



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2025 – 12:08 AM JST

PDB ID : 8WL2
EMDB ID : EMD-37611
Title : Cryo-EM structure of the membrane-anchored part of the flagellar motor-hook complex in the CW state.
Authors : Tan, J.X.; Zhang, L.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2023-09-29
Resolution : 3.40 Å (reported)
Based on initial models : ?, .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

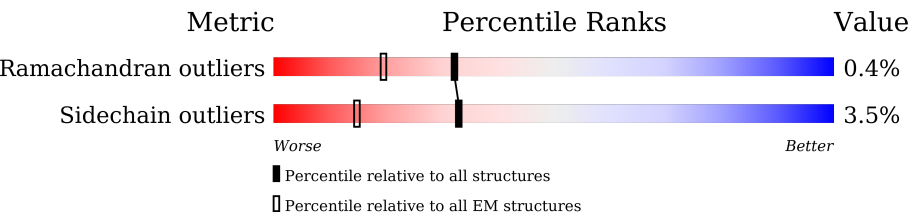
EMDB validation analysis : 0.0.1.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	A	232	
1	B	232	
1	C	232	
1	D	232	
1	E	232	
1	F	232	
1	G	232	
1	H	232	
1	I	232	

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Mol	Chain	Length	Quality of chain	
1	J	232	45%	88% 9%
1	K	232	41%	88% 9%
1	L	232	44%	88% 9%
1	M	232	47%	88% 9%
1	N	232	44%	88% 9%
1	O	232	50%	88% 9%
1	P	232	41%	88% 9%
1	Q	232	46%	88% 9%
1	R	232	42%	88% 9%
1	S	232	47%	88% 9%
1	T	232	49%	88% 9%
1	U	232	47%	88% 9%
1	V	232	47%	88% 9%
1	W	232	50%	88% 9%
1	X	232	46%	88% 9%
1	Y	232	48%	88% 9%
1	Z	232	47%	88% 9%
2	a	365	56%	80% 17%
2	b	365	55%	80% 17%
2	c	365	54%	80% 17%
2	d	365	55%	80% 17%
2	e	365	55%	80% 17%
2	f	365	55%	80% 17%
2	g	365	52%	80% 17%
2	h	365	57%	80% 17%

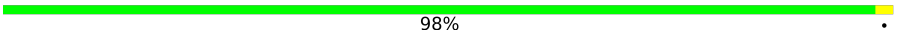
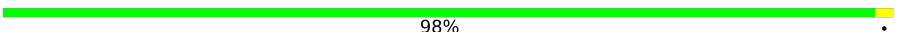
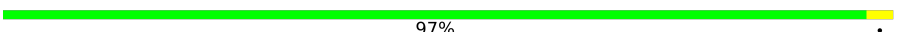
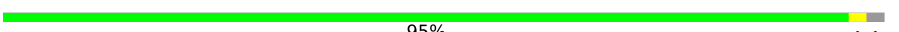
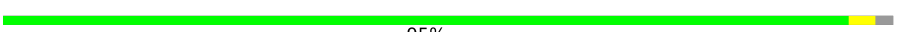







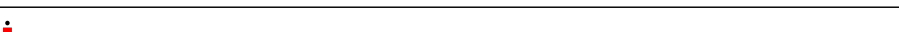

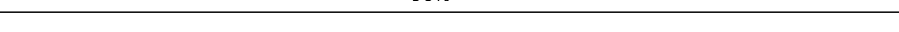
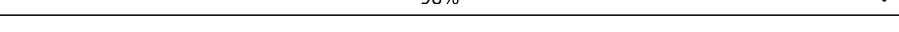
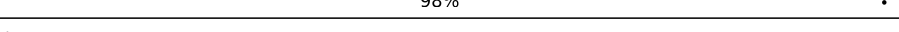
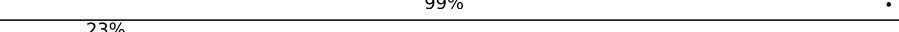
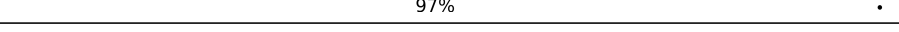
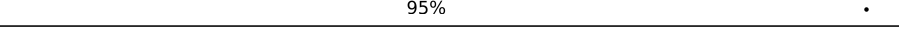
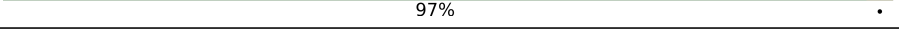
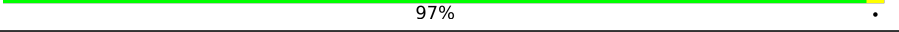
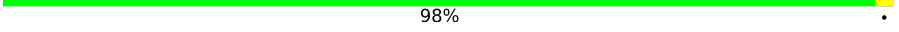
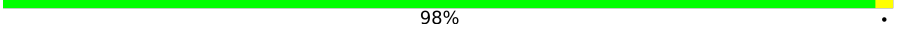
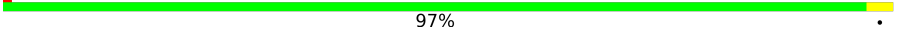
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Mol	Chain	Length	Quality of chain
2	i	365	
2	j	365	
2	k	365	
2	l	365	
2	m	365	
2	n	365	
2	o	365	
2	p	365	
2	q	365	
2	r	365	
2	s	365	
2	t	365	
2	u	365	
2	v	365	
2	w	365	
2	x	365	
2	y	365	
2	z	365	
3	0	260	
3	1	260	
3	2	260	
3	3	260	
3	4	260	
3	5	260	
3	6	260	

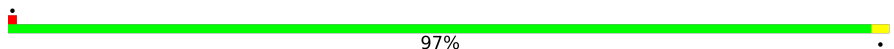
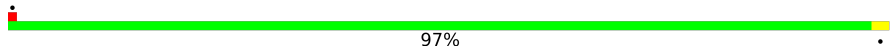
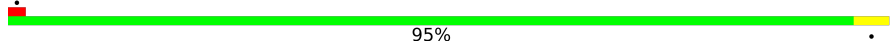
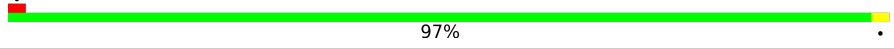
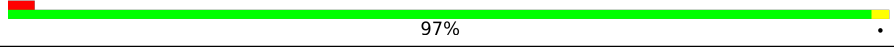
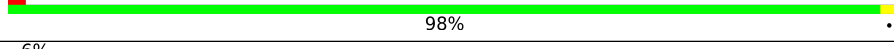
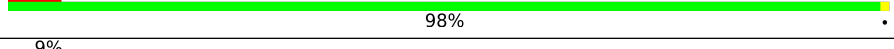
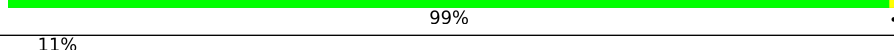
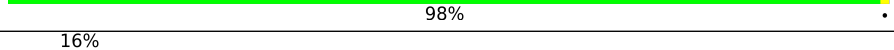
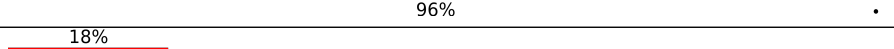
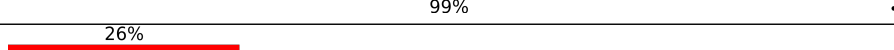
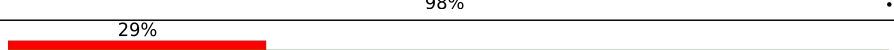
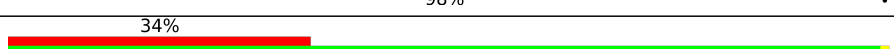
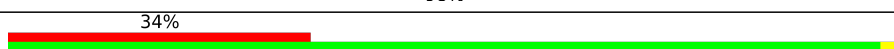
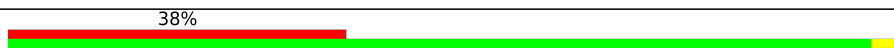
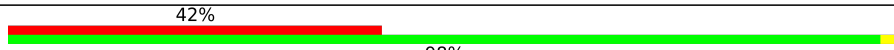
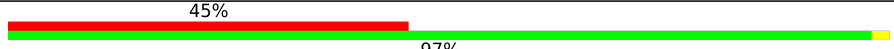
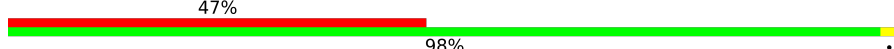
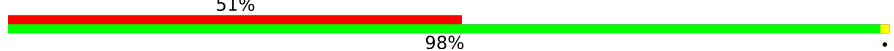
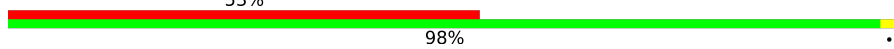
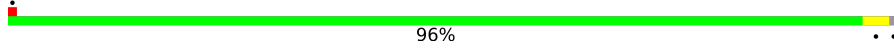
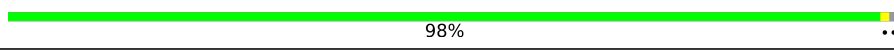
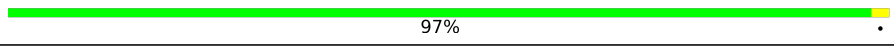
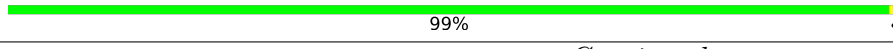

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Mol	Chain	Length	Quality of chain
3	7	260	 98%
3	8	260	 98%
3	9	260	 97%
3	AF	260	 95%
3	AG	260	 95%
3	AH	260	 94%
3	AI	260	 93%
3	AJ	260	 95%
3	AK	260	 92%
3	AL	260	 92%
3	AM	260	 92%
3	AN	260	 93%
3	ZA	260	 98%
3	ZB	260	 96%
3	ZC	260	 98%
3	ZD	260	 98%
3	ZE	260	 99%
4	ZF	403	 23% 97%
4	ZG	403	 95%
4	ZH	403	 97%
4	ZI	403	 97%
4	ZJ	403	 98%
4	ZK	403	 98%
4	ZL	403	 97%
4	ZM	403	 97%

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Mol	Chain	Length	Quality of chain
4	ZN	403	 97%
4	ZO	403	 97%
4	ZP	403	 95%
4	ZQ	403	 97%
4	ZR	403	 97%
4	ZS	403	 98%
4	ZT	403	 98%
4	ZU	403	 99%
4	ZV	403	 98%
4	ZW	403	 96%
4	ZX	403	 99%
4	ZY	403	 98%
4	ZZ	403	 98%
4	Za	403	 98%
4	Zb	403	 98%
4	Zc	403	 97%
4	Zd	403	 98%
4	Ze	403	 97%
4	Zf	403	 98%
4	Zg	403	 98%
4	Zh	403	 98%
5	AA	251	 96%
5	AB	251	 98%
5	AC	251	 97%
5	AD	251	 99%

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Mol	Chain	Length	Quality of chain
5	AE	251	98%
6	AO	560	18% 28% 71%
6	AP	560	18% 28% 71%
6	AQ	560	19% 28% 71%
6	AR	560	14% 28% 71%
6	AS	560	17% 28% 71%
6	AT	560	15% 28% 71%
6	AU	560	14% 28% 71%
6	AV	560	15% 28% 71%
6	AW	560	15% 28% 71%
6	AX	560	13% 28% 71%
6	AY	560	14% 28% 71%
6	AZ	560	14% 28% 71%
6	Aa	560	14% 28% 71%
6	Ac	560	17% 28% 71%
6	Ad	560	15% 28% 71%
6	Ae	560	16% 28% 71%
6	Af	560	17% 28% 71%
6	Ag	560	17% 28% 71%
6	Ah	560	18% 28% 71%
6	Ai	560	20% 28% 71%
6	Aj	560	18% 28% 71%
6	Ak	560	19% 28% 71%
6	Al	560	18% 28% 71%
6	Am	560	16% 28% 71%

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Mol	Chain	Length	Quality of chain
6	An	560	
6	Ao	560	
6	Ap	560	
6	BG	560	
6	BH	560	
6	BI	560	
6	BJ	560	
6	BK	560	
6	BL	560	
6	BM	560	
6	BN	560	
6	BO	560	
6	BP	560	
6	BQ	560	
6	BR	560	
6	BS	560	
6	BT	560	
6	BU	560	
6	BV	560	
6	BW	560	
6	BX	560	
6	UI	560	
6	UJ	560	
6	UK	560	
6	UL	560	

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Mol	Chain	Length	Quality of chain	
6	UM	560	27% 25% .	72%
6	UN	560	27% 25% .	72%
6	UO	560	27% 25% .	72%
6	UP	560	27% 25% .	72%
6	WA	560	6% 18% .	80%
6	WB	560	7% 18% .	80%
6	WC	560	7% 17% .	81%
6	WD	560	9% 18% .	80%
6	WE	560	9% 18% .	80%
6	WF	560	11% 18% .	80%
6	WG	560	13% 18% .	80%
6	WH	560	11% 16% .	83%
6	WI	560	13% 15% .	83%
6	WJ	560	14% 16% .	82%
6	WK	560	14% 16% .	82%
6	WL	560	13% 14% .	85%
6	WM	560	12% 14% .	85%
6	WN	560	12% 14% .	85%
6	WO	560	10% 16% .	83%
6	WP	560	9% 16% .	82%
6	WQ	560	9% 18% .	80%
6	WR	560	10% 17% .	80%
6	WS	560	7% 18% .	80%
6	WT	560	6% 17% .	80%
6	WU	560	8% 19% .	80%


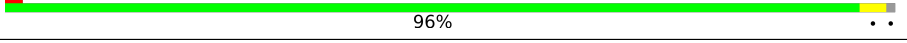
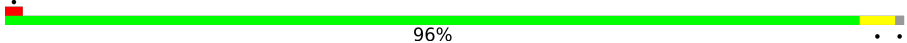
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Mol	Chain	Length	Quality of chain
6	WV	560	
6	WW	560	
7	Ab	89	
7	Aq	89	
7	Ar	89	
7	As	89	
8	At	264	
9	Au	245	
9	Av	245	
9	Aw	245	
9	Ax	245	
9	Ay	245	
10	A1	104	
10	A2	104	
10	A3	104	
10	A4	104	
10	A5	104	
10	Az	104	
11	A0	138	
11	A6	138	
11	A7	138	
11	A8	138	
11	A9	138	
12	BA	134	
12	BB	134	

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Mol	Chain	Length	Quality of chain
12	BC	134	 99% ..
12	BD	134	 96% ..
12	BE	134	 96% ..
12	BF	134	 96% ..

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 338677 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 L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	B	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	C	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	D	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	E	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	F	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	G	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	H	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	I	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	J	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	K	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	L	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	M	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	N	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	O	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	P	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	Q	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	S	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	T	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	U	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	V	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	W	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	X	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	Y	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		
1	Z	211	Total	C	N	O	S	0	0
			1580	985	282	309	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	b	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	c	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	d	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	e	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	f	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	g	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	h	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	i	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	j	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	k	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	l	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	m	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	n	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	o	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	p	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	q	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	r	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	s	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	t	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	u	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	v	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	w	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	x	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	y	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		
2	z	303	Total	C	N	O	S	0	0
			2228	1364	405	446	13		

- Molecule 3 is a protein called Flagellar basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	0	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
3	1	252	Total	C	N	O	S	0	0
			1894	1172	331	385	6		
3	2	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	4	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	5	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	6	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	7	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	8	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	9	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZA	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZB	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZC	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZD	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	ZE	260	Total 1949	C 1202	N 341	O 400	S 6	0	0
3	AF	254	Total 1903	C 1175	N 334	O 389	S 5	0	0
3	AG	255	Total 1911	C 1181	N 335	O 390	S 5	0	0
3	AH	256	Total 1919	C 1186	N 336	O 391	S 6	0	0
3	AI	254	Total 1903	C 1175	N 334	O 389	S 5	0	0
3	AJ	255	Total 1911	C 1181	N 335	O 390	S 5	0	0
3	AK	243	Total 1823	C 1127	N 318	O 373	S 5	0	0
3	AL	248	Total 1866	C 1154	N 327	O 379	S 6	0	0
3	AM	248	Total 1866	C 1154	N 327	O 379	S 6	0	0
3	AN	248	Total 1866	C 1154	N 327	O 379	S 6	0	0

- Molecule 4 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	ZF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZH	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZI	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZJ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZK	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZL	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZM	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZN	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZO	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZP	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZQ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZR	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZS	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZT	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZU	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZV	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZW	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZX	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZY	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	ZZ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Za	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zb	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zc	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zd	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Ze	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zf	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zg	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
4	Zh	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

- Molecule 5 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AA	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
5	AB	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
5	AC	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
5	AD	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
5	AE	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

- Molecule 6 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AR	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AS	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AT	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AU	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AV	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AW	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AX	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AY	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AZ	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Aa	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ac	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ad	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ae	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Af	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ag	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ah	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ai	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Aj	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ak	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Al	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Am	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	An	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ao	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	Ap	164	Total 1275	C 776	N 237	O 259	S 3	0	0
6	AO	164	Total 1275	C 776	N 237	O 259	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AP	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	AQ	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	UI	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UJ	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UK	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UL	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UM	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UN	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UO	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	UP	155	Total	C	N	O	S	0	0
			1172	733	211	226	2		
6	WA	113	Total	C	N	O	S	0	0
			849	534	148	166	1		
6	WB	111	Total	C	N	O	S	0	0
			836	526	146	163	1		
6	WC	108	Total	C	N	O	S	0	0
			812	510	142	159	1		
6	WD	110	Total	C	N	O	S	0	0
			827	522	144	160	1		
6	WE	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WF	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WG	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WH	95	Total	C	N	O	S	0	0
			703	439	126	137	1		
6	WI	95	Total	C	N	O	S	0	0
			703	439	126	137	1		
6	WJ	99	Total	C	N	O	S	0	0
			737	462	131	143	1		
6	WK	98	Total	C	N	O	S	0	0
			729	456	130	142	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	WL	85	Total	C	N	O	S	0	0
			622	389	110	122	1		
6	WM	82	Total	C	N	O	S	0	0
			596	372	107	116	1		
6	WN	84	Total	C	N	O	S	0	0
			611	380	109	121	1		
6	WO	96	Total	C	N	O	S	0	0
			714	448	127	138	1		
6	WP	100	Total	C	N	O	S	0	0
			741	464	132	144	1		
6	WQ	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WR	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WS	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WT	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	WU	112	Total	C	N	O	S	0	0
			843	531	147	164	1		
6	WV	110	Total	C	N	O	S	0	0
			827	521	144	161	1		
6	WW	111	Total	C	N	O	S	0	0
			834	526	145	162	1		
6	BG	13	Total	C	N	O		0	0
			81	50	15	16			
6	BH	16	Total	C	N	O		0	0
			103	64	19	20			
6	BI	20	Total	C	N	O		0	0
			133	83	23	27			
6	BJ	16	Total	C	N	O		0	0
			103	64	19	20			
6	BK	21	Total	C	N	O		0	0
			140	88	24	28			
6	BL	16	Total	C	N	O		0	0
			103	64	19	20			
6	BM	21	Total	C	N	O		0	0
			140	88	24	28			
6	BN	16	Total	C	N	O		0	0
			103	64	19	20			
6	BO	20	Total	C	N	O		0	0
			133	83	23	27			

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	BP	16	Total	C	N	O		0	0
			103	64	19	20			
6	BQ	21	Total	C	N	O		0	0
			140	88	24	28			
6	BR	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BS	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BT	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BU	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BV	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BW	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		
6	BX	164	Total	C	N	O	S	0	0
			1275	776	237	259	3		

- Molecule 7 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Ab	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	Aq	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	Ar	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
7	As	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

- Molecule 8 is a protein called Flagellar biosynthetic protein FliR.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	At	253	Total	C	N	O	S	0	0
			1945	1305	307	318	15		

- Molecule 9 is a protein called Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Au	207	Total	C	N	O	S	0	0
			1605	1072	249	272	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	Av	209	Total	C	N	O	S	0	0
			1626	1086	252	276	12		
9	Aw	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
9	Ax	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
9	Ay	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 10 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Az	59	Total	C	N	O	S	0	0
			429	265	74	83	7		
10	A1	91	Total	C	N	O	S	0	0
			672	415	121	129	7		
10	A2	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
10	A3	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
10	A4	93	Total	C	N	O	S	0	0
			686	424	123	132	7		
10	A5	92	Total	C	N	O	S	0	0
			679	420	122	130	7		

- Molecule 11 is a protein called Flagellar basal body rod protein FlgB.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A6	134	Total	C	N	O	S	0	0
			1030	633	189	203	5		
11	A7	121	Total	C	N	O	S	0	0
			942	583	172	182	5		
11	A8	125	Total	C	N	O	S	0	0
			967	598	177	187	5		
11	A9	127	Total	C	N	O	S	0	0
			982	606	182	189	5		
11	A0	123	Total	C	N	O	S	0	0
			950	588	172	185	5		

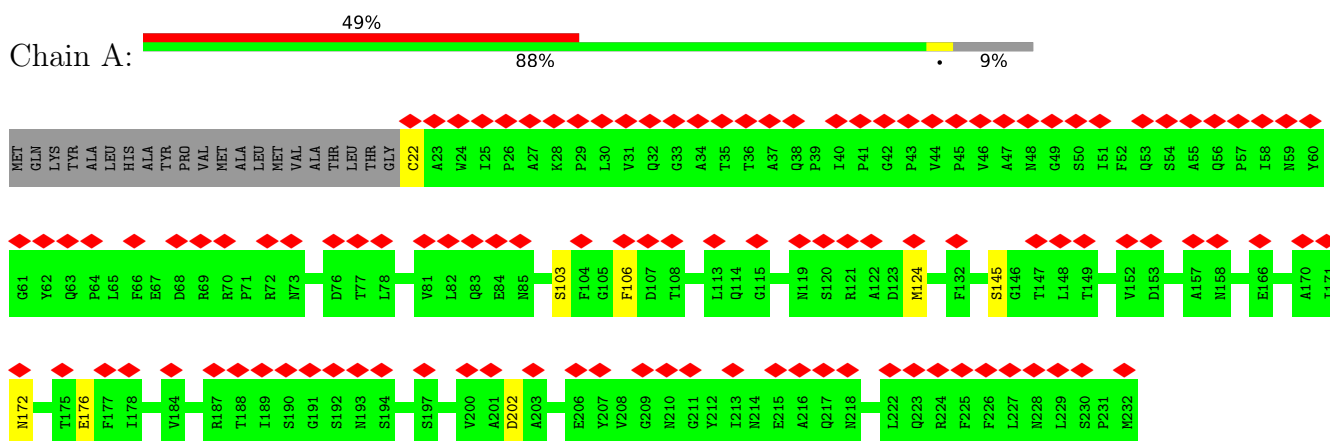
- Molecule 12 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BA	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BB	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
12	BC	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BD	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BE	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
12	BF	133	Total	C	N	O	S	0	0
			969	604	167	193	5		

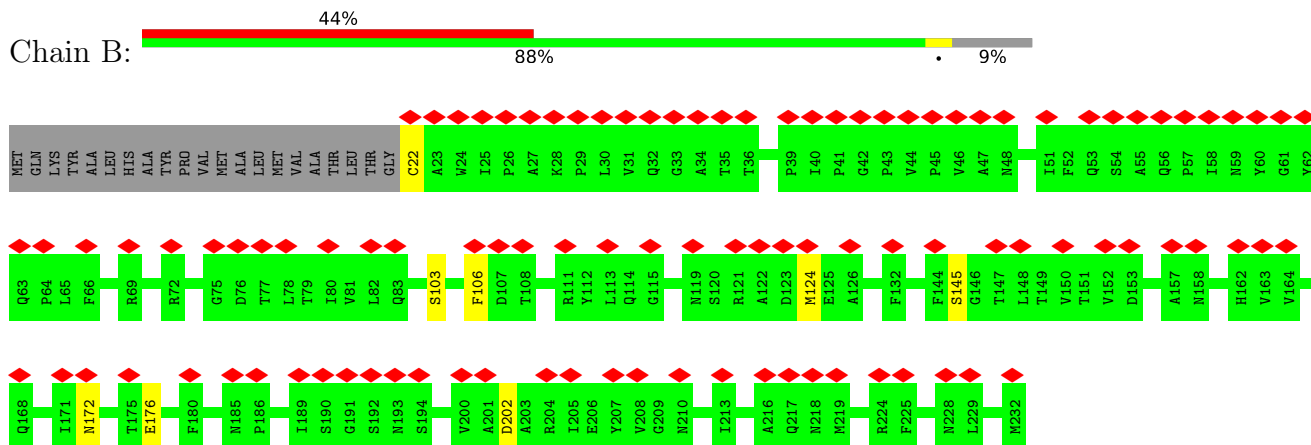
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

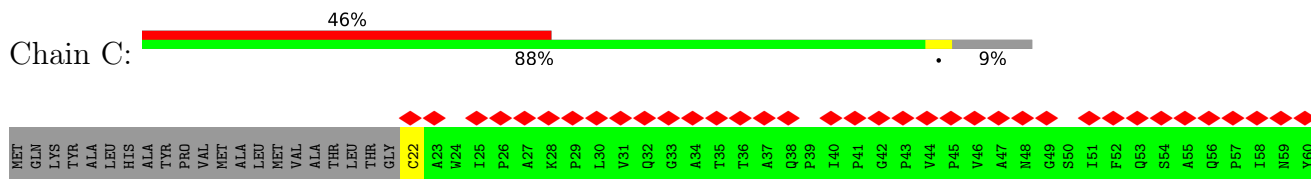
• Molecule 1: Flagellar L-ring protein

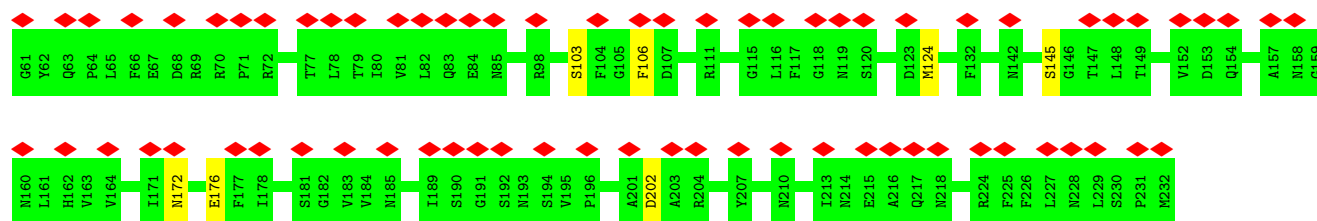


• Molecule 1: Flagellar L-ring protein

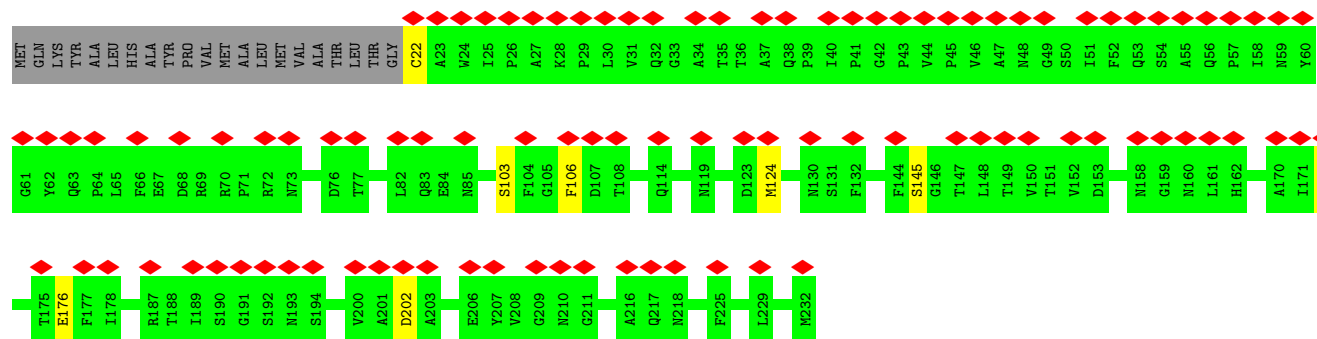
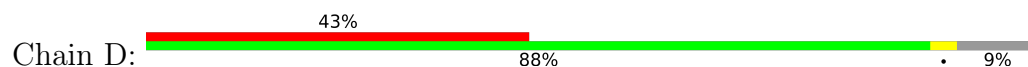


• Molecule 1: Flagellar L-ring protein

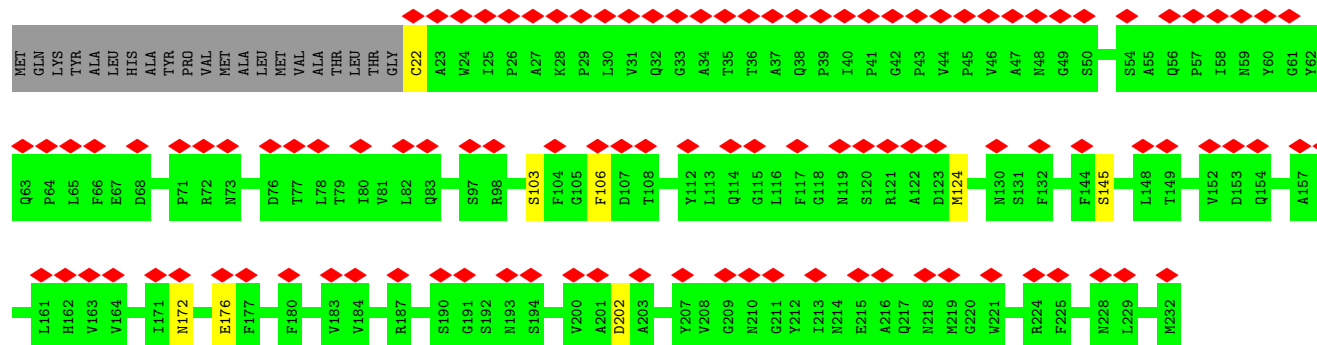
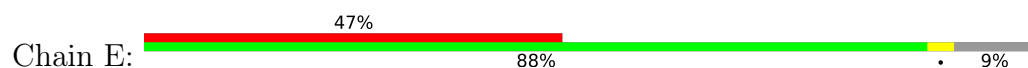




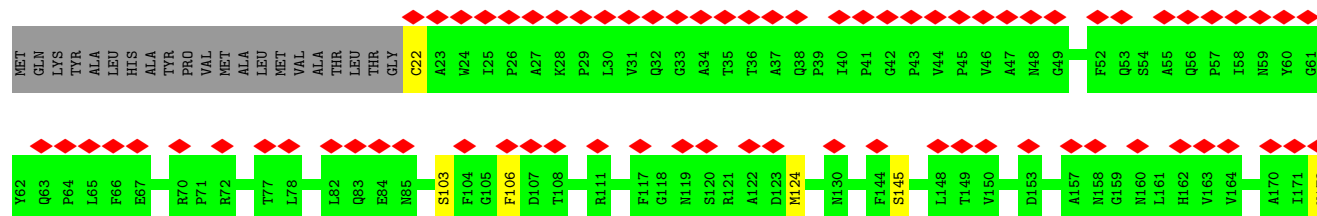
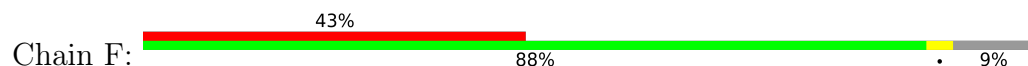
• Molecule 1: Flagellar L-ring protein



• Molecule 1: Flagellar L-ring protein

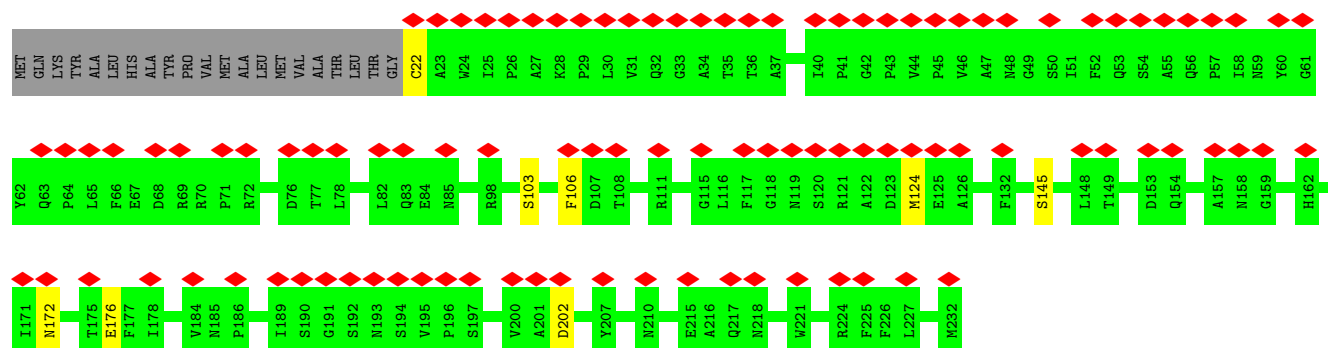
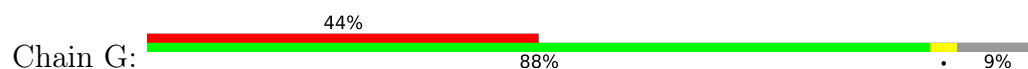


• Molecule 1: Flagellar L-ring protein

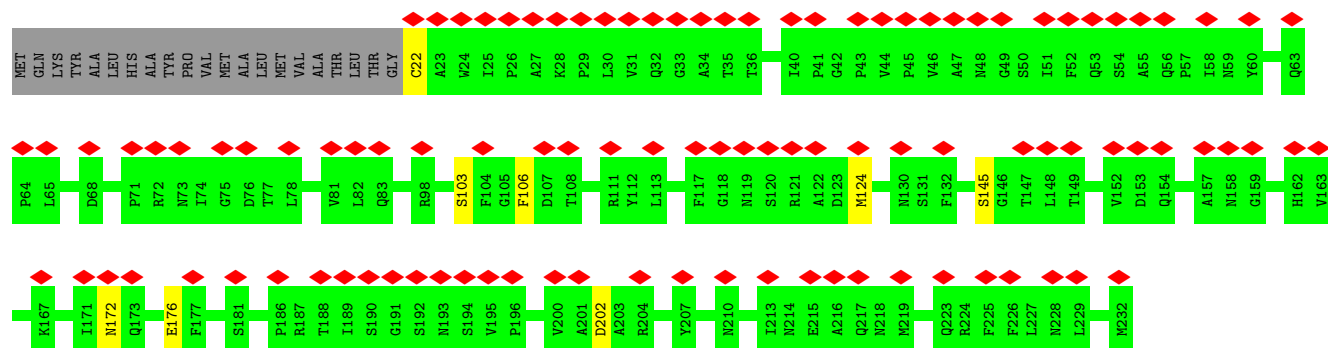
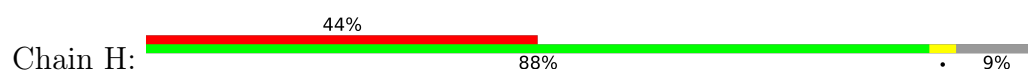




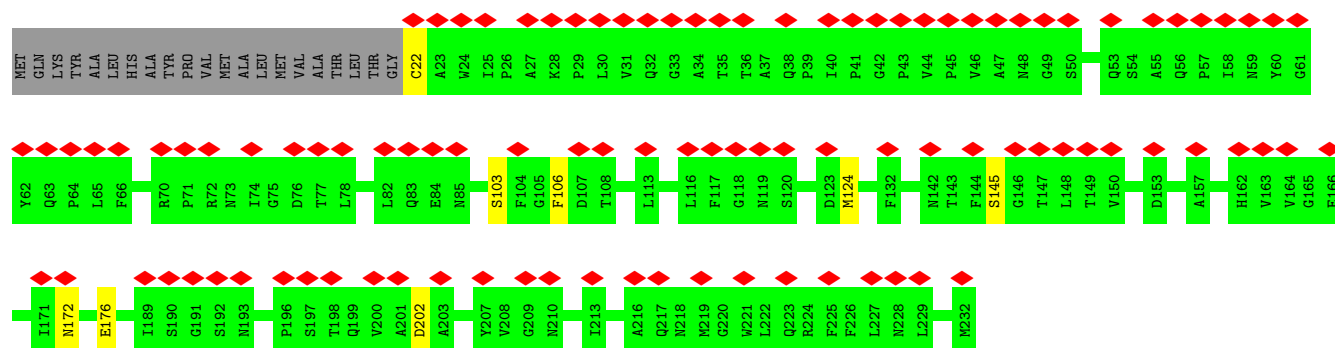
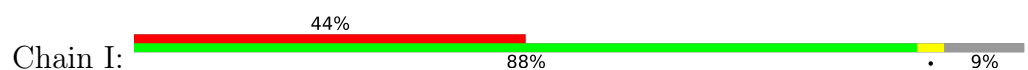
- Molecule 1: Flagellar L-ring protein



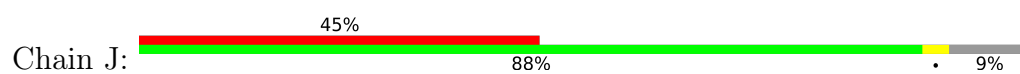
- Molecule 1: Flagellar L-ring protein



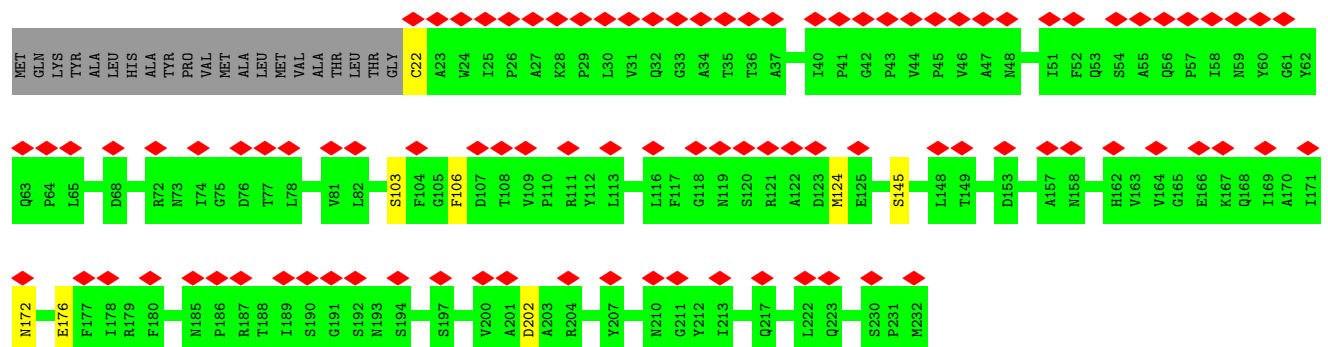
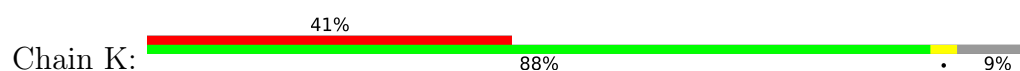
- Molecule 1: Flagellar L-ring protein



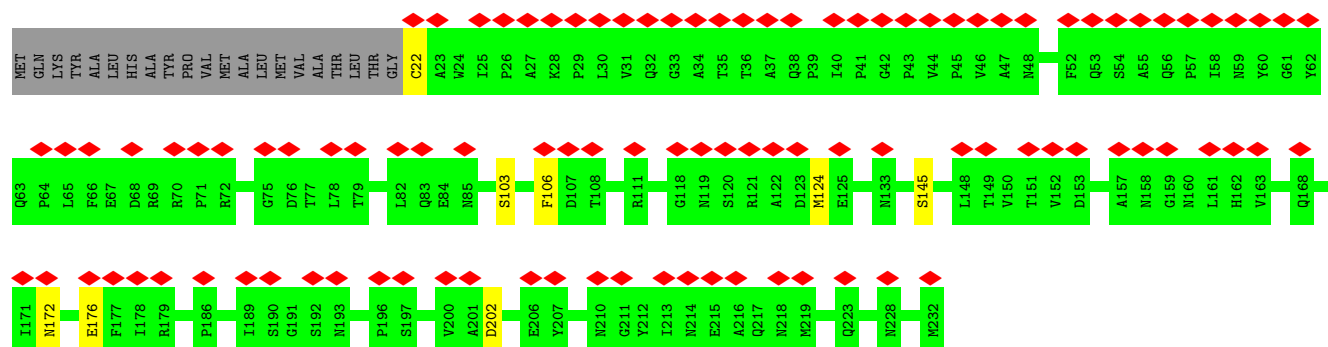
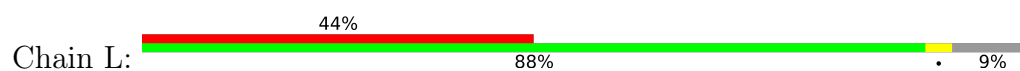
- Molecule 1: Flagellar L-ring protein



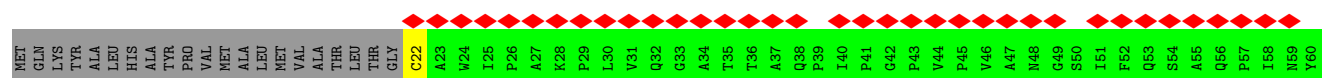
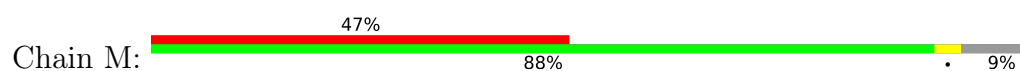
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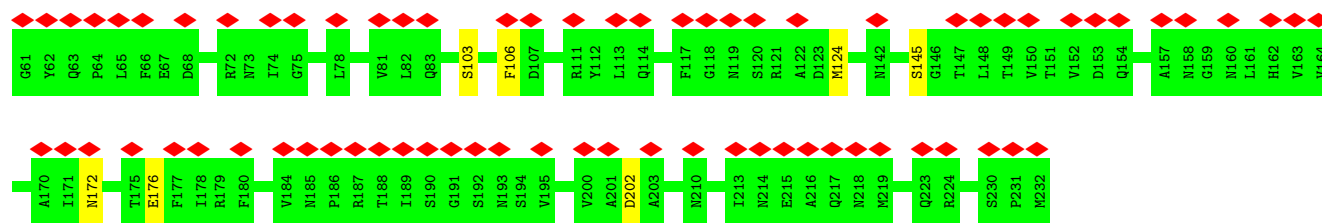


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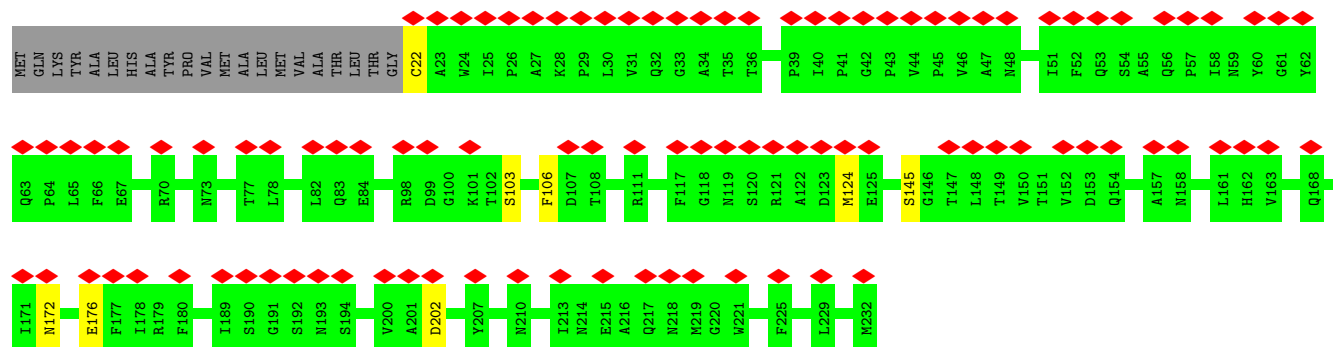
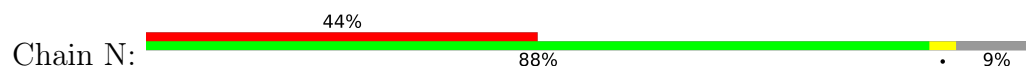


