



wwPDB EM Validation Summary Report ⓘ

May 7, 2026 – 04:46 PM JST

PDB ID : 8Z5N / pdb_00008z5n
EMDB ID : EMD-39776
Title : Cryo-EM structure of the LPHT ring
Authors : Zhang, L.; Tan, J.X.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2024-04-18
Resolution : 2.95 Å(reported)
Based on initial model : .

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

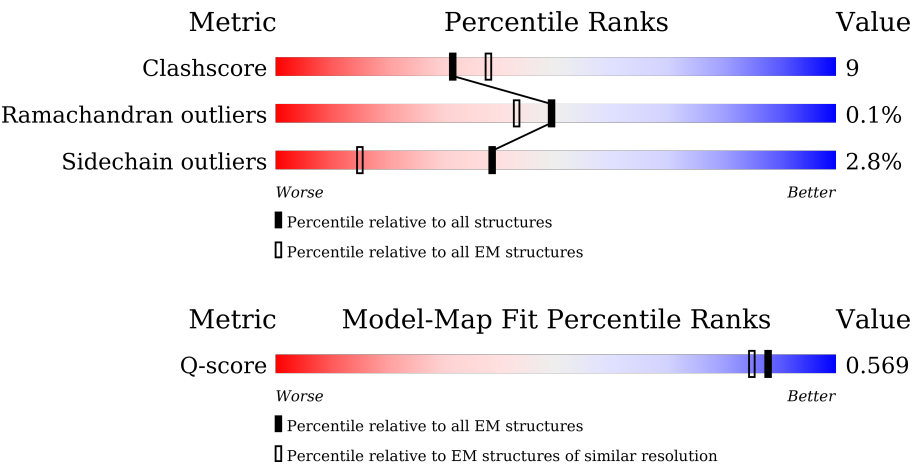
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.95 Å.

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



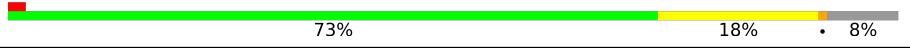
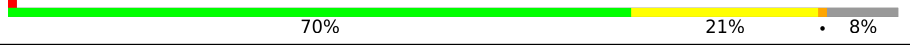
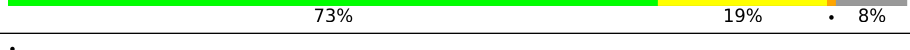
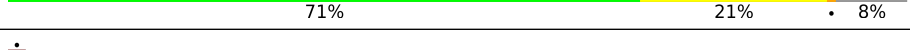
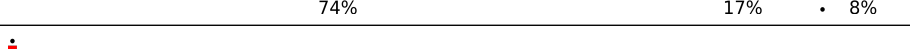
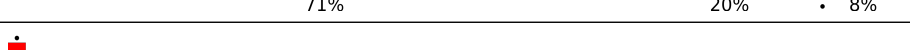
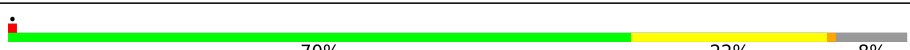
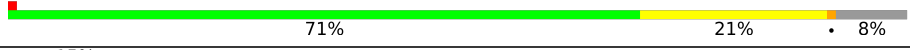
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13114 (2.45 - 3.45)

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	293	
1	B	293	
1	E	293	
1	F	293	

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Mol	Chain	Length	Quality of chain
1	I	293	
1	J	293	
1	M	293	
1	N	293	
1	Q	293	
1	R	293	
1	U	293	
1	V	293	
1	Y	293	
1	Z	293	
1	c	293	
1	d	293	
1	g	293	
1	h	293	
1	k	293	
1	l	293	
1	o	293	
1	p	293	
1	s	293	
1	t	293	
1	w	293	
1	x	293	
2	C	211	
2	D	211	
2	G	211	

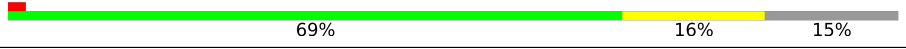
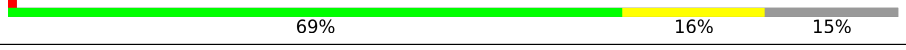
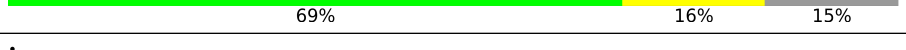
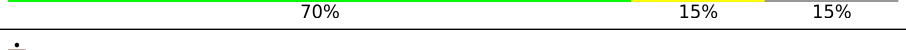
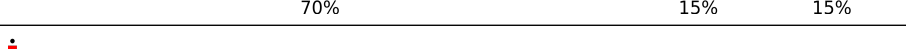
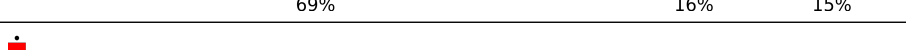
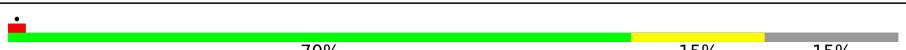
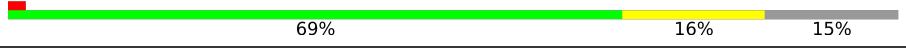
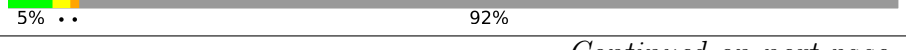
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Mol	Chain	Length	Quality of chain
2	H	211	
2	K	211	
2	L	211	
2	O	211	
2	P	211	
2	S	211	
2	T	211	
2	W	211	
2	X	211	
2	a	211	
2	b	211	
2	e	211	
2	f	211	
2	i	211	
2	j	211	
2	m	211	
2	n	211	
2	q	211	
2	r	211	
2	u	211	
2	v	211	
2	y	211	
2	z	211	
3	1	259	
3	6	259	

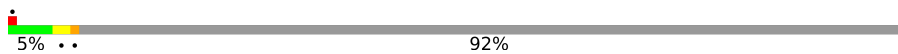
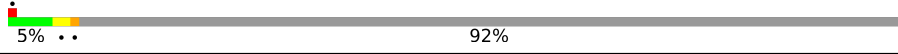
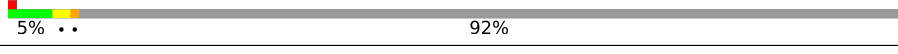
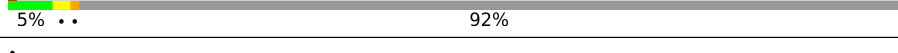
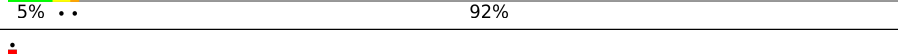
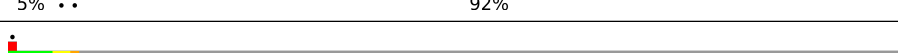
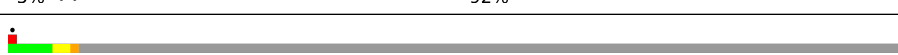
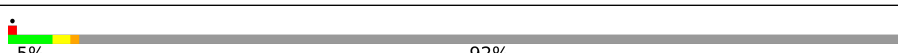
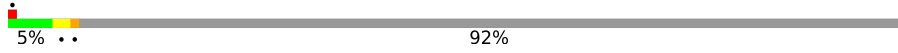
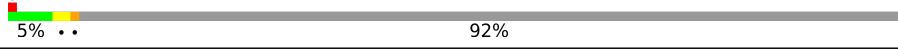
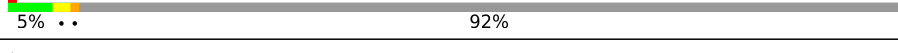
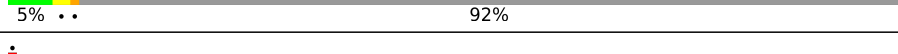
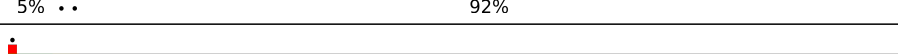
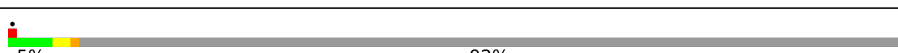
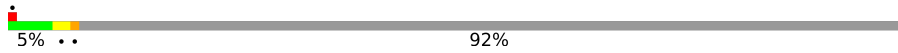
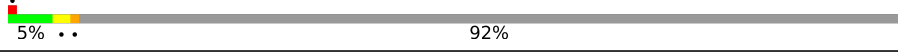
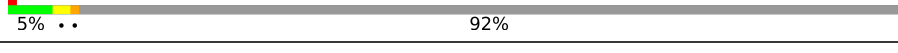
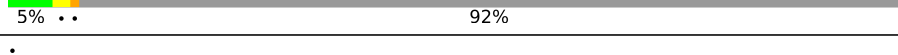
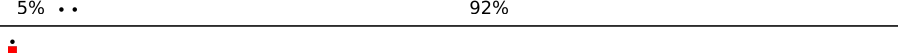
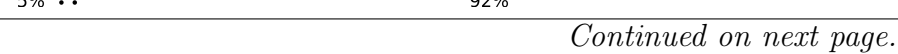
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Mol	Chain	Length	Quality of chain
3	A4	259	
3	A9	259	
3	AA	259	
3	AF	259	
3	AK	259	
3	AP	259	
3	AU	259	
3	AZ	259	
3	Ae	259	
3	Aj	259	
3	Ao	259	
3	At	259	
3	Ay	259	
3	B2	259	
3	BD	259	
3	BI	259	
3	BN	259	
3	BS	259	
3	BX	259	
3	Bc	259	
3	Bh	259	
3	Bm	259	
3	Br	259	
3	Bw	259	
4	2	143	

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Mol	Chain	Length	Quality of chain
4	7	143	 5% .. 92%
4	A0	143	 5% .. 92%
4	A5	143	 5% .. 92%
4	AB	143	 5% .. 92%
4	AG	143	 5% .. 92%
4	AL	143	 5% .. 92%
4	AQ	143	 5% .. 92%
4	AV	143	 5% .. 92%
4	Aa	143	 5% .. 92%
4	Af	143	 5% .. 92%
4	Ak	143	 5% .. 92%
4	Ap	143	 5% .. 92%
4	Au	143	 5% .. 92%
4	Az	143	 5% .. 92%
4	B3	143	 5% .. 92%
4	BE	143	 5% .. 92%
4	BJ	143	 5% .. 92%
4	BO	143	 5% .. 92%
4	BT	143	 5% .. 92%
4	BY	143	 5% .. 92%
4	Bd	143	 5% .. 92%
4	Bi	143	 5% .. 92%
4	Bn	143	 5% .. 92%
4	Bs	143	 5% .. 92%
4	Bx	143	 5% .. 92%

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Mol	Chain	Length	Quality of chain
5	3	13	
5	8	13	
5	A1	13	
5	A6	13	
5	AC	13	
5	AH	13	
5	AM	13	
5	AR	13	
5	AW	13	
5	Ab	13	
5	Ag	13	
5	Al	13	
5	Aq	13	
5	Av	13	
5	B4	13	
5	BA	13	
5	BF	13	
5	BK	13	
5	BP	13	
5	BU	13	
5	BZ	13	
5	Be	13	
5	Bj	13	
5	Bo	13	
5	Bt	13	

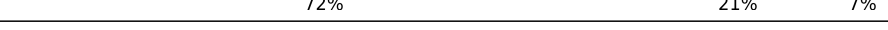
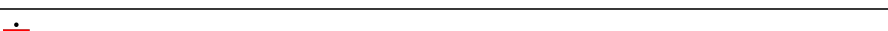
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Mol	Chain	Length	Quality of chain
5	By	13	
6	4	363	
6	9	363	
6	A2	363	
6	A7	363	
6	AD	363	
6	AI	363	
6	AN	363	
6	AS	363	
6	AX	363	
6	Ac	363	
6	Ah	363	
6	Am	363	
6	Ar	363	
6	Aw	363	
6	B5	363	
6	BB	363	
6	BG	363	
6	BL	363	
6	BQ	363	
6	BV	363	
6	Ba	363	
6	Bf	363	
6	Bk	363	
6	Bp	363	

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Mol	Chain	Length	Quality of chain
6	Bu	363	
6	Bz	363	
7	0	377	
7	5	377	
7	A3	377	
7	A8	377	
7	AE	377	
7	AJ	377	
7	AO	377	
7	AT	377	
7	AY	377	
7	Ad	377	
7	Ai	377	
7	An	377	
7	As	377	
7	Ax	377	
7	B1	377	
7	B6	377	
7	BC	377	
7	BH	377	
7	BM	377	
7	BR	377	
7	BW	377	
7	Bb	377	
7	Bg	377	

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Mol	Chain	Length	Quality of chain
7	Bl	377	72%21%7%
7	Bq	377	72%21%7%
7	Bv	377	73%20%7%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 269711 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 Component of sodium-driven polar flagellar motor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	B	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	E	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	F	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	I	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	J	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	M	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	N	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	Q	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	R	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	U	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	V	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	Y	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	Z	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	c	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	d	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	g	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	h	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	k	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	l	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	o	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	p	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	s	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	t	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		
1	w	270	Total	C	N	O	S	0	0
			2183	1372	394	410	7		
1	x	271	Total	C	N	O	S	0	0
			2190	1377	395	411	7		

- Molecule 2 is a protein called Sodium-type flagellar motor component.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	D	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	G	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	H	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	K	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	L	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	O	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	P	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	S	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		
2	T	179	Total	C	N	O	S	0	0
			1471	927	270	269	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	W	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	X	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	a	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	b	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	e	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	f	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	i	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	j	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	m	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	n	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	q	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	r	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	u	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	v	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	y	179	Total 1471	C 927	N 270	O 269	S 5	0	0
2	z	179	Total 1471	C 927	N 270	O 269	S 5	0	0

- Molecule 3 is a protein called Flagellar L-ring protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	6	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	AA	221	Total 1678	C 1038	N 288	O 349	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	AF	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	AK	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	AP	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	AU	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	AZ	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Ae	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Aj	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Ao	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	At	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Ay	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	A4	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	A9	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	BD	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	BI	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	BN	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	BS	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	BX	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Bc	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Bh	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Bm	221	Total 1678	C 1038	N 288	O 349	S 3	0	0
3	Br	221	Total 1678	C 1038	N 288	O 349	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Bw	221	Total	C	N	O	S	0	0
			1678	1038	288	349	3		
3	B2	221	Total	C	N	O	S	0	0
			1678	1038	288	349	3		

- Molecule 4 is a protein called Flagellar assembly lipoprotein FlgP.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	2	11	Total	C	N	O	0	0
			97	61	18	18		
4	7	11	Total	C	N	O	0	0
			97	61	18	18		
4	AB	11	Total	C	N	O	0	0
			97	61	18	18		
4	AG	11	Total	C	N	O	0	0
			97	61	18	18		
4	AL	11	Total	C	N	O	0	0
			97	61	18	18		
4	AQ	11	Total	C	N	O	0	0
			97	61	18	18		
4	AV	11	Total	C	N	O	0	0
			97	61	18	18		
4	Aa	11	Total	C	N	O	0	0
			97	61	18	18		
4	Af	11	Total	C	N	O	0	0
			97	61	18	18		
4	Ak	11	Total	C	N	O	0	0
			97	61	18	18		
4	Ap	11	Total	C	N	O	0	0
			97	61	18	18		
4	Au	11	Total	C	N	O	0	0
			97	61	18	18		
4	Az	11	Total	C	N	O	0	0
			97	61	18	18		
4	A5	11	Total	C	N	O	0	0
			97	61	18	18		
4	A0	11	Total	C	N	O	0	0
			97	61	18	18		
4	BE	11	Total	C	N	O	0	0
			97	61	18	18		
4	BJ	11	Total	C	N	O	0	0
			97	61	18	18		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	BO	11	Total	C	N	O	0	0
			97	61	18	18		
4	BT	11	Total	C	N	O	0	0
			97	61	18	18		
4	BY	11	Total	C	N	O	0	0
			97	61	18	18		
4	Bd	11	Total	C	N	O	0	0
			97	61	18	18		
4	Bi	11	Total	C	N	O	0	0
			97	61	18	18		
4	Bn	11	Total	C	N	O	0	0
			97	61	18	18		
4	Bs	11	Total	C	N	O	0	0
			97	61	18	18		
4	Bx	11	Total	C	N	O	0	0
			97	61	18	18		
4	B3	11	Total	C	N	O	0	0
			97	61	18	18		

- Molecule 5 is a protein called The N-terminus of Flagellar L-ring protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	3	13	Total	C	N	O	0	0
			65	39	13	13		
5	8	13	Total	C	N	O	0	0
			65	39	13	13		
5	AC	13	Total	C	N	O	0	0
			65	39	13	13		
5	AH	13	Total	C	N	O	0	0
			65	39	13	13		
5	AM	13	Total	C	N	O	0	0
			65	39	13	13		
5	AR	13	Total	C	N	O	0	0
			65	39	13	13		
5	AW	13	Total	C	N	O	0	0
			65	39	13	13		
5	Ab	13	Total	C	N	O	0	0
			65	39	13	13		
5	Ag	13	Total	C	N	O	0	0
			65	39	13	13		
5	Al	13	Total	C	N	O	0	0
			65	39	13	13		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	Aq	13	Total	C	N	O	0	0
			65	39	13	13		
5	Av	13	Total	C	N	O	0	0
			65	39	13	13		
5	A1	13	Total	C	N	O	0	0
			65	39	13	13		
5	A6	13	Total	C	N	O	0	0
			65	39	13	13		
5	BA	13	Total	C	N	O	0	0
			65	39	13	13		
5	BF	13	Total	C	N	O	0	0
			65	39	13	13		
5	BK	13	Total	C	N	O	0	0
			65	39	13	13		
5	BP	13	Total	C	N	O	0	0
			65	39	13	13		
5	BU	13	Total	C	N	O	0	0
			65	39	13	13		
5	BZ	13	Total	C	N	O	0	0
			65	39	13	13		
5	Be	13	Total	C	N	O	0	0
			65	39	13	13		
5	Bj	13	Total	C	N	O	0	0
			65	39	13	13		
5	Bo	13	Total	C	N	O	0	0
			65	39	13	13		
5	Bt	13	Total	C	N	O	0	0
			65	39	13	13		
5	By	13	Total	C	N	O	0	0
			65	39	13	13		
5	B4	13	Total	C	N	O	0	0
			65	39	13	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	9	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	AD	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	AI	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	AN	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	AS	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	AX	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Ac	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Ah	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Am	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Ar	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Aw	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	A2	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	A7	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	BB	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	BG	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	BL	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	BQ	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	BV	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Ba	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Bf	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Bk	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Bp	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	Bu	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	Bz	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		
6	B5	287	Total	C	N	O	S	0	0
			2102	1324	371	400	7		

- Molecule 7 is a protein called Flagella basal-body protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	0	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	AE	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	AJ	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	AO	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	AT	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	AY	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Ad	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Ai	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	An	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	As	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Ax	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	A3	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	A8	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	BC	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	BH	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	BM	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		

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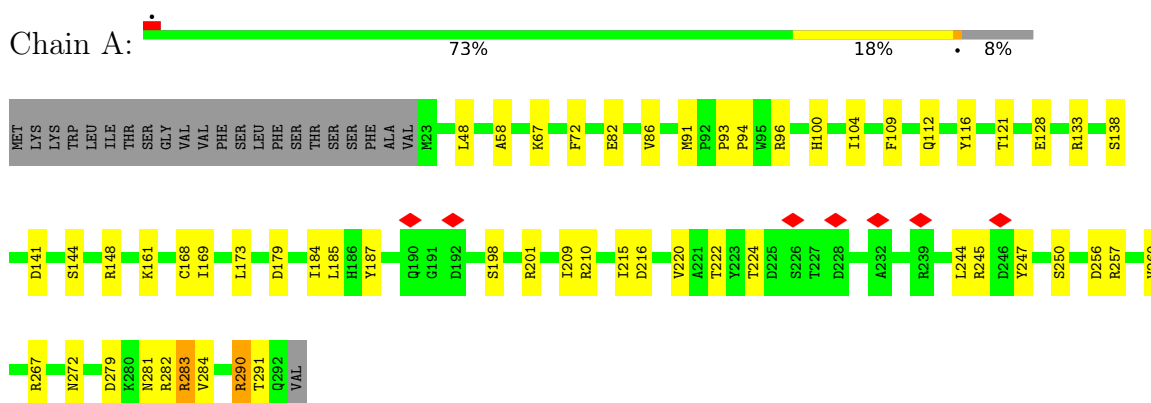
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Mol	Chain	Residues	Atoms					AltConf	Trace
7	BR	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	BW	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Bb	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Bg	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Bl	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Bq	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	Bv	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	B1	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		
7	B6	352	Total	C	N	O	S	0	0
			2774	1735	483	544	12		

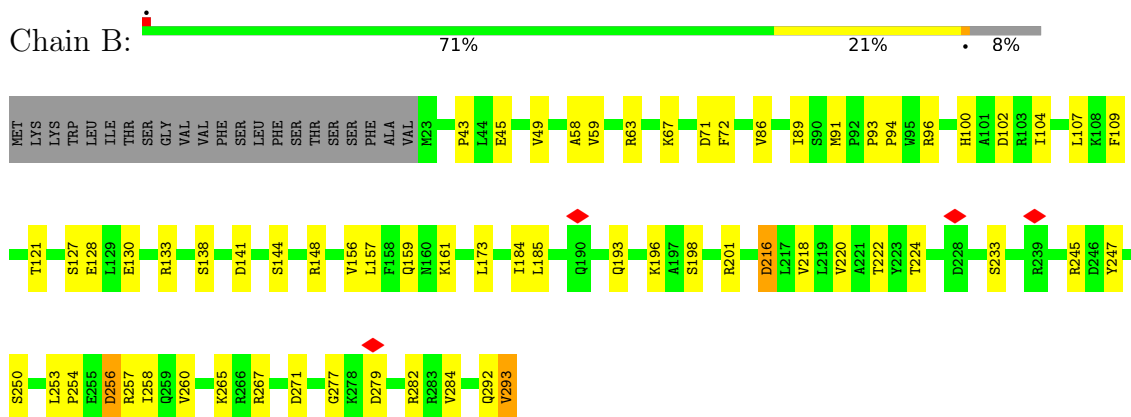
3 Residue-property plots

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.

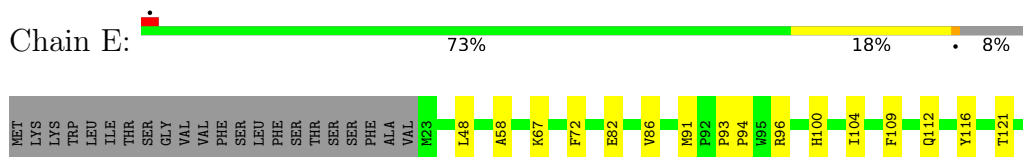
- Molecule 1: Component of sodium-driven polar flagellar motor

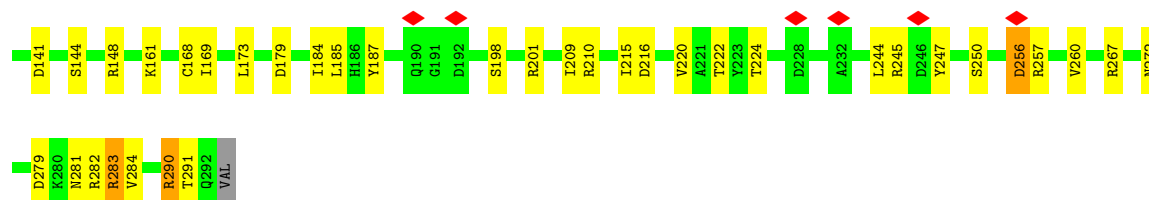


- Molecule 1: Component of sodium-driven polar flagellar motor



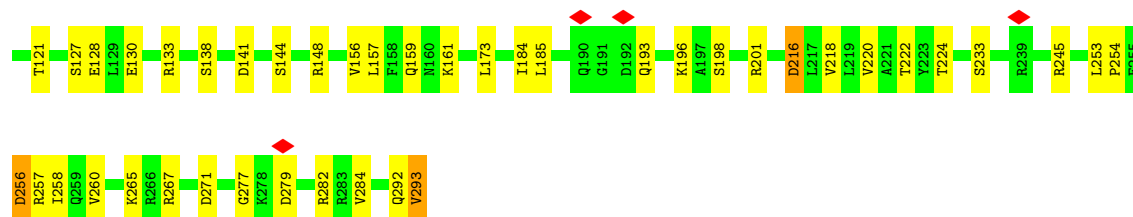
- Molecule 1: Component of sodium-driven polar flagellar motor





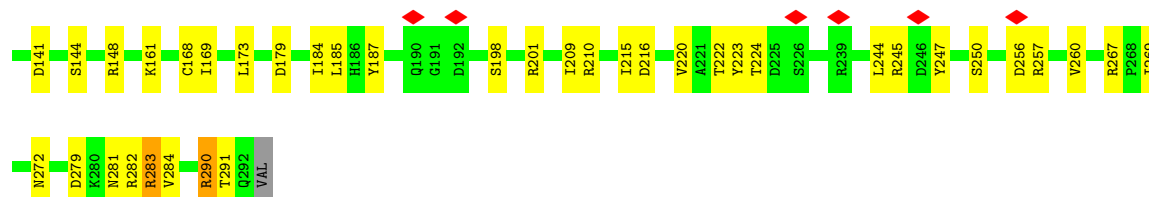
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain F: 71% 20% 8%



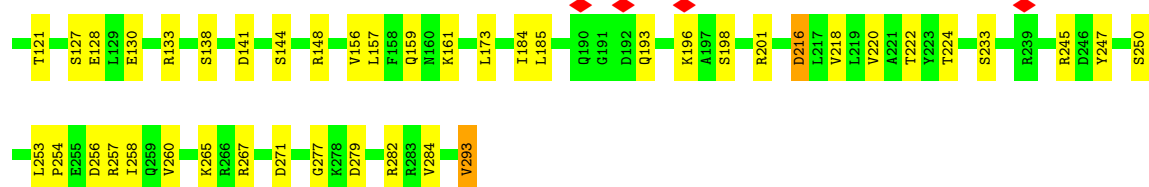
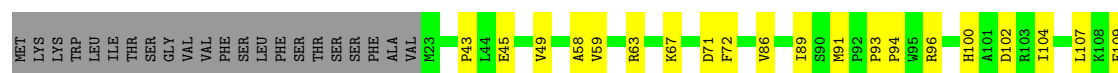
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain I: 73% 19% 8%



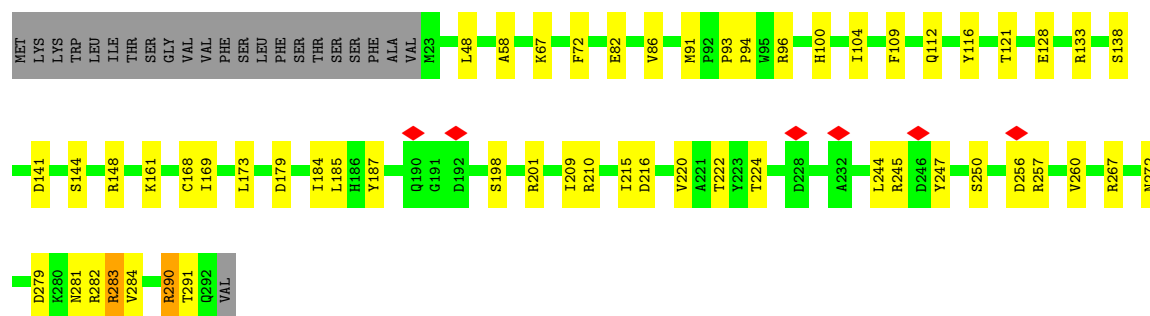
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain J: 71% 21% 8%



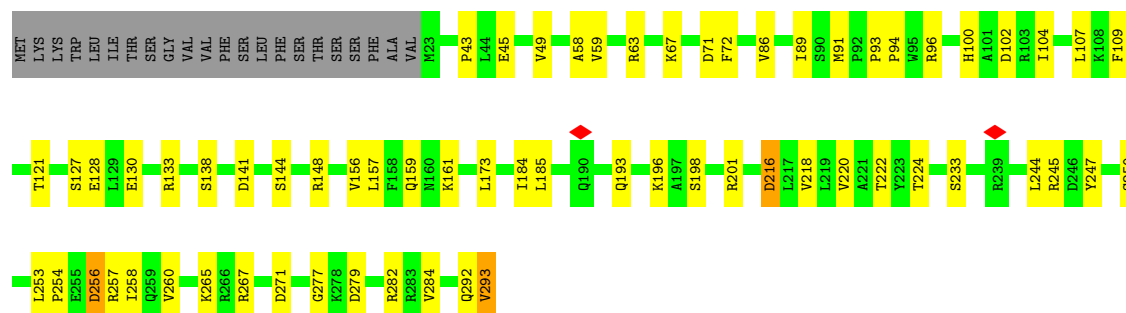
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain M: 



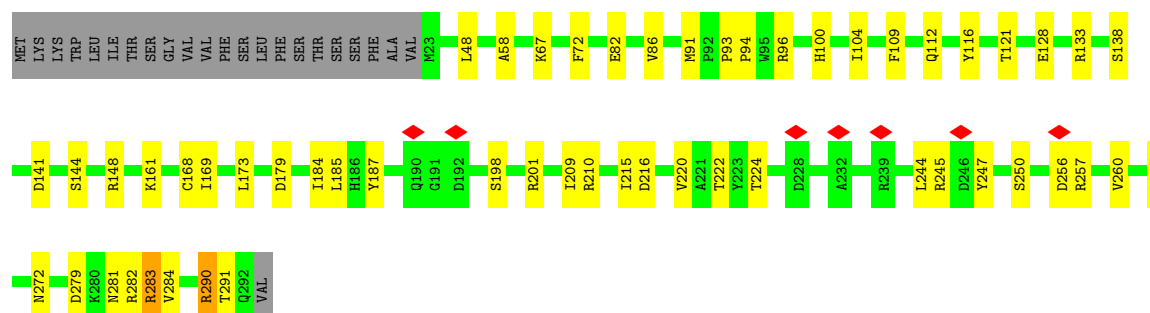
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain N: 



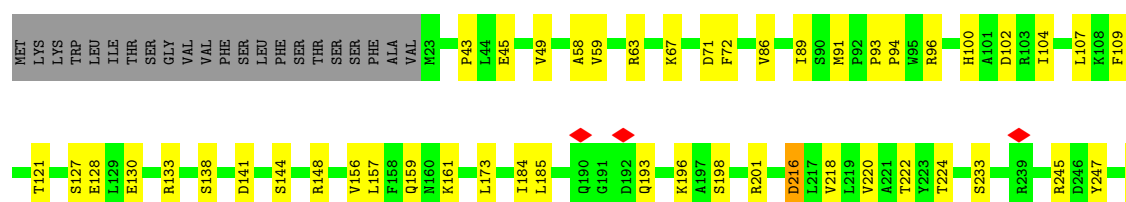
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain Q: 



- Molecule 1: Component of sodium-driven polar flagellar motor

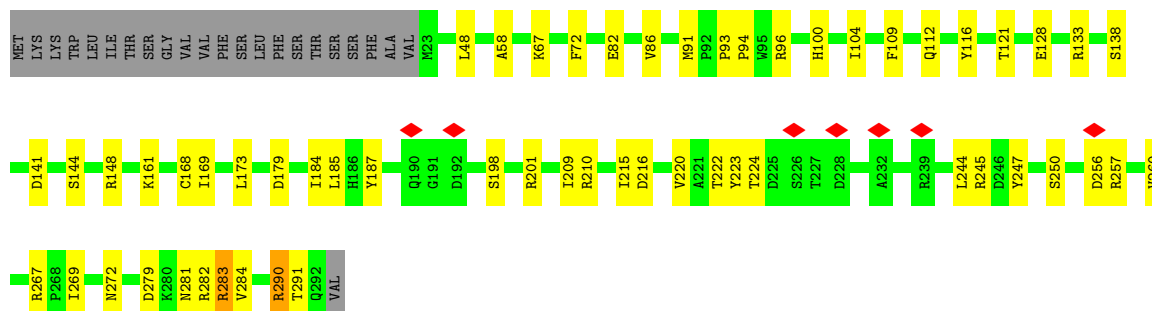
Chain R: 





