



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 03:07 PM UTC

PDB ID : 8VKR / pdb_00008vkr
EMDB ID : EMD-43328
Title : CW Flagellar Switch Complex with extra density - FliF, FliG, FliM, and FliN forming the C-ring from Salmonella
Authors : Singh, P.K.; Iverson, T.M.
Deposited on : 2024-01-09
Resolution : 5.90 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

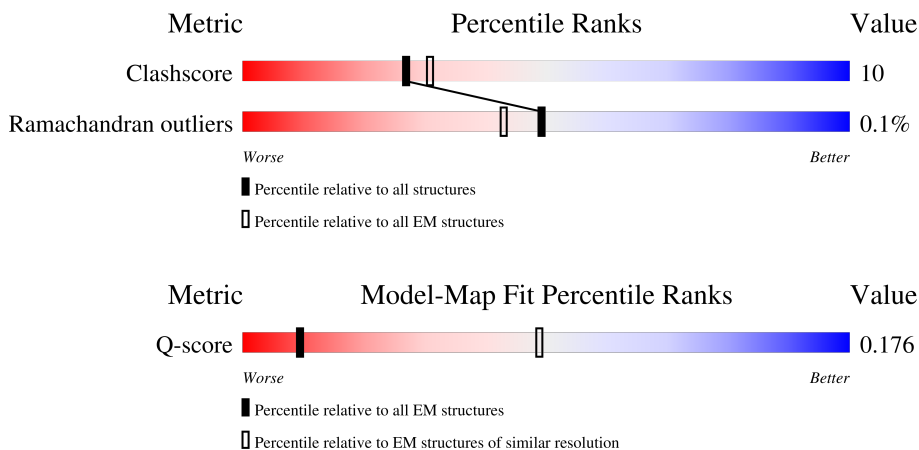
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	501 (5.40 - 6.40)

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

Mol	Chain	Length	Quality of chain
1	A	560	7% 8% 92%
1	BC	560	7% 8% 92%
1	BF	560	7% 8% 92%
1	DB	560	7% 8% 92%
1	DE	560	7% 8% 92%

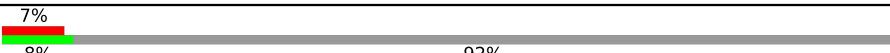
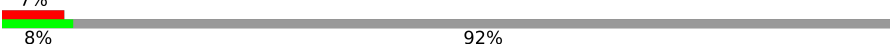
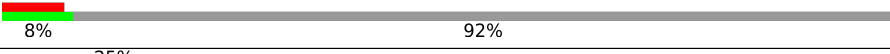
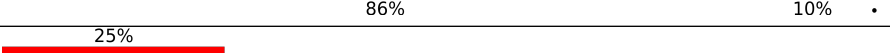
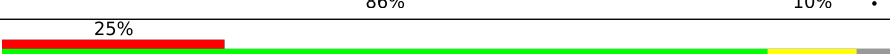
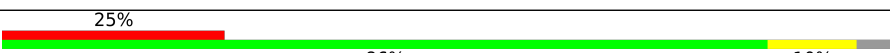
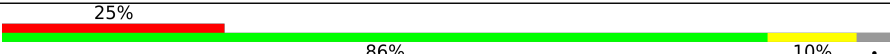
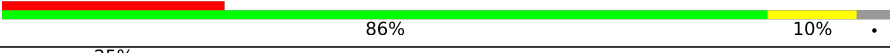
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Mol	Chain	Length	Quality of chain	
1	F	560		92%
1	FA	560		92%
1	FD	560		92%
1	FG	560		92%
1	HC	560		92%
1	HF	560		92%
1	I	560		92%
1	JB	560		92%
1	JE	560		92%
1	LA	560		92%
1	LD	560		92%
1	LG	560		92%
1	NC	560		92%
1	NF	560		92%
1	PB	560		92%
1	PE	560		92%
1	RA	560		92%
1	RD	560		92%
1	RG	560		92%
1	S	560		92%
1	TC	560		92%
1	TF	560		92%
1	VB	560		92%
1	VE	560		92%
1	XA	560		92%

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Mol	Chain	Length	Quality of chain
1	XD	560	
1	Z	560	
1	ZC	560	
1	ZF	560	
2	AA	331	
2	AD	331	
2	AG	331	
2	B	331	
2	CC	331	
2	CF	331	
2	EB	331	
2	EE	331	
2	G	331	
2	GA	331	
2	GD	331	
2	GG	331	
2	IC	331	
2	IF	331	
2	J	331	
2	KB	331	
2	KE	331	
2	MA	331	
2	MD	331	
2	MG	331	
2	OC	331	

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Mol	Chain	Length	Quality of chain
2	OF	331	25% 86% 10% .
2	QB	331	25% 85% 11% .
2	QE	331	26% 85% 11% .
2	SA	331	25% 86% 10% .
2	SD	331	25% 86% 10% .
2	SG	331	25% 86% 10% .
2	T	331	25% 86% 10% .
2	UC	331	25% 85% 11% .
2	UF	331	25% 86% 10% .
2	WB	331	25% 86% 10% .
2	WE	331	25% 86% 10% .
2	YA	331	25% 86% 10% .
2	YD	331	25% 86% 10% .
3	BA	334	23% 78% 8% 14%
3	BD	334	23% 78% 8% 14%
3	BG	334	23% 78% 8% 14%
3	C	334	23% 78% 8% 14%
3	DC	334	23% 78% 8% 14%
3	DF	334	23% 78% 8% 14%
3	FB	334	23% 78% 8% 14%
3	FE	334	23% 78% 8% 14%
3	HA	334	23% 78% 8% 14%
3	HD	334	23% 78% 8% 14%
3	HG	334	23% 78% 8% 14%
3	JC	334	23% 78% 8% 14%

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Mol	Chain	Length	Quality of chain
3	JF	334	23% 78% 8% 14%
3	K	334	23% 78% 8% 14%
3	LB	334	23% 78% 8% 14%
3	LE	334	23% 78% 8% 14%
3	M	334	23% 78% 8% 14%
3	NA	334	23% 78% 8% 14%
3	ND	334	23% 78% 8% 14%
3	NG	334	23% 78% 8% 14%
3	PC	334	23% 78% 8% 14%
3	PF	334	23% 78% 8% 14%
3	RB	334	23% 78% 8% 14%
3	RE	334	23% 78% 8% 14%
3	TA	334	23% 78% 8% 14%
3	TD	334	23% 78% 8% 14%
3	TG	334	23% 78% 8% 14%
3	V	334	23% 78% 8% 14%
3	VC	334	23% 78% 8% 14%
3	VF	334	23% 78% 8% 14%
3	XB	334	23% 78% 8% 14%
3	XE	334	23% 78% 8% 14%
3	ZA	334	23% 78% 8% 14%
3	ZD	334	23% 78% 8% 14%
4	AB	137	36% 63% 5% 32%
4	AC	137	50% 9% 41%
4	AE	137	36% 61% 7% 32%

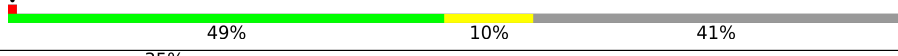
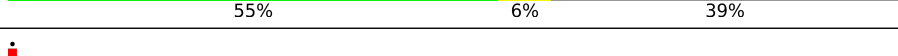
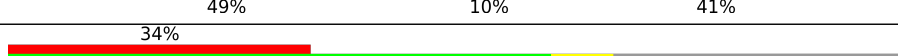
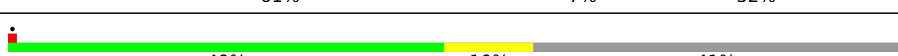
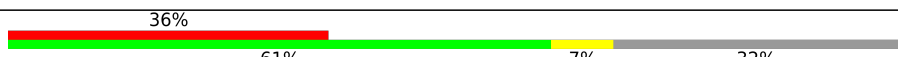
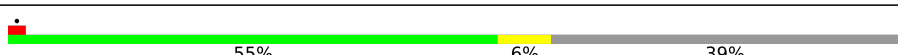
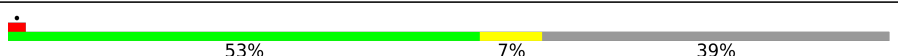
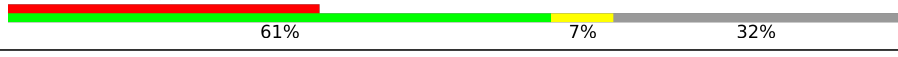
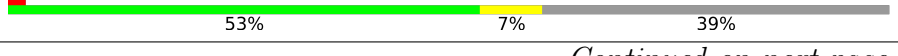
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Mol	Chain	Length	Quality of chain
4	AF	137	
4	BB	137	
4	BE	137	
4	CA	137	
4	CB	137	
4	CD	137	
4	CE	137	
4	CG	137	
4	D	137	
4	DA	137	
4	DD	137	
4	DG	137	
4	E	137	
4	EA	137	
4	EC	137	
4	ED	137	
4	EF	137	
4	EG	137	
4	FC	137	
4	FF	137	
4	GB	137	
4	GC	137	
4	GE	137	
4	GF	137	
4	H	137	

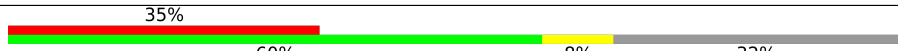
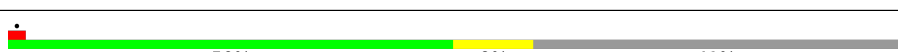
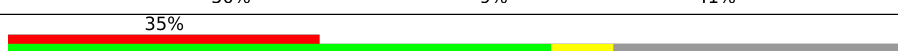
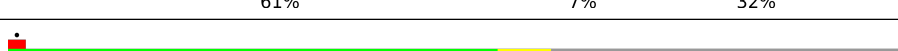
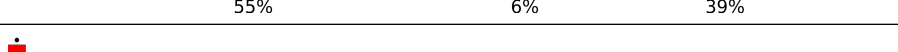
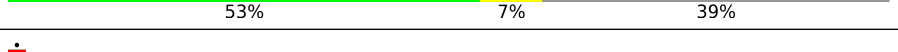
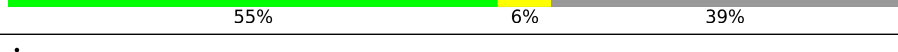
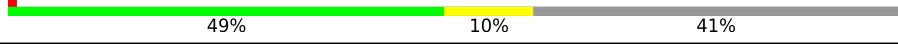
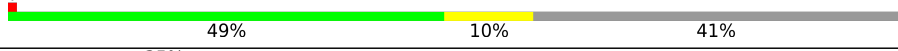
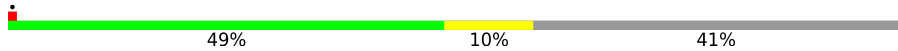
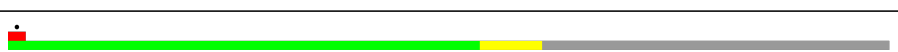
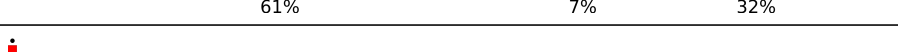
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Mol	Chain	Length	Quality of chain
4	HB	137	
4	HE	137	
4	IA	137	
4	IB	137	
4	ID	137	
4	IE	137	
4	IG	137	
4	JA	137	
4	JD	137	
4	JG	137	
4	KA	137	
4	KC	137	
4	KD	137	
4	KF	137	
4	KG	137	
4	L	137	
4	LC	137	
4	LF	137	
4	MB	137	
4	MC	137	
4	ME	137	
4	MF	137	
4	N	137	
4	NB	137	
4	NE	137	

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Mol	Chain	Length	Quality of chain
4	O	137	
4	OA	137	
4	OB	137	
4	OD	137	
4	OE	137	
4	OG	137	
4	P	137	
4	PA	137	
4	PD	137	
4	PG	137	
4	Q	137	
4	QA	137	
4	QC	137	
4	QD	137	
4	QF	137	
4	QG	137	
4	R	137	
4	RC	137	
4	RF	137	
4	SB	137	
4	SC	137	
4	SE	137	
4	SF	137	
4	TB	137	
4	TE	137	

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Mol	Chain	Length	Quality of chain
4	UA	137	
4	UB	137	
4	UD	137	
4	UE	137	
4	UG	137	
4	VA	137	
4	VD	137	
4	VG	137	
4	W	137	
4	WA	137	
4	WC	137	
4	WD	137	
4	WF	137	
4	WG	137	
4	X	137	
4	XC	137	
4	XF	137	
4	Y	137	
4	YB	137	
4	YC	137	
4	YE	137	
4	YF	137	
4	ZB	137	
4	ZE	137	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 152898 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	F	47	Total 234	C 140	N 47	O 47	0	0
1	A	47	Total 234	C 140	N 47	O 47	0	0
1	I	47	Total 234	C 140	N 47	O 47	0	0
1	S	47	Total 234	C 140	N 47	O 47	0	0
1	Z	47	Total 234	C 140	N 47	O 47	0	0
1	FA	47	Total 234	C 140	N 47	O 47	0	0
1	LA	47	Total 234	C 140	N 47	O 47	0	0
1	RA	47	Total 234	C 140	N 47	O 47	0	0
1	XA	47	Total 234	C 140	N 47	O 47	0	0
1	DB	47	Total 234	C 140	N 47	O 47	0	0
1	JB	47	Total 234	C 140	N 47	O 47	0	0
1	PB	47	Total 234	C 140	N 47	O 47	0	0
1	VB	47	Total 234	C 140	N 47	O 47	0	0
1	BC	47	Total 234	C 140	N 47	O 47	0	0
1	HC	47	Total 234	C 140	N 47	O 47	0	0
1	NC	47	Total 234	C 140	N 47	O 47	0	0
1	TC	47	Total 234	C 140	N 47	O 47	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	ZC	47	Total	C	N	O	0	0
			234	140	47	47		
1	FD	47	Total	C	N	O	0	0
			234	140	47	47		
1	LD	47	Total	C	N	O	0	0
			234	140	47	47		
1	RD	47	Total	C	N	O	0	0
			234	140	47	47		
1	XD	47	Total	C	N	O	0	0
			234	140	47	47		
1	DE	47	Total	C	N	O	0	0
			234	140	47	47		
1	JE	47	Total	C	N	O	0	0
			234	140	47	47		
1	PE	47	Total	C	N	O	0	0
			234	140	47	47		
1	VE	47	Total	C	N	O	0	0
			234	140	47	47		
1	BF	47	Total	C	N	O	0	0
			234	140	47	47		
1	HF	47	Total	C	N	O	0	0
			234	140	47	47		
1	NF	47	Total	C	N	O	0	0
			234	140	47	47		
1	TF	47	Total	C	N	O	0	0
			234	140	47	47		
1	ZF	47	Total	C	N	O	0	0
			234	140	47	47		
1	FG	47	Total	C	N	O	0	0
			234	140	47	47		
1	LG	47	Total	C	N	O	0	0
			234	140	47	47		
1	RG	47	Total	C	N	O	0	0
			234	140	47	47		

- Molecule 2 is a protein called Flagellar motor switch protein FliG.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	319	Total	C	N	O	0	0
			1579	941	319	319		
2	B	319	Total	C	N	O	0	0
			1579	941	319	319		

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	J	319	Total 1579	C 941	N 319	O 319	0	0
2	T	319	Total 1579	C 941	N 319	O 319	0	0
2	AA	319	Total 1579	C 941	N 319	O 319	0	0
2	GA	319	Total 1579	C 941	N 319	O 319	0	0
2	MA	319	Total 1579	C 941	N 319	O 319	0	0
2	SA	319	Total 1579	C 941	N 319	O 319	0	0
2	YA	319	Total 1579	C 941	N 319	O 319	0	0
2	EB	319	Total 1579	C 941	N 319	O 319	0	0
2	KB	319	Total 1579	C 941	N 319	O 319	0	0
2	QB	319	Total 1579	C 941	N 319	O 319	0	0
2	WB	319	Total 1579	C 941	N 319	O 319	0	0
2	CC	319	Total 1579	C 941	N 319	O 319	0	0
2	IC	319	Total 1579	C 941	N 319	O 319	0	0
2	OC	319	Total 1579	C 941	N 319	O 319	0	0
2	UC	319	Total 1579	C 941	N 319	O 319	0	0
2	AD	319	Total 1579	C 941	N 319	O 319	0	0
2	GD	319	Total 1579	C 941	N 319	O 319	0	0
2	MD	319	Total 1579	C 941	N 319	O 319	0	0
2	SD	319	Total 1579	C 941	N 319	O 319	0	0
2	YD	319	Total 1579	C 941	N 319	O 319	0	0
2	EE	319	Total 1579	C 941	N 319	O 319	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	KE	319	Total 1579	C 941	N 319	O 319	0	0
2	QE	319	Total 1579	C 941	N 319	O 319	0	0
2	WE	319	Total 1579	C 941	N 319	O 319	0	0
2	CF	319	Total 1579	C 941	N 319	O 319	0	0
2	IF	319	Total 1579	C 941	N 319	O 319	0	0
2	OF	319	Total 1579	C 941	N 319	O 319	0	0
2	UF	319	Total 1579	C 941	N 319	O 319	0	0
2	AG	319	Total 1579	C 941	N 319	O 319	0	0
2	GG	319	Total 1579	C 941	N 319	O 319	0	0
2	MG	319	Total 1579	C 941	N 319	O 319	0	0
2	SG	319	Total 1579	C 941	N 319	O 319	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
3	M	287	Total 1420	C 846	N 287	O 287	0	0
3	C	287	Total 1420	C 846	N 287	O 287	0	0
3	K	287	Total 1420	C 846	N 287	O 287	0	0
3	V	287	Total 1420	C 846	N 287	O 287	0	0
3	BA	287	Total 1420	C 846	N 287	O 287	0	0
3	HA	287	Total 1420	C 846	N 287	O 287	0	0
3	NA	287	Total 1420	C 846	N 287	O 287	0	0
3	TA	287	Total 1420	C 846	N 287	O 287	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	ZA	287	Total	C	N	O	0	0
			1420	846	287	287		
3	FB	287	Total	C	N	O	0	0
			1420	846	287	287		
3	LB	287	Total	C	N	O	0	0
			1420	846	287	287		
3	RB	287	Total	C	N	O	0	0
			1420	846	287	287		
3	XB	287	Total	C	N	O	0	0
			1420	846	287	287		
3	DC	287	Total	C	N	O	0	0
			1420	846	287	287		
3	JC	287	Total	C	N	O	0	0
			1420	846	287	287		
3	PC	287	Total	C	N	O	0	0
			1420	846	287	287		
3	VC	287	Total	C	N	O	0	0
			1420	846	287	287		
3	BD	287	Total	C	N	O	0	0
			1420	846	287	287		
3	HD	287	Total	C	N	O	0	0
			1420	846	287	287		
3	ND	287	Total	C	N	O	0	0
			1420	846	287	287		
3	TD	287	Total	C	N	O	0	0
			1420	846	287	287		
3	ZD	287	Total	C	N	O	0	0
			1420	846	287	287		
3	FE	287	Total	C	N	O	0	0
			1420	846	287	287		
3	LE	287	Total	C	N	O	0	0
			1420	846	287	287		
3	RE	287	Total	C	N	O	0	0
			1420	846	287	287		
3	XE	287	Total	C	N	O	0	0
			1420	846	287	287		
3	DF	287	Total	C	N	O	0	0
			1420	846	287	287		
3	JF	287	Total	C	N	O	0	0
			1420	846	287	287		
3	PF	287	Total	C	N	O	0	0
			1420	846	287	287		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	VF	287	Total	C	N	O	0	0
			1420	846	287	287		
3	BG	287	Total	C	N	O	0	0
			1420	846	287	287		
3	HG	287	Total	C	N	O	0	0
			1420	846	287	287		
3	NG	287	Total	C	N	O	0	0
			1420	846	287	287		
3	TG	287	Total	C	N	O	0	0
			1420	846	287	287		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	N	93	Total	C	N	O	0	0
			456	270	93	93		
4	P	83	Total	C	N	O	0	0
			409	242	83	84		
4	Q	81	Total	C	N	O	0	0
			399	236	81	82		
4	D	93	Total	C	N	O	0	0
			456	270	93	93		
4	E	83	Total	C	N	O	0	0
			409	242	83	84		
4	H	81	Total	C	N	O	0	0
			399	236	81	82		
4	L	93	Total	C	N	O	0	0
			456	270	93	93		
4	O	83	Total	C	N	O	0	0
			409	242	83	84		
4	R	81	Total	C	N	O	0	0
			399	236	81	82		
4	W	93	Total	C	N	O	0	0
			456	270	93	93		
4	X	83	Total	C	N	O	0	0
			409	242	83	84		
4	Y	81	Total	C	N	O	0	0
			399	236	81	82		
4	CA	93	Total	C	N	O	0	0
			456	270	93	93		
4	DA	83	Total	C	N	O	0	0
			409	242	83	84		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	EA	81	Total	C	N	O	0	0
			399	236	81	82		
4	IA	93	Total	C	N	O	0	0
			456	270	93	93		
4	JA	83	Total	C	N	O	0	0
			409	242	83	84		
4	KA	81	Total	C	N	O	0	0
			399	236	81	82		
4	OA	93	Total	C	N	O	0	0
			456	270	93	93		
4	PA	83	Total	C	N	O	0	0
			409	242	83	84		
4	QA	81	Total	C	N	O	0	0
			399	236	81	82		
4	UA	93	Total	C	N	O	0	0
			456	270	93	93		
4	VA	83	Total	C	N	O	0	0
			409	242	83	84		
4	WA	81	Total	C	N	O	0	0
			399	236	81	82		
4	AB	93	Total	C	N	O	0	0
			456	270	93	93		
4	BB	83	Total	C	N	O	0	0
			409	242	83	84		
4	CB	81	Total	C	N	O	0	0
			399	236	81	82		
4	GB	93	Total	C	N	O	0	0
			456	270	93	93		
4	HB	83	Total	C	N	O	0	0
			409	242	83	84		
4	IB	81	Total	C	N	O	0	0
			399	236	81	82		
4	MB	93	Total	C	N	O	0	0
			456	270	93	93		
4	NB	83	Total	C	N	O	0	0
			409	242	83	84		
4	OB	81	Total	C	N	O	0	0
			399	236	81	82		
4	SB	93	Total	C	N	O	0	0
			456	270	93	93		
4	TB	83	Total	C	N	O	0	0
			409	242	83	84		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	UB	81	Total	C	N	O	0	0
			399	236	81	82		
4	YB	93	Total	C	N	O	0	0
			456	270	93	93		
4	ZB	83	Total	C	N	O	0	0
			409	242	83	84		
4	AC	81	Total	C	N	O	0	0
			399	236	81	82		
4	EC	93	Total	C	N	O	0	0
			456	270	93	93		
4	FC	83	Total	C	N	O	0	0
			409	242	83	84		
4	GC	81	Total	C	N	O	0	0
			399	236	81	82		
4	KC	93	Total	C	N	O	0	0
			456	270	93	93		
4	LC	83	Total	C	N	O	0	0
			409	242	83	84		
4	MC	81	Total	C	N	O	0	0
			399	236	81	82		
4	QC	93	Total	C	N	O	0	0
			456	270	93	93		
4	RC	83	Total	C	N	O	0	0
			409	242	83	84		
4	SC	81	Total	C	N	O	0	0
			399	236	81	82		
4	WC	93	Total	C	N	O	0	0
			456	270	93	93		
4	XC	83	Total	C	N	O	0	0
			409	242	83	84		
4	YC	81	Total	C	N	O	0	0
			399	236	81	82		
4	CD	93	Total	C	N	O	0	0
			456	270	93	93		
4	DD	83	Total	C	N	O	0	0
			409	242	83	84		
4	ED	81	Total	C	N	O	0	0
			399	236	81	82		
4	ID	93	Total	C	N	O	0	0
			456	270	93	93		
4	JD	83	Total	C	N	O	0	0
			409	242	83	84		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	KD	81	Total	C	N	O	0	0
			399	236	81	82		
4	OD	93	Total	C	N	O	0	0
			456	270	93	93		
4	PD	83	Total	C	N	O	0	0
			409	242	83	84		
4	QD	81	Total	C	N	O	0	0
			399	236	81	82		
4	UD	93	Total	C	N	O	0	0
			456	270	93	93		
4	VD	83	Total	C	N	O	0	0
			409	242	83	84		
4	WD	81	Total	C	N	O	0	0
			399	236	81	82		
4	AE	93	Total	C	N	O	0	0
			456	270	93	93		
4	BE	83	Total	C	N	O	0	0
			409	242	83	84		
4	CE	81	Total	C	N	O	0	0
			399	236	81	82		
4	GE	93	Total	C	N	O	0	0
			456	270	93	93		
4	HE	83	Total	C	N	O	0	0
			409	242	83	84		
4	IE	81	Total	C	N	O	0	0
			399	236	81	82		
4	ME	93	Total	C	N	O	0	0
			456	270	93	93		
4	NE	83	Total	C	N	O	0	0
			409	242	83	84		
4	OE	81	Total	C	N	O	0	0
			399	236	81	82		
4	SE	93	Total	C	N	O	0	0
			456	270	93	93		
4	TE	83	Total	C	N	O	0	0
			409	242	83	84		
4	UE	81	Total	C	N	O	0	0
			399	236	81	82		
4	YE	93	Total	C	N	O	0	0
			456	270	93	93		
4	ZE	83	Total	C	N	O	0	0
			409	242	83	84		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	AF	81	Total	C	N	O	0	0
			399	236	81	82		
4	EF	93	Total	C	N	O	0	0
			456	270	93	93		
4	FF	83	Total	C	N	O	0	0
			409	242	83	84		
4	GF	81	Total	C	N	O	0	0
			399	236	81	82		
4	KF	93	Total	C	N	O	0	0
			456	270	93	93		
4	LF	83	Total	C	N	O	0	0
			409	242	83	84		
4	MF	81	Total	C	N	O	0	0
			399	236	81	82		
4	QF	93	Total	C	N	O	0	0
			456	270	93	93		
4	RF	83	Total	C	N	O	0	0
			409	242	83	84		
4	SF	81	Total	C	N	O	0	0
			399	236	81	82		
4	WF	93	Total	C	N	O	0	0
			456	270	93	93		
4	XF	83	Total	C	N	O	0	0
			409	242	83	84		
4	YF	81	Total	C	N	O	0	0
			399	236	81	82		
4	CG	93	Total	C	N	O	0	0
			456	270	93	93		
4	DG	83	Total	C	N	O	0	0
			409	242	83	84		
4	EG	81	Total	C	N	O	0	0
			399	236	81	82		
4	IG	93	Total	C	N	O	0	0
			456	270	93	93		
4	JG	83	Total	C	N	O	0	0
			409	242	83	84		
4	KG	81	Total	C	N	O	0	0
			399	236	81	82		
4	OG	93	Total	C	N	O	0	0
			456	270	93	93		
4	PG	83	Total	C	N	O	0	0
			409	242	83	84		

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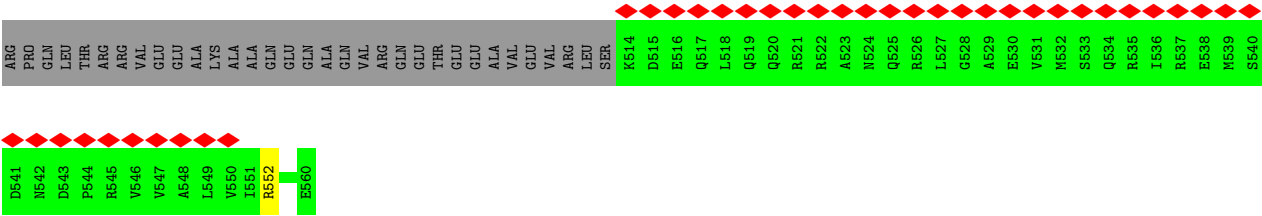
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Mol	Chain	Residues	Atoms				AltConf	Trace
4	QG	81	Total	C	N	O	0	0
			399	236	81	82		
4	UG	93	Total	C	N	O	0	0
			456	270	93	93		
4	VG	83	Total	C	N	O	0	0
			409	242	83	84		
4	WG	81	Total	C	N	O	0	0
			399	236	81	82		

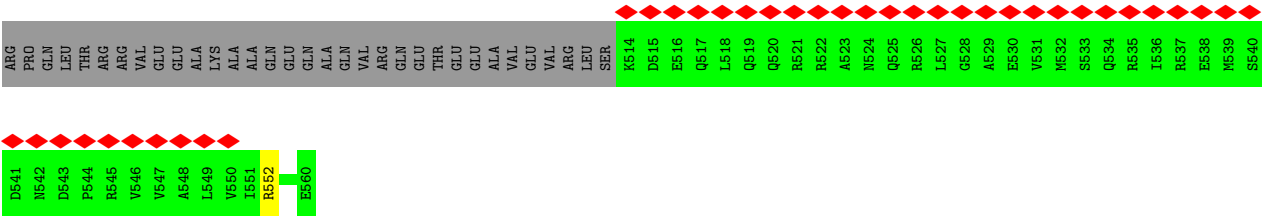
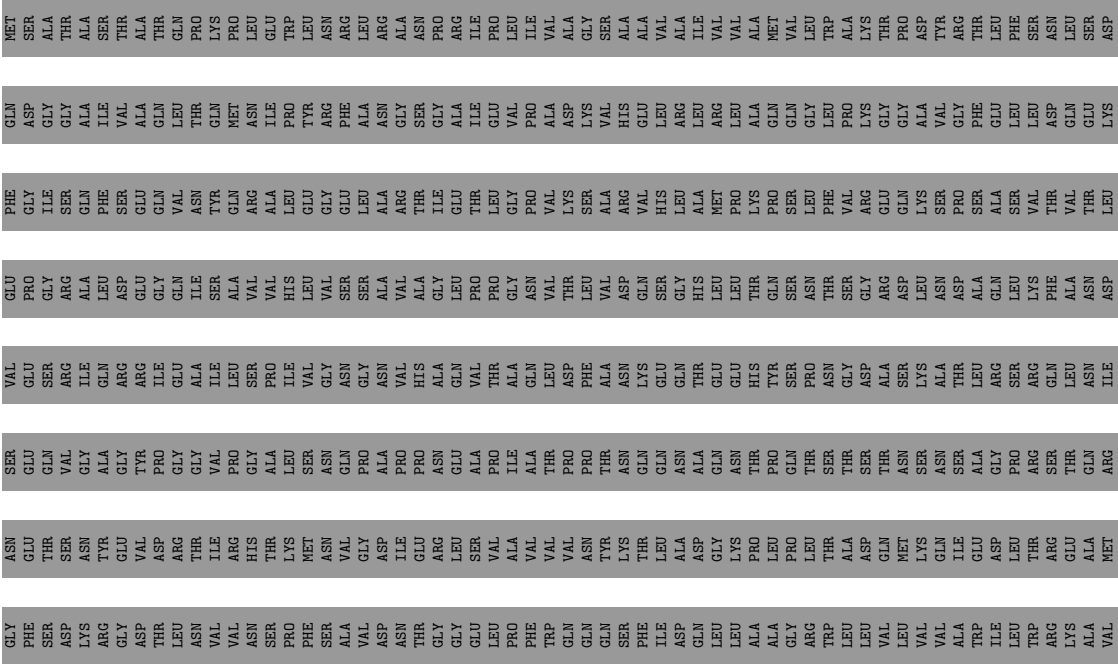
D541 N542 D543 P544 R545 V546 V547 A548 L549 V550 I551 R552 E560

Chain I: 7% 8% 92%

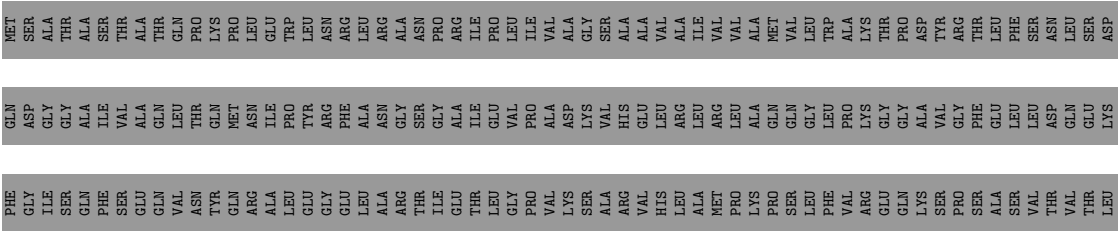




• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein



Chain LA:



D641	D642	D643	P644	R645	V646	V647	A648	L649	V650	R652	E660	ARG	PRO	GLN	LEU	THR	ARG	ARG	VAL	GLU	GLU	ALA	LYS	ALA	ALA	GLN	GLN	GLN	VAL	ARG	GLN	GLU	THR	GLU	ALA	ALA	VAL	GLU	VAL	ARG	LEU	SER	K514	D615	E516	Q617	L518	Q619	Q620	R621	R622	A623	N624	Q625	R626	L627	G628	A629	E630	V631	M632	S633	Q634	R635	I636	R637	E638	M639	S640
------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Chain XA:

[illegible]

Chain DB:

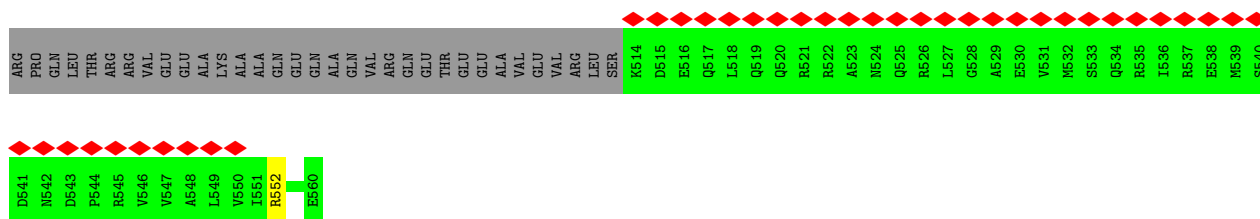
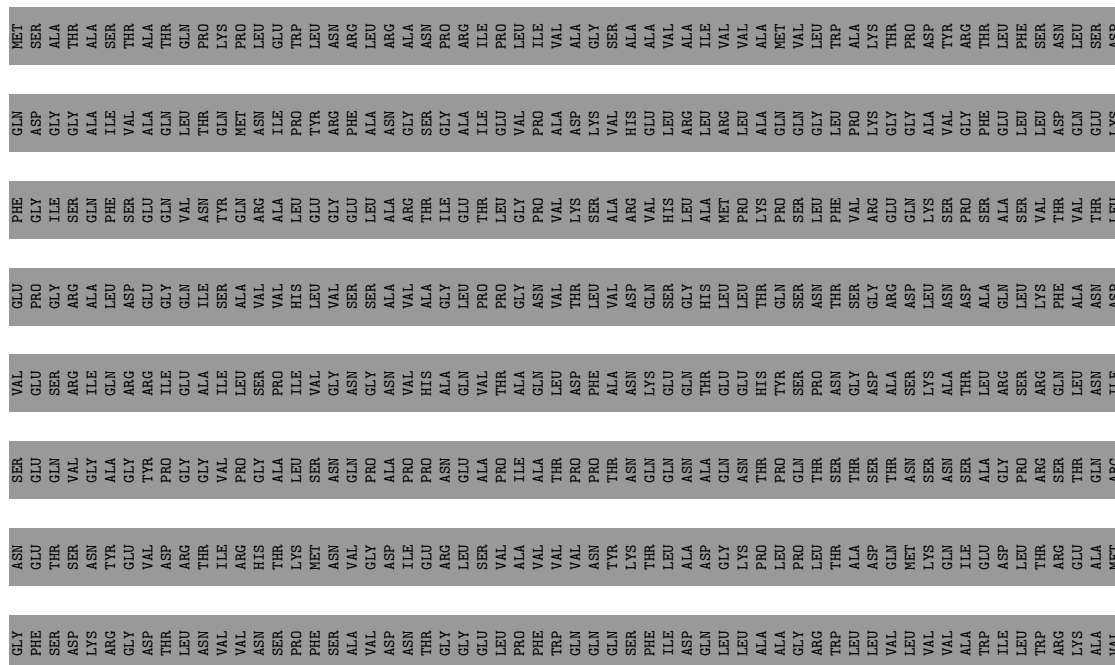
MET SER ALA ALA THR THR PRO PRO LYS LEU LEU TRP LEU ASN ARG ANG ARG ARG ASN ARG ARG ILE PRO PRO ILE LEU VAL VAL GLY SER SER ALA VAL VAL ALA ALA ILE VAL VAL VAL MET MET VAL VAL LEU TRP TYR THR THR LEU PHE SER ASN LEU SER SER

D541
N542
D543
P544
R545
V546
V547
A548
L549
V550
I551
R552
E560

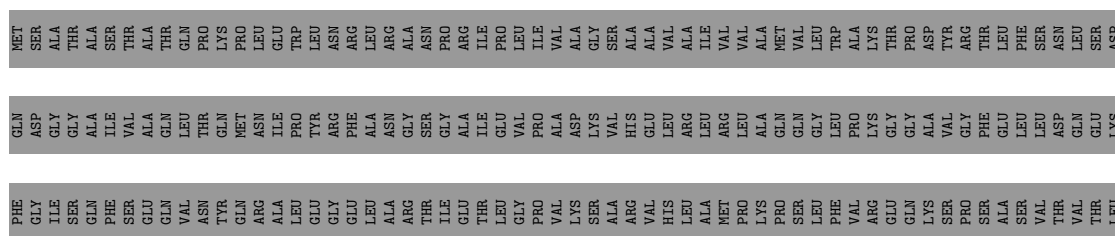
Chain JB:

[illegible]

- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein



Chain HC: 7% 8% 92%



D541	N542	D543	P544	R545	V546	V547	A548	L549	V550	I551	R552	E560
------	------	------	------	------	------	------	------	------	------	------	------	------

D541
N542
D543
P544
R545
V546
V547
A548
L549
V550
I551
R552
E560

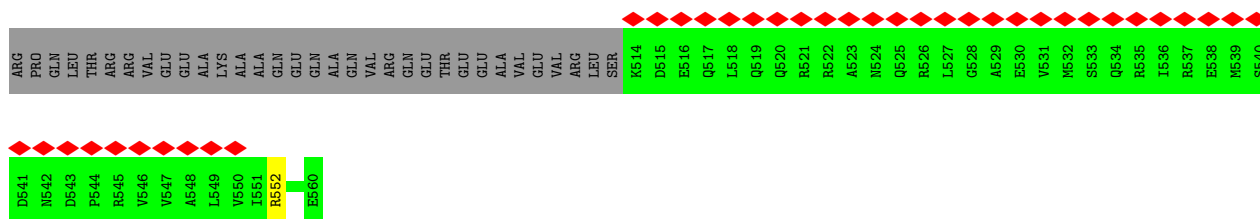
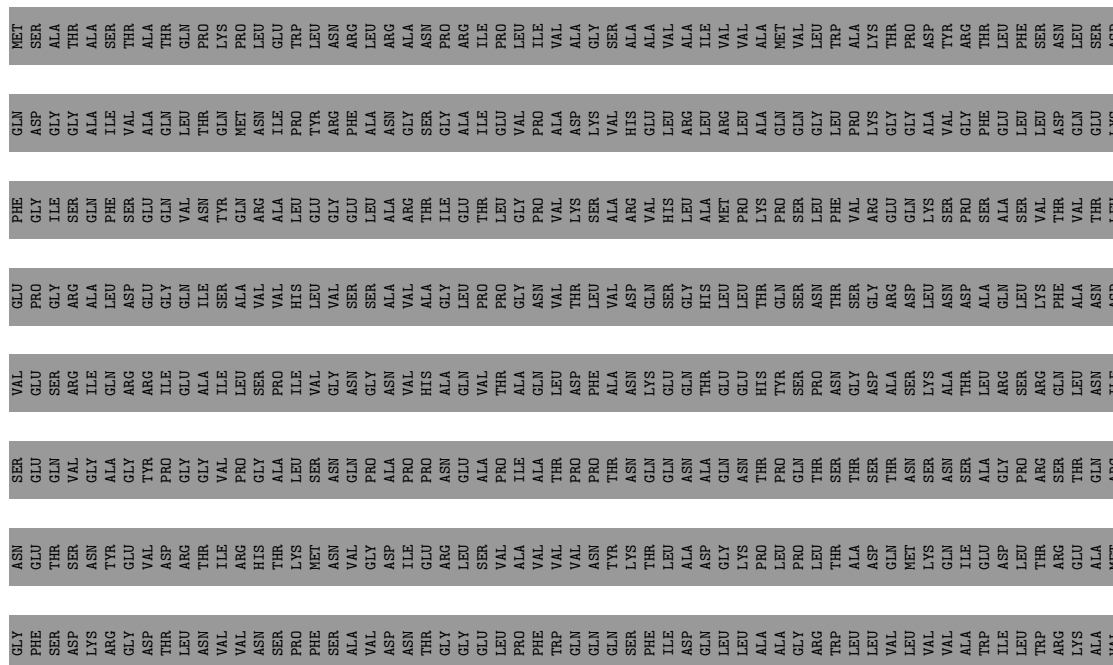
MET	SER	ALA	THR	ALA	SER	THR	THR	GLN	PRO	LYS	PRO	LEU	GLY	TRP	LEU	ASN	ARG	LEU	ALA	ARG	ALA	ASN	PRO	ARG	ILE	PRO	PRO	LEU	ILE	VAL	ALA	GLY	SER	ALA	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	THR	ALA	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER
-----	-----	-----	-----	-----	-----	-----	-----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

Diagram illustrating a 16-bit bus structure. The bus is divided into 16 segments, labeled D541, N542, D543, P544, R545, V546, V547, A548, L549, V550, I551, R552, and E560. The segments are connected sequentially, with a green arrow indicating the flow from the 15th segment to the 16th segment.