- Molecule 1: Flagellar L-ring protein

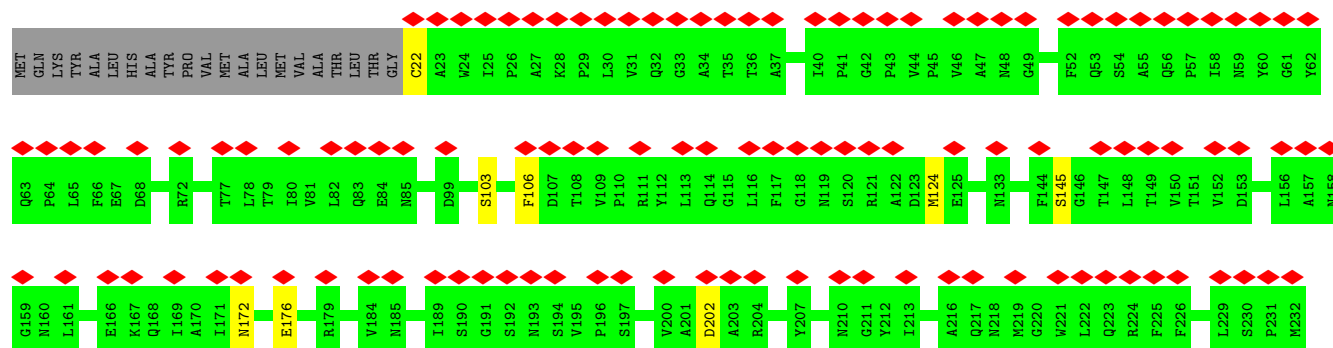
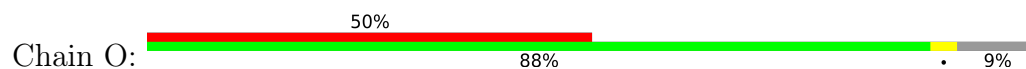




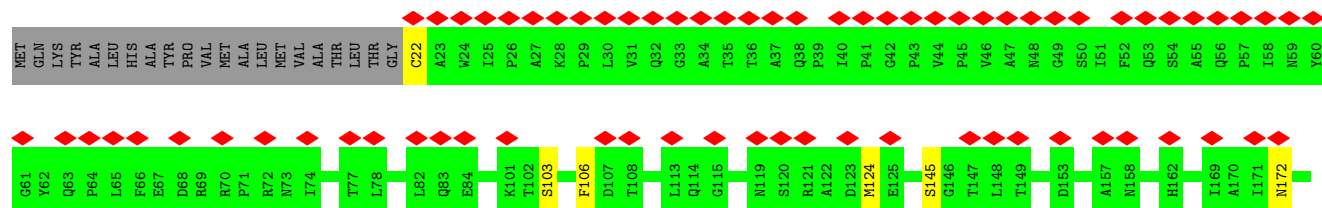
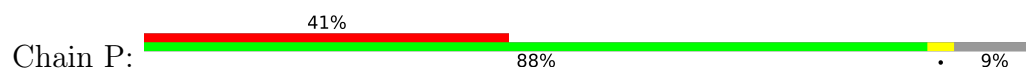
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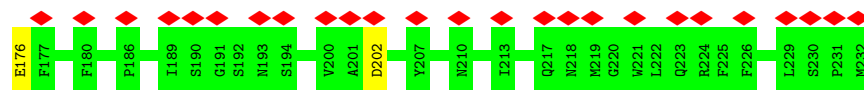


• Molecule 1: Flagellar L-ring protein

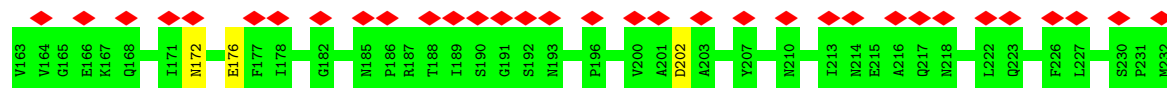
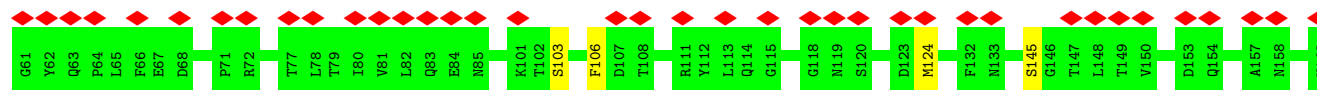
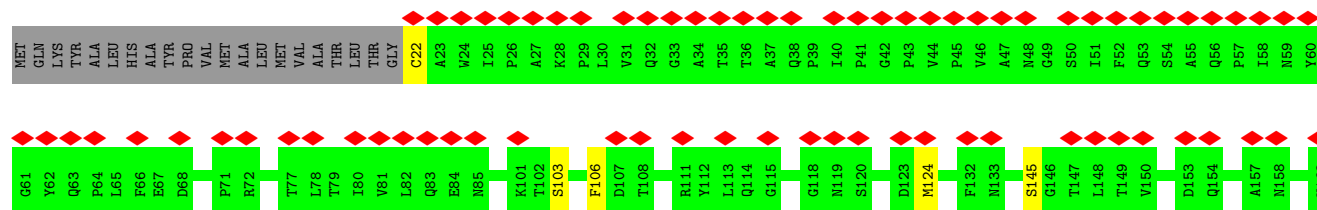
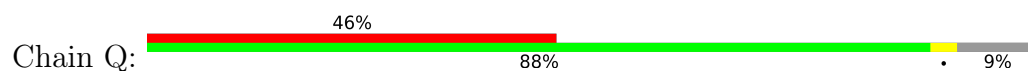


• Molecule 1: Flagellar L-ring protein

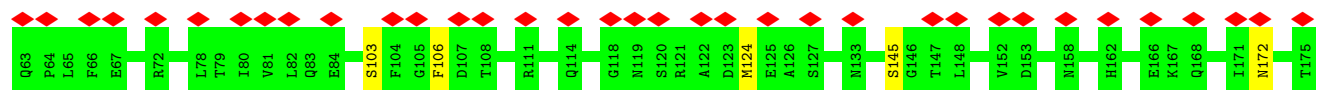
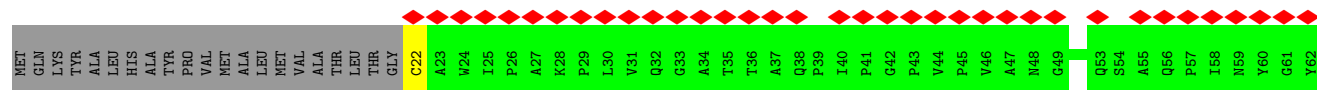
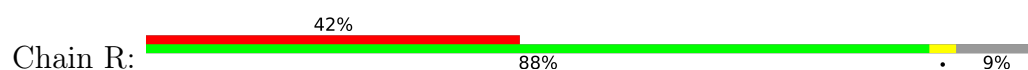




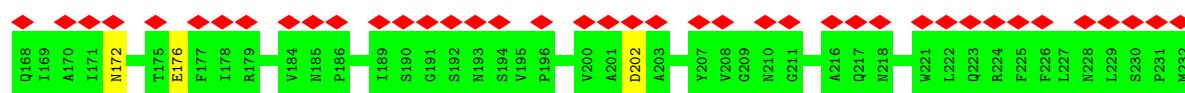
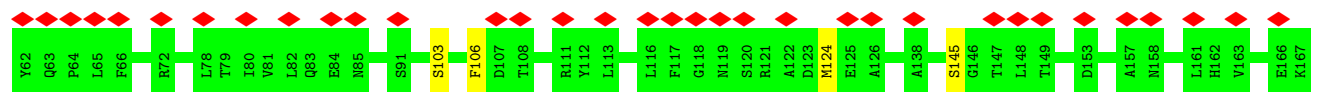
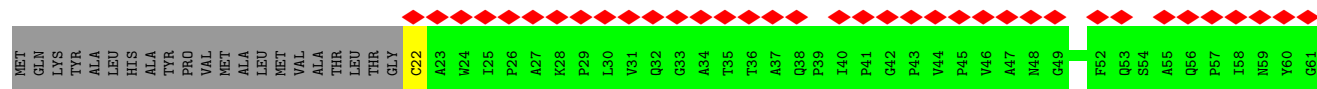
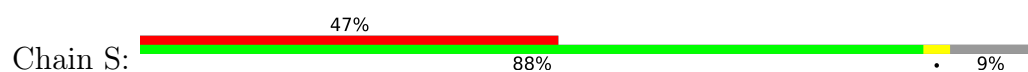
• Molecule 1: Flagellar L-ring protein



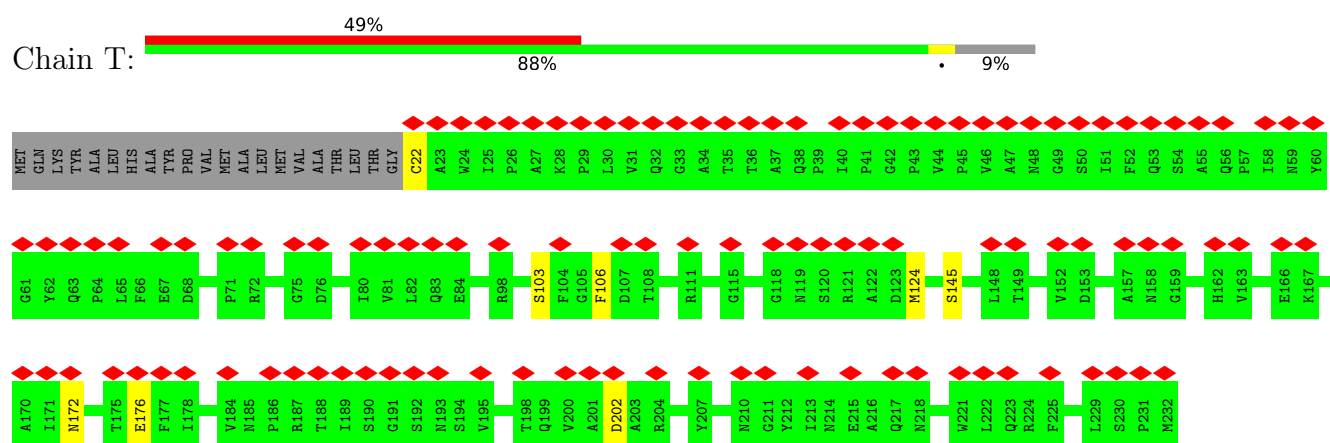
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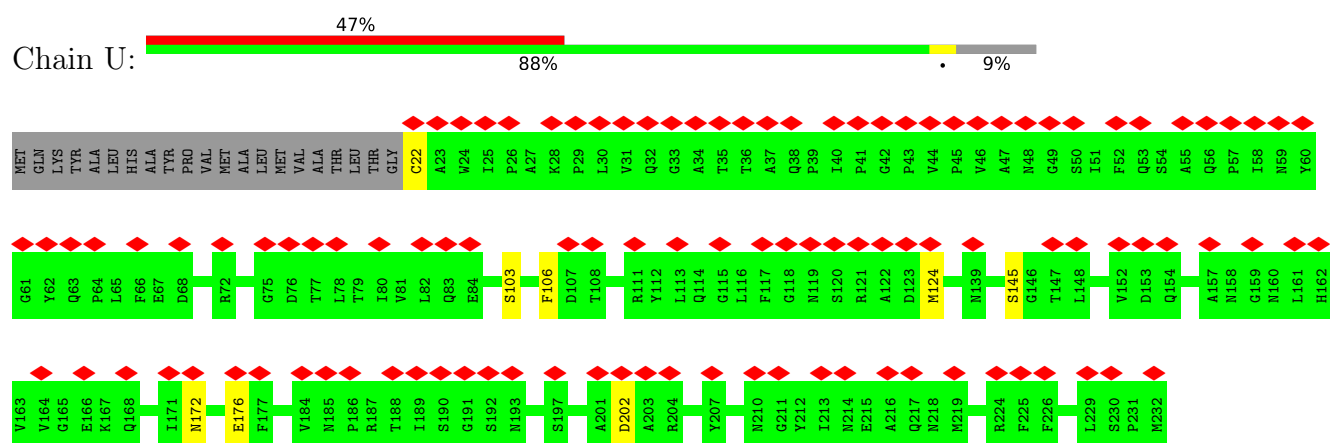
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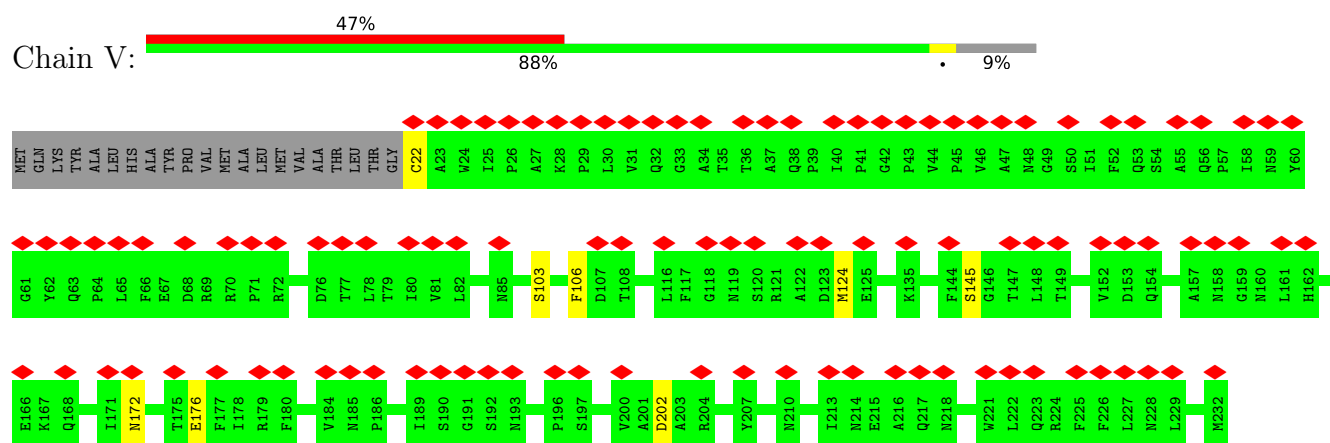
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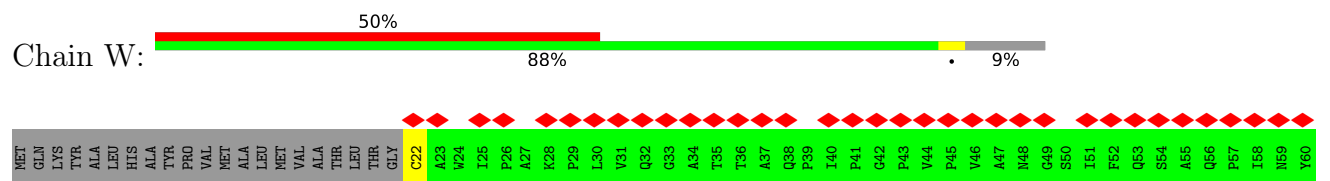
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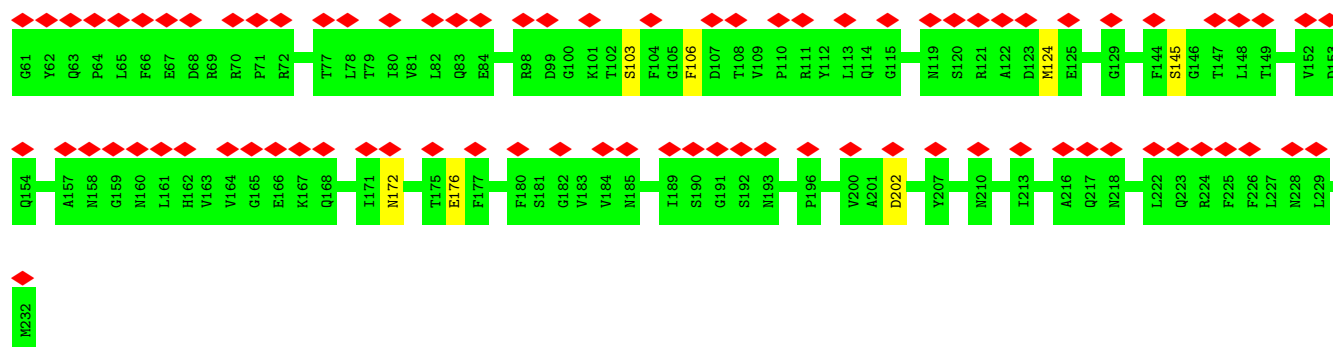


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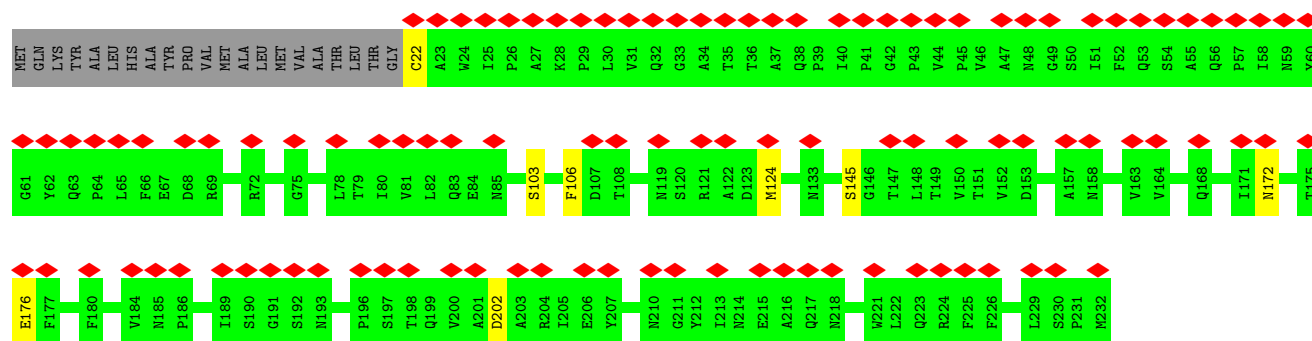
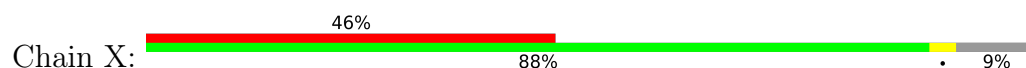


- Molecule 1: Flagellar L-ring protein

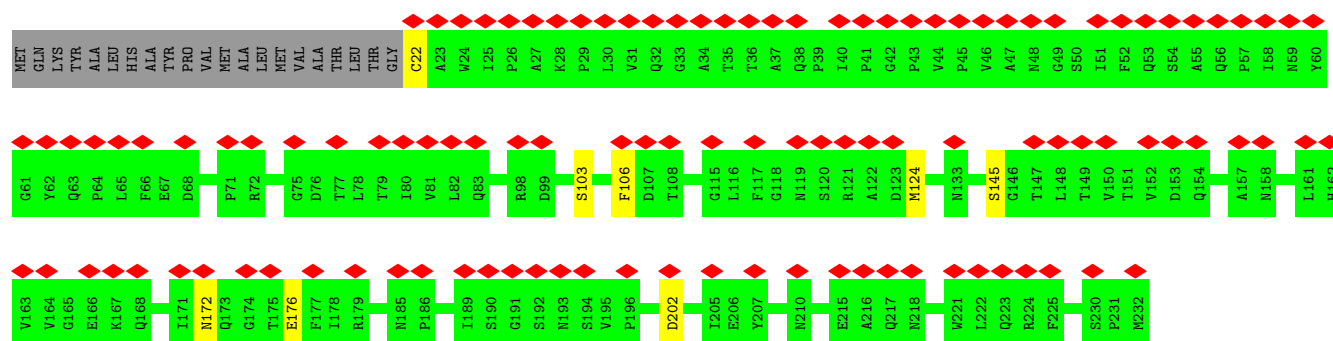
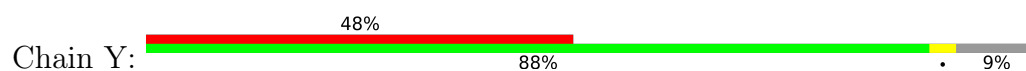




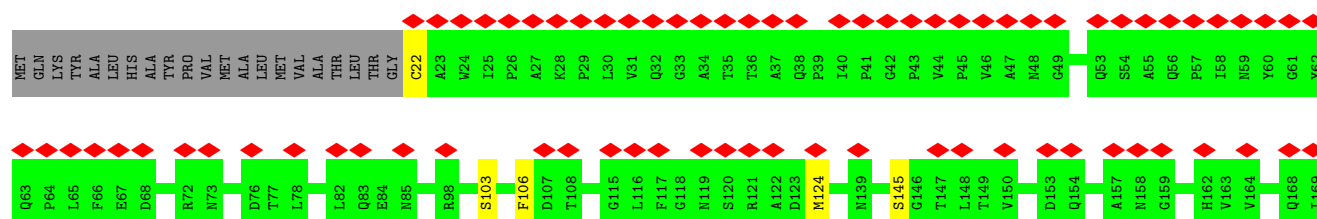
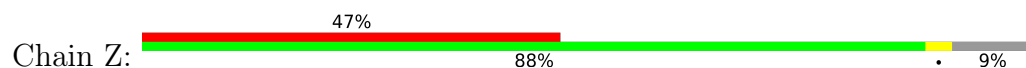
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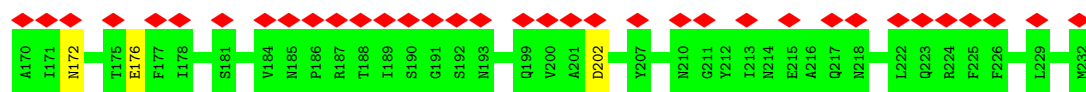


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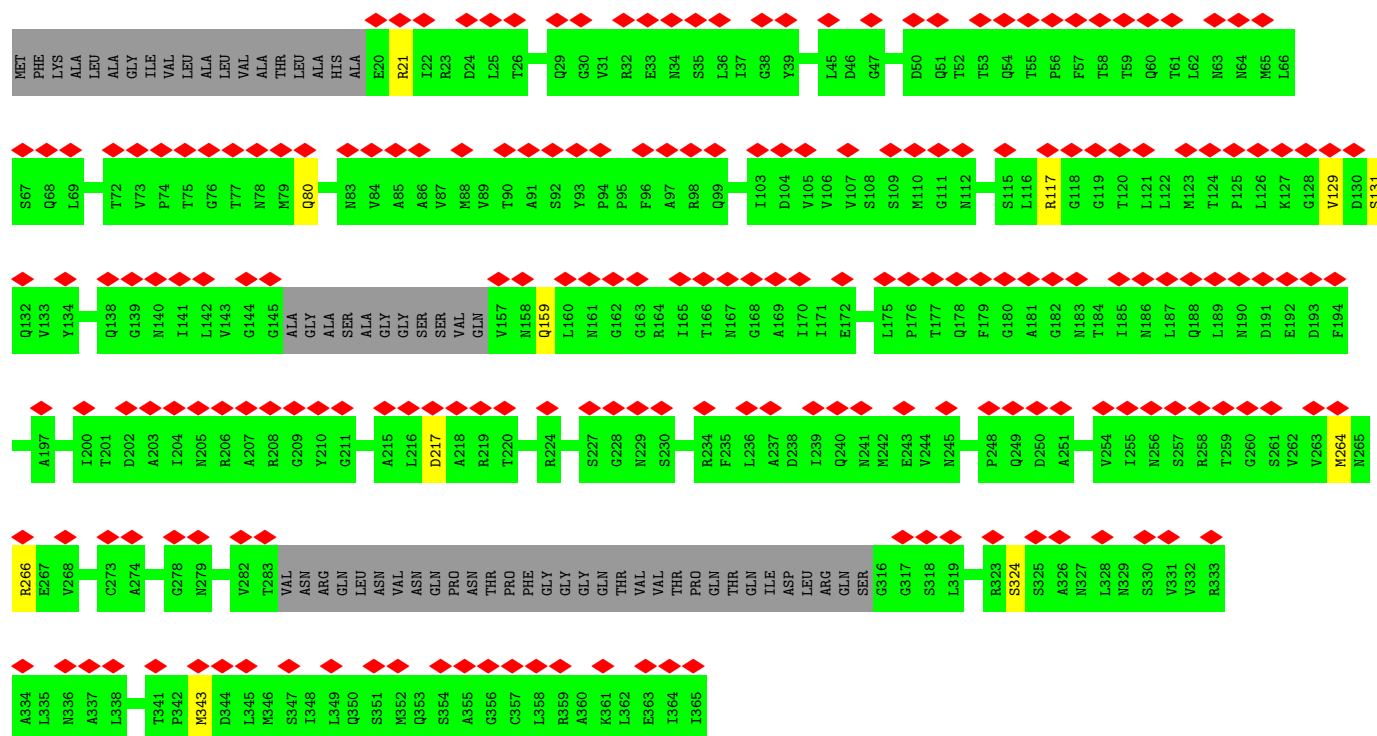
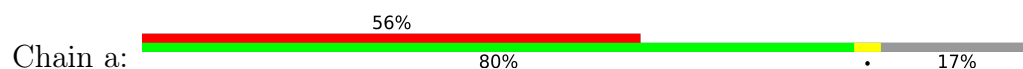


• Molecule 1: Flagellar L-ring protein

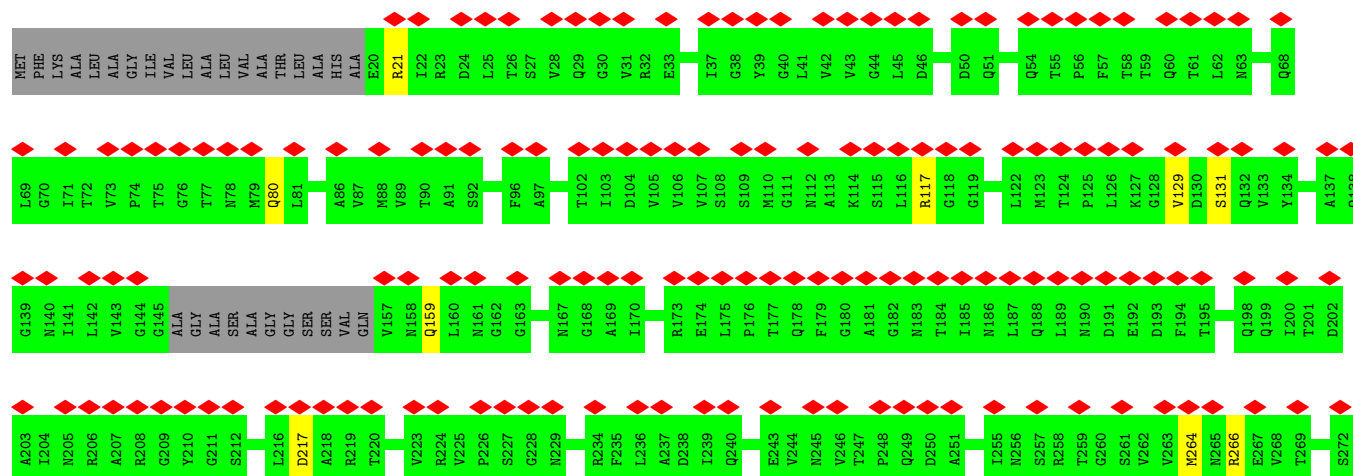
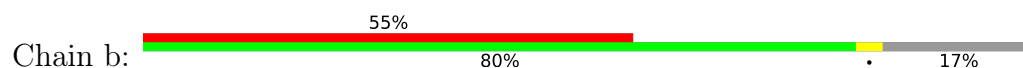


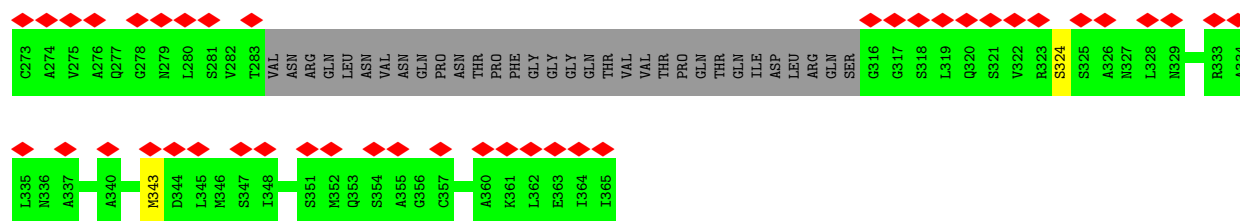


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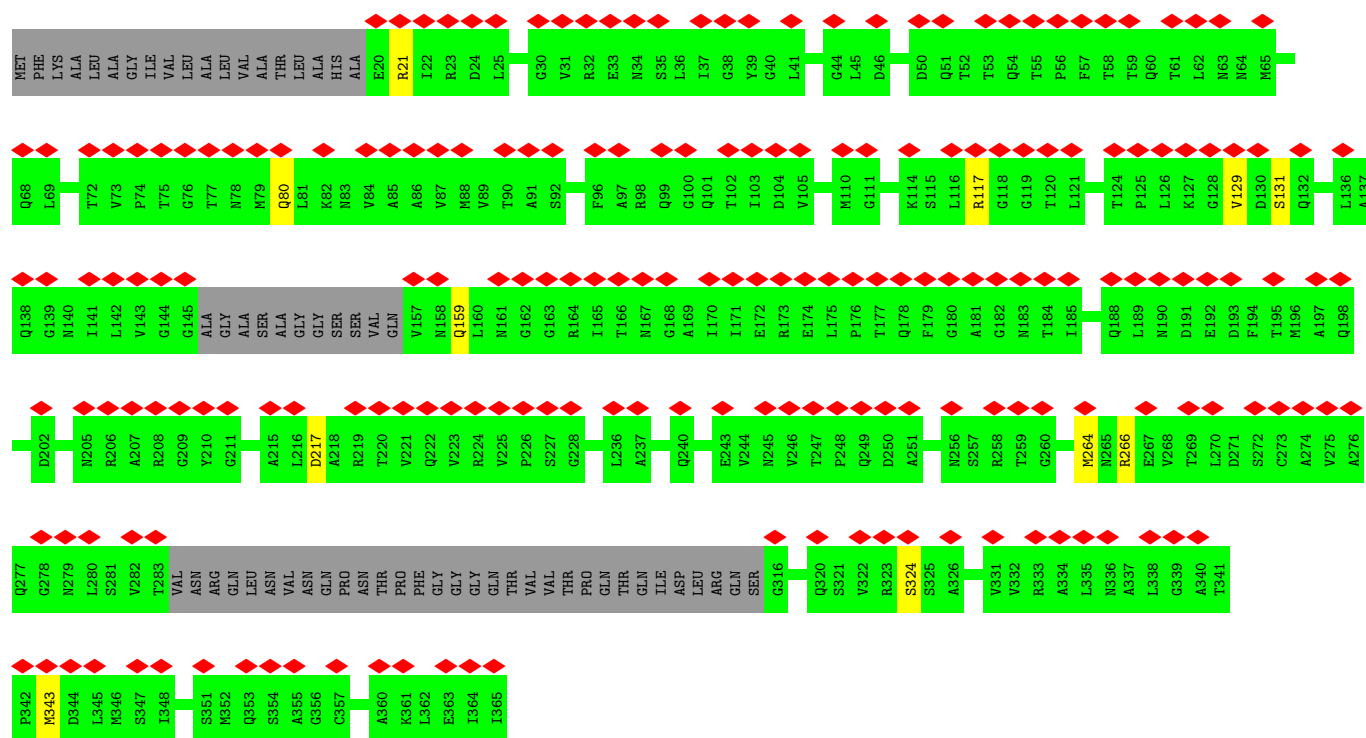
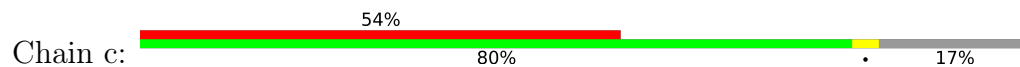


• Molecule 2: Flagellar P-ring protein

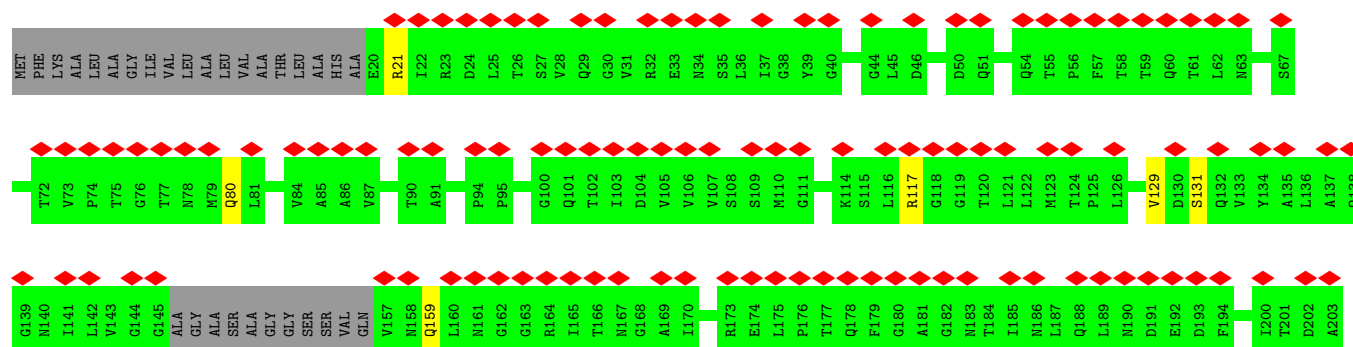
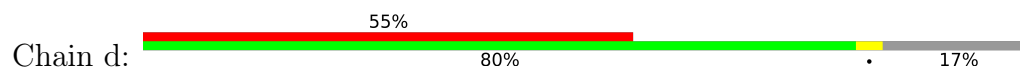




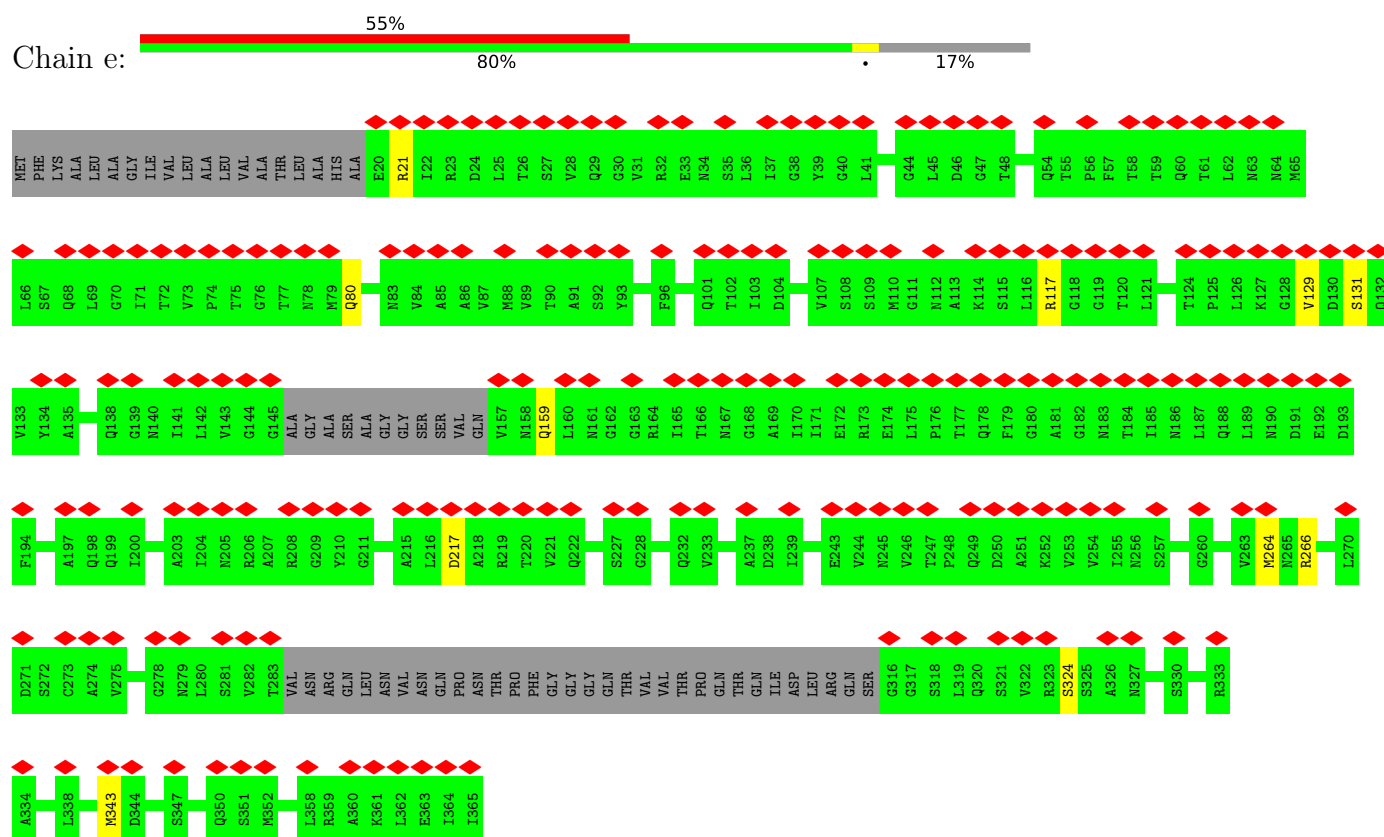
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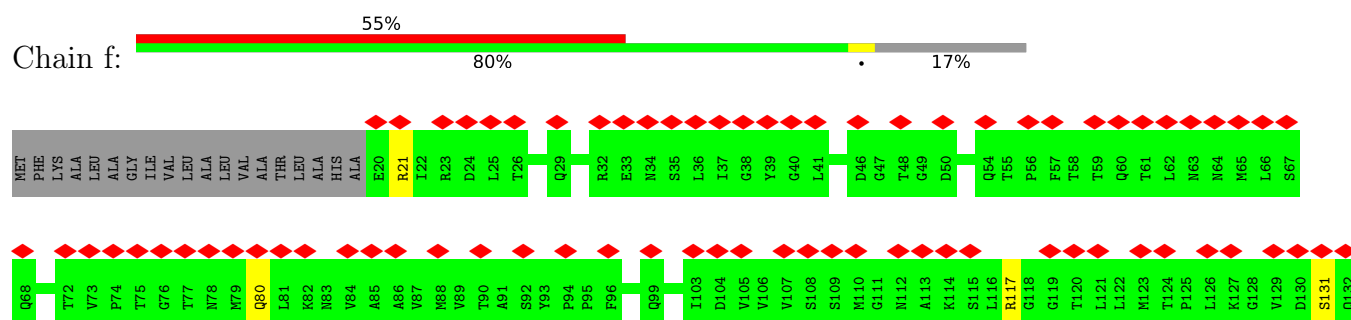
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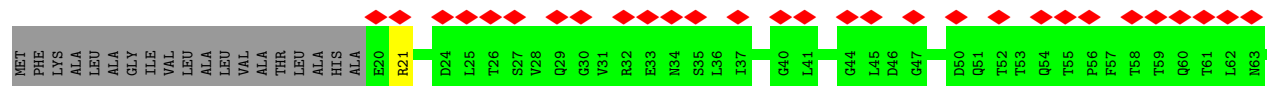


- Molecule 2: Flagellar P-ring protein



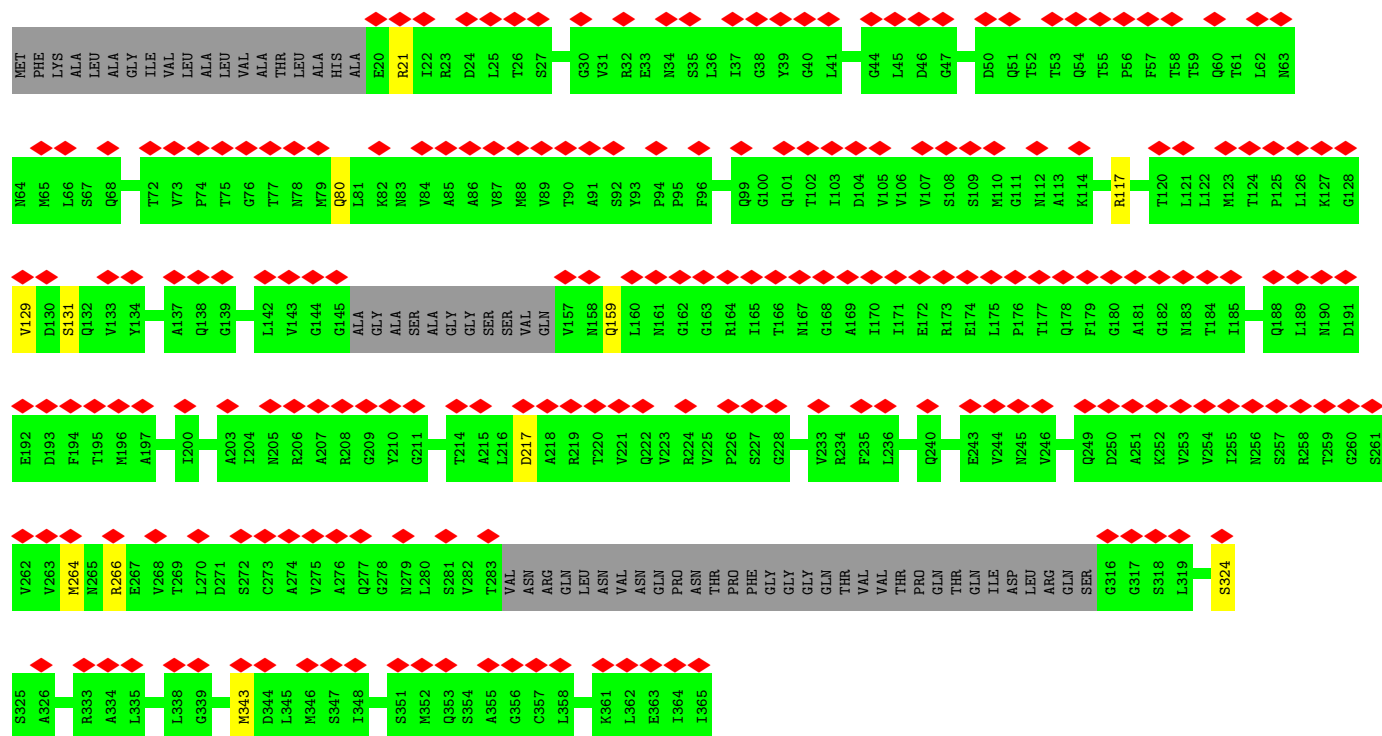
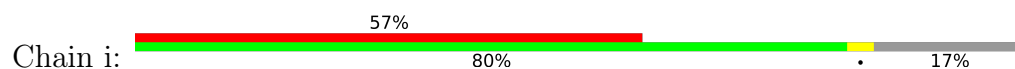
- Molecule 2: Flagellar P-ring protein