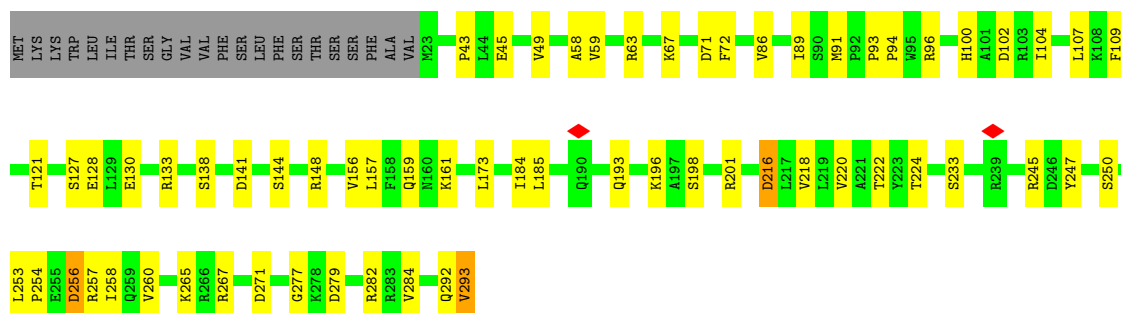
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain U: 73% 19% 8%



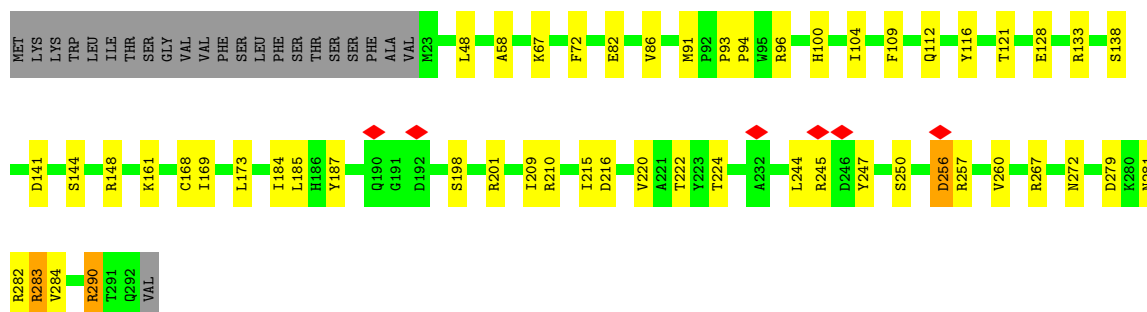
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain V: 71% 21% 8%



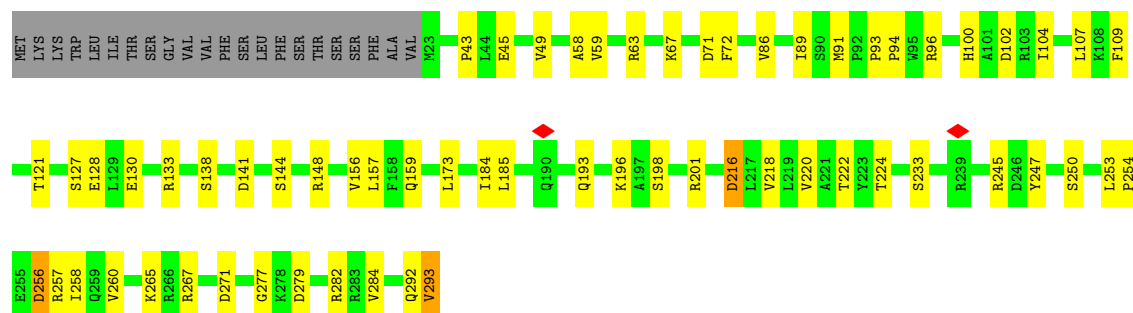
- Molecule 1: Component of sodium-driven polar flagellar motor

Chain Y: 74% 17% 8%

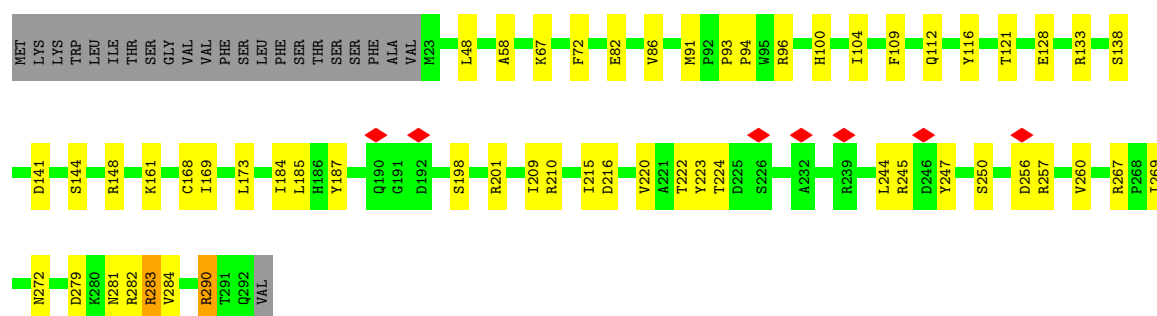


- Molecule 1: Component of sodium-driven polar flagellar motor

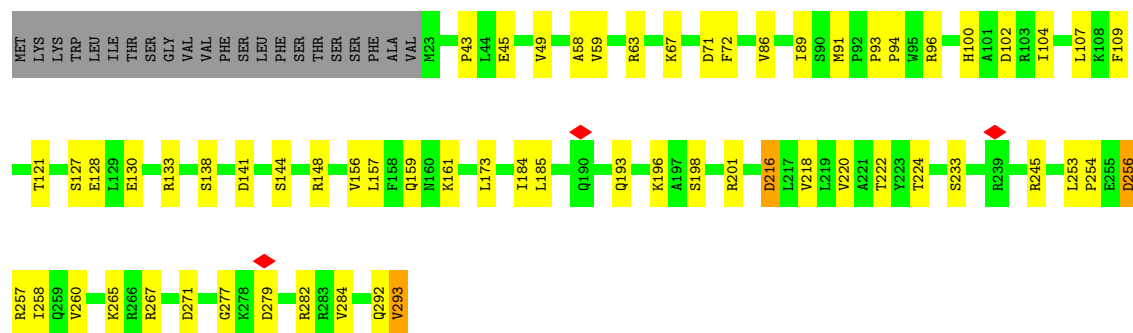
Chain Z: 71% 20% 8%



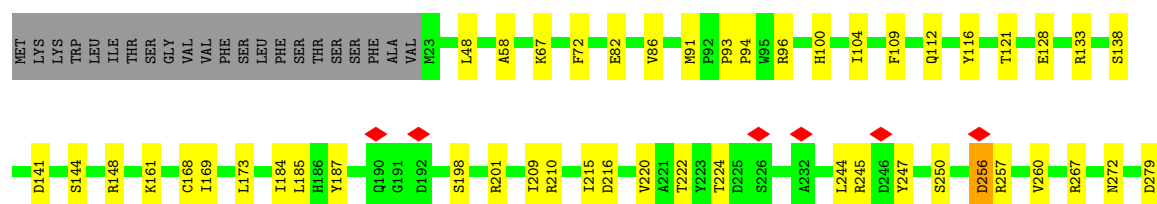
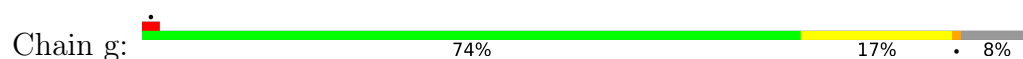
- Molecule 1: Component of sodium-driven polar flagellar motor

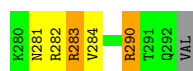


- Molecule 1: Component of sodium-driven polar flagellar motor

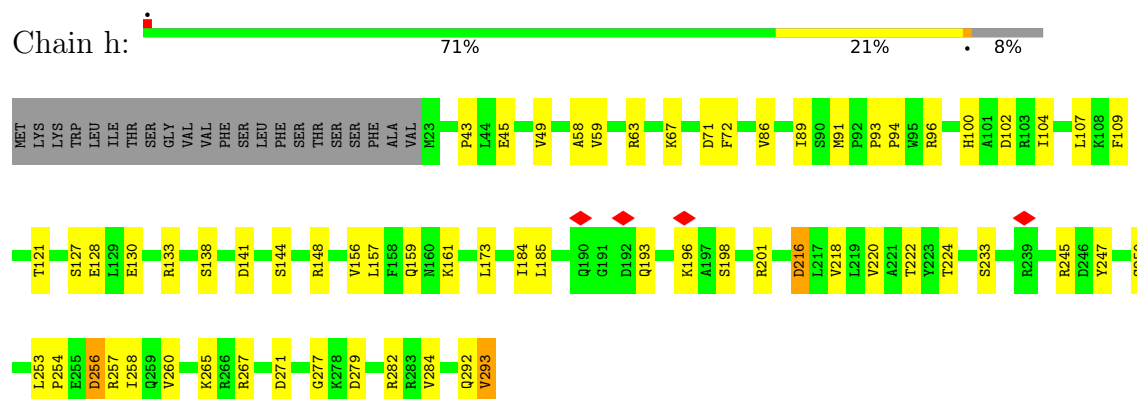


- Molecule 1: Component of sodium-driven polar flagellar motor

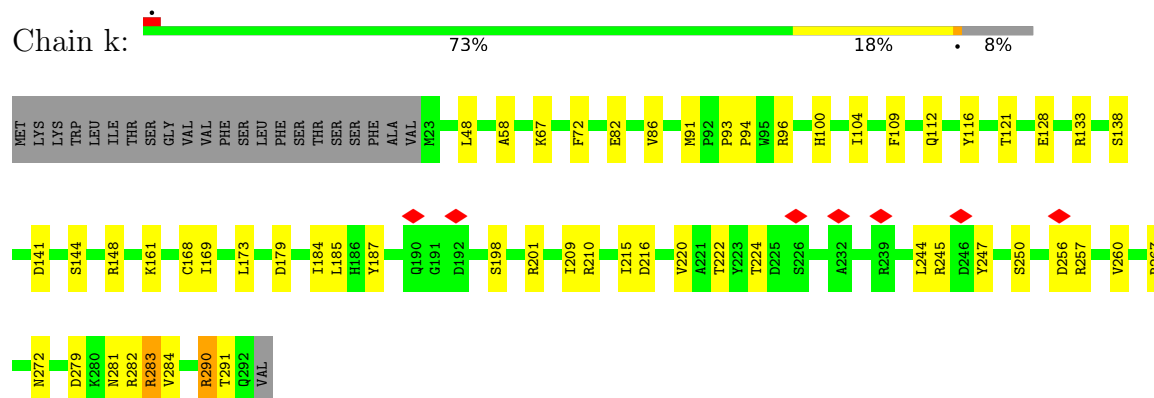




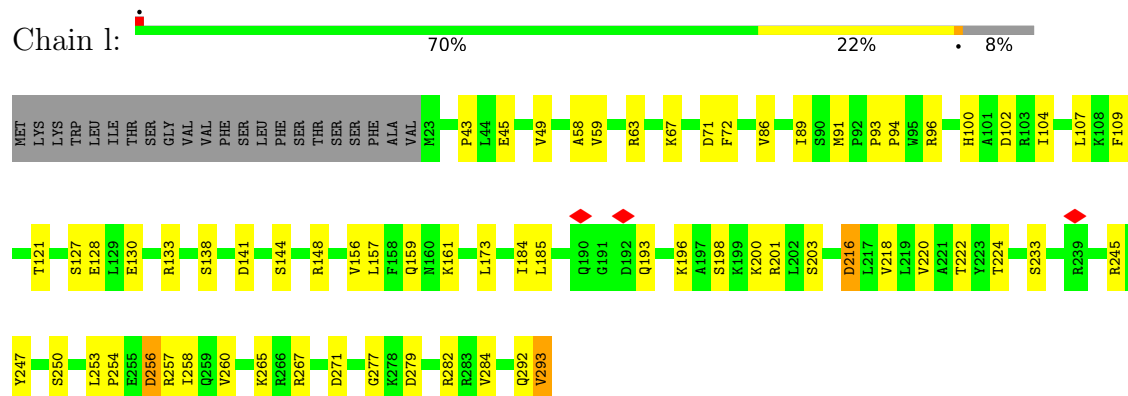
- Molecule 1: Component of sodium-driven polar flagellar motor



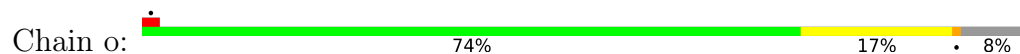
- Molecule 1: Component of sodium-driven polar flagellar motor

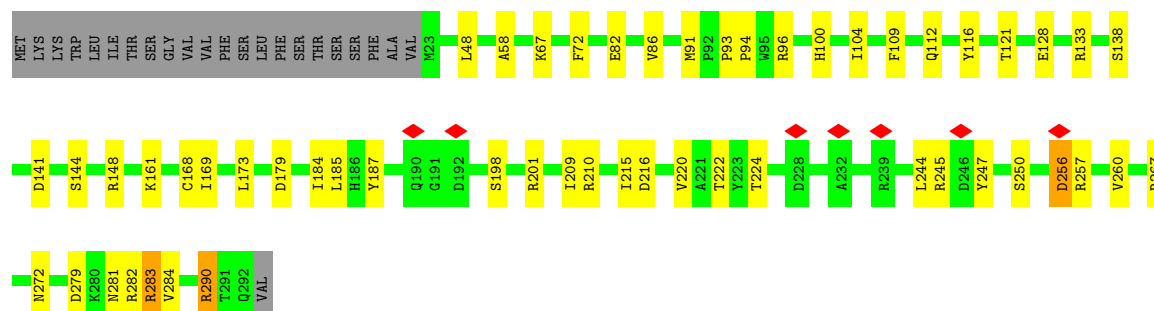


- Molecule 1: Component of sodium-driven polar flagellar motor

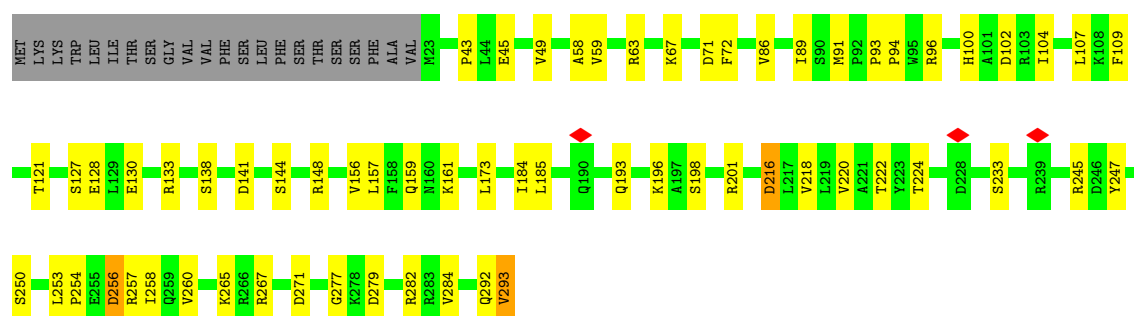


- Molecule 1: Component of sodium-driven polar flagellar motor

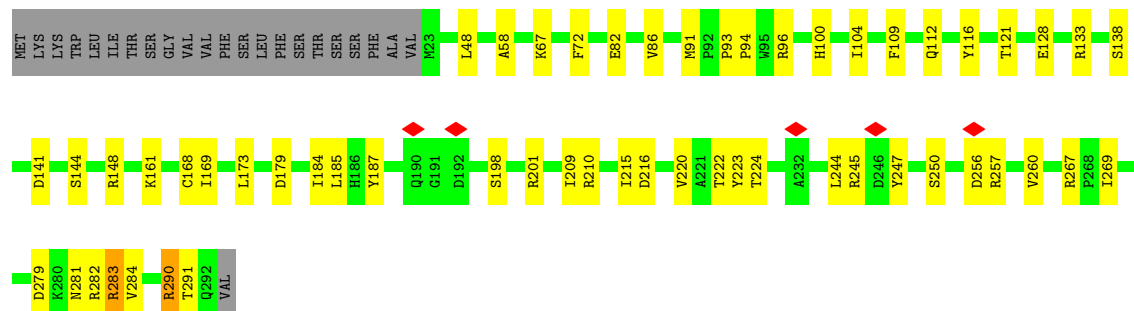




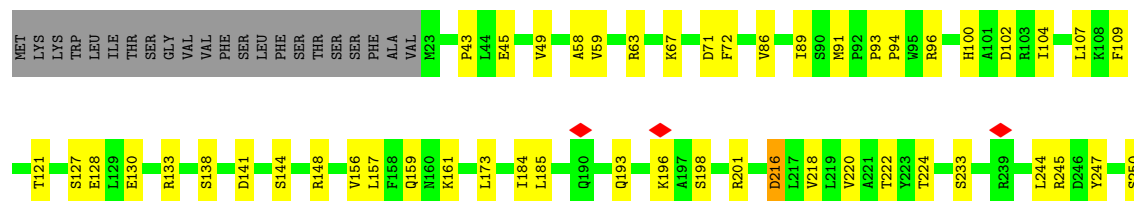
- Molecule 1: Component of sodium-driven polar flagellar motor



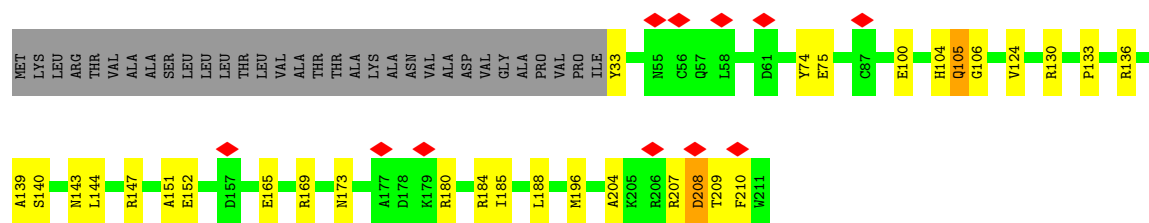
- Molecule 1: Component of sodium-driven polar flagellar motor



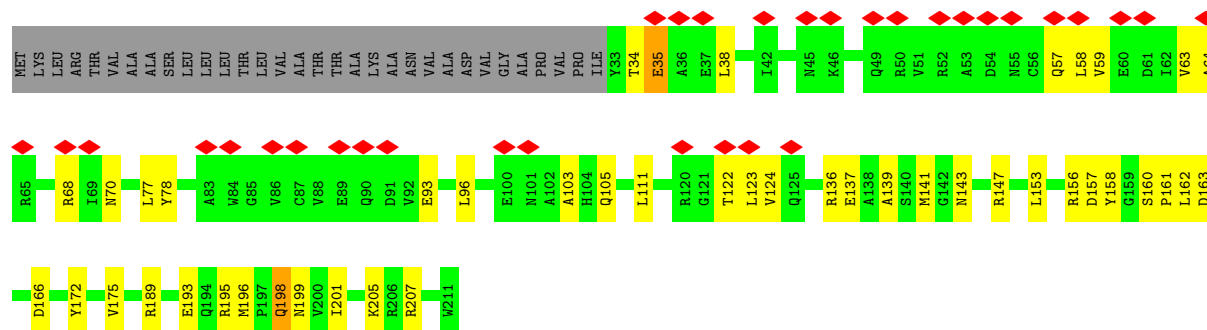
- Molecule 1: Component of sodium-driven polar flagellar motor



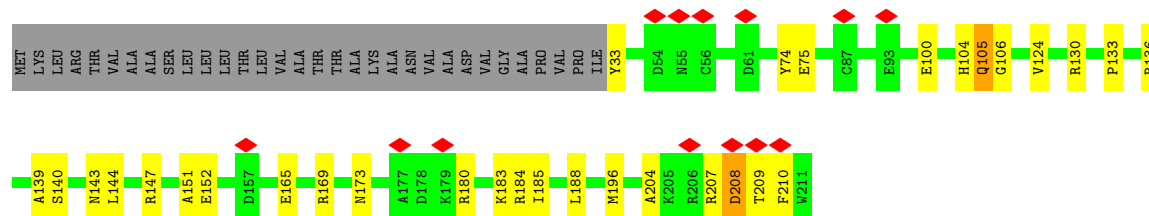




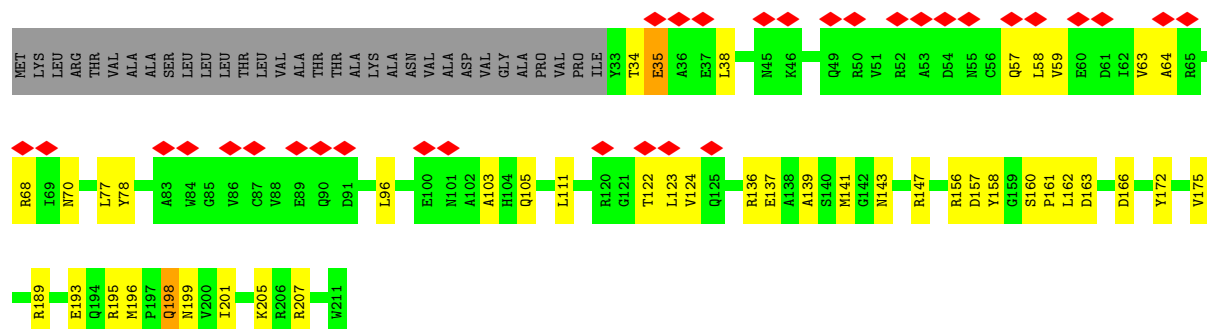
• Molecule 2: Sodium-type flagellar motor component



• Molecule 2: Sodium-type flagellar motor component

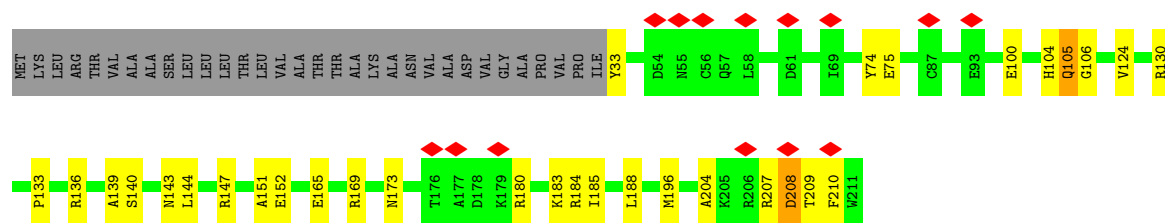


• Molecule 2: Sodium-type flagellar motor component

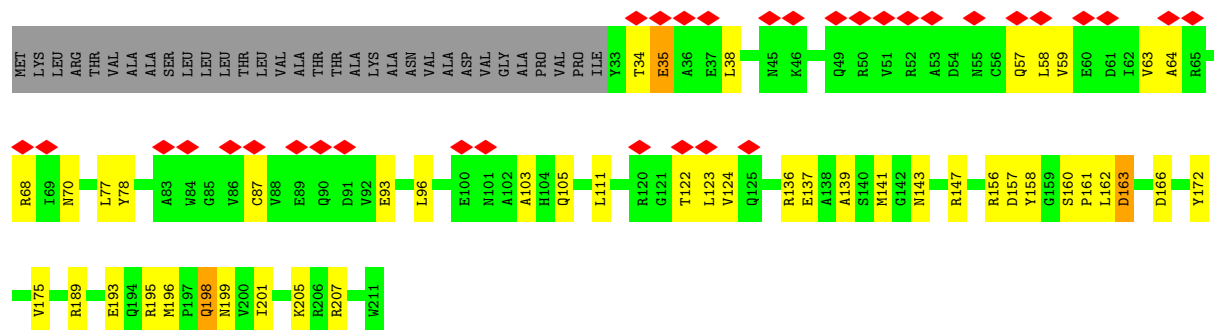


• Molecule 2: Sodium-type flagellar motor component

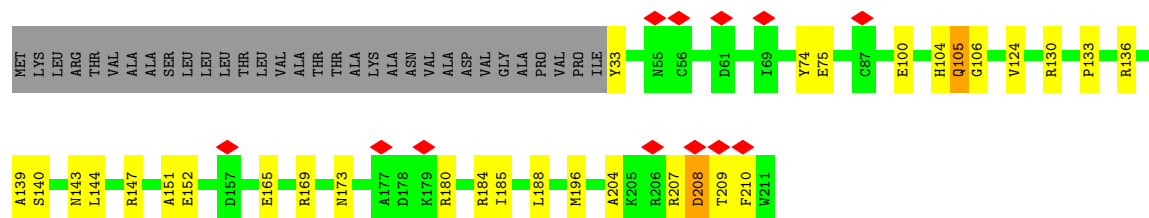




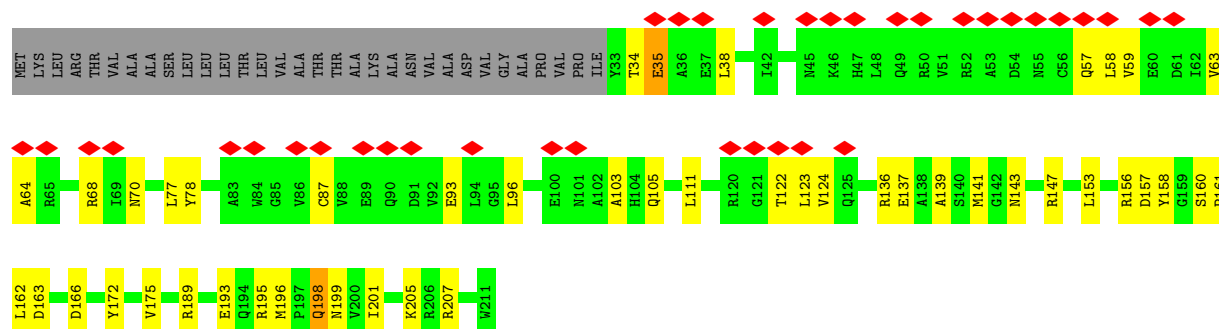
• Molecule 2: Sodium-type flagellar motor component



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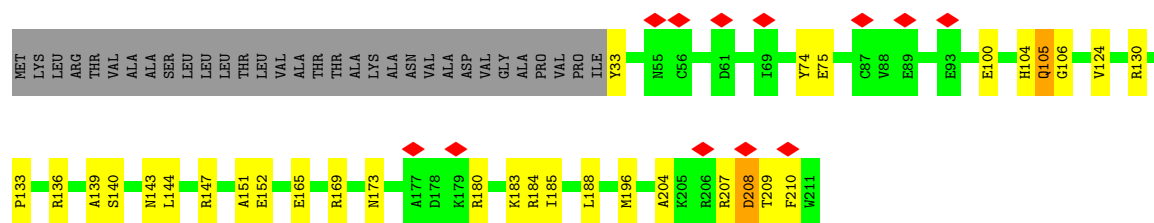


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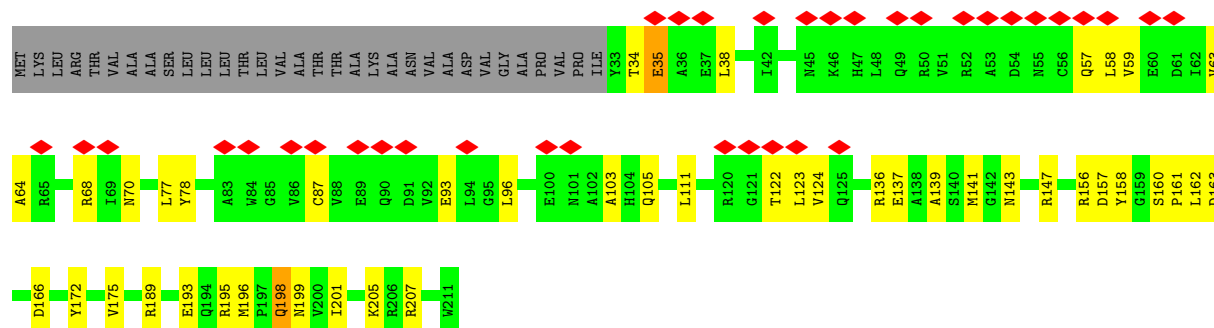


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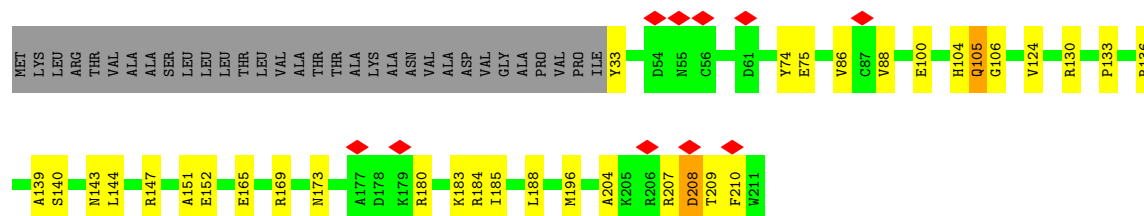




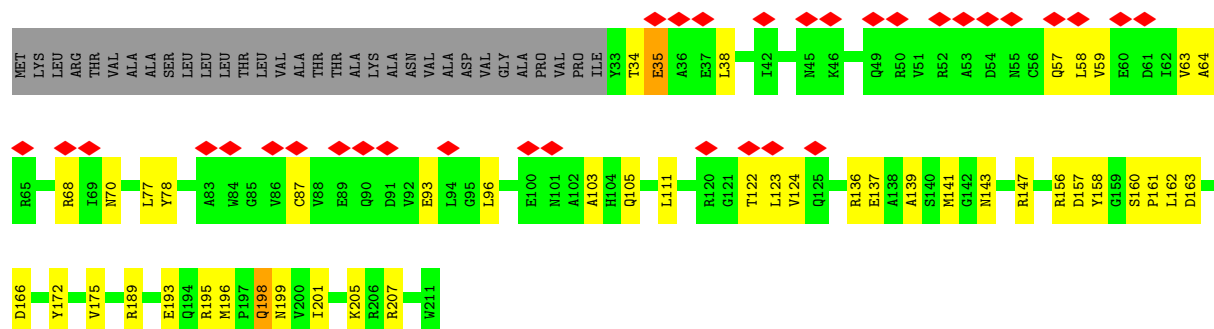
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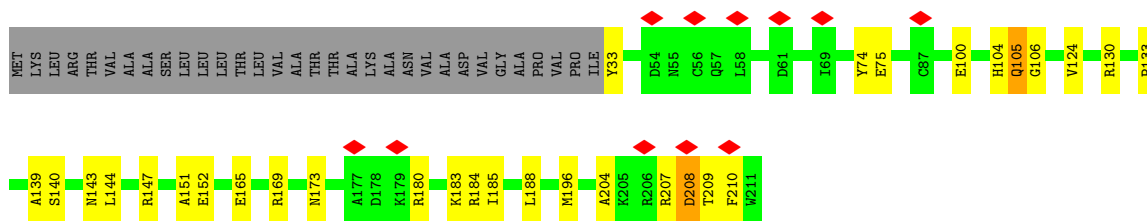


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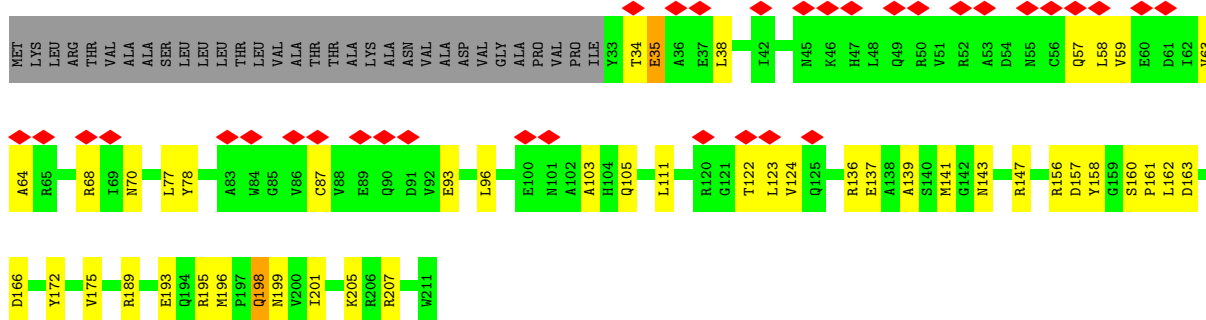


