



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 02:30 PM UTC

PDB ID : 9N4Z / pdb_00009n4z
EMDB ID : EMD-48916
Title : CCW Flagellar Switch Complex - FliF, FliG, FliM, and FliN forming 34-mer C-ring from Salmonella
Authors : Singh, P.K.; Iverson, T.M.
Deposited on : 2025-02-03
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

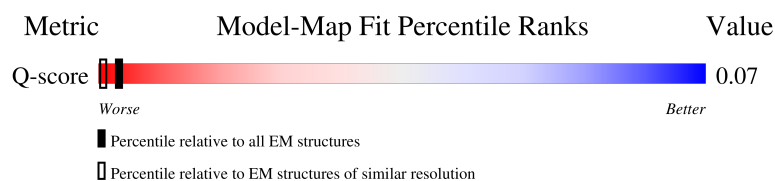
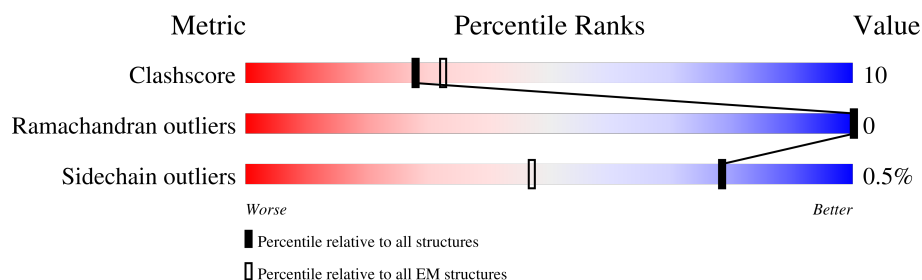
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	6% 8% 92%
1	BC	560	7% 8% 92%
1	BF	560	7% 8% 92%
1	DB	560	7% 8% 92%

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Mol	Chain	Length	Quality of chain	
1	DE	560		92%
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%

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Mol	Chain	Length	Quality of chain
1	XA	560	7% 8% 92%
1	XD	560	7% 8% 92%
1	Z	560	6% 8% 92%
1	ZC	560	7% 8% 92%
1	ZF	560	6% 8% 92%
2	AA	331	49% 85% 11% ..
2	AD	331	49% 85% 11% ..
2	AG	331	39% 85% 11% ..
2	B	331	45% 85% 11% ..
2	CC	331	51% 86% 10% ..
2	CF	331	37% 86% 10% ..
2	EB	331	50% 85% 11% ..
2	EE	331	44% 86% 10% ..
2	G	331	44% 86% 10% ..
2	GA	331	50% 85% 11% ..
2	GD	331	50% 85% 10% ..
2	GG	331	40% 85% 11% ..
2	IC	331	52% 86% 10% ..
2	IF	331	36% 86% 10% ..
2	J	331	46% 85% 11% ..
2	KB	331	51% 85% 11% ..
2	KE	331	42% 86% 10% ..
2	MA	331	50% 86% 10% ..
2	MD	331	47% 86% 10% ..
2	MG	331	41% 86% 10% ..

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Mol	Chain	Length	Quality of chain
2	OC	331	
2	OF	331	
2	QB	331	
2	QE	331	
2	SA	331	
2	SD	331	
2	SG	331	
2	T	331	
2	UC	331	
2	UF	331	
2	WB	331	
2	WE	331	
2	YA	331	
2	YD	331	
3	BA	334	
3	BD	334	
3	BG	334	
3	C	334	
3	DC	334	
3	DF	334	
3	FB	334	
3	FE	334	
3	HA	334	
3	HD	334	
3	HG	334	

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Mol	Chain	Length	Quality of chain
3	JC	334	
3	JF	334	
3	K	334	
3	LB	334	
3	LE	334	
3	M	334	
3	NA	334	
3	ND	334	
3	NG	334	
3	PC	334	
3	PF	334	
3	RB	334	
3	RE	334	
3	TA	334	
3	TD	334	
3	TG	334	
3	V	334	
3	VC	334	
3	VF	334	
3	XB	334	
3	XE	334	
3	ZA	334	
3	ZD	334	
4	AB	137	
4	AC	137	

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Mol	Chain	Length	Quality of chain
4	AE	137	
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	

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Mol	Chain	Length	Quality of chain
4	H	137	
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	

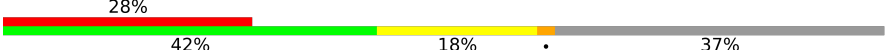
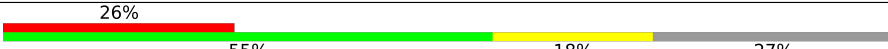
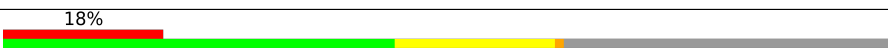
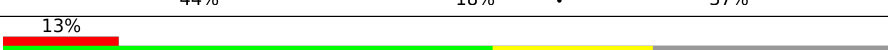
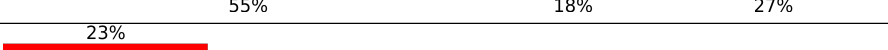
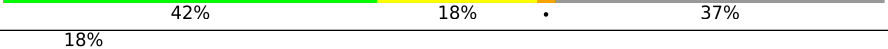
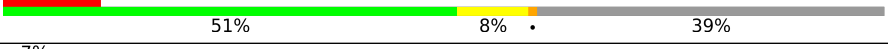
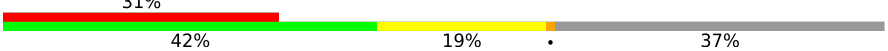
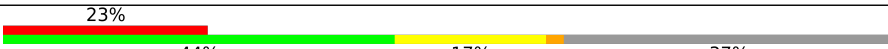
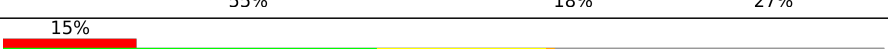
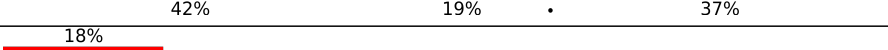
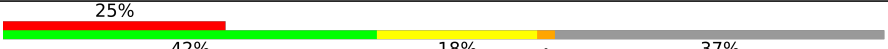
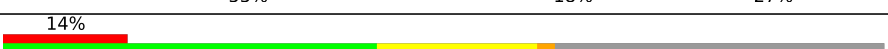
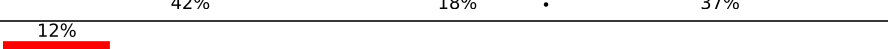
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Mol	Chain	Length	Quality of chain
4	NE	137	
4	O	137	
4	OA	137	
4	OB	137	
4	OD	137	
4	OE	137	
4	OG	137	
4	P	137	
4	PA	137	
4	PD	137	
4	PG	137	
4	Q	137	
4	QA	137	
4	QC	137	
4	QD	137	
4	QF	137	
4	QG	137	
4	R	137	
4	RC	137	
4	RF	137	
4	SB	137	
4	SC	137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

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Mol	Chain	Length	Quality of chain
4	TE	137	
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 218722 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	46	Total	C	N	O	0	0
			229	137	46	46		
1	A	46	Total	C	N	O	0	0
			229	137	46	46		
1	I	46	Total	C	N	O	0	0
			229	137	46	46		
1	S	46	Total	C	N	O	0	0
			229	137	46	46		
1	Z	46	Total	C	N	O	0	0
			229	137	46	46		
1	FA	46	Total	C	N	O	0	0
			229	137	46	46		
1	LA	46	Total	C	N	O	0	0
			229	137	46	46		
1	RA	46	Total	C	N	O	0	0
			229	137	46	46		
1	XA	46	Total	C	N	O	0	0
			229	137	46	46		
1	DB	46	Total	C	N	O	0	0
			229	137	46	46		
1	JB	46	Total	C	N	O	0	0
			229	137	46	46		
1	PB	46	Total	C	N	O	0	0
			229	137	46	46		
1	VB	46	Total	C	N	O	0	0
			229	137	46	46		
1	BC	46	Total	C	N	O	0	0
			229	137	46	46		
1	HC	46	Total	C	N	O	0	0
			229	137	46	46		
1	NC	46	Total	C	N	O	0	0
			229	137	46	46		
1	TC	46	Total	C	N	O	0	0
			229	137	46	46		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	ZC	46	Total	C	N	O	0	0
			229	137	46	46		
1	FD	46	Total	C	N	O	0	0
			229	137	46	46		
1	LD	46	Total	C	N	O	0	0
			229	137	46	46		
1	RD	46	Total	C	N	O	0	0
			229	137	46	46		
1	XD	46	Total	C	N	O	0	0
			229	137	46	46		
1	DE	46	Total	C	N	O	0	0
			229	137	46	46		
1	JE	46	Total	C	N	O	0	0
			229	137	46	46		
1	PE	46	Total	C	N	O	0	0
			229	137	46	46		
1	VE	46	Total	C	N	O	0	0
			229	137	46	46		
1	BF	46	Total	C	N	O	0	0
			229	137	46	46		
1	HF	46	Total	C	N	O	0	0
			229	137	46	46		
1	NF	46	Total	C	N	O	0	0
			229	137	46	46		
1	TF	46	Total	C	N	O	0	0
			229	137	46	46		
1	ZF	46	Total	C	N	O	0	0
			229	137	46	46		
1	FG	46	Total	C	N	O	0	0
			229	137	46	46		
1	LG	46	Total	C	N	O	0	0
			229	137	46	46		
1	RG	46	Total	C	N	O	0	0
			229	137	46	46		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	B	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	T	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	AA	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	GA	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	MA	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	SA	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	YA	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	EB	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	KB	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	QB	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	WB	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	CC	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	IC	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	OC	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	UC	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	AD	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	GD	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	MD	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	SD	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	YD	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	EE	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	KE	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	QE	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	WE	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	CF	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	IF	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	OF	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	UF	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	AG	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	GG	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	MG	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		
2	SG	319	Total	C	N	O	S	0	0
			1893	1157	357	376	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	C	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	K	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	V	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	BA	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	HA	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	NA	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	TA	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	ZA	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	FB	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	LB	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	RB	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	XB	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	DC	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	JC	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	PC	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	VC	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	BD	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	HD	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	ND	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	TD	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	ZD	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	FE	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	LE	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	RE	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	XE	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	DF	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	JF	291	Total 2287	C 1456	N 407	O 420	S 4	0	0
3	PF	291	Total 2287	C 1456	N 407	O 420	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	VF	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	BG	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	HG	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	NG	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		
3	TG	291	Total	C	N	O	S	0	0
			2287	1456	407	420	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	P	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	Q	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	D	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	E	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	H	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	L	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	O	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	R	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	W	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	X	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	Y	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	CA	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	DA	83	Total	C	N	O	S	0	0
			629	399	107	120	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	EA	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	IA	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	JA	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	KA	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	OA	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	PA	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	QA	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	UA	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	VA	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	WA	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	AB	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	BB	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	CB	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	GB	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	HB	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	IB	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	MB	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	NB	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	OB	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	SB	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	TB	83	Total 629	C 399	N 107	O 120	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	UB	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	YB	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	ZB	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	AC	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	EC	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	FC	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	GC	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	KC	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	LC	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	MC	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	QC	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	RC	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	SC	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	WC	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	XC	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	YC	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	CD	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	DD	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	ED	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	ID	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	JD	83	Total 629	C 399	N 107	O 120	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	KD	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	OD	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	PD	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	QD	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	UD	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	VD	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	WD	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	AE	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	BE	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	CE	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	GE	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	HE	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	IE	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	ME	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	NE	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	OE	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	SE	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	TE	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	UE	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	YE	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	ZE	83	Total	C	N	O	S	0	0
			629	399	107	120	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	AF	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	EF	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	FF	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	GF	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	KF	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	LF	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	MF	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	QF	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	RF	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	SF	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	WF	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	XF	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	YF	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	CG	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	DG	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	EG	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	IG	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	JG	83	Total 629	C 399	N 107	O 120	S 3	0	0
4	KG	100	Total 746	C 468	N 130	O 144	S 4	0	0
4	OG	86	Total 649	C 412	N 111	O 123	S 3	0	0
4	PG	83	Total 629	C 399	N 107	O 120	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	QG	100	Total	C	N	O	S	0	0
			746	468	130	144	4		
4	UG	86	Total	C	N	O	S	0	0
			649	412	111	123	3		
4	VG	83	Total	C	N	O	S	0	0
			629	399	107	120	3		
4	WG	100	Total	C	N	O	S	0	0
			746	468	130	144	4		

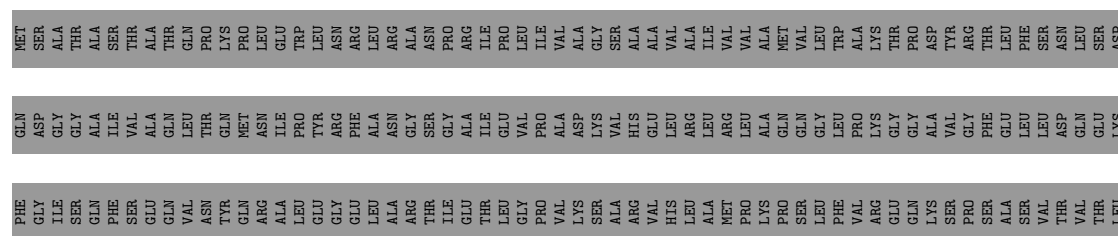
- Molecule 1: Flagellar M-ring protein

[illegible]

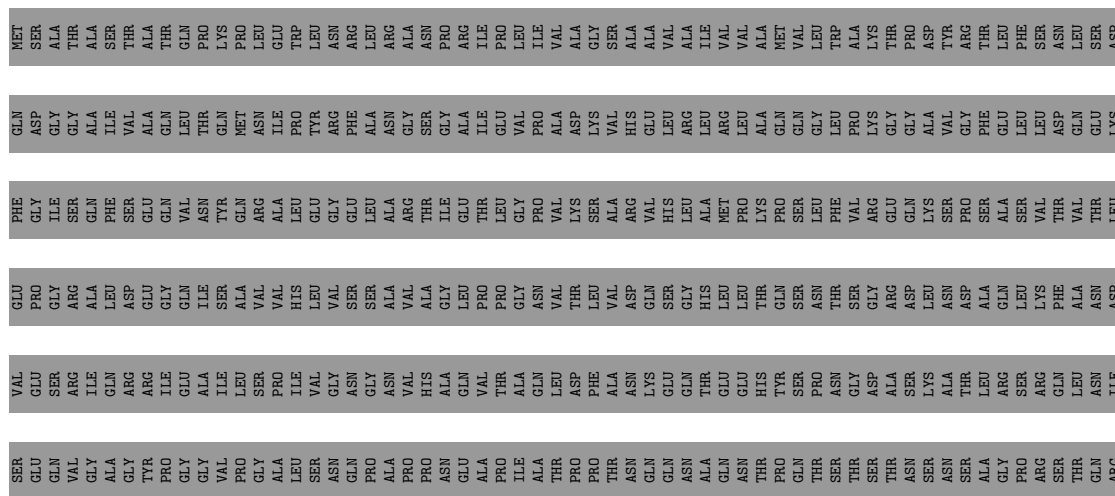
- Molecule 1: Flagellar M-ring protein

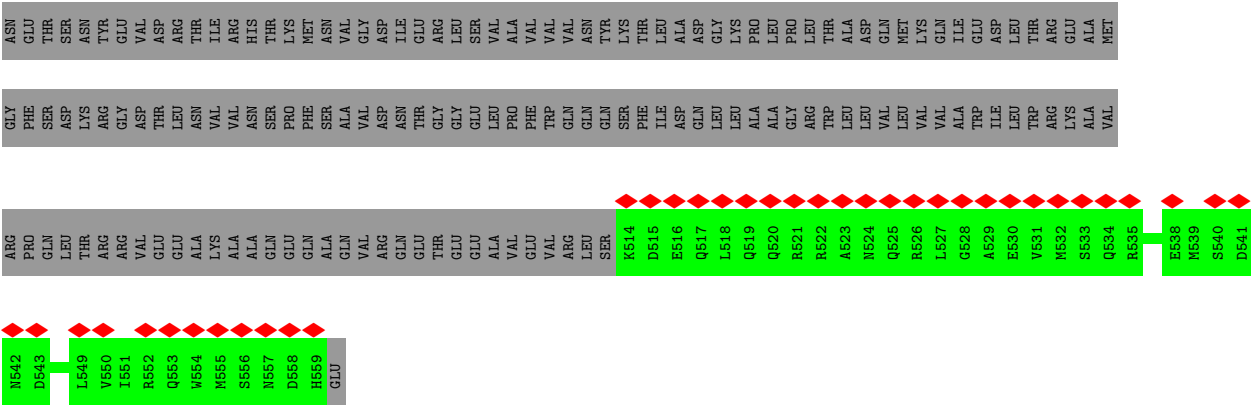


- Molecule 1: Flagellar M-ring protein

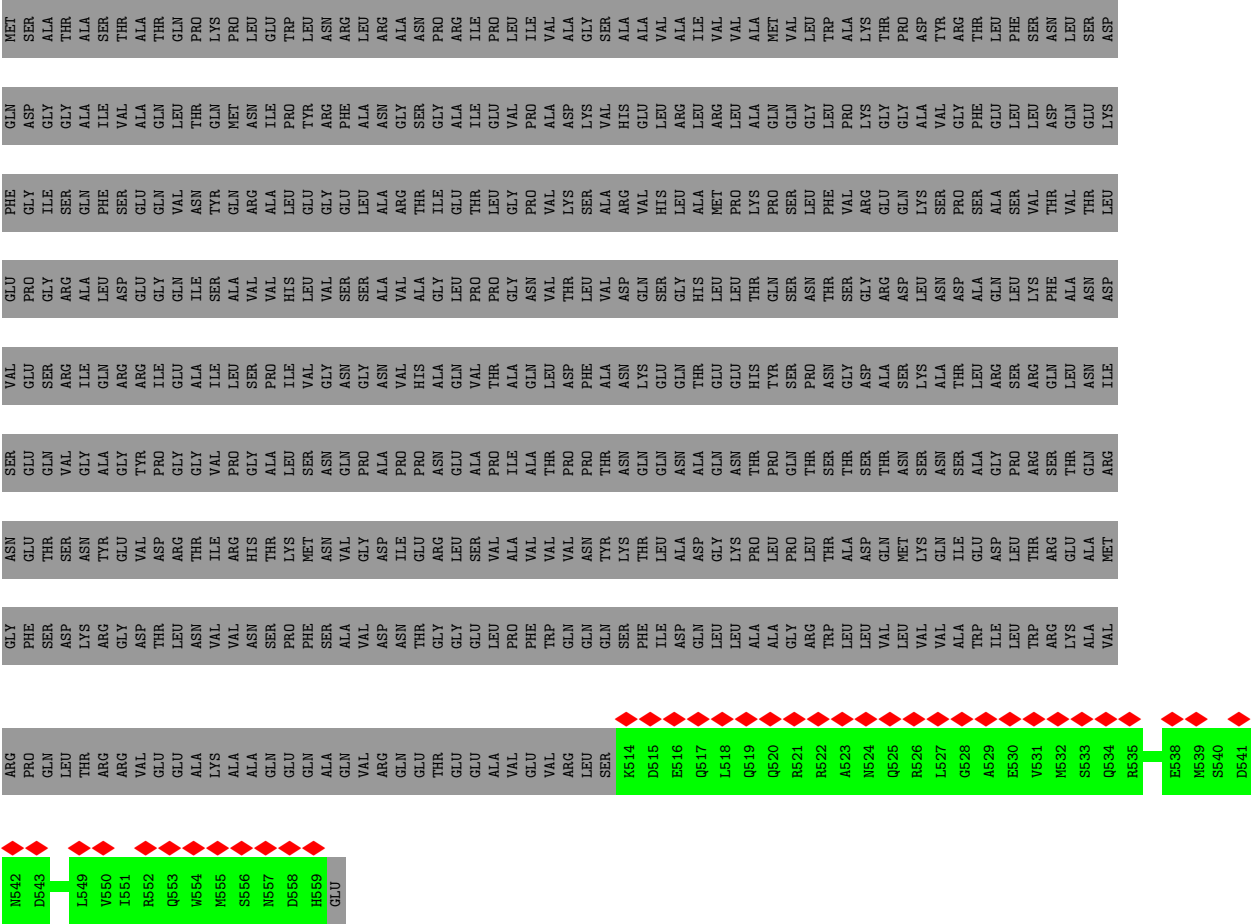


Chain LA:





● Molecule 1: Flagellar M-ring protein



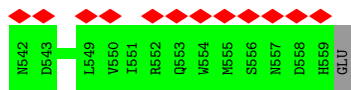
● Molecule 1: Flagellar M-ring protein



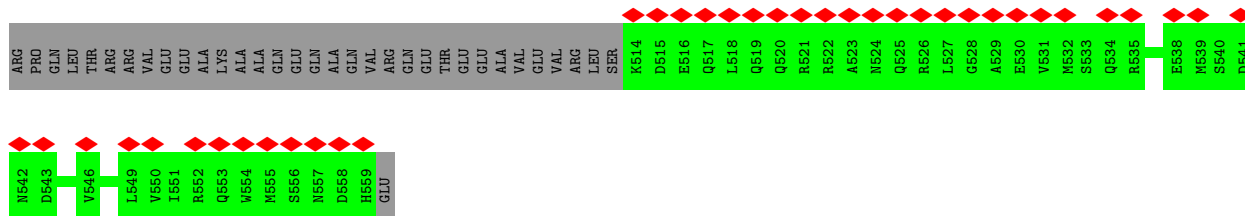
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Chain JB: 6% 8% 92%

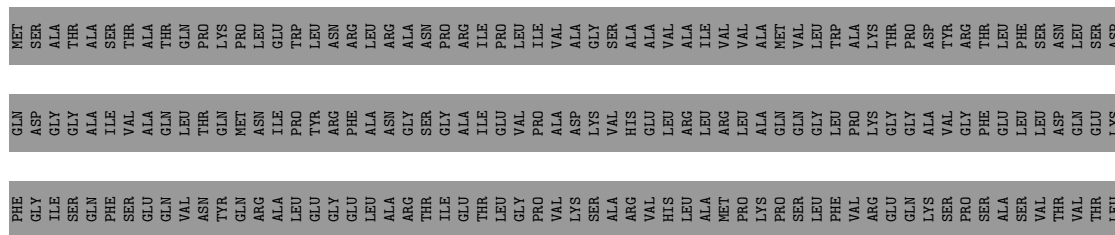


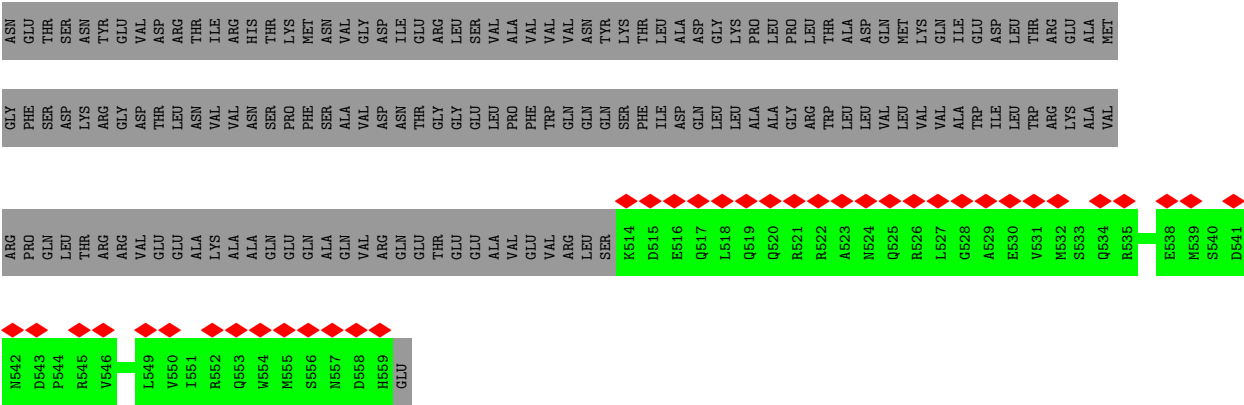


Chain PB:

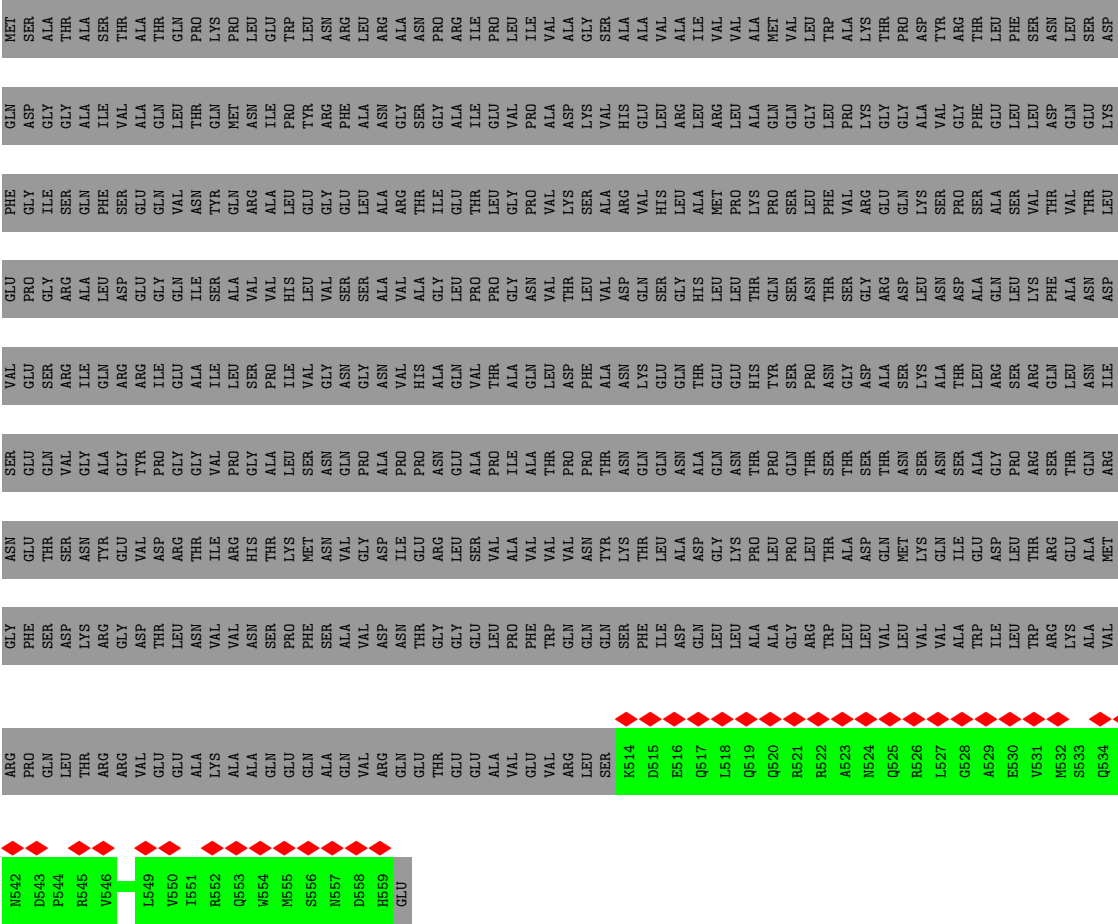


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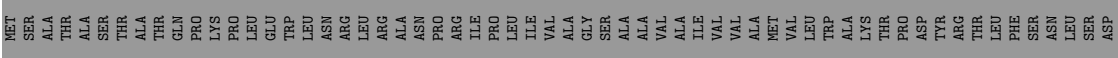




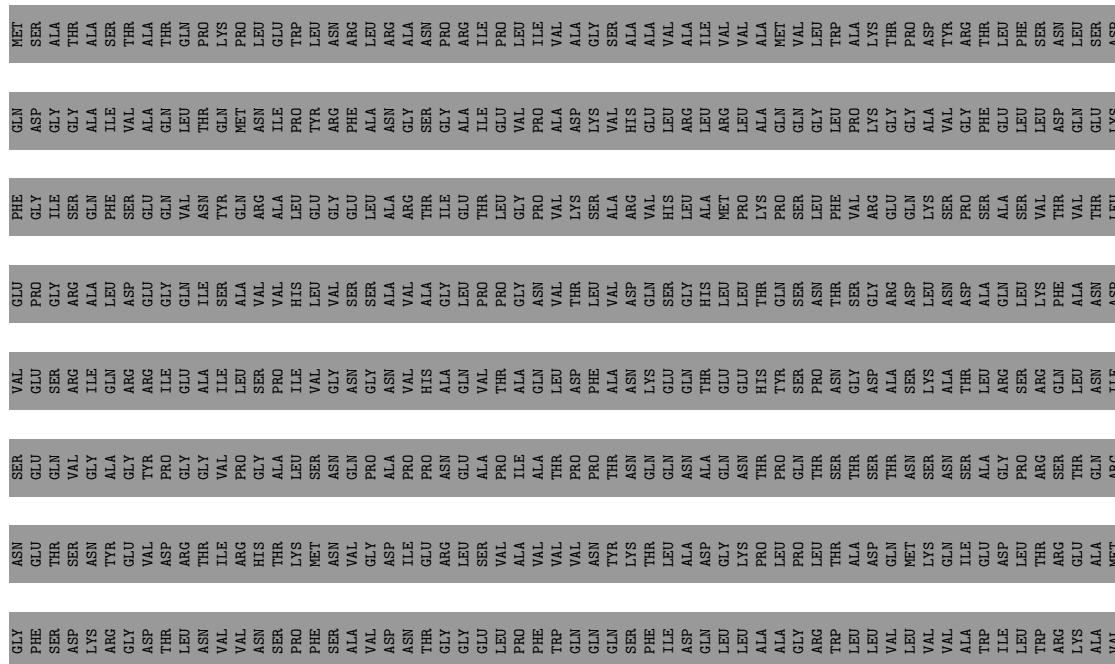
● Molecule 1: Flagellar M-ring protein

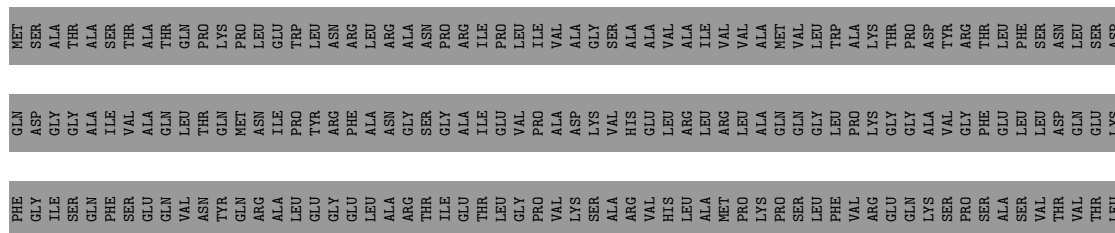


● Molecule 1: Flagellar M-ring protein

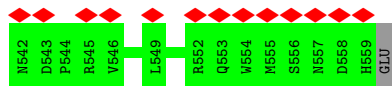


- Molecule 1: Flagellar M-ring protein

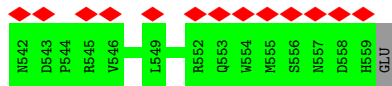




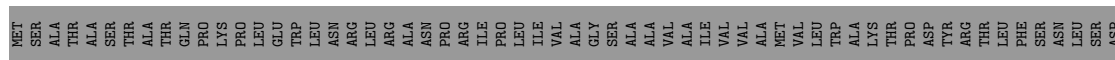
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Chain PE:



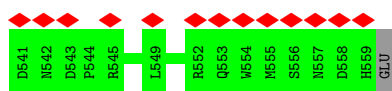
Chain VE:



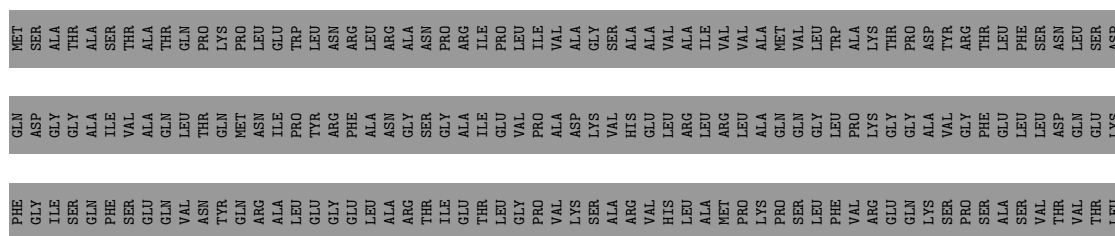
- Molecule 1: Flagellar M-ring protein

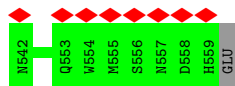


- Molecule 1: Flagellar M-ring protein

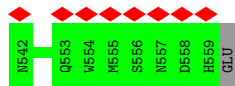


- Molecule 1: Flagellar M-ring protein

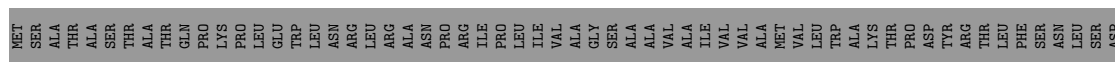


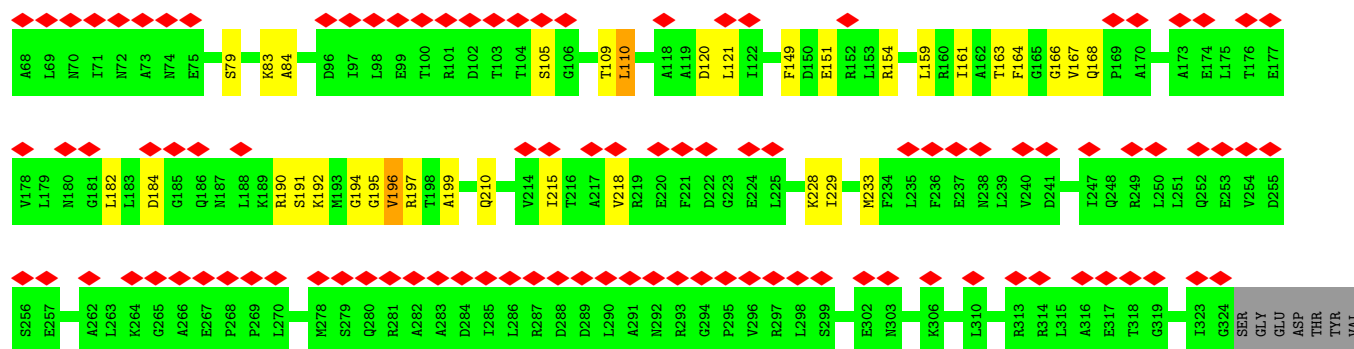


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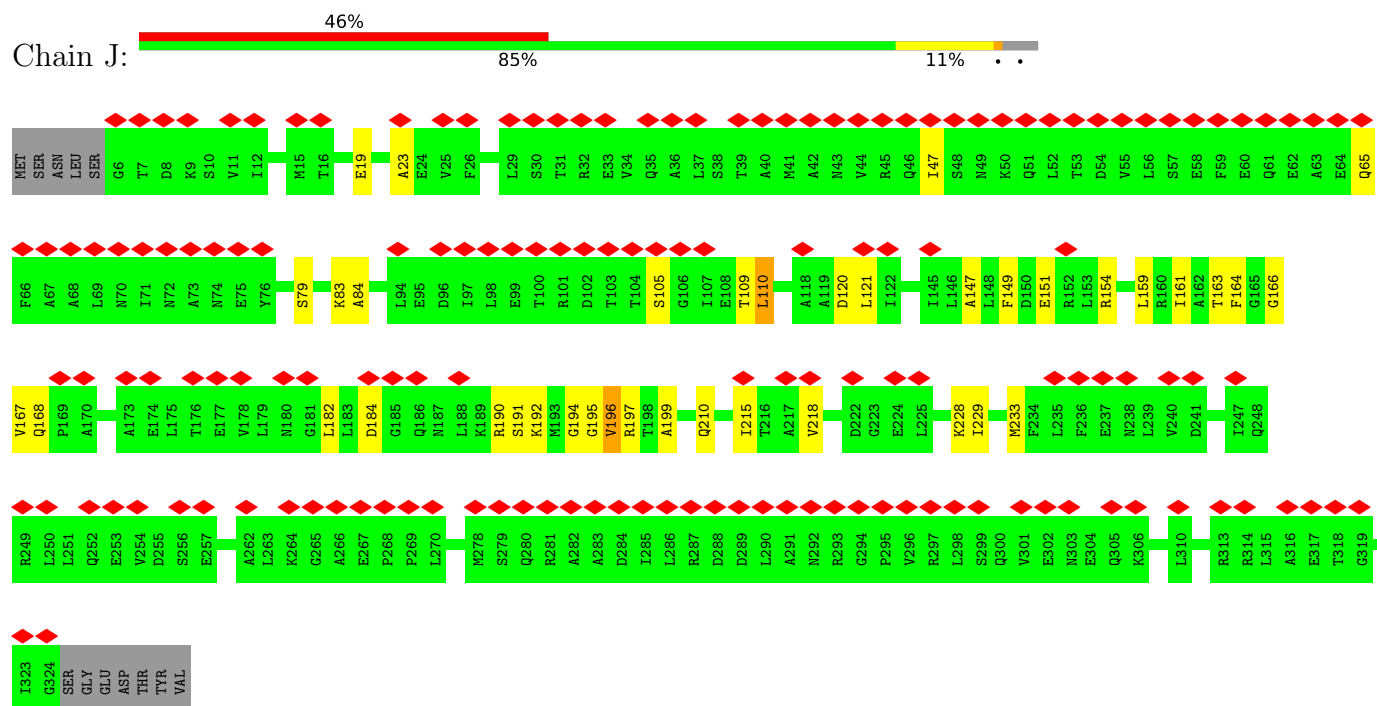


Chain RG:

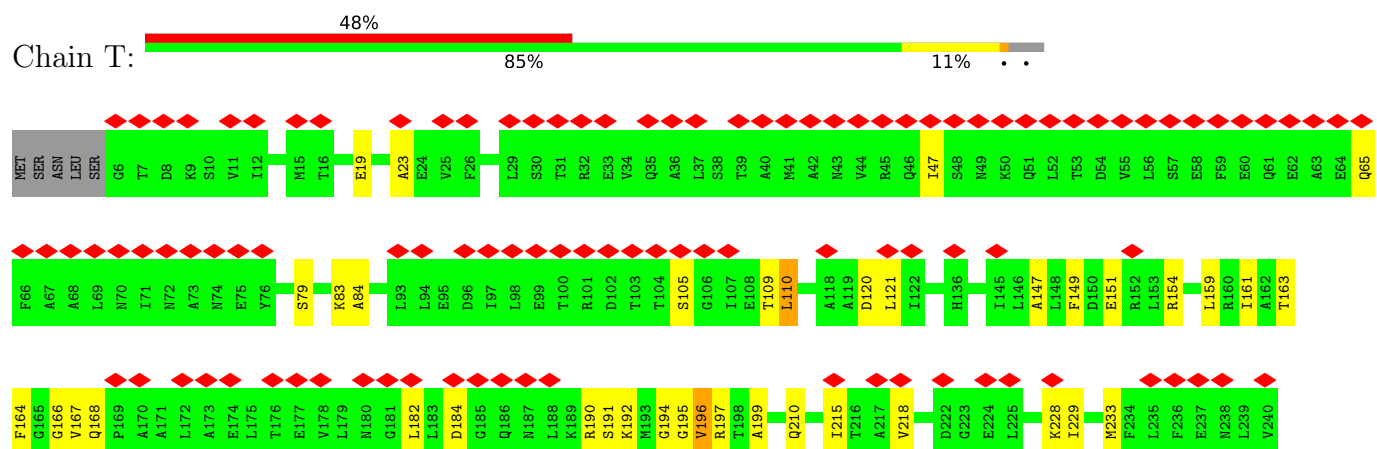


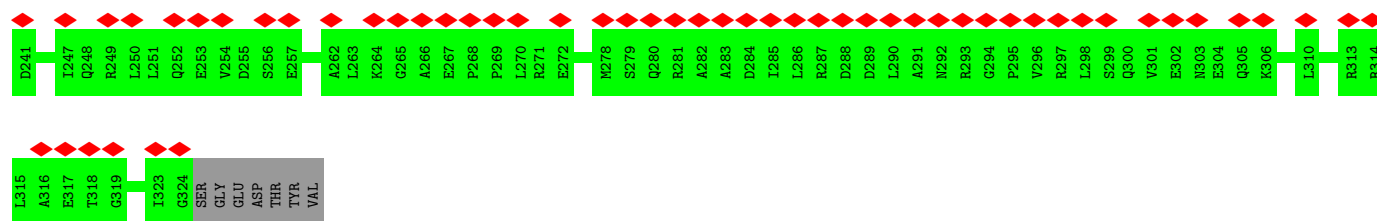


• Molecule 2: Flagellar motor switch protein FlhG

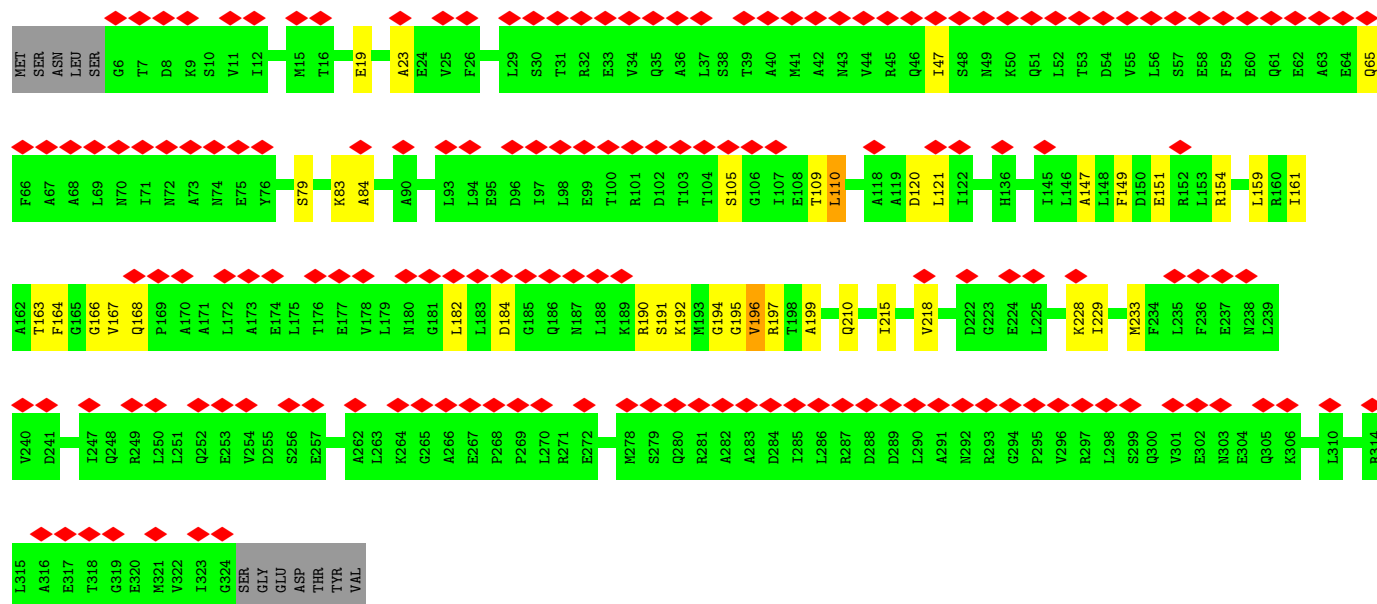
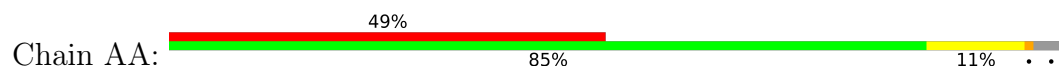


• Molecule 2: Flagellar motor switch protein FlhG

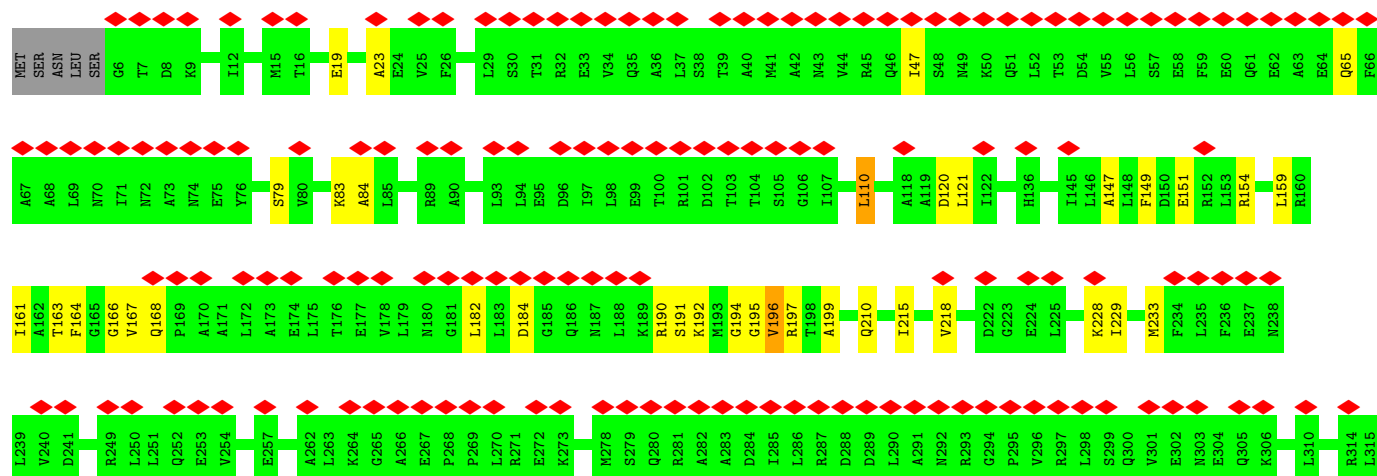
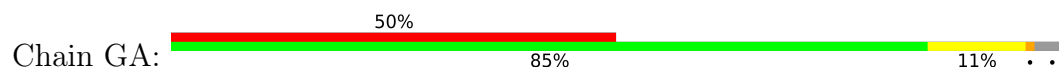


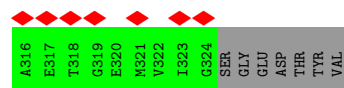


• Molecule 2: Flagellar motor switch protein FliG

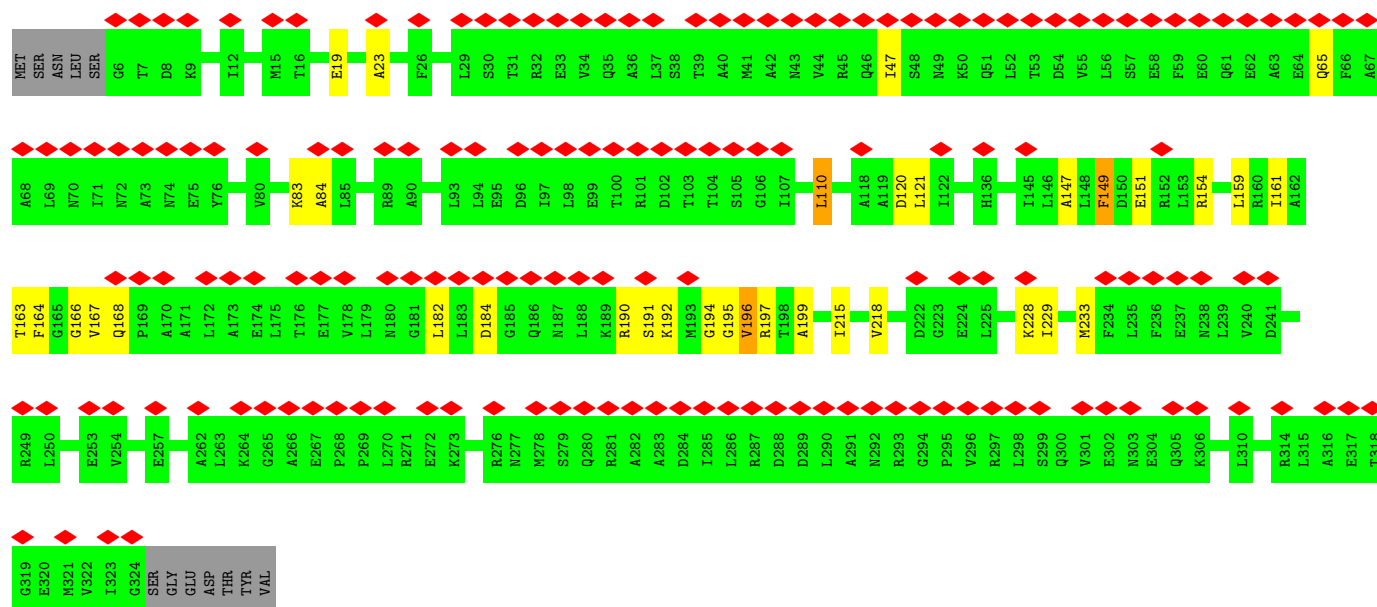
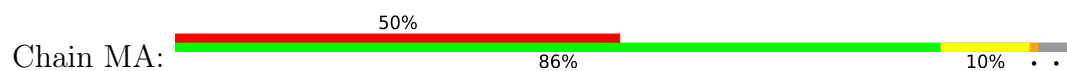


• Molecule 2: Flagellar motor switch protein FliG

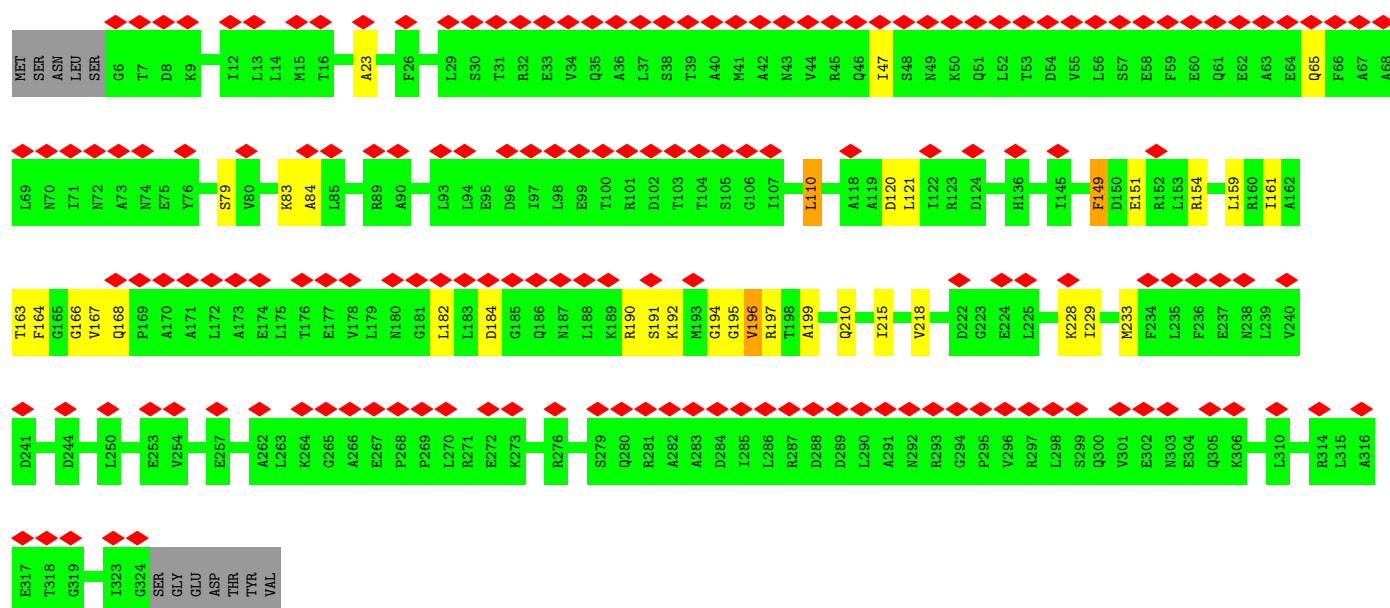
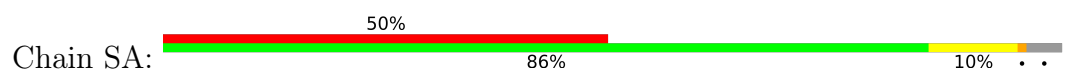




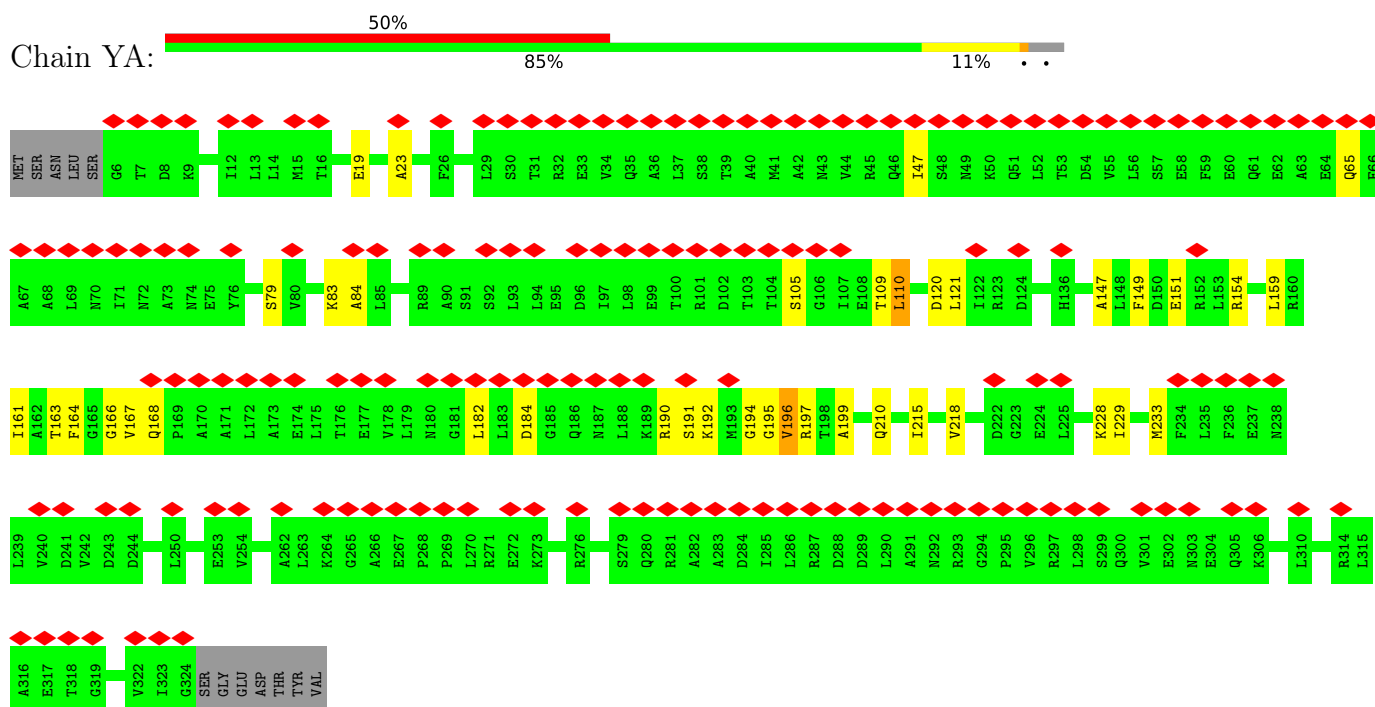
• Molecule 2: Flagellar motor switch protein FliG



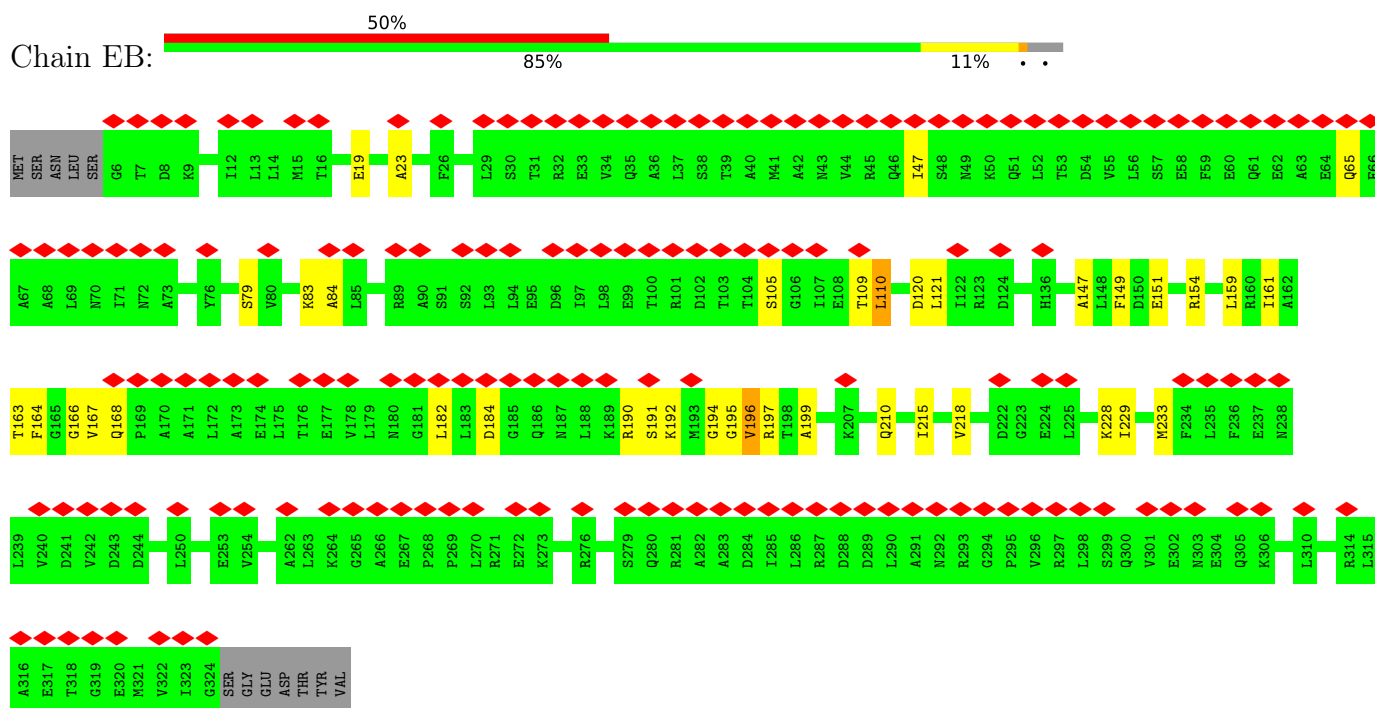
• Molecule 2: Flagellar motor switch protein FliG



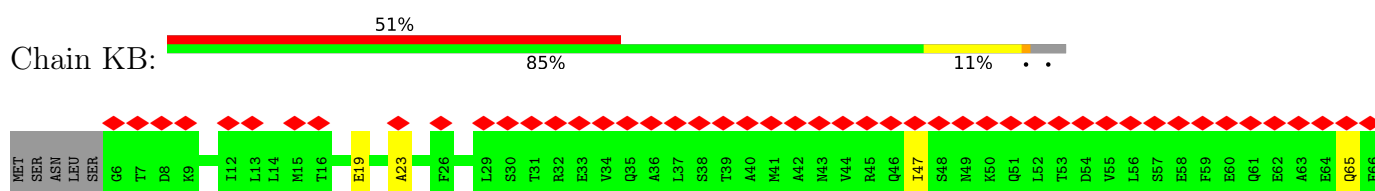
• Molecule 2: Flagellar motor switch protein FliG

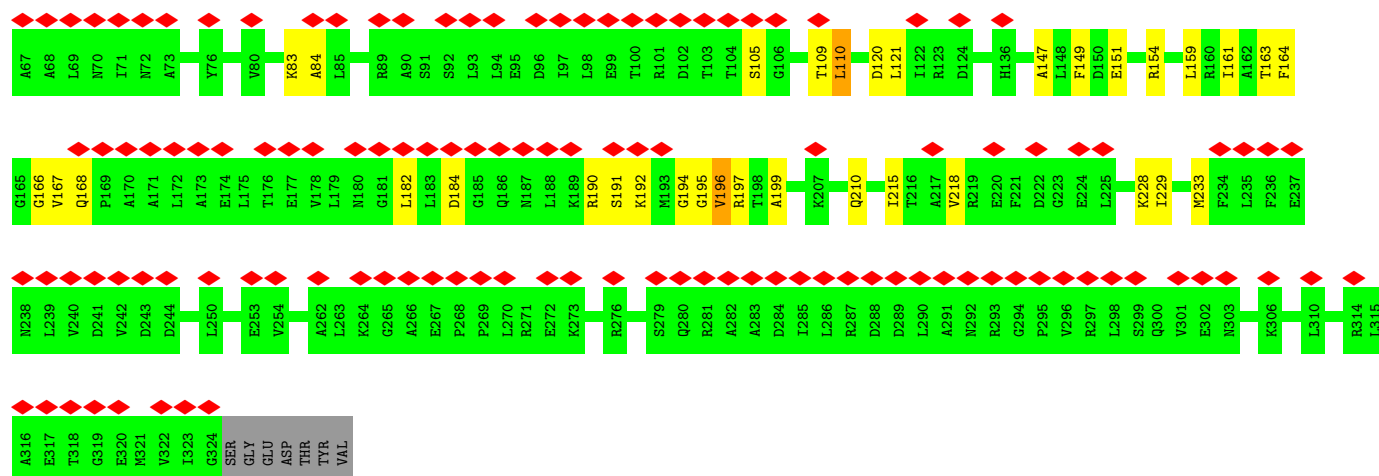


• Molecule 2: Flagellar motor switch protein FliG

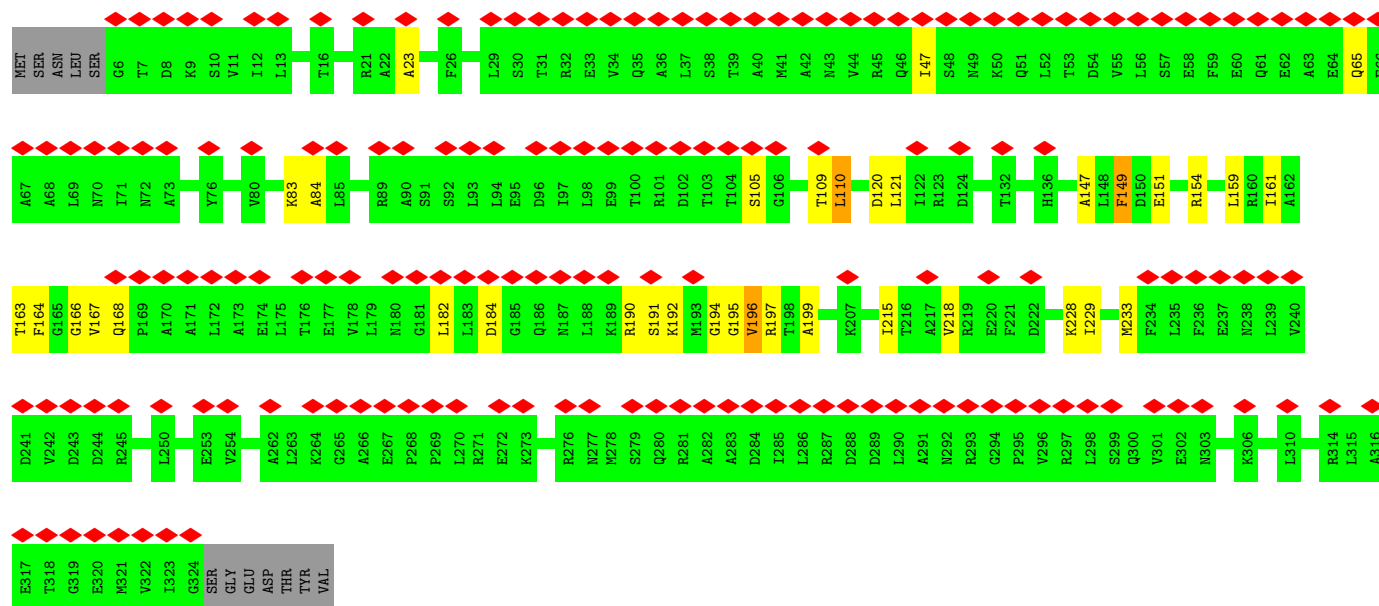
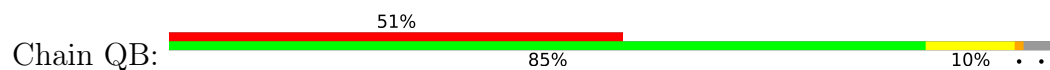


• Molecule 2: Flagellar motor switch protein FliG

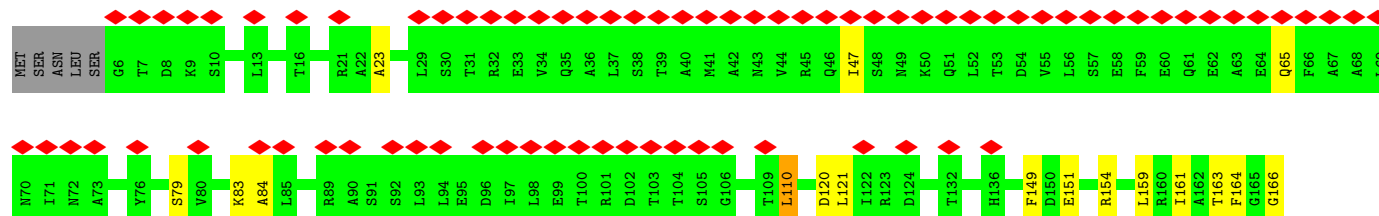
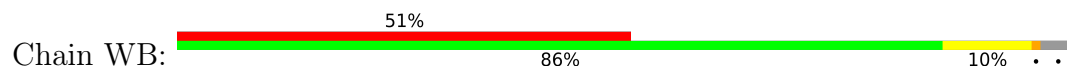


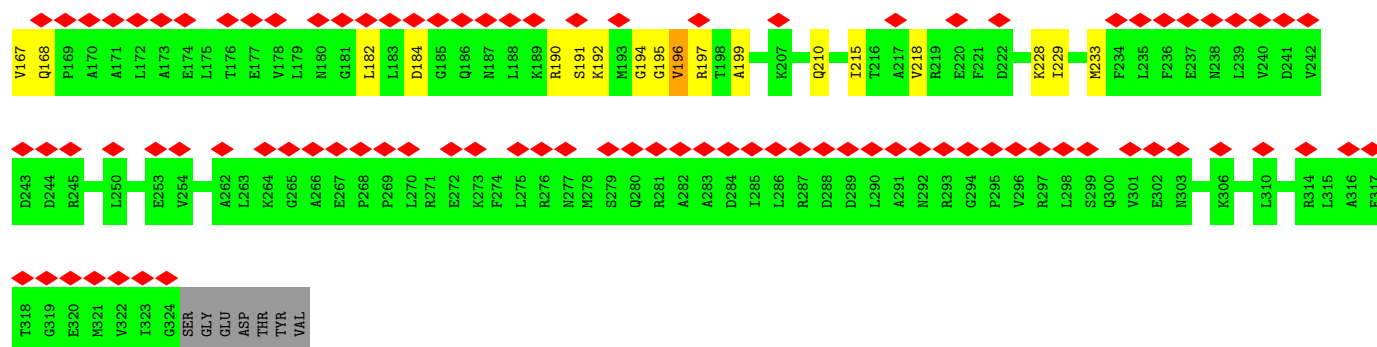


• Molecule 2: Flagellar motor switch protein FlhG

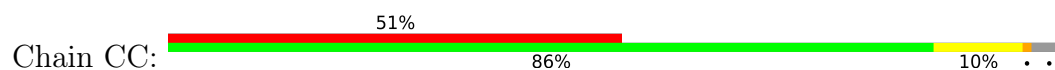


• Molecule 2: Flagellar motor switch protein FlhG

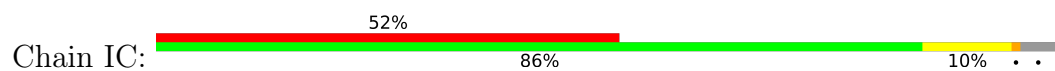


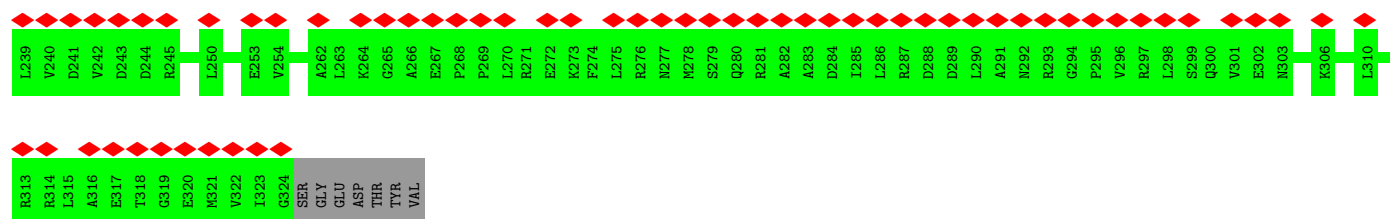


• Molecule 2: Flagellar motor switch protein FlhG

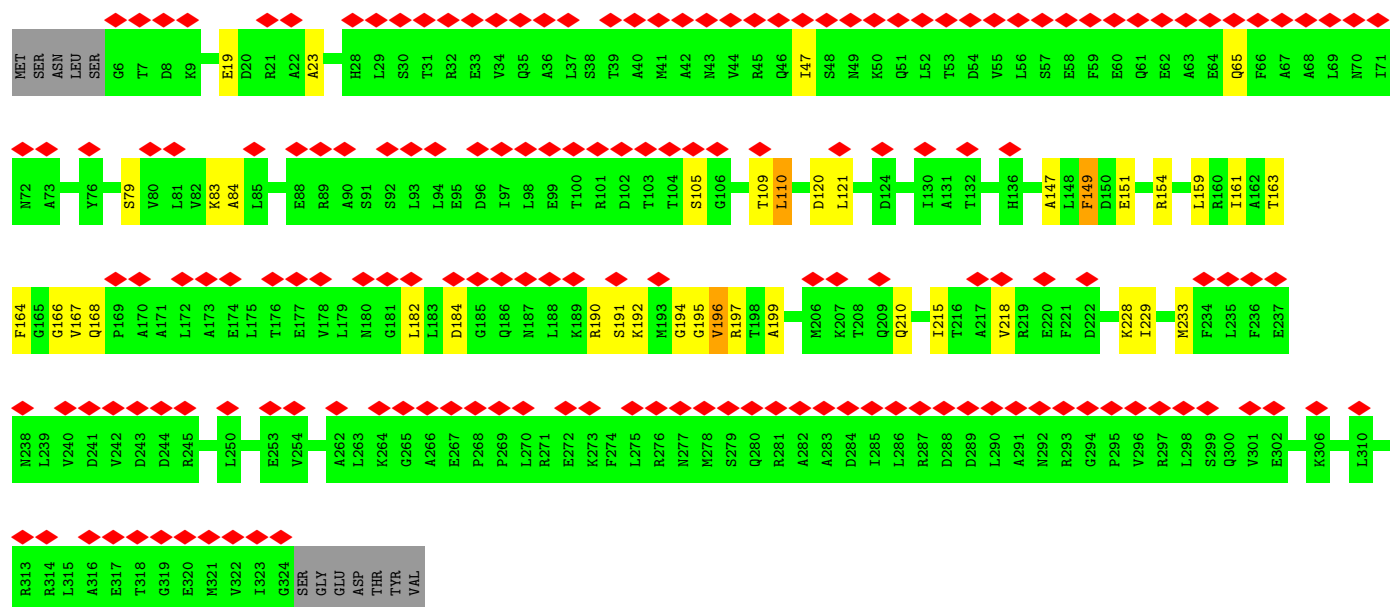
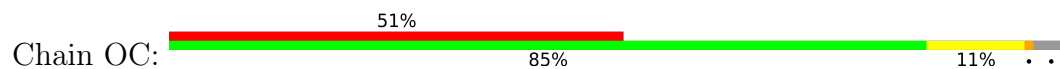


• Molecule 2: Flagellar motor switch protein FlhG

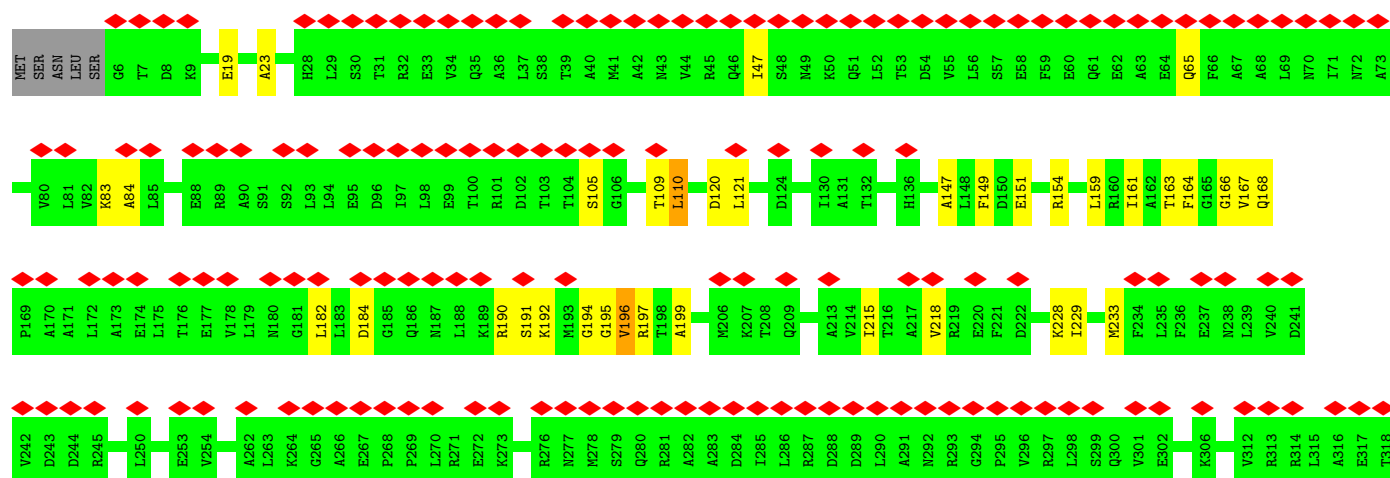
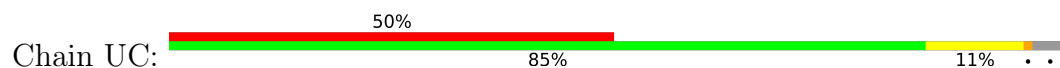


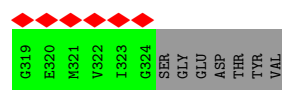


• Molecule 2: Flagellar motor switch protein FlhG

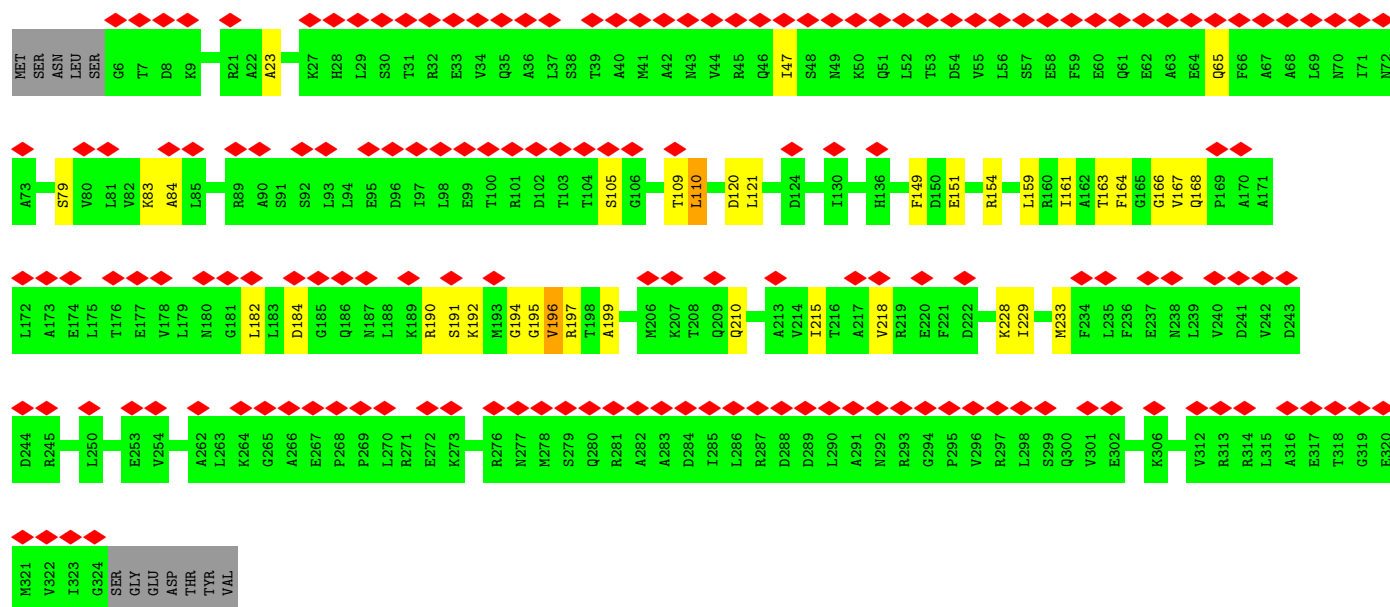
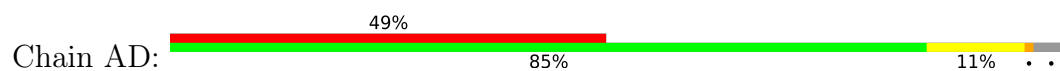


• Molecule 2: Flagellar motor switch protein FlhG

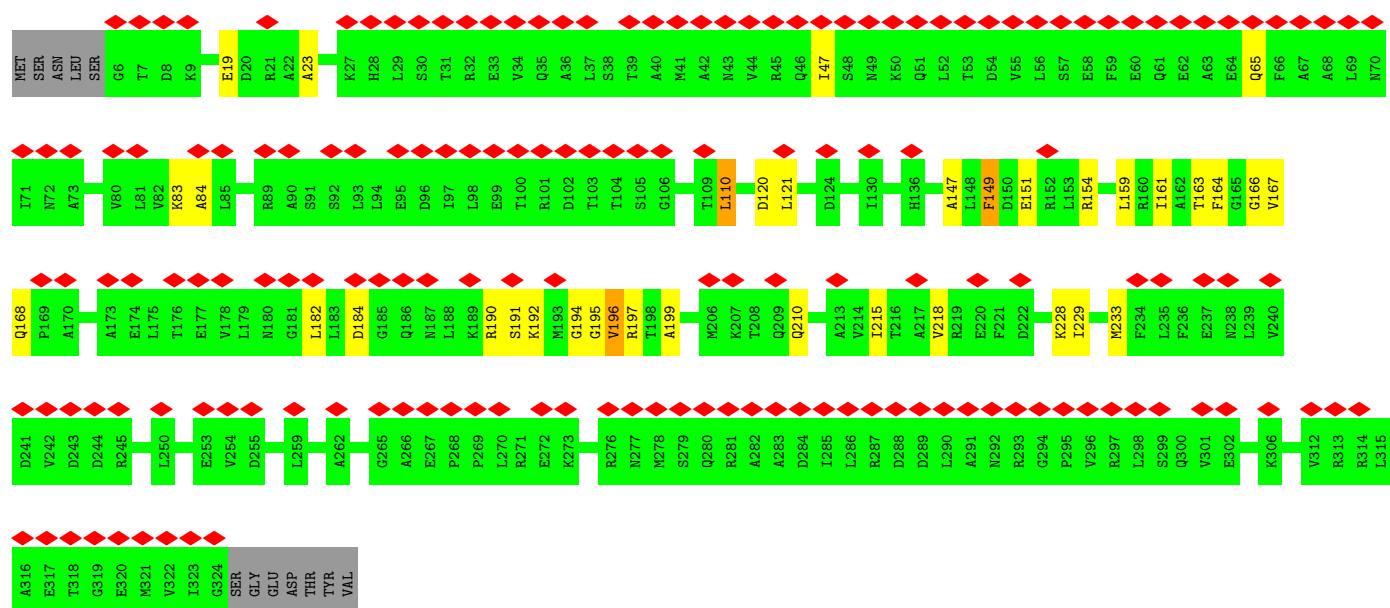
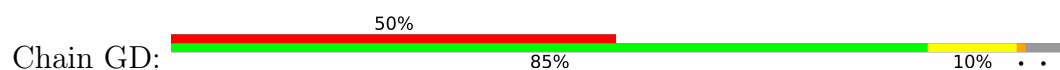




