



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:33 AM UTC

PDB ID : 8UOX / pdb_00008uox
EMDB ID : EMD-42439
Title : Cryo-EM structure of a Counterclockwise locked form of the Salmonella enterica Typhimurium flagellar C-ring, with C34 symmetry applied
Authors : Johnson, S.; Deme, J.C.; Lea, S.M.
Deposited on : 2023-10-20
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

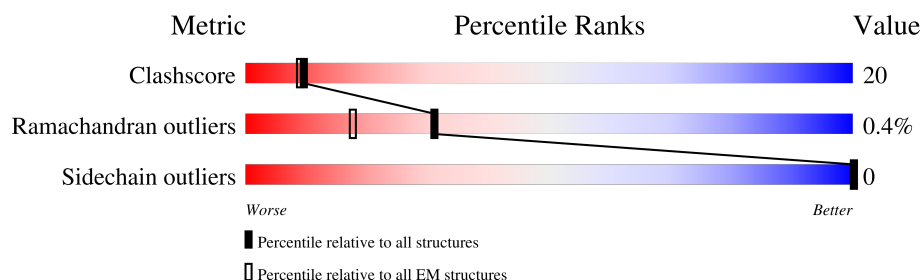
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

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



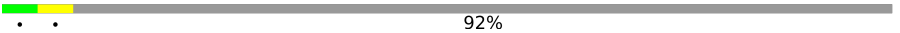
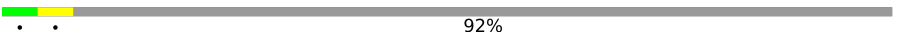
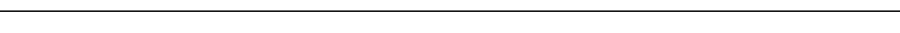
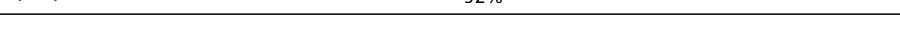
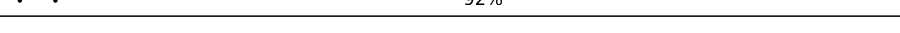
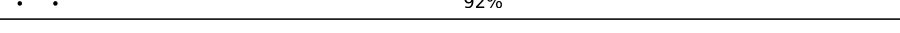
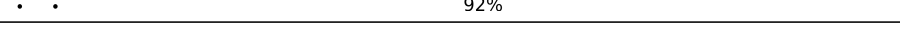
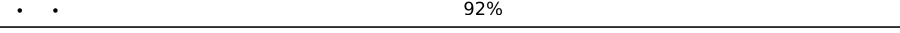
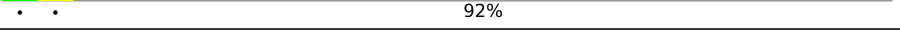
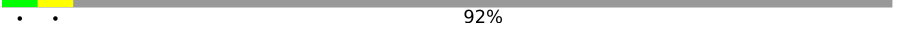
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A1	560	 92%
1	A2	560	 92%
1	A3	560	 92%
1	A4	560	 92%
1	A5	560	 92%
1	A6	560	 92%
1	A7	560	 92%
1	A8	560	 92%
1	A9	560	 92%

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Mol	Chain	Length	Quality of chain
1	AA	560	 92%
1	AB	560	 92%
1	AC	560	 92%
1	AD	560	 92%
1	AE	560	 92%
1	AF	560	 92%
1	AG	560	 92%
1	AH	560	 92%
1	AI	560	 92%
1	AJ	560	 92%
1	AK	560	 92%
1	AL	560	 92%
1	AM	560	 92%
1	AN	560	 92%
1	AO	560	 92%
1	AP	560	 92%
1	AQ	560	 92%
1	AR	560	 92%
1	AS	560	 92%
1	AT	560	 92%
1	AU	560	 92%
1	AV	560	 92%
1	AW	560	 92%
1	AX	560	 92%
1	AY	560	 92%

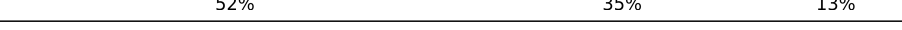
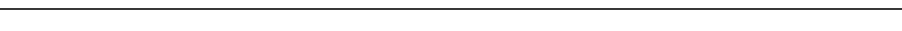
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Mol	Chain	Length	Quality of chain
2	B1	331	 60% 39% .
2	B2	331	 61% 38% .
2	B3	331	 61% 39% .
2	B4	331	 62% 37% .
2	B5	331	 64% 35% .
2	B6	331	 59% 40% .
2	B7	331	 62% 38% .
2	B8	331	 60% 39% .
2	B9	331	 63% 36% .
2	BA	331	 60% 40% .
2	BB	331	 60% 39% .
2	BC	331	 62% 38% .
2	BD	331	 63% 36% .
2	BE	331	 63% 36% .
2	BF	331	 63% 37% .
2	BG	331	 60% 40% .
2	BH	331	 59% 40% .
2	BI	331	 62% 38% .
2	BJ	331	 64% 36% .
2	BK	331	 61% 38% .
2	BL	331	 62% 37% .
2	BM	331	 65% 35% .
2	BN	331	 62% 38% .
2	BO	331	 62% 37% .
2	BP	331	 59% 41% .

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Mol	Chain	Length	Quality of chain
2	BQ	331	 60% 40% .
2	BR	331	 59% 41%
2	BS	331	 60% 40%
2	BT	331	 61% 38% .
2	BU	331	 61% 39% .
2	BV	331	 62% 38% .
2	BW	331	 62% 37% .
2	BX	331	 63% 37% .
2	BY	331	 58% 41% .
3	C1	334	 52% 35% 13%
3	C2	334	 50% 37% 13%
3	C3	334	 51% 36% 13%
3	C4	334	 49% 38% 13%
3	C5	334	 52% 35% 13%
3	C6	334	 50% 37% 13%
3	C7	334	 50% 37% 13%
3	C8	334	 52% 35% 13%
3	C9	334	 50% 37% 13%
3	CA	334	 51% 35% 13%
3	CB	334	 51% 36% 13%
3	CC	334	 51% 35% 13%
3	CD	334	 50% 37% 13%
3	CE	334	 51% 36% 13%
3	CF	334	 50% 37% 13%
3	CG	334	 51% 36% 13%

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Mol	Chain	Length	Quality of chain
3	CH	334	
3	CI	334	
3	CJ	334	
3	CK	334	
3	CL	334	
3	CM	334	
3	CN	334	
3	CO	334	
3	CP	334	
3	CQ	334	
3	CR	334	
3	CS	334	
3	CT	334	
3	CU	334	
3	CV	334	
3	CW	334	
3	CX	334	
3	CY	334	
4	D1	137	
4	D2	137	
4	D3	137	
4	D4	137	
4	D5	137	
4	D6	137	
4	D7	137	

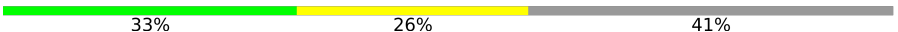
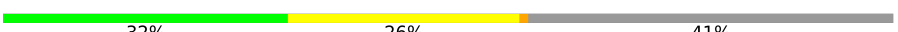
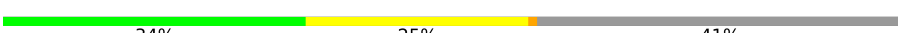
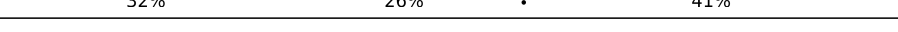
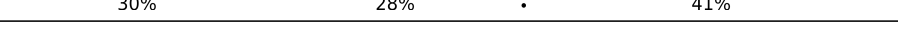
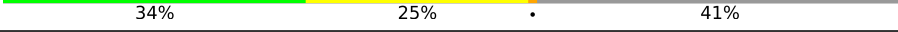
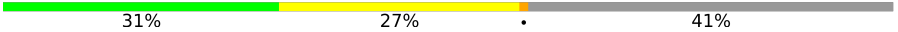
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Mol	Chain	Length	Quality of chain		
4	D8	137	32%	27%	41%
4	D9	137	31%	28%	41%
4	DA	137	33%	26%	41%
4	DB	137	34%	25%	41%
4	DC	137	32%	27%	41%
4	DD	137	31%	28%	41%
4	DE	137	31%	28%	41%
4	DF	137	33%	26%	41%
4	DG	137	34%	26%	41%
4	DH	137	34%	26%	41%
4	DI	137	32%	27%	41%
4	DJ	137	34%	26%	41%
4	DK	137	33%	26%	41%
4	DL	137	34%	26%	41%
4	DM	137	32%	27%	41%
4	DN	137	34%	25%	41%
4	DO	137	36%	23%	41%
4	DP	137	32%	27%	41%
4	DQ	137	33%	26%	41%
4	DR	137	31%	28%	41%
4	DS	137	33%	26%	41%
4	DT	137	32%	27%	41%
4	DU	137	34%	26%	41%
4	DV	137	34%	26%	41%
4	DW	137	31%	28%	41%