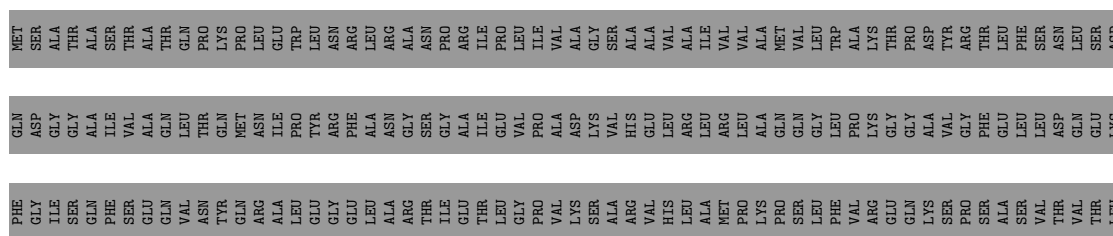
Chain FD: 7% 8% 92%



- Molecule 1: Flagellar M-ring protein



- Molecule 1: Flagellar M-ring protein



D541	N542	D543	P544	R545	V546	V547	A548	L549	V550	I551	R552	E560
------	------	------	------	------	------	------	------	------	------	------	------	------

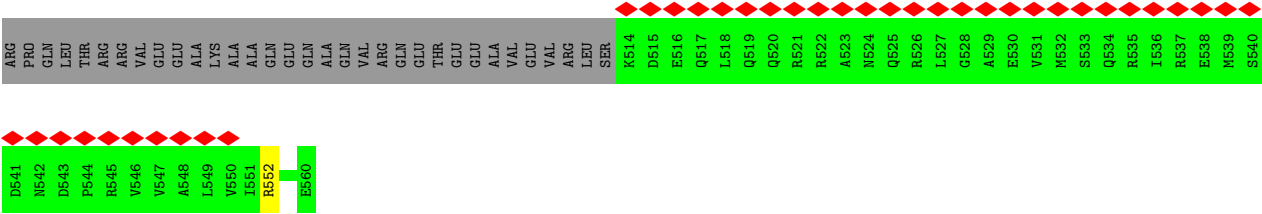
D541	N542	D543	P544	R545	V546	V547	A548	L549	V550	I551	R552	E560
------	------	------	------	------	------	------	------	------	------	------	------	------

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

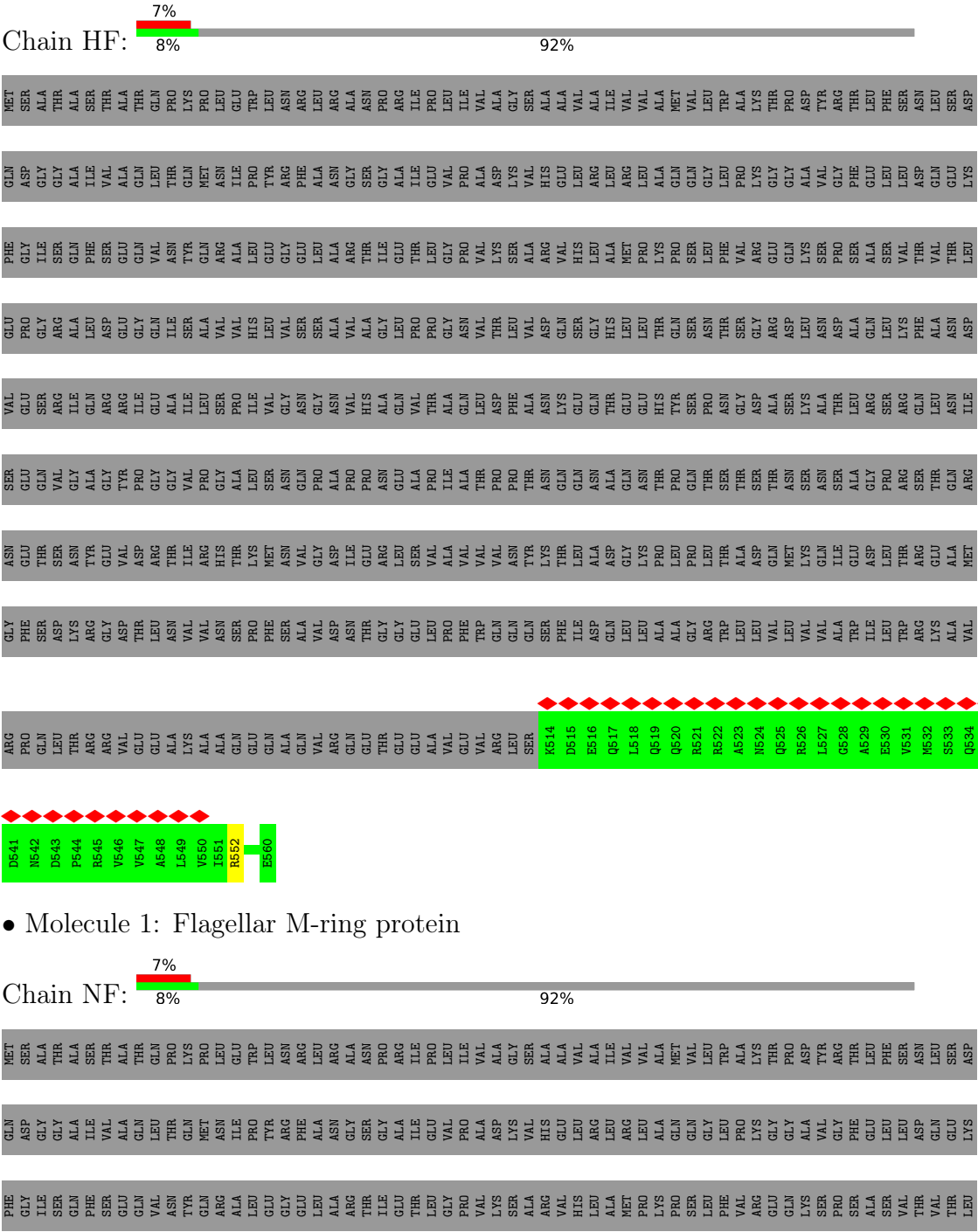
Diagram illustrating a 16-bit bus structure. The bus is divided into 16 segments, labeled D541, N542, D543, P544, R545, V546, V547, A548, L549, V550, I551, R552, and E560. The segments are color-coded: D541, N542, D543, P544, R545, V546, V547, A548, L549, V550, I551, and R552 are green; E560 is blue. A green arrow points from the R552 segment to the E560 segment.

Chain BF:

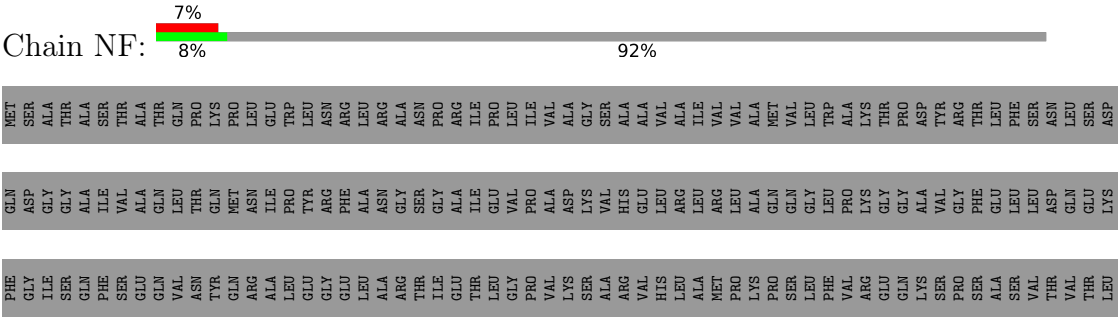




• Molecule 1: Flagellar M-ring protein



• Molecule 1: Flagellar M-ring protein



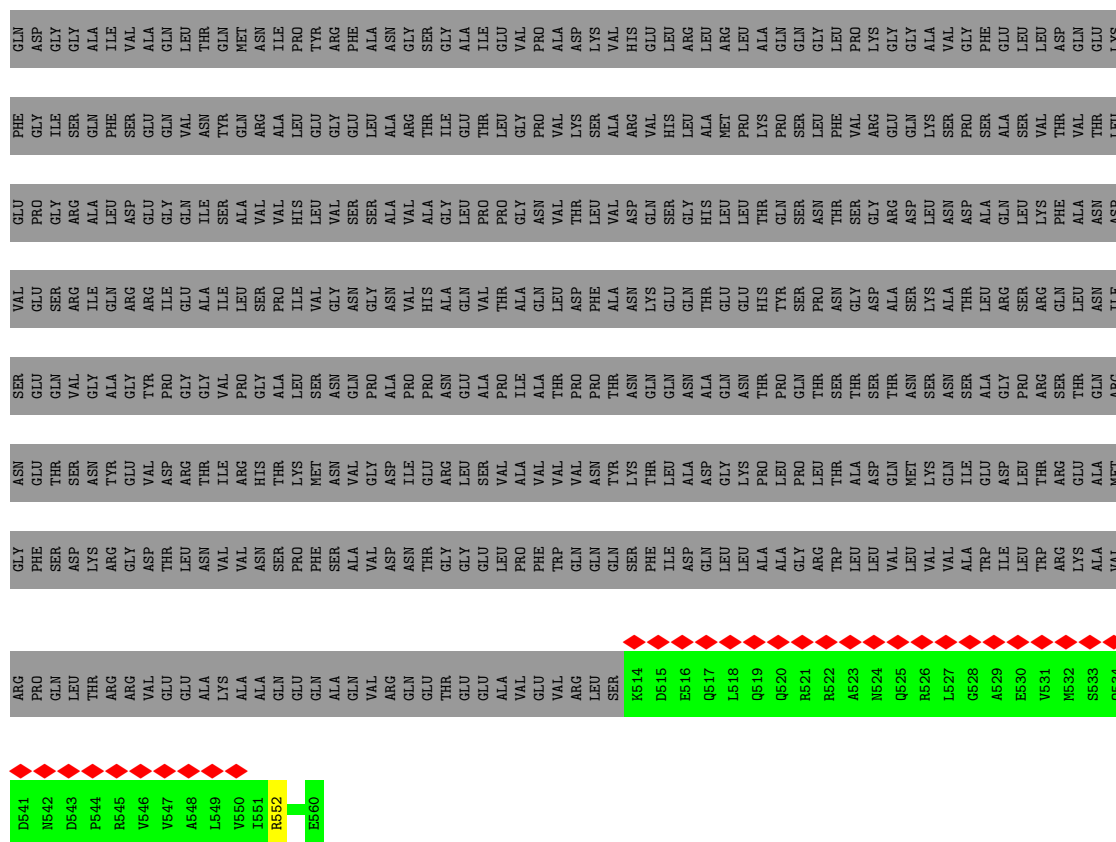
D641	D542	D643	P544	R545	V546	V547	A548	L549	V550	I551	R552	E560	ARG	PRO	GLN	LEU	THR	ARG	ARG	VAL	GLU	GLU	ALA	LYS	ALA	ALA	GLN	GLN	GLN	VAL	ARG	GLN	GLU	THR	GLU	GLU	ALA	VAL	VAL	ARG	LEU	SER	K514	D515	E516	Q517	L518	Q519	Q520	R521	R522	A523	N524	Q525	R526	L527	G528	A529	E530	V531	M532	S533	Q534	R535	I536	R537	E538	M539	S540
------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Chain LG:

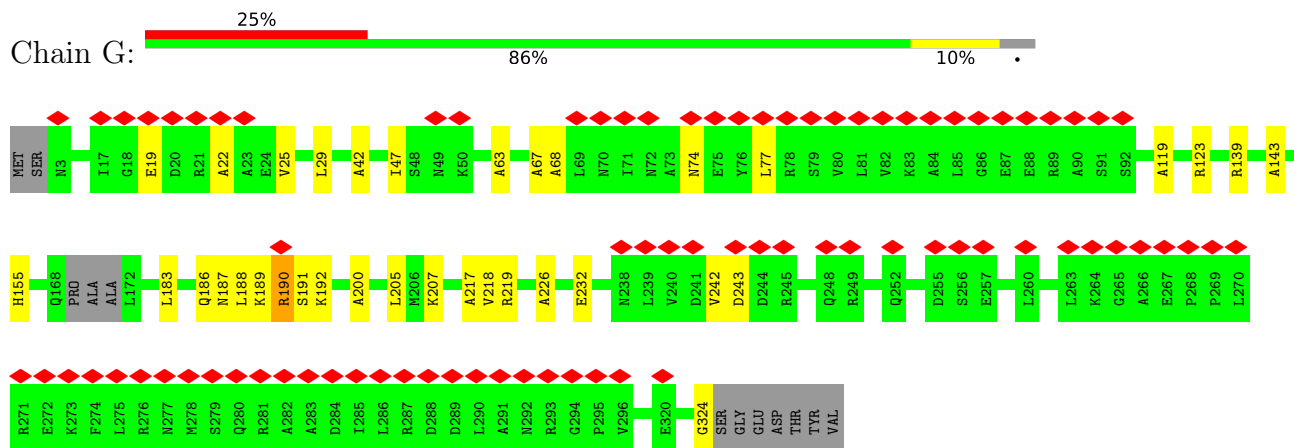
[illegible]

Chain RG:

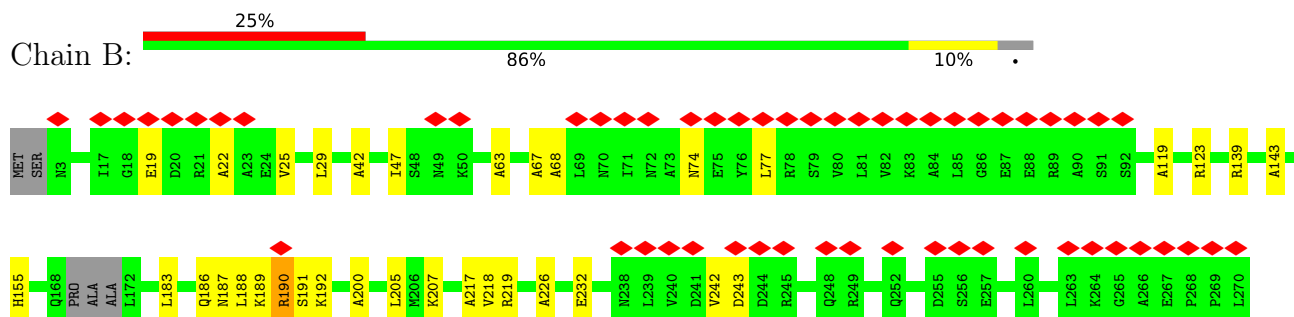
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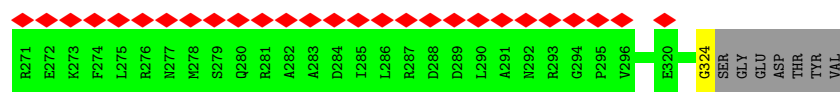


• Molecule 2: Flagellar motor switch protein FliG



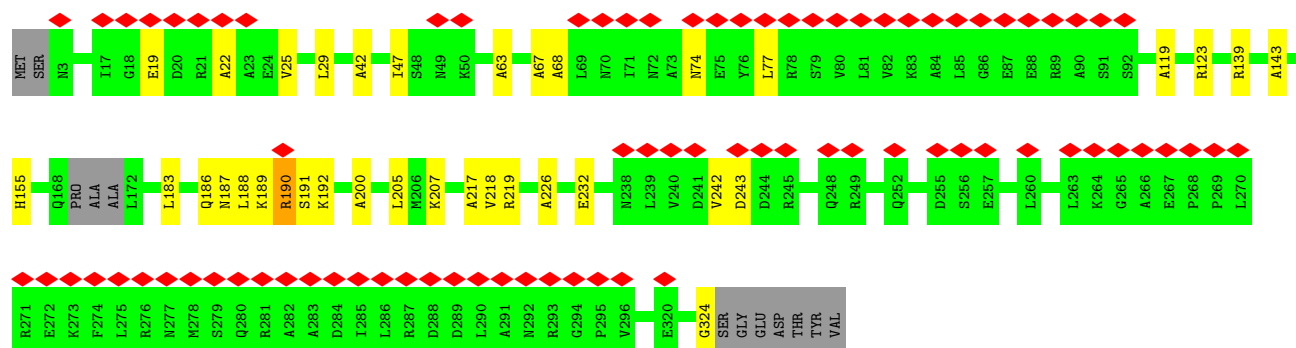
• Molecule 2: Flagellar motor switch protein FliG





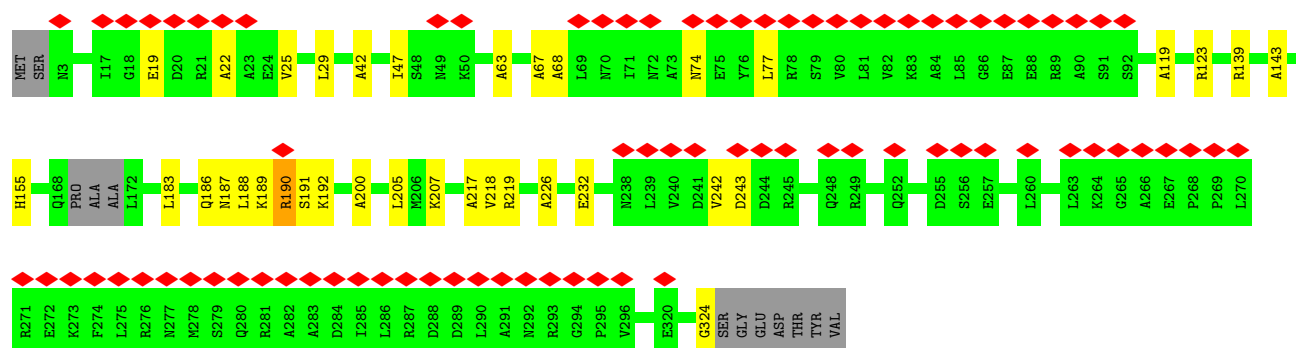
• Molecule 2: Flagellar motor switch protein FlhG

Chain J: 25% 86% 10% .



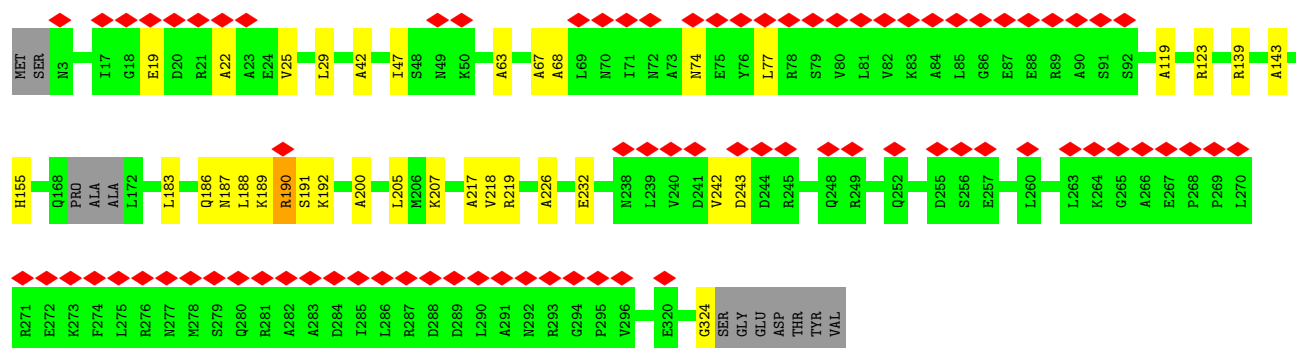
• Molecule 2: Flagellar motor switch protein FlhG

Chain T: 25% 86% 10% .



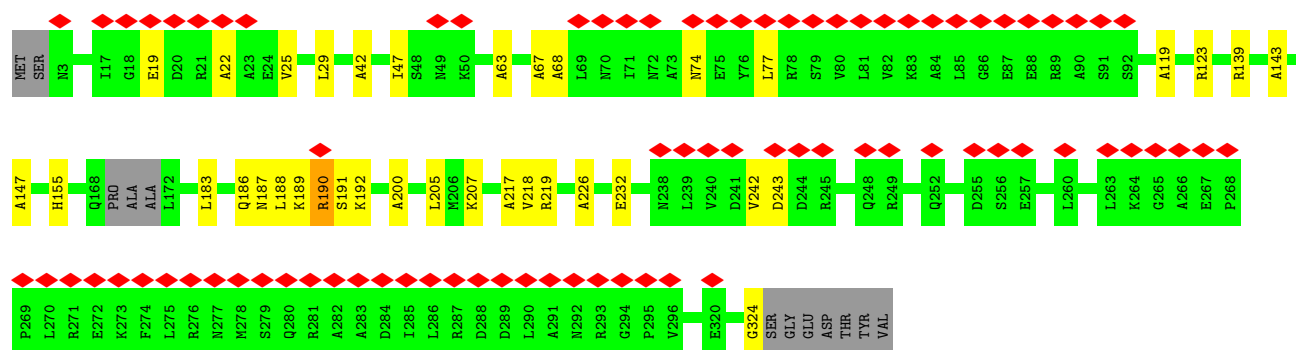
• Molecule 2: Flagellar motor switch protein FlhG

Chain AA: 25% 86% 10% .



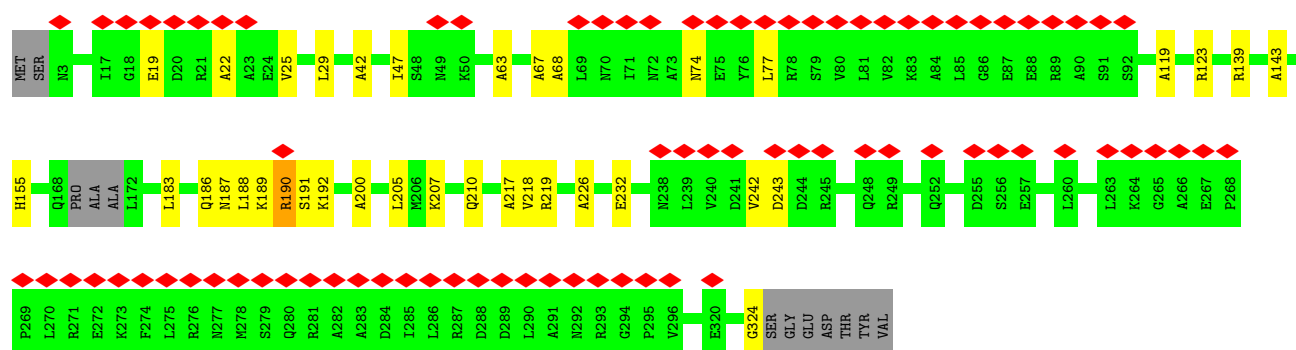
• Molecule 2: Flagellar motor switch protein FlhG

Chain GA: 



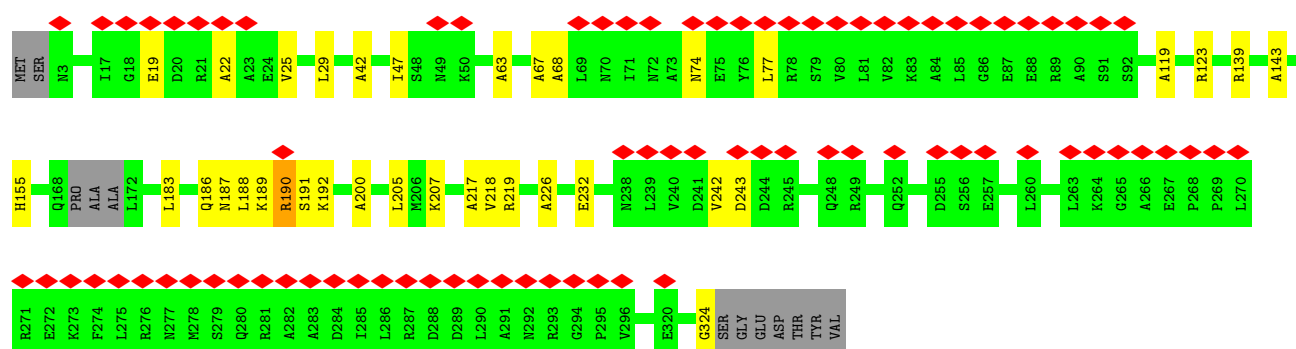
• Molecule 2: Flagellar motor switch protein FlgG

Chain MA: 



• Molecule 2: Flagellar motor switch protein FlgG

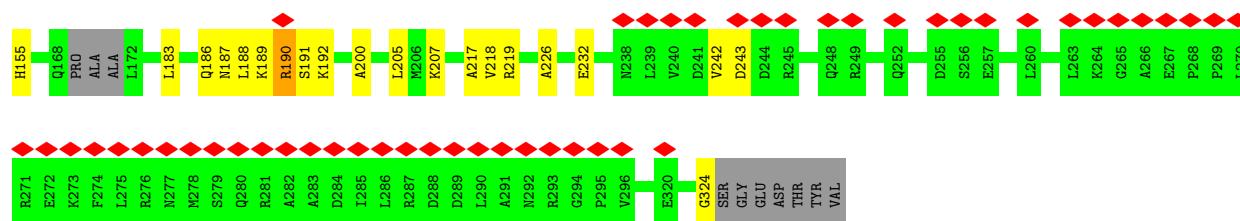
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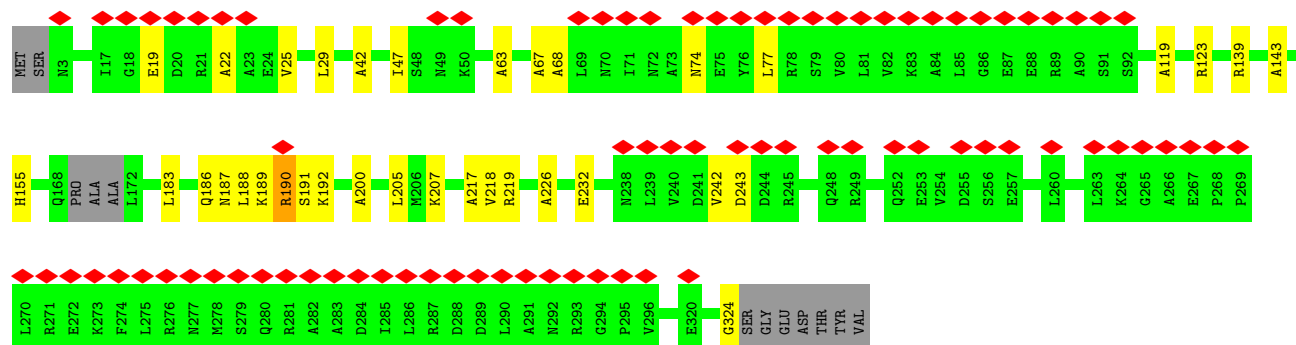
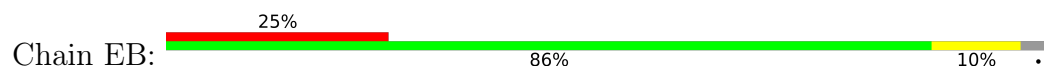
• Molecule 2: Flagellar motor switch protein FlgG

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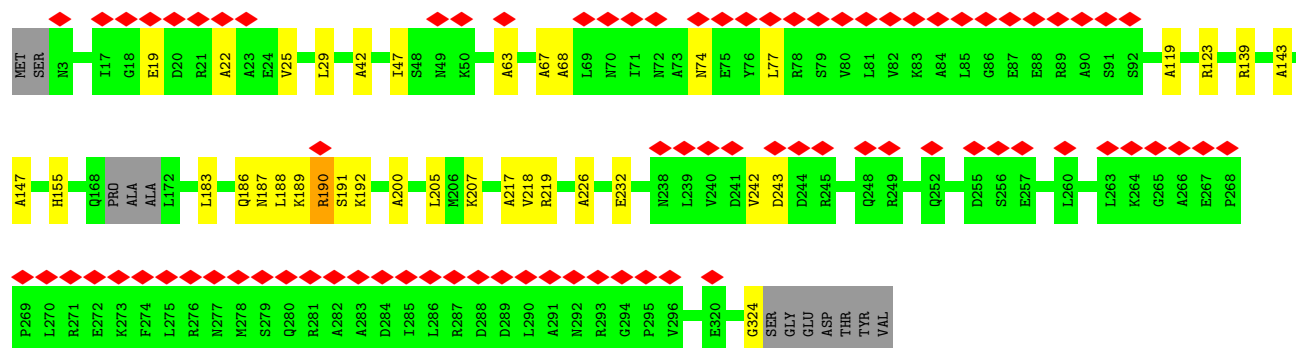
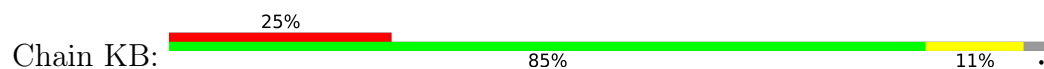




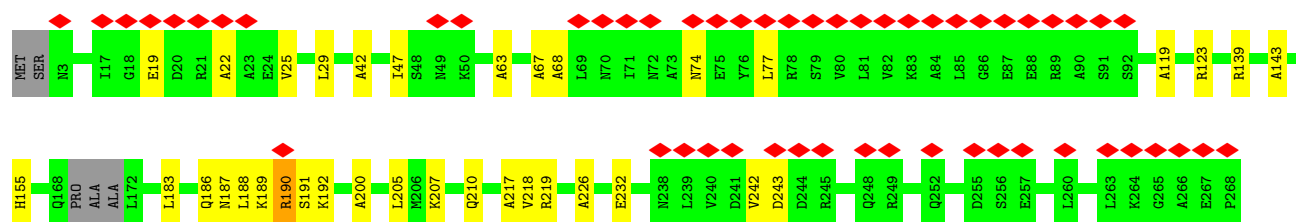
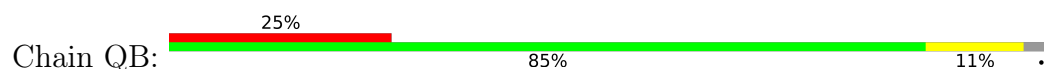
• Molecule 2: Flagellar motor switch protein FlhG

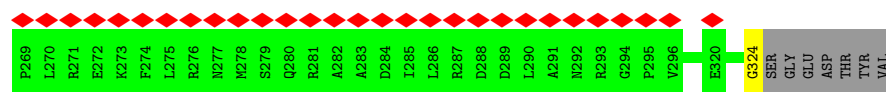


• Molecule 2: Flagellar motor switch protein FlhG

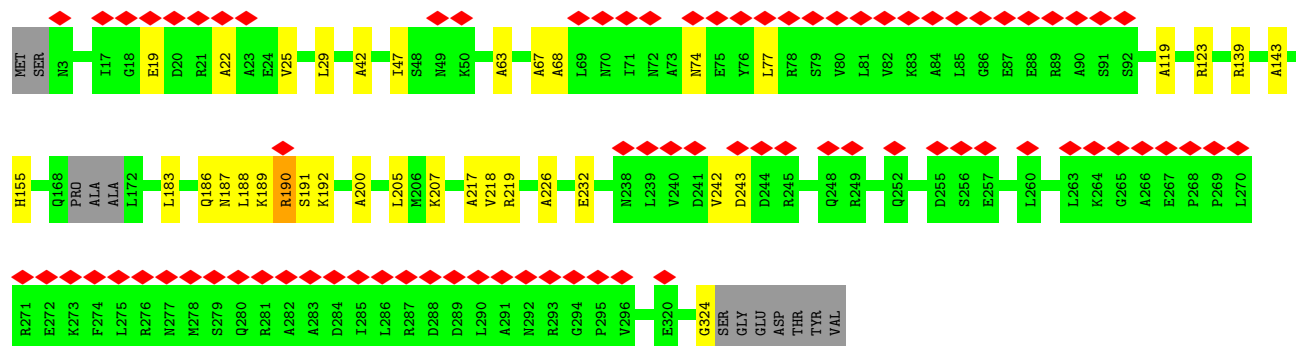
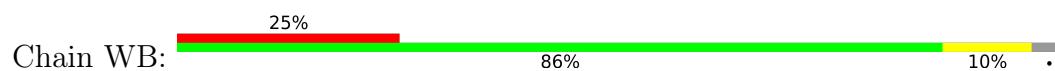