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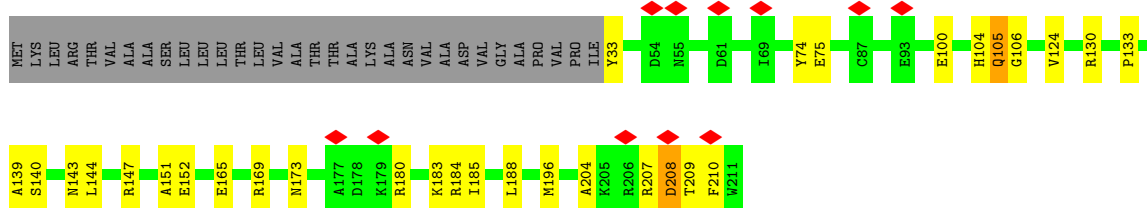




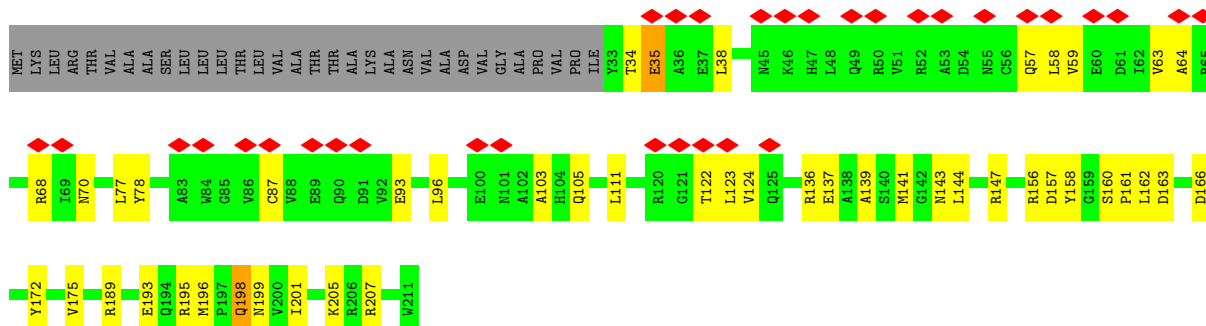
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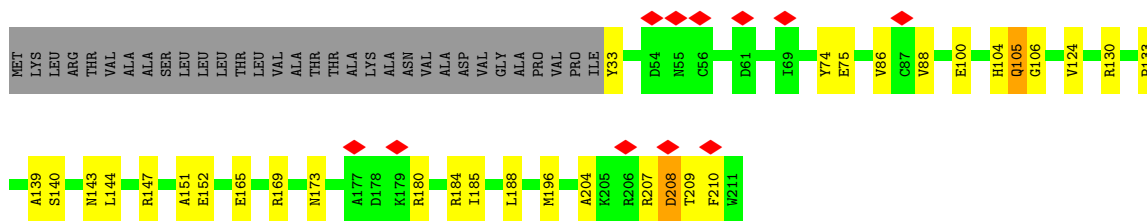


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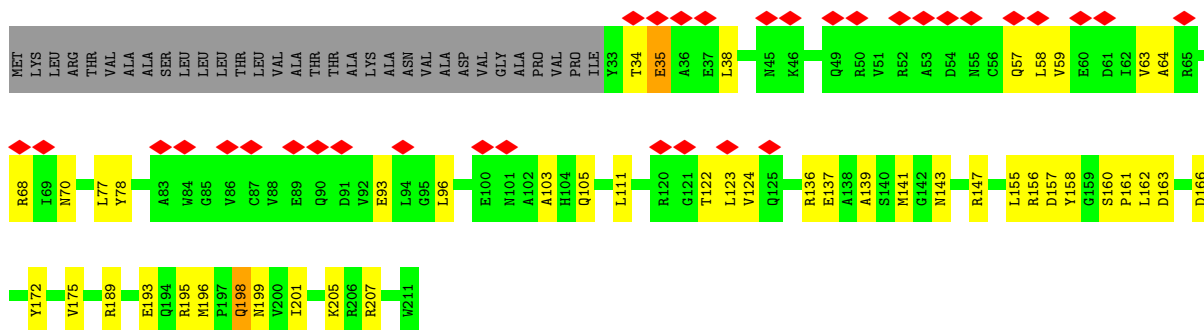


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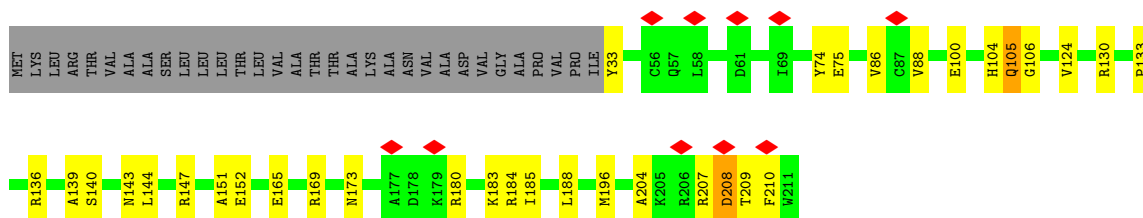




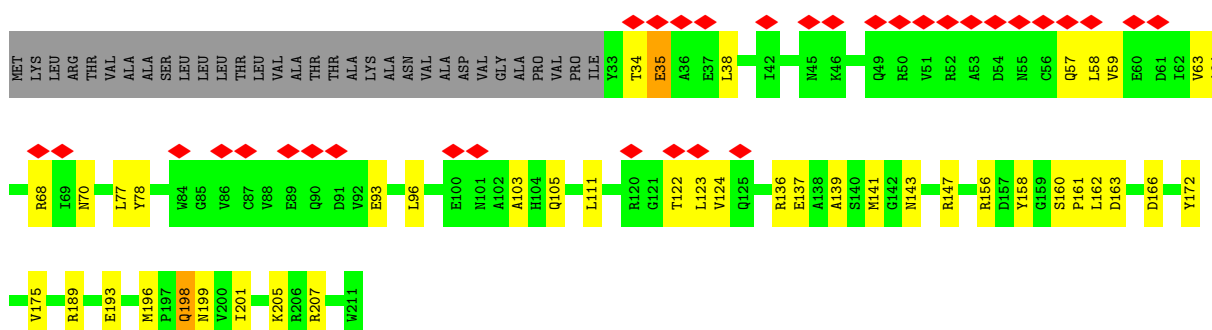
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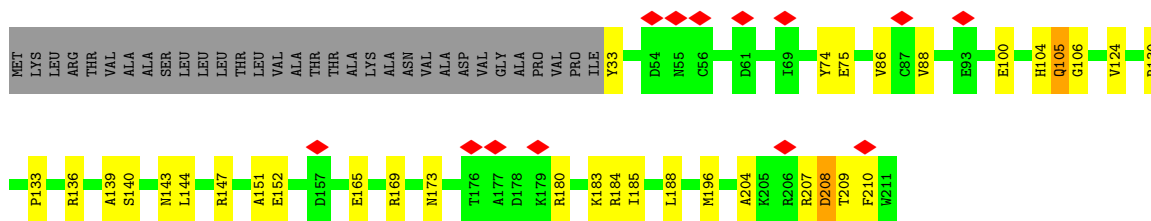


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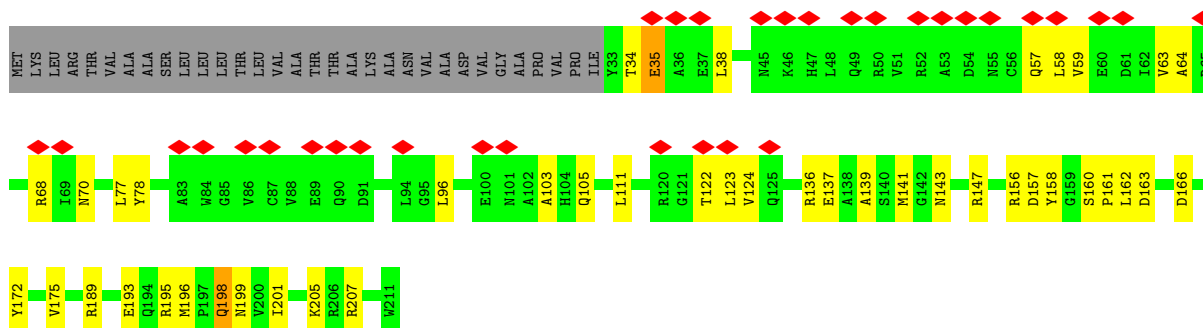


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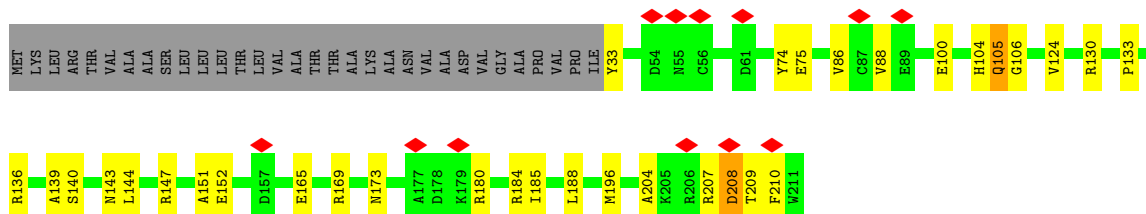




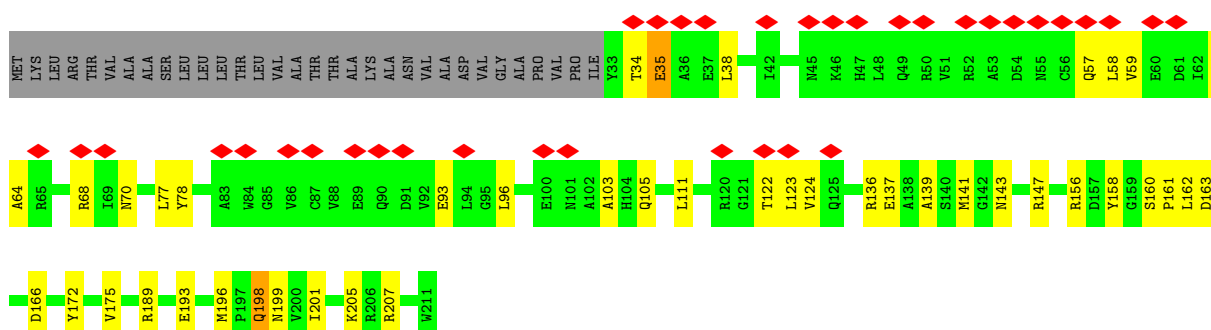
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• Molecule 3: Flagellar L-ring protein



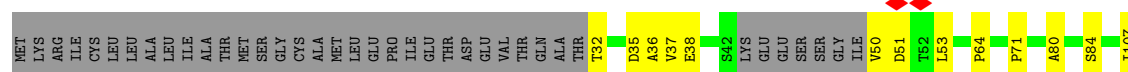
• Molecule 3: Flagellar L-ring protein



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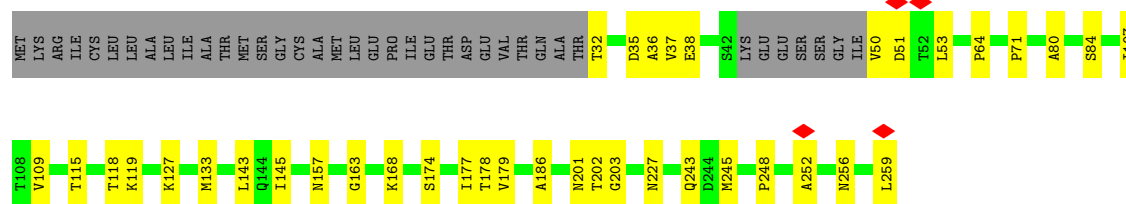


• Molecule 3: Flagellar L-ring protein



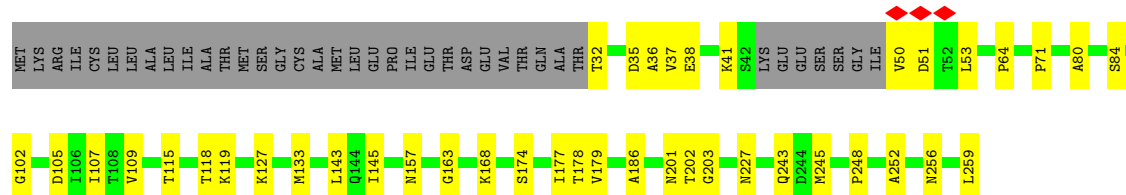
• Molecule 3: Flagellar L-ring protein

Chain Ae: 



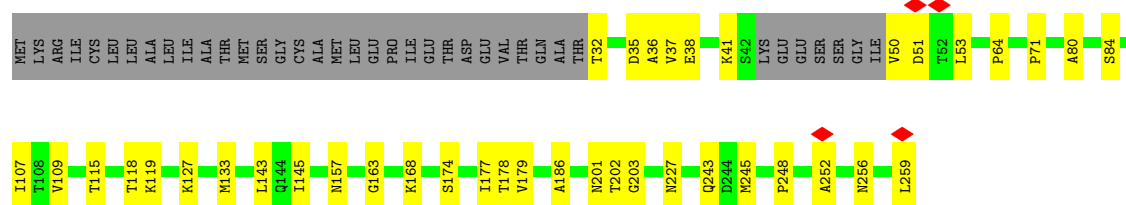
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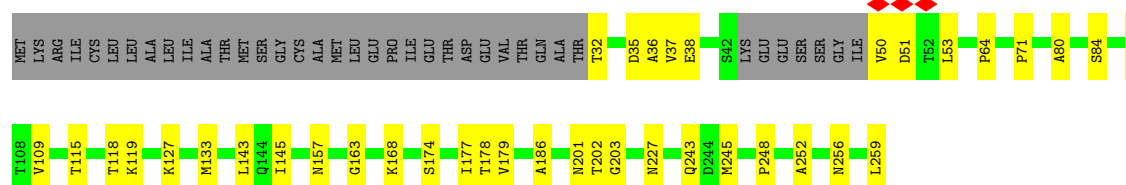
- Molecule 3: Flagellar L-ring protein

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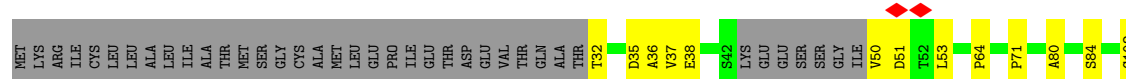
- Molecule 3: Flagellar L-ring protein

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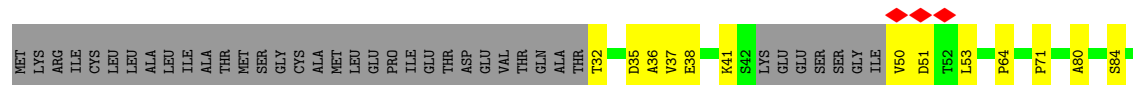
- Molecule 3: Flagellar L-ring protein

Chain Ay: 





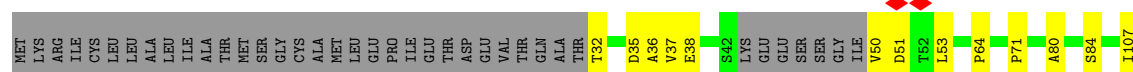
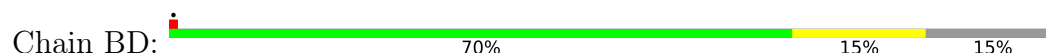
• Molecule 3: Flagellar L-ring protein



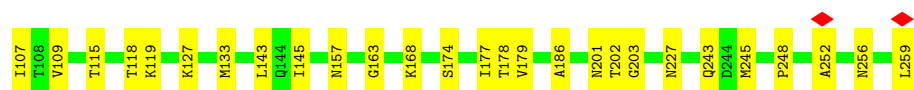
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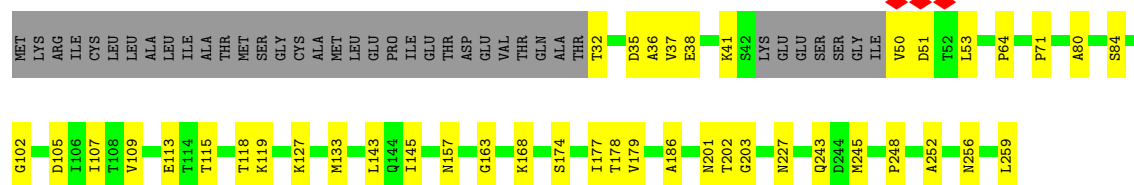


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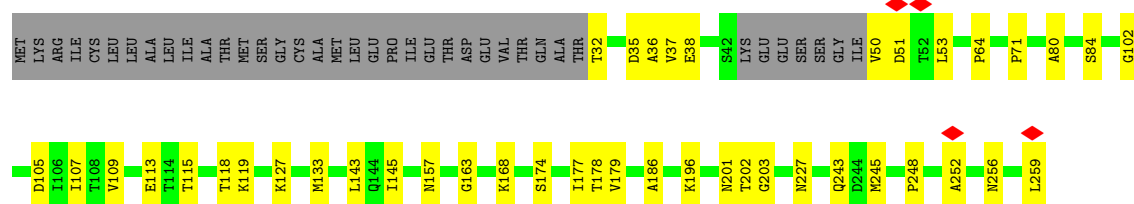
• Molecule 3: Flagellar L-ring protein

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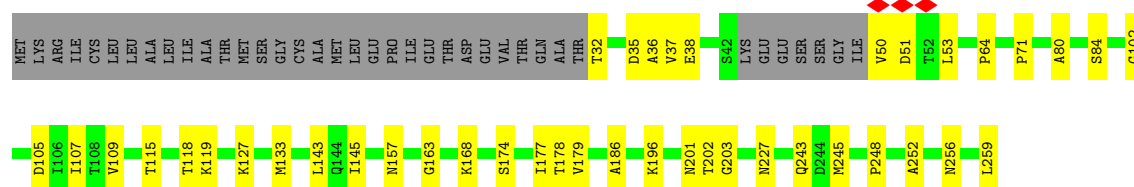
- Molecule 3: Flagellar L-ring protein

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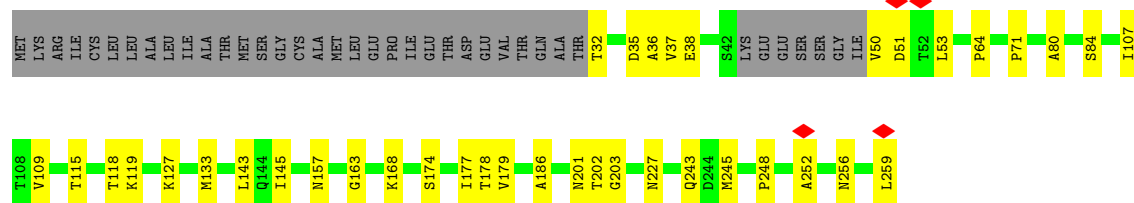
- Molecule 3: Flagellar L-ring protein

Chain BX: 



- Molecule 3: Flagellar L-ring protein

Chain Bc: 



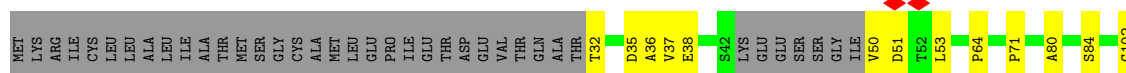
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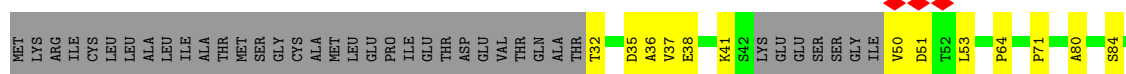




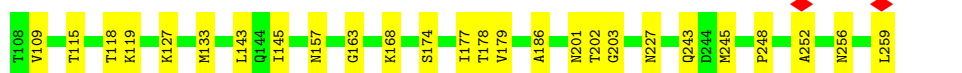
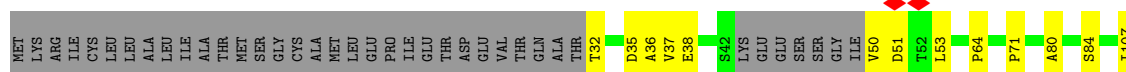
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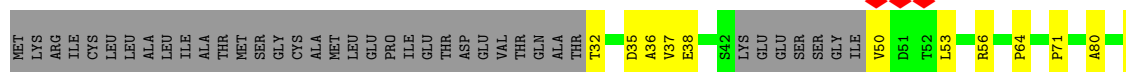
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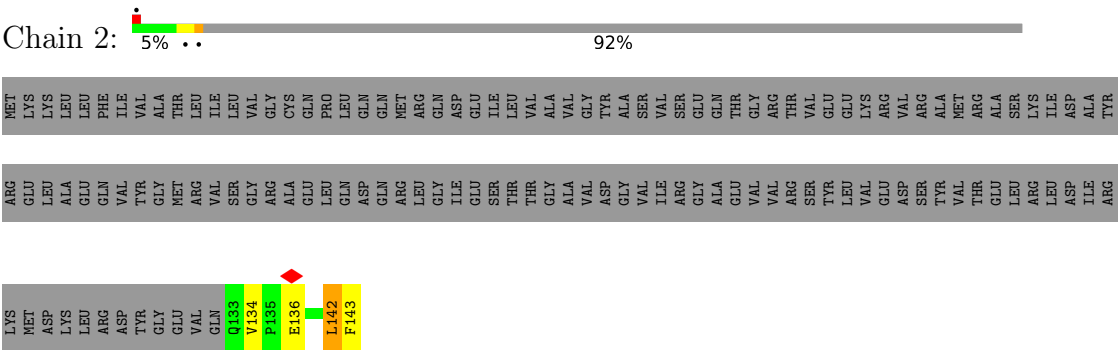
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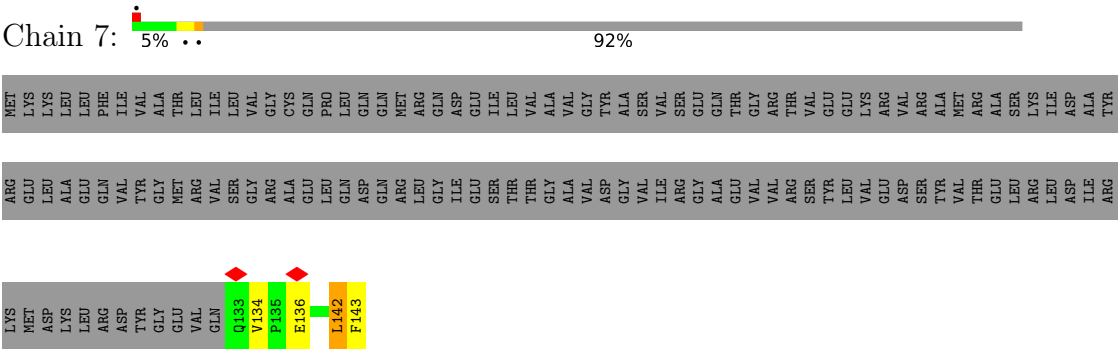
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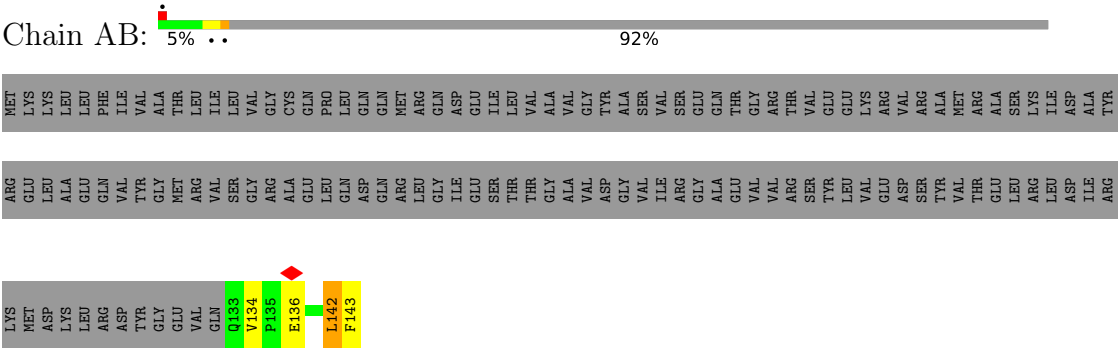
- Molecule 4: Flagellar assembly lipoprotein FlgP



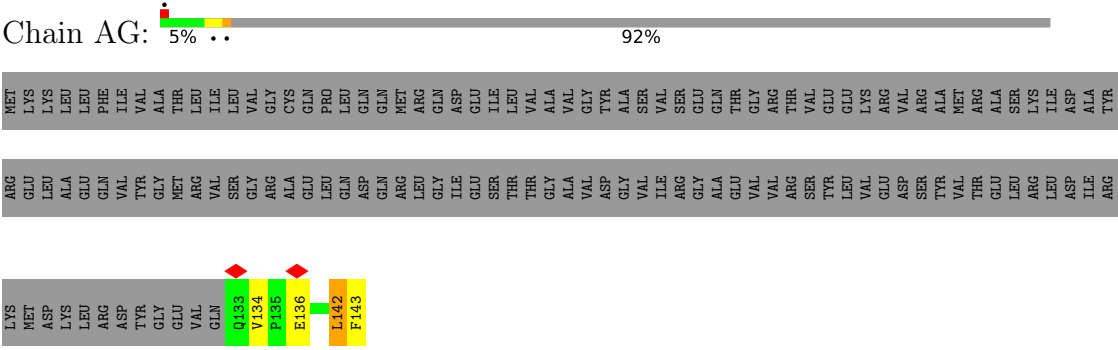
● Molecule 4: Flagellar assembly lipoprotein FlgP



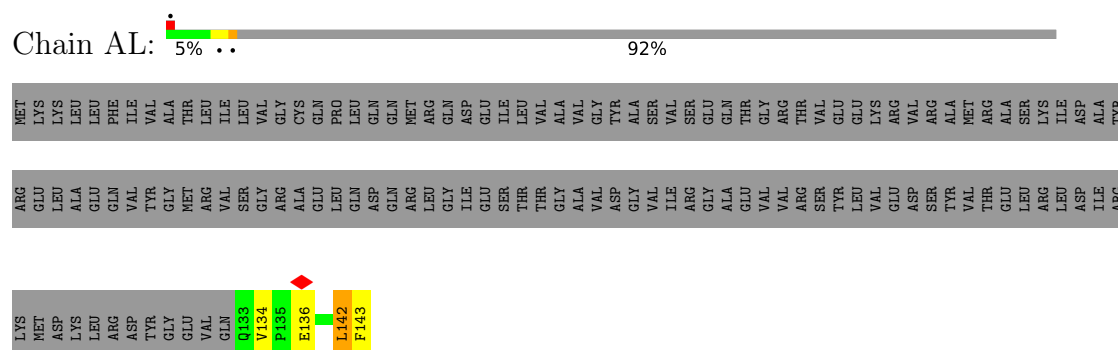
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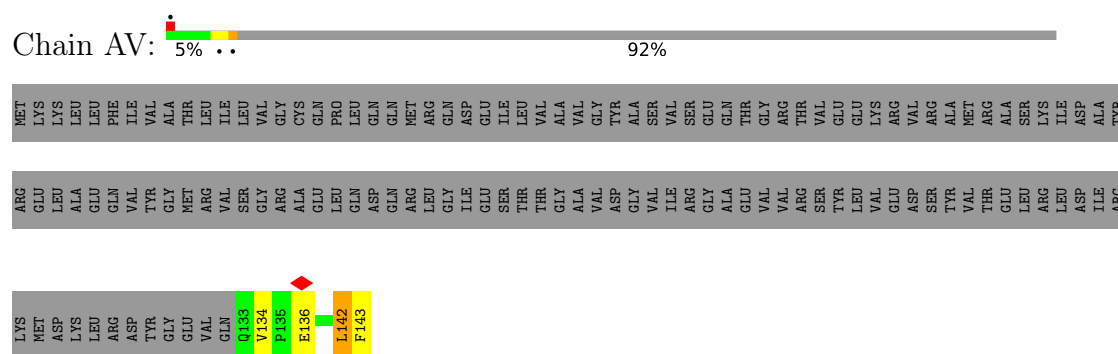
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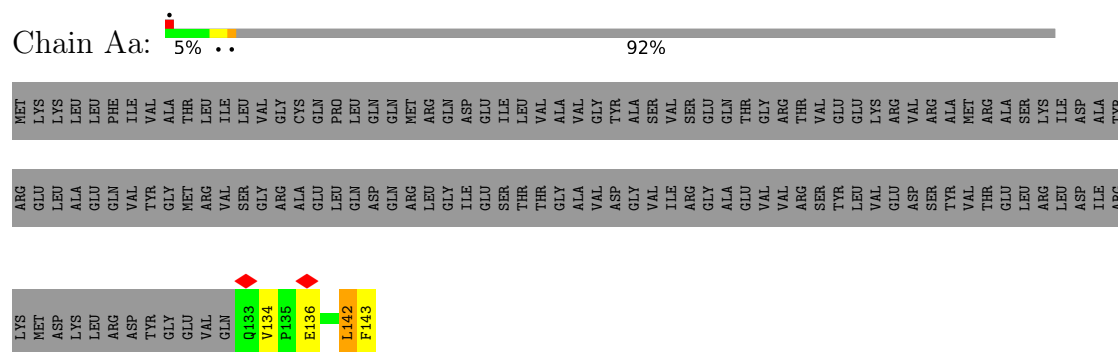
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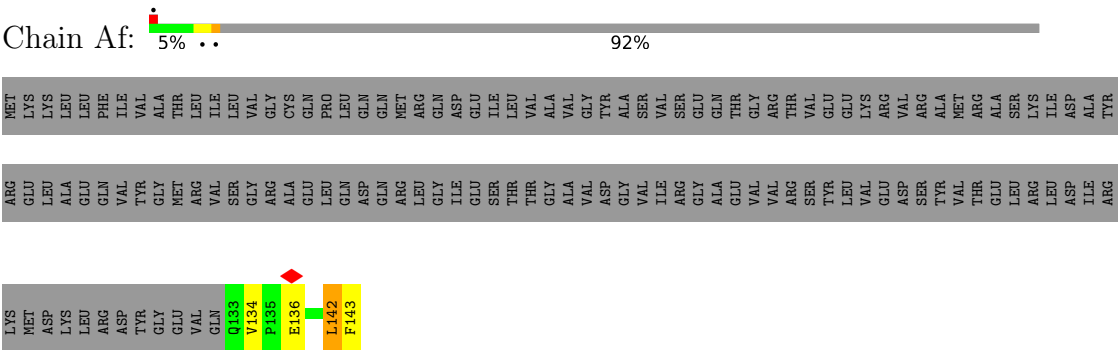
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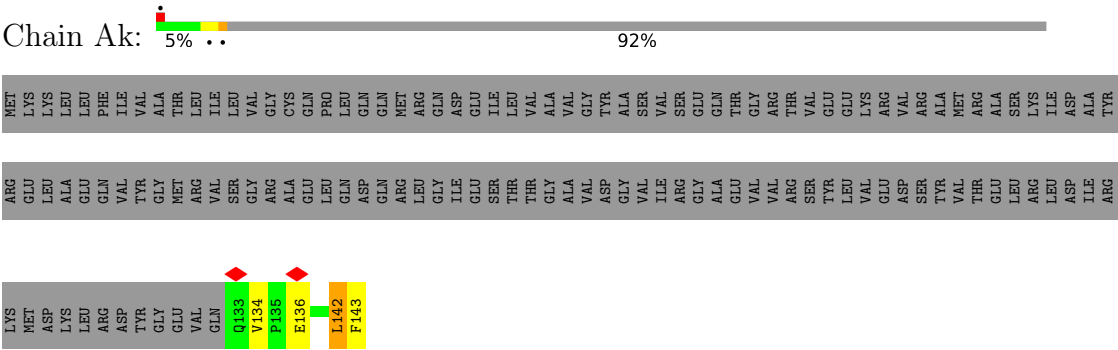
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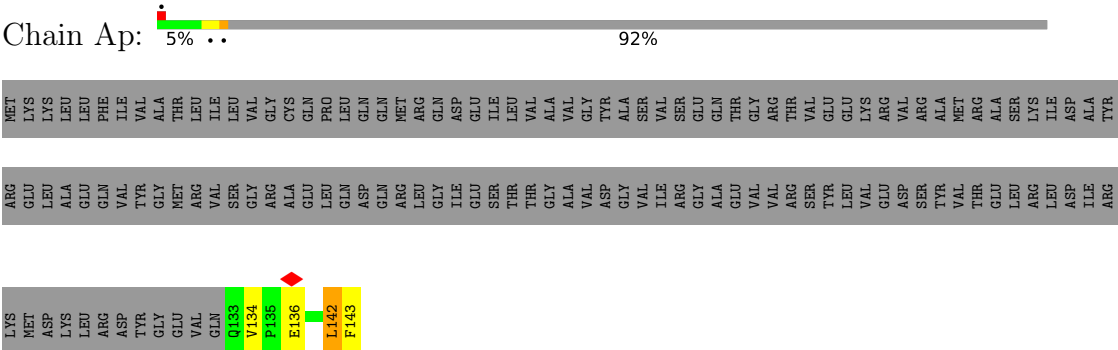
- Molecule 4: Flagellar assembly lipoprotein FlgP



