



## wwPDB EM Validation Summary Report ⓘ

Feb 22, 2024 – 02:31 PM EST

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

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

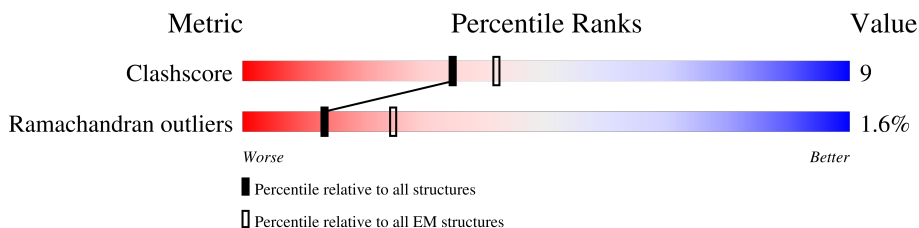
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.90 Å.

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



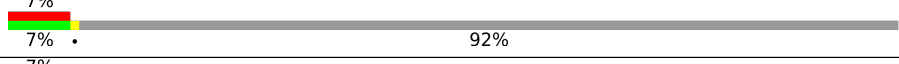
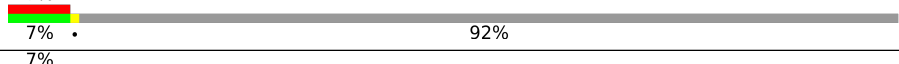
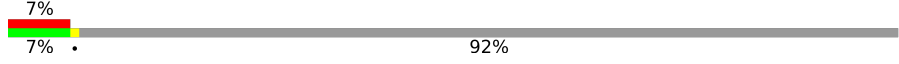
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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  $\geq 3$ , 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	
1	BC	560	
1	BF	560	
1	DB	560	
1	DE	560	
1	F	560	
1	FA	560	
1	FD	560	
1	FG	560	

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Mol	Chain	Length	Quality of chain
1	HC	560	 7% 7% • 92%
1	HF	560	 7% 7% • 92%
1	I	560	 7% 7% • 92%
1	JB	560	 7% 7% • 92%
1	JE	560	 7% 7% • 92%
1	LA	560	 7% 7% • 92%
1	LD	560	 7% 7% • 92%
1	LG	560	 7% 7% • 92%
1	NC	560	 7% 7% • 92%
1	NF	560	 7% 7% • 92%
1	PB	560	 7% 7% • 92%
1	PE	560	 7% 7% • 92%
1	RA	560	 7% 7% • 92%
1	RD	560	 7% 7% • 92%
1	RG	560	 7% 7% • 92%
1	S	560	 7% 7% • 92%
1	TC	560	 7% 7% • 92%
1	TF	560	 7% 7% • 92%
1	VB	560	 7% 7% • 92%
1	VE	560	 7% 7% • 92%
1	XA	560	 7% 7% • 92%
1	XD	560	 7% 7% • 92%
1	Z	560	 7% 7% • 92%
1	ZC	560	 7% 7% • 92%
1	ZF	560	 7% 7% • 92%

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Mol	Chain	Length	Quality of chain			
2	AA	331	28%	83%	10%	5%
2	AD	331	28%	83%	11%	5%
2	AG	331	28%	83%	11%	5%
2	B	331	28%	83%	10%	5%
2	CC	331	28%	83%	11%	5%
2	CF	331	28%	83%	11%	5%
2	EB	331	28%	83%	10%	5%
2	EE	331	28%	83%	11%	5%
2	G	331	28%	83%	10%	5%
2	GA	331	28%	83%	10%	5%
2	GD	331	28%	83%	11%	5%
2	GG	331	29%	83%	11%	5%
2	IC	331	28%	83%	11%	5%
2	IF	331	28%	83%	11%	5%
2	J	331	29%	83%	10%	5%
2	KB	331	28%	83%	11%	5%
2	KE	331	28%	83%	11%	5%
2	MA	331	28%	83%	10%	5%
2	MD	331	28%	83%	11%	5%
2	MG	331	28%	83%	11%	5%
2	OC	331	28%	82%	11%	5%
2	OF	331	28%	83%	11%	5%
2	QB	331	28%	83%	11%	5%
2	QE	331	28%	83%	11%	5%
2	SA	331	28%	83%	10%	5%

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Mol	Chain	Length	Quality of chain
2	SD	331	28% 83% 11% • 5%
2	SG	331	28% 83% 11% • 5%
2	T	331	28% 83% 10% • 5%
2	UC	331	28% 83% 11% • 5%
2	UF	331	28% 83% 11% • 5%
2	WB	331	28% 83% 11% • 5%
2	WE	331	29% 83% 11% • 5%
2	YA	331	28% 83% 10% • 5%
2	YD	331	28% 83% 11% • 5%
3	BA	291	28% 93% 5% •
3	BD	291	28% 93% 5% •
3	BG	291	28% 93% 5% •
3	C	291	28% 93% 5% •
3	DC	291	28% 93% 5% •
3	DF	291	28% 93% 5% •
3	FB	291	28% 93% 5% •
3	FE	291	28% 93% 5% •
3	HA	291	29% 93% 5% •
3	HD	291	28% 93% 5% •
3	HG	291	28% 93% 5% •
3	JC	291	28% 93% 5% •
3	JF	291	28% 93% 5% •
3	K	291	28% 93% 5% •
3	LB	291	29% 93% 5% •
3	LE	291	29% 93% 5% •

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Mol	Chain	Length	Quality of chain
3	M	291	28% 93% 5%
3	NA	291	29% 93% 5%
3	ND	291	29% 93% 5%
3	NG	291	28% 93% 5%
3	PC	291	28% 93% 5%
3	PF	291	28% 93% 5%
3	RB	291	28% 93% 5%
3	RE	291	28% 93% 5%
3	TA	291	28% 93% 5%
3	TD	291	28% 93% 5%
3	TG	291	28% 93% 5%
3	V	291	28% 93% 5%
3	VC	291	28% 93% 5%
3	VF	291	28% 93% 5%
3	XB	291	28% 93% 5%
3	XE	291	29% 93% 5%
3	ZA	291	29% 93% 5%
3	ZD	291	28% 93% 5%
4	AB	137	40% 64% 32%
4	AC	137	9% 53% 45%
4	AE	137	39% 64% 32%
4	AF	137	9% 53% 45%
4	BB	137	57% 42%
4	BE	137	57% 42%
4	CA	137	39% 64% 32%

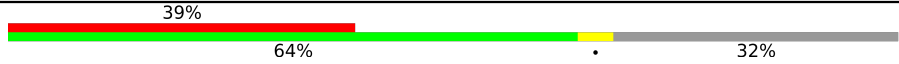
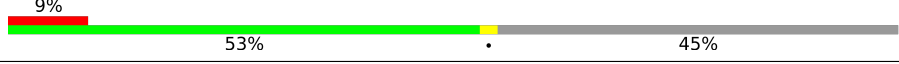
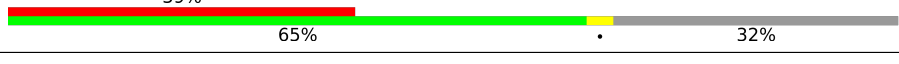



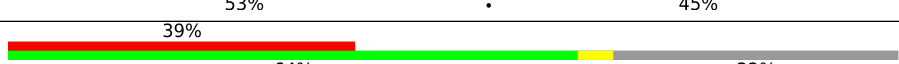

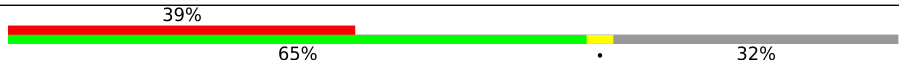


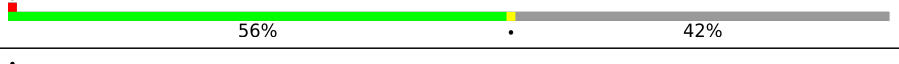
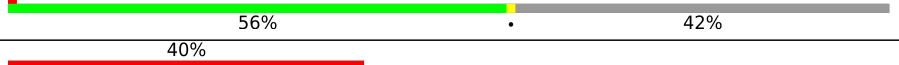

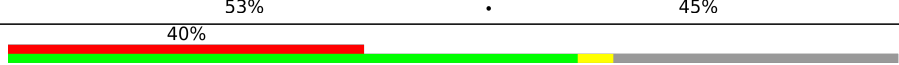
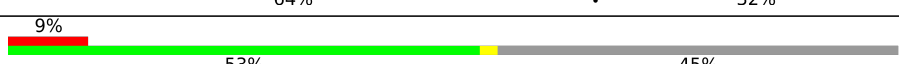









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Mol	Chain	Length	Quality of chain
4	CB	137	
4	CD	137	
4	CE	137	
4	CG	137	
4	D	137	
4	DA	137	
4	DD	137	
4	DG	137	
4	E	137	
4	EA	137	
4	EC	137	
4	ED	137	
4	EF	137	
4	EG	137	
4	FC	137	
4	FF	137	
4	GB	137	
4	GC	137	
4	GE	137	
4	GF	137	
4	H	137	
4	HB	137	
4	HE	137	
4	IA	137	
4	IB	137	

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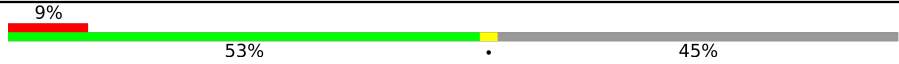
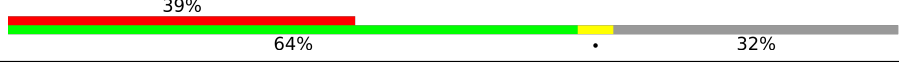
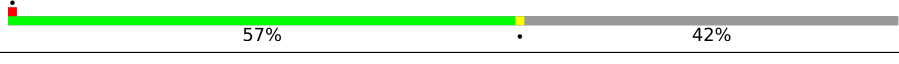




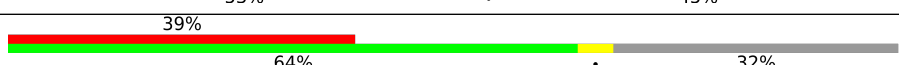


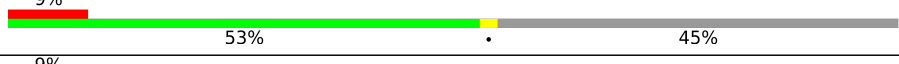
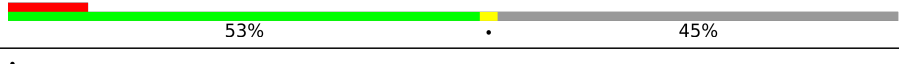
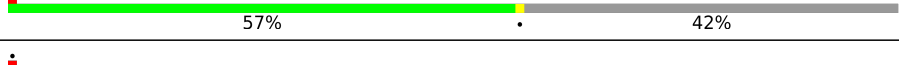



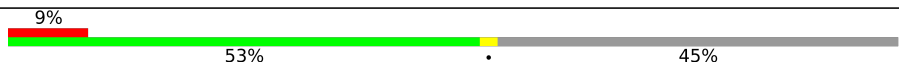



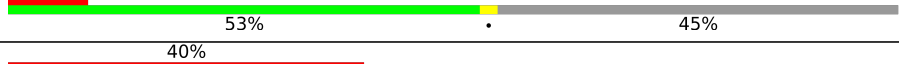




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Mol	Chain	Length	Quality of chain
4	ID	137	
4	IE	137	
4	IG	137	
4	JA	137	
4	JD	137	
4	JG	137	
4	KA	137	
4	KC	137	
4	KD	137	
4	KF	137	
4	KG	137	
4	L	137	
4	LC	137	
4	LF	137	
4	MB	137	
4	MC	137	
4	ME	137	
4	MF	137	
4	N	137	
4	NB	137	
4	NE	137	
4	O	137	
4	OA	137	
4	OB	137	
4	OD	137	

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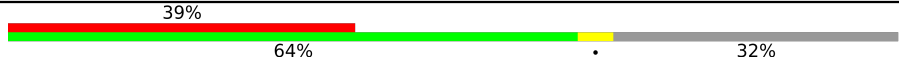
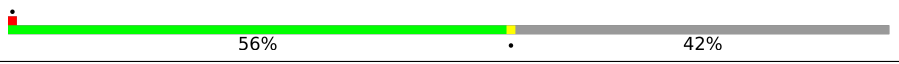





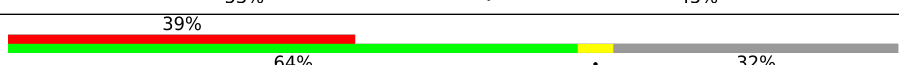

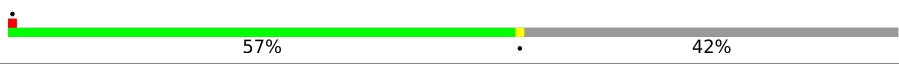
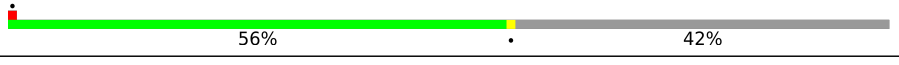
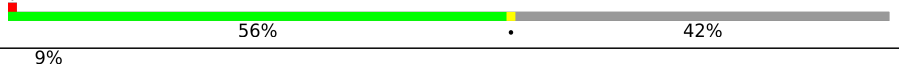


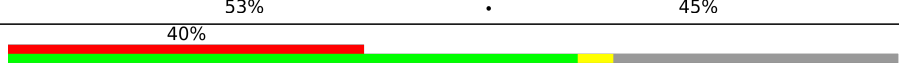
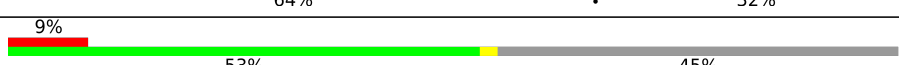






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Mol	Chain	Length	Quality of chain
4	OE	137	
4	OG	137	
4	P	137	
4	PA	137	
4	PD	137	
4	PG	137	
4	Q	137	
4	QA	137	
4	QC	137	
4	QD	137	
4	QF	137	
4	QG	137	
4	R	137	
4	RC	137	
4	RF	137	
4	SB	137	
4	SC	137	
4	SE	137	
4	SF	137	
4	TB	137	
4	TE	137	
4	UA	137	
4	UB	137	
4	UD	137	
4	UE	137	

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Mol	Chain	Length	Quality of chain
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 [i](#)

There are 4 unique types of molecules in this entry. The entry contains 150348 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
			Total	C	N	O		
1	F	47	234	140	47	47	0	0
1	A	47	234	140	47	47	0	0
1	I	47	234	140	47	47	0	0
1	S	47	234	140	47	47	0	0
1	Z	47	234	140	47	47	0	0
1	FA	47	234	140	47	47	0	0
1	LA	47	234	140	47	47	0	0
1	RA	47	234	140	47	47	0	0
1	XA	47	234	140	47	47	0	0
1	DB	47	234	140	47	47	0	0
1	JB	47	234	140	47	47	0	0
1	PB	47	234	140	47	47	0	0
1	VB	47	234	140	47	47	0	0
1	BC	47	234	140	47	47	0	0
1	HC	47	234	140	47	47	0	0
1	NC	47	234	140	47	47	0	0
1	TC	47	234	140	47	47	0	0

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	314	Total 1554	C 926	N 314	O 314	0	0
2	B	314	Total 1554	C 926	N 314	O 314	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	J	314	Total 1554	C 926	N 314	O 314	0	0
2	T	314	Total 1554	C 926	N 314	O 314	0	0
2	AA	314	Total 1554	C 926	N 314	O 314	0	0
2	GA	314	Total 1554	C 926	N 314	O 314	0	0
2	MA	314	Total 1554	C 926	N 314	O 314	0	0
2	SA	314	Total 1554	C 926	N 314	O 314	0	0
2	YA	314	Total 1554	C 926	N 314	O 314	0	0
2	EB	314	Total 1554	C 926	N 314	O 314	0	0
2	KB	314	Total 1554	C 926	N 314	O 314	0	0
2	QB	314	Total 1554	C 926	N 314	O 314	0	0
2	WB	314	Total 1554	C 926	N 314	O 314	0	0
2	CC	314	Total 1554	C 926	N 314	O 314	0	0
2	IC	314	Total 1554	C 926	N 314	O 314	0	0
2	OC	314	Total 1554	C 926	N 314	O 314	0	0
2	UC	314	Total 1554	C 926	N 314	O 314	0	0
2	AD	314	Total 1554	C 926	N 314	O 314	0	0
2	GD	314	Total 1554	C 926	N 314	O 314	0	0
2	MD	314	Total 1554	C 926	N 314	O 314	0	0
2	SD	314	Total 1554	C 926	N 314	O 314	0	0
2	YD	314	Total 1554	C 926	N 314	O 314	0	0
2	EE	314	Total 1554	C 926	N 314	O 314	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	KE	314	Total 1554	C 926	N 314	O 314	0	0
2	QE	314	Total 1554	C 926	N 314	O 314	0	0
2	WE	314	Total 1554	C 926	N 314	O 314	0	0
2	CF	314	Total 1554	C 926	N 314	O 314	0	0
2	IF	314	Total 1554	C 926	N 314	O 314	0	0
2	OF	314	Total 1554	C 926	N 314	O 314	0	0
2	UF	314	Total 1554	C 926	N 314	O 314	0	0
2	AG	314	Total 1554	C 926	N 314	O 314	0	0
2	GG	314	Total 1554	C 926	N 314	O 314	0	0
2	MG	314	Total 1554	C 926	N 314	O 314	0	0
2	SG	314	Total 1554	C 926	N 314	O 314	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
4	N	93	Total	C	N	O	0	0
			456	270	93	93		
4	P	79	Total	C	N	O	0	0
			389	230	79	80		
4	Q	75	Total	C	N	O	0	0
			369	218	75	76		
4	D	93	Total	C	N	O	0	0
			456	270	93	93		
4	E	79	Total	C	N	O	0	0
			389	230	79	80		
4	H	75	Total	C	N	O	0	0
			369	218	75	76		
4	L	93	Total	C	N	O	0	0
			456	270	93	93		
4	O	79	Total	C	N	O	0	0
			389	230	79	80		
4	R	75	Total	C	N	O	0	0
			369	218	75	76		
4	W	93	Total	C	N	O	0	0
			456	270	93	93		
4	X	79	Total	C	N	O	0	0
			389	230	79	80		
4	Y	75	Total	C	N	O	0	0
			369	218	75	76		
4	CA	93	Total	C	N	O	0	0
			456	270	93	93		
4	DA	79	Total	C	N	O	0	0
			389	230	79	80		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	EA	75	Total	C	N	O	0	0
			369	218	75	76		
4	IA	93	Total	C	N	O	0	0
			456	270	93	93		
4	JA	79	Total	C	N	O	0	0
			389	230	79	80		
4	KA	75	Total	C	N	O	0	0
			369	218	75	76		
4	OA	93	Total	C	N	O	0	0
			456	270	93	93		
4	PA	79	Total	C	N	O	0	0
			389	230	79	80		
4	QA	75	Total	C	N	O	0	0
			369	218	75	76		
4	UA	93	Total	C	N	O	0	0
			456	270	93	93		
4	VA	79	Total	C	N	O	0	0
			389	230	79	80		
4	WA	75	Total	C	N	O	0	0
			369	218	75	76		
4	AB	93	Total	C	N	O	0	0
			456	270	93	93		
4	BB	79	Total	C	N	O	0	0
			389	230	79	80		
4	CB	75	Total	C	N	O	0	0
			369	218	75	76		
4	GB	93	Total	C	N	O	0	0
			456	270	93	93		
4	HB	79	Total	C	N	O	0	0
			389	230	79	80		
4	IB	75	Total	C	N	O	0	0
			369	218	75	76		
4	MB	93	Total	C	N	O	0	0
			456	270	93	93		
4	NB	79	Total	C	N	O	0	0
			389	230	79	80		
4	OB	75	Total	C	N	O	0	0
			369	218	75	76		
4	SB	93	Total	C	N	O	0	0
			456	270	93	93		
4	TB	79	Total	C	N	O	0	0
			389	230	79	80		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	UB	75	Total	C	N	O	0	0
			369	218	75	76		
4	YB	93	Total	C	N	O	0	0
			456	270	93	93		
4	ZB	79	Total	C	N	O	0	0
			389	230	79	80		
4	AC	75	Total	C	N	O	0	0
			369	218	75	76		
4	EC	93	Total	C	N	O	0	0
			456	270	93	93		
4	FC	79	Total	C	N	O	0	0
			389	230	79	80		
4	GC	75	Total	C	N	O	0	0
			369	218	75	76		
4	KC	93	Total	C	N	O	0	0
			456	270	93	93		
4	LC	79	Total	C	N	O	0	0
			389	230	79	80		
4	MC	75	Total	C	N	O	0	0
			369	218	75	76		
4	QC	93	Total	C	N	O	0	0
			456	270	93	93		
4	RC	79	Total	C	N	O	0	0
			389	230	79	80		
4	SC	75	Total	C	N	O	0	0
			369	218	75	76		
4	WC	93	Total	C	N	O	0	0
			456	270	93	93		
4	XC	79	Total	C	N	O	0	0
			389	230	79	80		
4	YC	75	Total	C	N	O	0	0
			369	218	75	76		
4	CD	93	Total	C	N	O	0	0
			456	270	93	93		
4	DD	79	Total	C	N	O	0	0
			389	230	79	80		
4	ED	75	Total	C	N	O	0	0
			369	218	75	76		
4	ID	93	Total	C	N	O	0	0
			456	270	93	93		
4	JD	79	Total	C	N	O	0	0
			389	230	79	80		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	KD	75	Total	C	N	O	0	0
			369	218	75	76		
4	OD	93	Total	C	N	O	0	0
			456	270	93	93		
4	PD	79	Total	C	N	O	0	0
			389	230	79	80		
4	QD	75	Total	C	N	O	0	0
			369	218	75	76		
4	UD	93	Total	C	N	O	0	0
			456	270	93	93		
4	VD	79	Total	C	N	O	0	0
			389	230	79	80		
4	WD	75	Total	C	N	O	0	0
			369	218	75	76		
4	AE	93	Total	C	N	O	0	0
			456	270	93	93		
4	BE	79	Total	C	N	O	0	0
			389	230	79	80		
4	CE	75	Total	C	N	O	0	0
			369	218	75	76		
4	GE	93	Total	C	N	O	0	0
			456	270	93	93		
4	HE	79	Total	C	N	O	0	0
			389	230	79	80		
4	IE	75	Total	C	N	O	0	0
			369	218	75	76		
4	ME	93	Total	C	N	O	0	0
			456	270	93	93		
4	NE	79	Total	C	N	O	0	0
			389	230	79	80		
4	OE	75	Total	C	N	O	0	0
			369	218	75	76		
4	SE	93	Total	C	N	O	0	0
			456	270	93	93		
4	TE	79	Total	C	N	O	0	0
			389	230	79	80		
4	UE	75	Total	C	N	O	0	0
			369	218	75	76		
4	YE	93	Total	C	N	O	0	0
			456	270	93	93		
4	ZE	79	Total	C	N	O	0	0
			389	230	79	80		

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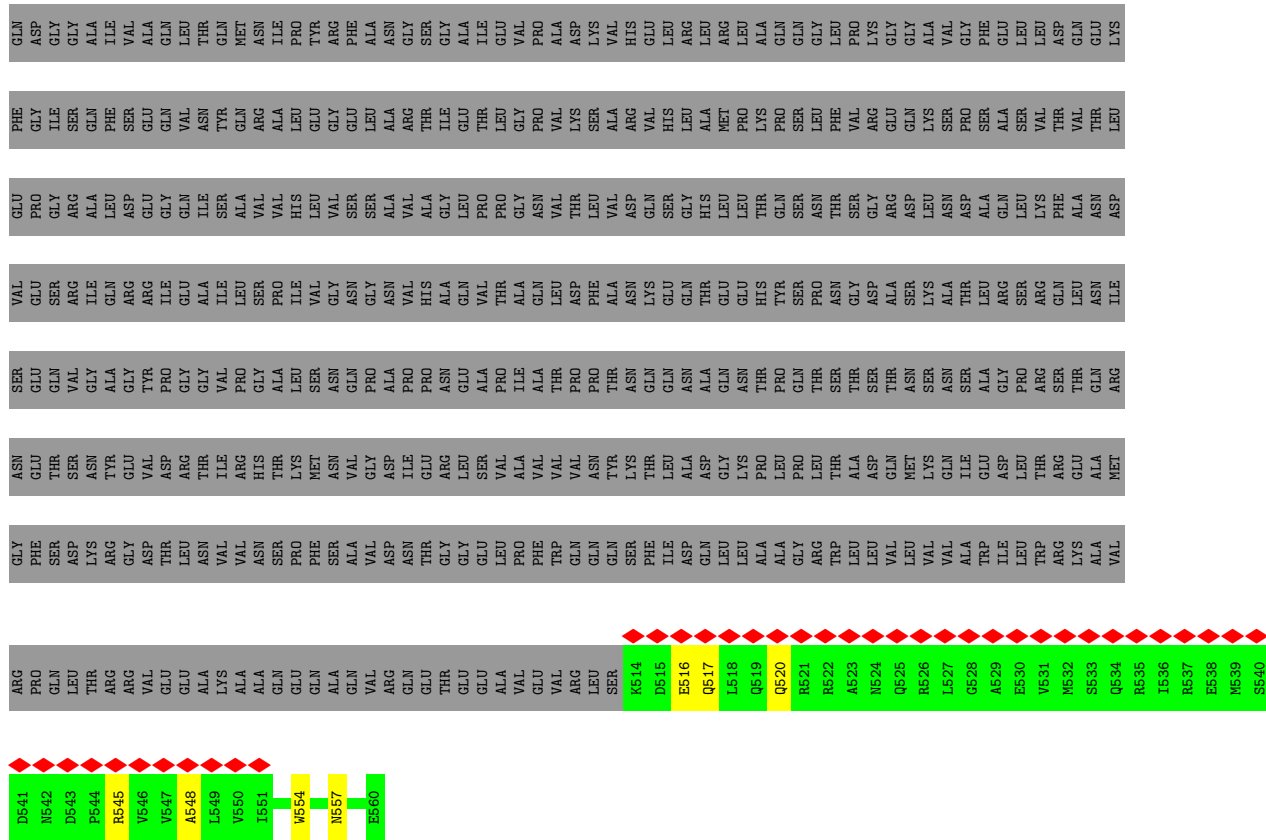
Mol	Chain	Residues	Atoms				AltConf	Trace
4	AF	75	Total	C	N	O	0	0
			369	218	75	76		
4	EF	93	Total	C	N	O	0	0
			456	270	93	93		
4	FF	79	Total	C	N	O	0	0
			389	230	79	80		
4	GF	75	Total	C	N	O	0	0
			369	218	75	76		
4	KF	93	Total	C	N	O	0	0
			456	270	93	93		
4	LF	79	Total	C	N	O	0	0
			389	230	79	80		
4	MF	75	Total	C	N	O	0	0
			369	218	75	76		
4	QF	93	Total	C	N	O	0	0
			456	270	93	93		
4	RF	79	Total	C	N	O	0	0
			389	230	79	80		
4	SF	75	Total	C	N	O	0	0
			369	218	75	76		
4	WF	93	Total	C	N	O	0	0
			456	270	93	93		
4	XF	79	Total	C	N	O	0	0
			389	230	79	80		
4	YF	75	Total	C	N	O	0	0
			369	218	75	76		
4	CG	93	Total	C	N	O	0	0
			456	270	93	93		
4	DG	79	Total	C	N	O	0	0
			389	230	79	80		
4	EG	75	Total	C	N	O	0	0
			369	218	75	76		
4	IG	93	Total	C	N	O	0	0
			456	270	93	93		
4	JG	79	Total	C	N	O	0	0
			389	230	79	80		
4	KG	75	Total	C	N	O	0	0
			369	218	75	76		
4	OG	93	Total	C	N	O	0	0
			456	270	93	93		
4	PG	79	Total	C	N	O	0	0
			389	230	79	80		

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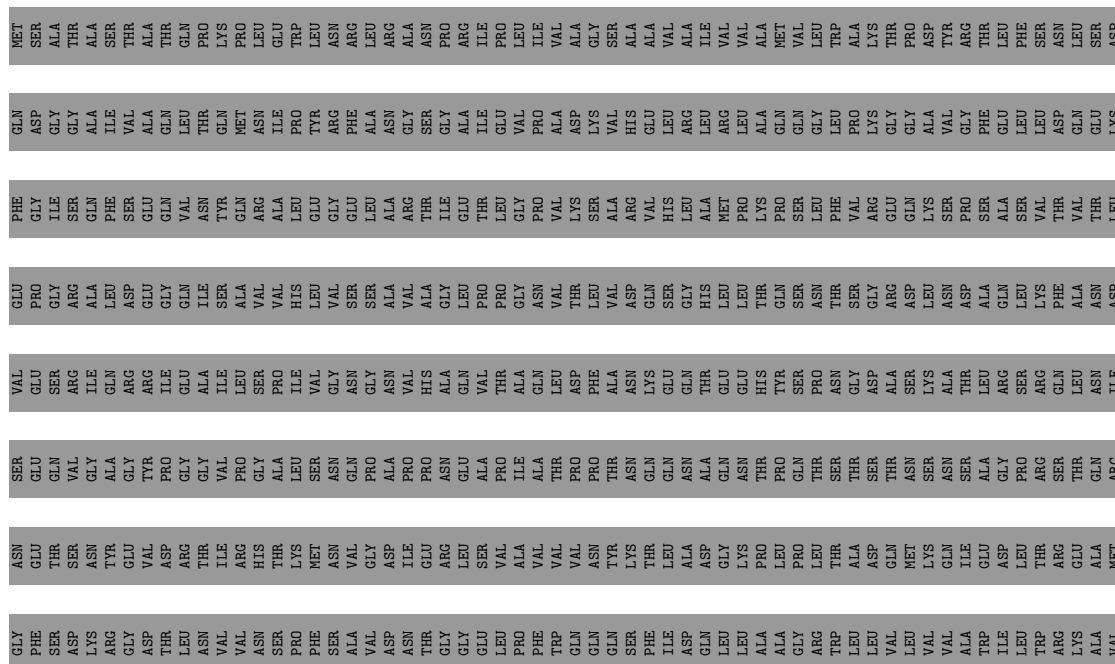
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>				<b>AltConf</b>	<b>Trace</b>
4	QG	75	Total 369	C 218	N 75	O 76	0	0
4	UG	93	Total 456	C 270	N 93	O 93	0	0
4	VG	79	Total 389	C 230	N 79	O 80	0	0
4	WG	75	Total 369	C 218	N 75	O 76	0	0





