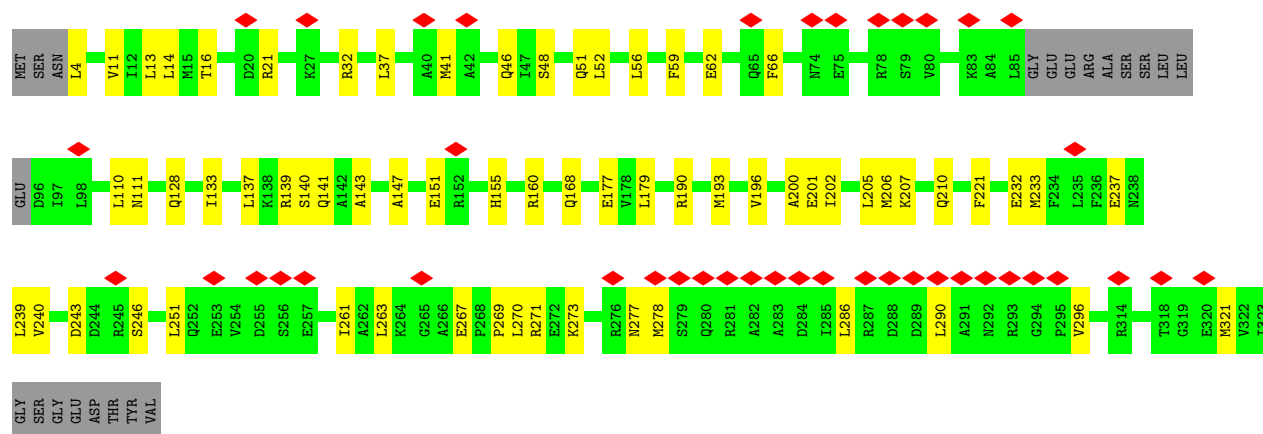


• Molecule 4: Flagellar motor switch protein FlgG

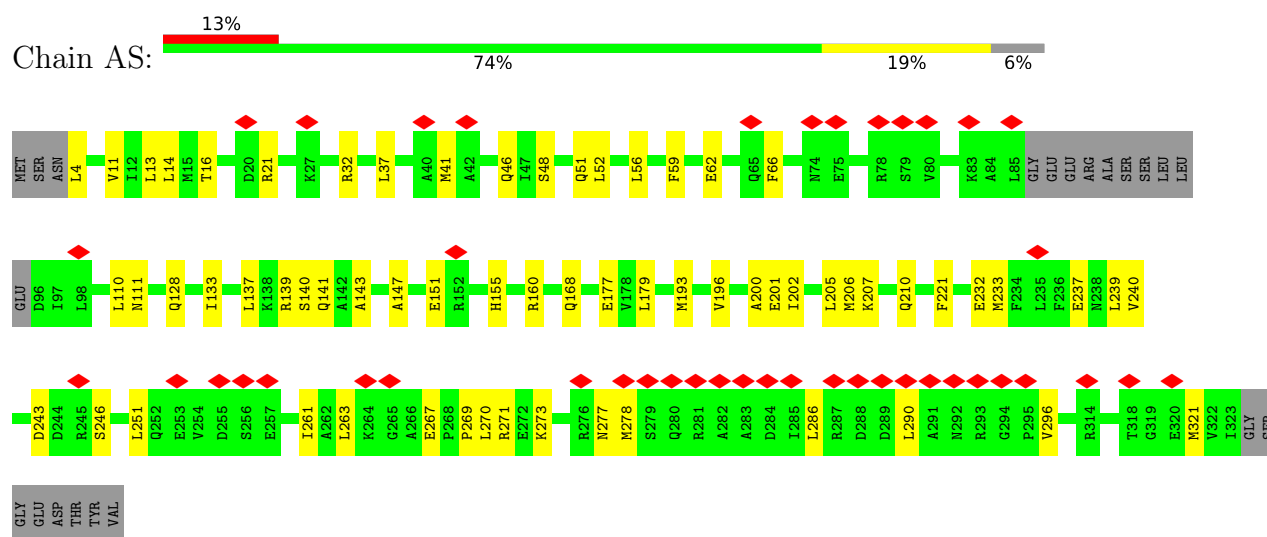


• Molecule 4: Flagellar motor switch protein FlgG

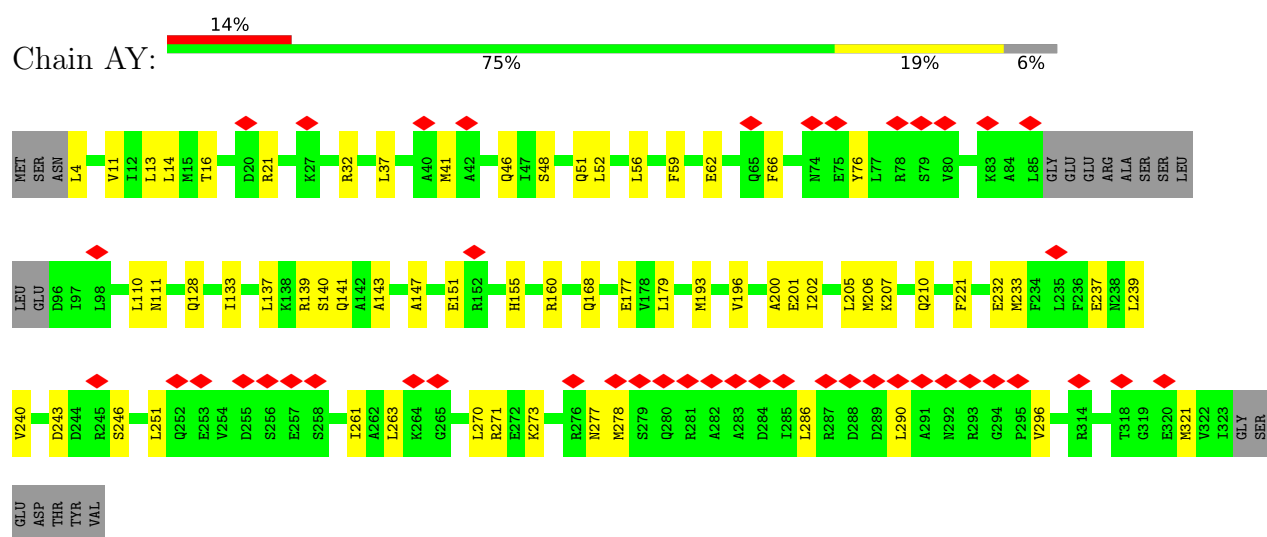




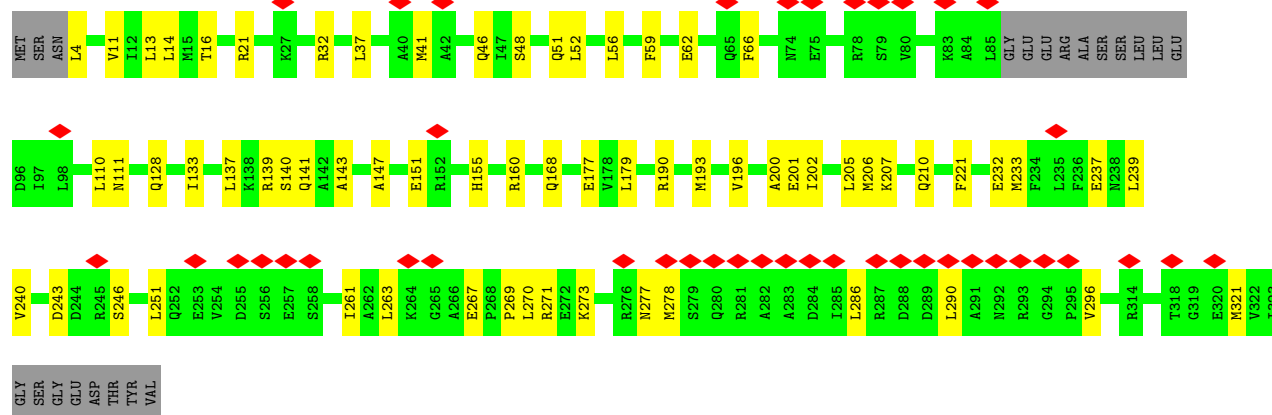
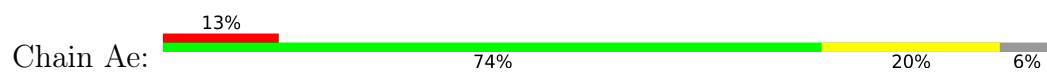
• Molecule 4: Flagellar motor switch protein Flig



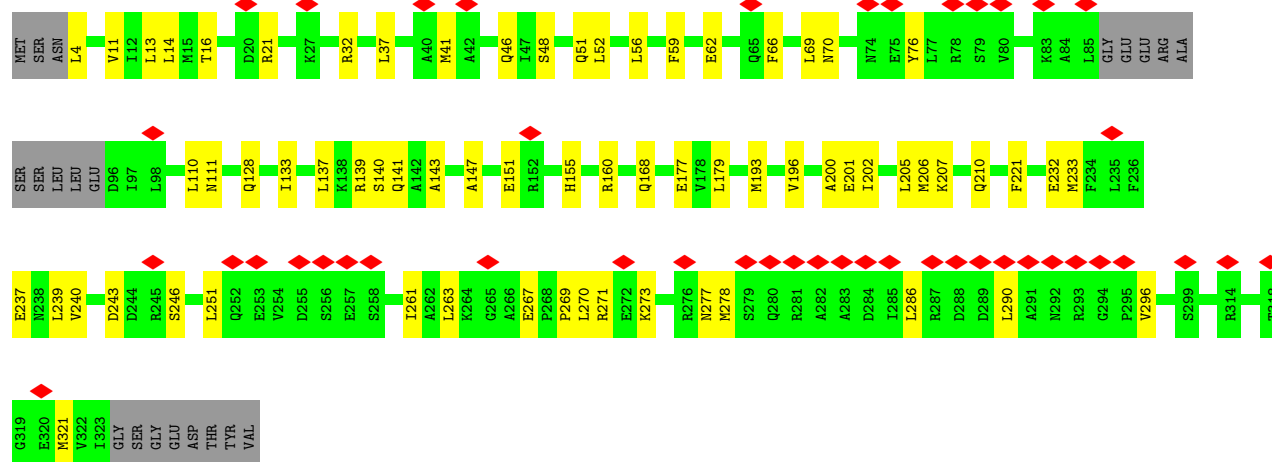
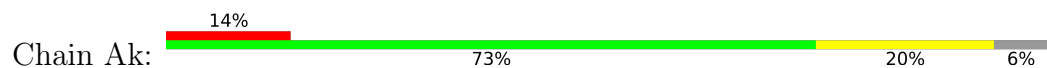
• Molecule 4: Flagellar motor switch protein Flig



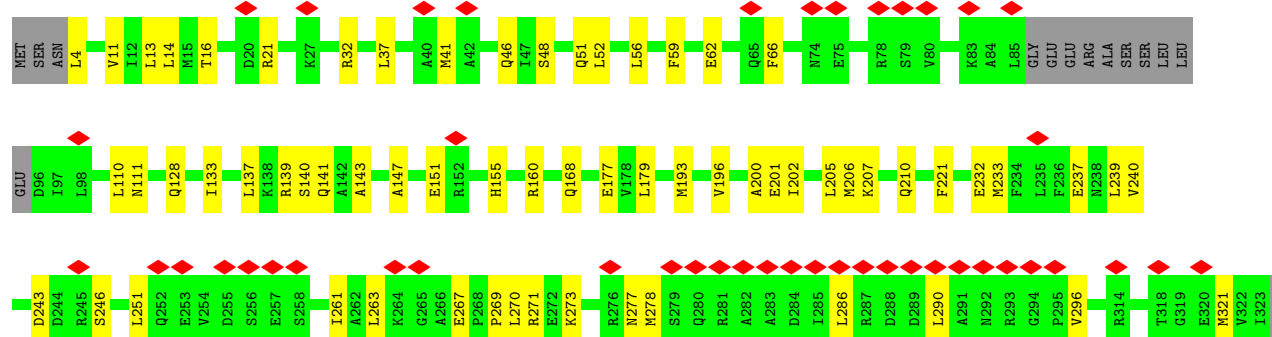
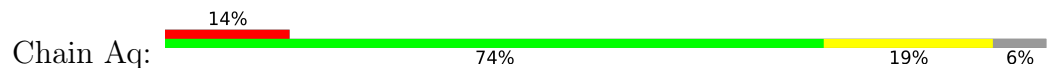
• Molecule 4: Flagellar motor switch protein Flig



• Molecule 4: Flagellar motor switch protein FlIG



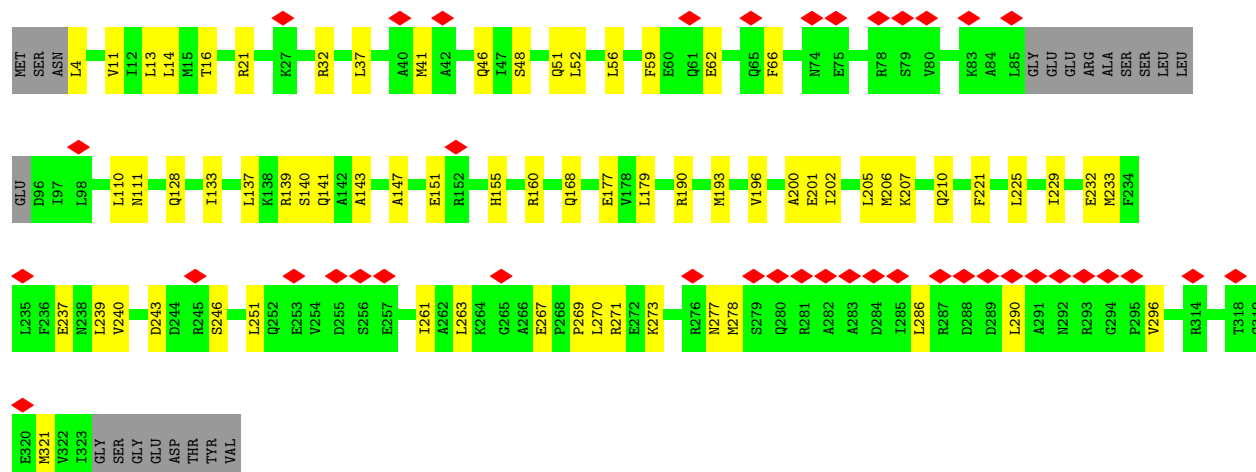
• Molecule 4: Flagellar motor switch protein FlIG



SER
GLY
GLU
ASP
THR
TYR
VAL

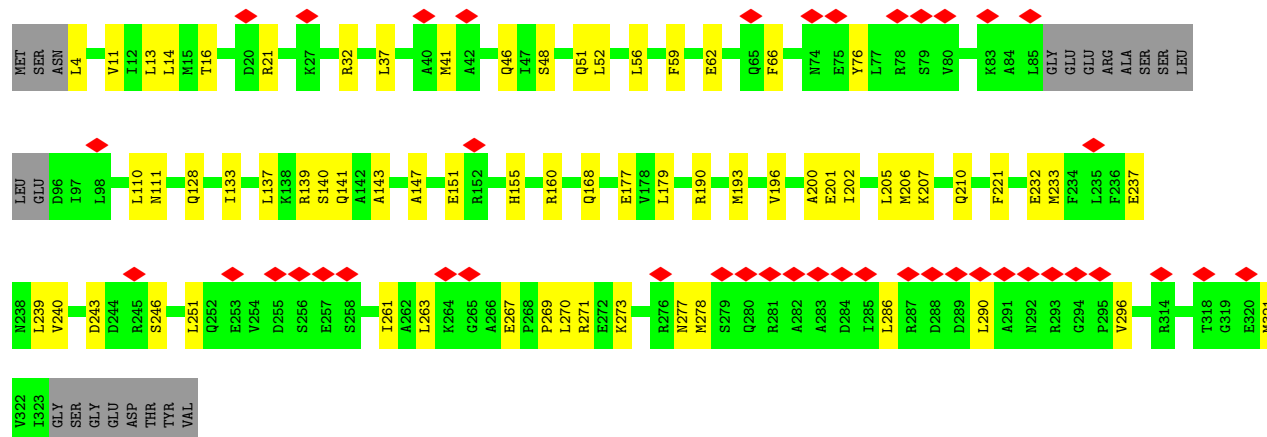
• Molecule 4: Flagellar motor switch protein FlIG

Chain Aw: 12% 73% 20% 6%



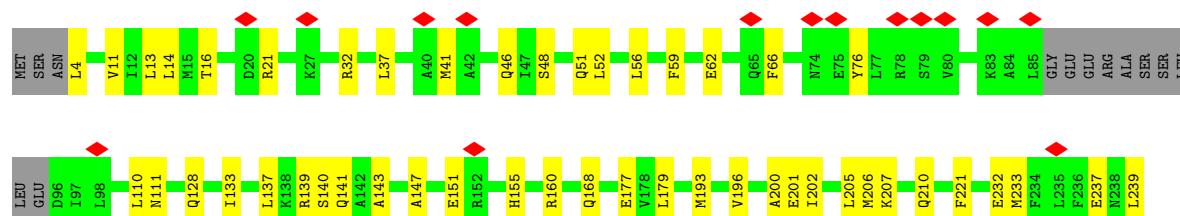
• Molecule 4: Flagellar motor switch protein FlIG

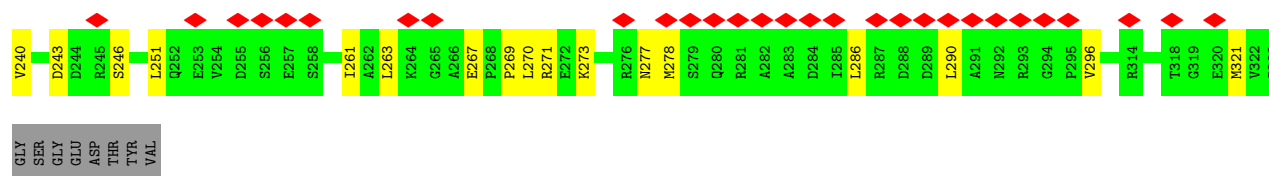
Chain A4: 13% 74% 20% 6%



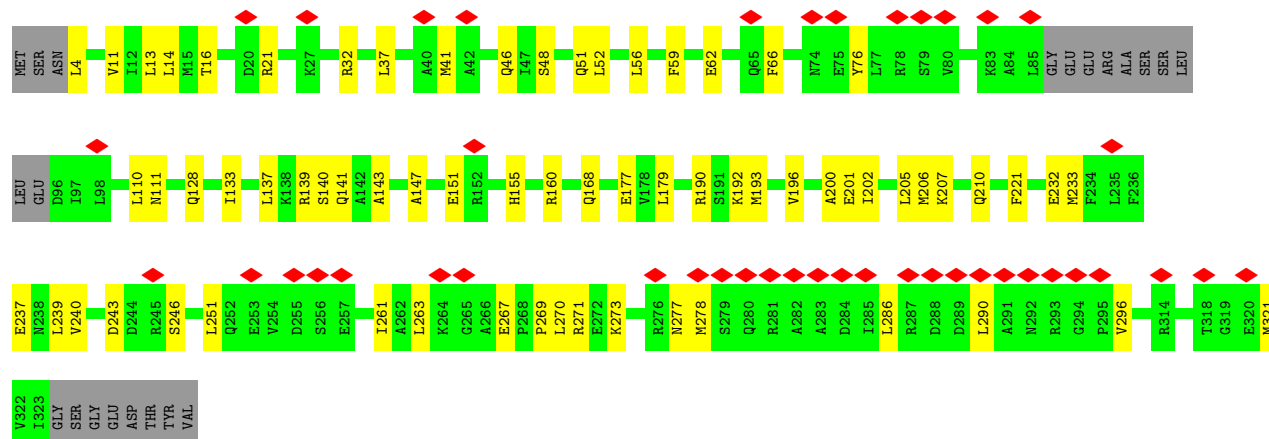
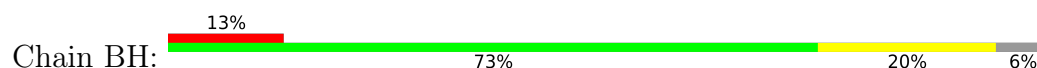
• Molecule 4: Flagellar motor switch protein FlIG