• Molecule 2: Flagellar motor switch protein FlhG

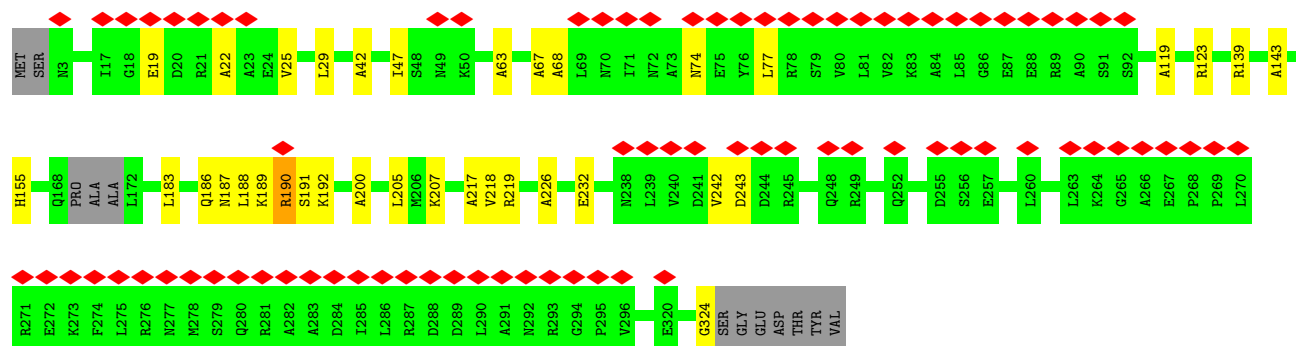
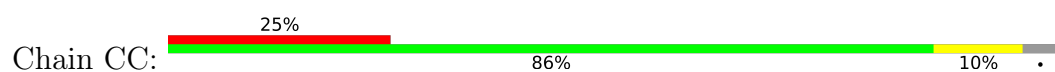




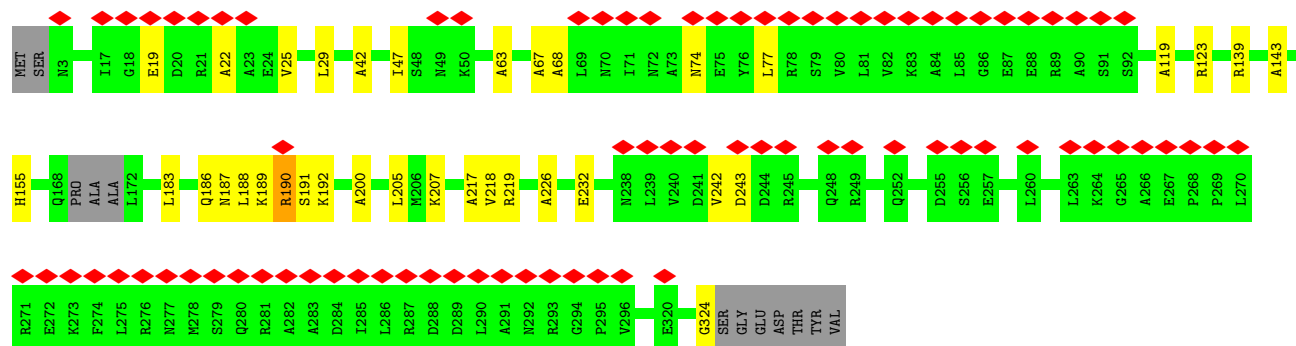
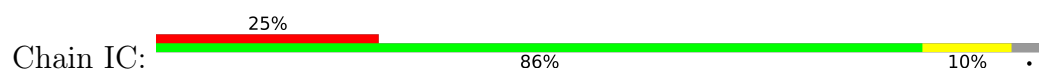
• Molecule 2: Flagellar motor switch protein FliG



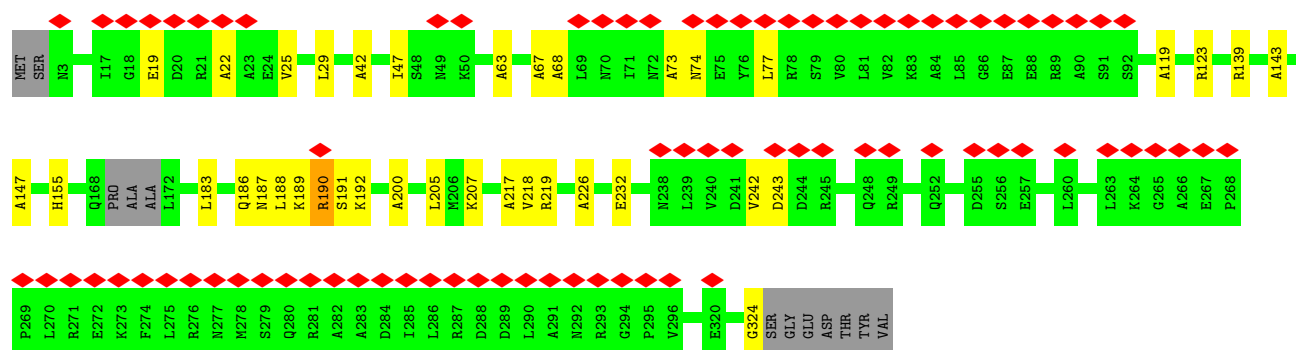
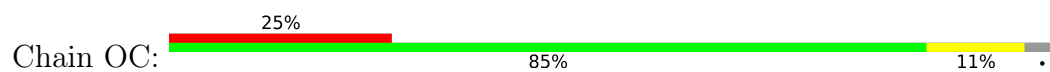
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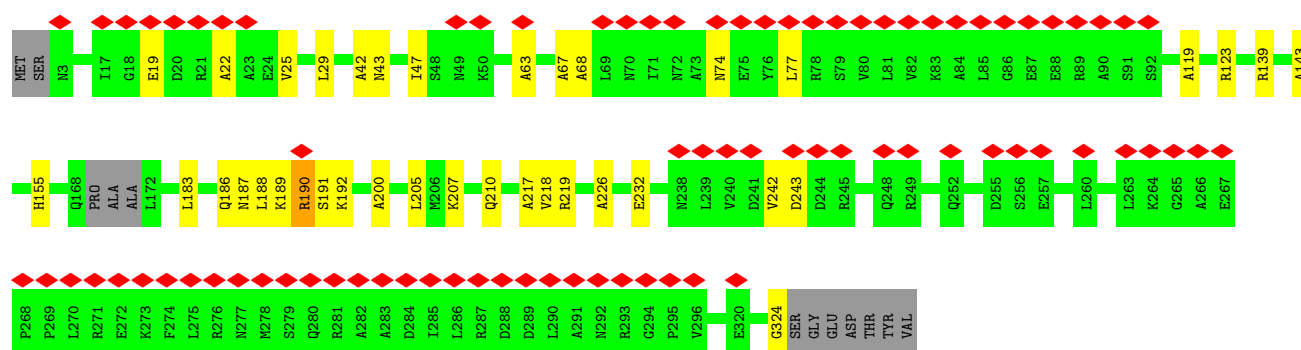
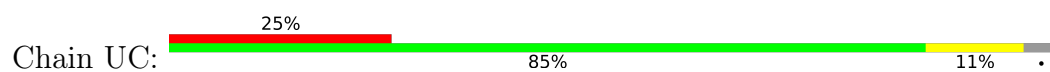
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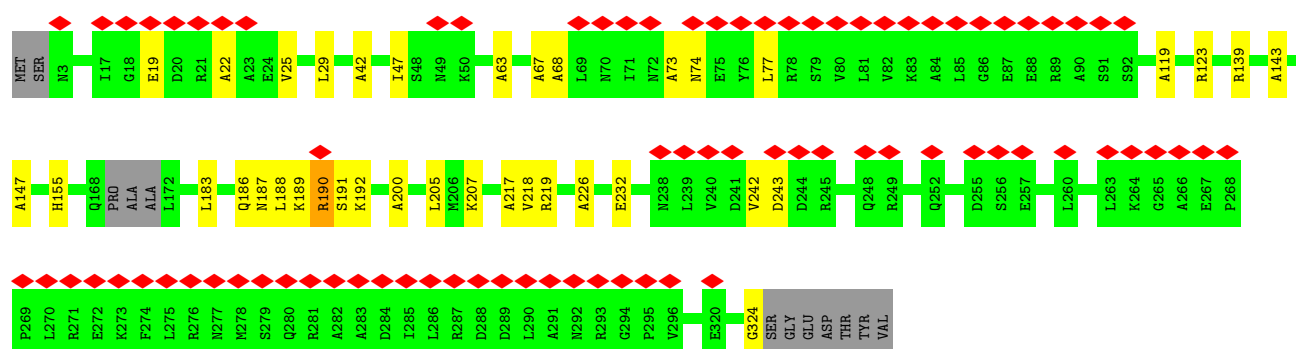
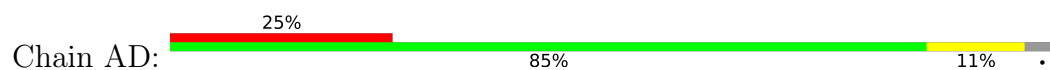
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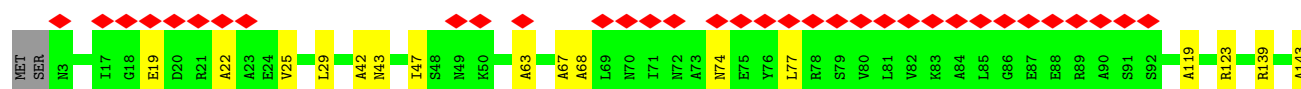
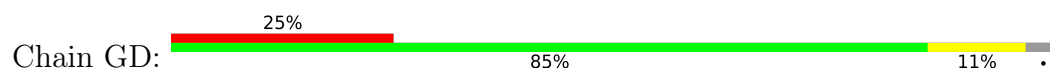
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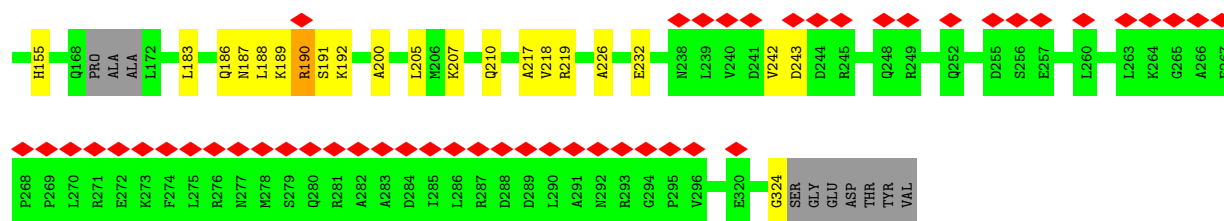


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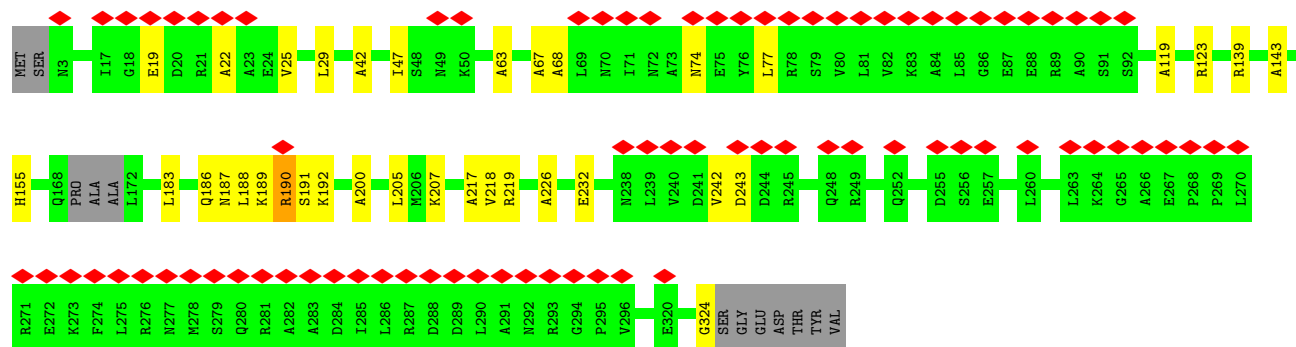
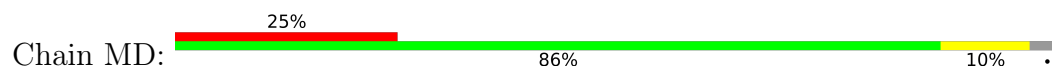


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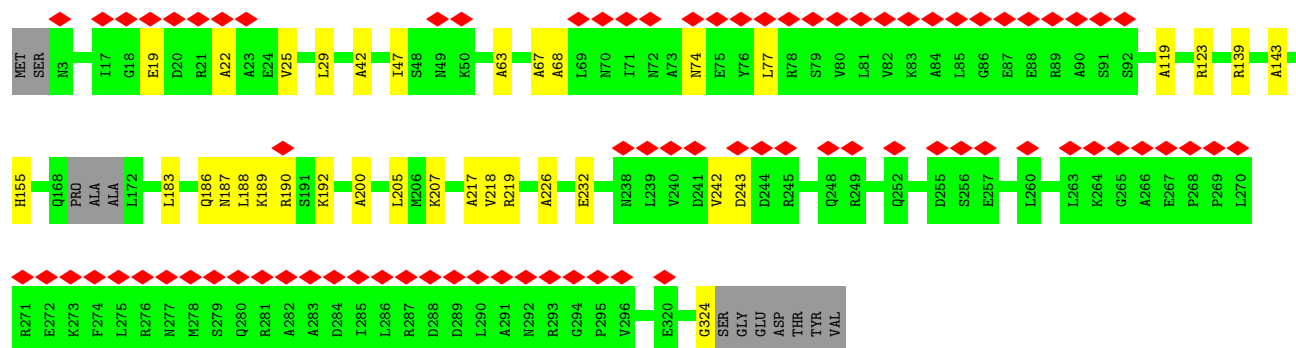
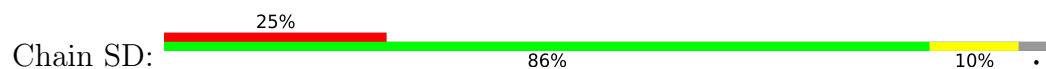




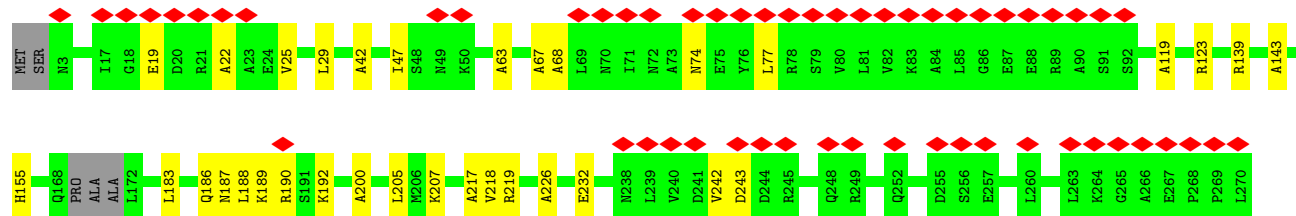
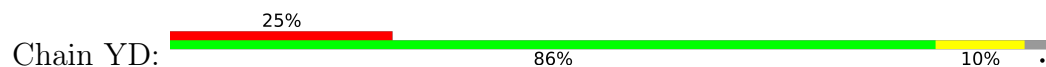
• Molecule 2: Flagellar motor switch protein FlhG

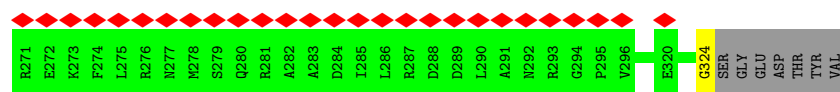


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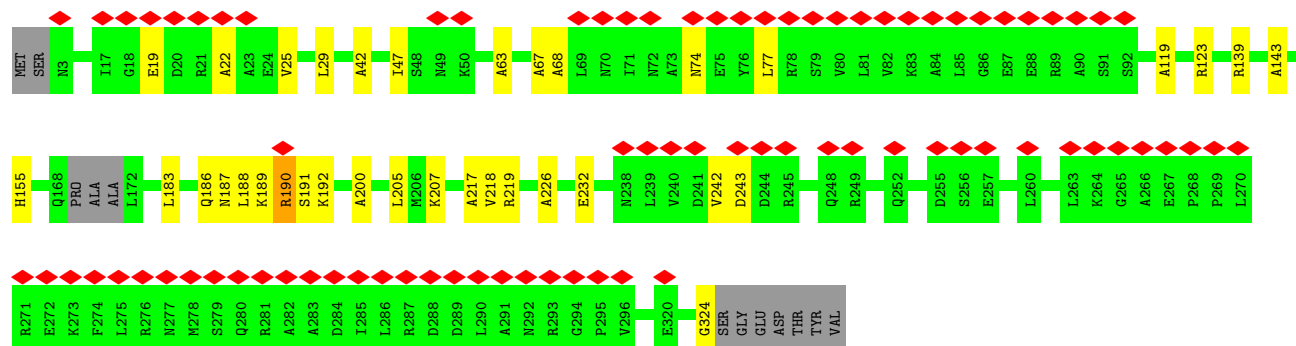
• Molecule 2: Flagellar motor switch protein FlhG





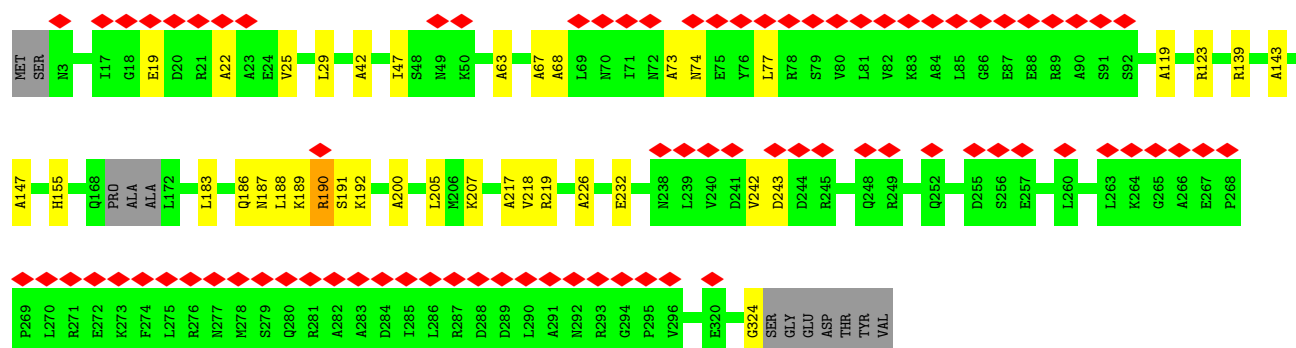
• Molecule 2: Flagellar motor switch protein FlIG

Chain EE: 25% 86% 10% .



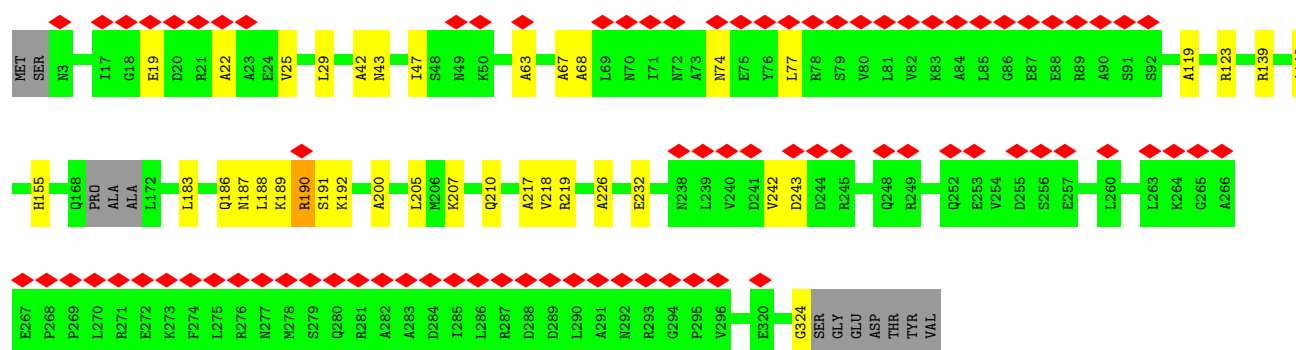
• Molecule 2: Flagellar motor switch protein FlIG

Chain KE: 25% 85% 11% .

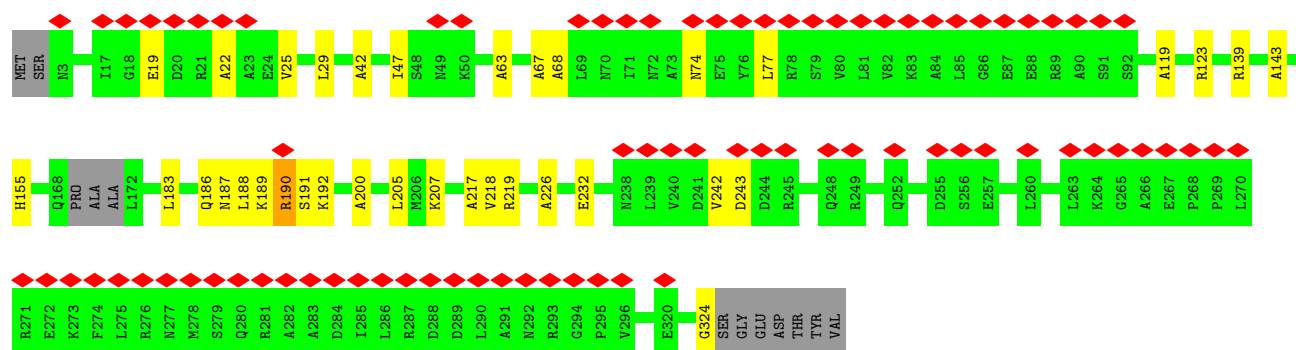
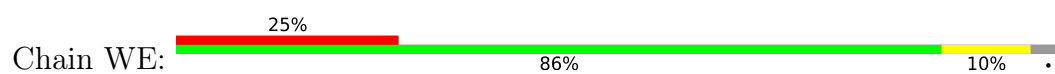


• Molecule 2: Flagellar motor switch protein FlIG

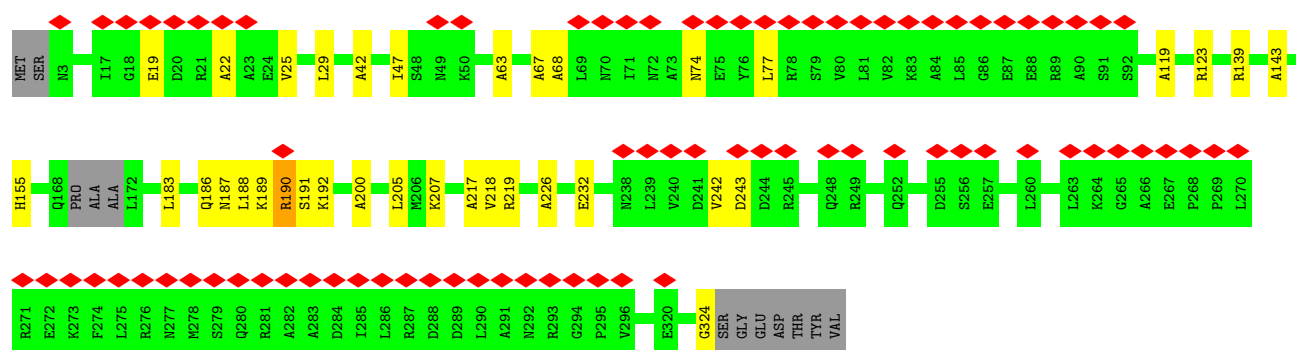
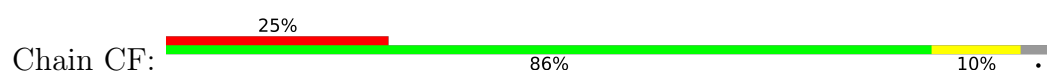
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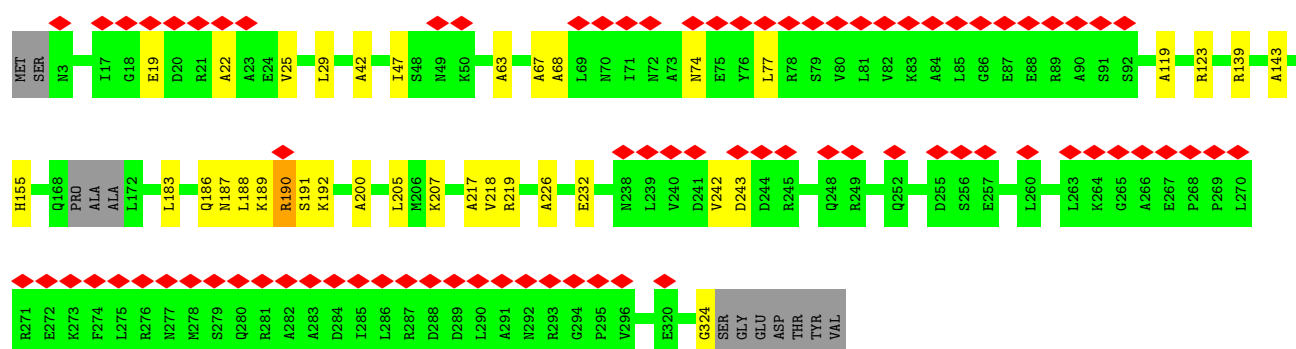
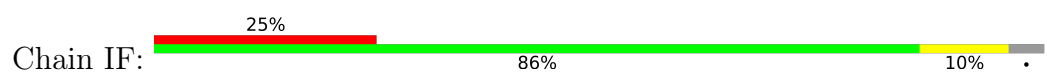
• Molecule 2: Flagellar motor switch protein FlIG



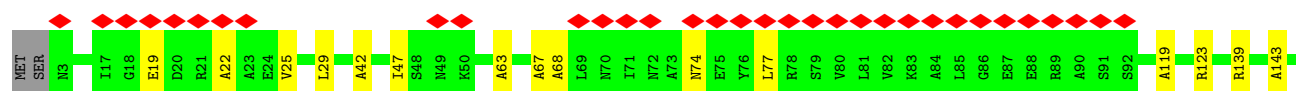
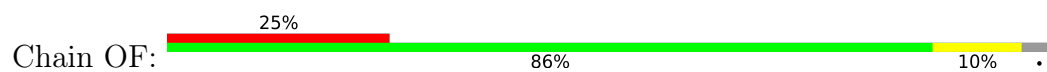
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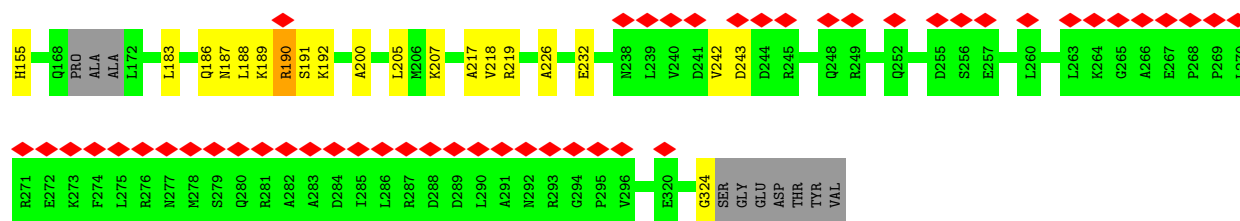


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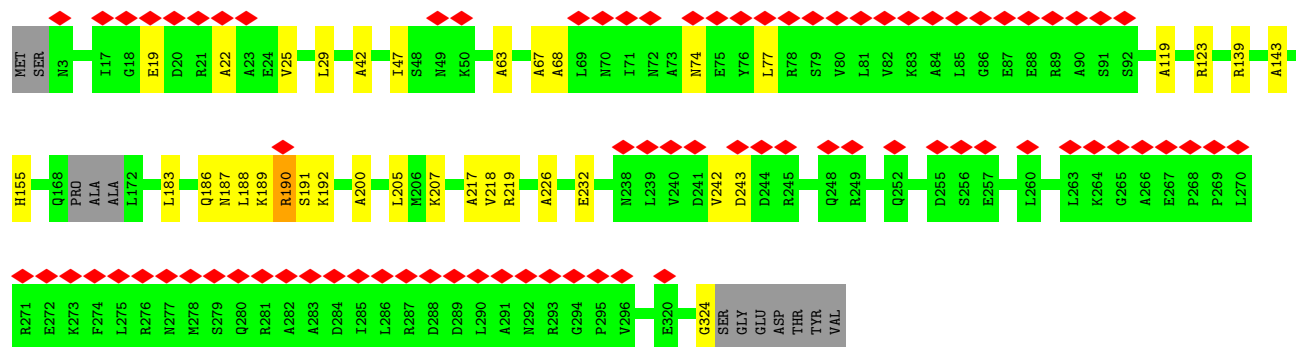
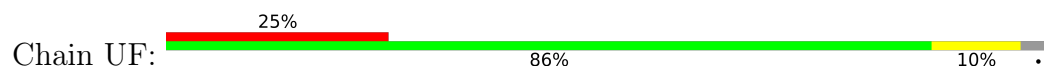


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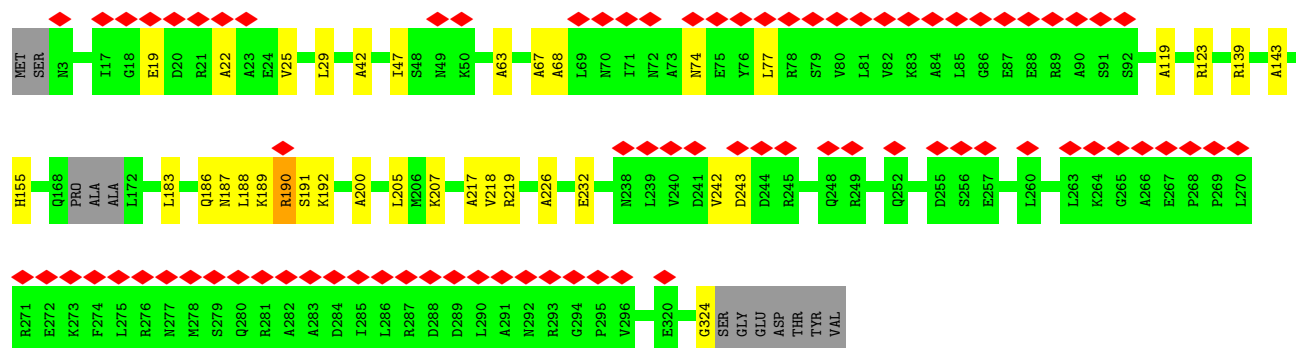
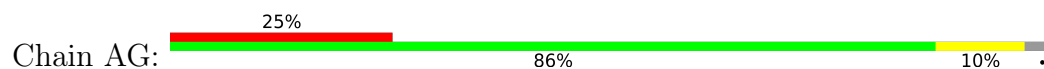




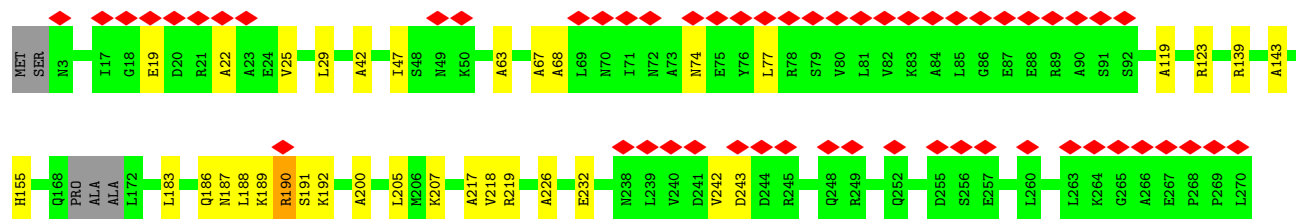
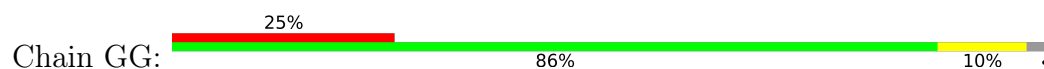
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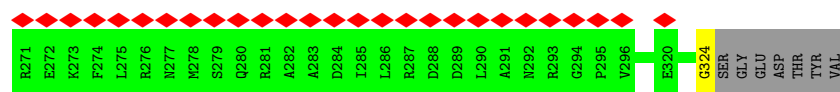


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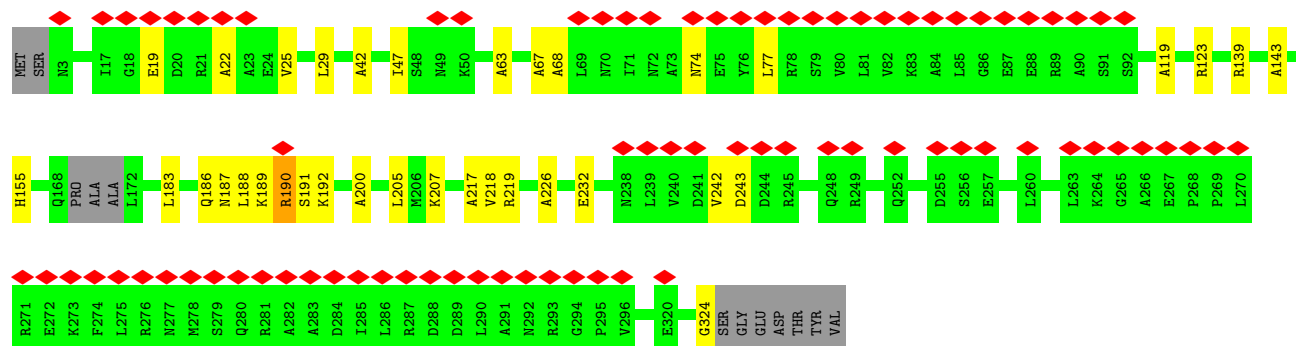
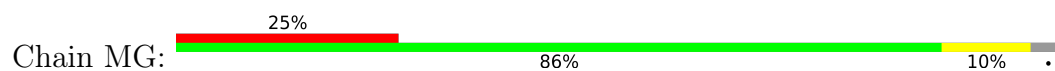


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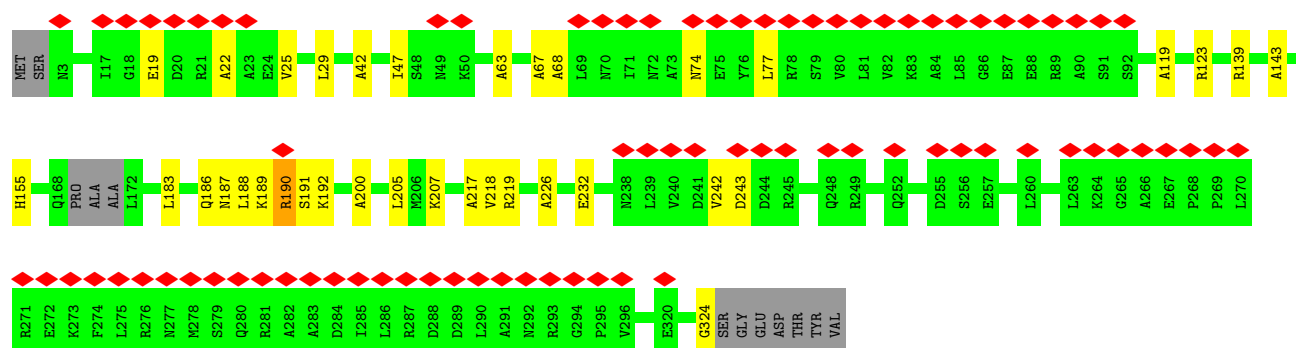
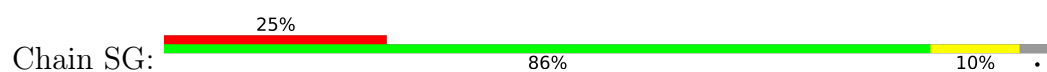




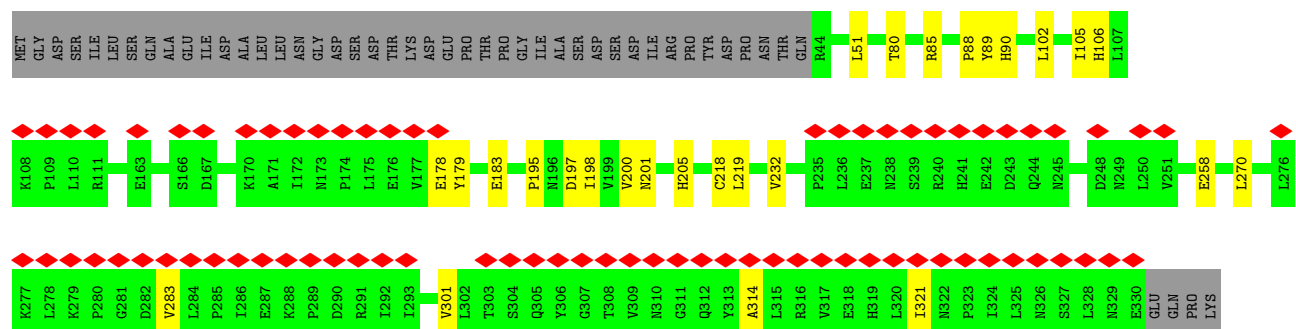
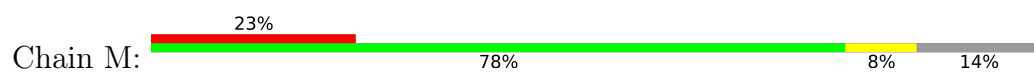
• Molecule 2: Flagellar motor switch protein FlIG