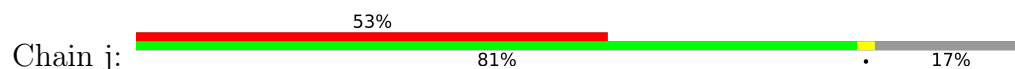


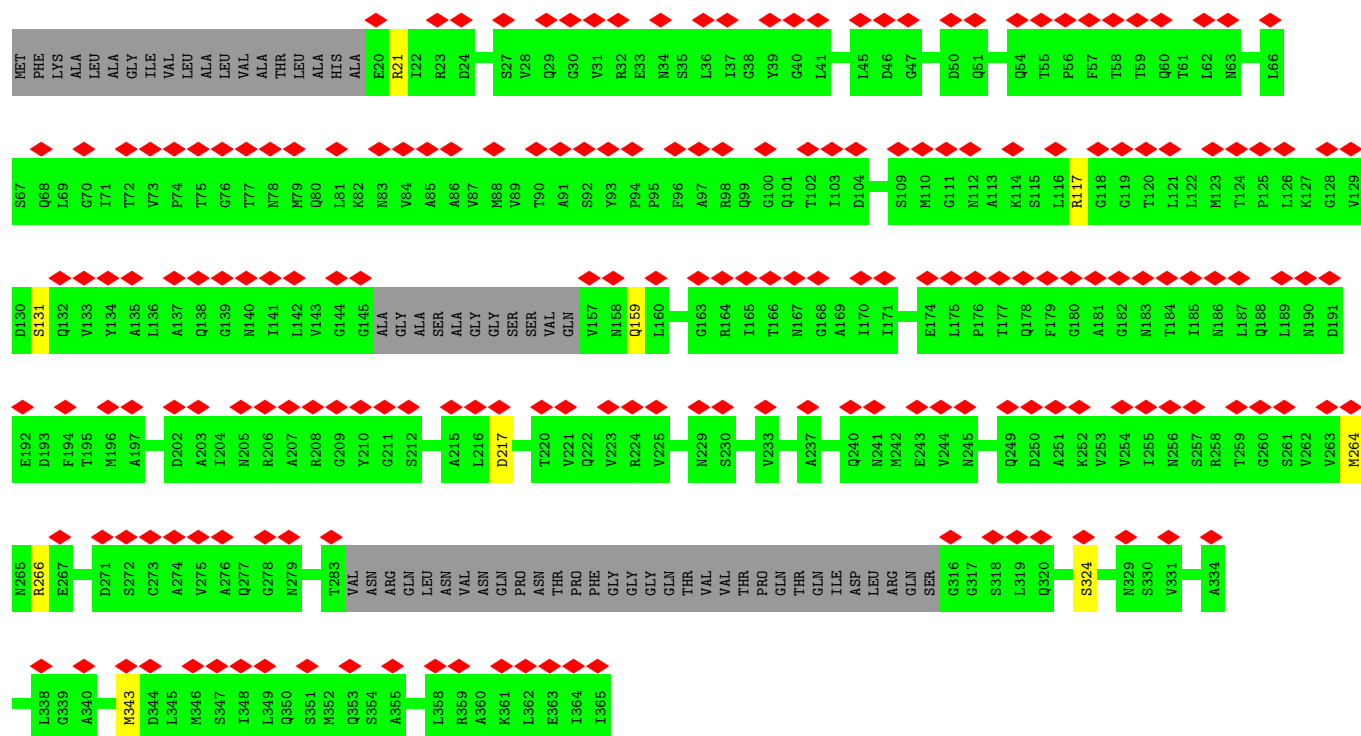


- Molecule 2: Flagellar P-ring protein

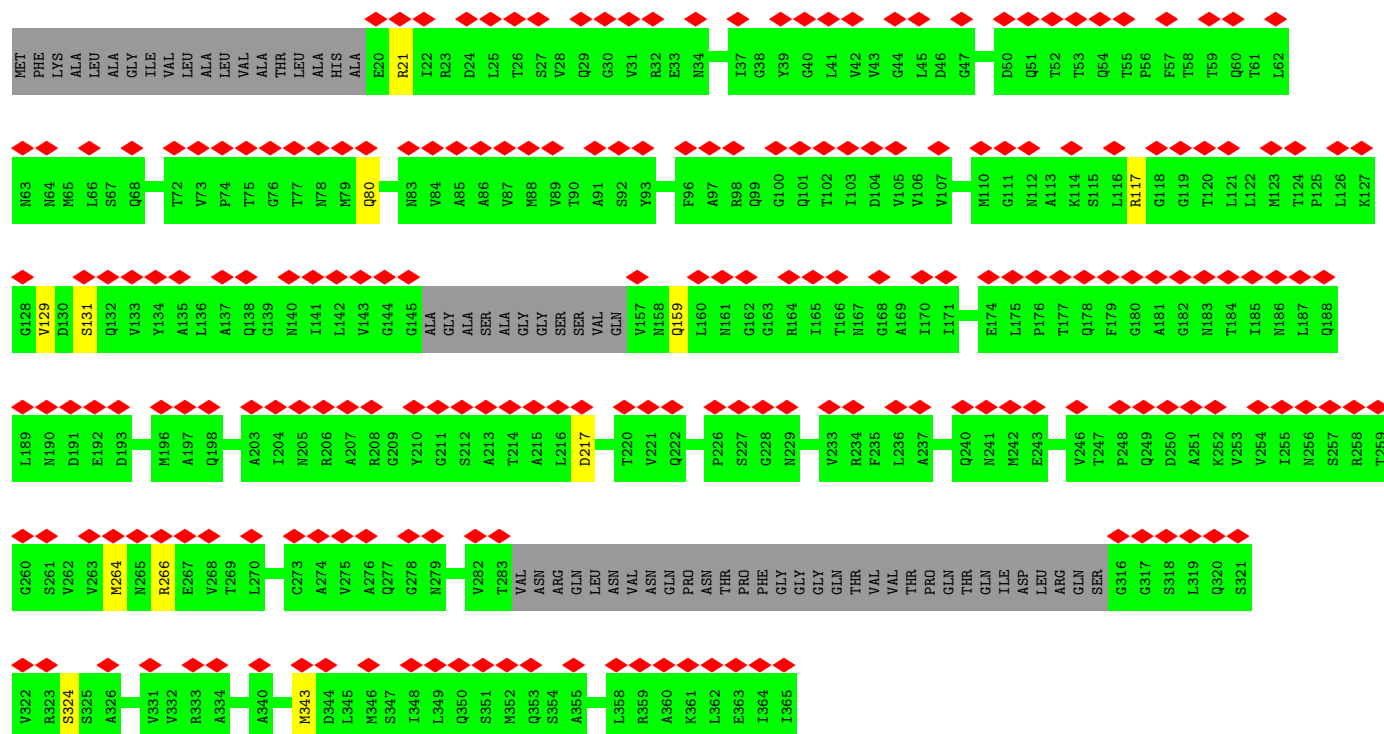
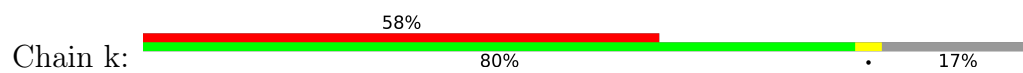


- Molecule 2: Flagellar P-ring protein





• Molecule 2: Flagellar P-ring protein



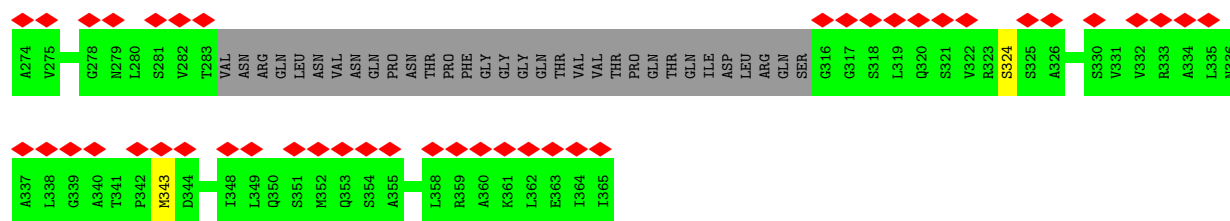
• Molecule 2: Flagellar P-ring protein

Response	Percentage
Good job	57%
Not doing a good job	43%

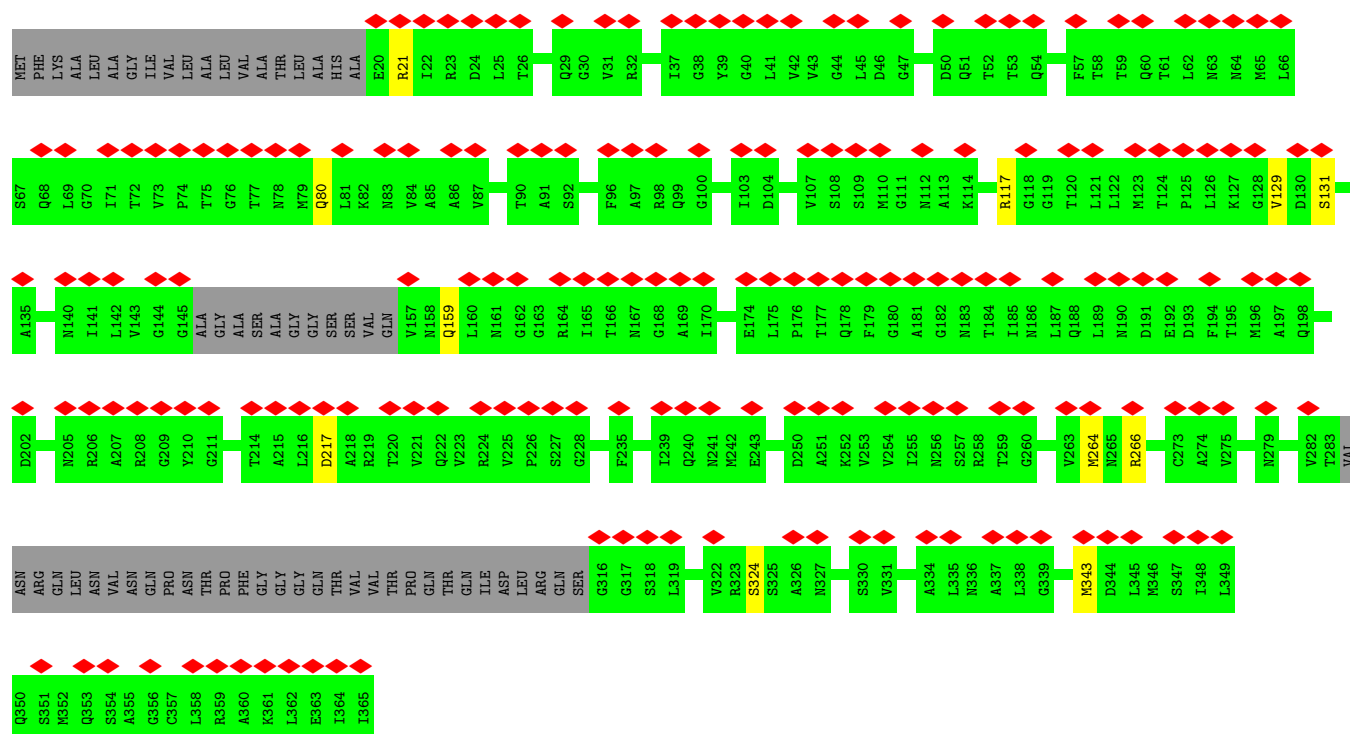
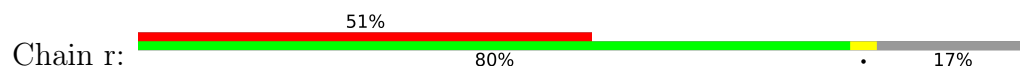


Category	Percentage
Red Bar	54%
Green Bar	80%
Grey Bar	17%

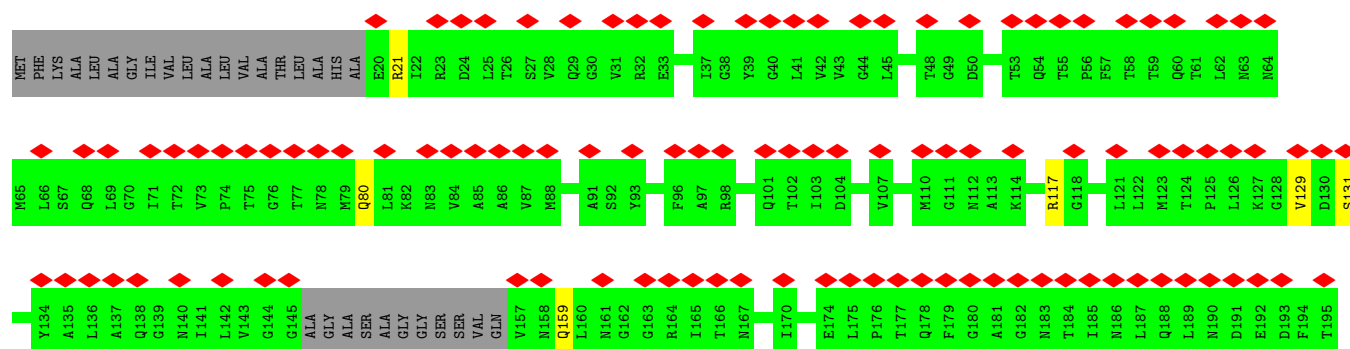


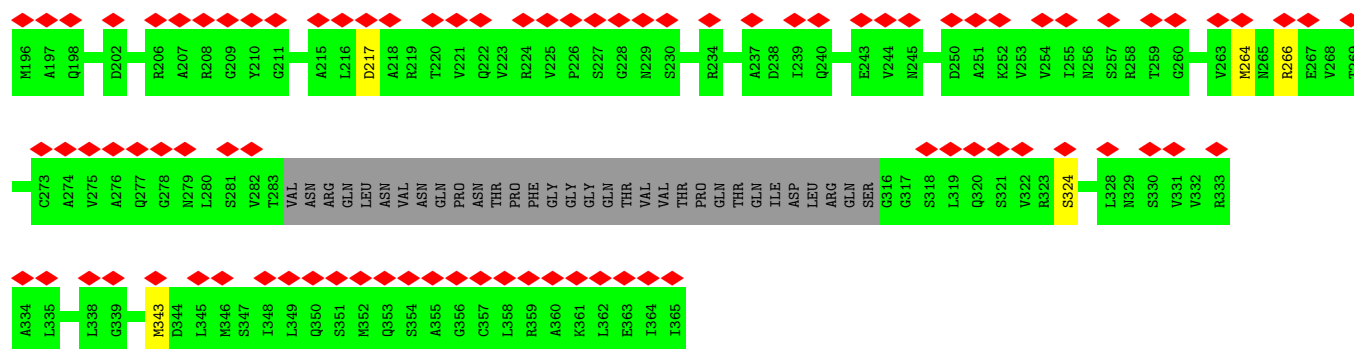


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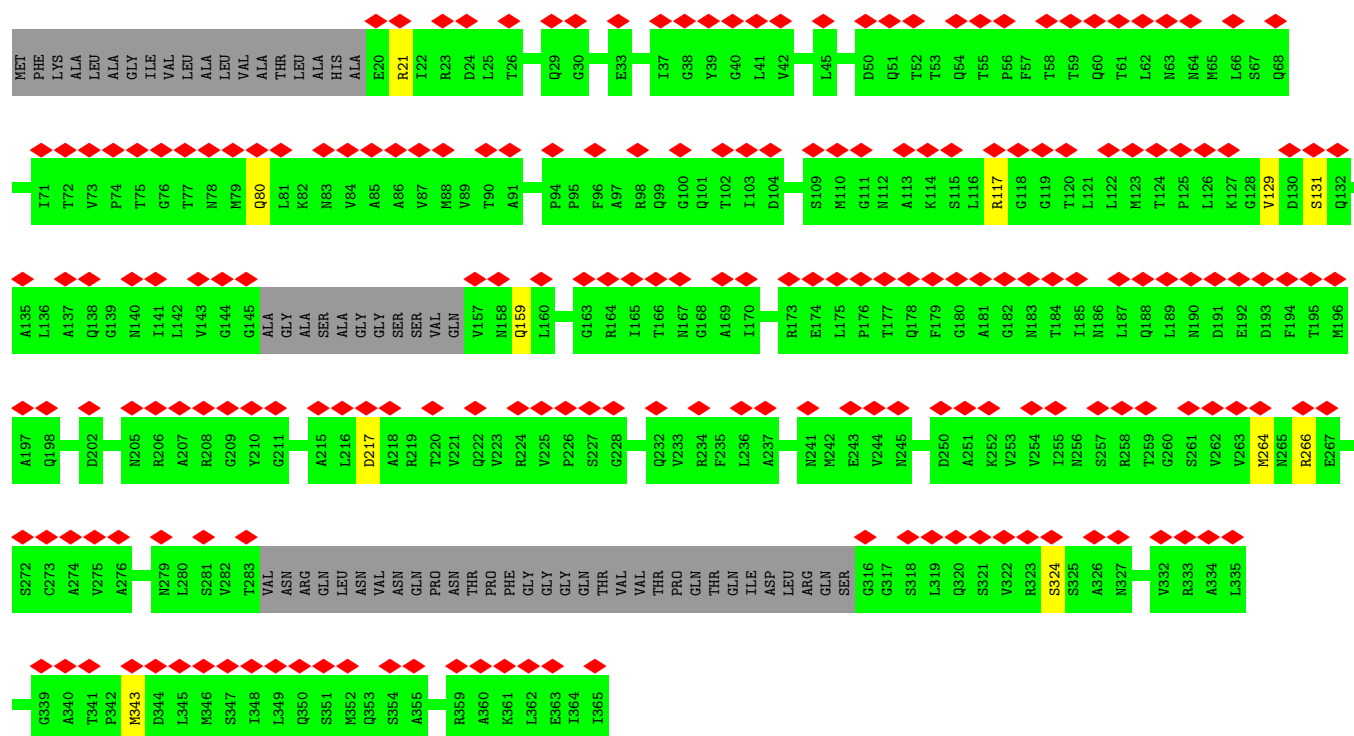
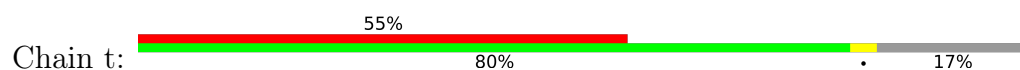


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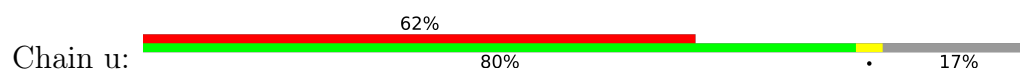


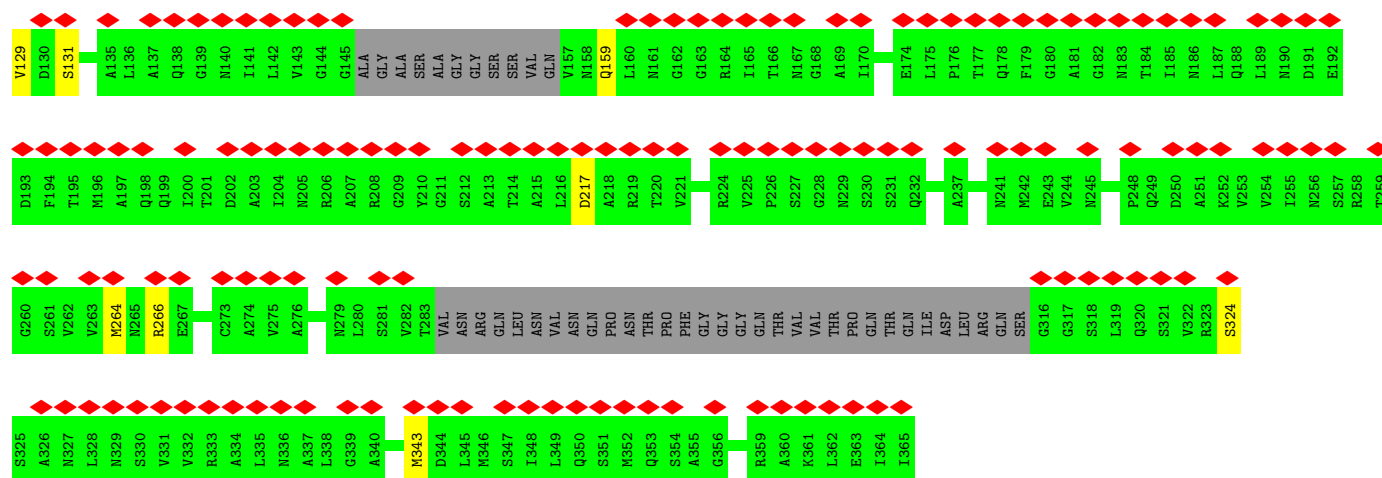


• Molecule 2: Flagellar P-ring protein

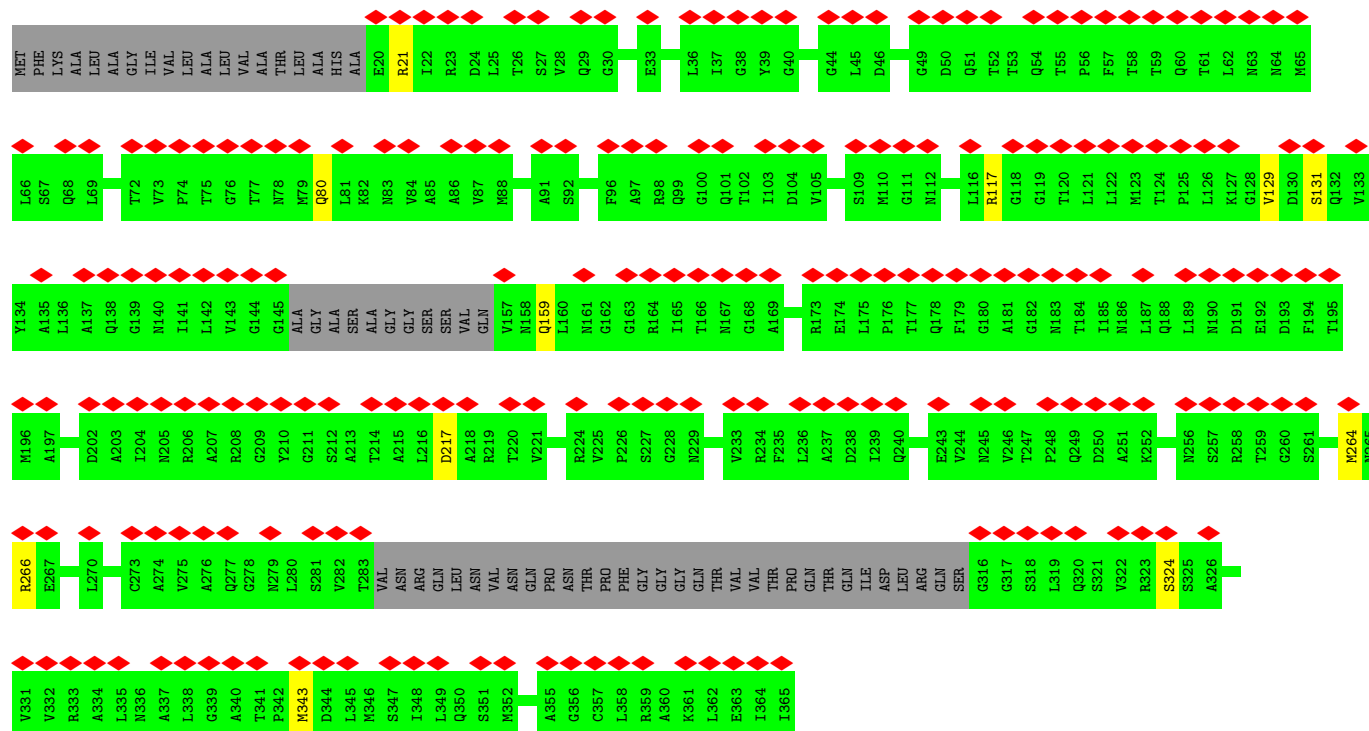
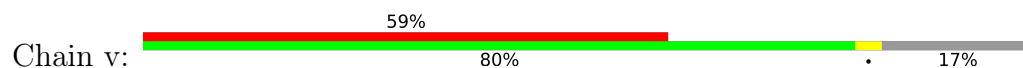


• Molecule 2: Flagellar P-ring protein

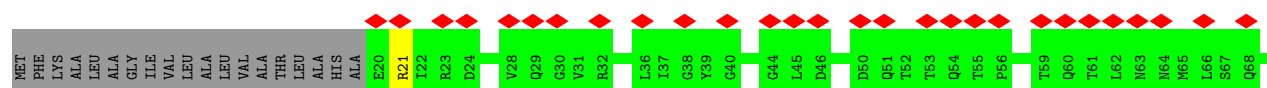


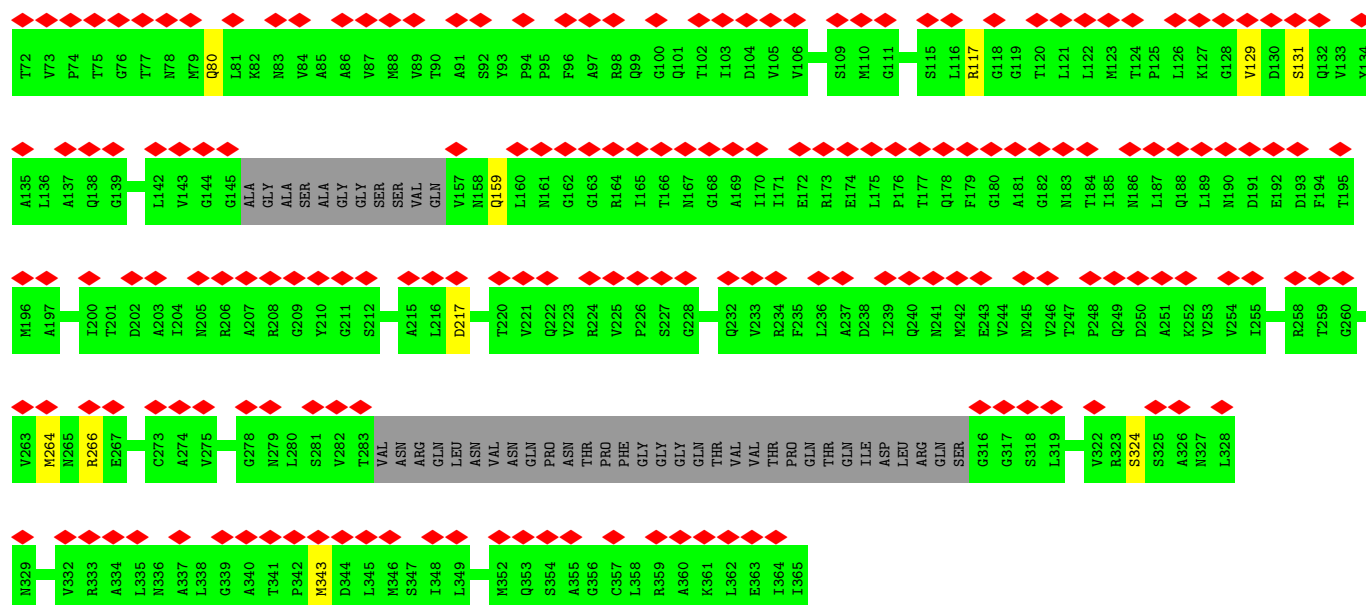


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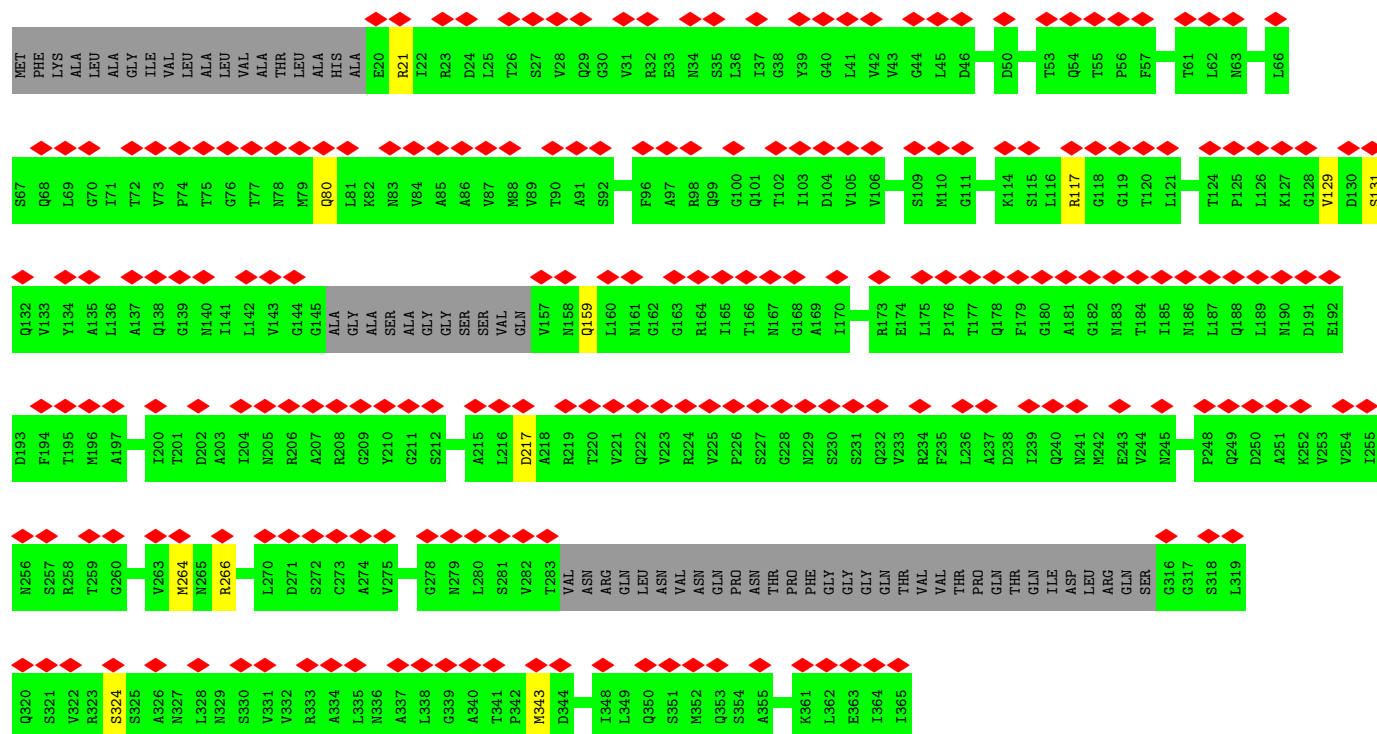
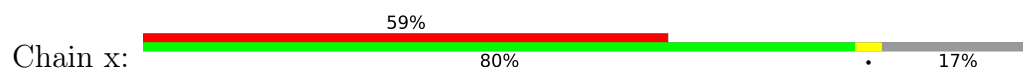


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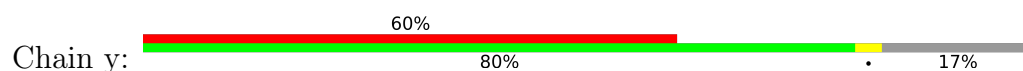


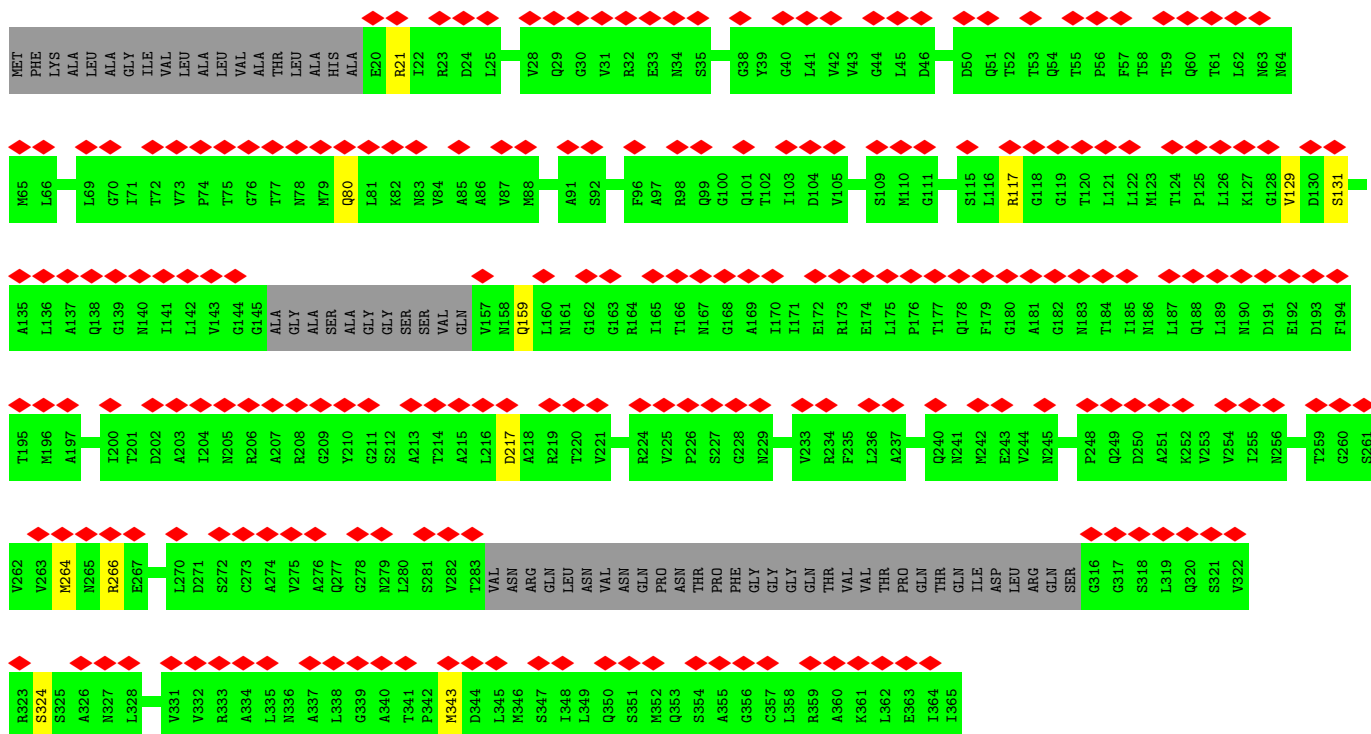


• Molecule 2: Flagellar P-ring protein

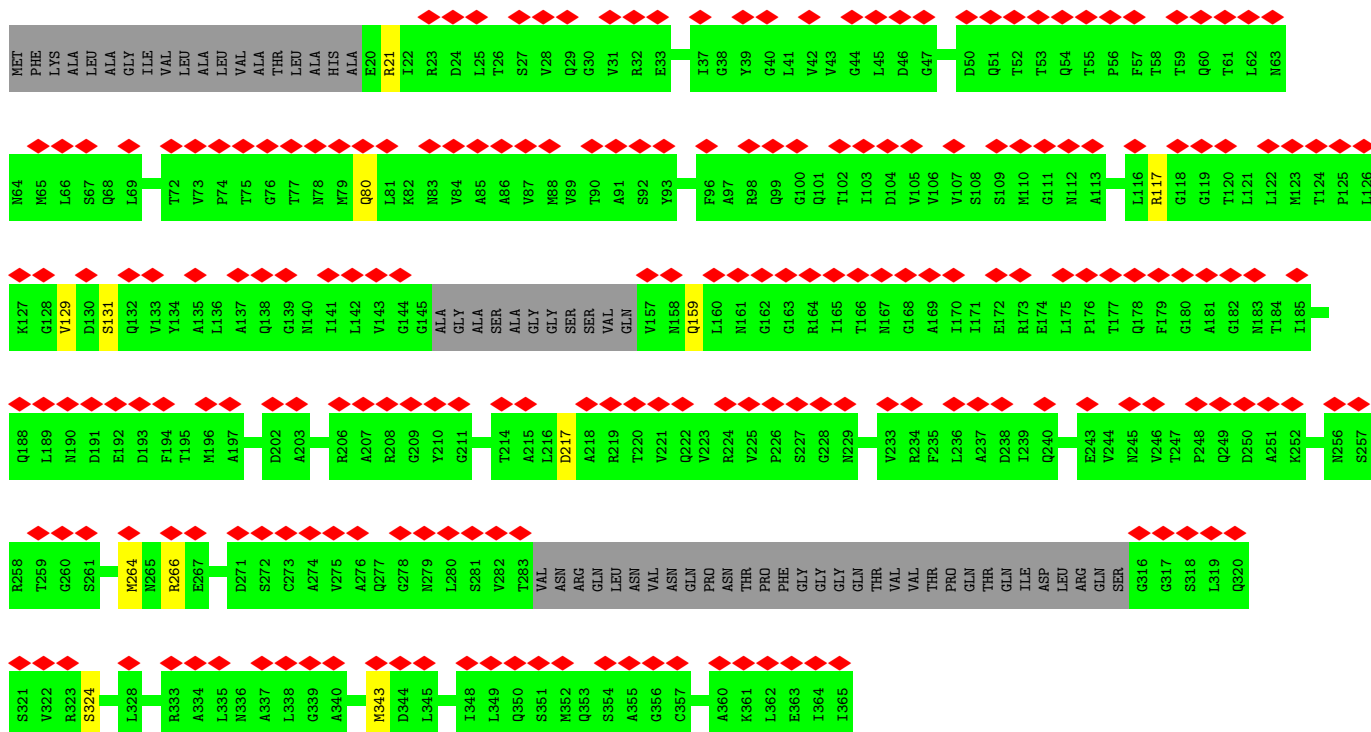
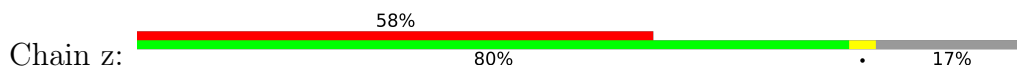


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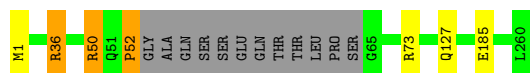


• Molecule 2: Flagellar P-ring protein



• Molecule 3: Flagellar basal-body rod protein FlgG

Chain 0:  93% .. 5%



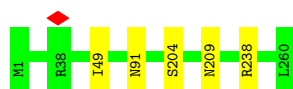
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 1:  93% ..



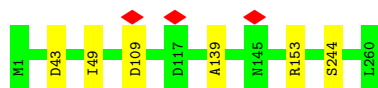
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 2:  98% .



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 3:  98% .



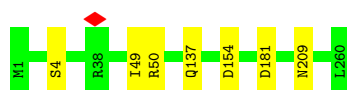
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 4:  97% .



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 5:  97% .



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 6:  97% .