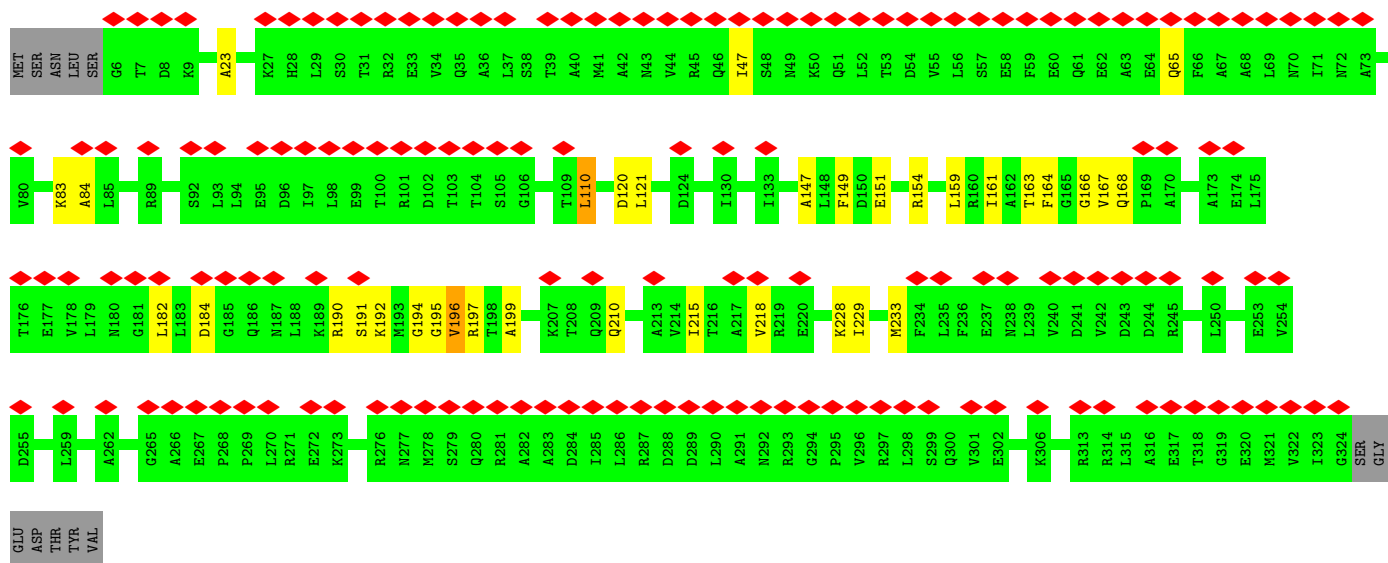
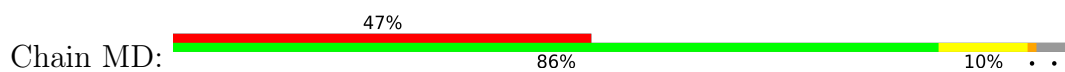
• Molecule 2: Flagellar motor switch protein FliG



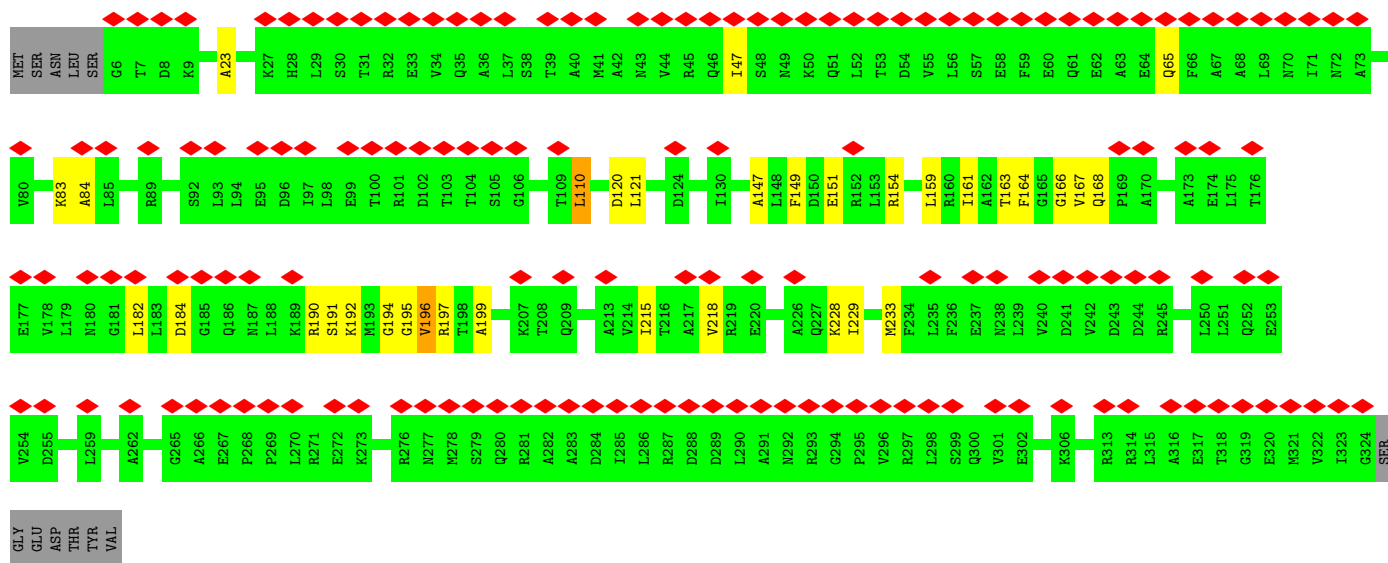
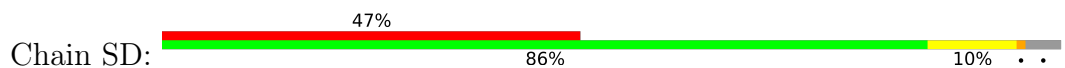
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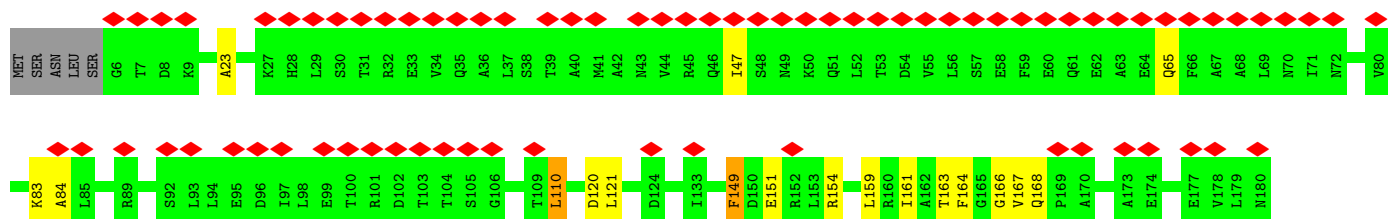
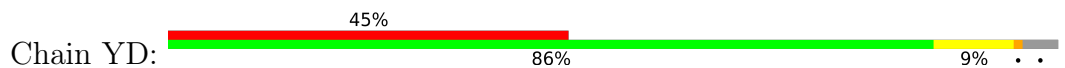
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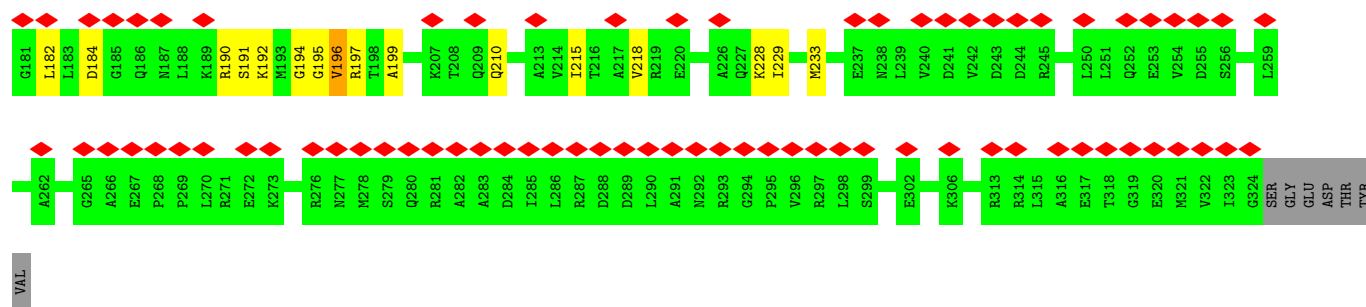


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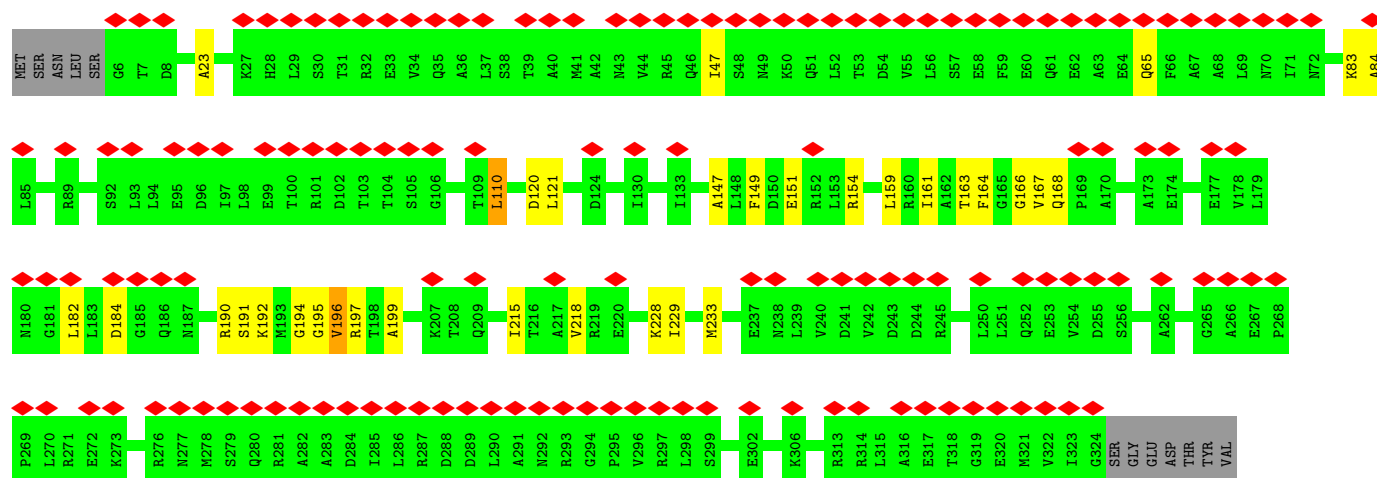
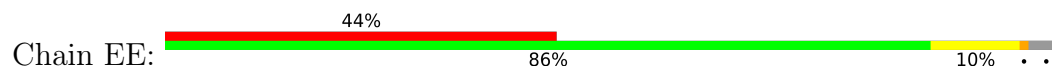


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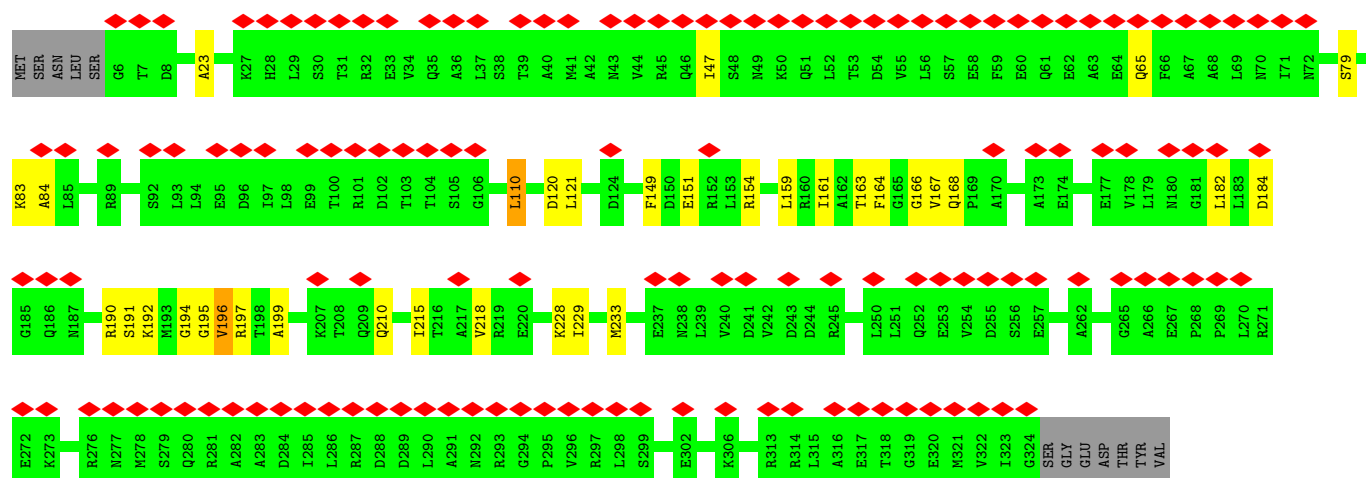
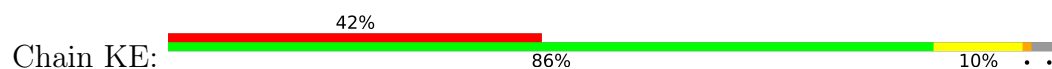




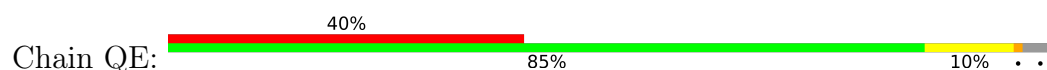
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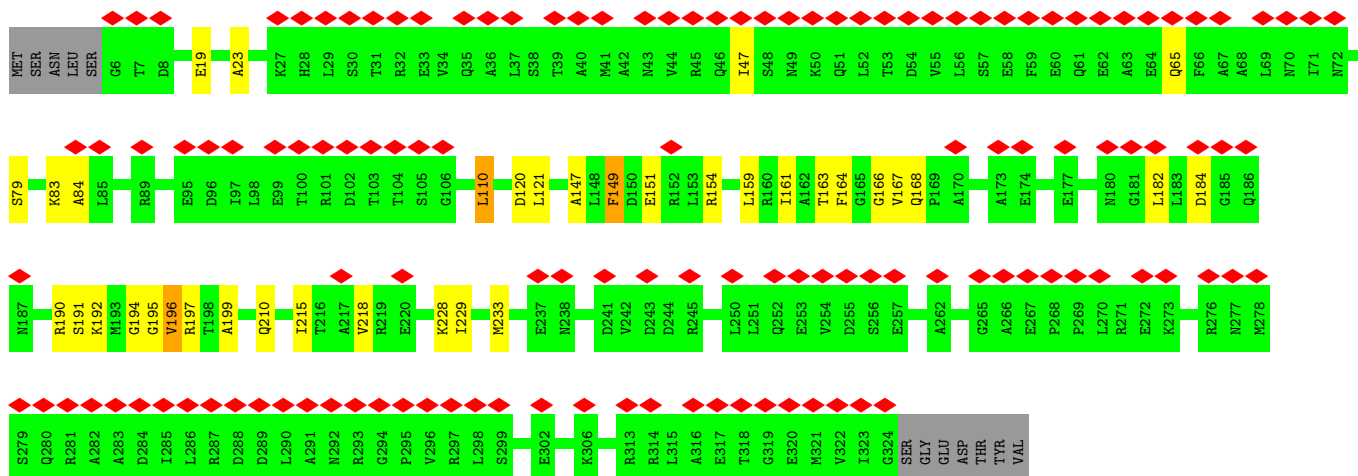


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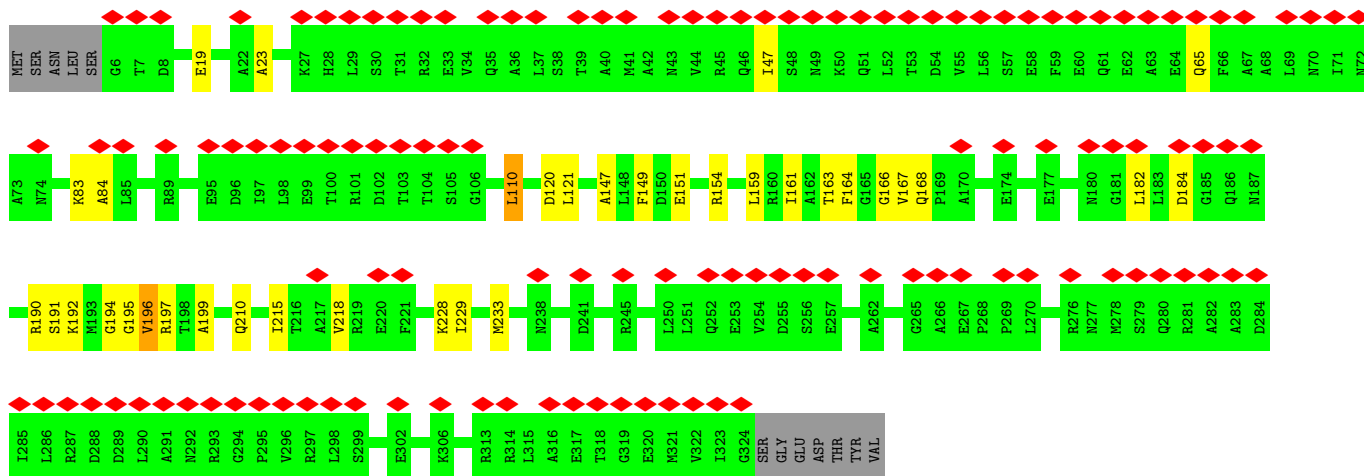
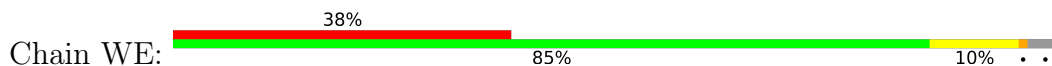


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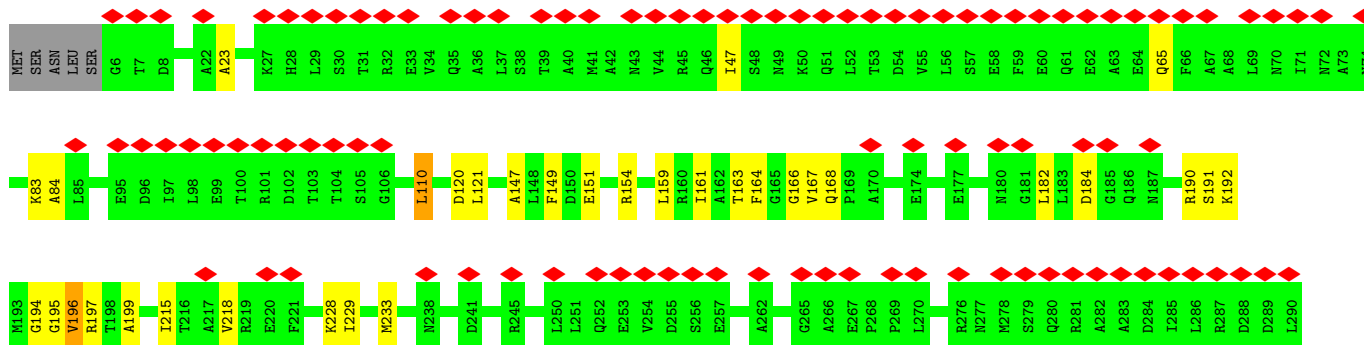
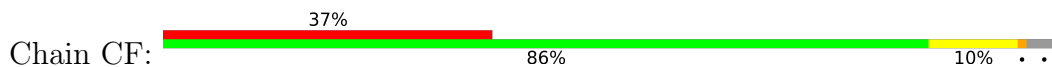


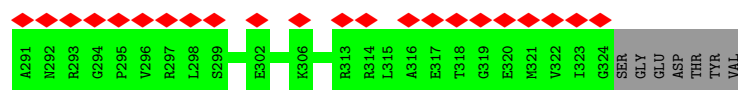


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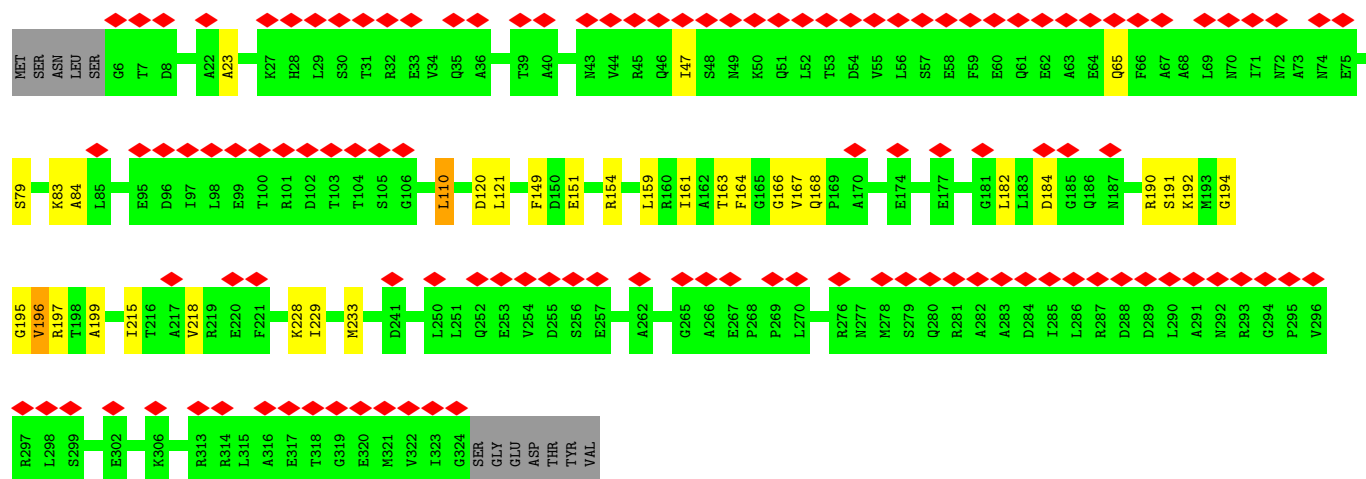
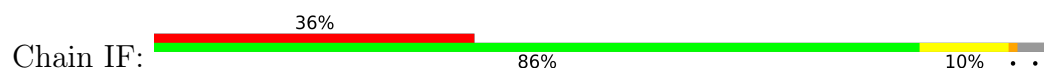


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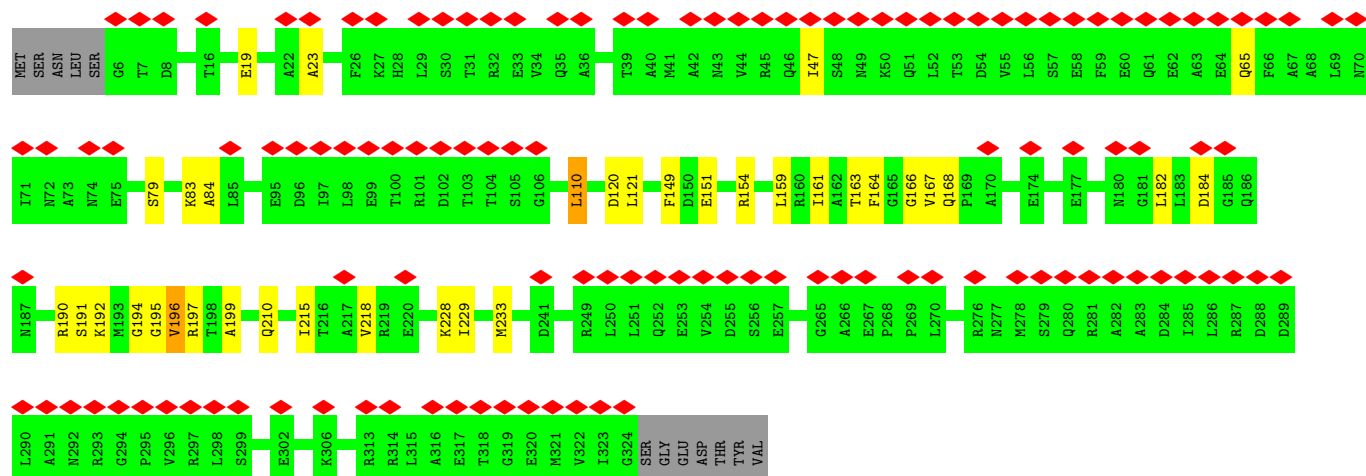
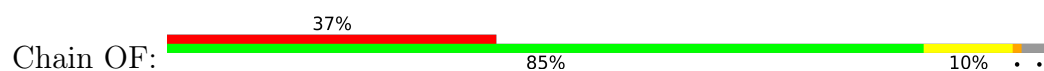




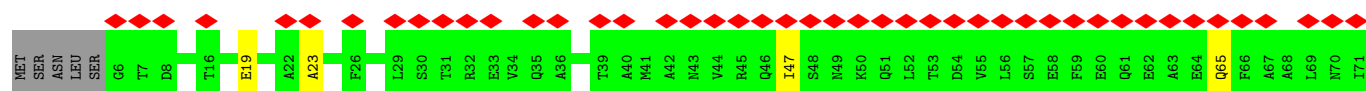
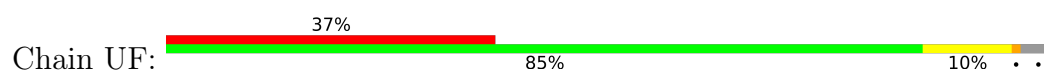
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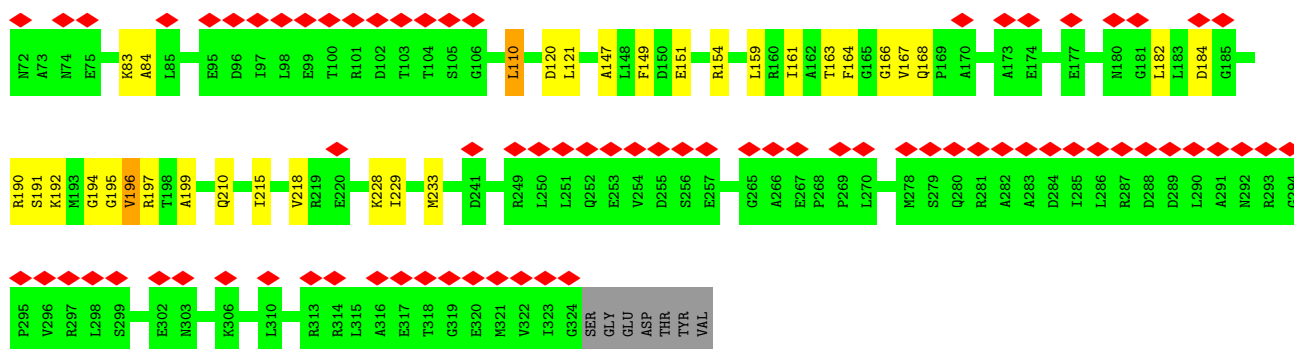


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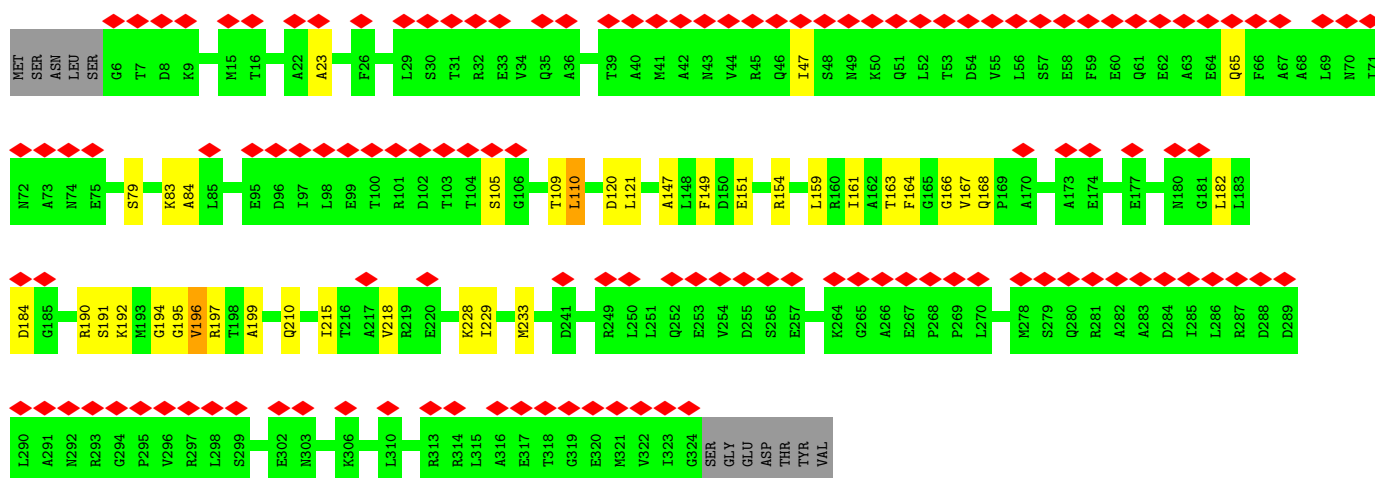
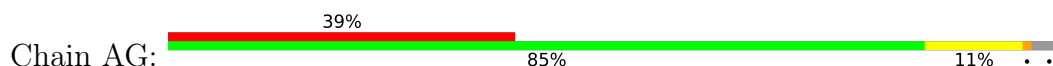


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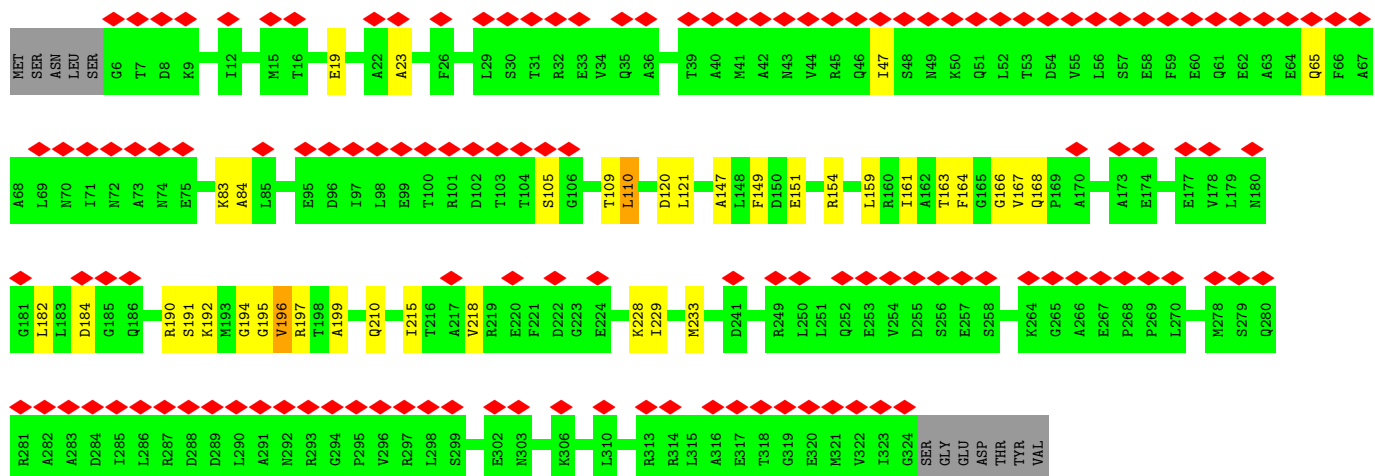
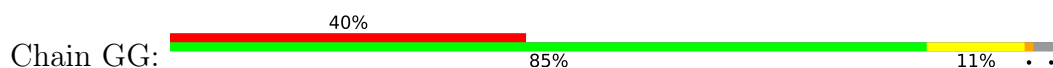




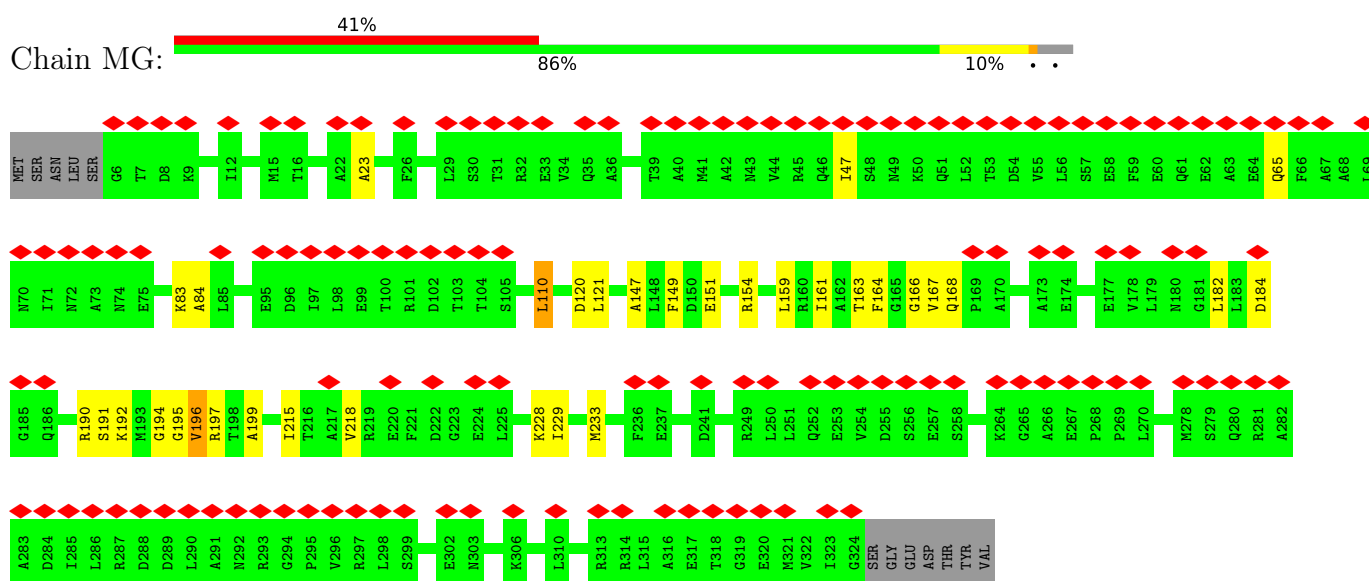
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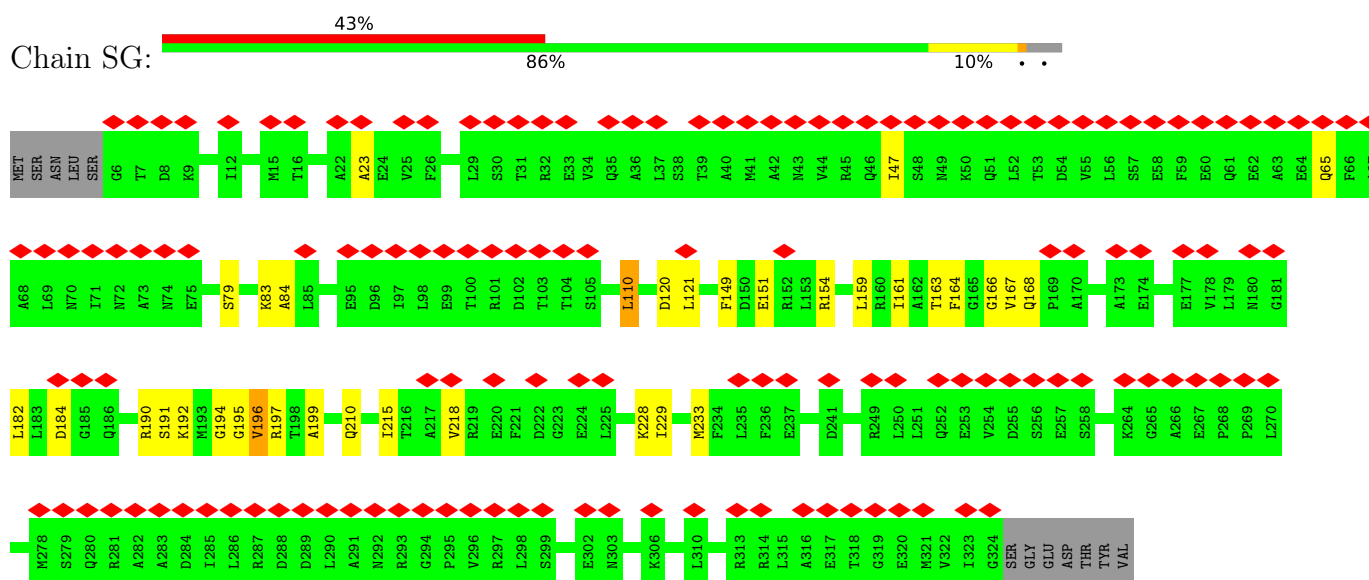
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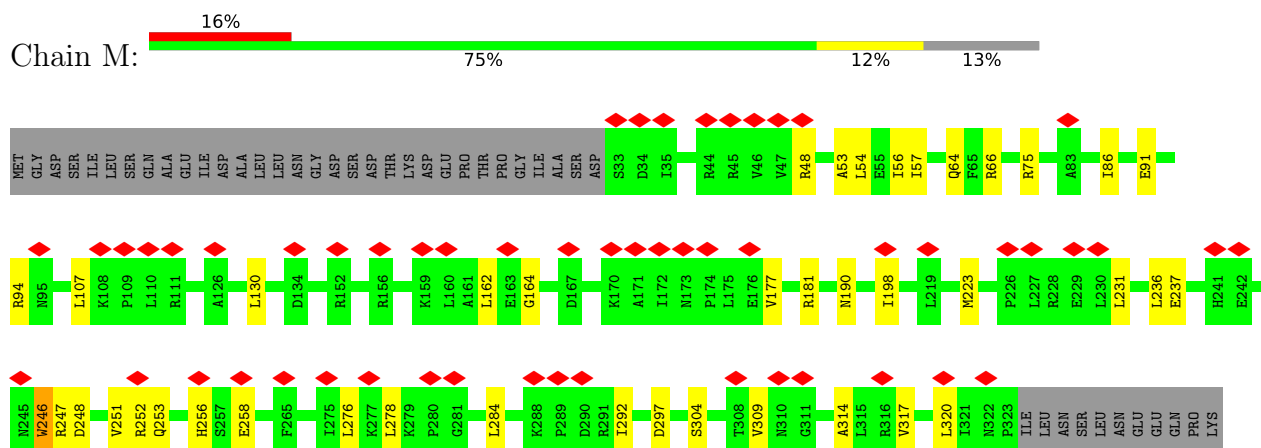
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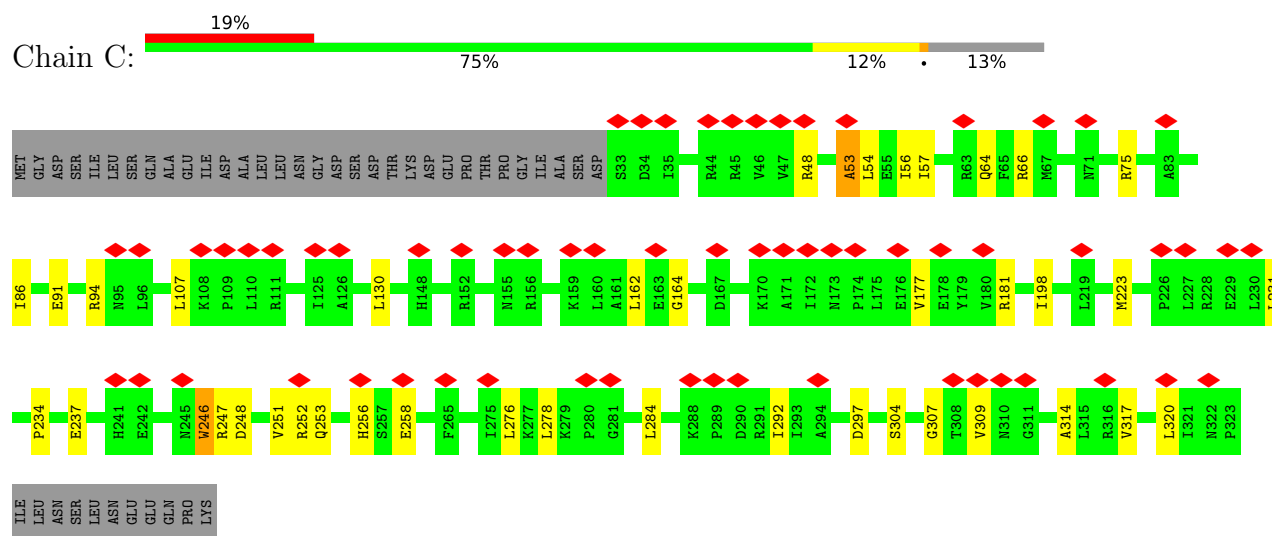
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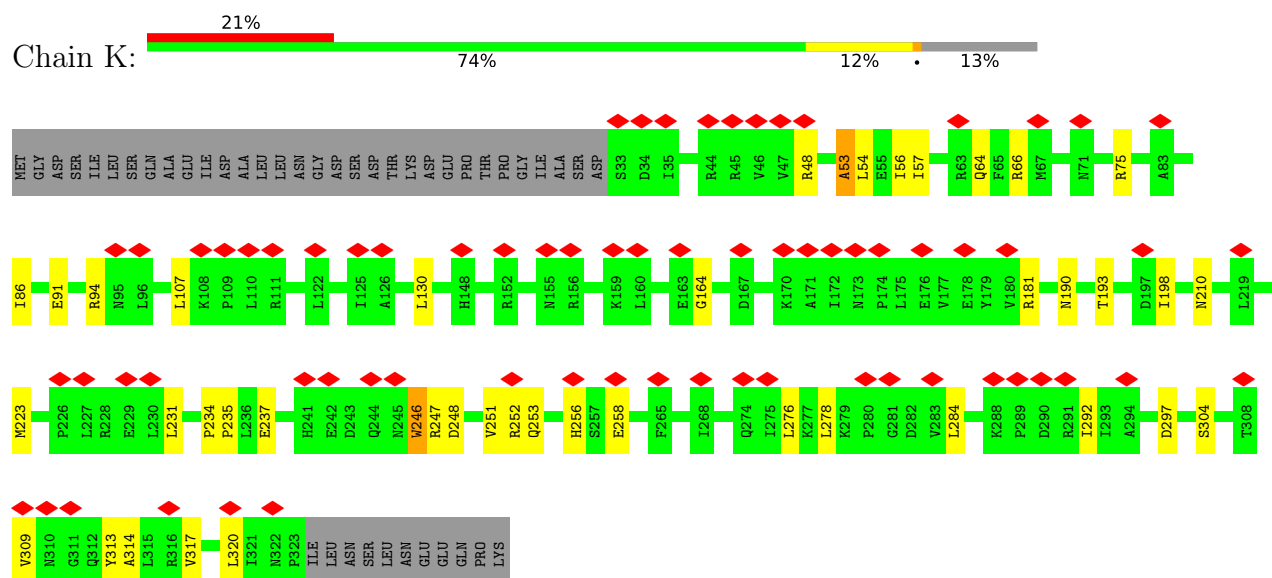
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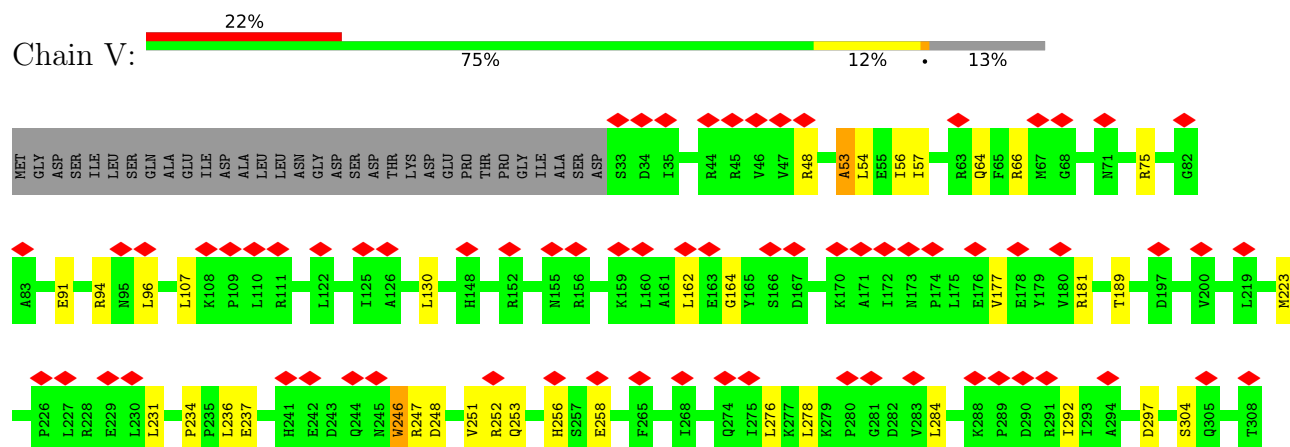
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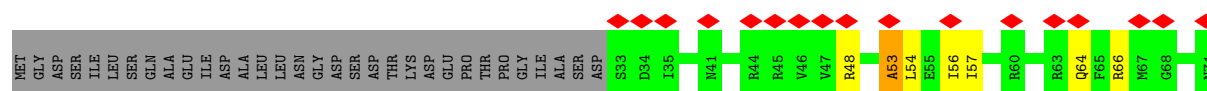