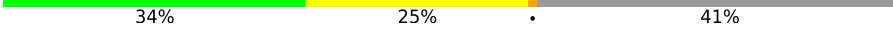
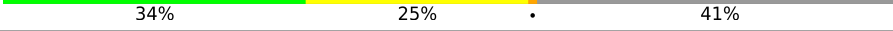
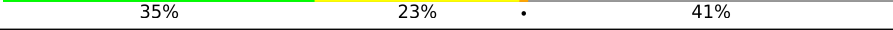
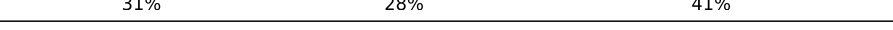
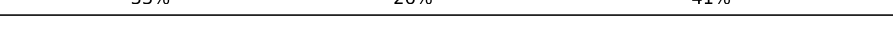
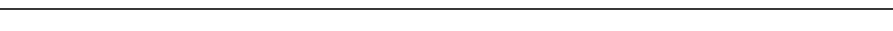
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Mol	Chain	Length	Quality of chain		
4	DX	137		33%	26%
4	DY	137		29%	30%
4	E1	137		30%	28%
4	E2	137		32%	26%
4	E3	137		34%	25%
4	E4	137		33%	26%
4	E5	137		36%	23%
4	E6	137		29%	29%
4	E7	137		34%	24%
4	E8	137		34%	25%
4	E9	137		30%	28%
4	EA	137		33%	26%
4	EB	137		31%	26%
4	EC	137		33%	26%
4	ED	137		31%	27%
4	EE	137		32%	26%
4	EF	137		30%	28%
4	EG	137		28%	31%
4	EH	137		29%	29%
4	EI	137		31%	27%
4	EJ	137		34%	25%
4	EK	137		33%	26%
4	EL	137		33%	26%
4	EM	137		31%	27%
4	EN	137		31%	28%

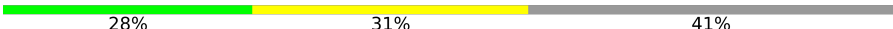
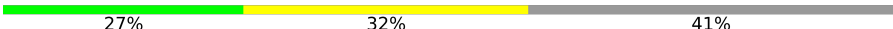
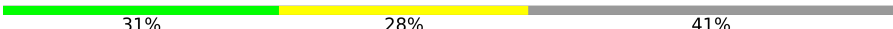
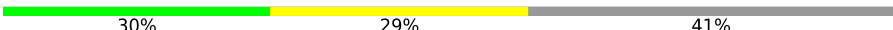
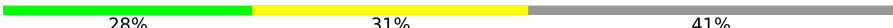
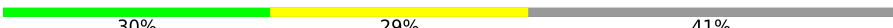
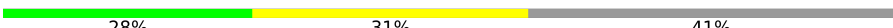
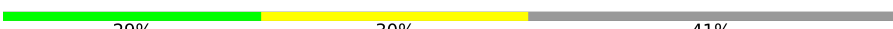
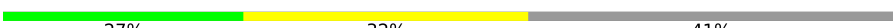
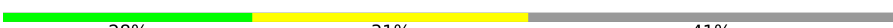
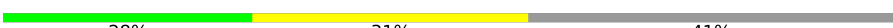
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Mol	Chain	Length	Quality of chain
4	EO	137	
4	EP	137	
4	EQ	137	
4	ER	137	
4	ES	137	
4	ET	137	
4	EU	137	
4	EV	137	
4	EW	137	
4	EX	137	
4	EY	137	
4	F1	137	
4	F2	137	
4	F3	137	
4	F4	137	
4	F5	137	
4	F6	137	
4	F7	137	
4	F8	137	
4	F9	137	
4	FA	137	
4	FB	137	
4	FC	137	
4	FD	137	
4	FE	137	

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Mol	Chain	Length	Quality of chain		
4	FF	137		28%	31%
4	FG	137		28%	31%
4	FH	137		27%	32%
4	FI	137		31%	28%
4	FJ	137		30%	29%
4	FK	137		28%	31%
4	FL	137		31%	28%
4	FM	137		28%	31%
4	FN	137		30%	29%
4	FO	137		29%	30%
4	FP	137		28%	31%
4	FQ	137		29%	30%
4	FR	137		27%	32%
4	FS	137		28%	31%
4	FT	137		29%	30%
4	FU	137		28%	31%
4	FV	137		27%	32%
4	FW	137		28%	31%
4	FX	137		28%	31%
4	FY	137		28%	31%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 244834 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A2	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A3	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A4	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A5	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A6	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A7	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A8	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	A9	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AA	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AB	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AC	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AD	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AE	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AF	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AG	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AH	47	Total	C	N	O	S	0	0
			393	233	81	76	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AI	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AJ	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AK	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AL	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AM	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AN	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AO	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AP	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AQ	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AR	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AS	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AT	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AU	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AV	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AW	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AX	47	Total	C	N	O	S	0	0
			393	233	81	76	3		
1	AY	47	Total	C	N	O	S	0	0
			393	233	81	76	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B1	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B2	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	B3	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B4	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B5	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B6	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B7	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B8	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	B9	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BA	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BB	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BC	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BD	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BE	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BF	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BG	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BH	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BI	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BJ	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BK	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BL	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BM	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BN	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	BO	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BP	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BQ	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BR	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BS	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BT	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BU	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BV	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BW	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BX	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		
2	BY	331	Total	C	N	O	S	0	0
			2583	1605	455	513	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C1	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C2	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C3	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C4	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C5	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C6	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C7	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	C8	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	C9	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CA	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CB	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CC	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CD	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CE	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CF	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CG	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CH	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CI	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CJ	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CK	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CL	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CM	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CN	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CO	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CP	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CQ	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CR	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CS	290	Total 2348	C 1497	N 424	O 422	S 5	0	0
3	CT	290	Total 2348	C 1497	N 424	O 422	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	CU	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	CV	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	CW	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	CX	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		
3	CY	290	Total	C	N	O	S	0	0
			2348	1497	424	422	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D1	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	E1	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	F1	81	Total	C	N	O	S	0	0
			627	397	111	116	3		
4	D2	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	E2	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	F2	81	Total	C	N	O	S	0	0
			627	397	111	116	3		
4	D3	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	E3	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	F3	81	Total	C	N	O	S	0	0
			627	397	111	116	3		
4	D4	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	E4	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	F4	81	Total	C	N	O	S	0	0
			627	397	111	116	3		
4	D5	81	Total	C	N	O	S	0	0
			625	398	108	116	3		
4	E5	81	Total	C	N	O	S	0	0
			625	398	108	116	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	F5	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	D6	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	E6	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	F6	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	D7	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	E7	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	F7	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	D8	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	E8	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	F8	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	D9	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	E9	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	F9	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DA	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EA	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FA	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DB	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EB	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FB	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DC	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EC	81	Total 625	C 398	N 108	O 116	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	FC	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DD	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	ED	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FD	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DE	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EE	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FE	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DF	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EF	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FF	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DG	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EG	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FG	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DH	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EH	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FH	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DI	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EI	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FI	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DJ	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EJ	81	Total 625	C 398	N 108	O 116	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	FJ	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DK	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EK	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FK	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DL	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EL	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FL	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DM	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EM	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FM	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DN	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EN	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FN	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DO	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EO	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FO	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DP	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EP	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FP	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DQ	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EQ	81	Total 625	C 398	N 108	O 116	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	FQ	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DR	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	ER	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FR	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DS	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	ES	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FS	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DT	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	ET	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FT	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DU	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EU	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FU	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DV	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EV	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FV	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DW	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EW	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FW	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DX	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EX	81	Total 625	C 398	N 108	O 116	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	FX	81	Total 627	C 397	N 111	O 116	S 3	0	0
4	DY	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	EY	81	Total 625	C 398	N 108	O 116	S 3	0	0
4	FY	81	Total 627	C 397	N 111	O 116	S 3	0	0

- Molecule 1: Flagellar M-ring protein

Chain A3: 92%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain A4: 92%

- Molecule 1: Flagellar M-ring protein

92%





- Molecule 1: Flagellar M-ring protein

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain AA: 92%

A548	L549	V550	I551	R552	Q553	W554	M555	S556	N557	D558	H559	E560
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Chain AB: 92%