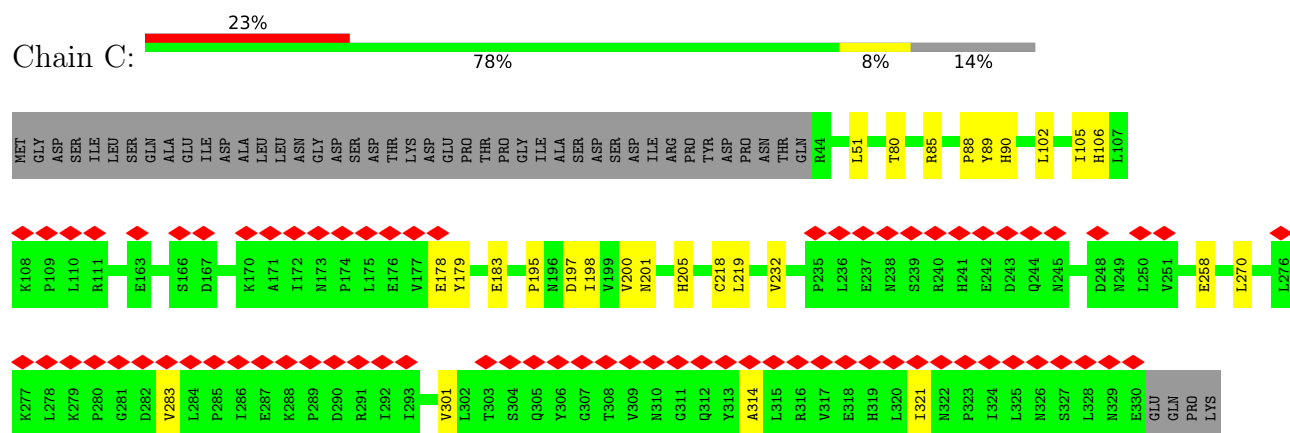
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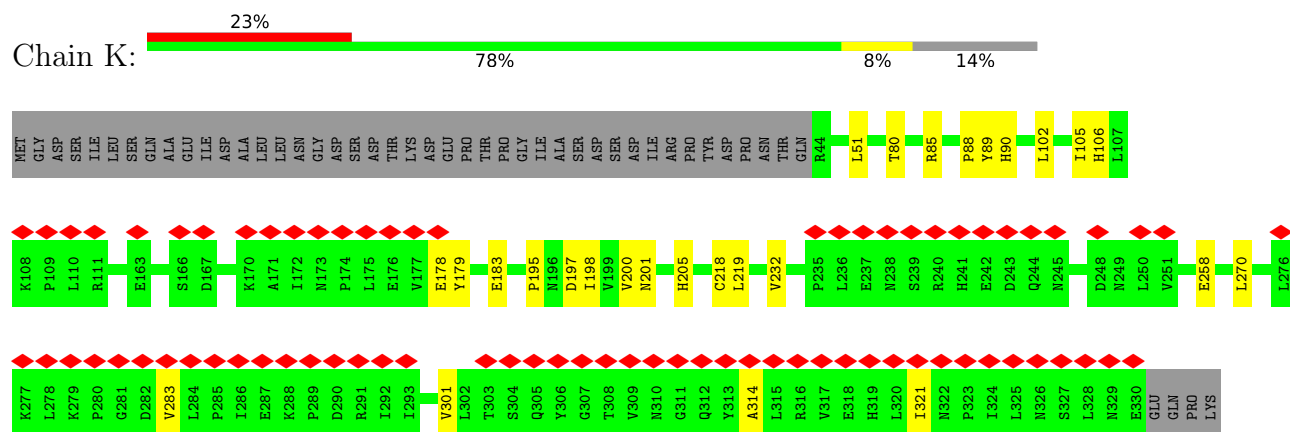
• Molecule 3: Flagellar motor switch protein FlIM



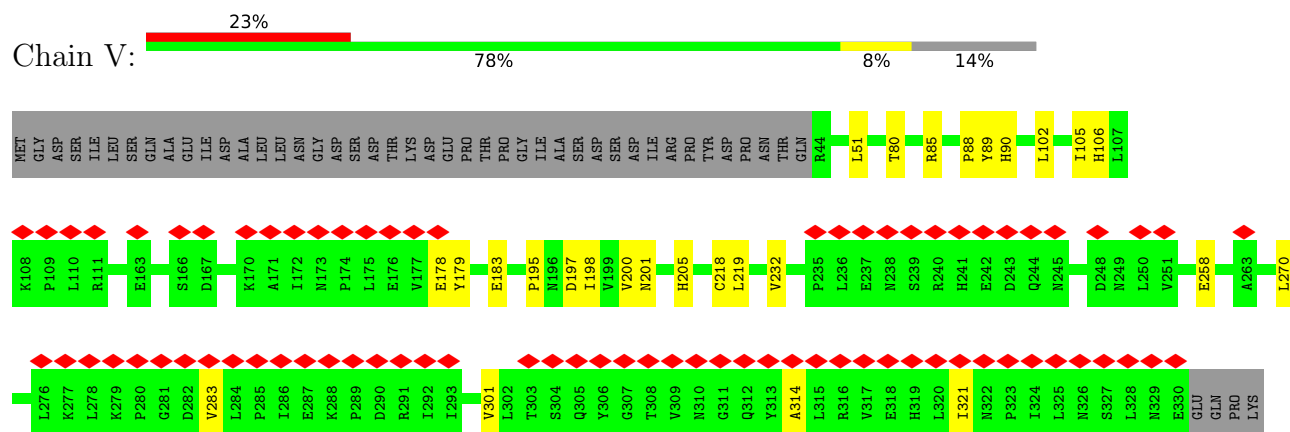
• Molecule 3: Flagellar motor switch protein FlIM



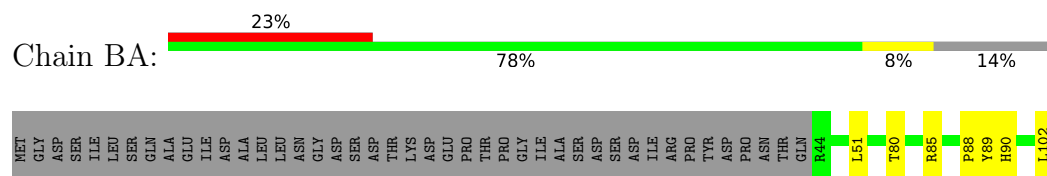
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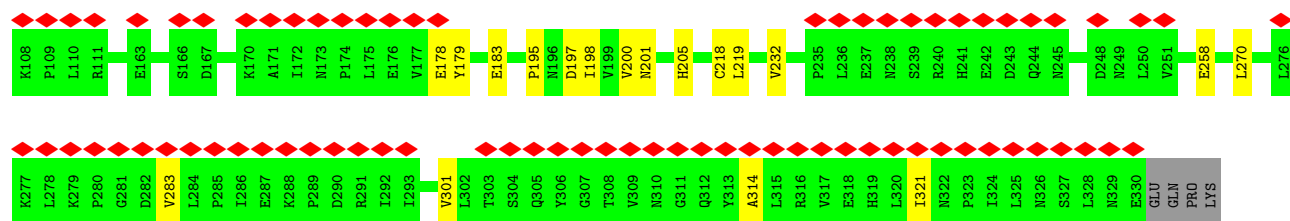


• Molecule 3: Flagellar motor switch protein FliM

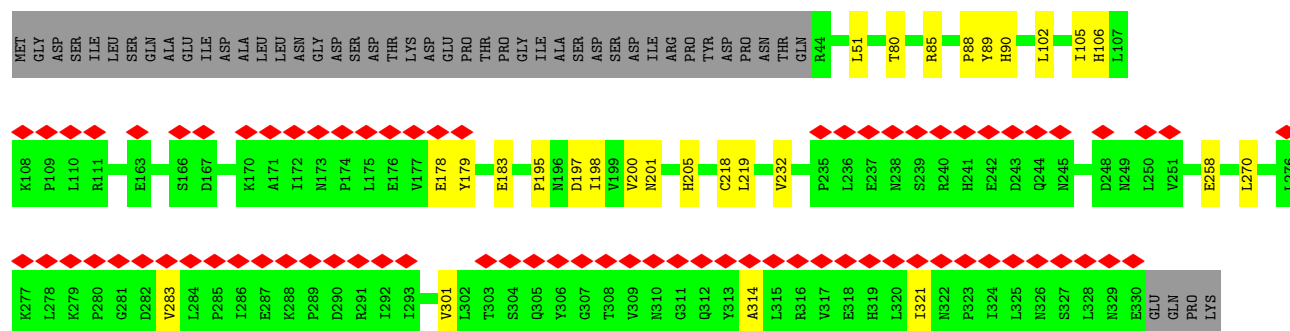
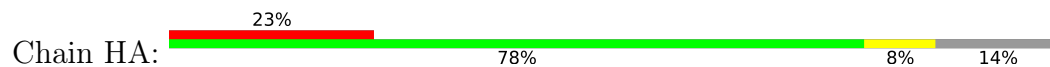


• Molecule 3: Flagellar motor switch protein FliM

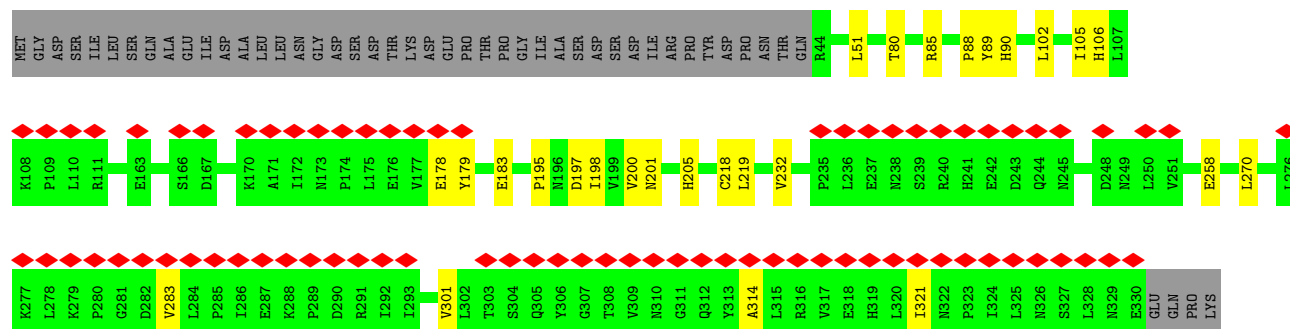
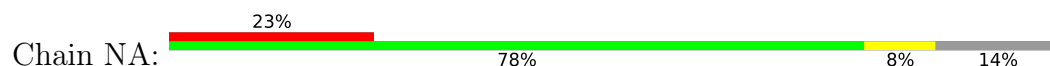




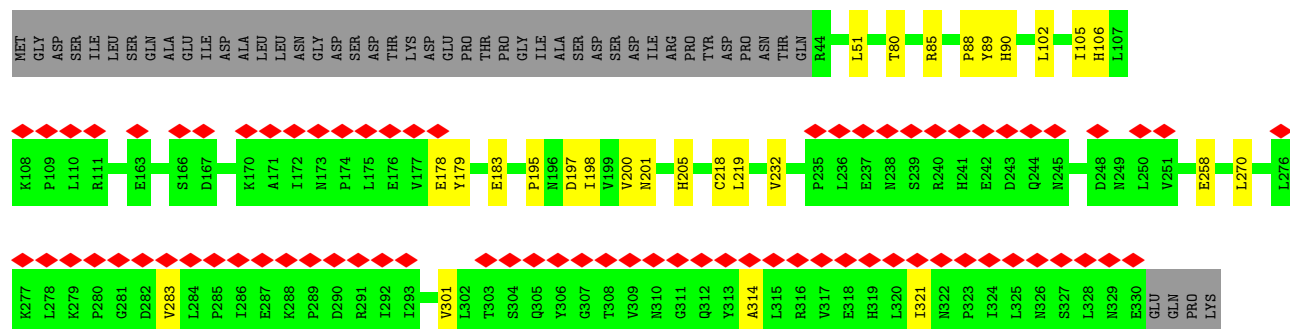
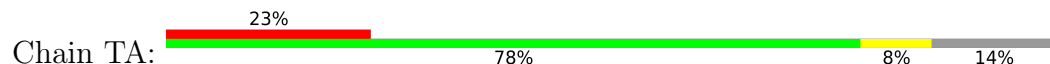
• Molecule 3: Flagellar motor switch protein FlIM



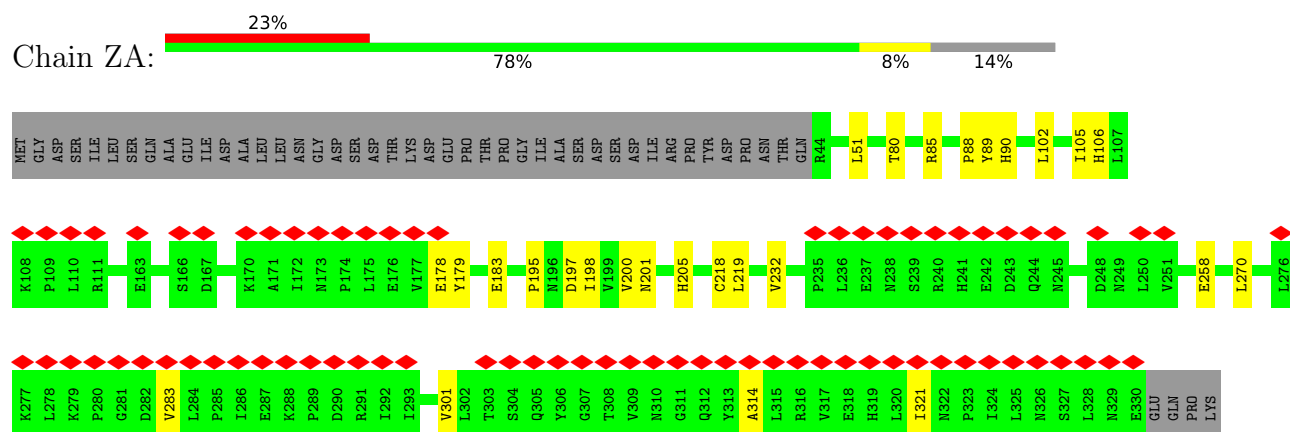
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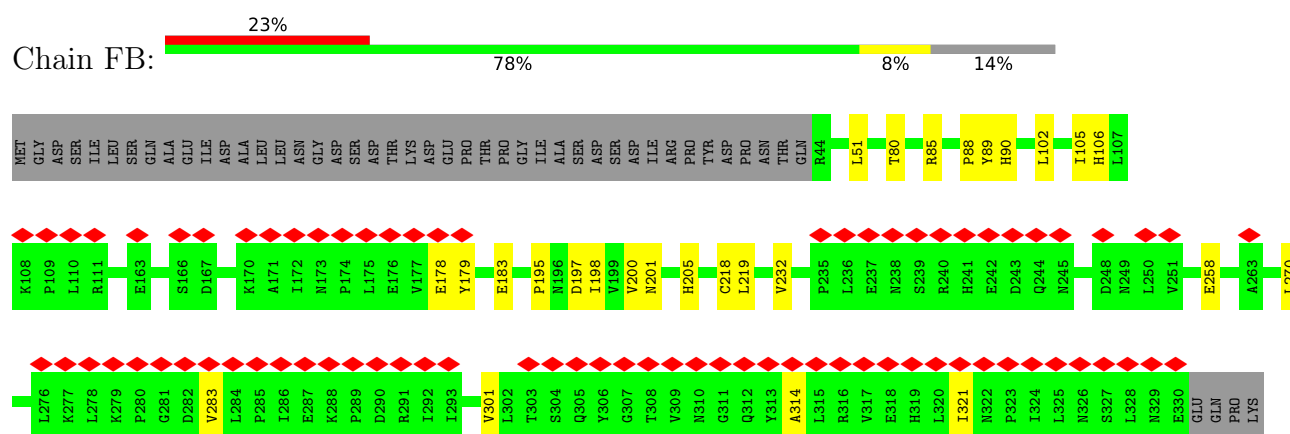
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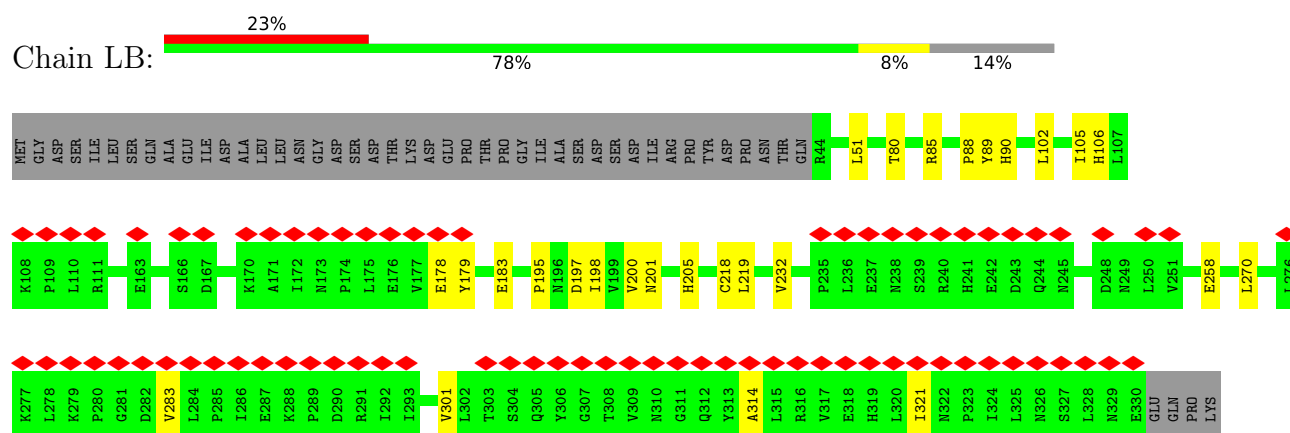
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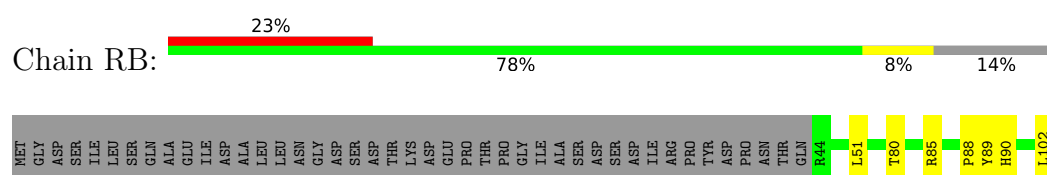
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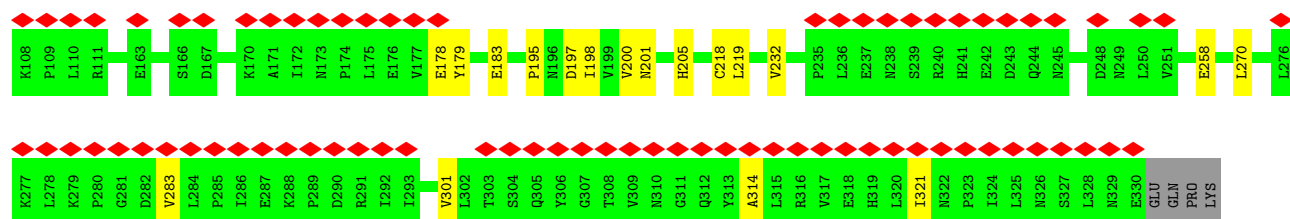


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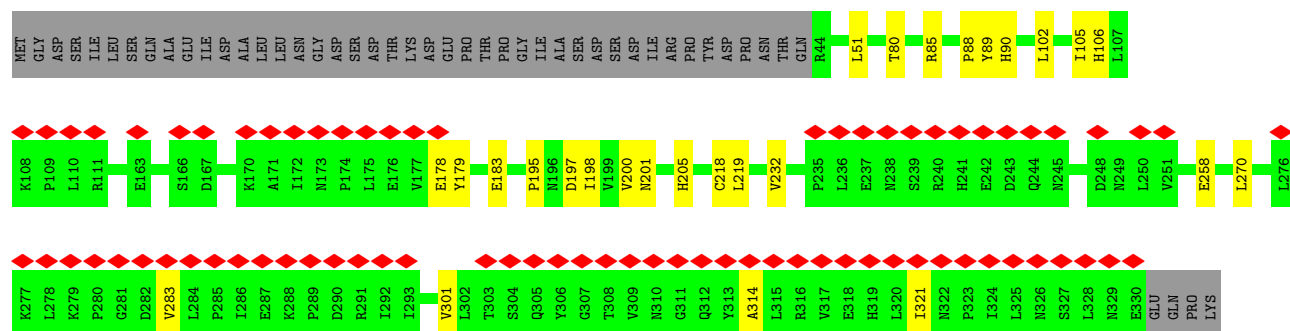
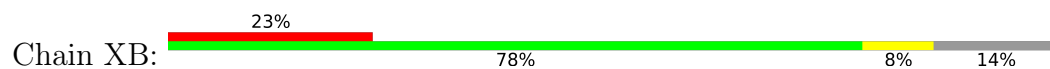


• Molecule 3: Flagellar motor switch protein FlIM

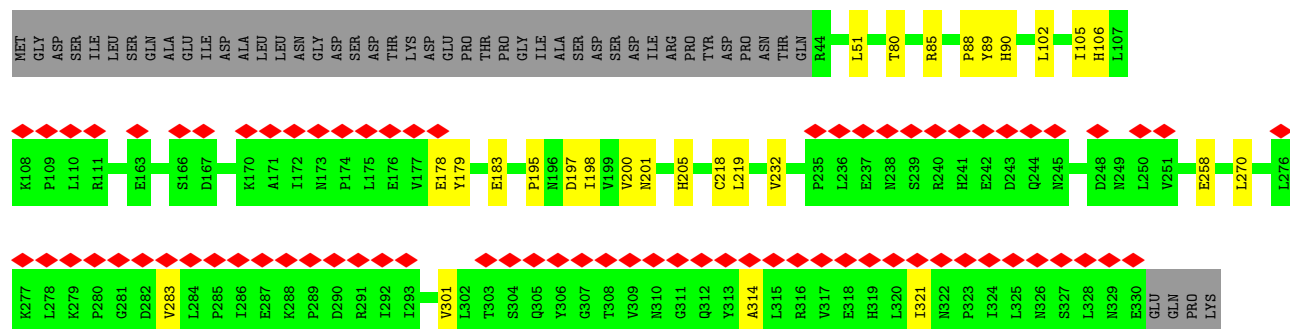
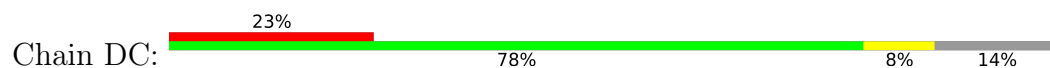




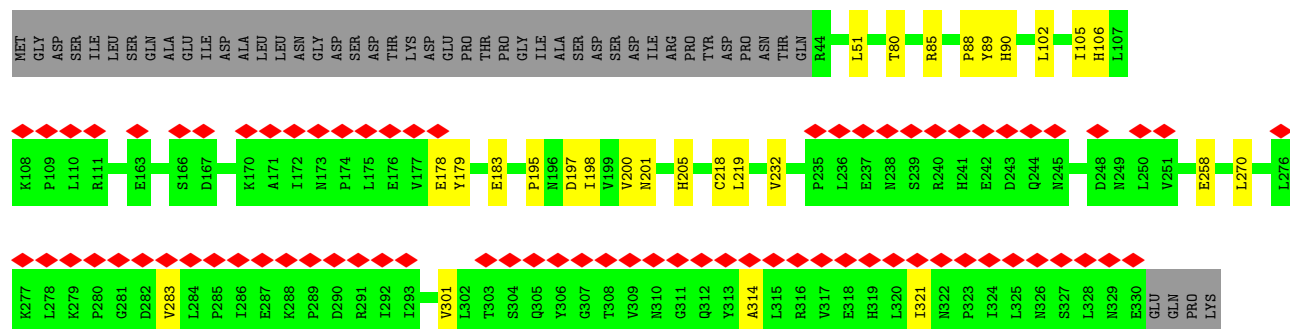
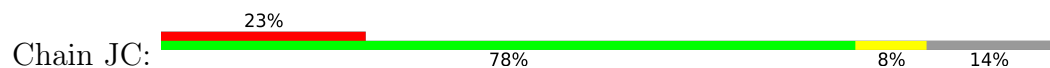
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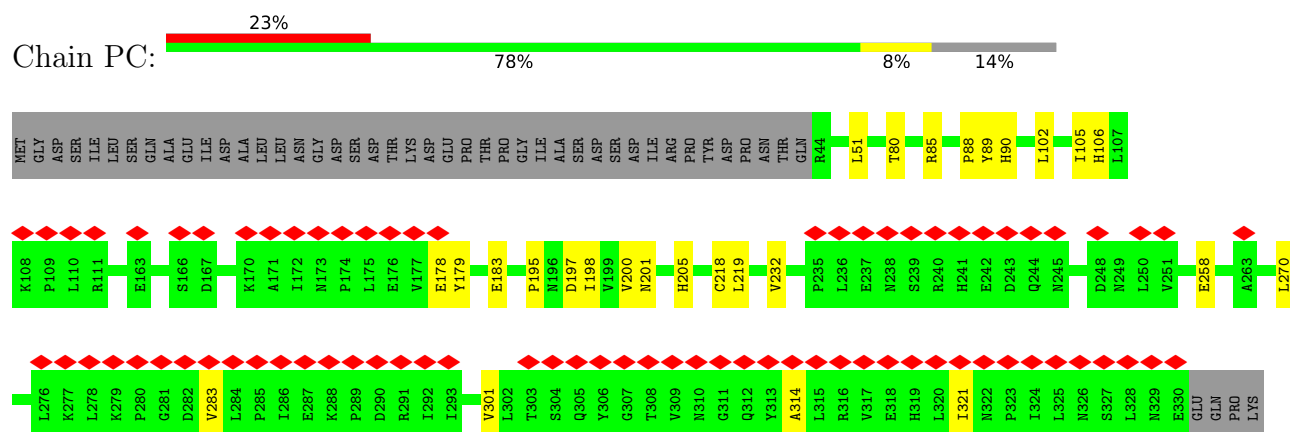
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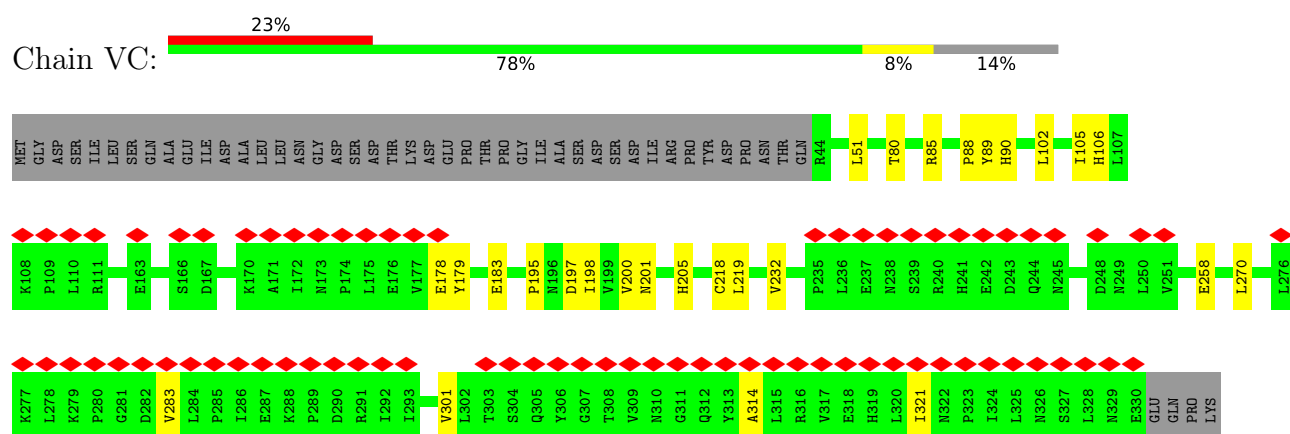
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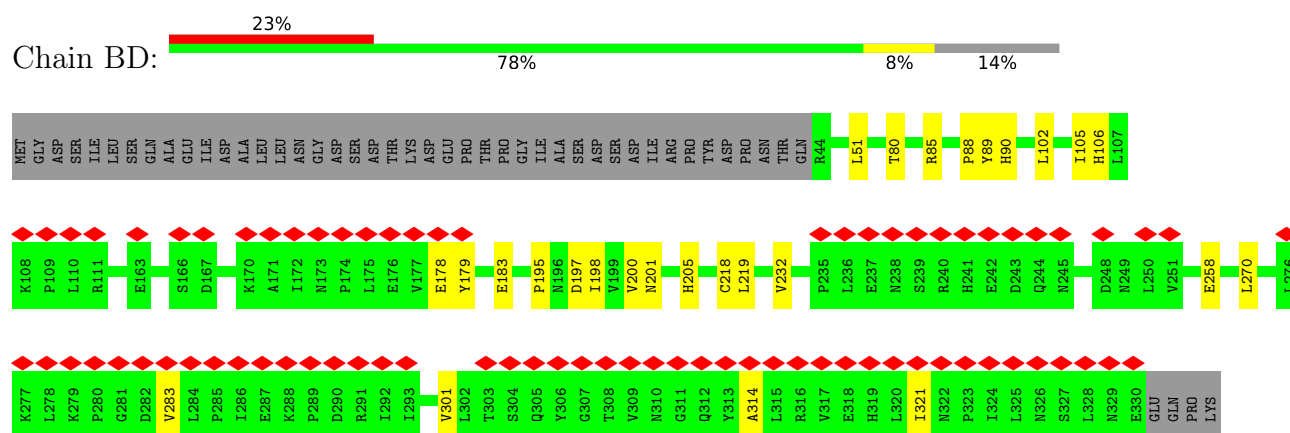
- Molecule 3: Flagellar motor switch protein FlIM



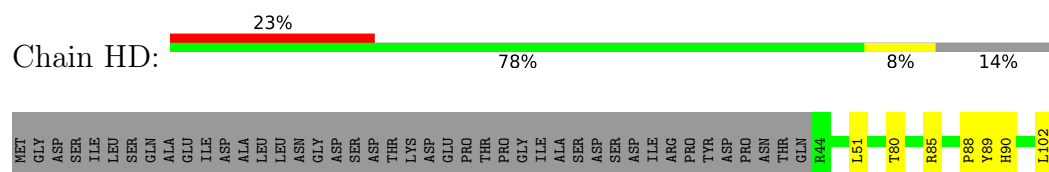
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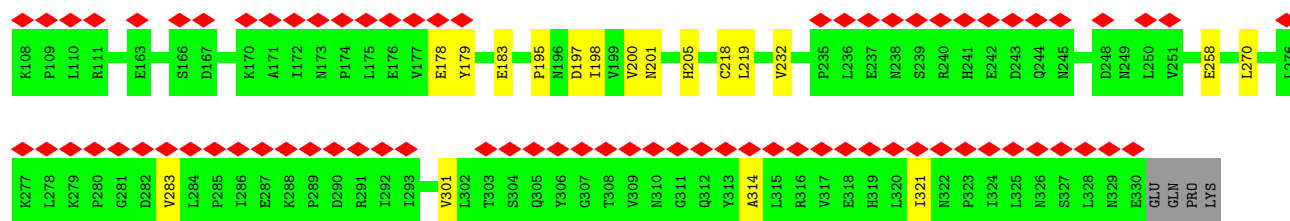


- Molecule 3: Flagellar motor switch protein FlIM

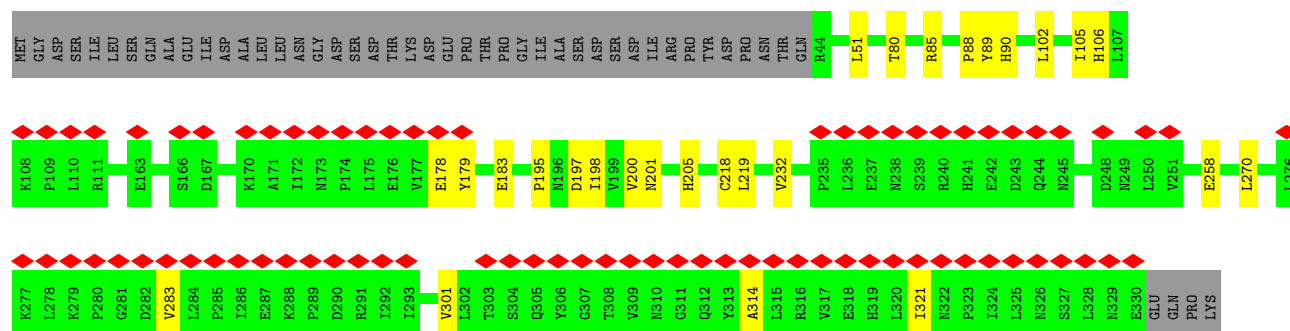
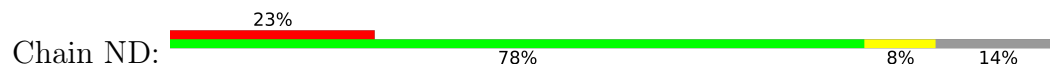


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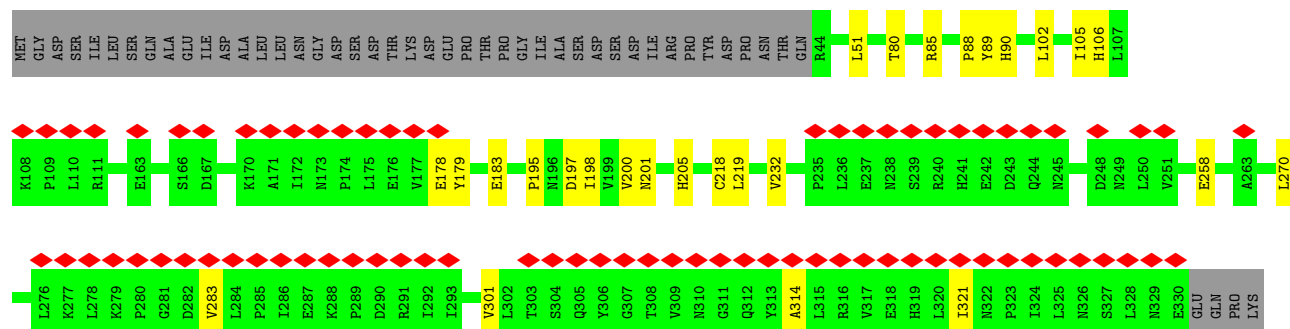
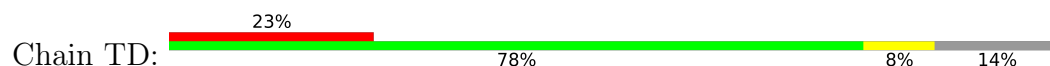




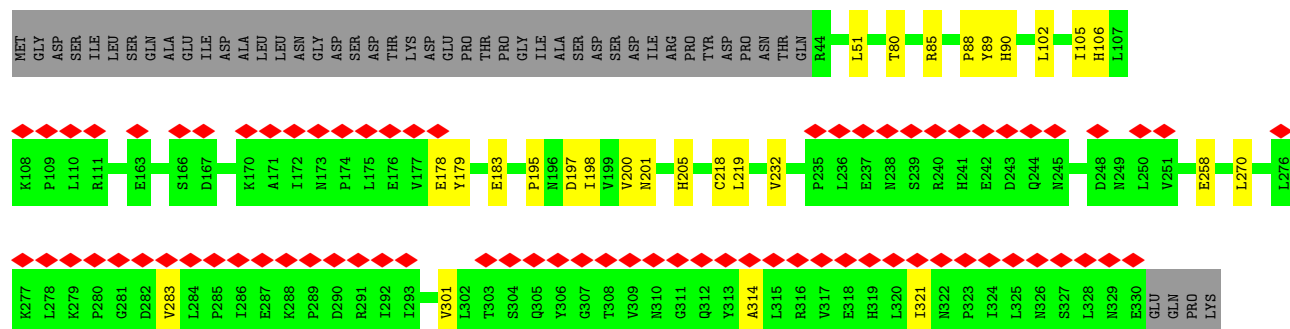
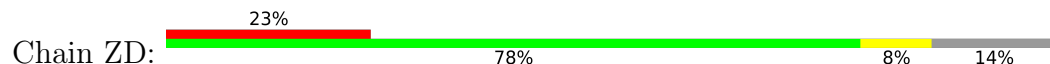
• Molecule 3: Flagellar motor switch protein FliM