• Molecule 1: Flagellar M-ring protein



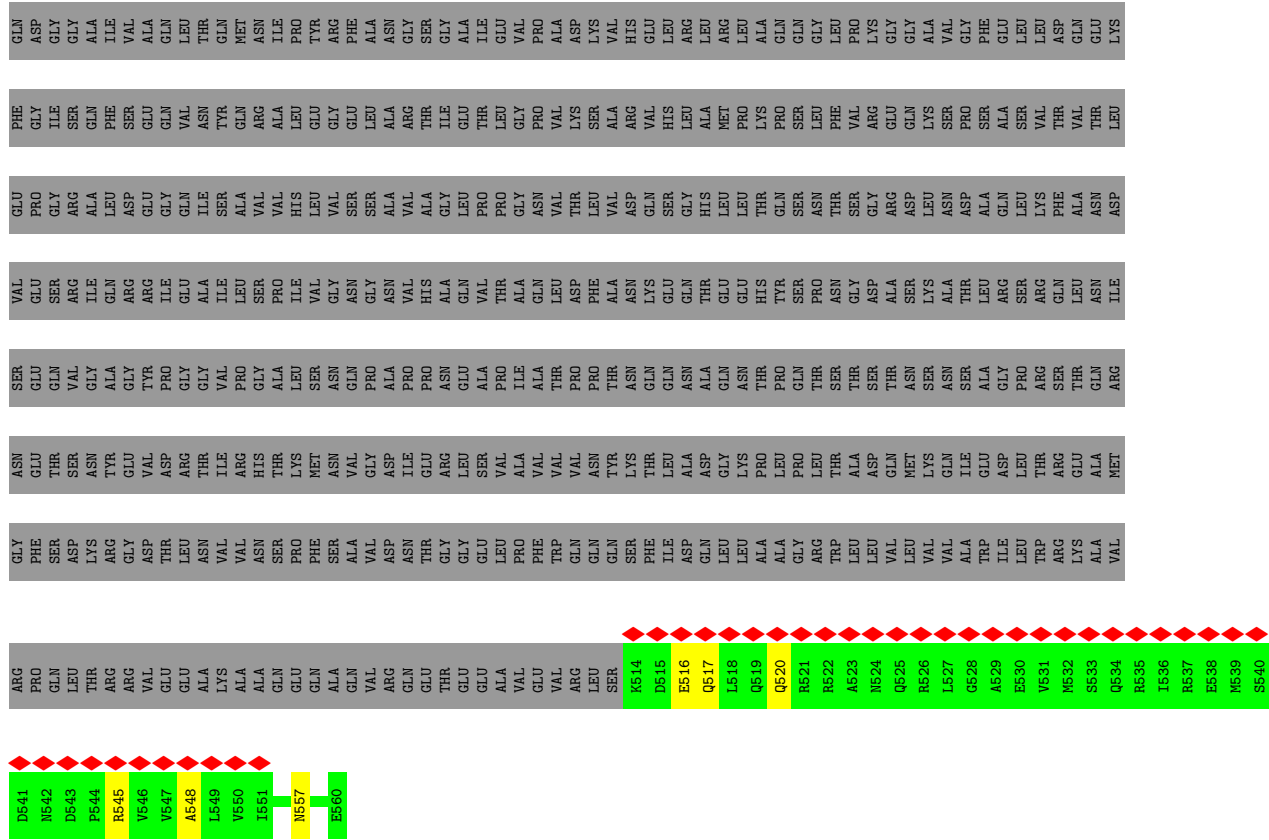




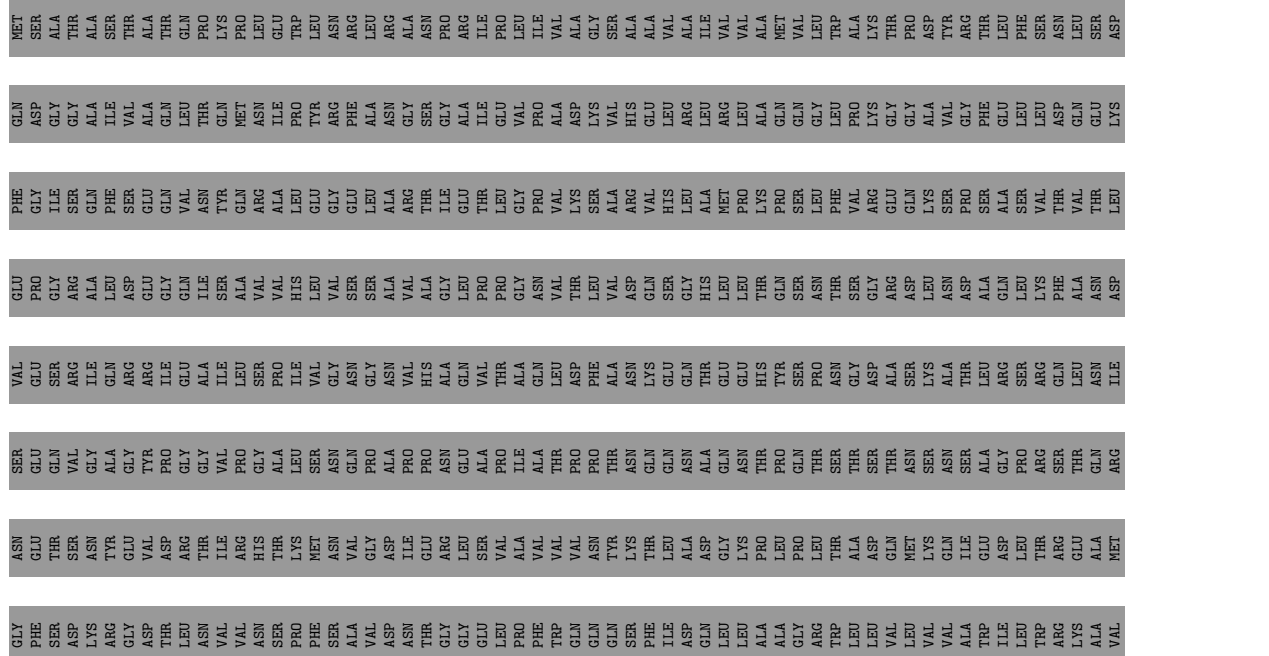




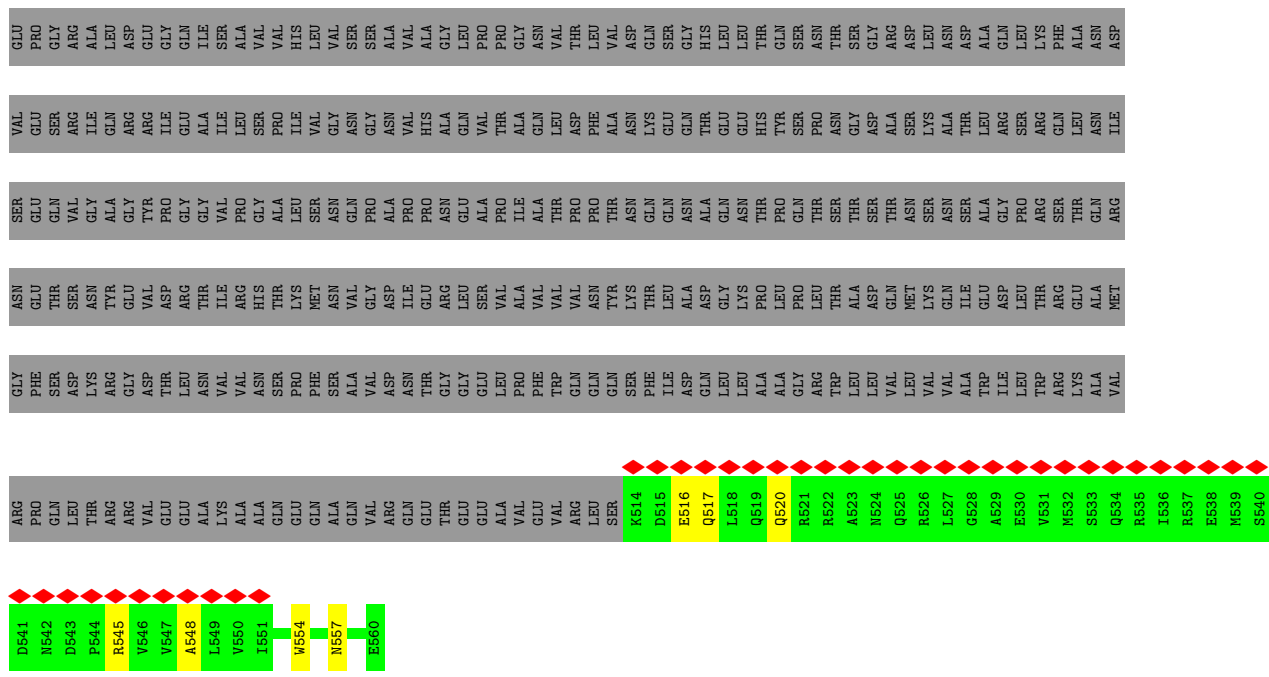




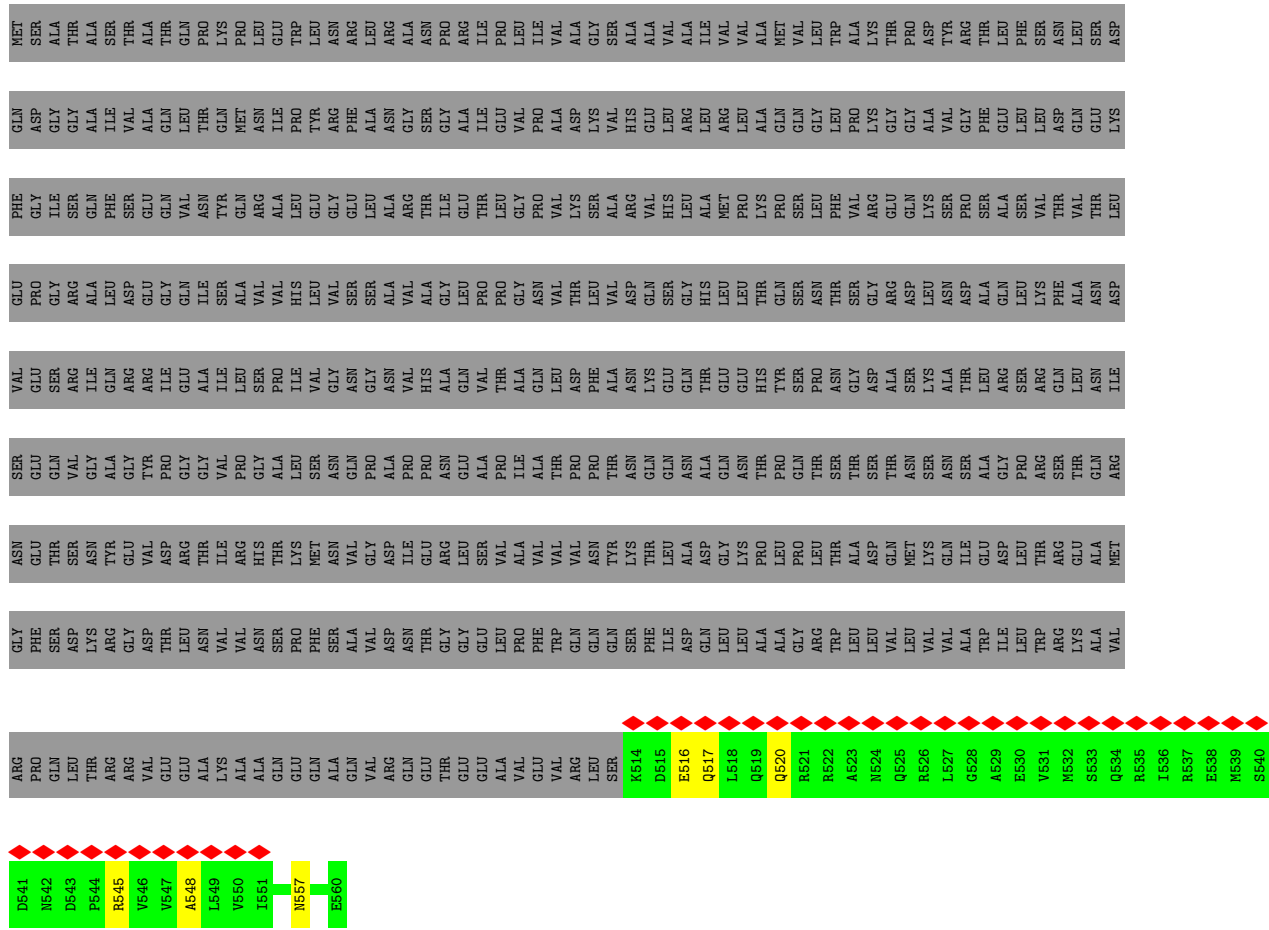
• Molecule 1: Flagellar M-ring protein







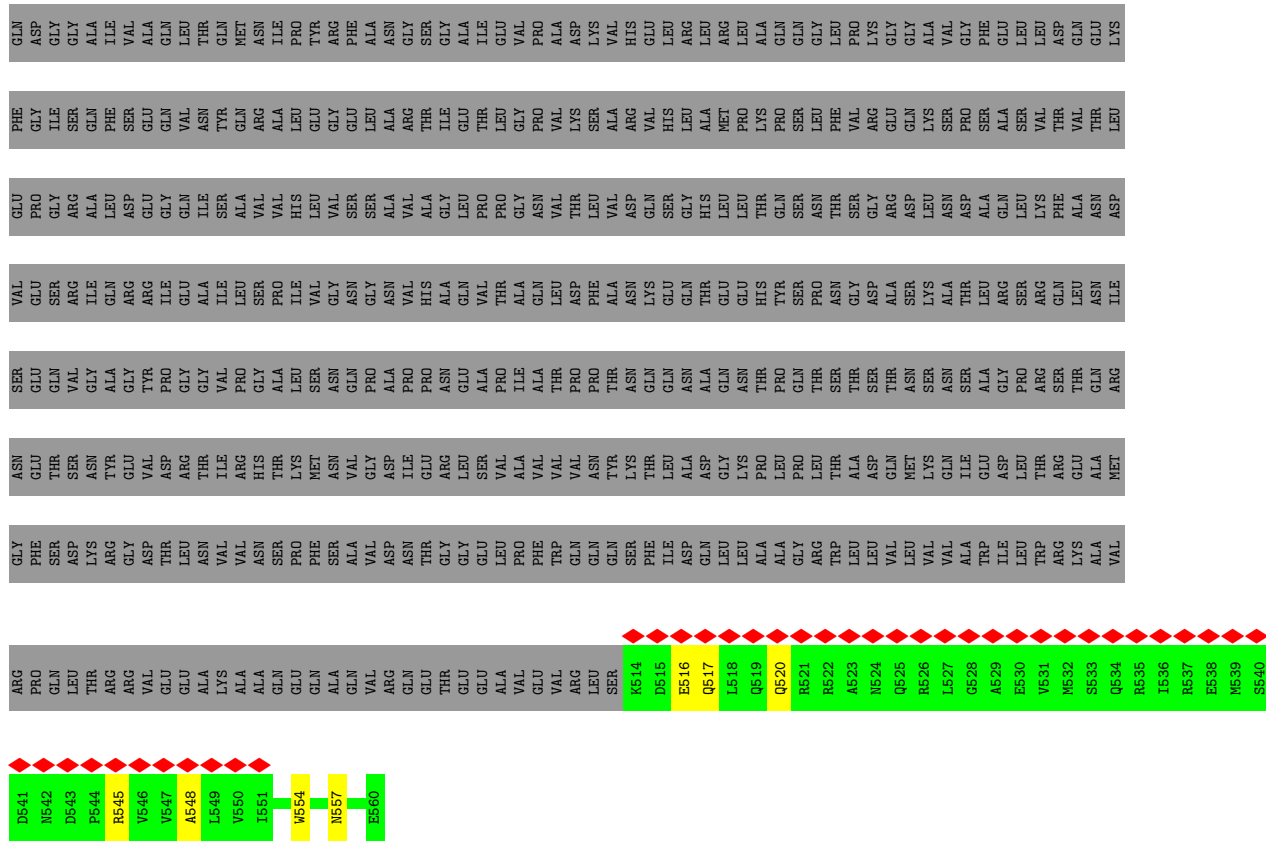
• Molecule 1: Flagellar M-ring protein



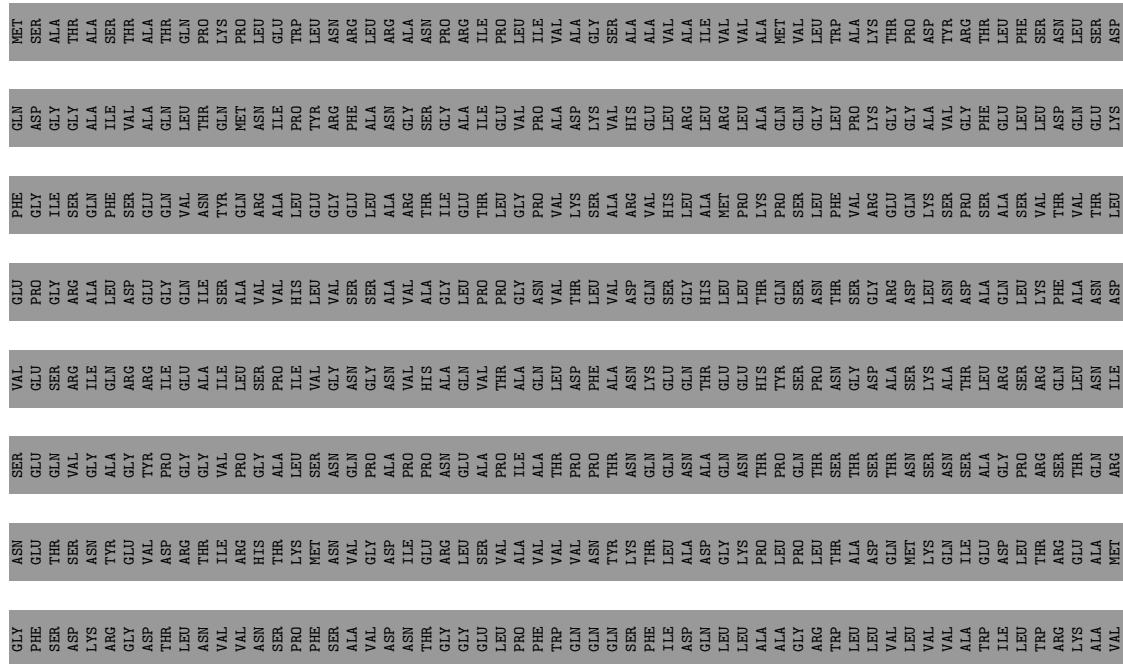


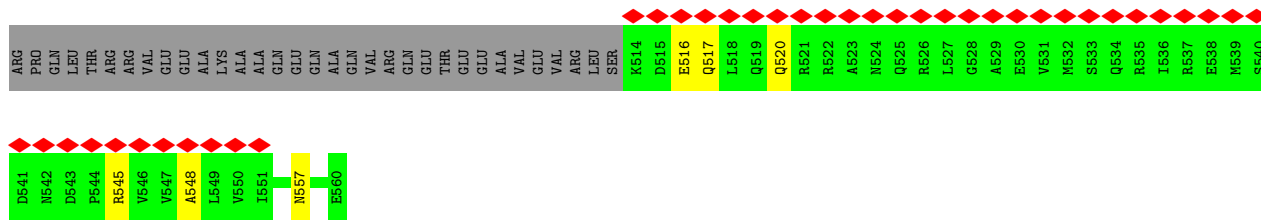




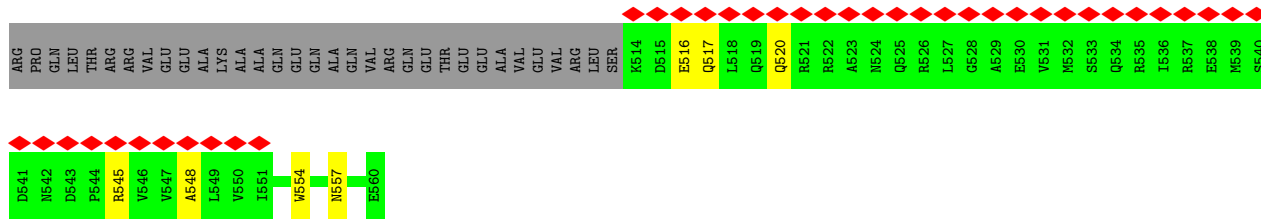
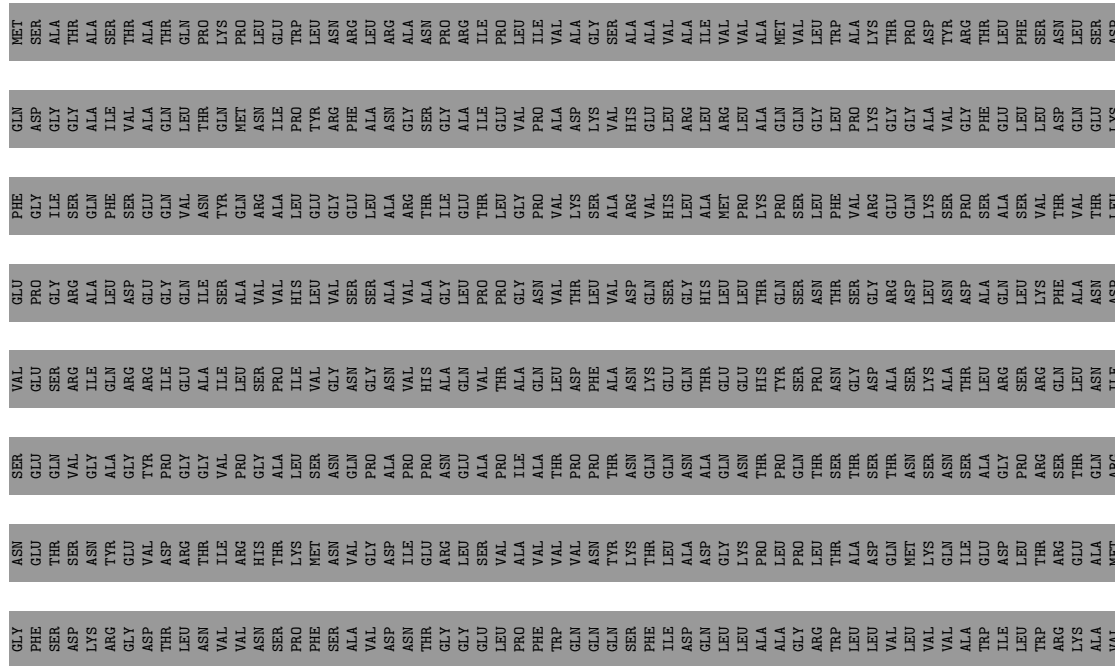


• Molecule 1: Flagellar M-ring protein

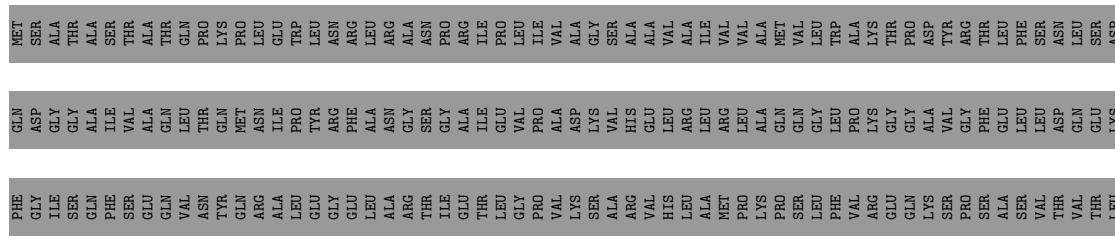


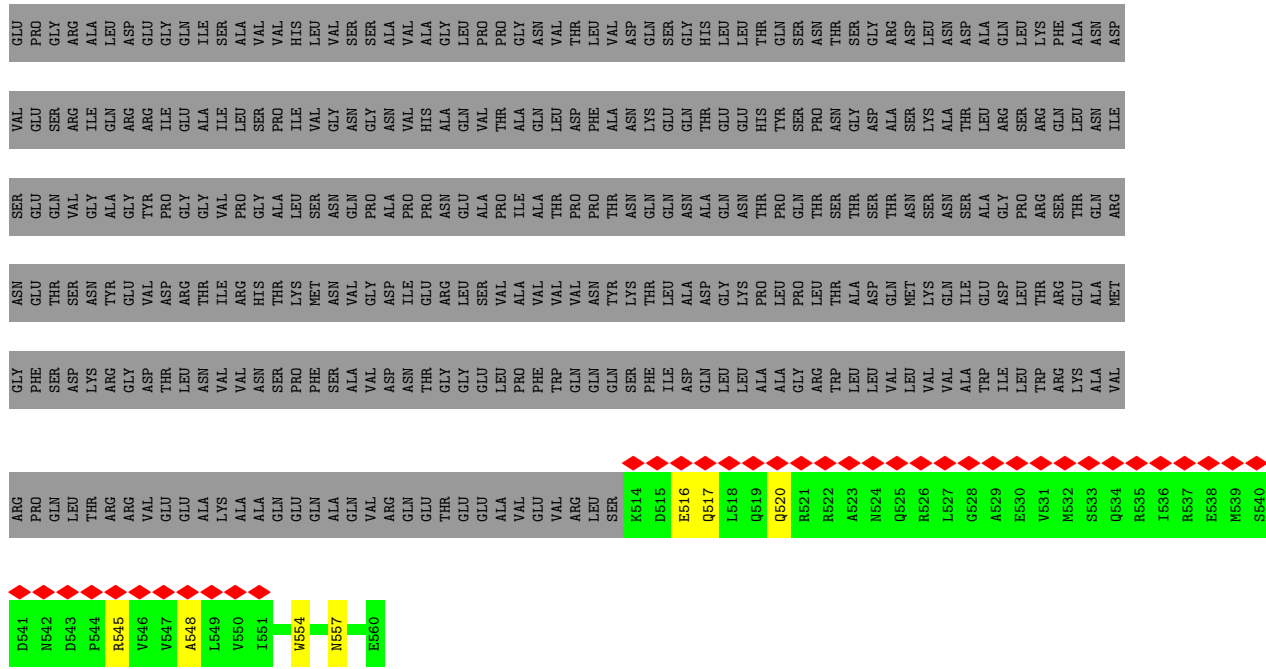


● Molecule 1: Flagellar M-ring protein

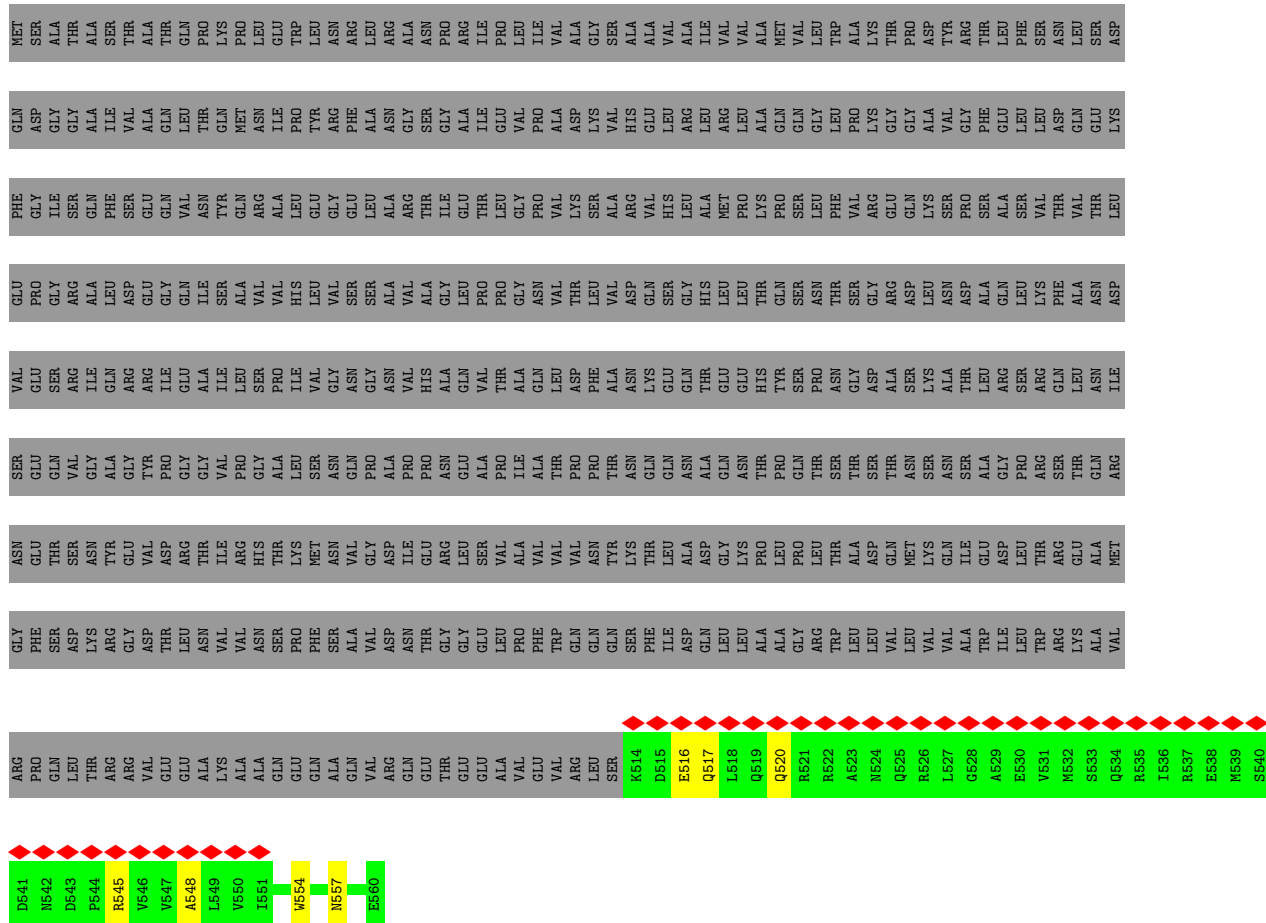


● Molecule 1: Flagellar M-ring protein





• Molecule 1: Flagellar M-ring protein

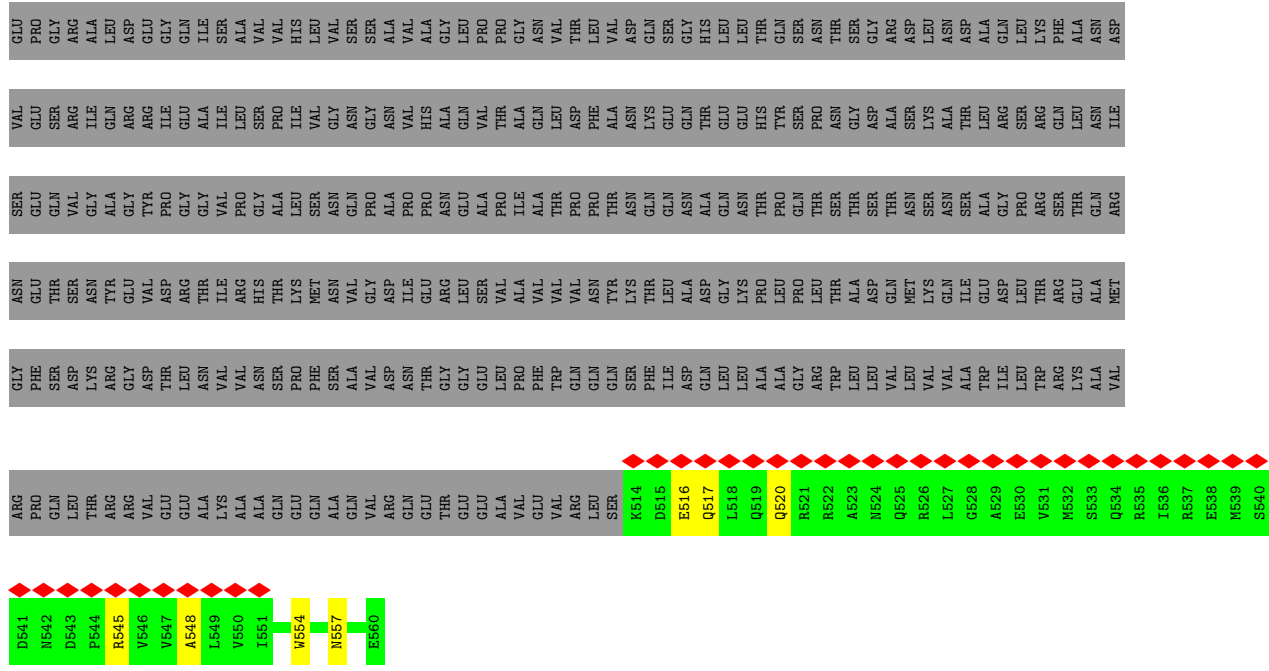




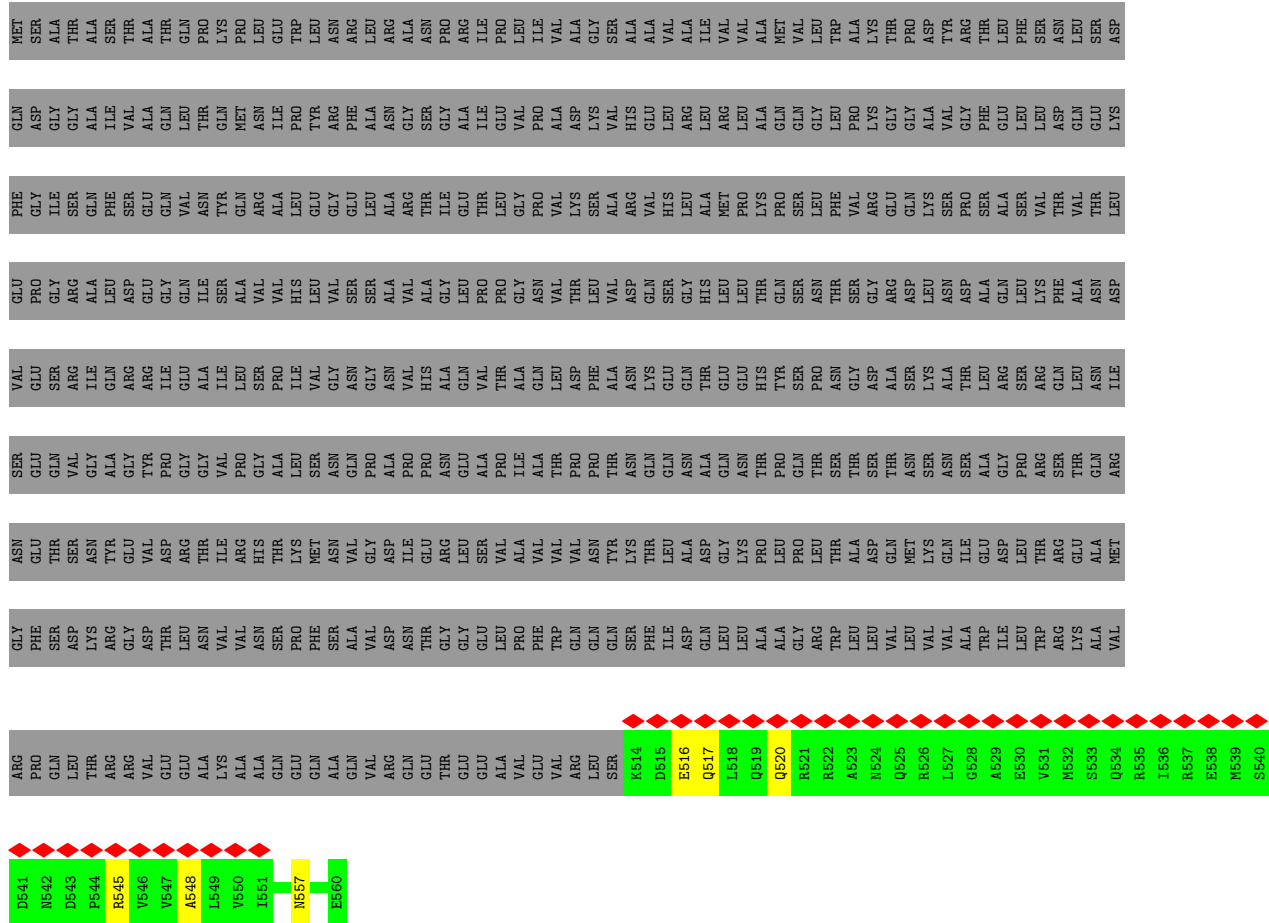








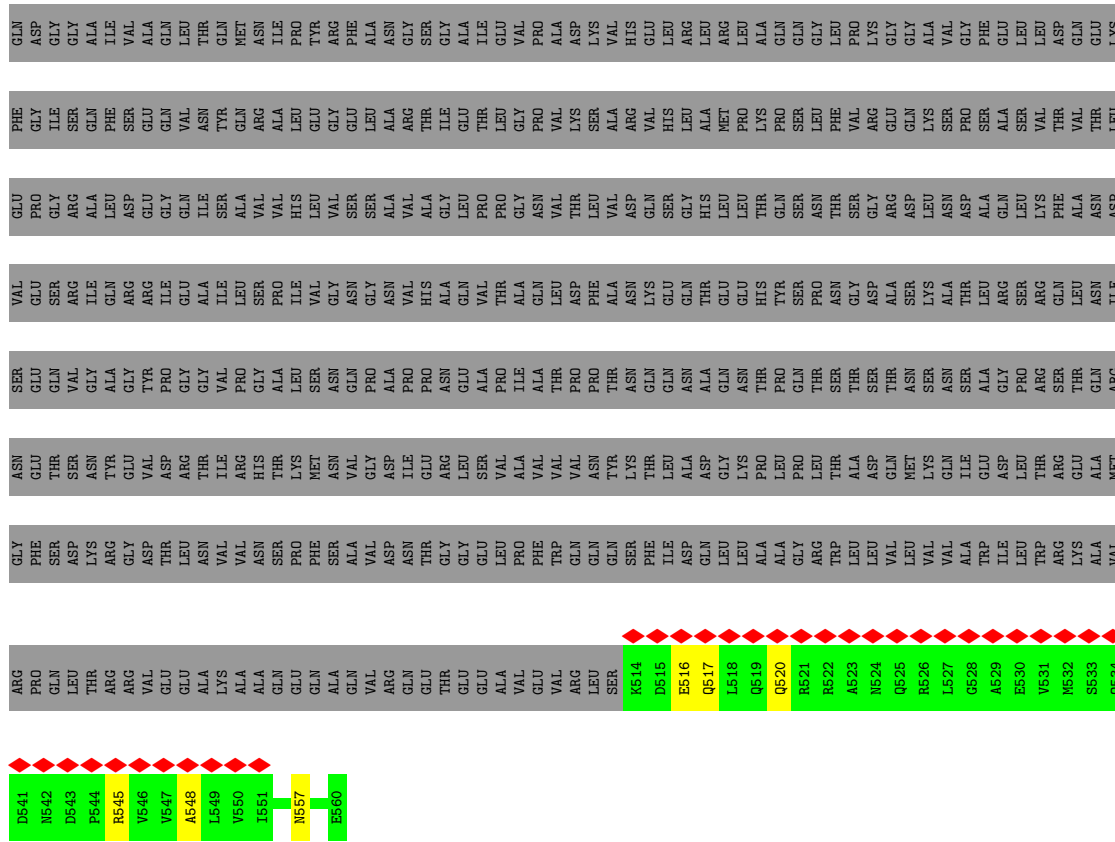
• Molecule 1: Flagellar M-ring protein



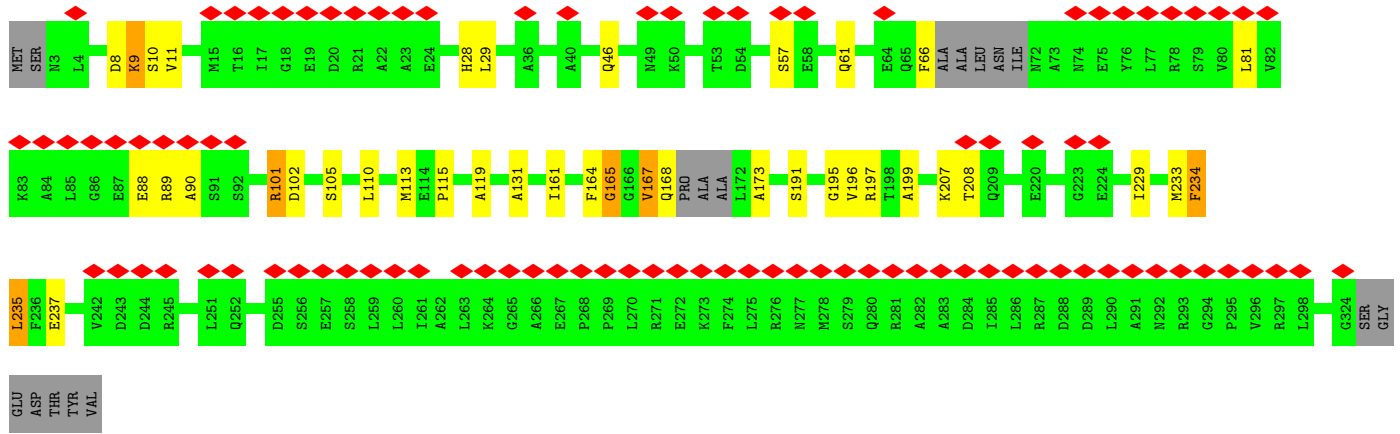
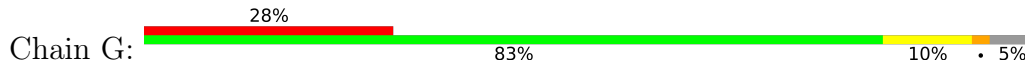




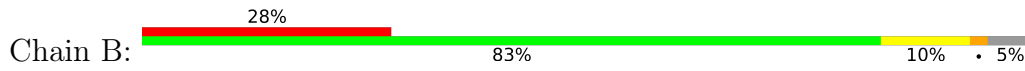


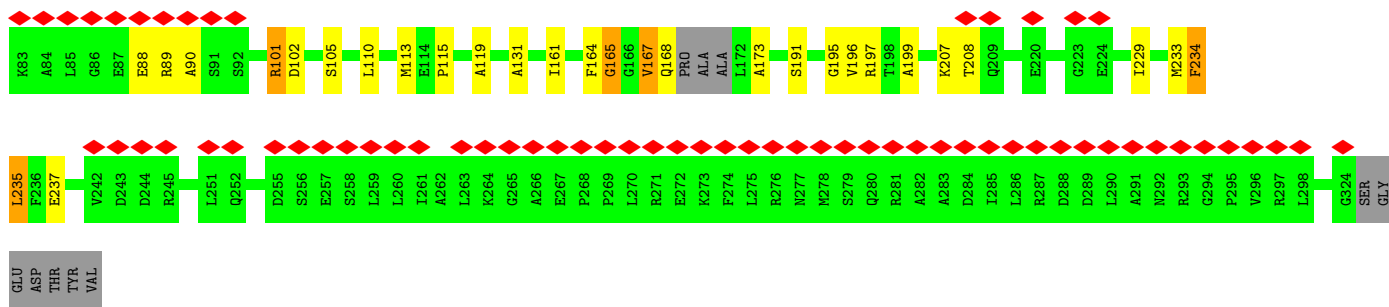


• Molecule 2: Flagellar motor switch protein FlIG

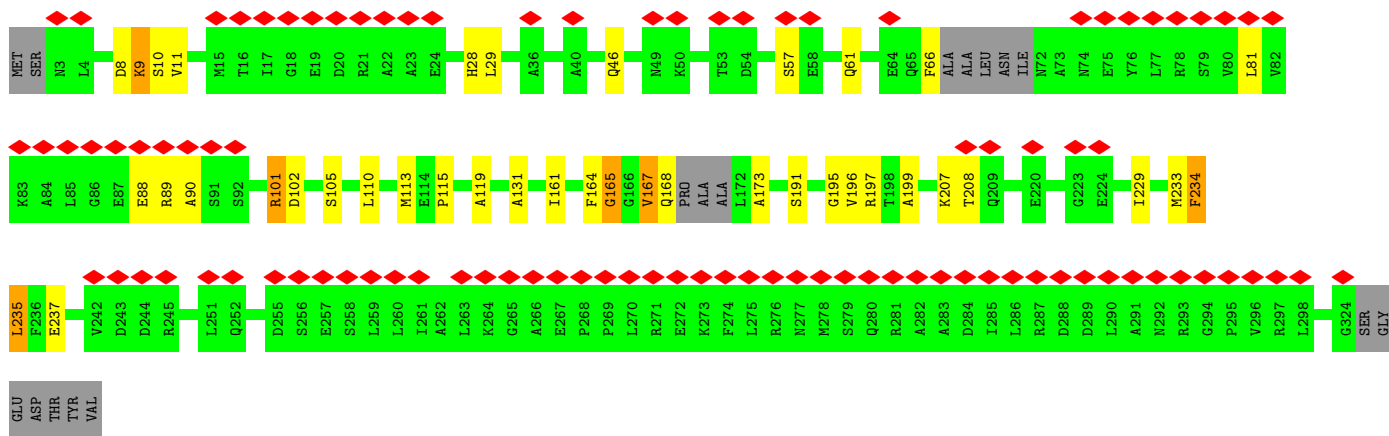
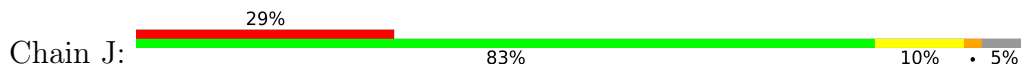