- Molecule 1: Flagellar M-ring protein

Chain AC: 92%



1561	ARG	GLY	ASN	SER	VAL	GLU	PHE	GLN
	PRO	PHE	GLU	GLU	GLU	GLU	ILE	ASP
1562	GLN	SER	THR	GLN	SER	GLY	ILE	GLY
	GLN	ASP	SER	VAL	ARG	GLY	SER	GLY
1563	LEU	LYS	ASN	GLY	ILE	ALA	GLN	ALA
1564	THR	ARG	TYR	ALA	GLN	LEU	PHE	ILE
1565	ARG	GLY	GLU	GLY	ARG	ASP	SER	VAL
1566	VAL	ASP	VAL	TYR	ARG	GLU	GLU	ALA
1567	GLU	THR	ASP	PRO	ILE	GLY	GLN	GLN
1568	GLU	LEU	ARG	GLY	GLU	GLY	VAL	LEU
1569	ALA	ASN	THR	GLY	ILE	ILE	ASN	THR
1570	LYS	VAL	THR	VAL	ILE	SER	TYR	GLN
1571	ALA	VAL	ARG	PRO	LEU	ALA	GLN	MET
	ALA	ASN	HIS	GLY	SER	VAL	ARG	ASN
1572	GLN	SER	THR	ALA	PRO	ILE	ALA	ILE
1573	GLU	PRO	LYS	LEU	ILE	HIS	PRO	LEU
1574	GLN	PHE	MET	SER	VAL	VAL	GLY	THR
1575	ALA	SER	ASN	ASN	GLY	VAL	GLY	ARG
1576	ALA	ALA	VAL	GLN	ASN	SER	GLY	PHE
1577	VAL	VAL	GLY	PRO	GLY	SER	LEU	ARG
1578	ARG	ASP	ASP	ALA	ASN	ALA	ALA	ASN
1579	GLN	ASN	ILE	PRO	VAL	VAL	ARG	GLY
1580	GLU	THR	GLU	PRO	HIS	ALA	THR	SER
1581	THR	GLY	ARG	ASN	ALA	GLY	ILE	GLY
1582	GLU	GLY	LEU	GLU	GLN	LEU	GLU	ALA
1583	GLU	LEU	SER	ALA	VAL	PRO	THR	ILE
1584	ALA	PRO	VAL	ILE	ALA	GLY	ILE	GLU
1585	GLU	PHE	VAL	ALA	GLN	ASN	PRO	PRO
1586	VAL	TRP	VAL	VAL	LEU	VAL	VAL	ALA
1587	ARG	GLN	VAL	VAL	THR	THR	LYS	ASP
1588	LEU	GLN	ASN	THR	PHE	PHE	VAL	SER
1589	SER	GLN	TYR	THR	ASN	ASN	ALA	LYS
1590	PHE	ILE	THR	GLN	GLY	GLY	VAL	LEU
1591	GLY	ASP	ALA	GLN	GLN	SER	HIS	LEU
1592	GLN	ASP	ALA	ALA	GLN	GLY	LEU	ARG
1593	LEU	GLN	ASP	GLN	THR	HIS	ALA	LEU
1594	GLY	LEU	GLY	GLM	GLU	LEU	MET	ARG
1595	ALA	LEU	LYS	GLM	GLU	LEU	PRO	LEU
1596	LEU	ALA	PRO	THR	HIS	THR	LYS	ALA
1597	ALA	ALA	LEU	PRO	TYR	GLN	GLN	GLN
1598	GLY	ARG	PRO	GLM	SER	SER	PRO	GLN
1599	THR	TRP	THR	THR	THR	THR	PHE	LEU
1600	LEU	LEU	ALA	THR	GLY	GLY	VAL	GLY
1601	VAL	VAL	GLN	THR	ASP	ARG	GLY	LYS
1602	LEU	LEU	MET	THR	ALA	ASP	GLY	GLY
1603	VAL	VAL	ASN	THR	ALA	ASP	GLY	GLY
1604	GLY	VAL	LYS	SER	LYS	GLN	VAL	VAL
1605	THR	THR	THR	GLM	GLN	GLY	VAL	HIS
1606	ASP	ILE	ALA	GLN	GLN	GLY	LEU	LEU
1607	GLN	GLN	ASP	GLM	THR	HIS	ALA	LEU
1608	LEU	GLN	GLY	GLM	GLU	MET	ALA	LEU
1609	GLY	LEU	LYS	GLM	GLU	PRO	ASN	LEU
1610	ALA	ALA	PRO	THR	HIS	THR	LYS	ALA
1611	ALA	ALA	LEU	PRO	TYR	GLN	PRO	GLN
1612	GLY	ARG	PRO	GLM	SER	SER	GLN	SER
1613	THR	THR	THR	THR	THR	THR	PHE	VAL
1614	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1615	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1616	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1617	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1618	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1619	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1620	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1621	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1622	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1623	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1624	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1625	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1626	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1627	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1628	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1629	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1630	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1631	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1632	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1633	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1634	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1635	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1636	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1637	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1638	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1639	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1640	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1641	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1642	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1643	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1644	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1645	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1646	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1647	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1648	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1649	GLU	GLU	THR	THR	THR	THR	VAL	VAL
1650	GLU	GLU	THR	THR	THR	THR	VAL	VAL

- Molecule 1: Flagellar M-ring protein

Chain AH: 92%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain AM: 92%

[illegible]

- Molecule 1: Flagellar M-ring protein

Chain AN: 92%

- Molecule 1: Flagellar M-ring protein

92%



ARG	PRO	GLN	LEU	THR	ARG	ARG	VAL	GLU	GLU	ALA	LYS	ALA	ALA	GLN	GLN	GLN	ALA	GLN	VAL	ARG	GLN	THR	GLU	GLU	ALA	VAL	GLU	VAL	ARG	LEU	SER	K514	D515	E516	Q517	I518	Q519	Q520	R521	R522	A523	R526	M532	S533	Q534	R535	I536	R537	E538	M539	S540	P544	R545	V546	V547																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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● Molecule 1: Flagellar M-ring protein

Chain AP: . . 92%

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● Molecule 1: Flagellar M-ring protein

Chain AQ: . . 92%

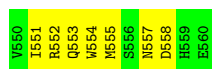
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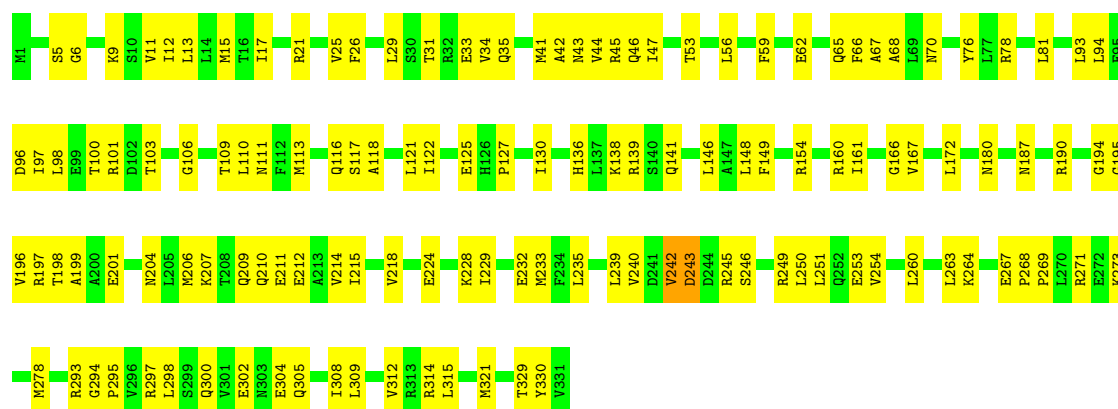


V550
I551
R552
Q553
W554
M555
S556
N557
D558
H559
E560

Chain AY: 92%



Chain B1: 60% 39% .



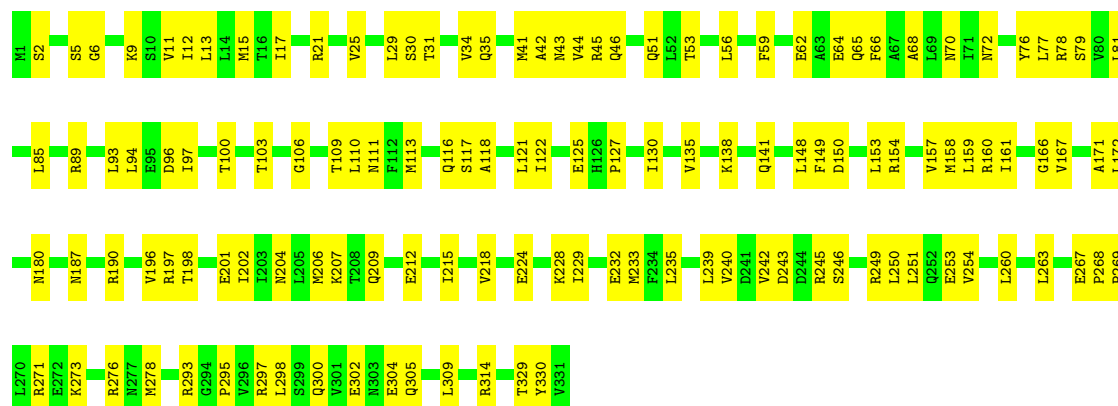
• Molecule 2: Flagellar motor switch protein FliG

Chain B2:



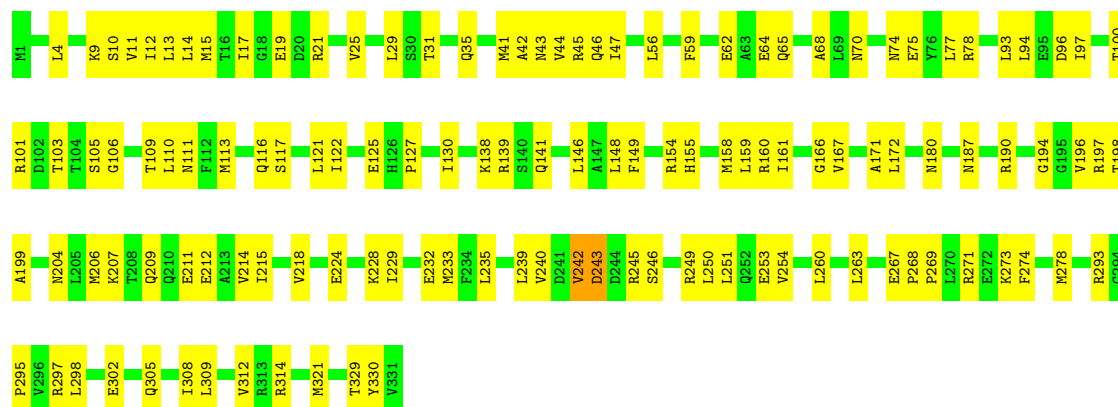
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Chain B3:

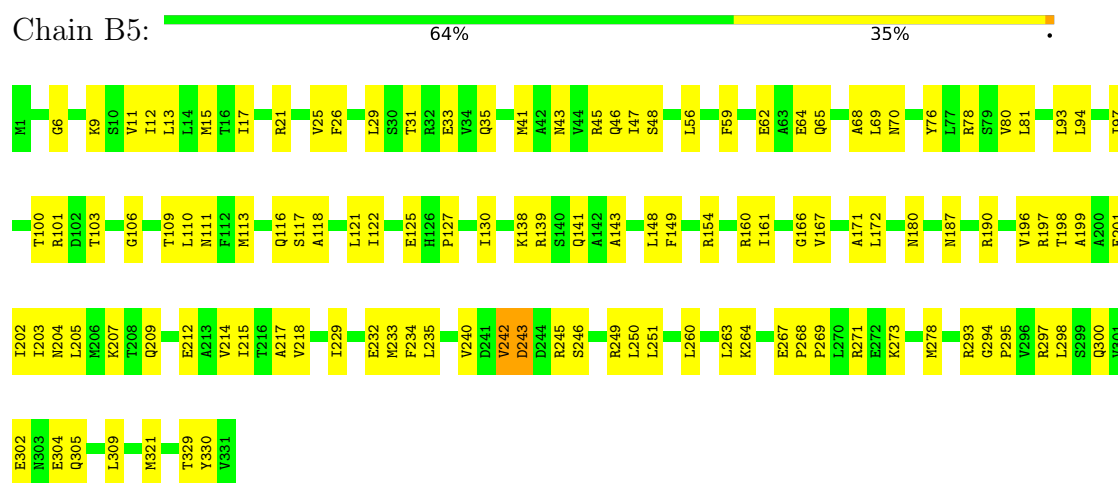


• Molecule 2: Flagellar motor switch protein FliG

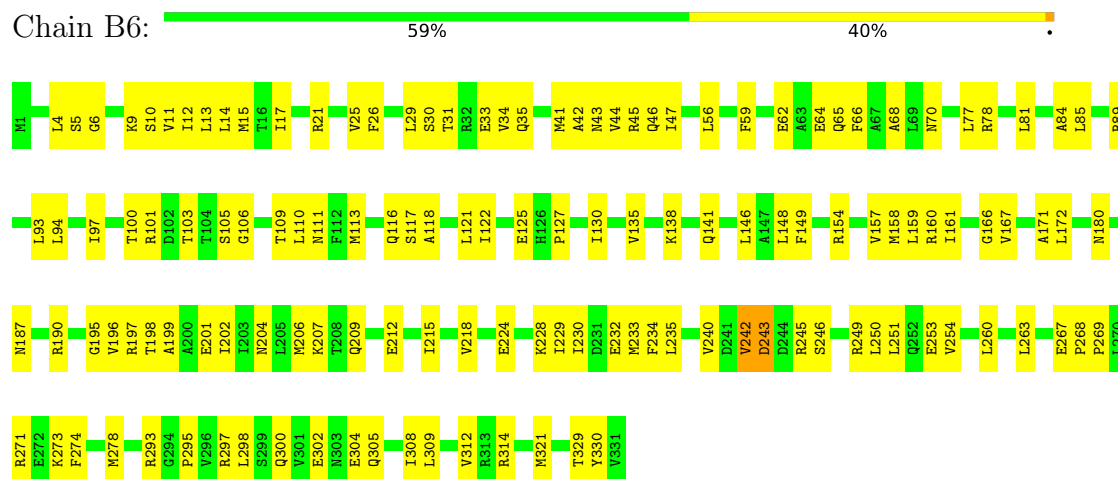
Chain B4:



• Molecule 2: Flagellar motor switch protein FliG

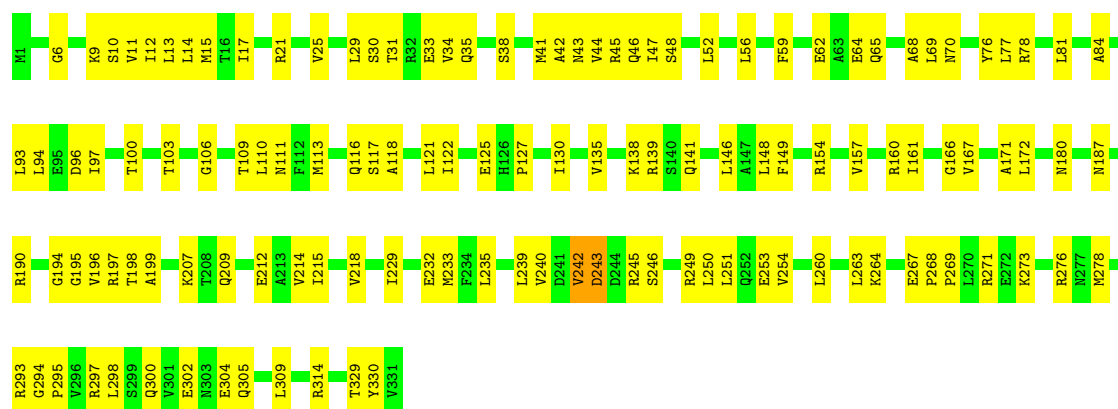


• Molecule 2: Flagellar motor switch protein FliG

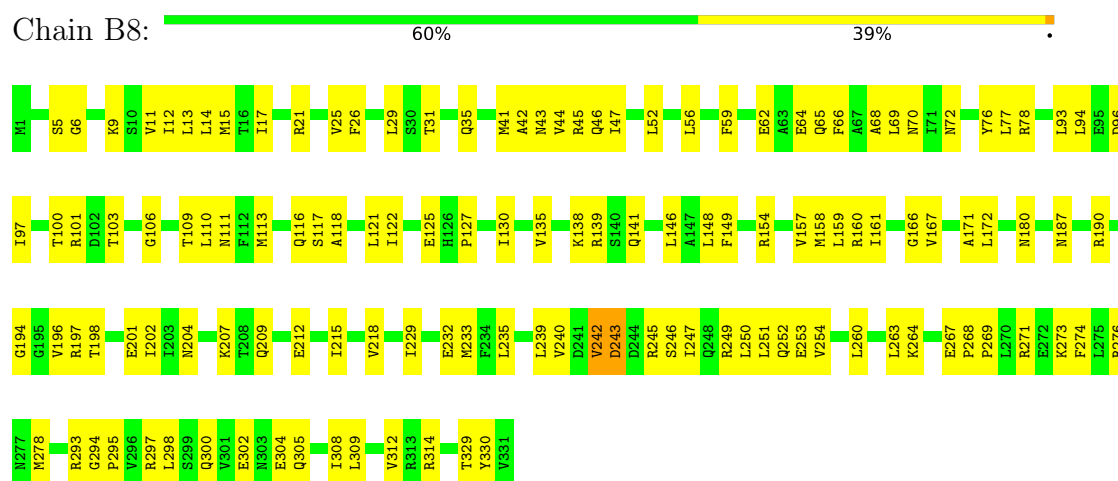


• Molecule 2: Flagellar motor switch protein FliG

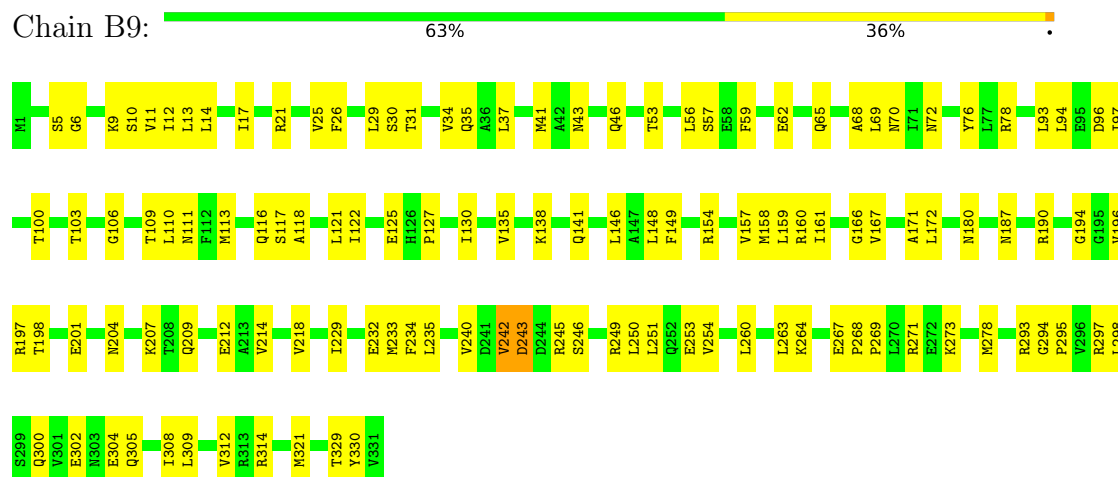




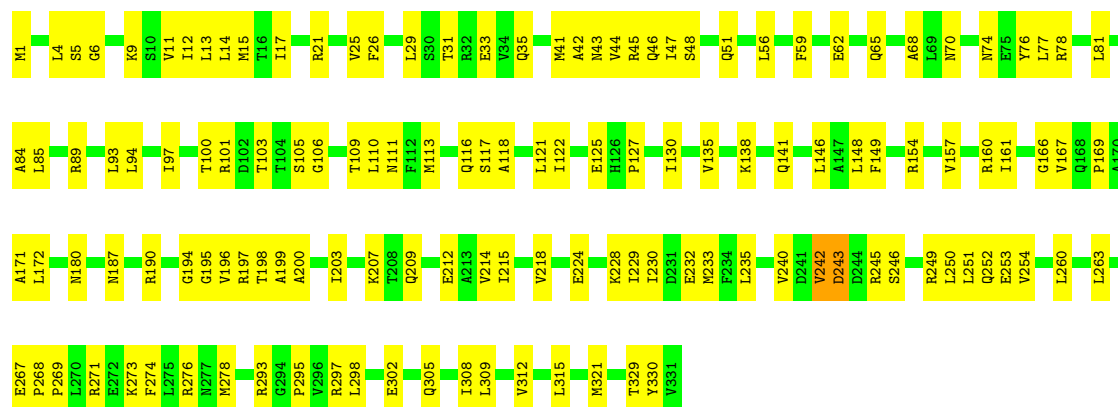
• Molecule 2: Flagellar motor switch protein FliG