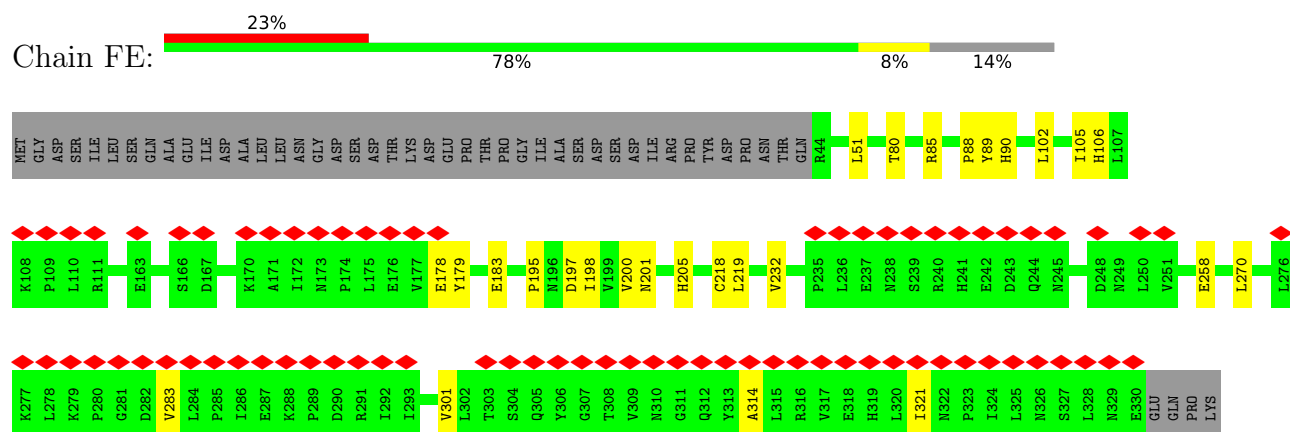
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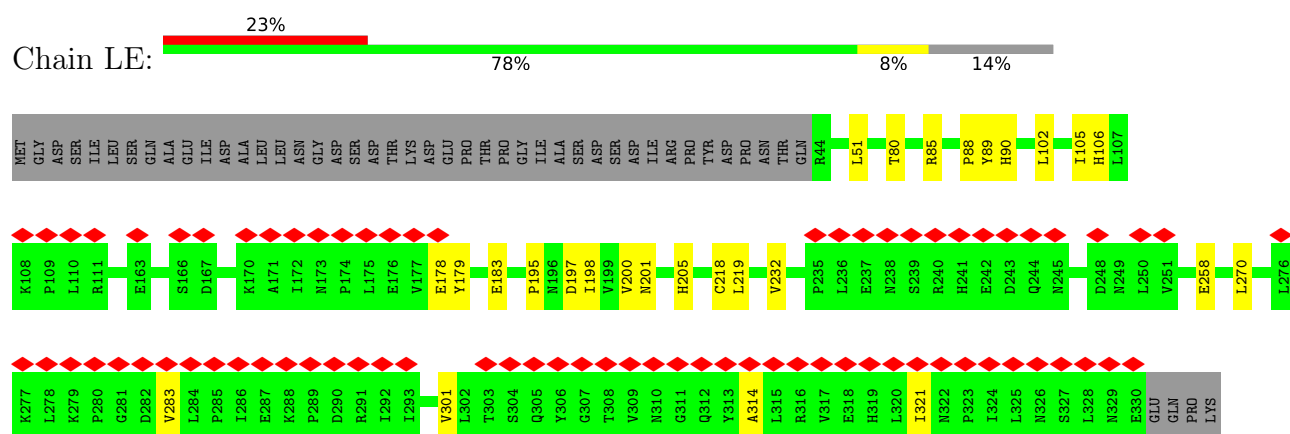
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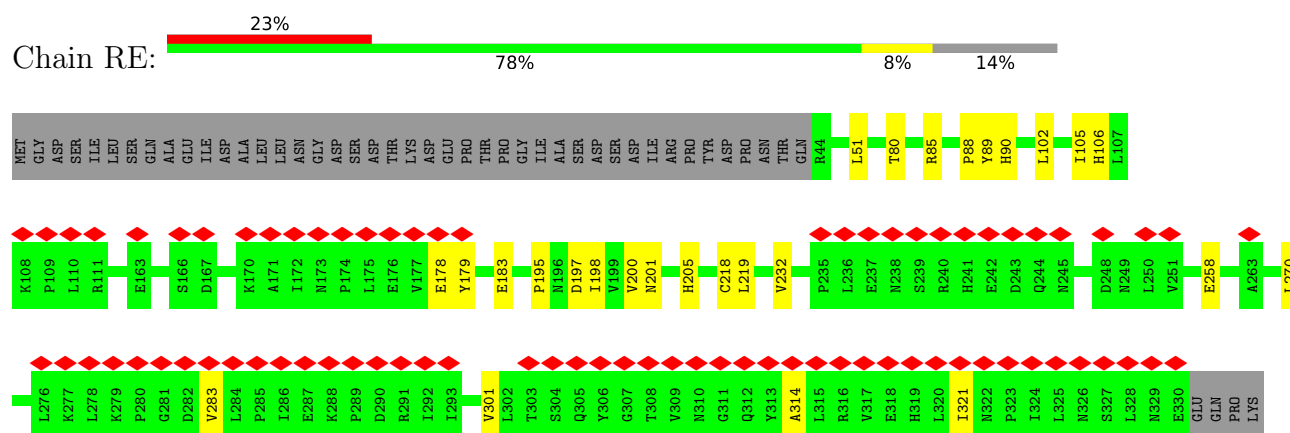
- Molecule 3: Flagellar motor switch protein FlIM



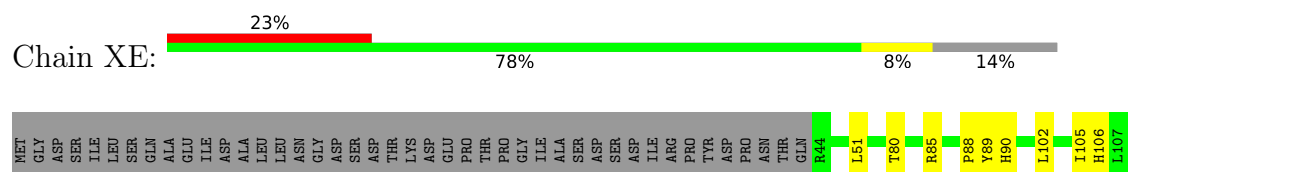
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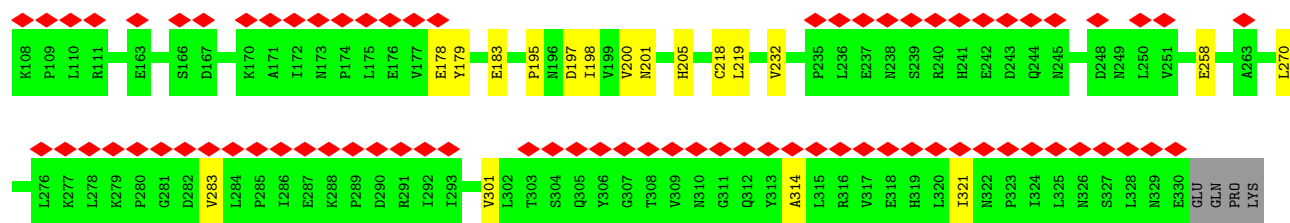


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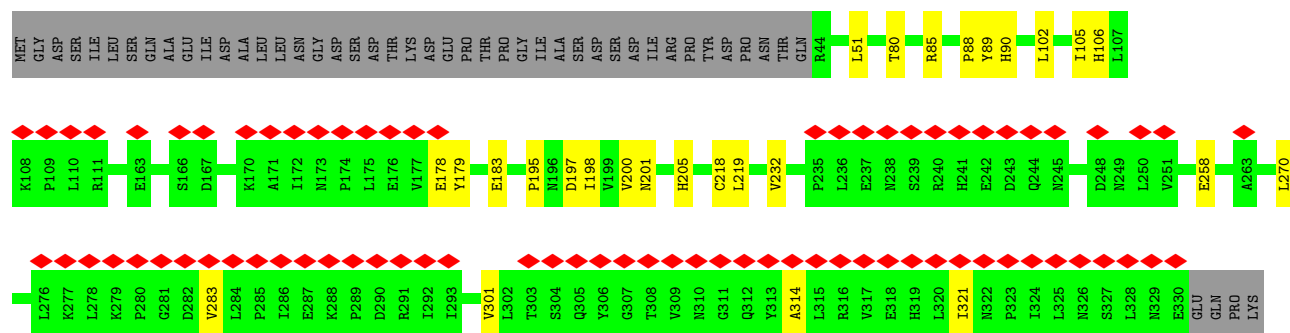
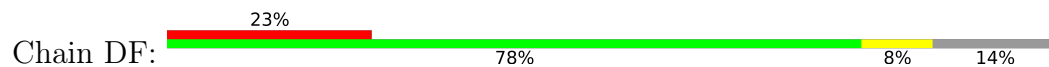


- Molecule 3: Flagellar motor switch protein FlIM

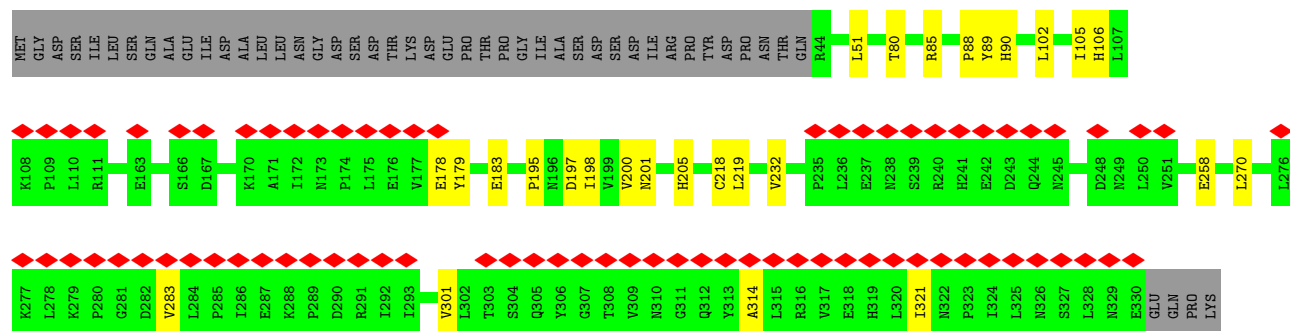
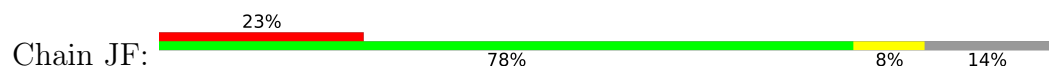




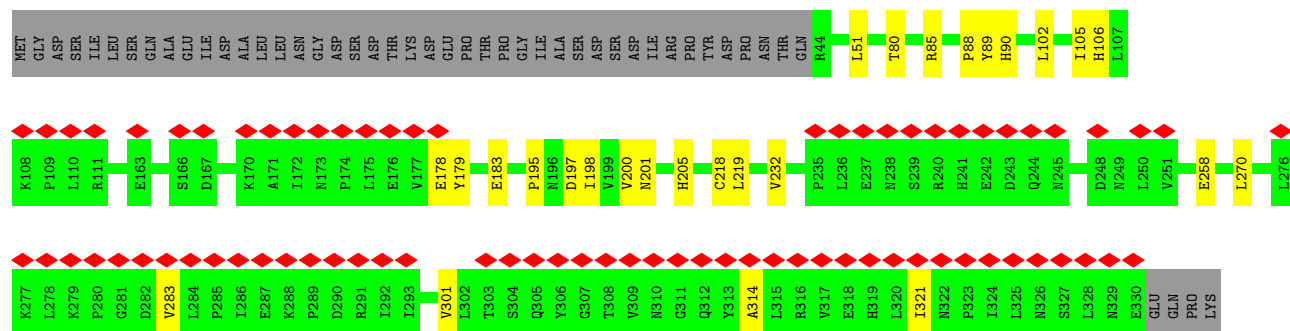
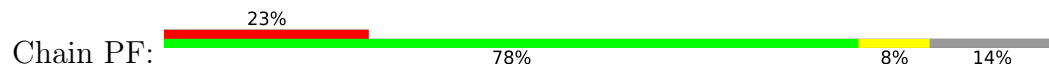
• Molecule 3: Flagellar motor switch protein FliM



• Molecule 3: Flagellar motor switch protein FliM

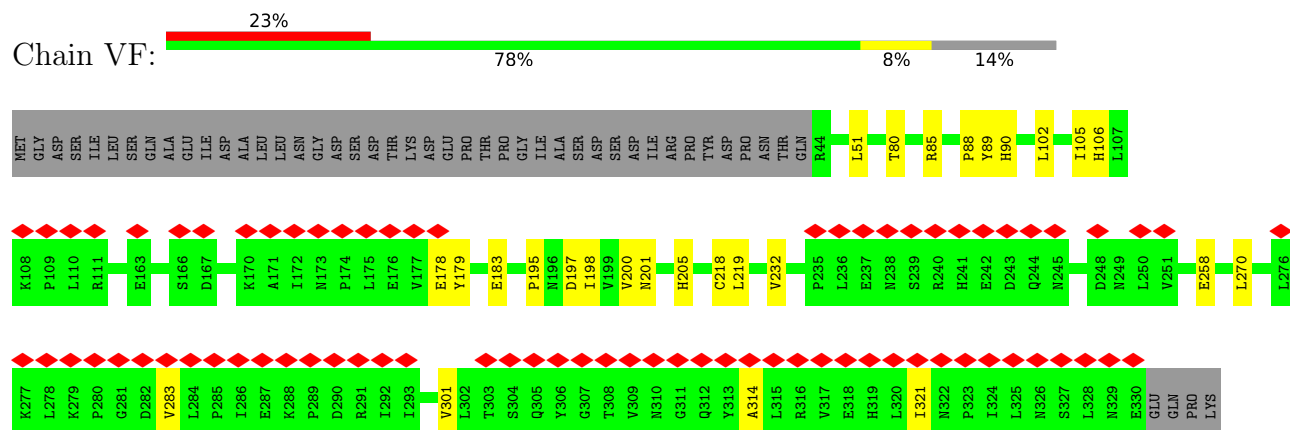


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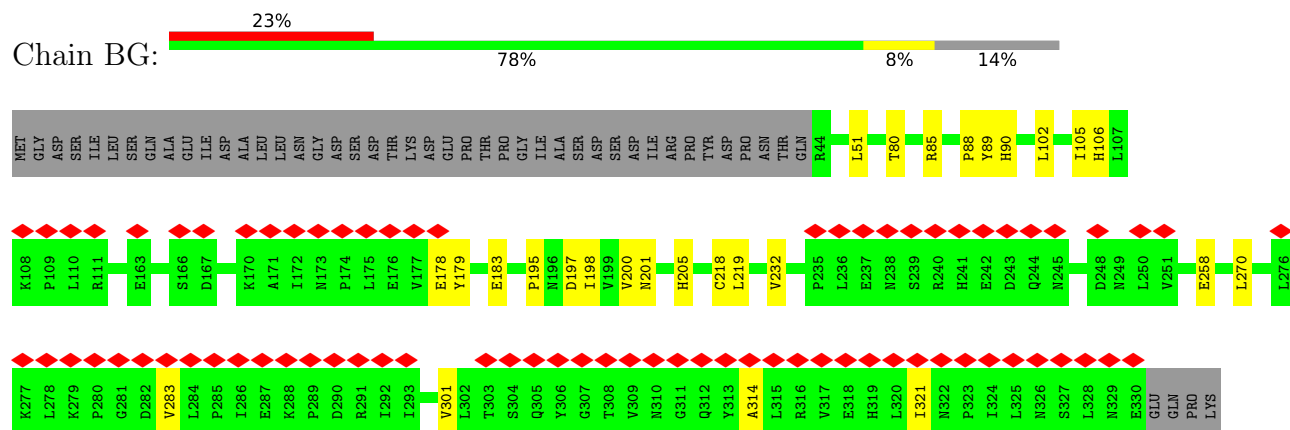
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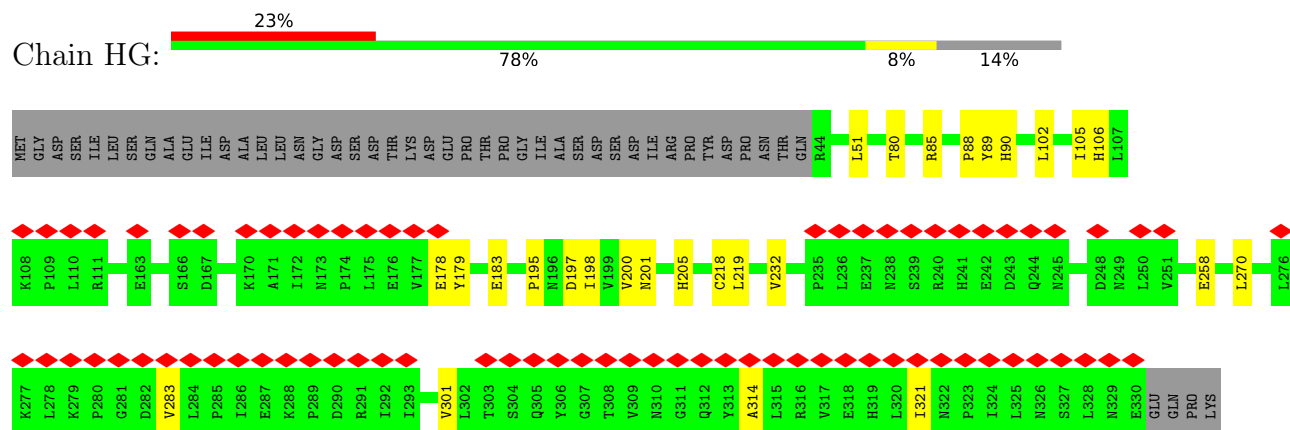
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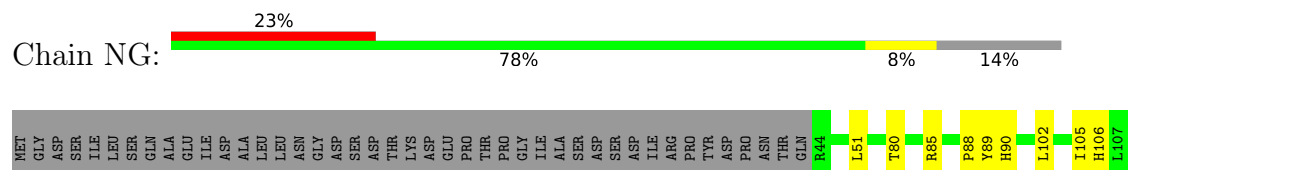
- Molecule 3: Flagellar motor switch protein FlIM

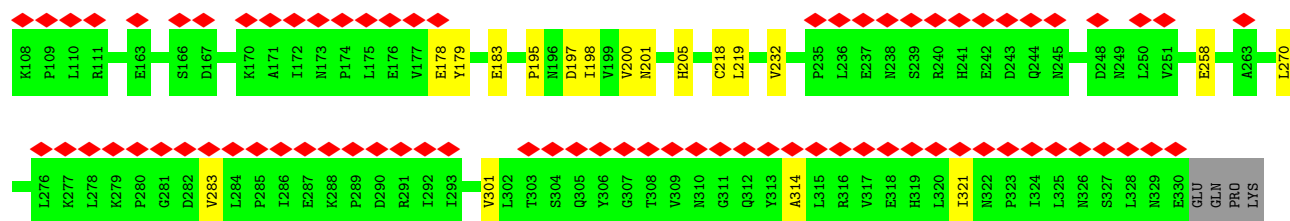
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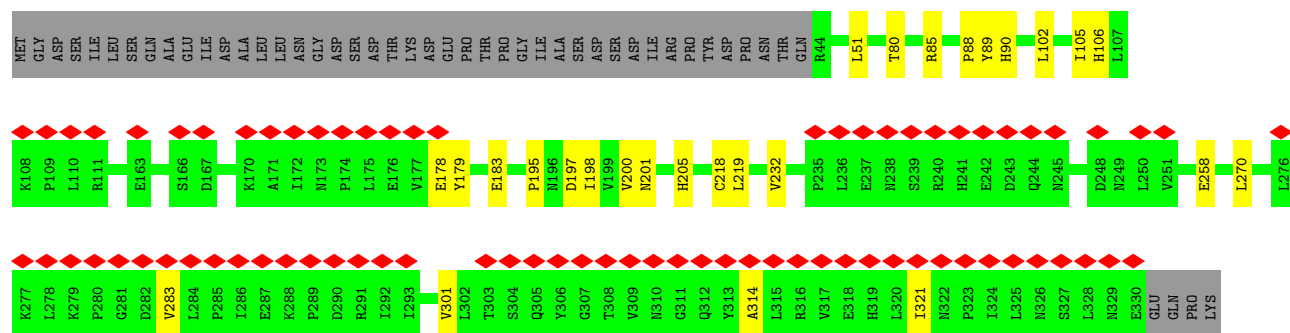
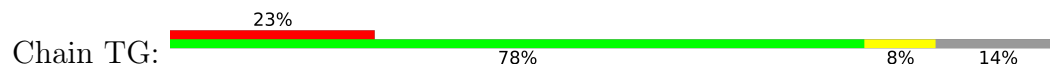
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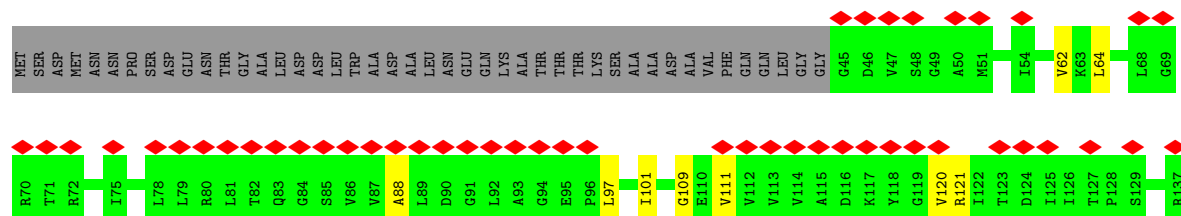




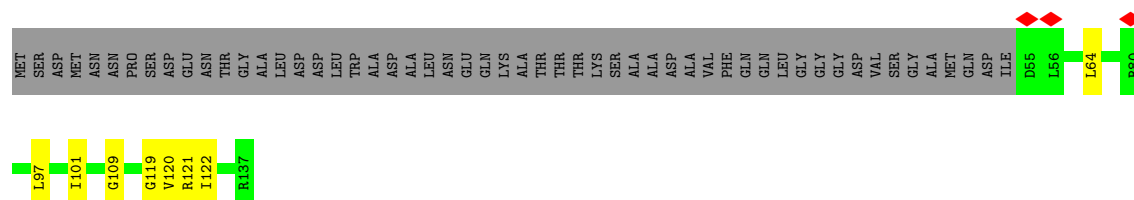
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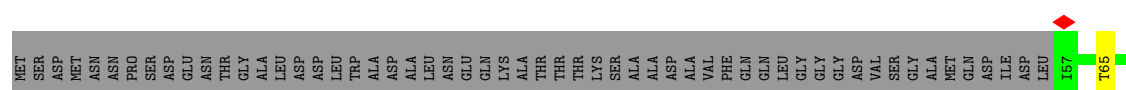
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• Molecule 4: Flagellar motor switch protein FliN

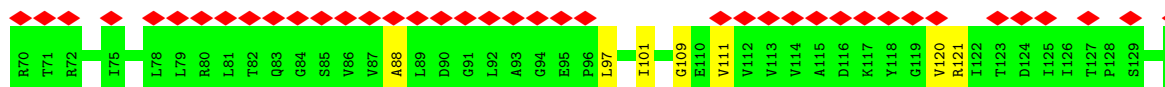
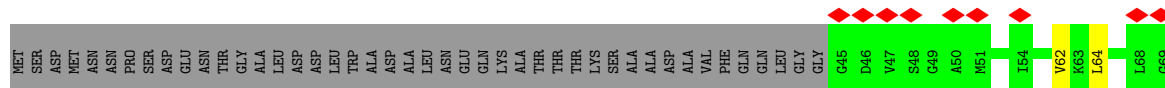


• Molecule 4: Flagellar motor switch protein FliN

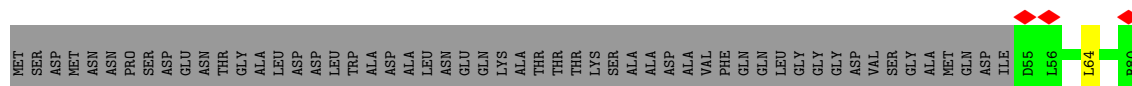




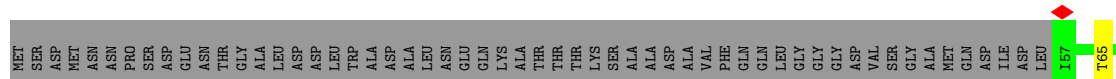
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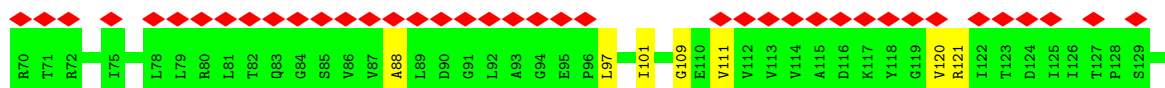
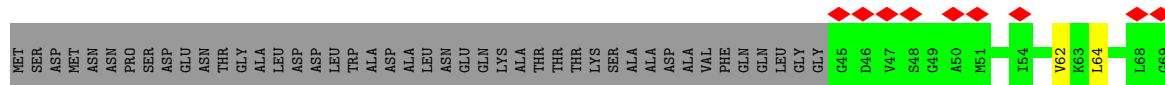
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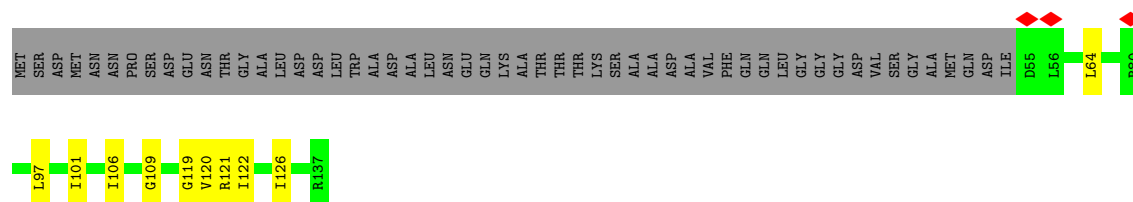
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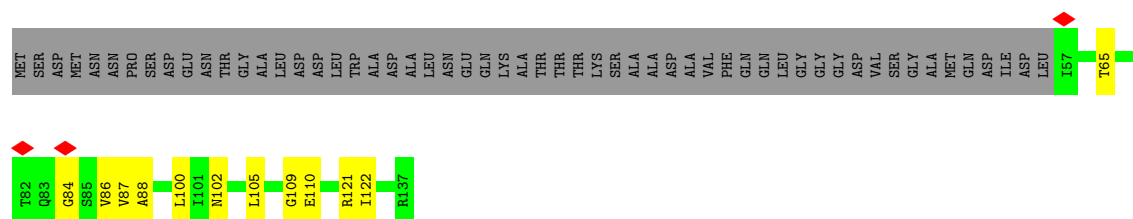
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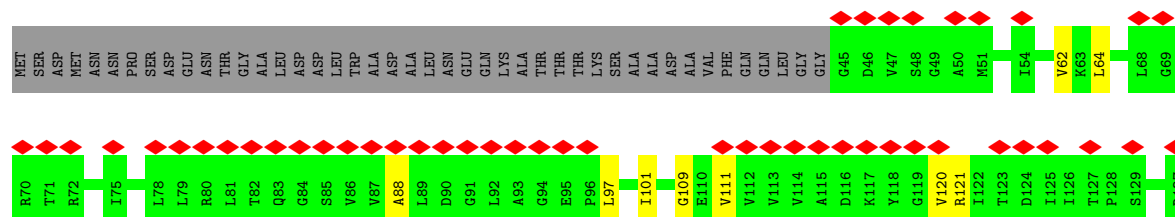
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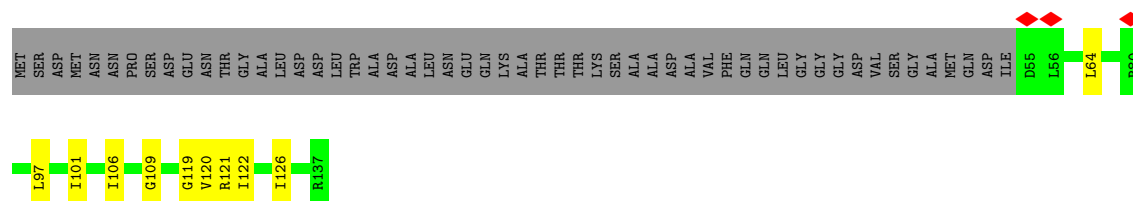
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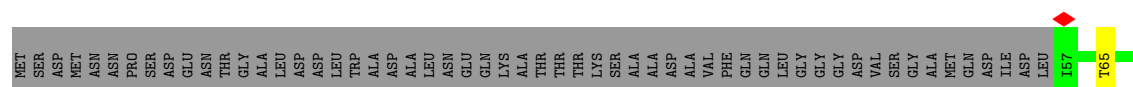
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• Molecule 4: Flagellar motor switch protein FlhN

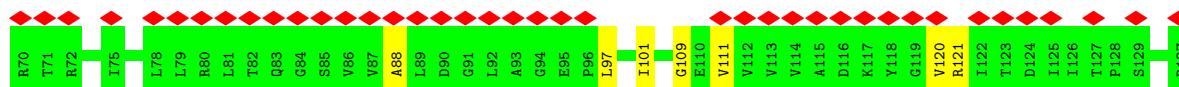
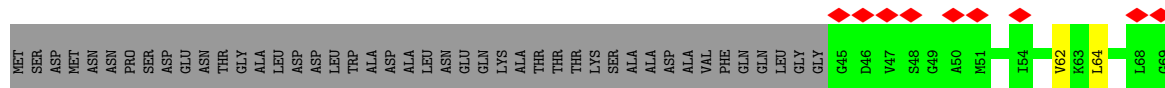
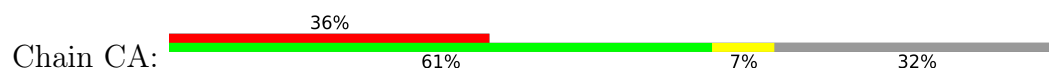


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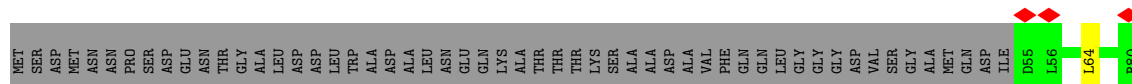




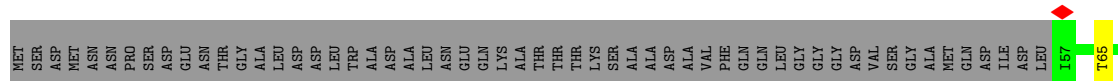
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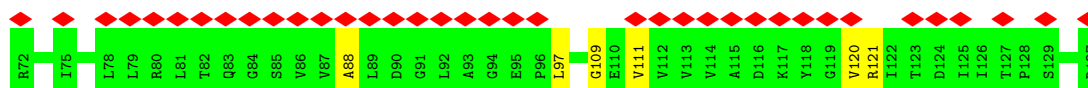
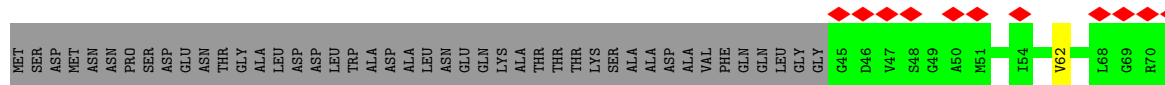
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- Molecule 4: Flagellar motor switch protein FliN

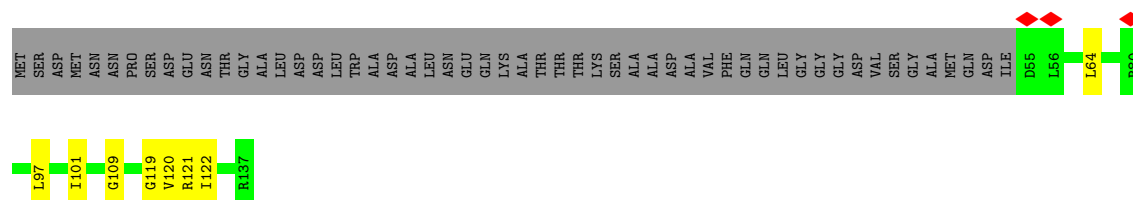


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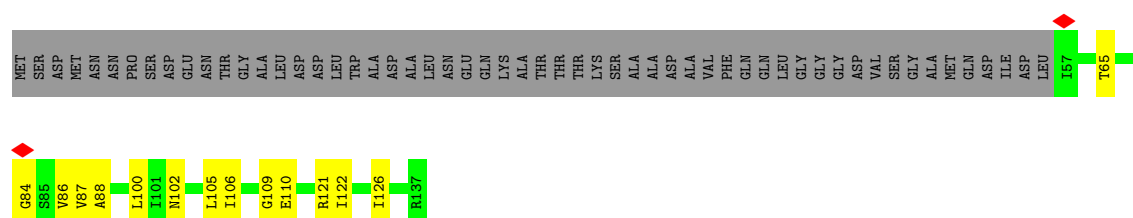
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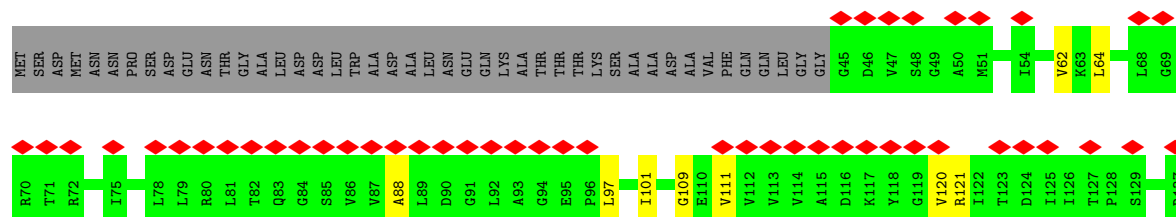
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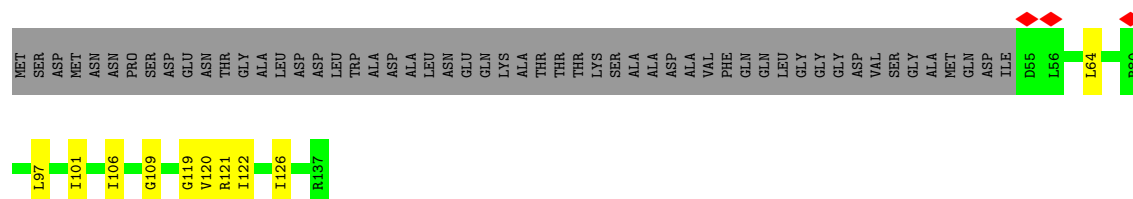
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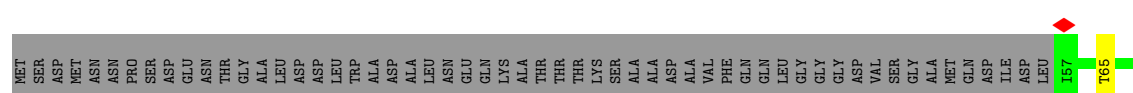
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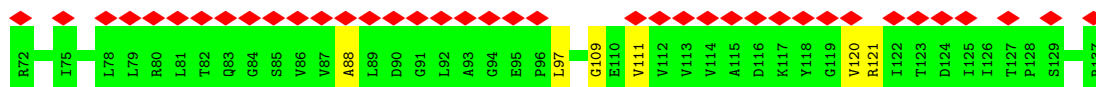
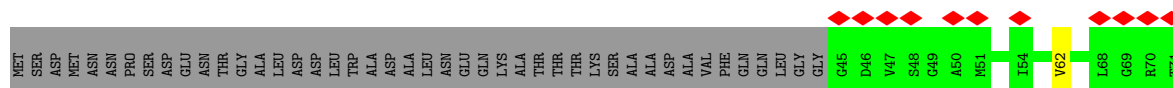
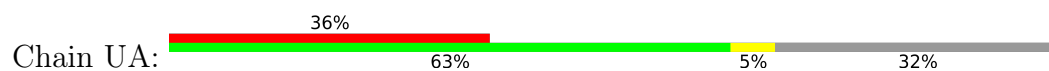
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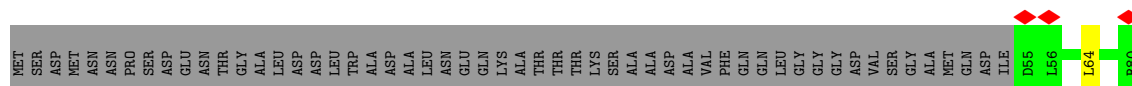