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 7:  98%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 8:  98%



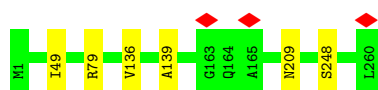
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain 9:  97%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZA:  98%



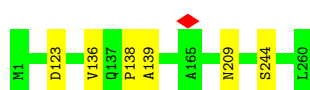
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZB:  96%



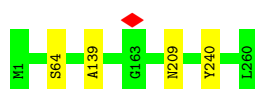
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZC:  98%



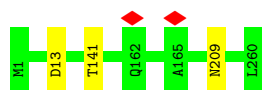
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZD:  98%



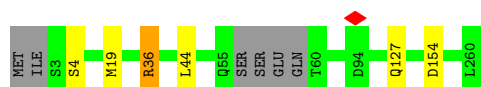
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain ZE:  99%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AF:  95%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AG:  95%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AH:  94%



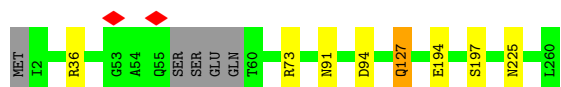
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AI:  93%



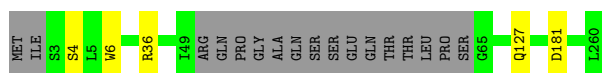
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AJ:  95%



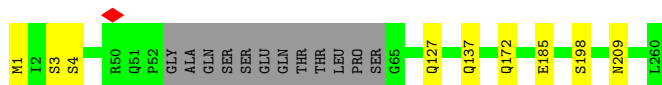
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AK:  92%



- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AL: 92% 5%



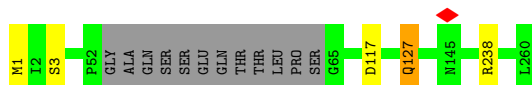
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AM: 92% 5%



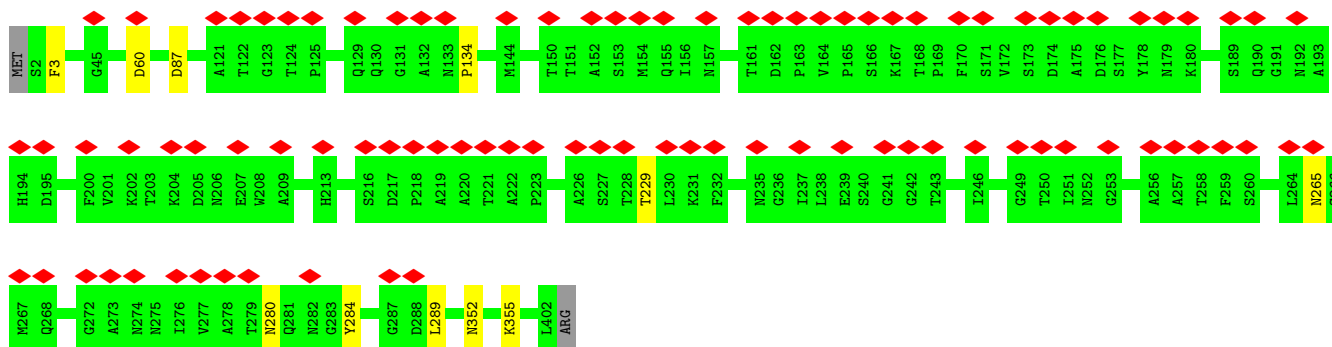
- Molecule 3: Flagellar basal-body rod protein FlgG

Chain AN: 93% 5%



- Molecule 4: Flagellar hook protein FlgE

Chain ZF: 23% 97% 5%



- Molecule 4: Flagellar hook protein FlgE

Chain ZG: 95% 5%



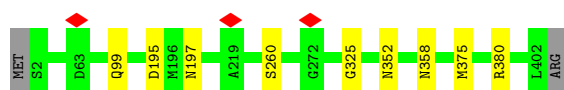
- Molecule 4: Flagellar hook protein FlgE

Chain ZH:  97%



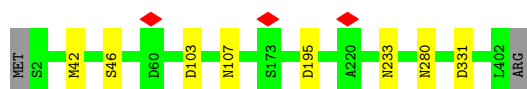
- Molecule 4: Flagellar hook protein FlgE

Chain ZI:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZJ:  98%



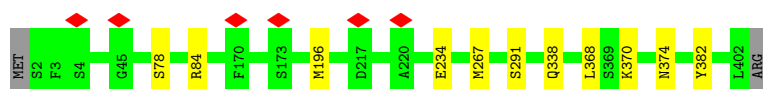
- Molecule 4: Flagellar hook protein FlgE

Chain ZK:  98%



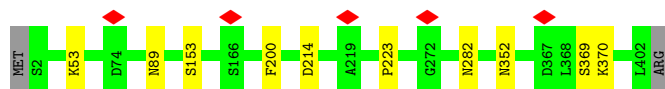
- Molecule 4: Flagellar hook protein FlgE

Chain ZL:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZM:  97%



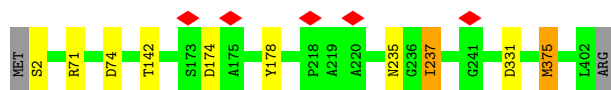
- Molecule 4: Flagellar hook protein FlgE

Chain ZN:  97%



- Molecule 4: Flagellar hook protein FlgE

Chain ZO:  97%



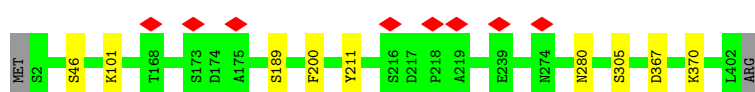
- Molecule 4: Flagellar hook protein FlgE

Chain ZP:  95%



- Molecule 4: Flagellar hook protein FlgE

Chain ZQ:  97%



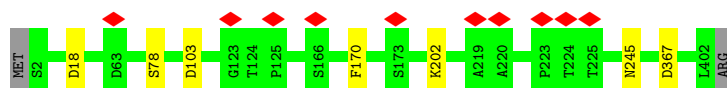
- Molecule 4: Flagellar hook protein FlgE

Chain ZR:  97%



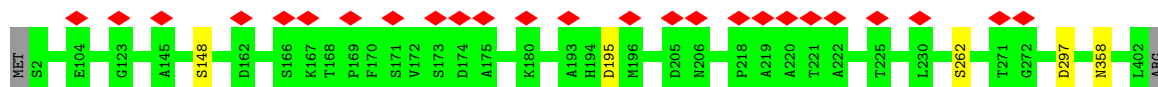
- Molecule 4: Flagellar hook protein FlgE

Chain ZS:  98%



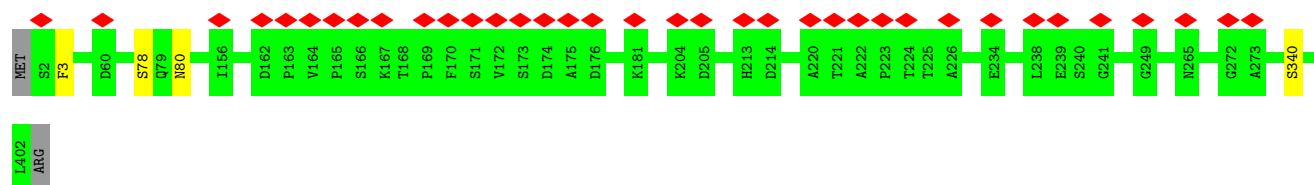
- Molecule 4: Flagellar hook protein FlgE

Chain ZT:  98%

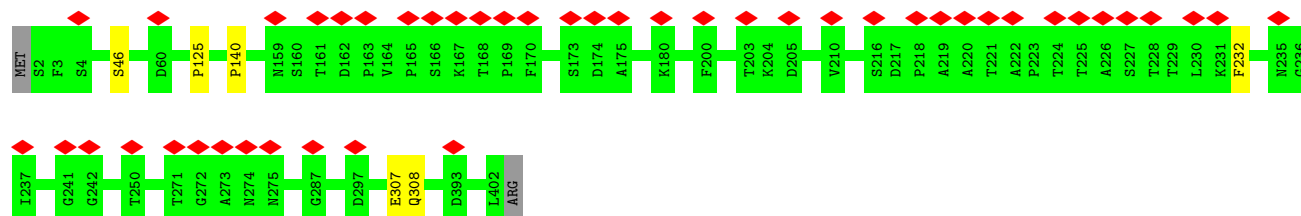


- Molecule 4: Flagellar hook protein FlgE

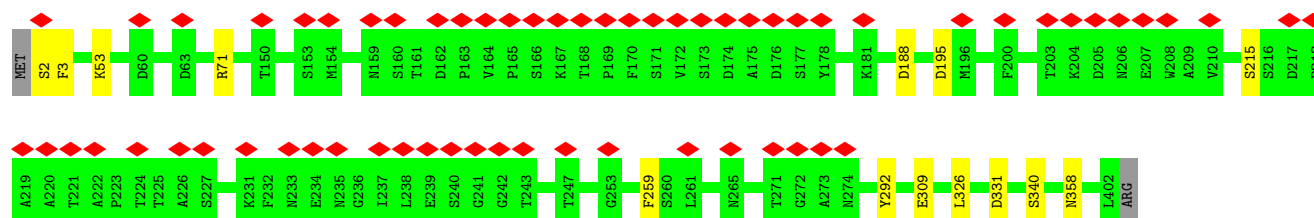
Chain ZU:  99%



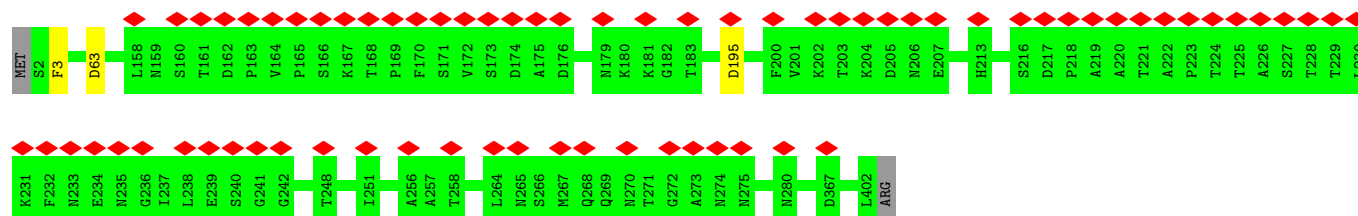
• Molecule 4: Flagellar hook protein FlgE



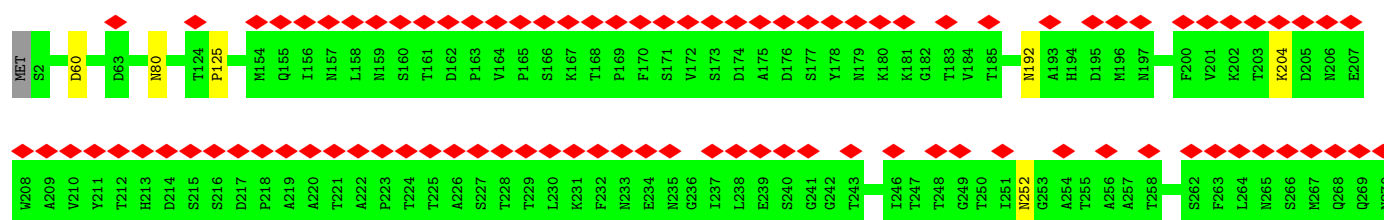
• Molecule 4: Flagellar hook protein FlgE

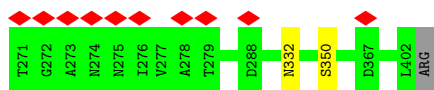


• Molecule 4: Flagellar hook protein FlgE

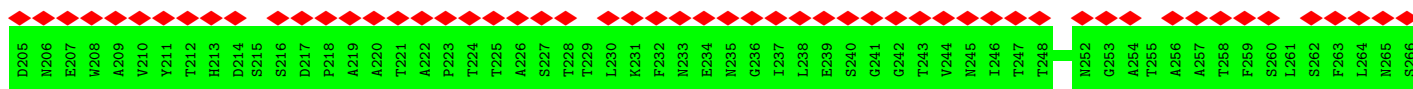
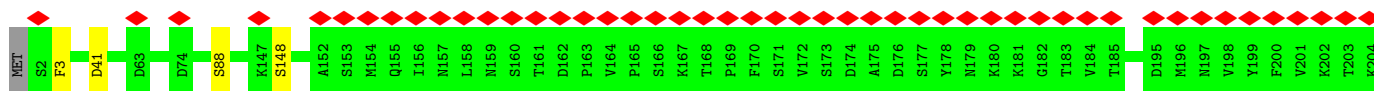


• Molecule 4: Flagellar hook protein FlgE

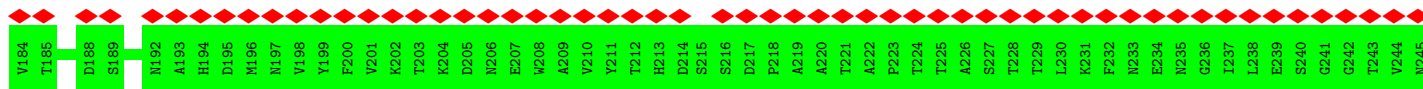
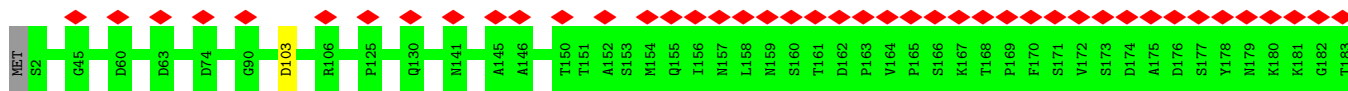




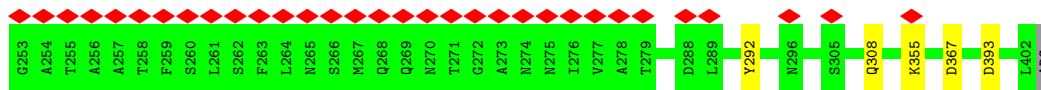
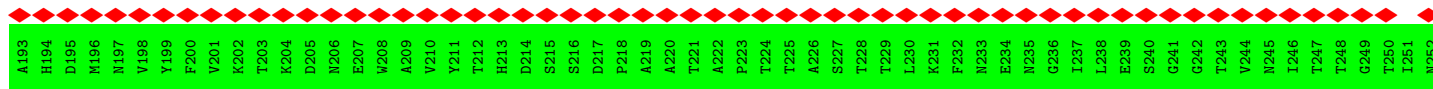
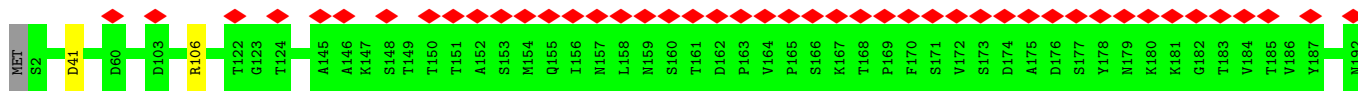
• Molecule 4: Flagellar hook protein FlgE



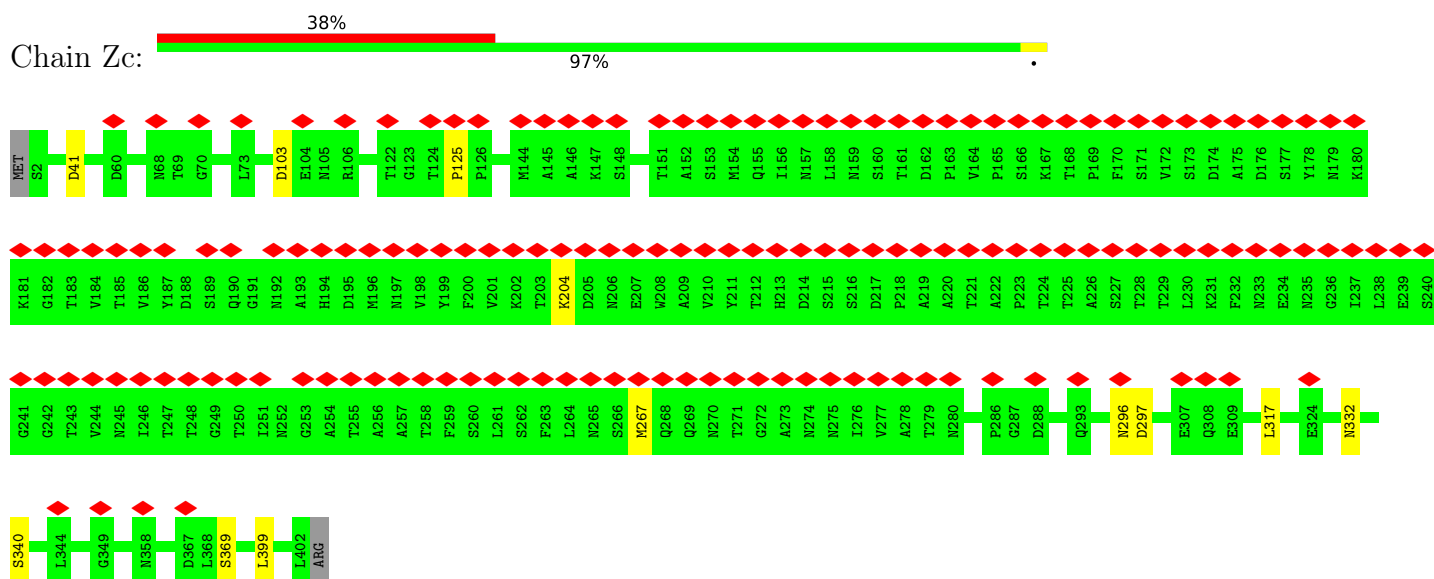
• Molecule 4: Flagellar hook protein FlgE



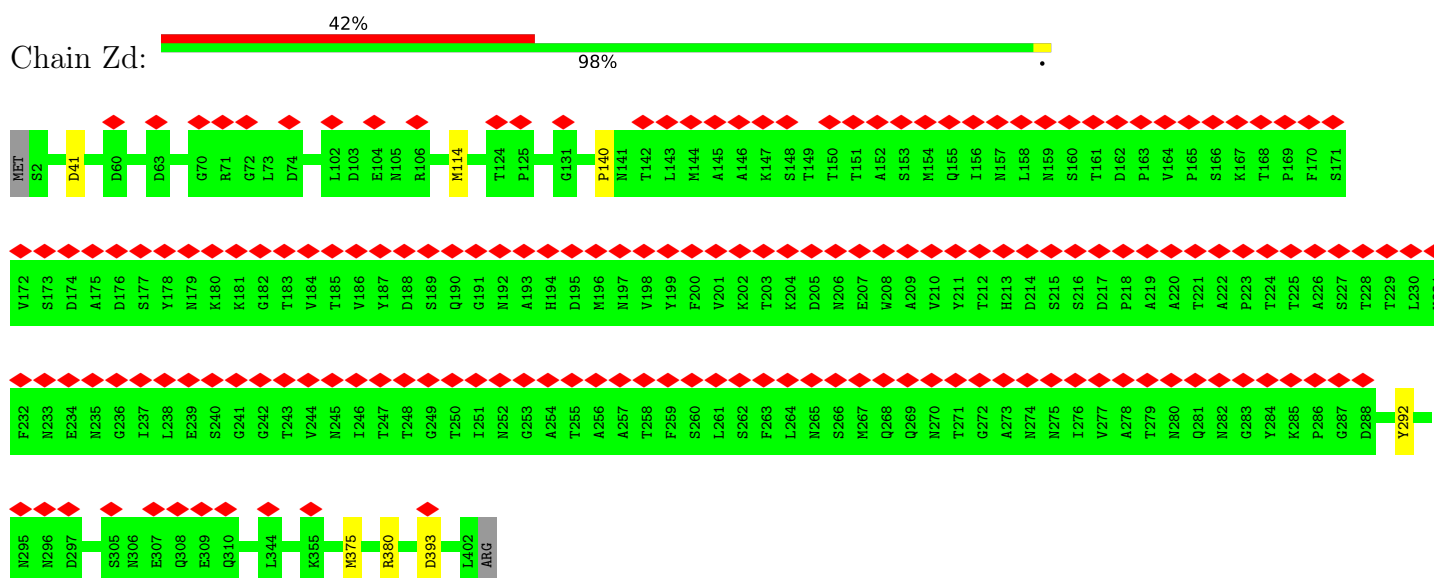
• Molecule 4: Flagellar hook protein FlgE



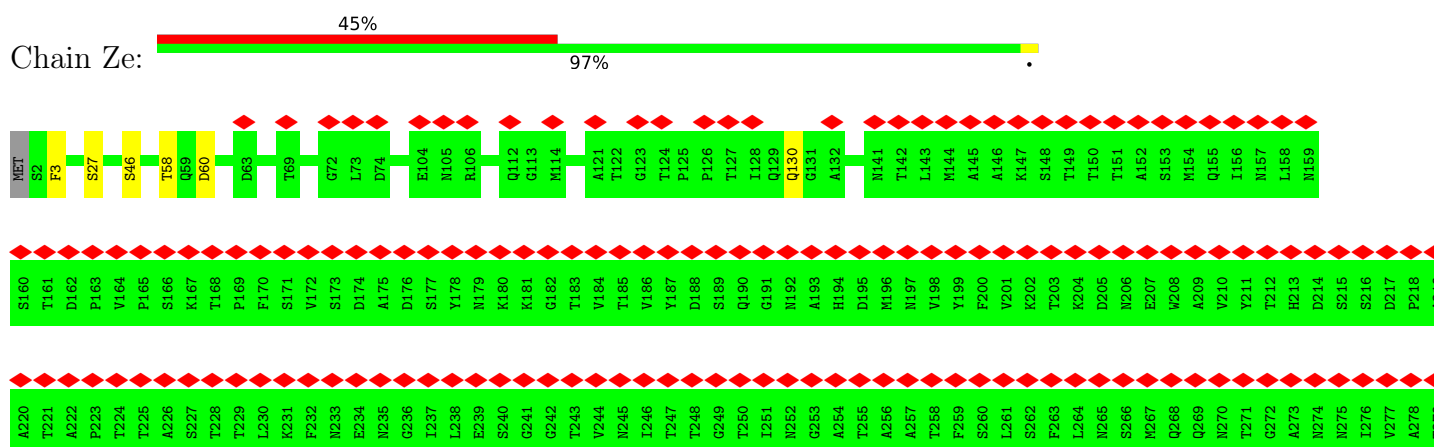
• Molecule 4: Flagellar hook protein FlgE

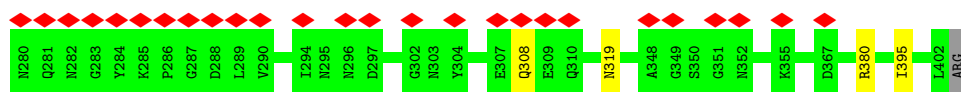


• Molecule 4: Flagellar hook protein FlgE

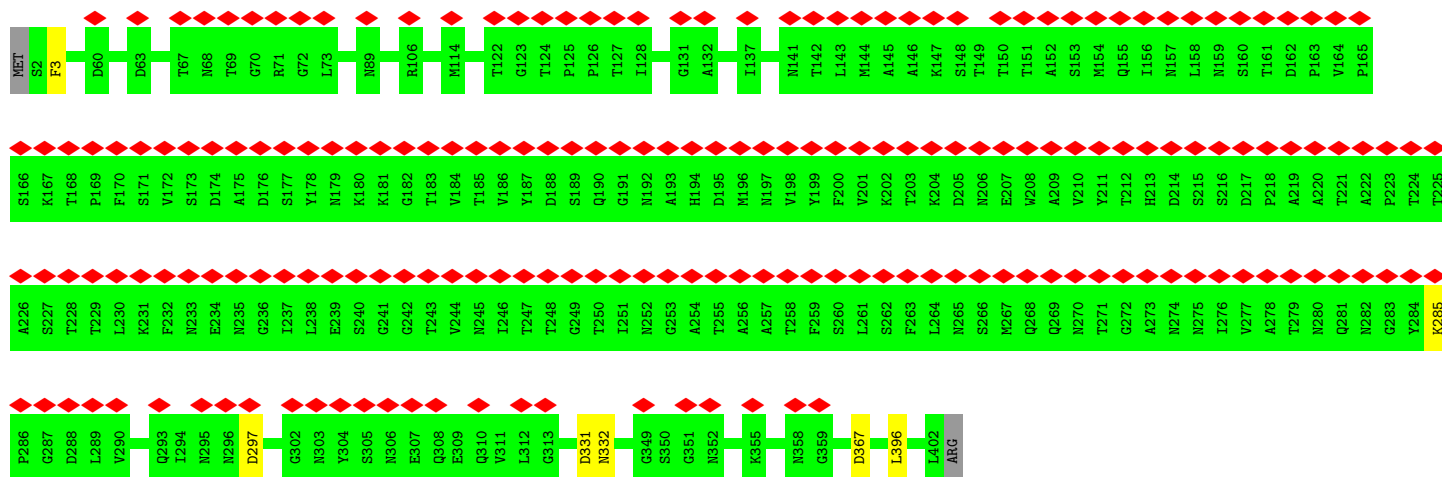


• Molecule 4: Flagellar hook protein FlgE

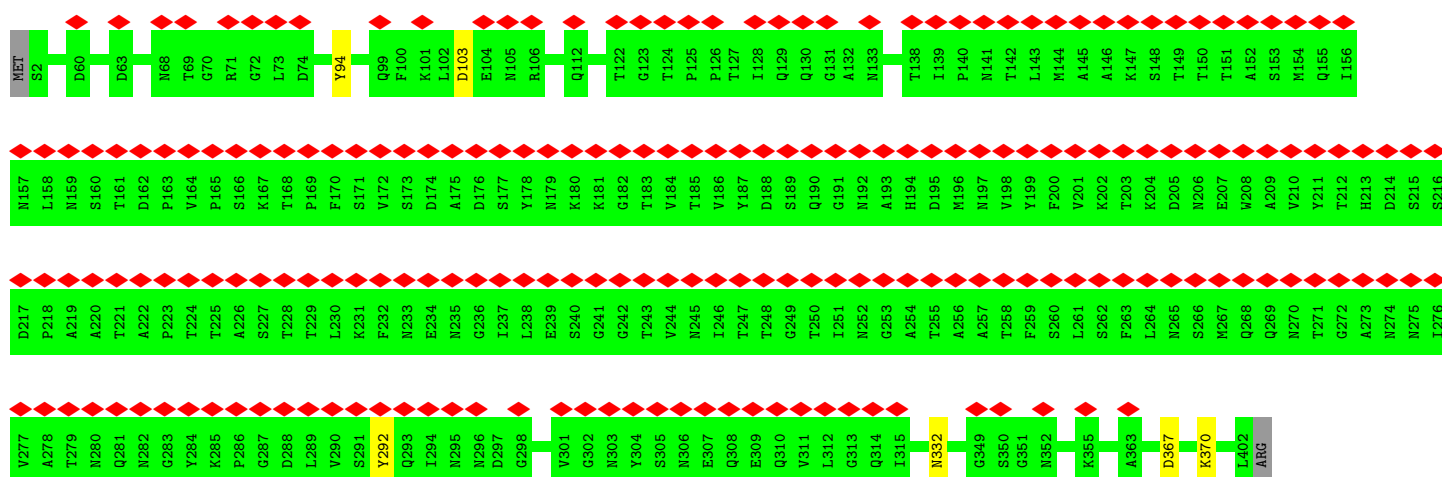




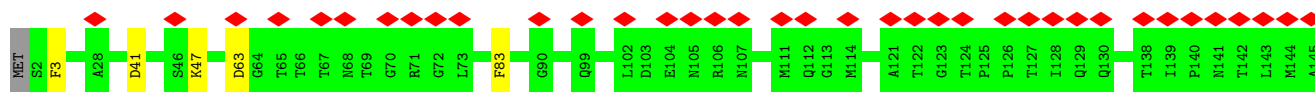
• Molecule 4: Flagellar hook protein FlgE

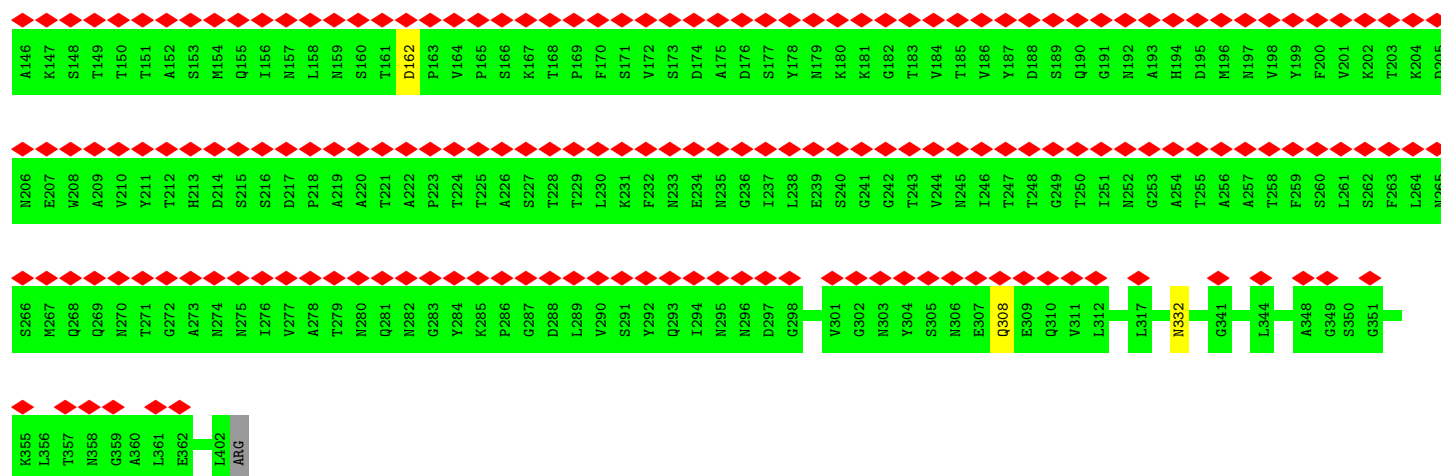


• Molecule 4: Flagellar hook protein FlgE



• Molecule 4: Flagellar hook protein FlgE





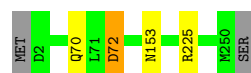
- Molecule 5: Flagellar basal-body rod protein FlgF

Chain AA:  96%



- Molecule 5: Flagellar basal-body rod protein FlgF

Chain AB:  98%



- Molecule 5: Flagellar basal-body rod protein FlgF

Chain AC:  97%



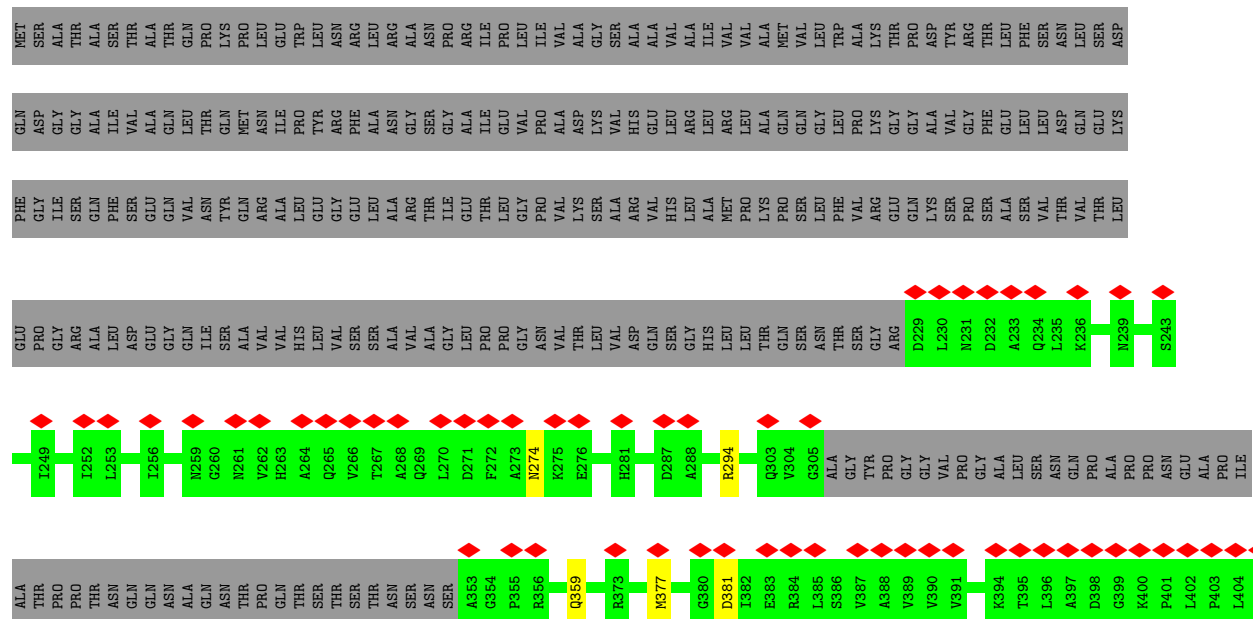
- Molecule 5: Flagellar basal-body rod protein FlgF

Chain AD:  99%

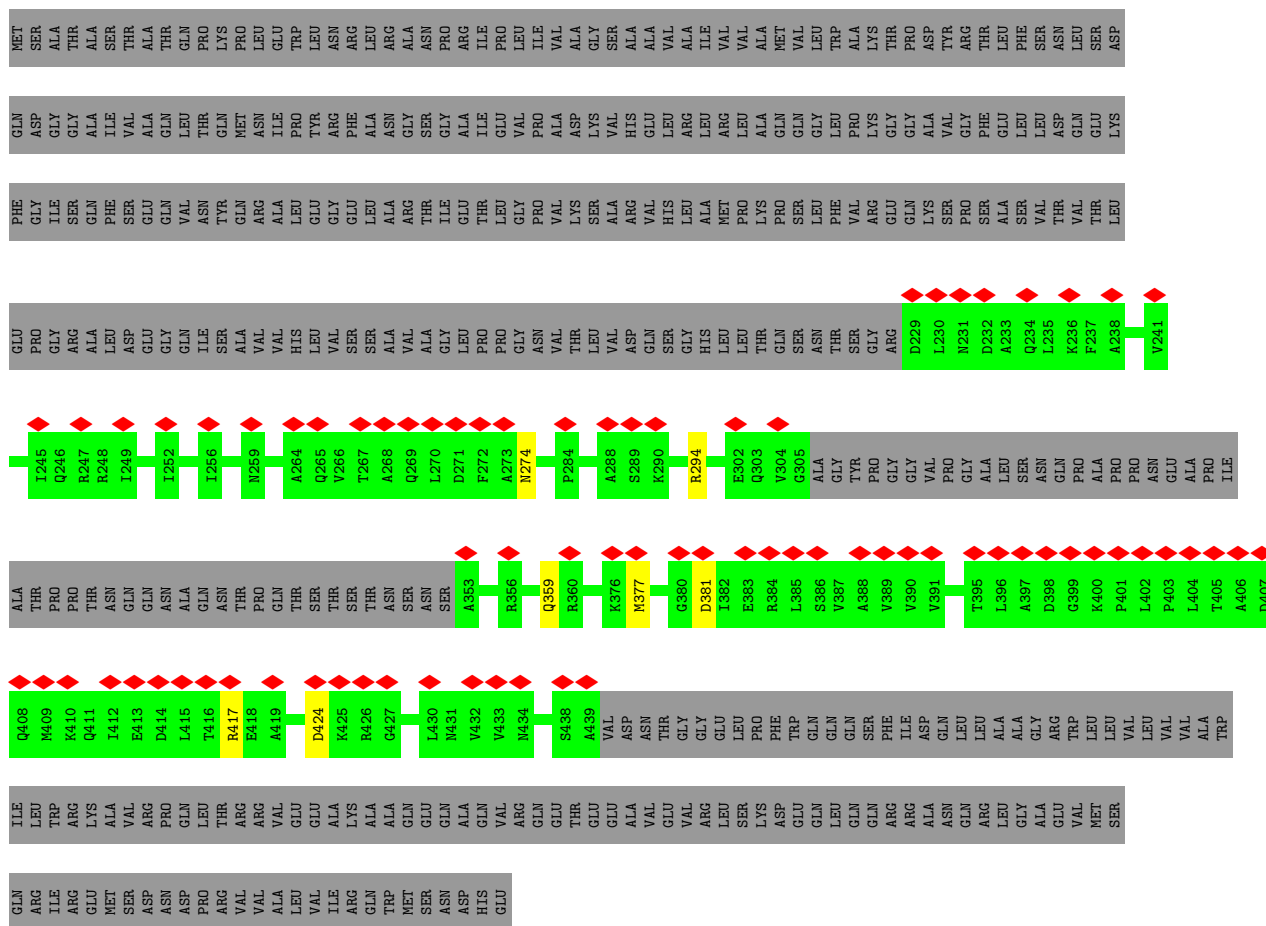


- Molecule 5: Flagellar basal-body rod protein FlgF

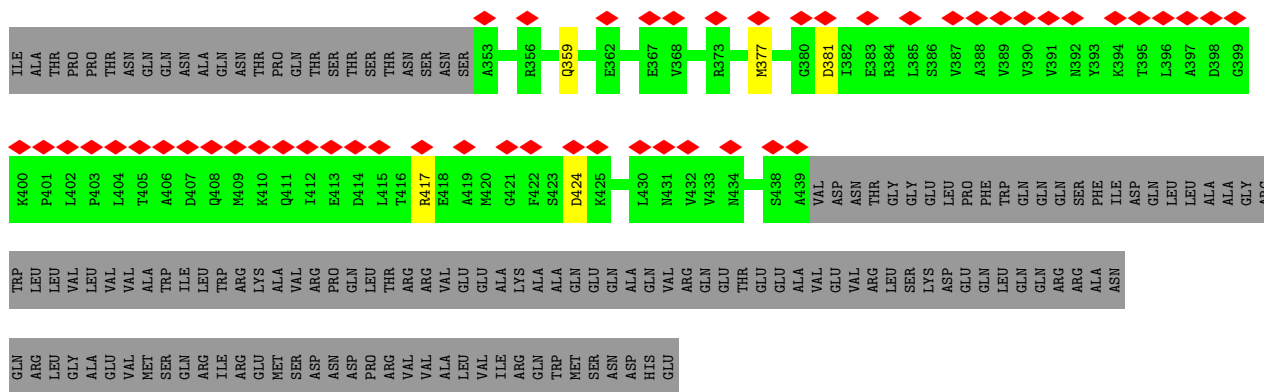
Chain AE:  98%



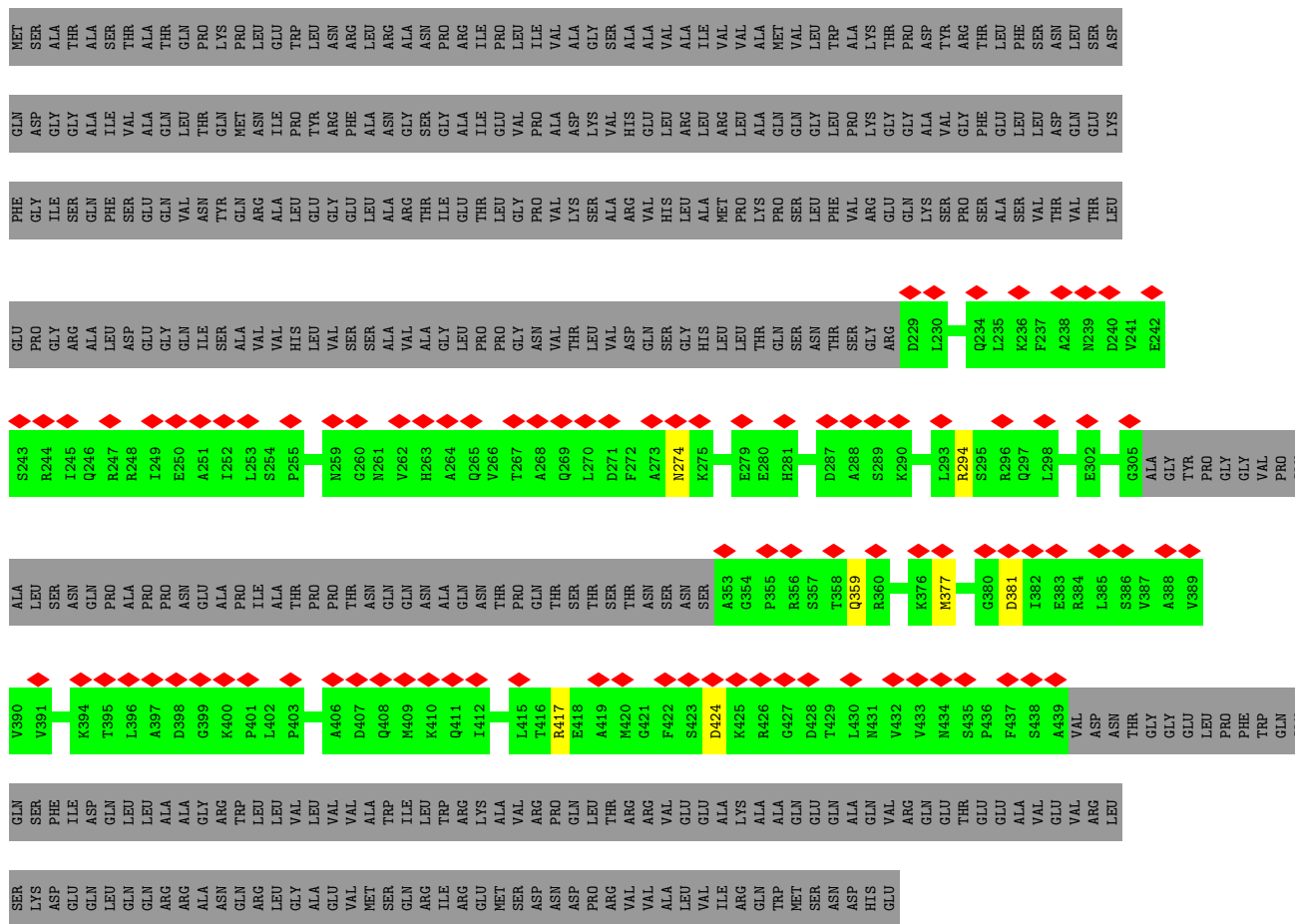
- Molecule 6: Flagellar M-ring protein



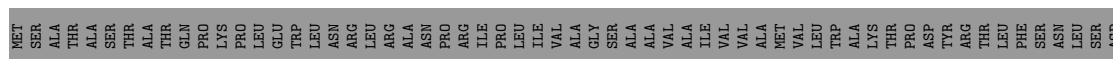
Protein ID	Amino Acid Count (approx.)
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R247	10
R248	10
I249	10
I252	10
I256	10
N259	10
A264	10
Q265	10
V266	10
T267	10
A268	10
Q269	10
L270	10
D271	10
F272	10
A273	10
N274	10
E279	10
E280	10
H281	10
S289	10
R294	10
S295	10
Q296	10
Q297	10
L298	10
E302	10
G305	10
ALA	10
TYR	10
PRO	10
GLY	10
VAL	10
PRO	10
GLY	10
ALA	10
LEU	10
SER	10
ASN	10
GLN	10
PRO	10
ALA	10
PRO	10
ASN	10
GLU	10
ALA	10
PRO	10



- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein





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

- Molecule 6: Flagellar M-ring protein



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

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

GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	ALA	GLY	LEU	PRO	PRO	GLY	ASN	GLY	THR	LEU	VAL	ASP	GLN	SER	SER	ASN	THR	SER	GLY	ARG	D229	L230	A233	Q234	L235	K236	F237	A238	N239	D240	WT44
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E242	E243	R244	R245	R246	R247	A251	L252	L253	S254	P255	T256	N259	G260	M261	V262	H263	A264	Q265	V266	T267	A268	Q269	L270	L271	D272	A273	N274	K275	E279	S283	D287	A288	S289	R290	A291	R294	L298	N299	I300	S301	E302	Q303	Q304	V304	G305	ALA	GLY	TYR	PRO	GLY	GLY	VAL	PRO
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[illegible]

R384	L385	A386	V389	Y393	K394	T395	L396	A397	D398	G399	K400	P401	L402	P403	L404	T405	A406	D407	K408	M409	K410	Q411	L412	F413	D414	L415	T416	R417	E418	A419	M420	D424	K425	D426	T429	L430	M431	V432	V433	M434	VAL	ASP	ASN	THR	GLY	GLU	LEU	PRO	PHE	PER
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GLN GLN GLN SER PHE ILE ASP GLN GLN LEU LEU ALA ALA GLY ARG TRP TRP LEU LEU VAL VAL VAL VAL VAL VAL ILE LEU TRP ARG ARG LYS LEU LEU THR ARG ARG VAL VAL GLU GLU ALA ALA LYS ALA ALA GLN GLN ALA GLN VAL ARG ARG GLN GLN THR GLU GLU VAL VAL VAL

ARG	LEU	SER	LYS	ASP	GLU	GLN	LEU	GLN	GLN	ARG	ARG	ALA	ASN	GLN	ARG	LEU	GLY	ALA	ALA	GLU	VAL	MET	SER	GLN	ARG	ILE	ARG	GLU	MET	ASP	ASN	ASP	PRO	ARG	VAL	VAL	ALA	LEU	VAL	ILE	ARG	GLN	TRP	MET	SER	ASN	ASP	GLU
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- Molecule 6: Flagellar M-ring protein