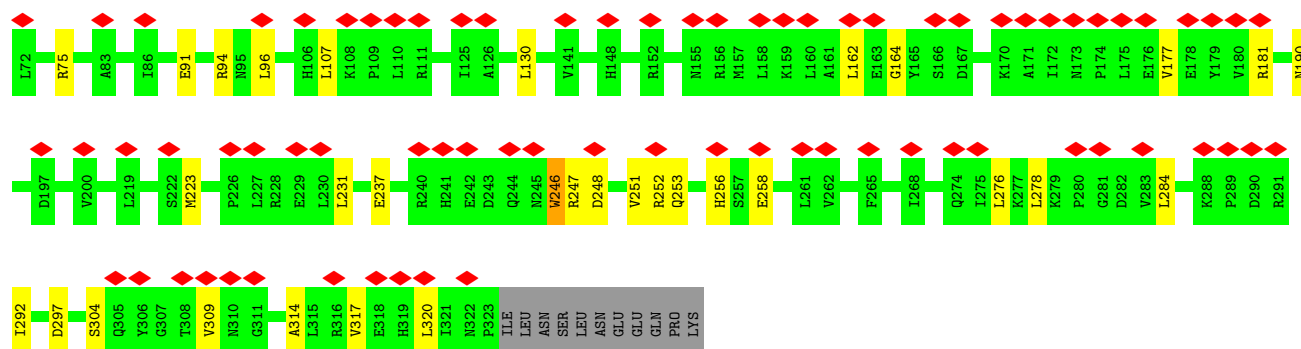
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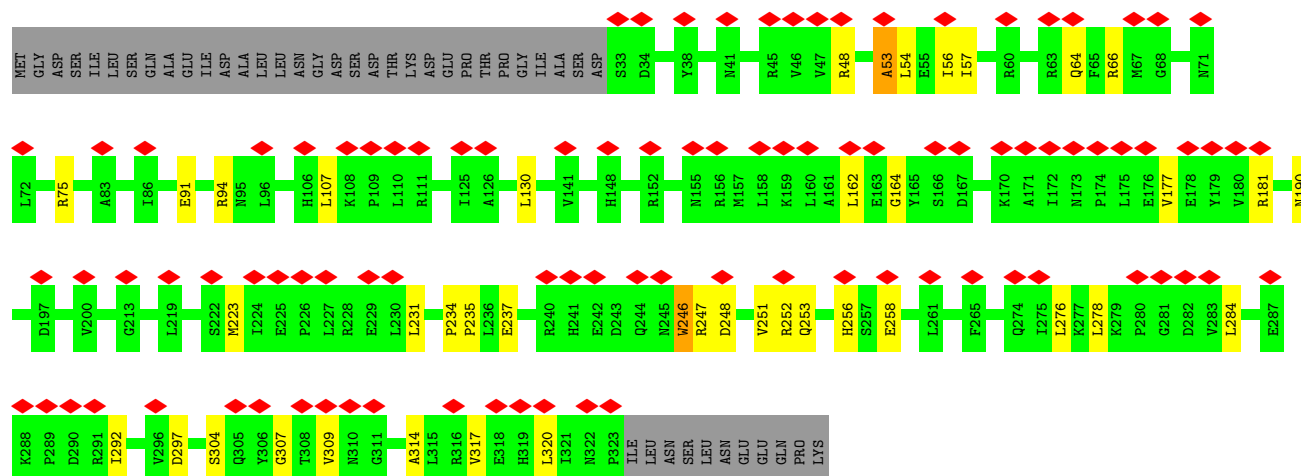
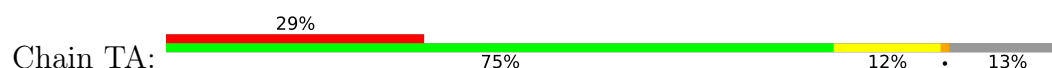
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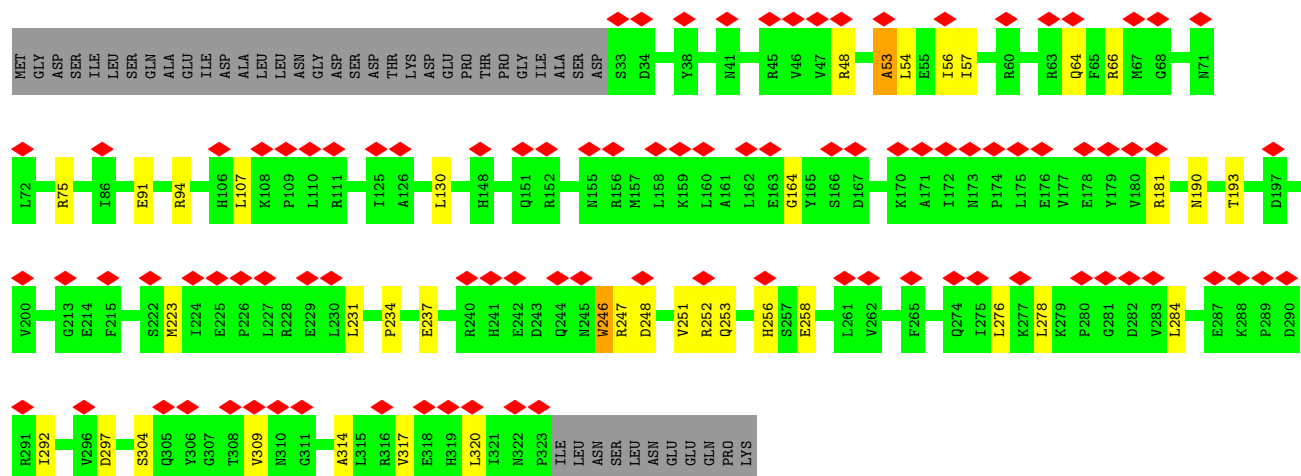
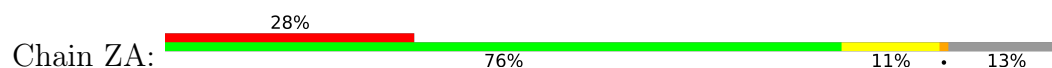




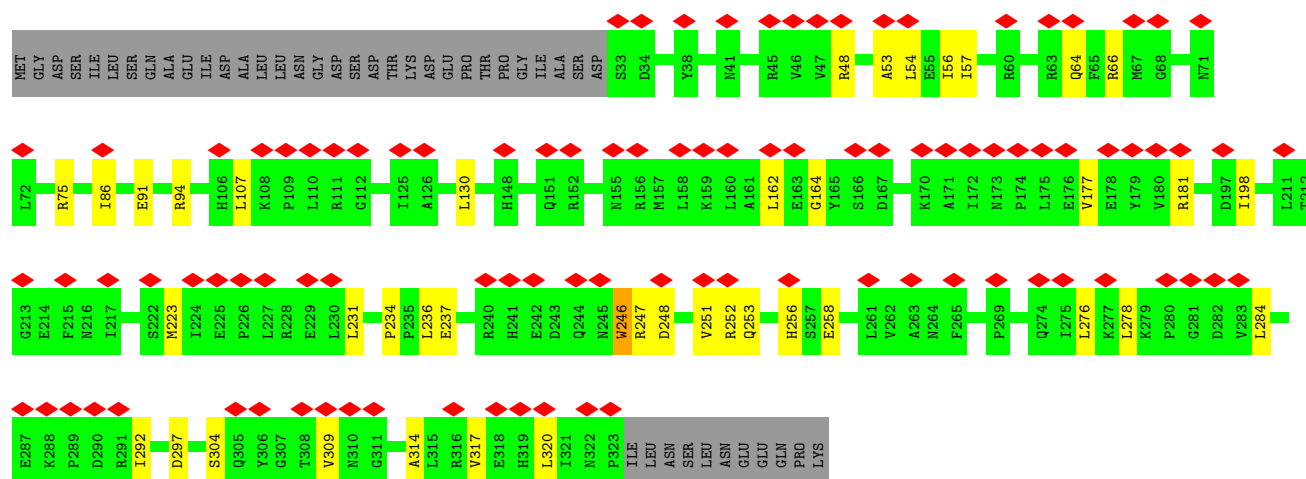
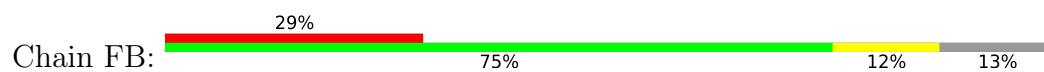
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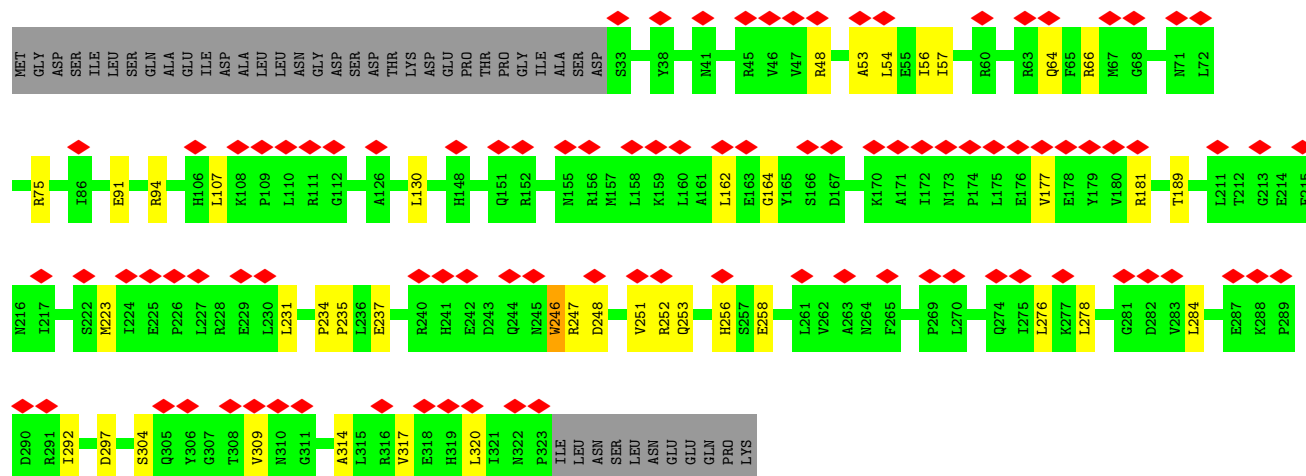
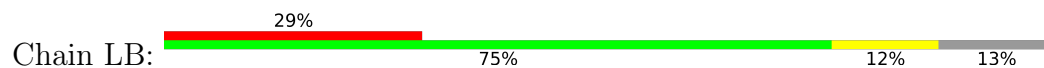
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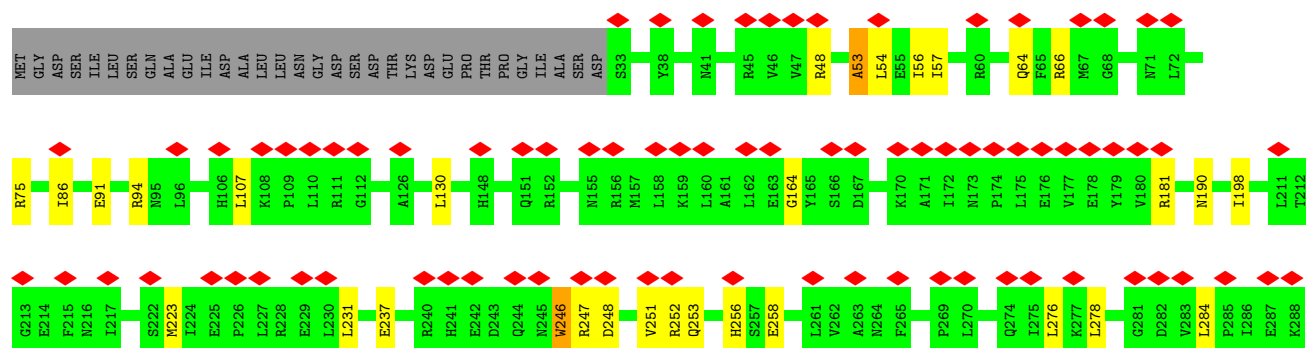
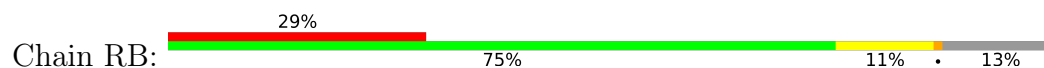
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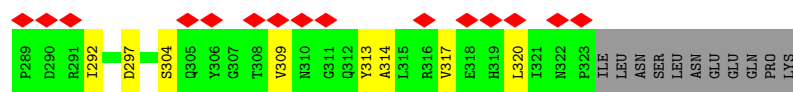


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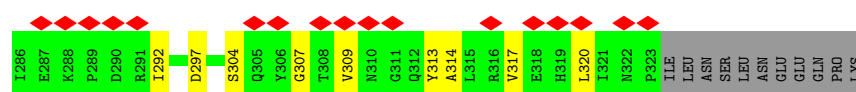
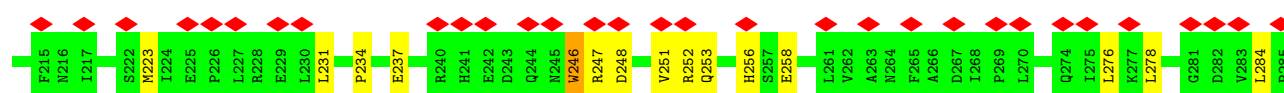
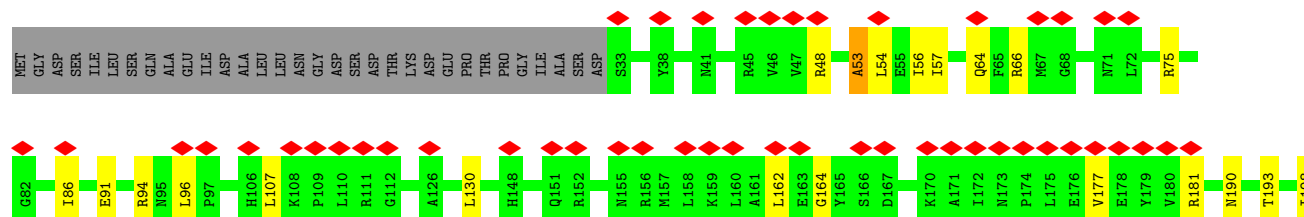
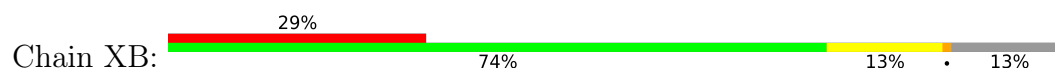


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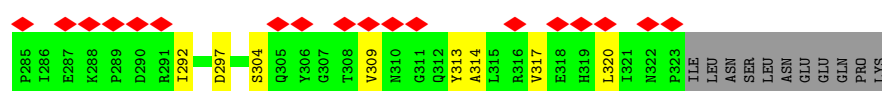
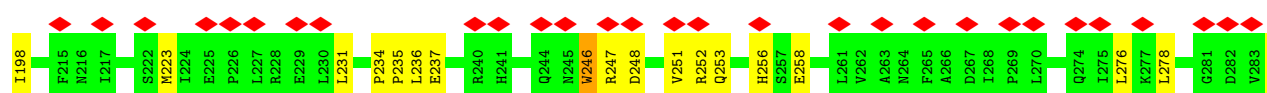
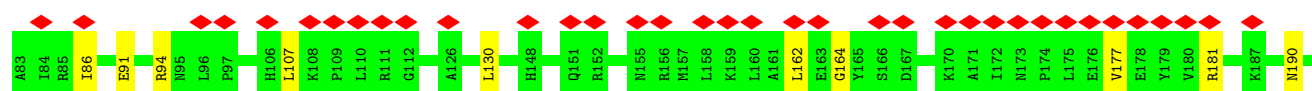
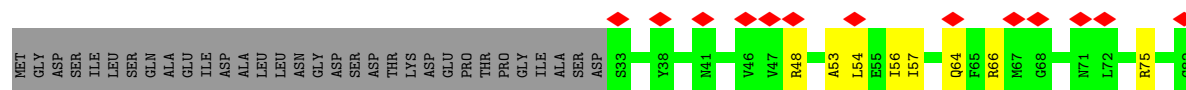
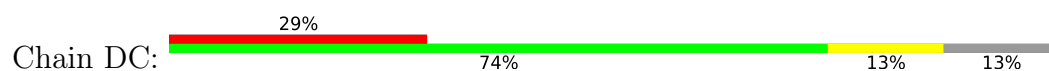




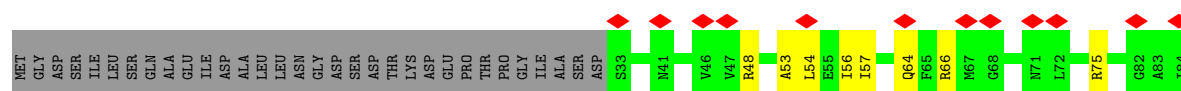
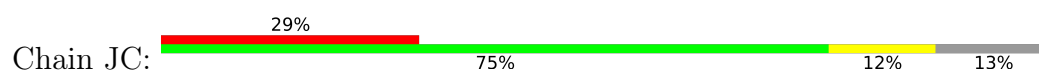
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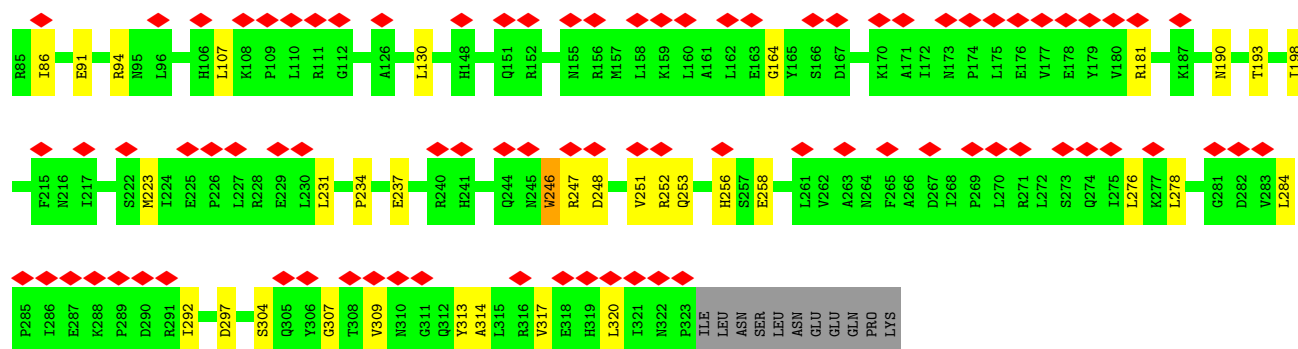


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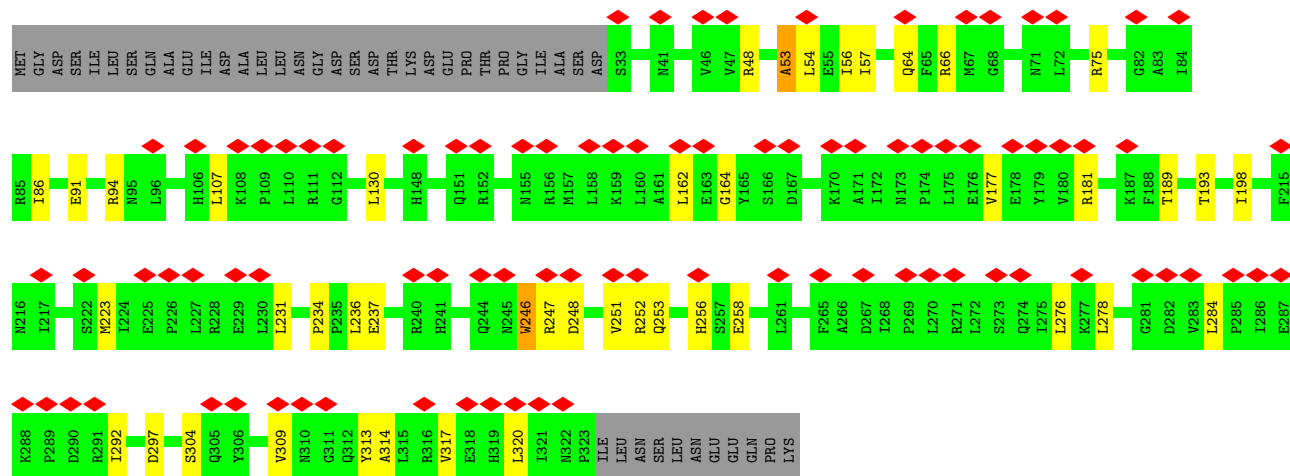
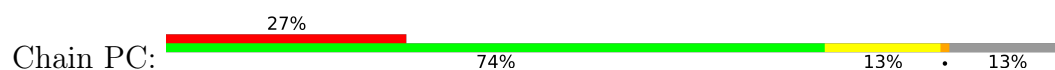


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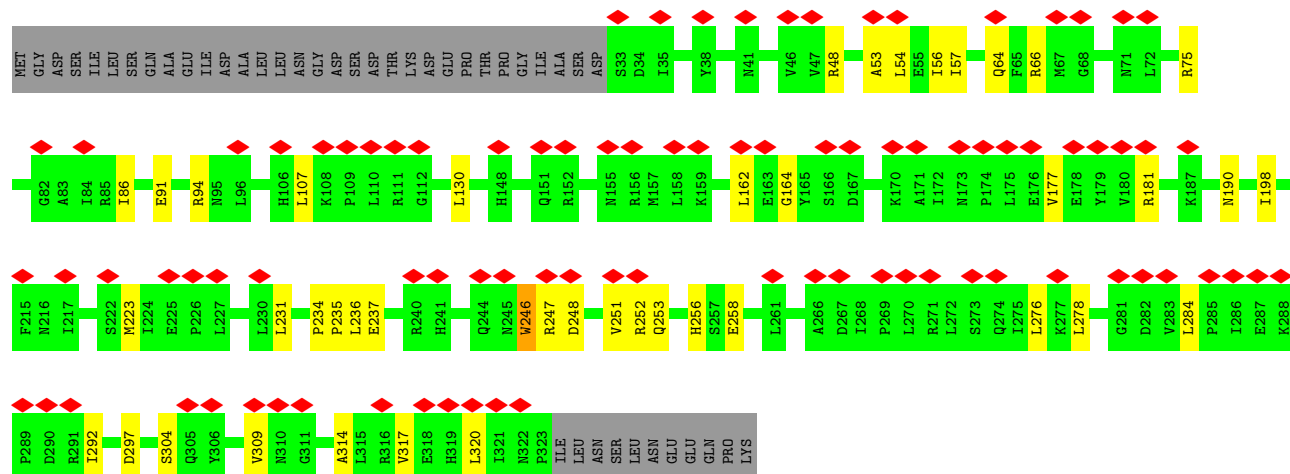
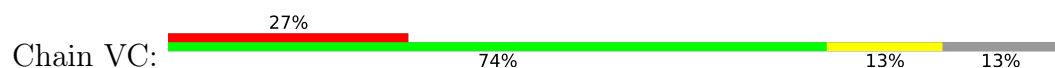




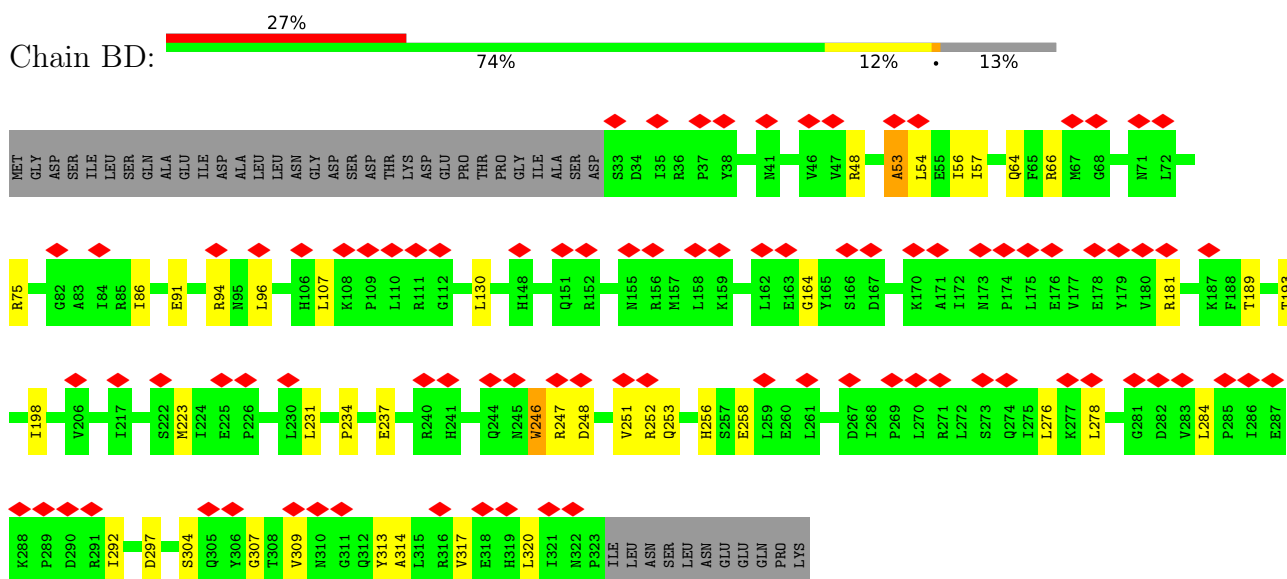
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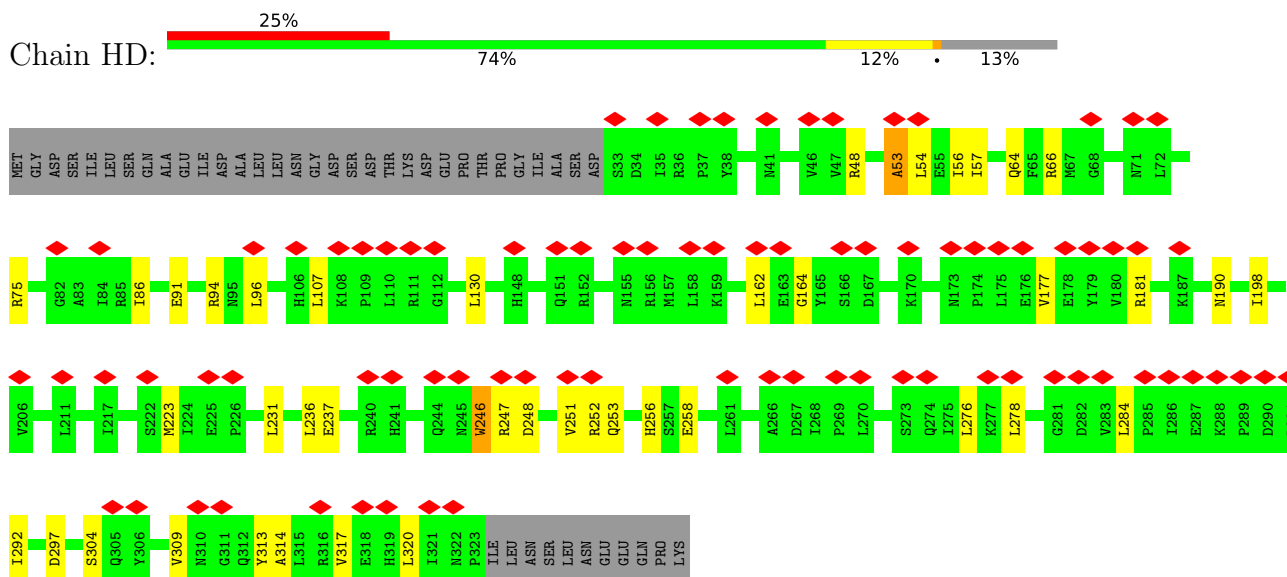
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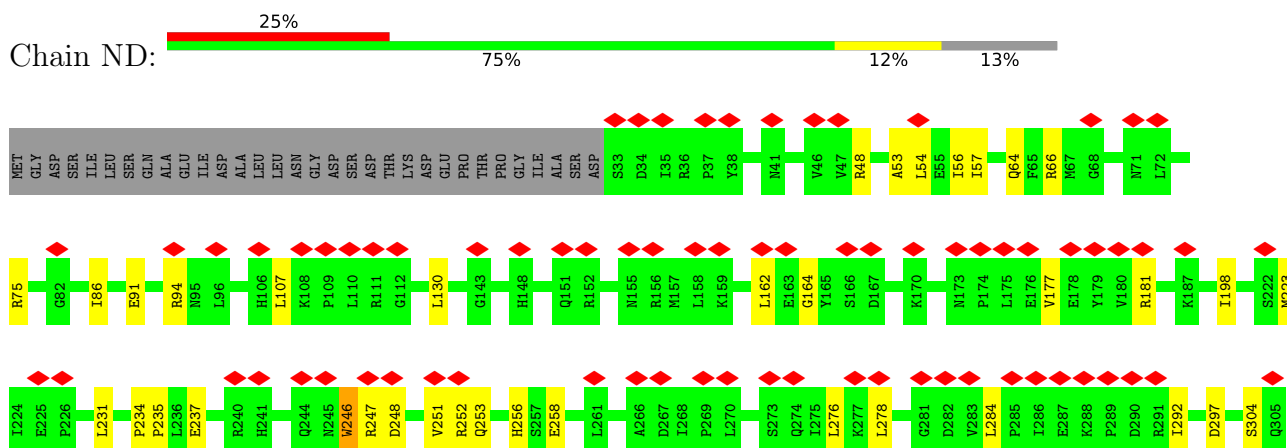
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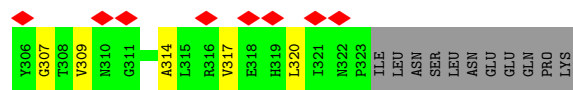


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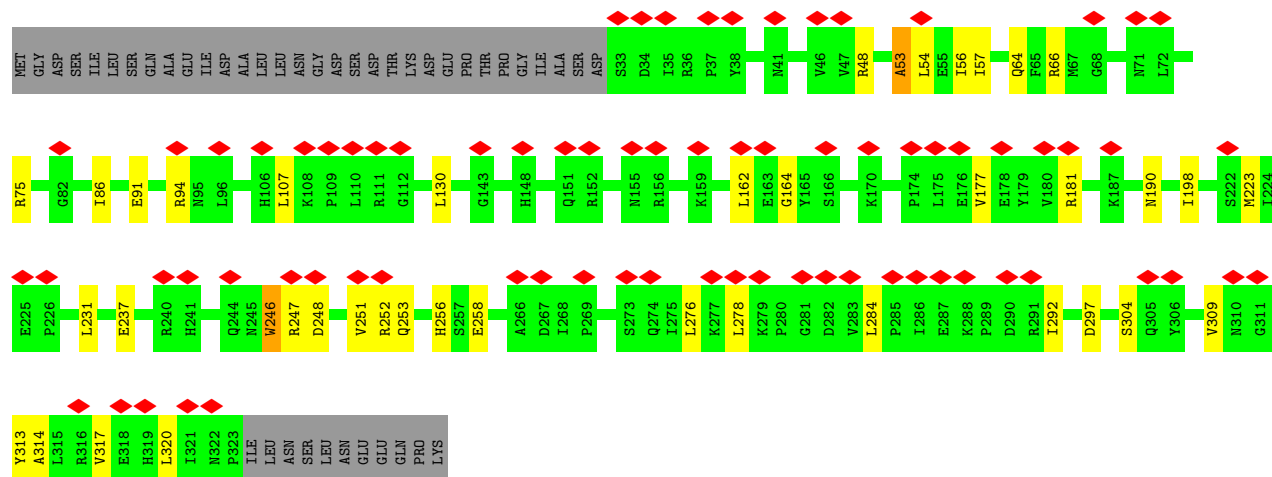
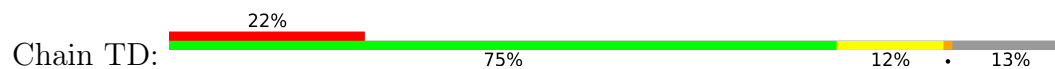


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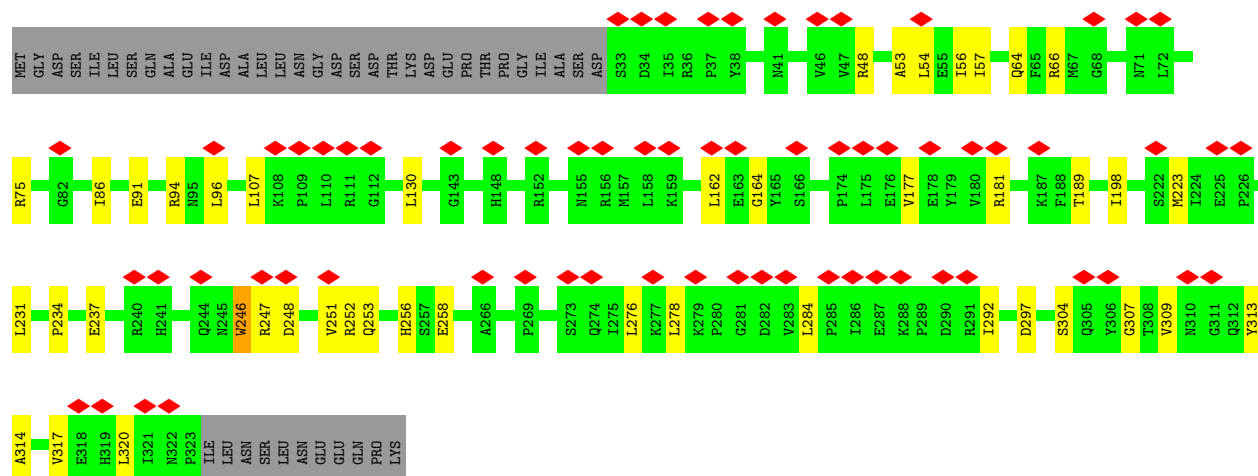
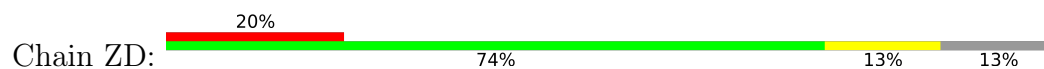