• Molecule 2: Flagellar motor switch protein FlIG

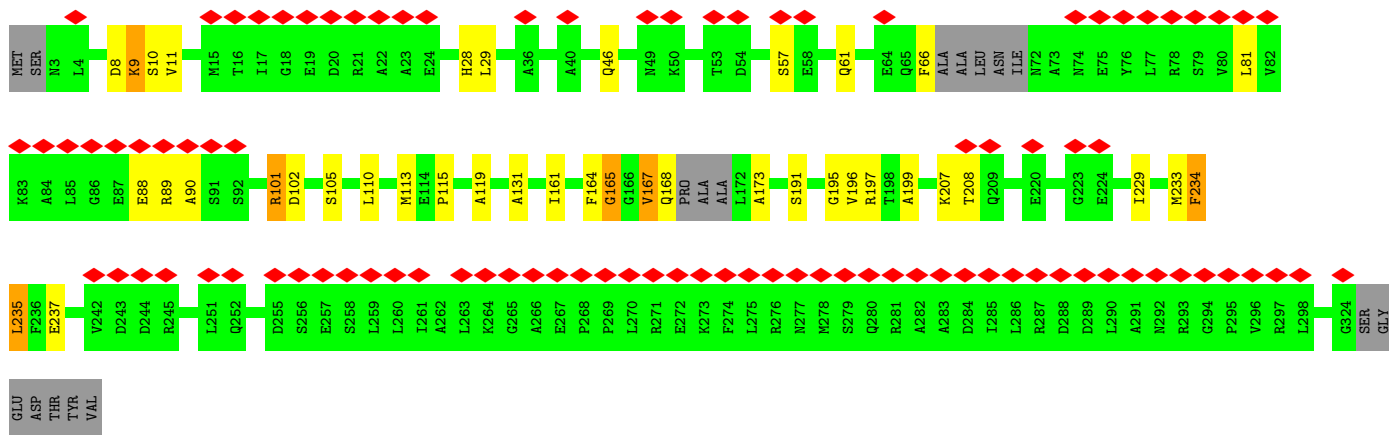
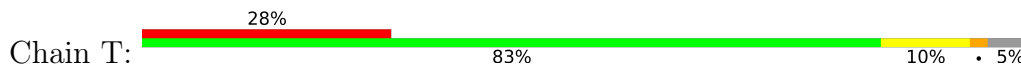




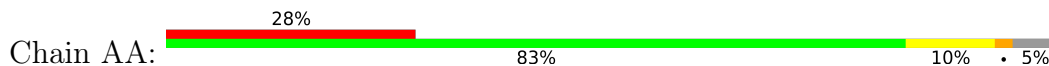
• Molecule 2: Flagellar motor switch protein Flig

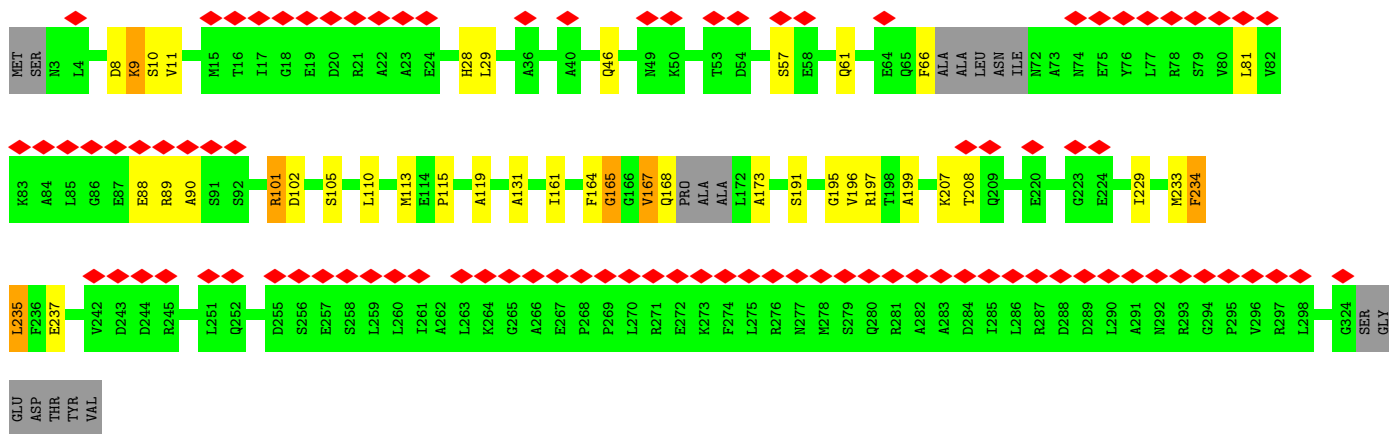


• Molecule 2: Flagellar motor switch protein Flig

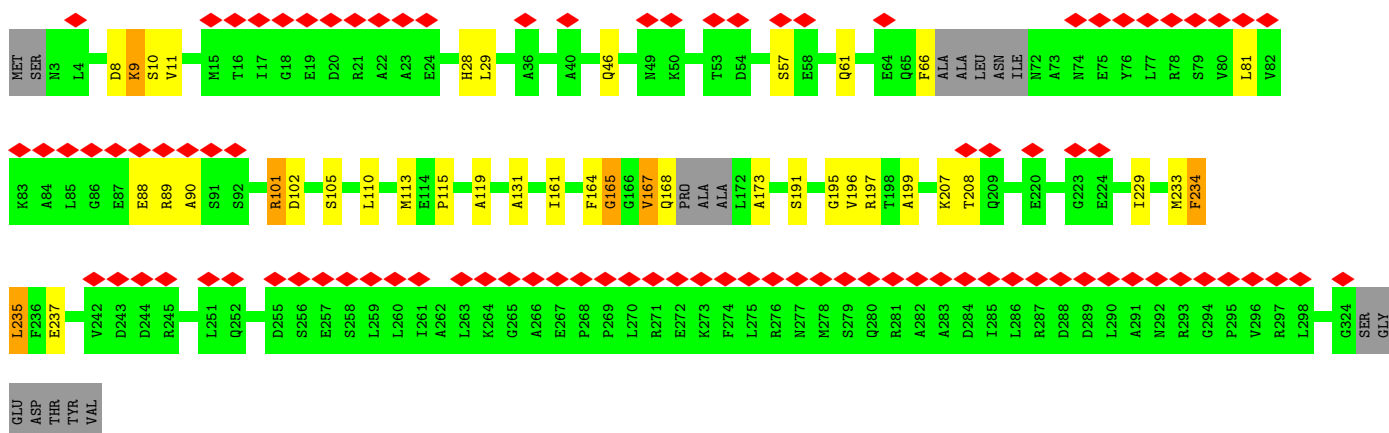
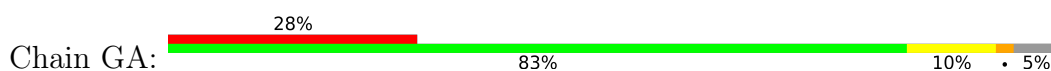


• Molecule 2: Flagellar motor switch protein Flig

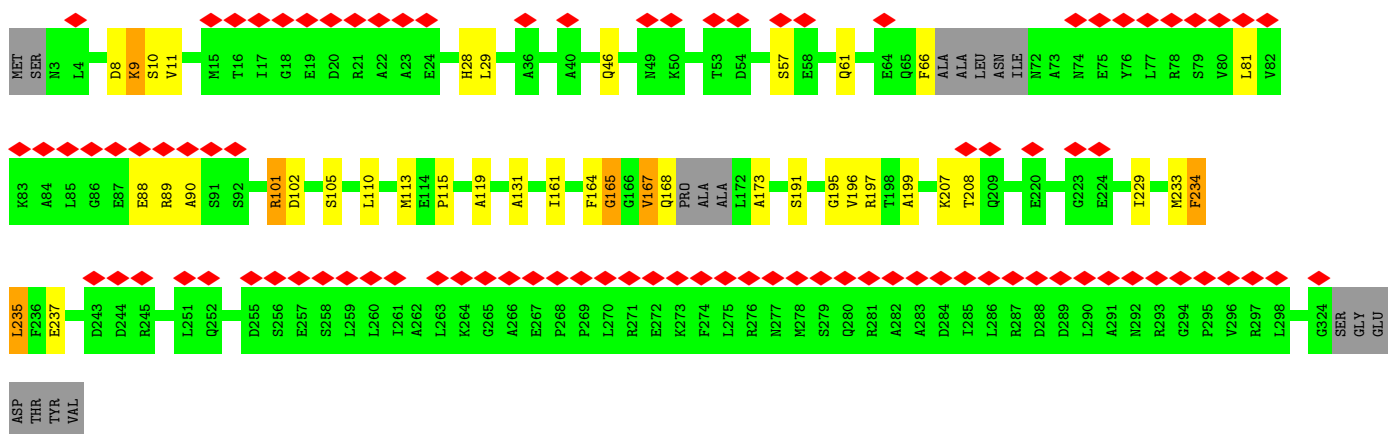
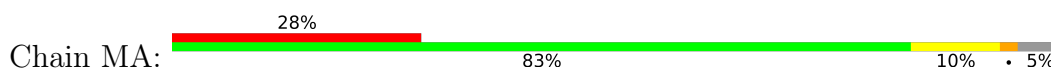




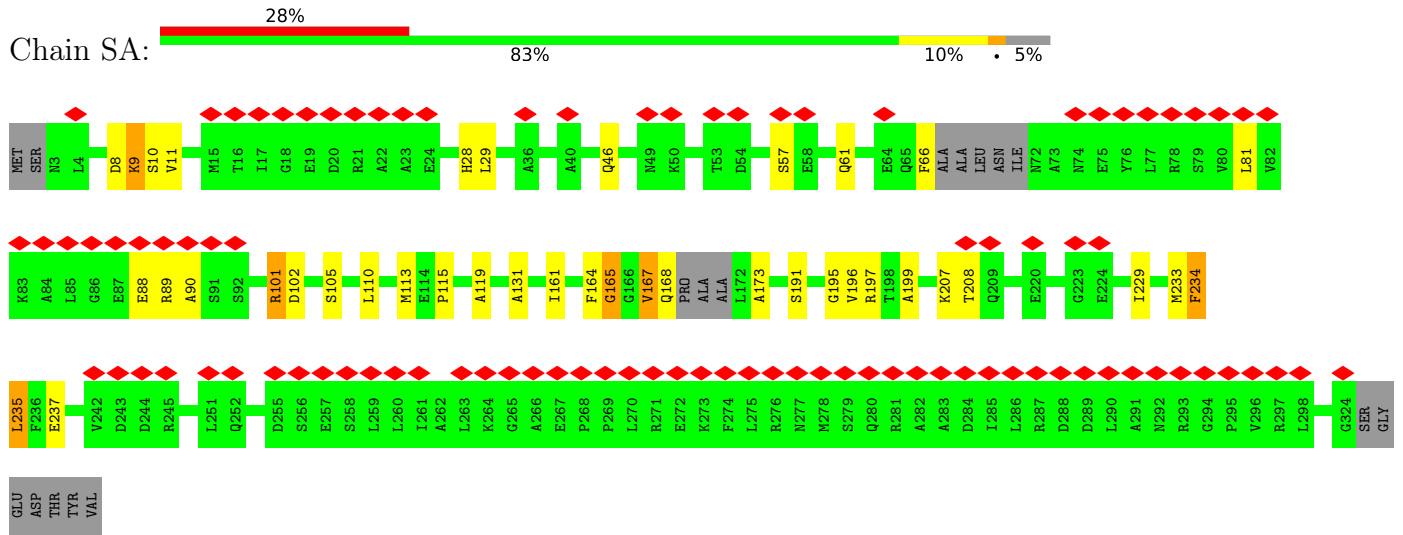
• Molecule 2: Flagellar motor switch protein FliG



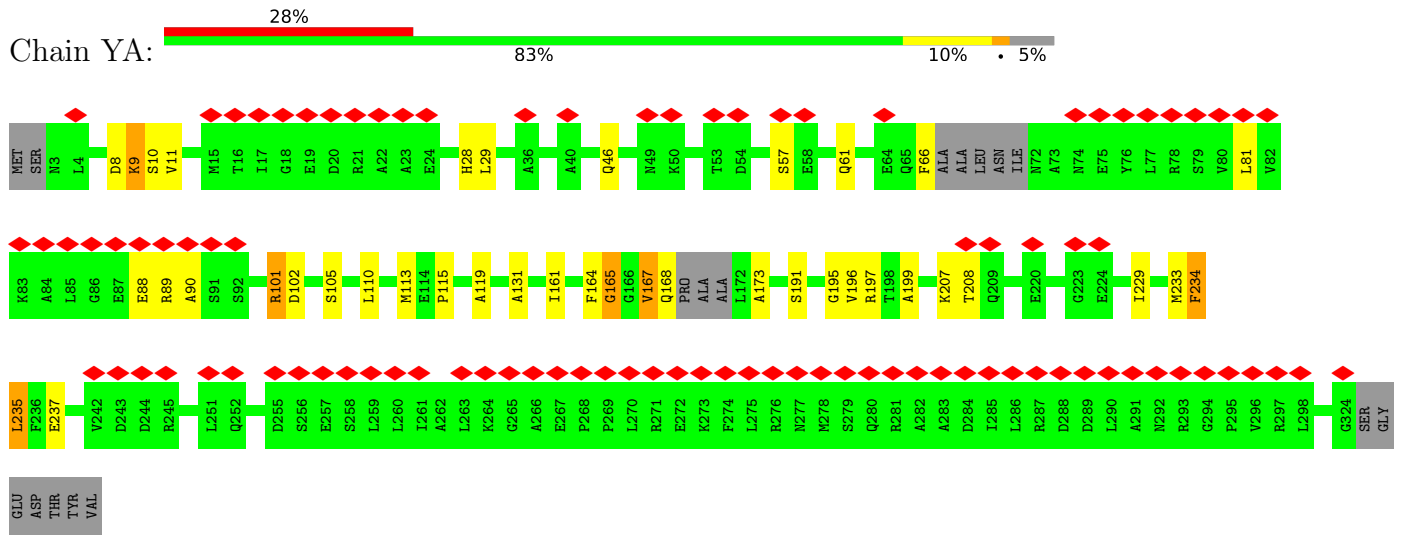
• Molecule 2: Flagellar motor switch protein FliG



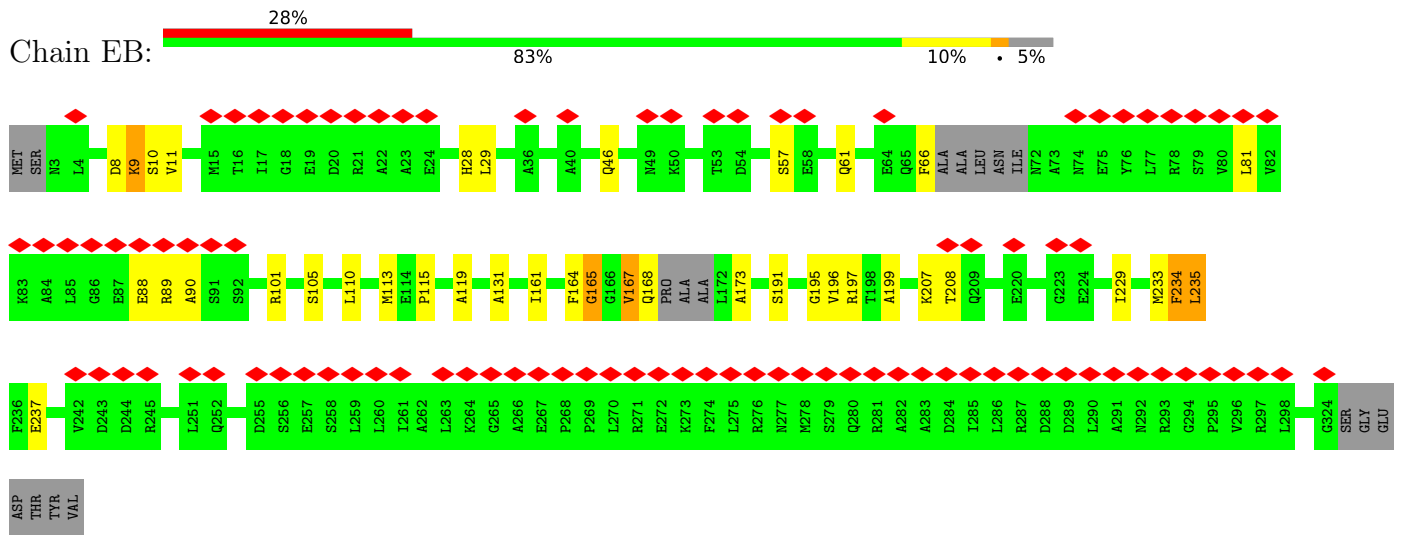
• Molecule 2: Flagellar motor switch protein FliG



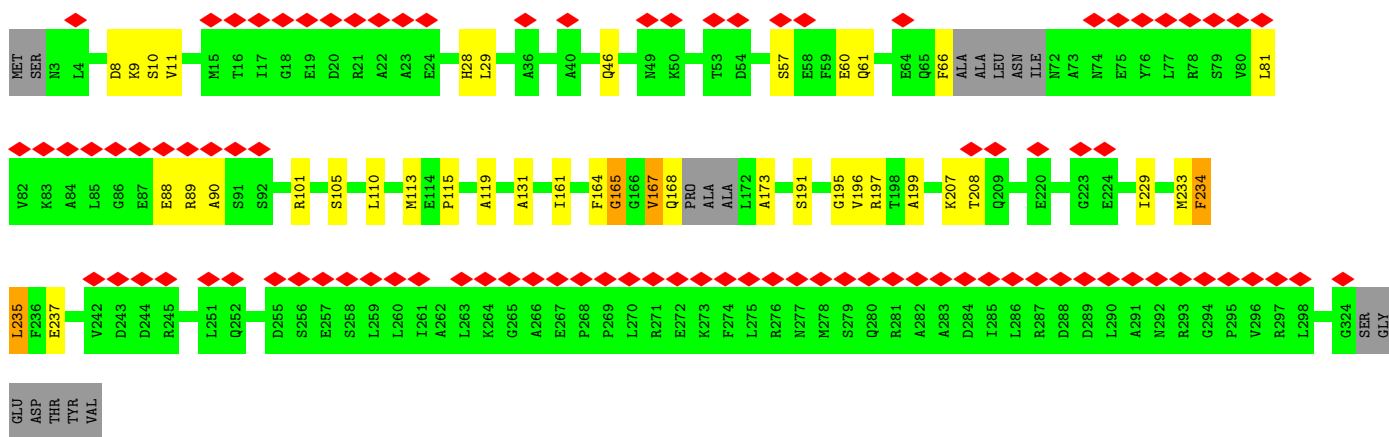
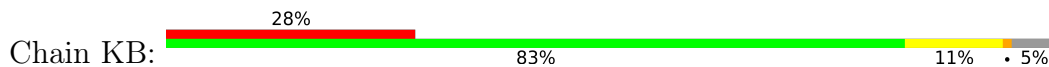
• Molecule 2: Flagellar motor switch protein FliG



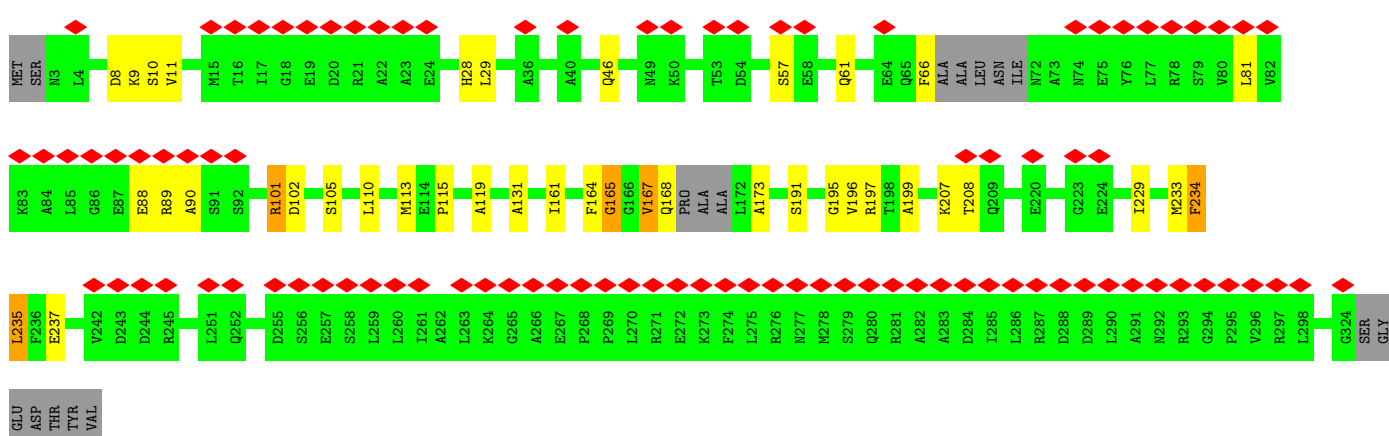
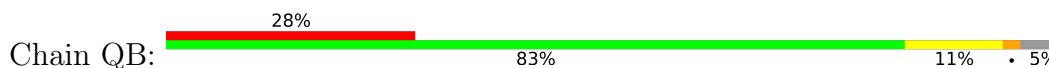
• Molecule 2: Flagellar motor switch protein FliG



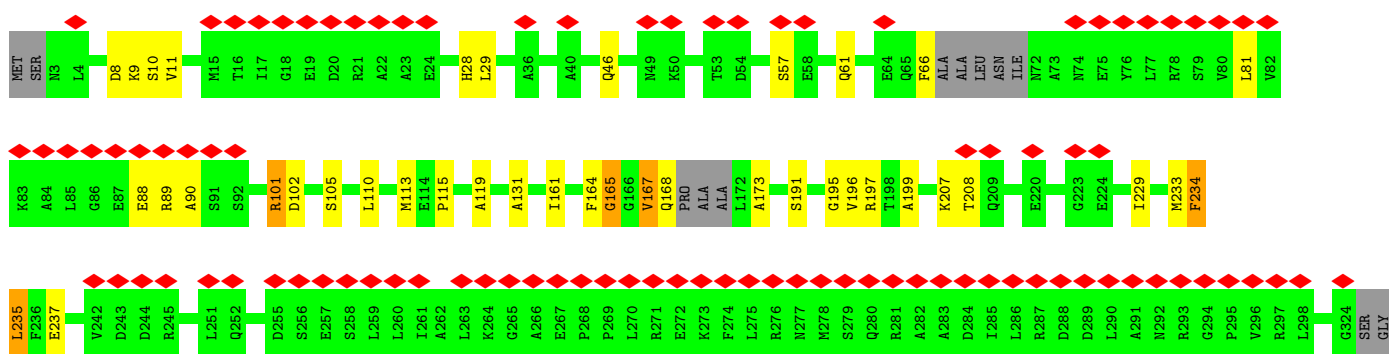
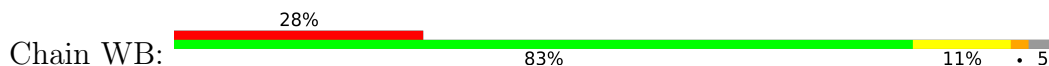
• Molecule 2: Flagellar motor switch protein Flig



• Molecule 2: Flagellar motor switch protein Flig

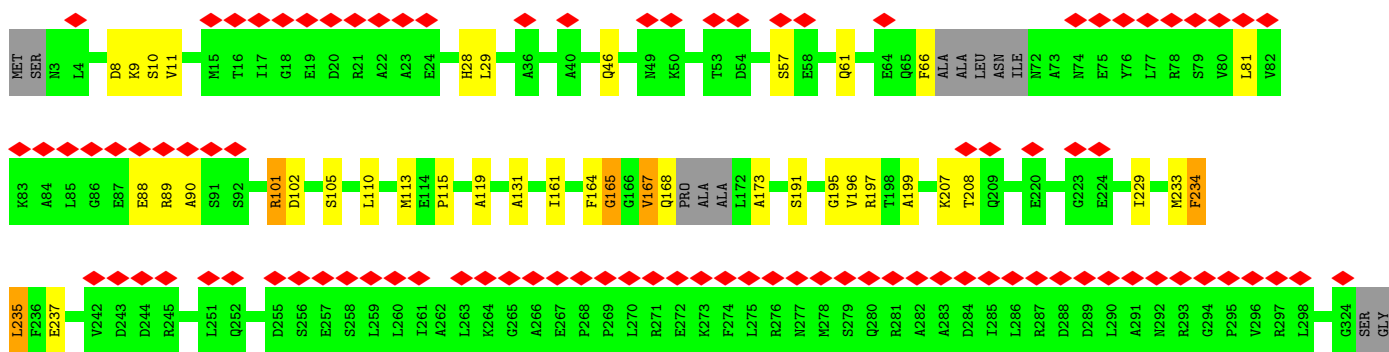
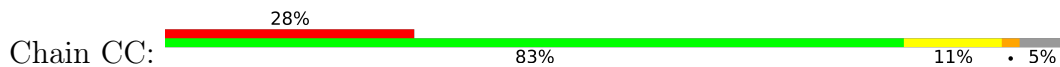


• Molecule 2: Flagellar motor switch protein Flig



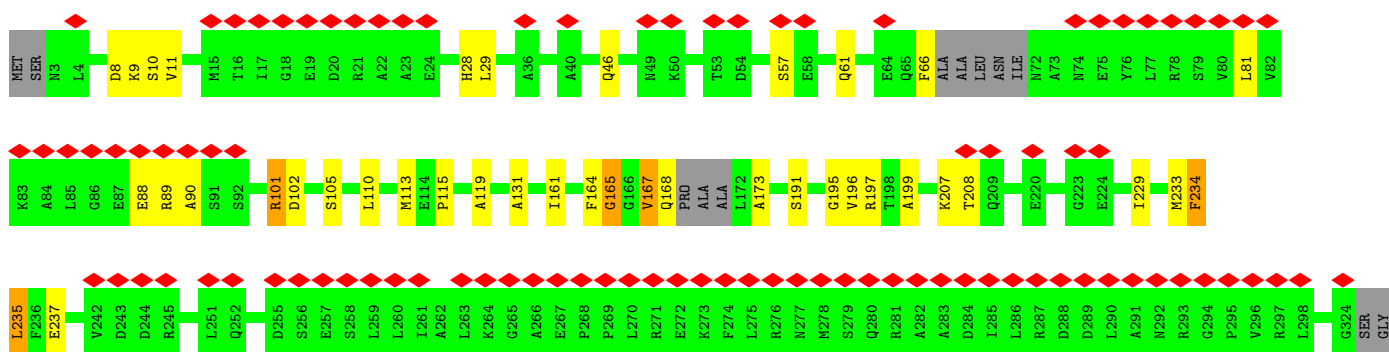
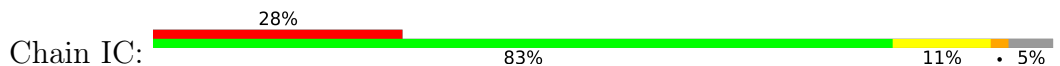
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ASP  
THR  
TYR  
VAL

• Molecule 2: Flagellar motor switch protein FlIG



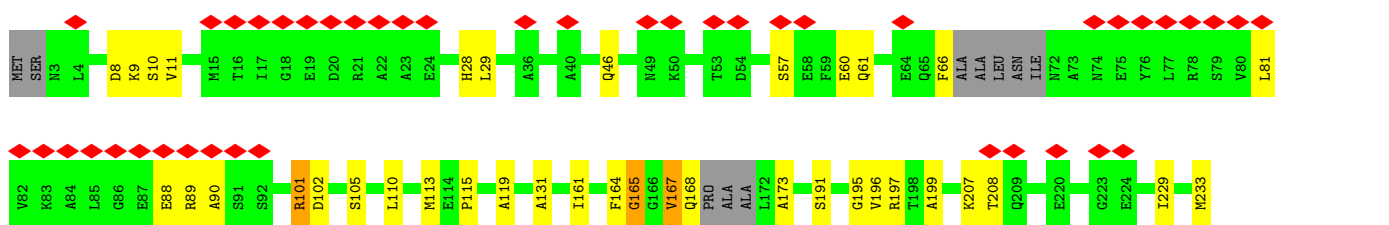
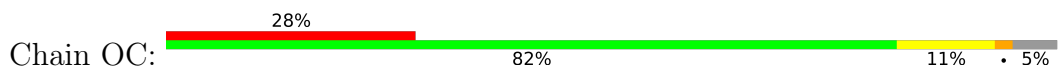
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• Molecule 2: Flagellar motor switch protein FlIG

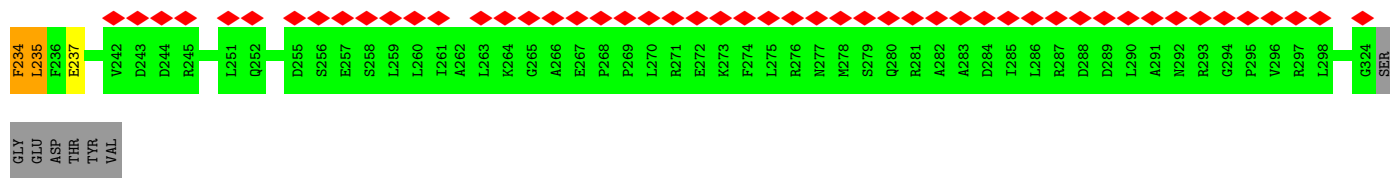


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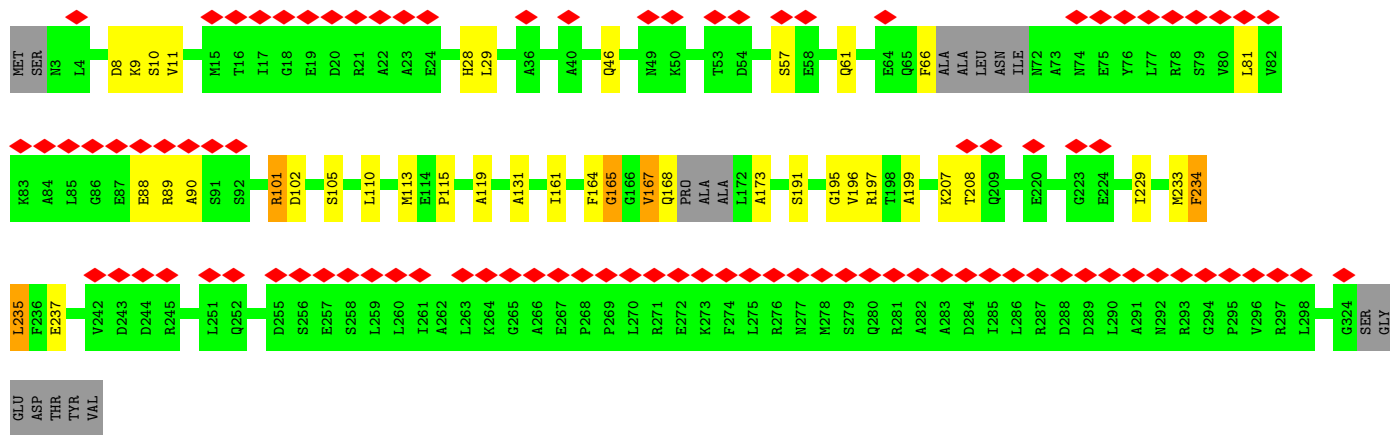
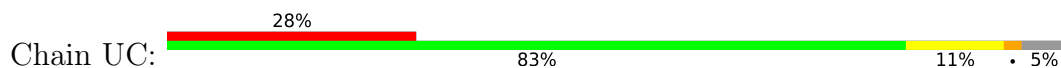
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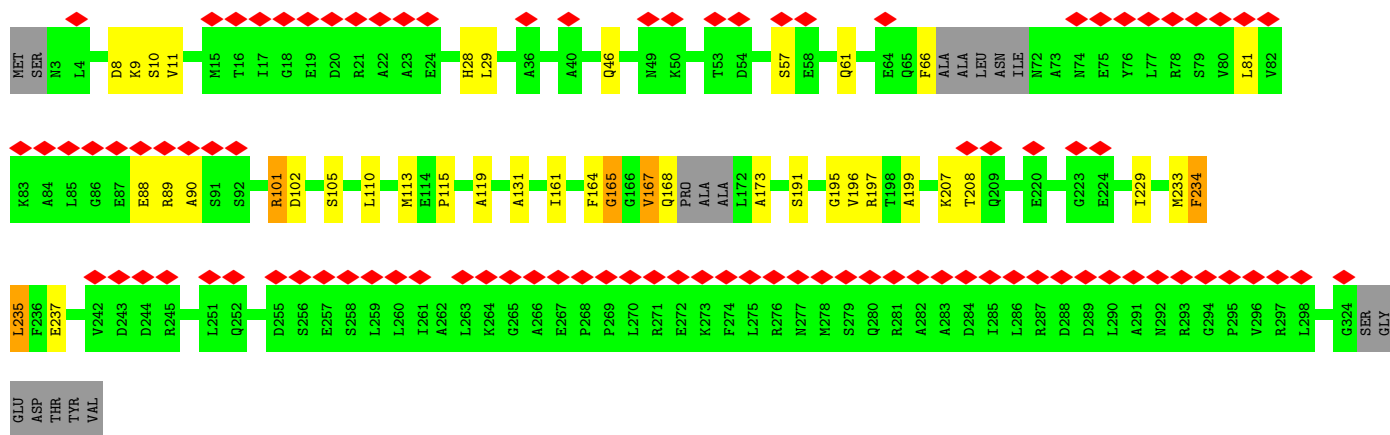
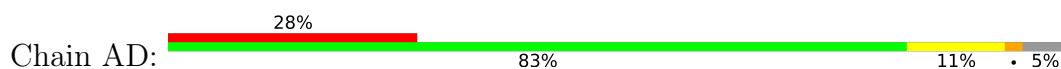




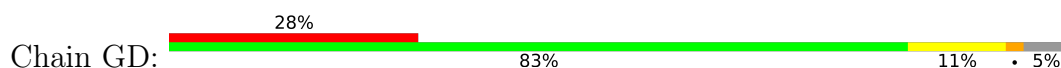
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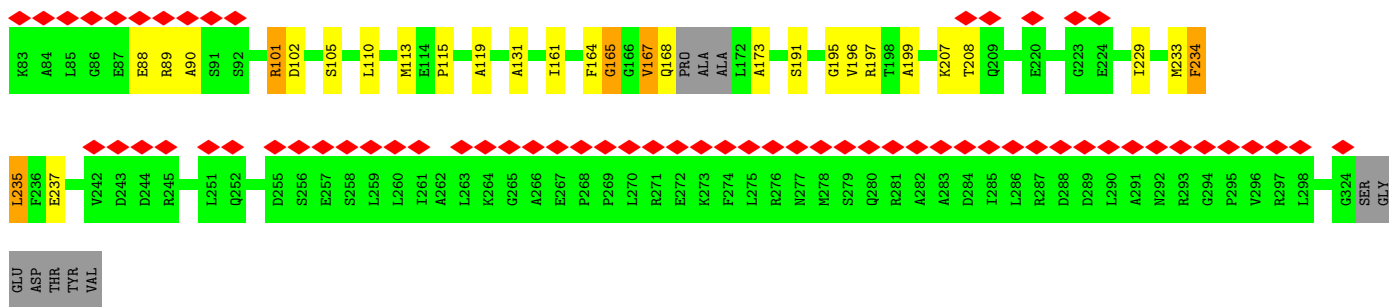


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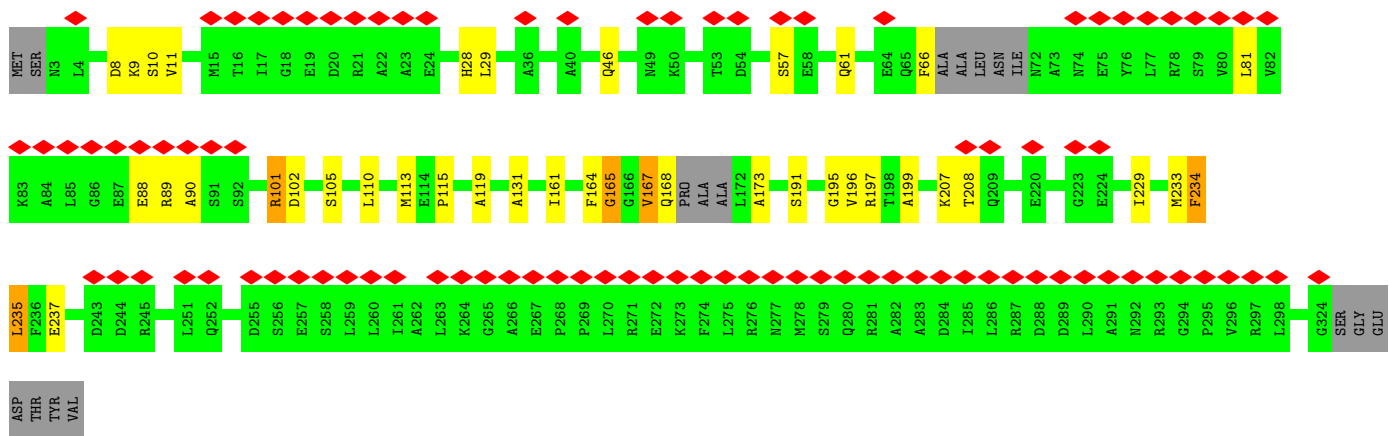
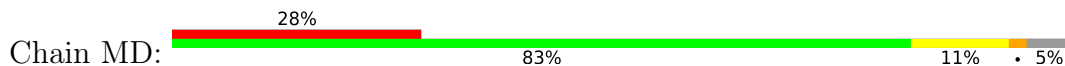