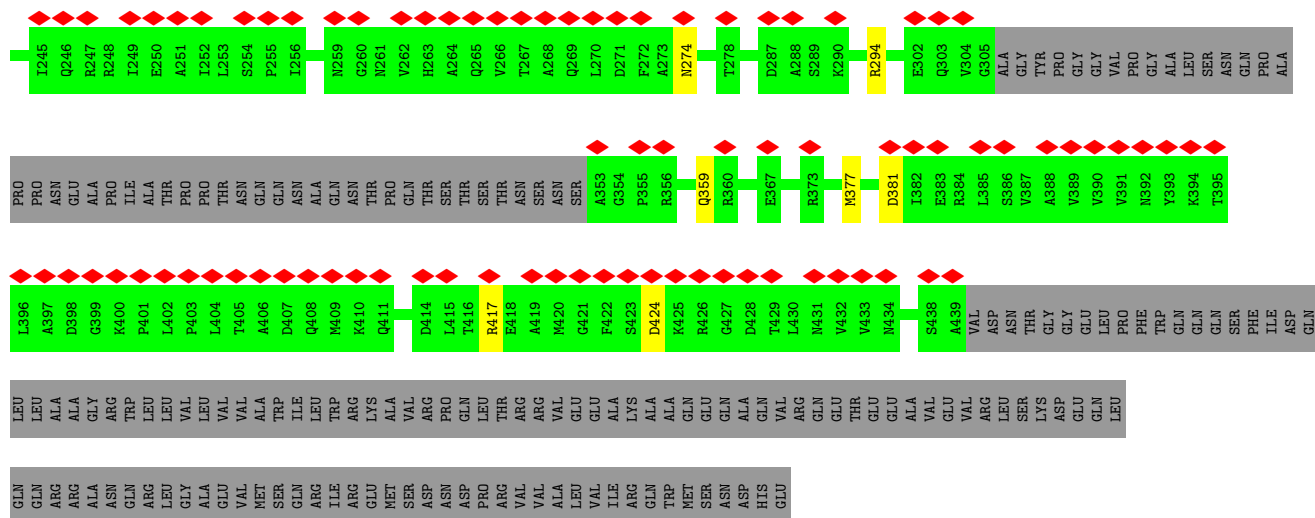


MET	SER	ALA	THR	THR	PRO	LYS	LEU	GLU	TRP	ASN	ARG	LEU	ARG	ALA	ASN	PRO	ARG	ILE	PRO	PRO	LEU	ILE	VAL	GLY	ALA	SER	ALA	ALA	VAL	VAL	ALA	ALA	ILE	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	SER
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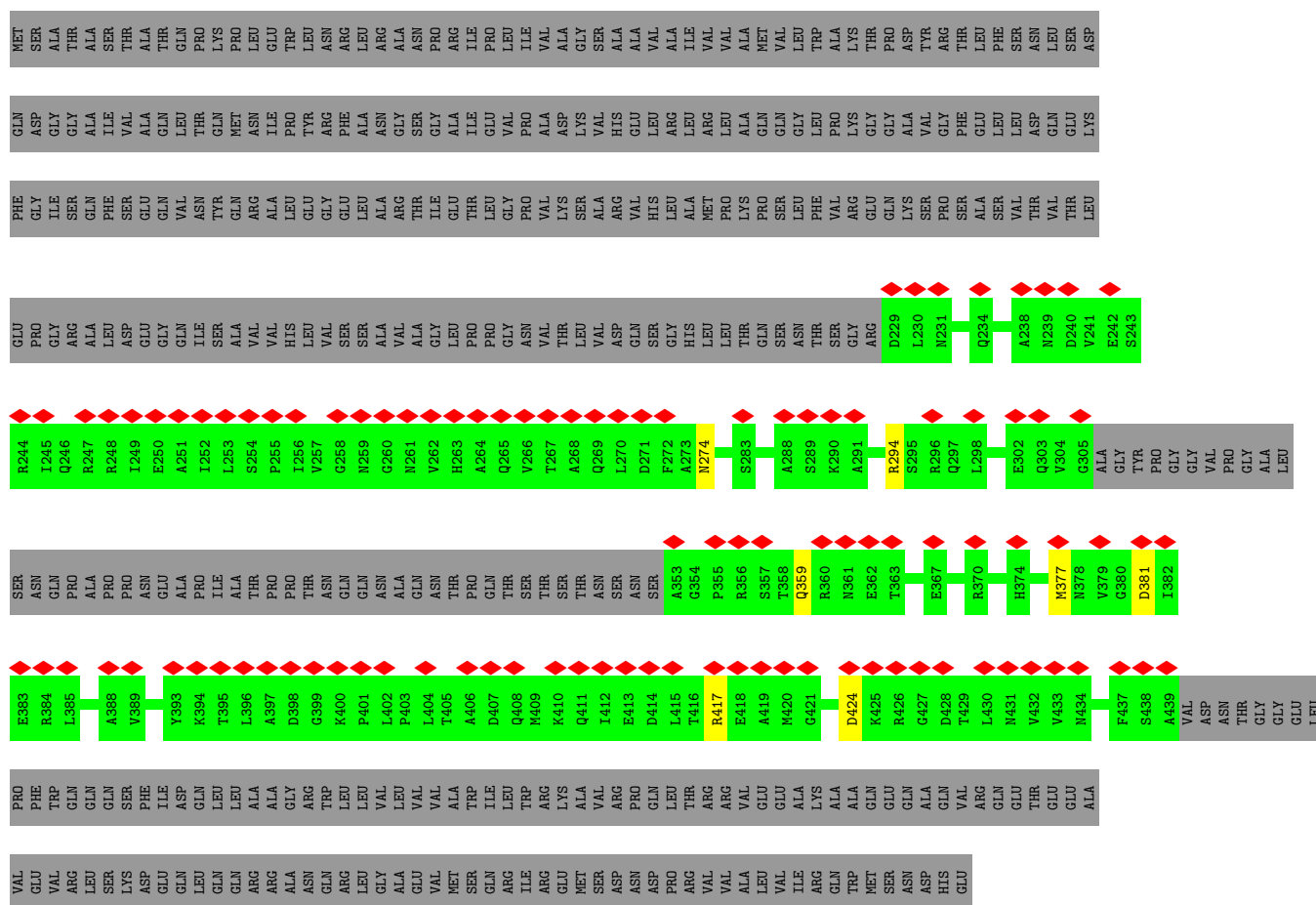
GLN ASP GLY GLY ILE VAL ALA ALA ALA LEU THR GLN MET ASN ILE PRO TYR ARG ARG PHE ALA ALA ASN GLY SER GLY ALA ILE GLU VAL VAL PRO PRO ALA ASP LYS VAL VAL HIS HIS LEU LEU LEU LEU LEU GLN GLN GLY GLY LEU VAL VAL LYS LYS GLY GLY GLY GLY LEU LEU LEU LEU LEU ASP ASP GLN GLN LYS

[illegible]

GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	SER	VAL	ALA	VAL	VAL	HIS	LEU	SER	SER	ALA	VAL	GLY	GLN	THR	LEU	VAL	ASP	GLN	SER	GLY	HIS	LEU	THR	GLN	SER	ASN	THR	LEU	VAL	VAL	PRO	GLY	ASN	GLY	HIS	LEU	THR	THR	SER	GLY	ARG	D229	D230	N231	D232	A233	K236	F237	A238	V241	F242
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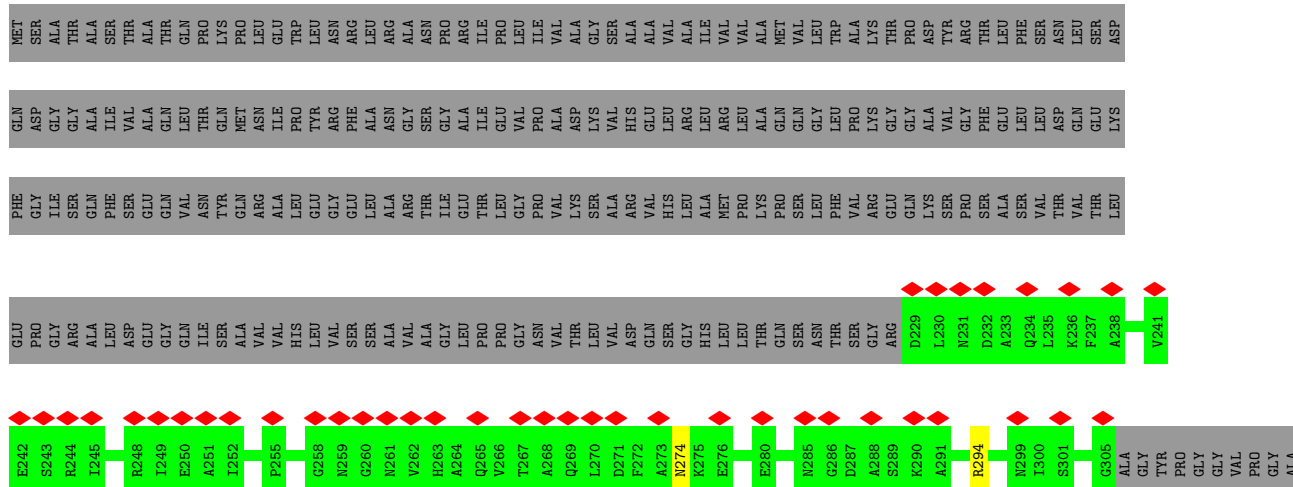


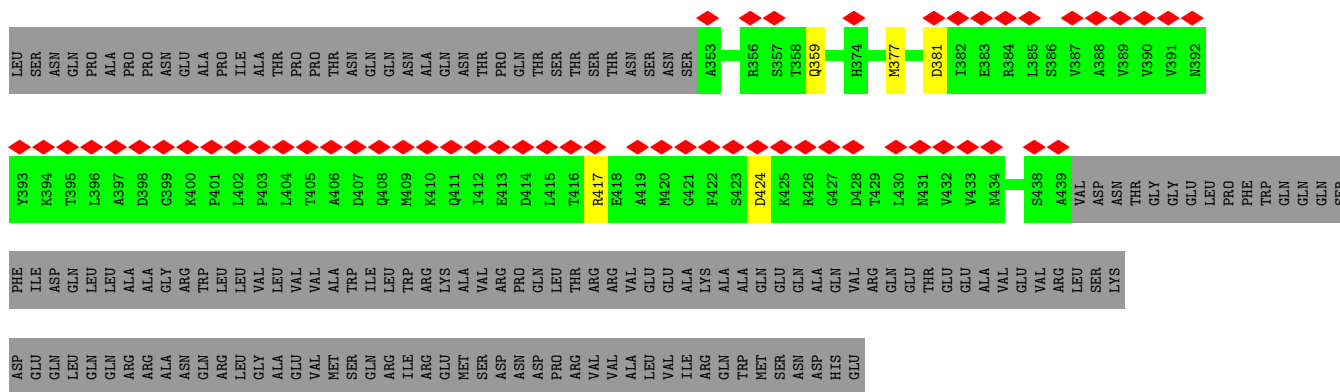
• Molecule 6: Flagellar M-ring protein



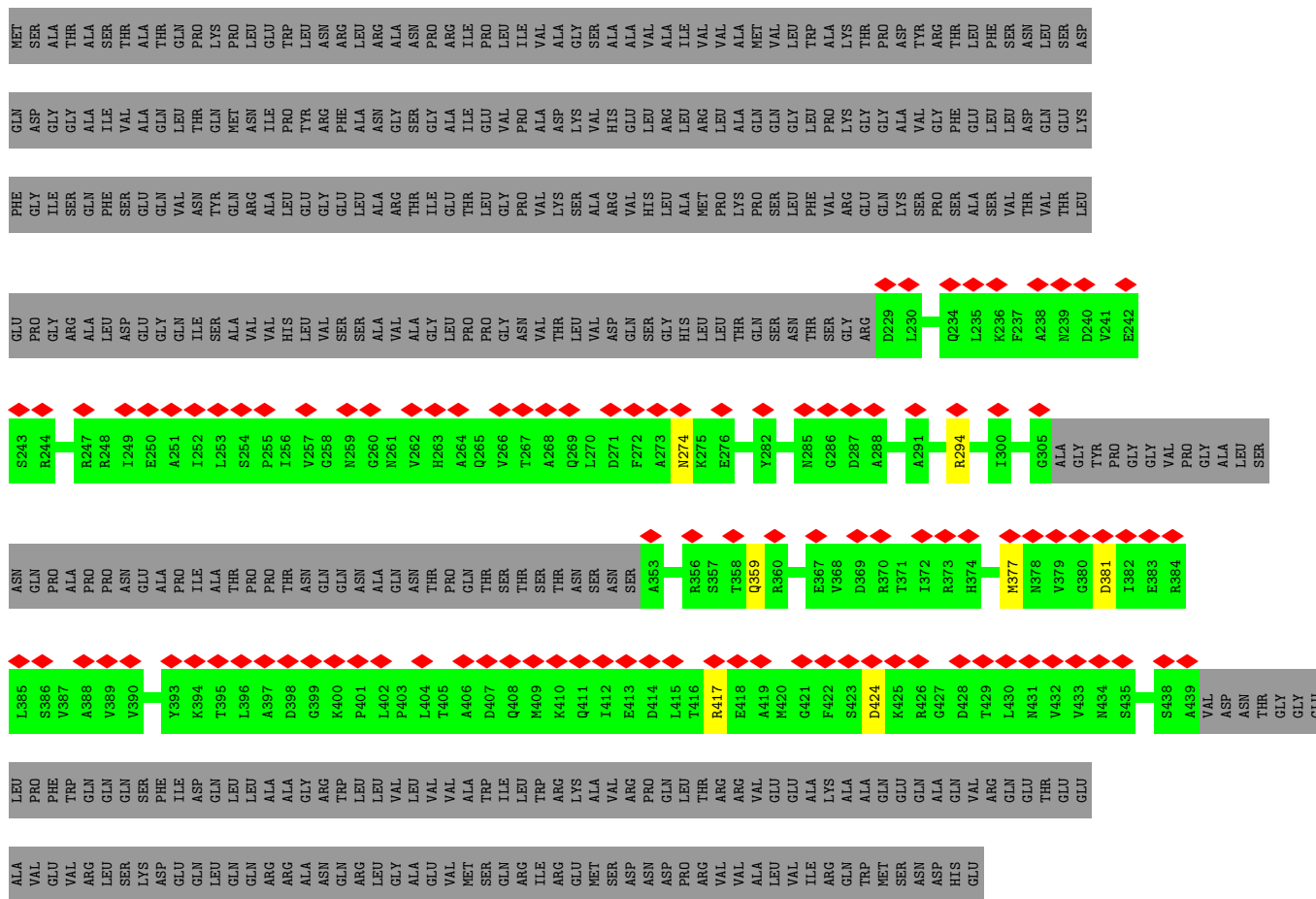
• Molecule 6: Flagellar M-ring protein



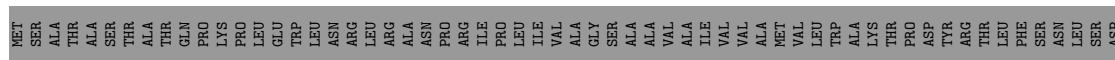


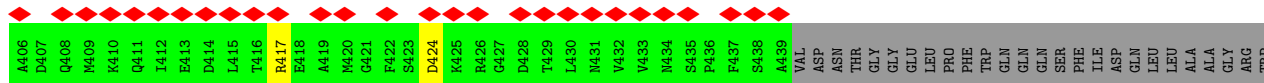


- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein





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

- Molecule 6: Flagellar M-ring protein



NET	SER	ALA	THR	ALA	SER	THR	ALA	THR	GLN	PRO	PRO	LYS	PRO	LEU	GLU	TRP	LEU	ASN	ARG	ARG	LEU	ARG	ALA	ALA	ASN	PRO	ARG	ILE	ILE	VAL	ALA	GLY	SER	ALA	ALA	ALA	VAL	VAL	ALA	ILE	VAL	VAL	VAL	VAL	MET	VAL	VAL	LEU	TRP	ALA	ALA	LYS	THR	PRO	ASP	SER	ASN	LEU	LEU	SER	ARG	THR	LEU	PHE	SER	ASN	LEU	LEU	SER	ARG
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- Molecule 6: Flagellar M-ring protein

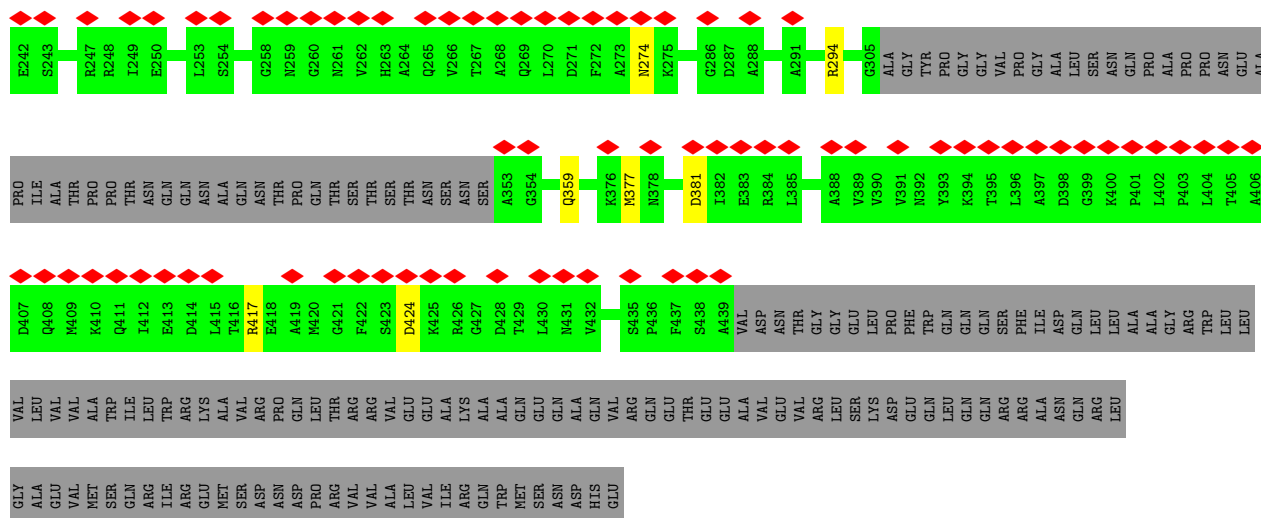


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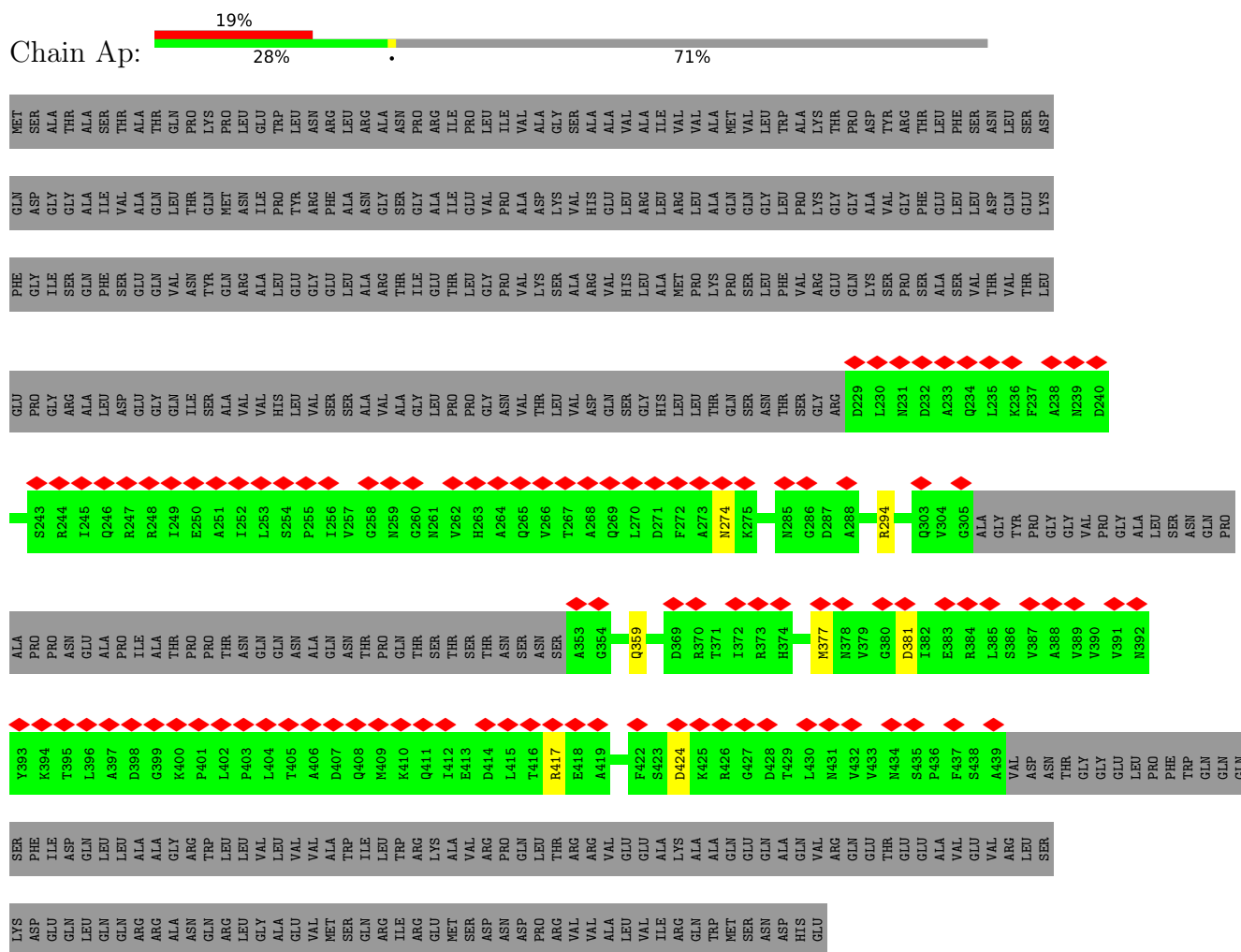
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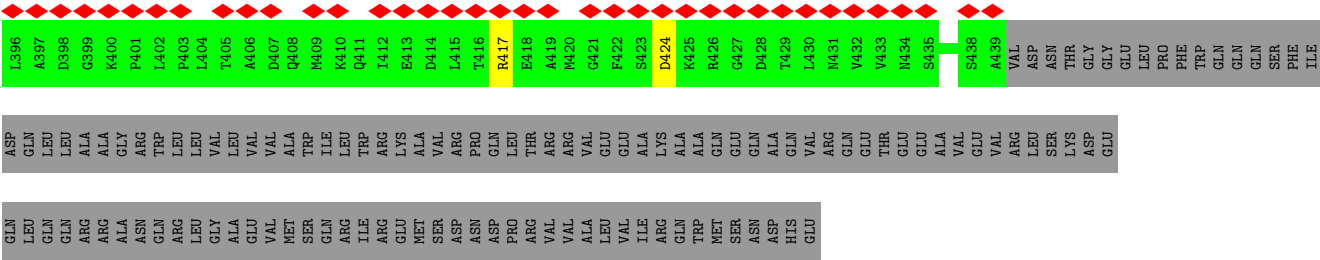


• Molecule 6: Flagellar M-ring protein

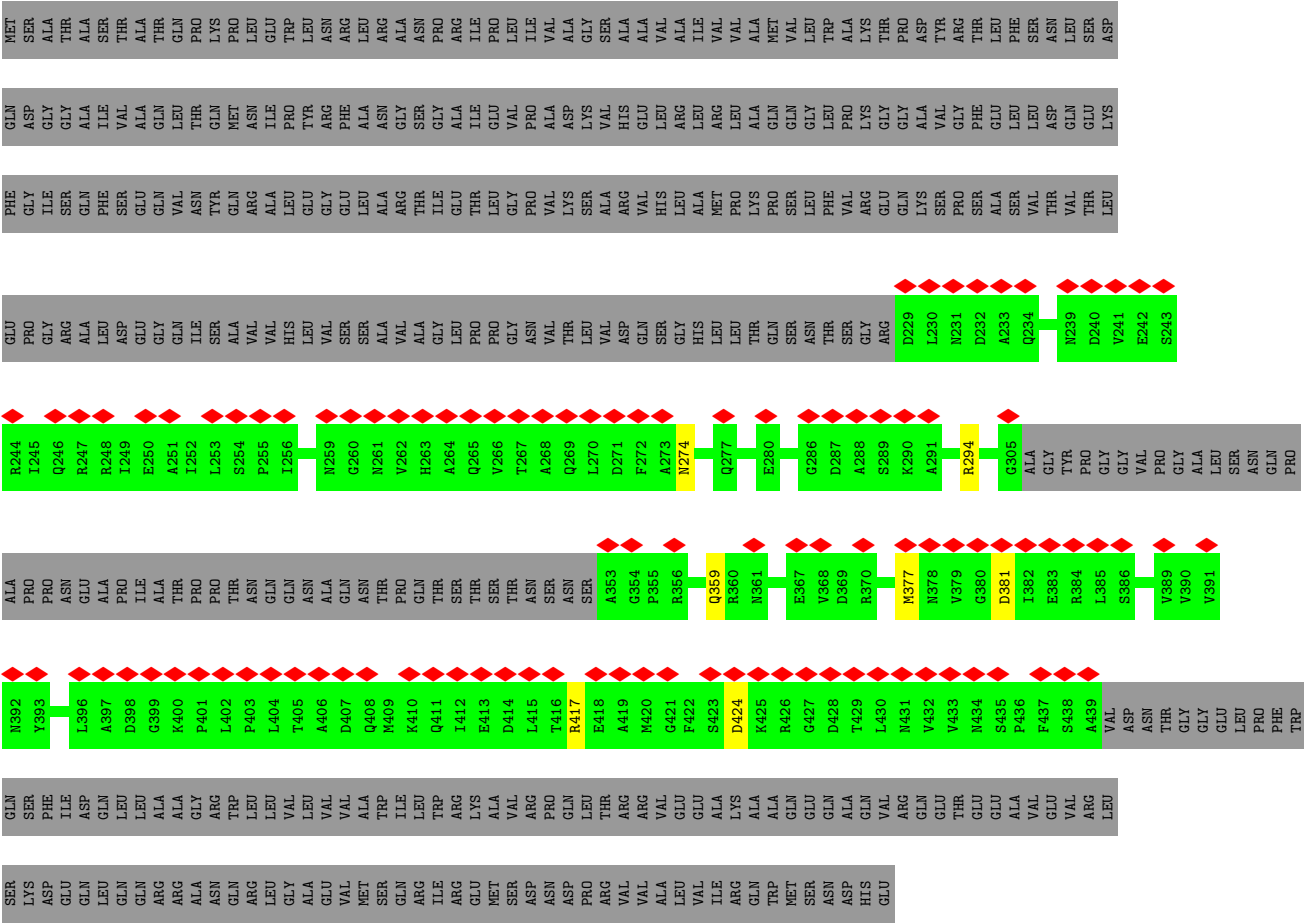


• Molecule 6: Flagellar M-ring protein

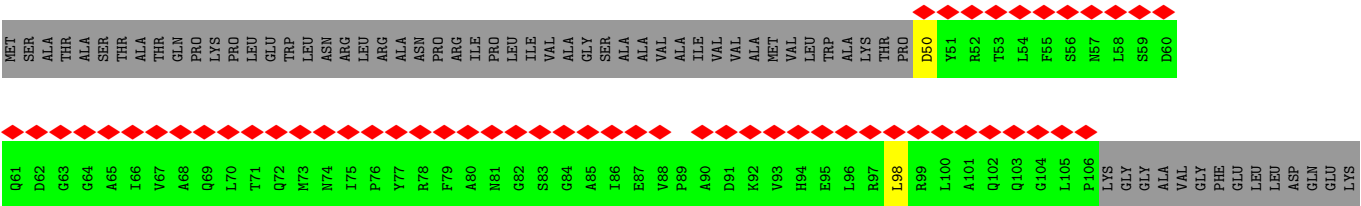




• Molecule 6: Flagellar M-ring protein

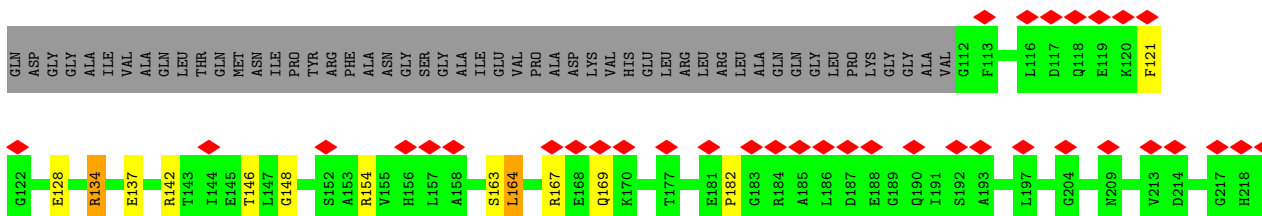
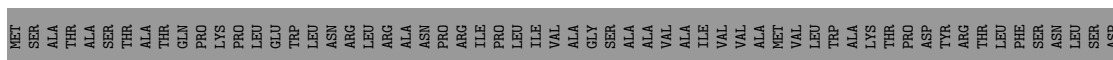
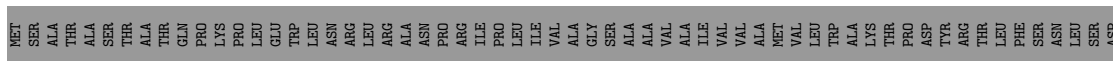


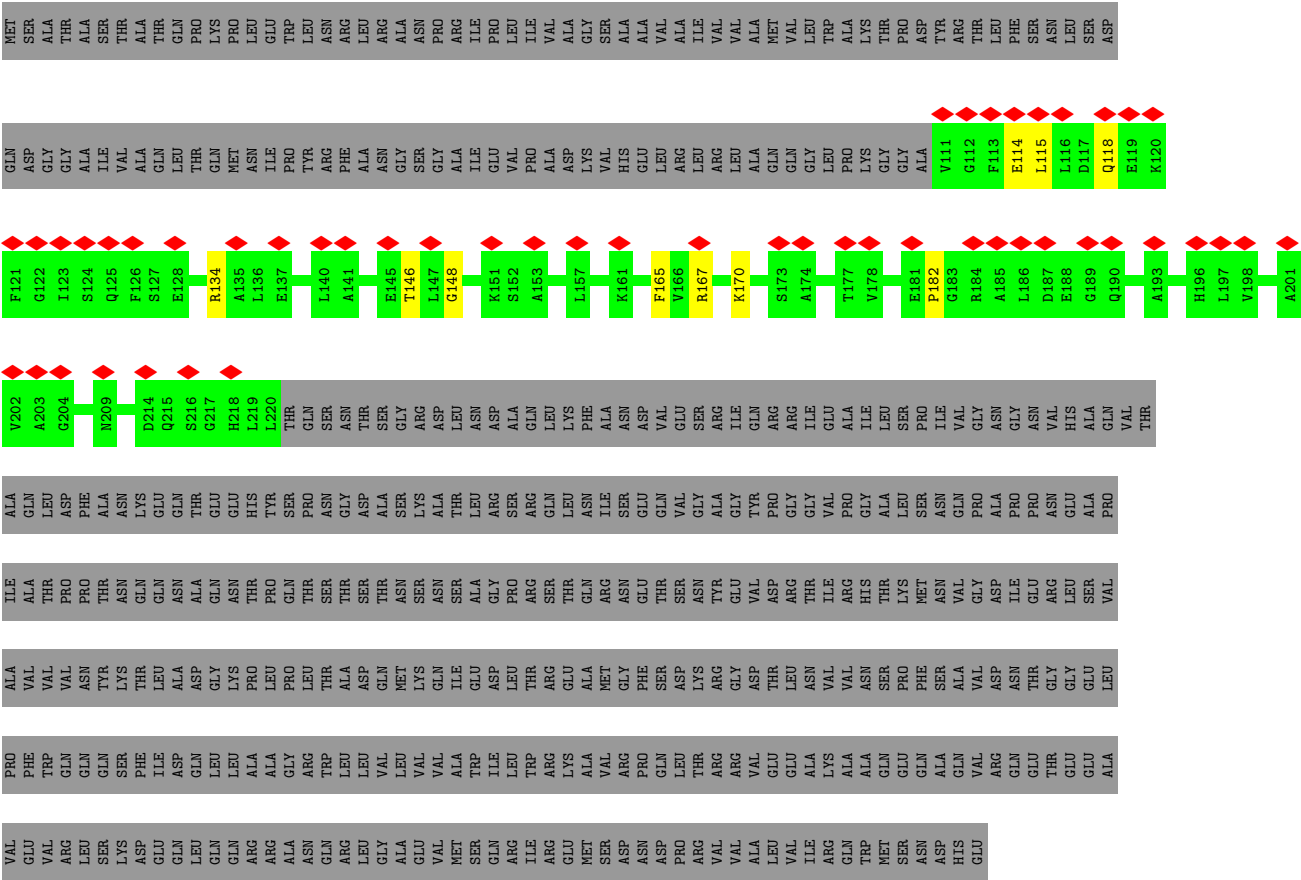
• Molecule 6: Flagellar M-ring protein



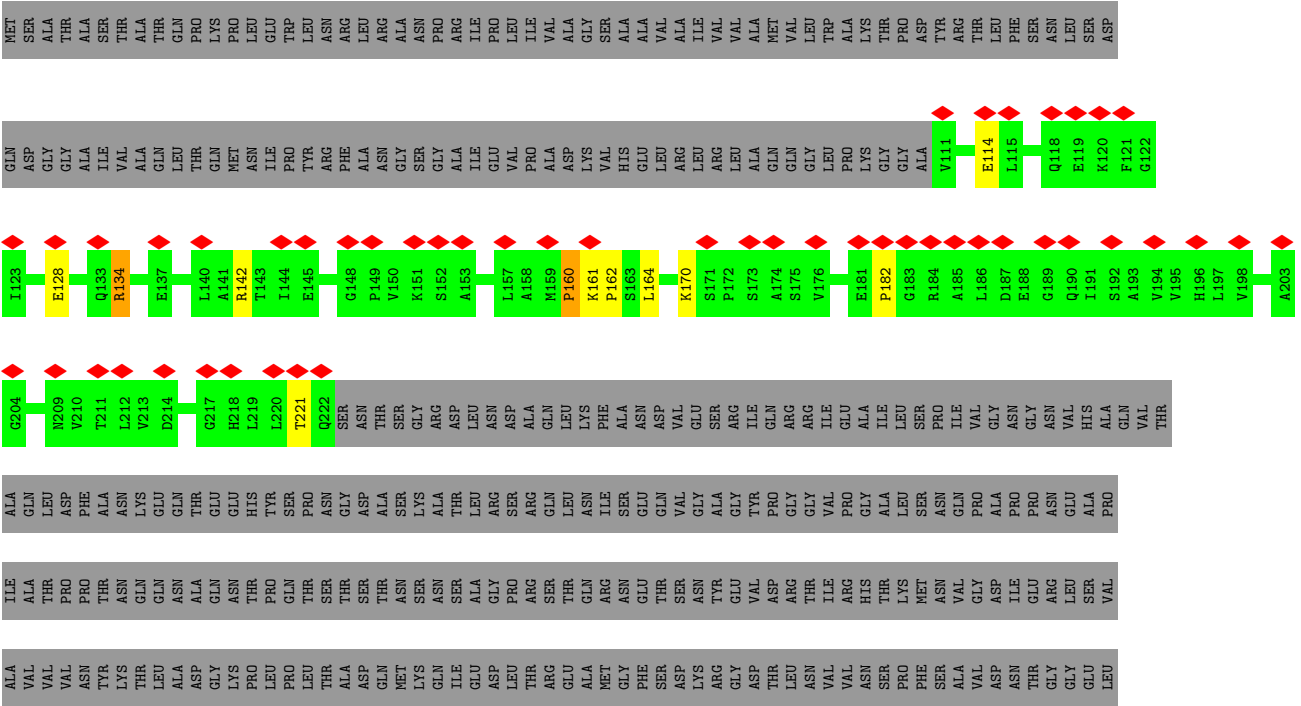
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- Molecule 6: Flagellar M-ring protein





● Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein



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GLN	ASP	GLY	GLY	ALA	ILE	VAL	ALA	GLN	LEU	THR	GLN	MET	ASN	ILE	PRO	TYR	ARG	PHE	ALA	ASN	GLY	SER	GLY	ALA	ILE	GLU	VAL	PRO	ALA	ASP	LYS	VAL	HIS	GLU	LEU	ARG	LEU	ARG	LEU	ALA	GLN	GLY	LEU	PRO	LYS	GLY	ALA	GLN	V111	G112	E114	L115	L116	D117	Q118	E119	V120
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S200	A201	A202	A203	G204	L205	P206	P207	G208	N209	V210	T211	L212	V213	D214	H218	L219	L220	T221	GLN	SER	ASN	THR	SER	GLY	ARG	ASP	LEU	ASN	ASP	ALA	ALA	GLN	LEU	LYS	PHE	ASP	ASN	ASN	ASP	ASP	VAL	GLU	SER	SER	ARG	ILE	ILE	GLN	ARG	ARG	ILE	GLU	ALA	ALA	ILE	LEU	SER	PRO	ILE	VAL	GLY	ASN	GLY
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- Molecule 6: Flagellar M-ring protein

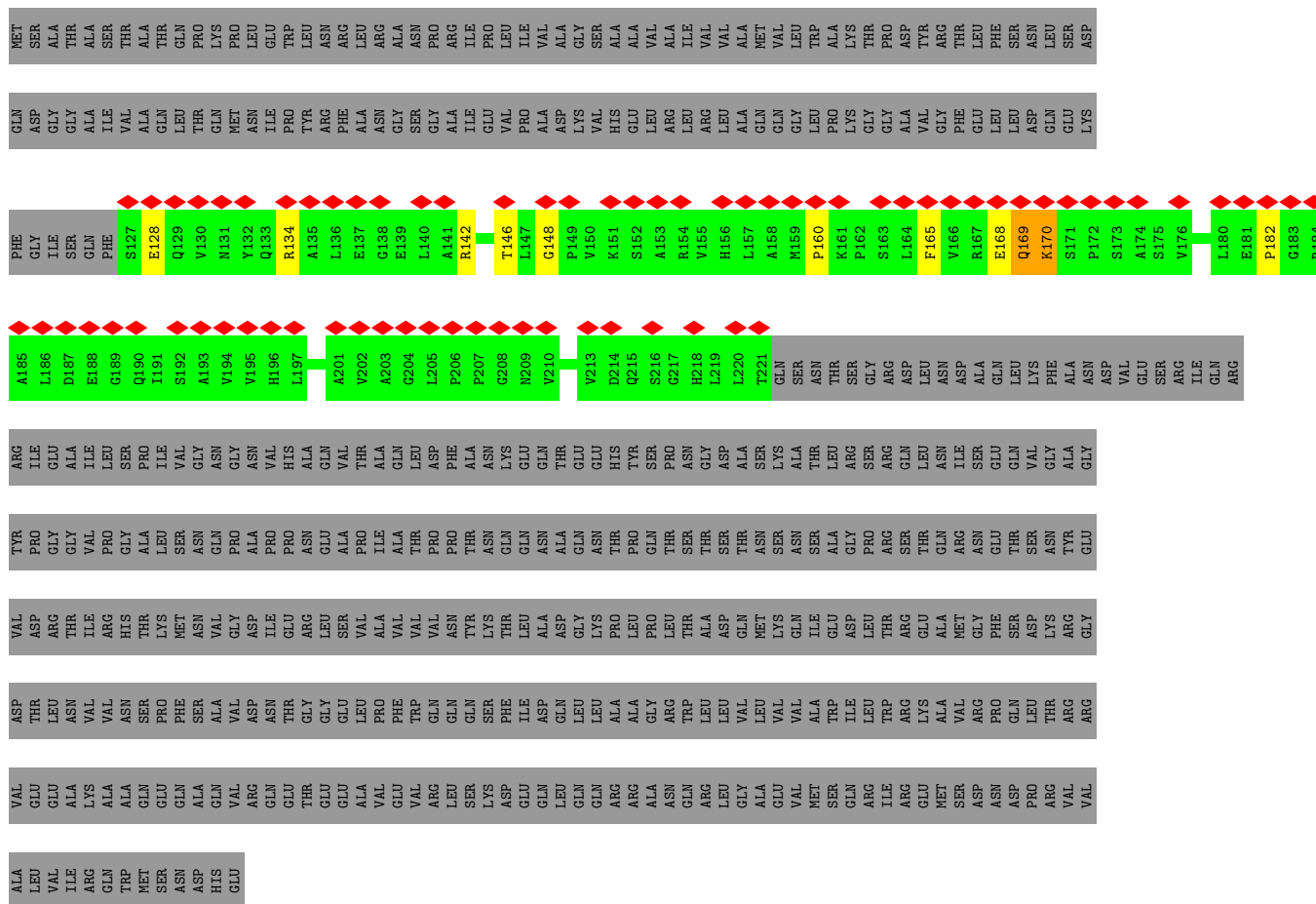


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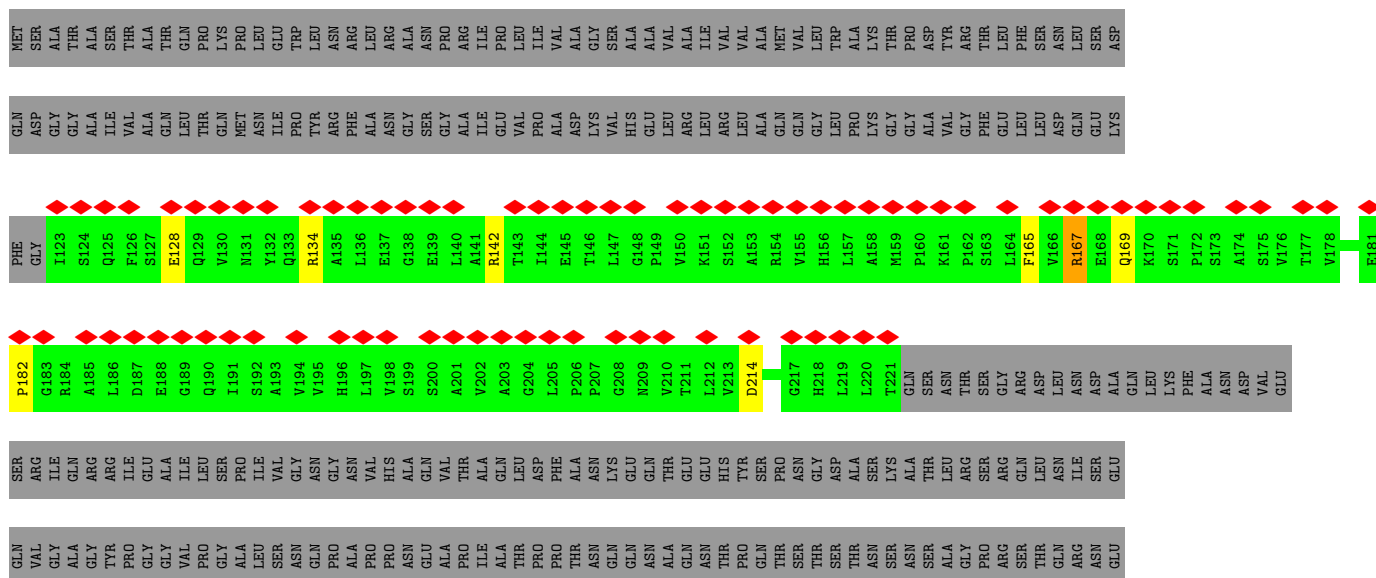
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- Molecule 6: Flagellar M-ring protein



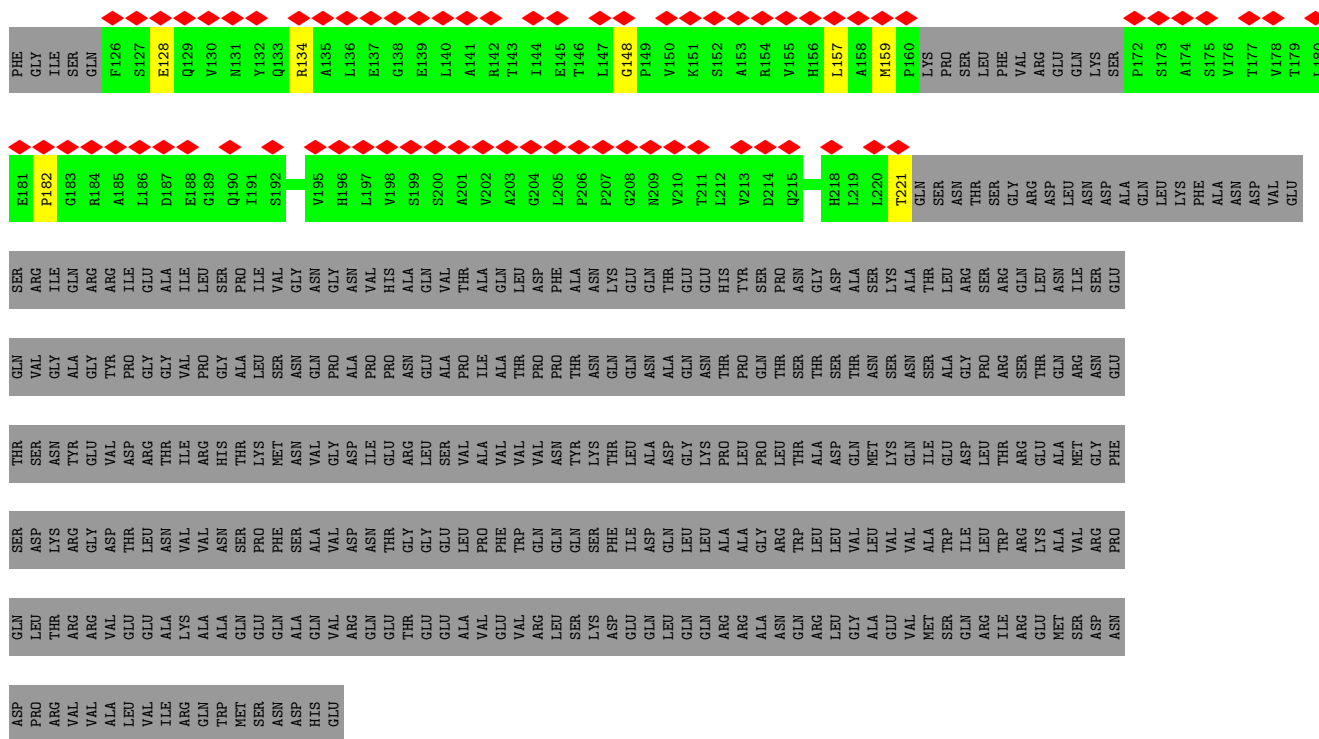
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- Molecule 6: Flagellar M-ring protein