Chain BA: 13% 74% 20% 6%

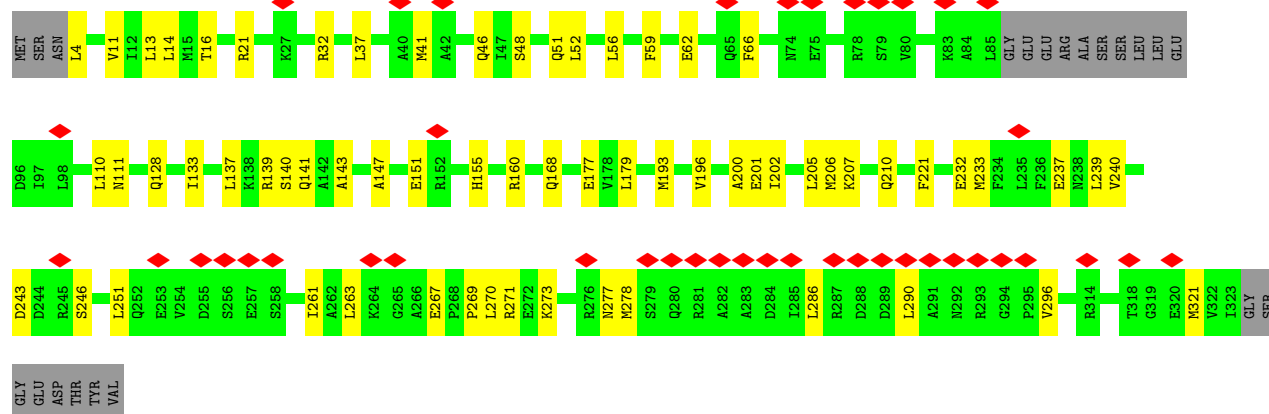
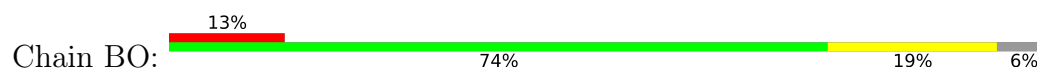




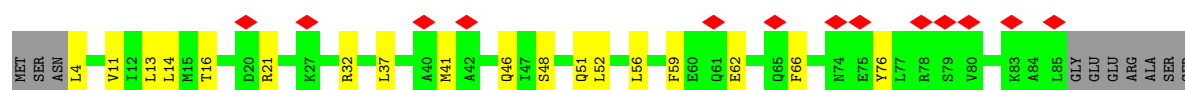
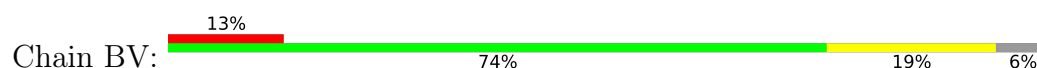
• Molecule 4: Flagellar motor switch protein FlgG

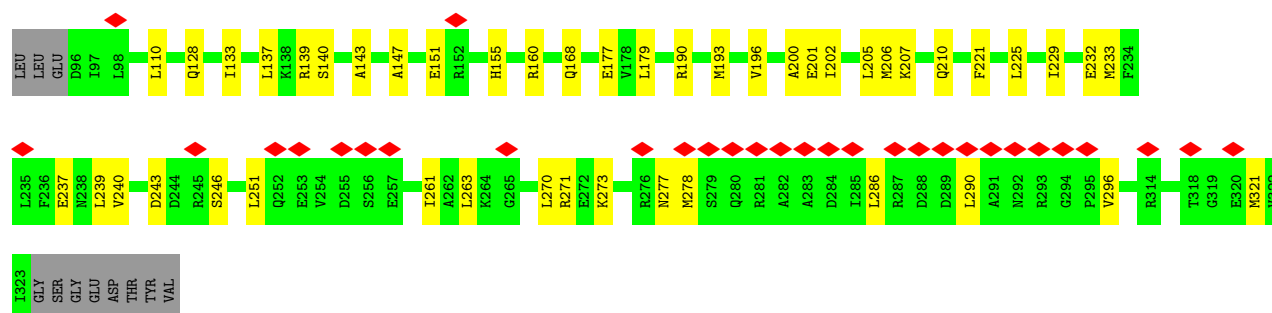


• Molecule 4: Flagellar motor switch protein FlgG

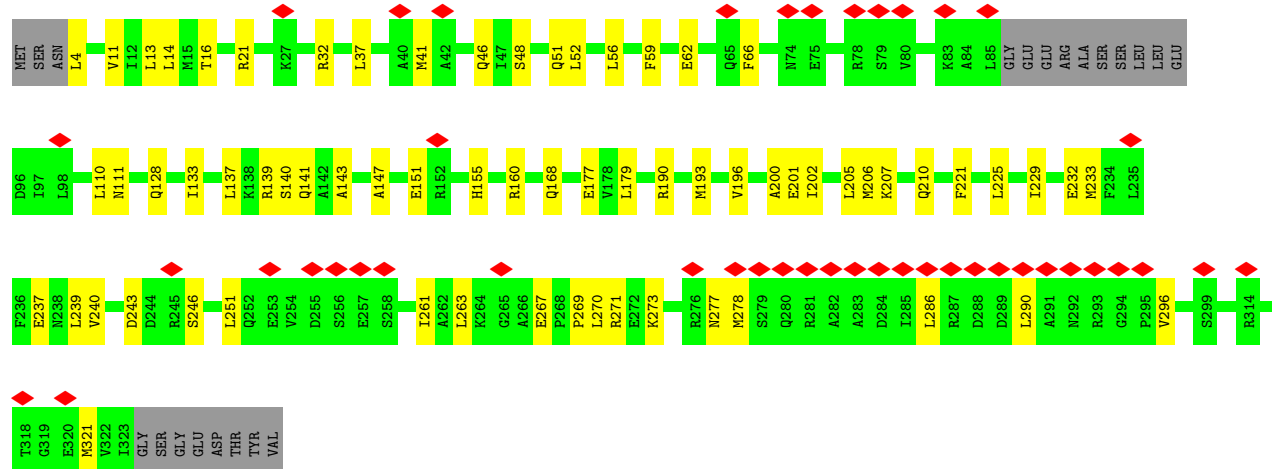
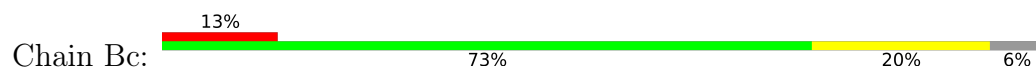


• Molecule 4: Flagellar motor switch protein FlgG

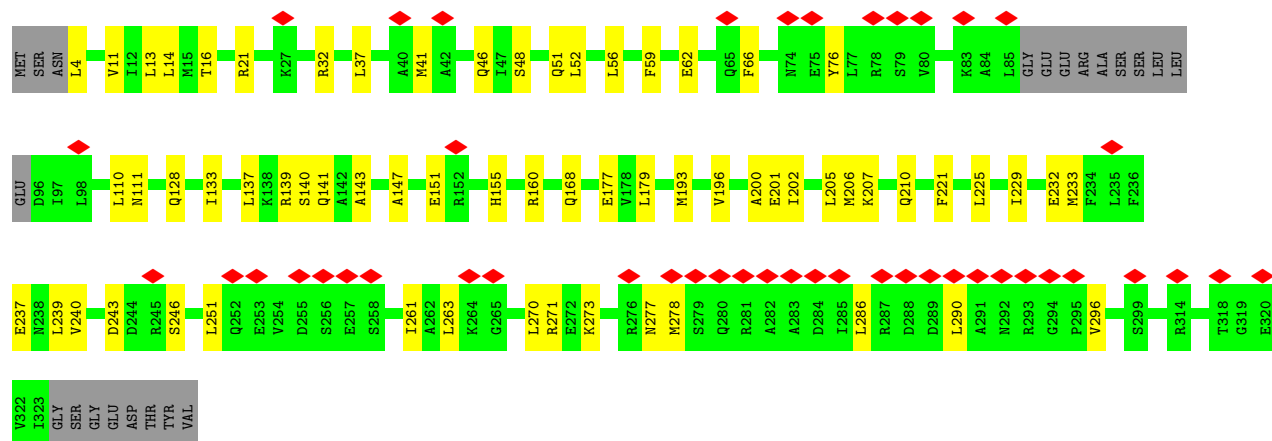
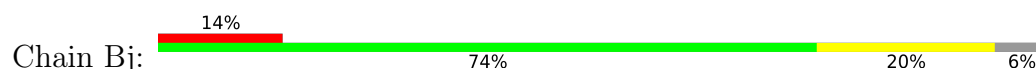




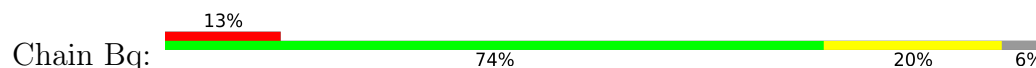
• Molecule 4: Flagellar motor switch protein FlIG

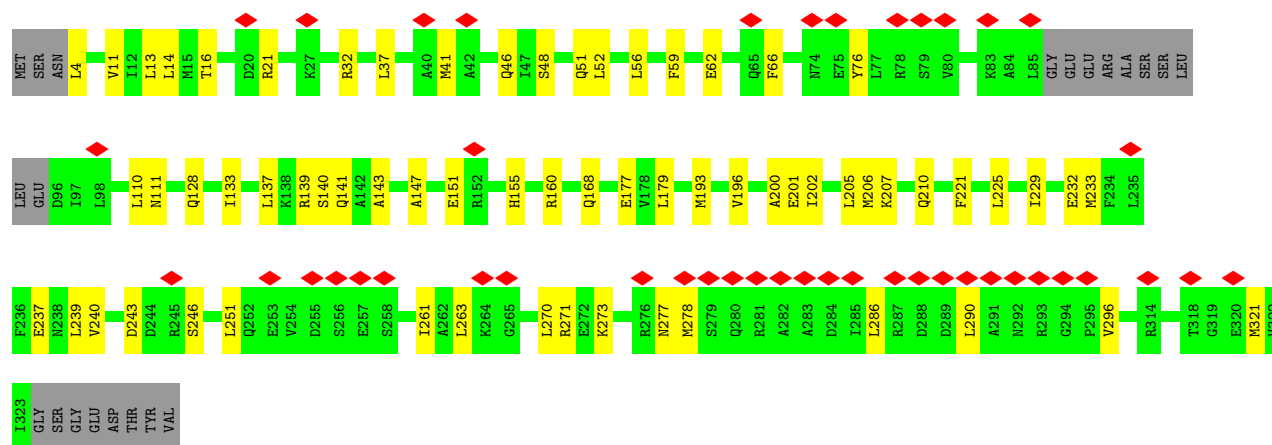


• Molecule 4: Flagellar motor switch protein FlIG

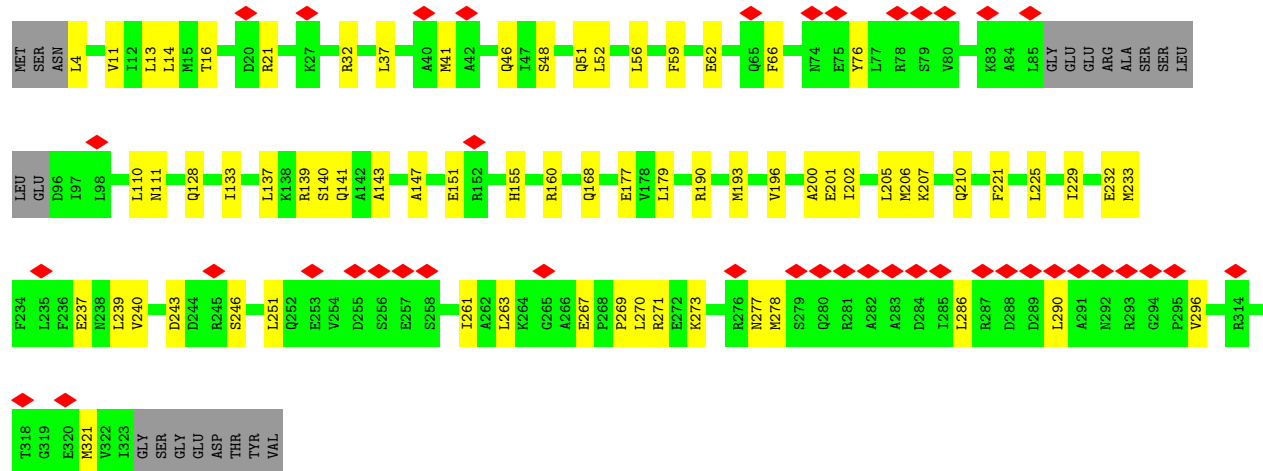
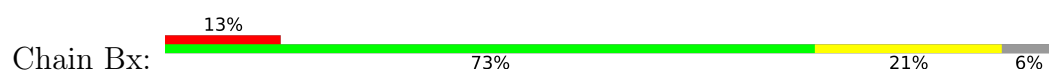


• Molecule 4: Flagellar motor switch protein FlIG

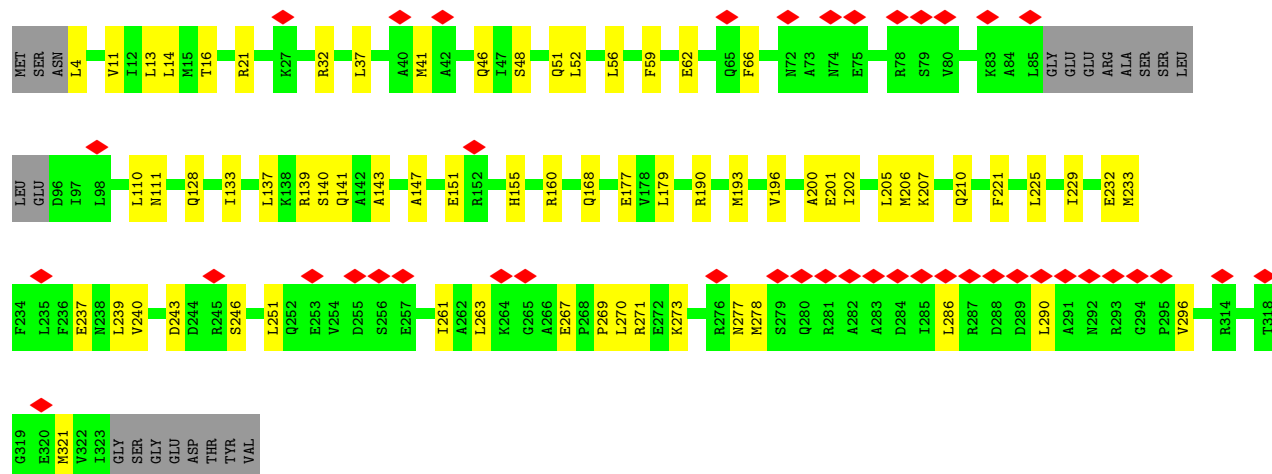
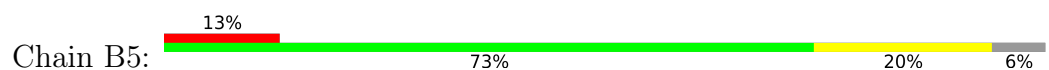




• Molecule 4: Flagellar motor switch protein FliG

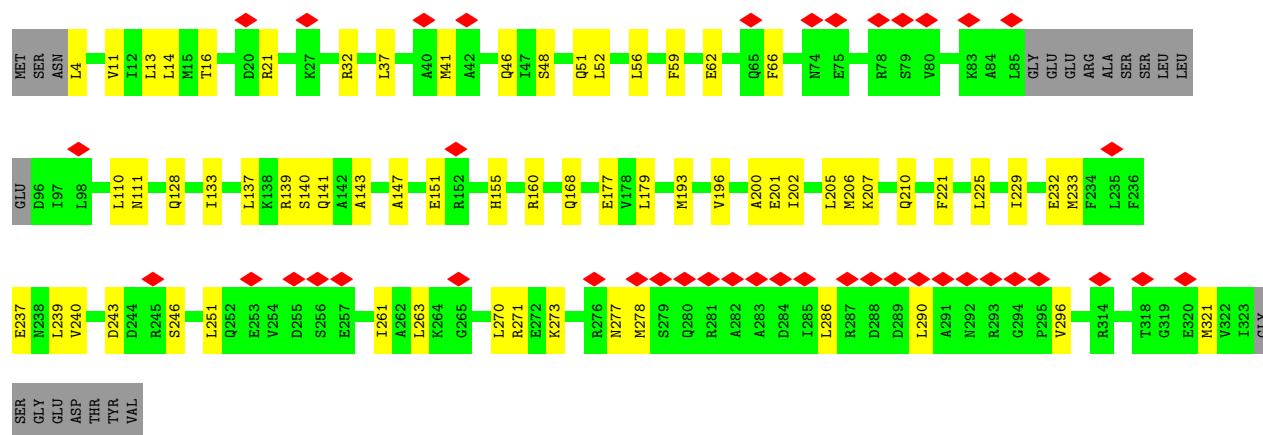


• Molecule 4: Flagellar motor switch protein FliG



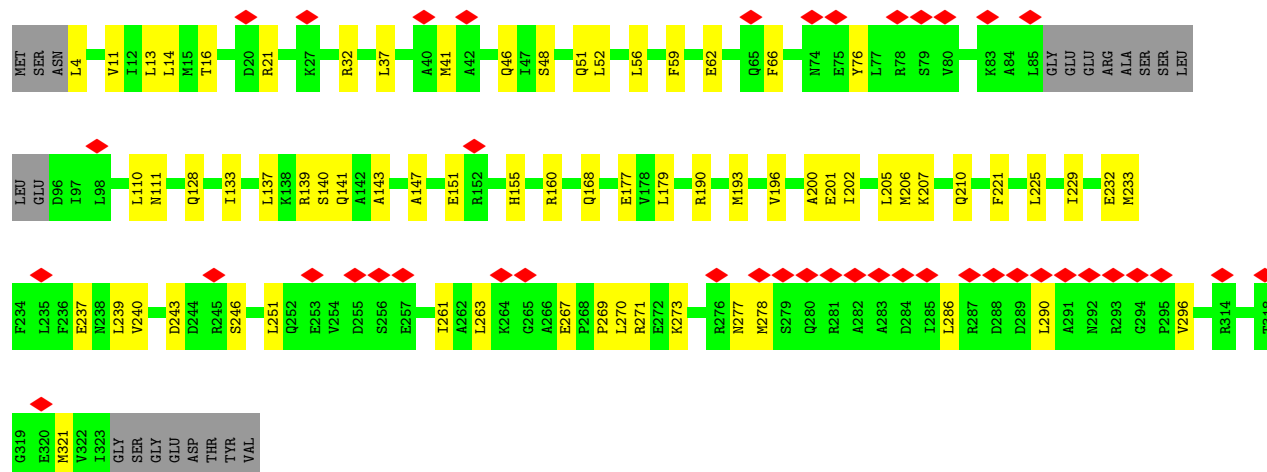
- Molecule 4: Flagellar motor switch protein FlhG

Chain CB: 