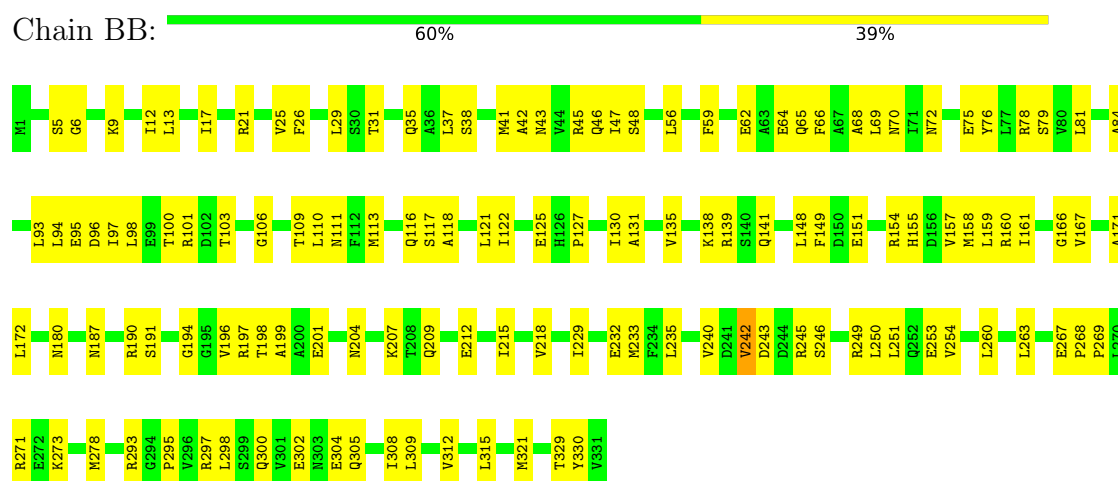
• Molecule 2: Flagellar motor switch protein FliG



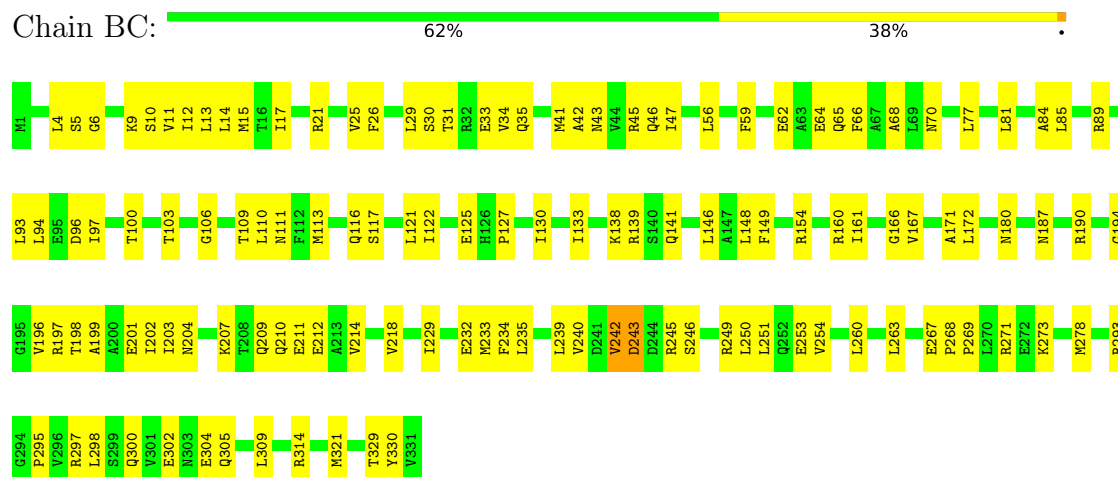
• Molecule 2: Flagellar motor switch protein FliG