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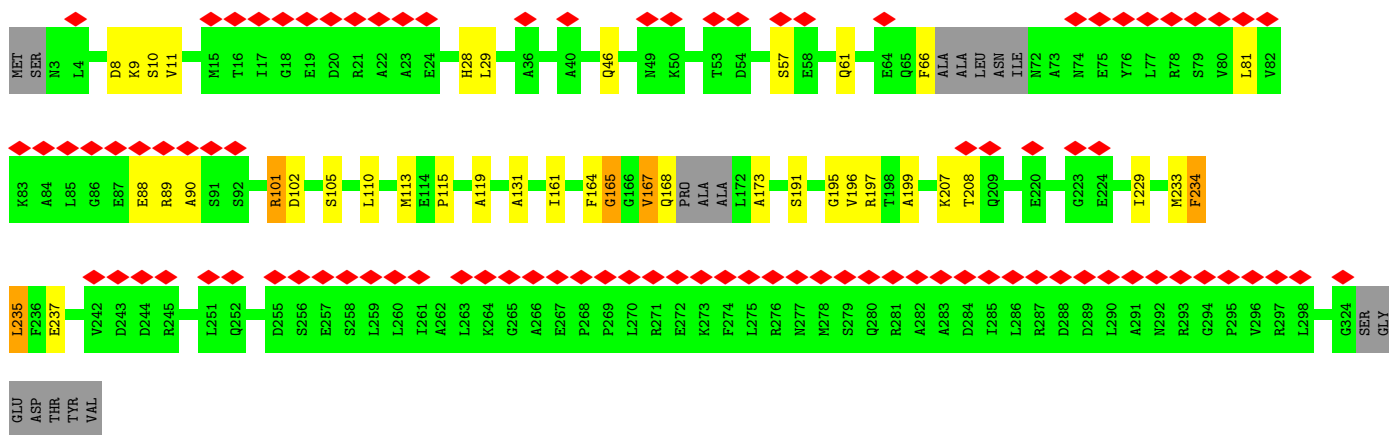
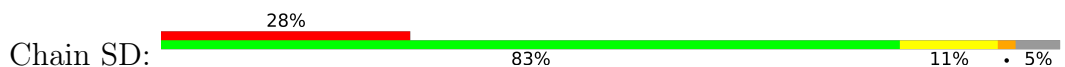




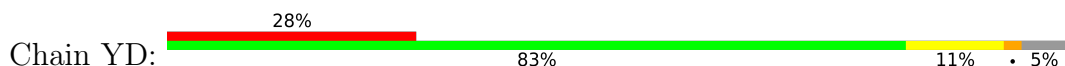
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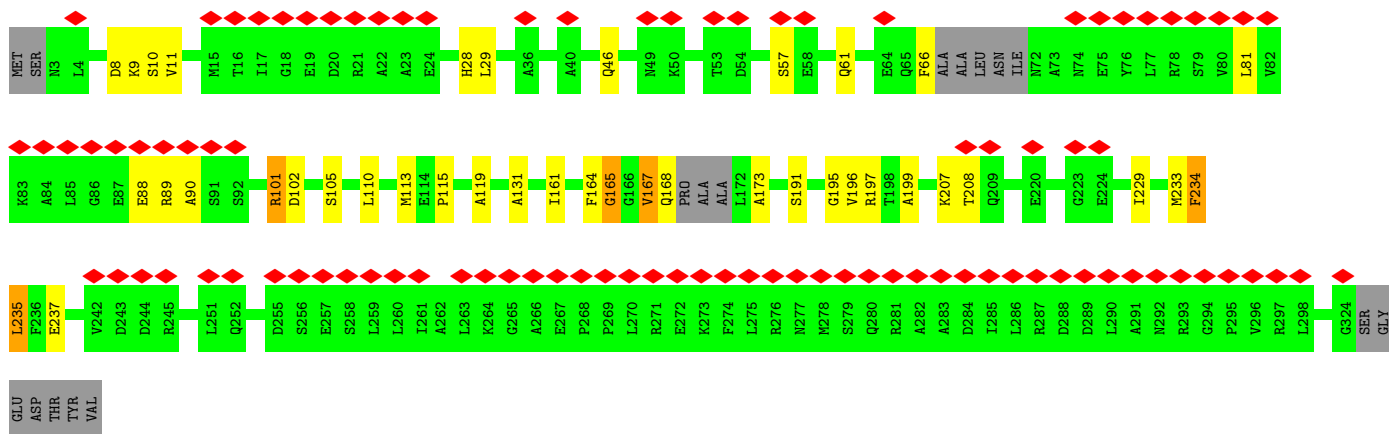


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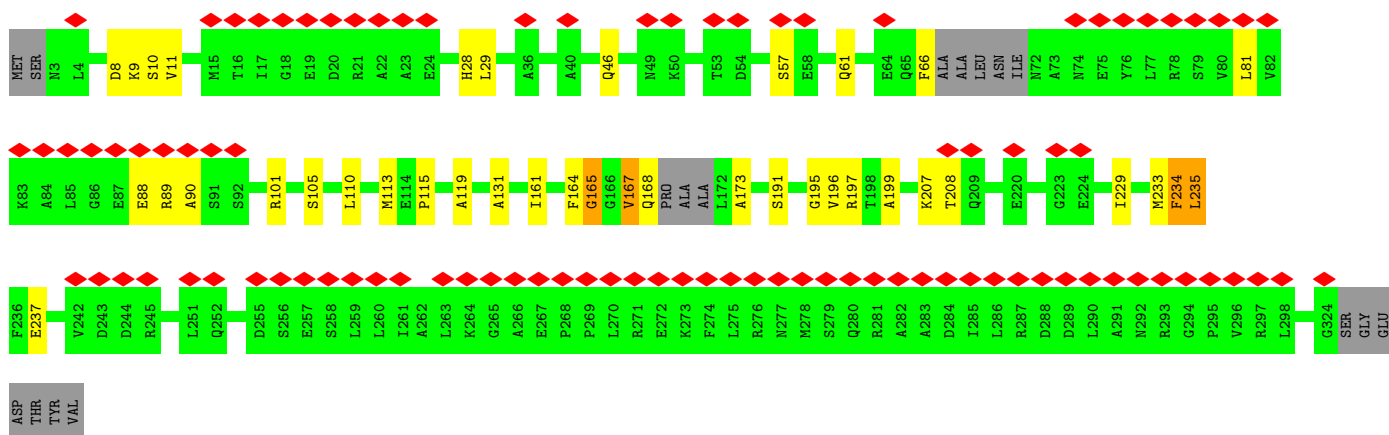
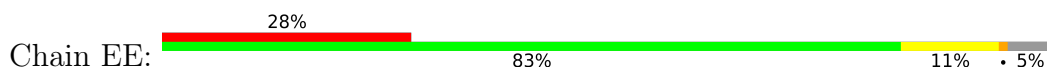


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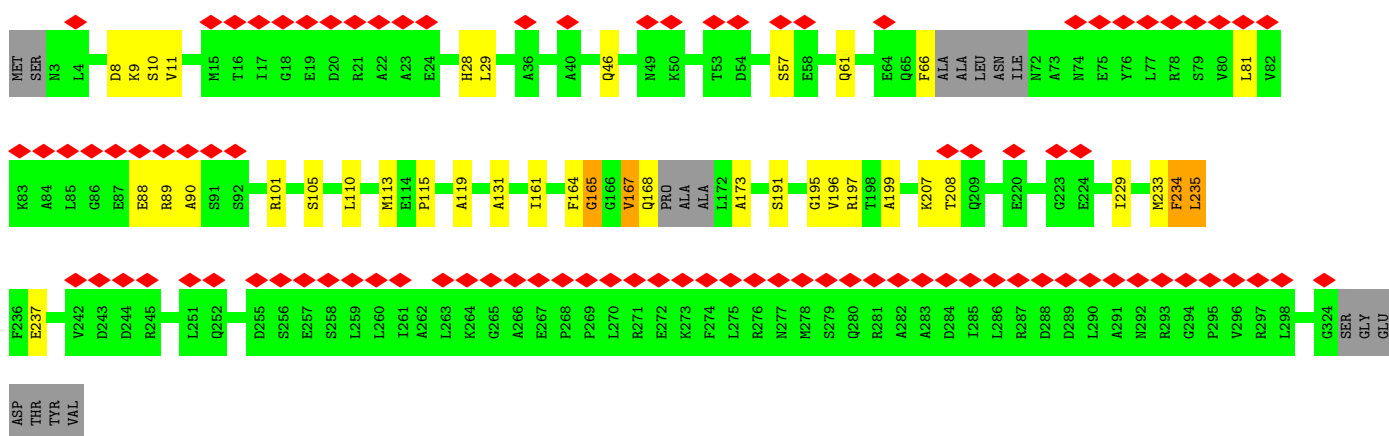
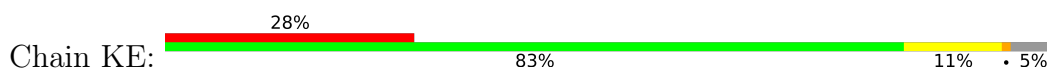




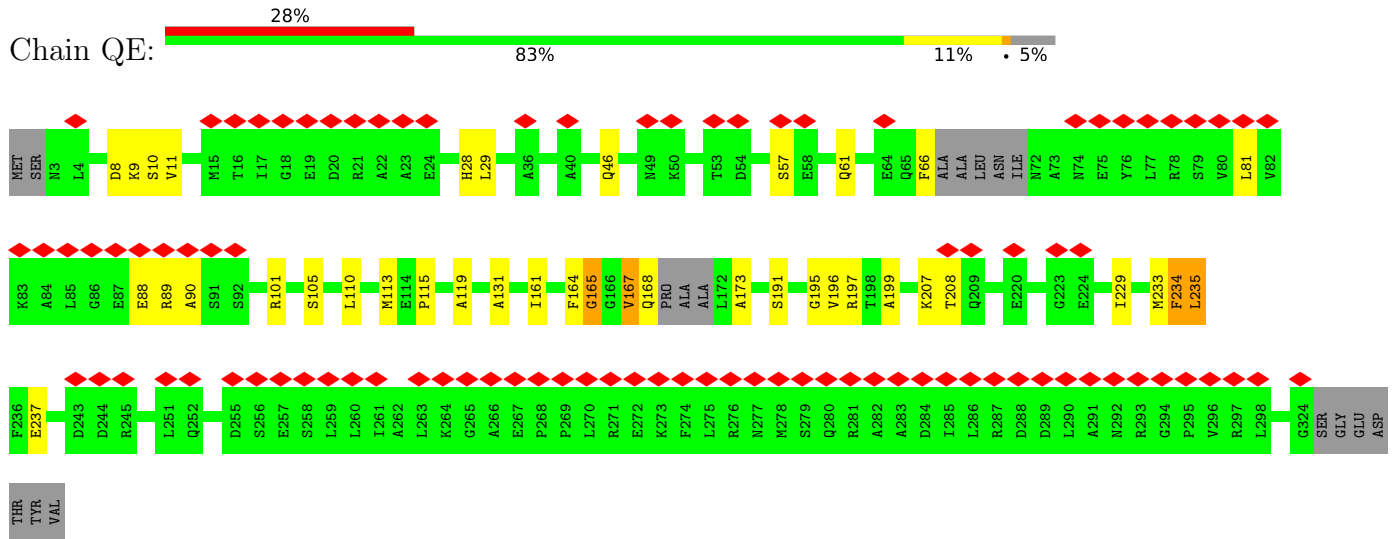
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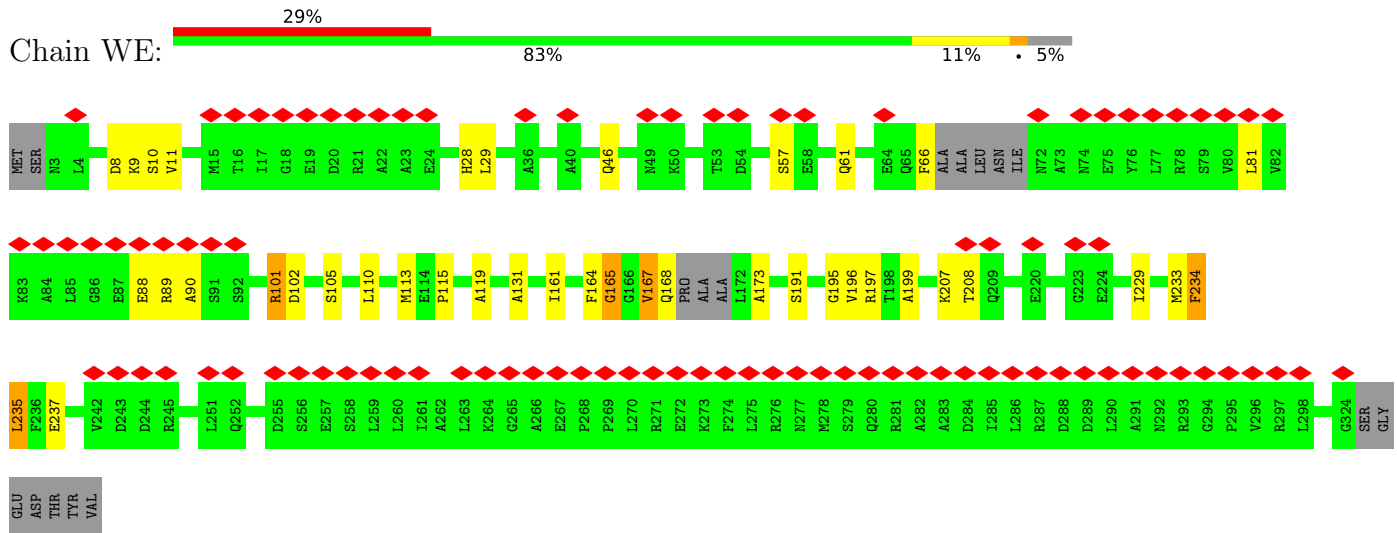
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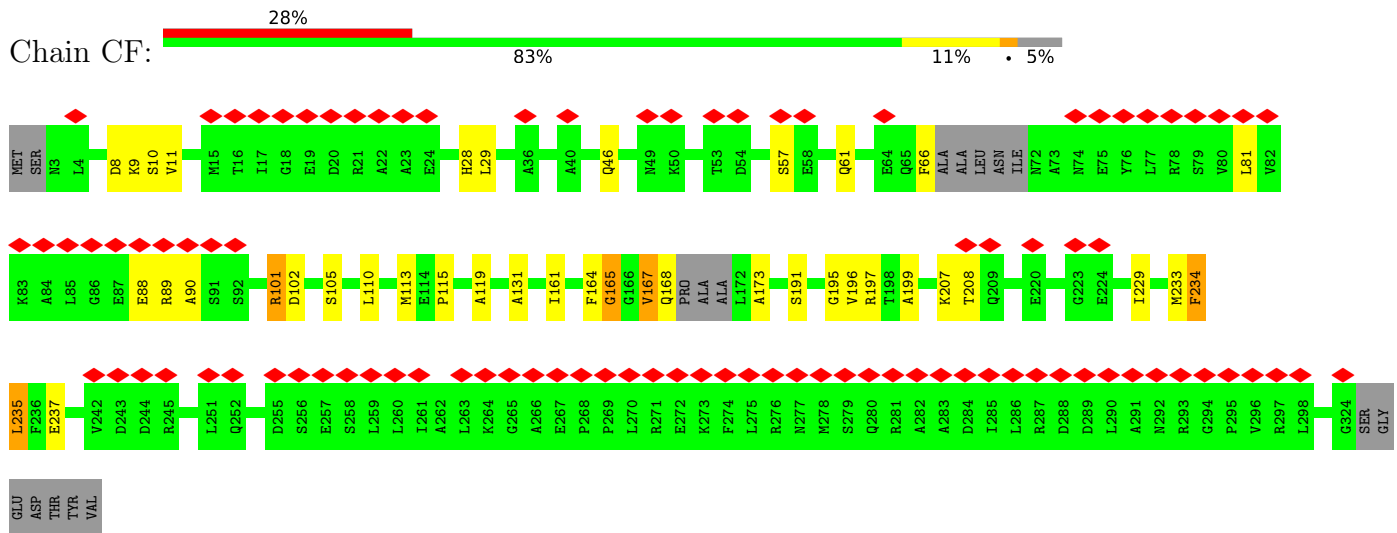
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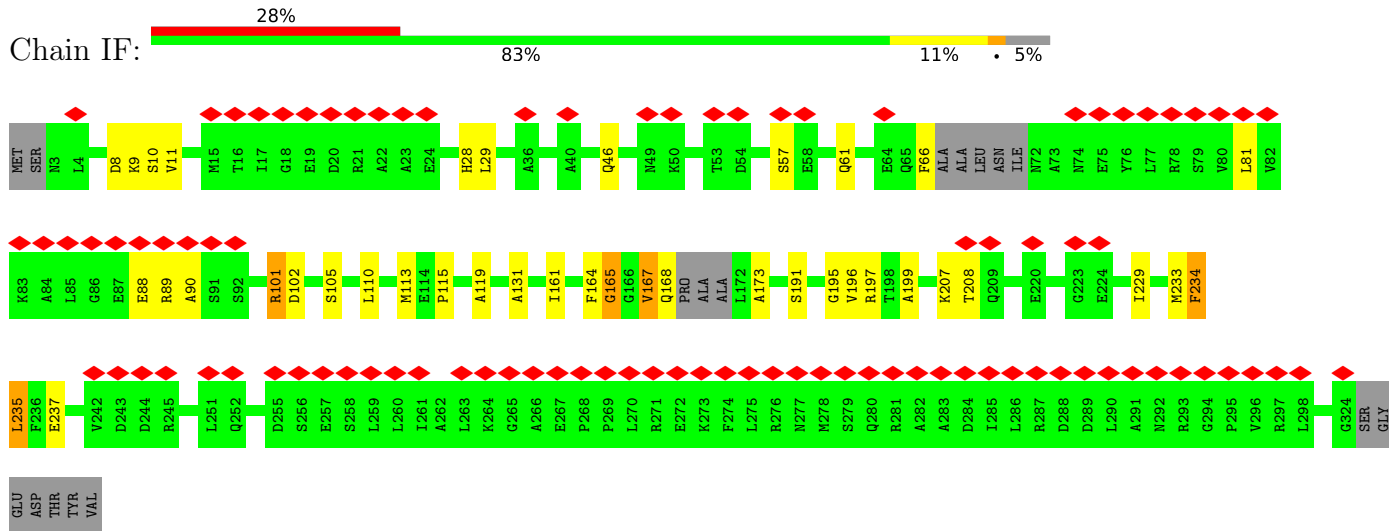
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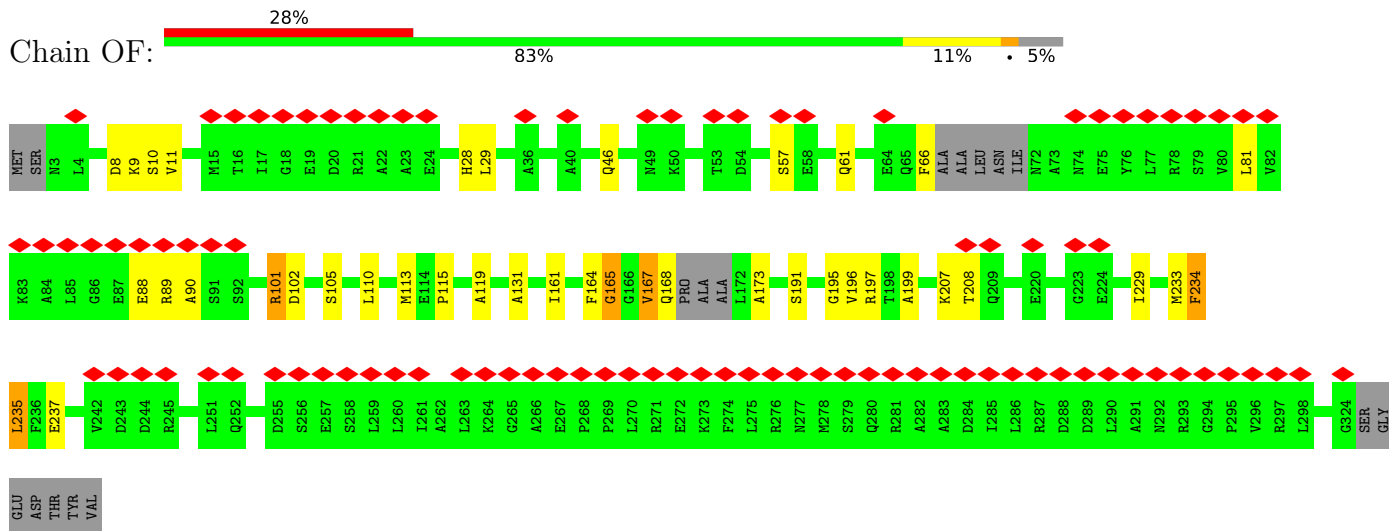
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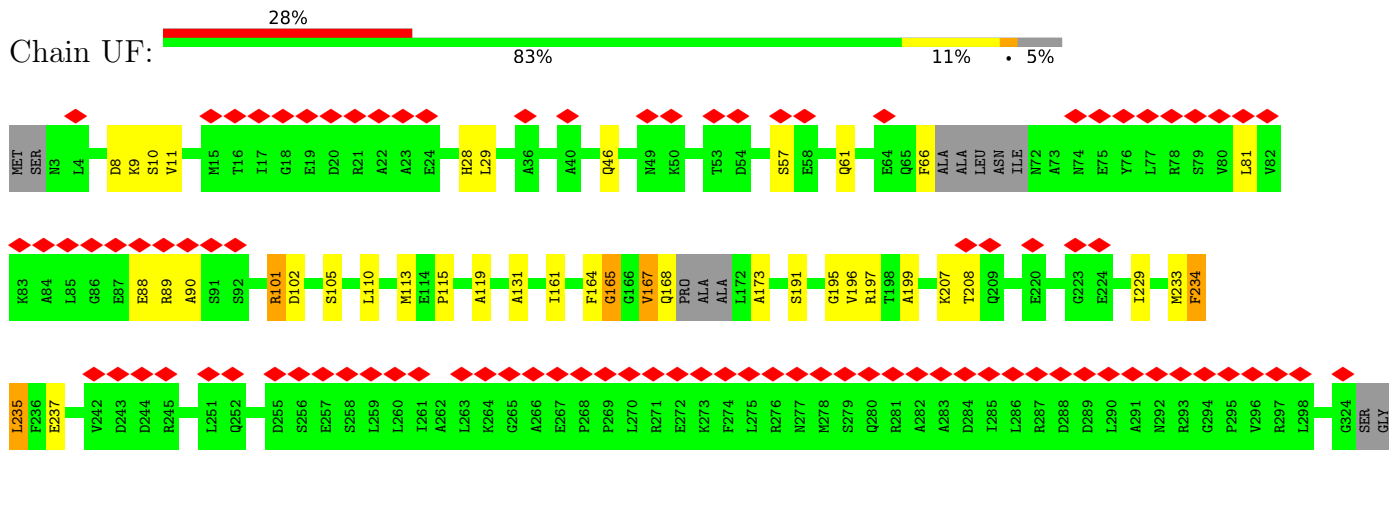
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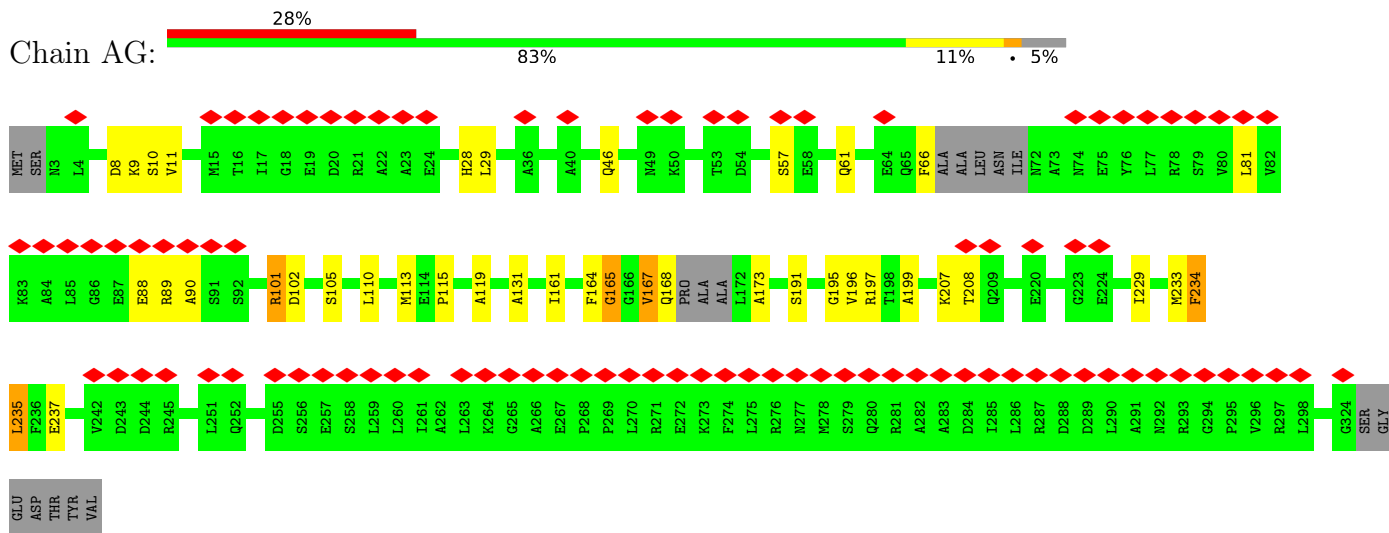


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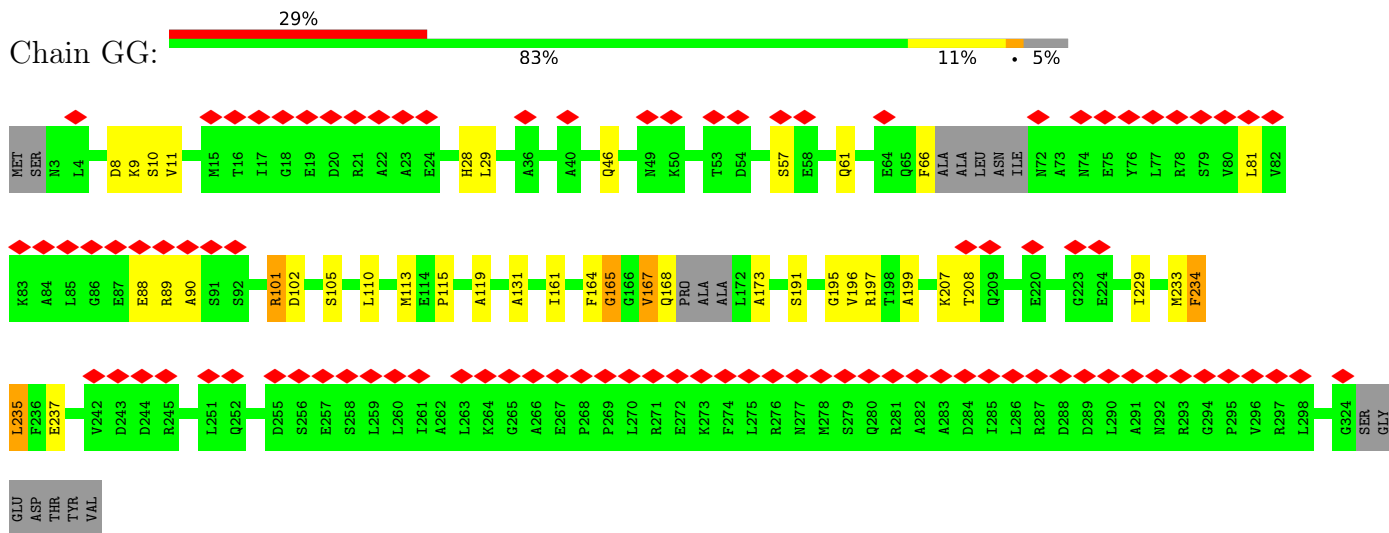


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TYR  
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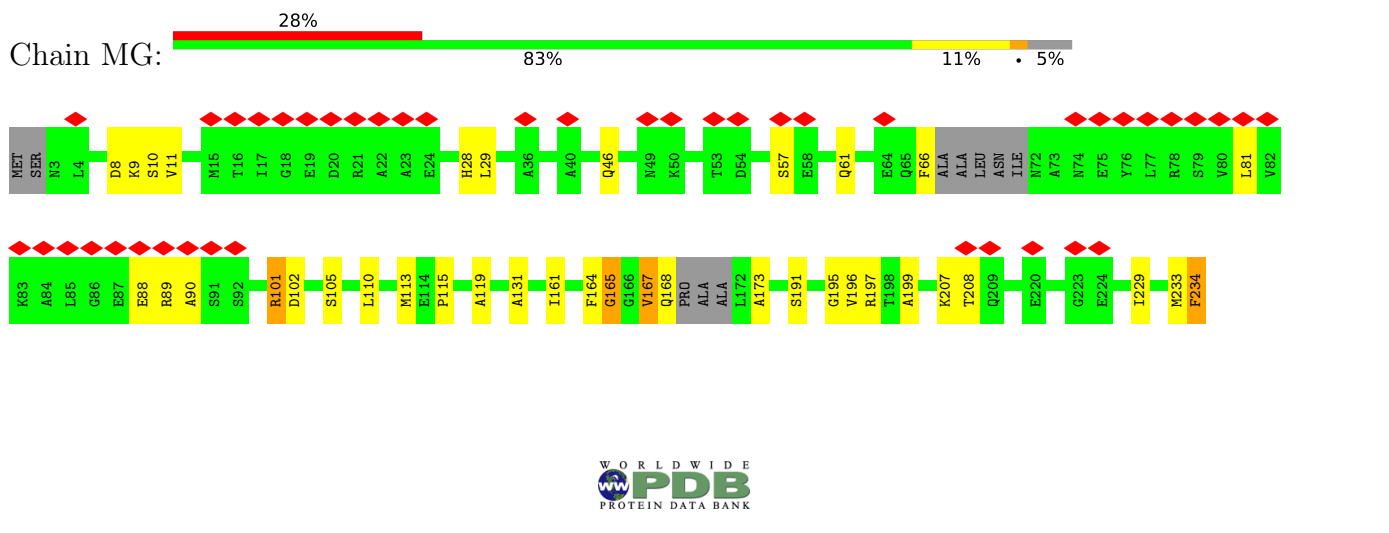
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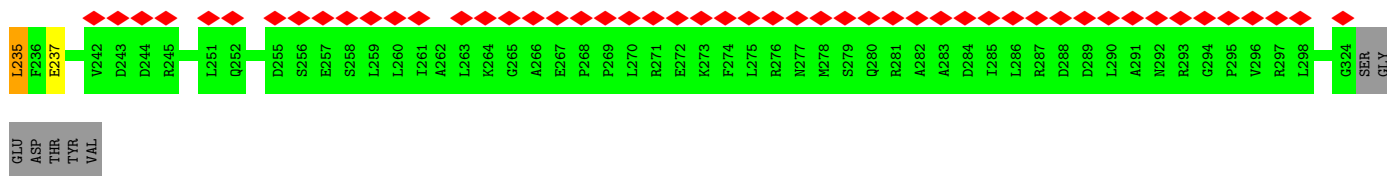


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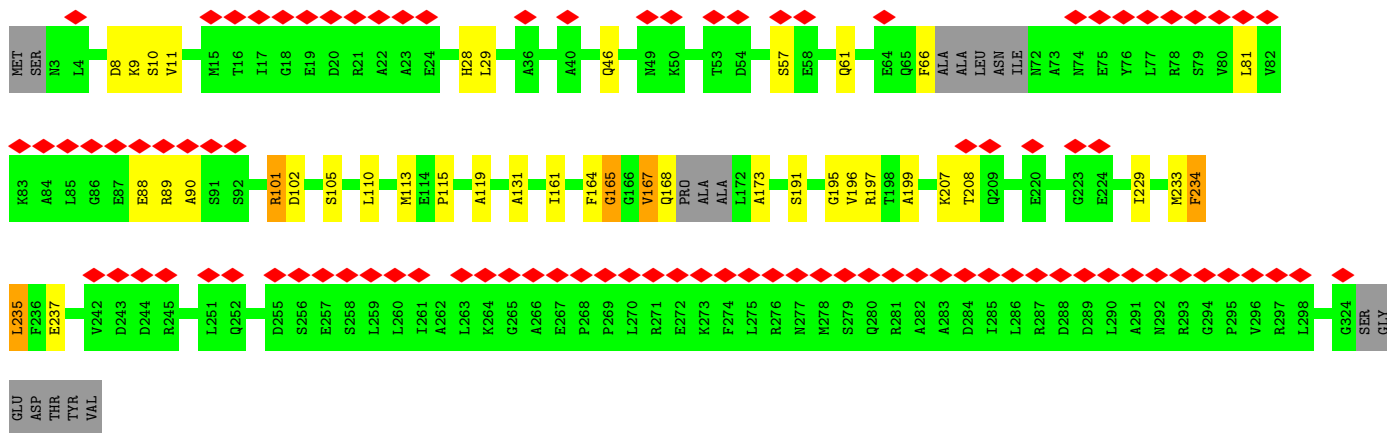
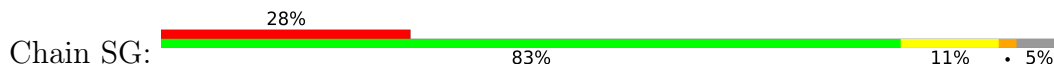


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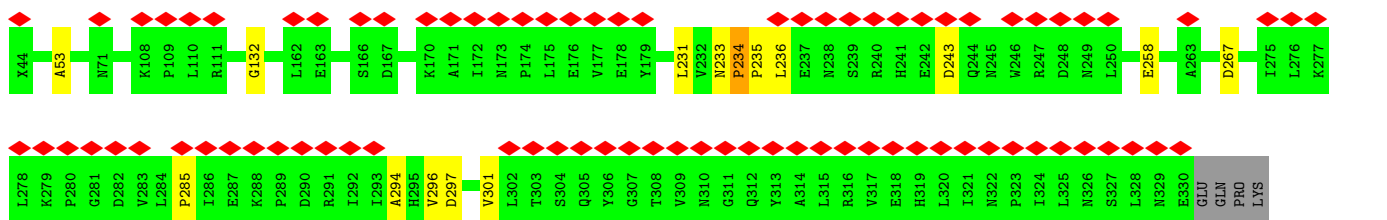




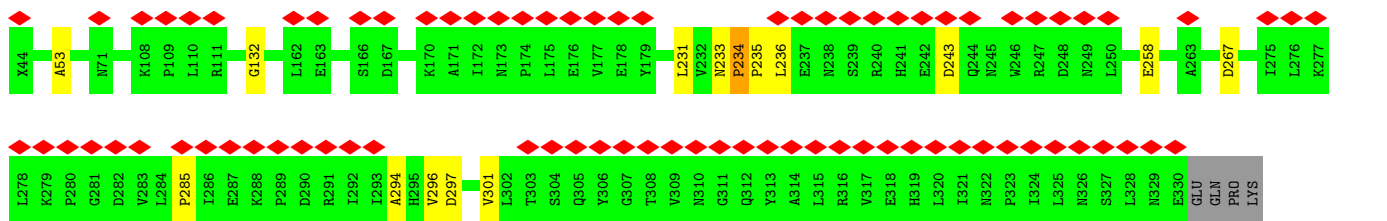
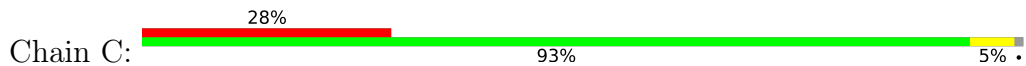
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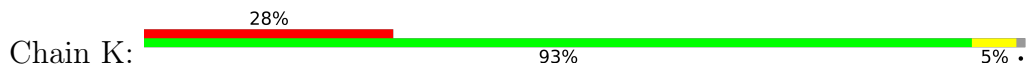
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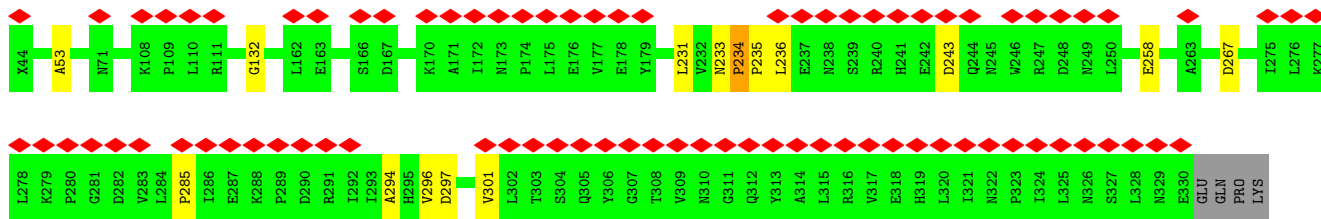