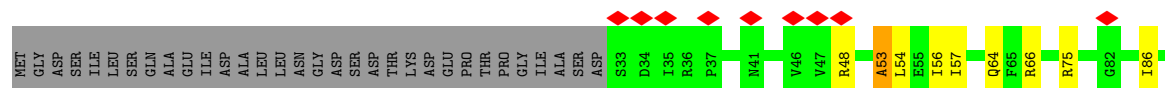
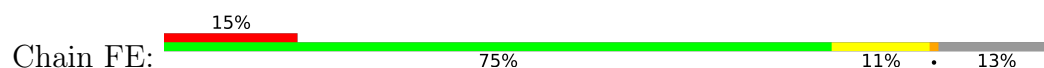
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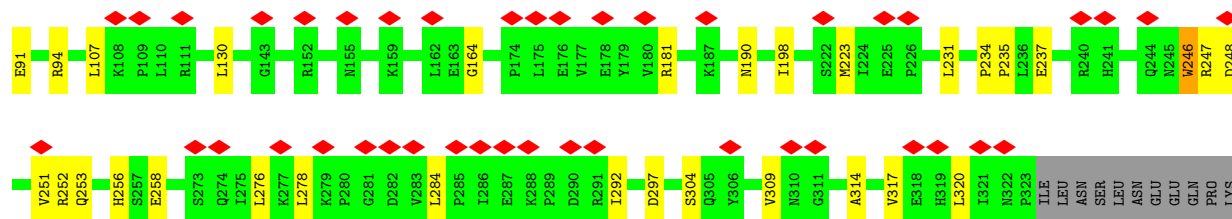


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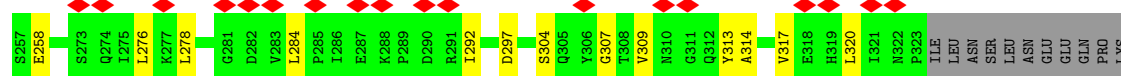
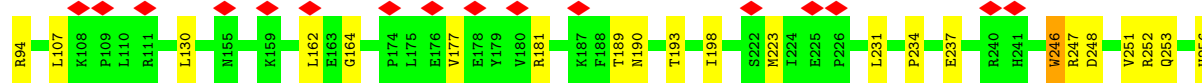
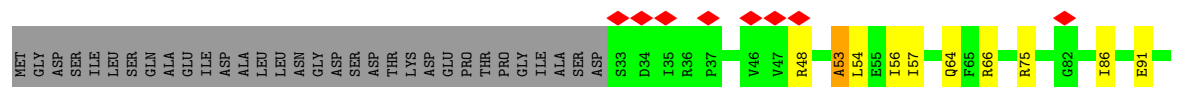
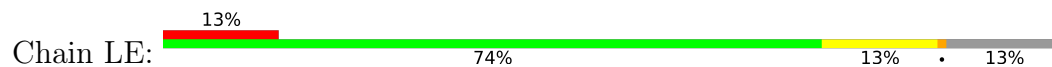


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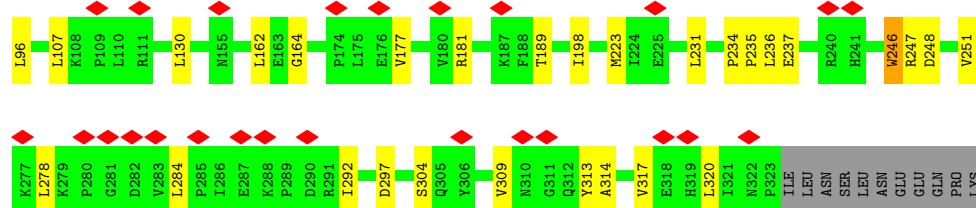
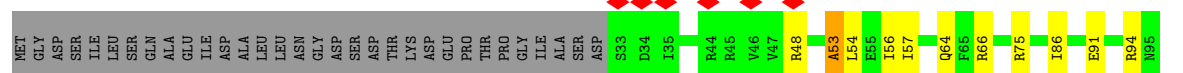
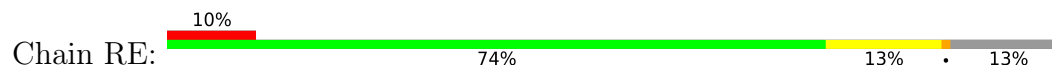




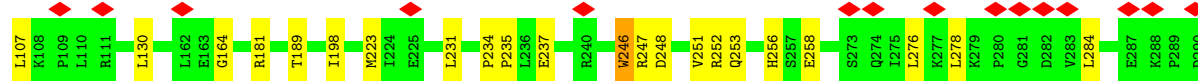
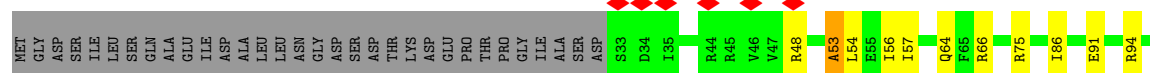
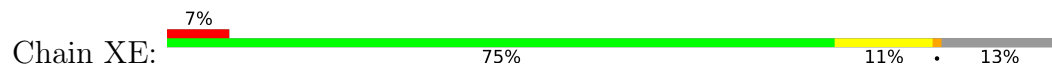
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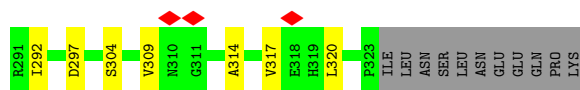


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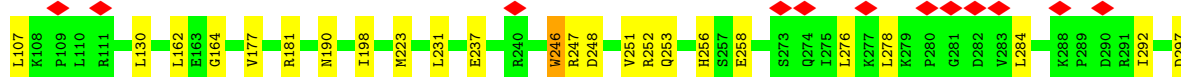
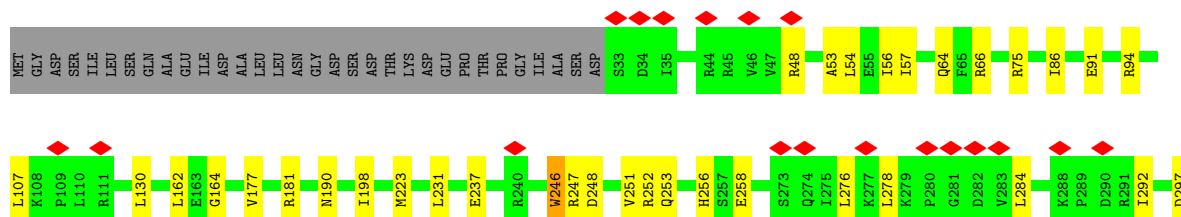
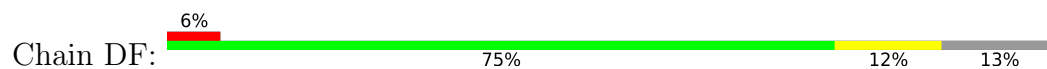


• Molecule 3: Flagellar motor switch protein FlIM

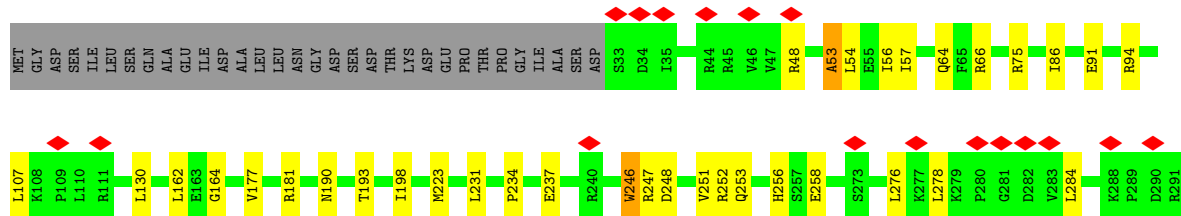
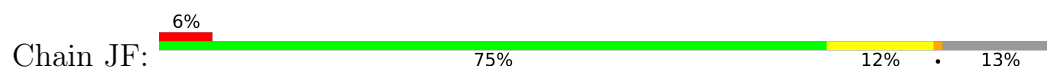




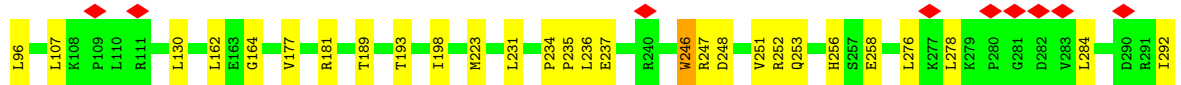
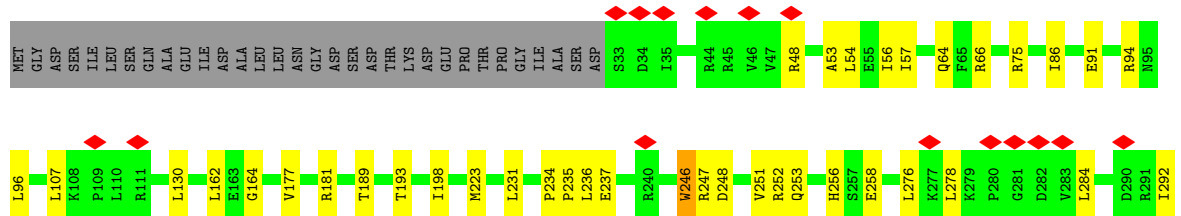
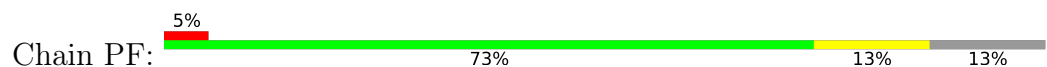
- Molecule 3: Flagellar motor switch protein FlIM



- Molecule 3: Flagellar motor switch protein FlIM

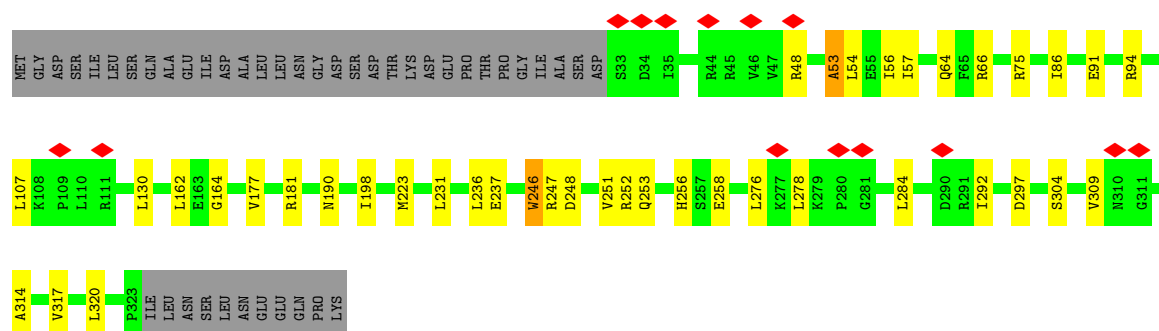


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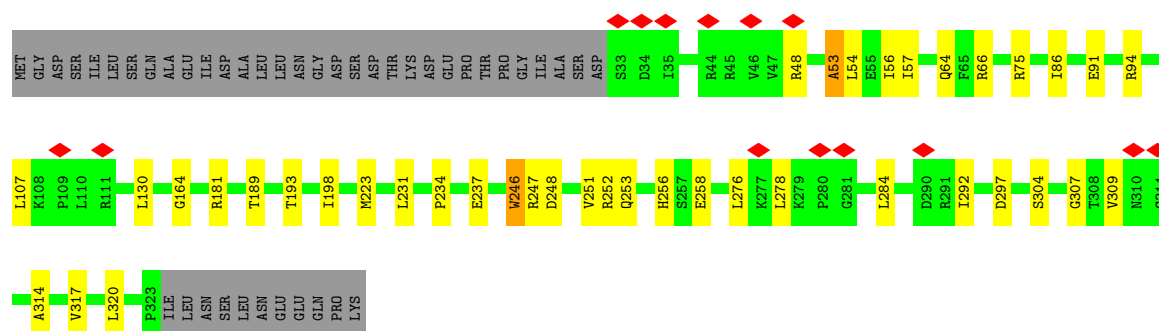
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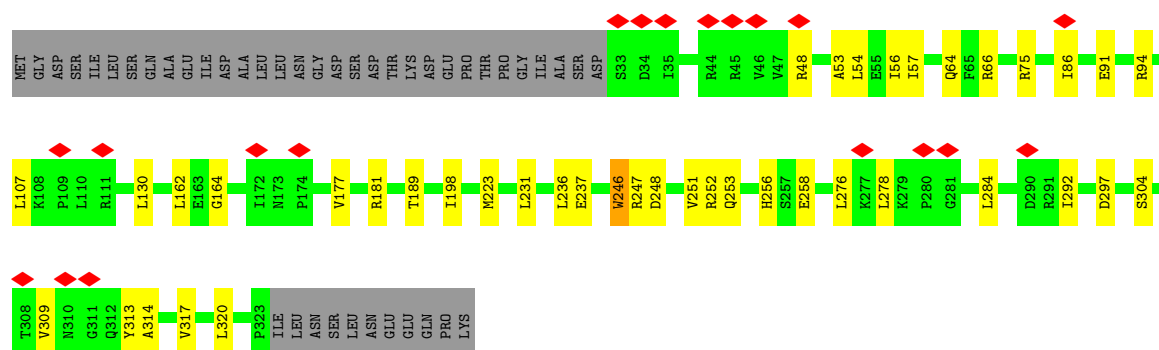
• Molecule 3: Flagellar motor switch protein FlIM

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• Molecule 3: Flagellar motor switch protein FlIM

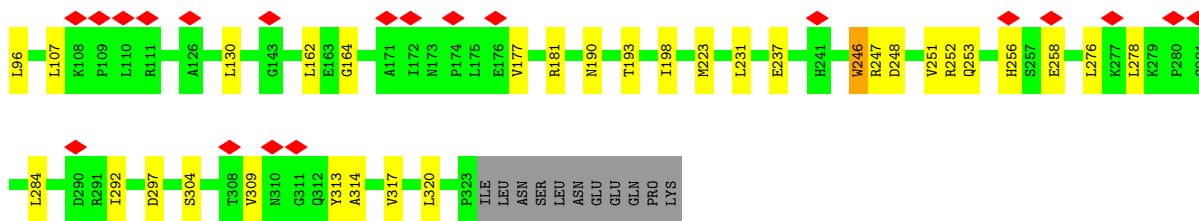
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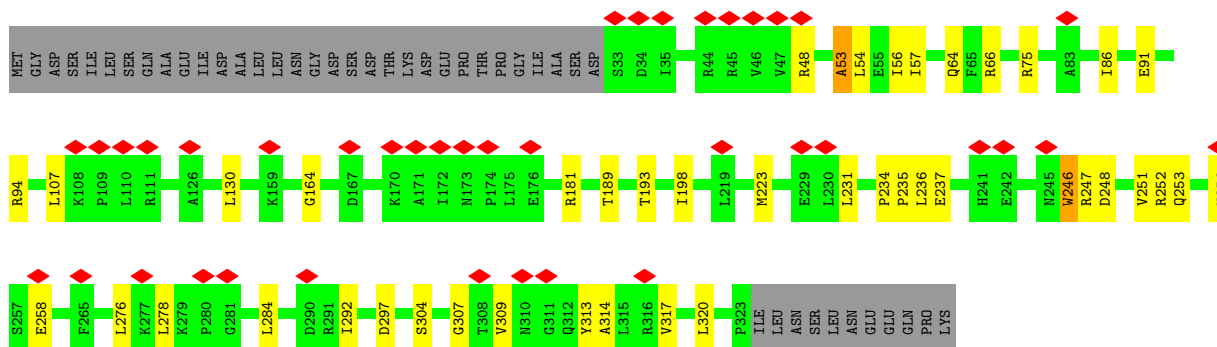
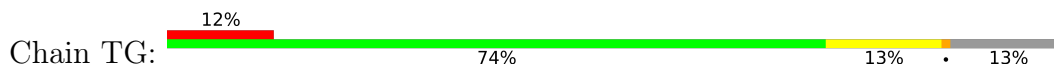
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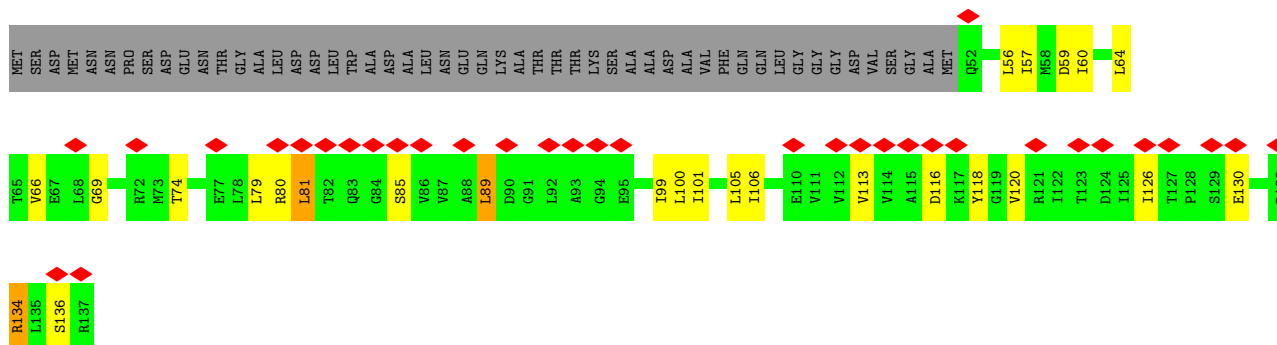
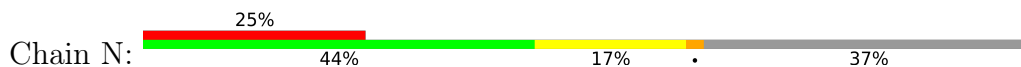




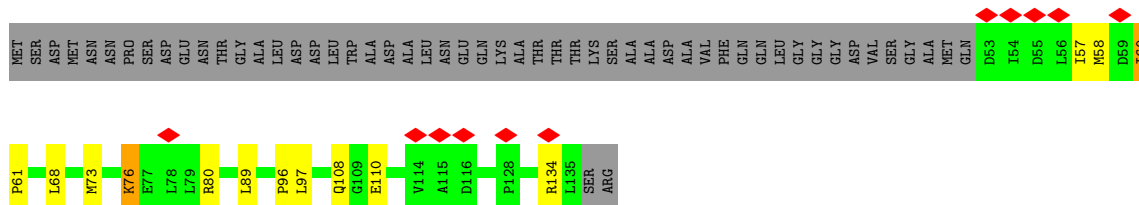
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• Molecule 4: Flagellar motor switch protein FliN

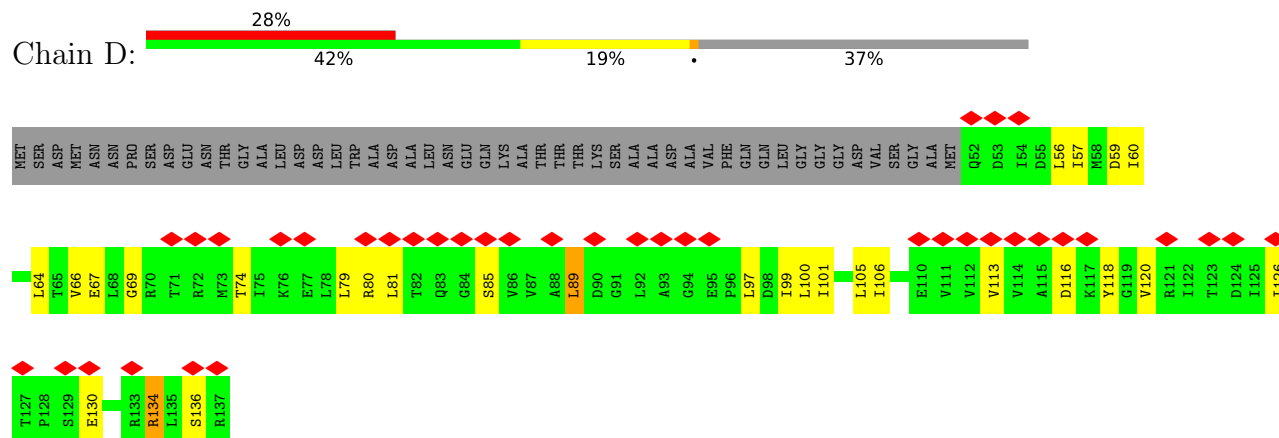


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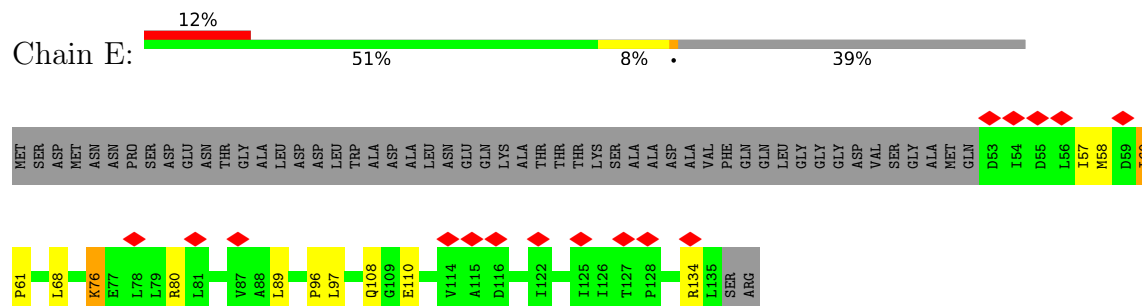


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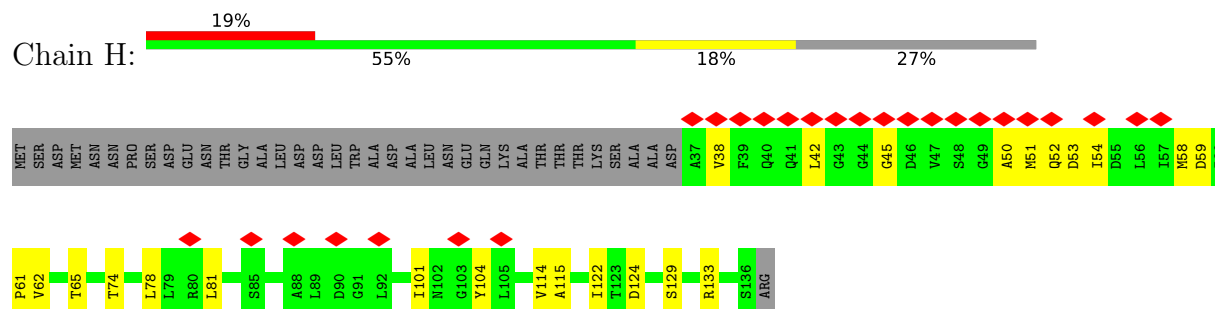
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- Molecule 4: Flagellar motor switch protein FliN

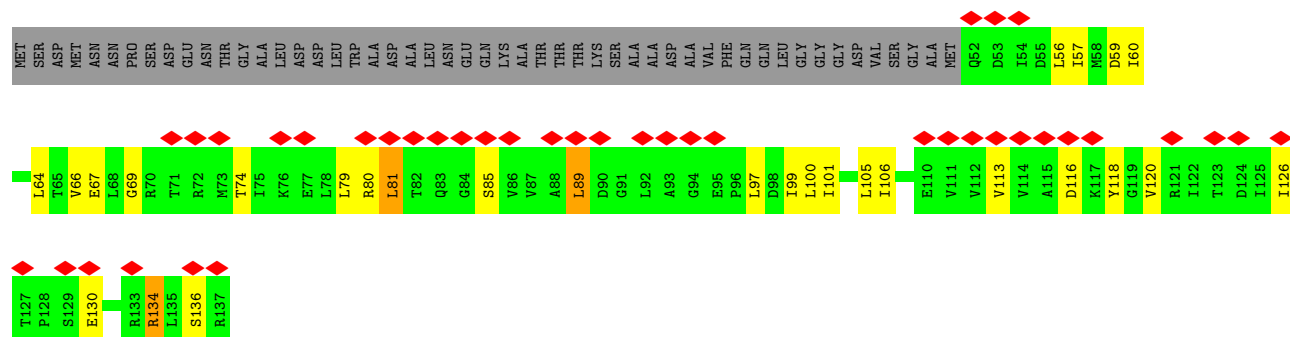


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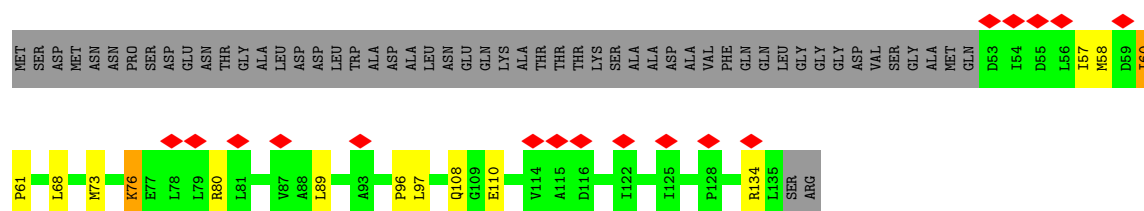


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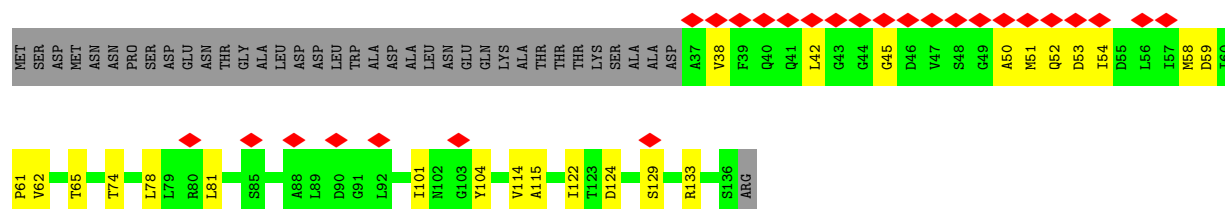




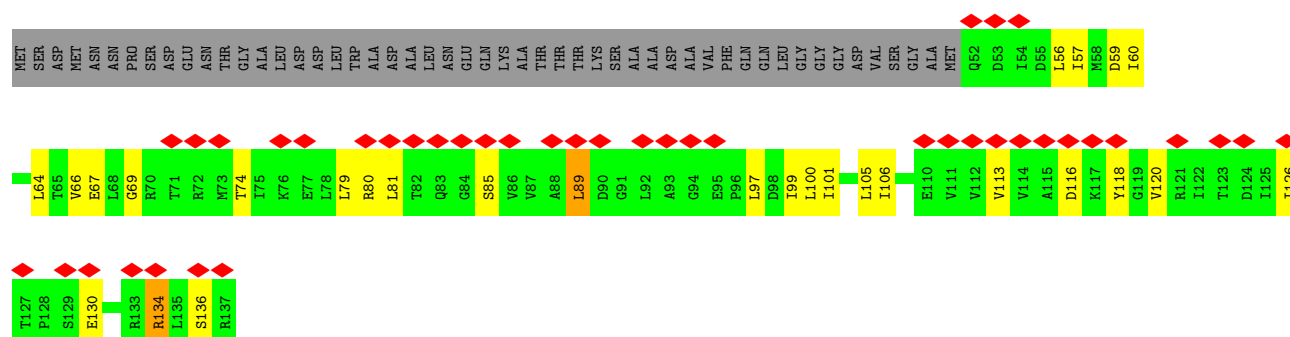
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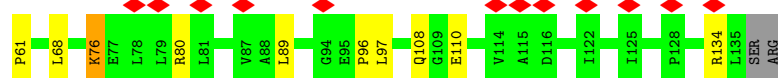
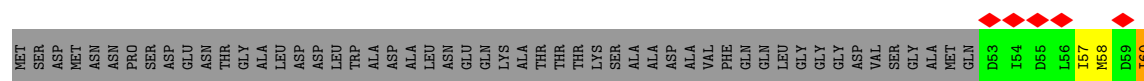


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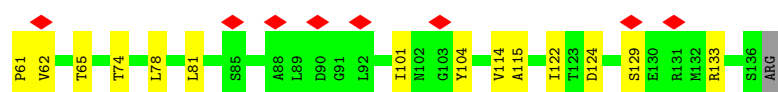
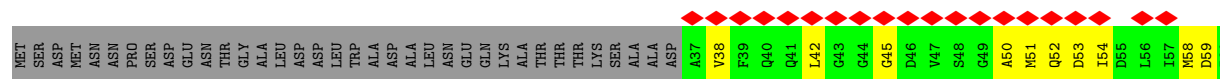


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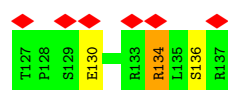
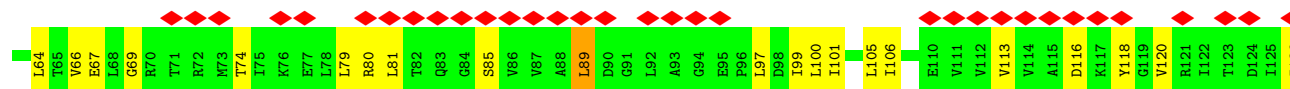
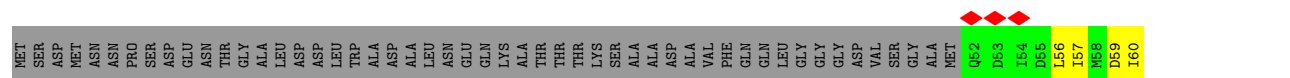




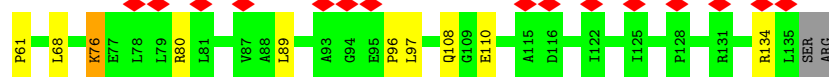
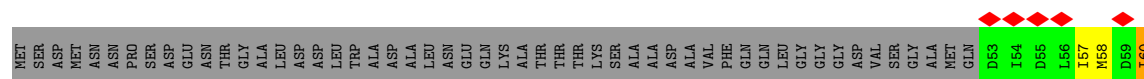
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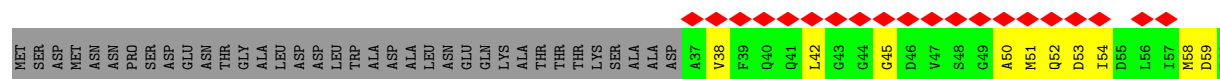
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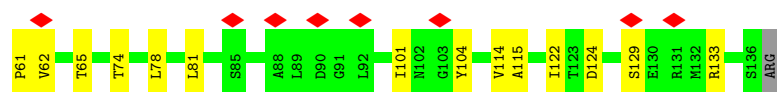


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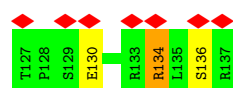
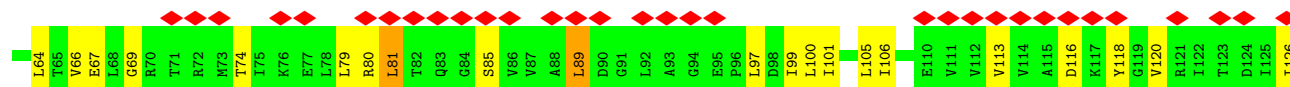
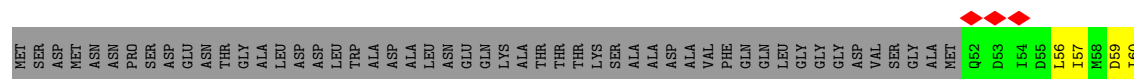
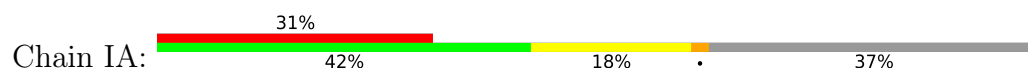


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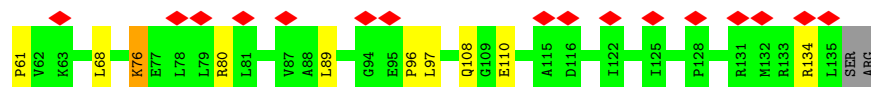
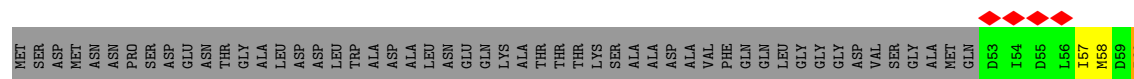




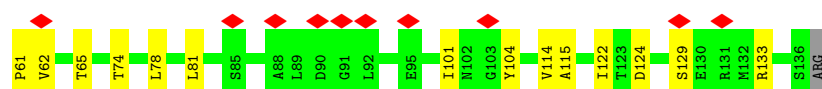
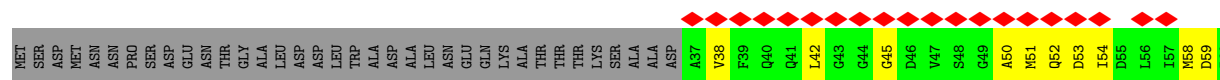
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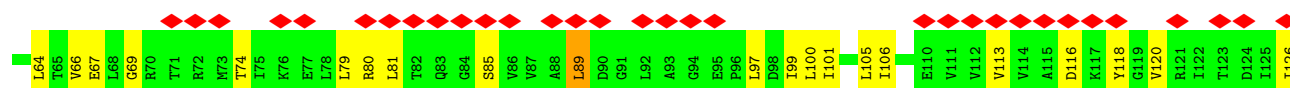
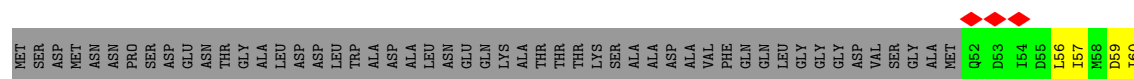
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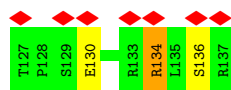


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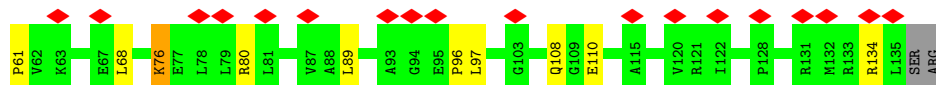
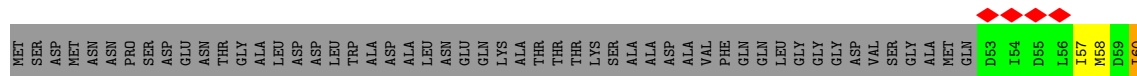


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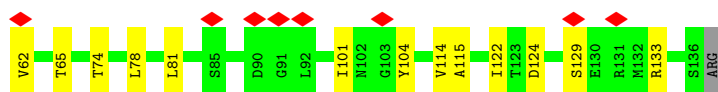
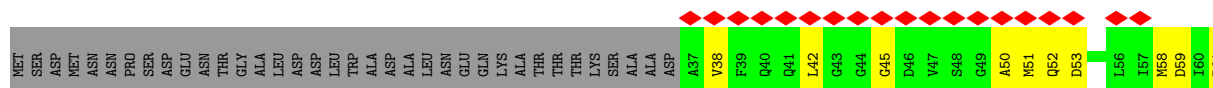




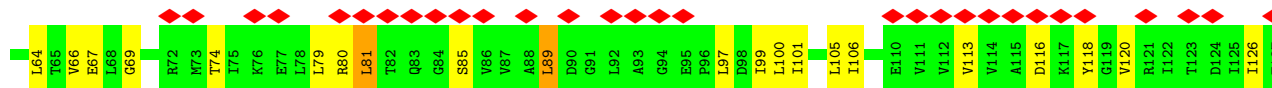
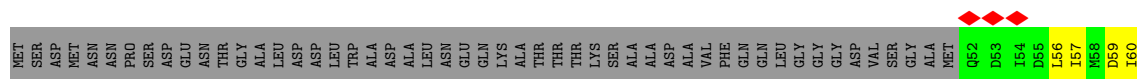
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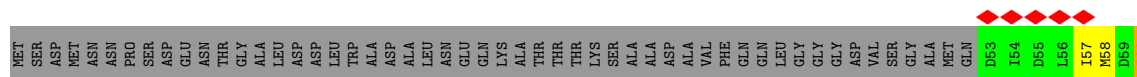
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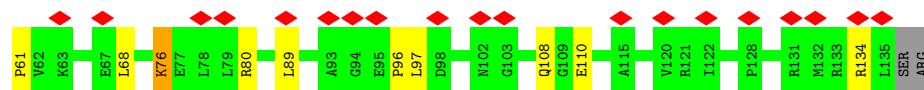


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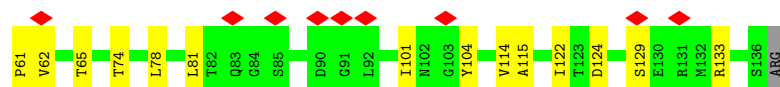
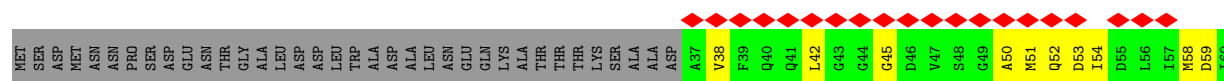


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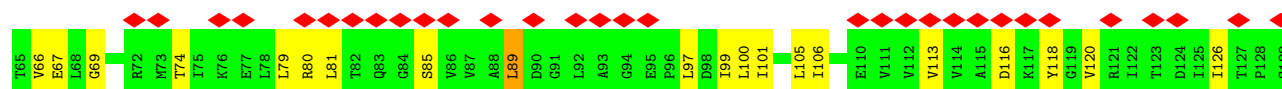
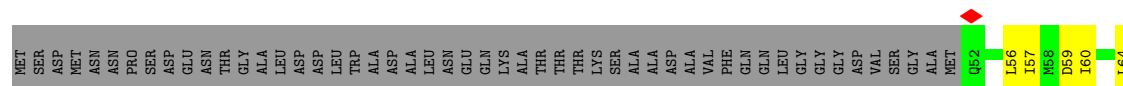
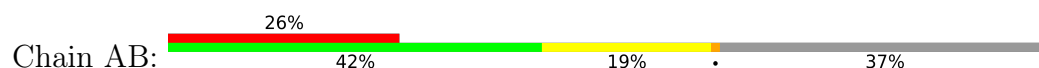




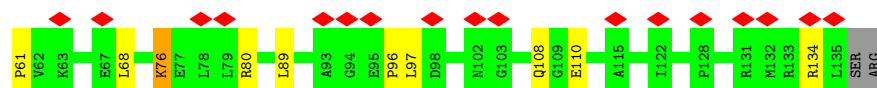
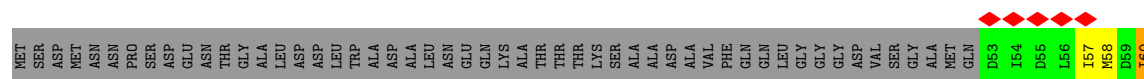
- Molecule 4: Flagellar motor switch protein FliN



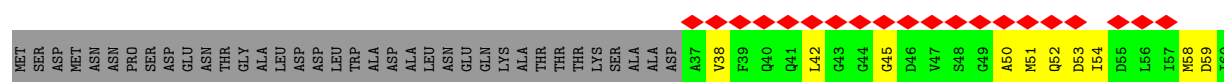
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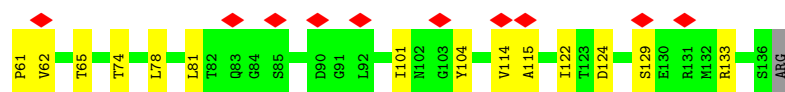


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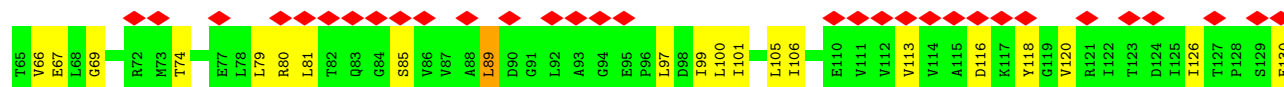
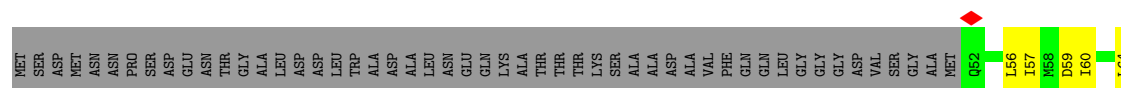
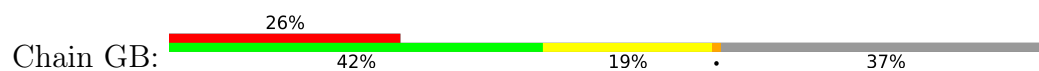