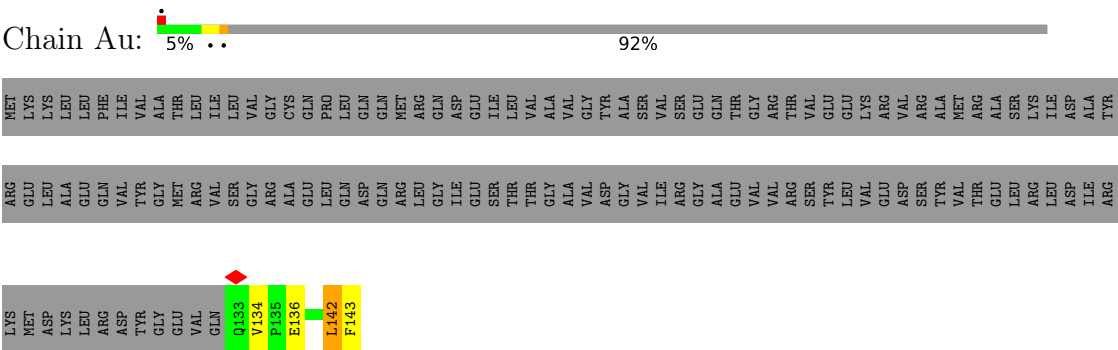
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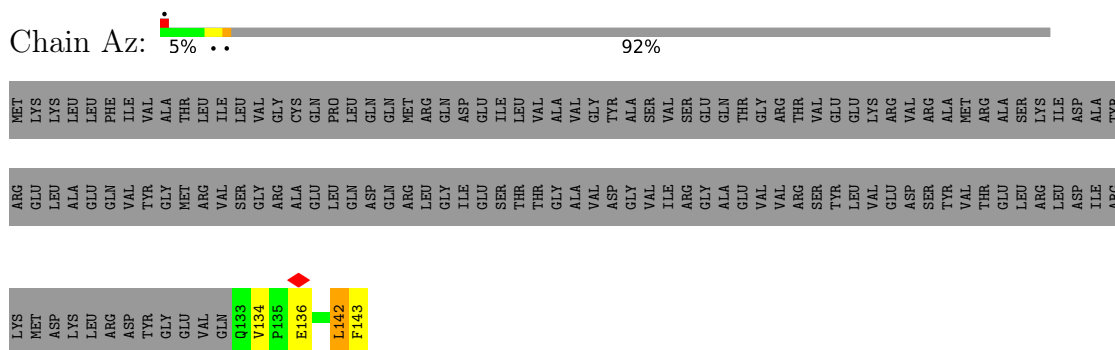
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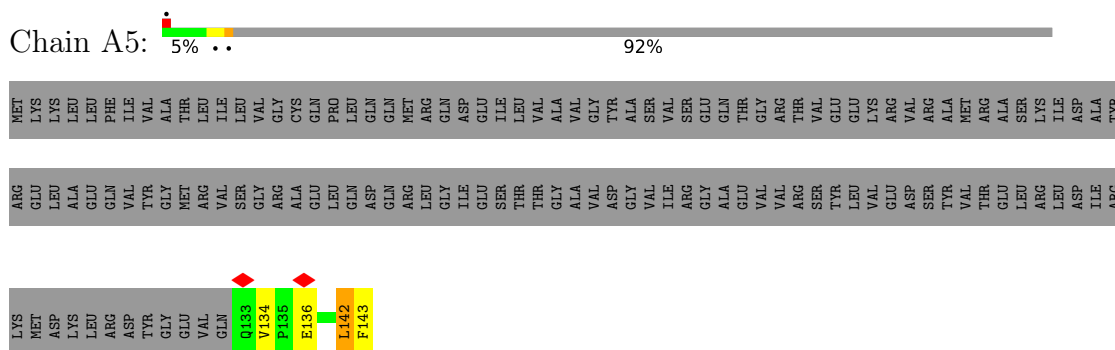
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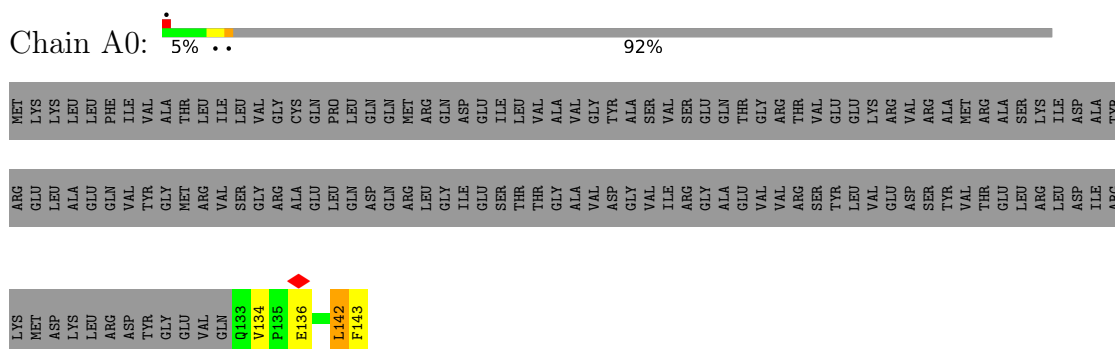
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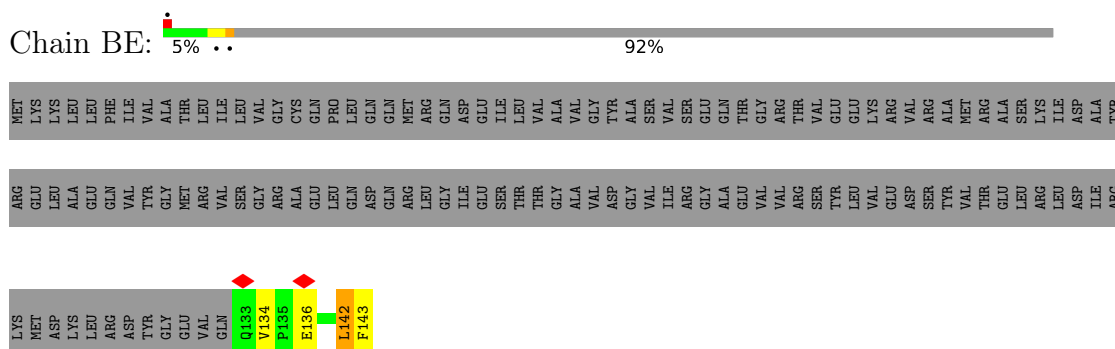
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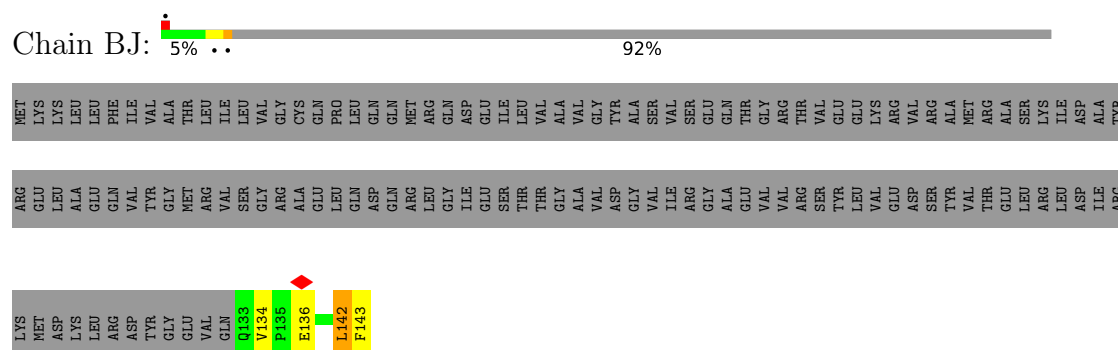
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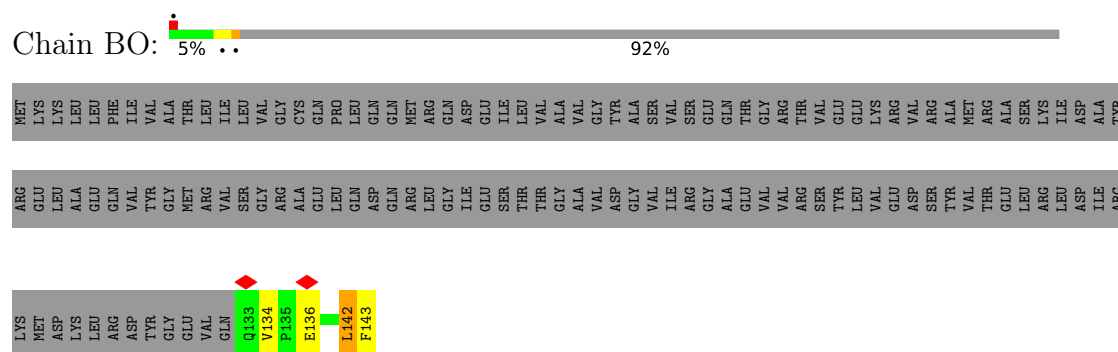
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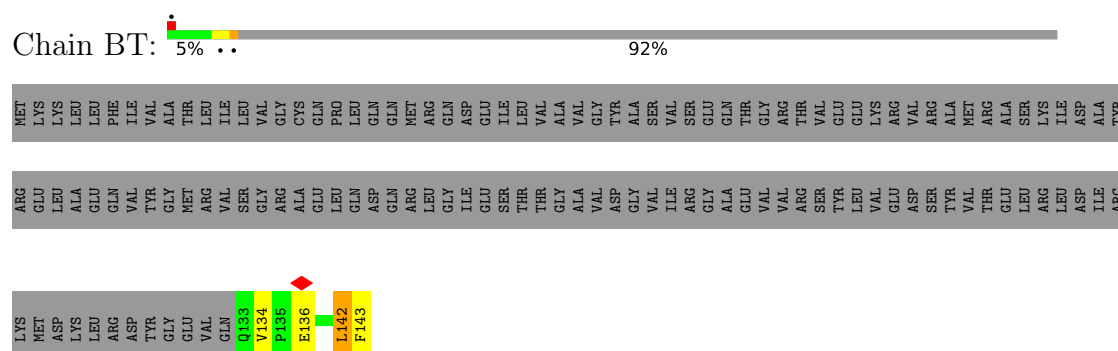
- Molecule 4: Flagellar assembly lipoprotein FlgP



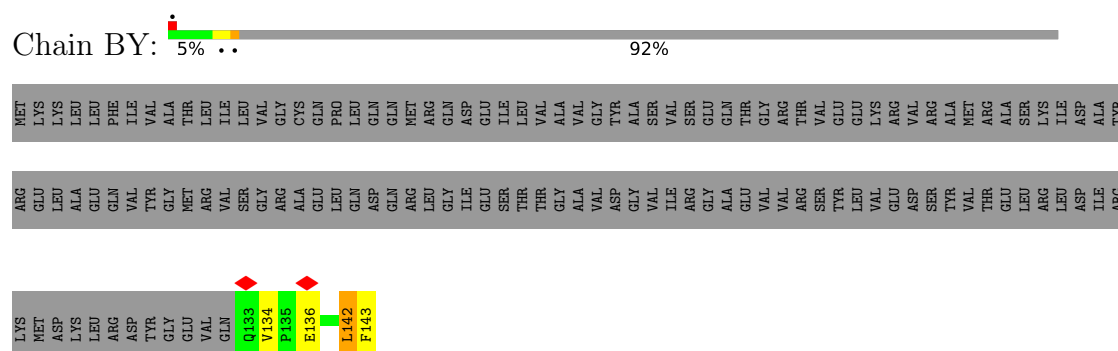
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MET	LYS	LYS	LEU	LEU	PHE	ILE	VAL	ALA	THR	LEU	ILE	LEU	VAL	GLY	CYS	GLN	PRO	LEU	GLN	GLN	MET	ARG	GLN	ASP	GLU	ILE	LEU	VAL	ALA	VAL	GLY	TYR	ALA	SER	VAL	ILE	SER	GLU	GLN	THR	GLY	ARG	THR	VAL	GLU	LYS	ARG	VAL	ARG	ALA	MET	ARG	ALA	LYS	ILE	ASP	ALA	TYR		
ARG	GLU	LEU	ALA	GLU	GLN	VAL	TYR	GLY	MET	ARG	VAL	GLN	SER	GLY	ARG	ALA	GLU	LEU	GLN	ASP	GLN	ARG	LEU	GLY	ILE	GLU	THR	THR	GLY	ALA	VAL	ASP	GLY	VAL	ILE	ARG	GLY	ALA	GLU	VAL	VAL	ARG	ASP	SER	TYR	LEU	VAL	GLU	ASP	SER	TYR	VAL	GLU	THR	GLU	ILE	ASP	ILE	ARG	
LYS	MET	ASP	LYS	LEU	ARG	ASP	TYR	GLY	GLU	VAL	GLN	Q133	V134	P135	E136	L142	F143																																											

● Molecule 4: Flagellar assembly lipoprotein FlgP



MET	LYS	LYS	LEU	LEU	PHE	ILE	VAL	ALA	THR	THR	LEU	ILE	LEU	VAL	GLY	CYS	GLN	PRO	LEU	GLN	GLN	MET	ARG	GLY	ASP	GLU	ILE	LEU	THR	THR	VAL	ALA	VAL	GLY	TYR	ALA	SER	VAL	ILE	SER	GLU	GLN	THR	GLY	ARG	THR	VAL	GLU	LYS	ARG	VAL	ARG	ALA	MET	ARG	ALA	LYS	ILE	ASP	ALA	TYR
ARG	GLU	LEU	ALA	GLU	GLN	VAL	TYR	GLY	MET	ARG	VAL	SER	GLY	ARG	ALA	GLU	LEU	GLN	GLN	ASP	GLN	ARG	LEU	GLY	ILE	GLU	SER	THR	THR	VAL	ALA	VAL	ASP	GLY	VAL	ILE	SER	ARG	GLY	ALA	VAL	ARG	THR	SER	TYR	LEU	VAL	ASP	SER	TYR	VAL	GLU	THR	GLU	ILE	ASP	ILE	ARG	TYR		
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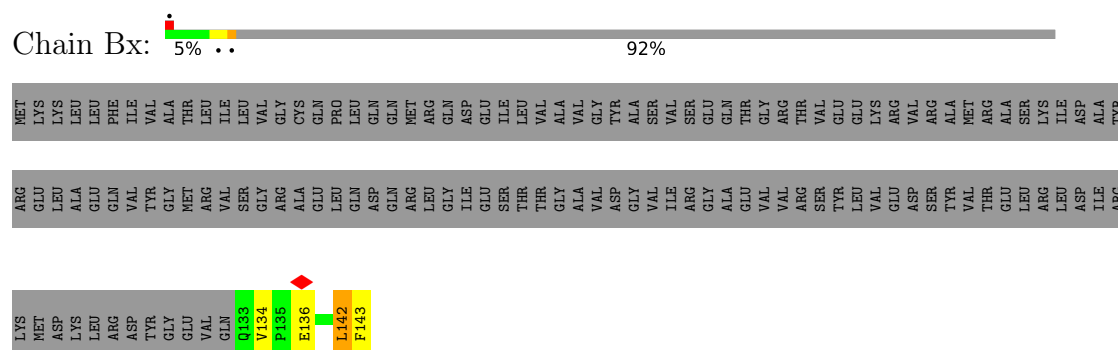
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ARG	GLU	LEU	ALA	GLU	GLN	VAL	TYR	GLY	MET	ARG	VAL	SER	GLY	ARG	ALA	GLU	LEU	GLN	ASP	GLN	ARG	LEU	GLY	ILE	GLU	SER	THR	THR	THR	VAL	ALA	VAL	ASP	GLY	VAL	ILE	SER	ARG	GLY	ALA	VAL	ARG	THR	SER	TYR	LEU	VAL	ASP	SER	TYR	VAL	GLU	THR	GLU	ILE	ASP	ILE	ARG	TYR		
LYS	MET	ASP	LYS	LEU	ARG	ASP	TYR	GLY	GLU	VAL	GLN	Q133	V134	P135	E136	L142	F143																																												

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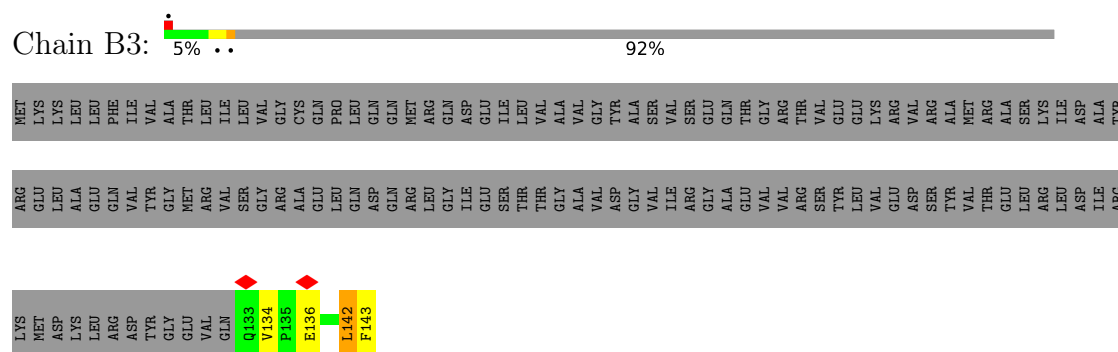


MET	LYS	LYS	LEU	LEU	PHE	ILE	VAL	ALA	THR	THR	LEU	ILE	LEU	VAL	GLY	CYS	GLN	PRO	LEU	GLN	GLN	MET	ARG	GLY	ASP	GLU	ILE	LEU	THR	THR	VAL	ALA	VAL	GLY	TYR	ALA	SER	VAL	ILE	SER	GLU	GLN	THR	GLY	ARG	THR	VAL	GLU	LYS	ARG	VAL	ARG	ALA	MET	ARG	ALA	LYS	ILE	ASP	ALA	TYR
ARG	GLU	LEU	ALA	GLU	GLN	VAL	TYR	GLY	MET	ARG	VAL	SER	GLY	ARG	ALA	GLU	LEU	GLN	ASP	GLN	ARG	LEU	GLY	ILE	GLU	SER	THR	THR	VAL	ALA	VAL	ASP	GLY	VAL	ILE	SER	ARG	GLY	ALA	VAL	ARG	THR	SER	TYR	LEU	VAL	ASP	SER	TYR	VAL	GLU	THR	GLU	ILE	ASP	ILE	ARG	TYR			
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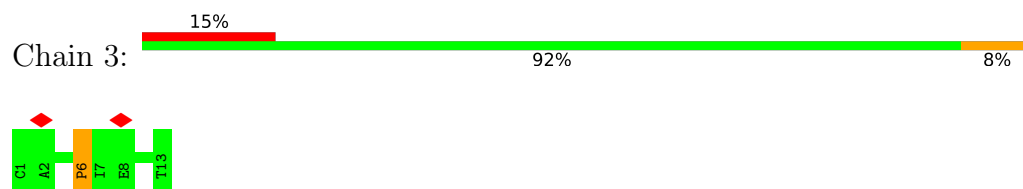
● Molecule 4: Flagellar assembly lipoprotein FlgP



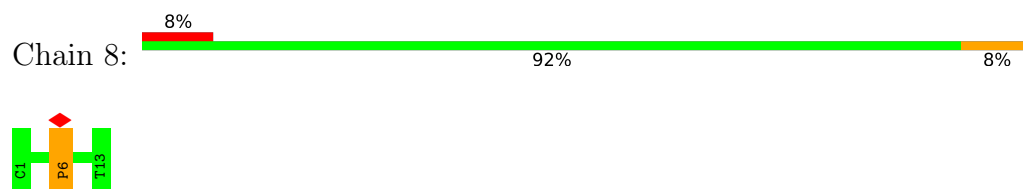
- Molecule 4: Flagellar assembly lipoprotein FlgP



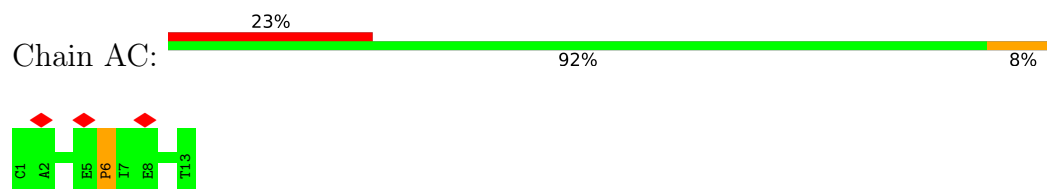
- Molecule 5: The N-terminus of Flagellar L-ring protein



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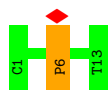


- Molecule 5: The N-terminus of Flagellar L-ring protein

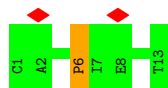


- Molecule 5: The N-terminus of Flagellar L-ring protein

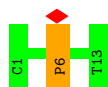




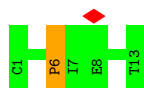
- Molecule 5: The N-terminus of Flagellar L-ring protein



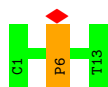
- Molecule 5: The N-terminus of Flagellar L-ring protein



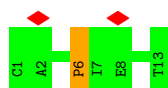
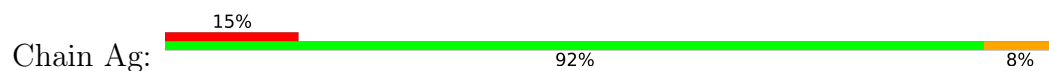
- Molecule 5: The N-terminus of Flagellar L-ring protein



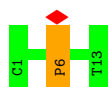
- Molecule 5: The N-terminus of Flagellar L-ring protein



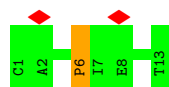
- Molecule 5: The N-terminus of Flagellar L-ring protein



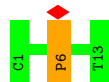
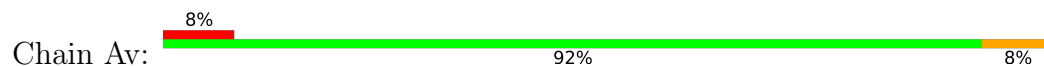
- Molecule 5: The N-terminus of Flagellar L-ring protein



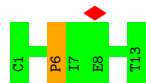
- Molecule 5: The N-terminus of Flagellar L-ring protein



- Molecule 5: The N-terminus of Flagellar L-ring protein



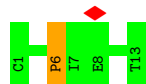
- Molecule 5: The N-terminus of Flagellar L-ring protein



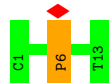
- Molecule 5: The N-terminus of Flagellar L-ring protein



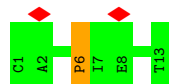
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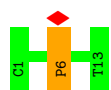
- Molecule 5: The N-terminus of Flagellar L-ring protein



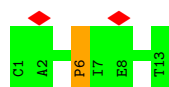
- Molecule 5: The N-terminus of Flagellar L-ring protein



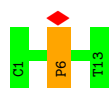
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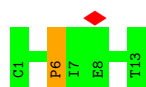
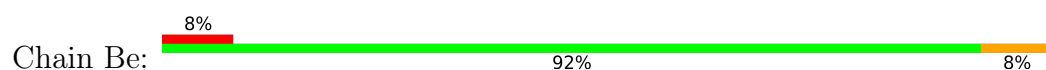
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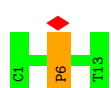
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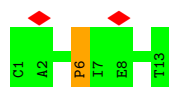
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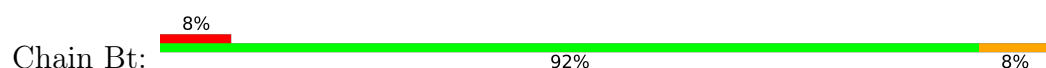
- Molecule 5: The N-terminus of Flagellar L-ring protein

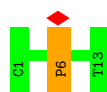


- Molecule 5: The N-terminus of Flagellar L-ring protein

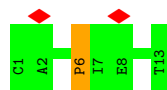


- Molecule 5: The N-terminus of Flagellar L-ring protein

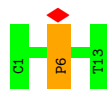




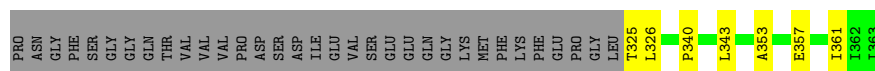
- Molecule 5: The N-terminus of Flagellar L-ring protein



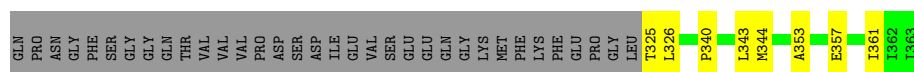
- Molecule 5: The N-terminus of Flagellar L-ring protein



- Molecule 6: Flagellar P-ring protein

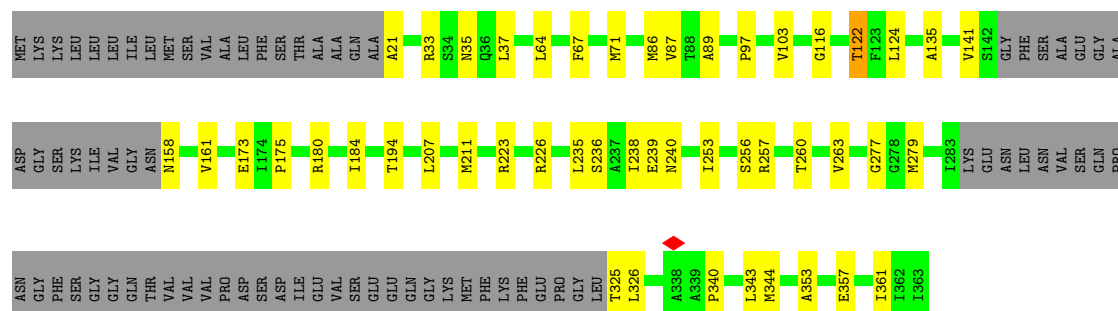


- Molecule 6: Flagellar P-ring protein

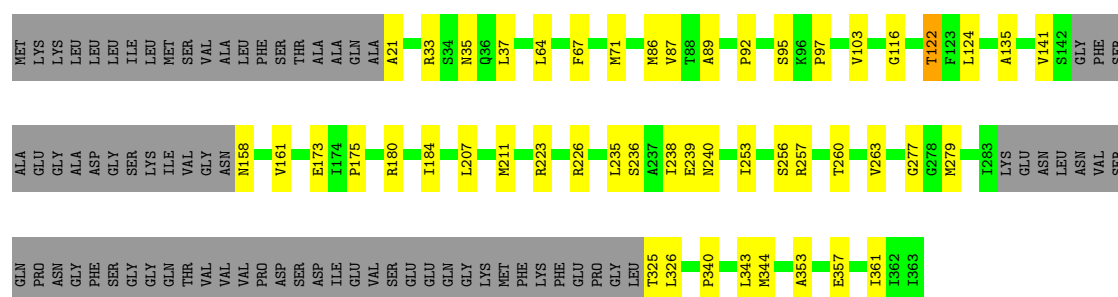


- Molecule 6: Flagellar P-ring protein

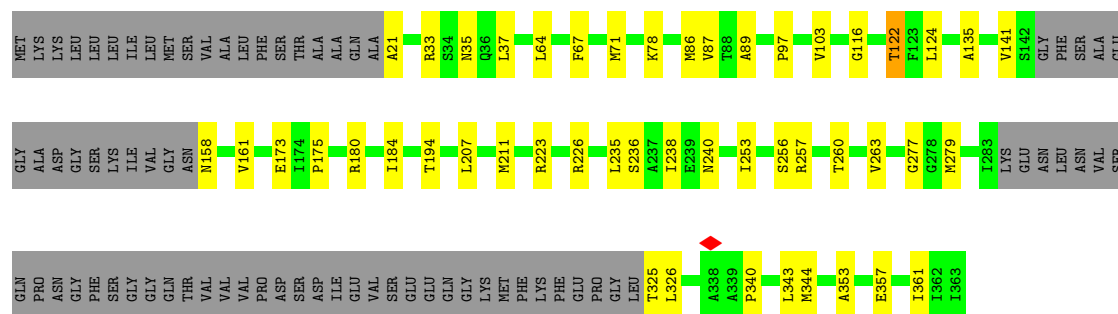




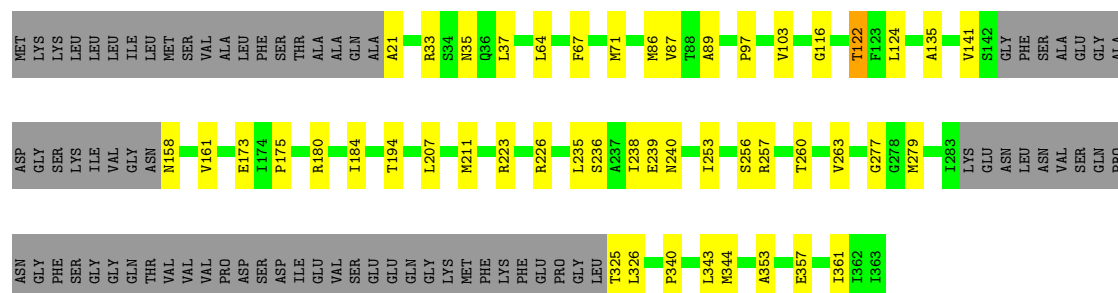
• Molecule 6: Flagellar P-ring protein



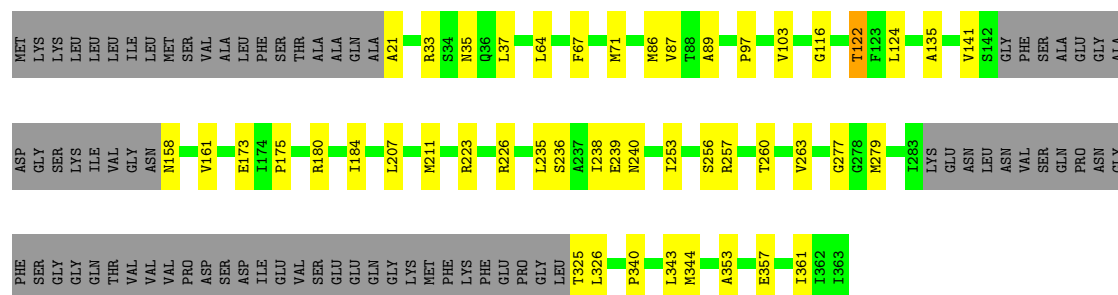
• Molecule 6: Flagellar P-ring protein



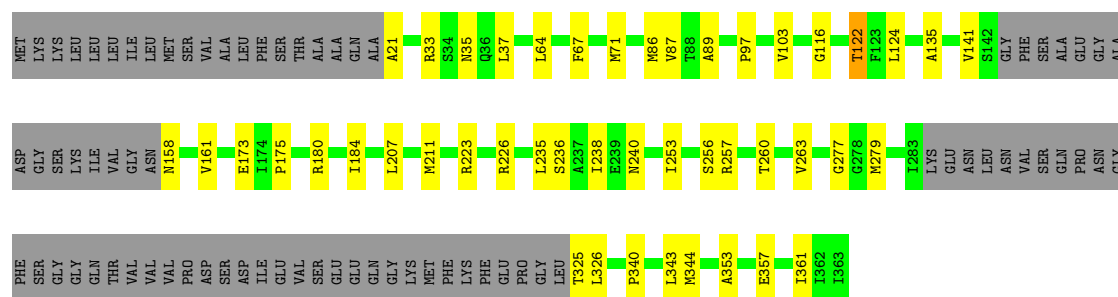
• Molecule 6: Flagellar P-ring protein



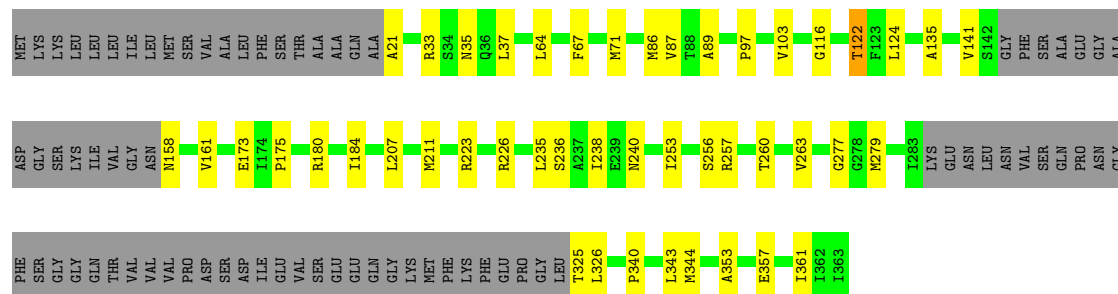
• Molecule 6: Flagellar P-ring protein

Chain AX:  66% 13% 21%

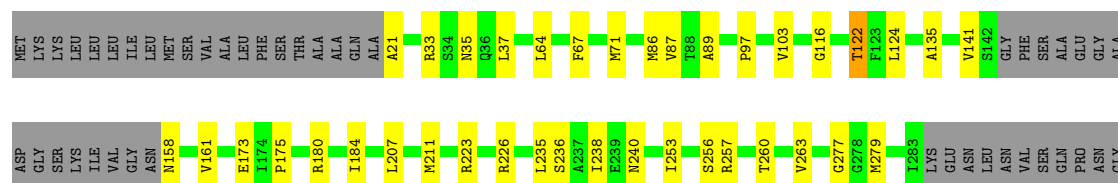
• Molecule 6: Flagellar P-ring protein

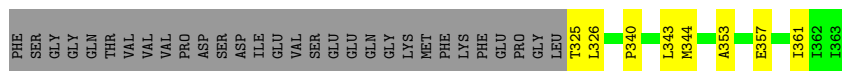
Chain Ac:  66% 12% 21%

• Molecule 6: Flagellar P-ring protein

Chain Ah:  66% 12% 21%

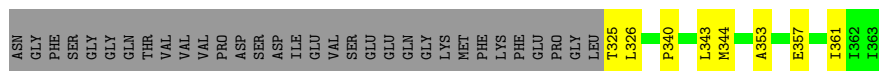
• Molecule 6: Flagellar P-ring protein

Chain Am:  66% 12% 21%



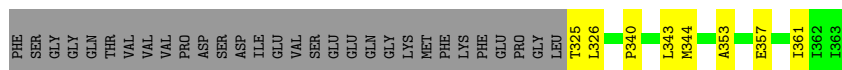
• Molecule 6: Flagellar P-ring protein

Chain Ar: 66% 13% 21%



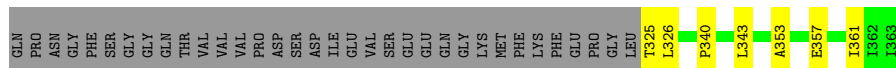
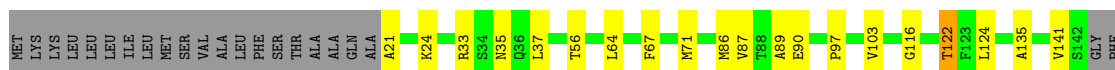
• Molecule 6: Flagellar P-ring protein