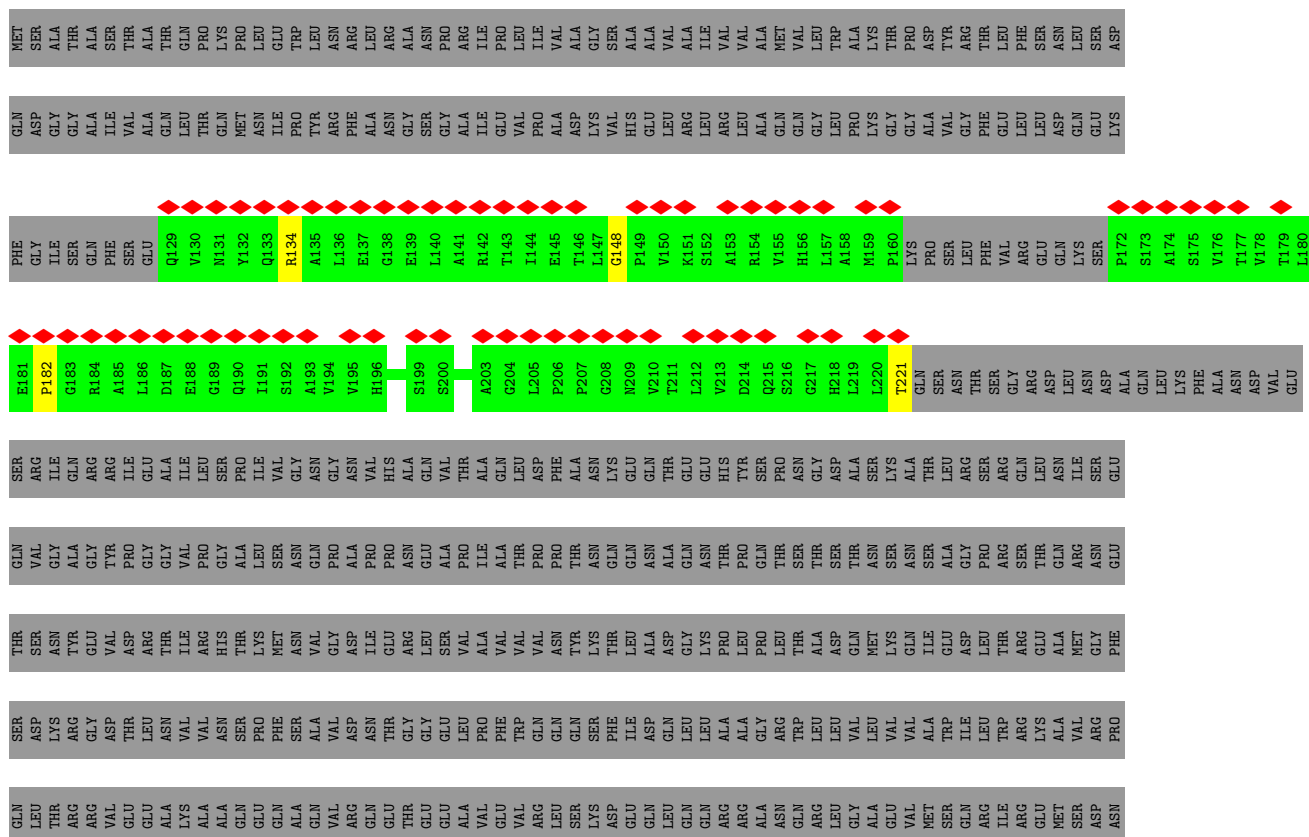
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- Molecule 6: Flagellar M-ring protein

[illegible]



- Molecule 6: Flagellar M-ring protein



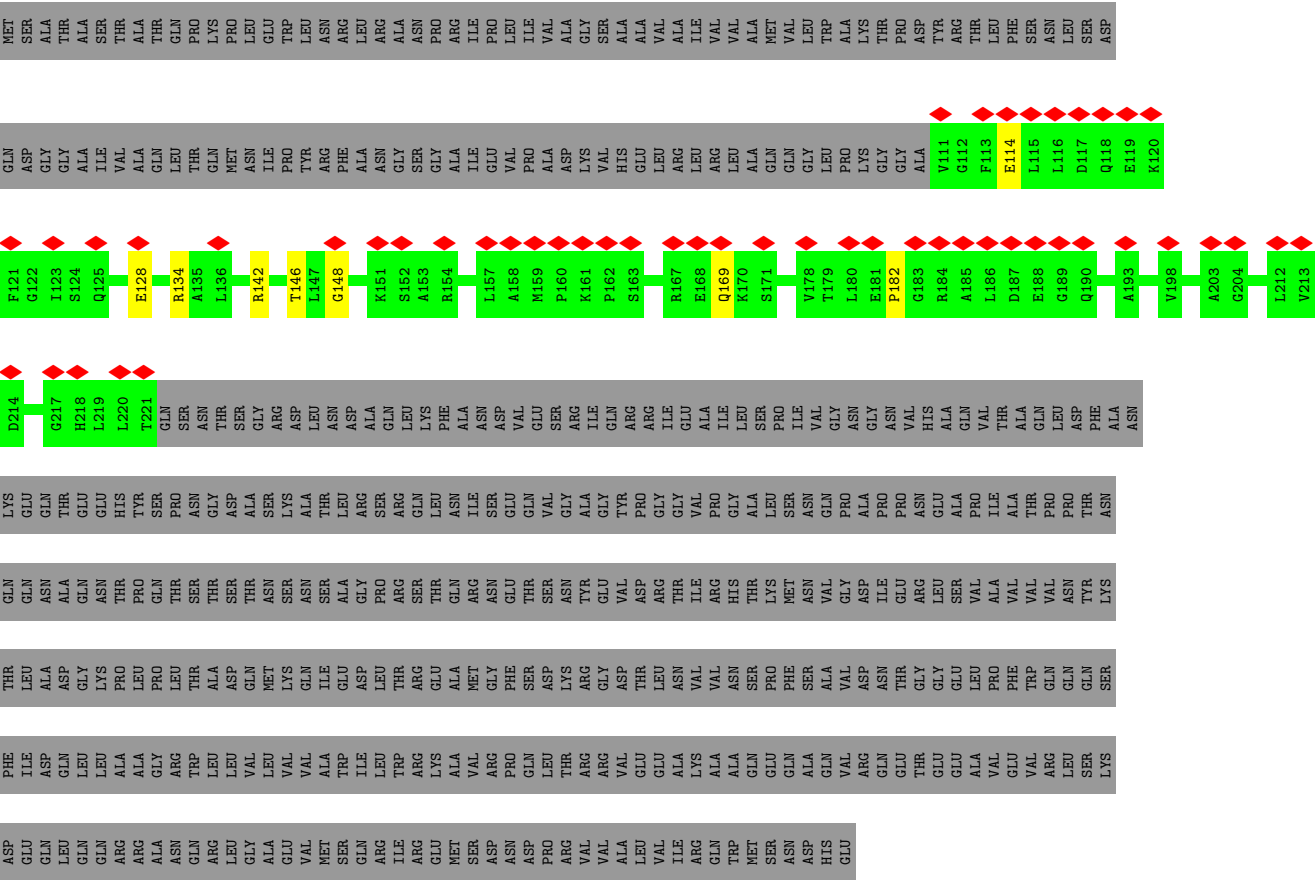
- Molecule 6: Flagellar M-ring protein



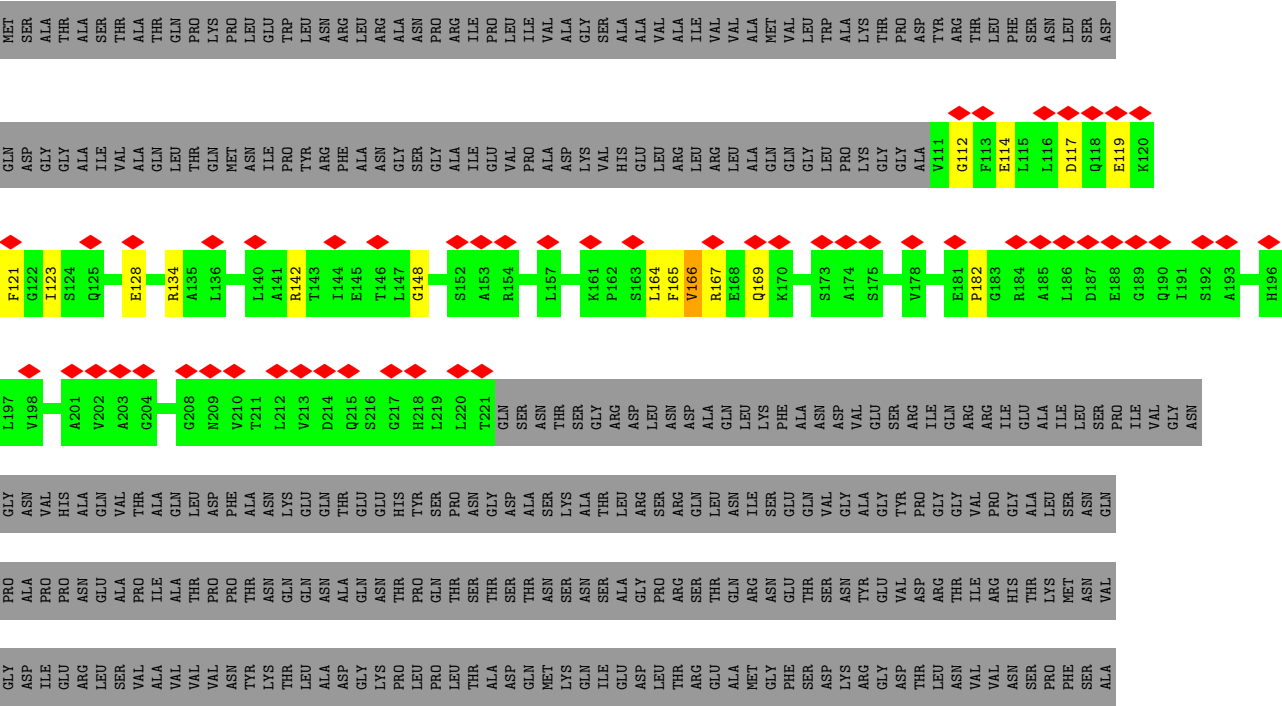
GLU	VAL	VAL	GLY	PRO	GLY	H196 L197	PHE G122 I123 E128 R134 G138 E139 L140 A141 R142 E145 L146 T147 G148 P149 V150 K151 S152 A153 R154 L157 A158 M159 P160 K161 L164 F165 V166 Q169 K170 S173 A174 S175 V176 T177 V178 T179 L180 E181 P182 G183 R184 A185 L186	GLN	MET
ARG	ASP	ASP	ASN	ALA	ASN	L197	G122	ASP	SER
GLN	ASN	ILE	ASN	PRO	VAL		I123	GLY	ALA
THR	THR	GLU	GLY	ASN	ALA	A201	E128	ALA	SER
GLU	GLY	LEU	SER	GLN	VAL	V202	R134	VAL	THR
GLU	VAL	VAL	VAL	ALA	THR	A203		ALA	
ALA	VAL	VAL	VAL	PRO	ALA	G204		GLN	GLN
VAL	PHE	VAL	VAL	ILE	ALA	L205		ALA	PRO
VAL	TRP	VAL	VAL	THR	LEU	N209		THR	LYS
ARG	GLN	GLN	ASN	PRO	ASP	V210		GLN	PRO
LEU	GLN	GLN	THR	THR	PHE	T211		MET	LEU
SER	LYS	SER	LYS	ASN	ALA	L212		ILE	LEU
ASP	PHE	THR	THR	GLN	GLY	V213		PRO	TRP
GLU	ILE	LEU	LEU	GLN	GLN	L214		TYR	LEU
GLN	ASP	ALA	ALA	ASN	GLN	D214		ARG	ASN
LEU	GLN	GLY	GLY	GLN	THR	Q215		ALA	ARG
GLN	LEU	LYS	LYS	ASN	GLU	S216		LEU	LEU
ARG	ALA	ALA	PRO	THR	THR	G217		ALA	ASN
ALA	LEU	LEU	GLN	PRO	GLN	TYR		ALA	ASN
GLY	GLY	GLY	PRO	ALA	SER	H218		GLY	PRO
ASN	ARG	ARG	LEU	THR	SER	L219		ALA	ARG
GLN	TRP	TRP	THR	THR	ASN	L220		GLU	ILE
LEU	LEU	LEU	ALA	THR	GLY	T221		VAL	ILE
GLY	VAL	VAL	GLN	THR	ASP	GLN		GLN	LEU
ALA	LEU	LEU	MET	ASN	ALA	SER		PRO	ILE
GLU	VAL	VAL	LYS	ASN	SER	THR		ALA	VAL
VAL	VAL	VAL	GLN	ASN	LYS	THR		ASP	ALA
VAL	VAL	ILE	ILE	SER	THR	GLY		VAL	GLY
SER	TRP	ILE	ASP	ALA	LEU	ARG		HIS	SER
GLN	ILE	LEU	LEU	GLY	ARG	ASP		GLU	ALA
ARG	TRP	TRP	THR	PRO	SER	LEU		LEU	VAL
ILE	TRP	ARG	THR	ARG	ASN	ASN		ARG	VAL
GLU	LYS	GLU	ARG	SER	GLN	ASP		ALA	MET
MET	MET	MET	ALA	GLN	ASN	GLN		ALA	VAL
SER	VAL	VAL	MET	ARG	ASN	LYS		ALA	VAL
ASP	ARG	ARG	GLY	ASN	SER	PHE		GLN	MET
ASN	PRO	GLN	SER	THR	GLU	ALA		GLN	VAL
ASN	ASN	ASP	THR	THR	GLN	ALA		GLY	LEU
PRO	THR	LEU	ASP	SER	VAL	ASN		LEU	TRP
ARG	THR	THR	LYS	ASN	GLY	VAL		LYS	LYS
VAL	ARG	ARG	ARG	TYR	ALA	GLU		GLY	THR
VAL	ARG	ARG	GLY	GLU	GLY	TYR		GLY	PRO
ALA	VAL	VAL	ASP	VAL	THR	SER		ARG	ASN
LEU	VAL	GLU	THR	THR	PRO	ILE		GLY	TYR
VAL	VAL	ILE	ALA	THR	GLY	GLN		ARG	THR
ARG	ARG	VAL	VAL	ILE	VAL	ARG		GLU	LEU
GLN	ALA	ALA	VAL	ARG	PRO	ILE		LEU	PHE
TRP	TRP	ALA	ASN	HIS	GLY	ILE		LEU	ASN
ALA	ASN	GLN	ASN	ALA	GLY	THR		LEU	SER
MET	MET	GLN	SER	THR	ALA	GLU		LEU	ASN
SER	GLU	GLU	PRO	THR	LEU	ALA		GLN	LEU
ASN	GLU	GLU	ASN	LYS	SER	ILE		ASN	GLU
ASN	GLN	LYS	PHE	MET	SER	ILE		GLY	THR
ASP	ALA	ALA	SER	VAL	ASN	ARG		GLU	LEU
THR	CTR	CTR	CTR	VAL	CTR	SER		CTR	SER

- Molecule 6: Flagellar M-ring protein





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

● Molecule 6: Flagellar M-ring protein

Chain BG: . 98%

ILE	ARG	ALA	ASN	VAL	THR	SER	GLU	VAL	GLU	PRO	PHE	GLY	ASP	GLN	MET
ARG	GLN	ALA	VAL	VAL	ARG	GLN	GLN	VAL	GLU	GLY	ILE	GLY	ASP	GLY	ALA
TRP	GLN	ALA	ASN	ASN	HIS	VAL	GLY	ARG	VAL	ARG	SER	THR	GLY	THR	ALA
GLN	GLN	GLN	PRO	PRO	LYS	ALA	GLY	GLN	GLN	LEU	PHE	ILE	ILE	SER	ALA
ASN	ASN	GLN	SER	SER	MET	TYR	TYR	ARG	ARG	ASP	GLU	ALA	VAL	ALA	THR
ASP	ASN	ASN	ALA	ALA	ASN	VAL	PRO	ILE	ILE	GLY	GLN	GLN	GLY	GLN	THR
HIS	GLN	VAL	SER	SER	VAL	GLU	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLN
GLU	VAL	VAL	ASP	VAL	GLY	GLN	ALA	ALA	ALA	GLN	VAL	VAL	VAL	LEU	THR
P322	GLN	GLN	ASP	LEU	ASP	GLY	ASN	ALA	ALA	ILE	VAL	HIS	ILE	GLN	PRO
	GLN	ASN	ASN	LEU	ILE	GLY	PRO	GLY	GLY	VAL	VAL	ASN	ASN	GLN	TYR
	GLN	THR	THR	GLY	GLU	ARG	ASN	SER	SER	VAL	VAL	VAL	VAL	ASN	PRO
	GLU	GLU	GLU	GLY	LEU	LEU	ASN	ILE	VAL	PRO	GLY	GLY	GLY	ILE	THR
	GLU	GLU	GLU	GLY	SER	ALA	ALA	VAL	GLY	VAL	GLY	LEU	GLY	THR	LEU
	ALA	VAL	PRO	PRO	VAL	ILE	VAL	VAL	GLY	ASN	SER	GLY	GLY	THR	LEU
	VAL	VAL	TRP	VAL	VAL	THR	ALA	GLY	ASN	ALA	GLY	LEU	GLY	THR	LEU
	ARG	ARG	GLN	GLN	ASN	PRO	PRO	VAL	ASN	ALA	ALA	VAL	VAL	ARG	ALA
	LEU	LEU	GLN	GLN	THR	THR	THR	HIS	HIS	VAL	VAL	ALA	THR	THR	ALA
	SER	SER	LYS	SER	LYS	THR	ASN	ALA	ALA	ALA	GLY	GLY	ILE	GLY	ASN
ASP	ASP	GLU	PHE	ILE	THR	GLN	GLN	VAL	GLN	PRO	THR	THR	ALA	ALA	PRO
GLU	GLN	GLN	ILE	LEU	ALA	ASN	ALA	THR	THR	PRO	PHE	THR	ILE	ILE	ILE
GLN	GLN	GLN	ASP	ALA	ALA	GLN	GLN	GLN	THR	THR	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	ASP	ALA	ASN	ALA	ALA	THR	GLY	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	ASP	ASN	ALA	ASN	GLN	GLY	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	ALA	ALA	GLY	GLN	GLY	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
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LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
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LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
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LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
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LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY	GLY	GLY	GLY
LEU	LEU	LEU	GLN	GLN	GLY	GLN	GLN	GLY	GLN	ASN	GLY	GLY</			

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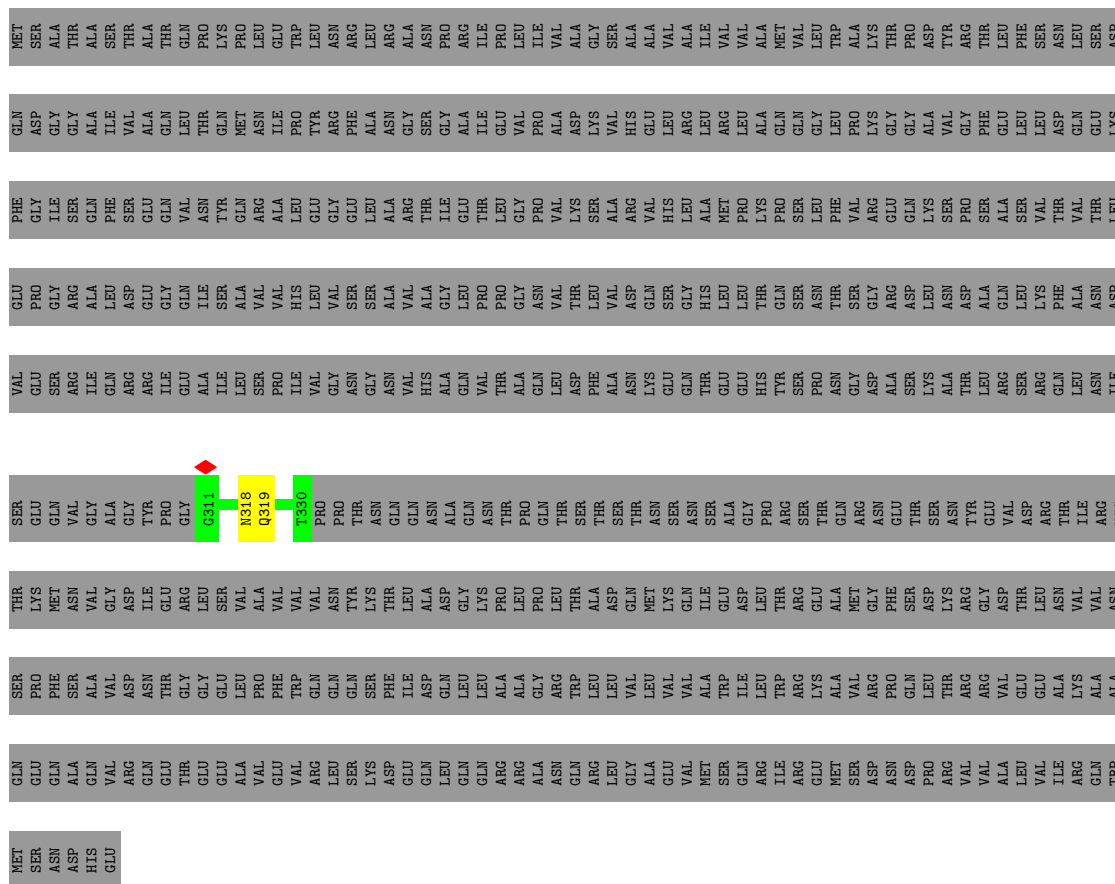
Chain BH: . 97%

MET	SER	GLN	ASP	GLY	PHE	GLU	GLY	ILE	SER	GLY	PRO	VAL	ALA	THR	ALA	THR	ALA	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GL
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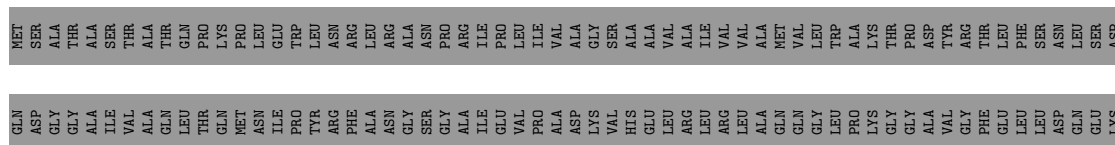
- Molecule 6: Flagellar M-ring protein

Chain BI: 96%



- Molecule 6: Flagellar M-ring protein

Chain BJ: 97%



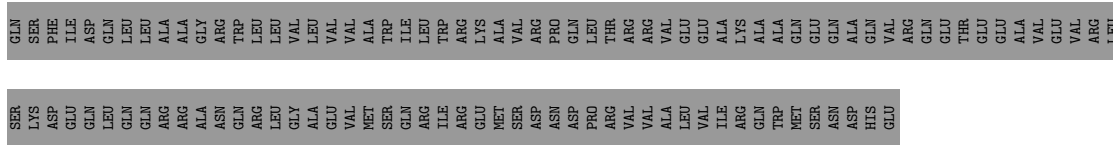
97%

SER
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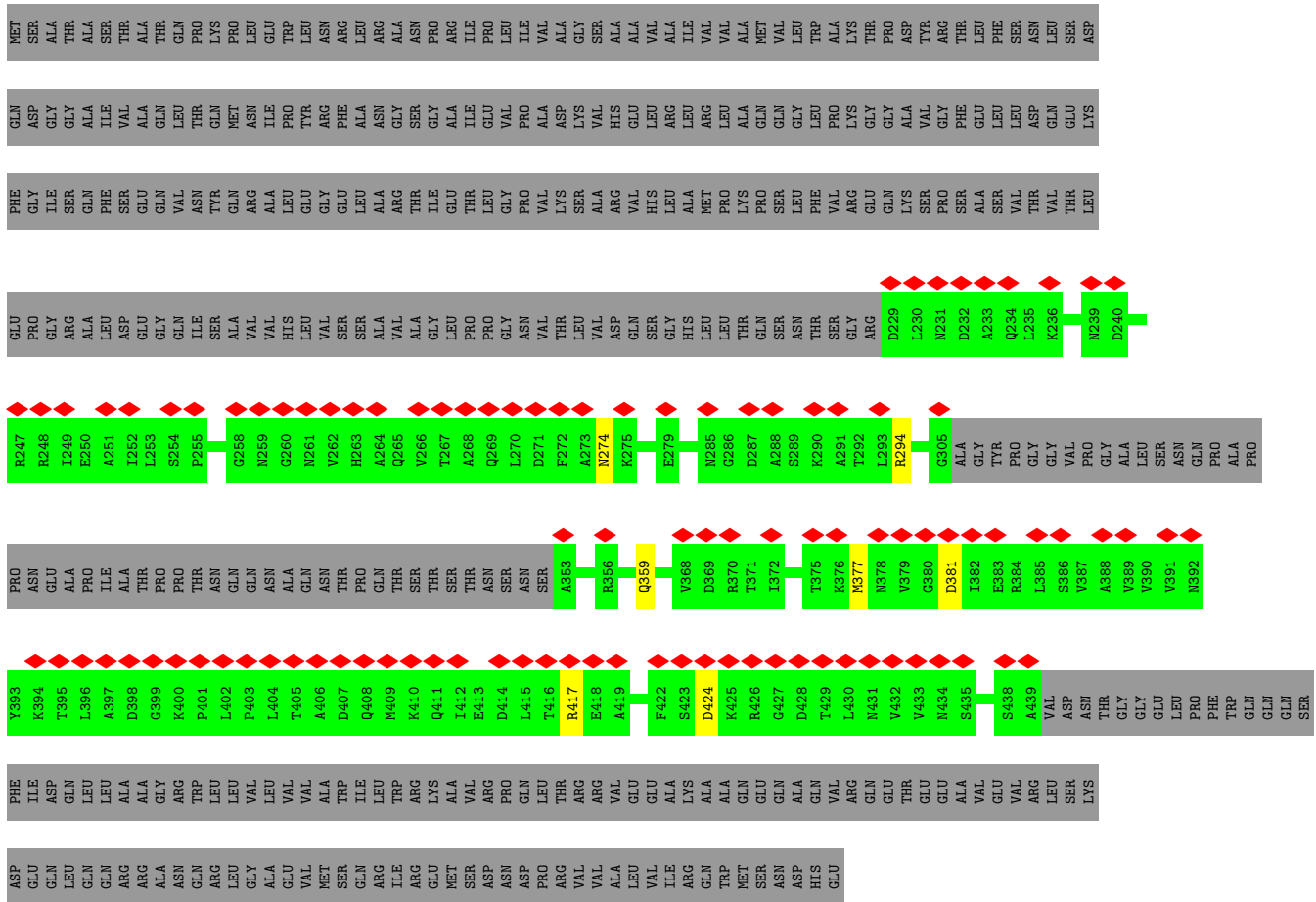
96%

SER	GLU	GLN	VAL	GLY	ALA	GLY	TYR	PRO	GLY	G311	F381	PRO	THR	ASN	GLN	ASN	ALA	GLN	ASN	THR	PRO	GLN	THR	SER	SER	SER	SER	SER	ALA	GLY	PRO	ARG	THR	THR	GLN	ARG	ASN	VAL	ASP	ARG	THR	THR	ILE	ARG	HIS	THR	LYS	THR	MET	ASN
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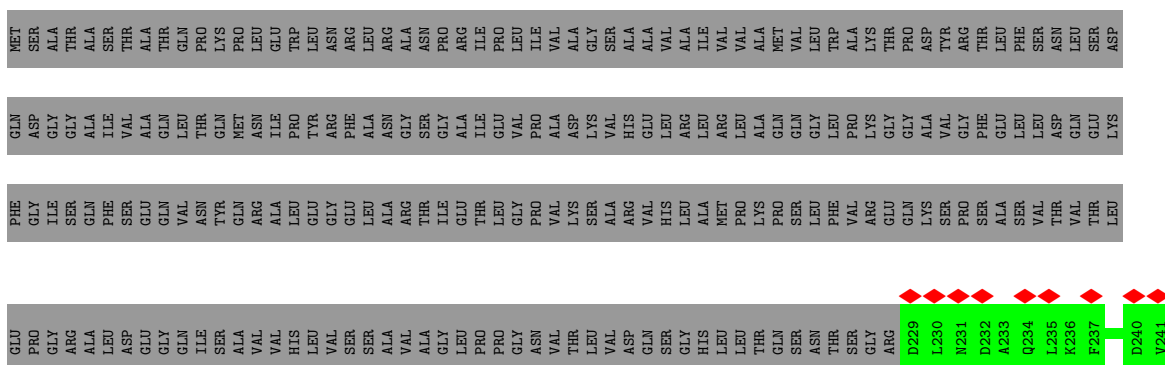




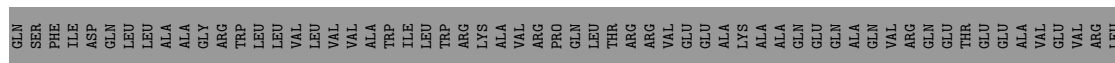
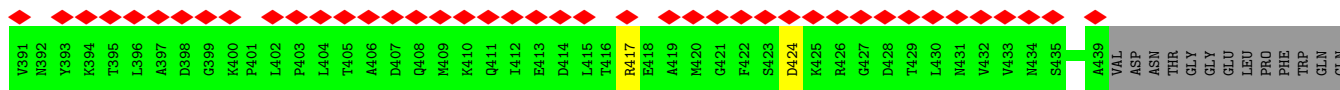
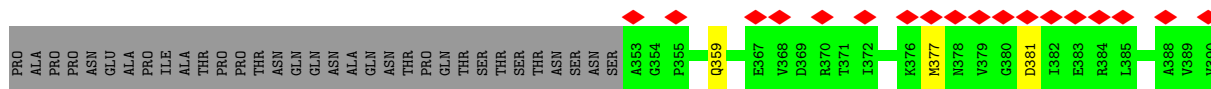
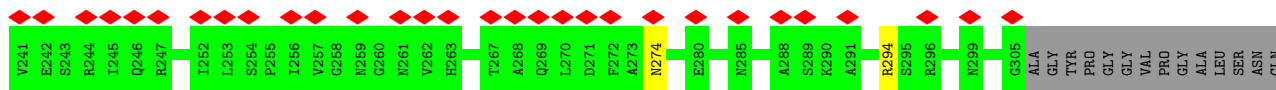
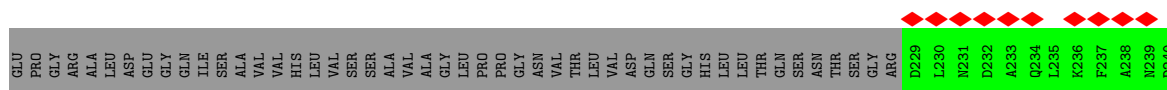
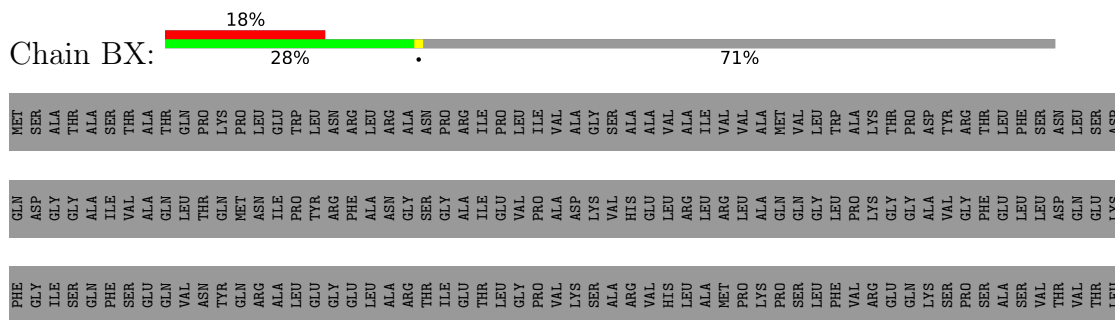
- Molecule 6: Flagellar M-ring protein



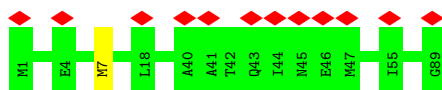
- Molecule 6: Flagellar M-ring protein



- Molecule 6: Flagellar M-ring protein

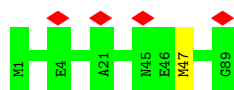


- Molecule 7: Flagellar biosynthetic protein FliQ

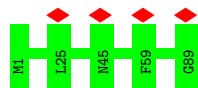
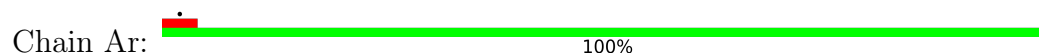


- Molecule 7: Flagellar biosynthetic protein FliQ

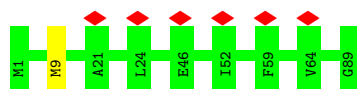




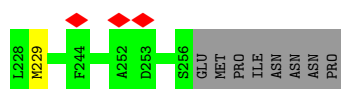
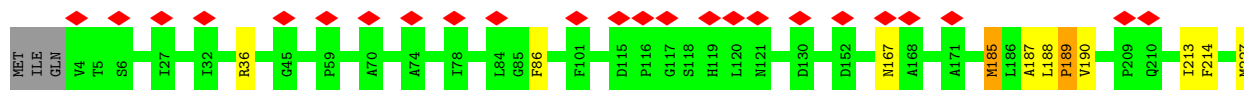
- Molecule 7: Flagellar biosynthetic protein FliQ



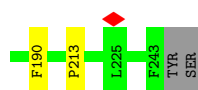
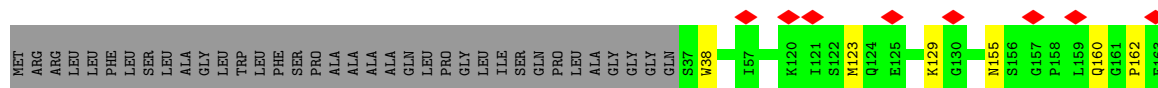
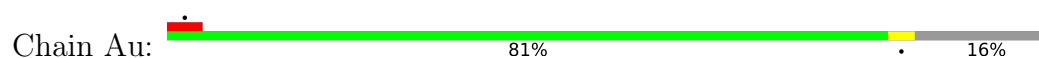
- Molecule 7: Flagellar biosynthetic protein FliQ



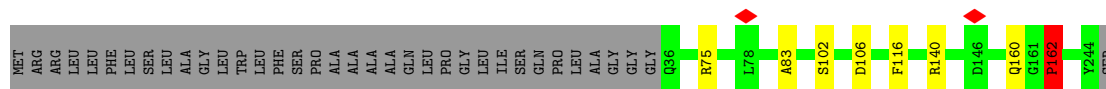
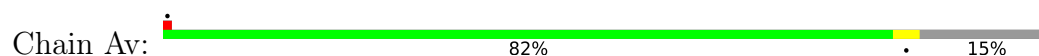
- Molecule 8: Flagellar biosynthetic protein FliR




- Molecule 9: Flagellar biosynthetic protein FliP

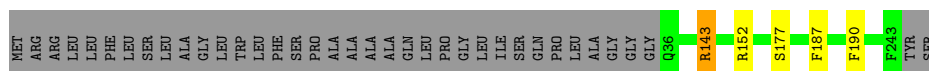


- Molecule 9: Flagellar biosynthetic protein FliP




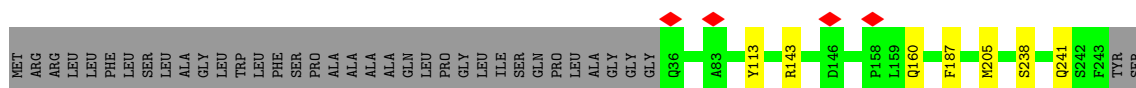
- Molecule 9: Flagellar biosynthetic protein FliP

Chain Aw:  83% 15%




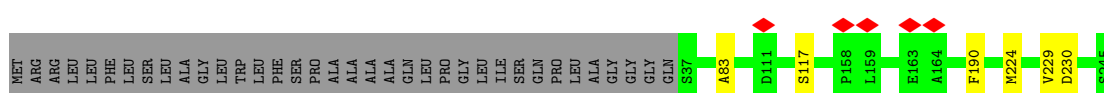
- Molecule 9: Flagellar biosynthetic protein FliP

Chain Ax:  82% 15%



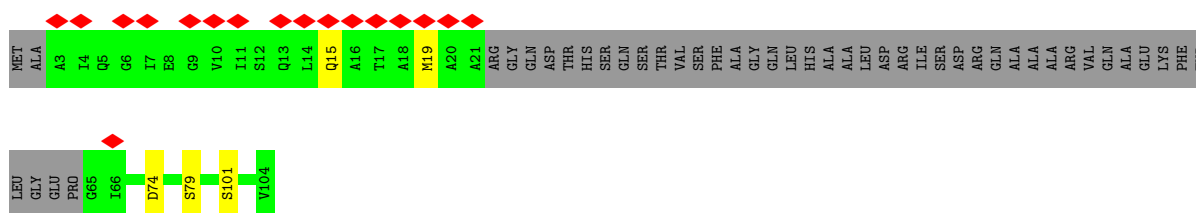
- Molecule 9: Flagellar biosynthetic protein FliP

Chain Ay:  83% 15%




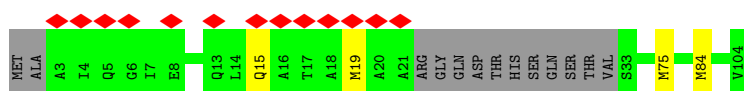
- Molecule 10: Flagellar hook-basal body complex protein FliE

Chain Az:  16% 52% 5% 43%




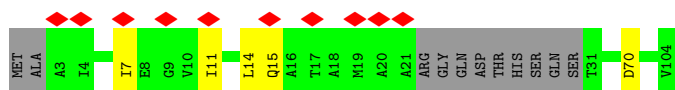
- Molecule 10: Flagellar hook-basal body complex protein FliE

Chain A1:  12% 84% 12%




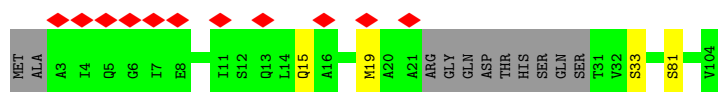
- Molecule 10: Flagellar hook-basal body complex protein FliE

Chain A2:  10% 85% 5% 11%

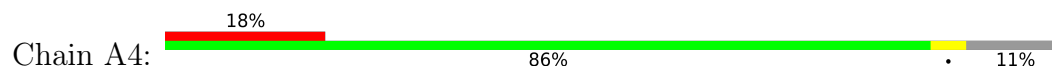


- Molecule 10: Flagellar hook-basal body complex protein FliE

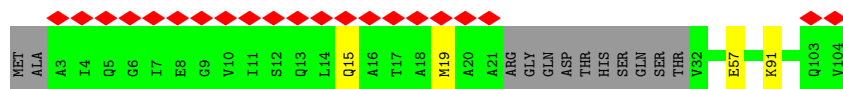
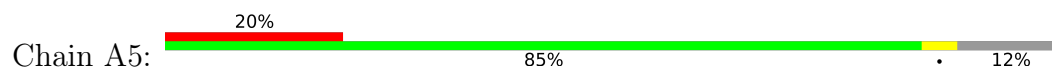
Chain A3:  11% 86% 11%



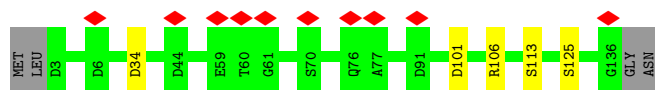
- Molecule 10: Flagellar hook-basal body complex protein FliE



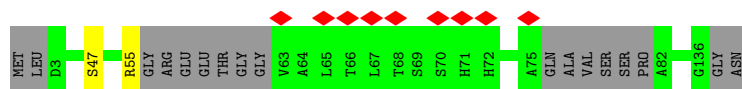
- Molecule 10: Flagellar hook-basal body complex protein FliE



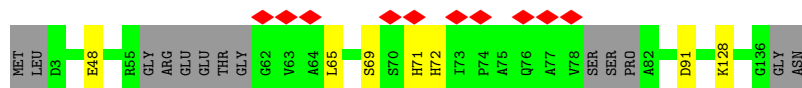
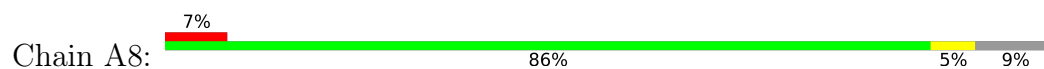
- Molecule 11: Flagellar basal body rod protein FlgB



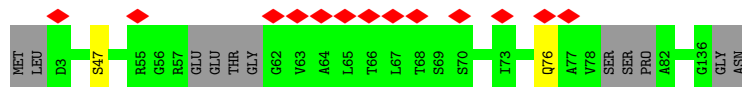
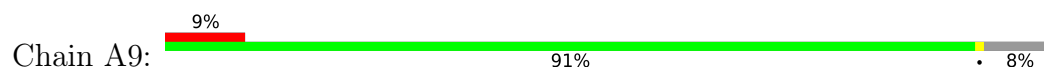
- Molecule 11: Flagellar basal body rod protein FlgB



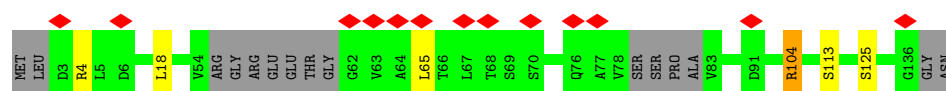
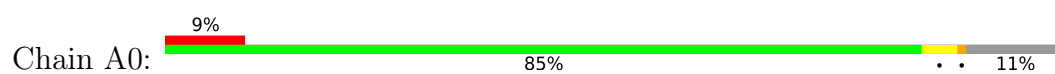
- Molecule 11: Flagellar basal body rod protein FlgB



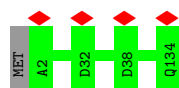
- Molecule 11: Flagellar basal body rod protein FlgB



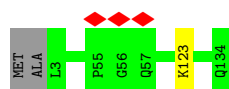
- Molecule 11: Flagellar basal body rod protein FlgB



- Molecule 12: Flagellar basal-body rod protein FlgC



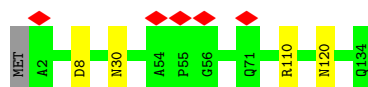
- Molecule 12: Flagellar basal-body rod protein FlgC