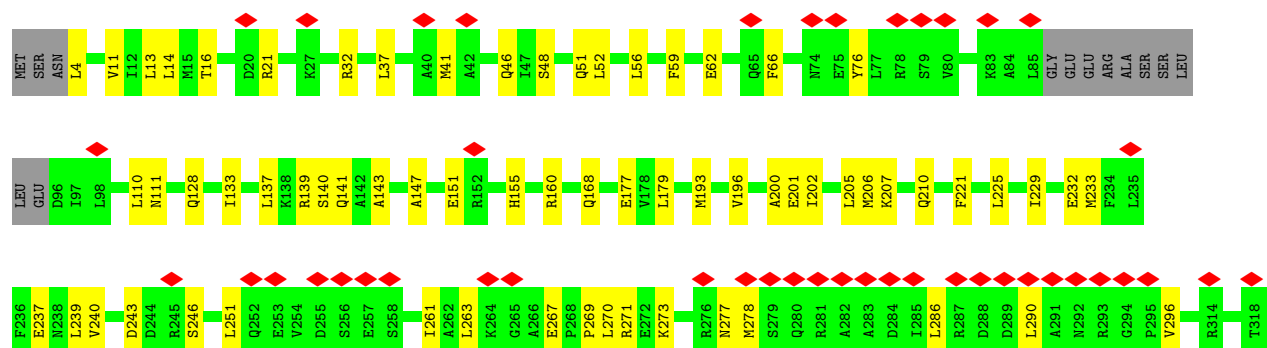
- Molecule 4: Flagellar motor switch protein FlhG

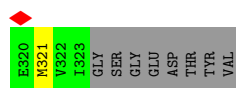
Chain CI: 



- Molecule 4: Flagellar motor switch protein FlhG

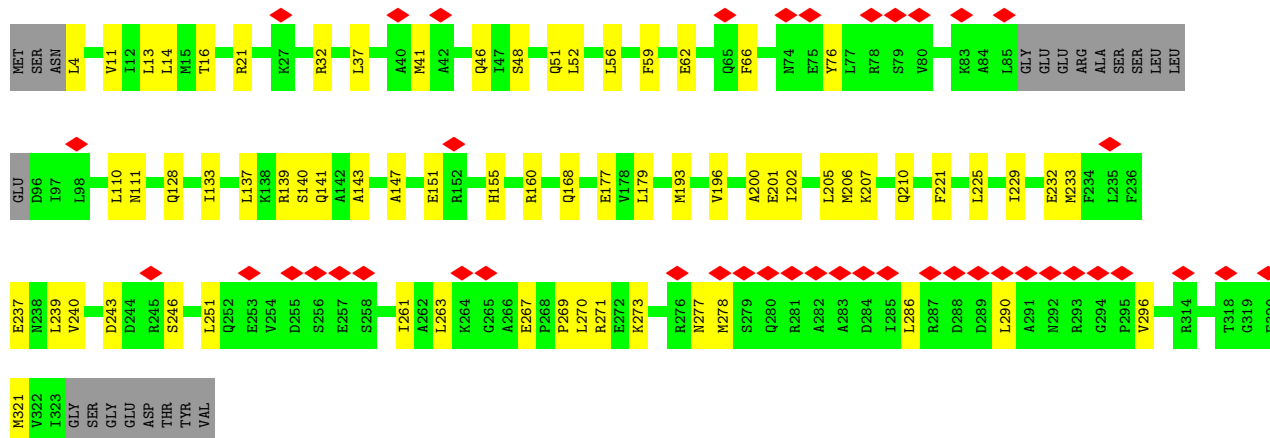
Chain CP: 





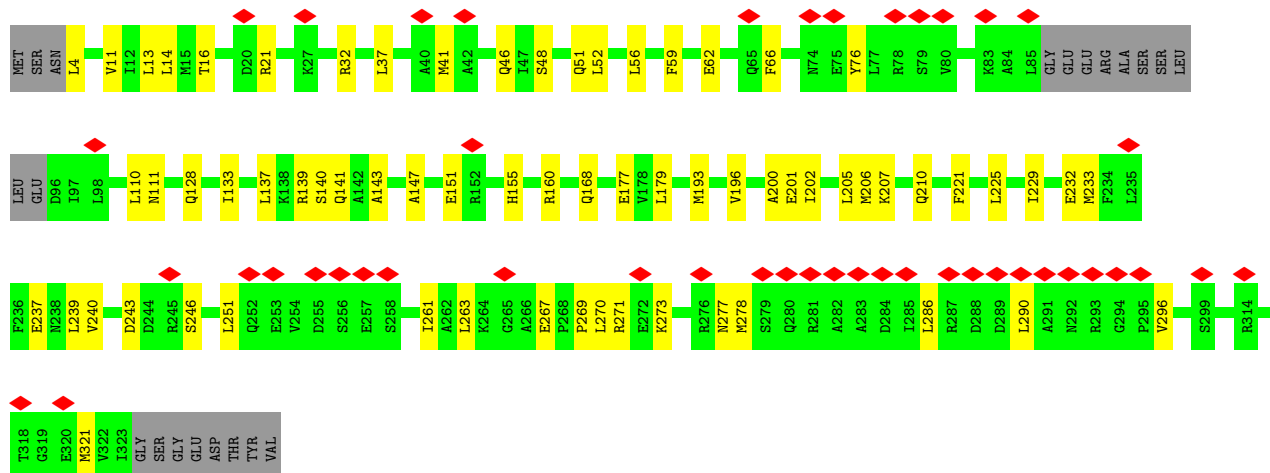
• Molecule 4: Flagellar motor switch protein FliG

Chain CW: 13% 73% 20% 6%



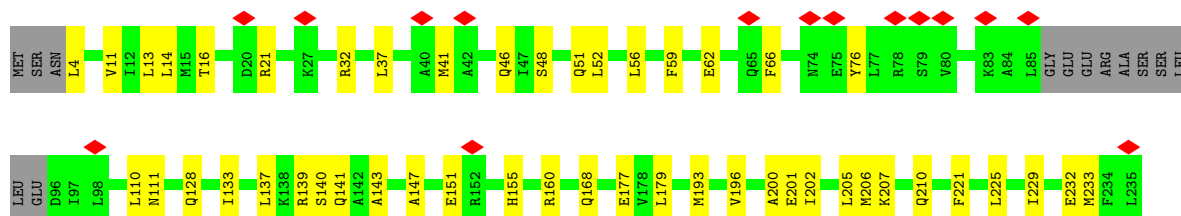
• Molecule 4: Flagellar motor switch protein FliG

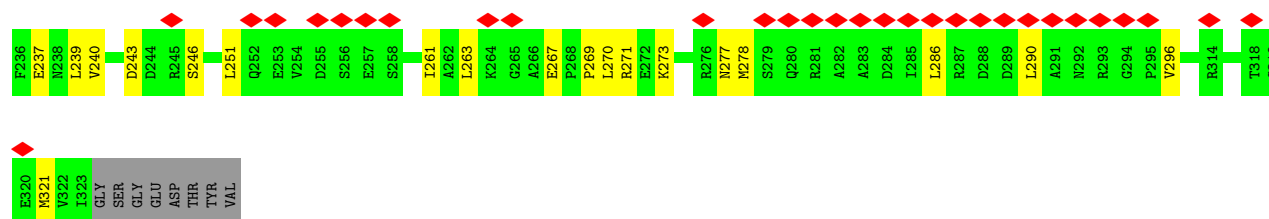
Chain Cd: 14% 73% 20% 6%



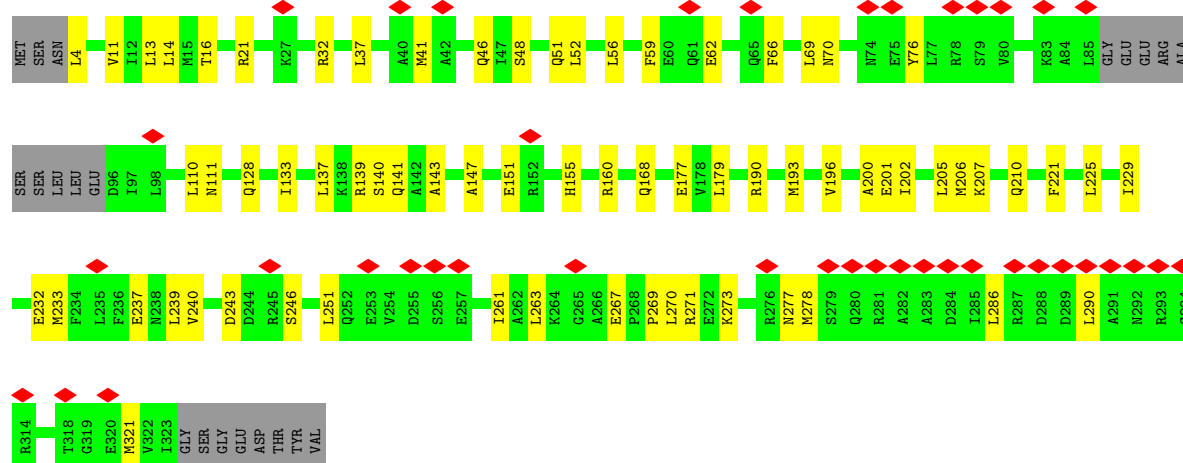
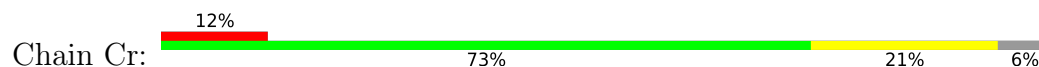
• Molecule 4: Flagellar motor switch protein FliG

Chain Ck: 14% 73% 20% 6%

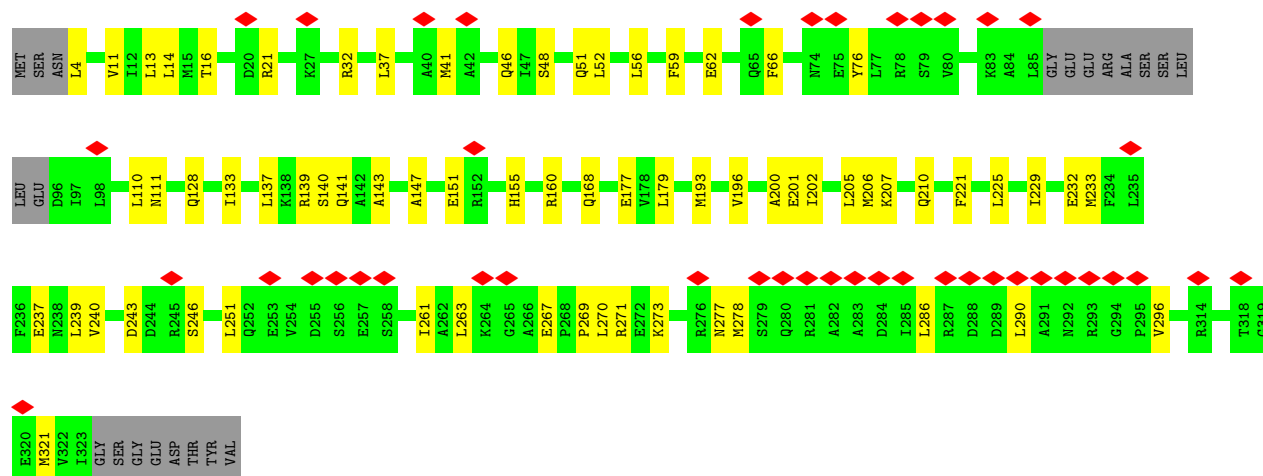
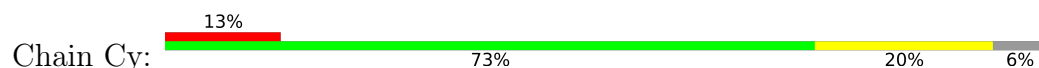




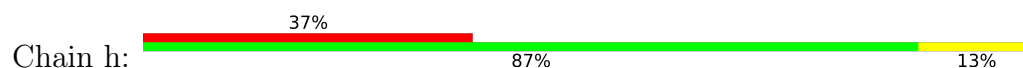
• Molecule 4: Flagellar motor switch protein FliG

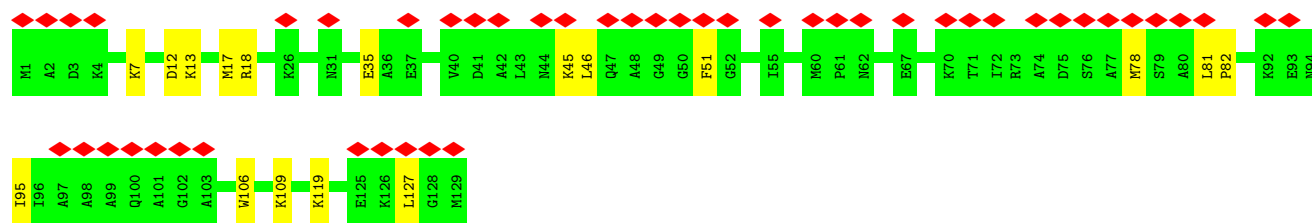


• Molecule 4: Flagellar motor switch protein FliG

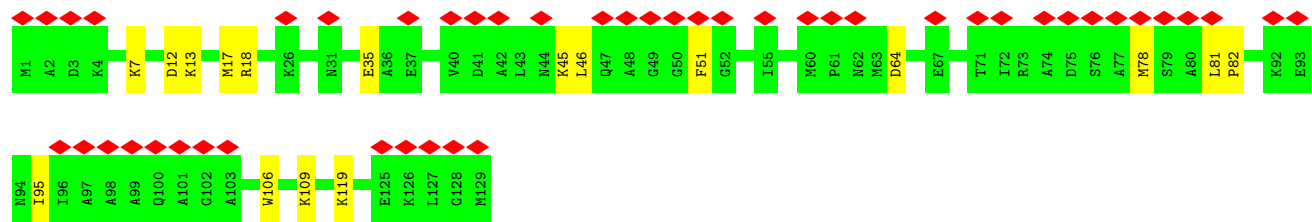
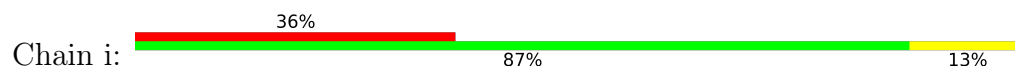


• Molecule 5: Chemotaxis protein CheY

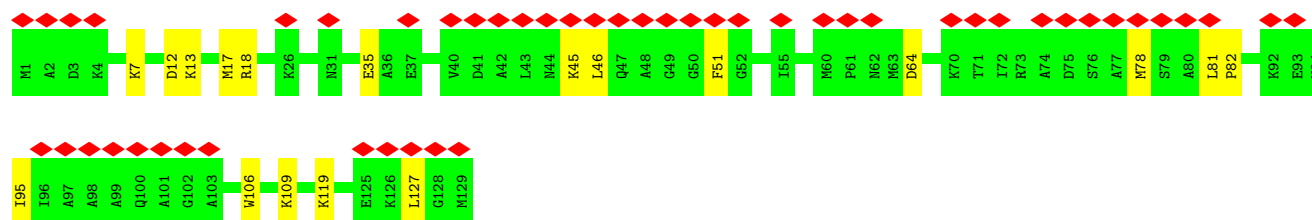
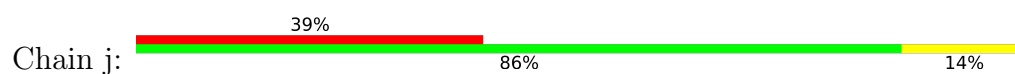




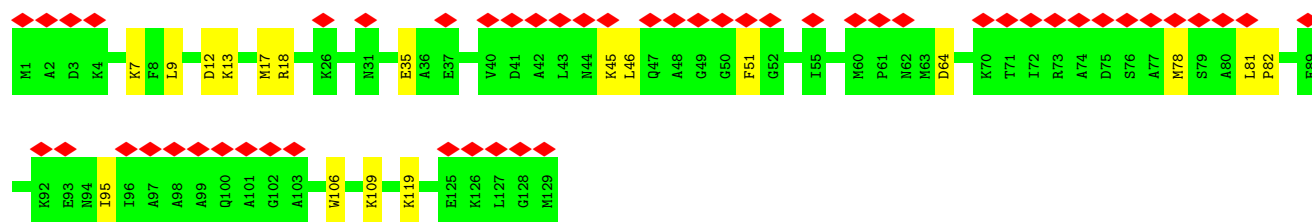
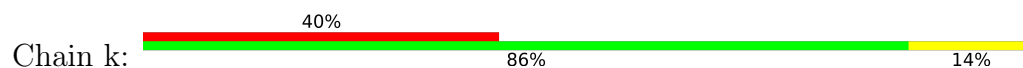
- Molecule 5: Chemotaxis protein CheY



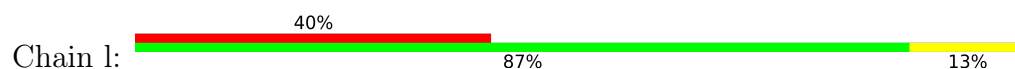
- Molecule 5: Chemotaxis protein CheY

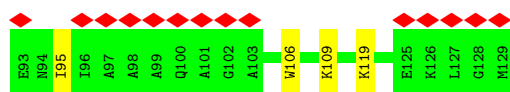


- Molecule 5: Chemotaxis protein CheY

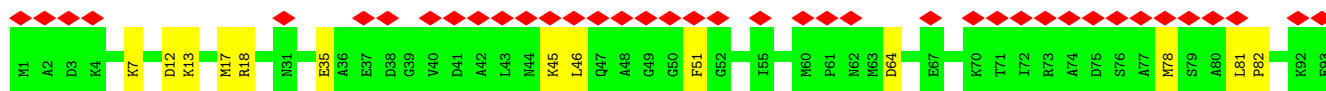
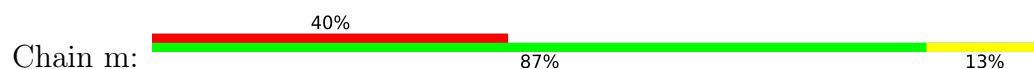


- Molecule 5: Chemotaxis protein CheY

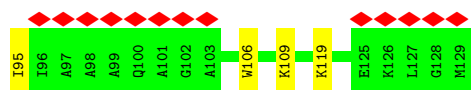
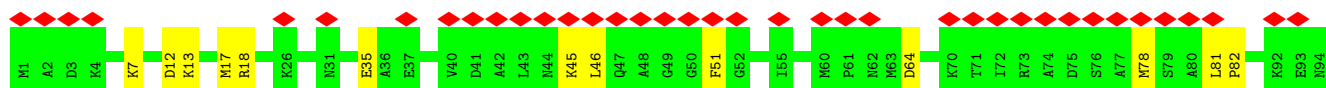
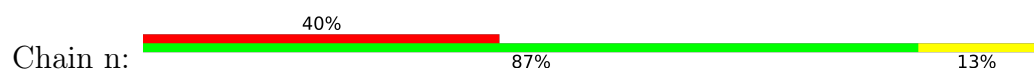




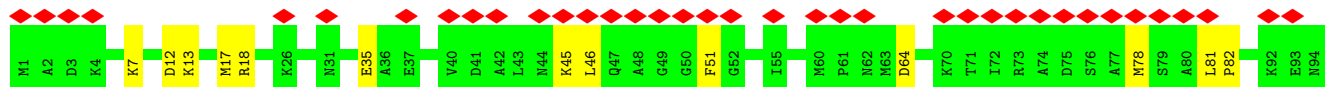
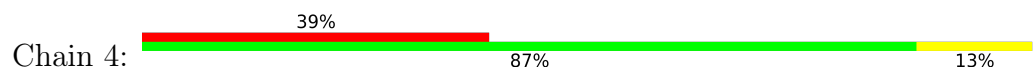
• Molecule 5: Chemotaxis protein CheY



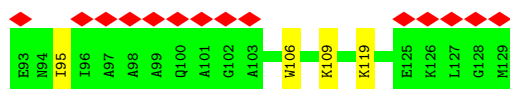
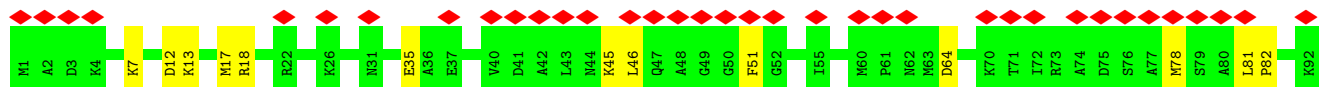
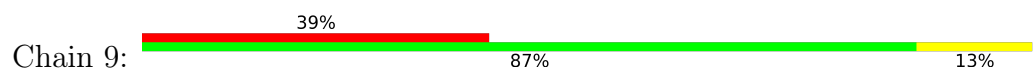
• Molecule 5: Chemotaxis protein CheY