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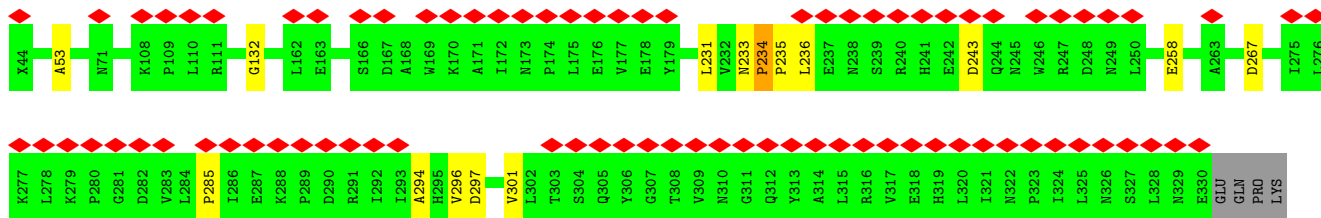
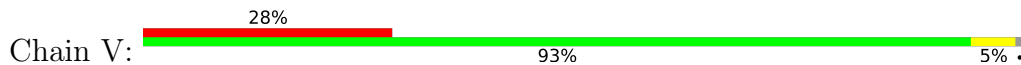


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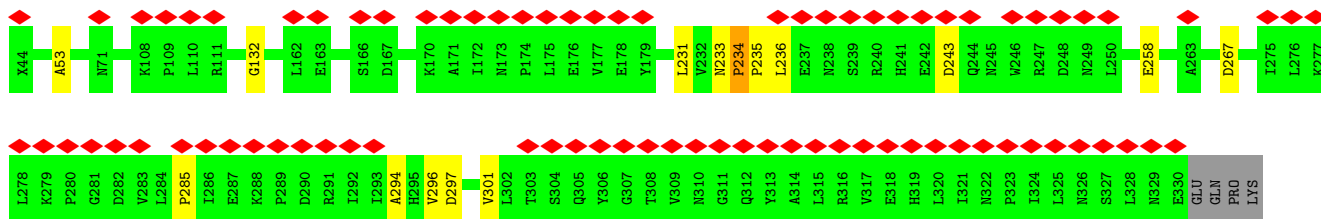




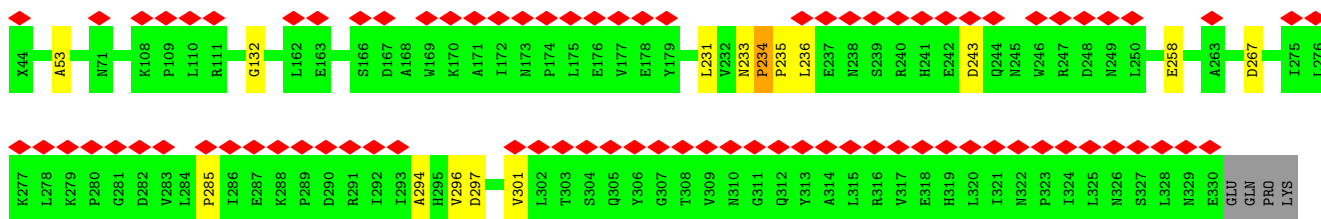
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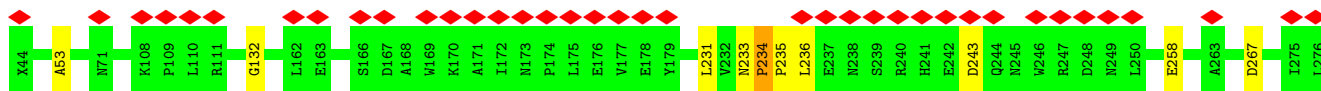
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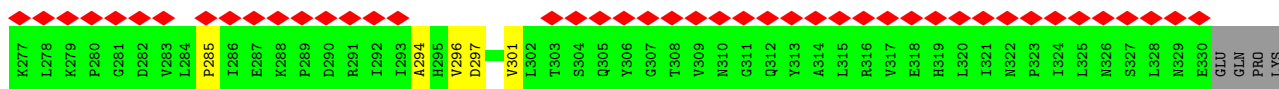
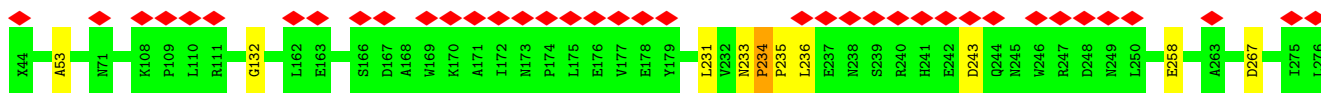
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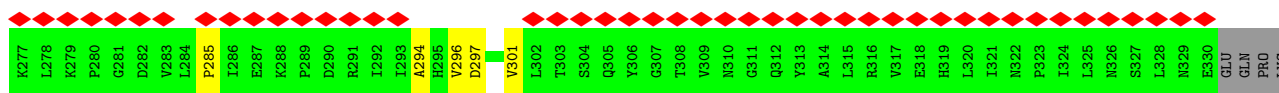
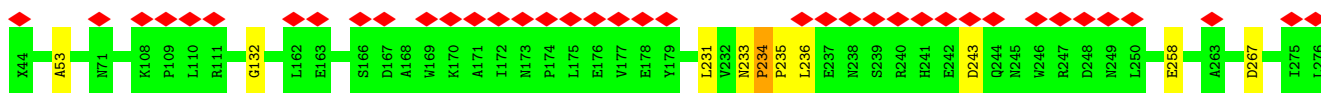




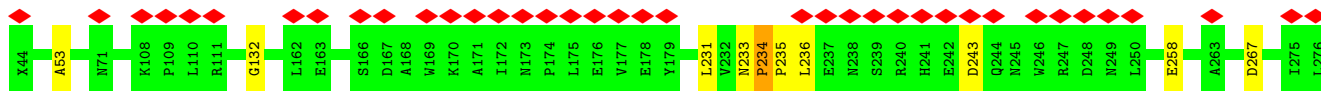
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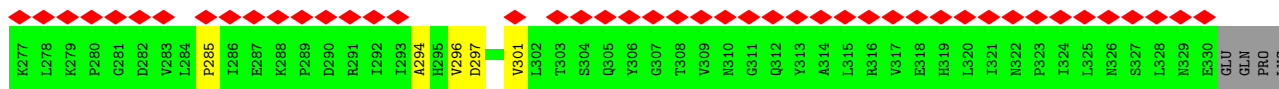
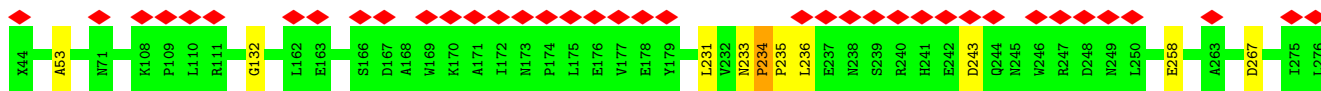
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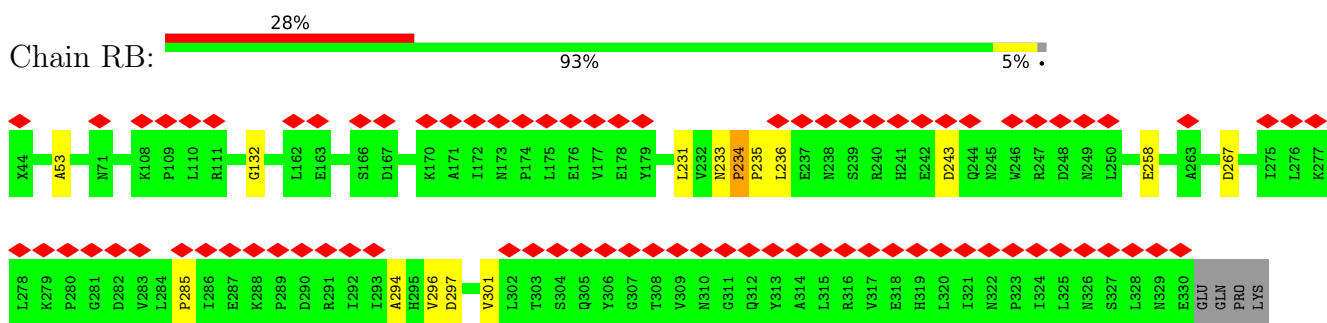
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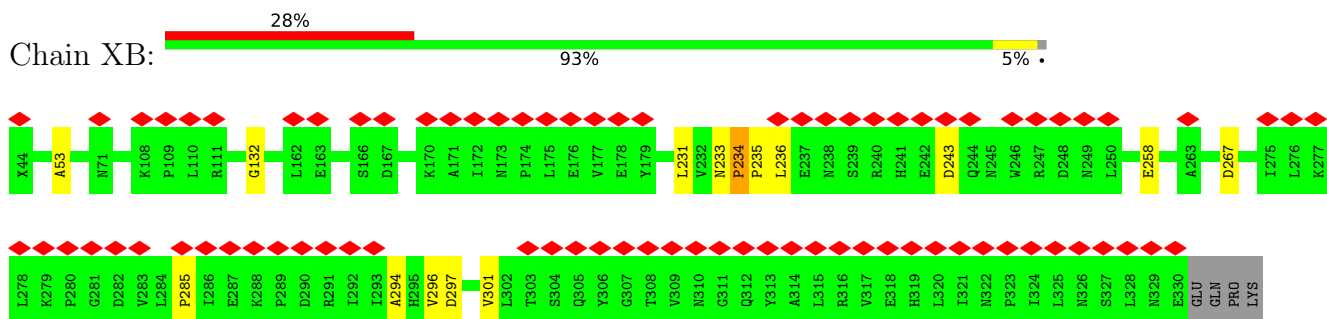
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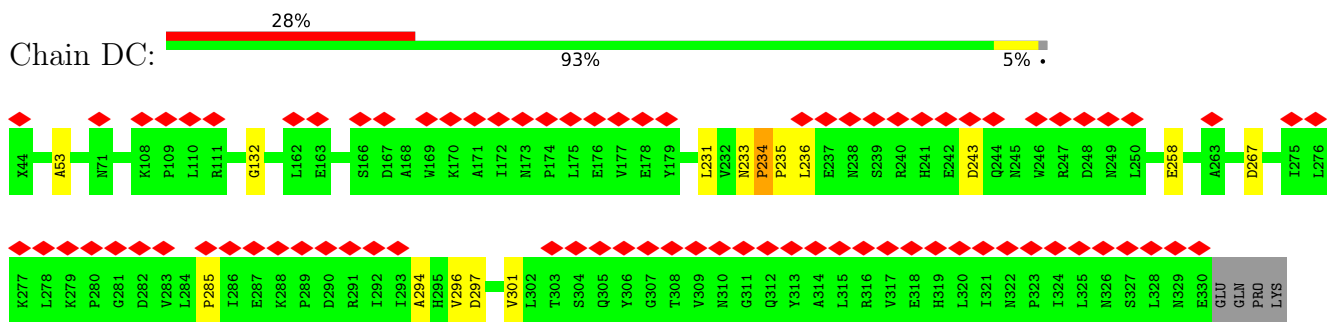
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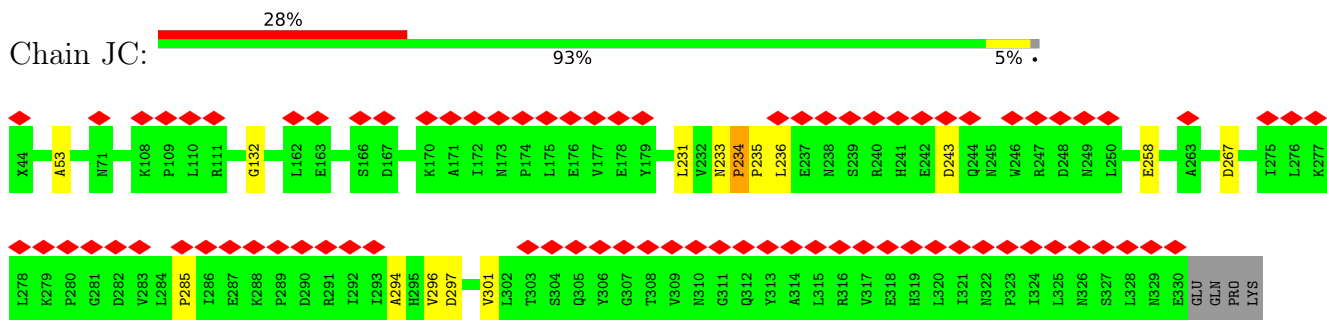
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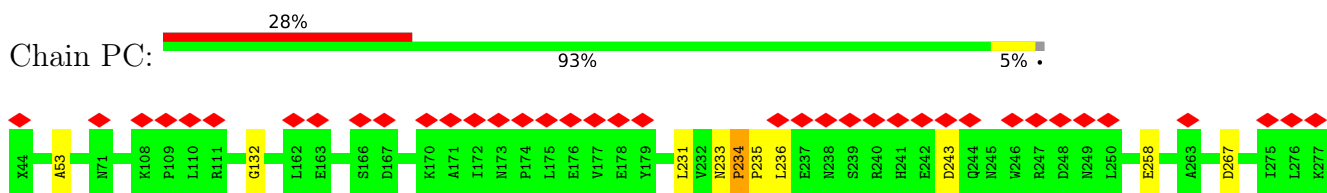
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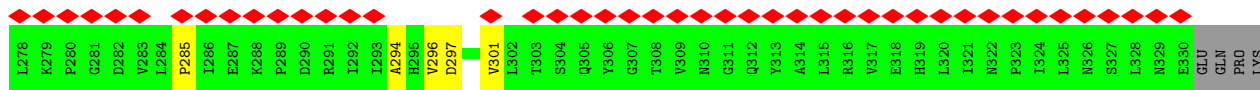


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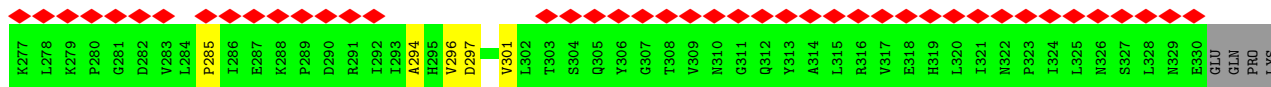
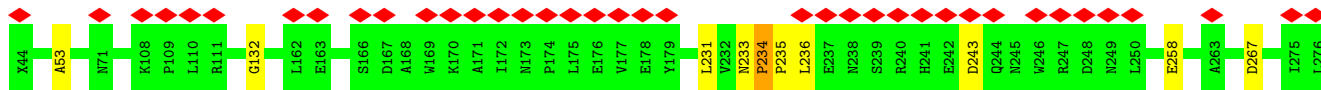


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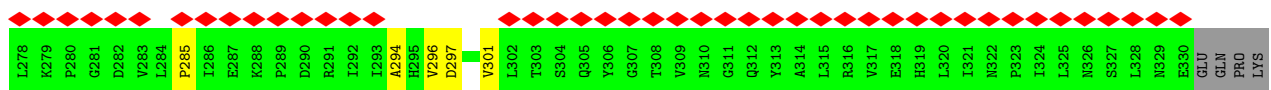
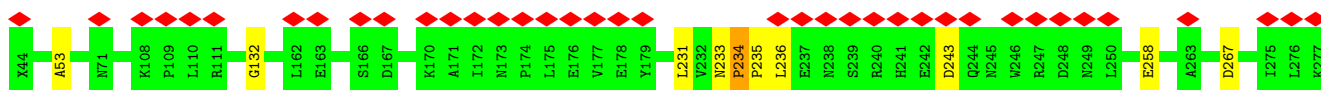




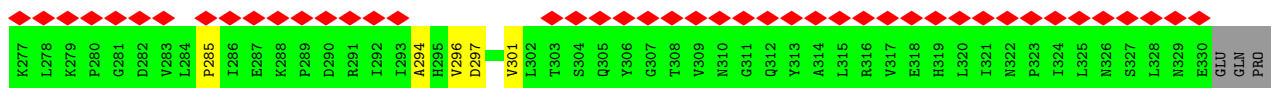
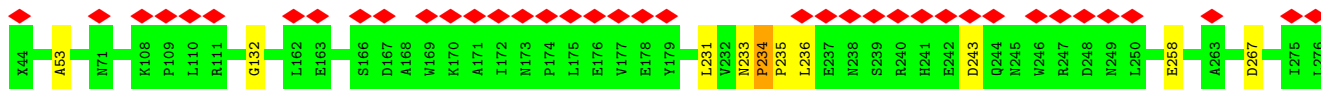
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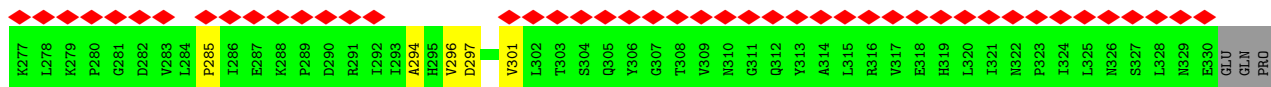
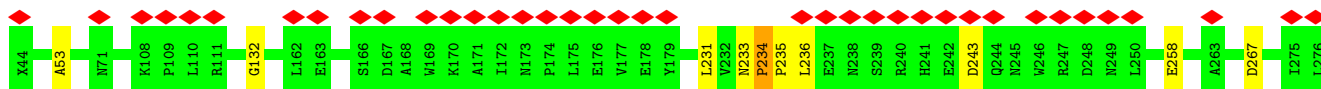
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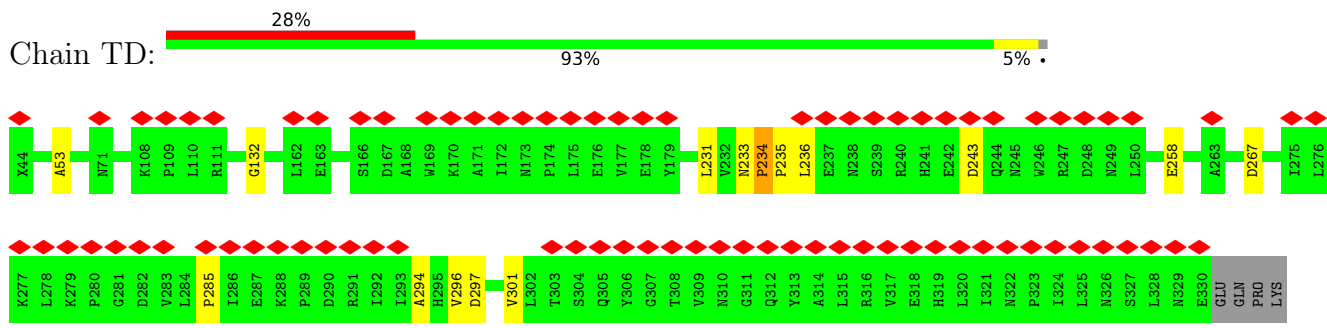
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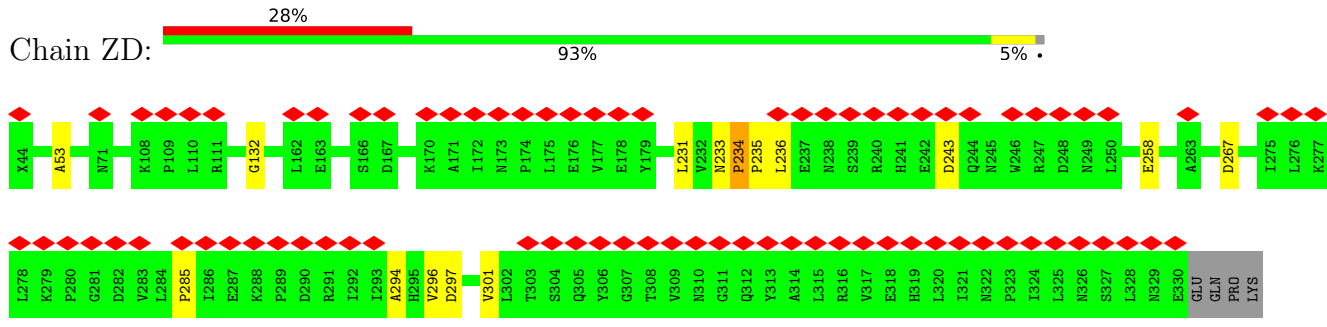
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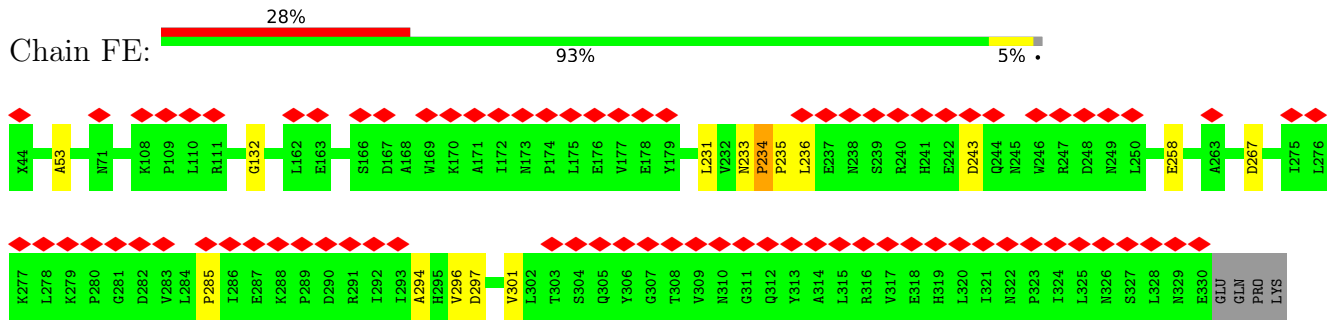
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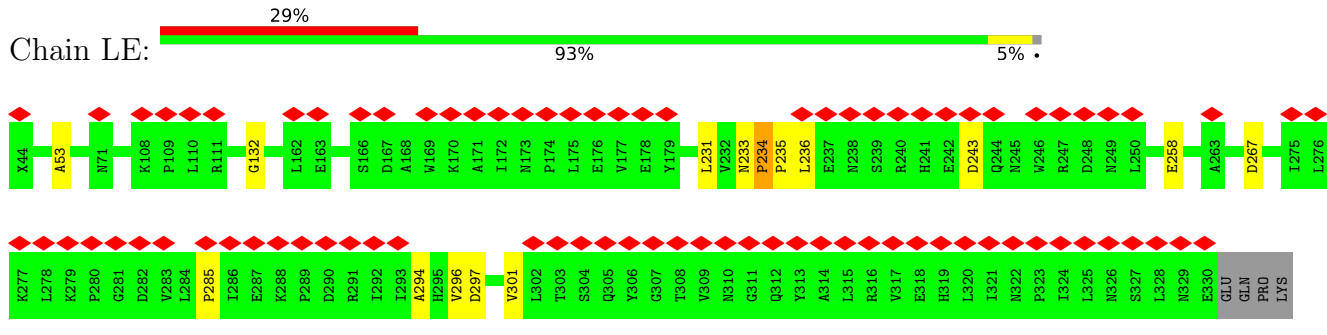
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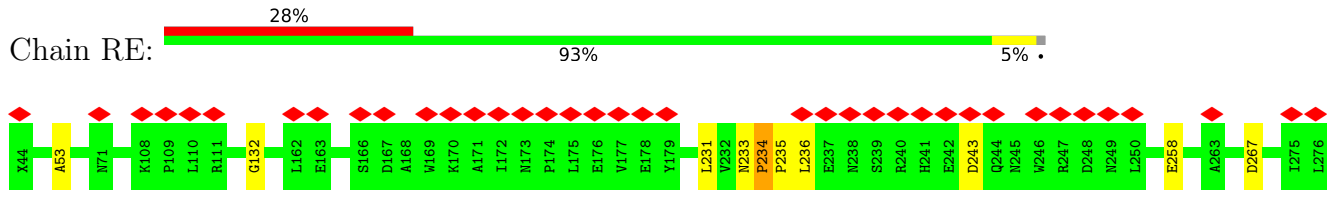
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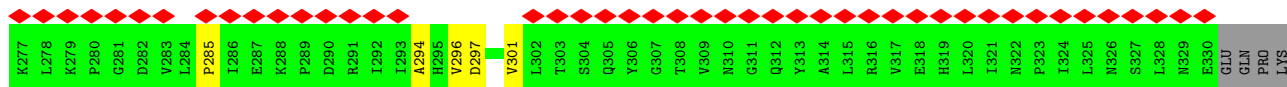
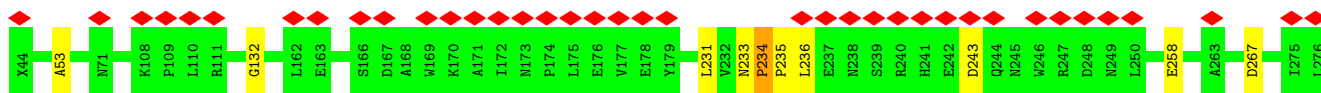


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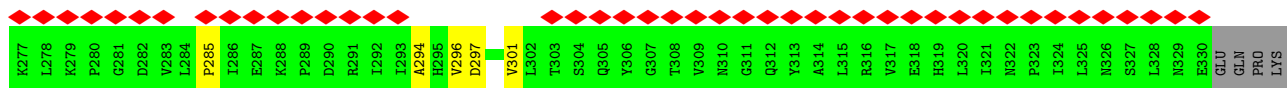
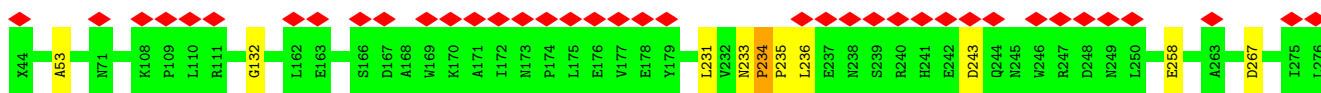




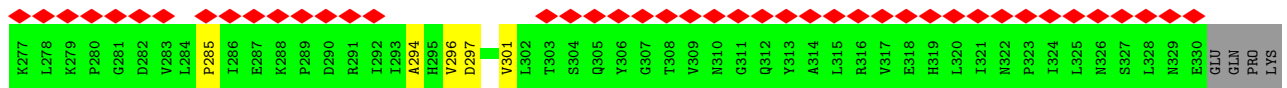
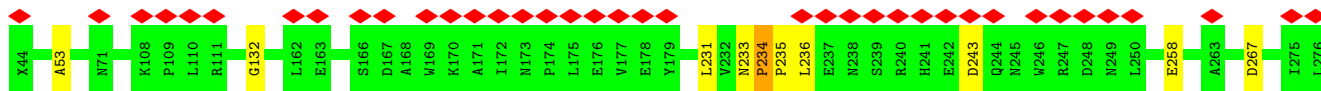
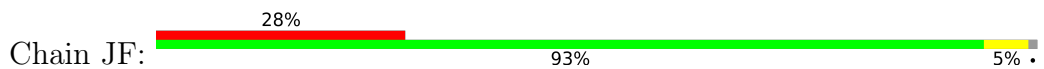
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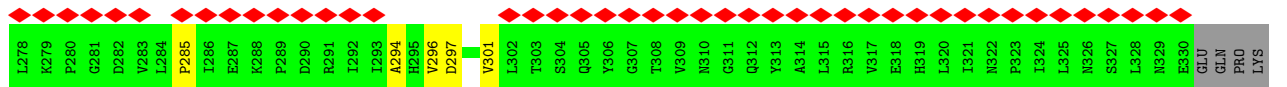
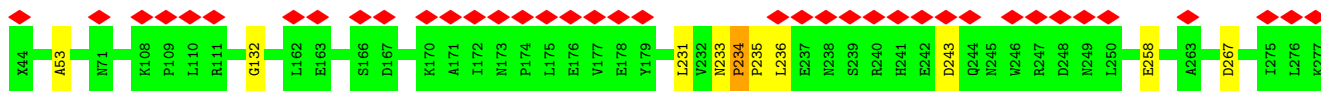
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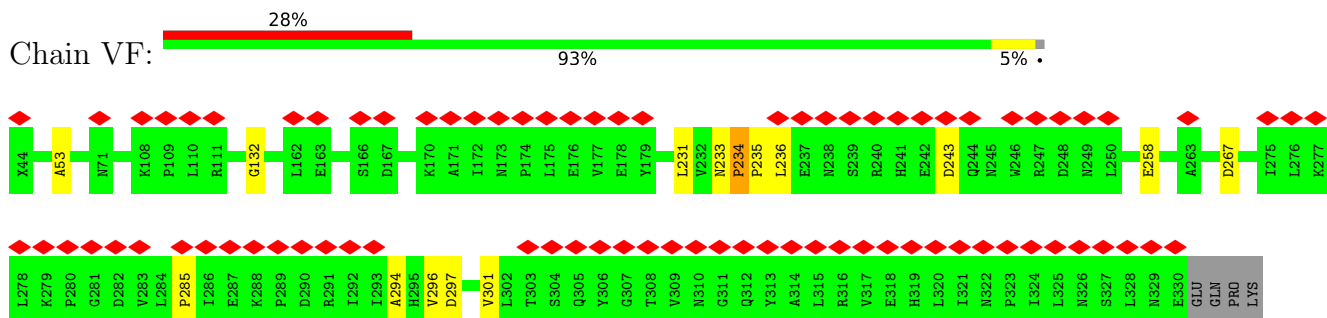
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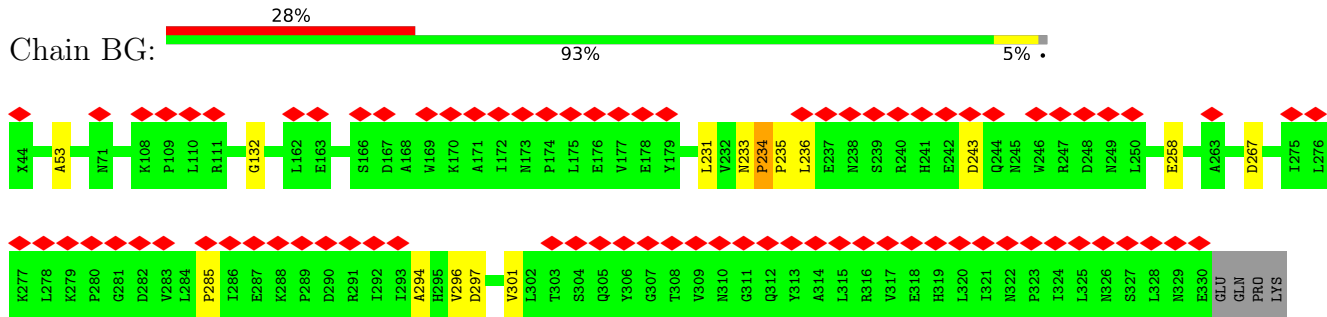
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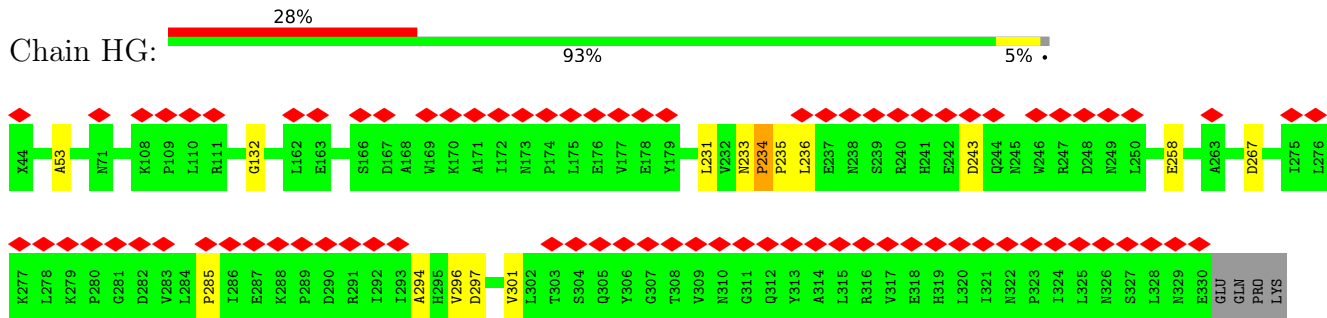
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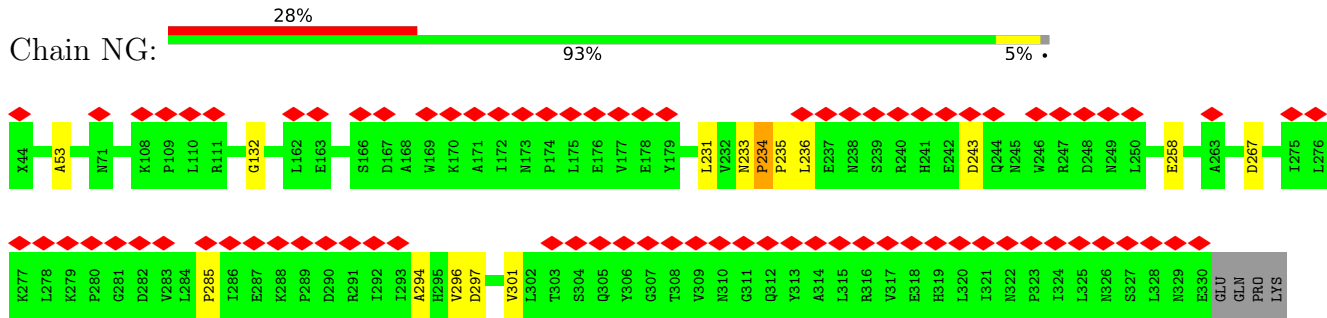
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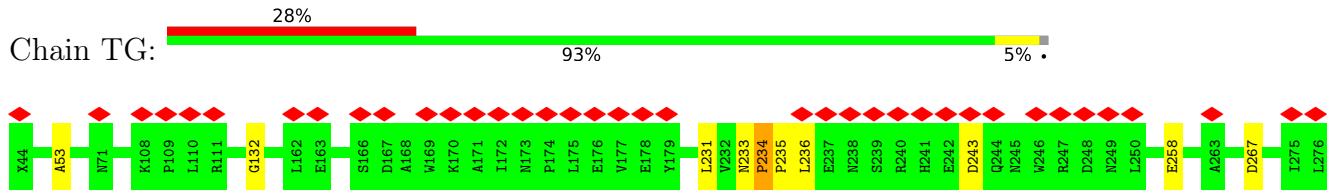
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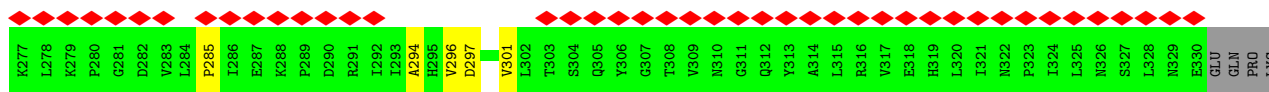


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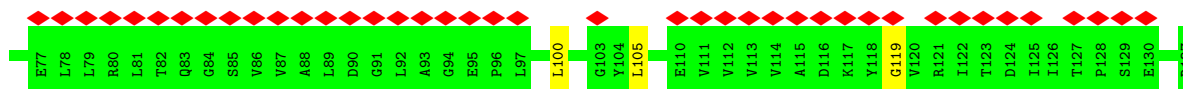
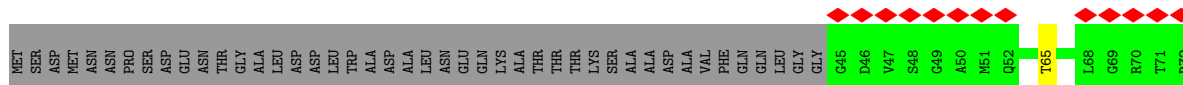
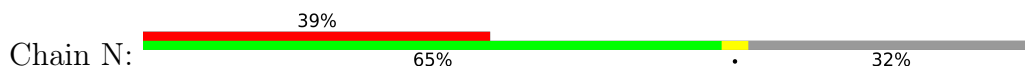


• Molecule 3: Flagellar motor switch protein FliM

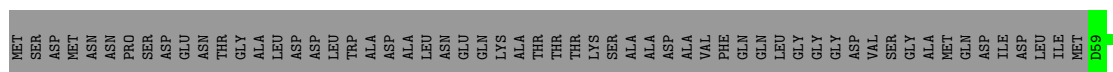




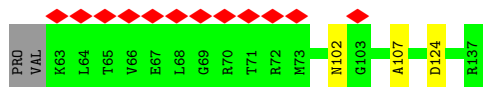
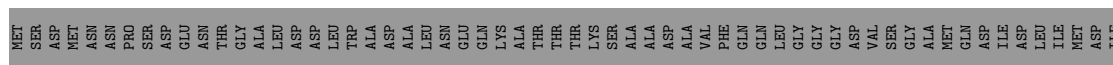
• Molecule 4: Flagellar motor switch protein FliN



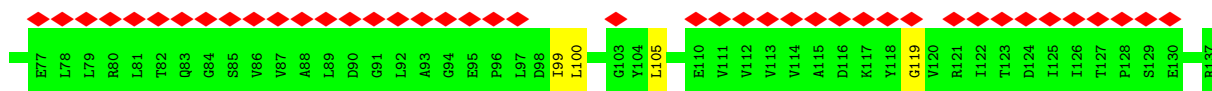
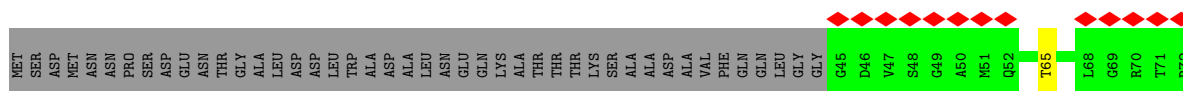
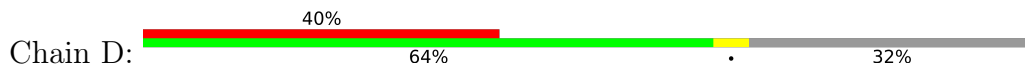
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN

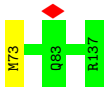
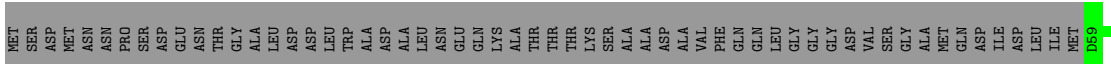