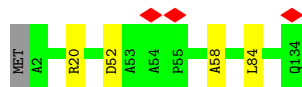
- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC



- Molecule 12: Flagellar basal-body rod protein FlgC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24191	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.118	Depositor
Minimum map value	-0.684	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.18	Depositor
Map size (Å)	614.4, 614.4, 614.4	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.27	0/1613	0.51	0/2194
1	B	0.27	0/1613	0.51	0/2194
1	C	0.27	0/1613	0.51	0/2194
1	D	0.27	0/1613	0.51	0/2194
1	E	0.27	0/1613	0.51	0/2194
1	F	0.27	0/1613	0.51	0/2194
1	G	0.27	0/1613	0.51	0/2194
1	H	0.27	0/1613	0.51	0/2194
1	I	0.27	0/1613	0.51	0/2194
1	J	0.27	0/1613	0.51	0/2194
1	K	0.27	0/1613	0.51	0/2194
1	L	0.27	0/1613	0.51	0/2194
1	M	0.27	0/1613	0.51	0/2194
1	N	0.27	0/1613	0.51	0/2194
1	O	0.27	0/1613	0.51	0/2194
1	P	0.27	0/1613	0.51	0/2194
1	Q	0.27	0/1613	0.51	0/2194
1	R	0.27	0/1613	0.51	0/2194
1	S	0.27	0/1613	0.51	0/2194
1	T	0.27	0/1613	0.51	0/2194
1	U	0.27	0/1613	0.51	0/2194
1	V	0.27	0/1613	0.51	0/2194
1	W	0.27	0/1613	0.51	0/2194
1	X	0.27	0/1613	0.51	0/2194
1	Y	0.27	0/1613	0.51	0/2194
1	Z	0.27	0/1613	0.51	0/2194
2	a	0.26	0/2243	0.51	0/3041
2	b	0.26	0/2243	0.51	0/3041
2	c	0.26	0/2243	0.51	0/3041
2	d	0.26	0/2243	0.51	0/3041
2	e	0.26	0/2243	0.51	0/3041
2	f	0.26	0/2243	0.51	0/3041
2	g	0.26	0/2243	0.51	0/3041
2	h	0.26	0/2243	0.51	0/3041

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	i	0.26	0/2243	0.51	0/3041
2	j	0.26	0/2243	0.51	0/3041
2	k	0.26	0/2243	0.51	0/3041
2	l	0.26	0/2243	0.51	0/3041
2	m	0.26	0/2243	0.51	0/3041
2	n	0.26	0/2243	0.51	0/3041
2	o	0.26	0/2243	0.51	0/3041
2	p	0.26	0/2243	0.51	0/3041
2	q	0.25	0/2243	0.51	0/3041
2	r	0.26	0/2243	0.51	0/3041
2	s	0.26	0/2243	0.51	0/3041
2	t	0.26	0/2243	0.51	0/3041
2	u	0.26	0/2243	0.51	0/3041
2	v	0.26	0/2243	0.51	0/3041
2	w	0.26	0/2243	0.51	0/3041
2	x	0.26	0/2243	0.51	0/3041
2	y	0.26	0/2243	0.51	0/3041
2	z	0.26	0/2243	0.51	0/3041
3	0	0.30	0/1888	0.52	1/2564 (0.0%)
3	1	0.31	0/1917	0.50	0/2605
3	2	0.27	0/1973	0.48	0/2682
3	3	0.28	0/1973	0.50	0/2682
3	4	0.28	0/1973	0.50	0/2682
3	5	0.32	0/1973	0.52	0/2682
3	6	0.30	0/1973	0.52	0/2682
3	7	0.28	0/1973	0.51	0/2682
3	8	0.30	0/1973	0.52	0/2682
3	9	0.29	0/1973	0.54	1/2682 (0.0%)
3	AF	0.33	0/1926	0.53	0/2618
3	AG	0.36	0/1934	0.56	0/2629
3	AH	0.33	0/1942	0.55	0/2639
3	AI	0.32	0/1926	0.57	1/2618 (0.0%)
3	AJ	0.30	0/1934	0.51	0/2629
3	AK	0.32	0/1844	0.51	0/2505
3	AL	0.31	0/1888	0.51	0/2564
3	AM	0.30	0/1888	0.54	1/2564 (0.0%)
3	AN	0.30	0/1888	0.51	0/2564
3	ZA	0.29	0/1973	0.52	0/2682
3	ZB	0.29	0/1973	0.49	0/2682
3	ZC	0.28	0/1973	0.51	0/2682
3	ZD	0.28	0/1973	0.51	0/2682
3	ZE	0.28	0/1973	0.50	1/2682 (0.0%)
4	ZF	0.28	0/2991	0.49	0/4076

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ZG	0.31	0/2991	0.50	0/4076
4	ZH	0.28	0/2991	0.50	0/4076
4	ZI	0.30	0/2991	0.51	0/4076
4	ZJ	0.31	0/2991	0.51	0/4076
4	ZK	0.26	0/2991	0.48	0/4076
4	ZL	0.28	0/2991	0.49	0/4076
4	ZM	0.29	0/2991	0.53	1/4076 (0.0%)
4	ZN	0.28	0/2991	0.51	0/4076
4	ZO	0.30	0/2991	0.50	0/4076
4	ZP	0.28	0/2991	0.50	1/4076 (0.0%)
4	ZQ	0.29	0/2991	0.51	0/4076
4	ZR	0.30	1/2991 (0.0%)	0.55	3/4076 (0.1%)
4	ZS	0.29	0/2991	0.52	1/4076 (0.0%)
4	ZT	0.26	0/2991	0.47	0/4076
4	ZU	0.28	0/2991	0.50	0/4076
4	ZV	0.50	4/2991 (0.1%)	0.67	6/4076 (0.1%)
4	ZW	0.25	0/2991	0.48	0/4076
4	ZX	0.28	0/2991	0.48	0/4076
4	ZY	0.30	1/2991 (0.0%)	0.54	2/4076 (0.0%)
4	ZZ	0.25	0/2991	0.46	0/4076
4	Za	0.27	0/2991	0.49	0/4076
4	Zb	0.29	0/2991	0.50	0/4076
4	Zc	0.29	0/2991	0.53	2/4076 (0.0%)
4	Zd	0.29	0/2991	0.50	0/4076
4	Ze	0.27	0/2991	0.48	0/4076
4	Zf	0.27	0/2991	0.48	0/4076
4	Zg	0.27	0/2991	0.49	0/4076
4	Zh	0.26	0/2991	0.48	0/4076
5	AA	0.33	0/1828	0.56	0/2492
5	AB	0.29	0/1836	0.54	1/2502 (0.0%)
5	AC	0.28	0/1844	0.54	0/2512
5	AD	0.27	0/1844	0.53	0/2512
5	AE	0.31	0/1836	0.55	0/2502
6	AO	0.27	0/1289	0.53	0/1741
6	AP	0.27	0/1289	0.53	0/1741
6	AQ	0.27	0/1289	0.53	0/1741
6	AR	0.26	0/1289	0.53	0/1741
6	AS	0.27	0/1289	0.53	0/1741
6	AT	0.27	0/1289	0.53	0/1741
6	AU	0.27	0/1289	0.53	0/1741
6	AV	0.27	0/1289	0.53	0/1741
6	AW	0.27	0/1289	0.53	0/1741
6	AX	0.27	0/1289	0.53	0/1741

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	AY	0.27	0/1289	0.53	0/1741
6	AZ	0.27	0/1289	0.53	0/1741
6	Aa	0.27	0/1289	0.53	0/1741
6	Ac	0.27	0/1289	0.53	0/1741
6	Ad	0.27	0/1289	0.53	0/1741
6	Ae	0.27	0/1289	0.53	0/1741
6	Af	0.27	0/1289	0.53	0/1741
6	Ag	0.27	0/1289	0.53	0/1741
6	Ah	0.26	0/1289	0.53	0/1741
6	Ai	0.27	0/1289	0.53	0/1741
6	Aj	0.27	0/1289	0.53	0/1741
6	Ak	0.26	0/1289	0.53	0/1741
6	Al	0.27	0/1289	0.53	0/1741
6	Am	0.27	0/1289	0.53	0/1741
6	An	0.27	0/1289	0.53	0/1741
6	Ao	0.27	0/1289	0.53	0/1741
6	Ap	0.26	0/1289	0.53	0/1741
6	BG	0.52	0/83	0.63	0/114
6	BH	0.27	0/107	0.38	0/148
6	BI	0.30	0/137	0.49	0/191
6	BJ	0.28	0/107	0.56	0/148
6	BK	1.36	1/145 (0.7%)	1.49	3/203 (1.5%)
6	BL	0.33	0/107	0.51	0/148
6	BM	0.26	0/145	0.44	0/203
6	BN	0.30	0/107	0.38	0/148
6	BO	0.30	0/137	0.57	0/191
6	BP	0.30	0/107	0.37	0/148
6	BQ	0.29	0/145	0.45	0/203
6	BR	0.27	0/1289	0.52	0/1741
6	BS	0.27	0/1289	0.53	0/1741
6	BT	0.27	0/1289	0.53	0/1741
6	BU	0.27	0/1289	0.53	0/1741
6	BV	0.27	0/1289	0.53	0/1741
6	BW	0.26	0/1289	0.52	0/1741
6	BX	0.27	0/1289	0.53	0/1741
6	UI	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UJ	0.84	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UK	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UL	0.82	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UM	0.84	3/1191 (0.3%)	0.82	4/1618 (0.2%)
6	UN	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UO	0.83	2/1191 (0.2%)	0.82	4/1618 (0.2%)
6	UP	0.84	2/1191 (0.2%)	0.82	4/1618 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	WA	0.61	0/863	0.72	1/1172 (0.1%)
6	WB	0.59	0/850	0.69	0/1154
6	WC	0.59	0/825	0.68	0/1121
6	WD	0.61	0/841	0.68	0/1142
6	WE	0.60	0/857	0.71	0/1164
6	WF	0.60	0/848	0.69	0/1152
6	WG	0.60	0/857	0.68	0/1164
6	WH	0.60	0/714	0.69	0/973
6	WI	0.60	0/714	0.74	0/973
6	WJ	0.61	0/749	0.72	1/1020 (0.1%)
6	WK	0.60	0/741	0.69	0/1009
6	WL	0.60	0/631	0.70	0/860
6	WM	0.59	0/604	0.70	0/824
6	WN	0.60	0/619	0.70	0/844
6	WO	0.60	0/726	0.72	1/989 (0.1%)
6	WP	0.60	0/753	0.69	0/1025
6	WQ	0.60	0/848	0.69	0/1152
6	WR	0.60	0/848	0.69	0/1152
6	WS	0.60	0/848	0.69	0/1152
6	WT	0.60	0/848	0.70	0/1152
6	WU	0.60	0/857	0.67	0/1164
6	WV	0.61	0/841	0.69	0/1142
6	WW	0.60	0/848	0.70	0/1152
7	Ab	0.29	0/681	0.47	0/930
7	Aq	0.26	0/681	0.49	0/930
7	Ar	0.28	0/681	0.48	0/930
7	As	0.29	0/681	0.49	0/930
8	At	0.38	1/1994 (0.1%)	0.56	1/2724 (0.0%)
9	Au	0.36	0/1643	0.62	2/2237 (0.1%)
9	Av	0.29	0/1665	0.49	1/2267 (0.0%)
9	Aw	0.29	0/1652	0.48	0/2249
9	Ax	0.28	0/1652	0.46	0/2249
9	Ay	0.31	0/1662	0.49	0/2263
10	A1	0.36	0/675	0.49	0/905
10	A2	0.37	0/689	0.52	0/925
10	A3	0.36	0/689	0.50	0/925
10	A4	0.37	0/689	0.53	0/925
10	A5	0.37	0/682	0.51	0/915
10	Az	0.42	0/428	0.53	0/572
11	A0	0.34	0/959	0.50	0/1293
11	A6	0.36	0/1042	0.55	0/1408
11	A7	0.33	0/951	0.49	0/1282
11	A8	0.35	0/976	0.57	0/1316

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	A9	0.34	0/991	0.54	0/1335
12	BA	0.28	0/981	0.44	0/1334
12	BB	0.26	0/976	0.46	0/1327
12	BC	0.57	2/981 (0.2%)	0.95	3/1334 (0.2%)
12	BD	0.28	0/981	0.52	1/1334 (0.1%)
12	BE	0.26	0/981	0.47	0/1334
12	BF	0.28	0/981	0.47	0/1334
All	All	0.34	27/343262 (0.0%)	0.54	68/466341 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	a	0	1
2	b	0	1
2	c	0	1
2	d	0	1
2	e	0	1
2	f	0	1
2	g	0	1
2	h	0	1
2	i	0	1
2	j	0	1
2	k	0	1
2	l	0	1
2	m	0	1
2	n	0	1
2	o	0	1
2	p	0	1
2	q	0	1
2	r	0	1
2	s	0	1
2	t	0	1
2	u	0	1
2	v	0	1
2	w	0	1
2	x	0	1
2	y	0	1
2	z	0	1
3	0	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	1	0	1
3	5	0	1
3	6	0	1
3	8	0	1
3	AF	0	1
3	AI	0	1
3	AM	0	2
3	AN	0	1
3	ZA	0	1
4	ZG	0	1
4	ZI	0	1
4	ZK	0	1
4	ZO	0	1
4	ZW	0	1
4	Zb	0	1
4	Zd	0	1
4	Ze	0	1
5	AA	0	2
5	AB	0	1
5	AC	0	1
5	AE	0	1
6	UI	0	2
6	UJ	0	2
6	UK	0	3
6	UL	0	3
6	UM	0	2
6	UN	0	2
6	UO	0	2
6	UP	0	3
6	WA	0	3
6	WB	0	4
6	WC	0	3
6	WD	0	1
6	WE	0	2
6	WF	0	3
6	WG	0	3
6	WI	0	1
6	WJ	0	3
6	WK	0	2
6	WL	0	2
6	WM	0	1
6	WN	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	WO	0	1
6	WP	0	3
6	WQ	0	2
6	WR	0	3
6	WS	0	1
6	WT	0	2
6	WU	0	2
6	WV	0	3
6	WW	0	2
9	Aw	0	1
11	A0	0	1
11	A6	0	1
12	BD	0	1
12	BF	0	1
All	All	0	123

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	ZV	140	PRO	CG-CD	-16.09	0.97	1.50
6	BK	331	PRO	CG-CD	-14.22	1.03	1.50
12	BC	73	PRO	CG-CD	-12.75	1.08	1.50
4	ZV	125	PRO	CG-CD	-10.16	1.17	1.50
6	UM	172	PRO	N-CD	-9.55	1.34	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	BC	73	PRO	N-CD-CG	-18.82	74.97	103.20
12	BC	73	PRO	CB-CG-CD	18.82	179.88	106.50
4	ZV	140	PRO	N-CD-CG	-17.33	77.21	103.20
6	BK	331	PRO	N-CD-CG	-16.14	78.99	103.20
12	BC	73	PRO	CA-CB-CG	-14.02	77.37	104.00

There are no chirality outliers.

5 of 123 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	a	117	ARG	Sidechain
2	b	117	ARG	Sidechain
2	c	117	ARG	Sidechain

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Mol	Chain	Res	Type	Group
2	d	117	ARG	Sidechain
2	e	117	ARG	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	B	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	C	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	D	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	E	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	F	209/232 (90%)	204 (98%)	4 (2%)	1 (0%)	25	54
1	G	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	H	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	I	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	J	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	K	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	L	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	M	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	N	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	O	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	P	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	Q	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	S	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	T	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	U	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	V	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	W	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	X	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	Y	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
1	Z	209/232 (90%)	205 (98%)	3 (1%)	1 (0%)	25	54
2	a	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	b	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	c	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	d	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	e	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	f	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	g	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	h	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	i	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	j	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	k	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	l	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	m	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	n	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	o	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	p	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	q	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	r	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	s	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	t	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	u	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	v	297/365 (81%)	293 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	w	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	x	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	y	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
2	z	297/365 (81%)	293 (99%)	4 (1%)	0	100	100
3	0	244/260 (94%)	237 (97%)	6 (2%)	1 (0%)	30	60
3	1	248/260 (95%)	238 (96%)	9 (4%)	1 (0%)	30	60
3	2	258/260 (99%)	247 (96%)	9 (4%)	2 (1%)	16	44
3	3	258/260 (99%)	248 (96%)	8 (3%)	2 (1%)	16	44
3	4	258/260 (99%)	248 (96%)	7 (3%)	3 (1%)	11	35
3	5	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	44
3	6	258/260 (99%)	244 (95%)	12 (5%)	2 (1%)	16	44
3	7	258/260 (99%)	245 (95%)	10 (4%)	3 (1%)	11	35
3	8	258/260 (99%)	247 (96%)	9 (4%)	2 (1%)	16	44
3	9	258/260 (99%)	245 (95%)	11 (4%)	2 (1%)	16	44
3	AF	250/260 (96%)	237 (95%)	12 (5%)	1 (0%)	30	60
3	AG	251/260 (96%)	237 (94%)	13 (5%)	1 (0%)	30	60
3	AH	252/260 (97%)	241 (96%)	10 (4%)	1 (0%)	30	60
3	AI	250/260 (96%)	242 (97%)	6 (2%)	2 (1%)	16	44
3	AJ	251/260 (96%)	241 (96%)	9 (4%)	1 (0%)	30	60
3	AK	239/260 (92%)	232 (97%)	6 (2%)	1 (0%)	30	60
3	AL	244/260 (94%)	237 (97%)	4 (2%)	3 (1%)	11	35
3	AM	244/260 (94%)	237 (97%)	6 (2%)	1 (0%)	30	60
3	AN	244/260 (94%)	240 (98%)	3 (1%)	1 (0%)	30	60
3	ZA	258/260 (99%)	242 (94%)	13 (5%)	3 (1%)	11	35
3	ZB	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	11	35
3	ZC	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	11	35
3	ZD	258/260 (99%)	244 (95%)	12 (5%)	2 (1%)	16	44
3	ZE	258/260 (99%)	245 (95%)	12 (5%)	1 (0%)	30	60
4	ZF	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZG	399/403 (99%)	392 (98%)	6 (2%)	1 (0%)	37	66
4	ZH	399/403 (99%)	388 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	ZI	399/403 (99%)	387 (97%)	10 (2%)	2 (0%)	25	54
4	ZJ	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZK	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	ZL	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	37	66
4	ZM	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZN	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZO	399/403 (99%)	381 (96%)	15 (4%)	3 (1%)	16	44
4	ZP	399/403 (99%)	385 (96%)	13 (3%)	1 (0%)	37	66
4	ZQ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
4	ZR	399/403 (99%)	390 (98%)	8 (2%)	1 (0%)	37	66
4	ZS	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	ZT	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
4	ZU	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	ZV	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	ZW	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
4	ZX	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	ZY	399/403 (99%)	384 (96%)	15 (4%)	0	100	100
4	ZZ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
4	Za	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	Zb	399/403 (99%)	392 (98%)	7 (2%)	0	100	100
4	Zc	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
4	Zd	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
4	Ze	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
4	Zf	399/403 (99%)	386 (97%)	13 (3%)	0	100	100
4	Zg	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
4	Zh	399/403 (99%)	393 (98%)	6 (2%)	0	100	100
5	AA	246/251 (98%)	232 (94%)	11 (4%)	3 (1%)	11	35
5	AB	247/251 (98%)	241 (98%)	6 (2%)	0	100	100
5	AC	248/251 (99%)	239 (96%)	9 (4%)	0	100	100
5	AD	248/251 (99%)	239 (96%)	9 (4%)	0	100	100
5	AE	247/251 (98%)	233 (94%)	13 (5%)	1 (0%)	30	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AO	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AP	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AQ	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AR	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AS	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AT	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AU	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AV	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AW	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AX	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AY	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	AZ	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Aa	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ac	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ad	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ae	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Af	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ag	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ah	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ai	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Aj	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ak	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Al	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Am	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	An	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ao	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	Ap	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BG	11/560 (2%)	10 (91%)	1 (9%)	0	100	100
6	BH	14/560 (2%)	12 (86%)	2 (14%)	0	100	100
6	BI	18/560 (3%)	18 (100%)	0	0	100	100
6	BJ	14/560 (2%)	14 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	BK	19/560 (3%)	19 (100%)	0	0	100	100
6	BL	14/560 (2%)	12 (86%)	2 (14%)	0	100	100
6	BM	19/560 (3%)	19 (100%)	0	0	100	100
6	BN	14/560 (2%)	14 (100%)	0	0	100	100
6	BO	18/560 (3%)	17 (94%)	1 (6%)	0	100	100
6	BP	14/560 (2%)	14 (100%)	0	0	100	100
6	BQ	19/560 (3%)	19 (100%)	0	0	100	100
6	BR	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BS	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BT	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BU	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BV	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BW	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	BX	160/560 (29%)	158 (99%)	2 (1%)	0	100	100
6	UI	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	UJ	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	UK	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	UL	151/560 (27%)	142 (94%)	7 (5%)	2 (1%)	10	33
6	UM	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	UN	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	UO	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	UP	151/560 (27%)	146 (97%)	3 (2%)	2 (1%)	10	33
6	WA	111/560 (20%)	99 (89%)	9 (8%)	3 (3%)	4	21
6	WB	109/560 (20%)	94 (86%)	10 (9%)	5 (5%)	2	12
6	WC	106/560 (19%)	96 (91%)	9 (8%)	1 (1%)	14	41
6	WD	108/560 (19%)	99 (92%)	4 (4%)	5 (5%)	2	12
6	WE	110/560 (20%)	98 (89%)	8 (7%)	4 (4%)	3	16
6	WF	109/560 (20%)	98 (90%)	8 (7%)	3 (3%)	4	20
6	WG	110/560 (20%)	98 (89%)	10 (9%)	2 (2%)	7	27
6	WH	93/560 (17%)	86 (92%)	5 (5%)	2 (2%)	5	24
6	WI	93/560 (17%)	82 (88%)	5 (5%)	6 (6%)	1	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	WJ	97/560 (17%)	89 (92%)	7 (7%)	1 (1%)	13	39
6	WK	96/560 (17%)	84 (88%)	9 (9%)	3 (3%)	3	18
6	WL	81/560 (14%)	75 (93%)	4 (5%)	2 (2%)	4	22
6	WM	78/560 (14%)	72 (92%)	4 (5%)	2 (3%)	4	22
6	WN	80/560 (14%)	75 (94%)	2 (2%)	3 (4%)	2	15
6	WO	94/560 (17%)	85 (90%)	7 (7%)	2 (2%)	5	24
6	WP	98/560 (18%)	87 (89%)	6 (6%)	5 (5%)	1	11
6	WQ	109/560 (20%)	100 (92%)	5 (5%)	4 (4%)	2	16
6	WR	109/560 (20%)	94 (86%)	8 (7%)	7 (6%)	1	7
6	WS	109/560 (20%)	96 (88%)	7 (6%)	6 (6%)	1	10
6	WT	109/560 (20%)	97 (89%)	5 (5%)	7 (6%)	1	7
6	WU	110/560 (20%)	101 (92%)	8 (7%)	1 (1%)	14	41
6	WV	108/560 (19%)	97 (90%)	9 (8%)	2 (2%)	6	26
6	WW	109/560 (20%)	95 (87%)	9 (8%)	5 (5%)	2	12
7	Ab	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
7	Aq	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
7	Ar	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
7	As	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
8	At	251/264 (95%)	231 (92%)	14 (6%)	6 (2%)	5	23
9	Au	205/245 (84%)	195 (95%)	10 (5%)	0	100	100
9	Av	207/245 (84%)	199 (96%)	6 (3%)	2 (1%)	13	39
9	Aw	206/245 (84%)	201 (98%)	5 (2%)	0	100	100
9	Ax	206/245 (84%)	199 (97%)	6 (3%)	1 (0%)	25	54
9	Ay	207/245 (84%)	201 (97%)	4 (2%)	2 (1%)	13	39
10	A1	87/104 (84%)	87 (100%)	0	0	100	100
10	A2	89/104 (86%)	87 (98%)	2 (2%)	0	100	100
10	A3	89/104 (86%)	89 (100%)	0	0	100	100
10	A4	89/104 (86%)	89 (100%)	0	0	100	100
10	A5	88/104 (85%)	88 (100%)	0	0	100	100
10	Az	55/104 (53%)	53 (96%)	2 (4%)	0	100	100
11	A0	117/138 (85%)	115 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	A6	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
11	A7	115/138 (83%)	114 (99%)	1 (1%)	0	100	100
11	A8	119/138 (86%)	116 (98%)	3 (2%)	0	100	100
11	A9	121/138 (88%)	118 (98%)	3 (2%)	0	100	100
12	BA	131/134 (98%)	123 (94%)	8 (6%)	0	100	100
12	BB	130/134 (97%)	124 (95%)	6 (5%)	0	100	100
12	BC	131/134 (98%)	126 (96%)	5 (4%)	0	100	100
12	BD	131/134 (98%)	127 (97%)	4 (3%)	0	100	100
12	BE	131/134 (98%)	125 (95%)	5 (4%)	1 (1%)	16	44
12	BF	131/134 (98%)	126 (96%)	5 (4%)	0	100	100
All	All	44708/81227 (55%)	43390 (97%)	1126 (2%)	192 (0%)	32	60

5 of 192 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	209	ASN
3	5	209	ASN
3	8	209	ASN
3	ZA	209	ASN
3	ZB	164	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	B	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	C	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	D	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	E	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	F	170/186 (91%)	163 (96%)	7 (4%)	26	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	H	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	I	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	J	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	K	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	L	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	M	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	N	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	O	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	P	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	Q	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	R	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	S	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	T	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	U	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	V	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	W	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	X	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	Y	170/186 (91%)	163 (96%)	7 (4%)	26	51
1	Z	170/186 (91%)	163 (96%)	7 (4%)	26	51
2	a	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	b	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	c	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	d	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	e	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	f	248/294 (84%)	239 (96%)	9 (4%)	30	56
2	g	248/294 (84%)	239 (96%)	9 (4%)	30	56
2	h	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	i	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	j	248/294 (84%)	240 (97%)	8 (3%)	34	59
2	k	248/294 (84%)	238 (96%)	10 (4%)	27	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	l	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	m	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	n	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	o	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	p	248/294 (84%)	239 (96%)	9 (4%)	30	56
2	q	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	r	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	s	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	t	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	u	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	v	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	w	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	x	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	y	248/294 (84%)	238 (96%)	10 (4%)	27	52
2	z	248/294 (84%)	238 (96%)	10 (4%)	27	52
3	0	205/215 (95%)	199 (97%)	6 (3%)	37	61
3	1	209/215 (97%)	201 (96%)	8 (4%)	28	54
3	2	215/215 (100%)	212 (99%)	3 (1%)	62	77
3	3	215/215 (100%)	211 (98%)	4 (2%)	52	71
3	4	215/215 (100%)	211 (98%)	4 (2%)	52	71
3	5	215/215 (100%)	211 (98%)	4 (2%)	52	71
3	6	215/215 (100%)	210 (98%)	5 (2%)	45	67
3	7	215/215 (100%)	214 (100%)	1 (0%)	86	91
3	8	215/215 (100%)	213 (99%)	2 (1%)	75	86
3	9	215/215 (100%)	211 (98%)	4 (2%)	52	71
3	AF	209/215 (97%)	204 (98%)	5 (2%)	44	66
3	AG	210/215 (98%)	203 (97%)	7 (3%)	33	58
3	AH	211/215 (98%)	201 (95%)	10 (5%)	22	49
3	AI	209/215 (97%)	200 (96%)	9 (4%)	25	50
3	AJ	210/215 (98%)	202 (96%)	8 (4%)	28	54
3	AK	200/215 (93%)	196 (98%)	4 (2%)	50	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AL	205/215 (95%)	199 (97%)	6 (3%)	37	61
3	AM	205/215 (95%)	197 (96%)	8 (4%)	27	53
3	AN	205/215 (95%)	201 (98%)	4 (2%)	50	70
3	ZA	215/215 (100%)	213 (99%)	2 (1%)	75	86
3	ZB	215/215 (100%)	207 (96%)	8 (4%)	29	54
3	ZC	215/215 (100%)	212 (99%)	3 (1%)	62	77
3	ZD	215/215 (100%)	213 (99%)	2 (1%)	75	86
3	ZE	215/215 (100%)	214 (100%)	1 (0%)	86	91
4	ZF	321/323 (99%)	310 (97%)	11 (3%)	32	57
4	ZG	321/323 (99%)	306 (95%)	15 (5%)	22	49
4	ZH	321/323 (99%)	309 (96%)	12 (4%)	29	54
4	ZI	321/323 (99%)	315 (98%)	6 (2%)	52	71
4	ZJ	321/323 (99%)	313 (98%)	8 (2%)	42	65
4	ZK	321/323 (99%)	315 (98%)	6 (2%)	52	71
4	ZL	321/323 (99%)	311 (97%)	10 (3%)	35	60
4	ZM	321/323 (99%)	312 (97%)	9 (3%)	38	62
4	ZN	321/323 (99%)	311 (97%)	10 (3%)	35	60
4	ZO	321/323 (99%)	313 (98%)	8 (2%)	42	65
4	ZP	321/323 (99%)	306 (95%)	15 (5%)	22	49
4	ZQ	321/323 (99%)	312 (97%)	9 (3%)	38	62
4	ZR	321/323 (99%)	313 (98%)	8 (2%)	42	65
4	ZS	321/323 (99%)	315 (98%)	6 (2%)	52	71
4	ZT	321/323 (99%)	316 (98%)	5 (2%)	58	75
4	ZU	321/323 (99%)	317 (99%)	4 (1%)	67	80
4	ZV	321/323 (99%)	317 (99%)	4 (1%)	67	80
4	ZW	321/323 (99%)	308 (96%)	13 (4%)	27	52
4	ZX	321/323 (99%)	318 (99%)	3 (1%)	75	86
4	ZY	321/323 (99%)	314 (98%)	7 (2%)	47	68
4	ZZ	321/323 (99%)	316 (98%)	5 (2%)	58	75
4	Za	321/323 (99%)	316 (98%)	5 (2%)	58	75
4	Zb	321/323 (99%)	315 (98%)	6 (2%)	52	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Zc	321/323 (99%)	310 (97%)	11 (3%)	32	57
4	Zd	321/323 (99%)	315 (98%)	6 (2%)	52	71
4	Ze	321/323 (99%)	312 (97%)	9 (3%)	38	62
4	Zf	321/323 (99%)	314 (98%)	7 (2%)	47	68
4	Zg	321/323 (99%)	315 (98%)	6 (2%)	52	71
4	Zh	321/323 (99%)	313 (98%)	8 (2%)	42	65
5	AA	190/193 (98%)	187 (98%)	3 (2%)	58	75
5	AB	191/193 (99%)	188 (98%)	3 (2%)	58	75
5	AC	192/193 (100%)	187 (97%)	5 (3%)	41	64
5	AD	192/193 (100%)	190 (99%)	2 (1%)	73	83
5	AE	191/193 (99%)	190 (100%)	1 (0%)	86	91
6	AO	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AP	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AQ	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AR	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AS	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AT	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AU	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AV	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AW	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AX	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AY	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	AZ	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Aa	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ac	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ad	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ae	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Af	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ag	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ah	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ai	141/467 (30%)	134 (95%)	7 (5%)	20	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Aj	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ak	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Al	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Am	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	An	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ao	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	Ap	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BG	8/467 (2%)	8 (100%)	0	100	100
6	BH	11/467 (2%)	10 (91%)	1 (9%)	7	26
6	BI	14/467 (3%)	12 (86%)	2 (14%)	2	10
6	BJ	11/467 (2%)	11 (100%)	0	100	100
6	BK	15/467 (3%)	15 (100%)	0	100	100
6	BL	11/467 (2%)	11 (100%)	0	100	100
6	BM	15/467 (3%)	15 (100%)	0	100	100
6	BN	11/467 (2%)	11 (100%)	0	100	100
6	BO	14/467 (3%)	13 (93%)	1 (7%)	12	37
6	BP	11/467 (2%)	11 (100%)	0	100	100
6	BQ	15/467 (3%)	14 (93%)	1 (7%)	13	38
6	BR	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BS	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BT	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BU	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BV	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BW	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	BX	141/467 (30%)	134 (95%)	7 (5%)	20	46
6	UI	128/467 (27%)	123 (96%)	5 (4%)	27	53
6	UJ	128/467 (27%)	123 (96%)	5 (4%)	27	53
6	UK	128/467 (27%)	123 (96%)	5 (4%)	27	53
6	UL	128/467 (27%)	122 (95%)	6 (5%)	22	49
6	UM	128/467 (27%)	123 (96%)	5 (4%)	27	53
6	UN	128/467 (27%)	123 (96%)	5 (4%)	27	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	UO	128/467 (27%)	123 (96%)	5 (4%)	27	53
6	UP	128/467 (27%)	122 (95%)	6 (5%)	22	49
6	WA	95/467 (20%)	91 (96%)	4 (4%)	25	51
6	WB	93/467 (20%)	87 (94%)	6 (6%)	14	39
6	WC	91/467 (20%)	83 (91%)	8 (9%)	8	28
6	WD	92/467 (20%)	88 (96%)	4 (4%)	25	50
6	WE	94/467 (20%)	87 (93%)	7 (7%)	11	35
6	WF	93/467 (20%)	86 (92%)	7 (8%)	11	35
6	WG	94/467 (20%)	87 (93%)	7 (7%)	11	35
6	WH	79/467 (17%)	75 (95%)	4 (5%)	20	46
6	WI	79/467 (17%)	73 (92%)	6 (8%)	11	34
6	WJ	83/467 (18%)	79 (95%)	4 (5%)	21	48
6	WK	82/467 (18%)	77 (94%)	5 (6%)	15	40
6	WL	69/467 (15%)	66 (96%)	3 (4%)	25	50
6	WM	66/467 (14%)	65 (98%)	1 (2%)	60	76
6	WN	68/467 (15%)	66 (97%)	2 (3%)	37	61
6	WO	80/467 (17%)	76 (95%)	4 (5%)	20	46
6	WP	83/467 (18%)	77 (93%)	6 (7%)	12	37
6	WQ	93/467 (20%)	91 (98%)	2 (2%)	47	68
6	WR	93/467 (20%)	86 (92%)	7 (8%)	11	35
6	WS	93/467 (20%)	87 (94%)	6 (6%)	14	39
6	WT	93/467 (20%)	86 (92%)	7 (8%)	11	35
6	WU	94/467 (20%)	90 (96%)	4 (4%)	25	50
6	WV	92/467 (20%)	83 (90%)	9 (10%)	6	23
6	WW	93/467 (20%)	85 (91%)	8 (9%)	8	29
7	Ab	74/74 (100%)	73 (99%)	1 (1%)	62	77
7	Aq	74/74 (100%)	73 (99%)	1 (1%)	62	77
7	Ar	74/74 (100%)	74 (100%)	0	100	100
7	As	74/74 (100%)	73 (99%)	1 (1%)	62	77
8	At	210/221 (95%)	204 (97%)	6 (3%)	37	61
9	Au	177/204 (87%)	170 (96%)	7 (4%)	27	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Av	179/204 (88%)	172 (96%)	7 (4%)	27	53
9	Aw	178/204 (87%)	173 (97%)	5 (3%)	38	62
9	Ax	178/204 (87%)	172 (97%)	6 (3%)	32	57
9	Ay	179/204 (88%)	175 (98%)	4 (2%)	47	68
10	A1	68/79 (86%)	64 (94%)	4 (6%)	16	41
10	A2	70/79 (89%)	65 (93%)	5 (7%)	12	37
10	A3	70/79 (89%)	66 (94%)	4 (6%)	17	43
10	A4	70/79 (89%)	66 (94%)	4 (6%)	17	43
10	A5	69/79 (87%)	65 (94%)	4 (6%)	17	42
10	Az	45/79 (57%)	40 (89%)	5 (11%)	5	18
11	A0	102/113 (90%)	96 (94%)	6 (6%)	16	41
11	A6	110/113 (97%)	106 (96%)	4 (4%)	30	56
11	A7	101/113 (89%)	99 (98%)	2 (2%)	50	70
11	A8	103/113 (91%)	96 (93%)	7 (7%)	13	38
11	A9	104/113 (92%)	102 (98%)	2 (2%)	52	71
12	BA	104/105 (99%)	104 (100%)	0	100	100
12	BB	104/105 (99%)	103 (99%)	1 (1%)	73	83
12	BC	104/105 (99%)	104 (100%)	0	100	100
12	BD	104/105 (99%)	102 (98%)	2 (2%)	52	71
12	BE	104/105 (99%)	101 (97%)	3 (3%)	37	61
12	BF	104/105 (99%)	100 (96%)	4 (4%)	28	54
All	All	37085/66670 (56%)	35783 (96%)	1302 (4%)	33	56

5 of 1302 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	Aj	417	ARG
6	WE	170	LYS
6	An	381	ASP
6	Aj	381	ASP
10	A2	15	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1144 such sidechains are listed below:

Mol	Chain	Res	Type
3	AG	223	ASN
3	AK	127	GLN
3	AG	145	ASN
6	AO	303	GLN
2	1	198	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

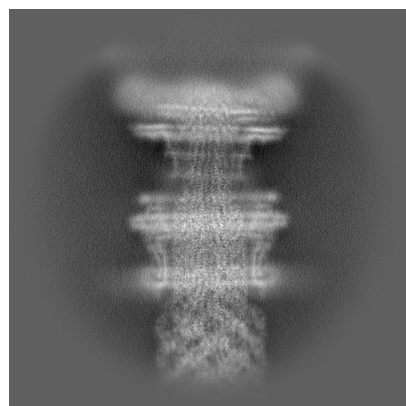
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37611. These allow visual inspection of the internal detail of the map and identification of artifacts.

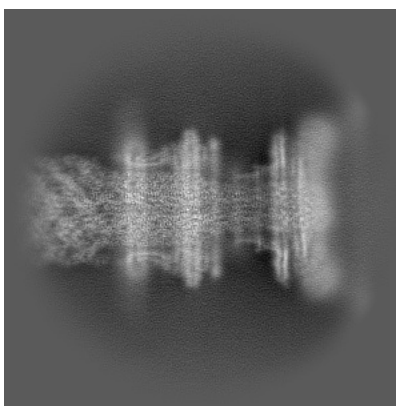
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

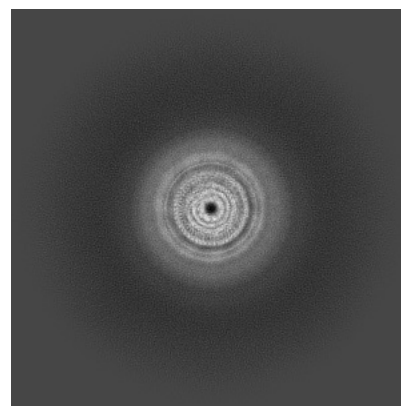
6.1.1 Primary map



X

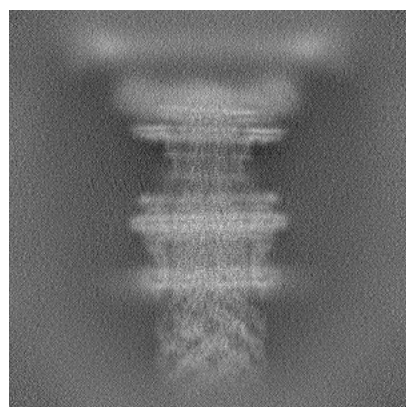


Y

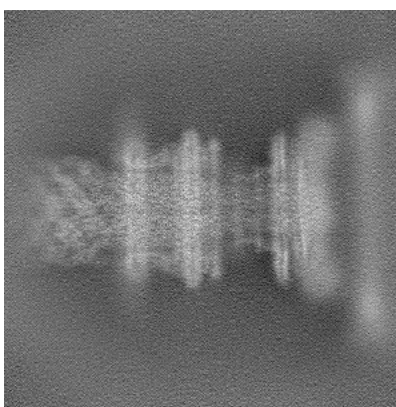


Z

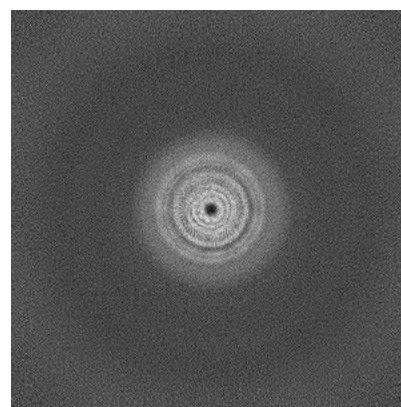
6.1.2 Raw map



X



Y

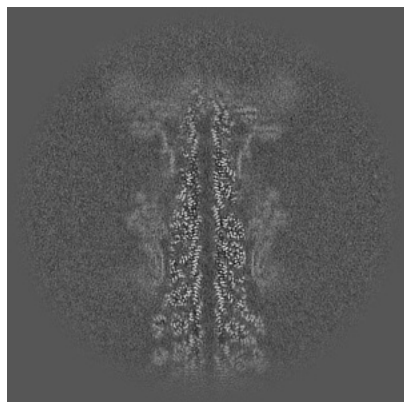


Z

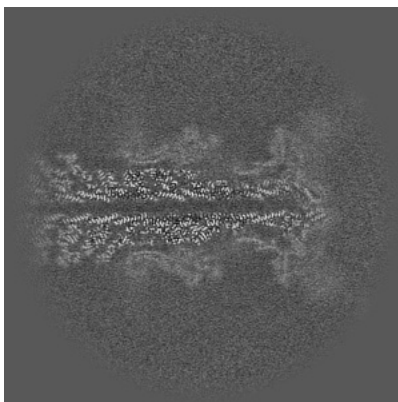
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

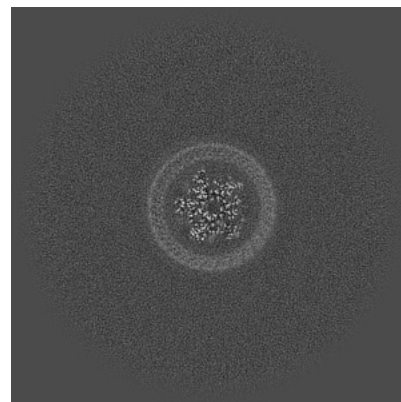
6.2.1 Primary map



X Index: 256

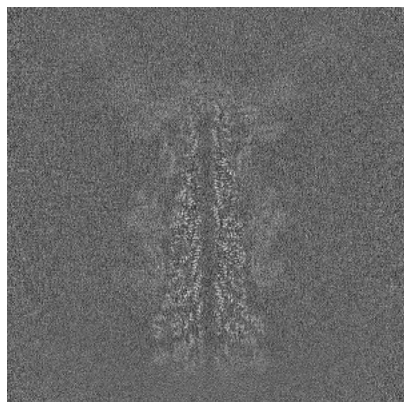


Y Index: 256

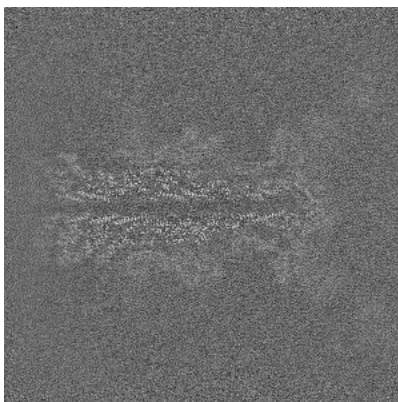


Z Index: 256

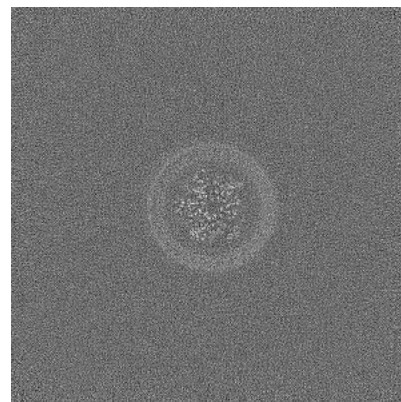
6.2.2 Raw map



X Index: 256



Y Index: 256

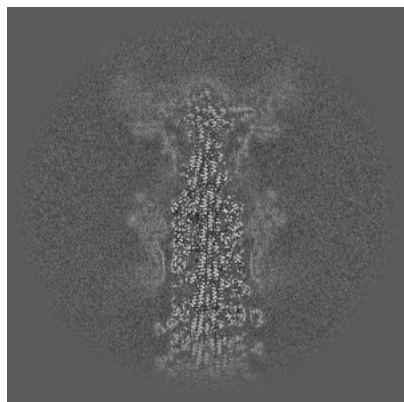


Z Index: 256

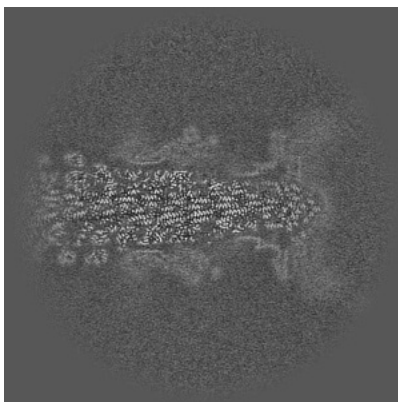
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

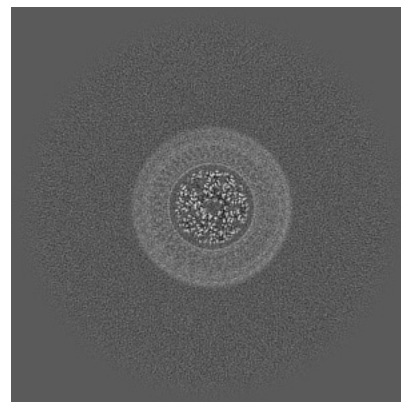
6.3.1 Primary map



X Index: 242

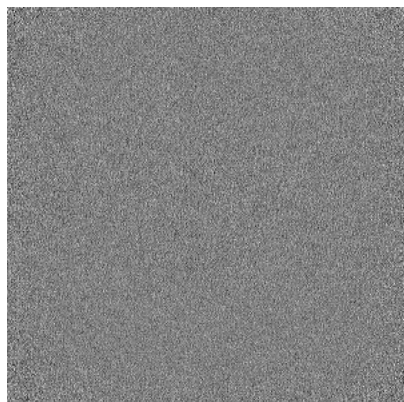


Y Index: 268

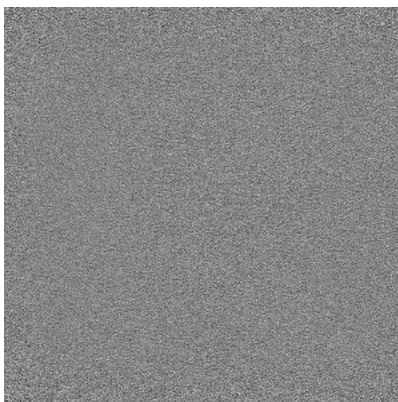


Z Index: 234

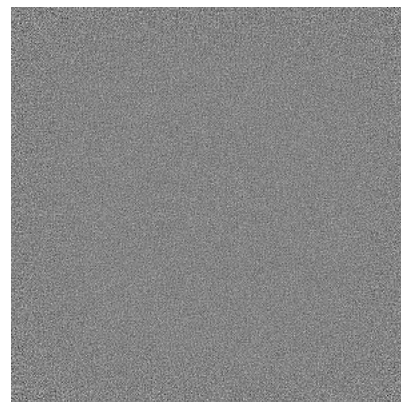
6.3.2 Raw map



X Index: 0



Y Index: 0

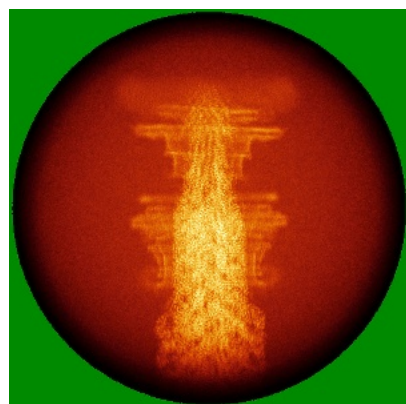


Z Index: 0

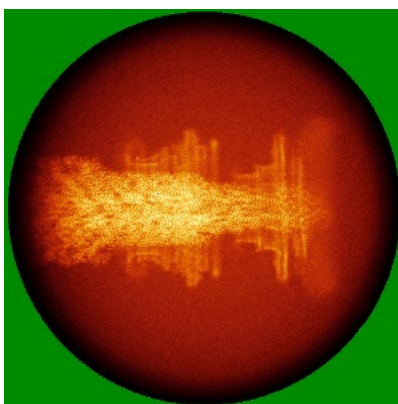
The images above show the largest variance slices of the map in three orthogonal directions.