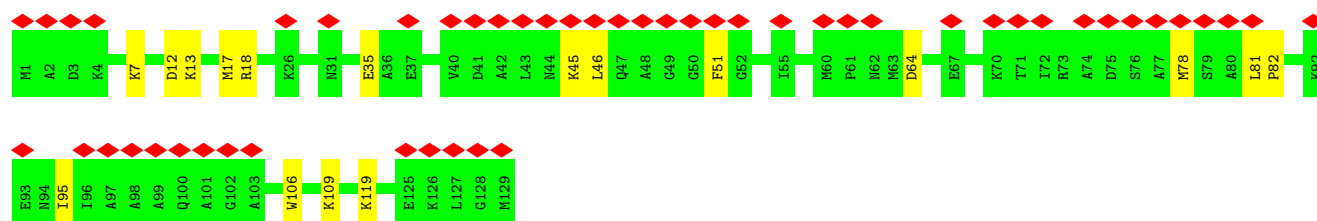
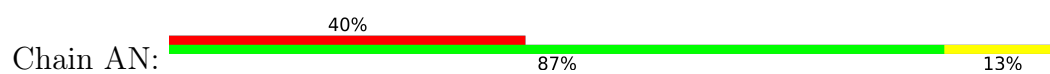
• Molecule 5: Chemotaxis protein CheY



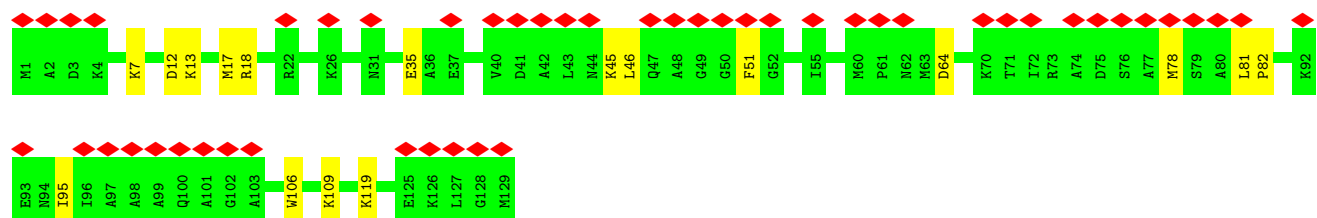
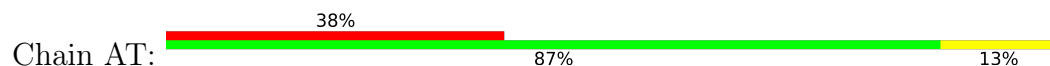
• Molecule 5: Chemotaxis protein CheY



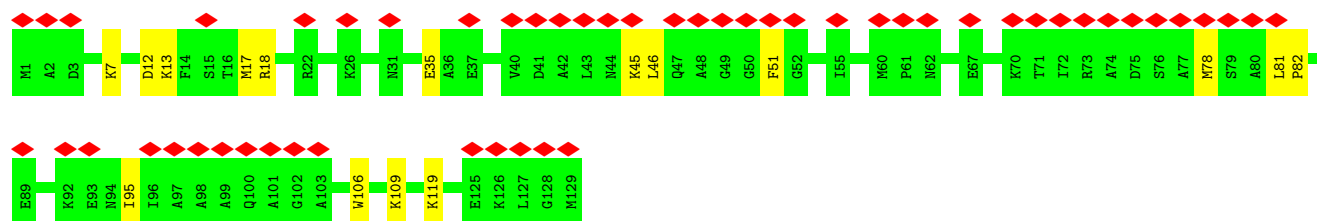
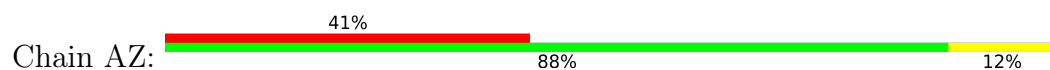
• Molecule 5: Chemotaxis protein CheY



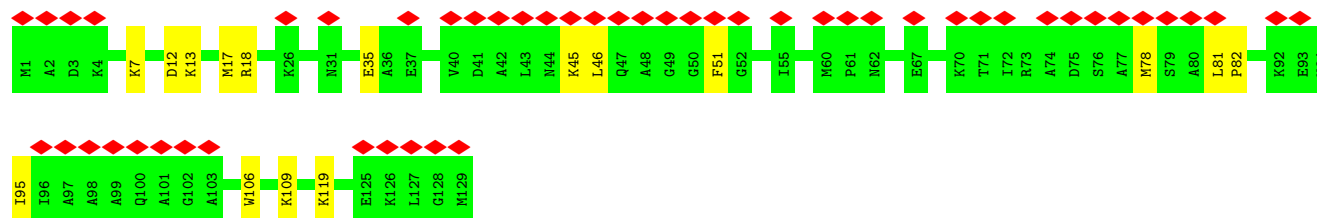
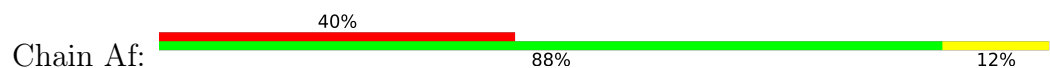
• Molecule 5: Chemotaxis protein CheY



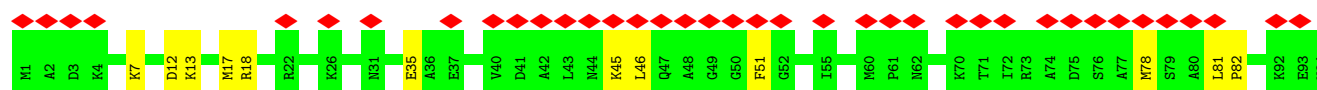
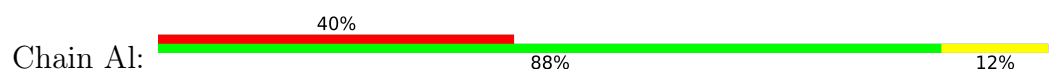
• Molecule 5: Chemotaxis protein CheY

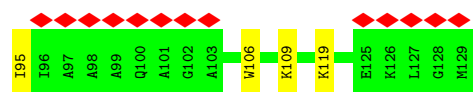


• Molecule 5: Chemotaxis protein CheY

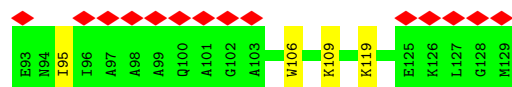
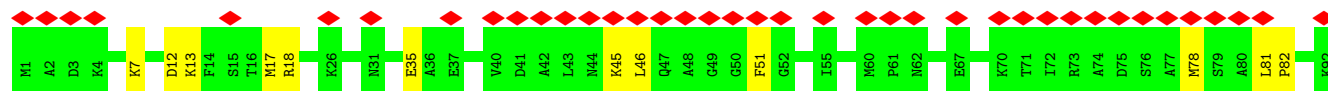
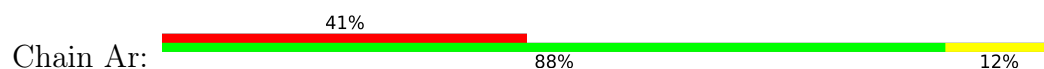


• Molecule 5: Chemotaxis protein CheY

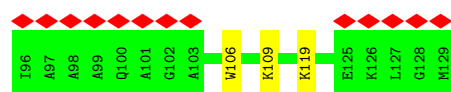
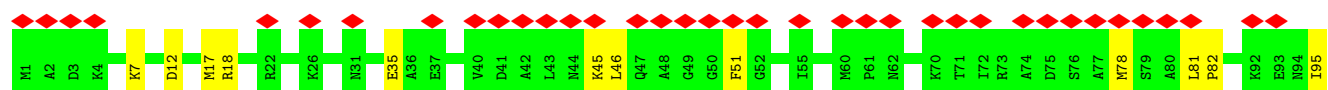
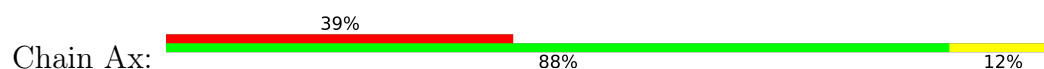




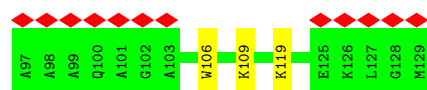
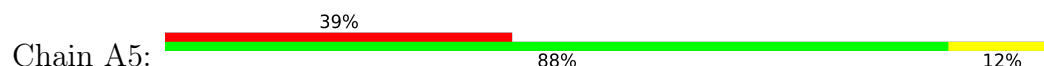
- Molecule 5: Chemotaxis protein CheY



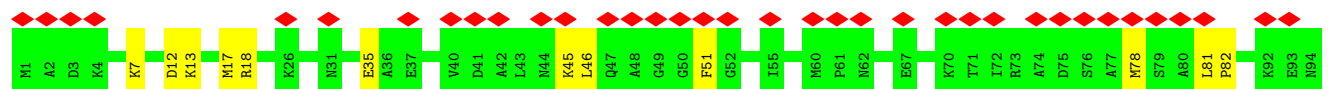
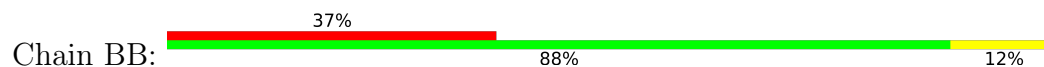
- Molecule 5: Chemotaxis protein CheY



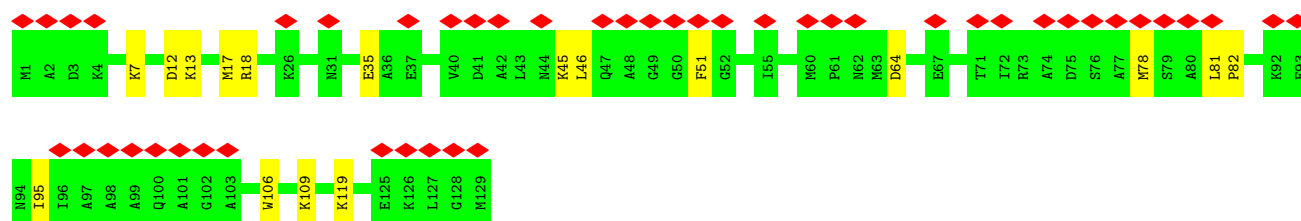
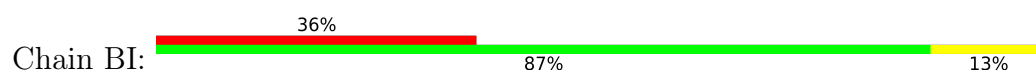
- Molecule 5: Chemotaxis protein CheY



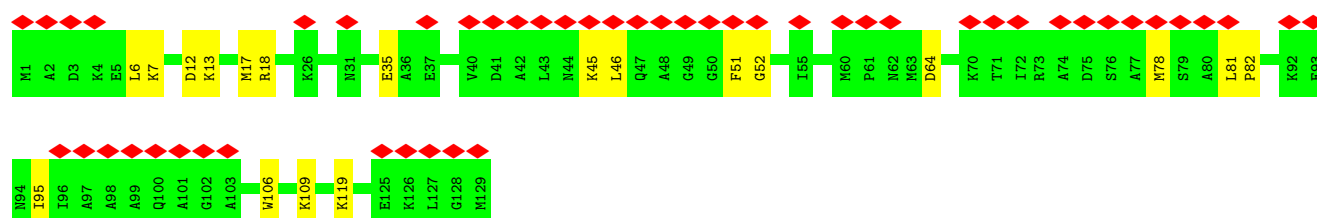
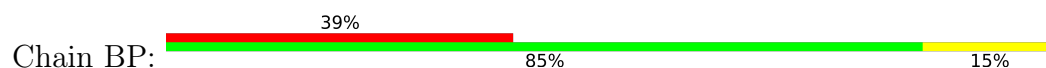
- Molecule 5: Chemotaxis protein CheY



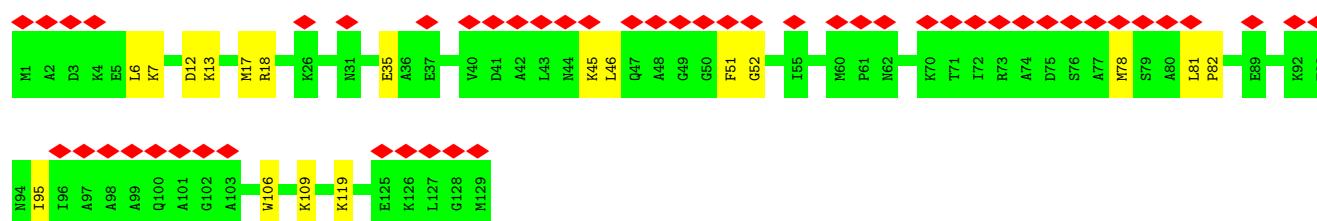
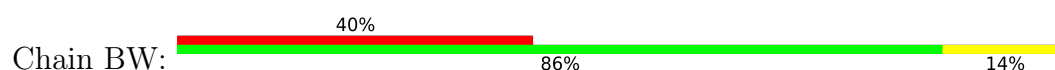
- Molecule 5: Chemotaxis protein CheY



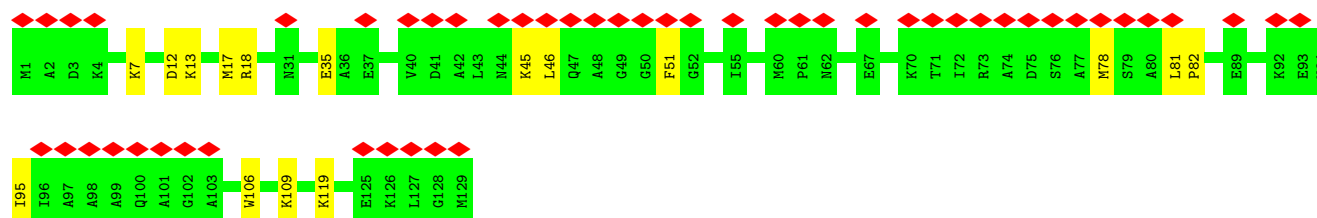
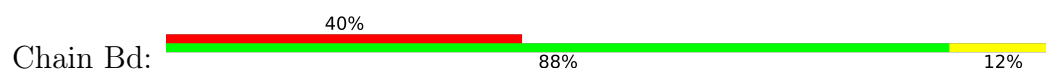
• Molecule 5: Chemotaxis protein CheY



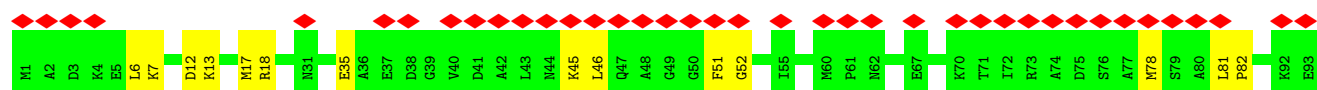
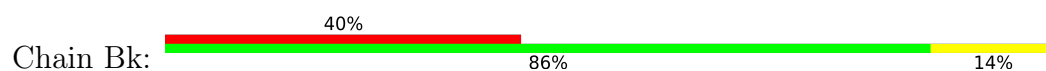
• Molecule 5: Chemotaxis protein CheY

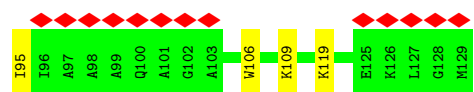


• Molecule 5: Chemotaxis protein CheY

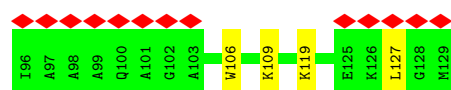
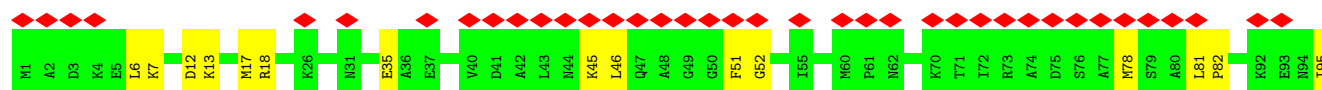
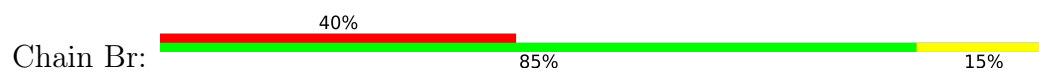


• Molecule 5: Chemotaxis protein CheY

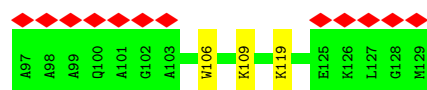
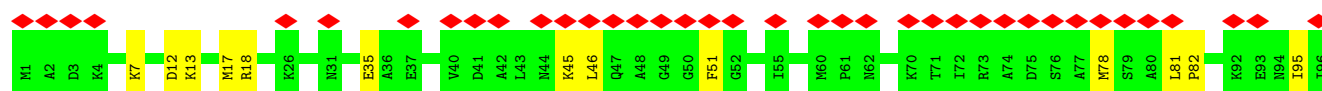
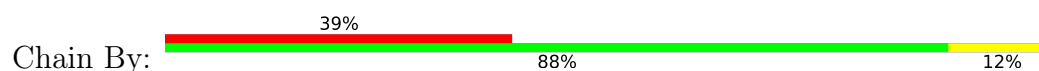




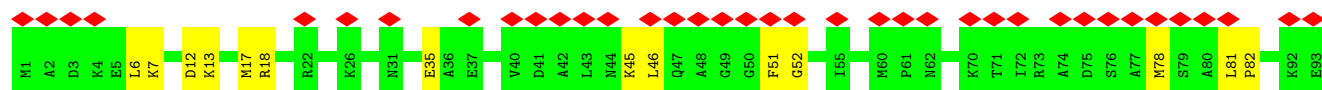
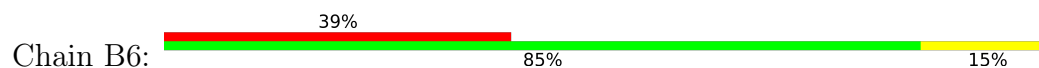
• Molecule 5: Chemotaxis protein CheY



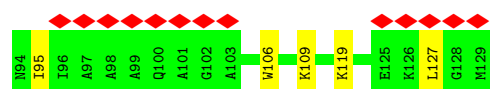
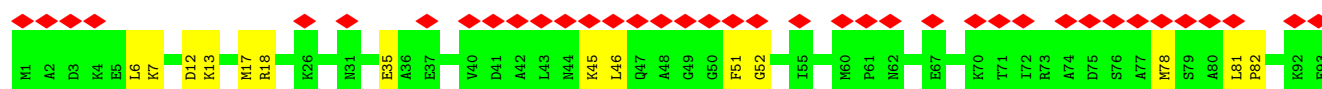
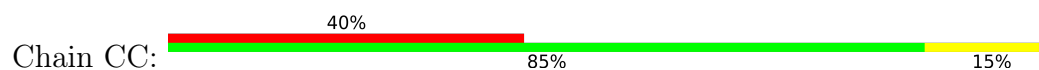
• Molecule 5: Chemotaxis protein CheY