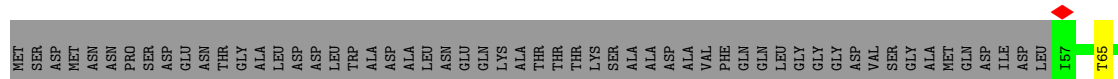
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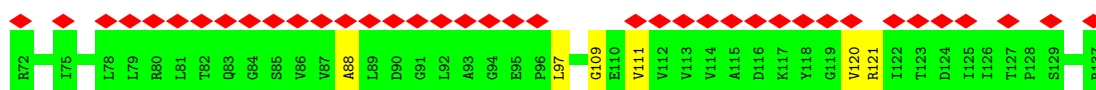
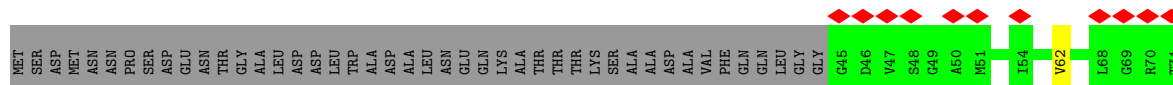
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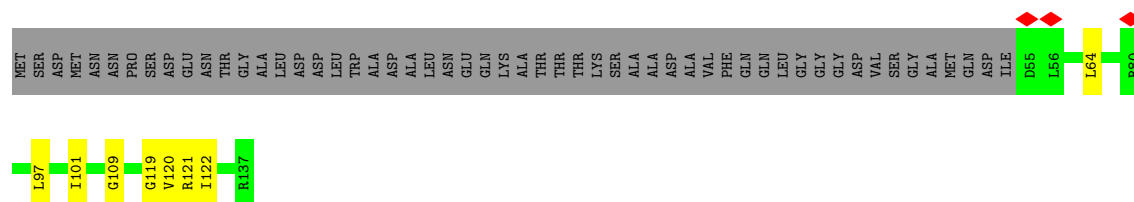


- Molecule 4: Flagellar motor switch protein FliN



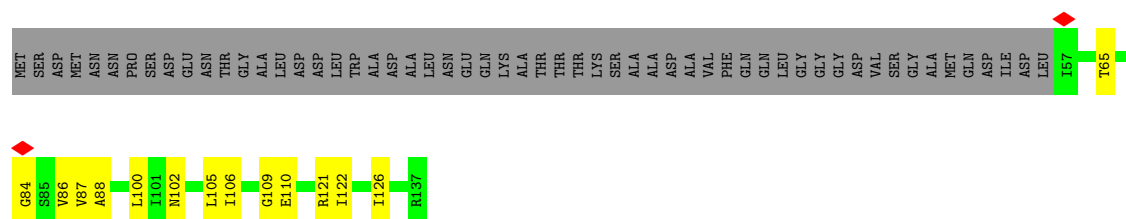
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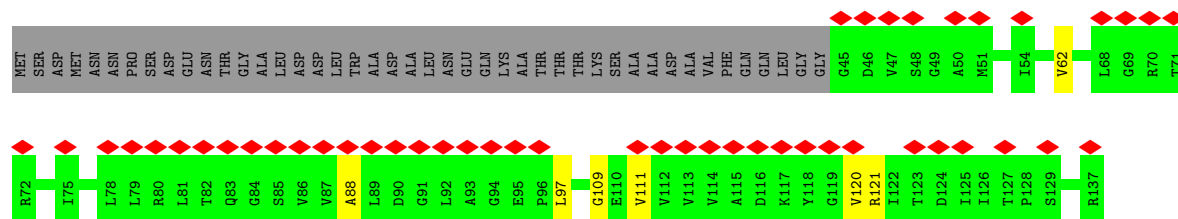
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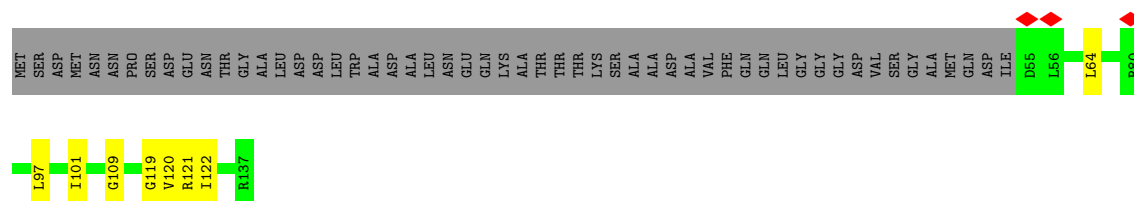
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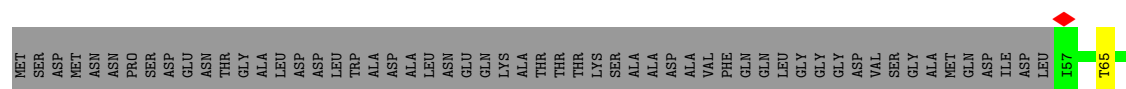
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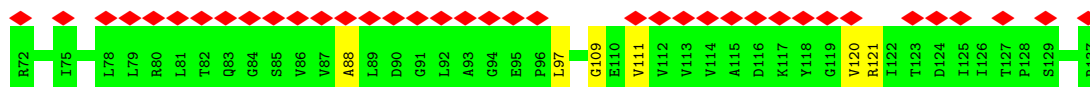
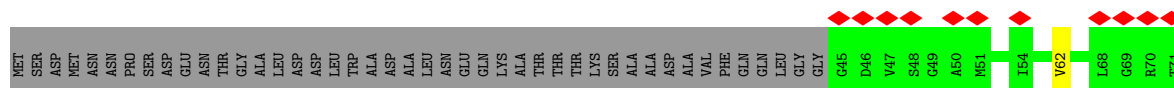
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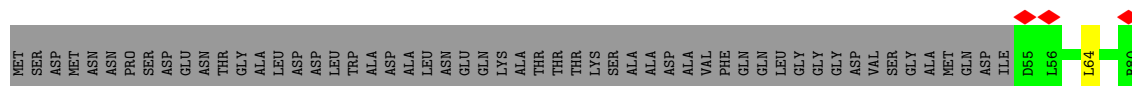




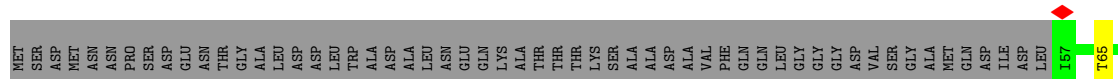
- Molecule 4: Flagellar motor switch protein FliN



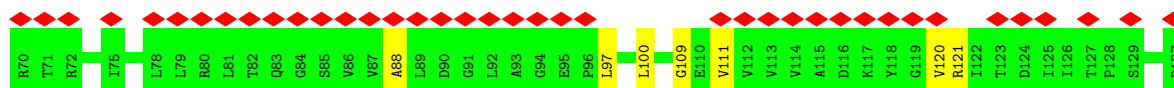
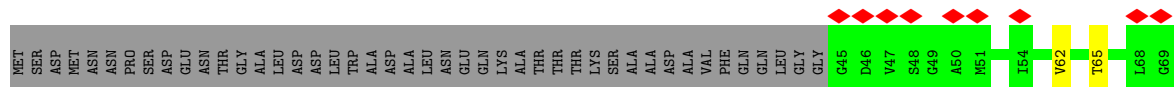
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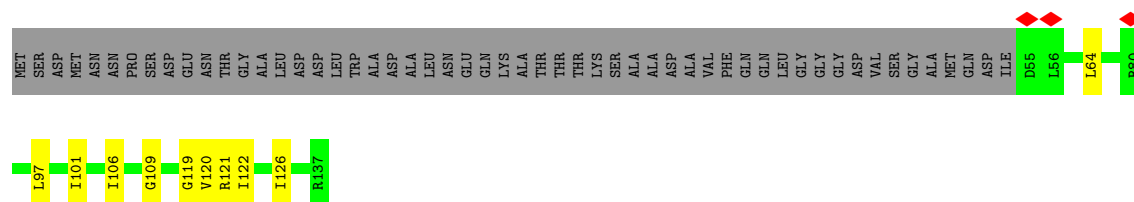
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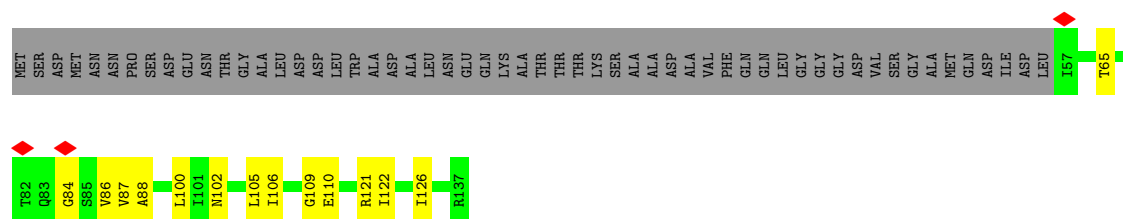
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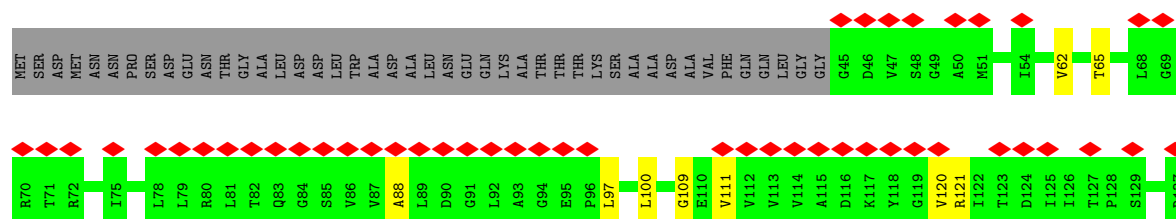
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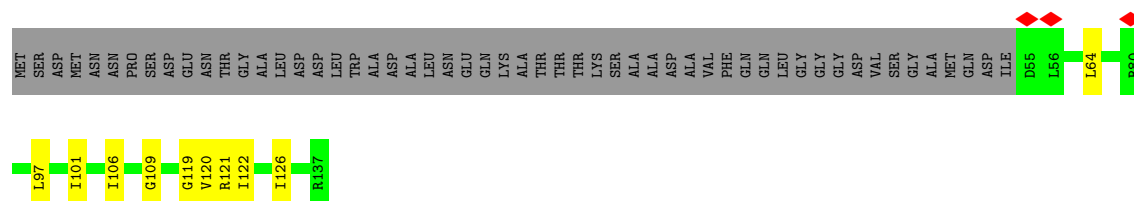
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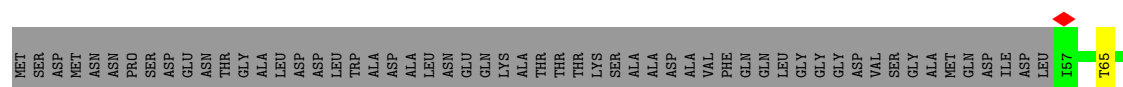
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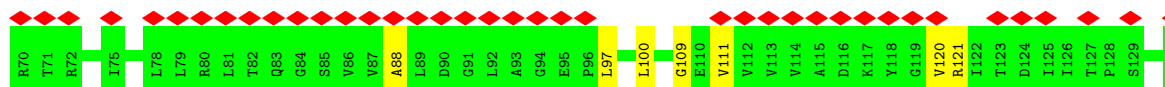
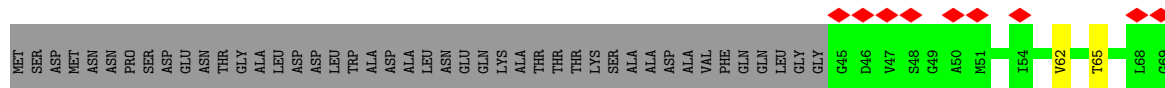


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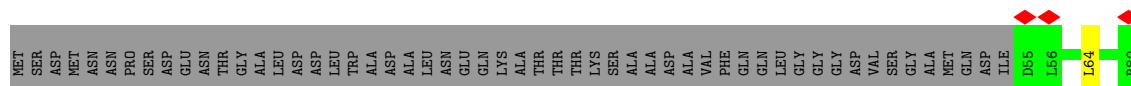




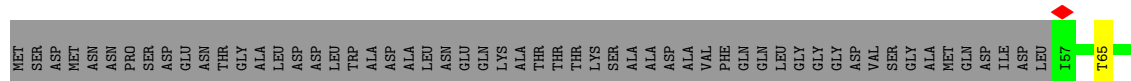
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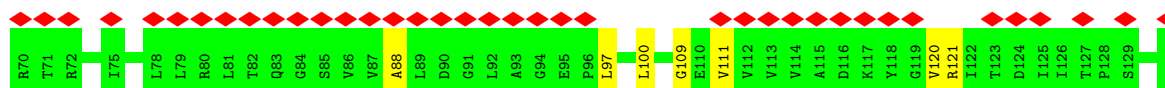
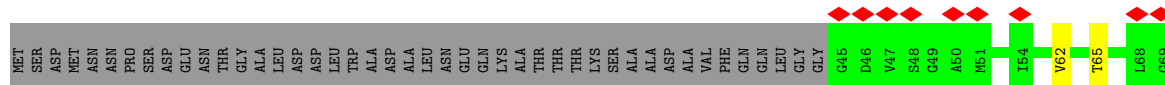
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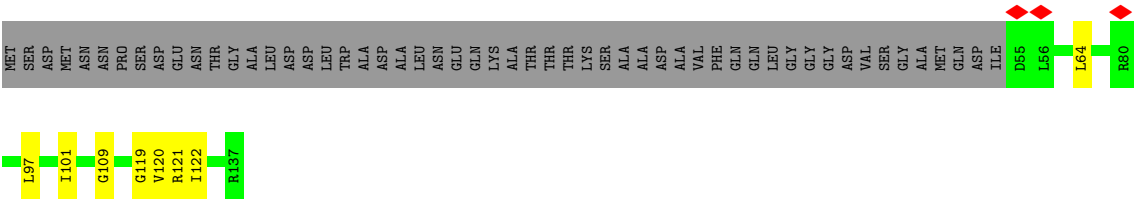
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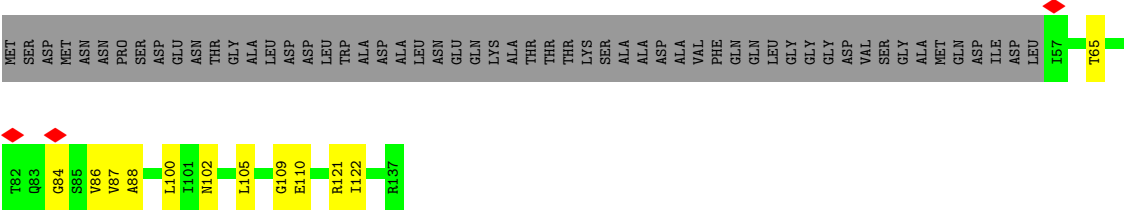
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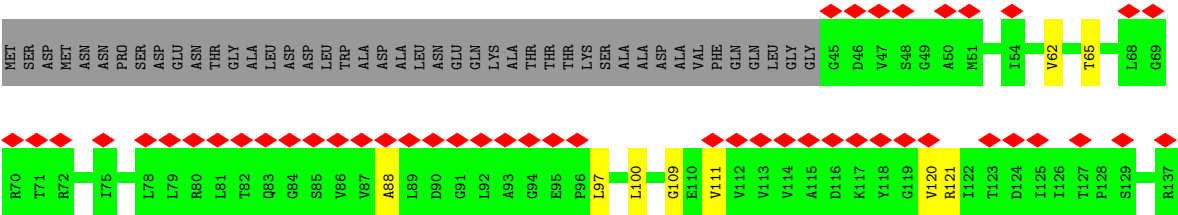
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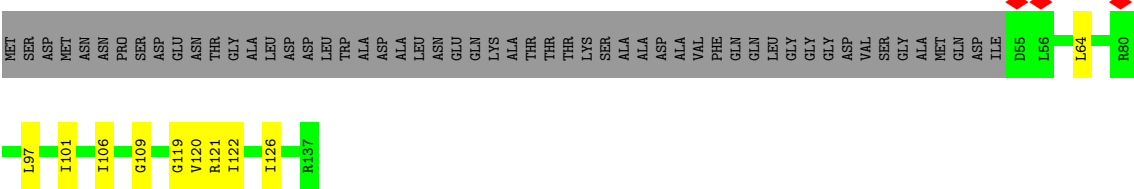
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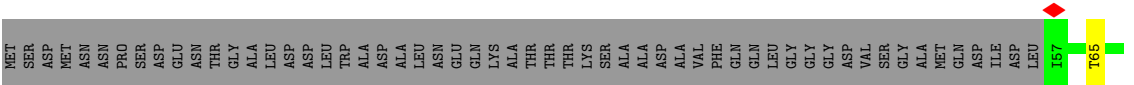
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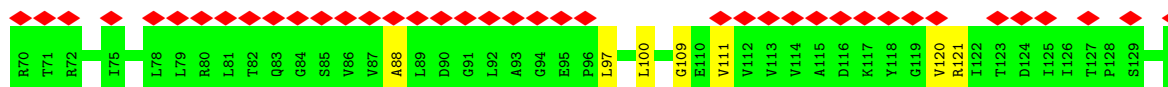
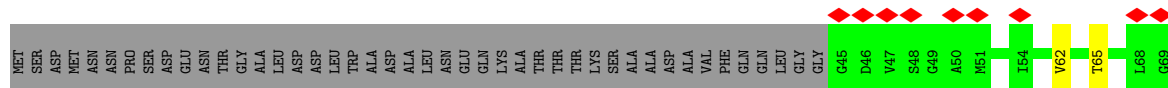


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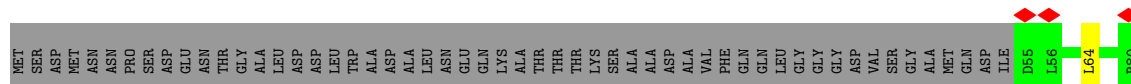




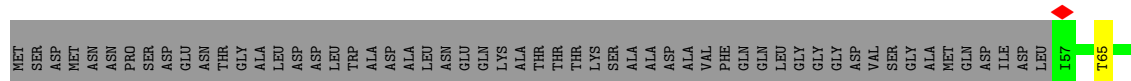
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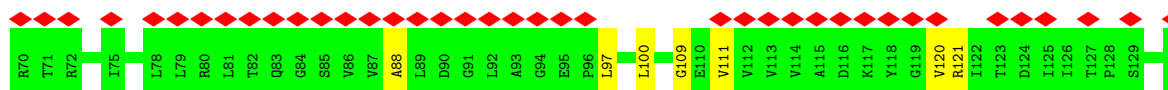
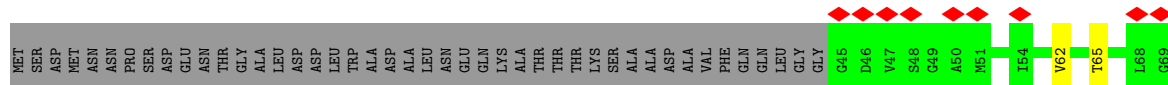
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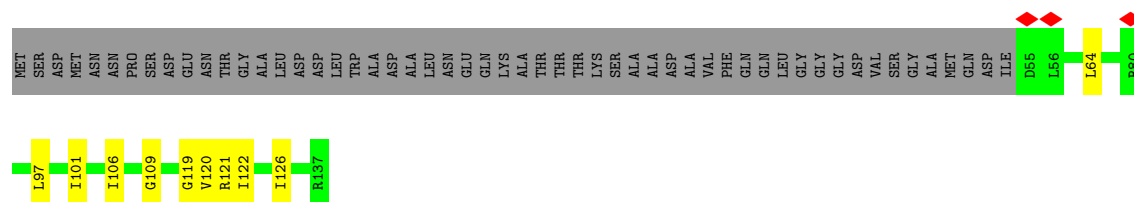


- Molecule 4: Flagellar motor switch protein FliN



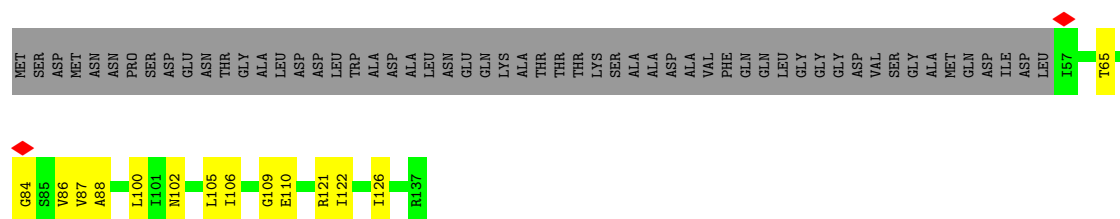
- Molecule 4: Flagellar motor switch protein FliN

Chain DD: 



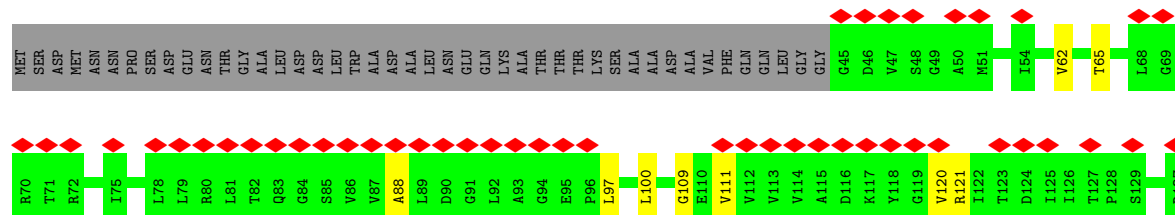
- Molecule 4: Flagellar motor switch protein FliN

Chain ED: 



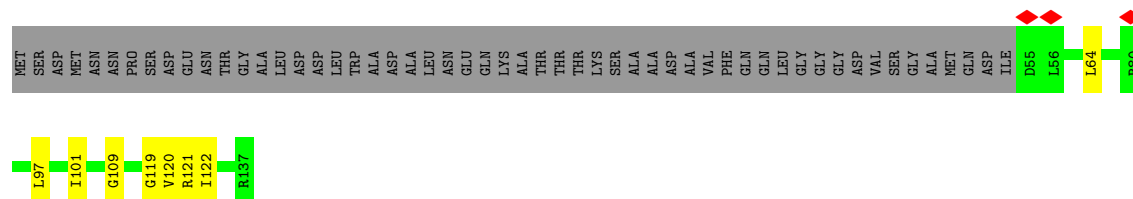
- Molecule 4: Flagellar motor switch protein FliN

Chain ID: 



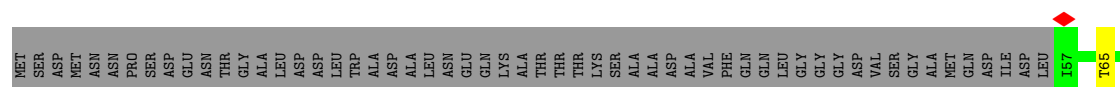
- Molecule 4: Flagellar motor switch protein FliN

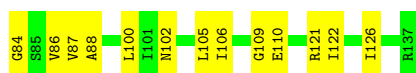
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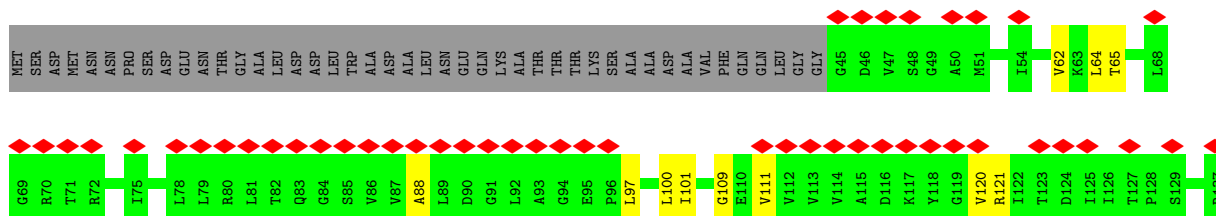
- Molecule 4: Flagellar motor switch protein FliN

Chain KD: 

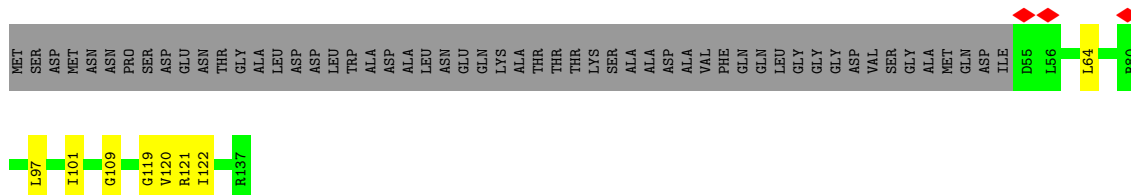




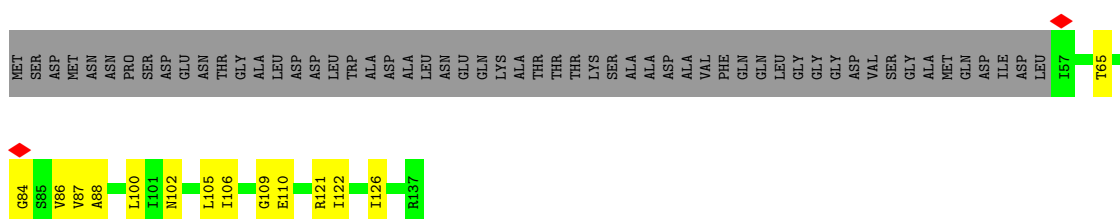
- Molecule 4: Flagellar motor switch protein FliN



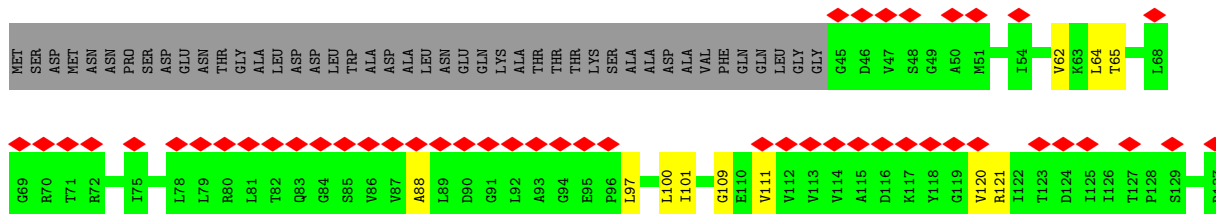
- Molecule 4: Flagellar motor switch protein FliN



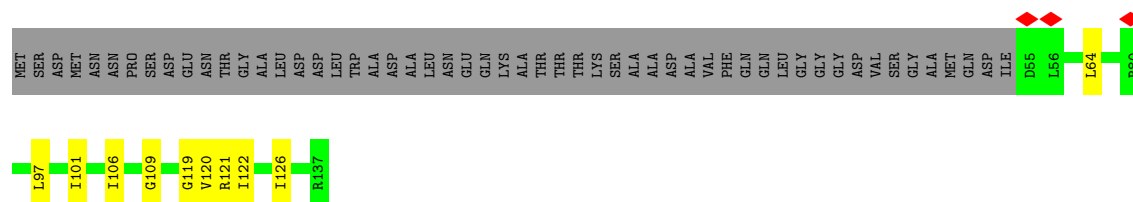
- Molecule 4: Flagellar motor switch protein FliN



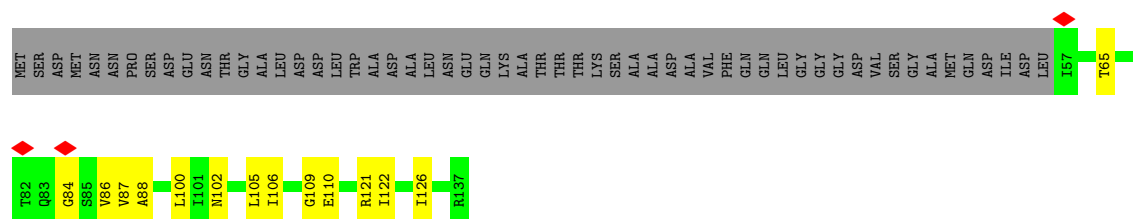
- Molecule 4: Flagellar motor switch protein FliN



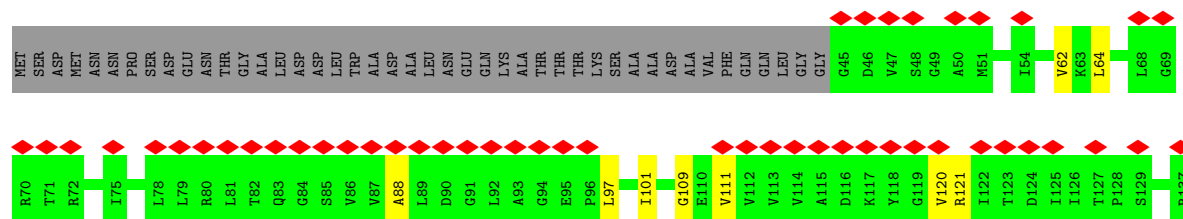
- Molecule 4: Flagellar motor switch protein FliN



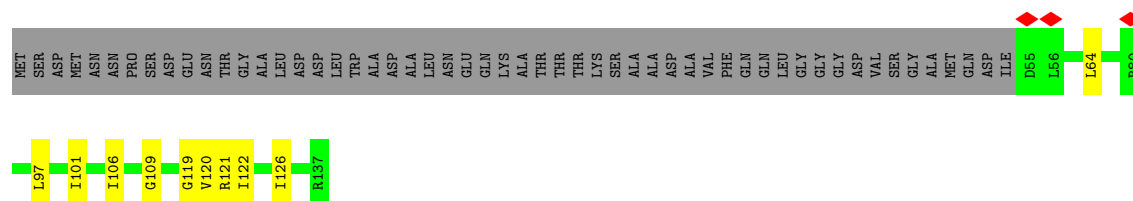
• Molecule 4: Flagellar motor switch protein FliN



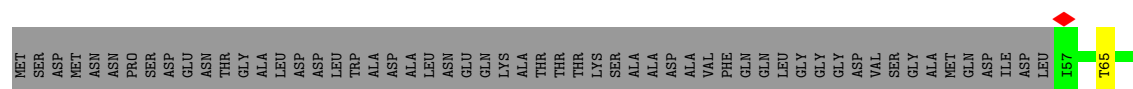
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN

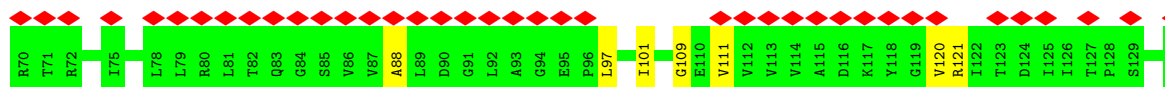
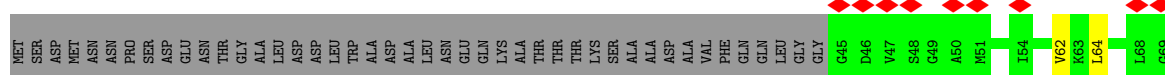


• Molecule 4: Flagellar motor switch protein FliN

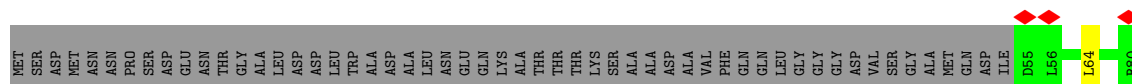




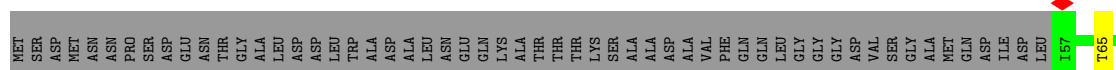
- Molecule 4: Flagellar motor switch protein FliN



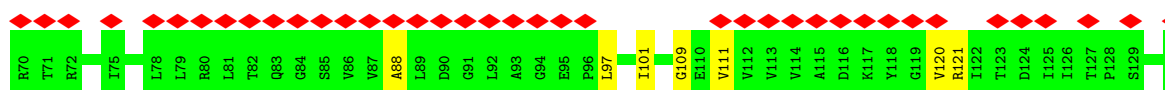
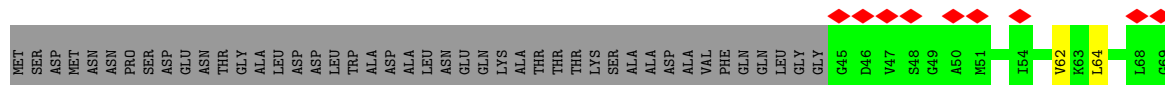
- Molecule 4: Flagellar motor switch protein FliN



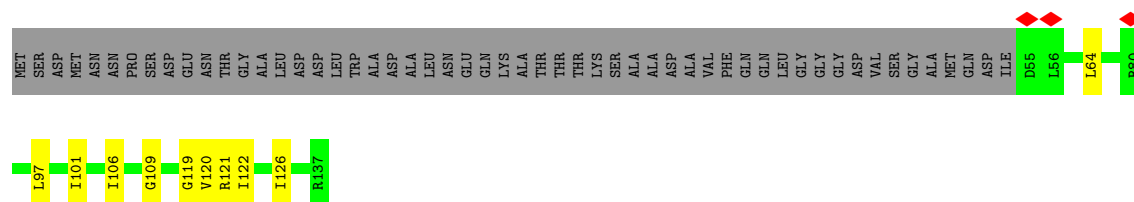
- Molecule 4: Flagellar motor switch protein FliN



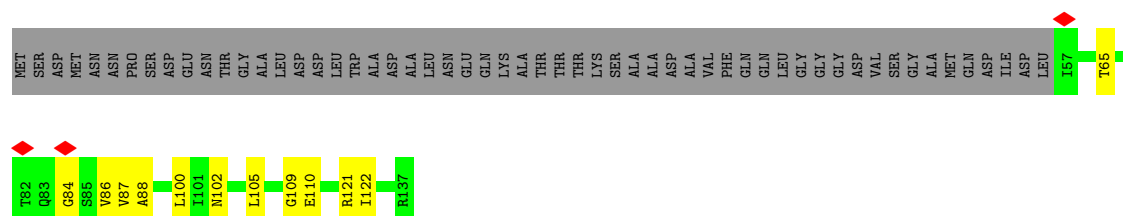
- Molecule 4: Flagellar motor switch protein FliN



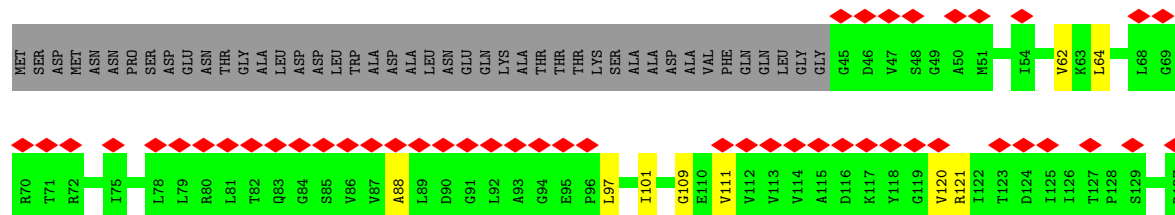
- Molecule 4: Flagellar motor switch protein FliN



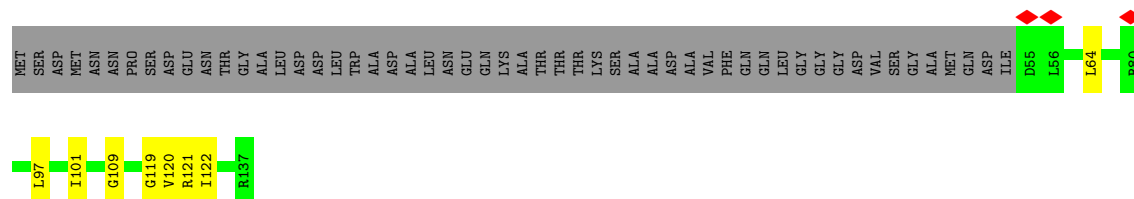
- Molecule 4: Flagellar motor switch protein FlhN