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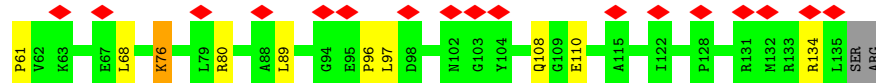
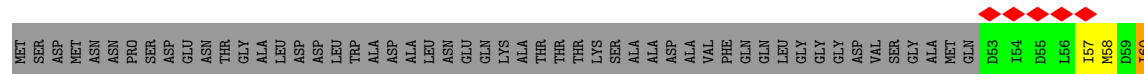




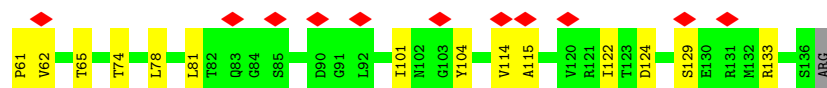
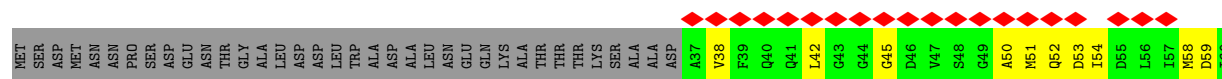
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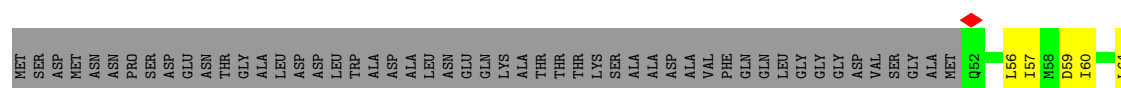
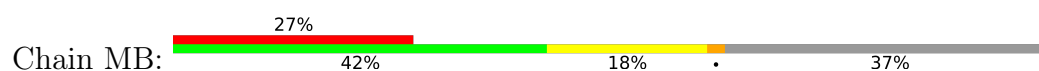
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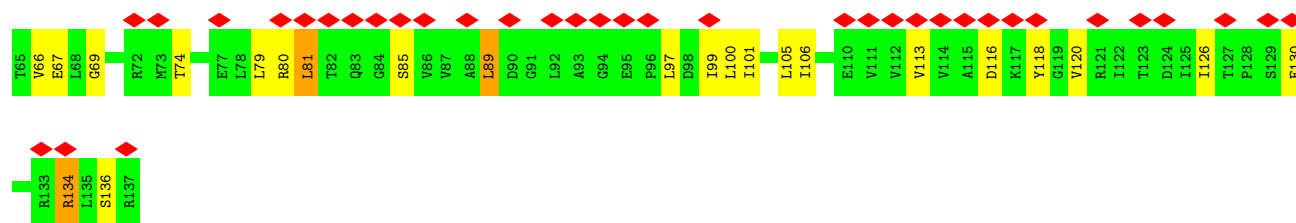


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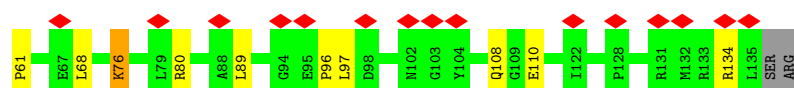
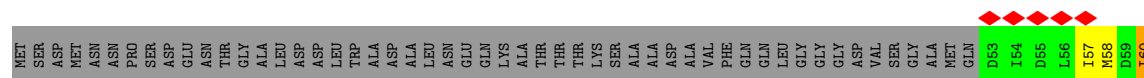


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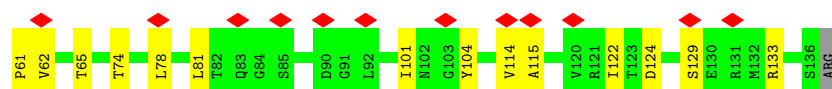
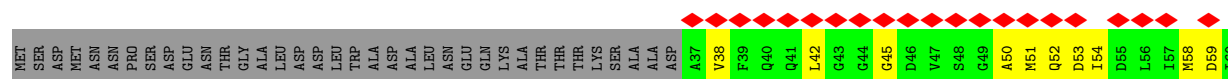




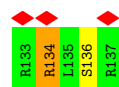
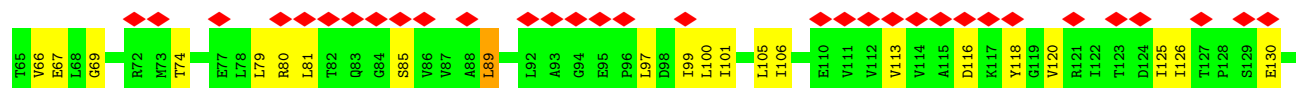
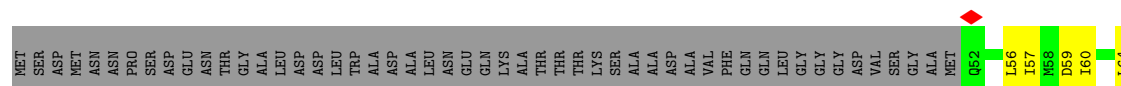
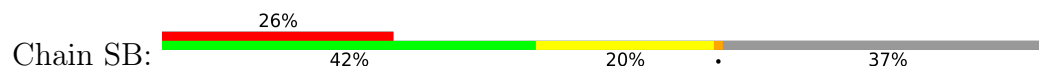
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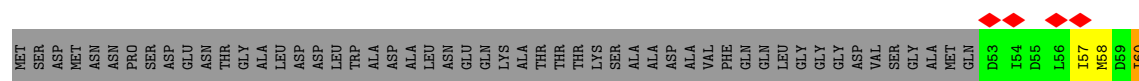


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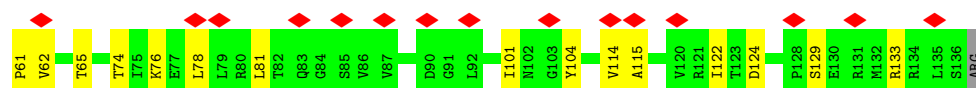
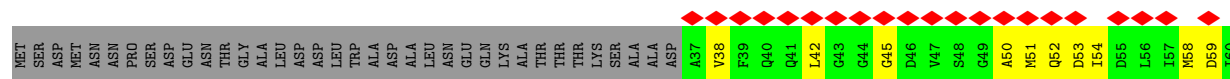


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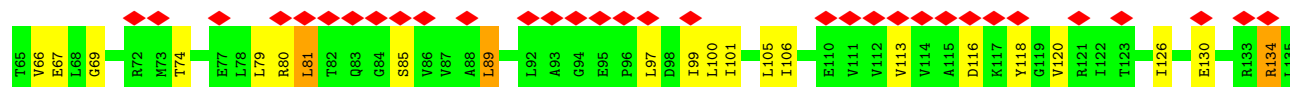
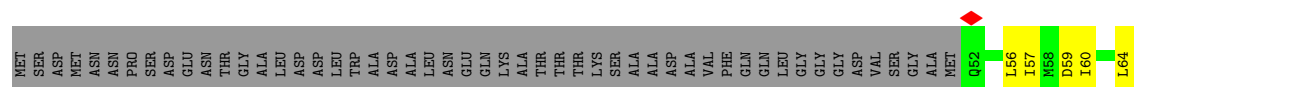
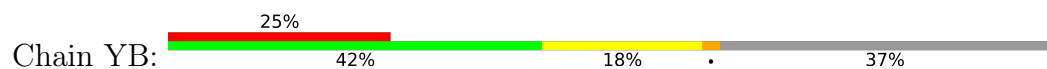




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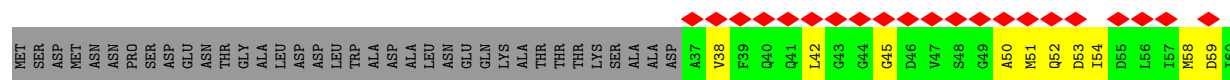
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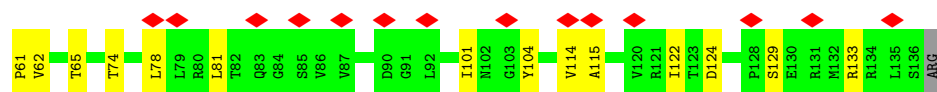


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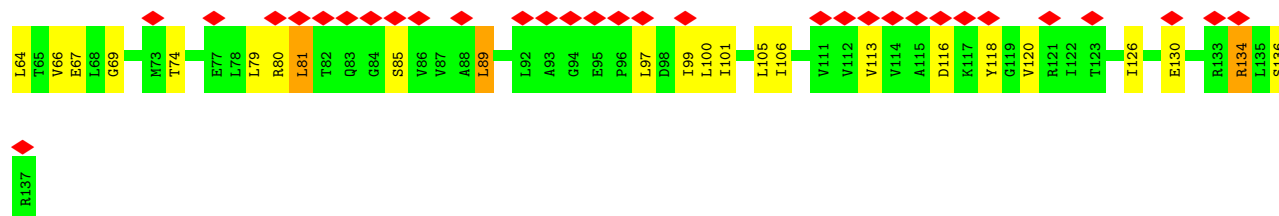
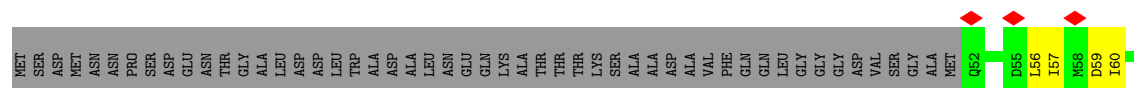
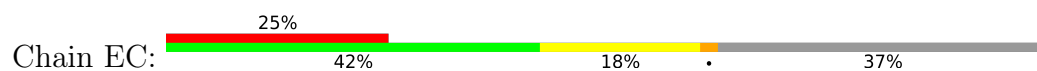


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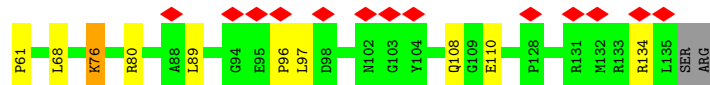
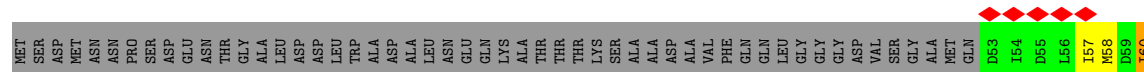




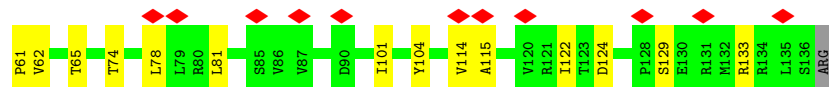
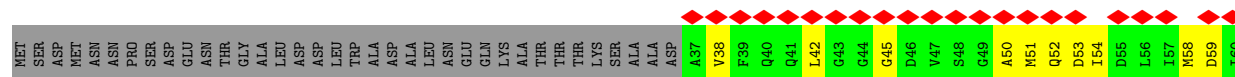
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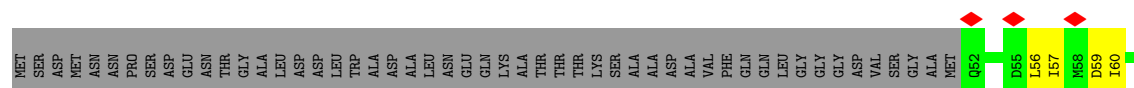
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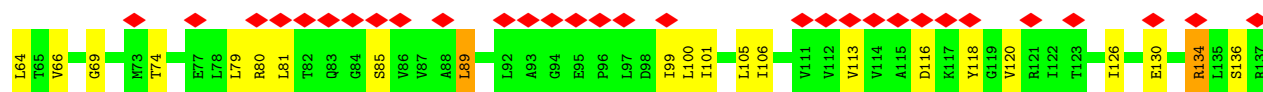


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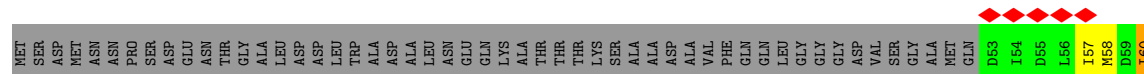


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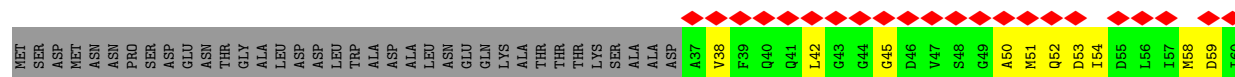




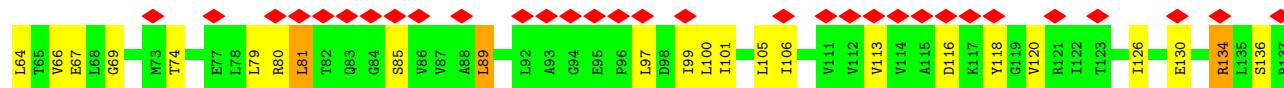
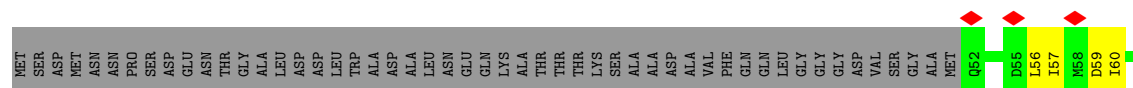
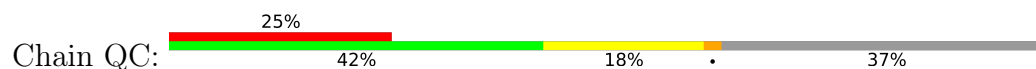
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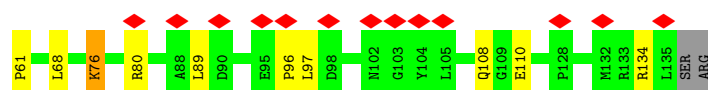
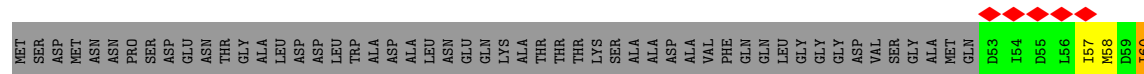
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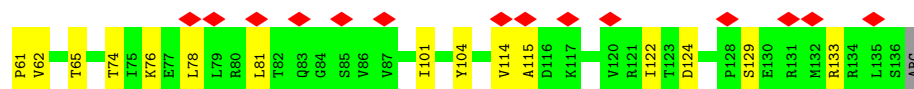
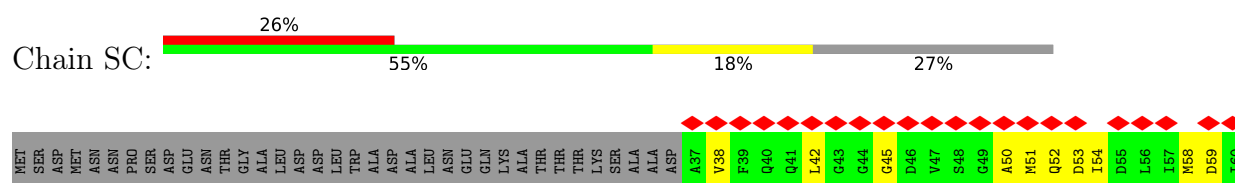
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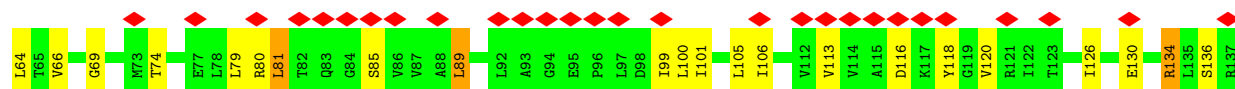
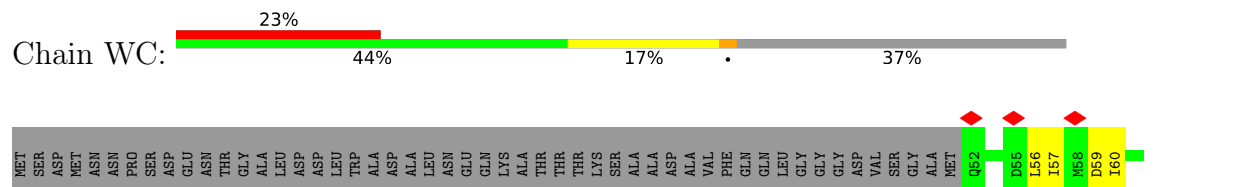
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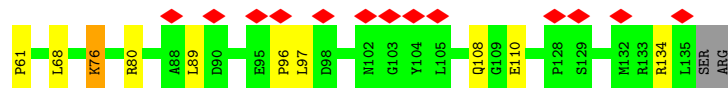
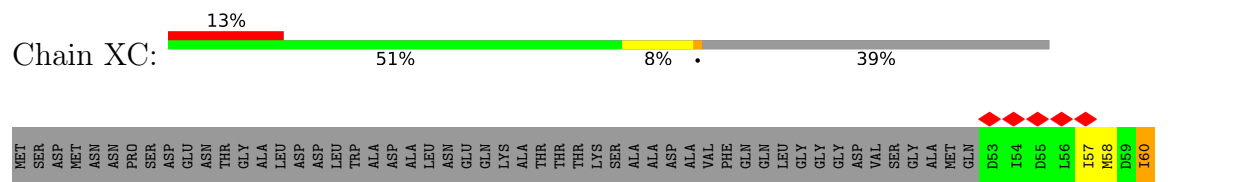
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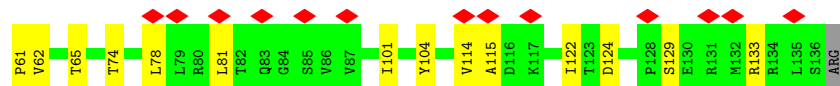
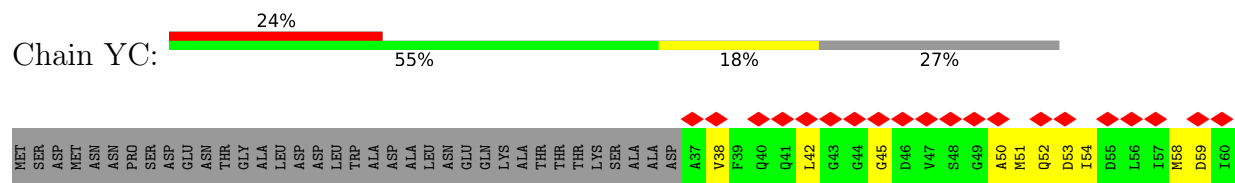
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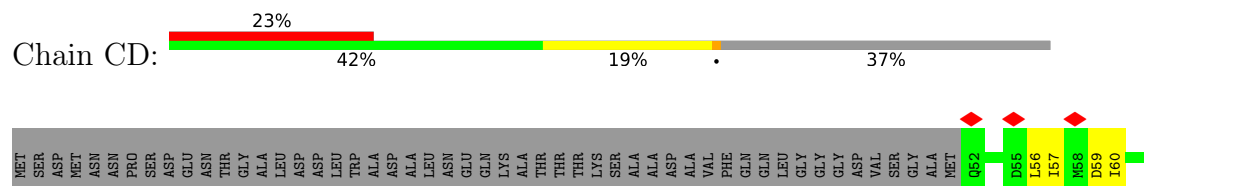
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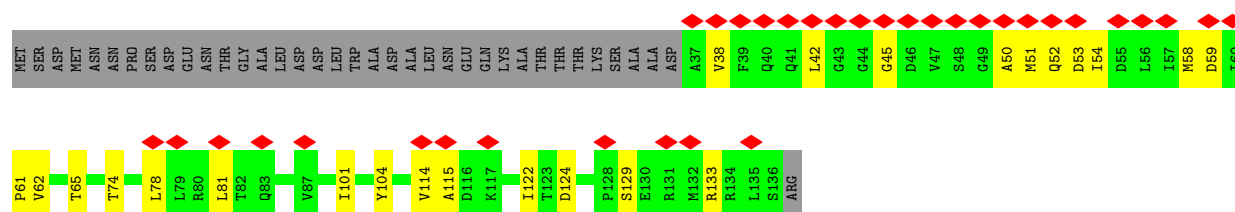


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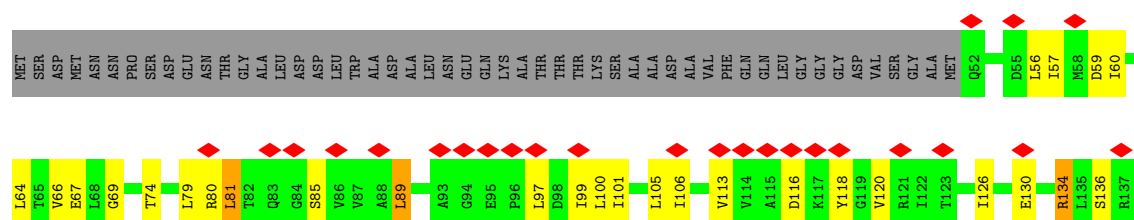
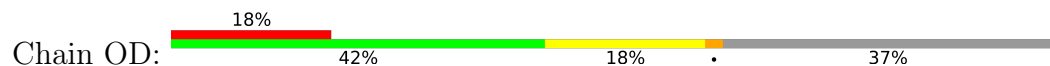


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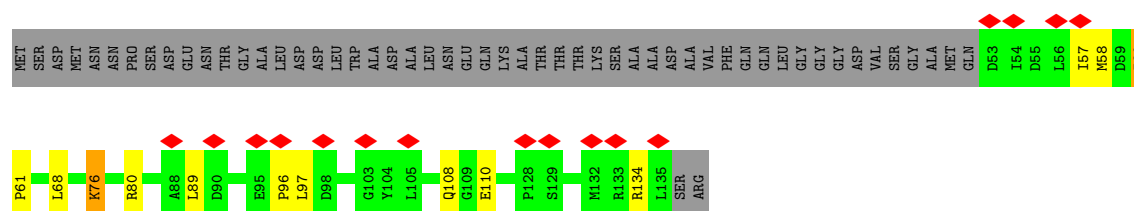




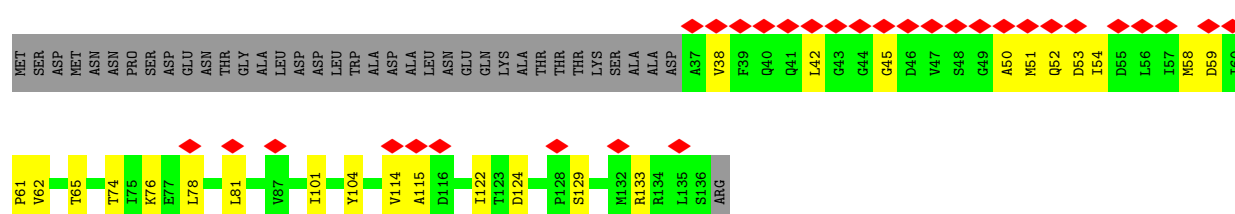
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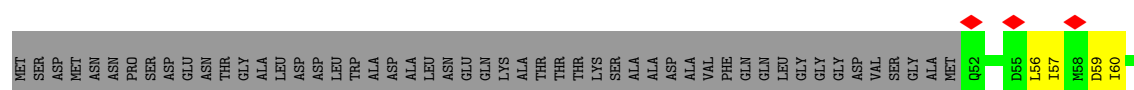
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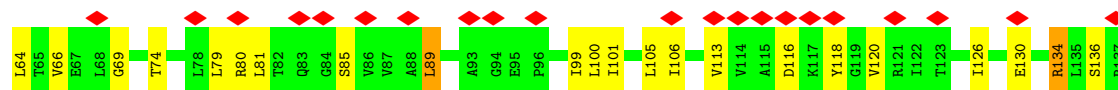


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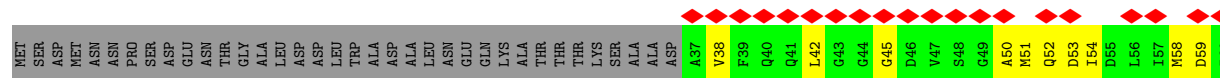




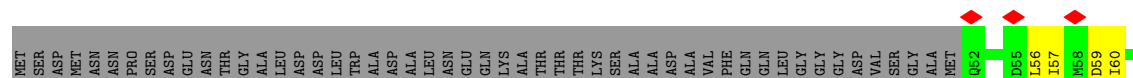
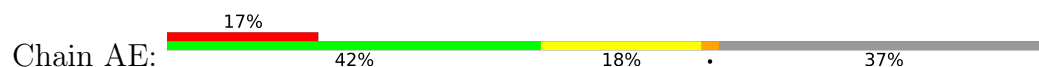
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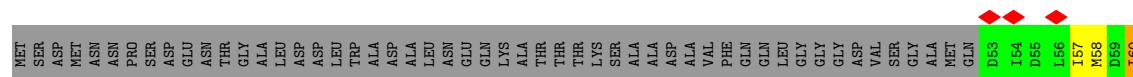
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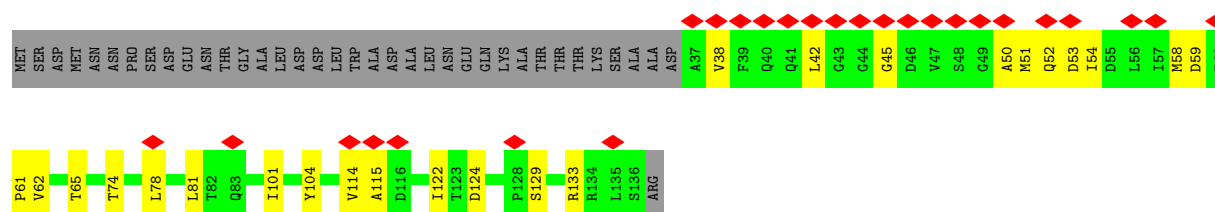


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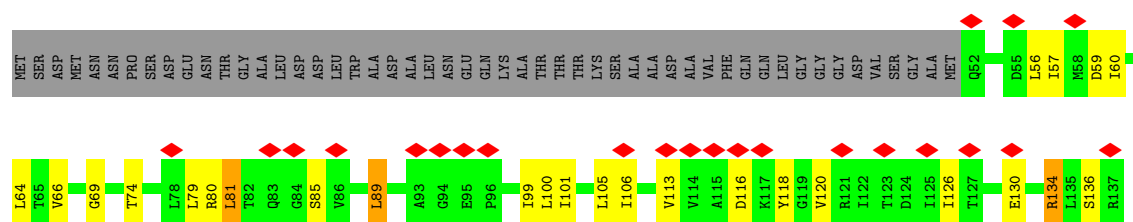


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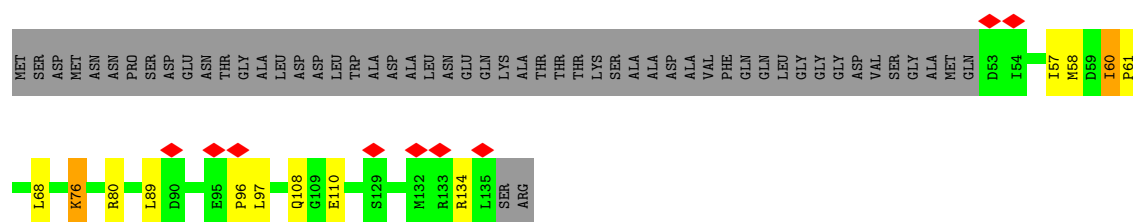




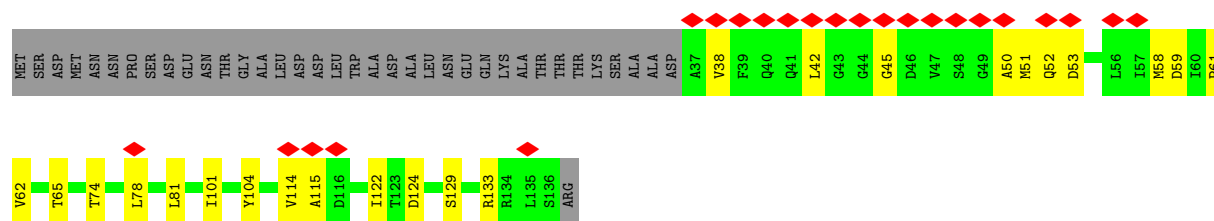
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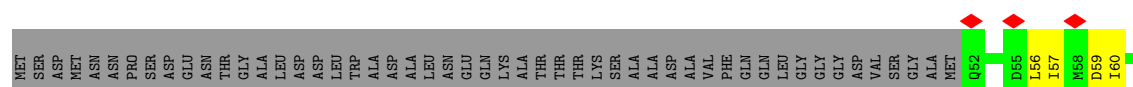
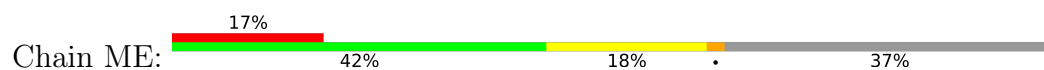
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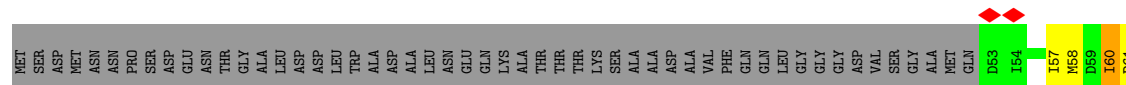


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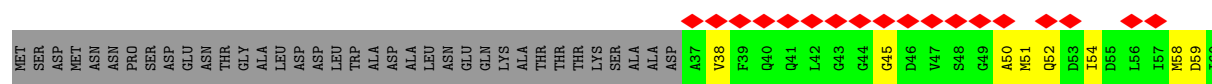




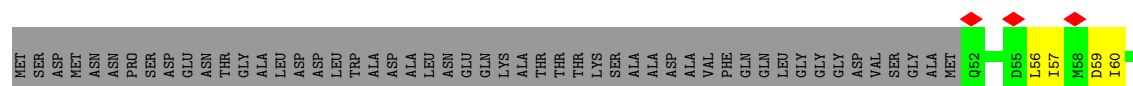
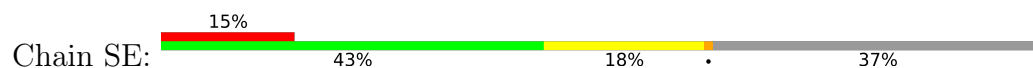
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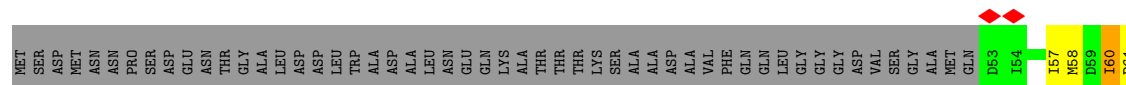
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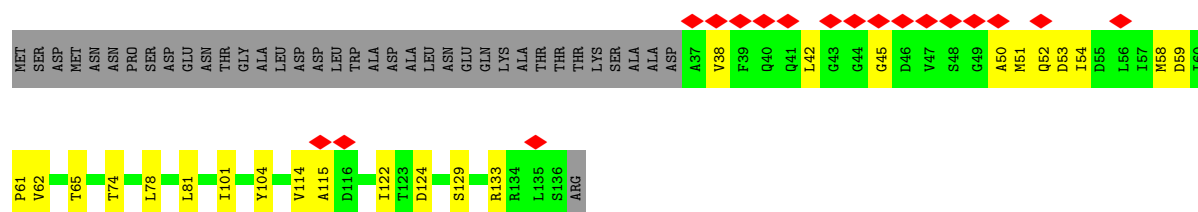
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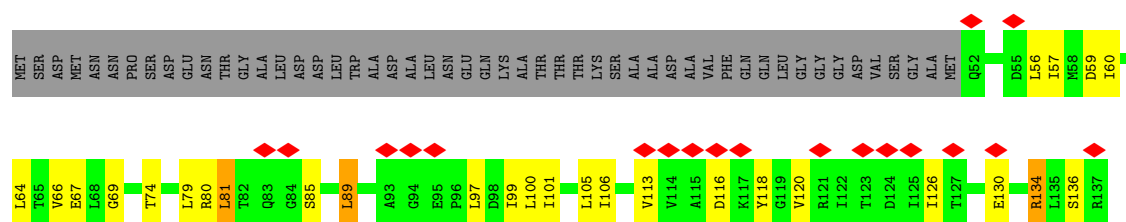
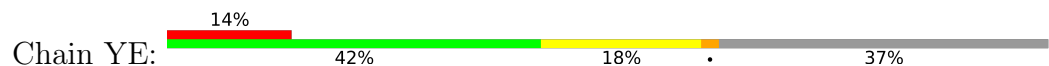
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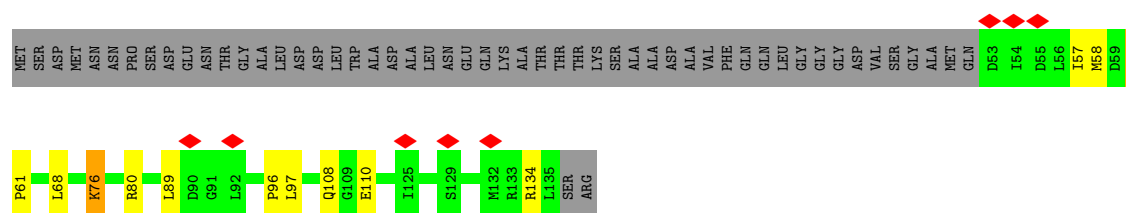
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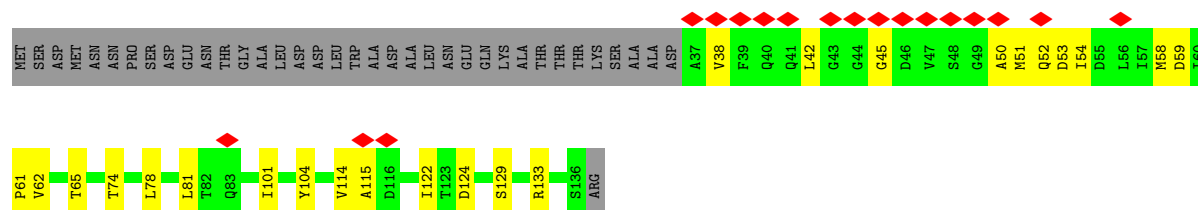
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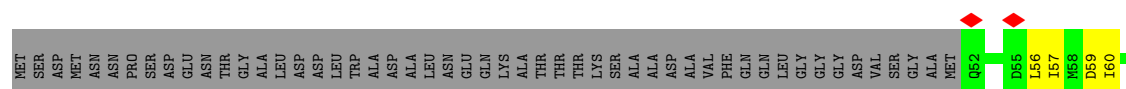
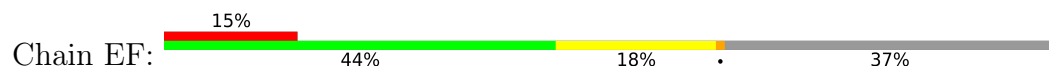
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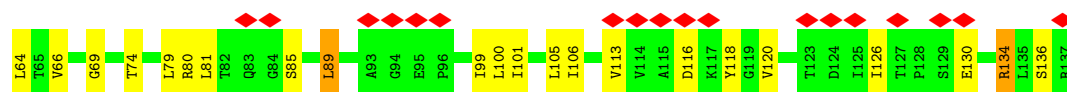


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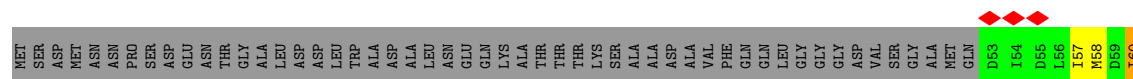


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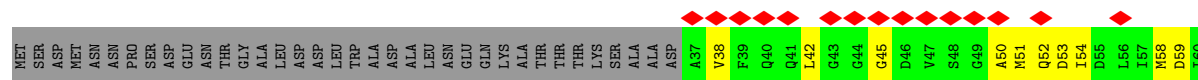




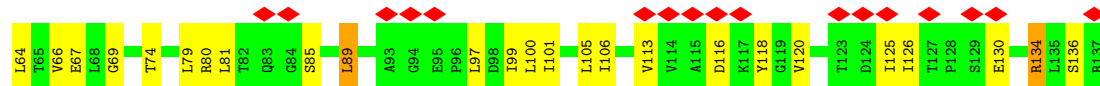
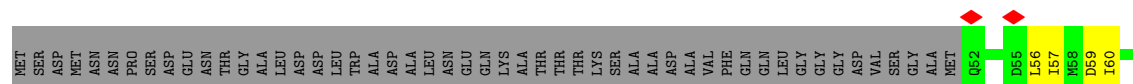
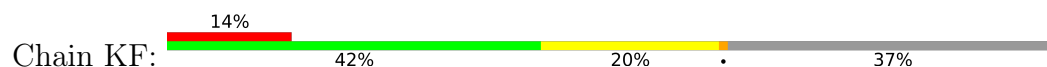
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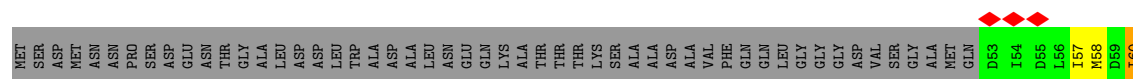
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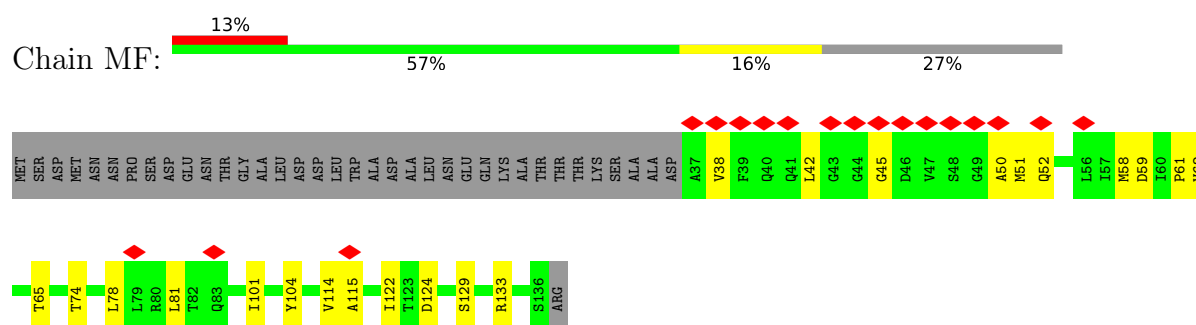
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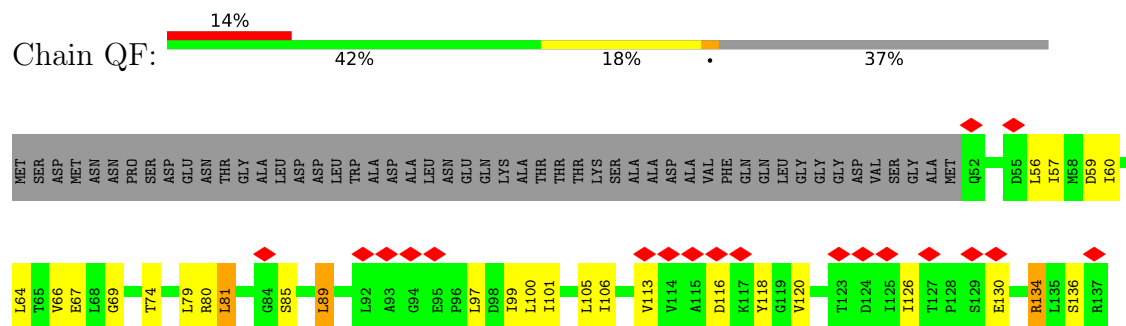
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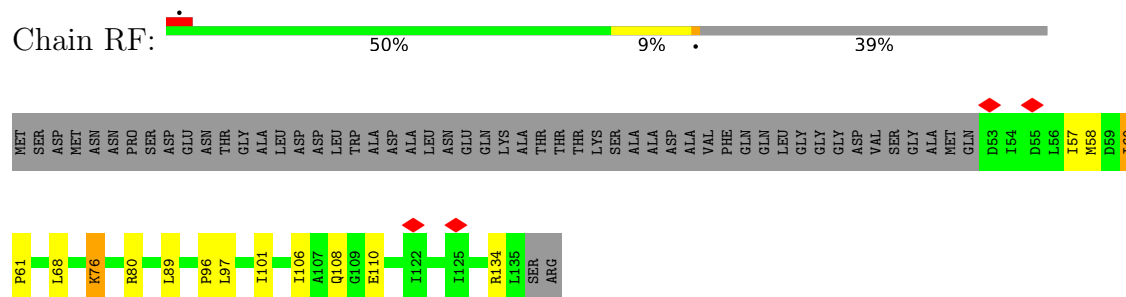
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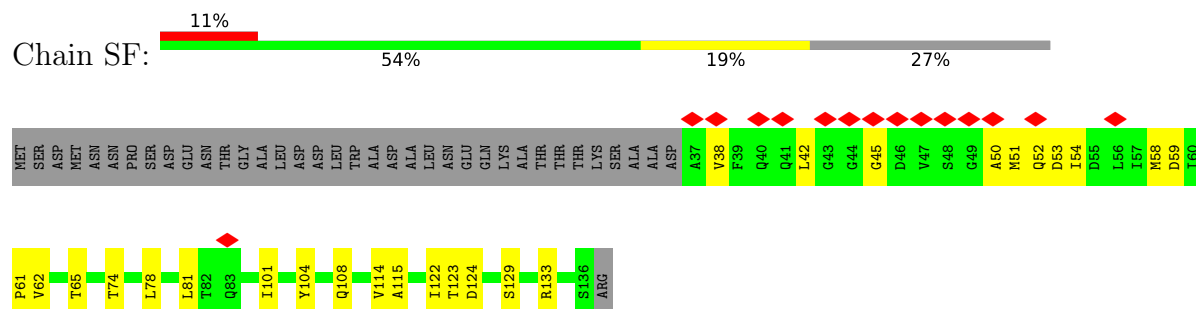
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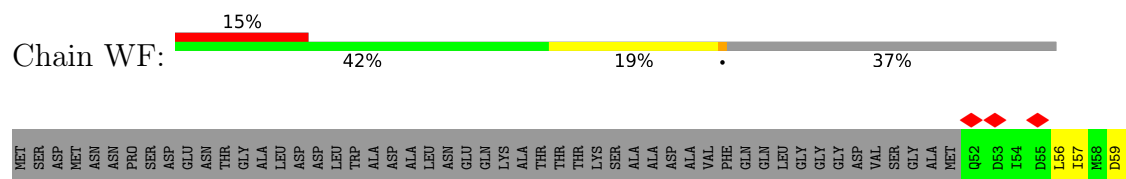
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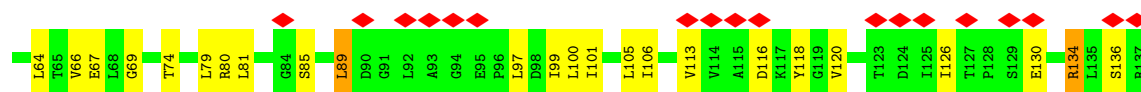