• Molecule 2: Flagellar motor switch protein FliG



• Molecule 2: Flagellar motor switch protein FliG

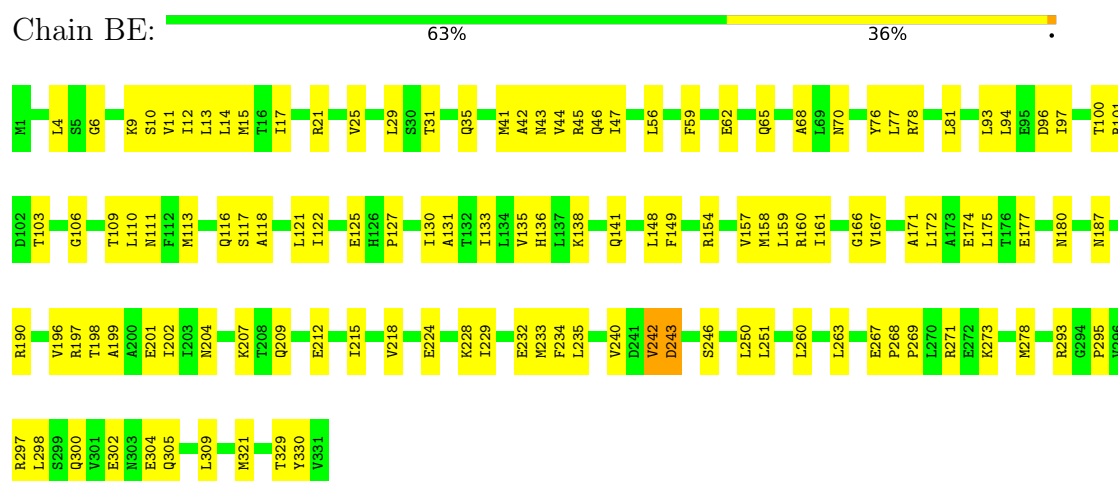


• Molecule 2: Flagellar motor switch protein FliG

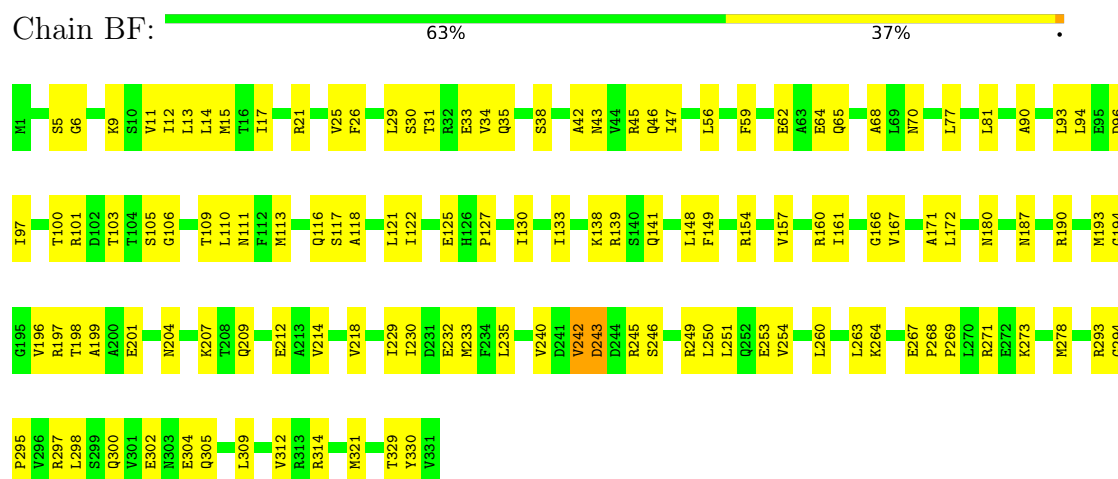




• Molecule 2: Flagellar motor switch protein FliG



• Molecule 2: Flagellar motor switch protein FliG

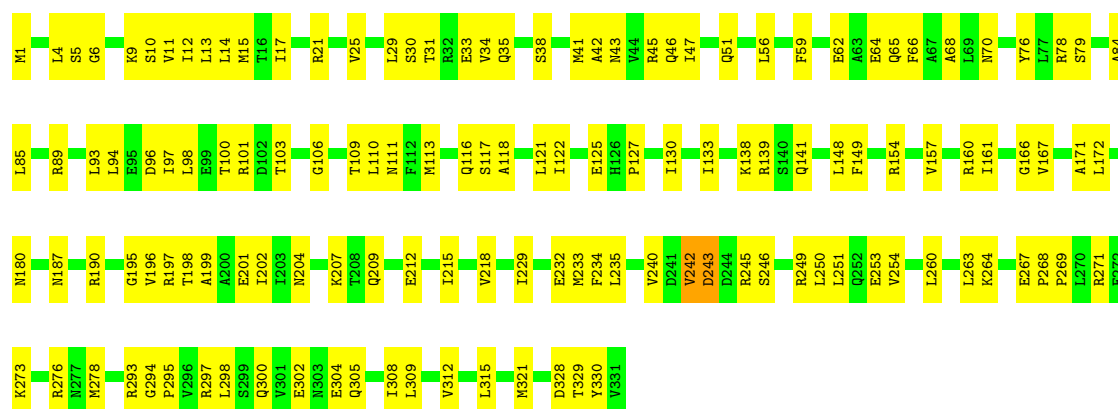


• Molecule 2: Flagellar motor switch protein FliG



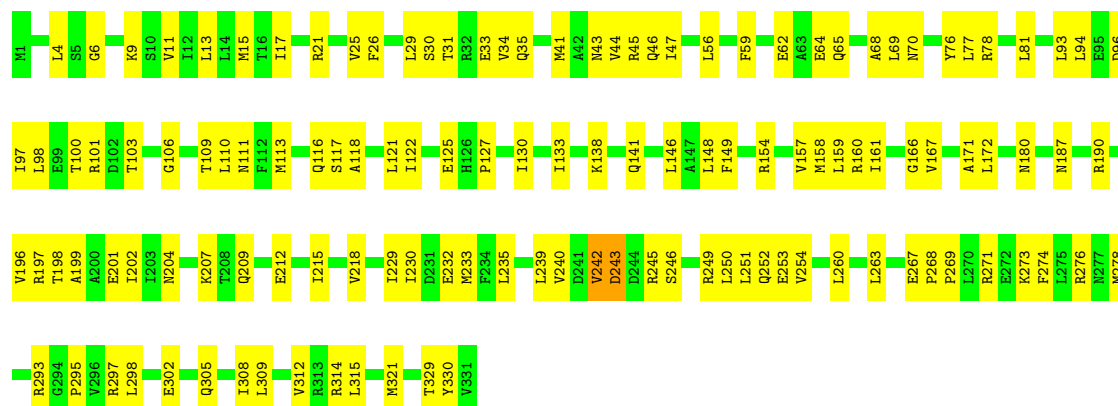
• Molecule 2: Flagellar motor switch protein FliG

Chain BH: 59% 40% .



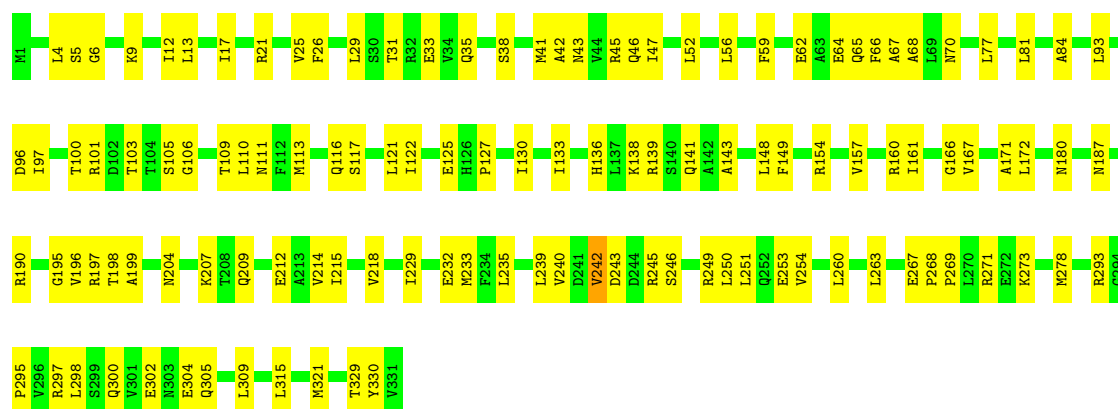
• Molecule 2: Flagellar motor switch protein FliG

Chain BI: 62% 38% .

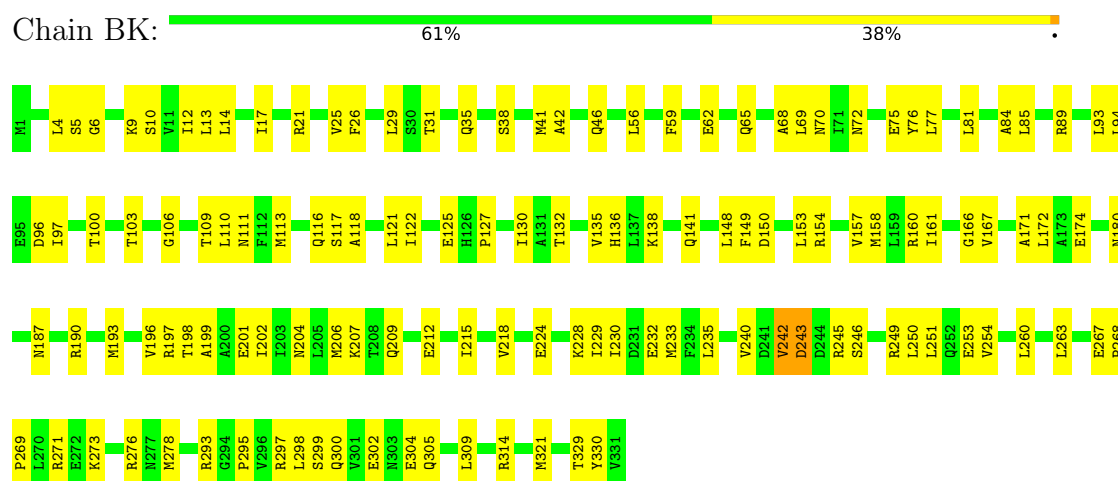


• Molecule 2: Flagellar motor switch protein FliG

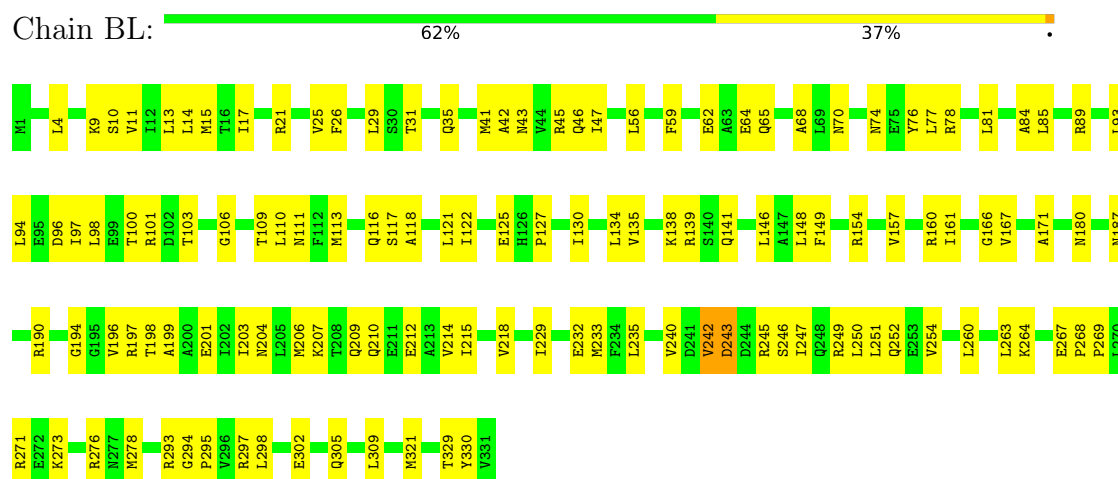
Chain BJ: 64% 36%



• Molecule 2: Flagellar motor switch protein FliG

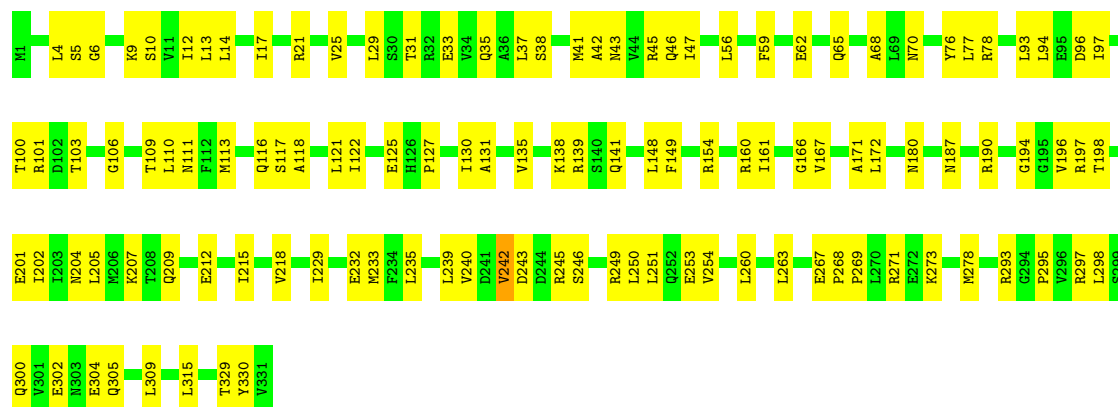


• Molecule 2: Flagellar motor switch protein FliG



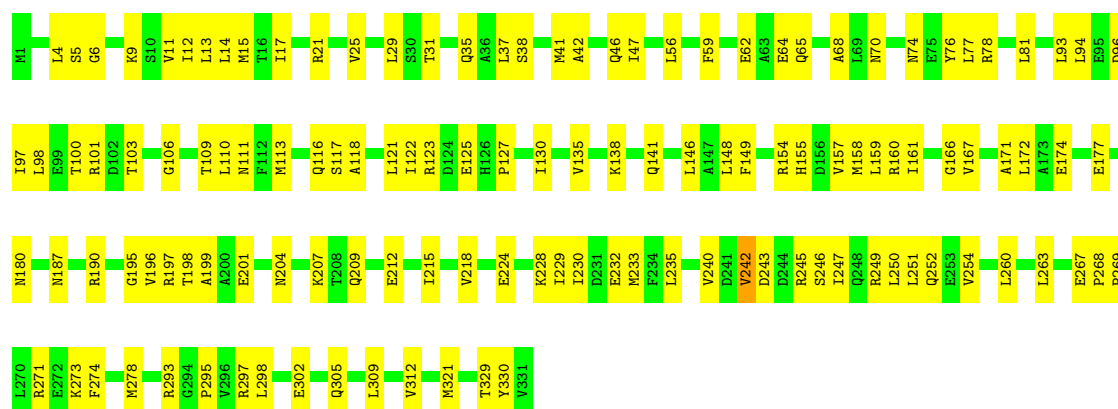
• Molecule 2: Flagellar motor switch protein FliG