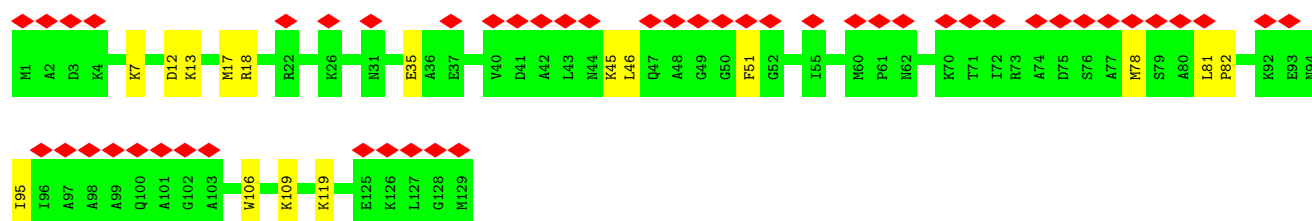
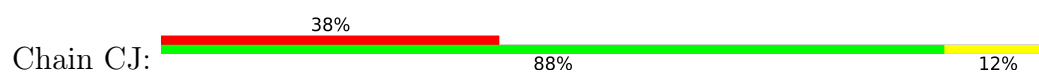
• Molecule 5: Chemotaxis protein CheY



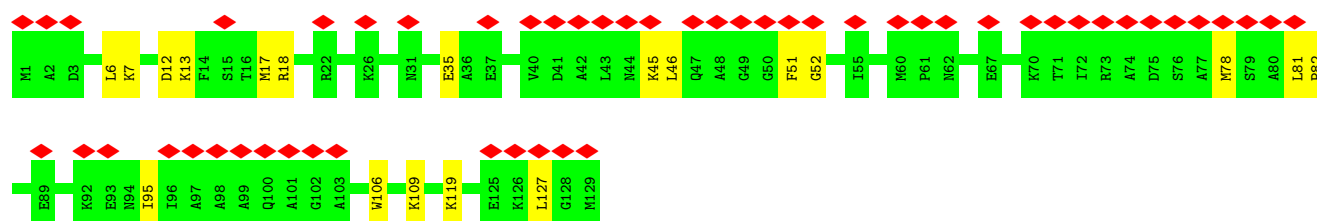
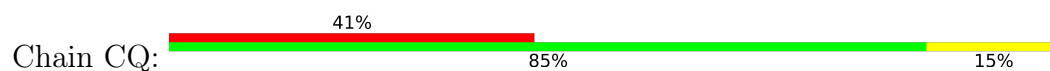
• Molecule 5: Chemotaxis protein CheY



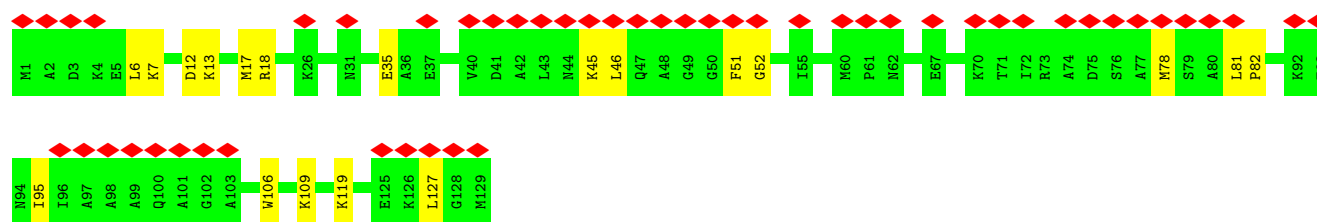
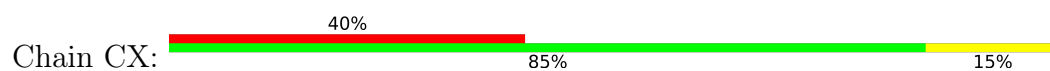
• Molecule 5: Chemotaxis protein CheY



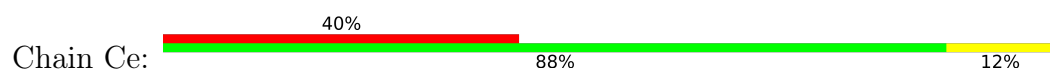
• Molecule 5: Chemotaxis protein CheY



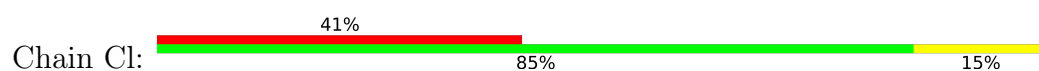
• Molecule 5: Chemotaxis protein CheY

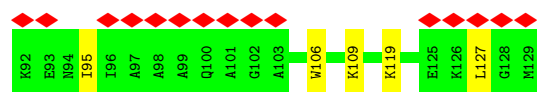


• Molecule 5: Chemotaxis protein CheY

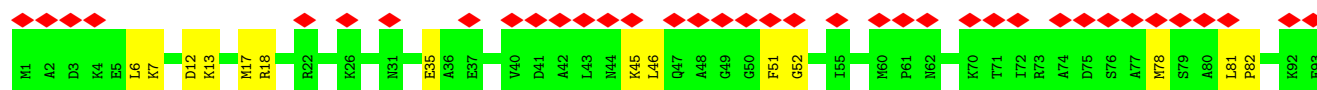
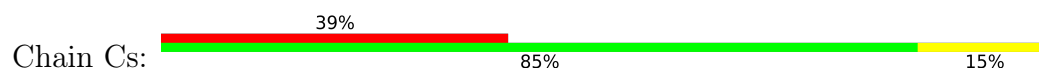


• Molecule 5: Chemotaxis protein CheY

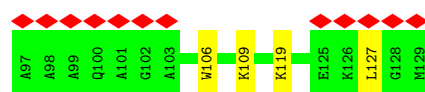
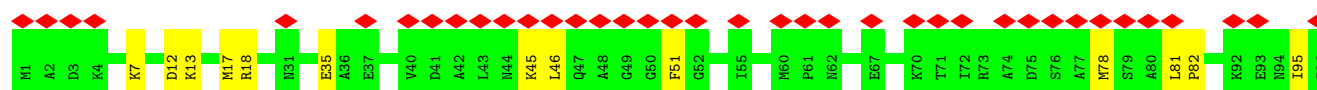
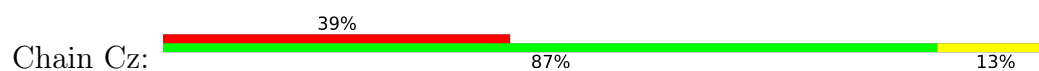




• Molecule 5: Chemotaxis protein CheY



• Molecule 5: Chemotaxis protein CheY



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C34	Depositor
Number of particles used	28119	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.438	Depositor
Minimum map value	-0.222	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	720.0, 720.0, 720.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	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	0.29	0/679	0.55	0/917
1	1	0.51	0/679	0.75	1/917 (0.1%)
1	2	0.33	0/679	0.61	1/917 (0.1%)
1	5	0.51	0/679	0.75	1/917 (0.1%)
1	6	0.33	0/679	0.61	1/917 (0.1%)
1	A1	0.29	0/679	0.55	0/917
1	A6	0.51	0/679	0.75	1/917 (0.1%)
1	A7	0.33	0/679	0.61	1/917 (0.1%)
1	A8	0.29	0/679	0.55	0/917
1	AA	0.29	0/679	0.55	0/917
1	AB	0.29	0/679	0.55	0/917
1	AC	0.29	0/679	0.55	0/917
1	AD	0.29	0/679	0.55	0/917
1	AE	0.29	0/679	0.55	0/917
1	AF	0.29	0/679	0.55	0/917
1	AG	0.29	0/679	0.55	0/917
1	AH	0.29	0/679	0.55	0/917
1	AI	0.51	0/679	0.75	1/917 (0.1%)
1	AJ	0.33	0/679	0.61	1/917 (0.1%)
1	AK	0.29	0/679	0.55	0/917
1	AO	0.51	0/679	0.75	1/917 (0.1%)
1	AP	0.33	0/679	0.61	1/917 (0.1%)
1	AQ	0.29	0/679	0.55	0/917
1	AU	0.51	0/679	0.75	1/917 (0.1%)
1	AV	0.33	0/679	0.61	1/917 (0.1%)
1	AW	0.29	0/679	0.55	0/917
1	Aa	0.51	0/679	0.75	1/917 (0.1%)
1	Ab	0.33	0/679	0.61	1/917 (0.1%)
1	Ac	0.29	0/679	0.55	0/917
1	Ag	0.51	0/679	0.75	1/917 (0.1%)
1	Ah	0.32	0/679	0.61	1/917 (0.1%)
1	Ai	0.29	0/679	0.55	0/917
1	Am	0.51	0/679	0.75	1/917 (0.1%)
1	An	0.33	0/679	0.61	1/917 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Ao	0.29	0/679	0.55	0/917
1	As	0.51	0/679	0.75	1/917 (0.1%)
1	At	0.33	0/679	0.61	1/917 (0.1%)
1	Au	0.29	0/679	0.55	0/917
1	Ay	0.51	0/679	0.75	1/917 (0.1%)
1	Az	0.33	0/679	0.61	1/917 (0.1%)
1	B1	0.33	0/679	0.61	1/917 (0.1%)
1	B2	0.29	0/679	0.55	0/917
1	B7	0.51	0/679	0.75	1/917 (0.1%)
1	B8	0.33	0/679	0.61	1/917 (0.1%)
1	B9	0.29	0/679	0.55	0/917
1	BC	0.51	0/679	0.75	1/917 (0.1%)
1	BD	0.33	0/679	0.61	1/917 (0.1%)
1	BE	0.29	0/679	0.55	0/917
1	BJ	0.51	0/679	0.75	1/917 (0.1%)
1	BK	0.33	0/679	0.61	1/917 (0.1%)
1	BL	0.29	0/679	0.55	0/917
1	BQ	0.51	0/679	0.75	1/917 (0.1%)
1	BR	0.33	0/679	0.61	1/917 (0.1%)
1	BS	0.29	0/679	0.55	0/917
1	BX	0.51	0/679	0.75	1/917 (0.1%)
1	BY	0.33	0/679	0.61	1/917 (0.1%)
1	BZ	0.29	0/679	0.55	0/917
1	Be	0.51	0/679	0.75	1/917 (0.1%)
1	Bf	0.33	0/679	0.61	1/917 (0.1%)
1	Bg	0.29	0/679	0.55	0/917
1	Bl	0.51	0/679	0.75	1/917 (0.1%)
1	Bm	0.33	0/679	0.61	1/917 (0.1%)
1	Bn	0.29	0/679	0.55	0/917
1	Bs	0.51	0/679	0.75	1/917 (0.1%)
1	Bt	0.33	0/679	0.61	1/917 (0.1%)
1	Bu	0.29	0/679	0.55	0/917
1	Bz	0.51	0/679	0.75	1/917 (0.1%)
1	C1	0.51	0/679	0.75	1/917 (0.1%)
1	C2	0.33	0/679	0.61	1/917 (0.1%)
1	CD	0.51	0/679	0.75	1/917 (0.1%)
1	CE	0.33	0/679	0.61	1/917 (0.1%)
1	CF	0.29	0/679	0.55	0/917
1	CK	0.51	0/679	0.75	1/917 (0.1%)
1	CL	0.33	0/679	0.61	1/917 (0.1%)
1	CM	0.29	0/679	0.55	0/917
1	CR	0.51	0/679	0.75	1/917 (0.1%)
1	CS	0.33	0/679	0.61	1/917 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CT	0.29	0/679	0.55	0/917
1	CY	0.51	0/679	0.75	1/917 (0.1%)
1	CZ	0.32	0/679	0.61	1/917 (0.1%)
1	Ca	0.29	0/679	0.55	0/917
1	Cf	0.51	0/679	0.75	1/917 (0.1%)
1	Cg	0.33	0/679	0.61	1/917 (0.1%)
1	Ch	0.29	0/679	0.55	0/917
1	Cm	0.51	0/679	0.75	1/917 (0.1%)
1	Cn	0.33	0/679	0.61	1/917 (0.1%)
1	Co	0.29	0/679	0.55	0/917
1	Ct	0.51	0/679	0.75	1/917 (0.1%)
1	Cu	0.33	0/679	0.61	1/917 (0.1%)
1	Cv	0.29	0/679	0.55	0/917
1	o	0.51	0/679	0.75	1/917 (0.1%)
1	p	0.51	0/679	0.75	1/917 (0.1%)
1	q	0.51	0/679	0.75	1/917 (0.1%)
1	r	0.51	0/679	0.75	1/917 (0.1%)
1	s	0.51	0/679	0.75	1/917 (0.1%)
1	t	0.51	0/679	0.75	1/917 (0.1%)
1	u	0.33	0/679	0.61	1/917 (0.1%)
1	v	0.33	0/679	0.61	1/917 (0.1%)
1	w	0.33	0/679	0.61	1/917 (0.1%)
1	x	0.33	0/679	0.61	1/917 (0.1%)
1	y	0.33	0/679	0.61	1/917 (0.1%)
1	z	0.33	0/679	0.61	1/917 (0.1%)
2	A2	0.08	0/226	0.20	0/303
2	A9	0.08	0/226	0.20	0/303
2	B0	0.08	0/226	0.20	0/303
2	B3	0.08	0/226	0.20	0/303
2	BF	0.08	0/226	0.20	0/303
2	BM	0.08	0/226	0.20	0/303
2	BT	0.08	0/226	0.20	0/303
2	Ba	0.08	0/226	0.20	0/303
2	Bh	0.08	0/226	0.21	0/303
2	Bo	0.08	0/226	0.20	0/303
2	Bv	0.08	0/226	0.20	0/303
2	C	0.08	0/226	0.20	0/303
2	CG	0.08	0/226	0.20	0/303
2	CN	0.08	0/226	0.20	0/303
2	CU	0.08	0/226	0.20	0/303
2	Cb	0.08	0/226	0.20	0/303
2	Ci	0.08	0/226	0.20	0/303
2	Cp	0.08	0/226	0.20	0/303

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
2	Cw	0.08	0/226	0.20	0/303
2	D	0.08	0/226	0.20	0/303
2	E	0.08	0/226	0.20	0/303
2	F	0.08	0/226	0.20	0/303
2	G	0.08	0/226	0.20	0/303
2	H	0.08	0/226	0.21	0/303
2	I	0.08	0/226	0.20	0/303
2	J	0.08	0/226	0.20	0/303
2	K	0.08	0/226	0.20	0/303
2	L	0.08	0/226	0.20	0/303
2	M	0.08	0/226	0.20	0/303
2	N	0.08	0/226	0.20	0/303
2	O	0.08	0/226	0.20	0/303
2	P	0.08	0/226	0.20	0/303
2	Q	0.08	0/226	0.20	0/303
2	R	0.08	0/226	0.20	0/303
3	7	0.24	0/2482	0.39	0/3375
3	A0	0.24	0/2482	0.39	0/3375
3	A3	0.24	0/2482	0.39	0/3375
3	AL	0.24	0/2482	0.39	0/3375
3	AR	0.24	0/2482	0.39	0/3375
3	AX	0.24	0/2482	0.39	0/3375
3	Ad	0.24	0/2482	0.39	0/3375
3	Aj	0.24	0/2482	0.39	0/3375
3	Ap	0.24	0/2482	0.39	0/3375
3	Av	0.24	0/2482	0.39	0/3375
3	B4	0.24	0/2482	0.39	0/3375
3	BG	0.24	0/2482	0.39	0/3375
3	BN	0.24	0/2482	0.39	0/3375
3	BU	0.24	0/2482	0.39	0/3375
3	Bb	0.24	0/2482	0.39	0/3375
3	Bi	0.24	0/2482	0.39	0/3375
3	Bp	0.24	0/2482	0.39	0/3375
3	Bw	0.24	0/2482	0.39	0/3375
3	CA	0.24	0/2482	0.39	0/3375
3	CH	0.24	0/2482	0.39	0/3375
3	CO	0.24	0/2482	0.39	0/3375
3	CV	0.24	0/2482	0.39	0/3375
3	Cc	0.24	0/2482	0.39	0/3375
3	Cj	0.24	0/2482	0.39	0/3375
3	Cq	0.24	0/2482	0.39	0/3375
3	Cx	0.24	0/2482	0.39	0/3375
3	S	0.24	0/2482	0.39	0/3375

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	T	0.24	0/2482	0.39	0/3375
3	U	0.24	0/2482	0.39	0/3375
3	V	0.24	0/2482	0.39	0/3375
3	W	0.24	0/2482	0.39	0/3375
3	X	0.24	0/2482	0.39	0/3375
3	Y	0.24	0/2482	0.39	0/3375
3	g	0.24	0/2482	0.39	0/3375
4	3	0.08	0/2447	0.22	0/3300
4	8	0.08	0/2447	0.22	0/3300
4	A4	0.08	0/2447	0.22	0/3300
4	AM	0.08	0/2447	0.22	0/3300
4	AS	0.08	0/2447	0.22	0/3300
4	AY	0.08	0/2447	0.22	0/3300
4	Ae	0.08	0/2447	0.22	0/3300
4	Ak	0.08	0/2447	0.22	0/3300
4	Aq	0.08	0/2447	0.22	0/3300
4	Aw	0.08	0/2447	0.22	0/3300
4	B5	0.08	0/2447	0.22	0/3300
4	BA	0.08	0/2447	0.22	0/3300
4	BH	0.08	0/2447	0.22	0/3300
4	BO	0.08	0/2447	0.22	0/3300
4	BV	0.08	0/2447	0.22	0/3300
4	Bc	0.08	0/2447	0.22	0/3300
4	Bj	0.08	0/2447	0.22	0/3300
4	Bq	0.08	0/2447	0.22	0/3300
4	Bx	0.08	0/2447	0.22	0/3300
4	CB	0.08	0/2447	0.22	0/3300
4	CI	0.08	0/2447	0.22	0/3300
4	CP	0.08	0/2447	0.22	0/3300
4	CW	0.08	0/2447	0.22	0/3300
4	Cd	0.08	0/2447	0.22	0/3300
4	Ck	0.08	0/2447	0.22	0/3300
4	Cr	0.08	0/2447	0.22	0/3300
4	Cy	0.08	0/2447	0.22	0/3300
4	Z	0.08	0/2447	0.22	0/3300
4	a	0.08	0/2447	0.22	0/3300
4	b	0.08	0/2447	0.22	0/3300
4	c	0.08	0/2447	0.22	0/3300
4	d	0.08	0/2447	0.22	0/3300
4	e	0.08	0/2447	0.22	0/3300
4	f	0.08	0/2447	0.22	0/3300
5	4	0.06	0/1004	0.19	0/1349
5	9	0.06	0/1004	0.19	0/1349

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	A5	0.06	0/1004	0.19	0/1349
5	AN	0.06	0/1004	0.19	0/1349
5	AT	0.06	0/1004	0.19	0/1349
5	AZ	0.06	0/1004	0.19	0/1349
5	Af	0.06	0/1004	0.19	0/1349
5	Al	0.06	0/1004	0.19	0/1349
5	Ar	0.06	0/1004	0.19	0/1349
5	Ax	0.06	0/1004	0.19	0/1349
5	B6	0.06	0/1004	0.19	0/1349
5	BB	0.06	0/1004	0.19	0/1349
5	BI	0.06	0/1004	0.19	0/1349
5	BP	0.06	0/1004	0.19	0/1349
5	BW	0.06	0/1004	0.19	0/1349
5	Bd	0.06	0/1004	0.19	0/1349
5	Bk	0.06	0/1004	0.19	0/1349
5	Br	0.06	0/1004	0.19	0/1349
5	By	0.06	0/1004	0.19	0/1349
5	CC	0.06	0/1004	0.19	0/1349
5	CJ	0.06	0/1004	0.19	0/1349
5	CQ	0.06	0/1004	0.19	0/1349
5	CX	0.06	0/1004	0.19	0/1349
5	Ce	0.06	0/1004	0.19	0/1349
5	Cl	0.06	0/1004	0.19	0/1349
5	Cs	0.06	0/1004	0.19	0/1349
5	Cz	0.06	0/1004	0.19	0/1349
5	h	0.06	0/1004	0.19	0/1349
5	i	0.06	0/1004	0.19	0/1349
5	j	0.06	0/1004	0.19	0/1349
5	k	0.06	0/1004	0.19	0/1349
5	l	0.06	0/1004	0.19	0/1349
5	m	0.06	0/1004	0.19	0/1349
5	n	0.06	0/1004	0.19	0/1349
All	All	0.24	0/278664	0.41	68/376652 (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	1
1	1	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2	0	1
1	5	0	1
1	6	0	1
1	A1	0	1
1	A6	0	1
1	A7	0	1
1	A8	0	1
1	AA	0	1
1	AB	0	1
1	AC	0	1
1	AD	0	1
1	AE	0	1
1	AF	0	1
1	AG	0	1
1	AH	0	1
1	AI	0	1
1	AJ	0	1
1	AK	0	1
1	AO	0	1
1	AP	0	1
1	AQ	0	1
1	AU	0	1
1	AV	0	1
1	AW	0	1
1	Aa	0	1
1	Ab	0	1
1	Ac	0	1
1	Ag	0	1
1	Ah	0	1
1	Ai	0	1
1	Am	0	1
1	An	0	1
1	Ao	0	1
1	As	0	1
1	At	0	1
1	Au	0	1
1	Ay	0	1
1	Az	0	1
1	B1	0	1
1	B2	0	1
1	B7	0	1
1	B8	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B9	0	1
1	BC	0	1
1	BD	0	1
1	BE	0	1
1	BJ	0	1
1	BK	0	1
1	BL	0	1
1	BQ	0	1
1	BR	0	1
1	BS	0	1
1	BX	0	1
1	BY	0	1
1	BZ	0	1
1	Be	0	1
1	Bf	0	1
1	Bg	0	1
1	Bl	0	1
1	Bm	0	1
1	Bn	0	1
1	Bs	0	1
1	Bt	0	1
1	Bu	0	1
1	Bz	0	1
1	C1	0	1
1	C2	0	1
1	CD	0	1
1	CE	0	1
1	CF	0	1
1	CK	0	1
1	CL	0	1
1	CM	0	1
1	CR	0	1
1	CS	0	1
1	CT	0	1
1	CY	0	1
1	CZ	0	1
1	Ca	0	1
1	Cf	0	1
1	Cg	0	1
1	Ch	0	1
1	Cm	0	1
1	Cn	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Co	0	1
1	Ct	0	1
1	Cu	0	1
1	Cv	0	1
1	o	0	1
1	p	0	1
1	q	0	1
1	r	0	1
1	s	0	1
1	t	0	1
1	u	0	1
1	v	0	1
1	w	0	1
1	x	0	1
1	y	0	1
1	z	0	1
3	7	0	2
3	A0	0	2
3	A3	0	2
3	AL	0	2
3	AR	0	2
3	AX	0	2
3	Ad	0	2
3	Aj	0	2
3	Ap	0	2
3	Av	0	2
3	B4	0	2
3	BG	0	2
3	BN	0	2
3	BU	0	2
3	Bb	0	2
3	Bi	0	2
3	Bp	0	2
3	Bw	0	2
3	CA	0	2
3	CH	0	2
3	CO	0	2
3	CV	0	2
3	Cc	0	2
3	Cj	0	2
3	Cq	0	2
3	Cx	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
3	S	0	2
3	T	0	2
3	U	0	2
3	V	0	2
3	W	0	2
3	X	0	2
3	Y	0	2
3	g	0	2
All	All	0	170

There are no bond length outliers.