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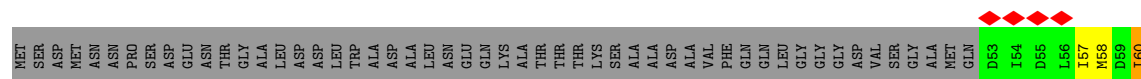


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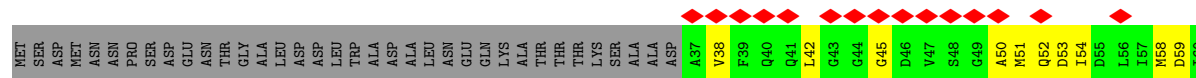




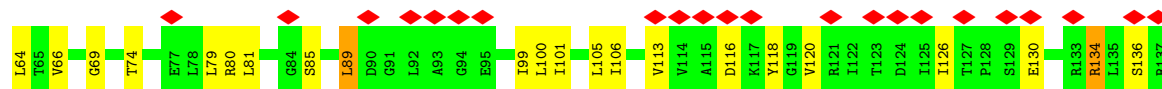
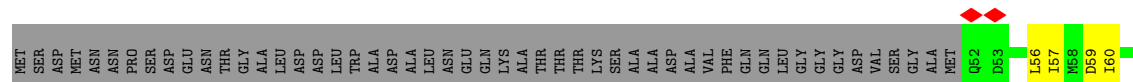
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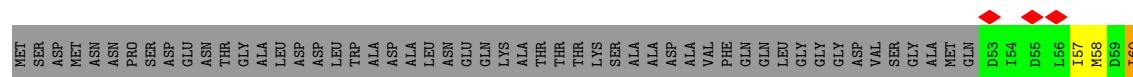
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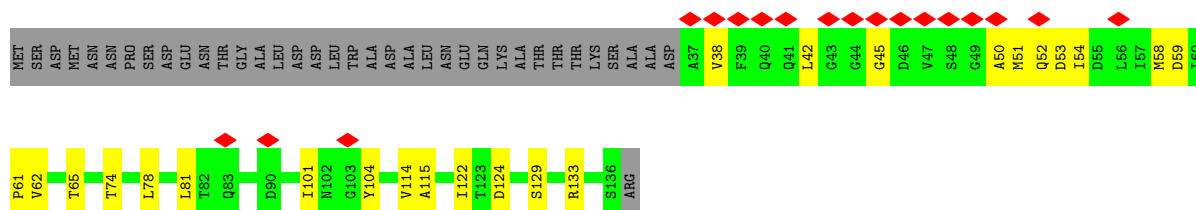
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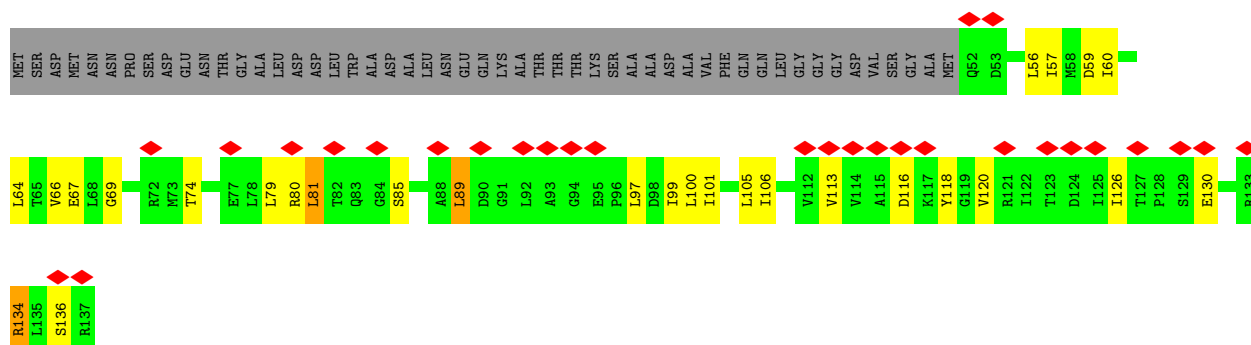
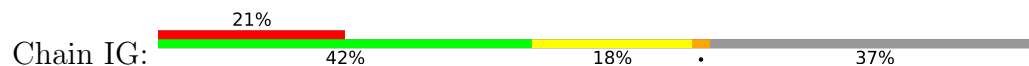
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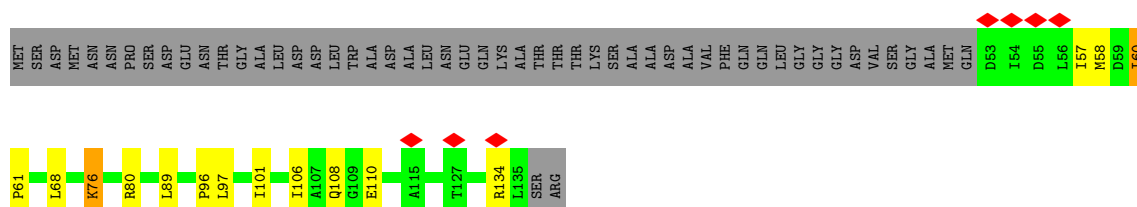
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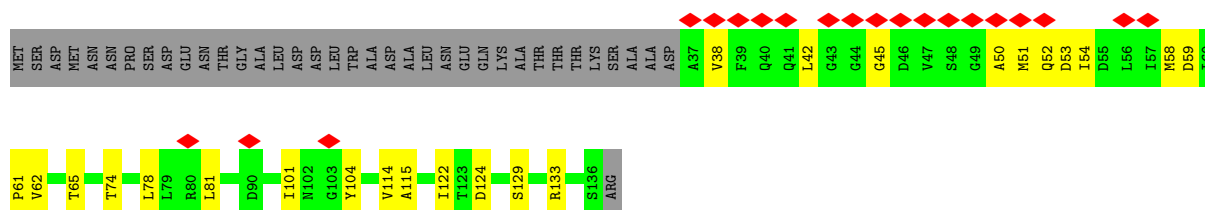
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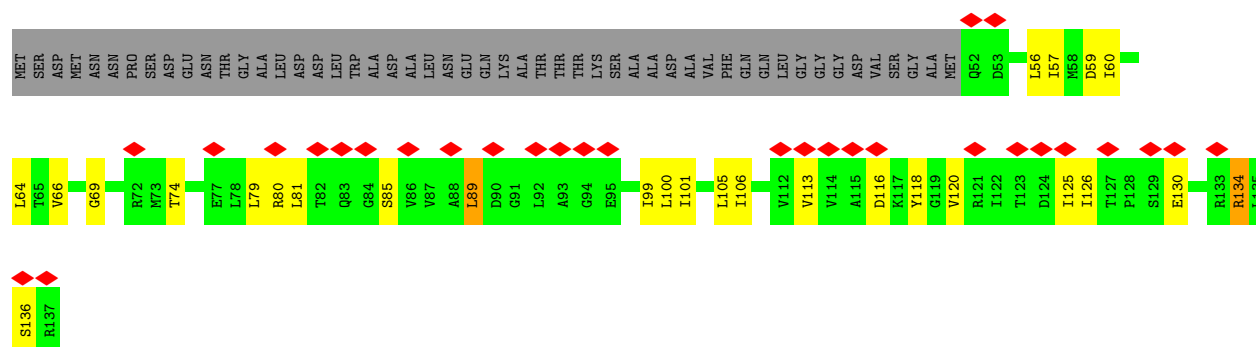


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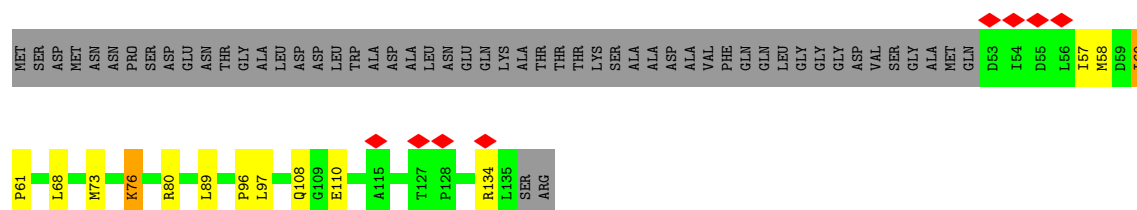


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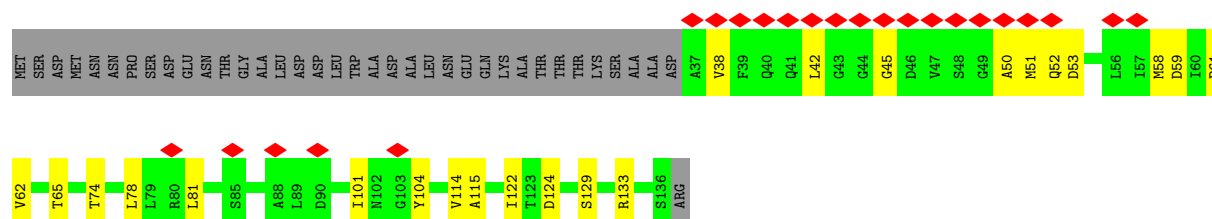




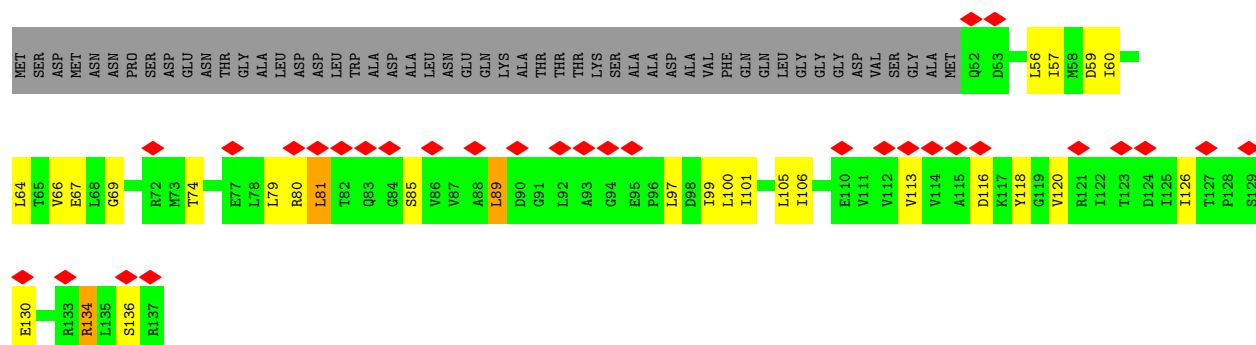
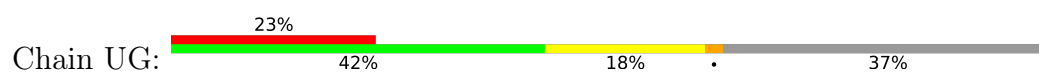
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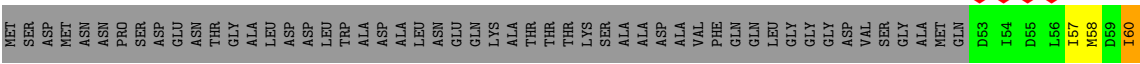
- Molecule 4: Flagellar motor switch protein FliN



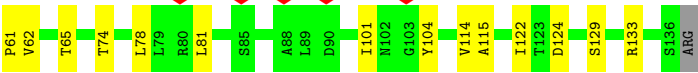
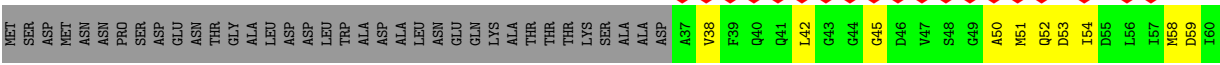
- Molecule 4: Flagellar motor switch protein FliN



- 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	20863	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 ($e^-/\text{\AA}^2$)	51.557	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	0.322	Depositor
Minimum map value	-0.054	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.135	Depositor
Map size (Å)	1044.48, 1044.48, 1044.48	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.57	0/228	0.87	0/317
1	BC	0.57	0/228	0.87	0/317
1	BF	0.57	0/228	0.87	0/317
1	DB	0.57	0/228	0.87	0/317
1	DE	0.57	0/228	0.87	0/317
1	F	0.57	0/228	0.87	0/317
1	FA	0.57	0/228	0.87	0/317
1	FD	0.57	0/228	0.87	0/317
1	FG	0.57	0/228	0.87	0/317
1	HC	0.57	0/228	0.87	0/317
1	HF	0.57	0/228	0.87	0/317
1	I	0.57	0/228	0.87	0/317
1	JB	0.57	0/228	0.87	0/317
1	JE	0.57	0/228	0.87	0/317
1	LA	0.57	0/228	0.87	0/317
1	LD	0.57	0/228	0.87	0/317
1	LG	0.57	0/228	0.87	0/317
1	NC	0.56	0/228	0.87	0/317
1	NF	0.57	0/228	0.87	0/317
1	PB	0.57	0/228	0.87	0/317
1	PE	0.57	0/228	0.87	0/317
1	RA	0.57	0/228	0.87	0/317
1	RD	0.57	0/228	0.87	0/317
1	RG	0.57	0/228	0.87	0/317
1	S	0.57	0/228	0.87	0/317
1	TC	0.57	0/228	0.87	0/317
1	TF	0.57	0/228	0.87	0/317
1	VB	0.57	0/228	0.87	0/317
1	VE	0.57	0/228	0.87	0/317
1	XA	0.57	0/228	0.86	0/317
1	XD	0.57	0/228	0.87	0/317
1	Z	0.57	0/228	0.87	0/317
1	ZC	0.57	0/228	0.87	0/317
1	ZF	0.57	0/228	0.87	0/317

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AA	0.44	0/1902	0.68	3/2617 (0.1%)
2	AD	0.44	0/1902	0.68	3/2617 (0.1%)
2	AG	0.44	0/1902	0.68	3/2617 (0.1%)
2	B	0.44	0/1902	0.69	3/2617 (0.1%)
2	CC	0.44	0/1902	0.68	3/2617 (0.1%)
2	CF	0.45	0/1902	0.68	3/2617 (0.1%)
2	EB	0.44	0/1902	0.68	3/2617 (0.1%)
2	EE	0.45	0/1902	0.68	3/2617 (0.1%)
2	G	0.44	0/1902	0.68	3/2617 (0.1%)
2	GA	0.45	0/1902	0.68	3/2617 (0.1%)
2	GD	0.44	0/1902	0.68	3/2617 (0.1%)
2	GG	0.44	0/1902	0.68	3/2617 (0.1%)
2	IC	0.45	0/1902	0.69	3/2617 (0.1%)
2	IF	0.45	0/1902	0.68	3/2617 (0.1%)
2	J	0.44	0/1902	0.68	3/2617 (0.1%)
2	KB	0.45	0/1902	0.69	3/2617 (0.1%)
2	KE	0.45	0/1902	0.68	3/2617 (0.1%)
2	MA	0.44	0/1902	0.68	3/2617 (0.1%)
2	MD	0.45	0/1902	0.69	3/2617 (0.1%)
2	MG	0.45	0/1902	0.69	3/2617 (0.1%)
2	OC	0.44	0/1902	0.68	3/2617 (0.1%)
2	OF	0.44	0/1902	0.68	3/2617 (0.1%)
2	QB	0.44	0/1902	0.68	3/2617 (0.1%)
2	QE	0.45	0/1902	0.68	3/2617 (0.1%)
2	SA	0.45	0/1902	0.69	3/2617 (0.1%)
2	SD	0.45	0/1902	0.69	3/2617 (0.1%)
2	SG	0.45	0/1902	0.68	3/2617 (0.1%)
2	T	0.44	0/1902	0.68	3/2617 (0.1%)
2	UC	0.44	0/1902	0.68	3/2617 (0.1%)
2	UF	0.45	0/1902	0.68	3/2617 (0.1%)
2	WB	0.45	0/1902	0.68	3/2617 (0.1%)
2	WE	0.44	0/1902	0.68	3/2617 (0.1%)
2	YA	0.44	0/1902	0.68	3/2617 (0.1%)
2	YD	0.44	0/1902	0.68	3/2617 (0.1%)
3	BA	0.44	0/2339	0.77	5/3192 (0.2%)
3	BD	0.43	0/2339	0.76	5/3192 (0.2%)
3	BG	0.44	0/2339	0.76	5/3192 (0.2%)
3	C	0.44	0/2339	0.76	5/3192 (0.2%)
3	DC	0.44	0/2339	0.76	4/3192 (0.1%)
3	DF	0.44	0/2339	0.76	4/3192 (0.1%)
3	FB	0.44	0/2339	0.76	4/3192 (0.1%)
3	FE	0.44	0/2339	0.76	5/3192 (0.2%)
3	HA	0.44	0/2339	0.76	5/3192 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	HD	0.44	0/2339	0.76	5/3192 (0.2%)
3	HG	0.44	0/2339	0.76	4/3192 (0.1%)
3	JC	0.44	0/2339	0.76	4/3192 (0.1%)
3	JF	0.44	0/2339	0.76	5/3192 (0.2%)
3	K	0.44	0/2339	0.76	5/3192 (0.2%)
3	LB	0.44	0/2339	0.76	4/3192 (0.1%)
3	LE	0.44	0/2339	0.76	5/3192 (0.2%)
3	M	0.44	0/2339	0.76	4/3192 (0.1%)
3	NA	0.44	0/2339	0.76	5/3192 (0.2%)
3	ND	0.44	0/2339	0.76	4/3192 (0.1%)
3	NG	0.44	0/2339	0.76	5/3192 (0.2%)
3	PC	0.44	0/2339	0.76	5/3192 (0.2%)
3	PF	0.44	0/2339	0.76	4/3192 (0.1%)
3	RB	0.44	0/2339	0.76	5/3192 (0.2%)
3	RE	0.44	0/2339	0.76	5/3192 (0.2%)
3	TA	0.44	0/2339	0.76	5/3192 (0.2%)
3	TD	0.44	0/2339	0.76	5/3192 (0.2%)
3	TG	0.44	0/2339	0.76	5/3192 (0.2%)
3	V	0.44	0/2339	0.76	5/3192 (0.2%)
3	VC	0.44	0/2339	0.76	4/3192 (0.1%)
3	VF	0.44	0/2339	0.76	5/3192 (0.2%)
3	XB	0.44	0/2339	0.77	5/3192 (0.2%)
3	XE	0.44	0/2339	0.77	5/3192 (0.2%)
3	ZA	0.44	0/2339	0.76	5/3192 (0.2%)
3	ZD	0.44	0/2339	0.76	4/3192 (0.1%)
4	AB	0.66	0/653	1.11	5/885 (0.6%)
4	AC	0.44	0/751	0.95	4/1015 (0.4%)
4	AE	0.66	0/653	1.11	5/885 (0.6%)
4	AF	0.44	0/751	0.95	4/1015 (0.4%)
4	BB	0.63	0/633	1.17	5/858 (0.6%)
4	BE	0.63	0/633	1.18	5/858 (0.6%)
4	CA	0.66	0/653	1.11	5/885 (0.6%)
4	CB	0.44	0/751	0.95	4/1015 (0.4%)
4	CD	0.65	0/653	1.11	5/885 (0.6%)
4	CE	0.44	0/751	0.96	4/1015 (0.4%)
4	CG	0.66	0/653	1.11	5/885 (0.6%)
4	D	0.66	0/653	1.11	4/885 (0.5%)
4	DA	0.63	0/633	1.17	5/858 (0.6%)
4	DD	0.63	0/633	1.17	5/858 (0.6%)
4	DG	0.63	0/633	1.17	5/858 (0.6%)
4	E	0.63	0/633	1.18	5/858 (0.6%)
4	EA	0.44	0/751	0.96	4/1015 (0.4%)
4	EC	0.65	0/653	1.11	5/885 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ED	0.44	0/751	0.95	4/1015 (0.4%)
4	EF	0.66	0/653	1.11	5/885 (0.6%)
4	EG	0.44	0/751	0.95	4/1015 (0.4%)
4	FC	0.63	0/633	1.17	5/858 (0.6%)
4	FF	0.63	0/633	1.17	5/858 (0.6%)
4	GB	0.66	0/653	1.11	5/885 (0.6%)
4	GC	0.44	0/751	0.95	4/1015 (0.4%)
4	GE	0.65	0/653	1.11	5/885 (0.6%)
4	GF	0.44	0/751	0.95	4/1015 (0.4%)
4	H	0.44	0/751	0.95	4/1015 (0.4%)
4	HB	0.63	0/633	1.17	5/858 (0.6%)
4	HE	0.63	0/633	1.18	5/858 (0.6%)
4	IA	0.65	0/653	1.11	5/885 (0.6%)
4	IB	0.44	0/751	0.95	4/1015 (0.4%)
4	ID	0.65	0/653	1.11	5/885 (0.6%)
4	IE	0.44	0/751	0.95	4/1015 (0.4%)
4	IG	0.65	0/653	1.11	5/885 (0.6%)
4	JA	0.63	0/633	1.18	5/858 (0.6%)
4	JD	0.63	0/633	1.18	5/858 (0.6%)
4	JG	0.63	0/633	1.18	5/858 (0.6%)
4	KA	0.44	0/751	0.95	4/1015 (0.4%)
4	KC	0.65	0/653	1.11	5/885 (0.6%)
4	KD	0.44	0/751	0.95	4/1015 (0.4%)
4	KF	0.65	0/653	1.11	5/885 (0.6%)
4	KG	0.44	0/751	0.95	4/1015 (0.4%)
4	L	0.65	0/653	1.11	5/885 (0.6%)
4	LC	0.64	0/633	1.17	5/858 (0.6%)
4	LF	0.63	0/633	1.17	5/858 (0.6%)
4	MB	0.65	0/653	1.11	5/885 (0.6%)
4	MC	0.44	0/751	0.95	4/1015 (0.4%)
4	ME	0.65	0/653	1.11	5/885 (0.6%)
4	MF	0.44	0/751	0.95	4/1015 (0.4%)
4	N	0.65	0/653	1.11	5/885 (0.6%)
4	NB	0.63	0/633	1.17	5/858 (0.6%)
4	NE	0.63	0/633	1.18	5/858 (0.6%)
4	O	0.64	0/633	1.17	5/858 (0.6%)
4	OA	0.65	0/653	1.11	5/885 (0.6%)
4	OB	0.44	0/751	0.95	4/1015 (0.4%)
4	OD	0.66	0/653	1.11	5/885 (0.6%)
4	OE	0.44	0/751	0.95	4/1015 (0.4%)
4	OG	0.65	0/653	1.11	5/885 (0.6%)
4	P	0.63	0/633	1.17	5/858 (0.6%)
4	PA	0.63	0/633	1.18	5/858 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	PD	0.63	0/633	1.17	5/858 (0.6%)
4	PG	0.63	0/633	1.18	5/858 (0.6%)
4	Q	0.44	0/751	0.96	4/1015 (0.4%)
4	QA	0.44	0/751	0.95	4/1015 (0.4%)
4	QC	0.66	0/653	1.11	5/885 (0.6%)
4	QD	0.44	0/751	0.95	4/1015 (0.4%)
4	QF	0.66	0/653	1.11	5/885 (0.6%)
4	QG	0.44	0/751	0.95	4/1015 (0.4%)
4	R	0.44	0/751	0.95	4/1015 (0.4%)
4	RC	0.63	0/633	1.18	5/858 (0.6%)
4	RF	0.63	0/633	1.17	5/858 (0.6%)
4	SB	0.65	0/653	1.11	5/885 (0.6%)
4	SC	0.44	0/751	0.95	4/1015 (0.4%)
4	SE	0.65	0/653	1.11	5/885 (0.6%)
4	SF	0.44	0/751	0.95	4/1015 (0.4%)
4	TB	0.63	0/633	1.17	5/858 (0.6%)
4	TE	0.63	0/633	1.18	5/858 (0.6%)
4	UA	0.66	0/653	1.11	5/885 (0.6%)
4	UB	0.44	0/751	0.95	4/1015 (0.4%)
4	UD	0.65	0/653	1.11	4/885 (0.5%)
4	UE	0.44	0/751	0.95	4/1015 (0.4%)
4	UG	0.65	0/653	1.11	5/885 (0.6%)
4	VA	0.63	0/633	1.17	5/858 (0.6%)
4	VD	0.63	0/633	1.18	5/858 (0.6%)
4	VG	0.63	0/633	1.18	5/858 (0.6%)
4	W	0.66	0/653	1.11	5/885 (0.6%)
4	WA	0.44	0/751	0.95	4/1015 (0.4%)
4	WC	0.66	0/653	1.11	4/885 (0.5%)
4	WD	0.44	0/751	0.95	4/1015 (0.4%)
4	WF	0.66	0/653	1.11	5/885 (0.6%)
4	WG	0.44	0/751	0.95	4/1015 (0.4%)
4	X	0.63	0/633	1.18	5/858 (0.6%)
4	XC	0.63	0/633	1.17	5/858 (0.6%)
4	XF	0.63	0/633	1.17	5/858 (0.6%)
4	Y	0.44	0/751	0.95	4/1015 (0.4%)
4	YB	0.65	0/653	1.11	5/885 (0.6%)
4	YC	0.43	0/751	0.95	4/1015 (0.4%)
4	YE	0.65	0/653	1.11	4/885 (0.5%)
4	YF	0.44	0/751	0.95	4/1015 (0.4%)
4	ZB	0.63	0/633	1.17	5/858 (0.6%)
4	ZE	0.63	0/633	1.17	5/858 (0.6%)
All	All	0.49	0/221204	0.86	733/302056 (0.2%)

There are no bond length outliers.

The worst 5 of 733 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	DG	58	MET	N-CA-C	-8.41	102.78	113.72
4	FC	58	MET	N-CA-C	-8.40	102.80	113.72
4	TE	58	MET	N-CA-C	-8.40	102.80	113.72
4	VG	58	MET	N-CA-C	-8.40	102.80	113.72
4	X	58	MET	N-CA-C	-8.40	102.81	113.72

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	229	0	100	0	0
1	BC	229	0	100	0	0
1	BF	229	0	100	0	0
1	DB	229	0	100	0	0
1	DE	229	0	100	0	0
1	F	229	0	100	0	0
1	FA	229	0	100	0	0
1	FD	229	0	100	0	0
1	FG	229	0	100	0	0
1	HC	229	0	100	0	0
1	HF	229	0	100	0	0
1	I	229	0	100	0	0
1	JB	229	0	100	0	0
1	JE	229	0	100	0	0
1	LA	229	0	100	0	0
1	LD	229	0	100	0	0
1	LG	229	0	100	0	0
1	NC	229	0	100	0	0
1	NF	229	0	100	0	0
1	PB	229	0	100	0	0
1	PE	229	0	100	0	0
1	RA	229	0	100	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RD	229	0	100	0	0
1	RG	229	0	100	0	0
1	S	229	0	100	0	0
1	TC	229	0	100	0	0
1	TF	229	0	100	0	0
1	VB	229	0	100	0	0
1	VE	229	0	100	0	0
1	XA	229	0	100	0	0
1	XD	229	0	100	0	0
1	Z	229	0	100	0	0
1	ZC	229	0	100	0	0
1	ZF	229	0	100	0	0
2	AA	1893	0	1356	61	0
2	AD	1893	0	1356	56	0
2	AG	1893	0	1356	57	0
2	B	1893	0	1356	60	0
2	CC	1893	0	1356	57	0
2	CF	1893	0	1356	55	0
2	EB	1893	0	1356	62	0
2	EE	1893	0	1356	56	0
2	G	1893	0	1356	59	0
2	GA	1893	0	1356	60	0
2	GD	1893	0	1356	57	0
2	GG	1893	0	1356	57	0
2	IC	1893	0	1356	59	0
2	IF	1893	0	1356	58	0
2	J	1893	0	1356	61	0
2	KB	1893	0	1356	57	0
2	KE	1893	0	1356	59	0
2	MA	1893	0	1356	56	0
2	MD	1893	0	1356	55	0
2	MG	1893	0	1356	56	0
2	OC	1893	0	1356	61	0
2	OF	1893	0	1356	58	0
2	QB	1893	0	1356	58	0
2	QE	1893	0	1356	60	0
2	SA	1893	0	1356	58	0
2	SD	1893	0	1356	56	0
2	SG	1893	0	1356	58	0
2	T	1893	0	1356	60	0
2	UC	1893	0	1356	55	0
2	UF	1893	0	1356	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	WB	1893	0	1356	59	0
2	WE	1893	0	1356	56	0
2	YA	1893	0	1356	63	0
2	YD	1893	0	1356	57	0
3	BA	2287	0	2246	45	0
3	BD	2287	0	2246	46	0
3	BG	2287	0	2246	45	0
3	C	2287	0	2246	44	0
3	DC	2287	0	2246	48	0
3	DF	2287	0	2246	43	0
3	FB	2287	0	2246	46	0
3	FE	2287	0	2246	44	0
3	HA	2287	0	2246	45	0
3	HD	2287	0	2246	48	0
3	HG	2287	0	2246	46	0
3	JC	2287	0	2246	46	0
3	JF	2287	0	2246	46	0
3	K	2287	0	2246	46	0
3	LB	2287	0	2246	42	0
3	LE	2287	0	2246	52	0
3	M	2287	0	2246	45	0
3	NA	2287	0	2246	43	0
3	ND	2287	0	2246	44	0
3	NG	2287	0	2246	46	0
3	PC	2287	0	2246	50	0
3	PF	2287	0	2246	52	0
3	RB	2287	0	2246	43	0
3	RE	2287	0	2246	52	0
3	TA	2287	0	2246	44	0
3	TD	2287	0	2246	43	0
3	TG	2287	0	2246	50	0
3	V	2287	0	2246	47	0
3	VC	2287	0	2246	47	0
3	VF	2287	0	2246	45	0
3	XB	2287	0	2246	49	0
3	XE	2287	0	2246	43	0
3	ZA	2287	0	2246	45	0
3	ZD	2287	0	2246	48	0
4	AB	649	0	684	31	0
4	AC	746	0	771	39	0
4	AE	649	0	684	35	0
4	AF	746	0	771	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	BB	629	0	662	9	0
4	BE	629	0	662	8	0
4	CA	649	0	684	32	0
4	CB	746	0	771	39	0
4	CD	649	0	684	33	0
4	CE	746	0	771	36	0
4	CG	649	0	684	31	0
4	D	649	0	684	32	0
4	DA	629	0	662	9	0
4	DD	629	0	662	9	0
4	DG	629	0	662	10	0
4	E	629	0	662	9	0
4	EA	746	0	771	40	0
4	EC	649	0	684	35	0
4	ED	746	0	771	40	0
4	EF	649	0	684	31	0
4	EG	746	0	771	37	0
4	FC	629	0	662	9	0
4	FF	629	0	662	10	0
4	GB	649	0	684	33	0
4	GC	746	0	771	38	0
4	GE	649	0	684	32	0
4	GF	746	0	771	38	0
4	H	746	0	771	37	0
4	HB	629	0	662	9	0
4	HE	629	0	662	9	0
4	IA	649	0	684	34	0
4	IB	746	0	771	36	0
4	ID	649	0	684	34	0
4	IE	746	0	771	38	0
4	IG	649	0	684	34	0
4	JA	629	0	662	9	0
4	JD	629	0	662	9	0
4	JG	629	0	662	10	0
4	KA	746	0	771	36	0
4	KC	649	0	684	32	0
4	KD	746	0	771	37	0
4	KF	649	0	684	33	0
4	KG	746	0	771	36	0
4	L	649	0	684	34	0
4	LC	629	0	662	9	0
4	LF	629	0	662	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	MB	649	0	684	33	0
4	MC	746	0	771	40	0
4	ME	649	0	684	33	0
4	MF	746	0	771	40	0
4	N	649	0	684	32	0
4	NB	629	0	662	9	0
4	NE	629	0	662	10	0
4	O	629	0	662	10	0
4	OA	649	0	684	32	0
4	OB	746	0	771	36	0
4	OD	649	0	684	33	0
4	OE	746	0	771	38	0
4	OG	649	0	684	33	0
4	P	629	0	662	10	0
4	PA	629	0	662	9	0
4	PD	629	0	662	9	0
4	PG	629	0	662	10	0
4	Q	746	0	771	38	0
4	QA	746	0	771	36	0
4	QC	649	0	684	35	0
4	QD	746	0	771	37	0
4	QF	649	0	684	33	0
4	QG	746	0	771	42	0
4	R	746	0	771	40	0
4	RC	629	0	662	9	0
4	RF	629	0	662	10	0
4	SB	649	0	684	34	0
4	SC	746	0	771	40	0
4	SE	649	0	684	32	0
4	SF	746	0	771	37	0
4	TB	629	0	662	9	0
4	TE	629	0	662	10	0
4	UA	649	0	684	32	0
4	UB	746	0	771	40	0
4	UD	649	0	684	32	0
4	UE	746	0	771	36	0
4	UG	649	0	684	34	0
4	VA	629	0	662	9	0
4	VD	629	0	662	9	0
4	VG	629	0	662	10	0
4	W	649	0	684	34	0
4	WA	746	0	771	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	WC	649	0	684	32	0
4	WD	746	0	771	40	0
4	WF	649	0	684	32	0
4	WG	746	0	771	37	0
4	X	629	0	662	9	0
4	XC	629	0	662	9	0
4	XF	629	0	662	9	0
4	Y	746	0	771	36	0
4	YB	649	0	684	34	0
4	YC	746	0	771	37	0
4	YE	649	0	684	33	0
4	YF	746	0	771	38	0
4	ZB	629	0	662	9	0
4	ZE	629	0	662	9	0
All	All	218722	0	197846	3993	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 3993 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)
3:PC:309:VAL:HG12	3:PC:314:ALA:HB2	1.32	1.12
3:BD:309:VAL:HG12	3:BD:314:ALA:HB2	1.32	1.12
3:NA:309:VAL:HG12	3:NA:314:ALA:HB2	1.32	1.11
3:ZA:309:VAL:HG12	3:ZA:314:ALA:HB2	1.32	1.11
3:V:309:VAL:HG12	3:V:314:ALA:HB2	1.32	1.11