• Molecule 4: Flagellar motor switch protein FliN

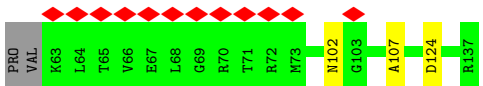
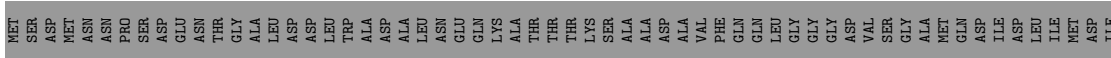


• Molecule 4: Flagellar motor switch protein FliN

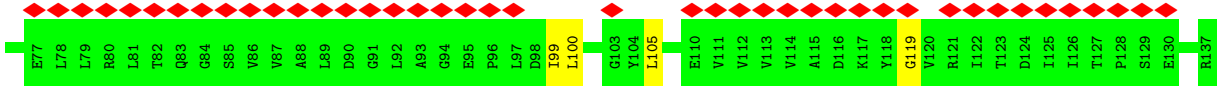
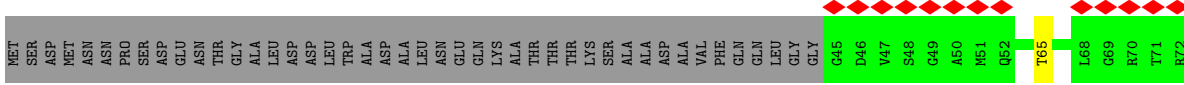
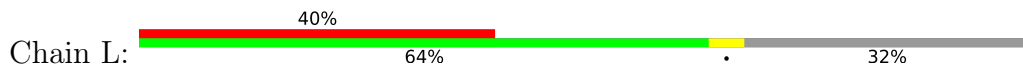




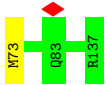
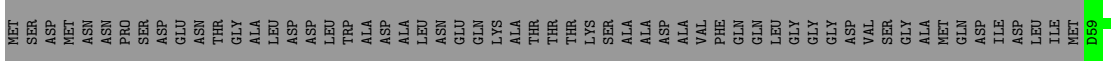
● Molecule 4: Flagellar motor switch protein FliN



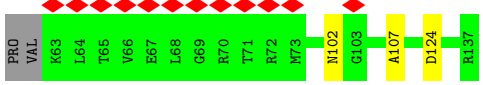
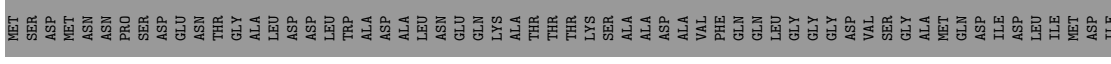
● Molecule 4: Flagellar motor switch protein FliN



● Molecule 4: Flagellar motor switch protein FliN

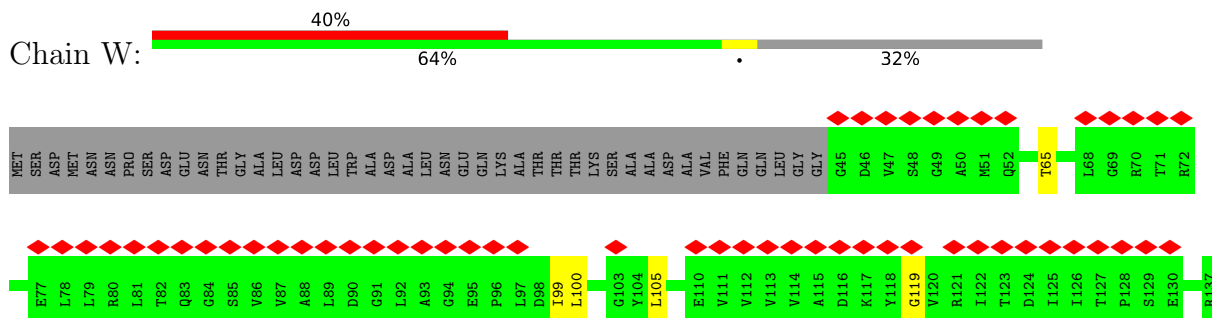


● Molecule 4: Flagellar motor switch protein FliN

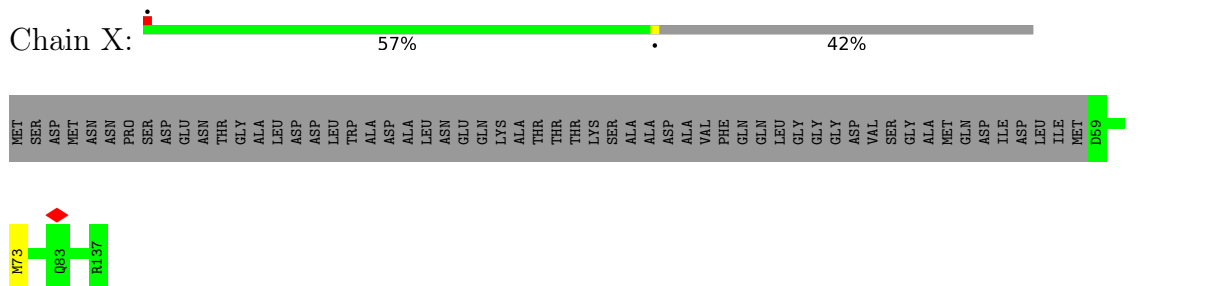


● Molecule 4: Flagellar motor switch protein FliN

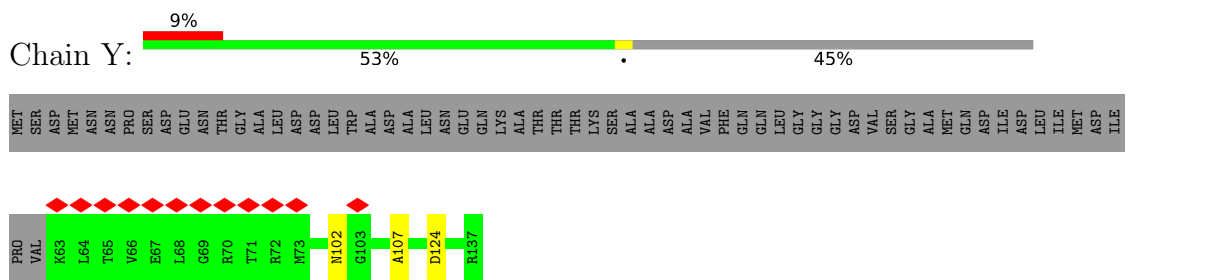




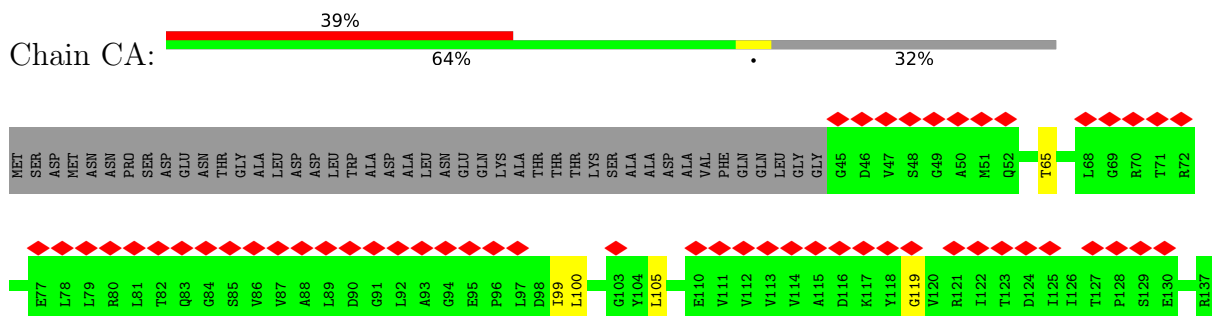
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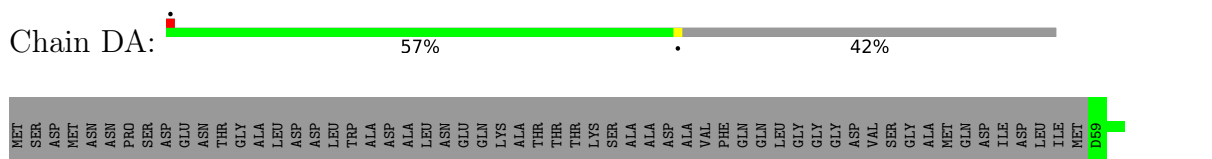
• Molecule 4: Flagellar motor switch protein FliN

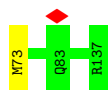


• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN

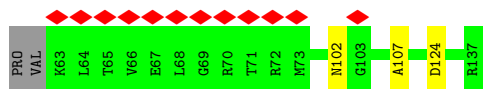




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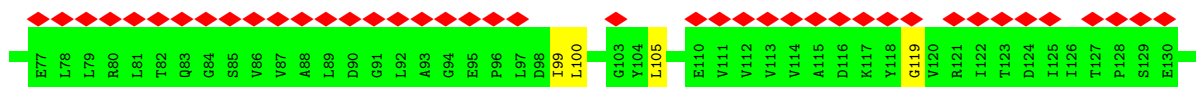
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• Molecule 4: Flagellar motor switch protein FliN



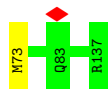
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• Molecule 4: Flagellar motor switch protein FliN



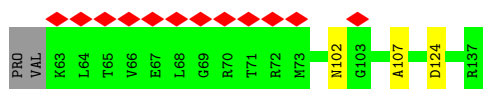
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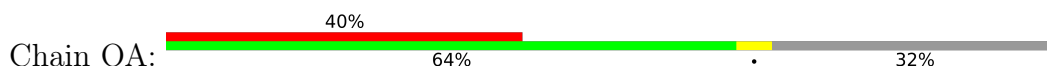
• Molecule 4: Flagellar motor switch protein FliN

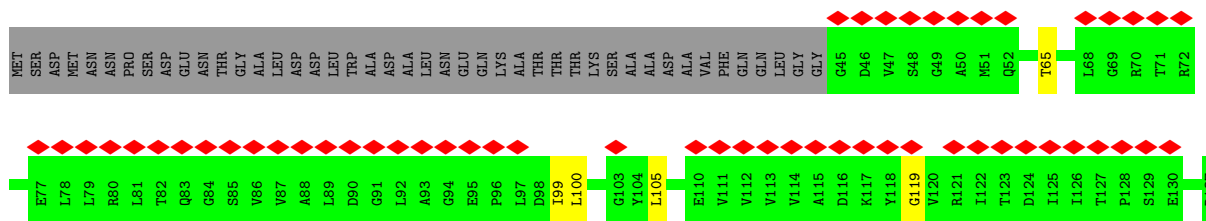


MET	SER	ASP	MET	ASN	ASN	PRO	SER	ASP	GLU	THR	GLY	ALA	LEU	ASP	LEU	TRP	ALA	ASP	ALA	LEU	ASN	GLU	GLN	LYS	ALA	ALA	THR	THR	THR	LYS	SER	ALA	ALA	ASP	ALA	VAL	PHE	GLN	GLN	LEU	LEU	GLY	GLY	GLY	ASP	VAL	SER	SER	GLY	ALA	ALA	MET	GLN	ASP	ASP	ILE	ILE	LEU	ILE	MET	ASP	ASP	ILE
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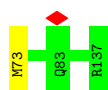
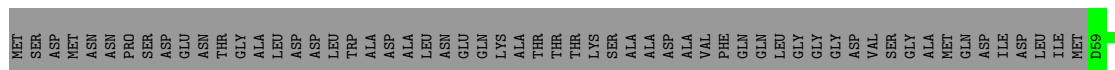


• Molecule 4: Flagellar motor switch protein FliN

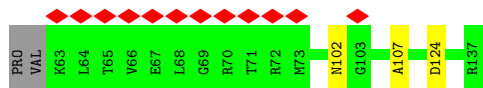
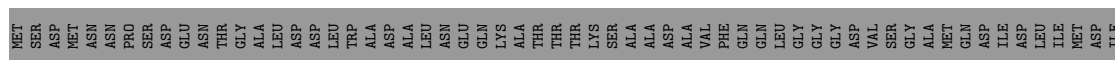




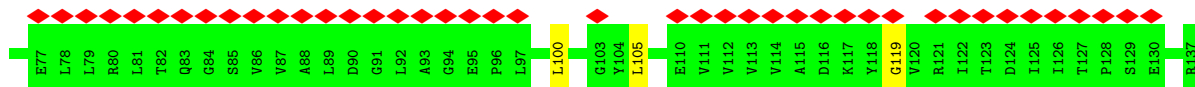
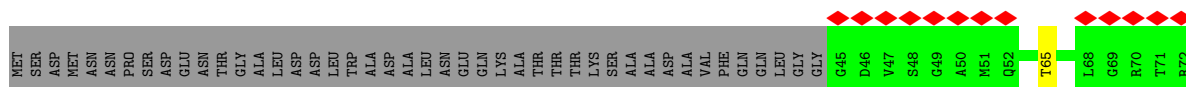
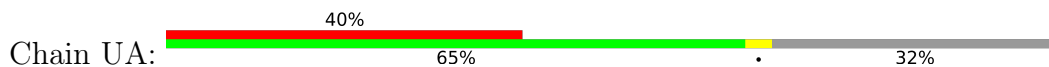
• Molecule 4: Flagellar motor switch protein FliN



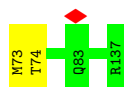
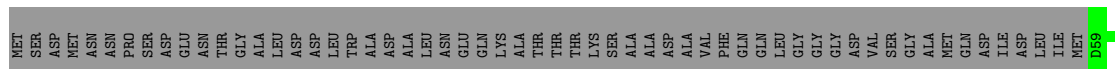
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN



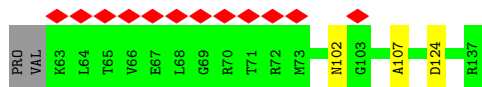
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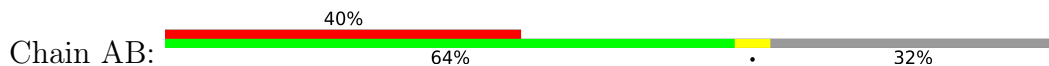
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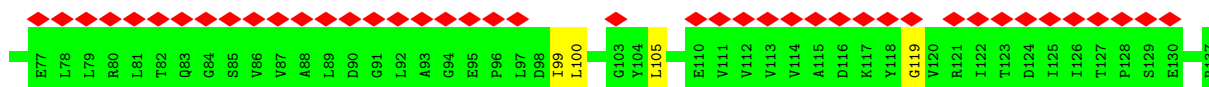
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• Molecule 4: Flagellar motor switch protein FliN



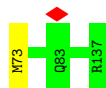
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• Molecule 4: Flagellar motor switch protein FliN



MET	SER	ASP	MET	ASN	ASN	PRO	SER	ASP	GLU	ASN	THR	GLY	ALA	LEU	ASP	LEU	TRP	ALA	ASP	LEU	LEU	GLN	LYS	THR	THR	THR	LYS	SER	ALA	ALA	ALA	ASP	VAL	VAL	PHE	GLN	GLN	LEU	LEU	GLY	GLY	GLY	ASP	VAL	SER	GLY	ALA	MET	GLN	ASP	ILE	ASP	LEU	ILE	MET	D59
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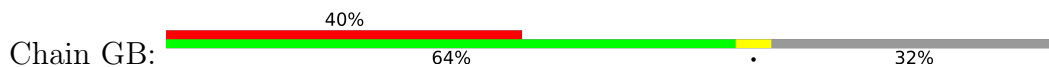
• Molecule 4: Flagellar motor switch protein FliN



MET	SER	ASP	MET	ASN	ASN	PRO	SER	ASP	GLU	ASN	THR	GLY	ALA	LEU	ASP	LEU	TRP	ALA	ASP	LEU	LEU	GLN	LYS	THR	THR	THR	LYS	SER	ALA	ALA	ALA	ASP	VAL	VAL	PHE	GLN	GLN	LEU	LEU	GLY	GLY	GLY	ASP	VAL	SER	GLY	ALA	MET	GLN	ASP	ILE	ASP	LEU	ILE	MET	ASP	ILE
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• Molecule 4: Flagellar motor switch protein FliN

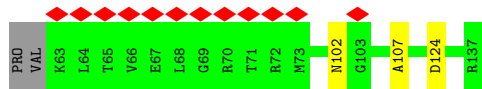


MET	SER	ASP	MET	ASN	ASN	PRO	SER	ASP	GLU	ASN	THR	GLY	ALA	LEU	ASP	LEU	TRP	ALA	ASP	LEU	LEU	GLN	LYS	THR	THR	THR	LYS	SER	ALA	ALA	ALA	ASP	VAL	VAL	PHE	GLN	GLN	LEU	LEU	GLY	GLY	G45	D46	V47	S48	G49	A50	M51	Q52	T65	L68	G69	R70	T71	R72
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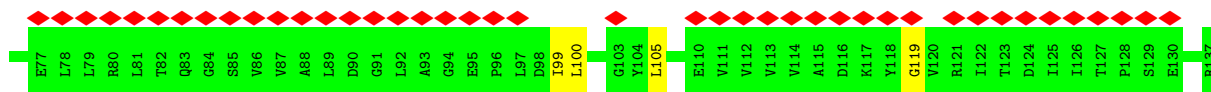
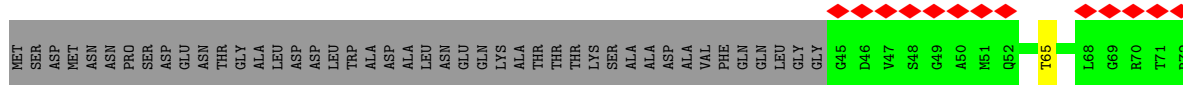
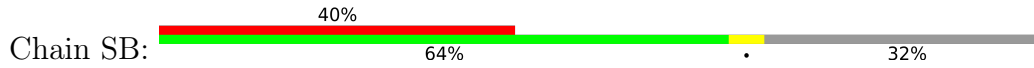




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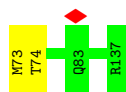
- Molecule 4: Flagellar motor switch protein FliN



- Molecule 4: Flagellar motor switch protein FliN



MET SER ASP MET MET ASN PRO PRO SER ASP GLU THR THR GLY LEU LEU ASP ASP TRP ALA ALA ALA LEU ASN ASN GLU GLN LYS THR THR THR THR LYS SER SER ALA ALA ALA ASP ASP VAL VAL PHE GLN GLN LEU LEU GLY GLY GLY ASP VAL VAL VAL GLY ALA MET GLN ASP ASP ILE ASP LEU LEU ILE MET ASP D59



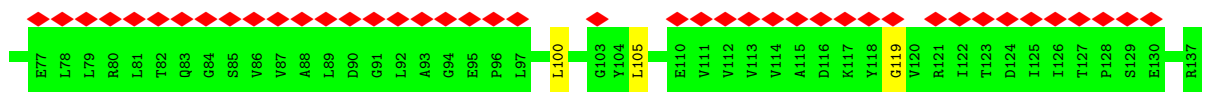
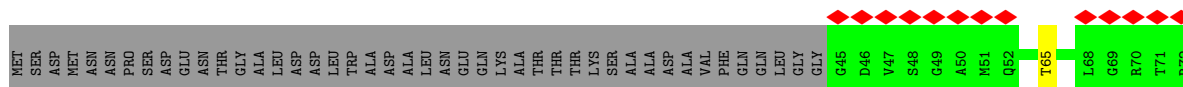
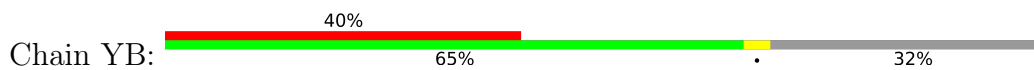
- Molecule 4: Flagellar motor switch protein FliN



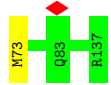
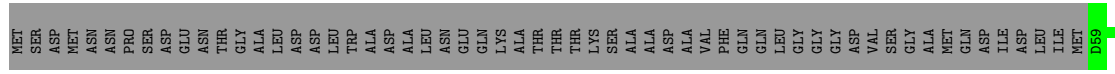
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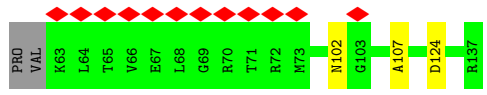
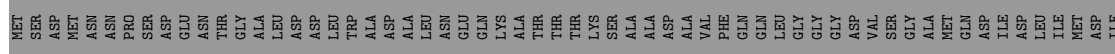
- Molecule 4: Flagellar motor switch protein FliN



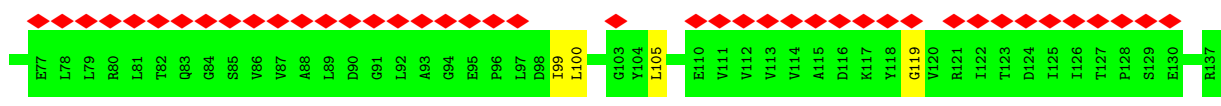
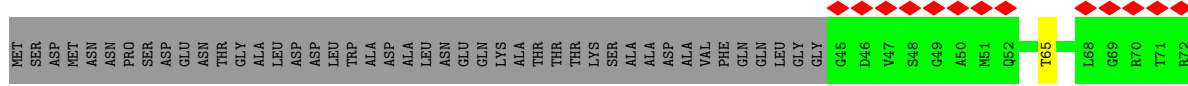
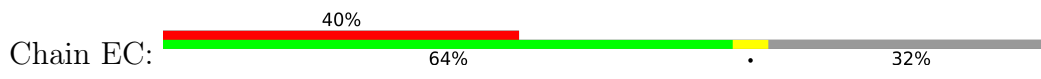
- Molecule 4: Flagellar motor switch protein FliN



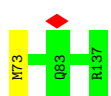
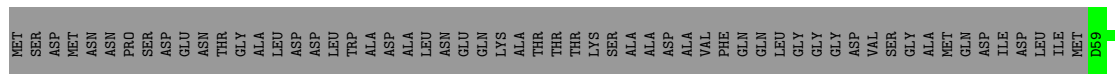
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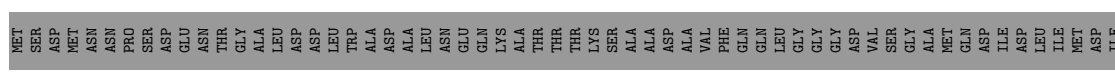
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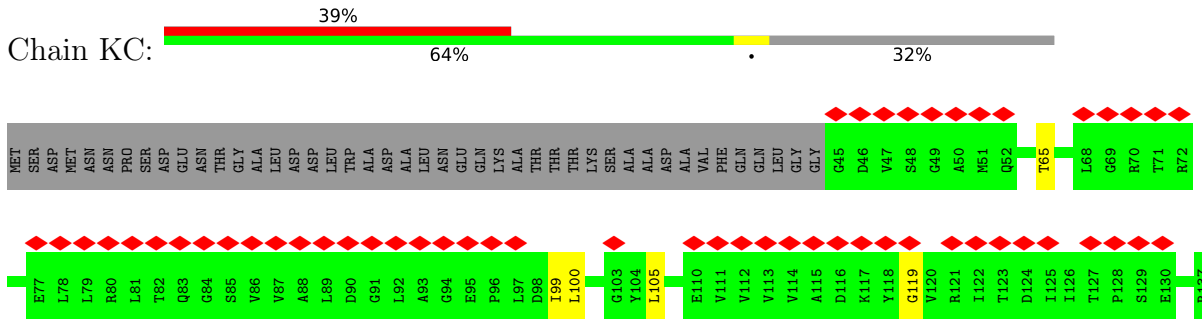
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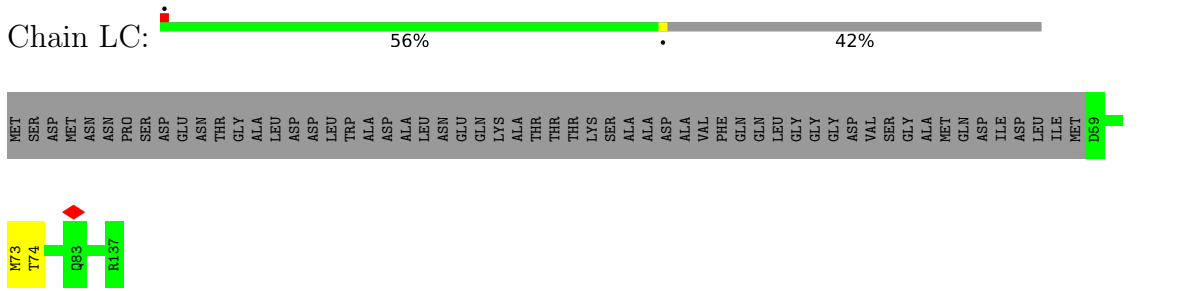
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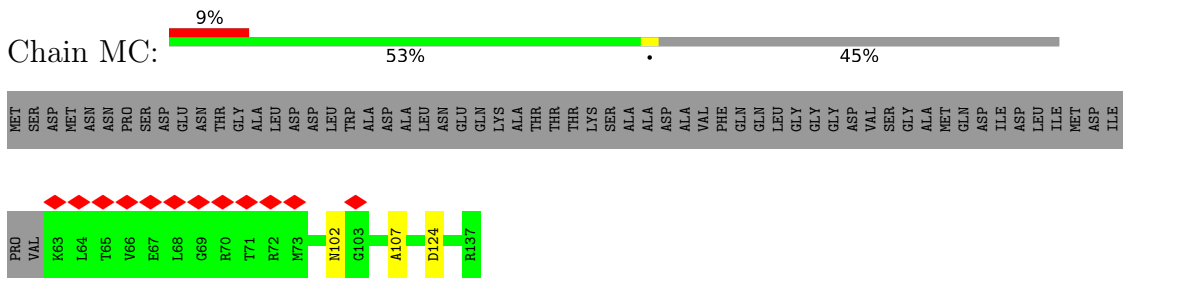
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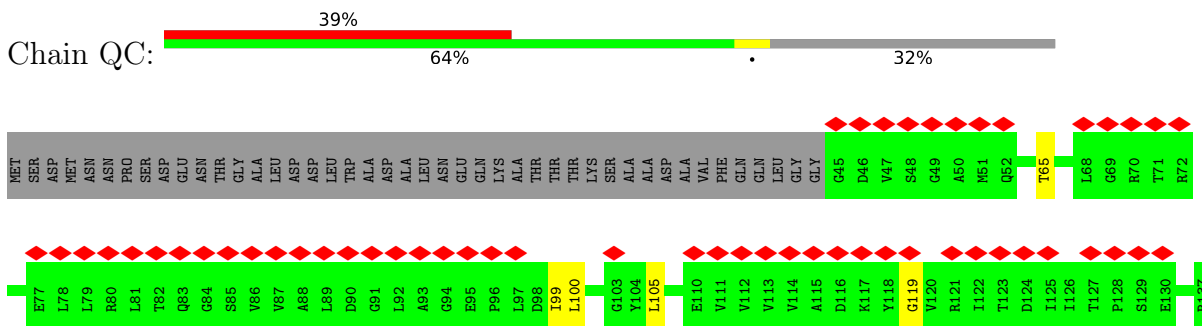
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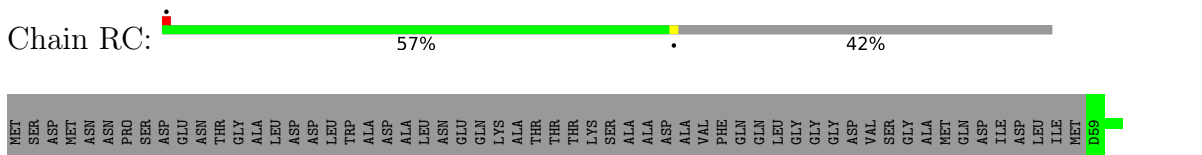
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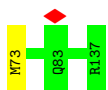
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● Molecule 4: Flagellar motor switch protein FliN



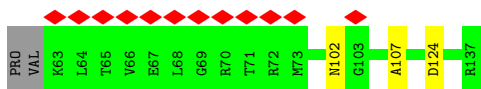




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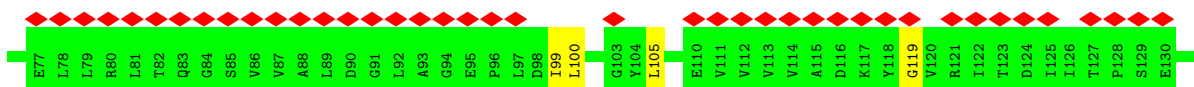
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• Molecule 4: Flagellar motor switch protein FliN



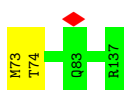
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• Molecule 4: Flagellar motor switch protein FliN



MET	SER	ASP	MET	ASN	ASN	PRO	SER	ASP	ASP	GLU	ASN	THR	GLY	ALA	LEU	ASP	LEU	TRP	ALA	ASP	ALA	LEU	ASN	GLU	GLN	LYS	ALA	ALA	THR	THR	THR	LYS	SER	ALA	ALA	ASP	ALA	VAL	PHE	GLN	GLN	LEU	LEU	GLY	GLY	GLY	ASP	VAL	SER	SER	GLY	ALA	MET	GLN	ASP	ILE	ASP	LEU	ILE	MET	D69
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• Molecule 4: Flagellar motor switch protein FliN

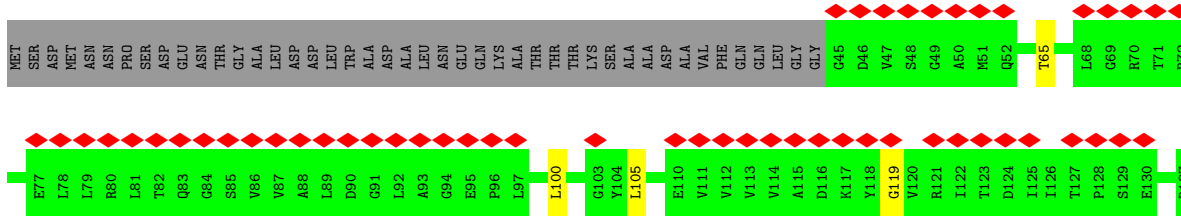


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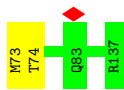


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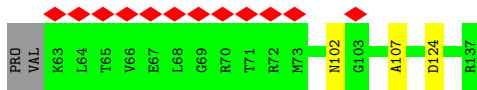




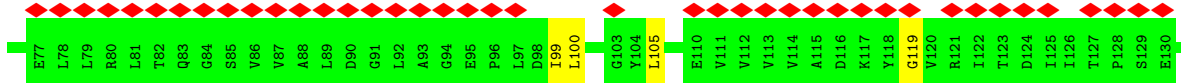
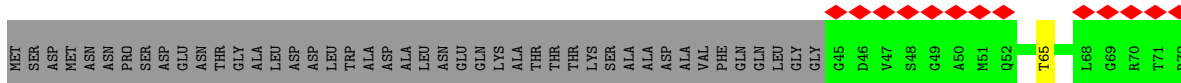
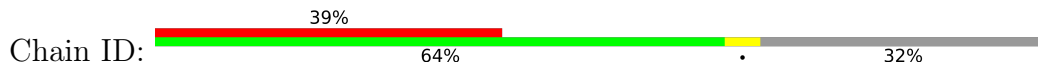
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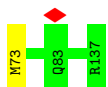
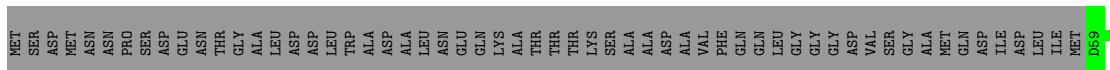
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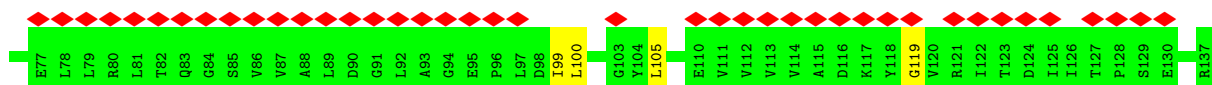
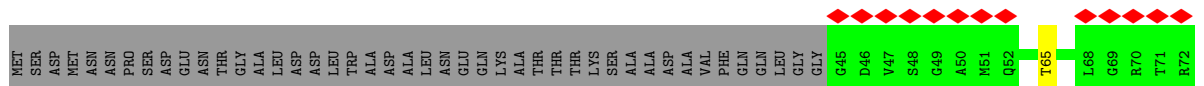
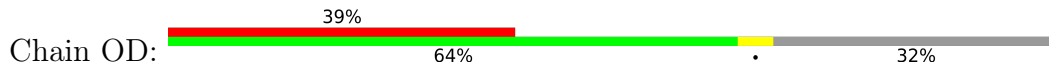
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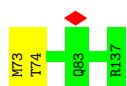
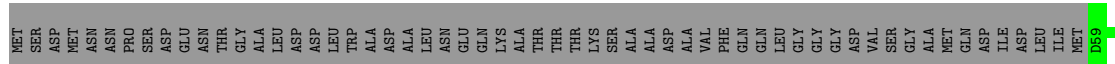
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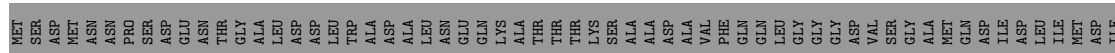
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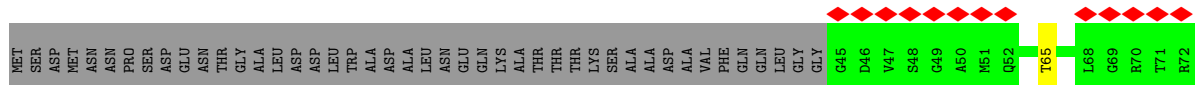
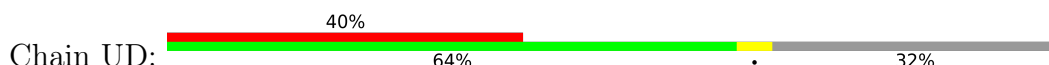
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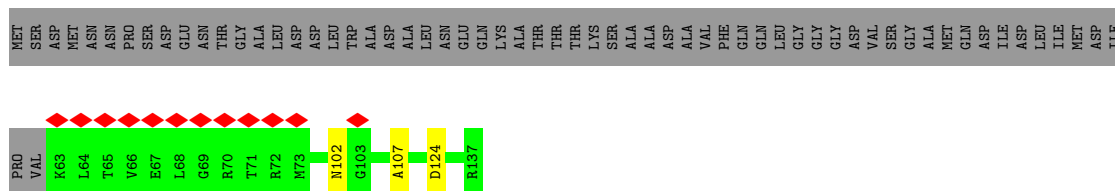
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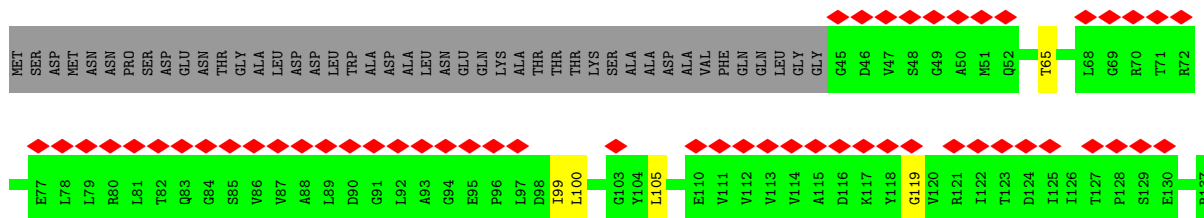
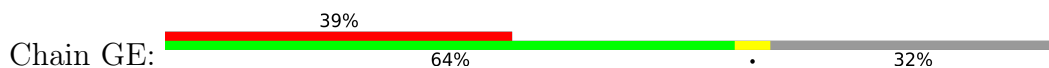
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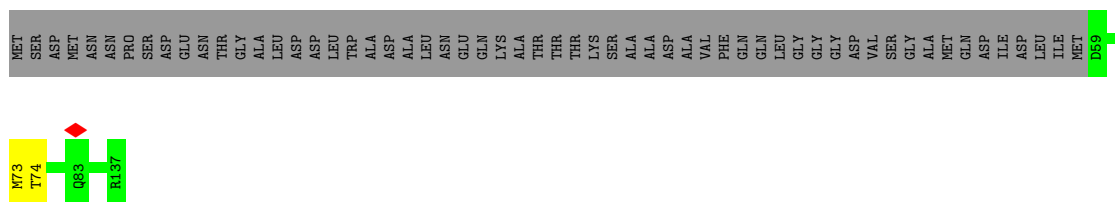