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	w	128	PRO	N-CA-C	6.10	121.56	113.57
1	z	128	PRO	N-CA-C	6.10	121.56	113.57
1	BR	128	PRO	N-CA-C	6.10	121.56	113.57
1	Bm	128	PRO	N-CA-C	6.10	121.56	113.57
1	6	128	PRO	N-CA-C	6.10	121.56	113.57

There are no chirality outliers.

5 of 170 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	131	ARG	Sidechain
3	S	60	ARG	Sidechain
3	S	63	ARG	Sidechain
1	o	131	ARG	Sidechain
1	u	131	ARG	Sidechain

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	0	675	0	726	22	0
1	1	675	0	726	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	675	0	726	20	0
1	5	675	0	726	33	0
1	6	675	0	726	23	0
1	A1	675	0	726	20	0
1	A6	675	0	726	28	0
1	A7	675	0	726	20	0
1	A8	675	0	726	21	0
1	AA	675	0	726	21	0
1	AB	675	0	726	23	0
1	AC	675	0	726	21	0
1	AD	675	0	726	22	0
1	AE	675	0	726	22	0
1	AF	675	0	726	22	0
1	AG	675	0	726	23	0
1	AH	675	0	726	22	0
1	AI	675	0	726	30	0
1	AJ	675	0	726	21	0
1	AK	675	0	726	22	0
1	AO	675	0	726	29	0
1	AP	675	0	726	21	0
1	AQ	675	0	726	22	0
1	AU	675	0	726	30	0
1	AV	675	0	726	23	0
1	AW	675	0	726	21	0
1	Aa	675	0	726	31	0
1	Ab	675	0	726	20	0
1	Ac	675	0	726	21	0
1	Ag	675	0	726	29	0
1	Ah	675	0	726	20	0
1	Ai	675	0	726	21	0
1	Am	675	0	726	30	0
1	An	675	0	726	21	0
1	Ao	675	0	726	20	0
1	As	675	0	726	30	0
1	At	675	0	726	19	0
1	Au	675	0	726	19	0
1	Ay	675	0	726	30	0
1	Az	675	0	726	22	0
1	B1	675	0	726	21	0
1	B2	675	0	726	22	0
1	B7	675	0	726	29	0
1	B8	675	0	726	21	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B9	675	0	726	20	0
1	BC	675	0	726	29	0
1	BD	675	0	726	21	0
1	BE	675	0	726	21	0
1	BJ	675	0	726	30	0
1	BK	675	0	726	22	0
1	BL	675	0	726	21	0
1	BQ	675	0	726	30	0
1	BR	675	0	726	21	0
1	BS	675	0	726	21	0
1	BX	675	0	726	29	0
1	BY	675	0	726	22	0
1	BZ	675	0	726	21	0
1	Be	675	0	726	29	0
1	Bf	675	0	726	22	0
1	Bg	675	0	726	21	0
1	Bl	675	0	726	28	0
1	Bm	675	0	726	22	0
1	Bn	675	0	726	22	0
1	Bs	675	0	726	29	0
1	Bt	675	0	726	22	0
1	Bu	675	0	726	22	0
1	Bz	675	0	726	30	0
1	C1	675	0	726	29	0
1	C2	675	0	726	23	0
1	CD	675	0	726	29	0
1	CE	675	0	726	20	0
1	CF	675	0	726	21	0
1	CK	675	0	726	29	0
1	CL	675	0	726	21	0
1	CM	675	0	726	20	0
1	CR	675	0	726	28	0
1	CS	675	0	726	21	0
1	CT	675	0	726	21	0
1	CY	675	0	726	31	0
1	CZ	675	0	726	21	0
1	Ca	675	0	726	21	0
1	Cf	675	0	726	30	0
1	Cg	675	0	726	20	0
1	Ch	675	0	726	21	0
1	Cm	675	0	726	29	0
1	Cn	675	0	726	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Co	675	0	726	19	0
1	Ct	675	0	726	30	0
1	Cu	675	0	726	20	0
1	Cv	675	0	726	22	0
1	o	675	0	726	30	0
1	p	675	0	726	31	0
1	q	675	0	726	28	0
1	r	675	0	726	30	0
1	s	675	0	726	31	0
1	t	675	0	726	30	0
1	u	675	0	726	20	0
1	v	675	0	726	21	0
1	w	675	0	726	22	0
1	x	675	0	726	20	0
1	y	675	0	726	22	0
1	z	675	0	726	22	0
2	A2	224	0	221	10	0
2	A9	224	0	221	10	0
2	B0	224	0	221	9	0
2	B3	224	0	221	9	0
2	BF	224	0	221	10	0
2	BM	224	0	221	9	0
2	BT	224	0	221	9	0
2	Ba	224	0	221	9	0
2	Bh	224	0	221	10	0
2	Bo	224	0	221	10	0
2	Bv	224	0	221	10	0
2	C	224	0	221	10	0
2	CG	224	0	221	9	0
2	CN	224	0	221	10	0
2	CU	224	0	221	10	0
2	Cb	224	0	221	10	0
2	Ci	224	0	221	9	0
2	Cp	224	0	221	9	0
2	Cw	224	0	221	8	0
2	D	224	0	221	10	0
2	E	224	0	221	8	0
2	F	224	0	221	9	0
2	G	224	0	221	9	0
2	H	224	0	221	10	0
2	I	224	0	221	10	0
2	J	224	0	221	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	224	0	221	9	0
2	L	224	0	221	9	0
2	M	224	0	221	10	0
2	N	224	0	221	10	0
2	O	224	0	221	10	0
2	P	224	0	221	9	0
2	Q	224	0	221	9	0
2	R	224	0	221	9	0
3	7	2431	0	2462	49	0
3	A0	2431	0	2462	48	0
3	A3	2431	0	2462	47	0
3	AL	2431	0	2462	48	0
3	AR	2431	0	2462	50	0
3	AX	2431	0	2462	48	0
3	Ad	2431	0	2462	47	0
3	Aj	2431	0	2462	48	0
3	Ap	2431	0	2462	49	0
3	Av	2431	0	2462	48	0
3	B4	2431	0	2462	48	0
3	BG	2431	0	2462	48	0
3	BN	2431	0	2462	50	0
3	BU	2431	0	2462	49	0
3	Bb	2431	0	2462	49	0
3	Bi	2431	0	2462	50	0
3	Bp	2431	0	2462	48	0
3	Bw	2431	0	2462	49	0
3	CA	2431	0	2462	47	0
3	CH	2431	0	2462	48	0
3	CO	2431	0	2462	47	0
3	CV	2431	0	2462	48	0
3	Cc	2431	0	2462	47	0
3	Cj	2431	0	2462	47	0
3	Cq	2431	0	2462	48	0
3	Cx	2431	0	2462	48	0
3	S	2431	0	2462	47	0
3	T	2431	0	2462	48	0
3	U	2431	0	2462	49	0
3	V	2431	0	2462	50	0
3	W	2431	0	2462	49	0
3	X	2431	0	2462	49	0
3	Y	2431	0	2462	49	0
3	g	2431	0	2462	49	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	3	2428	0	2491	62	0
4	8	2428	0	2491	62	0
4	A4	2428	0	2491	64	0
4	AM	2428	0	2491	62	0
4	AS	2428	0	2491	61	0
4	AY	2428	0	2491	61	0
4	Ae	2428	0	2491	63	0
4	Ak	2428	0	2491	62	0
4	Aq	2428	0	2491	61	0
4	Aw	2428	0	2491	62	0
4	B5	2428	0	2491	63	0
4	BA	2428	0	2491	63	0
4	BH	2428	0	2491	66	0
4	BO	2428	0	2491	61	0
4	BV	2428	0	2491	61	0
4	Bc	2428	0	2491	63	0
4	Bj	2428	0	2491	62	0
4	Bq	2428	0	2491	63	0
4	Bx	2428	0	2491	65	0
4	CB	2428	0	2491	60	0
4	CI	2428	0	2491	63	0
4	CP	2428	0	2491	64	0
4	CW	2428	0	2491	65	0
4	Cd	2428	0	2491	64	0
4	Ck	2428	0	2491	63	0
4	Cr	2428	0	2491	65	0
4	Cy	2428	0	2491	62	0
4	Z	2428	0	2491	63	0
4	a	2428	0	2491	64	0
4	b	2428	0	2491	64	0
4	c	2428	0	2491	61	0
4	d	2428	0	2491	63	0
4	e	2428	0	2491	65	0
4	f	2428	0	2491	63	0
5	4	991	0	1025	12	0
5	9	991	0	1025	12	0
5	A5	991	0	1025	11	0
5	AN	991	0	1025	12	0
5	AT	991	0	1025	12	0
5	AZ	991	0	1025	11	0
5	Af	991	0	1025	11	0
5	Al	991	0	1025	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	Ar	991	0	1025	11	0
5	Ax	991	0	1025	10	0
5	B6	991	0	1025	13	0
5	BB	991	0	1025	11	0
5	BI	991	0	1025	12	0
5	BP	991	0	1025	13	0
5	BW	991	0	1025	12	0
5	Bd	991	0	1025	11	0
5	Bk	991	0	1025	12	0
5	Br	991	0	1025	13	0
5	By	991	0	1025	11	0
5	CC	991	0	1025	13	0
5	CJ	991	0	1025	11	0
5	CQ	991	0	1025	13	0
5	CX	991	0	1025	13	0
5	Ce	991	0	1025	11	0
5	Cl	991	0	1025	13	0
5	Cs	991	0	1025	13	0
5	Cz	991	0	1025	12	0
5	h	991	0	1025	12	0
5	i	991	0	1025	12	0
5	j	991	0	1025	13	0
5	k	991	0	1025	13	0
5	l	991	0	1025	12	0
5	m	991	0	1025	12	0
5	n	991	0	1025	12	0
All	All	275366	0	284818	5062	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 9.

The worst 5 of 5062 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)
4:d:143:ALA:HB1	4:e:206:MET:HG2	1.31	1.13
4:BA:143:ALA:HB1	4:BH:206:MET:HG2	1.31	1.13
4:3:143:ALA:HB1	4:8:206:MET:HG2	1.31	1.12
4:Aq:143:ALA:HB1	4:Aw:206:MET:HG2	1.31	1.12
4:8:143:ALA:HB1	4:AM:206:MET:HG2	1.31	1.12

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

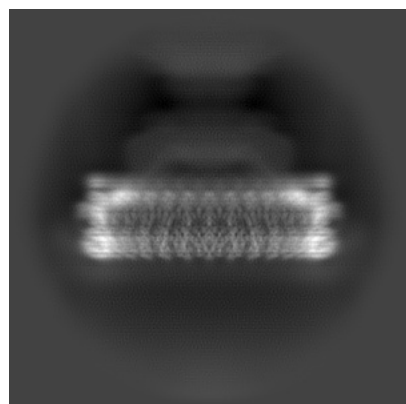
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37570. These allow visual inspection of the internal detail of the map and identification of artifacts.

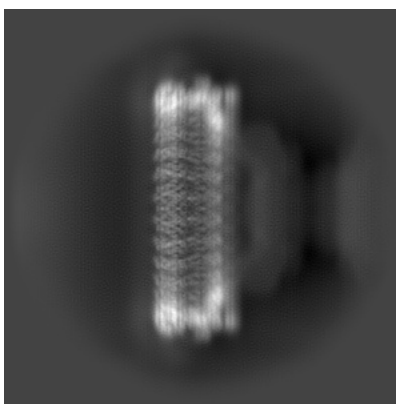
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

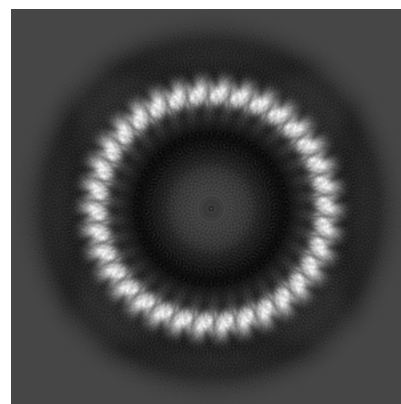
6.1.1 Primary map



X

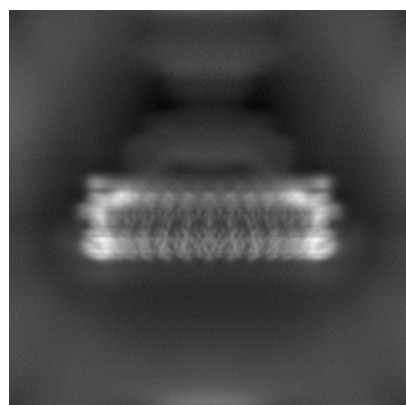


Y

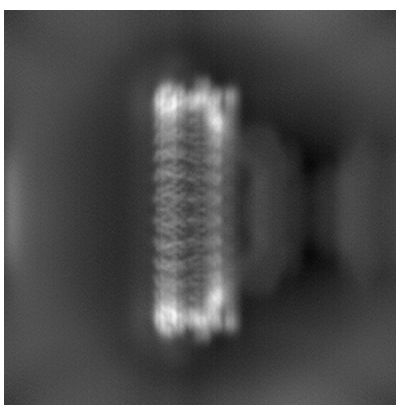


Z

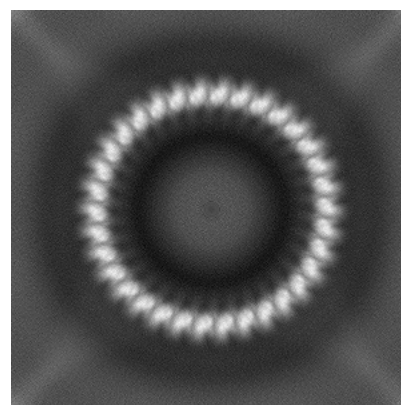
6.1.2 Raw map



X



Y

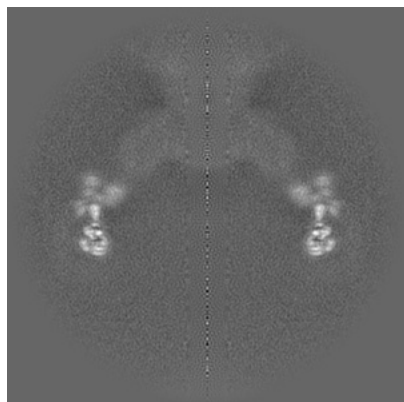


Z

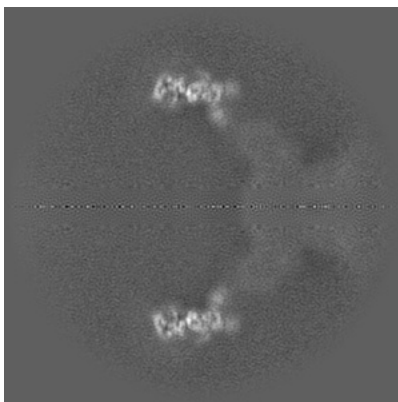
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

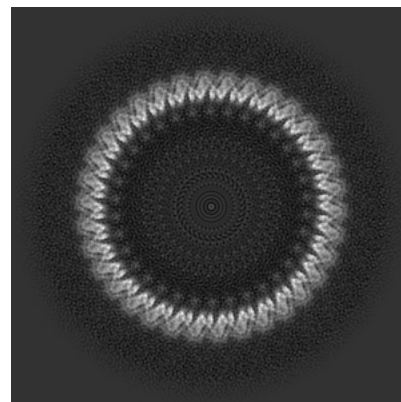
6.2.1 Primary map



X Index: 300



Y Index: 300

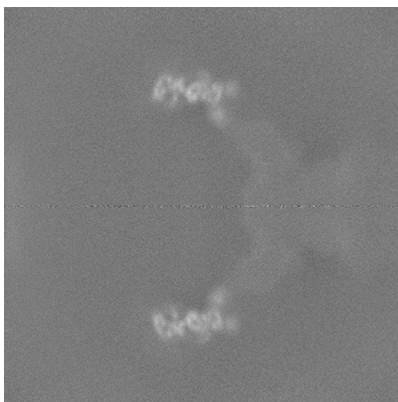


Z Index: 300

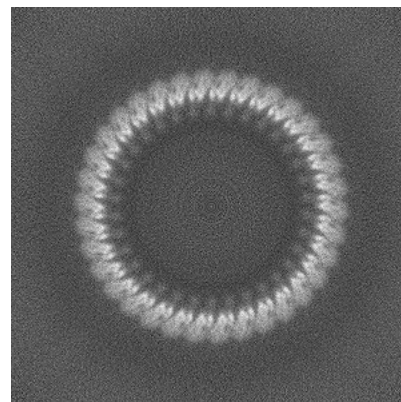
6.2.2 Raw map



X Index: 300



Y Index: 300

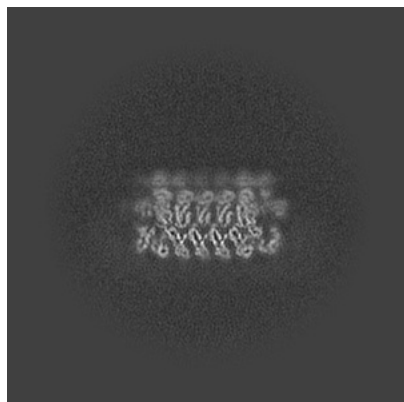


Z Index: 300

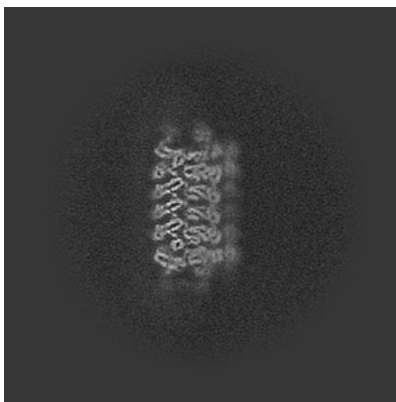
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