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	BC	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	BF	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	DB	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	DE	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	F	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	FA	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	FD	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	FG	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	HC	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	HF	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	I	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	JB	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	JE	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	LA	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	LD	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	LG	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	NC	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	NF	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	PB	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	PE	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	RA	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	RD	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	RG	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	S	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	TC	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	TF	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	VB	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	VE	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	XA	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	XD	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	Z	44/560 (8%)	43 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ZC	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
1	ZF	44/560 (8%)	43 (98%)	1 (2%)	0	100	100
2	AA	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	AD	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	AG	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	B	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	CC	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	CF	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	EB	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	EE	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	G	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	GA	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	GD	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	GG	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	IC	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	IF	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	J	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	KB	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	KE	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	MA	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	MD	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	MG	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	OC	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	OF	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	QB	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	QE	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	SA	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	SD	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	SG	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	T	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	UC	317/331 (96%)	310 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	UF	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	WB	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	WE	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	YA	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
2	YD	317/331 (96%)	310 (98%)	7 (2%)	0	100	100
3	BA	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	BD	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	BG	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	C	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	DC	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	DF	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	FB	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	FE	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	HA	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	HD	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	HG	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	JC	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	JF	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	K	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	LB	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	LE	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	M	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	NA	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	ND	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	NG	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	PC	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	PF	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	RB	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	RE	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	TA	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	TD	289/334 (86%)	276 (96%)	13 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	TG	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	V	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	VC	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	VF	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	XB	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	XE	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	ZA	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
3	ZD	289/334 (86%)	276 (96%)	13 (4%)	0	100	100
4	AB	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	AC	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	AE	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	AF	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	BB	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	BE	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	CA	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	CB	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	CD	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	CE	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	CG	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	D	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	DA	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	DD	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	DG	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	E	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	EA	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	EC	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	ED	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	EF	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	EG	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	FC	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	FF	81/137 (59%)	76 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	GB	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	GC	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	GE	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	GF	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	H	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	HB	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	HE	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	IA	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	IB	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	ID	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	IE	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	IG	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	JA	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	JD	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	JG	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	KA	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	KC	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	KD	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	KF	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	KG	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	L	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	LC	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	LF	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	MB	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	MC	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	ME	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	MF	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	N	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	NB	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	NE	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	O	81/137 (59%)	76 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	OA	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	OB	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	OD	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	OE	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	OG	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	P	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	PA	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	PD	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	PG	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	Q	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	QA	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	QC	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	QD	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	QF	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	QG	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	R	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	RC	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	RF	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	SB	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	SC	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	SE	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	SF	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	TB	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	TE	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	UA	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	UB	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	UD	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	UE	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	UG	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	VA	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	VD	81/137 (59%)	76 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	VG	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	W	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	WA	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	WC	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	WD	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	WF	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	WG	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	X	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	XC	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	XF	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	Y	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	YB	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	YC	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	YE	84/137 (61%)	76 (90%)	8 (10%)	0	100	100
4	YF	98/137 (72%)	92 (94%)	6 (6%)	0	100	100
4	ZB	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
4	ZE	81/137 (59%)	76 (94%)	5 (6%)	0	100	100
All	All	31042/55624 (56%)	29682 (96%)	1360 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AA	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	AD	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	AG	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	B	92/282 (33%)	90 (98%)	2 (2%)	45	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	CC	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	CF	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	EB	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	EE	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	G	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	GA	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	GD	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	GG	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	IC	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	IF	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	J	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	KB	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	KE	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	MA	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	MD	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	MG	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	OC	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	OF	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	QB	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	QE	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	SA	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	SD	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	SG	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	T	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	UC	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	UF	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	WB	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	WE	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	YA	92/282 (33%)	90 (98%)	2 (2%)	45	74
2	YD	92/282 (33%)	90 (98%)	2 (2%)	45	74
3	BA	248/301 (82%)	248 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BD	248/301 (82%)	248 (100%)	0	100	100
3	BG	248/301 (82%)	248 (100%)	0	100	100
3	C	248/301 (82%)	248 (100%)	0	100	100
3	DC	248/301 (82%)	248 (100%)	0	100	100
3	DF	248/301 (82%)	248 (100%)	0	100	100
3	FB	248/301 (82%)	248 (100%)	0	100	100
3	FE	248/301 (82%)	248 (100%)	0	100	100
3	HA	248/301 (82%)	248 (100%)	0	100	100
3	HD	248/301 (82%)	248 (100%)	0	100	100
3	HG	248/301 (82%)	248 (100%)	0	100	100
3	JC	248/301 (82%)	248 (100%)	0	100	100
3	JF	248/301 (82%)	248 (100%)	0	100	100
3	K	248/301 (82%)	248 (100%)	0	100	100
3	LB	248/301 (82%)	248 (100%)	0	100	100
3	LE	248/301 (82%)	248 (100%)	0	100	100
3	M	248/301 (82%)	248 (100%)	0	100	100
3	NA	248/301 (82%)	248 (100%)	0	100	100
3	ND	248/301 (82%)	248 (100%)	0	100	100
3	NG	248/301 (82%)	248 (100%)	0	100	100
3	PC	248/301 (82%)	248 (100%)	0	100	100
3	PF	248/301 (82%)	248 (100%)	0	100	100
3	RB	248/301 (82%)	248 (100%)	0	100	100
3	RE	248/301 (82%)	248 (100%)	0	100	100
3	TA	248/301 (82%)	248 (100%)	0	100	100
3	TD	248/301 (82%)	248 (100%)	0	100	100
3	TG	248/301 (82%)	248 (100%)	0	100	100
3	V	248/301 (82%)	248 (100%)	0	100	100
3	VC	248/301 (82%)	248 (100%)	0	100	100
3	VF	248/301 (82%)	248 (100%)	0	100	100
3	XB	248/301 (82%)	248 (100%)	0	100	100
3	XE	248/301 (82%)	248 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	ZA	248/301 (82%)	248 (100%)	0	100	100
3	ZD	248/301 (82%)	248 (100%)	0	100	100
4	AB	71/113 (63%)	71 (100%)	0	100	100
4	AC	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	AE	71/113 (63%)	71 (100%)	0	100	100
4	AF	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	BB	69/113 (61%)	69 (100%)	0	100	100
4	BE	69/113 (61%)	69 (100%)	0	100	100
4	CA	71/113 (63%)	71 (100%)	0	100	100
4	CB	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	CD	71/113 (63%)	71 (100%)	0	100	100
4	CE	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	CG	71/113 (63%)	71 (100%)	0	100	100
4	D	71/113 (63%)	71 (100%)	0	100	100
4	DA	69/113 (61%)	69 (100%)	0	100	100
4	DD	69/113 (61%)	69 (100%)	0	100	100
4	DG	69/113 (61%)	69 (100%)	0	100	100
4	E	69/113 (61%)	69 (100%)	0	100	100
4	EA	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	EC	71/113 (63%)	71 (100%)	0	100	100
4	ED	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	EF	71/113 (63%)	71 (100%)	0	100	100
4	EG	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	FC	69/113 (61%)	69 (100%)	0	100	100
4	FF	69/113 (61%)	69 (100%)	0	100	100
4	GB	71/113 (63%)	71 (100%)	0	100	100
4	GC	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	GE	71/113 (63%)	71 (100%)	0	100	100
4	GF	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	H	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	HB	69/113 (61%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	HE	69/113 (61%)	69 (100%)	0	100	100
4	IA	71/113 (63%)	71 (100%)	0	100	100
4	IB	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	ID	71/113 (63%)	71 (100%)	0	100	100
4	IE	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	IG	71/113 (63%)	71 (100%)	0	100	100
4	JA	69/113 (61%)	69 (100%)	0	100	100
4	JD	69/113 (61%)	69 (100%)	0	100	100
4	JG	69/113 (61%)	69 (100%)	0	100	100
4	KA	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	KC	71/113 (63%)	71 (100%)	0	100	100
4	KD	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	KF	71/113 (63%)	71 (100%)	0	100	100
4	KG	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	L	71/113 (63%)	71 (100%)	0	100	100
4	LC	69/113 (61%)	69 (100%)	0	100	100
4	LF	69/113 (61%)	69 (100%)	0	100	100
4	MB	71/113 (63%)	71 (100%)	0	100	100
4	MC	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	ME	71/113 (63%)	71 (100%)	0	100	100
4	MF	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	N	71/113 (63%)	71 (100%)	0	100	100
4	NB	69/113 (61%)	69 (100%)	0	100	100
4	NE	69/113 (61%)	69 (100%)	0	100	100
4	O	69/113 (61%)	69 (100%)	0	100	100
4	OA	71/113 (63%)	71 (100%)	0	100	100
4	OB	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	OD	71/113 (63%)	71 (100%)	0	100	100
4	OE	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	OG	71/113 (63%)	71 (100%)	0	100	100
4	P	69/113 (61%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	PA	69/113 (61%)	69 (100%)	0	100	100
4	PD	69/113 (61%)	69 (100%)	0	100	100
4	PG	69/113 (61%)	69 (100%)	0	100	100
4	Q	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	QA	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	QC	71/113 (63%)	71 (100%)	0	100	100
4	QD	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	QF	71/113 (63%)	71 (100%)	0	100	100
4	QG	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	R	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	RC	69/113 (61%)	69 (100%)	0	100	100
4	RF	69/113 (61%)	69 (100%)	0	100	100
4	SB	71/113 (63%)	71 (100%)	0	100	100
4	SC	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	SE	71/113 (63%)	71 (100%)	0	100	100
4	SF	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	TB	69/113 (61%)	69 (100%)	0	100	100
4	TE	69/113 (61%)	69 (100%)	0	100	100
4	UA	71/113 (63%)	71 (100%)	0	100	100
4	UB	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	UD	71/113 (63%)	71 (100%)	0	100	100
4	UE	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	UG	71/113 (63%)	71 (100%)	0	100	100
4	VA	69/113 (61%)	69 (100%)	0	100	100
4	VD	69/113 (61%)	69 (100%)	0	100	100
4	VG	69/113 (61%)	69 (100%)	0	100	100
4	W	71/113 (63%)	71 (100%)	0	100	100
4	WA	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	WC	71/113 (63%)	71 (100%)	0	100	100
4	WD	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	WF	71/113 (63%)	71 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	WG	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	X	69/113 (61%)	69 (100%)	0	100	100
4	XC	69/113 (61%)	69 (100%)	0	100	100
4	XF	69/113 (61%)	69 (100%)	0	100	100
4	Y	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	YB	71/113 (63%)	71 (100%)	0	100	100
4	YC	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	YE	71/113 (63%)	71 (100%)	0	100	100
4	YF	80/113 (71%)	79 (99%)	1 (1%)	61	81
4	ZB	69/113 (61%)	69 (100%)	0	100	100
4	ZE	69/113 (61%)	69 (100%)	0	100	100
All	All	19040/31348 (61%)	18938 (100%)	102 (0%)	78	89

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	MD	149	PHE
4	OE	122	ILE
2	SG	149	PHE
4	QD	122	ILE
4	CE	122	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
4	TE	108	GLN
4	XF	108	GLN
3	XE	58	ASN
2	IF	136	HIS
3	HG	185	GLN

5.3.3 RNA ⓘ

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.

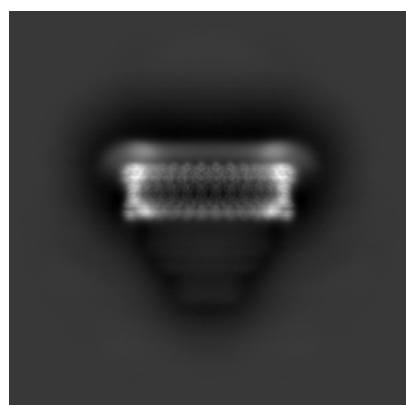
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48916. These allow visual inspection of the internal detail of the map and identification of artifacts.

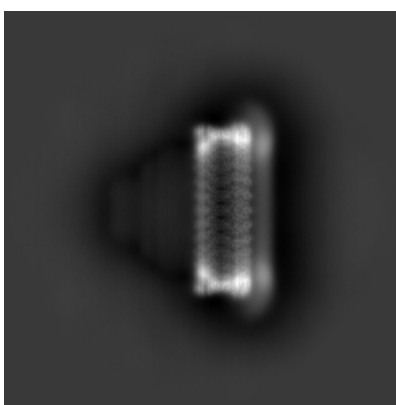
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

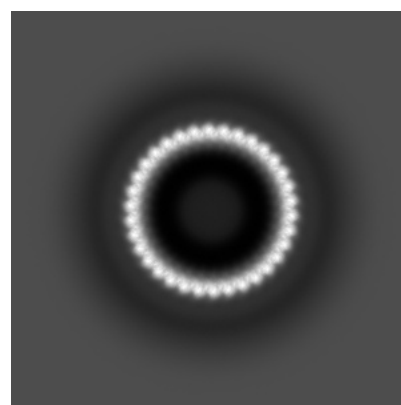
6.1.1 Primary map



X



Y

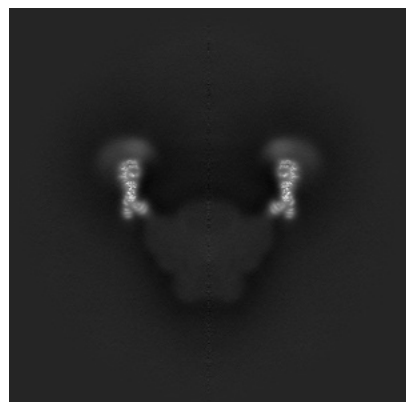


Z

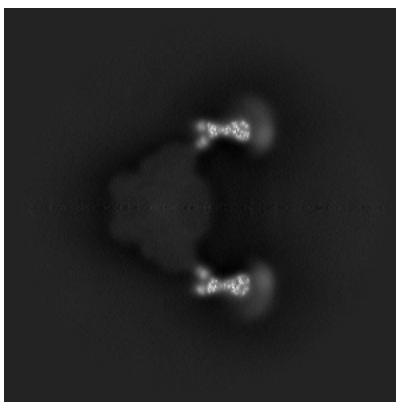
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

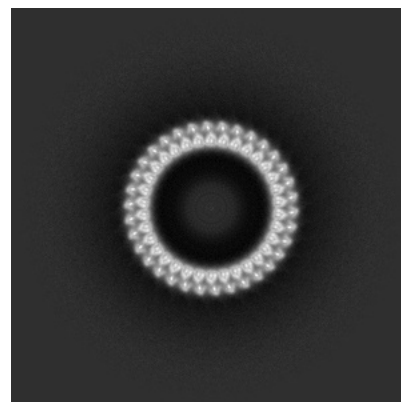
6.2.1 Primary map



X Index: 384



Y Index: 384

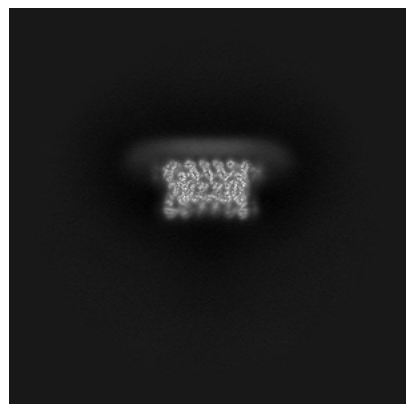


Z Index: 384

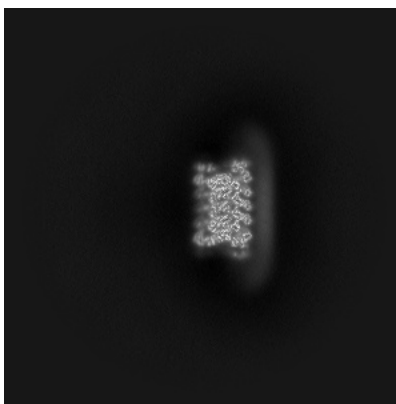
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

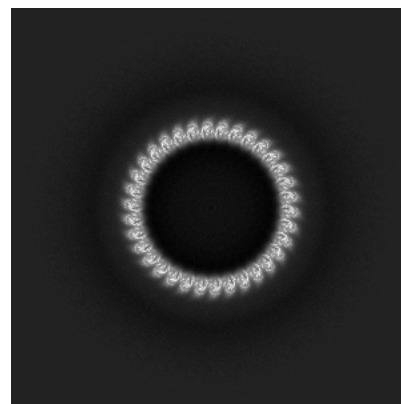
6.3.1 Primary map



X Index: 242



Y Index: 527

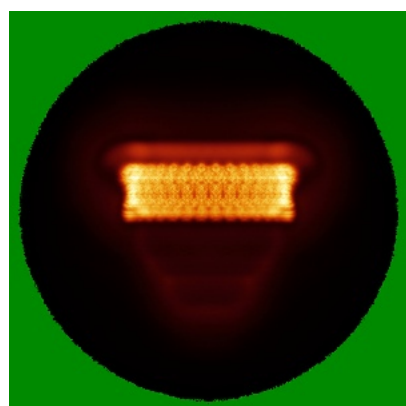


Z Index: 447

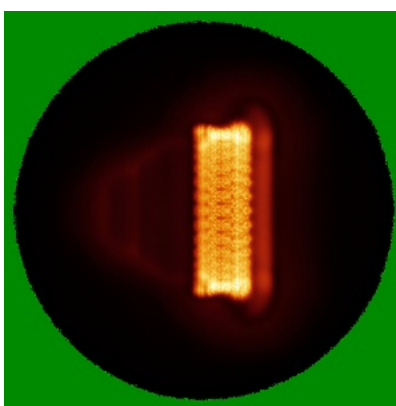
The images above show the largest variance slices of the map in three orthogonal directions.

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

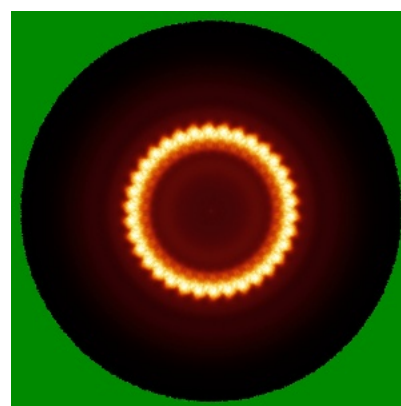
6.4.1 Primary map



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

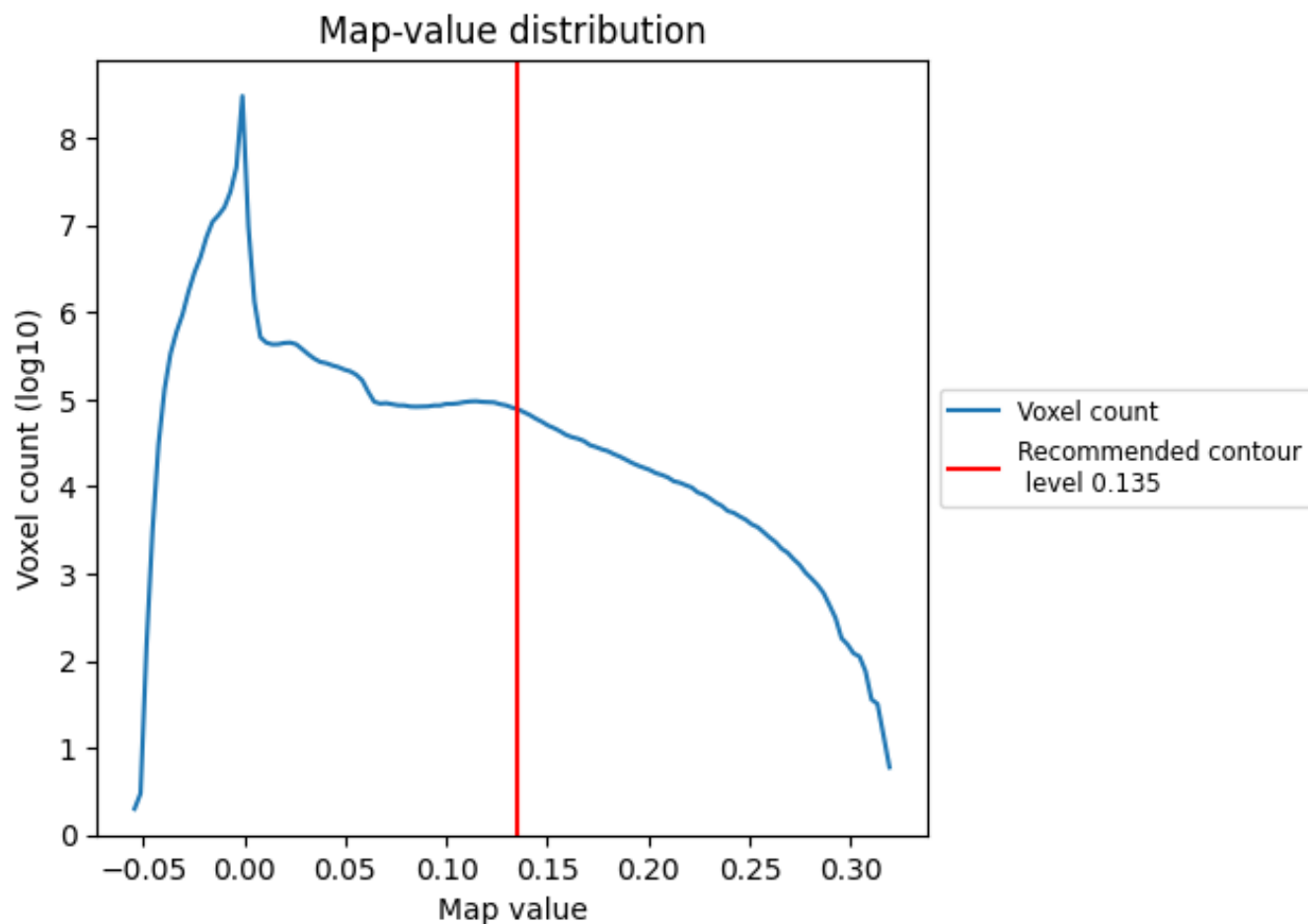
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

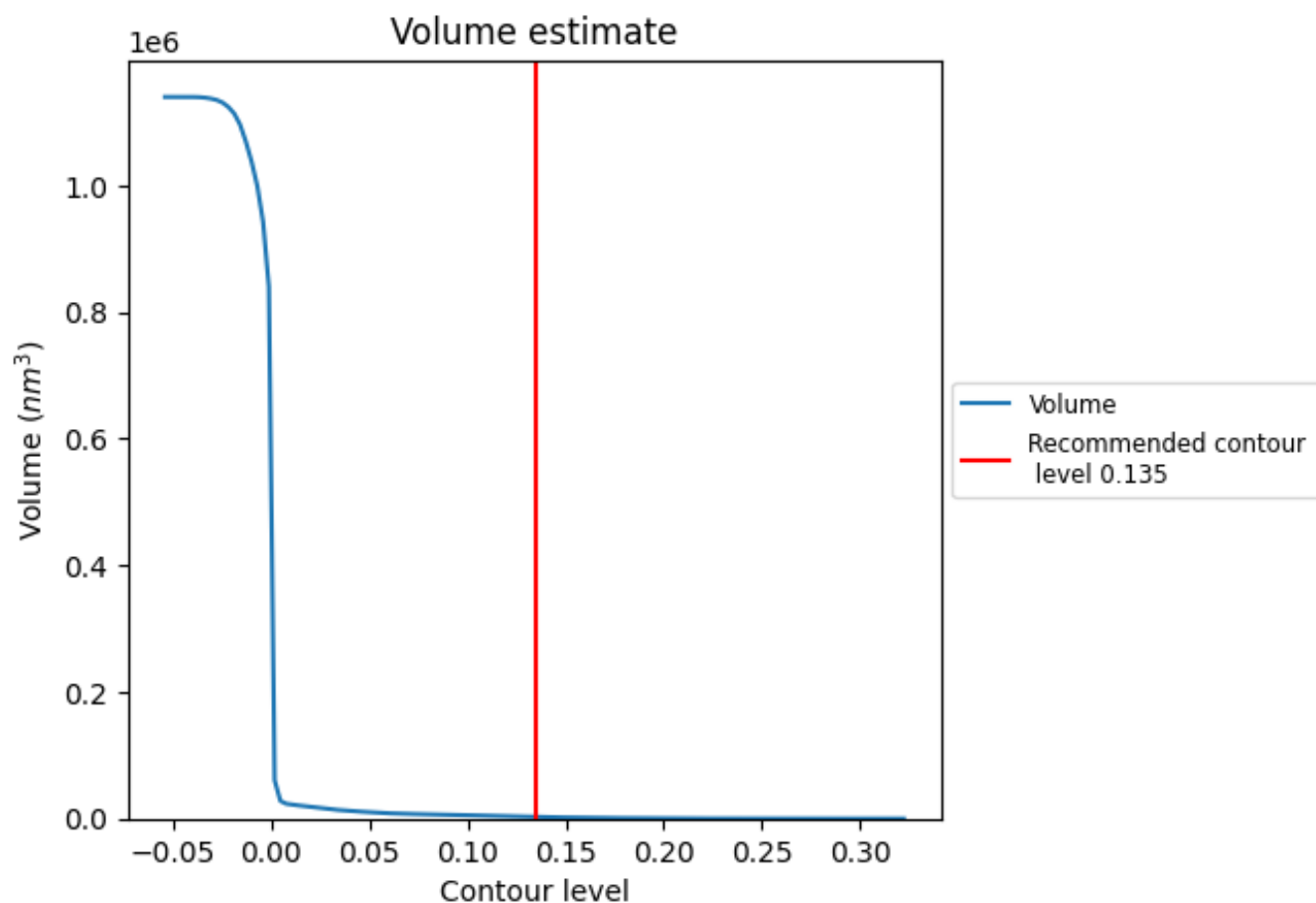
This section contains the results of statistical analysis of the map.

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.

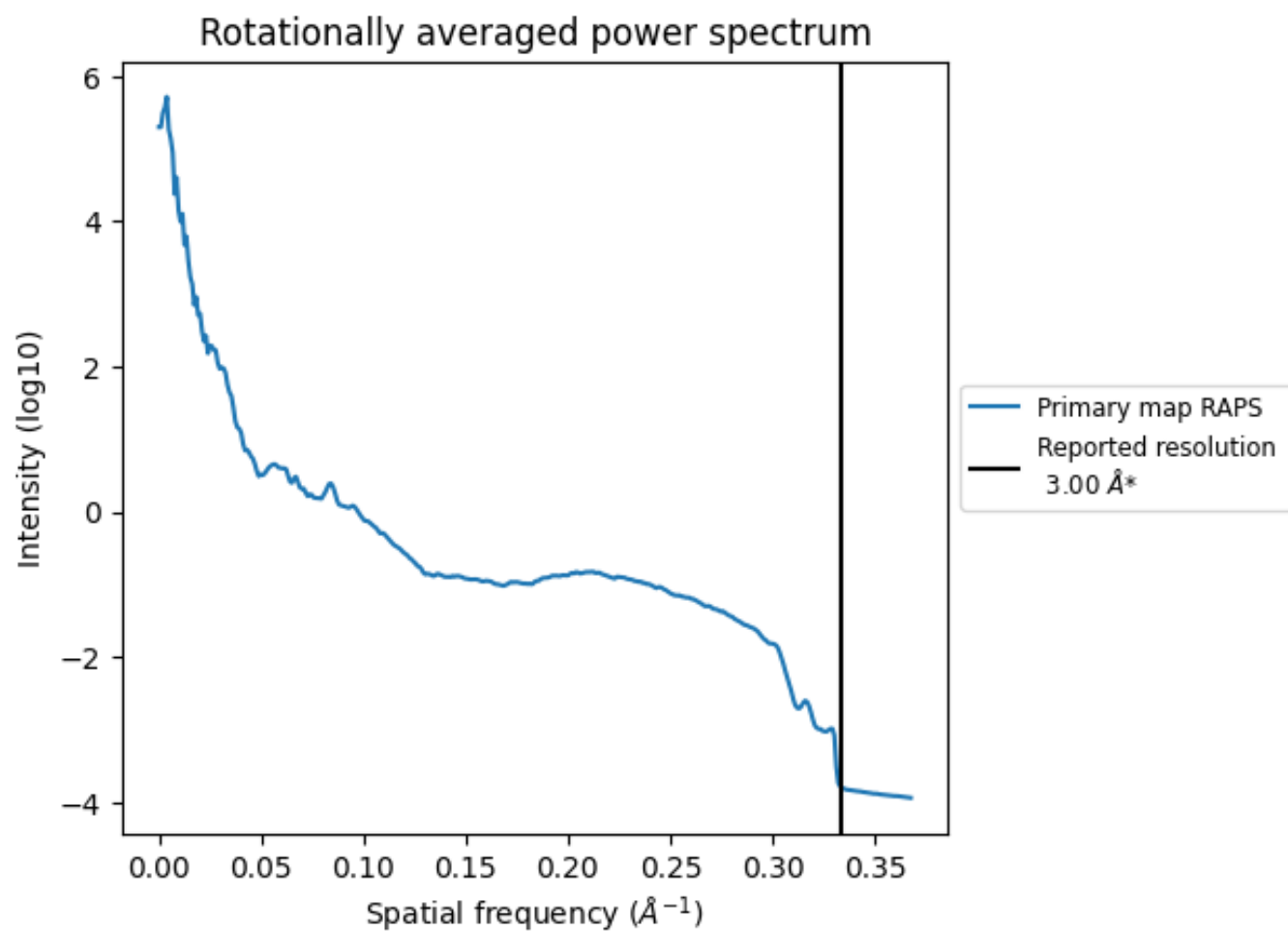
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2617 nm³; this corresponds to an approximate mass of 2364 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 0.333 Å⁻¹

8 Fourier-Shell correlation

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

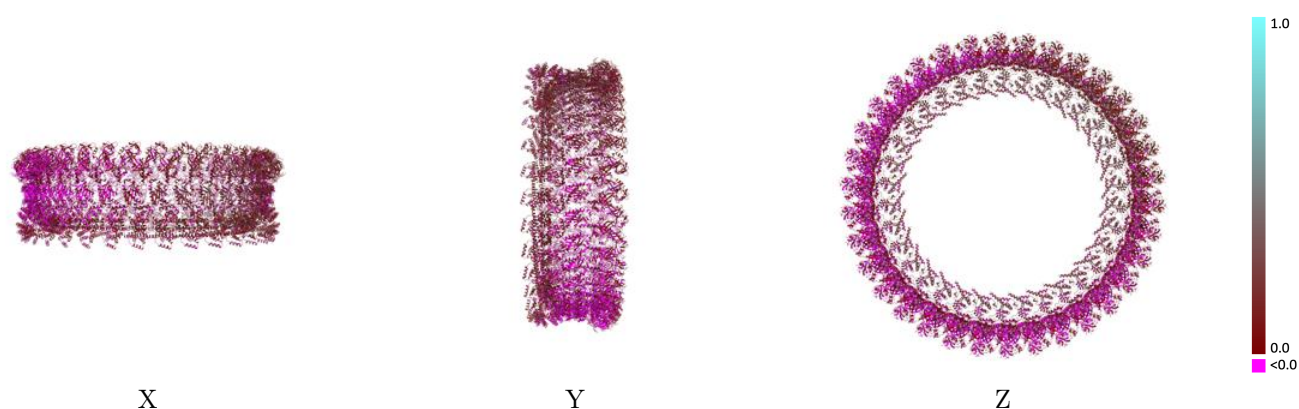
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48916 and PDB model 9N4Z. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)

This section was not generated.

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

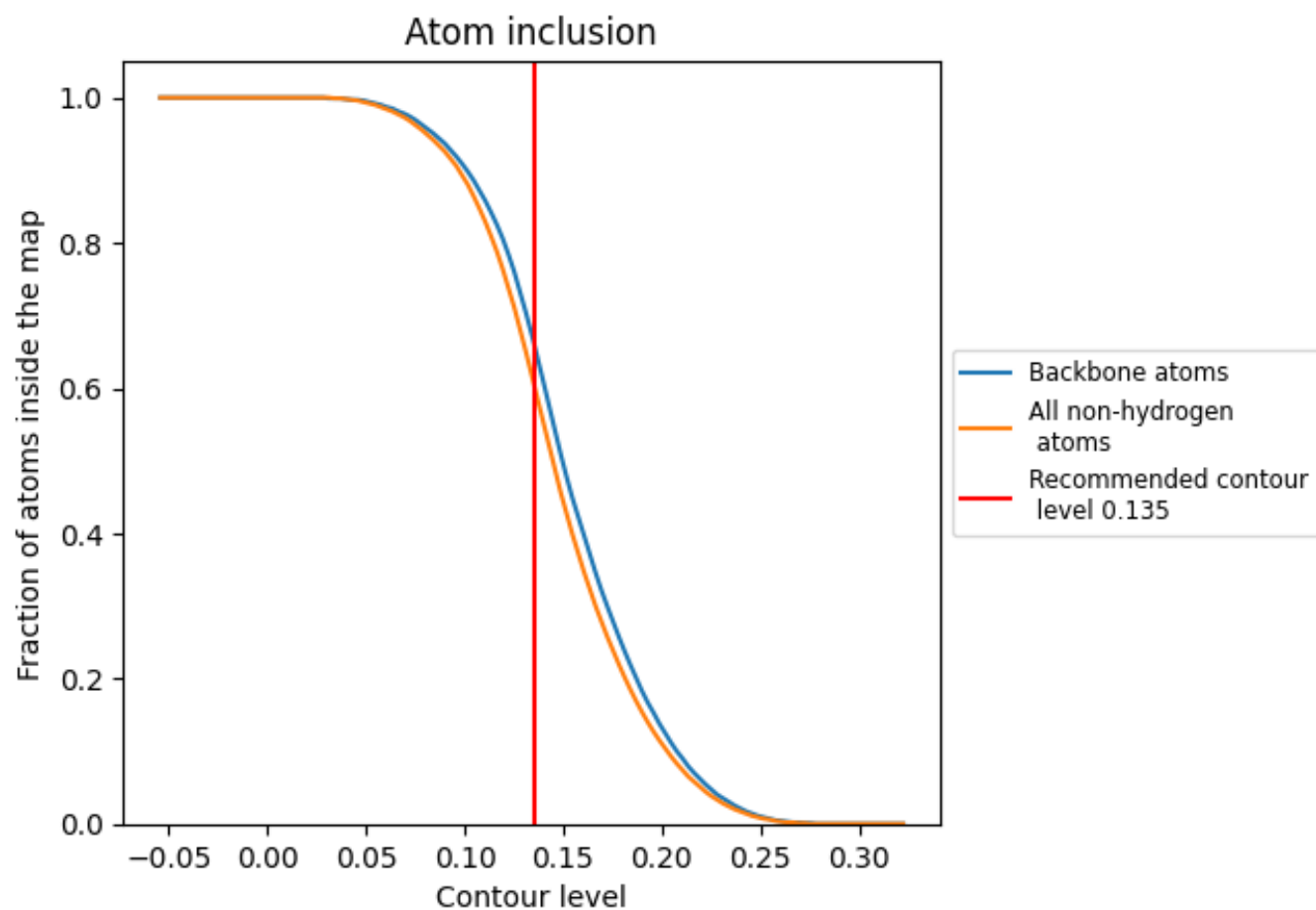


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 66% of all backbone atoms, 61% 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 (0.135) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6070	 0.0700
A	 0.2880	 0.1670
AA	 0.5040	 0.0700
AB	 0.4930	 0.0520
AC	 0.5960	 0.0230
AD	 0.4850	 0.0540
AE	 0.6190	 0.0660
AF	 0.7440	 0.1720
AG	 0.6090	 0.1630
B	 0.5320	 0.0860
BA	 0.6310	 -0.0090
BB	 0.6550	 -0.0230
BC	 0.1830	 0.1060
BD	 0.6140	 -0.0150
BE	 0.7040	 0.0590
BF	 0.1880	 0.1510
BG	 0.7950	 0.1490
C	 0.6730	 0.0060
CA	 0.4500	 0.0420
CB	 0.6230	 0.0320
CC	 0.4710	 0.0460
CD	 0.5810	 0.0470
CE	 0.6680	 0.0490
CF	 0.6200	 0.1880
CG	 0.6190	 0.1390
D	 0.4820	 0.0500
DA	 0.6670	 -0.0230
DB	 0.2100	 0.1390
DC	 0.5980	 -0.0020
DD	 0.6650	 -0.0030
DE	 0.1700	 0.1080
DF	 0.8030	 0.1910
DG	 0.7720	 0.1610
E	 0.7170	 0.0160
EA	 0.6140	 0.0180



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Chain	Atom inclusion	Q-score
EB	 0.4850	 0.0500
EC	 0.5530	 0.0590
ED	 0.6010	 0.0040
EE	 0.5570	 0.1090
EF	 0.6550	 0.1440
EG	 0.7340	 0.1650
F	 0.2800	 0.1710
FA	 0.2710	 0.1600
FB	 0.5940	 0.0000
FC	 0.6810	 0.0010
FD	 0.1750	 0.0900
FE	 0.7190	 0.0490
FF	 0.7800	 0.1930
FG	 0.2580	 0.1780
G	 0.5500	 0.0970
GA	 0.5020	 0.0630
GB	 0.5020	 0.0550
GC	 0.5960	 0.0170
GD	 0.5030	 0.0590
GE	 0.6280	 0.0750
GF	 0.7510	 0.1910
GG	 0.5940	 0.1460
H	 0.6250	 0.0290
HA	 0.6180	 -0.0070
HB	 0.6520	 -0.0160
HC	 0.1790	 0.0920
HD	 0.6260	 -0.0140
HE	 0.7190	 0.0820
HF	 0.2180	 0.1600
HG	 0.7820	 0.1150
I	 0.2930	 0.1640
IA	 0.4600	 0.0470
IB	 0.6140	 0.0310
IC	 0.4690	 0.0460
ID	 0.5940	 0.0450
IE	 0.6950	 0.0750
IF	 0.6240	 0.1940
IG	 0.5860	 0.1200
J	 0.5250	 0.0800
JA	 0.6540	 -0.0280
JB	 0.2180	 0.1240
JC	 0.5990	 -0.0050

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Chain	Atom inclusion	Q-score
JD	 0.6700	 0.0070
JE	 0.1830	 0.1200
JF	 0.8110	 0.2050
JG	 0.7670	 0.1360
K	 0.6600	 -0.0030
KA	 0.6080	 0.0190
KB	 0.4760	 0.0490
KC	 0.5570	 0.0600
KD	 0.6120	 0.0110
KE	 0.5730	 0.1280
KF	 0.6520	 0.1530
KG	 0.7120	 0.1360
L	 0.4720	 0.0430
LA	 0.2530	 0.1580
LB	 0.5930	 0.0020
LC	 0.6580	 0.0000
LD	 0.1750	 0.1000
LE	 0.7430	 0.0820
LF	 0.7970	 0.2040
LG	 0.2620	 0.1740
M	 0.6950	 0.0230
MA	 0.4930	 0.0590
MB	 0.5130	 0.0560
MC	 0.5950	 0.0130
MD	 0.5180	 0.0680
ME	 0.6350	 0.0890
MF	 0.7620	 0.2050
MG	 0.5830	 0.1290
N	 0.5050	 0.0640
NA	 0.6070	 -0.0060
NB	 0.6580	 -0.0130
NC	 0.1790	 0.0910
ND	 0.6400	 -0.0090
NE	 0.7420	 0.1150
NF	 0.2270	 0.1710
NG	 0.7580	 0.0830
O	 0.6960	 -0.0010
OA	 0.4710	 0.0470
OB	 0.6040	 0.0330
OC	 0.4740	 0.0470
OD	 0.6000	 0.0500
OE	 0.7110	 0.1050

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Chain	Atom inclusion	Q-score
OF	 0.6220	 0.1910
OG	 0.5650	 0.1040
P	 0.7380	 0.0430
PA	 0.6540	 -0.0250
PB	 0.2100	 0.1120
PC	 0.6040	 -0.0080
PD	 0.6850	 0.0240
PE	 0.1920	 0.1290
PF	 0.8120	 0.1980
PG	 0.7670	 0.1090
Q	 0.6470	 0.0480
QA	 0.6150	 0.0250
QB	 0.4780	 0.0480
QC	 0.5640	 0.0570
QD	 0.6290	 0.0190
QE	 0.5970	 0.1550
QF	 0.6420	 0.1580
QG	 0.6960	 0.1050
R	 0.6220	 0.0230
RA	 0.2400	 0.1470
RB	 0.5840	 0.0010
RC	 0.6730	 -0.0010
RD	 0.1620	 0.0990
RE	 0.7690	 0.1330
RF	 0.8000	 0.2010
RG	 0.2620	 0.1730
S	 0.2840	 0.1610
SA	 0.4880	 0.0550
SB	 0.5310	 0.0590
SC	 0.6010	 0.0070
SD	 0.5240	 0.0750
SE	 0.6440	 0.1110
SF	 0.7520	 0.2020
SG	 0.5590	 0.1090
T	 0.5120	 0.0750
TA	 0.6020	 -0.0040
TB	 0.6760	 -0.0040
TC	 0.1790	 0.0890
TD	 0.6600	 0.0020
TE	 0.7630	 0.1520
TF	 0.2310	 0.1720
TG	 0.7220	 0.0450

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Chain	Atom inclusion	Q-score
UA	 0.4800	 0.0500
UB	 0.6030	 0.0290
UC	 0.4810	 0.0520
UD	 0.6130	 0.0540
UE	 0.7340	 0.1420
UF	 0.6210	 0.1810
UG	 0.5290	 0.0820
V	 0.6460	 -0.0060
VA	 0.6410	 -0.0280
VB	 0.2100	 0.1090
VC	 0.6130	 -0.0130
VD	 0.6890	 0.0380
VE	 0.1750	 0.1430
VF	 0.8070	 0.1800
VG	 0.7530	 0.0690
W	 0.4570	 0.0440
WA	 0.6160	 0.0300
WB	 0.4750	 0.0460
WC	 0.5730	 0.0540
WD	 0.6470	 0.0320
WE	 0.6070	 0.1740
WF	 0.6310	 0.1510
WG	 0.6590	 0.0730
X	 0.6780	 -0.0150
XA	 0.2310	 0.1440
XB	 0.5900	 -0.0000
XC	 0.6700	 -0.0040
XD	 0.1530	 0.1030
XE	 0.7910	 0.1690
XF	 0.7870	 0.1860
Y	 0.6210	 0.0180
YA	 0.4890	 0.0520
YB	 0.5460	 0.0600
YC	 0.6040	 0.0030
YD	 0.5400	 0.0900
YE	 0.6530	 0.1300
YF	 0.7510	 0.1900
Z	 0.2800	 0.1610
ZA	 0.5970	 -0.0020
ZB	 0.6910	 -0.0010
ZC	 0.1830	 0.0880
ZD	 0.6870	 0.0230

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Chain	Atom inclusion	Q-score
ZE	 0.7770	 0.1780
ZF	 0.2440	 0.1810