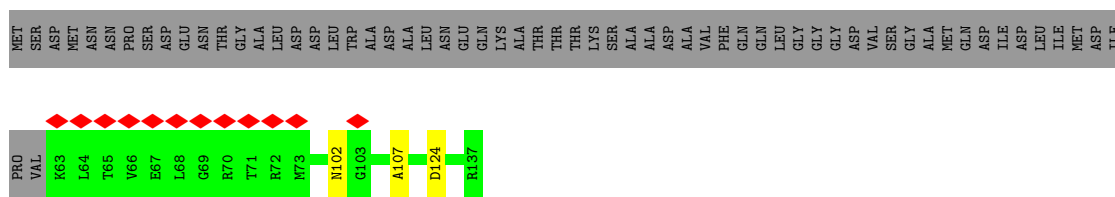
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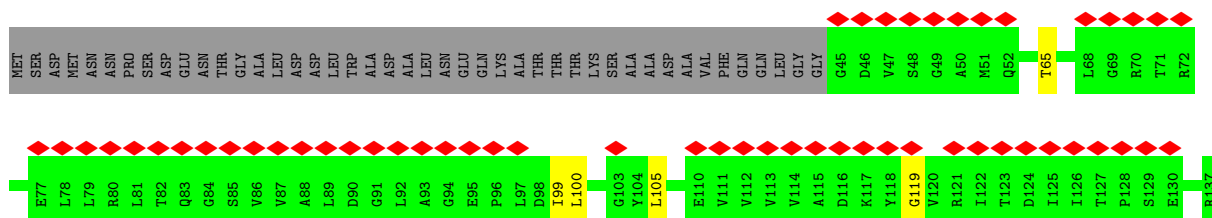
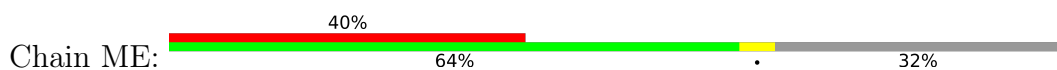
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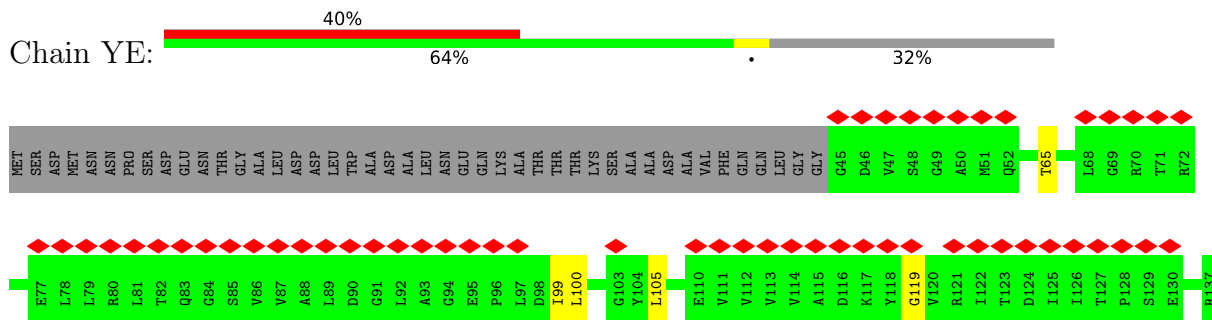
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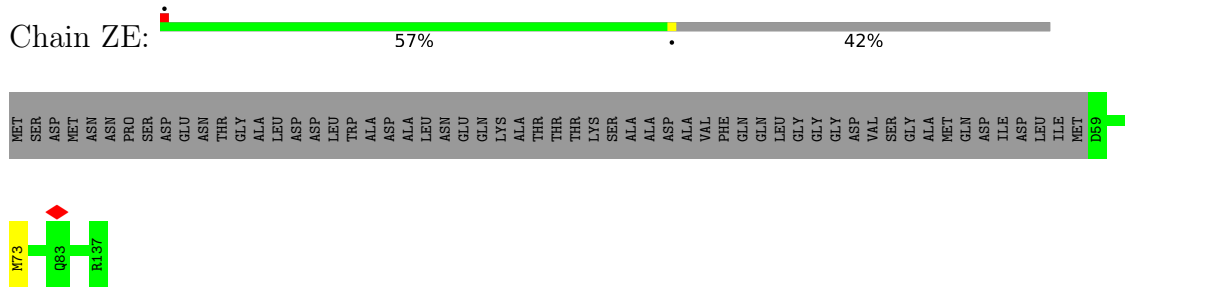
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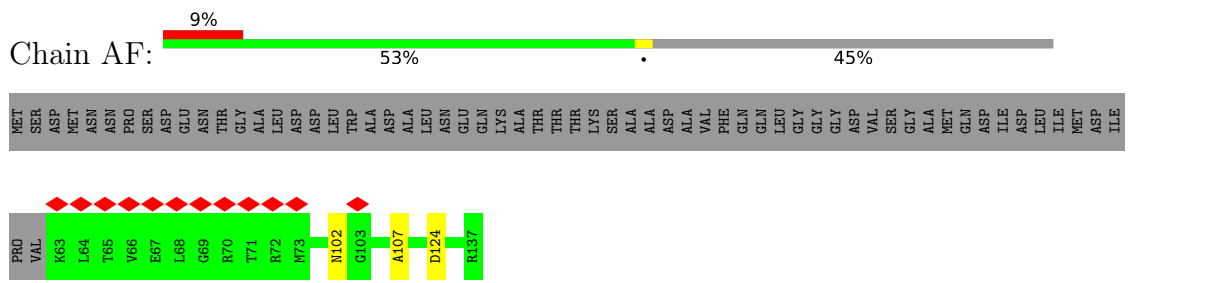
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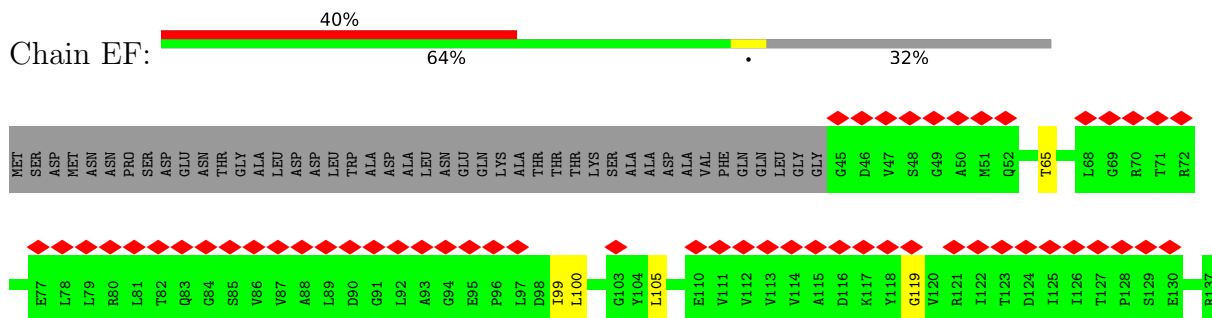
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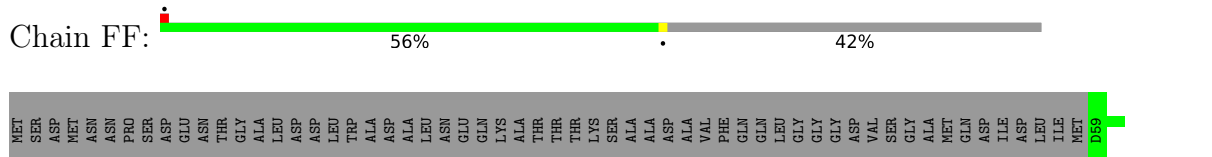
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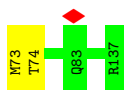


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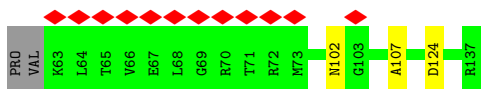
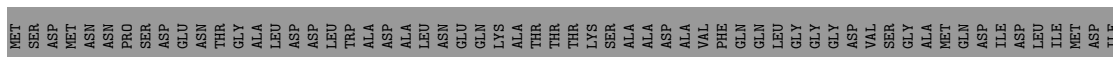


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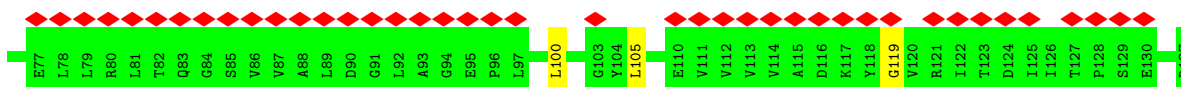
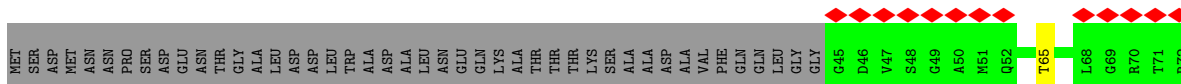




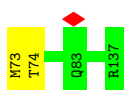
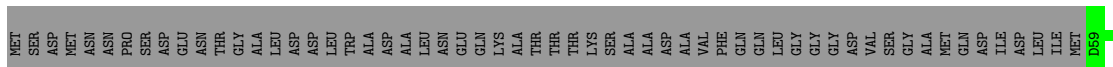
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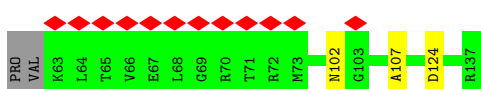
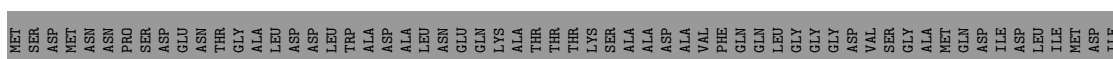
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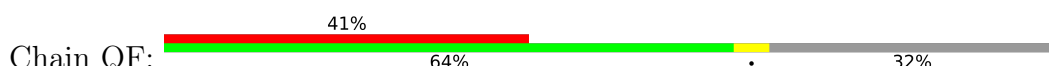
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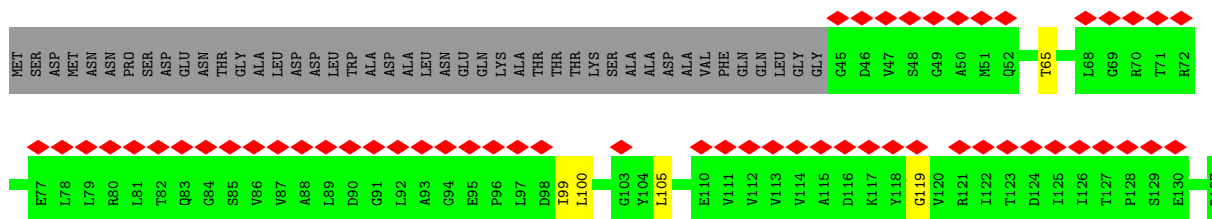
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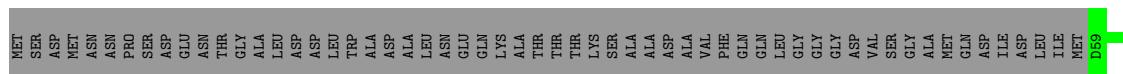
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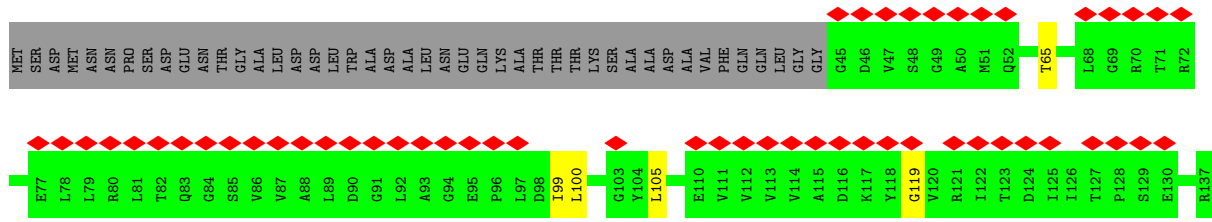
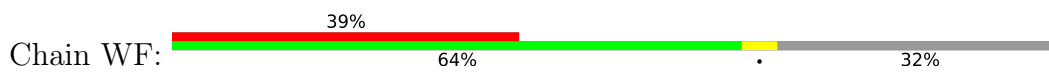
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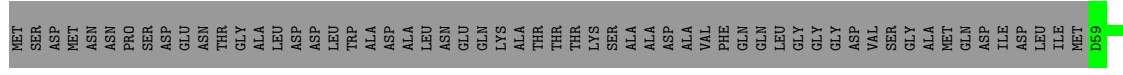
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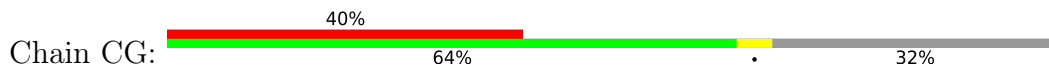
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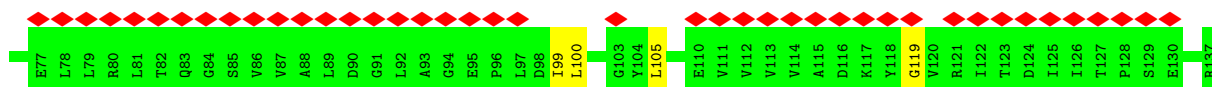
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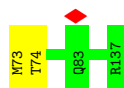
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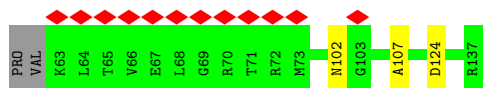
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• Molecule 4: Flagellar motor switch protein FliN



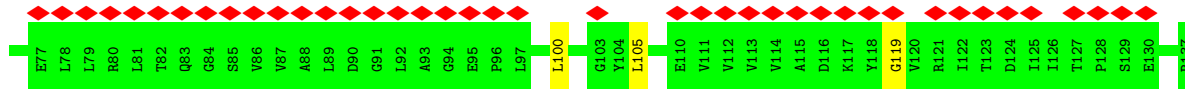
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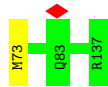
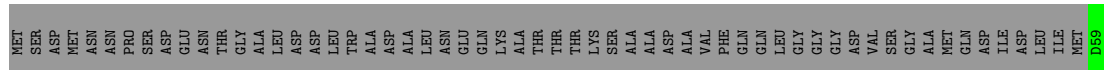
• Molecule 4: Flagellar motor switch protein FliN



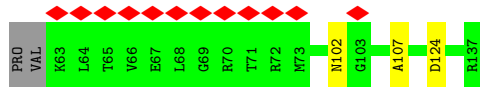
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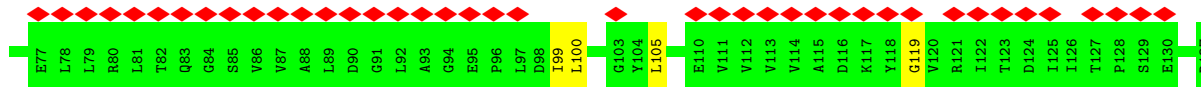
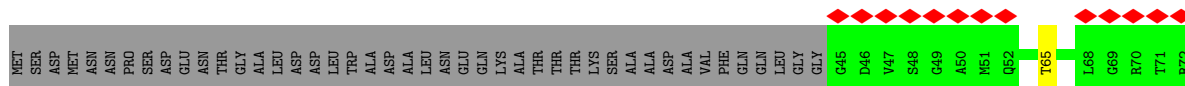
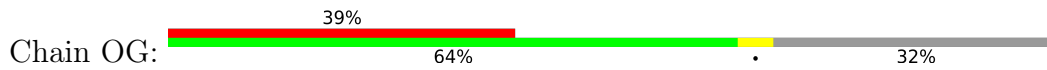
• Molecule 4: Flagellar motor switch protein FliN



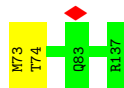
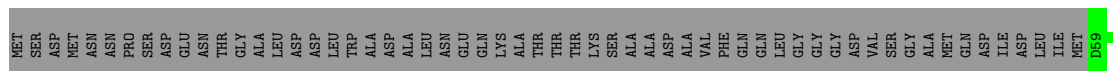
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN



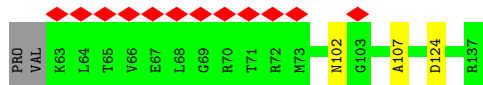
• Molecule 4: Flagellar motor switch protein FliN



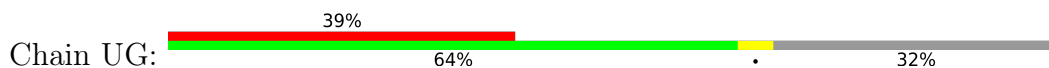
• Molecule 4: Flagellar motor switch protein FliN



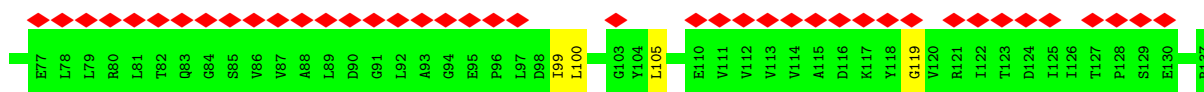
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• Molecule 4: Flagellar motor switch protein FliN



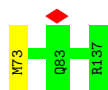
MET SER ASP MET MET ASN PRO SER ASP GLU THR GLY LEU ASP ASP TRP ALA ALA ALA LEU ASN ASN GLU GLN LYS SER SER ALA ALA ALA ASP ASP VAL PHE GLN GLN LEU LEU GLY GLY G45 D46 V47 S48 G49 A50 M51 Q52 T65 L68 G69 R70 T71 R72



• Molecule 4: Flagellar motor switch protein FliN



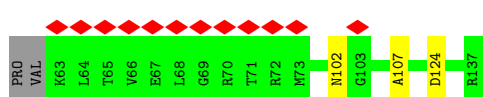
MET SER ASP MET MET ASN PRO SER ASP GLU THR GLY LEU ASP ASP TRP ALA ALA ALA LEU ASN ASN GLU GLN LYS SER SER ALA ALA ALA ASP ASP VAL PHE GLN GLN LEU LEU GLY GLY G45 D46 V47 S48 G49 A50 M51 Q52 T65 L68 G69 R70 T71 R72 D59 R137



• Molecule 4: Flagellar motor switch protein FliN



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



## 4 Experimental information

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.44	0/233	0.43	0/324
1	BC	0.44	0/233	0.43	0/324
1	BF	0.44	0/233	0.43	0/324
1	DB	0.44	0/233	0.43	0/324
1	DE	0.44	0/233	0.43	0/324
1	F	0.44	0/233	0.43	0/324
1	FA	0.44	0/233	0.43	0/324
1	FD	0.44	0/233	0.43	0/324
1	FG	0.44	0/233	0.43	0/324
1	HC	0.44	0/233	0.43	0/324
1	HF	0.44	0/233	0.43	0/324
1	I	0.44	0/233	0.43	0/324
1	JB	0.44	0/233	0.43	0/324
1	JE	0.44	0/233	0.43	0/324
1	LA	0.44	0/233	0.43	0/324
1	LD	0.44	0/233	0.43	0/324
1	LG	0.44	0/233	0.43	0/324
1	NC	0.44	0/233	0.43	0/324
1	NF	0.44	0/233	0.43	0/324
1	PB	0.45	0/233	0.43	0/324
1	PE	0.44	0/233	0.43	0/324
1	RA	0.44	0/233	0.43	0/324
1	RD	0.44	0/233	0.43	0/324
1	RG	0.44	0/233	0.43	0/324
1	S	0.44	0/233	0.43	0/324
1	TC	0.44	0/233	0.43	0/324
1	TF	0.44	0/233	0.43	0/324
1	VB	0.44	0/233	0.43	0/324
1	VE	0.44	0/233	0.43	0/324
1	XA	0.44	0/233	0.43	0/324
1	XD	0.44	0/233	0.43	0/324
1	Z	0.44	0/233	0.43	0/324
1	ZC	0.44	0/233	0.43	0/324
1	ZF	0.44	0/233	0.43	0/324

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	AA	0.53	0/1551	0.66	1/2157 (0.0%)
2	AD	0.52	0/1551	0.66	1/2157 (0.0%)
2	AG	0.53	0/1551	0.66	1/2157 (0.0%)
2	B	0.53	0/1551	0.66	1/2157 (0.0%)
2	CC	0.52	0/1551	0.66	1/2157 (0.0%)
2	CF	0.53	0/1551	0.66	1/2157 (0.0%)
2	EB	0.53	0/1551	0.66	1/2157 (0.0%)
2	EE	0.53	0/1551	0.66	1/2157 (0.0%)
2	G	0.52	0/1551	0.66	1/2157 (0.0%)
2	GA	0.53	0/1551	0.66	1/2157 (0.0%)
2	GD	0.52	0/1551	0.66	1/2157 (0.0%)
2	GG	0.53	0/1551	0.66	1/2157 (0.0%)
2	IC	0.53	0/1551	0.66	1/2157 (0.0%)
2	IF	0.53	0/1551	0.66	1/2157 (0.0%)
2	J	0.52	0/1551	0.66	1/2157 (0.0%)
2	KB	0.53	0/1551	0.66	1/2157 (0.0%)
2	KE	0.53	0/1551	0.66	1/2157 (0.0%)
2	MA	0.53	0/1551	0.66	1/2157 (0.0%)
2	MD	0.53	0/1551	0.66	1/2157 (0.0%)
2	MG	0.53	0/1551	0.66	1/2157 (0.0%)
2	OC	0.52	0/1551	0.66	1/2157 (0.0%)
2	OF	0.52	0/1551	0.66	1/2157 (0.0%)
2	QB	0.52	0/1551	0.66	1/2157 (0.0%)
2	QE	0.53	0/1551	0.66	1/2157 (0.0%)
2	SA	0.52	0/1551	0.66	1/2157 (0.0%)
2	SD	0.53	0/1551	0.66	1/2157 (0.0%)
2	SG	0.52	0/1551	0.66	1/2157 (0.0%)
2	T	0.53	0/1551	0.66	1/2157 (0.0%)
2	UC	0.52	0/1551	0.66	1/2157 (0.0%)
2	UF	0.53	0/1551	0.66	1/2157 (0.0%)
2	WB	0.52	0/1551	0.66	1/2157 (0.0%)
2	WE	0.53	0/1551	0.66	1/2157 (0.0%)
2	YA	0.53	0/1551	0.66	1/2157 (0.0%)
2	YD	0.52	0/1551	0.66	1/2157 (0.0%)
3	BA	0.39	0/1384	0.61	2/1927 (0.1%)
3	BD	0.38	0/1384	0.61	2/1927 (0.1%)
3	BG	0.39	0/1384	0.61	2/1927 (0.1%)
3	C	0.38	0/1384	0.61	2/1927 (0.1%)
3	DC	0.39	0/1384	0.61	2/1927 (0.1%)
3	DF	0.39	0/1384	0.61	2/1927 (0.1%)
3	FB	0.39	0/1384	0.61	2/1927 (0.1%)
3	FE	0.38	0/1384	0.61	2/1927 (0.1%)
3	HA	0.38	0/1384	0.61	2/1927 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
3	HD	0.39	0/1384	0.61	2/1927 (0.1%)
3	HG	0.39	0/1384	0.61	2/1927 (0.1%)
3	JC	0.39	0/1384	0.61	2/1927 (0.1%)
3	JF	0.38	0/1384	0.61	2/1927 (0.1%)
3	K	0.39	0/1384	0.61	2/1927 (0.1%)
3	LB	0.38	0/1384	0.61	2/1927 (0.1%)
3	LE	0.38	0/1384	0.61	2/1927 (0.1%)
3	M	0.38	0/1384	0.61	2/1927 (0.1%)
3	NA	0.38	0/1384	0.61	2/1927 (0.1%)
3	ND	0.39	0/1384	0.61	2/1927 (0.1%)
3	NG	0.38	0/1384	0.61	2/1927 (0.1%)
3	PC	0.38	0/1384	0.61	2/1927 (0.1%)
3	PF	0.38	0/1384	0.61	2/1927 (0.1%)
3	RB	0.39	0/1384	0.61	2/1927 (0.1%)
3	RE	0.38	0/1384	0.61	2/1927 (0.1%)
3	TA	0.38	0/1384	0.61	2/1927 (0.1%)
3	TD	0.39	0/1384	0.61	2/1927 (0.1%)
3	TG	0.39	0/1384	0.61	2/1927 (0.1%)
3	V	0.39	0/1384	0.61	2/1927 (0.1%)
3	VC	0.39	0/1384	0.61	2/1927 (0.1%)
3	VF	0.39	0/1384	0.61	2/1927 (0.1%)
3	XB	0.38	0/1384	0.61	2/1927 (0.1%)
3	XE	0.39	0/1384	0.61	2/1927 (0.1%)
3	ZA	0.39	0/1384	0.61	2/1927 (0.1%)
3	ZD	0.39	0/1384	0.61	2/1927 (0.1%)
4	AB	0.42	0/455	0.52	0/630
4	AC	0.44	0/368	0.54	0/508
4	AE	0.42	0/455	0.52	0/630
4	AF	0.44	0/368	0.54	0/508
4	BB	0.41	0/388	0.56	0/536
4	BE	0.41	0/388	0.56	0/536
4	CA	0.42	0/455	0.52	0/630
4	CB	0.44	0/368	0.54	0/508
4	CD	0.42	0/455	0.52	0/630
4	CE	0.44	0/368	0.54	0/508
4	CG	0.42	0/455	0.52	0/630
4	D	0.42	0/455	0.52	0/630
4	DA	0.41	0/388	0.56	0/536
4	DD	0.41	0/388	0.56	0/536
4	DG	0.41	0/388	0.56	0/536
4	E	0.41	0/388	0.56	0/536
4	EA	0.44	0/368	0.54	0/508
4	EC	0.42	0/455	0.52	0/630



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
4	ED	0.44	0/368	0.54	0/508
4	EF	0.42	0/455	0.52	0/630
4	EG	0.44	0/368	0.54	0/508
4	FC	0.41	0/388	0.56	0/536
4	FF	0.41	0/388	0.56	0/536
4	GB	0.42	0/455	0.52	0/630
4	GC	0.44	0/368	0.54	0/508
4	GE	0.42	0/455	0.52	0/630
4	GF	0.44	0/368	0.54	0/508
4	H	0.44	0/368	0.54	0/508
4	HB	0.41	0/388	0.56	0/536
4	HE	0.41	0/388	0.56	0/536
4	IA	0.42	0/455	0.52	0/630
4	IB	0.44	0/368	0.54	0/508
4	ID	0.42	0/455	0.52	0/630
4	IE	0.44	0/368	0.54	0/508
4	IG	0.42	0/455	0.52	0/630
4	JA	0.41	0/388	0.56	0/536
4	JD	0.41	0/388	0.56	0/536
4	JG	0.41	0/388	0.56	0/536
4	KA	0.44	0/368	0.54	0/508
4	KC	0.42	0/455	0.52	0/630
4	KD	0.44	0/368	0.54	0/508
4	KF	0.42	0/455	0.52	0/630
4	KG	0.44	0/368	0.54	0/508
4	L	0.42	0/455	0.52	0/630
4	LC	0.41	0/388	0.56	0/536
4	LF	0.41	0/388	0.56	0/536
4	MB	0.42	0/455	0.52	0/630
4	MC	0.44	0/368	0.54	0/508
4	ME	0.42	0/455	0.52	0/630
4	MF	0.44	0/368	0.54	0/508
4	N	0.42	0/455	0.52	0/630
4	NB	0.41	0/388	0.56	0/536
4	NE	0.41	0/388	0.56	0/536
4	O	0.41	0/388	0.56	0/536
4	OA	0.42	0/455	0.52	0/630
4	OB	0.44	0/368	0.54	0/508
4	OD	0.42	0/455	0.52	0/630
4	OE	0.44	0/368	0.54	0/508
4	OG	0.42	0/455	0.52	0/630
4	P	0.41	0/388	0.56	0/536
4	PA	0.41	0/388	0.56	0/536

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
4	PD	0.41	0/388	0.56	0/536
4	PG	0.41	0/388	0.56	0/536
4	Q	0.44	0/368	0.54	0/508
4	QA	0.44	0/368	0.54	0/508
4	QC	0.42	0/455	0.52	0/630
4	QD	0.44	0/368	0.54	0/508
4	QF	0.42	0/455	0.52	0/630
4	QG	0.44	0/368	0.54	0/508
4	R	0.44	0/368	0.54	0/508
4	RC	0.41	0/388	0.56	0/536
4	RF	0.41	0/388	0.56	0/536
4	SB	0.42	0/455	0.52	0/630
4	SC	0.44	0/368	0.54	0/508
4	SE	0.42	0/455	0.52	0/630
4	SF	0.44	0/368	0.54	0/508
4	TB	0.41	0/388	0.56	0/536
4	TE	0.41	0/388	0.56	0/536
4	UA	0.42	0/455	0.52	0/630
4	UB	0.44	0/368	0.54	0/508
4	UD	0.42	0/455	0.52	0/630
4	UE	0.44	0/368	0.54	0/508
4	UG	0.42	0/455	0.52	0/630
4	VA	0.41	0/388	0.56	0/536
4	VD	0.41	0/388	0.56	0/536
4	VG	0.41	0/388	0.56	0/536
4	W	0.42	0/455	0.52	0/630
4	WA	0.44	0/368	0.54	0/508
4	WC	0.42	0/455	0.52	0/630
4	WD	0.44	0/368	0.54	0/508
4	WF	0.42	0/455	0.52	0/630
4	WG	0.44	0/368	0.54	0/508
4	X	0.41	0/388	0.56	0/536
4	XC	0.41	0/388	0.56	0/536
4	XF	0.41	0/388	0.56	0/536
4	Y	0.44	0/368	0.54	0/508
4	YB	0.42	0/455	0.52	0/630
4	YC	0.44	0/368	0.54	0/508
4	YE	0.42	0/455	0.52	0/630
4	YF	0.44	0/368	0.54	0/508
4	ZB	0.41	0/388	0.56	0/536
4	ZE	0.41	0/388	0.56	0/536
All	All	0.45	0/148886	0.60	102/206788 (0.0%)

There are no bond length outliers.

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	TD	235	PRO	N-CA-C	-6.98	93.96	112.10
3	BA	235	PRO	N-CA-C	-6.97	93.97	112.10
3	NA	235	PRO	N-CA-C	-6.97	93.97	112.10
3	ZA	235	PRO	N-CA-C	-6.97	93.97	112.10
3	LB	235	PRO	N-CA-C	-6.97	93.97	112.10

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	234	0	102	19	0
1	BC	234	0	102	18	0
1	BF	234	0	102	19	0
1	DB	234	0	102	18	0
1	DE	234	0	102	19	0
1	F	234	0	102	18	0
1	FA	234	0	102	18	0
1	FD	234	0	102	18	0
1	FG	234	0	102	18	0
1	HC	234	0	102	18	0
1	HF	234	0	102	18	0
1	I	234	0	102	19	0
1	JB	234	0	102	19	0
1	JE	234	0	102	18	0
1	LA	234	0	102	19	0
1	LD	234	0	102	19	0
1	LG	234	0	102	19	0
1	NC	234	0	102	18	0
1	NF	234	0	102	19	0
1	PB	234	0	102	21	0
1	PE	234	0	102	19	0
1	RA	234	0	102	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	RD	234	0	102	19	0
1	RG	234	0	102	18	0
1	S	234	0	102	19	0
1	TC	234	0	102	20	0
1	TF	234	0	102	18	0
1	VB	234	0	102	19	0
1	VE	234	0	102	18	0
1	XA	234	0	102	19	0
1	XD	234	0	102	19	0
1	Z	234	0	102	18	0
1	ZC	234	0	102	19	0
1	ZF	234	0	102	19	0
2	AA	1554	0	723	47	0
2	AD	1554	0	723	47	0
2	AG	1554	0	723	47	0
2	B	1554	0	723	48	0
2	CC	1554	0	723	46	0
2	CF	1554	0	723	47	0
2	EB	1554	0	723	46	0
2	EE	1554	0	723	46	0
2	G	1554	0	723	47	0
2	GA	1554	0	723	47	0
2	GD	1554	0	723	46	0
2	GG	1554	0	723	46	0
2	IC	1554	0	723	46	0
2	IF	1554	0	723	46	0
2	J	1554	0	723	48	0
2	KB	1554	0	723	48	0
2	KE	1554	0	723	45	0
2	MA	1554	0	723	48	0
2	MD	1554	0	723	47	0
2	MG	1554	0	723	47	0
2	OC	1554	0	723	48	0
2	OF	1554	0	723	47	0
2	QB	1554	0	723	47	0
2	QE	1554	0	723	46	0
2	SA	1554	0	723	48	0
2	SD	1554	0	723	47	0
2	SG	1554	0	723	46	0
2	T	1554	0	723	48	0
2	UC	1554	0	723	46	0
2	UF	1554	0	723	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	WB	1554	0	723	47	0
2	WE	1554	0	723	46	0
2	YA	1554	0	723	48	0
2	YD	1554	0	723	47	0
3	BA	1420	0	604	9	0
3	BD	1420	0	604	9	0
3	BG	1420	0	604	9	0
3	C	1420	0	604	9	0
3	DC	1420	0	604	10	0
3	DF	1420	0	604	10	0
3	FB	1420	0	604	9	0
3	FE	1420	0	604	9	0
3	HA	1420	0	604	9	0
3	HD	1420	0	604	10	0
3	HG	1420	0	604	10	0
3	JC	1420	0	604	9	0
3	JF	1420	0	604	9	0
3	K	1420	0	604	9	0
3	LB	1420	0	604	10	0
3	LE	1420	0	604	9	0
3	M	1420	0	604	9	0
3	NA	1420	0	604	10	0
3	ND	1420	0	604	10	0
3	NG	1420	0	604	9	0
3	PC	1420	0	604	10	0
3	PF	1420	0	604	10	0
3	RB	1420	0	604	9	0
3	RE	1420	0	604	9	0
3	TA	1420	0	604	9	0
3	TD	1420	0	604	9	0
3	TG	1420	0	604	9	0
3	V	1420	0	604	9	0
3	VC	1420	0	604	10	0
3	VF	1420	0	604	10	0
3	XB	1420	0	604	9	0
3	XE	1420	0	604	10	0
3	ZA	1420	0	604	9	0
3	ZD	1420	0	604	10	0
4	AB	456	0	206	4	0
4	AC	369	0	166	2	0
4	AE	456	0	206	4	0
4	AF	369	0	166	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	BB	389	0	173	3	0
4	BE	389	0	173	3	0
4	CA	456	0	206	4	0
4	CB	369	0	166	2	0
4	CD	456	0	206	3	0
4	CE	369	0	166	2	0
4	CG	456	0	206	4	0
4	D	456	0	206	4	0
4	DA	389	0	173	3	0
4	DD	389	0	173	4	0
4	DG	389	0	173	4	0
4	E	389	0	173	3	0
4	EA	369	0	166	2	0
4	EC	456	0	206	4	0
4	ED	369	0	166	2	0
4	EF	456	0	206	4	0
4	EG	369	0	166	2	0
4	FC	389	0	173	3	0
4	FF	389	0	173	4	0
4	GB	456	0	206	4	0
4	GC	369	0	166	2	0
4	GE	456	0	206	4	0
4	GF	369	0	166	2	0
4	H	369	0	166	2	0
4	HB	389	0	173	3	0
4	HE	389	0	173	4	0
4	IA	456	0	206	4	0
4	IB	369	0	166	2	0
4	ID	456	0	206	4	0
4	IE	369	0	166	2	0
4	IG	456	0	206	3	0
4	JA	389	0	173	3	0
4	JD	389	0	173	3	0
4	JG	389	0	173	3	0
4	KA	369	0	166	2	0
4	KC	456	0	206	4	0
4	KD	369	0	166	2	0
4	KF	456	0	206	3	0
4	KG	369	0	166	2	0
4	L	456	0	206	4	0
4	LC	389	0	173	4	0
4	LF	389	0	173	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	MB	456	0	206	4	0
4	MC	369	0	166	2	0
4	ME	456	0	206	4	0
4	MF	369	0	166	2	0
4	N	456	0	206	3	0
4	NB	389	0	173	3	0
4	NE	389	0	173	3	0
4	O	389	0	173	3	0
4	OA	456	0	206	4	0
4	OB	369	0	166	2	0
4	OD	456	0	206	4	0
4	OE	369	0	166	2	0
4	OG	456	0	206	4	0
4	P	389	0	173	3	0
4	PA	389	0	173	3	0
4	PD	389	0	173	4	0
4	PG	389	0	173	4	0
4	Q	369	0	166	2	0
4	QA	369	0	166	2	0
4	QC	456	0	206	4	0
4	QD	369	0	166	2	0
4	QF	456	0	206	4	0
4	QG	369	0	166	2	0
4	R	369	0	166	2	0
4	RC	389	0	173	3	0
4	RF	389	0	173	3	0
4	SB	456	0	206	4	0
4	SC	369	0	166	2	0
4	SE	456	0	206	3	0
4	SF	369	0	166	2	0
4	TB	389	0	173	4	0
4	TE	389	0	173	3	0
4	UA	456	0	206	3	0
4	UB	369	0	166	2	0
4	UD	456	0	206	4	0
4	UE	369	0	166	2	0
4	UG	456	0	206	4	0
4	VA	389	0	173	4	0
4	VD	389	0	173	4	0
4	VG	389	0	173	3	0
4	W	456	0	206	4	0
4	WA	369	0	166	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	WC	456	0	206	4	0
4	WD	369	0	166	2	0
4	WF	456	0	206	4	0
4	WG	369	0	166	2	0
4	X	389	0	173	3	0
4	XC	389	0	173	4	0
4	XF	389	0	173	4	0
4	Y	369	0	166	2	0
4	YB	456	0	206	3	0
4	YC	369	0	166	2	0
4	YE	456	0	206	4	0
4	YF	369	0	166	2	0
4	ZB	389	0	173	3	0
4	ZE	389	0	173	3	0
All	All	150348	0	67116	1904	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 1904 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:UF:61:GLN:HA	1:ZF:520:GLN:CB	1.22	1.67
2:AG:61:GLN:HA	1:FG:520:GLN:CB	1.19	1.64
2:OF:61:GLN:HA	1:TF:520:GLN:CB	1.18	1.63
2:B:61:GLN:HA	1:I:520:GLN:CB	1.21	1.63
2:G:61:GLN:HA	1:A:520:GLN:CB	1.24	1.63