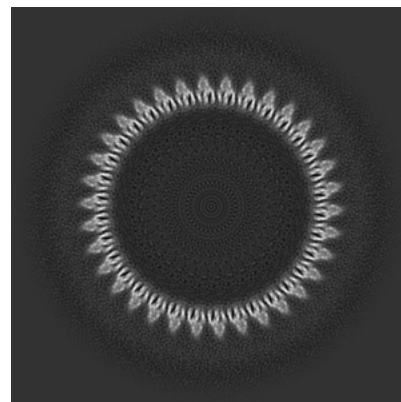
6.3.1 Primary map



X Index: 138

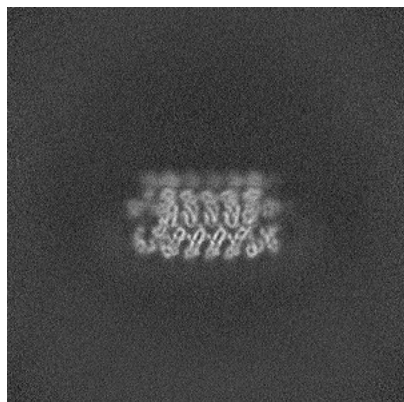


Y Index: 138

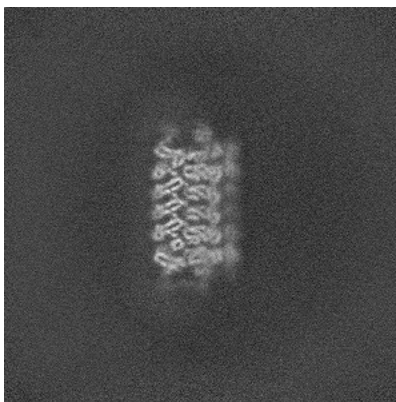


Z Index: 256

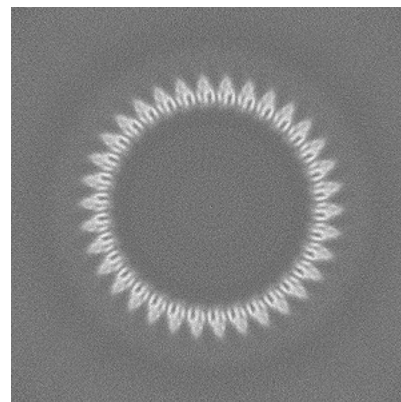
6.3.2 Raw map



X Index: 463



Y Index: 138

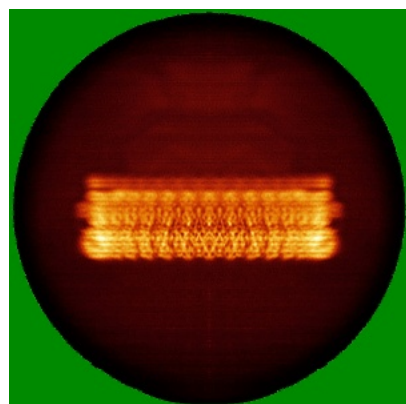


Z Index: 256

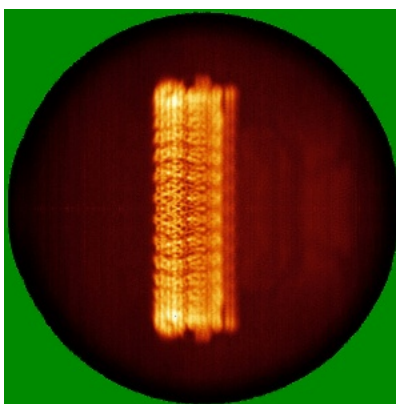
The images above show the largest variance slices of the map in three orthogonal directions.

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

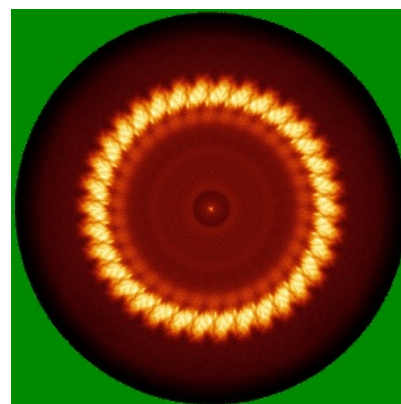
6.4.1 Primary map



X

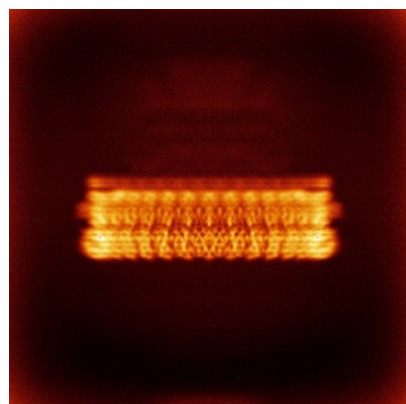


Y

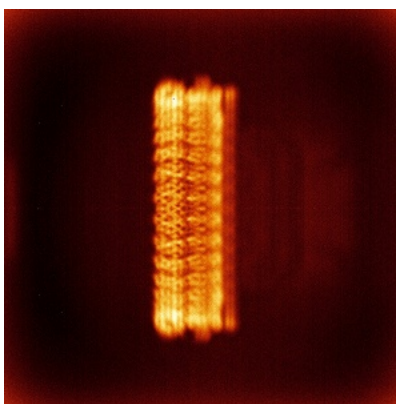


Z

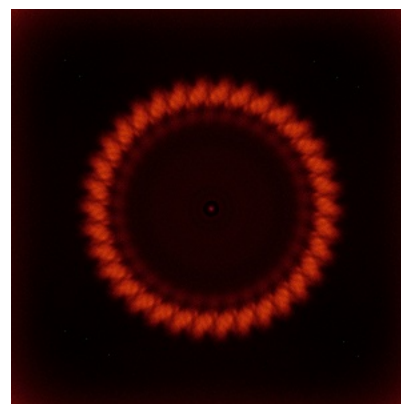
6.4.2 Raw map



X



Y

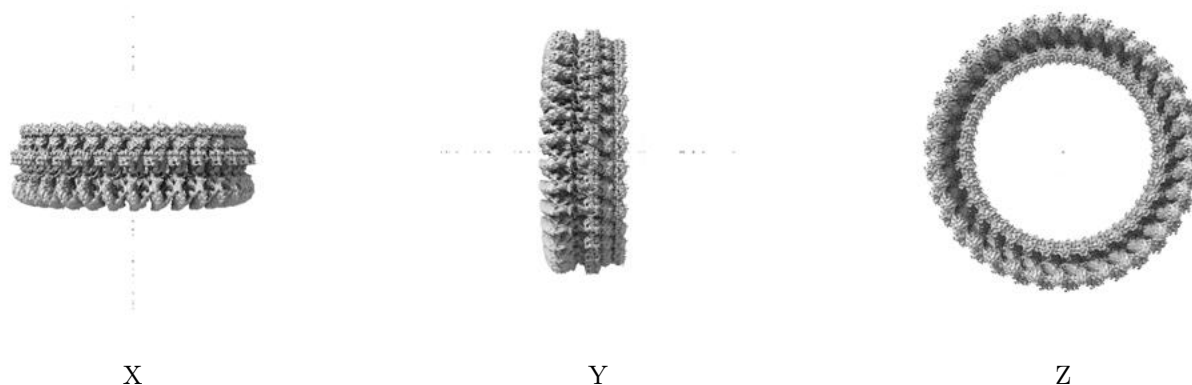


Z

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 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

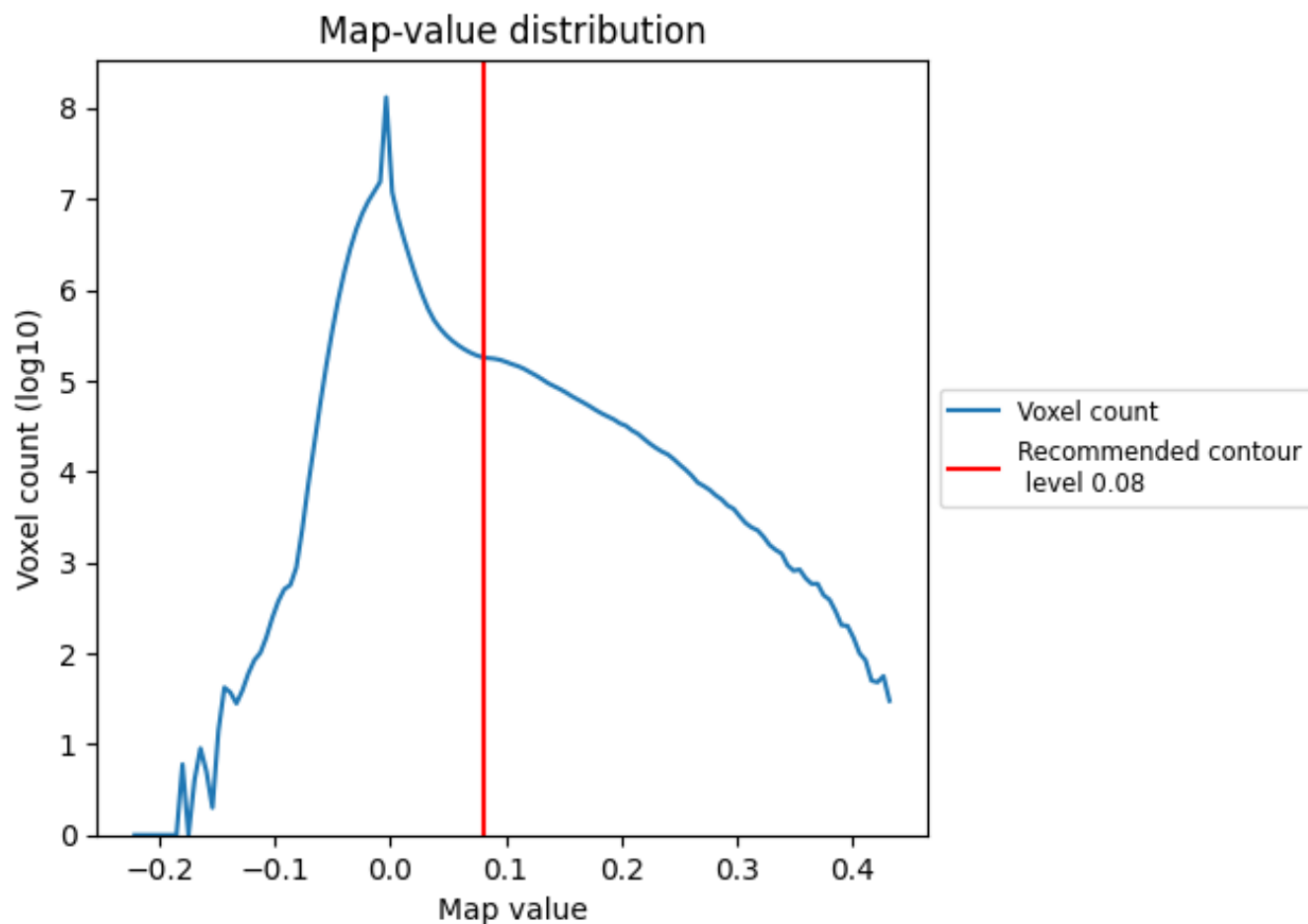
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

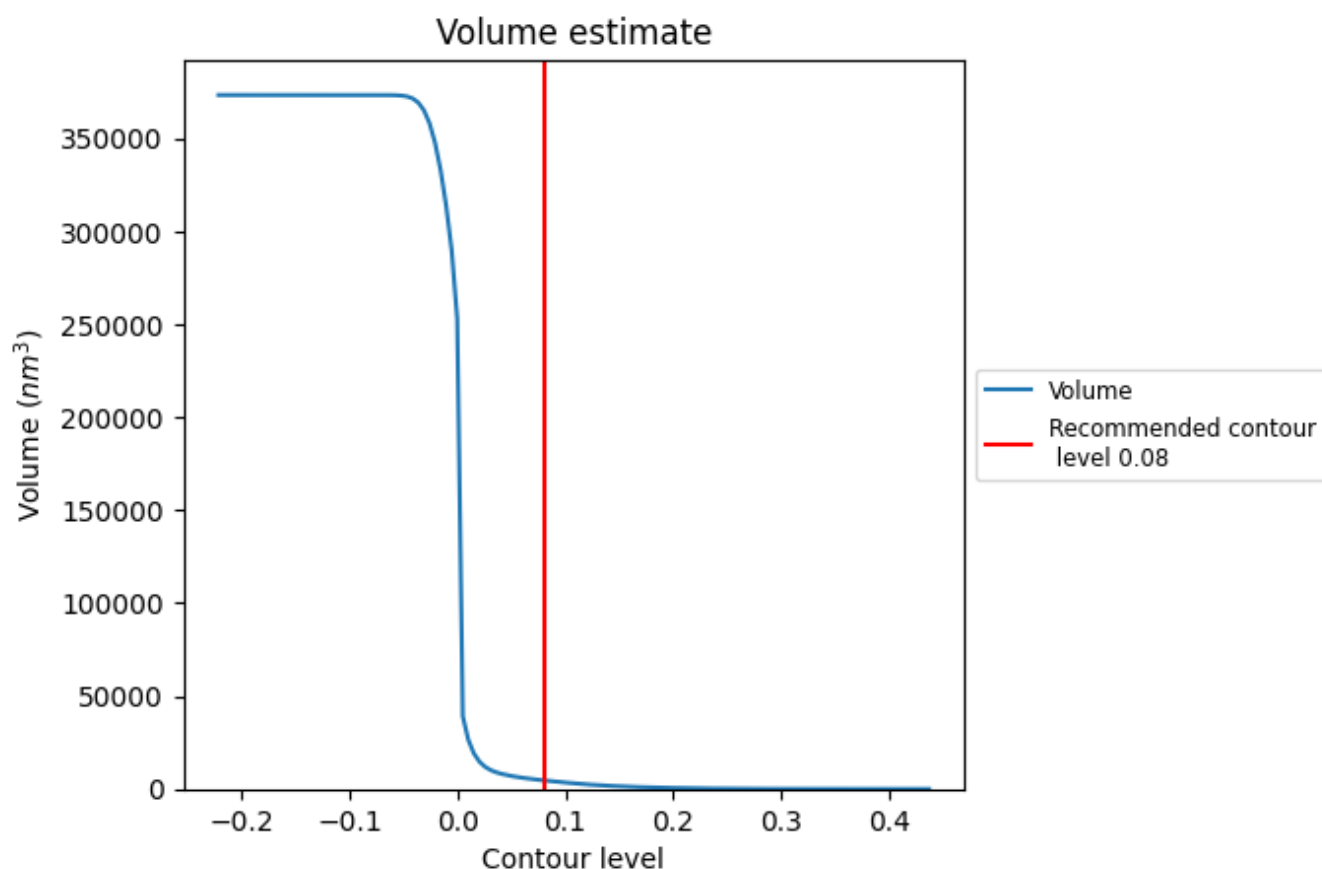
This section contains the results of statistical analysis of the map.

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.

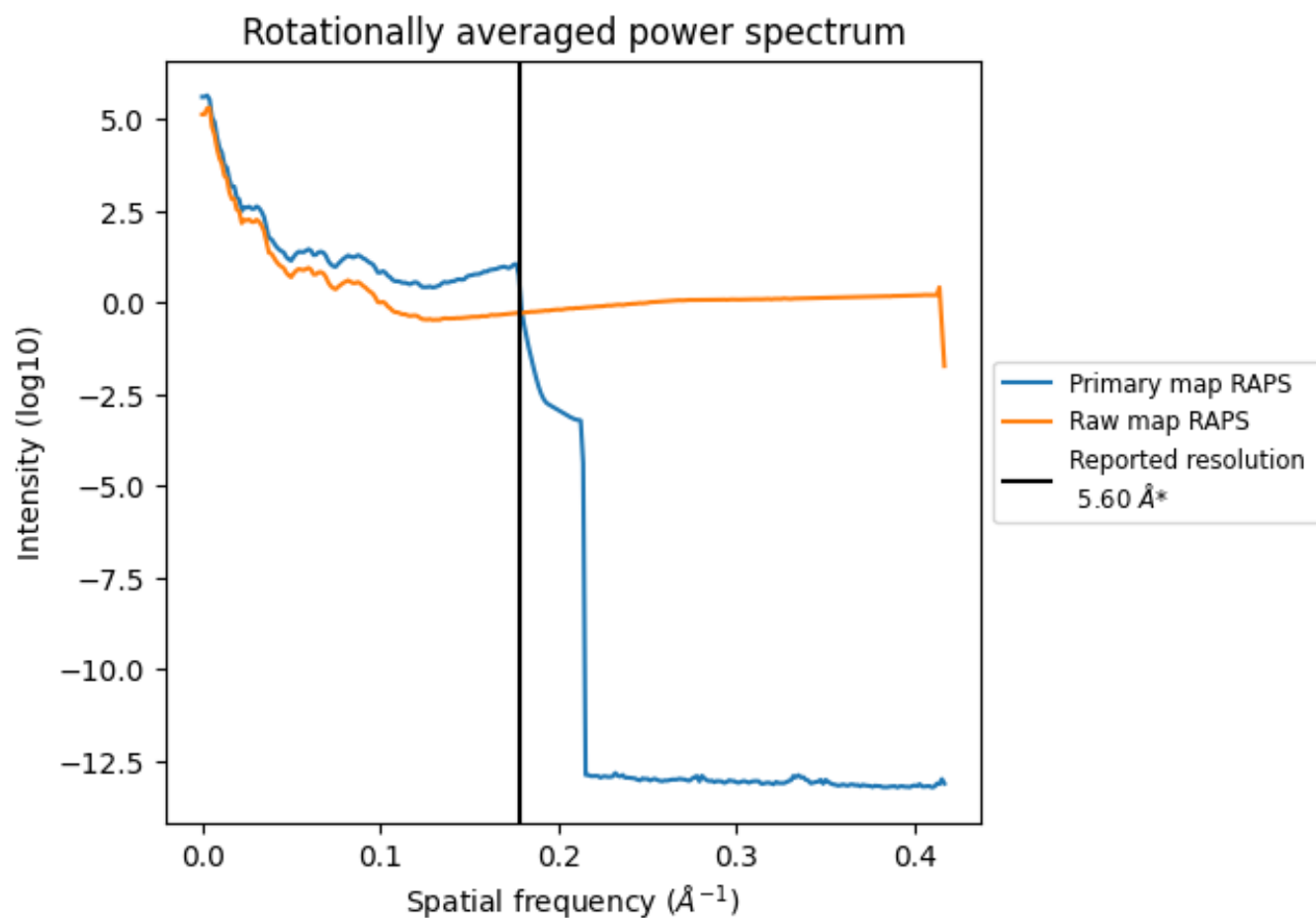
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4620 nm³; this corresponds to an approximate mass of 4173 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 ⓘ