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

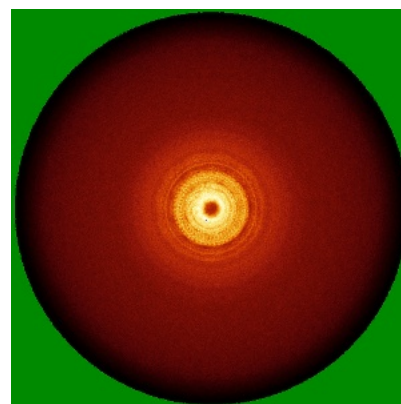
6.4.1 Primary map



X

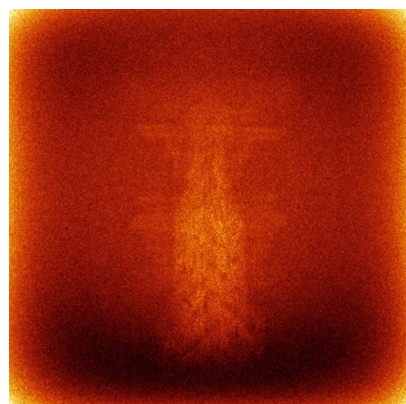


Y

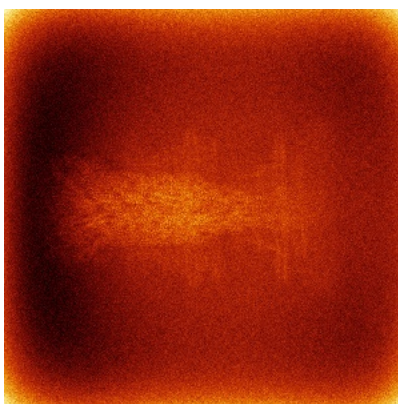


Z

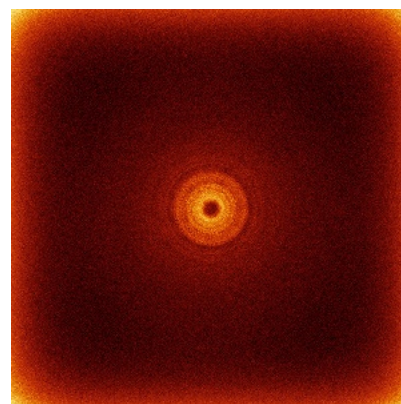
6.4.2 Raw map



X



Y

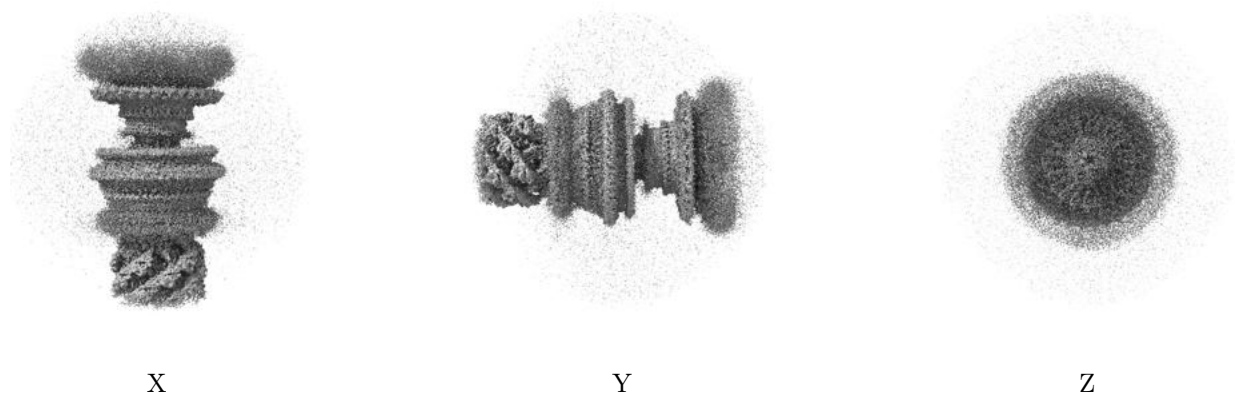


Z

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

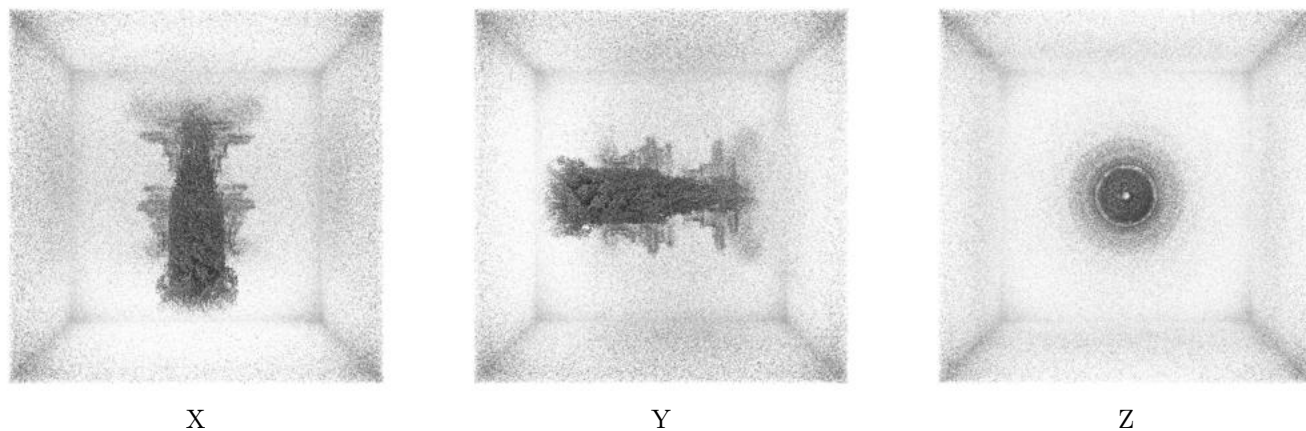
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.18. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

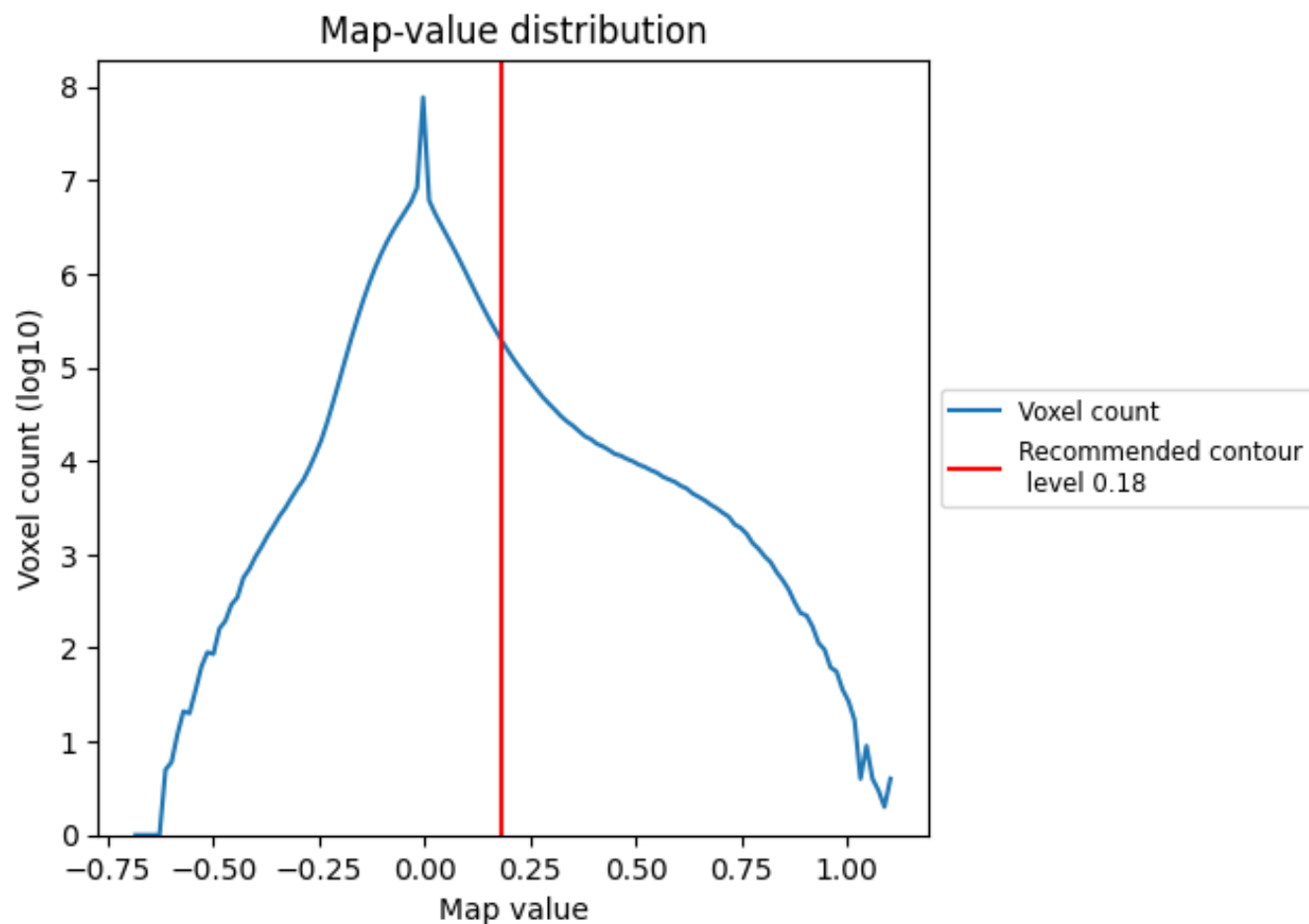
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

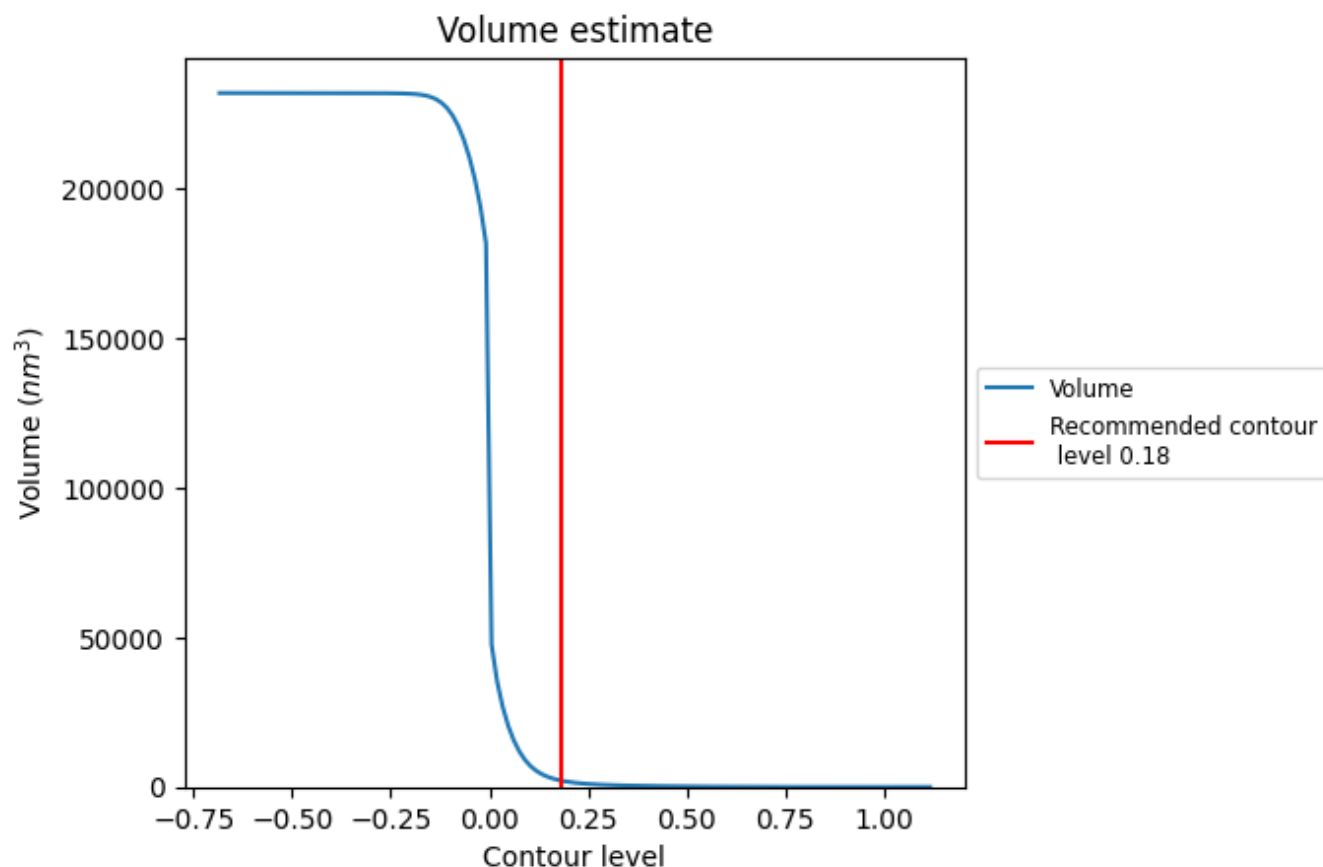
This section contains the results of statistical analysis of the map.

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.

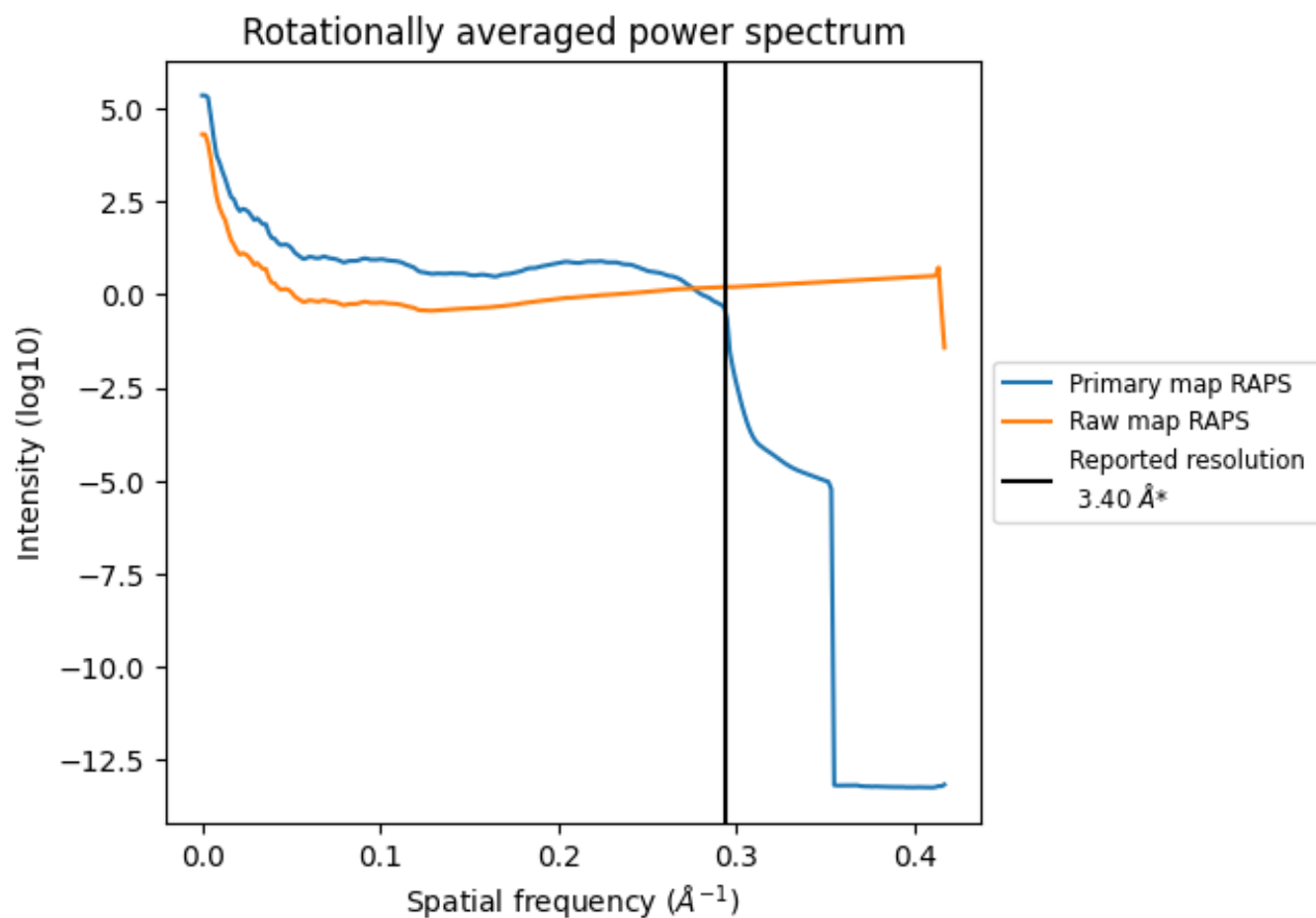
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2188 nm^3 ; this corresponds to an approximate mass of 1977 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

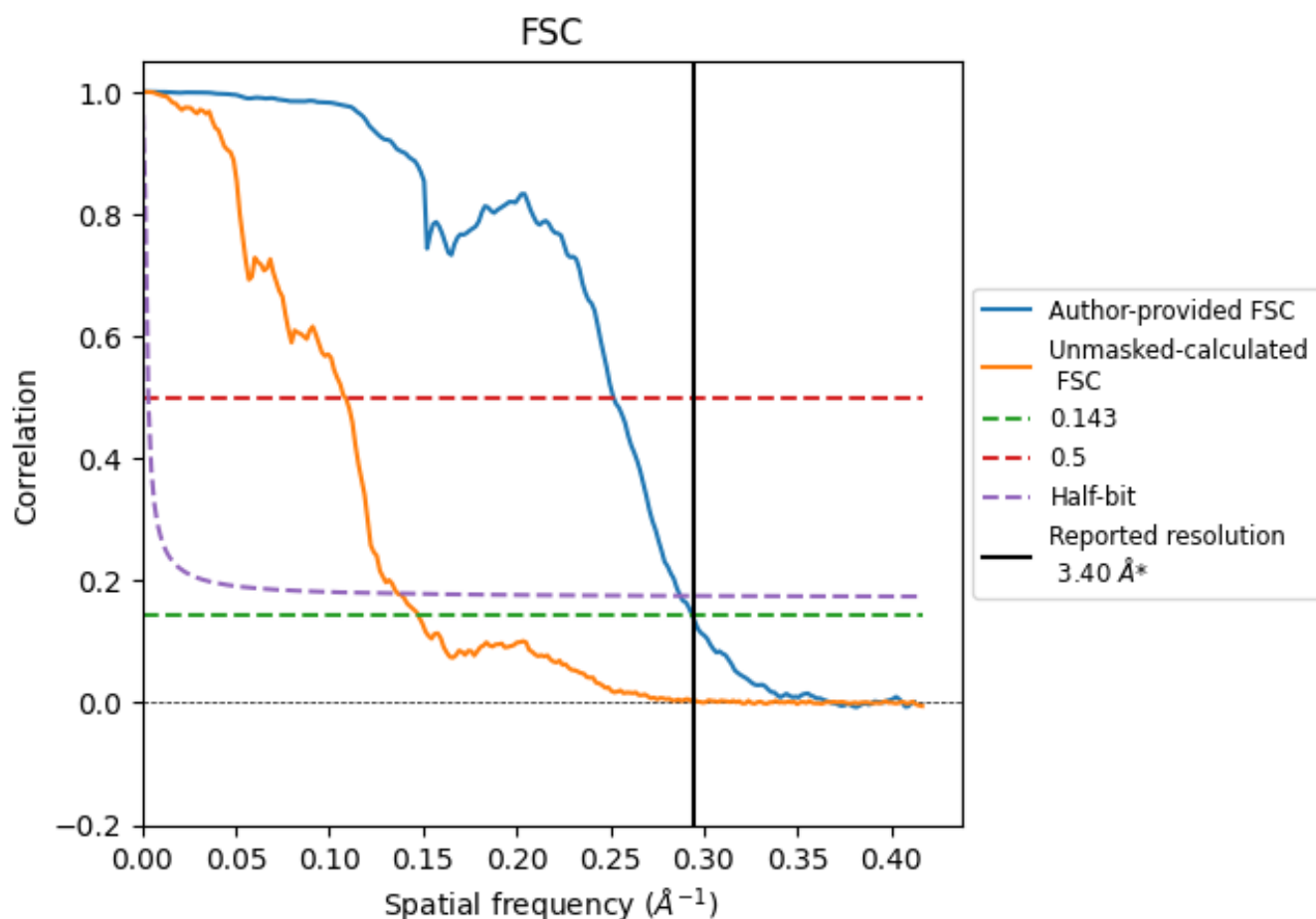


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

8.2 Resolution estimates [i](#)

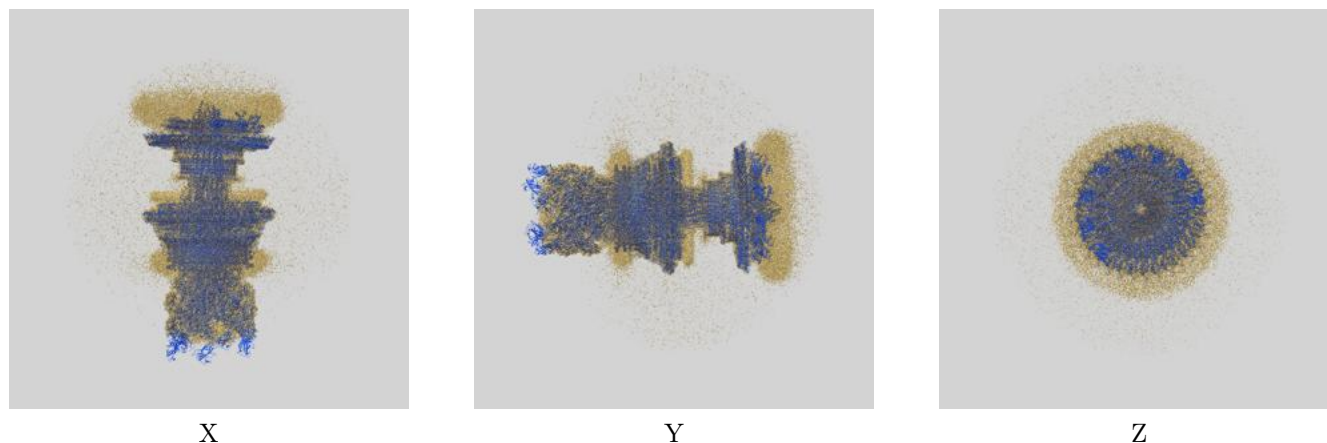
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.40	3.97	3.48
Unmasked-calculated*	6.78	9.23	7.33

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.78 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

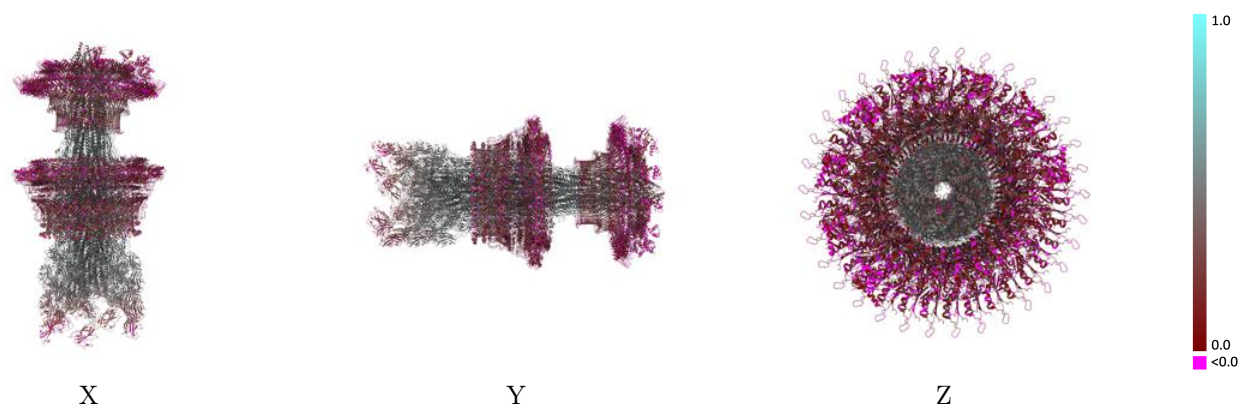
This section contains information regarding the fit between EMDB map EMD-37611 and PDB model 8WL2. Per-residue inclusion information can be found in section [3](#) on page [24](#).

9.1 Map-model overlay [i](#)



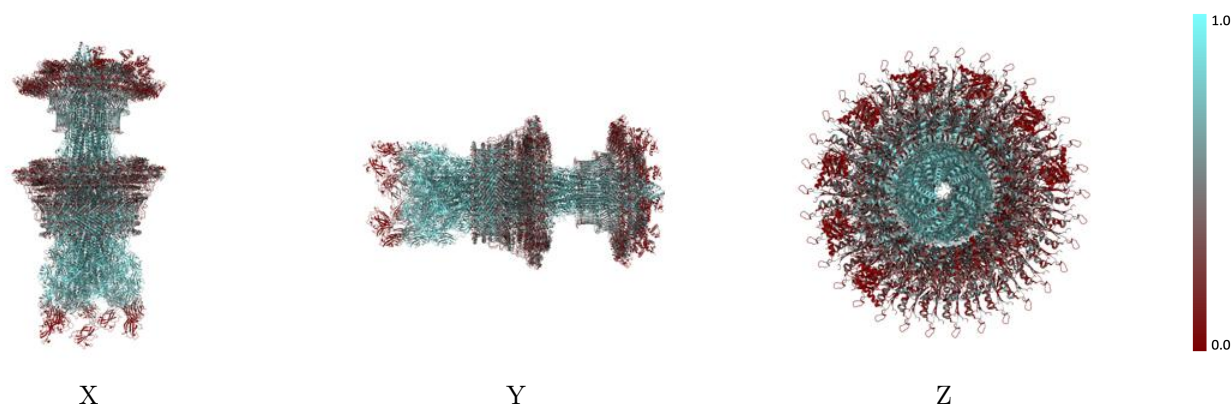
The images above show the 3D surface view of the map at the recommended contour level 0.18 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



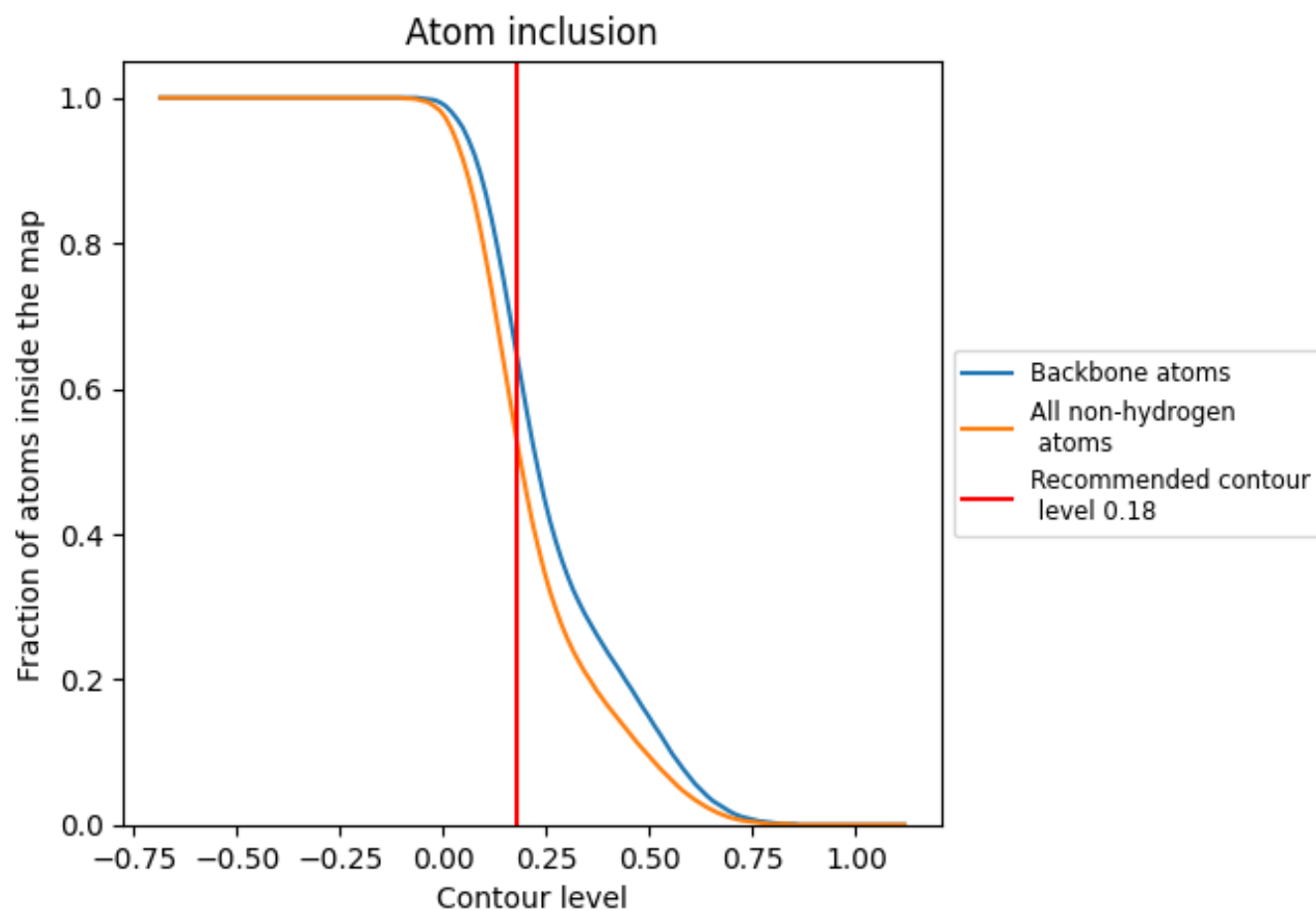
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.18).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 52% 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 (0.18) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5240	 0.3100
0	 0.8020	 0.5090
1	 0.7900	 0.5090
2	 0.7950	 0.5130
3	 0.7850	 0.5070
4	 0.7900	 0.5030
5	 0.7960	 0.5030
6	 0.8020	 0.5080
7	 0.7970	 0.5020
8	 0.7960	 0.5040
9	 0.8000	 0.5090
A	 0.3850	 0.2080
A0	 0.7190	 0.4510
A1	 0.6820	 0.4090
A2	 0.7020	 0.4120
A3	 0.7000	 0.4350
A4	 0.6560	 0.3930
A5	 0.6150	 0.3870
A6	 0.7010	 0.4630
A7	 0.7480	 0.4640
A8	 0.7500	 0.4690
A9	 0.7310	 0.4640
AA	 0.7600	 0.5010
AB	 0.8190	 0.5150
AC	 0.8150	 0.5130
AD	 0.8120	 0.5120
AE	 0.7910	 0.4970
AF	 0.7780	 0.5070
AG	 0.8070	 0.5130
AH	 0.8030	 0.5070
AI	 0.8010	 0.5170
AJ	 0.7940	 0.5080
AK	 0.7960	 0.5130
AL	 0.8000	 0.5060
AM	 0.7940	 0.5090























































































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Chain	Atom inclusion	Q-score
AN	 0.8010	 0.5120
AO	 0.3380	 0.1640
AP	 0.3490	 0.1710
AQ	 0.3360	 0.1640
AR	 0.4180	 0.1610
AS	 0.3560	 0.1480
AT	 0.3970	 0.1610
AU	 0.4010	 0.1700
AV	 0.4010	 0.1490
AW	 0.4060	 0.1660
AX	 0.4240	 0.1740
AY	 0.4270	 0.1780
AZ	 0.4290	 0.1660
Aa	 0.4270	 0.1780
Ab	 0.6140	 0.3500
Ac	 0.3860	 0.1240
Ad	 0.3920	 0.1320
Ae	 0.3650	 0.1210
Af	 0.3730	 0.1160
Ag	 0.3340	 0.0990
Ah	 0.3330	 0.0830
Ai	 0.3180	 0.0890
Aj	 0.3380	 0.1030
Ak	 0.3440	 0.1450
Al	 0.3450	 0.1410
Am	 0.3770	 0.1600
An	 0.3770	 0.1760
Ao	 0.3710	 0.1760
Ap	 0.3450	 0.1640
Aq	 0.7130	 0.3970
Ar	 0.7130	 0.3910
As	 0.6690	 0.3770
At	 0.6300	 0.3800
Au	 0.7040	 0.4150
Av	 0.7440	 0.4450
Aw	 0.7660	 0.4570
Ax	 0.7460	 0.4570
Ay	 0.7020	 0.4330
Az	 0.5680	 0.3510
B	 0.3860	 0.2100
BA	 0.7550	 0.4860
BB	 0.7870	 0.5020





















































































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Chain	Atom inclusion	Q-score
BC	 0.7890	 0.5030
BD	 0.7900	 0.4940
BE	 0.7900	 0.4970
BF	 0.7590	 0.4810
BG	 0.6170	 0.4660
BH	 0.7180	 0.4850
BI	 0.7370	 0.4830
BJ	 0.8160	 0.5020
BK	 0.7790	 0.4960
BL	 0.7570	 0.5110
BM	 0.8500	 0.5000
BN	 0.7280	 0.4740
BO	 0.8200	 0.4880
BP	 0.7090	 0.4900
BQ	 0.7790	 0.4970
BR	 0.3280	 0.1360
BS	 0.3230	 0.1370
BT	 0.3040	 0.1250
BU	 0.3200	 0.1330
BV	 0.3420	 0.1530
BW	 0.3410	 0.1290
BX	 0.3550	 0.1470
C	 0.3820	 0.2010
D	 0.4050	 0.2210
E	 0.3900	 0.1980
F	 0.4010	 0.2100
G	 0.3990	 0.2110
H	 0.4010	 0.1950
I	 0.3930	 0.1990
J	 0.3770	 0.1840
K	 0.4020	 0.2130
L	 0.3930	 0.1900
M	 0.3930	 0.1980
N	 0.3970	 0.1950
O	 0.3710	 0.1920
P	 0.4060	 0.2080
Q	 0.3950	 0.2020
R	 0.4030	 0.2000
S	 0.3840	 0.1850
T	 0.3800	 0.1880
U	 0.3720	 0.2040
UI	 0.0730	 0.0730





















































































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Chain	Atom inclusion	Q-score
UJ	 0.0820	 0.0660
UK	 0.0470	 0.0870
UL	 0.0550	 0.0410
UM	 0.0440	 0.0280
UN	 0.0700	 0.0480
UO	 0.0660	 0.0660
UP	 0.0720	 0.0510
V	 0.3900	 0.2060
W	 0.3700	 0.2020
WA	 0.5050	 0.2590
WB	 0.4920	 0.2350
WC	 0.4740	 0.2500
WD	 0.4420	 0.2190
WE	 0.4360	 0.2360
WF	 0.3890	 0.2250
WG	 0.3190	 0.1870
WH	 0.2930	 0.1630
WI	 0.2800	 0.1510
WJ	 0.2700	 0.1580
WK	 0.2070	 0.1260
WL	 0.1940	 0.0880
WM	 0.2250	 0.1040
WN	 0.2470	 0.1100
WO	 0.3410	 0.1590
WP	 0.4010	 0.1750
WQ	 0.4120	 0.2190
WR	 0.4230	 0.2080
WS	 0.4750	 0.2340
WT	 0.4910	 0.2460
WU	 0.4830	 0.2110
WV	 0.4840	 0.2430
WW	 0.4710	 0.2400
X	 0.3790	 0.2040
Y	 0.3830	 0.2120
Z	 0.3850	 0.2080
ZA	 0.7820	 0.4990
ZB	 0.8050	 0.5050
ZC	 0.8020	 0.5020
ZD	 0.7950	 0.4990
ZE	 0.7860	 0.4940
ZF	 0.6200	 0.4500
ZG	 0.7670	 0.4800























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Chain	Atom inclusion	Q-score
ZH	 0.8040	 0.4840
ZI	 0.8010	 0.4820
ZJ	 0.8020	 0.4780
ZK	 0.7950	 0.4740
ZL	 0.7990	 0.4730
ZM	 0.7980	 0.4730
ZN	 0.7960	 0.4690
ZO	 0.7900	 0.4690
ZP	 0.7840	 0.4620
ZQ	 0.7650	 0.4540
ZR	 0.7520	 0.4520
ZS	 0.7520	 0.4530
ZT	 0.7300	 0.4370
ZU	 0.7080	 0.4320
ZV	 0.6860	 0.4250
ZW	 0.6600	 0.4250
ZX	 0.6380	 0.4160
ZY	 0.5890	 0.4060
ZZ	 0.5560	 0.3950
Za	 0.5220	 0.3800
Zb	 0.5020	 0.3870
Zc	 0.4820	 0.3740
Zd	 0.4430	 0.3490
Ze	 0.4150	 0.3440
Zf	 0.3900	 0.3300
Zg	 0.3620	 0.3120
Zh	 0.3480	 0.3080
a	 0.3210	 0.1760
b	 0.3200	 0.1710
c	 0.3090	 0.1790
d	 0.3240	 0.1660
e	 0.3130	 0.1690
f	 0.3160	 0.1750
g	 0.3270	 0.1590
h	 0.3060	 0.1600
i	 0.3170	 0.1580
j	 0.3240	 0.1730
k	 0.3040	 0.1510
l	 0.3020	 0.1620
m	 0.3210	 0.1550
n	 0.3140	 0.1640
o	 0.3250	 0.1600

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Chain	Atom inclusion	Q-score
p	 0.3230	 0.1910
q	 0.3040	 0.1610
r	 0.3300	 0.1840
s	 0.3010	 0.1560
t	 0.3010	 0.1710
u	 0.2760	 0.1590
v	 0.3060	 0.1650
w	 0.2970	 0.1650
x	 0.2910	 0.1570
y	 0.2720	 0.1480
z	 0.3090	 0.1790