Chain Aw: 66% 12% 21%



• Molecule 6: Flagellar P-ring protein

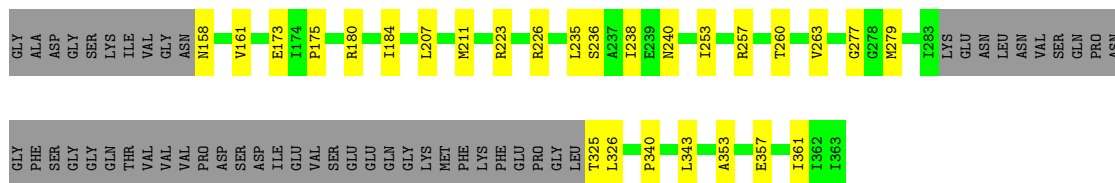
Chain A2: 66% 13% 21%



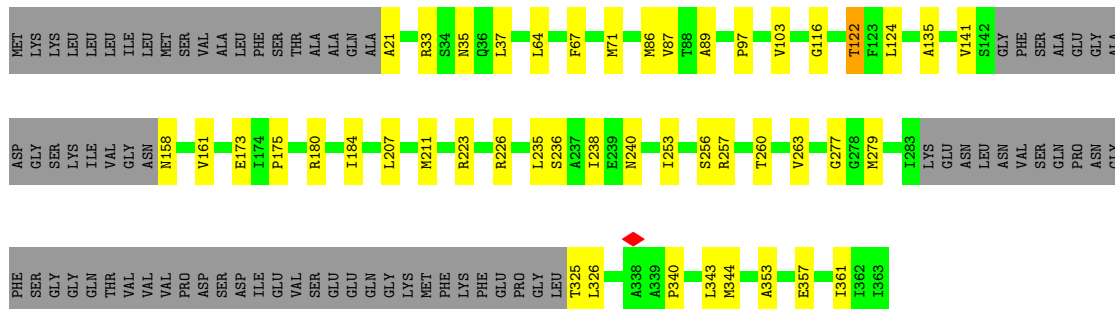
• Molecule 6: Flagellar P-ring protein

Chain A7: 67% 12% 21%

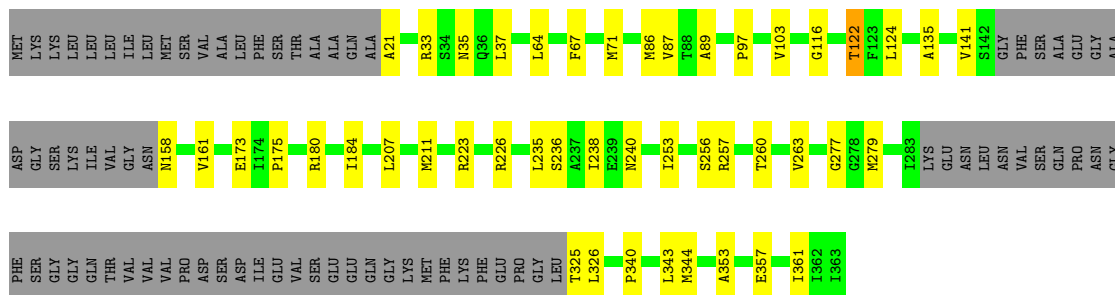




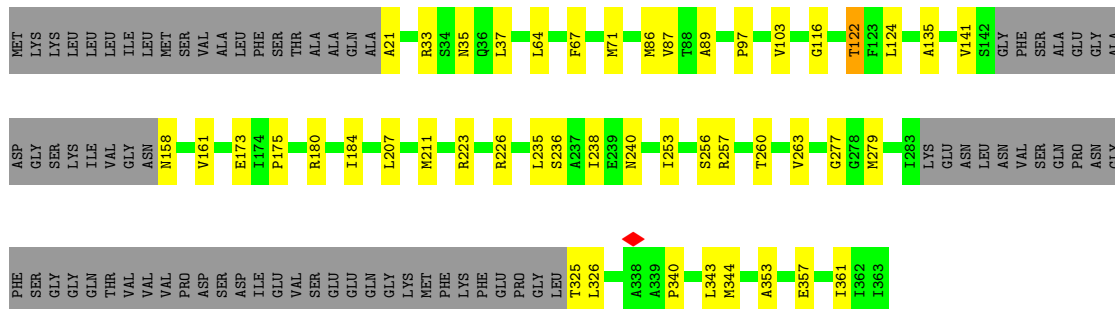
- Molecule 6: Flagellar P-ring protein



- Molecule 6: Flagellar P-ring protein

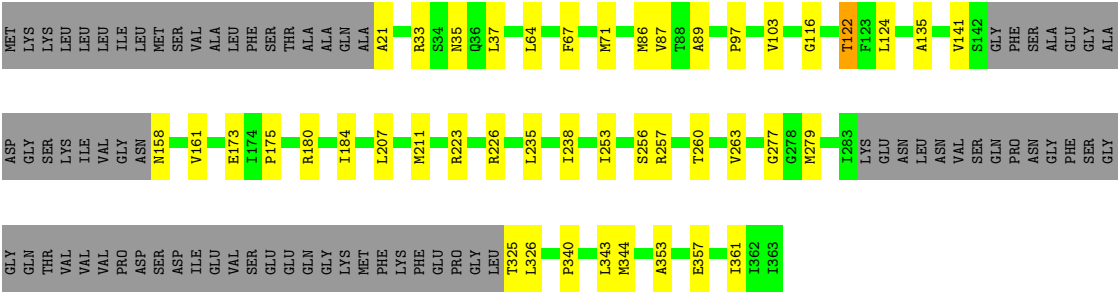


- Molecule 6: Flagellar P-ring protein

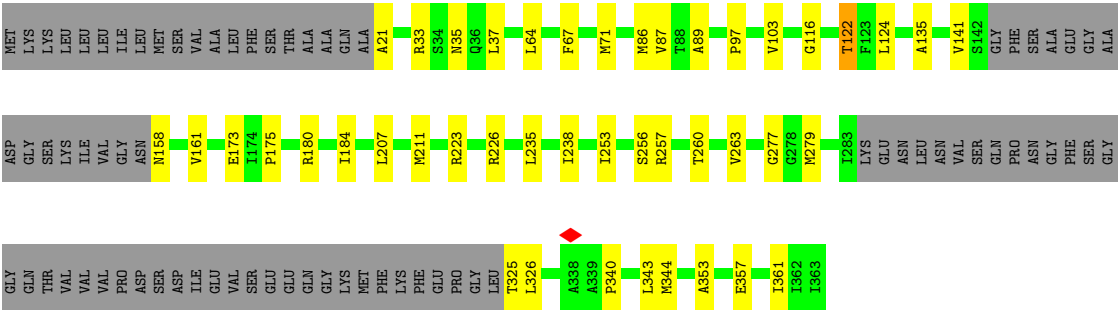


- Molecule 6: Flagellar P-ring protein

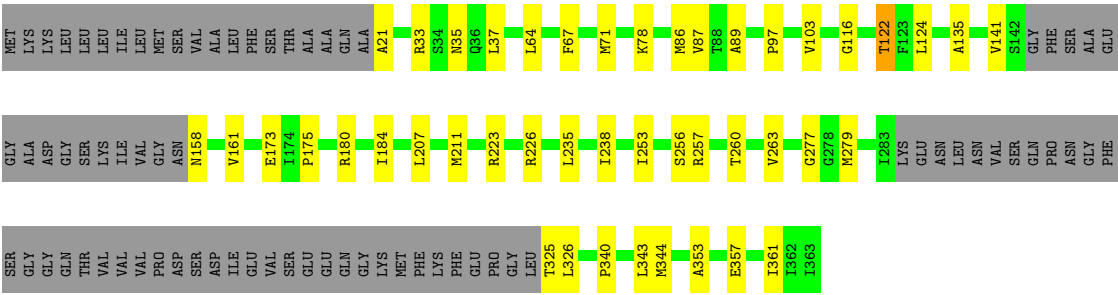




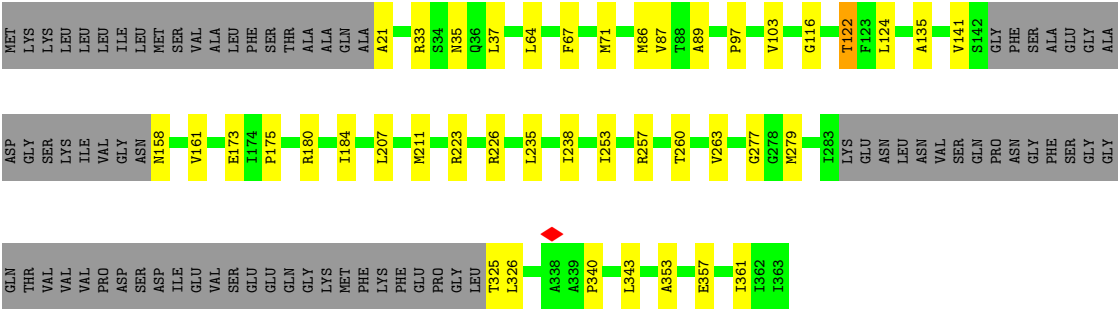
● Molecule 6: Flagellar P-ring protein



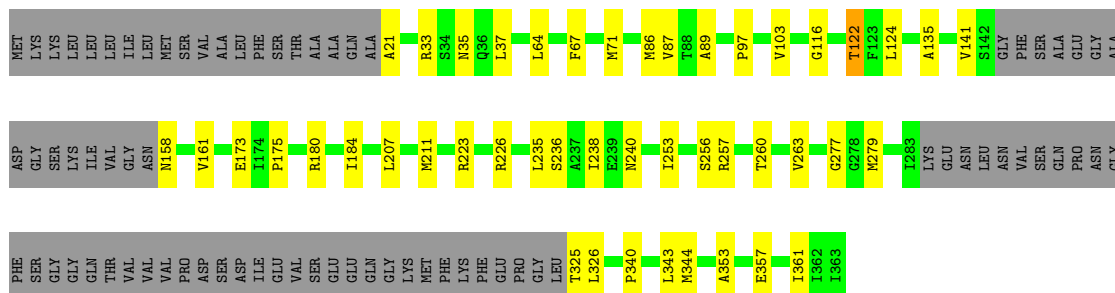
● Molecule 6: Flagellar P-ring protein



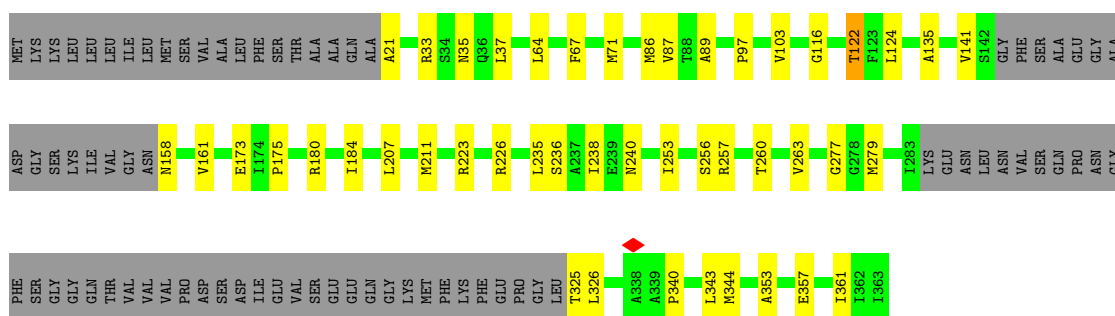
● Molecule 6: Flagellar P-ring protein



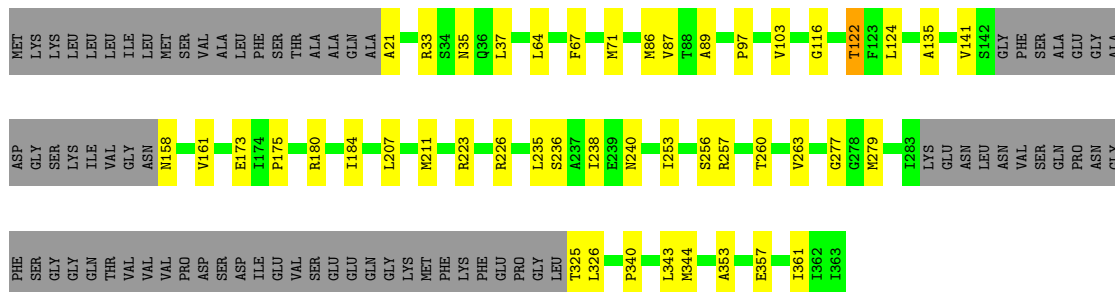
• Molecule 6: Flagellar P-ring protein

Chain Bk:  66% 12% 21%

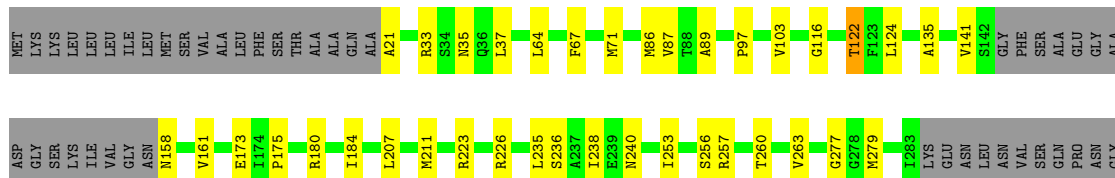
• Molecule 6: Flagellar P-ring protein

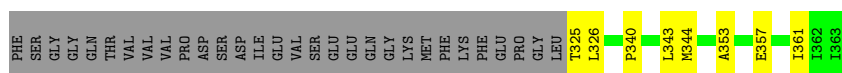
Chain Bp:  66% 12% 21%

• Molecule 6: Flagellar P-ring protein

Chain Bu:  66% 12% 21%

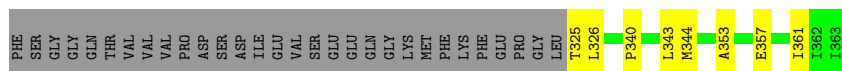
• Molecule 6: Flagellar P-ring protein

Chain Bz:  66% 12% 21%



- Molecule 6: Flagellar P-ring protein

Chain B5: 66% 12% 21%



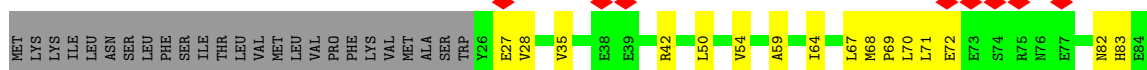
- Molecule 7: Flagella basal-body protein

Chain 5: 72% 21% 7%



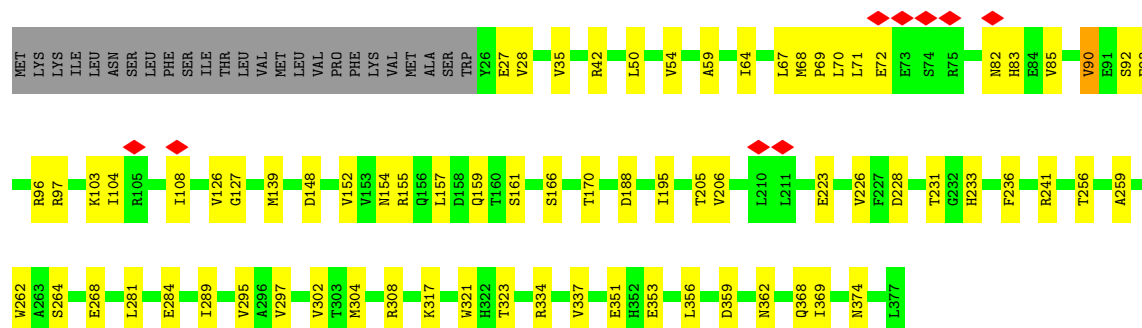
- Molecule 7: Flagella basal-body protein

Chain 0: 73% 20% 7%



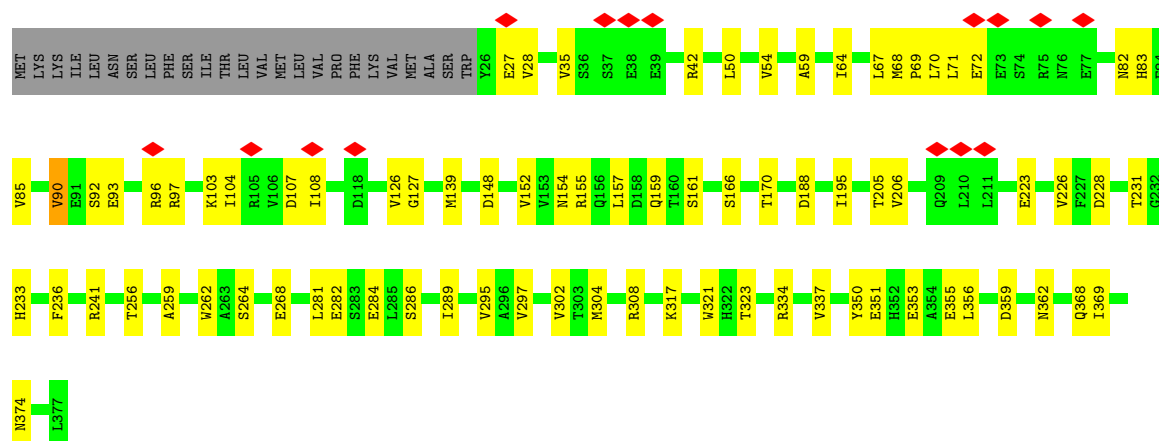
- Molecule 7: Flagella basal-body protein

Chain AE: 74% 19% 7%



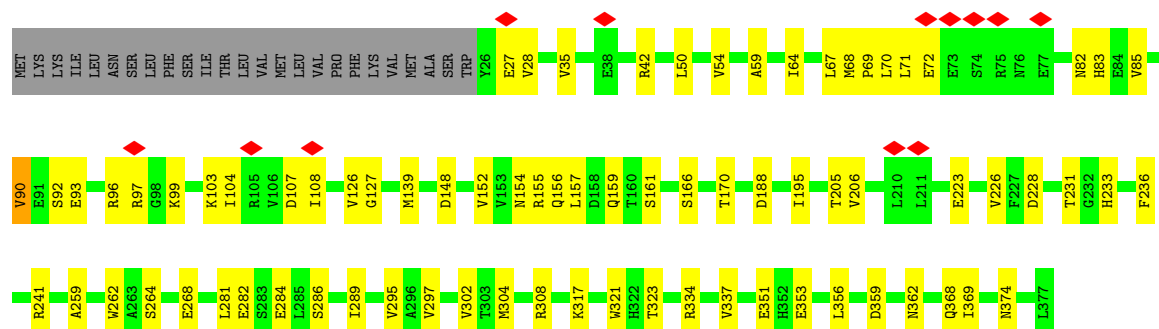
• Molecule 7: Flagella basal-body protein

Chain AJ: 72% 21% 7%



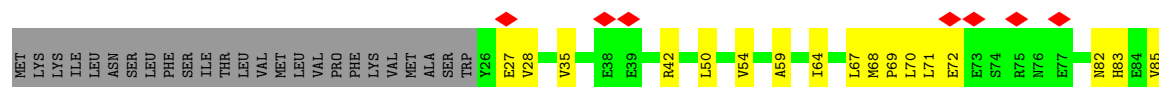
• Molecule 7: Flagella basal-body protein

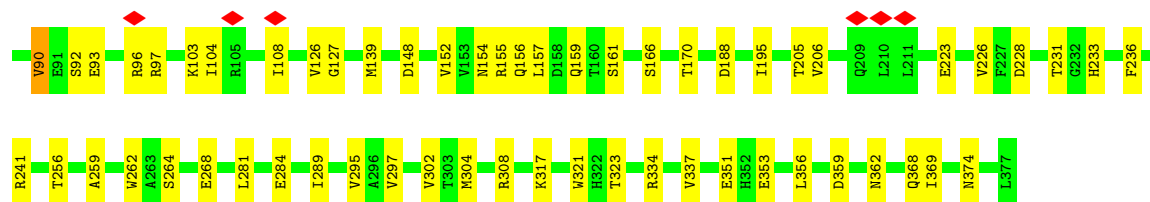
Chain AO: 73% 20% 7%



• Molecule 7: Flagella basal-body protein

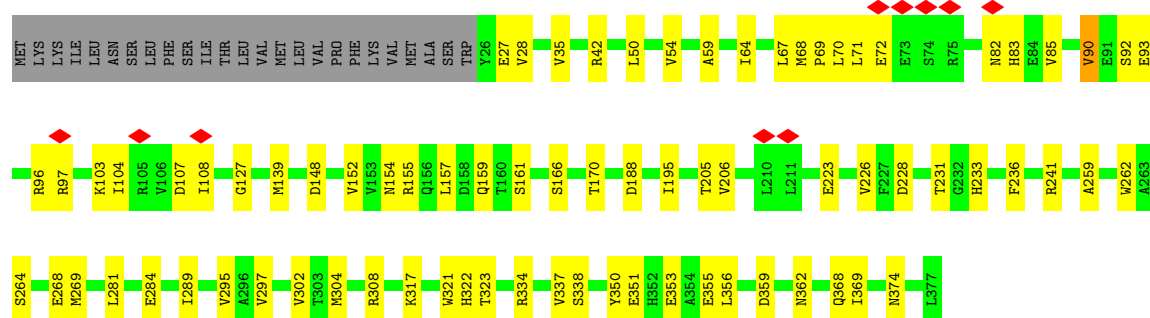
Chain AT: 73% 20% 7%





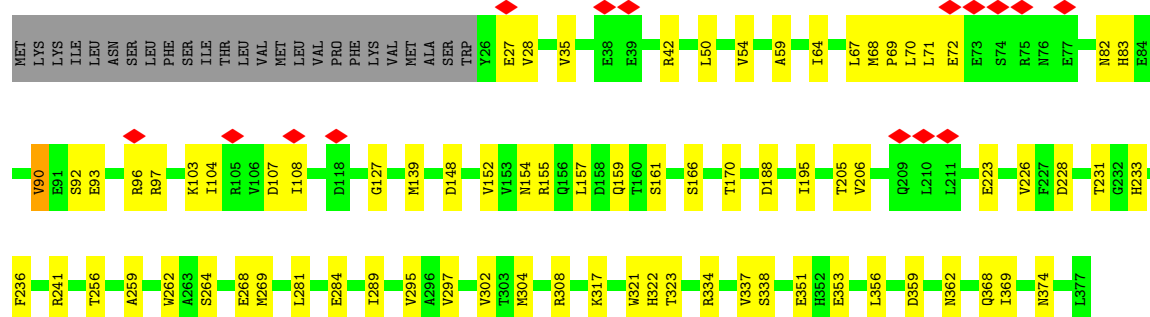
• Molecule 7: Flagella basal-body protein

Chain AY: 73% 20% 7%



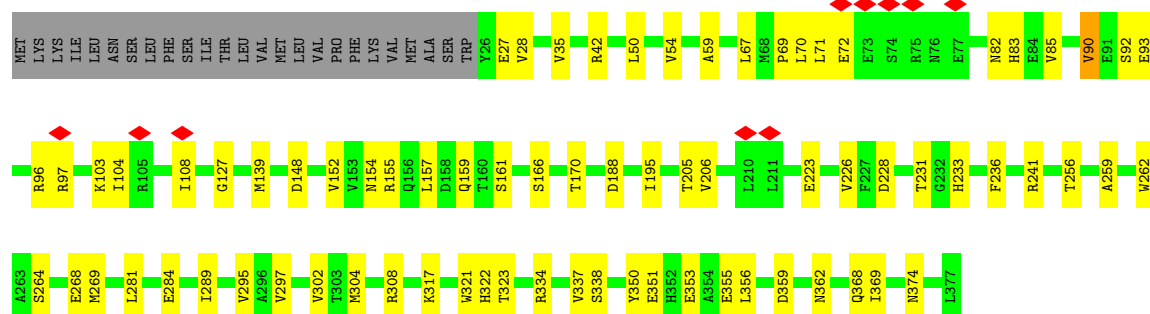
• Molecule 7: Flagella basal-body protein

Chain Ad: 73% 20% 7%



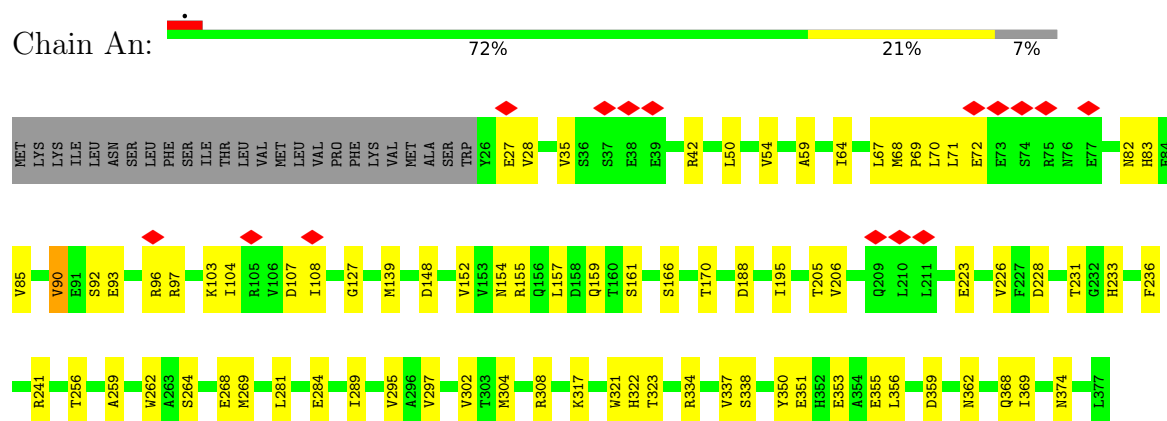
• Molecule 7: Flagella basal-body protein

Chain Ai: 73% 20% 7%



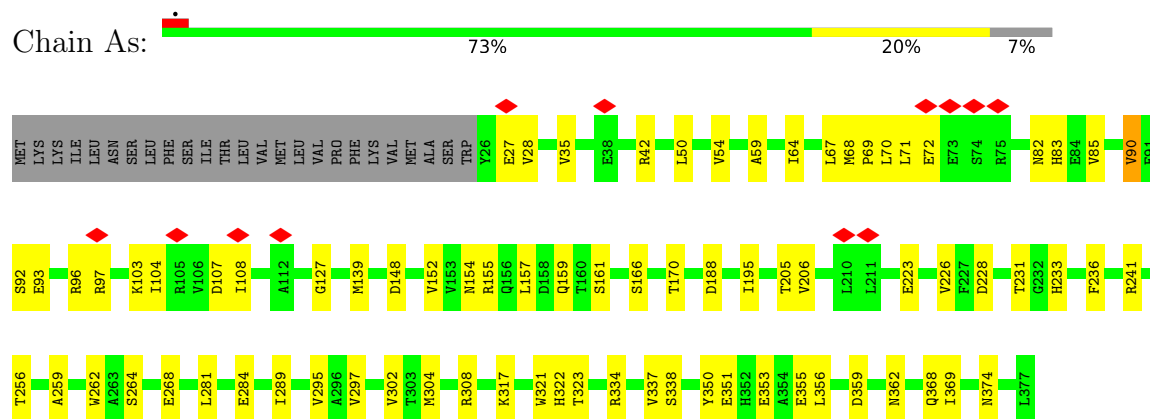
- Molecule 7: Flagella basal-body protein

Chain An:



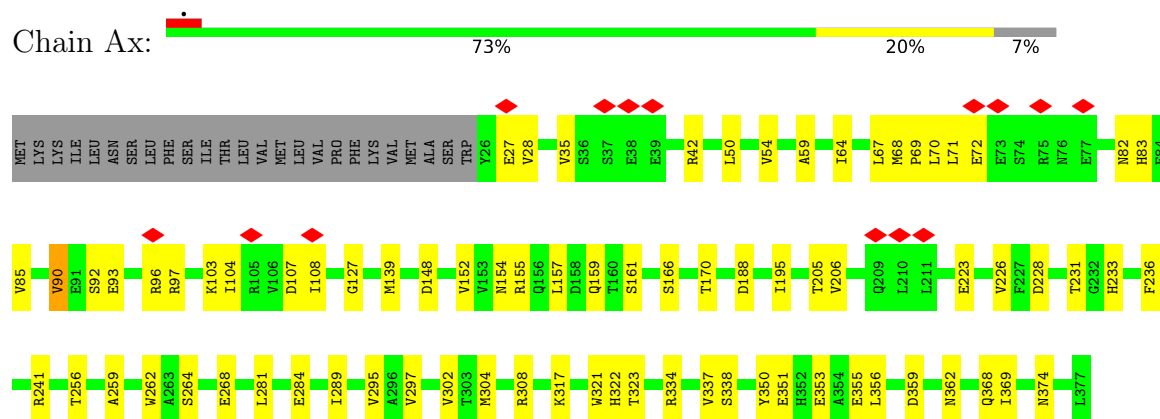
- Molecule 7: Flagella basal-body protein