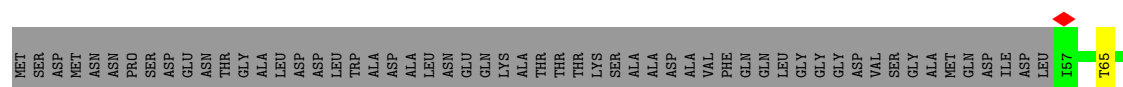
- Molecule 4: Flagellar motor switch protein FlhN



- Molecule 4: Flagellar motor switch protein FlhN

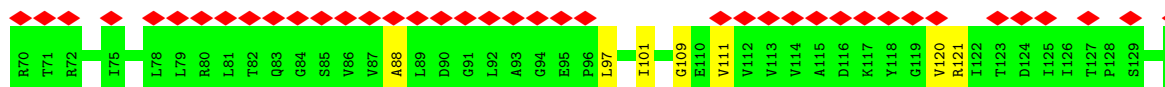
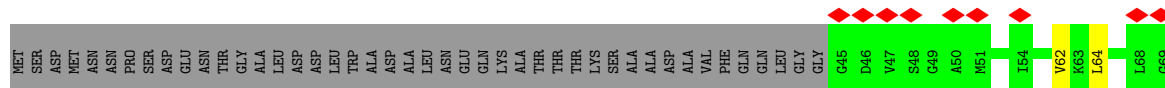


- Molecule 4: Flagellar motor switch protein FlhN

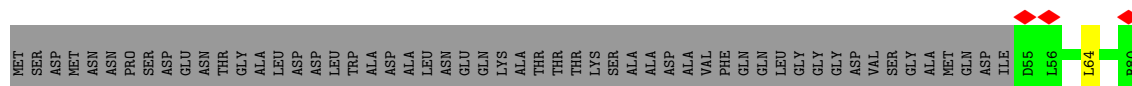




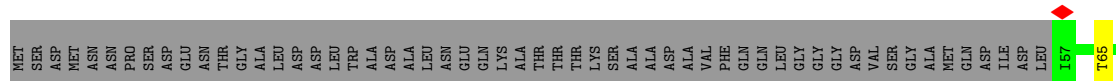
- Molecule 4: Flagellar motor switch protein FliN



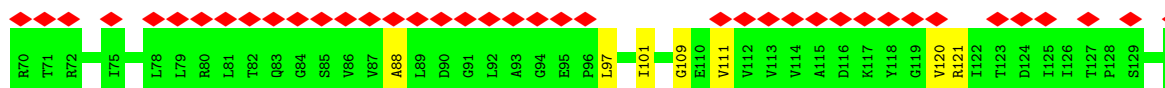
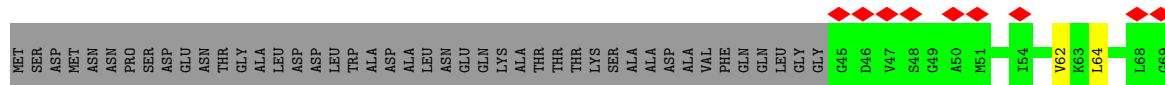
- Molecule 4: Flagellar motor switch protein FliN



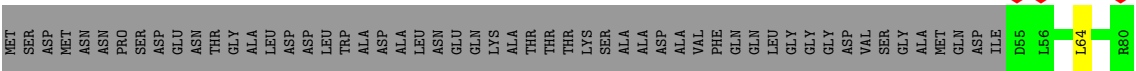
- Molecule 4: Flagellar motor switch protein FliN



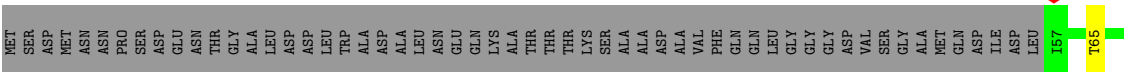
- Molecule 4: Flagellar motor switch protein FliN



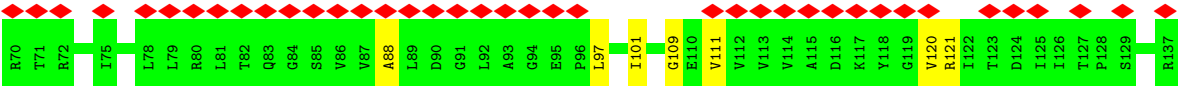
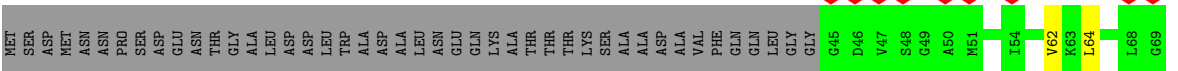
- Molecule 4: Flagellar motor switch protein FliN



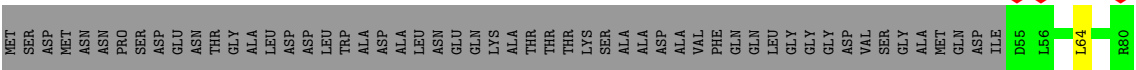
• Molecule 4: Flagellar motor switch protein FliN



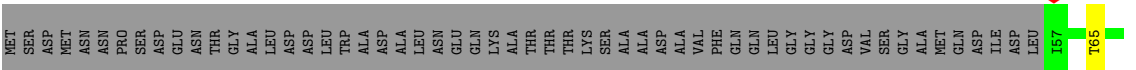
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN

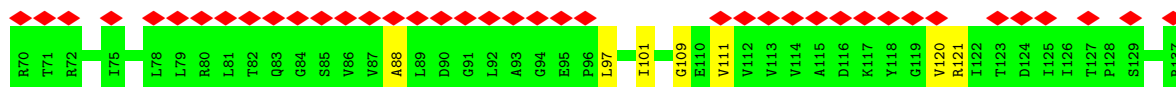
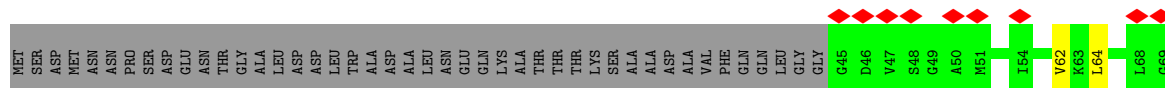


• Molecule 4: Flagellar motor switch protein FliN

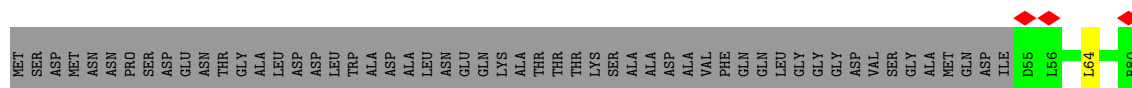




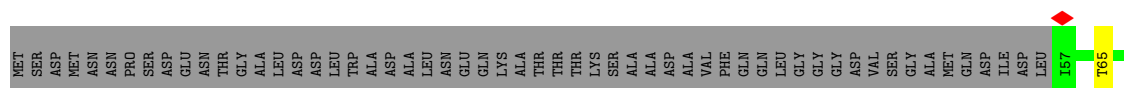
- Molecule 4: Flagellar motor switch protein FliN



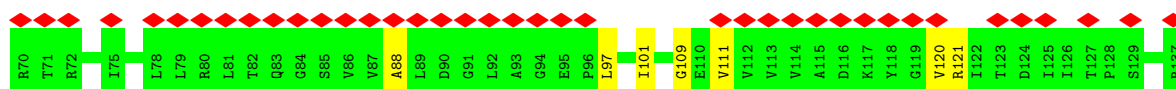
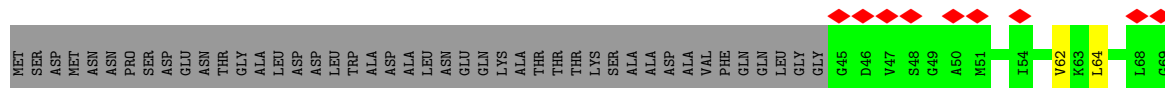
- Molecule 4: Flagellar motor switch protein FliN



- Molecule 4: Flagellar motor switch protein FliN

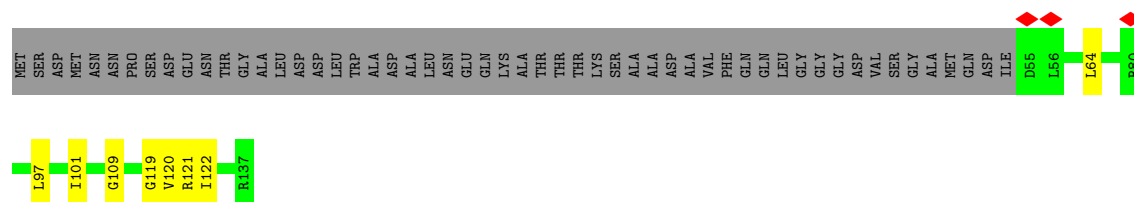


- Molecule 4: Flagellar motor switch protein FliN



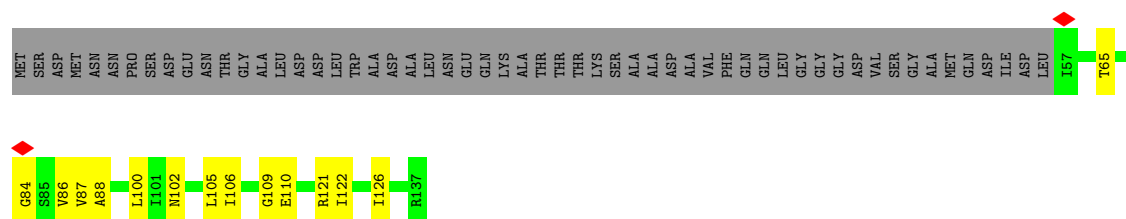
- Molecule 4: Flagellar motor switch protein FliN

Chain XF: 



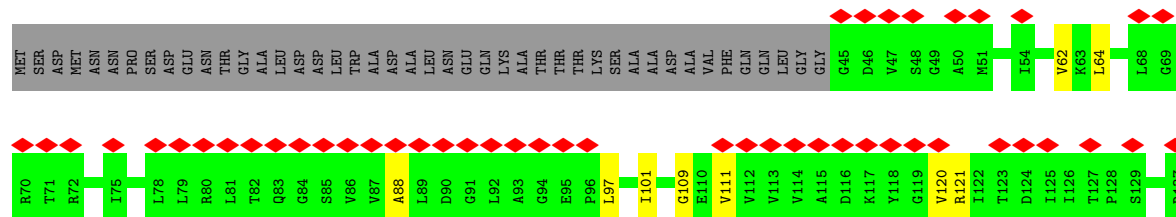
- Molecule 4: Flagellar motor switch protein FliN

Chain YF: 



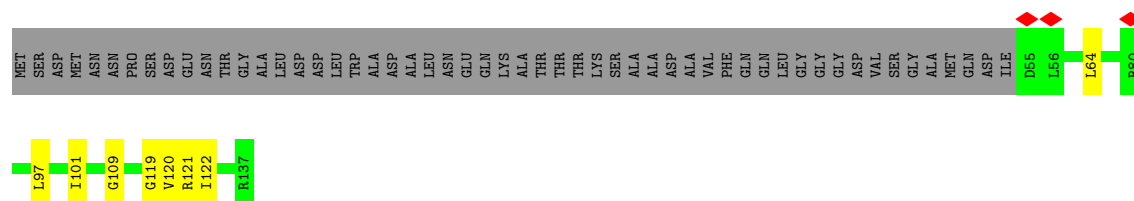
- Molecule 4: Flagellar motor switch protein FliN

Chain CG: 



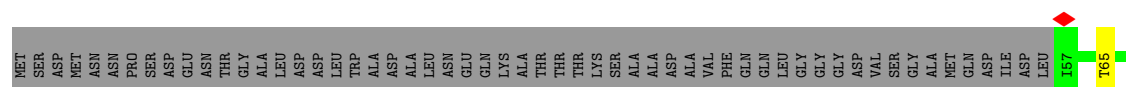
- Molecule 4: Flagellar motor switch protein FliN

Chain DG: 



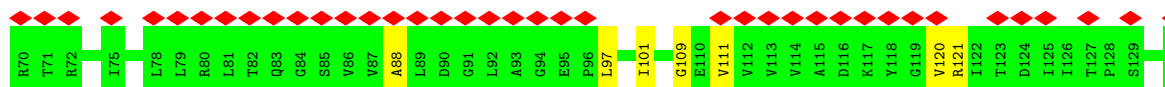
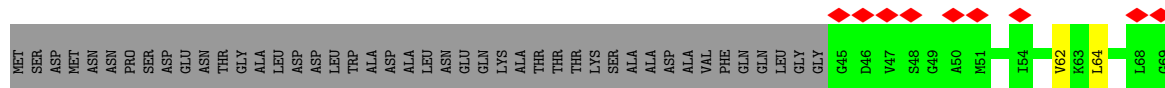
- Molecule 4: Flagellar motor switch protein FliN

Chain EG: 

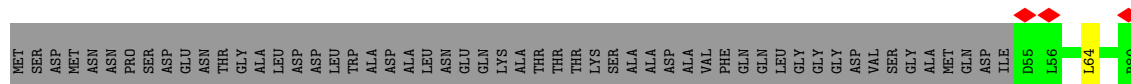




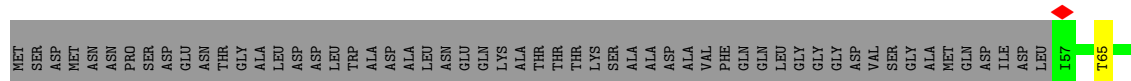
- Molecule 4: Flagellar motor switch protein FliN



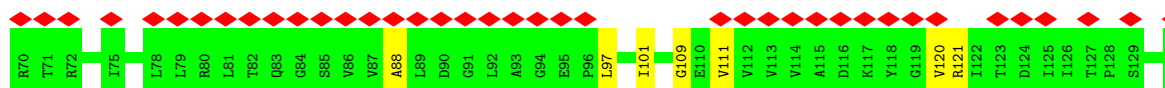
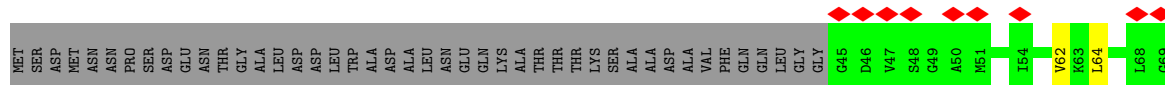
- Molecule 4: Flagellar motor switch protein FliN



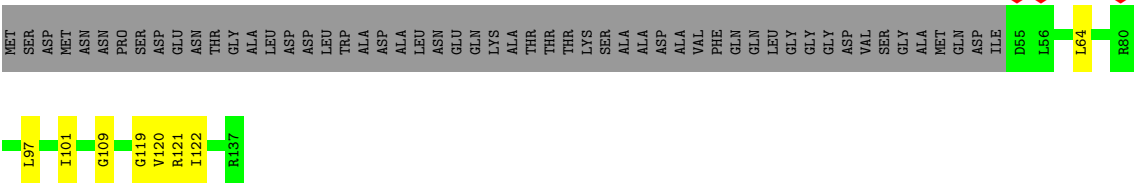
- Molecule 4: Flagellar motor switch protein FliN



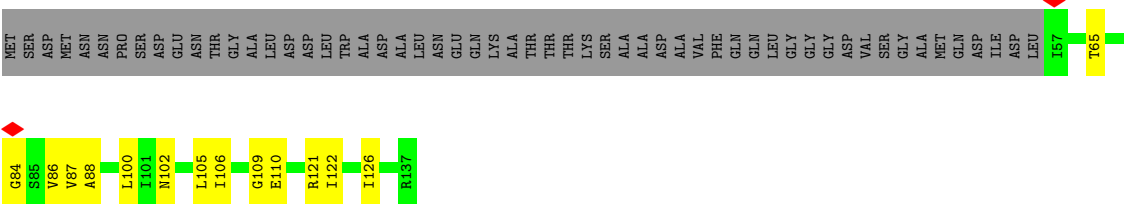
- Molecule 4: Flagellar motor switch protein FliN



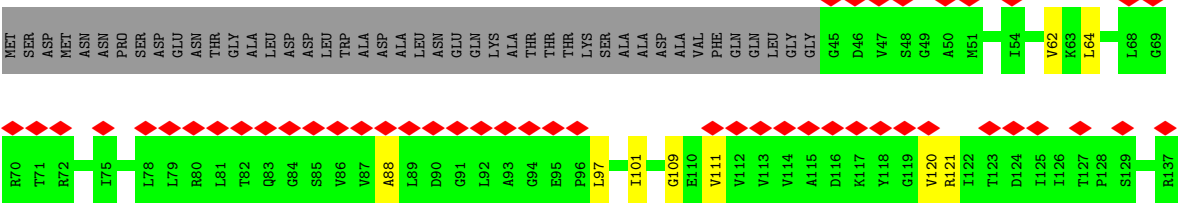
- Molecule 4: Flagellar motor switch protein FliN



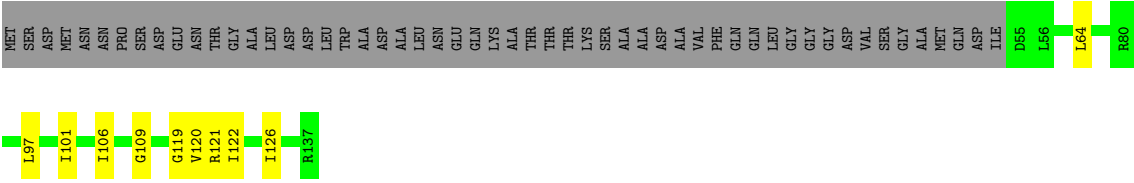
• Molecule 4: Flagellar motor switch protein FliN



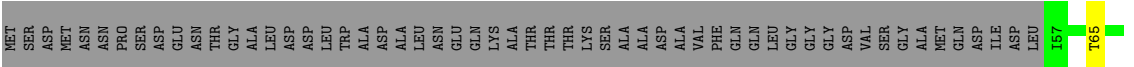
• Molecule 4: Flagellar motor switch protein FliN

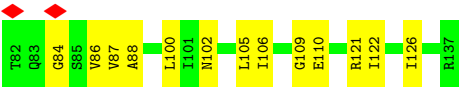


• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11106	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.242	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.283	Depositor
Minimum map value	-0.060	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.175	Depositor
Map size (Å)	1047.04, 1047.04, 1047.04	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.045, 2.045, 2.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.02	0/233	1.25	0/324
1	BC	1.02	0/233	1.25	0/324
1	BF	1.03	0/233	1.26	0/324
1	DB	1.02	0/233	1.26	0/324
1	DE	1.03	0/233	1.25	0/324
1	F	1.02	0/233	1.25	0/324
1	FA	1.02	0/233	1.26	0/324
1	FD	1.02	0/233	1.25	0/324
1	FG	1.02	0/233	1.26	0/324
1	HC	1.03	0/233	1.26	0/324
1	HF	1.02	0/233	1.25	0/324
1	I	1.02	0/233	1.26	0/324
1	JB	1.02	0/233	1.25	0/324
1	JE	1.03	0/233	1.26	0/324
1	LA	1.03	0/233	1.26	0/324
1	LD	1.02	0/233	1.26	0/324
1	LG	1.02	0/233	1.25	0/324
1	NC	1.02	0/233	1.25	0/324
1	NF	1.02	0/233	1.25	0/324
1	PB	1.02	0/233	1.25	0/324
1	PE	1.02	0/233	1.25	0/324
1	RA	1.03	0/233	1.26	0/324
1	RD	1.03	0/233	1.25	0/324
1	RG	1.02	0/233	1.25	0/324
1	S	1.02	0/233	1.25	0/324
1	TC	1.03	0/233	1.25	0/324
1	TF	1.03	0/233	1.25	0/324
1	VB	1.03	0/233	1.25	0/324
1	VE	1.02	0/233	1.25	0/324
1	XA	1.03	0/233	1.25	0/324
1	XD	1.02	0/233	1.25	0/324
1	Z	1.02	0/233	1.25	0/324
1	ZC	1.03	0/233	1.25	0/324
1	ZF	1.03	0/233	1.26	0/324

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AA	0.72	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	AD	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	AG	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	B	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	CC	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	CF	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	EB	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	EE	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	G	0.71	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	GA	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	GD	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	GG	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	IC	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	IF	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	J	0.71	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	KB	0.72	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	KE	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	MA	0.72	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	MD	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	MG	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	OC	0.71	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	OF	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	QB	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	QE	0.71	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	SA	0.71	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	SD	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	SG	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	T	0.72	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	UC	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	UF	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	WB	0.71	1/1577 (0.1%)	0.92	5/2195 (0.2%)
2	WE	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	YA	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
2	YD	0.72	1/1577 (0.1%)	0.93	5/2195 (0.2%)
3	BA	0.40	0/1419	0.54	0/1976
3	BD	0.40	0/1419	0.54	0/1976
3	BG	0.40	0/1419	0.54	0/1976
3	C	0.40	0/1419	0.54	0/1976
3	DC	0.40	0/1419	0.54	0/1976
3	DF	0.40	0/1419	0.54	0/1976
3	FB	0.40	0/1419	0.54	0/1976
3	FE	0.40	0/1419	0.54	0/1976
3	HA	0.40	0/1419	0.54	0/1976

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	HD	0.40	0/1419	0.54	0/1976
3	HG	0.40	0/1419	0.54	0/1976
3	JC	0.40	0/1419	0.54	0/1976
3	JF	0.40	0/1419	0.54	0/1976
3	K	0.40	0/1419	0.54	0/1976
3	LB	0.40	0/1419	0.54	0/1976
3	LE	0.40	0/1419	0.54	0/1976
3	M	0.40	0/1419	0.54	0/1976
3	NA	0.40	0/1419	0.54	0/1976
3	ND	0.40	0/1419	0.54	0/1976
3	NG	0.40	0/1419	0.55	0/1976
3	PC	0.40	0/1419	0.54	0/1976
3	PF	0.40	0/1419	0.54	0/1976
3	RB	0.40	0/1419	0.54	0/1976
3	RE	0.40	0/1419	0.54	0/1976
3	TA	0.40	0/1419	0.54	0/1976
3	TD	0.40	0/1419	0.54	0/1976
3	TG	0.40	0/1419	0.54	0/1976
3	V	0.40	0/1419	0.54	0/1976
3	VC	0.40	0/1419	0.54	0/1976
3	VF	0.40	0/1419	0.54	0/1976
3	XB	0.40	0/1419	0.54	0/1976
3	XE	0.40	0/1419	0.54	0/1976
3	ZA	0.40	0/1419	0.54	0/1976
3	ZD	0.40	0/1419	0.54	0/1976
4	AB	0.56	0/455	0.65	0/630
4	AC	0.31	0/398	0.42	0/550
4	AE	0.56	0/455	0.65	0/630
4	AF	0.31	0/398	0.42	0/550
4	BB	0.40	0/408	0.49	0/564
4	BE	0.40	0/408	0.49	0/564
4	CA	0.56	0/455	0.65	0/630
4	CB	0.31	0/398	0.42	0/550
4	CD	0.55	0/455	0.65	0/630
4	CE	0.31	0/398	0.42	0/550
4	CG	0.56	0/455	0.66	0/630
4	D	0.55	0/455	0.65	0/630
4	DA	0.40	0/408	0.48	0/564
4	DD	0.40	0/408	0.49	0/564
4	DG	0.40	0/408	0.49	0/564
4	E	0.40	0/408	0.49	0/564
4	EA	0.31	0/398	0.42	0/550
4	EC	0.56	0/455	0.66	0/630

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ED	0.31	0/398	0.42	0/550
4	EF	0.55	0/455	0.65	0/630
4	EG	0.31	0/398	0.42	0/550
4	FC	0.40	0/408	0.48	0/564
4	FF	0.40	0/408	0.49	0/564
4	GB	0.55	0/455	0.65	0/630
4	GC	0.31	0/398	0.42	0/550
4	GE	0.56	0/455	0.65	0/630
4	GF	0.31	0/398	0.42	0/550
4	H	0.31	0/398	0.42	0/550
4	HB	0.40	0/408	0.48	0/564
4	HE	0.40	0/408	0.49	0/564
4	IA	0.55	0/455	0.65	0/630
4	IB	0.31	0/398	0.42	0/550
4	ID	0.55	0/455	0.66	0/630
4	IE	0.31	0/398	0.42	0/550
4	IG	0.55	0/455	0.65	0/630
4	JA	0.40	0/408	0.49	0/564
4	JD	0.40	0/408	0.49	0/564
4	JG	0.40	0/408	0.49	0/564
4	KA	0.31	0/398	0.42	0/550
4	KC	0.55	0/455	0.66	0/630
4	KD	0.31	0/398	0.42	0/550
4	KF	0.55	0/455	0.66	0/630
4	KG	0.31	0/398	0.42	0/550
4	L	0.56	0/455	0.66	0/630
4	LC	0.40	0/408	0.49	0/564
4	LF	0.40	0/408	0.49	0/564
4	MB	0.56	0/455	0.65	0/630
4	MC	0.31	0/398	0.42	0/550
4	ME	0.56	0/455	0.65	0/630
4	MF	0.31	0/398	0.42	0/550
4	N	0.55	0/455	0.65	0/630
4	NB	0.40	0/408	0.49	0/564
4	NE	0.40	0/408	0.49	0/564
4	O	0.40	0/408	0.48	0/564
4	OA	0.55	0/455	0.65	0/630
4	OB	0.31	0/398	0.42	0/550
4	OD	0.55	0/455	0.65	0/630
4	OE	0.31	0/398	0.42	0/550
4	OG	0.55	0/455	0.66	0/630
4	P	0.40	0/408	0.49	0/564
4	PA	0.40	0/408	0.49	0/564

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	PD	0.40	0/408	0.48	0/564
4	PG	0.40	0/408	0.49	0/564
4	Q	0.31	0/398	0.42	0/550
4	QA	0.31	0/398	0.42	0/550
4	QC	0.56	0/455	0.65	0/630
4	QD	0.31	0/398	0.42	0/550
4	QF	0.56	0/455	0.65	0/630
4	QG	0.31	0/398	0.42	0/550
4	R	0.31	0/398	0.42	0/550
4	RC	0.40	0/408	0.49	0/564
4	RF	0.40	0/408	0.49	0/564
4	SB	0.56	0/455	0.65	0/630
4	SC	0.31	0/398	0.42	0/550
4	SE	0.56	0/455	0.65	0/630
4	SF	0.31	0/398	0.42	0/550
4	TB	0.40	0/408	0.49	0/564
4	TE	0.40	0/408	0.49	0/564
4	UA	0.55	0/455	0.65	0/630
4	UB	0.31	0/398	0.42	0/550
4	UD	0.56	0/455	0.65	0/630
4	UE	0.30	0/398	0.42	0/550
4	UG	0.55	0/455	0.65	0/630
4	VA	0.40	0/408	0.48	0/564
4	VD	0.40	0/408	0.49	0/564
4	VG	0.40	0/408	0.48	0/564
4	W	0.56	0/455	0.65	0/630
4	WA	0.31	0/398	0.42	0/550
4	WC	0.55	0/455	0.65	0/630
4	WD	0.31	0/398	0.42	0/550
4	WF	0.55	0/455	0.65	0/630
4	WG	0.31	0/398	0.42	0/550
4	X	0.40	0/408	0.49	0/564
4	XC	0.40	0/408	0.49	0/564
4	XF	0.40	0/408	0.49	0/564
4	Y	0.31	0/398	0.42	0/550
4	YB	0.56	0/455	0.66	0/630
4	YC	0.31	0/398	0.42	0/550
4	YE	0.56	0/455	0.66	0/630
4	YF	0.31	0/398	0.42	0/550
4	ZB	0.40	0/408	0.49	0/564
4	ZE	0.40	0/408	0.49	0/564
All	All	0.58	34/152660 (0.0%)	0.75	170/212126 (0.1%)

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	SG	207	LYS	C-N	-6.61	1.25	1.33
2	CC	207	LYS	C-N	-6.59	1.25	1.33
2	AG	207	LYS	C-N	-6.59	1.25	1.33
2	GD	207	LYS	C-N	-6.59	1.25	1.33
2	YA	207	LYS	C-N	-6.58	1.25	1.33

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	IC	186	GLN	N-CA-C	-7.41	103.38	114.64
2	SG	186	GLN	N-CA-C	-7.40	103.39	114.64
2	UC	186	GLN	N-CA-C	-7.38	103.42	114.64
2	SD	186	GLN	N-CA-C	-7.38	103.43	114.64
2	YA	186	GLN	N-CA-C	-7.37	103.43	114.64

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	234	0	102	1	0
1	BC	234	0	102	1	0
1	BF	234	0	102	1	0
1	DB	234	0	102	1	0
1	DE	234	0	102	1	0
1	F	234	0	102	1	0
1	FA	234	0	102	1	0
1	FD	234	0	102	1	0
1	FG	234	0	102	1	0
1	HC	234	0	102	1	0
1	HF	234	0	102	1	0
1	I	234	0	102	1	0
1	JB	234	0	102	1	0
1	JE	234	0	102	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	LA	234	0	102	1	0
1	LD	234	0	102	1	0
1	LG	234	0	102	1	0
1	NC	234	0	102	1	0
1	NF	234	0	102	1	0
1	PB	234	0	102	1	0
1	PE	234	0	102	1	0
1	RA	234	0	102	1	0
1	RD	234	0	102	1	0
1	RG	234	0	102	1	0
1	S	234	0	102	1	0
1	TC	234	0	102	1	0
1	TF	234	0	102	1	0
1	VB	234	0	102	1	0
1	VE	234	0	102	1	0
1	XA	234	0	102	1	0
1	XD	234	0	102	1	0
1	Z	234	0	102	1	0
1	ZC	234	0	102	1	0
1	ZF	234	0	102	1	0
2	AA	1579	0	738	50	0
2	AD	1579	0	738	49	0
2	AG	1579	0	738	49	0
2	B	1579	0	738	49	0
2	CC	1579	0	738	49	0
2	CF	1579	0	738	48	0
2	EB	1579	0	738	50	0
2	EE	1579	0	738	48	0
2	G	1579	0	738	49	0
2	GA	1579	0	738	51	0
2	GD	1579	0	738	51	0
2	GG	1579	0	738	48	0
2	IC	1579	0	738	50	0
2	IF	1579	0	738	49	0
2	J	1579	0	738	49	0
2	KB	1579	0	738	50	0
2	KE	1579	0	738	51	0
2	MA	1579	0	738	48	0
2	MD	1579	0	738	49	0
2	MG	1579	0	738	47	0
2	OC	1579	0	738	52	0
2	OF	1579	0	738	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	QB	1579	0	738	49	0
2	QE	1579	0	738	51	0
2	SA	1579	0	738	47	0
2	SD	1579	0	738	48	0
2	SG	1579	0	738	49	0
2	T	1579	0	738	49	0
2	UC	1579	0	738	50	0
2	UF	1579	0	738	49	0
2	WB	1579	0	738	48	0
2	WE	1579	0	738	49	0
2	YA	1579	0	738	49	0
2	YD	1579	0	738	48	0
3	BA	1420	0	604	16	0
3	BD	1420	0	604	17	0
3	BG	1420	0	604	16	0
3	C	1420	0	604	16	0
3	DC	1420	0	604	17	0
3	DF	1420	0	604	16	0
3	FB	1420	0	604	17	0
3	FE	1420	0	604	16	0
3	HA	1420	0	604	16	0
3	HD	1420	0	604	16	0
3	HG	1420	0	604	16	0
3	JC	1420	0	604	16	0
3	JF	1420	0	604	16	0
3	K	1420	0	604	16	0
3	LB	1420	0	604	17	0
3	LE	1420	0	604	17	0
3	M	1420	0	604	16	0
3	NA	1420	0	604	16	0
3	ND	1420	0	604	16	0
3	NG	1420	0	604	16	0
3	PC	1420	0	604	16	0
3	PF	1420	0	604	16	0
3	RB	1420	0	604	16	0
3	RE	1420	0	604	16	0
3	TA	1420	0	604	16	0
3	TD	1420	0	604	16	0
3	TG	1420	0	604	16	0
3	V	1420	0	604	16	0
3	VC	1420	0	604	17	0
3	VF	1420	0	604	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	XB	1420	0	604	16	0
3	XE	1420	0	604	16	0
3	ZA	1420	0	604	17	0
3	ZD	1420	0	604	16	0
4	AB	456	0	206	5	0
4	AC	399	0	177	9	0
4	AE	456	0	206	6	0
4	AF	399	0	177	9	0
4	BB	409	0	181	6	0
4	BE	409	0	181	7	0
4	CA	456	0	206	6	0
4	CB	399	0	177	10	0
4	CD	456	0	206	6	0
4	CE	399	0	177	9	0
4	CG	456	0	206	6	0
4	D	456	0	206	6	0
4	DA	409	0	181	6	0
4	DD	409	0	181	7	0
4	DG	409	0	181	6	0
4	E	409	0	181	6	0
4	EA	399	0	177	9	0
4	EC	456	0	206	6	0
4	ED	399	0	177	10	0
4	EF	456	0	206	6	0
4	EG	399	0	177	10	0
4	FC	409	0	181	6	0
4	FF	409	0	181	7	0
4	GB	456	0	206	5	0
4	GC	399	0	177	9	0
4	GE	456	0	206	6	0
4	GF	399	0	177	9	0
4	H	399	0	177	10	0
4	HB	409	0	181	6	0
4	HE	409	0	181	7	0
4	IA	456	0	206	5	0
4	IB	399	0	177	10	0
4	ID	456	0	206	6	0
4	IE	399	0	177	9	0
4	IG	456	0	206	6	0
4	JA	409	0	181	6	0
4	JD	409	0	181	6	0
4	JG	409	0	181	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	KA	399	0	177	10	0
4	KC	456	0	206	6	0
4	KD	399	0	177	10	0
4	KF	456	0	206	6	0
4	KG	399	0	177	10	0
4	L	456	0	206	6	0
4	LC	409	0	181	6	0
4	LF	409	0	181	7	0
4	MB	456	0	206	5	0
4	MC	399	0	177	9	0
4	ME	456	0	206	6	0
4	MF	399	0	177	9	0
4	N	456	0	206	6	0
4	NB	409	0	181	6	0
4	NE	409	0	181	7	0
4	O	409	0	181	7	0
4	OA	456	0	206	6	0
4	OB	399	0	177	10	0
4	OD	456	0	206	7	0
4	OE	399	0	177	9	0
4	OG	456	0	206	6	0
4	P	409	0	181	6	0
4	PA	409	0	181	7	0
4	PD	409	0	181	6	0
4	PG	409	0	181	6	0
4	Q	399	0	177	10	0
4	QA	399	0	177	10	0
4	QC	456	0	206	6	0
4	QD	399	0	177	10	0
4	QF	456	0	206	6	0
4	QG	399	0	177	10	0
4	R	399	0	177	9	0
4	RC	409	0	181	7	0
4	RF	409	0	181	7	0
4	SB	456	0	206	6	0
4	SC	399	0	177	9	0
4	SE	456	0	206	6	0
4	SF	399	0	177	9	0
4	TB	409	0	181	7	0
4	TE	409	0	181	6	0
4	UA	456	0	206	5	0
4	UB	399	0	177	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	UD	456	0	206	7	0
4	UE	399	0	177	10	0
4	UG	456	0	206	6	0
4	VA	409	0	181	6	0
4	VD	409	0	181	7	0
4	VG	409	0	181	7	0
4	W	456	0	206	6	0
4	WA	399	0	177	10	0
4	WC	456	0	206	6	0
4	WD	399	0	177	10	0
4	WF	456	0	206	6	0
4	WG	399	0	177	10	0
4	X	409	0	181	7	0
4	XC	409	0	181	7	0
4	XF	409	0	181	6	0
4	Y	399	0	177	9	0
4	YB	456	0	206	6	0
4	YC	399	0	177	9	0
4	YE	456	0	206	6	0
4	YF	399	0	177	10	0
4	ZB	409	0	181	7	0
4	ZE	409	0	181	6	0
All	All	152898	0	68272	2191	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 10.