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	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	BC	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	BF	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	DB	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	DE	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	F	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	FA	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	FD	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	FG	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	HC	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	HF	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	I	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	JB	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	JE	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	LA	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	LD	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	LG	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	NC	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	NF	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	PB	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	PE	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	RA	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	RD	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	RG	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	S	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	TC	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	TF	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	VB	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	VE	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	XA	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	XD	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	Z	45/560 (8%)	42 (93%)	3 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ZC	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
1	ZF	45/560 (8%)	42 (93%)	3 (7%)	0	100	100
2	AA	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	AD	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	AG	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	B	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	CC	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	CF	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	EB	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	EE	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	G	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	GA	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	GD	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	GG	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	IC	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	IF	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	J	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	KB	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	KE	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	MA	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	MD	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	MG	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	OC	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	OF	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	QB	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	QE	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	SA	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	SD	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	SG	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	T	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	UC	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	UF	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	WB	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	WE	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	YA	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
2	YD	308/331 (93%)	271 (88%)	27 (9%)	10 (3%)	4	26
3	BA	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	BD	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	BG	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	C	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	DC	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	DF	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	FB	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	FE	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	HA	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	HD	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	HG	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	JC	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	JF	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	K	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	LB	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	LE	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	M	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	NA	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	ND	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	NG	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	PC	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	PF	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	RB	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	RE	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	TA	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	TD	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	TG	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	V	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	VC	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	VF	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	XB	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	XE	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	ZA	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
3	ZD	279/291 (96%)	255 (91%)	20 (7%)	4 (1%)	11	46
4	AB	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	AC	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	AE	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	AF	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	BB	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	BE	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	CA	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	CB	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	CD	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	CE	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	CG	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	D	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	DA	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	DD	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	DG	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	E	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	EA	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	EC	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	ED	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	EF	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	EG	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	FC	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	FF	77/137 (56%)	69 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	GB	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	GC	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	GE	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	GF	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	H	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	HB	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	HE	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	IA	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	IB	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	ID	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	IE	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	IG	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	JA	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	JD	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	JG	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	KA	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	KC	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	KD	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	KF	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	KG	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	L	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	LC	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	LF	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	MB	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	MC	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	ME	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	MF	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	N	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	NB	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	NE	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	O	77/137 (56%)	69 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	OA	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	OB	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	OD	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	OE	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	OG	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	P	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	PA	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	PD	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	PG	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	Q	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	QA	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	QC	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	QD	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	QF	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	QG	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	R	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	RC	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	RF	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	SB	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	SC	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	SE	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	SF	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	TB	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	TE	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	UA	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	UB	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	UD	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	UE	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	UG	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	VA	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	VD	77/137 (56%)	69 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	VG	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	W	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	WA	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	WC	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	WD	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	WF	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	WG	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	X	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	XC	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	XF	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	Y	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	YB	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	YC	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	YE	91/137 (66%)	90 (99%)	1 (1%)	0	100	100
4	YF	73/137 (53%)	70 (96%)	3 (4%)	0	100	100
4	ZB	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
4	ZE	77/137 (56%)	69 (90%)	8 (10%)	0	100	100
All	All	29682/54162 (55%)	27098 (91%)	2108 (7%)	476 (2%)	13	43

5 of 476 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	9	LYS
2	G	89	ARG
2	G	167	VAL
3	M	233	ASN
2	B	9	LYS

### 5.3.2 Protein sidechains [i](#)

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



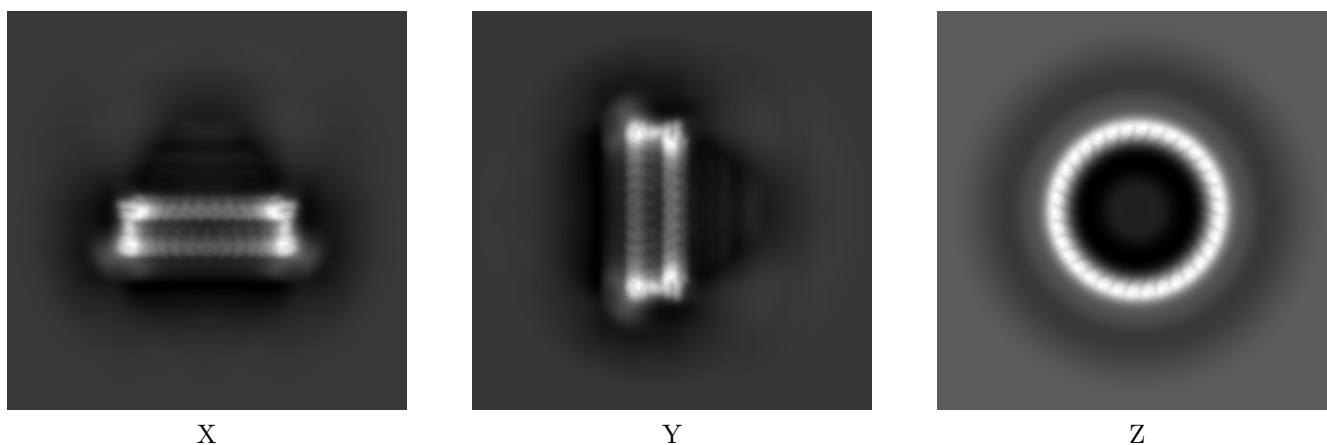
## 6 Map visualisation [i](#)

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

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

### 6.1 Orthogonal projections [i](#)

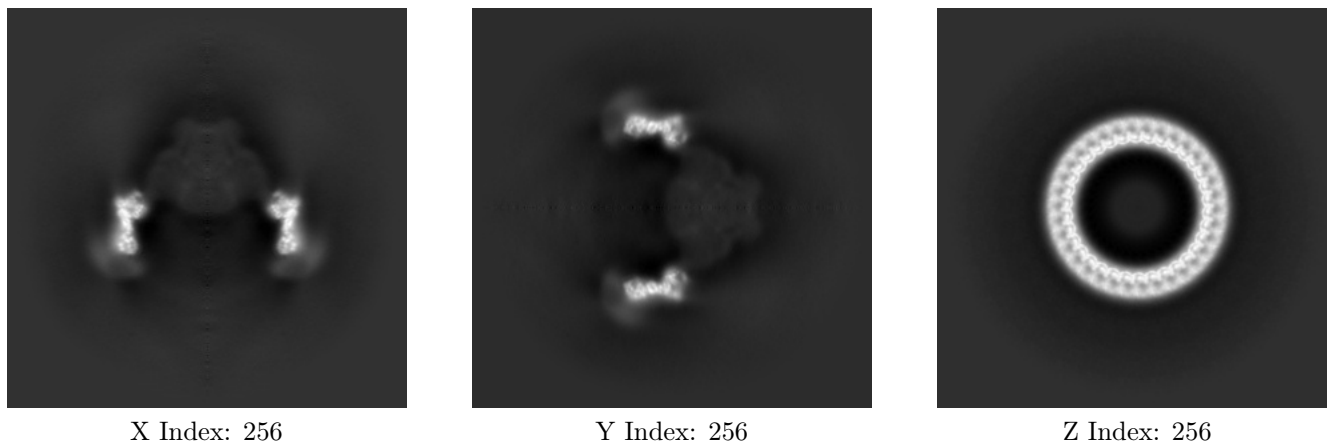
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

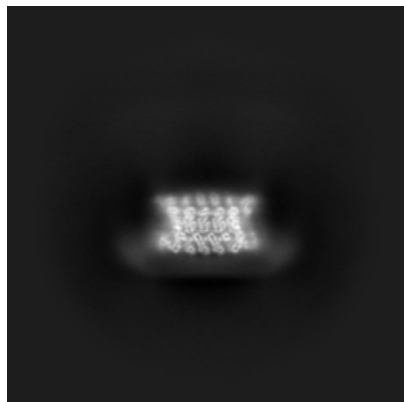
#### 6.2.1 Primary map



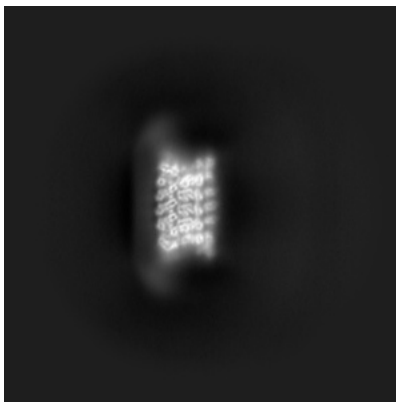
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

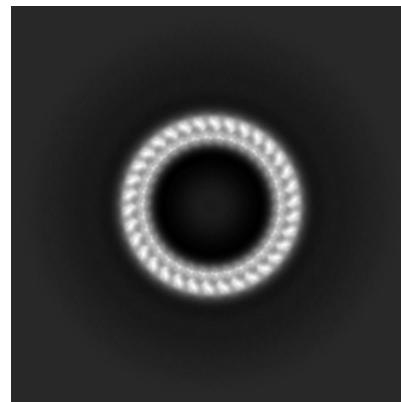
### 6.3.1 Primary map



X Index: 157



Y Index: 157

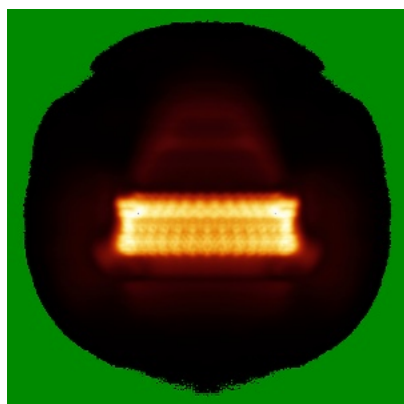


Z Index: 252

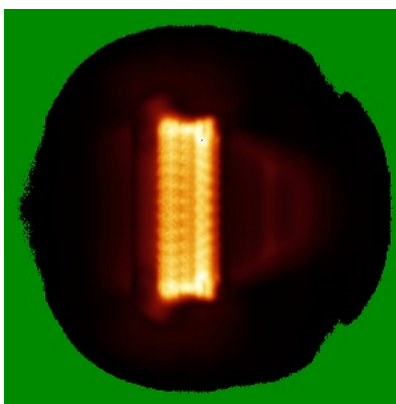
The images above show the largest variance slices of the map in three orthogonal directions.

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

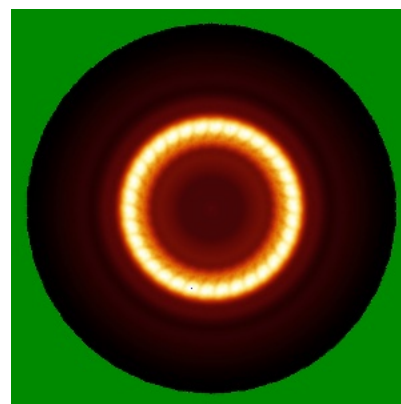
### 6.4.1 Primary map



X



Y



Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



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

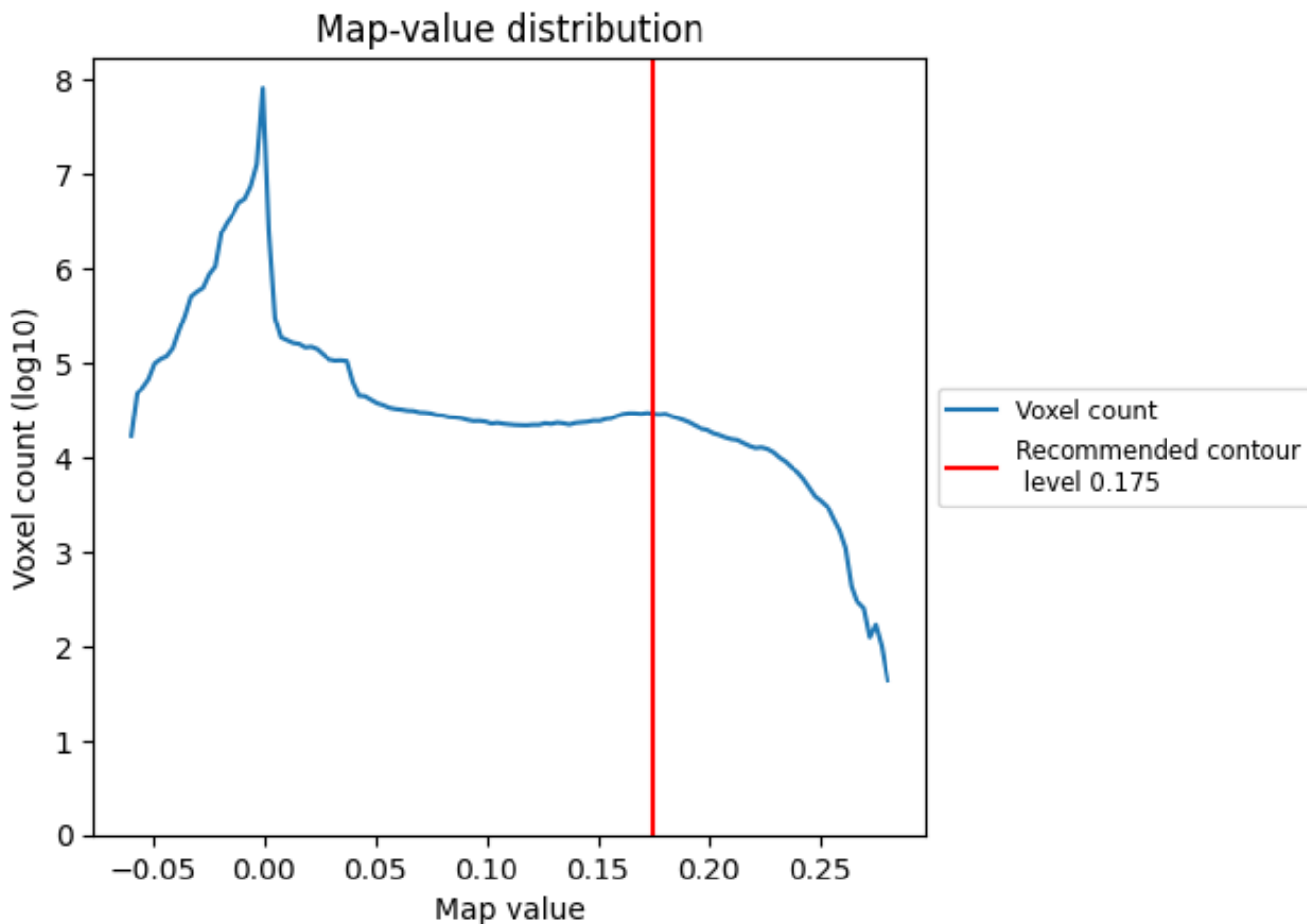
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

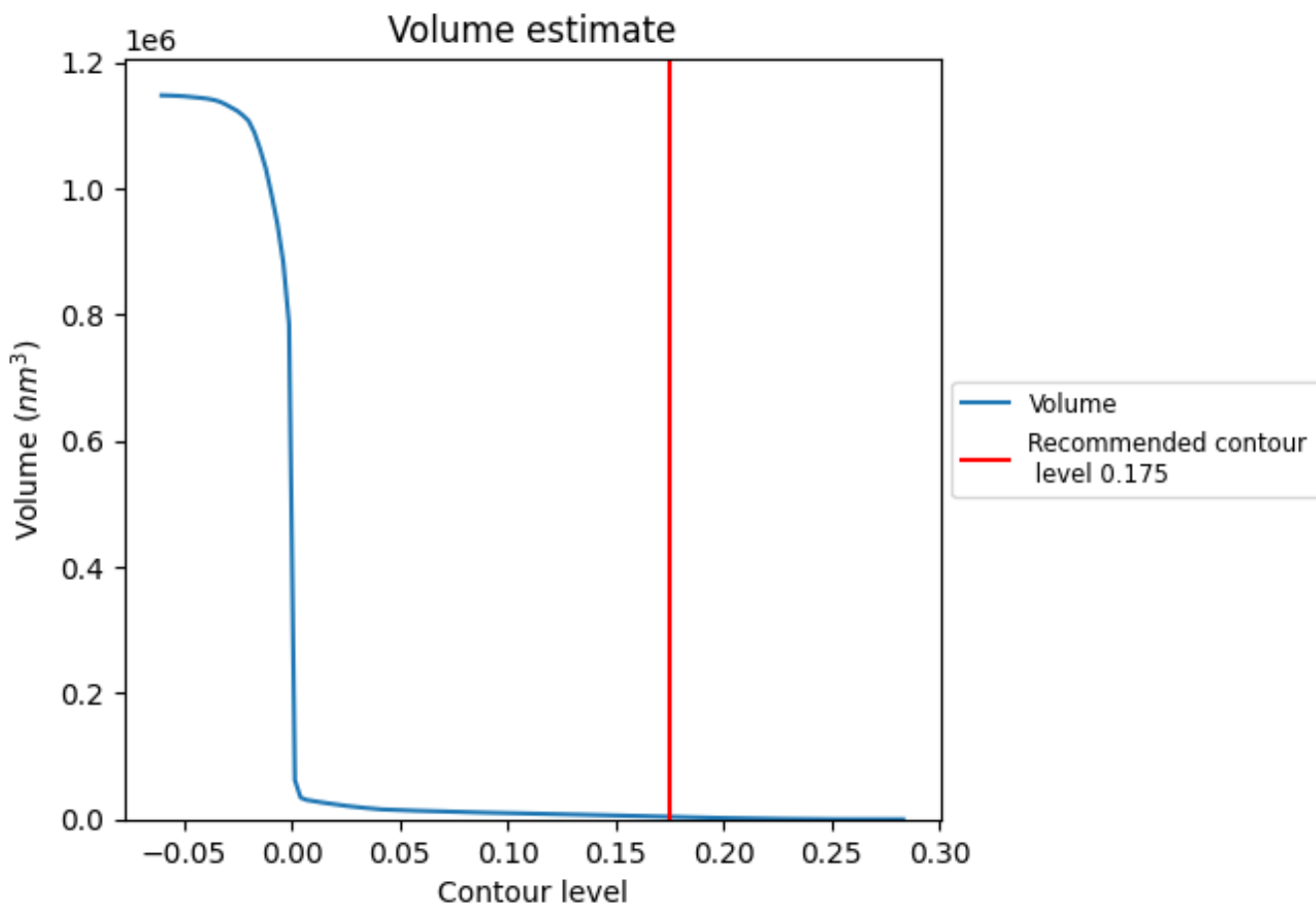
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

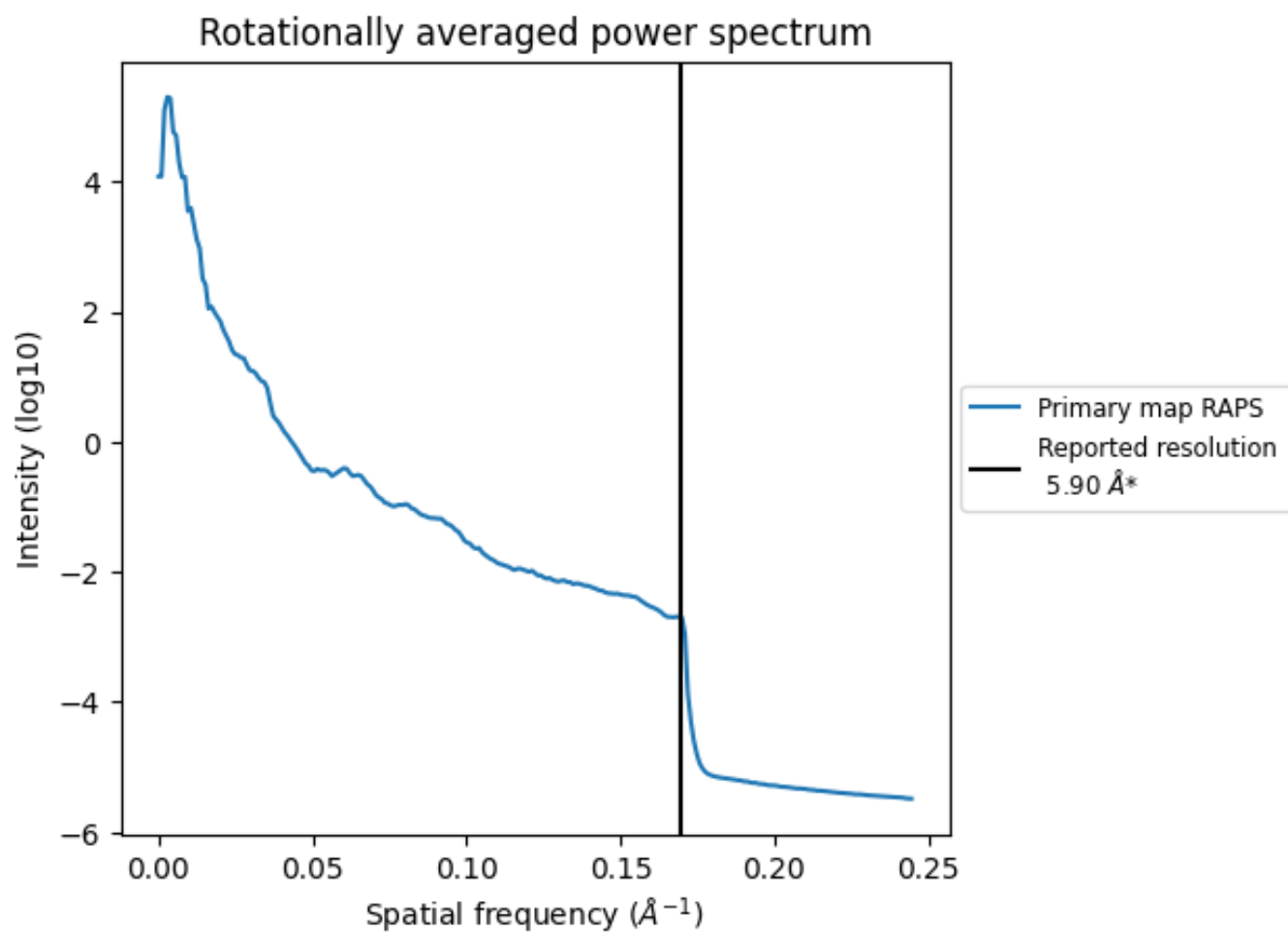
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is  $4028 \text{ nm}^3$ ; this corresponds to an approximate mass of 3639 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of 0.169 Å<sup>-1</sup>

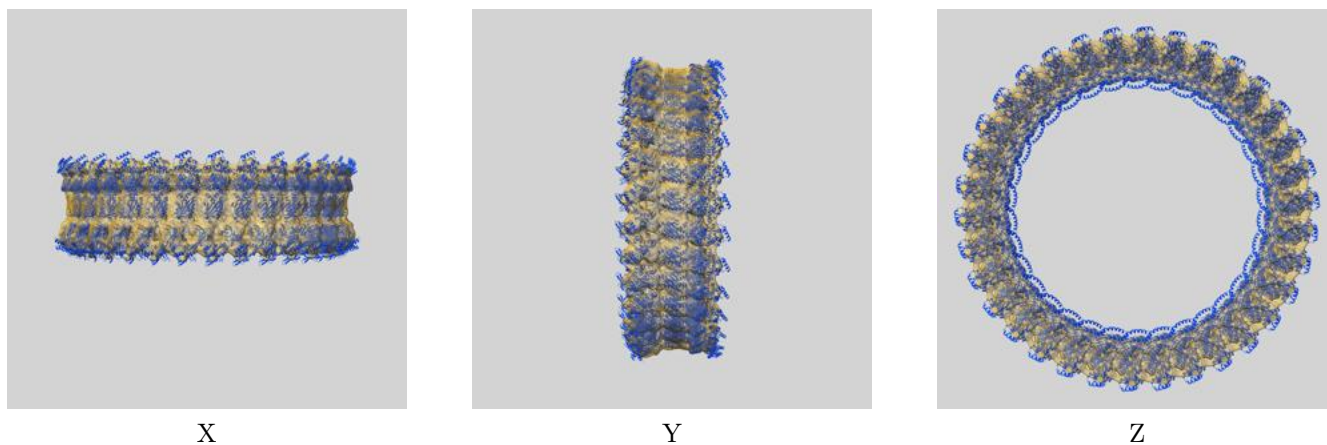
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

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

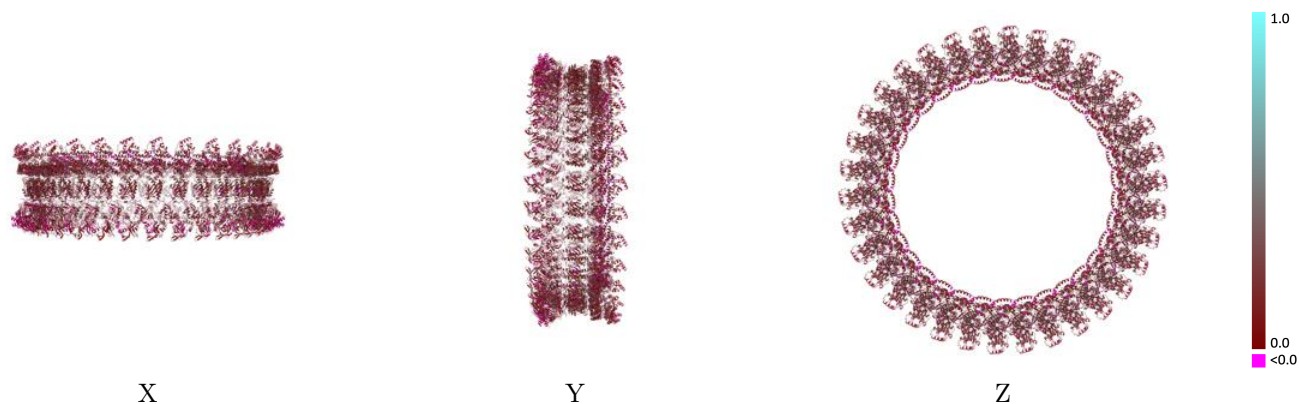
### 9.1 Map-model overlay [i](#)



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

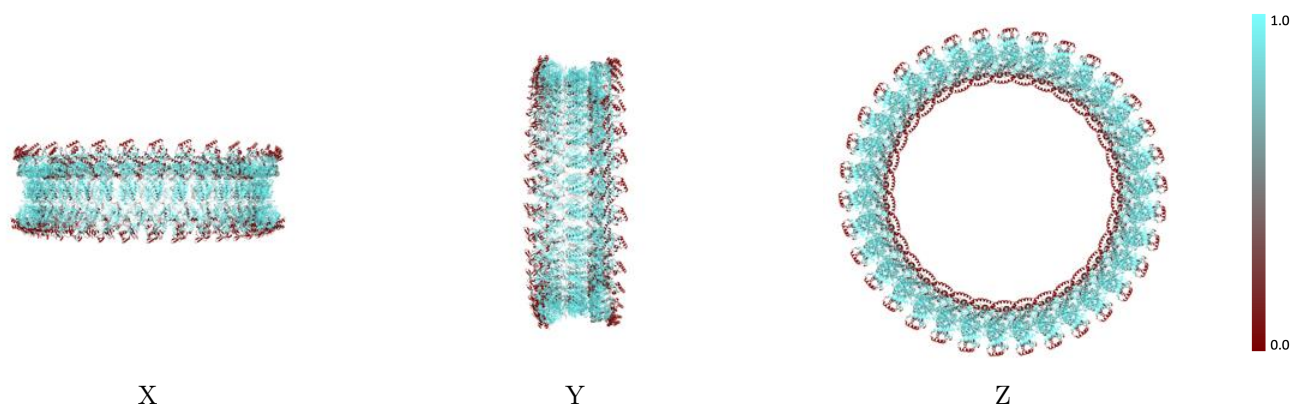


## 9.2 Q-score mapped to coordinate model [i](#)



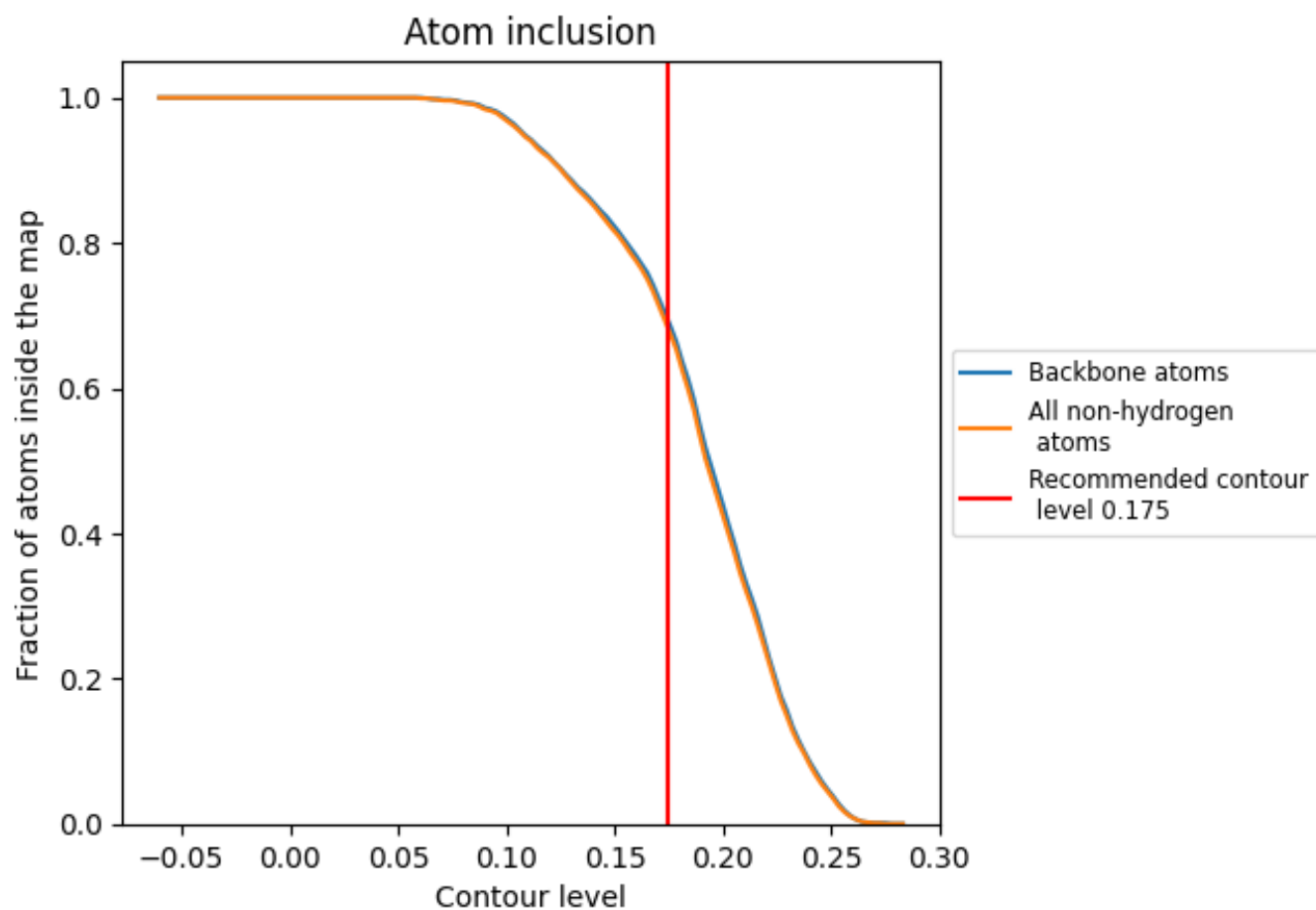
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6800	 0.1490
A	 0.2010	 0.0420
AA	 0.6980	 0.1640
AB	 0.4230	 0.1100
AC	 0.8180	 0.1300
AD	 0.6990	 0.1630
AE	 0.4320	 0.1200
AF	 0.8210	 0.1360
AG	 0.6970	 0.1680
B	 0.6970	 0.1670
BA	 0.7070	 0.1690
BB	 0.9590	 0.1320
BC	 0.2010	 0.0550
BD	 0.7090	 0.1720
BE	 0.9560	 0.1330
BF	 0.2010	 0.0410
BG	 0.7090	 0.1680
C	 0.7090	 0.1670
CA	 0.4320	 0.1140
CB	 0.8180	 0.1250
CC	 0.6970	 0.1630
CD	 0.4280	 0.1160
CE	 0.8210	 0.1330
CF	 0.6970	 0.1660
CG	 0.4280	 0.1180
D	 0.4250	 0.1150
DA	 0.9560	 0.1310
DB	 0.1970	 0.0560
DC	 0.7090	 0.1690
DD	 0.9510	 0.1320
DE	 0.2010	 0.0410
DF	 0.7080	 0.1680
DG	 0.9560	 0.1320
E	 0.9610	 0.1270
EA	 0.8210	 0.1280























































































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Chain	Atom inclusion	Q-score
EB	 0.6970	 0.1650
EC	 0.4280	 0.1140
ED	 0.8210	 0.1330
EE	 0.6980	 0.1640
EF	 0.4300	 0.1220
EG	 0.8240	 0.1330
F	 0.2010	 0.0430
FA	 0.2010	 0.0470
FB	 0.7090	 0.1700
FC	 0.9560	 0.1350
FD	 0.1970	 0.0530
FE	 0.7080	 0.1680
FF	 0.9560	 0.1310
FG	 0.2010	 0.0390
G	 0.6990	 0.1670
GA	 0.6970	 0.1640
GB	 0.4250	 0.1100
GC	 0.8210	 0.1290
GD	 0.6960	 0.1640
GE	 0.4280	 0.1210
GF	 0.8210	 0.1360
GG	 0.6960	 0.1650
H	 0.8180	 0.1320
HA	 0.7060	 0.1690
HB	 0.9560	 0.1310
HC	 0.2010	 0.0500
HD	 0.7060	 0.1680
HE	 0.9560	 0.1340
HF	 0.2010	 0.0360
HG	 0.7060	 0.1660
I	 0.2010	 0.0410
IA	 0.4210	 0.1080
IB	 0.8210	 0.1260
IC	 0.6970	 0.1620
ID	 0.4340	 0.1200
IE	 0.8210	 0.1360
IF	 0.6960	 0.1660
IG	 0.4340	 0.1170
J	 0.6980	 0.1690
JA	 0.9540	 0.1310
JB	 0.2010	 0.0530
JC	 0.7070	 0.1680





















































































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Chain	Atom inclusion	Q-score
JD	 0.9560	 0.1320
JE	 0.2010	 0.0420
JF	 0.7080	 0.1680
JG	 0.9590	 0.1270
K	 0.7090	 0.1680
KA	 0.8210	 0.1310
KB	 0.6960	 0.1640
KC	 0.4320	 0.1130
KD	 0.8240	 0.1360
KE	 0.6970	 0.1640
KF	 0.4340	 0.1200
KG	 0.8240	 0.1340
L	 0.4230	 0.1130
LA	 0.1970	 0.0480
LB	 0.7070	 0.1700
LC	 0.9590	 0.1280
LD	 0.2010	 0.0510
LE	 0.7060	 0.1680
LF	 0.9590	 0.1260
LG	 0.2010	 0.0380
M	 0.7090	 0.1710
MA	 0.6980	 0.1630
MB	 0.4230	 0.1120
MC	 0.8180	 0.1310
MD	 0.6980	 0.1660
ME	 0.4230	 0.1200
MF	 0.8210	 0.1350
MG	 0.6970	 0.1680
N	 0.4280	 0.1130
NA	 0.7040	 0.1700
NB	 0.9540	 0.1260
NC	 0.2010	 0.0510
ND	 0.7060	 0.1680
NE	 0.9560	 0.1300
NF	 0.2010	 0.0350
NG	 0.7090	 0.1700
O	 0.9560	 0.1250
OA	 0.4250	 0.1100
OB	 0.8210	 0.1290
OC	 0.6970	 0.1640
OD	 0.4320	 0.1190
OE	 0.8210	 0.1370

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Chain	Atom inclusion	Q-score
OF	 0.6980	 0.1660
OG	 0.4320	 0.1160
P	 0.9510	 0.1300
PA	 0.9560	 0.1300
PB	 0.2010	 0.0550
PC	 0.7090	 0.1710
PD	 0.9560	 0.1300
PE	 0.2010	 0.0450
PF	 0.7080	 0.1690
PG	 0.9560	 0.1300
Q	 0.8210	 0.1310
QA	 0.8210	 0.1320
QB	 0.6980	 0.1600
QC	 0.4300	 0.1120
QD	 0.8240	 0.1380
QE	 0.6980	 0.1650
QF	 0.4170	 0.1170
QG	 0.8240	 0.1350
R	 0.8210	 0.1320
RA	 0.2010	 0.0520
RB	 0.7090	 0.1690
RC	 0.9510	 0.1300
RD	 0.2010	 0.0500
RE	 0.7060	 0.1680
RF	 0.9540	 0.1300
RG	 0.2010	 0.0390
S	 0.2010	 0.0430
SA	 0.6980	 0.1620
SB	 0.4250	 0.1120
SC	 0.8240	 0.1340
SD	 0.6960	 0.1640
SE	 0.4280	 0.1200
SF	 0.8210	 0.1330
SG	 0.6960	 0.1670
T	 0.6960	 0.1670
TA	 0.7080	 0.1680
TB	 0.9590	 0.1310
TC	 0.2010	 0.0500
TD	 0.7060	 0.1670
TE	 0.9560	 0.1300
TF	 0.1970	 0.0390
TG	 0.7090	 0.1690


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Chain	Atom inclusion	Q-score
UA	0.4300	0.1100
UB	0.8240	0.1320
UC	0.6980	0.1640
UD	0.4250	0.1190
UE	0.8210	0.1360
UF	0.6970	0.1670
UG	0.4250	0.1120
V	0.7070	0.1680
VA	0.9560	0.1250
VB	0.1970	0.0570
VC	0.7080	0.1700
VD	0.9590	0.1320
VE	0.2010	0.0410
VF	0.7090	0.1660
VG	0.9590	0.1280
W	0.4250	0.1130
WA	0.8210	0.1260
WB	0.6970	0.1610
WC	0.4300	0.1150
WD	0.8210	0.1330
WE	0.6960	0.1670
WF	0.4280	0.1220
WG	0.8210	0.1320
X	0.9590	0.1280
XA	0.2010	0.0510
XB	0.7090	0.1670
XC	0.9560	0.1340
XD	0.2010	0.0460
XE	0.7050	0.1650
XF	0.9590	0.1350
Y	0.8210	0.1260
YA	0.6960	0.1630
YB	0.4300	0.1160
YC	0.8240	0.1330
YD	0.6980	0.1630
YE	0.4230	0.1210
YF	0.8240	0.1360
Z	0.2010	0.0430
ZA	0.7070	0.1660
ZB	0.9590	0.1320
ZC	0.2010	0.0560
ZD	0.7070	0.1680

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Chain	Atom inclusion	Q-score
ZE	 0.9590	 0.1350
ZF	 0.1970	 0.0390