Chain As:



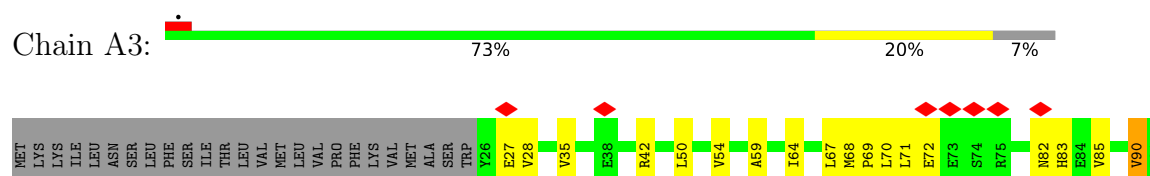
- Molecule 7: Flagella basal-body protein

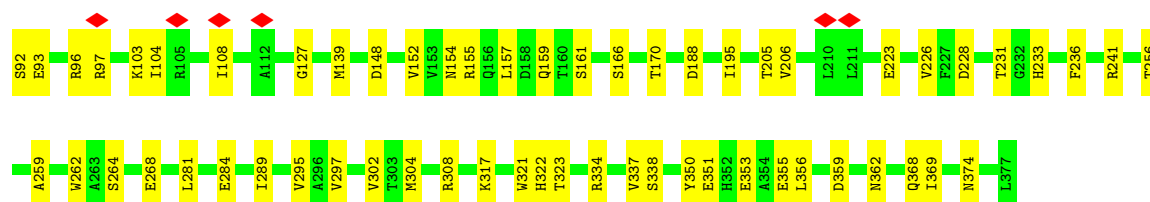
Chain Ax:



- Molecule 7: Flagella basal-body protein

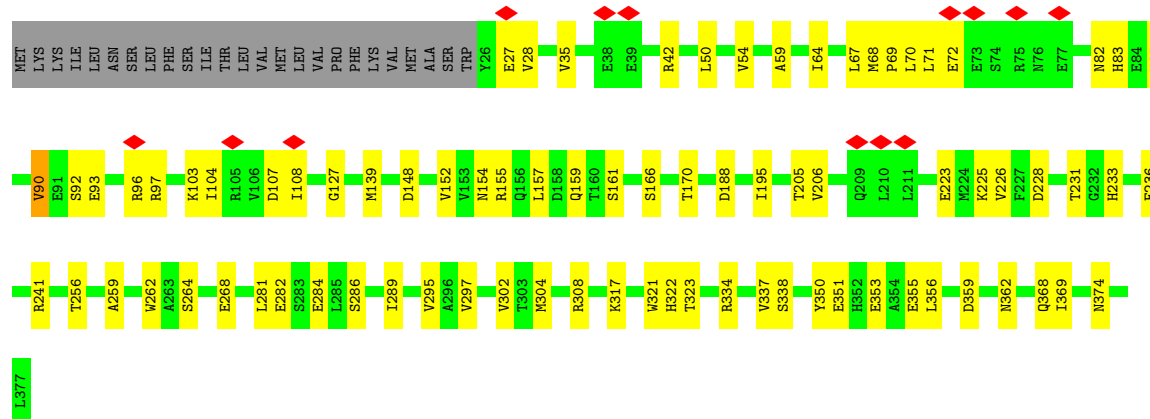
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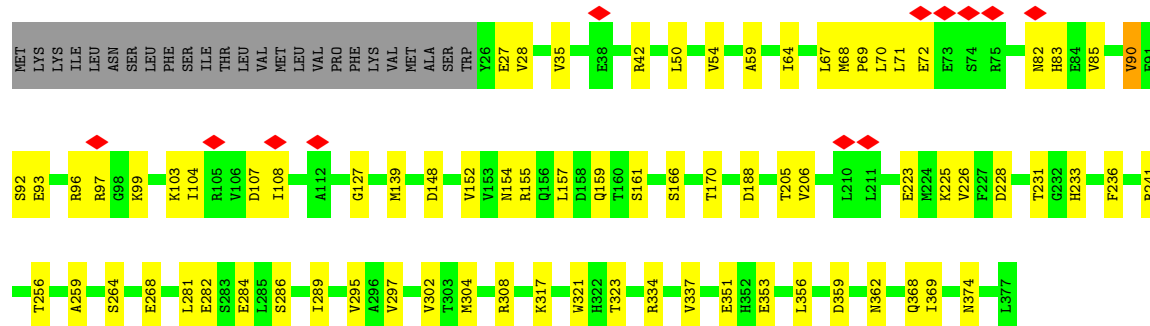
• Molecule 7: Flagella basal-body protein

Chain A8: 72% 21% 7%



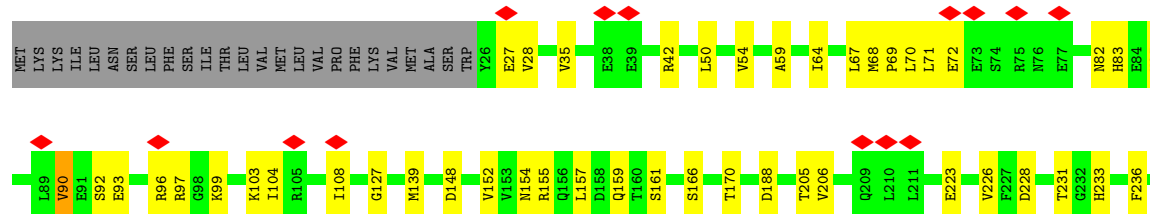
• Molecule 7: Flagella basal-body protein

Chain BC: 73% 20% 7%



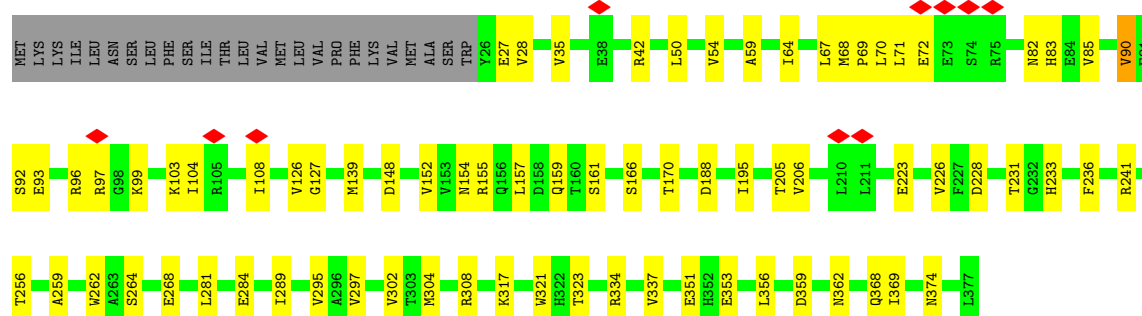
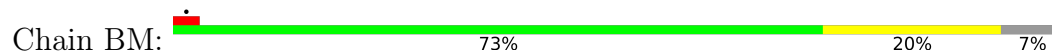
• Molecule 7: Flagella basal-body protein

Chain BH: 74% 19% 7%

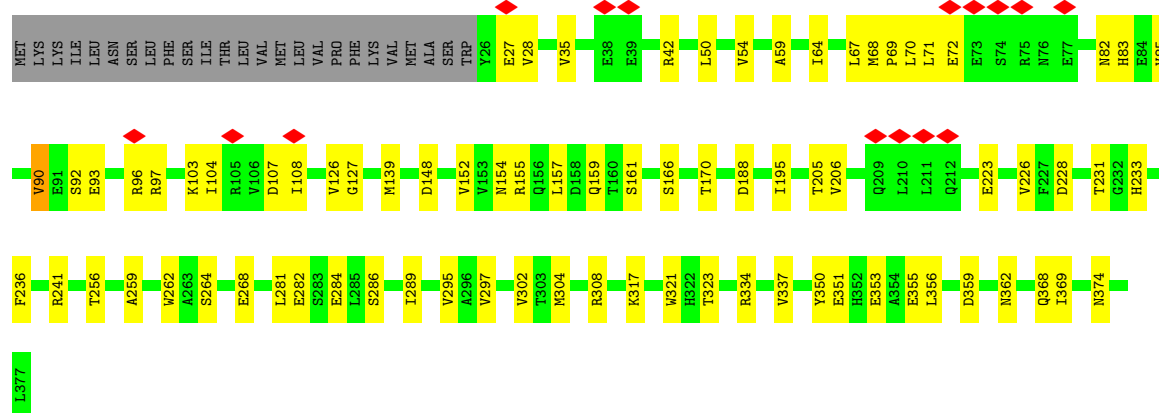
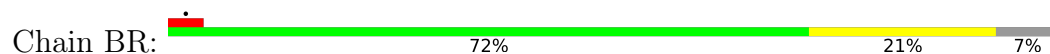




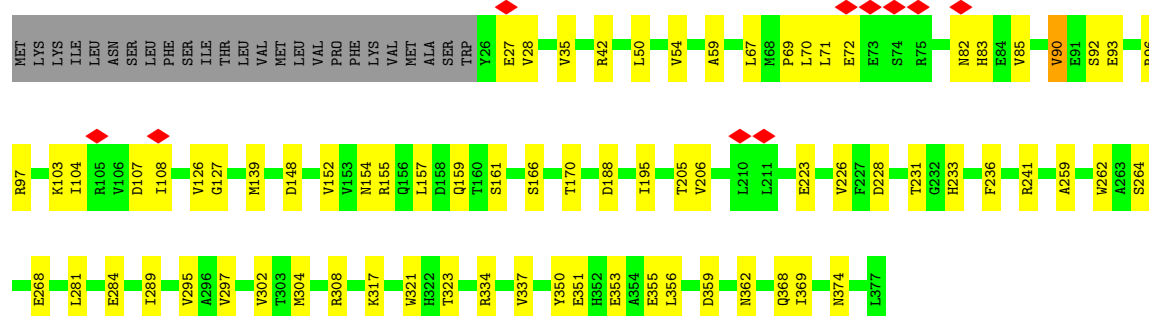
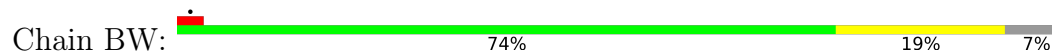
• Molecule 7: Flagella basal-body protein



• Molecule 7: Flagella basal-body protein

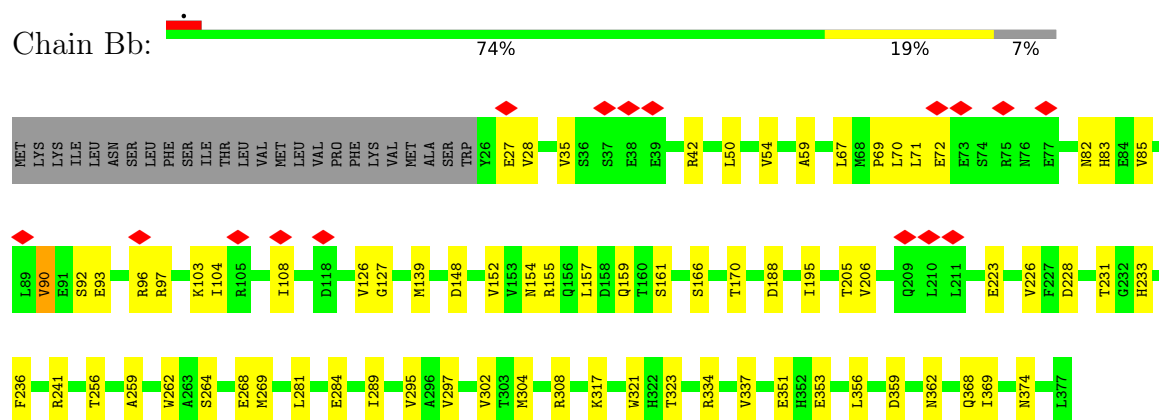


• Molecule 7: Flagella basal-body protein



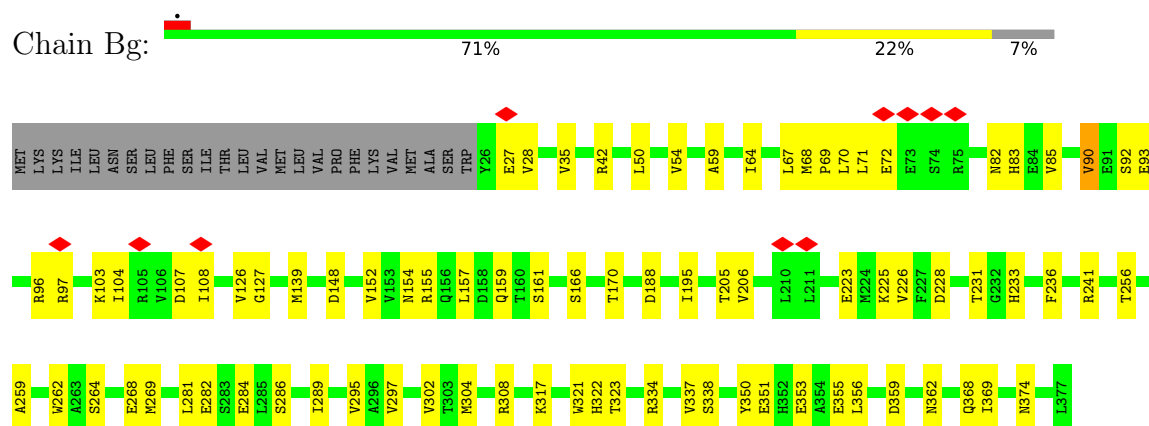
• Molecule 7: Flagella basal-body protein

Chain Bb:



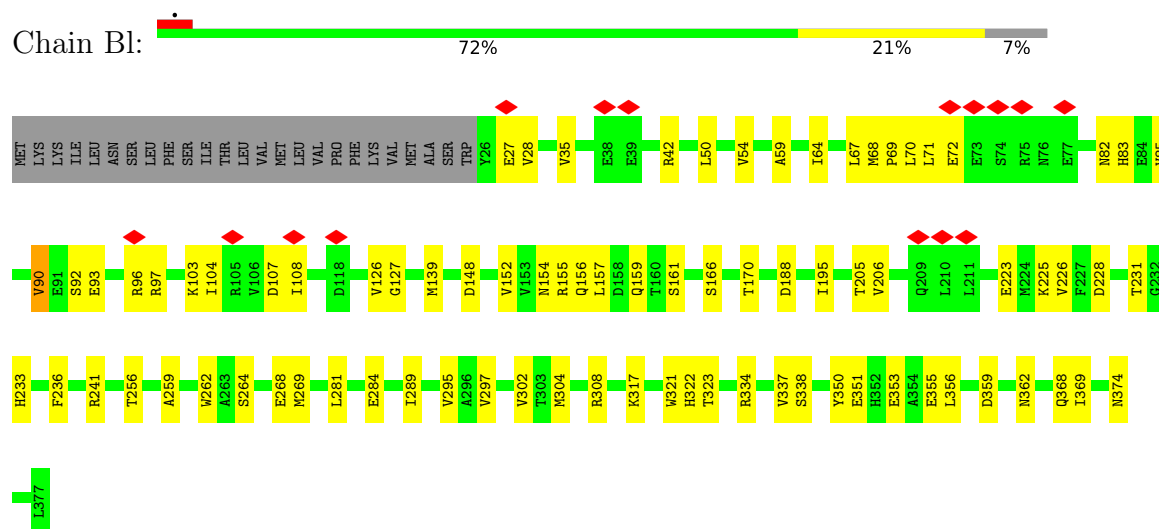
- Molecule 7: Flagella basal-body protein

Chain Bg:



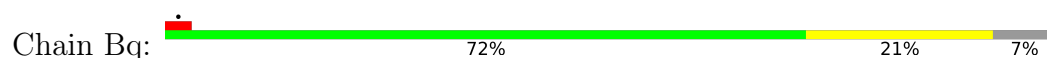
- Molecule 7: Flagella basal-body protein

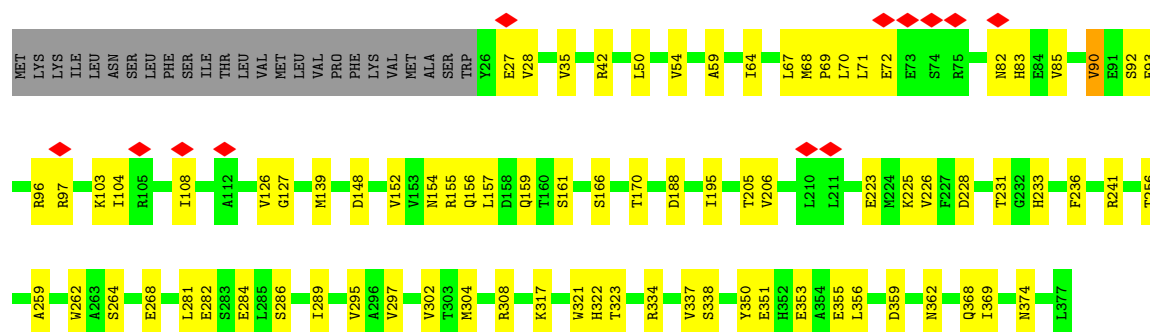
Chain Bl:



- Molecule 7: Flagella basal-body protein

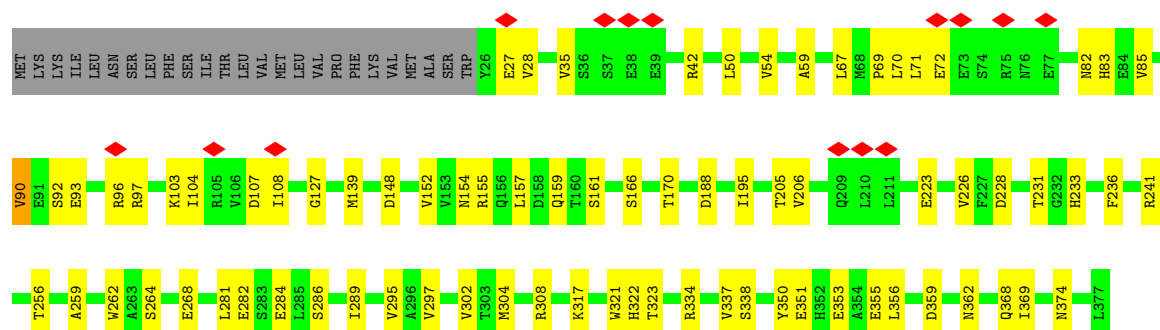
Chain Bq:





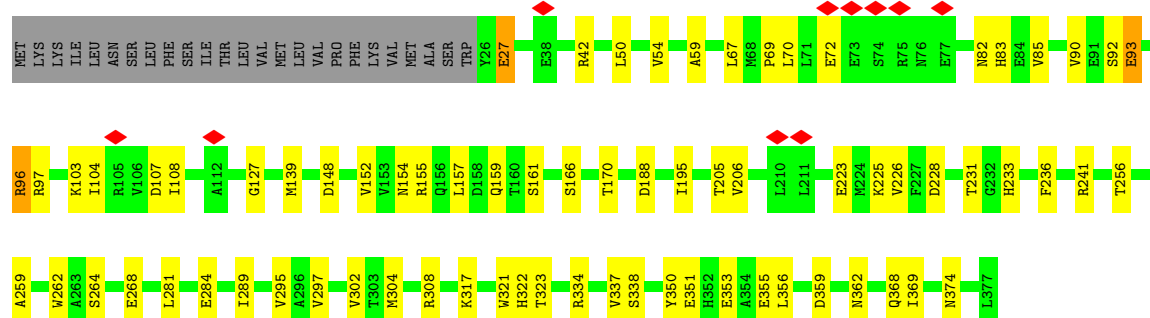
• Molecule 7: Flagella basal-body protein

Chain Bv: 73% 20% 7%



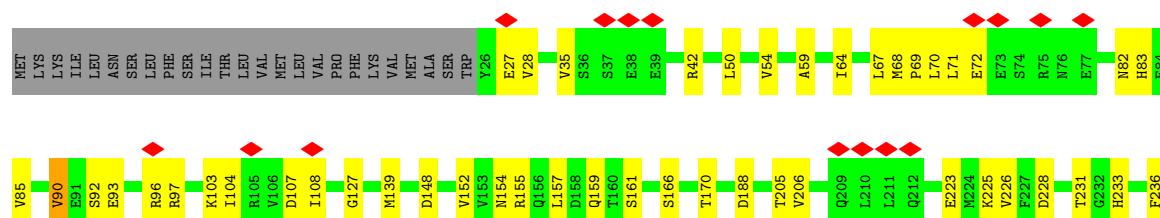
• Molecule 7: Flagella basal-body protein

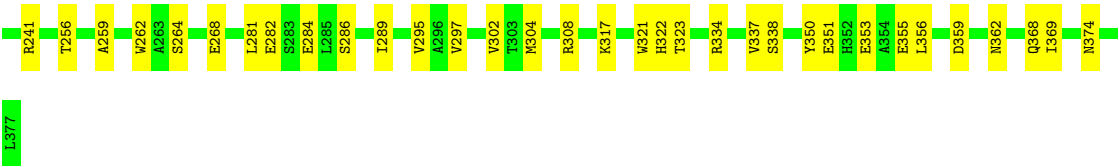
Chain B1: 74% 19% 7%



• Molecule 7: Flagella basal-body protein

Chain B6: 72% 21% 7%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C13	Depositor
Number of particles used	45233	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	3.861	Depositor
Minimum map value	-2.661	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.120	Depositor
Recommended contour level	0.34	Depositor
Map size (Å)	744.0, 744.0, 744.0	wwPDB
Map dimensions	620, 620, 620	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	0.23	0/2230	0.35	0/3009
1	B	0.22	0/2237	0.35	0/3019
1	E	0.23	0/2230	0.35	0/3009
1	F	0.22	0/2237	0.35	0/3019
1	I	0.23	0/2230	0.35	0/3009
1	J	0.22	0/2237	0.35	0/3019
1	M	0.23	0/2230	0.35	0/3009
1	N	0.22	0/2237	0.35	0/3019
1	Q	0.23	0/2230	0.35	0/3009
1	R	0.22	0/2237	0.35	0/3019
1	U	0.23	0/2230	0.35	0/3009
1	V	0.22	0/2237	0.35	0/3019
1	Y	0.23	0/2230	0.35	0/3009
1	Z	0.22	0/2237	0.35	0/3019
1	c	0.23	0/2230	0.35	0/3009
1	d	0.22	0/2237	0.35	0/3019
1	g	0.23	0/2230	0.35	0/3009
1	h	0.22	0/2237	0.35	0/3019
1	k	0.23	0/2230	0.35	0/3009
1	l	0.22	0/2237	0.35	0/3019
1	o	0.23	0/2230	0.35	0/3009
1	p	0.22	0/2237	0.36	0/3019
1	s	0.23	0/2230	0.35	0/3009
1	t	0.22	0/2237	0.35	0/3019
1	w	0.23	0/2230	0.35	0/3009
1	x	0.22	0/2237	0.35	0/3019
2	C	0.15	0/1499	0.39	0/2029
2	D	0.17	0/1499	0.38	0/2029
2	G	0.15	0/1499	0.39	0/2029
2	H	0.17	0/1499	0.38	0/2029
2	K	0.15	0/1499	0.39	0/2029
2	L	0.17	0/1499	0.38	0/2029
2	O	0.15	0/1499	0.39	0/2029
2	P	0.17	0/1499	0.38	0/2029

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
2	S	0.15	0/1499	0.39	0/2029
2	T	0.17	0/1499	0.38	0/2029
2	W	0.15	0/1499	0.39	0/2029
2	X	0.17	0/1499	0.38	0/2029
2	a	0.15	0/1499	0.39	0/2029
2	b	0.17	0/1499	0.38	0/2029
2	e	0.15	0/1499	0.39	0/2029
2	f	0.17	0/1499	0.38	0/2029
2	i	0.15	0/1499	0.39	0/2029
2	j	0.17	0/1499	0.38	0/2029
2	m	0.15	0/1499	0.39	0/2029
2	n	0.17	0/1499	0.38	0/2029
2	q	0.15	0/1499	0.39	0/2029
2	r	0.17	0/1499	0.38	0/2029
2	u	0.15	0/1499	0.39	0/2029
2	v	0.17	0/1499	0.38	0/2029
2	y	0.15	0/1499	0.39	0/2029
2	z	0.17	0/1499	0.38	0/2029
3	1	0.18	0/1706	0.29	0/2315
3	6	0.18	0/1706	0.29	0/2315
3	A4	0.18	0/1706	0.29	0/2315
3	A9	0.18	0/1706	0.29	0/2315
3	AA	0.18	0/1706	0.29	0/2315
3	AF	0.18	0/1706	0.29	0/2315
3	AK	0.18	0/1706	0.29	0/2315
3	AP	0.18	0/1706	0.29	0/2315
3	AU	0.18	0/1706	0.29	0/2315
3	AZ	0.18	0/1706	0.29	0/2315
3	Ae	0.18	0/1706	0.29	0/2315
3	Aj	0.18	0/1706	0.29	0/2315
3	Ao	0.18	0/1706	0.29	0/2315
3	At	0.18	0/1706	0.29	0/2315
3	Ay	0.18	0/1706	0.29	0/2315
3	B2	0.18	0/1706	0.29	0/2315
3	BD	0.18	0/1706	0.29	0/2315
3	BI	0.18	0/1706	0.29	0/2315
3	BN	0.18	0/1706	0.29	0/2315
3	BS	0.18	0/1706	0.29	0/2315
3	BX	0.18	0/1706	0.29	0/2315
3	Bc	0.18	0/1706	0.29	0/2315
3	Bh	0.18	0/1706	0.29	0/2315
3	Bm	0.18	0/1706	0.29	0/2315
3	Br	0.18	0/1706	0.29	0/2315

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	Bw	0.18	0/1706	0.29	0/2315
4	2	0.23	0/98	0.39	0/129
4	7	0.23	0/98	0.39	0/129
4	A0	0.23	0/98	0.39	0/129
4	A5	0.23	0/98	0.39	0/129
4	AB	0.23	0/98	0.39	0/129
4	AG	0.23	0/98	0.38	0/129
4	AL	0.23	0/98	0.38	0/129
4	AQ	0.23	0/98	0.39	0/129
4	AV	0.23	0/98	0.39	0/129
4	Aa	0.23	0/98	0.39	0/129
4	Af	0.23	0/98	0.39	0/129
4	Ak	0.23	0/98	0.38	0/129
4	Ap	0.23	0/98	0.38	0/129
4	Au	0.23	0/98	0.39	0/129
4	Az	0.23	0/98	0.39	0/129
4	B3	0.23	0/98	0.39	0/129
4	BE	0.23	0/98	0.39	0/129
4	BJ	0.23	0/98	0.38	0/129
4	BO	0.23	0/98	0.38	0/129
4	BT	0.23	0/98	0.39	0/129
4	BY	0.23	0/98	0.39	0/129
4	Bd	0.23	0/98	0.39	0/129
4	Bi	0.23	0/98	0.39	0/129
4	Bn	0.23	0/98	0.38	0/129
4	Bs	0.23	0/98	0.38	0/129
4	Bx	0.23	0/98	0.39	0/129
5	3	0.34	0/64	0.99	1/88 (1.1%)
5	8	0.34	0/64	0.99	1/88 (1.1%)
5	A1	0.35	0/64	0.99	1/88 (1.1%)
5	A6	0.34	0/64	0.99	1/88 (1.1%)
5	AC	0.34	0/64	0.99	1/88 (1.1%)
5	AH	0.34	0/64	0.99	1/88 (1.1%)
5	AM	0.34	0/64	0.99	1/88 (1.1%)
5	AR	0.34	0/64	0.99	1/88 (1.1%)
5	AW	0.34	0/64	0.98	1/88 (1.1%)
5	Ab	0.34	0/64	0.99	1/88 (1.1%)
5	Ag	0.34	0/64	0.99	1/88 (1.1%)
5	Al	0.34	0/64	0.99	1/88 (1.1%)
5	Aq	0.34	0/64	0.99	1/88 (1.1%)
5	Av	0.34	0/64	0.98	1/88 (1.1%)
5	B4	0.35	0/64	0.99	1/88 (1.1%)
5	BA	0.34	0/64	0.99	1/88 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	BF	0.34	0/64	0.99	1/88 (1.1%)
5	BK	0.34	0/64	0.99	1/88 (1.1%)
5	BP	0.34	0/64	0.99	1/88 (1.1%)
5	BU	0.34	0/64	0.99	1/88 (1.1%)
5	BZ	0.34	0/64	0.98	1/88 (1.1%)
5	Be	0.34	0/64	0.99	1/88 (1.1%)
5	Bj	0.34	0/64	0.99	1/88 (1.1%)
5	Bo	0.34	0/64	0.99	1/88 (1.1%)
5	Bt	0.34	0/64	0.99	1/88 (1.1%)
5	By	0.34	0/64	0.98	1/88 (1.1%)
6	4	0.18	0/2131	0.27	0/2894
6	9	0.18	0/2131	0.27	0/2894
6	A2	0.18	0/2131	0.27	0/2894
6	A7	0.18	0/2131	0.27	0/2894
6	AD	0.18	0/2131	0.27	0/2894
6	AI	0.18	0/2131	0.27	0/2894
6	AN	0.18	0/2131	0.27	0/2894
6	AS	0.18	0/2131	0.27	0/2894
6	AX	0.18	0/2131	0.27	0/2894
6	Ac	0.18	0/2131	0.27	0/2894
6	Ah	0.18	0/2131	0.27	0/2894
6	Am	0.18	0/2131	0.27	0/2894
6	Ar	0.18	0/2131	0.27	0/2894
6	Aw	0.18	0/2131	0.27	0/2894
6	B5	0.18	0/2131	0.27	0/2894
6	BB	0.18	0/2131	0.27	0/2894
6	BG	0.18	0/2131	0.27	0/2894
6	BL	0.18	0/2131	0.27	0/2894
6	BQ	0.18	0/2131	0.27	0/2894
6	BV	0.18	0/2131	0.27	0/2894
6	Ba	0.18	0/2131	0.27	0/2894
6	Bf	0.18	0/2131	0.27	0/2894
6	Bk	0.18	0/2131	0.27	0/2894
6	Bp	0.18	0/2131	0.27	0/2894
6	Bu	0.18	0/2131	0.27	0/2894
6	Bz	0.18	0/2131	0.27	0/2894
7	0	0.18	0/2818	0.28	0/3814
7	5	0.17	0/2818	0.28	0/3814
7	A3	0.18	0/2818	0.28	0/3814
7	A8	0.17	0/2818	0.28	0/3814
7	AE	0.17	0/2818	0.28	0/3814
7	AJ	0.17	0/2818	0.28	0/3814
7	AO	0.18	0/2818	0.28	0/3814

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	AT	0.18	0/2818	0.28	0/3814
7	AY	0.18	0/2818	0.28	0/3814
7	Ad	0.17	0/2818	0.28	0/3814
7	Ai	0.18	0/2818	0.28	0/3814
7	An	0.18	0/2818	0.28	0/3814
7	As	0.18	0/2818	0.28	0/3814
7	Ax	0.17	0/2818	0.28	0/3814
7	B1	0.17	0/2818	0.28	0/3814
7	B6	0.18	0/2818	0.28	0/3814
7	BC	0.18	0/2818	0.28	0/3814
7	BH	0.17	0/2818	0.28	0/3814
7	BM	0.17	0/2818	0.28	0/3814
7	BR	0.18	0/2818	0.28	0/3814
7	BW	0.18	0/2818	0.28	0/3814
7	Bb	0.18	0/2818	0.28	0/3814
7	Bg	0.17	0/2818	0.28	0/3814
7	Bl	0.18	0/2818	0.28	0/3814
7	Bq	0.18	0/2818	0.28	0/3814
7	Bv	0.18	0/2818	0.28	0/3814
All	All	0.19	0/274287	0.32	26/371358 (0.0%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	AM	6	PRO	N-CA-CB	7.71	110.17	103.31
5	BP	6	PRO	N-CA-CB	7.71	110.17	103.31
5	A1	6	PRO	N-CA-CB	7.69	110.16	103.31
5	B4	6	PRO	N-CA-CB	7.69	110.16	103.31
5	Ag	6	PRO	N-CA-CB	7.69	110.15	103.31