The worst 5 of 2191 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:KE:77:LEU:CB	2:QE:42:ALA:HA	1.55	1.35
2:MA:200:ALA:CB	2:MA:232:GLU:CB	2.05	1.35
2:QB:200:ALA:CB	2:QB:232:GLU:CB	2.05	1.35
2:WB:200:ALA:CB	2:WB:232:GLU:CB	2.05	1.35
2:GD:200:ALA:CB	2:GD:232:GLU:CB	2.05	1.35

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	BC	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	BF	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	DB	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	DE	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	F	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	FA	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	FD	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	FG	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	HC	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	HF	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	I	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	JB	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	JE	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	LA	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	LD	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	LG	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	NC	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	NF	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	PB	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	PE	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	RA	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	RD	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	RG	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	S	45/560 (8%)	44 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	TC	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	TF	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	VB	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	VE	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	XA	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	XD	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	Z	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	ZC	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	ZF	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
2	AA	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	AD	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	AG	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	B	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	CC	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	CF	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	EB	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	EE	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	G	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	GA	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	GD	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	GG	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	IC	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	IF	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	J	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	KB	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	KE	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	MA	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	MD	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	MG	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	OC	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	OF	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	QB	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	QE	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	SA	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	SD	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	SG	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	T	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	UC	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	UF	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	WB	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	WE	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	YA	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
2	YD	315/331 (95%)	299 (95%)	15 (5%)	1 (0%)	36	72
3	BA	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	BD	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	BG	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	C	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	DC	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	DF	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	FB	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	FE	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	HA	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	HD	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	HG	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	JC	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	JF	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	K	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	LB	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	LE	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	M	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	NA	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	ND	285/334 (85%)	274 (96%)	11 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	NG	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	PC	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	PF	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	RB	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	RE	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	TA	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	TD	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	TG	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	V	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	VC	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	VF	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	XB	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	XE	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	ZA	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
3	ZD	285/334 (85%)	274 (96%)	11 (4%)	0	100	100
4	AB	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	AC	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	AE	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	AF	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	BB	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	BE	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	CA	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	CB	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	CD	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	CE	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	CG	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	D	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	DA	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	DD	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	DG	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	E	81/137 (59%)	73 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	EA	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	EC	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	ED	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	EF	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	EG	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	FC	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	FF	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	GB	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	GC	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	GE	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	GF	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	H	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	HB	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	HE	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	IA	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	IB	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	ID	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	IE	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	IG	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	JA	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	JD	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	JG	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	KA	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	KC	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	KD	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	KF	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	KG	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	L	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	LC	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	LF	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	MB	91/137 (66%)	88 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	MC	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	ME	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	MF	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	N	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	NB	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	NE	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	O	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	OA	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	OB	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	OD	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	OE	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	OG	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	P	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	PA	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	PD	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	PG	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	Q	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	QA	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	QC	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	QD	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	QF	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	QG	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	R	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	RC	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	RF	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	SB	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	SC	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	SE	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	SF	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	TB	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	TE	81/137 (59%)	73 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	UA	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	UB	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	UD	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	UE	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	UG	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	VA	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	VD	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	VG	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	W	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	WA	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	WC	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	WD	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	WF	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	WG	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	X	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	XC	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	XF	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	Y	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	YB	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	YC	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	YE	91/137 (66%)	88 (97%)	3 (3%)	0	100	100
4	YF	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	ZB	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
4	ZE	81/137 (59%)	73 (90%)	8 (10%)	0	100	100
All	All	30464/55624 (55%)	28968 (95%)	1462 (5%)	34 (0%)	49	83

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	243	ASP
2	B	243	ASP
2	J	243	ASP
2	T	243	ASP
2	AA	243	ASP

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.

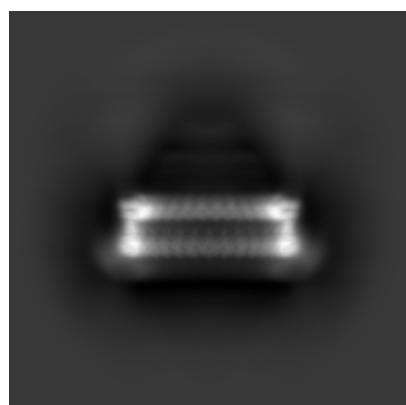
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43328. These allow visual inspection of the internal detail of the map and identification of artifacts.

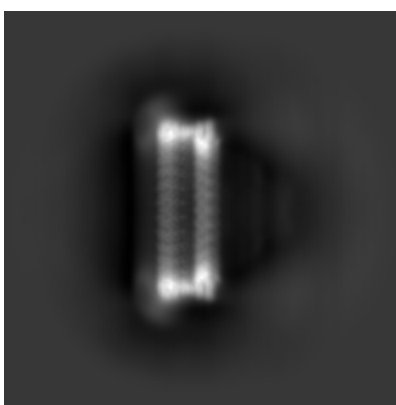
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

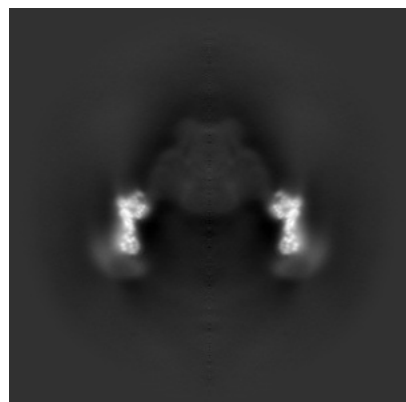


Z

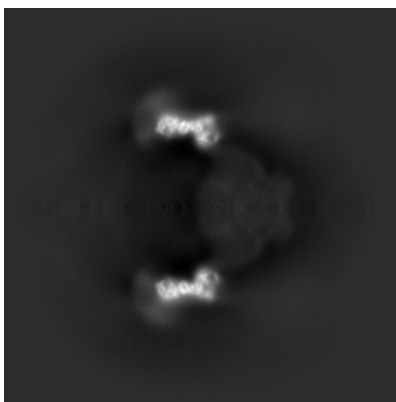
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

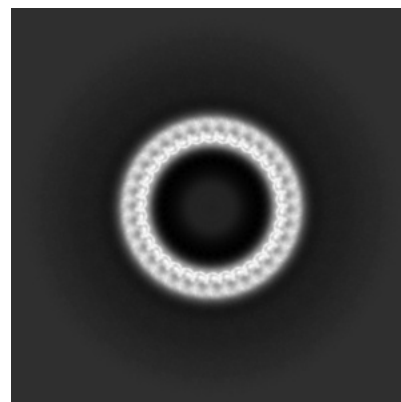
6.2.1 Primary map



X Index: 256



Y Index: 256

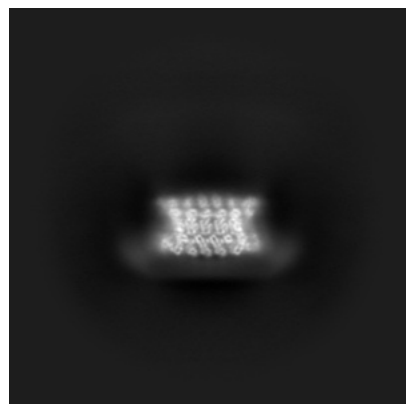


Z Index: 256

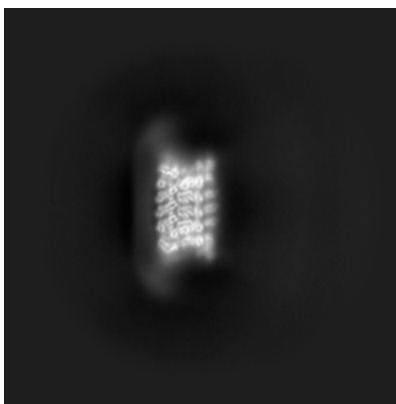
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

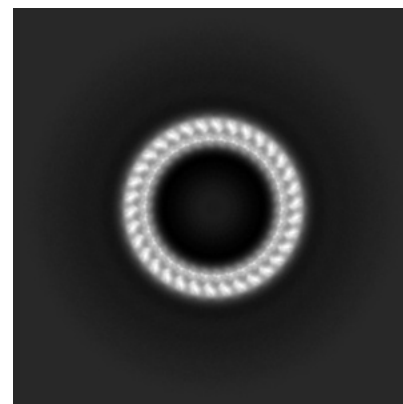
6.3.1 Primary map



X Index: 157



Y Index: 157

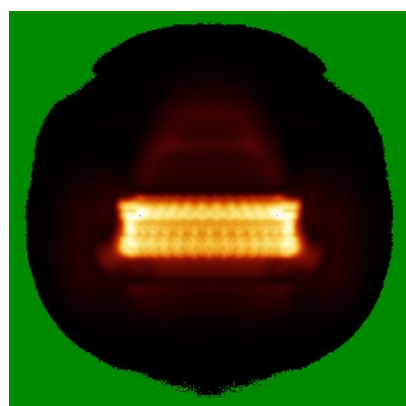


Z Index: 252

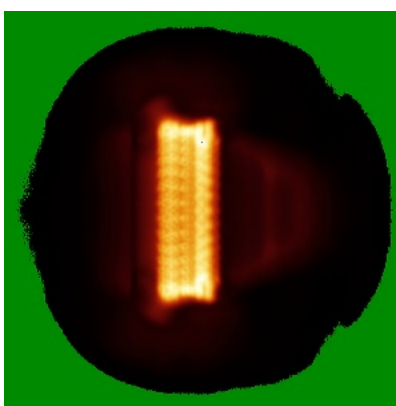
The images above show the largest variance slices of the map in three orthogonal directions.

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

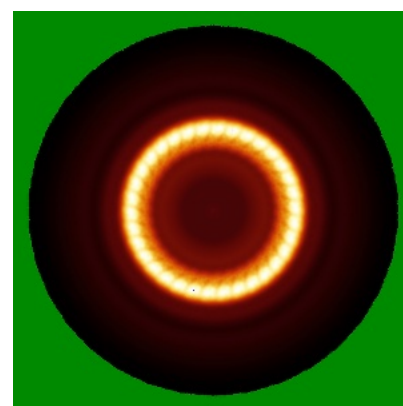
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.175. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

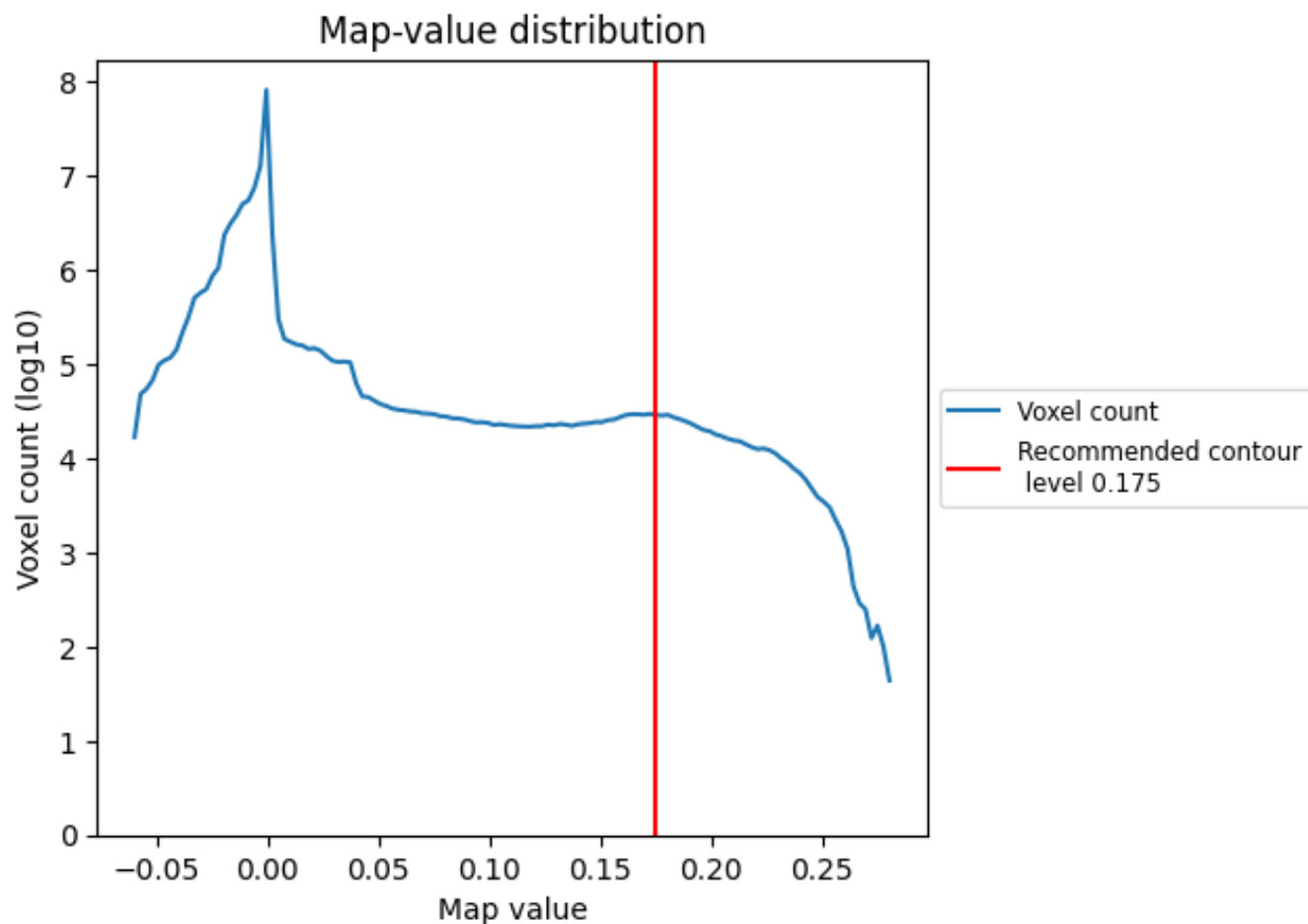
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

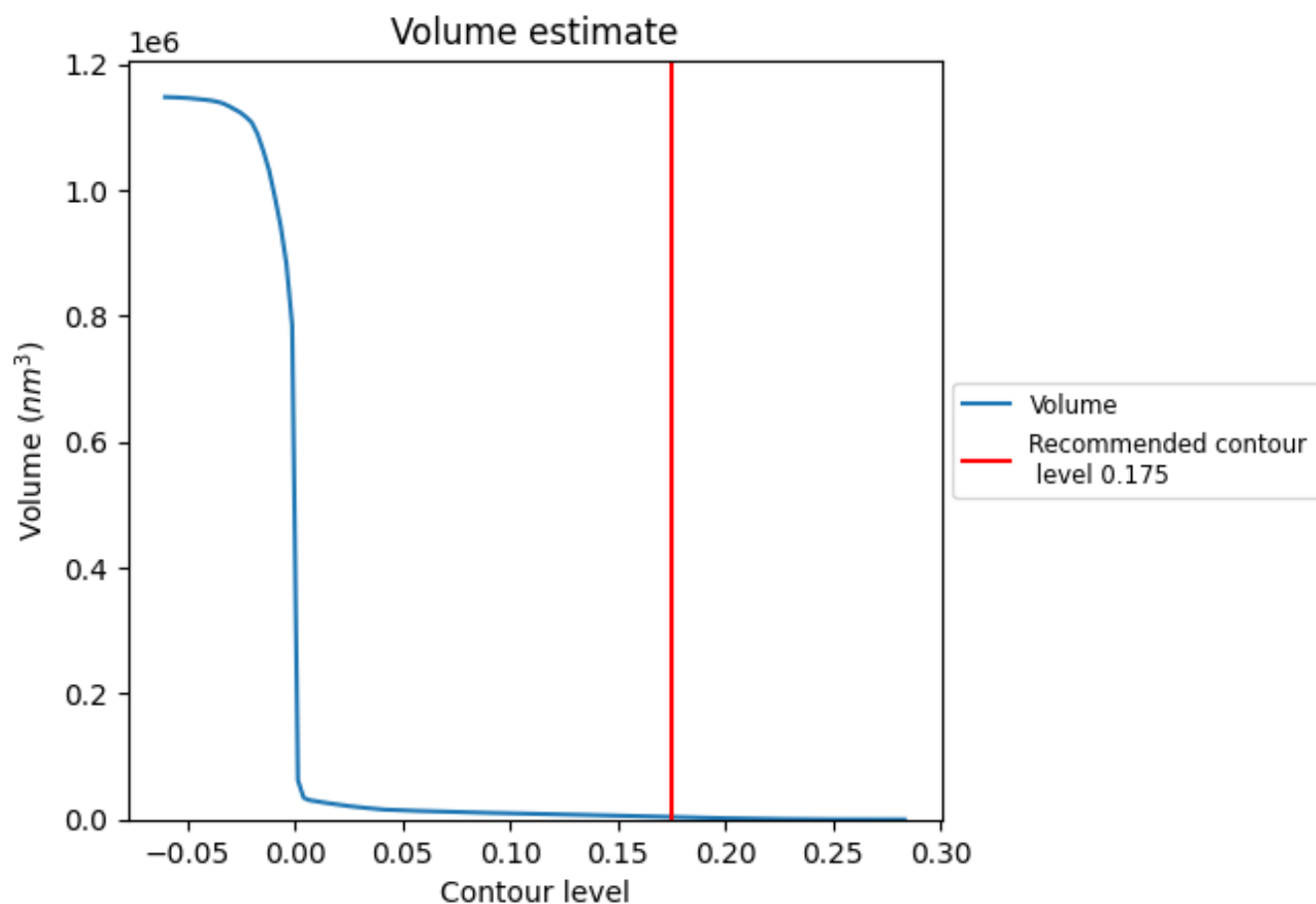
This section contains the results of statistical analysis of the map.

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.

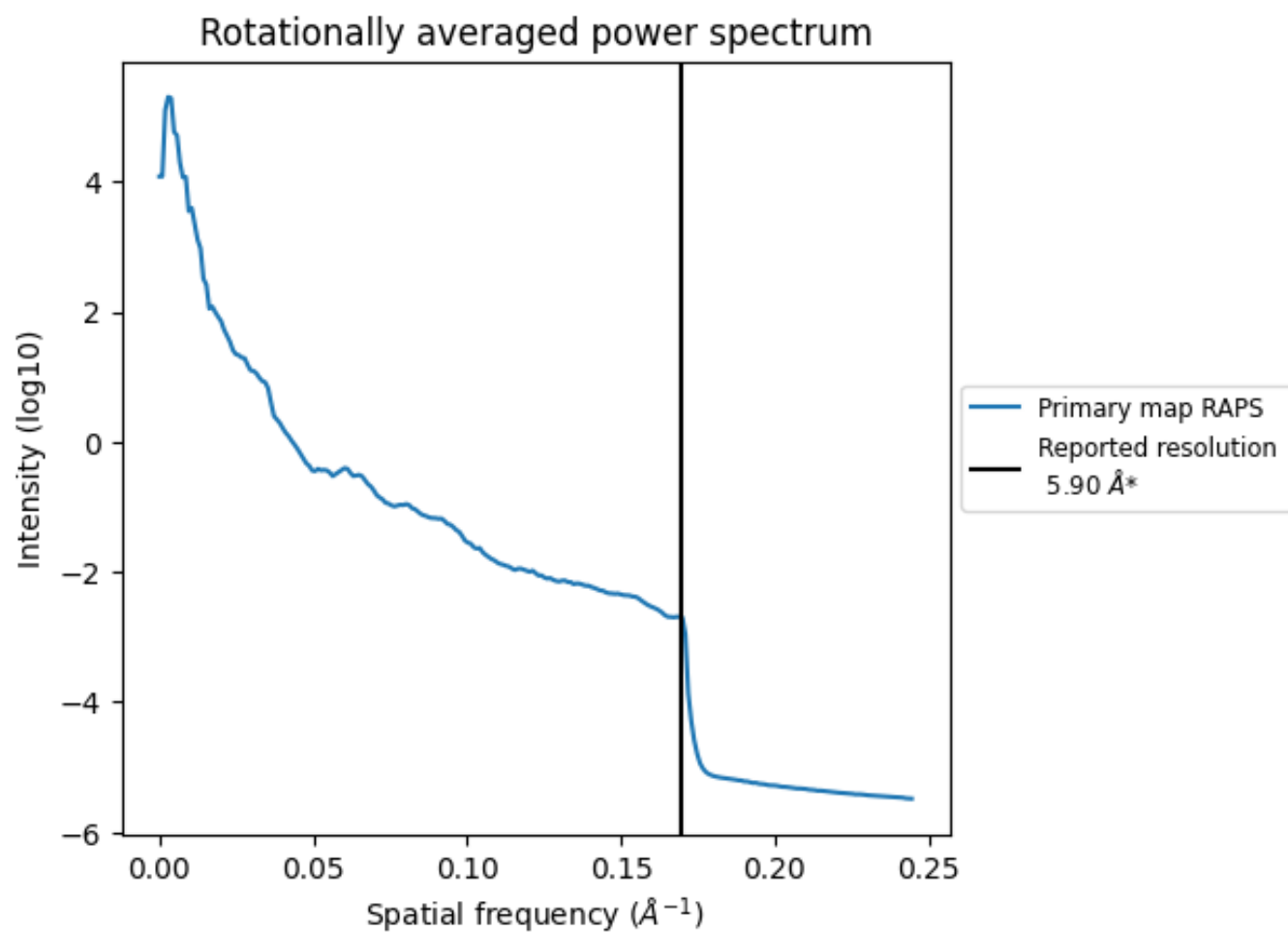
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4028 nm³; this corresponds to an approximate mass of 3639 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 0.169 Å⁻¹

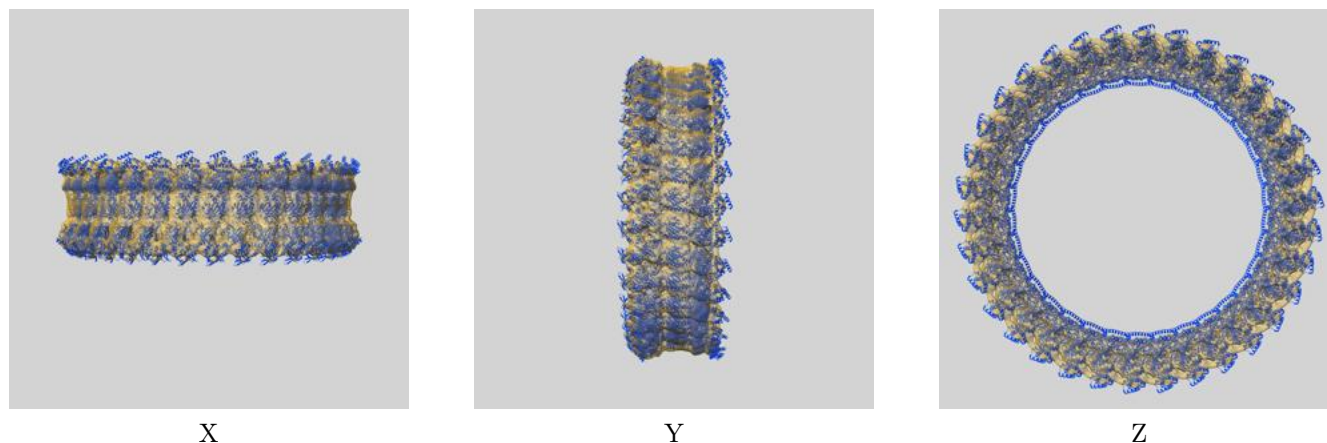
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

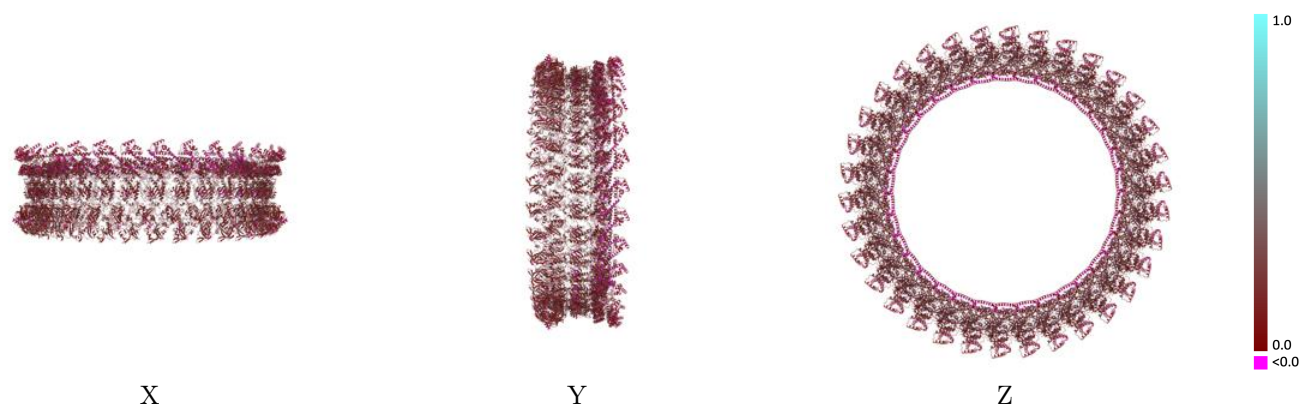
This section contains information regarding the fit between EMDB map EMD-43328 and PDB model 8VKR. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



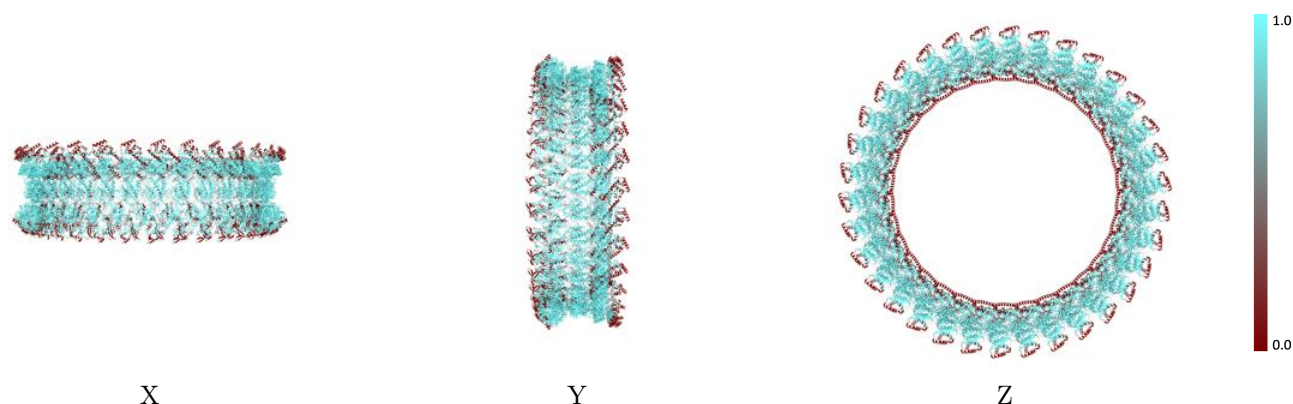
The images above show the 3D surface view of the map at the recommended contour level 0.175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



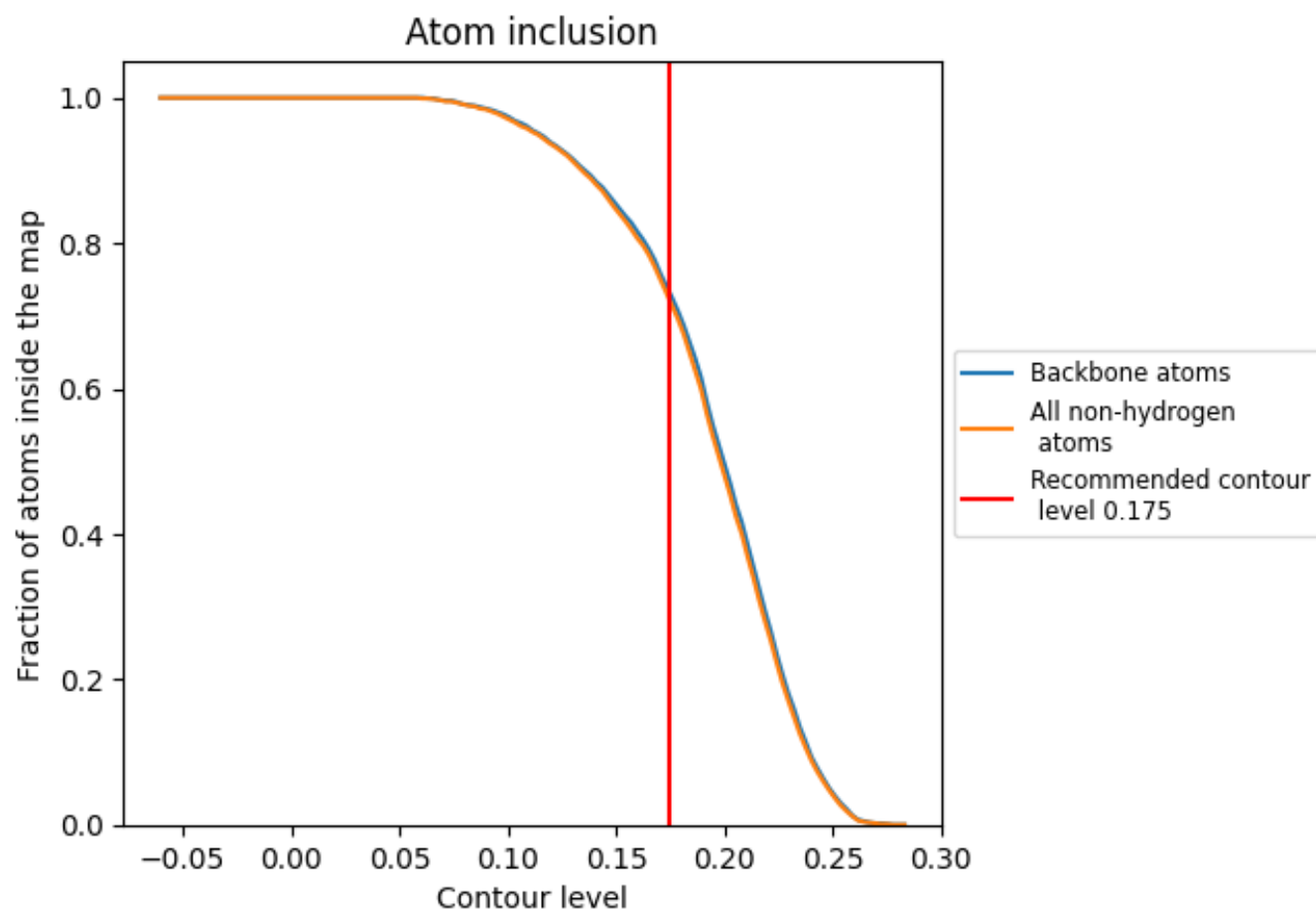
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.175).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 72% 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 (0.175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7200	 0.1760
A	 0.2270	 0.0810
AA	 0.7330	 0.1670
AB	 0.4850	 0.1760
AC	 0.9470	 0.2060
AD	 0.7320	 0.1650
AE	 0.4820	 0.1750
AF	 0.9520	 0.2090
AG	 0.7320	 0.1680
B	 0.7330	 0.1680
BA	 0.7280	 0.1930
BB	 0.9660	 0.1860
BC	 0.2270	 0.0900
BD	 0.7270	 0.1930
BE	 0.9660	 0.1860
BF	 0.2270	 0.0780
BG	 0.7280	 0.1900
C	 0.7270	 0.1920
CA	 0.4820	 0.1730
CB	 0.9500	 0.2020
CC	 0.7320	 0.1650
CD	 0.4870	 0.1790
CE	 0.9500	 0.2090
CF	 0.7310	 0.1680
CG	 0.4850	 0.1770
D	 0.4820	 0.1740
DA	 0.9660	 0.1880
DB	 0.2270	 0.0840
DC	 0.7280	 0.1910
DD	 0.9660	 0.1810
DE	 0.2270	 0.0880
DF	 0.7250	 0.1920
DG	 0.9660	 0.1890
E	 0.9660	 0.1900
EA	 0.9500	 0.2040



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Chain	Atom inclusion	Q-score
EB	 0.7310	 0.1640
EC	 0.4850	 0.1740
ED	 0.9500	 0.2100
EE	 0.7330	 0.1650
EF	 0.4820	 0.1830
EG	 0.9470	 0.2030
F	 0.2270	 0.0820
FA	 0.2270	 0.0820
FB	 0.7250	 0.1940
FC	 0.9660	 0.1850
FD	 0.2270	 0.0930
FE	 0.7260	 0.1900
FF	 0.9630	 0.1860
FG	 0.2270	 0.0770
G	 0.7330	 0.1690
GA	 0.7330	 0.1660
GB	 0.4820	 0.1790
GC	 0.9500	 0.1990
GD	 0.7320	 0.1640
GE	 0.4850	 0.1810
GF	 0.9450	 0.2060
GG	 0.7320	 0.1670
H	 0.9470	 0.2040
HA	 0.7260	 0.1930
HB	 0.9660	 0.1850
HC	 0.2270	 0.0920
HD	 0.7260	 0.1910
HE	 0.9660	 0.1850
HF	 0.2270	 0.0760
HG	 0.7300	 0.1930
I	 0.2270	 0.0790
IA	 0.4820	 0.1800
IB	 0.9500	 0.1970
IC	 0.7330	 0.1640
ID	 0.4850	 0.1770
IE	 0.9470	 0.2090
IF	 0.7330	 0.1680
IG	 0.4850	 0.1780
J	 0.7330	 0.1670
JA	 0.9660	 0.1890
JB	 0.2270	 0.0830
JC	 0.7300	 0.1950

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Chain	Atom inclusion	Q-score
JD	 0.9630	 0.1860
JE	 0.2270	 0.0880
JF	 0.7300	 0.1910
JG	 0.9630	 0.1850
K	 0.7260	 0.1920
KA	 0.9500	 0.2050
KB	 0.7330	 0.1630
KC	 0.4870	 0.1750
KD	 0.9550	 0.2060
KE	 0.7320	 0.1650
KF	 0.4850	 0.1780
KG	 0.9520	 0.2100
L	 0.4870	 0.1820
LA	 0.2220	 0.0850
LB	 0.7280	 0.1940
LC	 0.9660	 0.1810
LD	 0.2270	 0.0870
LE	 0.7260	 0.1910
LF	 0.9660	 0.1870
LG	 0.2270	 0.0760
M	 0.7280	 0.1930
MA	 0.7330	 0.1650
MB	 0.4850	 0.1730
MC	 0.9470	 0.2080
MD	 0.7330	 0.1650
ME	 0.4820	 0.1830
MF	 0.9470	 0.2100
MG	 0.7330	 0.1680
N	 0.4870	 0.1790
NA	 0.7250	 0.1940
NB	 0.9660	 0.1840
NC	 0.2270	 0.0870
ND	 0.7260	 0.1920
NE	 0.9660	 0.1880
NF	 0.2270	 0.0790
NG	 0.7280	 0.1900
O	 0.9660	 0.1930
OA	 0.4850	 0.1770
OB	 0.9520	 0.2000
OC	 0.7330	 0.1640
OD	 0.4870	 0.1820
OE	 0.9470	 0.2080

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Chain	Atom inclusion	Q-score
OF	 0.7330	 0.1670
OG	 0.4890	 0.1800
P	 0.9660	 0.1860
PA	 0.9630	 0.1900
PB	 0.2270	 0.0900
PC	 0.7280	 0.1940
PD	 0.9630	 0.1870
PE	 0.2270	 0.0860
PF	 0.7270	 0.1890
PG	 0.9660	 0.1890
Q	 0.9500	 0.2070
QA	 0.9520	 0.2020
QB	 0.7320	 0.1620
QC	 0.4850	 0.1820
QD	 0.9520	 0.2090
QE	 0.7310	 0.1660
QF	 0.4850	 0.1790
QG	 0.9500	 0.2050
R	 0.9470	 0.2030
RA	 0.2270	 0.0830
RB	 0.7280	 0.1900
RC	 0.9660	 0.1840
RD	 0.2270	 0.0850
RE	 0.7250	 0.1900
RF	 0.9660	 0.1890
RG	 0.2270	 0.0760
S	 0.2270	 0.0770
SA	 0.7320	 0.1650
SB	 0.4870	 0.1760
SC	 0.9500	 0.2080
SD	 0.7330	 0.1650
SE	 0.4870	 0.1810
SF	 0.9470	 0.2060
SG	 0.7320	 0.1680
T	 0.7330	 0.1670
TA	 0.7290	 0.1920
TB	 0.9630	 0.1850
TC	 0.2270	 0.0880
TD	 0.7260	 0.1900
TE	 0.9630	 0.1860
TF	 0.2270	 0.0810
TG	 0.7260	 0.1910

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Chain	Atom inclusion	Q-score
UA	0.4850	0.1760
UB	0.9470	0.2020
UC	0.7310	0.1630
UD	0.4870	0.1790
UE	0.9520	0.2100
UF	0.7330	0.1680
UG	0.4850	0.1780
V	0.7260	0.1910
VA	0.9630	0.1870
VB	0.2270	0.0900
VC	0.7250	0.1930
VD	0.9630	0.1820
VE	0.2270	0.0810
VF	0.7280	0.1930
VG	0.9660	0.1870
W	0.4850	0.1780
WA	0.9470	0.2030
WB	0.7330	0.1650
WC	0.4870	0.1820
WD	0.9470	0.2060
WE	0.7330	0.1660
WF	0.4850	0.1770
WG	0.9470	0.2070
X	0.9660	0.1890
XA	0.2270	0.0840
XB	0.7300	0.1940
XC	0.9660	0.1850
XD	0.2270	0.0860
XE	0.7250	0.1910
XF	0.9630	0.1890
Y	0.9470	0.2000
YA	0.7330	0.1630
YB	0.4850	0.1750
YC	0.9520	0.2120
YD	0.7330	0.1650
YE	0.4850	0.1770
YF	0.9520	0.2100
Z	0.2270	0.0800
ZA	0.7280	0.1930
ZB	0.9660	0.1830
ZC	0.2270	0.0890
ZD	0.7280	0.1920

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Chain	Atom inclusion	Q-score
ZE	 0.9630	 0.1880
ZF	 0.2270	 0.0790