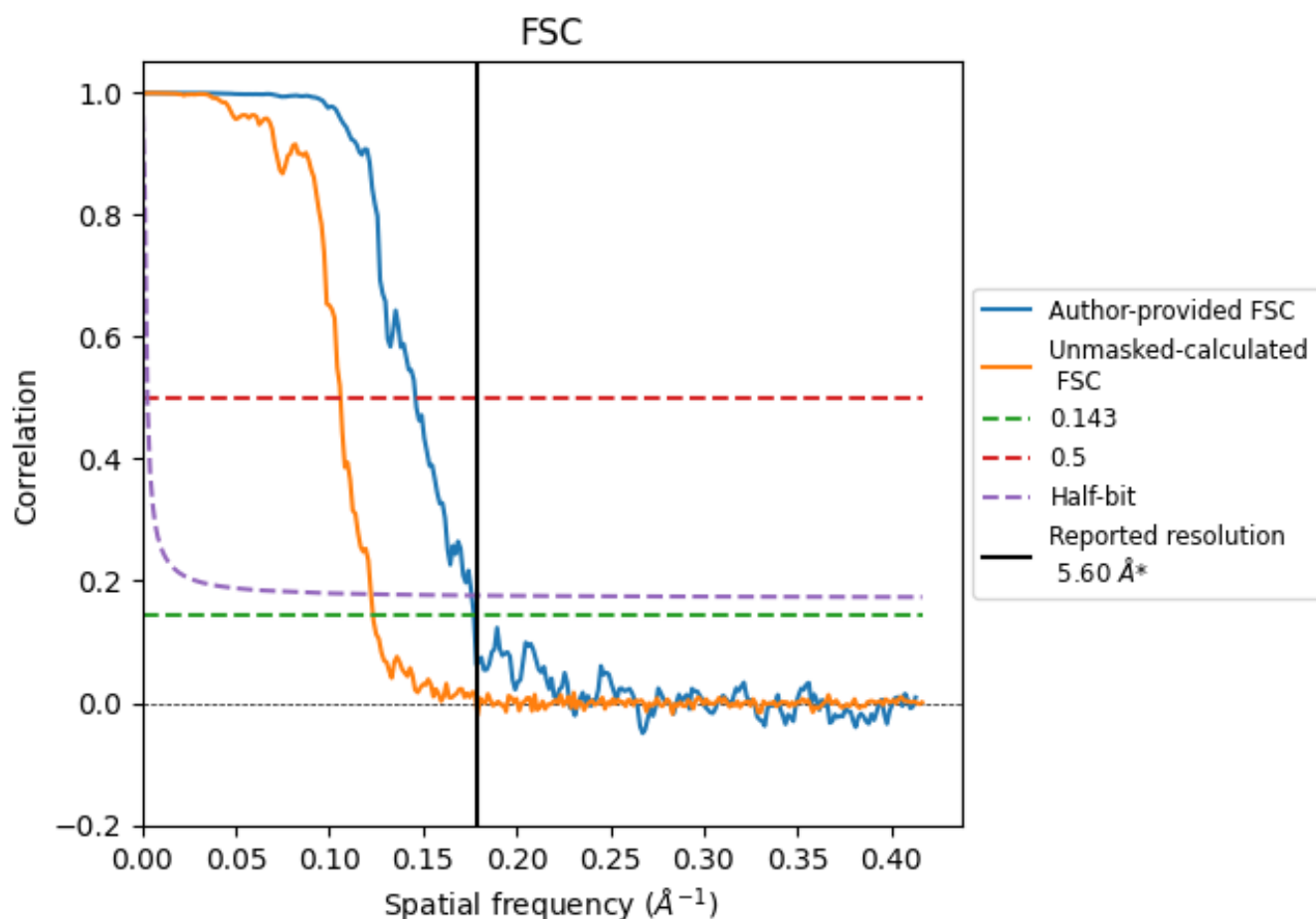


*Reported resolution corresponds to spatial frequency of 0.179 Å⁻¹

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 $0.179 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

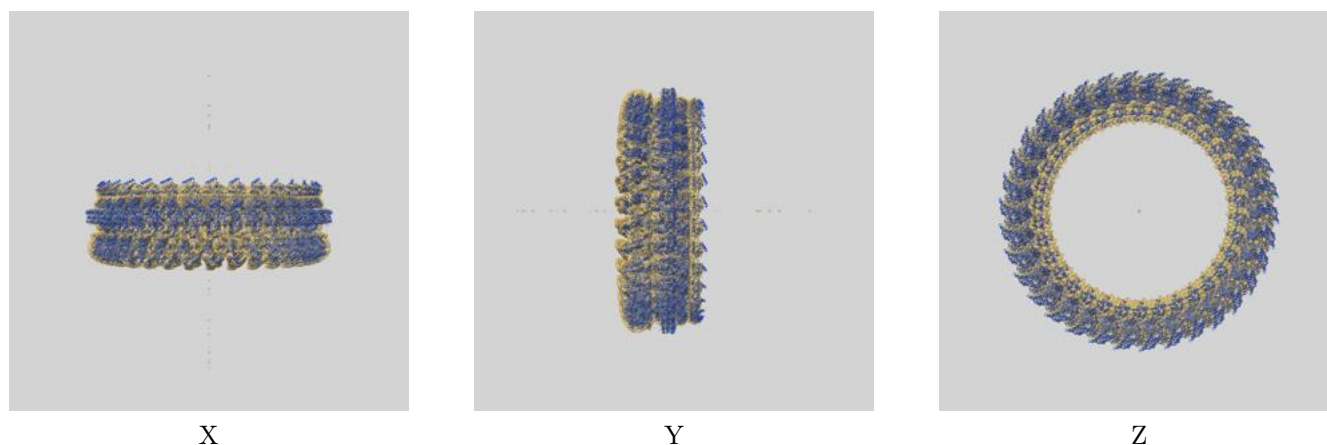
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.60	-	-
Author-provided FSC curve	5.64	6.85	5.68
Unmasked-calculated*	8.11	9.44	8.18

*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 8.11 differs from the reported value 5.6 by more than 10 %

9 Map-model fit [i](#)

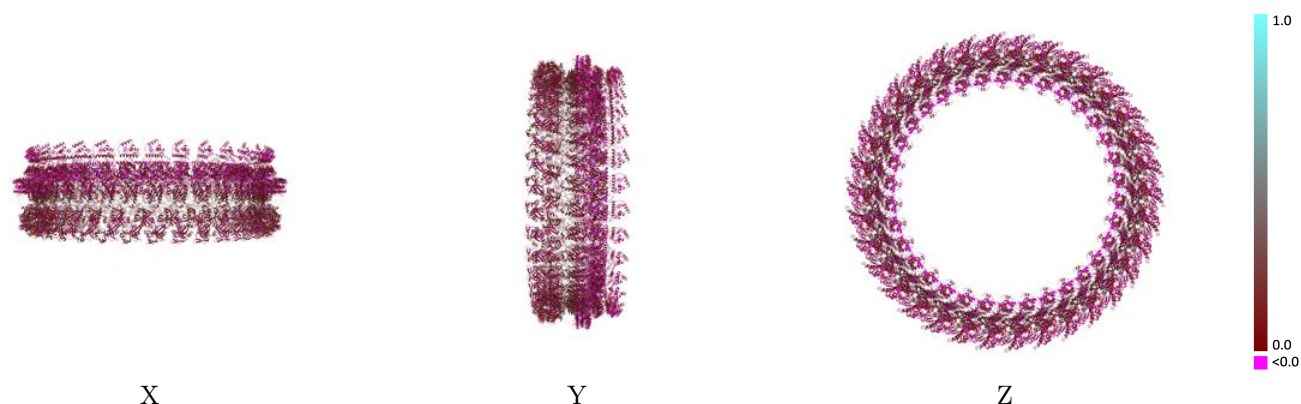
This section contains information regarding the fit between EMDB map EMD-37570 and PDB model 8WIW. Per-residue inclusion information can be found in section [3](#) on page [27](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.08 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](#)

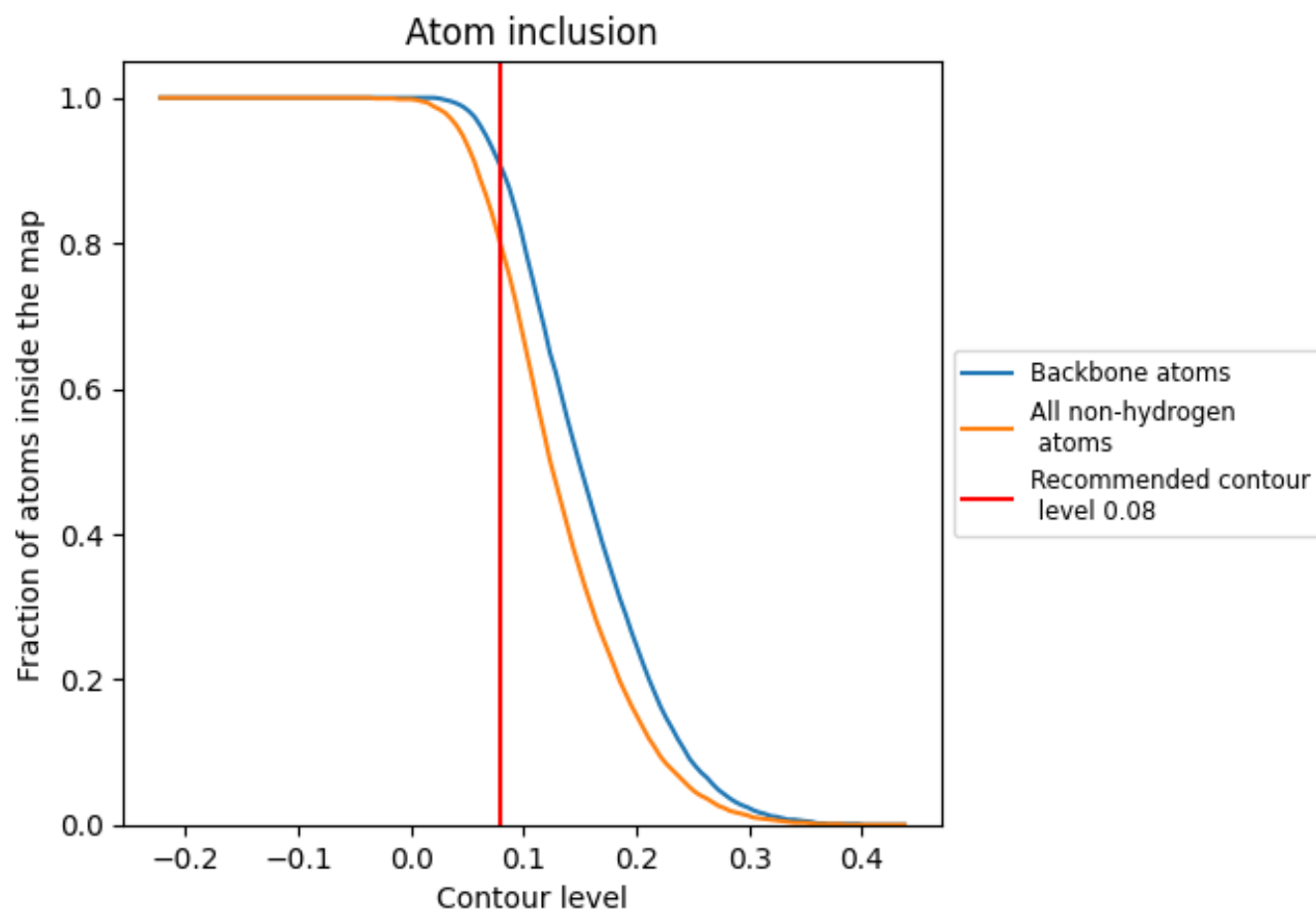


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 80% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.1300
0	 0.8680	 0.1720
1	 0.8660	 0.1660
2	 0.8750	 0.1640
3	 0.7770	 0.0820
4	 0.5350	 0.1050
5	 0.8660	 0.1670
6	 0.8780	 0.1620
7	 0.8670	 0.1670
8	 0.7720	 0.0800
9	 0.5430	 0.1070
A0	 0.8690	 0.1670
A1	 0.8690	 0.1710
A2	 0.8470	 0.0510
A3	 0.8680	 0.1670
A4	 0.7750	 0.0820
A5	 0.5410	 0.1050
A6	 0.8620	 0.1650
A7	 0.8740	 0.1650
A8	 0.8680	 0.1730
A9	 0.8370	 0.0510
AA	 0.8680	 0.1690
AB	 0.8660	 0.1700
AC	 0.8660	 0.1700
AD	 0.8600	 0.1680
AE	 0.8680	 0.1680
AF	 0.8660	 0.1690
AG	 0.8680	 0.1680
AH	 0.8680	 0.1690
AI	 0.8660	 0.1660
AJ	 0.8780	 0.1640
AK	 0.8650	 0.1690
AL	 0.8690	 0.1670
AM	 0.7740	 0.0780
AN	 0.5340	 0.1050



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
AO	 0.8650	 0.1650
AP	 0.8800	 0.1650
AQ	 0.8650	 0.1710
AR	 0.8690	 0.1670
AS	 0.7740	 0.0810
AT	 0.5410	 0.1040
AU	 0.8660	 0.1660
AV	 0.8780	 0.1630
AW	 0.8650	 0.1710
AX	 0.8670	 0.1660
AY	 0.7740	 0.0800
AZ	 0.5290	 0.1030
Aa	 0.8630	 0.1630
Ab	 0.8750	 0.1650
Ac	 0.8710	 0.1700
Ad	 0.8670	 0.1660
Ae	 0.7730	 0.0790
Af	 0.5210	 0.1040
Ag	 0.8630	 0.1640
Ah	 0.8720	 0.1630
Ai	 0.8630	 0.1710
Aj	 0.8660	 0.1680
Ak	 0.7700	 0.0800
Al	 0.5220	 0.1030
Am	 0.8600	 0.1660
An	 0.8660	 0.1640
Ao	 0.8660	 0.1700
Ap	 0.8680	 0.1660
Aq	 0.7730	 0.0810
Ar	 0.5220	 0.1030
As	 0.8600	 0.1640
At	 0.8750	 0.1660
Au	 0.8680	 0.1690
Av	 0.8680	 0.1670
Aw	 0.7730	 0.0800
Ax	 0.5290	 0.1040
Ay	 0.8660	 0.1650
Az	 0.8780	 0.1660
B0	 0.8560	 0.0530
B1	 0.8780	 0.1640
B2	 0.8680	 0.1740
B3	 0.8470	 0.0530

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
B4	 0.8670	 0.1670
B5	 0.7720	 0.0820
B6	 0.5430	 0.1050
B7	 0.8660	 0.1680
B8	 0.8780	 0.1630
B9	 0.8650	 0.1720
BA	 0.7710	 0.0800
BB	 0.5400	 0.1030
BC	 0.8620	 0.1670
BD	 0.8800	 0.1640
BE	 0.8680	 0.1710
BF	 0.8510	 0.0510
BG	 0.8660	 0.1660
BH	 0.7710	 0.0800
BI	 0.5410	 0.1030
BJ	 0.8660	 0.1670
BK	 0.8770	 0.1620
BL	 0.8660	 0.1740
BM	 0.8420	 0.0560
BN	 0.8690	 0.1660
BO	 0.7750	 0.0810
BP	 0.5280	 0.1020
BQ	 0.8650	 0.1690
BR	 0.8740	 0.1650
BS	 0.8660	 0.1750
BT	 0.8560	 0.0570
BU	 0.8670	 0.1660
BV	 0.7750	 0.0820
BW	 0.5180	 0.1030
BX	 0.8650	 0.1670
BY	 0.8720	 0.1650
BZ	 0.8600	 0.1710
Ba	 0.8510	 0.0560
Bb	 0.8650	 0.1670
Bc	 0.7740	 0.0810
Bd	 0.5270	 0.1030
Be	 0.8630	 0.1650
Bf	 0.8710	 0.1670
Bg	 0.8680	 0.1710
Bh	 0.8510	 0.0520
Bi	 0.8670	 0.1660
Bj	 0.7710	 0.0810

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bk	 0.5200	 0.1070
Bl	 0.8630	 0.1650
Bm	 0.8740	 0.1640
Bn	 0.8660	 0.1720
Bo	 0.8420	 0.0520
Bp	 0.8700	 0.1660
Bq	 0.7740	 0.0810
Br	 0.5240	 0.1080
Bs	 0.8660	 0.1660
Bt	 0.8750	 0.1650
Bu	 0.8680	 0.1720
Bv	 0.8510	 0.0530
Bw	 0.8680	 0.1670
Bx	 0.7770	 0.0820
By	 0.5350	 0.1050
Bz	 0.8660	 0.1690
C	 0.8370	 0.0560
C1	 0.8620	 0.1630
C2	 0.8740	 0.1620
CA	 0.8690	 0.1660
CB	 0.7740	 0.0820
CC	 0.5340	 0.1030
CD	 0.8650	 0.1650
CE	 0.8800	 0.1650
CF	 0.8650	 0.1720
CG	 0.8560	 0.0580
CH	 0.8690	 0.1650
CI	 0.7740	 0.0830
CJ	 0.5410	 0.1040
CK	 0.8660	 0.1650
CL	 0.8780	 0.1640
CM	 0.8650	 0.1730
CN	 0.8370	 0.0570
CO	 0.8670	 0.1640
CP	 0.7740	 0.0820
CQ	 0.5290	 0.1030
CR	 0.8630	 0.1620
CS	 0.8750	 0.1650
CT	 0.8710	 0.1710
CU	 0.8510	 0.0530
CV	 0.8670	 0.1640
CW	 0.7730	 0.0810

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
CX	 0.5210	 0.1050
CY	 0.8630	 0.1620
CZ	 0.8720	 0.1620
Ca	 0.8630	 0.1710
Cb	 0.8510	 0.0520
Cc	 0.8660	 0.1660
Cd	 0.7700	 0.0810
Ce	 0.5220	 0.1050
Cf	 0.8600	 0.1650
Cg	 0.8660	 0.1630
Ch	 0.8660	 0.1730
Ci	 0.8560	 0.0560
Cj	 0.8680	 0.1660
Ck	 0.7730	 0.0820
Cl	 0.5220	 0.1040
Cm	 0.8600	 0.1640
Cn	 0.8750	 0.1630
Co	 0.8680	 0.1720
Cp	 0.8420	 0.0560
Cq	 0.8680	 0.1670
Cr	 0.7730	 0.0810
Cs	 0.5290	 0.1040
Ct	 0.8660	 0.1640
Cu	 0.8780	 0.1610
Cv	 0.8690	 0.1710
Cw	 0.8470	 0.0540
Cx	 0.8680	 0.1670
Cy	 0.7750	 0.0820
Cz	 0.5410	 0.1050
D	 0.8510	 0.0530
E	 0.8420	 0.0550
F	 0.8560	 0.0600
G	 0.8510	 0.0580
H	 0.8510	 0.0510
I	 0.8420	 0.0510
J	 0.8510	 0.0510
K	 0.8470	 0.0550
L	 0.8560	 0.0550
M	 0.8560	 0.0550
N	 0.8370	 0.0550
O	 0.8510	 0.0520
P	 0.8510	 0.0490

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Q	 0.8560	 0.0560
R	 0.8420	 0.0540
S	 0.8690	 0.1660
T	 0.8660	 0.1660
U	 0.8690	 0.1650
V	 0.8670	 0.1670
W	 0.8650	 0.1690
X	 0.8670	 0.1680
Y	 0.8700	 0.1670
Z	 0.7710	 0.0810
a	 0.7710	 0.0820
b	 0.7750	 0.0820
c	 0.7750	 0.0820
d	 0.7740	 0.0790
e	 0.7710	 0.0810
f	 0.7740	 0.0800
g	 0.8680	 0.1680
h	 0.5400	 0.1040
i	 0.5410	 0.1030
j	 0.5280	 0.1020
k	 0.5180	 0.1010
l	 0.5270	 0.1040
m	 0.5200	 0.1050
n	 0.5240	 0.1080
o	 0.8620	 0.1630
p	 0.8660	 0.1650
q	 0.8650	 0.1650
r	 0.8650	 0.1630
s	 0.8630	 0.1630
t	 0.8630	 0.1630
u	 0.8800	 0.1620
v	 0.8770	 0.1610
w	 0.8740	 0.1640
x	 0.8720	 0.1630
y	 0.8710	 0.1630
z	 0.8740	 0.1630