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2183	0	2154	33	0
1	B	2190	0	2163	47	0
1	E	2183	0	2154	34	0
1	F	2190	0	2163	46	0
1	I	2183	0	2154	32	0
1	J	2190	0	2163	44	0
1	M	2183	0	2154	32	0
1	N	2190	0	2163	47	0
1	Q	2183	0	2154	34	0
1	R	2190	0	2163	47	0
1	U	2183	0	2154	34	0
1	V	2190	0	2163	47	0
1	Y	2183	0	2154	33	0
1	Z	2190	0	2163	46	0
1	c	2183	0	2154	33	0
1	d	2190	0	2163	46	0
1	g	2183	0	2154	32	0
1	h	2190	0	2163	47	0
1	k	2183	0	2154	33	0
1	l	2190	0	2163	48	0
1	o	2183	0	2154	33	0
1	p	2190	0	2163	47	0
1	s	2183	0	2154	35	0
1	t	2190	0	2163	48	0
1	w	2183	0	2154	35	0
1	x	2190	0	2163	46	0
2	C	1471	0	1457	27	0
2	D	1471	0	1457	26	0
2	G	1471	0	1457	28	0
2	H	1471	0	1457	27	0
2	K	1471	0	1457	26	0
2	L	1471	0	1457	27	0
2	O	1471	0	1457	29	0
2	P	1471	0	1457	26	0
2	S	1471	0	1457	29	0
2	T	1471	0	1457	27	0
2	W	1471	0	1457	28	0
2	X	1471	0	1457	28	0
2	a	1471	0	1457	28	0
2	b	1471	0	1457	27	0
2	e	1471	0	1457	28	0
2	f	1471	0	1457	26	0
2	i	1471	0	1457	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	j	1471	0	1457	26	0
2	m	1471	0	1457	28	0
2	n	1471	0	1457	27	0
2	q	1471	0	1457	26	0
2	r	1471	0	1457	29	0
2	u	1471	0	1457	27	0
2	v	1471	0	1457	27	0
2	y	1471	0	1457	26	0
2	z	1471	0	1457	28	0
3	1	1678	0	1612	64	0
3	6	1678	0	1612	64	0
3	A4	1678	0	1612	67	0
3	A9	1678	0	1612	65	0
3	AA	1678	0	1612	65	0
3	AF	1678	0	1612	67	0
3	AK	1678	0	1612	65	0
3	AP	1678	0	1612	66	0
3	AU	1678	0	1612	67	0
3	AZ	1678	0	1612	66	0
3	Ae	1678	0	1612	65	0
3	Aj	1678	0	1612	68	0
3	Ao	1678	0	1612	67	0
3	At	1678	0	1612	65	0
3	Ay	1678	0	1612	65	0
3	B2	1678	0	1612	64	0
3	BD	1678	0	1612	65	0
3	BI	1678	0	1612	64	0
3	BN	1678	0	1612	66	0
3	BS	1678	0	1612	67	0
3	BX	1678	0	1612	66	0
3	Bc	1678	0	1612	63	0
3	Bh	1678	0	1612	63	0
3	Bm	1678	0	1612	64	0
3	Br	1678	0	1612	65	0
3	Bw	1678	0	1612	64	0
4	2	97	0	98	6	0
4	7	97	0	98	6	0
4	A0	97	0	98	6	0
4	A5	97	0	98	6	0
4	AB	97	0	98	6	0
4	AG	97	0	98	6	0
4	AL	97	0	98	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AQ	97	0	98	6	0
4	AV	97	0	98	6	0
4	Aa	97	0	98	6	0
4	Af	97	0	98	6	0
4	Ak	97	0	98	6	0
4	Ap	97	0	98	6	0
4	Au	97	0	98	6	0
4	Az	97	0	98	6	0
4	B3	97	0	98	6	0
4	BE	97	0	98	6	0
4	BJ	97	0	98	6	0
4	BO	97	0	98	6	0
4	BT	97	0	98	6	0
4	BY	97	0	98	6	0
4	Bd	97	0	98	6	0
4	Bi	97	0	98	6	0
4	Bn	97	0	98	6	0
4	Bs	97	0	98	6	0
4	Bx	97	0	98	6	0
5	3	65	0	30	5	0
5	8	65	0	30	5	0
5	A1	65	0	30	5	0
5	A6	65	0	30	5	0
5	AC	65	0	30	5	0
5	AH	65	0	30	5	0
5	AM	65	0	30	5	0
5	AR	65	0	30	5	0
5	AW	65	0	30	5	0
5	Ab	65	0	30	5	0
5	Ag	65	0	30	5	0
5	Al	65	0	30	5	0
5	Aq	65	0	30	5	0
5	Av	65	0	30	5	0
5	B4	65	0	30	5	0
5	BA	65	0	30	5	0
5	BF	65	0	30	5	0
5	BK	65	0	30	5	0
5	BP	65	0	30	5	0
5	BU	65	0	30	5	0
5	BZ	65	0	30	5	0
5	Be	65	0	30	5	0
5	Bj	65	0	30	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	Bo	65	0	30	5	0
5	Bt	65	0	30	5	0
5	By	65	0	30	5	0
6	4	2102	0	2158	44	0
6	9	2102	0	2158	45	0
6	A2	2102	0	2158	42	0
6	A7	2102	0	2158	43	0
6	AD	2102	0	2158	45	0
6	AI	2102	0	2158	46	0
6	AN	2102	0	2158	45	0
6	AS	2102	0	2158	46	0
6	AX	2102	0	2158	45	0
6	Ac	2102	0	2158	45	0
6	Ah	2102	0	2158	43	0
6	Am	2102	0	2158	43	0
6	Ar	2102	0	2158	45	0
6	Aw	2102	0	2158	44	0
6	B5	2102	0	2158	44	0
6	BB	2102	0	2158	45	0
6	BG	2102	0	2158	44	0
6	BL	2102	0	2158	43	0
6	BQ	2102	0	2158	43	0
6	BV	2102	0	2158	43	0
6	Ba	2102	0	2158	45	0
6	Bf	2102	0	2158	41	0
6	Bk	2102	0	2158	44	0
6	Bp	2102	0	2158	44	0
6	Bu	2102	0	2158	43	0
6	Bz	2102	0	2158	43	0
7	0	2774	0	2747	73	0
7	5	2774	0	2747	72	0
7	A3	2774	0	2747	72	0
7	A8	2774	0	2747	76	0
7	AE	2774	0	2747	69	0
7	AJ	2774	0	2747	76	0
7	AO	2774	0	2747	74	0
7	AT	2774	0	2747	73	0
7	AY	2774	0	2747	72	0
7	Ad	2774	0	2747	77	0
7	Ai	2774	0	2747	72	0
7	An	2774	0	2747	76	0
7	As	2774	0	2747	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	Ax	2774	0	2747	74	0
7	B1	2774	0	2747	72	0
7	B6	2774	0	2747	76	0
7	BC	2774	0	2747	71	0
7	BH	2774	0	2747	73	0
7	BM	2774	0	2747	71	0
7	BR	2774	0	2747	76	0
7	BW	2774	0	2747	70	0
7	Bb	2774	0	2747	73	0
7	Bg	2774	0	2747	77	0
7	Bl	2774	0	2747	79	0
7	Bq	2774	0	2747	76	0
7	Bv	2774	0	2747	76	0
All	All	269711	0	266773	4658	0

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

The worst 5 of 4658 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BG:277:GLY:O	6:BL:340:PRO:HB2	1.64	0.98
6:BB:277:GLY:O	6:BG:340:PRO:HB2	1.64	0.98
6:Bf:277:GLY:O	6:Bk:340:PRO:HB2	1.64	0.98
6:Am:277:GLY:O	6:Ar:340:PRO:HB2	1.64	0.97
6:Bk:277:GLY:O	6:Bp:340:PRO:HB2	1.64	0.97

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	B	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	E	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	F	269/293 (92%)	266 (99%)	3 (1%)	0	100	100
1	I	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	J	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	M	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	N	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	Q	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	R	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	U	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	V	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	Y	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	Z	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	c	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	d	269/293 (92%)	266 (99%)	3 (1%)	0	100	100
1	g	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	h	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	k	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	l	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	o	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	p	269/293 (92%)	266 (99%)	3 (1%)	0	100	100
1	s	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	t	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
1	w	268/293 (92%)	259 (97%)	9 (3%)	0	100	100
1	x	269/293 (92%)	267 (99%)	2 (1%)	0	100	100
2	C	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	D	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	G	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	H	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	K	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	L	177/211 (84%)	172 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	O	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	P	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	S	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	T	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	W	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	X	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	a	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	b	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	e	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	f	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	i	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	j	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	m	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	n	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	q	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	r	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	u	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	v	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
2	y	177/211 (84%)	170 (96%)	6 (3%)	1 (1%)	21	45
2	z	177/211 (84%)	172 (97%)	5 (3%)	0	100	100
3	1	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	6	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	A4	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	A9	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	AA	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	AF	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	AK	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	AP	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	AU	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	AZ	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Ae	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Aj	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Ao	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	At	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Ay	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	B2	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	BD	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	BI	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	BN	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	BS	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	BX	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Bc	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Bh	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Bm	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Br	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
3	Bw	217/259 (84%)	212 (98%)	4 (2%)	1 (0%)	24	49
4	2	9/143 (6%)	9 (100%)	0	0	100	100
4	7	9/143 (6%)	9 (100%)	0	0	100	100
4	A0	9/143 (6%)	9 (100%)	0	0	100	100
4	A5	9/143 (6%)	9 (100%)	0	0	100	100
4	AB	9/143 (6%)	9 (100%)	0	0	100	100
4	AG	9/143 (6%)	9 (100%)	0	0	100	100
4	AL	9/143 (6%)	9 (100%)	0	0	100	100
4	AQ	9/143 (6%)	9 (100%)	0	0	100	100
4	AV	9/143 (6%)	9 (100%)	0	0	100	100
4	Aa	9/143 (6%)	9 (100%)	0	0	100	100
4	Af	9/143 (6%)	9 (100%)	0	0	100	100
4	Ak	9/143 (6%)	9 (100%)	0	0	100	100
4	Ap	9/143 (6%)	9 (100%)	0	0	100	100
4	Au	9/143 (6%)	9 (100%)	0	0	100	100
4	Az	9/143 (6%)	9 (100%)	0	0	100	100
4	B3	9/143 (6%)	9 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	BE	9/143 (6%)	9 (100%)	0	0	100	100
4	BJ	9/143 (6%)	9 (100%)	0	0	100	100
4	BO	9/143 (6%)	9 (100%)	0	0	100	100
4	BT	9/143 (6%)	9 (100%)	0	0	100	100
4	BY	9/143 (6%)	9 (100%)	0	0	100	100
4	Bd	9/143 (6%)	9 (100%)	0	0	100	100
4	Bi	9/143 (6%)	9 (100%)	0	0	100	100
4	Bn	9/143 (6%)	9 (100%)	0	0	100	100
4	Bs	9/143 (6%)	9 (100%)	0	0	100	100
4	Bx	9/143 (6%)	9 (100%)	0	0	100	100
5	3	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	8	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	A1	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	A6	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	AC	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	AH	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	AM	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	AR	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	AW	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Ab	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Ag	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Al	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Aq	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Av	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	B4	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	BA	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	BF	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	BK	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	BP	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	BU	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	BZ	11/13 (85%)	9 (82%)	2 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Be	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Bj	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Bo	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	Bt	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
5	By	11/13 (85%)	9 (82%)	2 (18%)	0	100	100
6	4	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	9	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	A2	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	A7	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	AD	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	AI	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	AN	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	AS	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	AX	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Ac	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Ah	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Am	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Ar	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Aw	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	B5	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	BB	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	BG	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	BL	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	BQ	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	BV	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Ba	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Bf	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Bk	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Bp	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Bu	281/363 (77%)	275 (98%)	6 (2%)	0	100	100
6	Bz	281/363 (77%)	275 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	0	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	5	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	A3	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	A8	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	AE	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	AJ	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	AO	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	AT	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	AY	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Ad	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Ai	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	An	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	As	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Ax	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	B1	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	B6	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	BC	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	BH	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	BM	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	BR	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	BW	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Bb	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Bg	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Bl	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Bq	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
7	Bv	350/377 (93%)	346 (99%)	4 (1%)	0	100	100
All	All	34151/43134 (79%)	33407 (98%)	705 (2%)	39 (0%)	49	72

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	35	GLU
2	G	35	GLU

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Mol	Chain	Res	Type
2	K	35	GLU
2	O	35	GLU
2	S	35	GLU

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	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	B	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	E	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	F	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	I	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	J	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	M	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	N	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	Q	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	R	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	U	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	V	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	Y	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	Z	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	c	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	d	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	g	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	h	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	k	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	l	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	o	239/260 (92%)	227 (95%)	12 (5%)	22	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	p	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	s	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	t	240/260 (92%)	231 (96%)	9 (4%)	29	55
1	w	239/260 (92%)	227 (95%)	12 (5%)	22	47
1	x	240/260 (92%)	231 (96%)	9 (4%)	29	55
2	C	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	D	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	G	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	H	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	K	151/175 (86%)	145 (96%)	6 (4%)	28	53
2	L	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	O	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	P	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	S	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	T	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	W	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	X	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	a	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	b	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	e	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	f	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	i	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	j	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	m	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	n	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	q	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	r	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	u	151/175 (86%)	145 (96%)	6 (4%)	28	53
2	v	151/175 (86%)	143 (95%)	8 (5%)	20	45
2	y	151/175 (86%)	144 (95%)	7 (5%)	24	50
2	z	151/175 (86%)	143 (95%)	8 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	1	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	6	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	A4	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	A9	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	AA	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	AF	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	AK	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	AP	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	AU	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	AZ	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Ae	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Aj	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Ao	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	At	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Ay	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	B2	183/215 (85%)	179 (98%)	4 (2%)	45	69
3	BD	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	BI	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	BN	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	BS	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	BX	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Bc	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Bh	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Bm	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Br	183/215 (85%)	180 (98%)	3 (2%)	55	75
3	Bw	183/215 (85%)	180 (98%)	3 (2%)	55	75
4	2	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	7	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	A0	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	A5	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	AB	11/123 (9%)	10 (91%)	1 (9%)	9	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AG	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	AL	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	AQ	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	AV	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Aa	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Af	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Ak	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Ap	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Au	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Az	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	B3	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	BE	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	BJ	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	BO	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	BT	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	BY	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Bd	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Bi	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Bn	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Bs	11/123 (9%)	10 (91%)	1 (9%)	9	23
4	Bx	11/123 (9%)	10 (91%)	1 (9%)	9	23
6	4	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	9	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	A2	224/285 (79%)	217 (97%)	7 (3%)	35	59
6	A7	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	AD	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	AI	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	AN	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	AS	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	AX	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Ac	224/285 (79%)	220 (98%)	4 (2%)	51	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Ah	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Am	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Ar	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Aw	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	B5	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	BB	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	BG	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	BL	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	BQ	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	BV	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Ba	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Bf	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Bk	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Bp	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Bu	224/285 (79%)	220 (98%)	4 (2%)	51	72
6	Bz	224/285 (79%)	220 (98%)	4 (2%)	51	72
7	0	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	5	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	A3	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	A8	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	AE	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	AJ	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	AO	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	AT	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	AY	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Ad	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Ai	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	An	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	As	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Ax	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	B1	308/332 (93%)	304 (99%)	4 (1%)	61	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	B6	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	BC	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	BH	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	BM	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	BR	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	BW	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Bb	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Bg	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Bl	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Bq	308/332 (93%)	303 (98%)	5 (2%)	55	75
7	Bv	308/332 (93%)	303 (98%)	5 (2%)	55	75
All	All	29029/36140 (80%)	28222 (97%)	807 (3%)	38	62

5 of 807 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	z	208	ASP
4	Af	142	LEU
6	B5	141	VAL
7	5	71	LEU
2	z	196	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 603 such sidechains are listed below:

Mol	Chain	Res	Type
6	BV	176	ASN
6	Bz	176	ASN
3	BX	222	ASN
6	BV	121	GLN
6	Bk	334	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

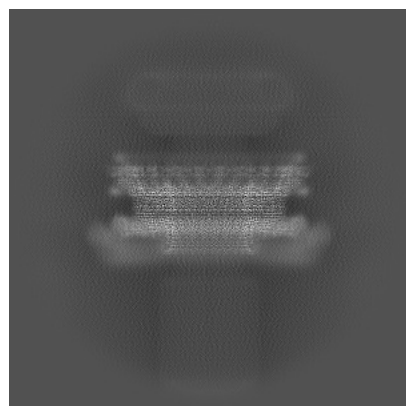
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39776. These allow visual inspection of the internal detail of the map and identification of artifacts.

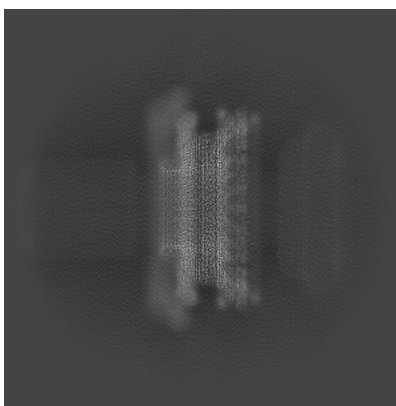
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

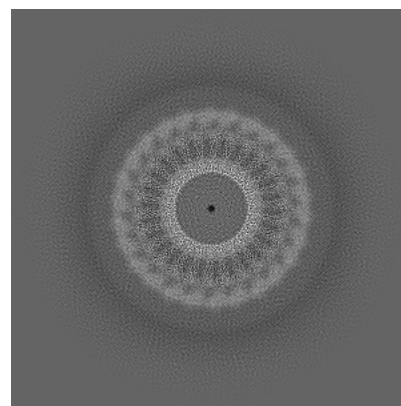
6.1.1 Primary map



X

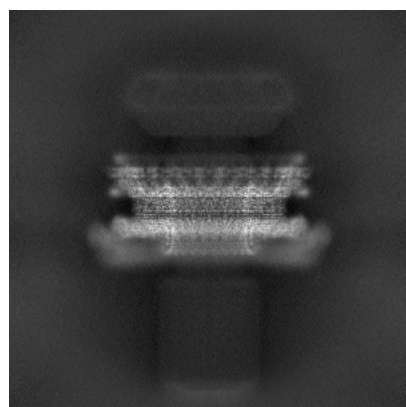


Y

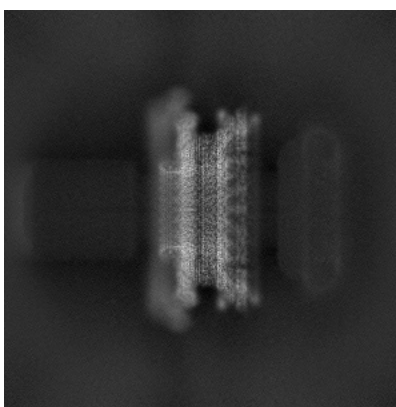


Z

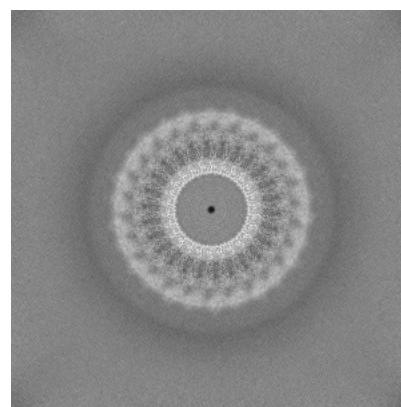
6.1.2 Raw map



X



Y

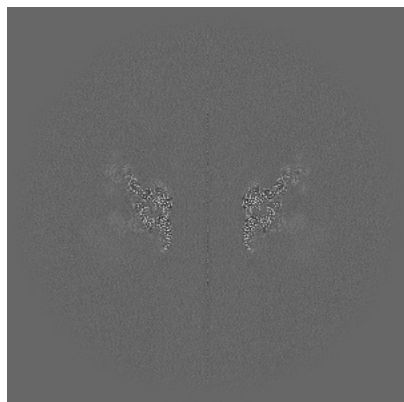


Z

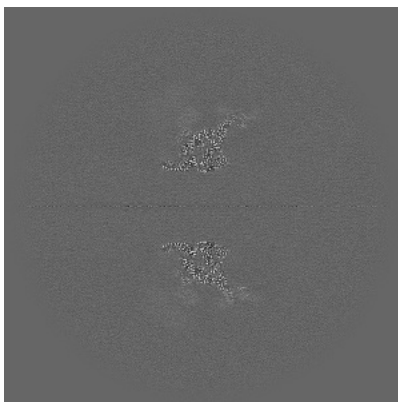
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

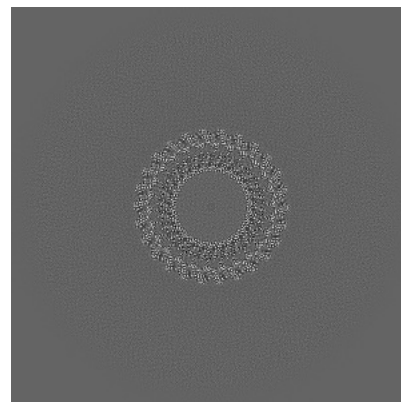
6.2.1 Primary map



X Index: 310

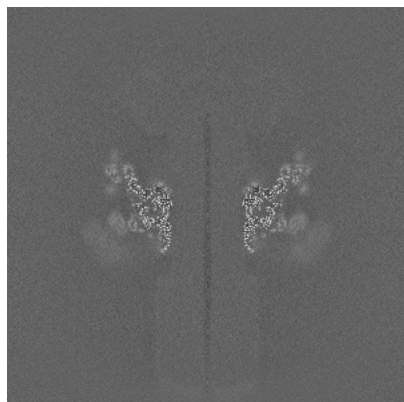


Y Index: 310

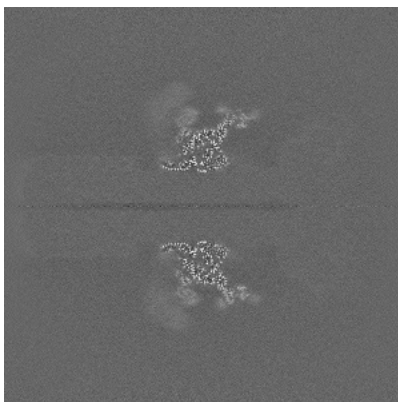


Z Index: 310

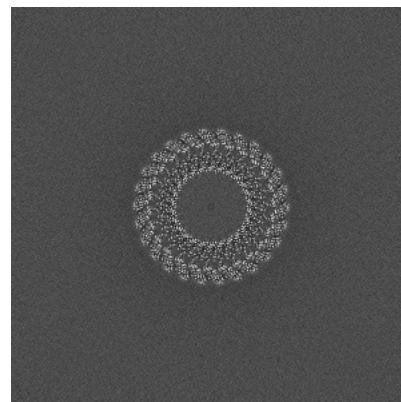
6.2.2 Raw map



X Index: 310



Y Index: 310

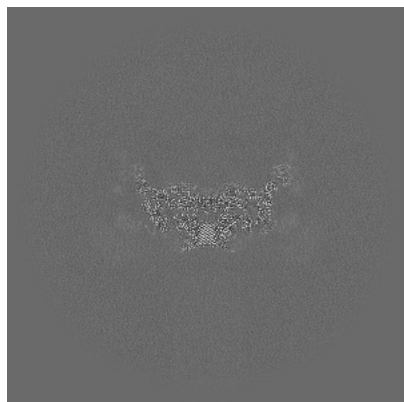


Z Index: 310

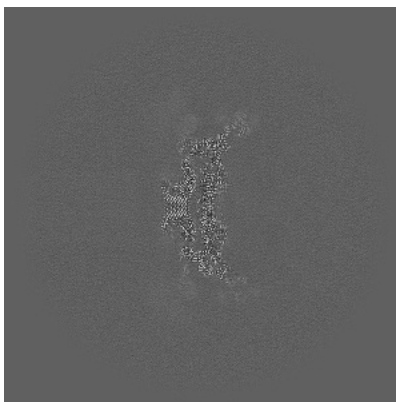
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

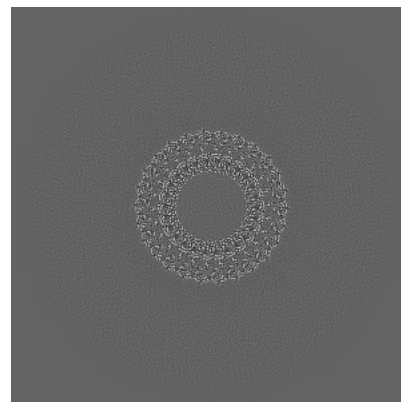
6.3.1 Primary map



X Index: 368



Y Index: 367

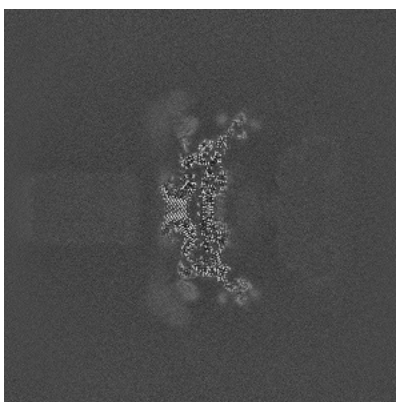


Z Index: 312

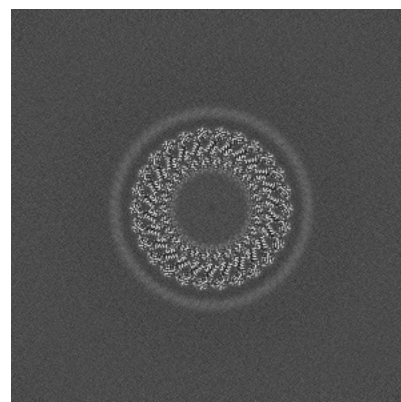
6.3.2 Raw map



X Index: 252



Y Index: 253

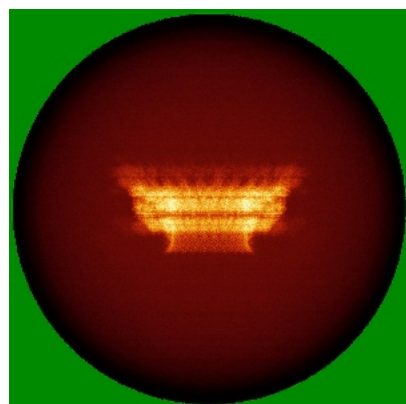


Z Index: 332

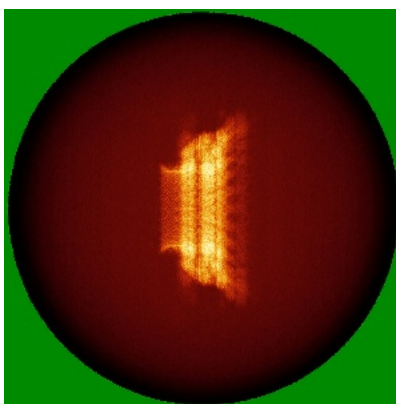
The images above show the largest variance slices of the map in three orthogonal directions.

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

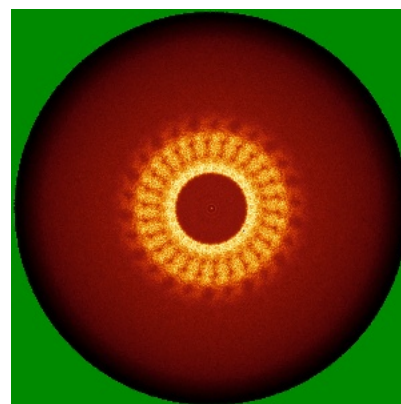
6.4.1 Primary map



X

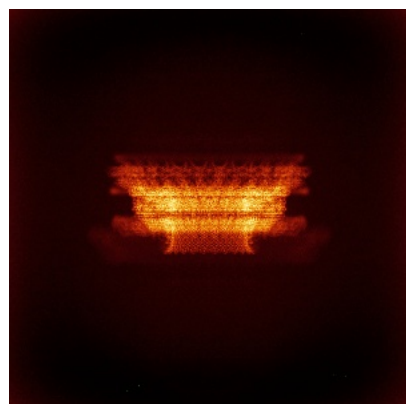


Y

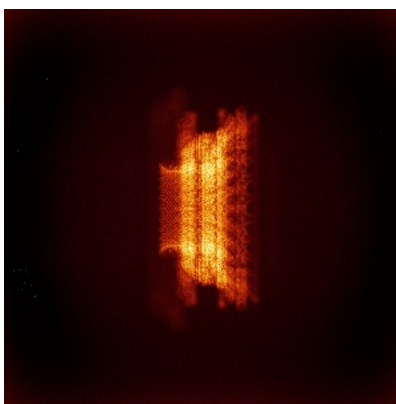


Z

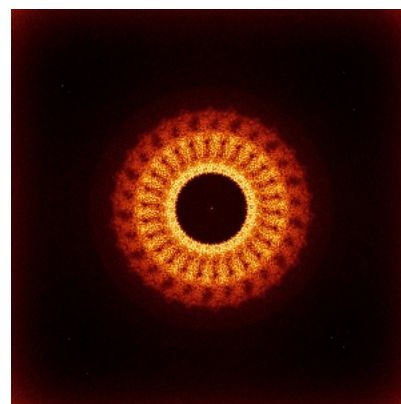
6.4.2 Raw map



X



Y

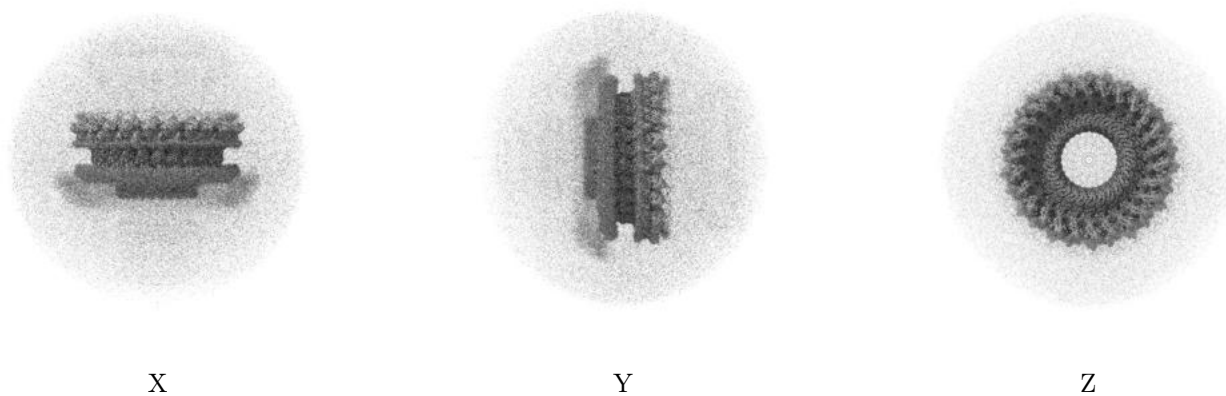


Z

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.

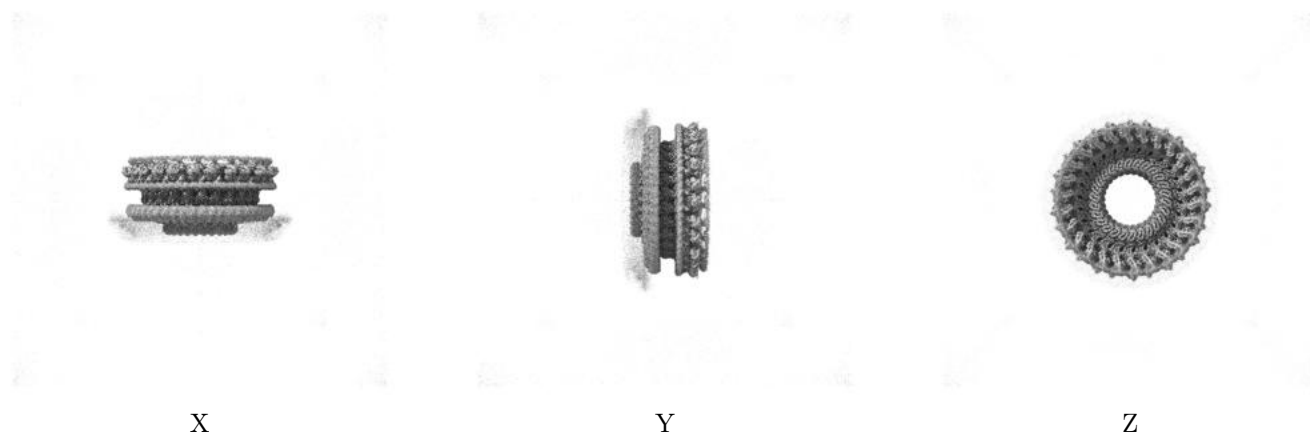
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.34. 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.

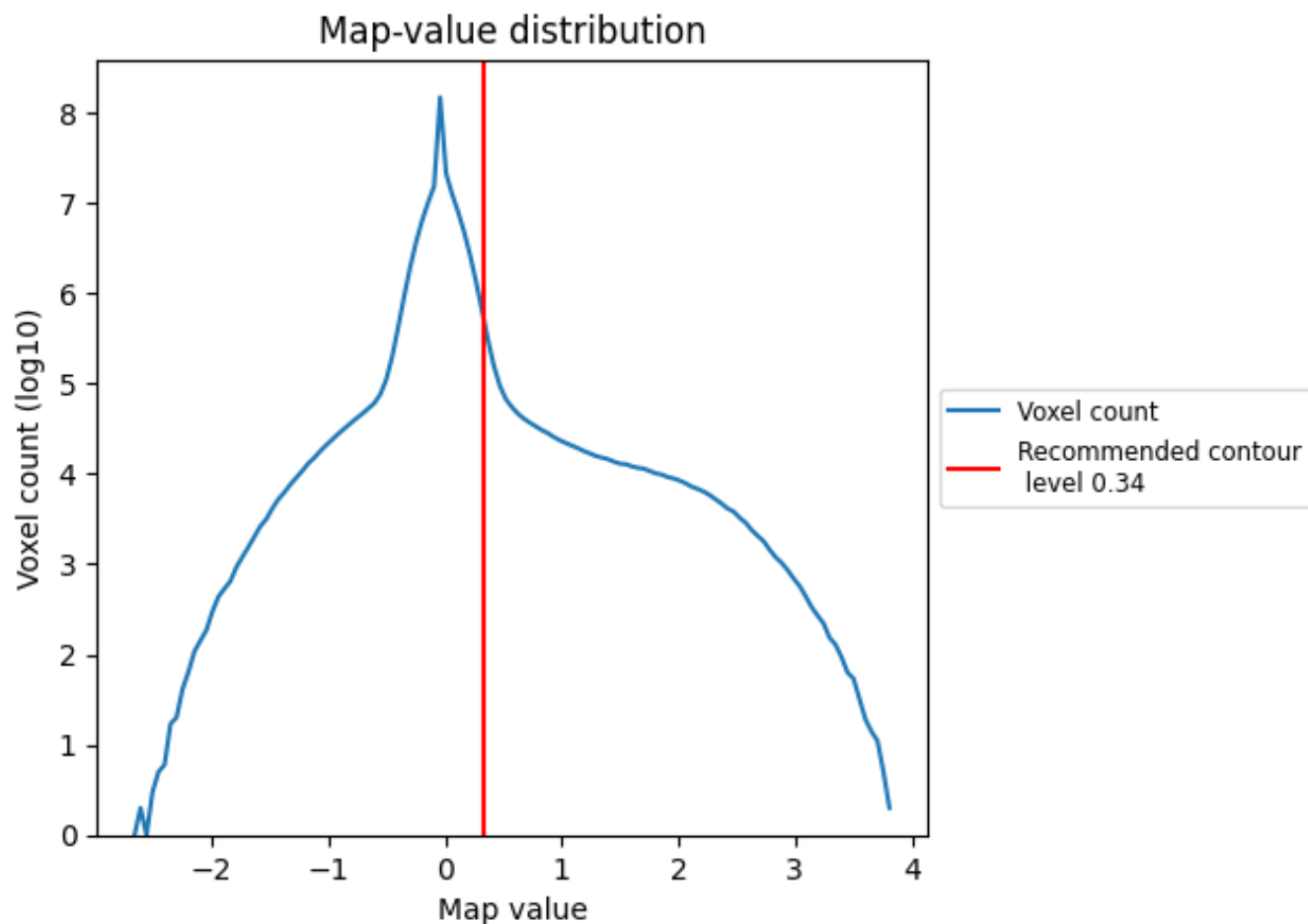
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

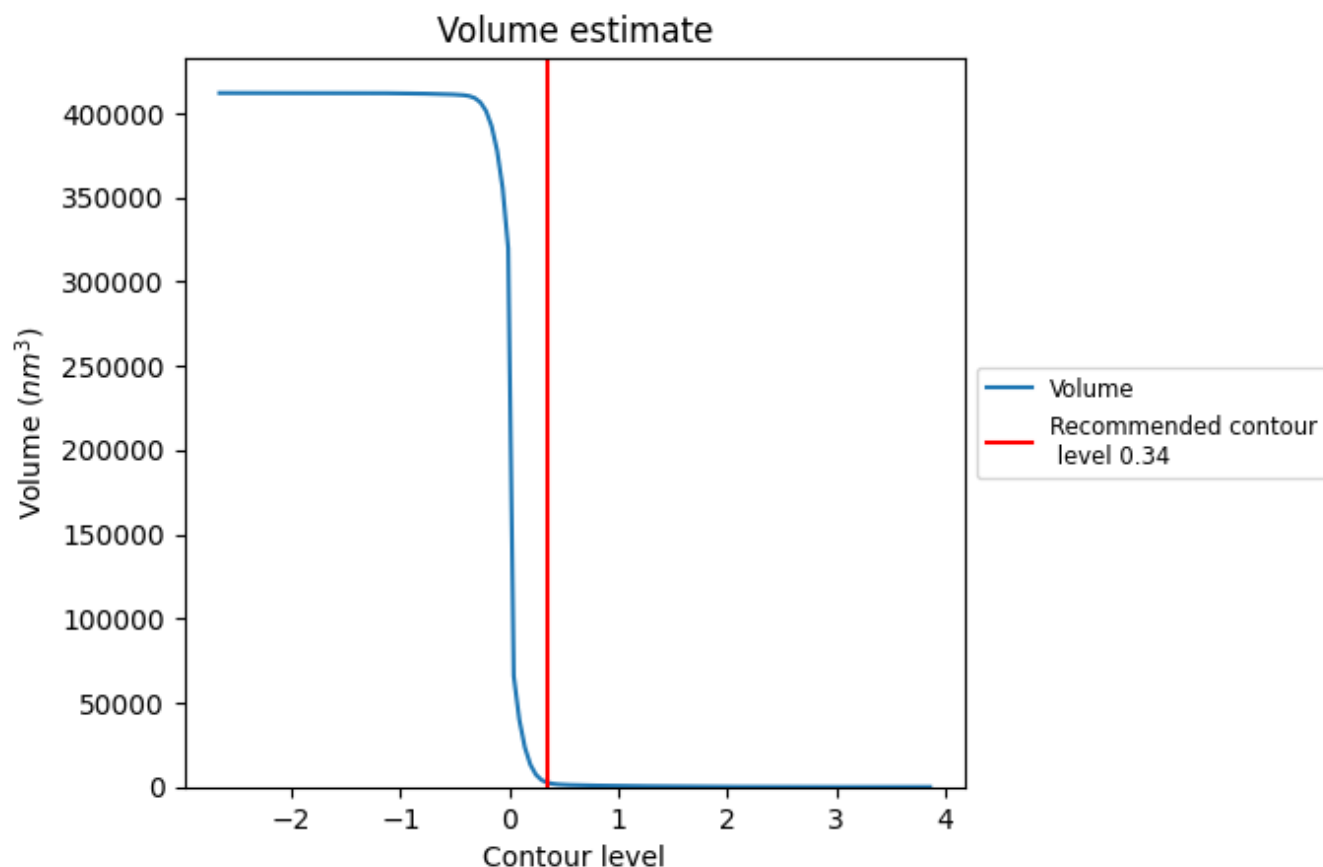
This section contains the results of statistical analysis of the map.

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.

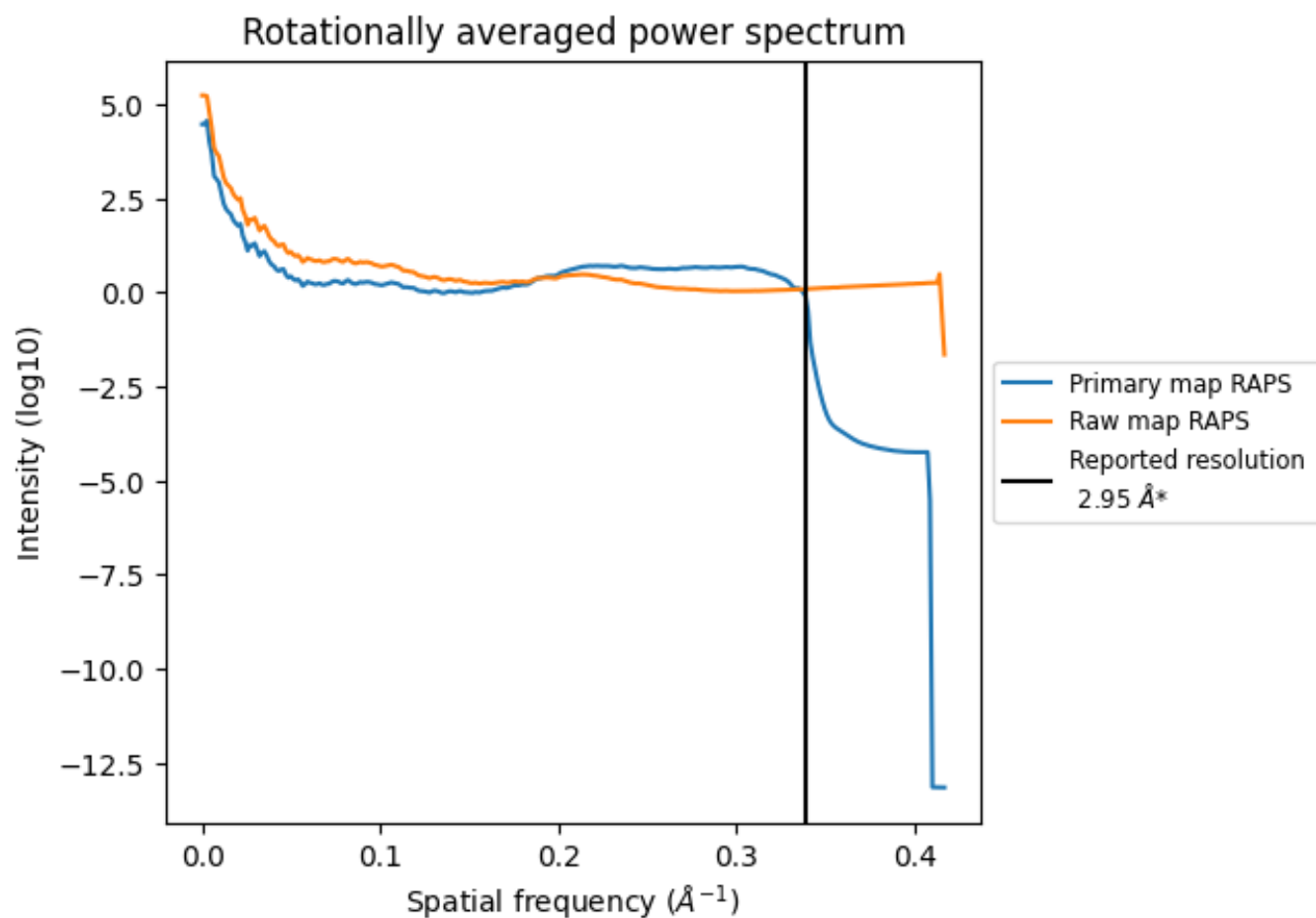
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2763 nm³; this corresponds to an approximate mass of 2496 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 ⓘ

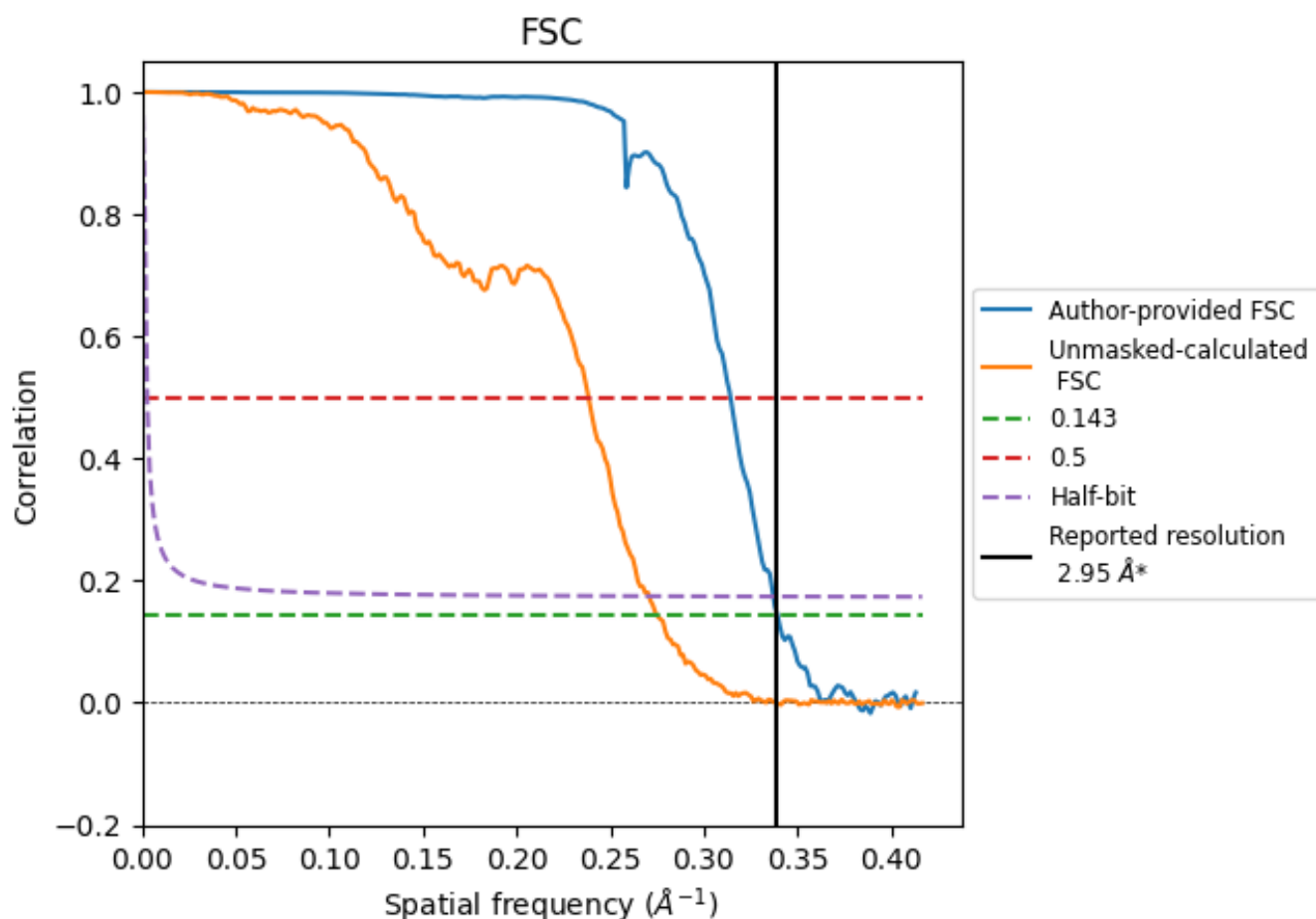


*Reported resolution corresponds to spatial frequency of 0.339 $\text{\AA}^{-1}$

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 $0.339 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

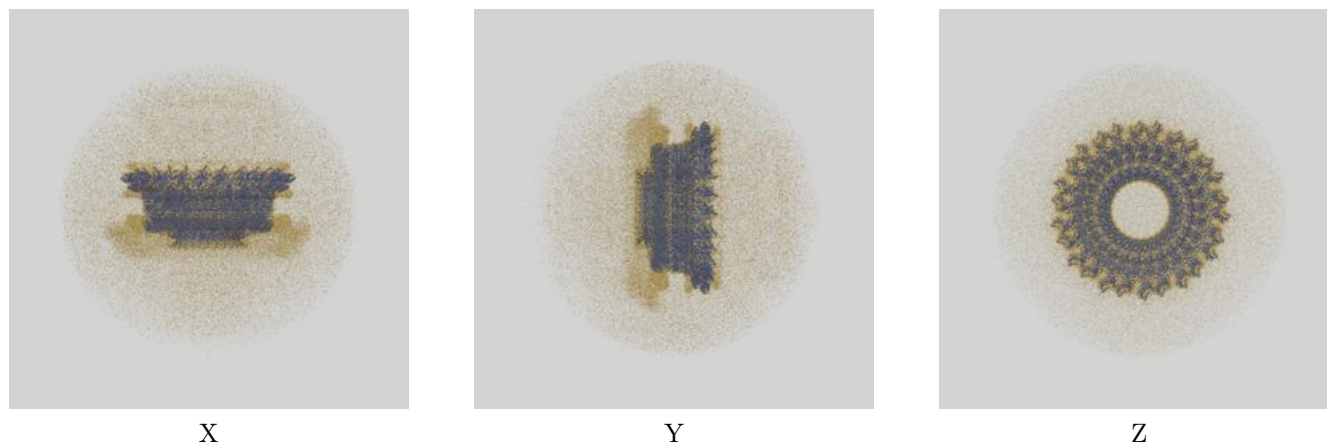
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.95	-	-
Author-provided FSC curve	2.95	3.18	2.97
Unmasked-calculated*	3.64	4.19	3.69

*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 3.64 differs from the reported value 2.95 by more than 10 %

9 Map-model fit [i](#)

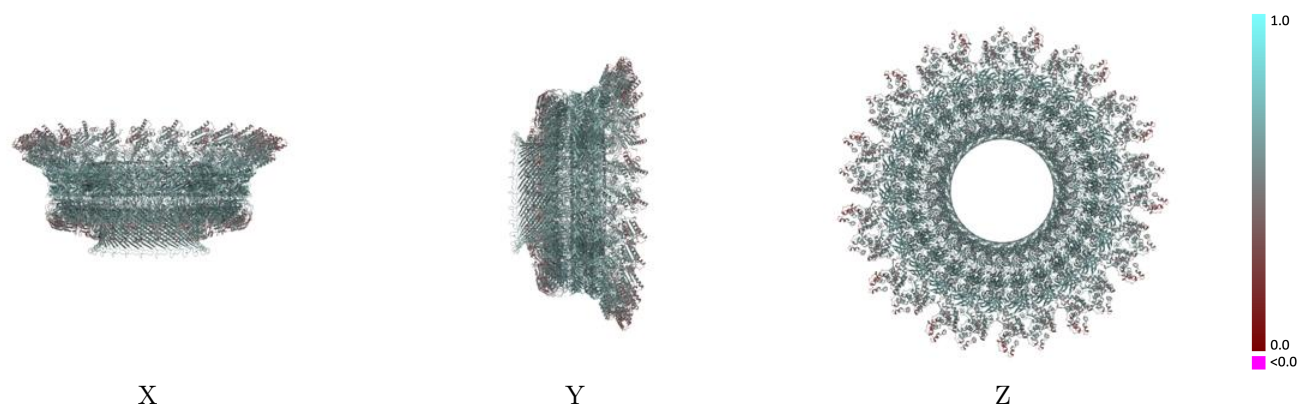
This section contains information regarding the fit between EMDB map EMD-39776 and PDB model 8Z5N. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



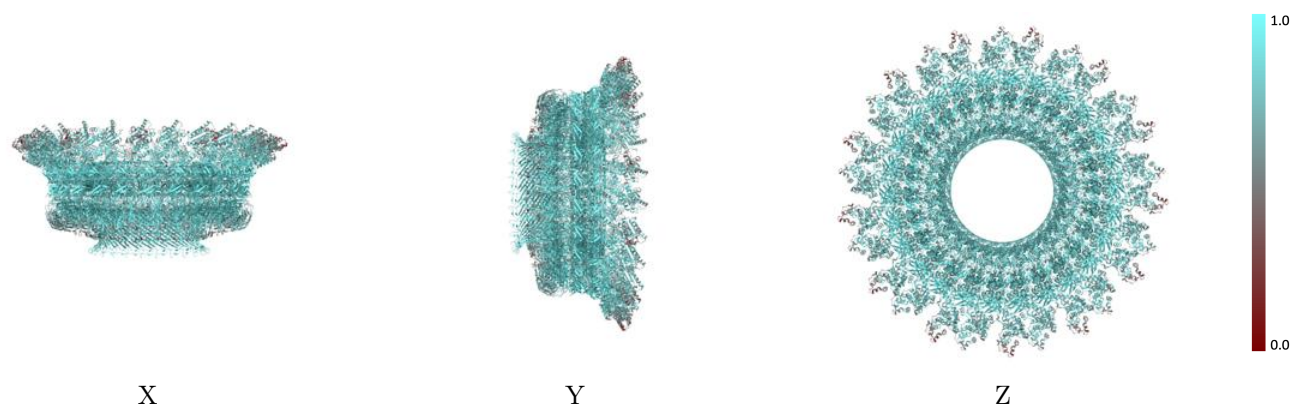
The images above show the 3D surface view of the map at the recommended contour level 0.34 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



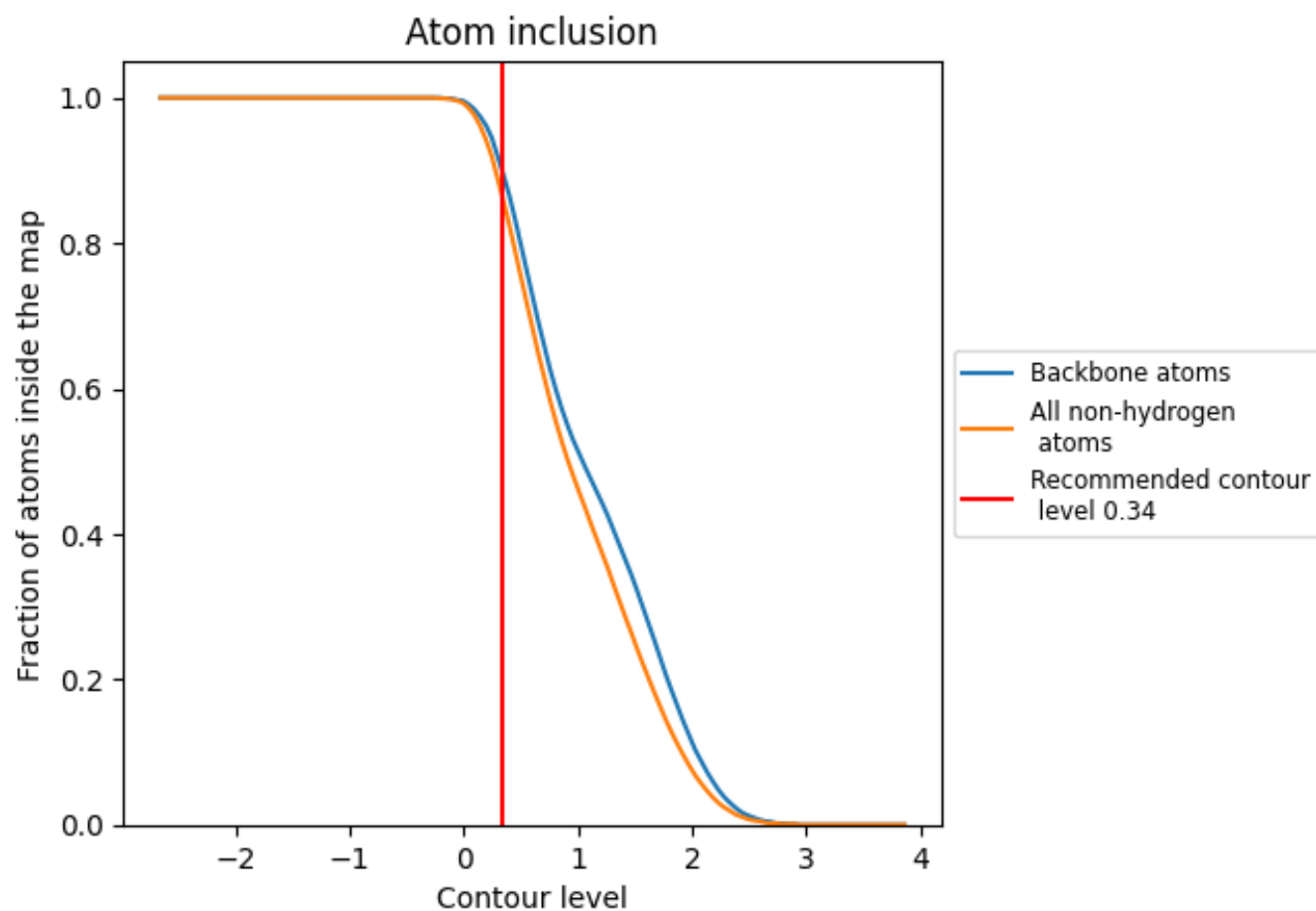
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.34).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% 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 (0.34) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.5690
0	 0.8610	 0.5640
1	 0.9100	 0.5960
2	 0.7050	 0.5170
3	 0.7390	 0.4450
4	 0.9430	 0.6100
5	 0.8680	 0.5710
6	 0.9070	 0.5900
7	 0.6840	 0.5030
8	 0.7230	 0.4460
9	 0.9320	 0.6020
A	 0.8630	 0.5790
A0	 0.7050	 0.5180
A1	 0.7690	 0.4340
A2	 0.9450	 0.6090
A3	 0.8640	 0.5690
A4	 0.9070	 0.5940
A5	 0.6950	 0.4940
A6	 0.7390	 0.4480
A7	 0.9360	 0.6060
A8	 0.8610	 0.5640
A9	 0.9040	 0.5950
AA	 0.9060	 0.5940
AB	 0.7260	 0.5260
AC	 0.7230	 0.4460
AD	 0.9440	 0.6060
AE	 0.8670	 0.5700
AF	 0.9090	 0.5910
AG	 0.7050	 0.4900
AH	 0.7390	 0.4500
AI	 0.9350	 0.6010
AJ	 0.8590	 0.5650
AK	 0.9050	 0.5950
AL	 0.7160	 0.5240
AM	 0.7390	 0.4380



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Chain	Atom inclusion	Q-score
AN	 0.9410	 0.6070
AO	 0.8650	 0.5710
AP	 0.9050	 0.5910
AQ	 0.7050	 0.4910
AR	 0.7390	 0.4500
AS	 0.9300	 0.6020
AT	 0.8610	 0.5640
AU	 0.9050	 0.5960
AV	 0.7160	 0.5290
AW	 0.7390	 0.4400
AX	 0.9440	 0.6070
AY	 0.8650	 0.5700
AZ	 0.9050	 0.5920
Aa	 0.6840	 0.4890
Ab	 0.7390	 0.4480
Ac	 0.9340	 0.6020
Ad	 0.8610	 0.5620
Ae	 0.9070	 0.5950
Af	 0.7260	 0.5230
Ag	 0.7690	 0.4410
Ah	 0.9440	 0.6080
Ai	 0.8690	 0.5700
Aj	 0.9070	 0.5910
Ak	 0.6950	 0.4940
Al	 0.7390	 0.4480
Am	 0.9340	 0.6020
An	 0.8590	 0.5620
Ao	 0.9090	 0.5950
Ap	 0.7370	 0.5210
Aq	 0.7540	 0.4390
Ar	 0.9430	 0.6080
As	 0.8680	 0.5690
At	 0.9060	 0.5920
Au	 0.7160	 0.4920
Av	 0.7390	 0.4430
Aw	 0.9360	 0.6040
Ax	 0.8590	 0.5630
Ay	 0.9090	 0.5960
Az	 0.7050	 0.5270
B	 0.8600	 0.5700
B1	 0.8700	 0.5700
B2	 0.9080	 0.5900

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Chain	Atom inclusion	Q-score
B3	 0.7050	 0.4970
B4	 0.7540	 0.4540
B5	 0.9360	 0.6020
B6	 0.8600	 0.5630
BA	 0.7540	 0.4280
BB	 0.9350	 0.6080
BC	 0.8690	 0.5700
BD	 0.9100	 0.5920
BE	 0.7050	 0.5000
BF	 0.7540	 0.4420
BG	 0.9320	 0.6020
BH	 0.8580	 0.5620
BI	 0.9060	 0.5970
BJ	 0.7260	 0.5250
BK	 0.7540	 0.4270
BL	 0.9380	 0.6070
BM	 0.8640	 0.5690
BN	 0.9100	 0.5920
BO	 0.6950	 0.4860
BP	 0.7230	 0.4520
BQ	 0.9360	 0.6020
BR	 0.8620	 0.5630
BS	 0.9100	 0.5950
BT	 0.7160	 0.5080
BU	 0.7390	 0.4440
BV	 0.9430	 0.6060
BW	 0.8700	 0.5690
BX	 0.9040	 0.5910
BY	 0.6950	 0.4950
BZ	 0.7390	 0.4530
Ba	 0.9360	 0.6030
Bb	 0.8610	 0.5640
Bc	 0.9020	 0.5950
Bd	 0.7160	 0.5110
Be	 0.7850	 0.4540
Bf	 0.9410	 0.6080
Bg	 0.8670	 0.5700
Bh	 0.9070	 0.5900
Bi	 0.7050	 0.4880
Bj	 0.7390	 0.4510
Bk	 0.9350	 0.6040
Bl	 0.8590	 0.5640

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Chain	Atom inclusion	Q-score
Bm	 0.9060	 0.5950
Bn	 0.7050	 0.5220
Bo	 0.7540	 0.4310
Bp	 0.9420	 0.6070
Bq	 0.8680	 0.5690
Br	 0.9100	 0.5910
Bs	 0.7050	 0.4950
Bt	 0.7540	 0.4570
Bu	 0.9330	 0.6020
Bv	 0.8590	 0.5630
Bw	 0.9070	 0.5940
Bx	 0.7260	 0.5180
By	 0.7540	 0.4420
Bz	 0.9430	 0.6060
C	 0.6660	 0.4840
D	 0.7580	 0.5210
E	 0.8620	 0.5770
F	 0.8600	 0.5690
G	 0.6590	 0.4790
H	 0.7510	 0.5200
I	 0.8630	 0.5770
J	 0.8620	 0.5680
K	 0.6700	 0.4820
L	 0.7490	 0.5200
M	 0.8630	 0.5770
N	 0.8630	 0.5680
O	 0.6650	 0.4800
P	 0.7570	 0.5210
Q	 0.8650	 0.5760
R	 0.8620	 0.5660
S	 0.6580	 0.4790
T	 0.7570	 0.5200
U	 0.8610	 0.5760
V	 0.8590	 0.5690
W	 0.6610	 0.4800
X	 0.7500	 0.5200
Y	 0.8630	 0.5750
Z	 0.8570	 0.5670
a	 0.6650	 0.4810
b	 0.7500	 0.5160
c	 0.8630	 0.5740
d	 0.8630	 0.5670

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Chain	Atom inclusion	Q-score
e	 0.6650	 0.4790
f	 0.7490	 0.5180
g	 0.8590	 0.5730
h	 0.8610	 0.5670
i	 0.6640	 0.4780
j	 0.7550	 0.5190
k	 0.8580	 0.5750
l	 0.8600	 0.5660
m	 0.6680	 0.4810
n	 0.7530	 0.5170
o	 0.8640	 0.5740
p	 0.8560	 0.5660
q	 0.6610	 0.4780
r	 0.7450	 0.5150
s	 0.8600	 0.5750
t	 0.8580	 0.5660
u	 0.6650	 0.4780
v	 0.7440	 0.5170
w	 0.8660	 0.5750
x	 0.8640	 0.5660
y	 0.6580	 0.4780
z	 0.7570	 0.5190