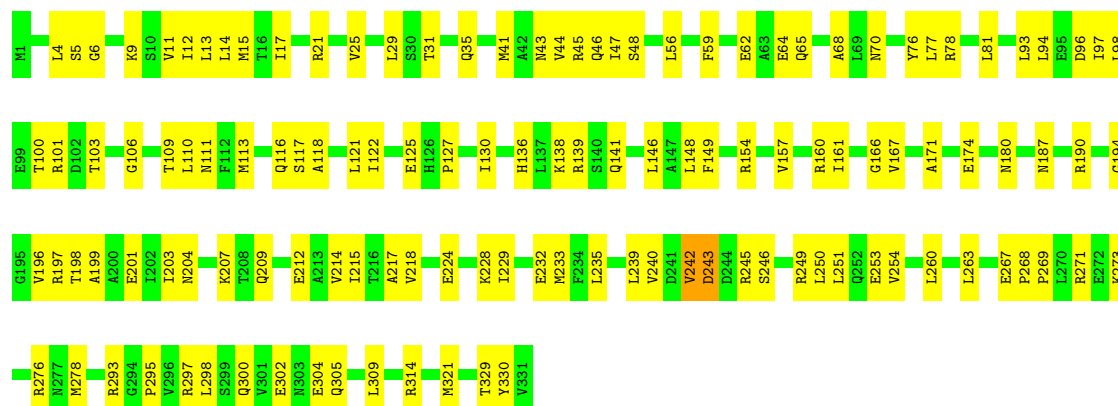
• Molecule 2: Flagellar motor switch protein FlhG

Chain BN: 62% 38%



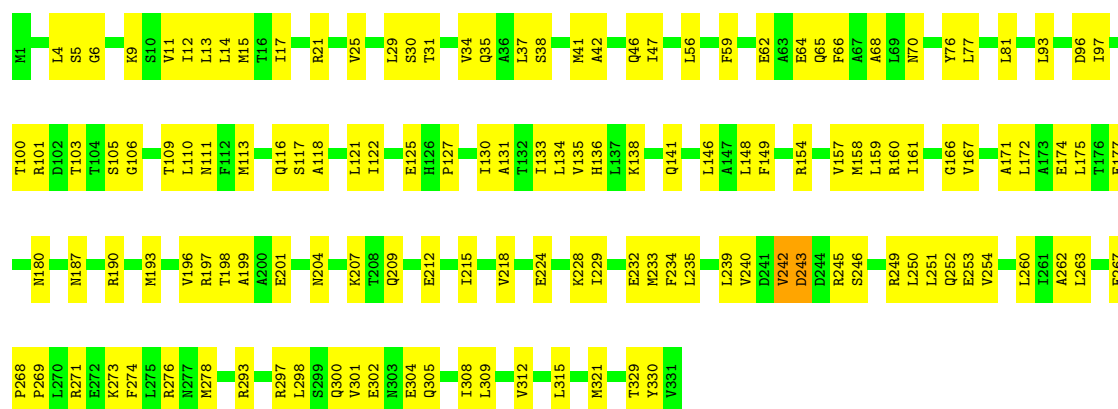
• Molecule 2: Flagellar motor switch protein FlhG

Chain BO: 62% 37%



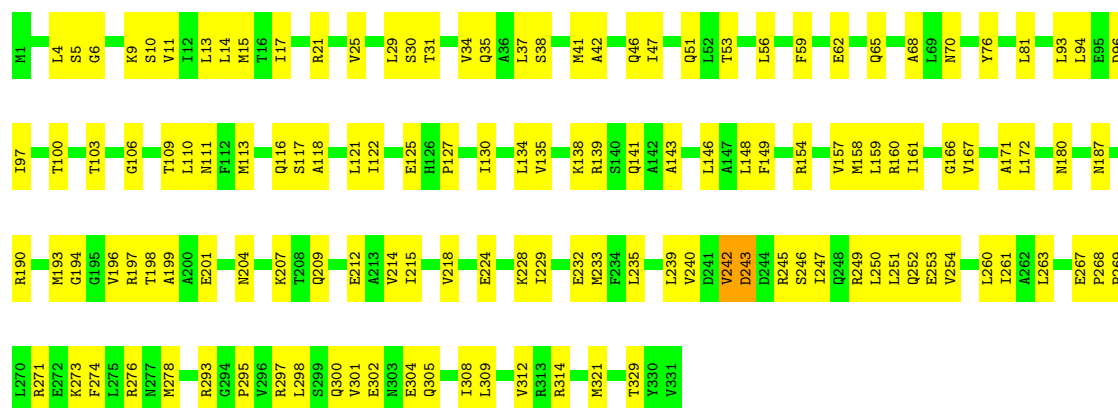
• Molecule 2: Flagellar motor switch protein FlhG

Chain BP: 59% 41%



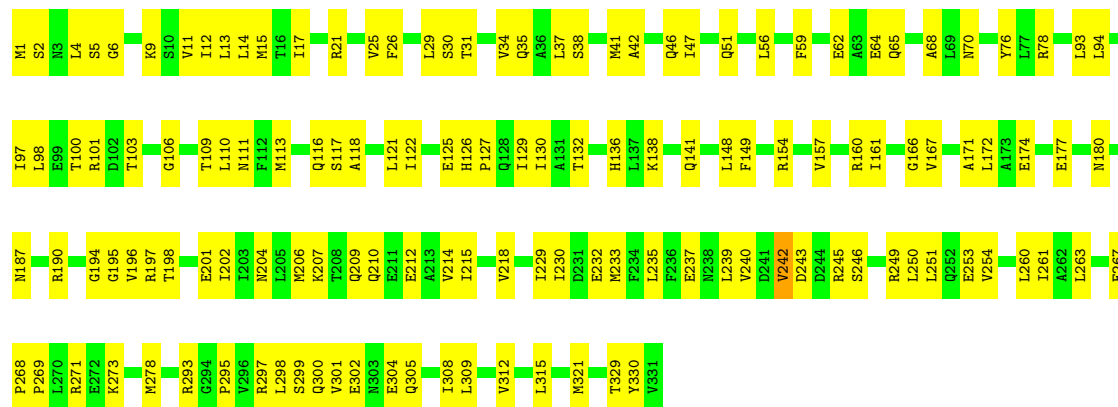
• Molecule 2: Flagellar motor switch protein FlIG

Chain BQ: .



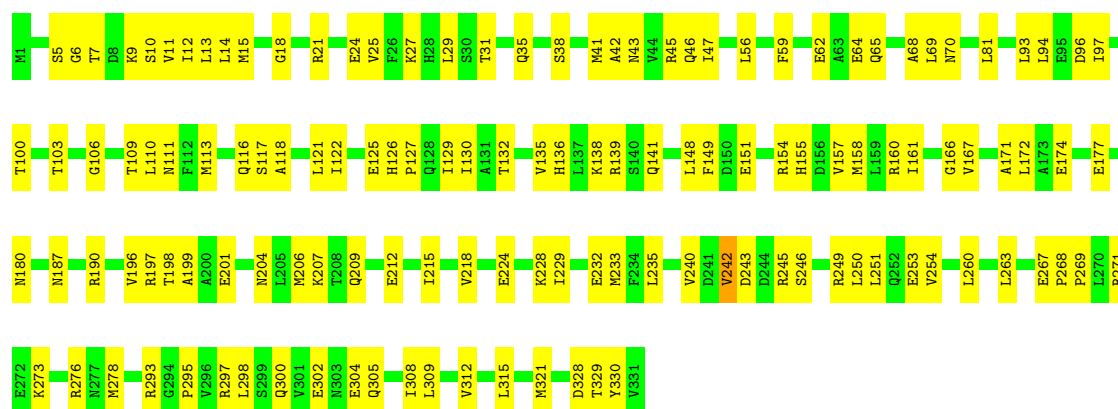
• Molecule 2: Flagellar motor switch protein FlIG

Chain BR:



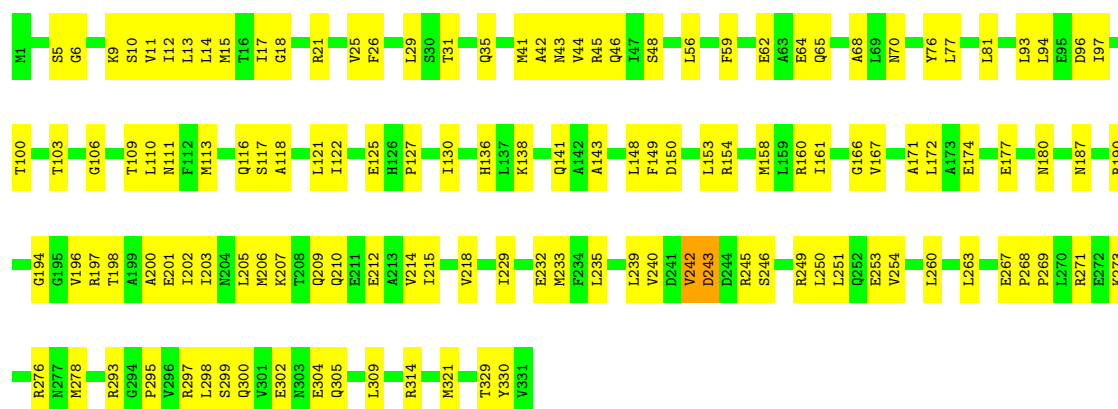
• Molecule 2: Flagellar motor switch protein FlIG

Chain BS:



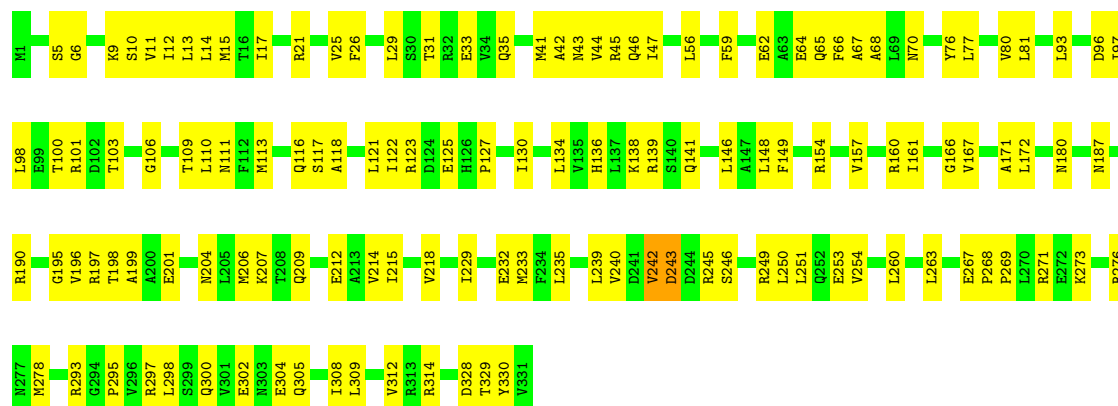
• Molecule 2: Flagellar motor switch protein FliG

Chain BT: 61% 38%



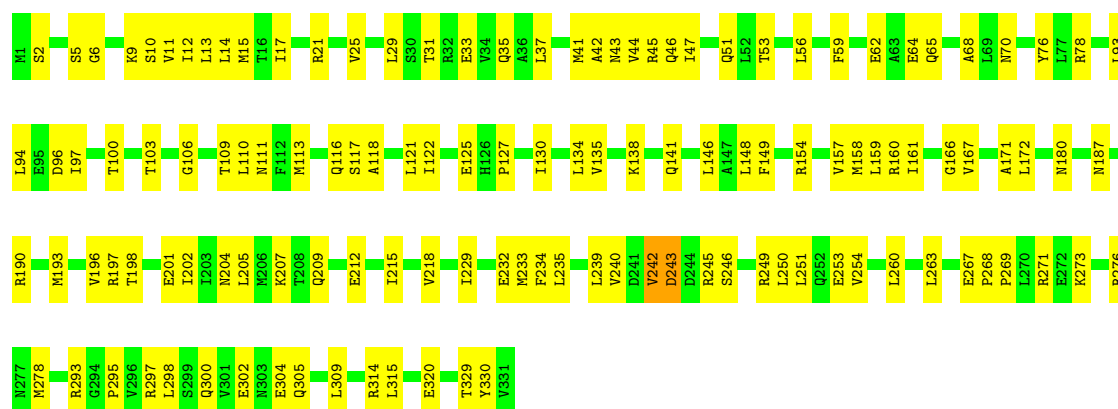
• Molecule 2: Flagellar motor switch protein FliG

Chain BU: 61% 39%



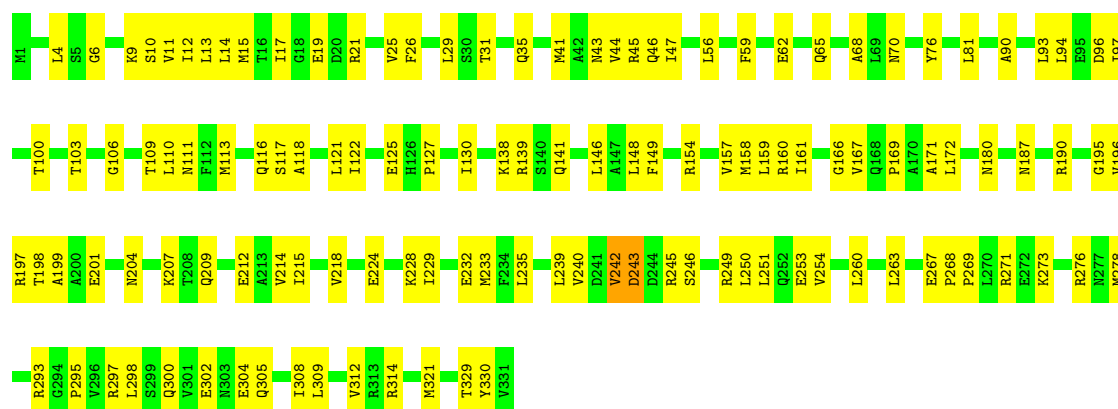
• Molecule 2: Flagellar motor switch protein FliG

Chain BV: 62% 38%



• Molecule 2: Flagellar motor switch protein FlhG

Chain BW: 62% 37% .



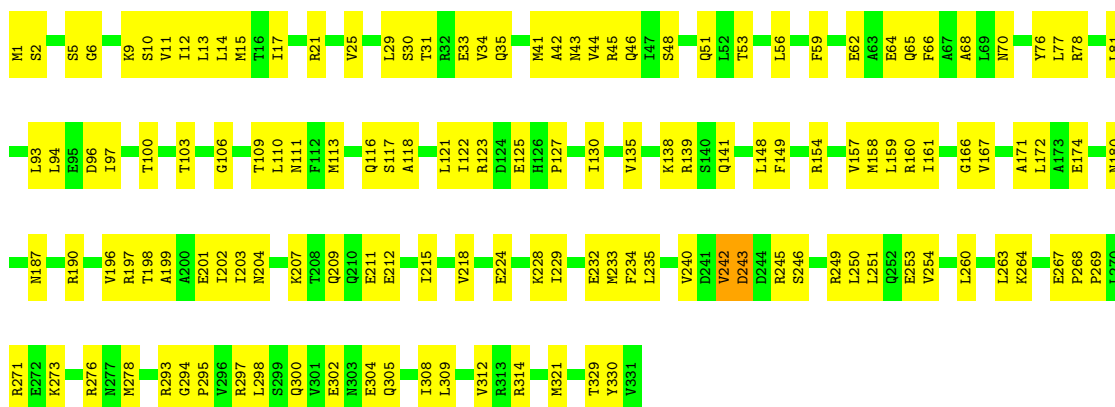
• Molecule 2: Flagellar motor switch protein FlhG

Chain BX: 63% 37% .



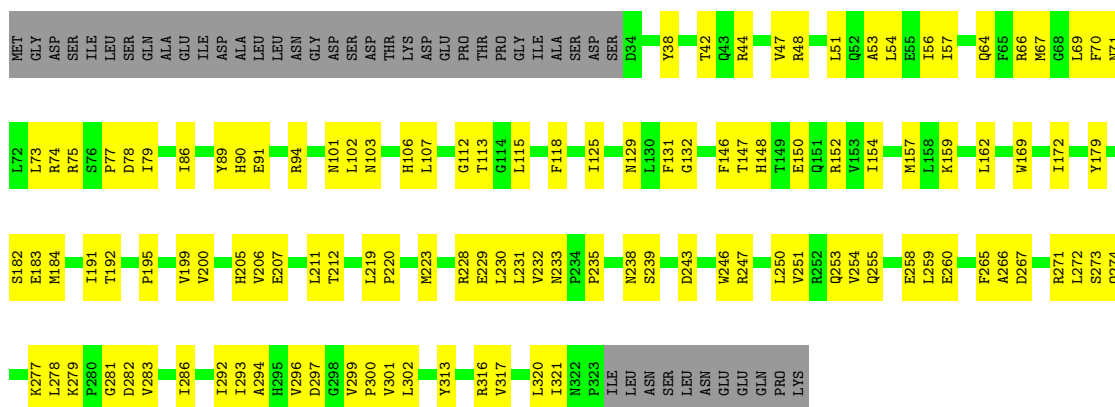
• Molecule 2: Flagellar motor switch protein FlhG

Chain BY: 58% 41% .



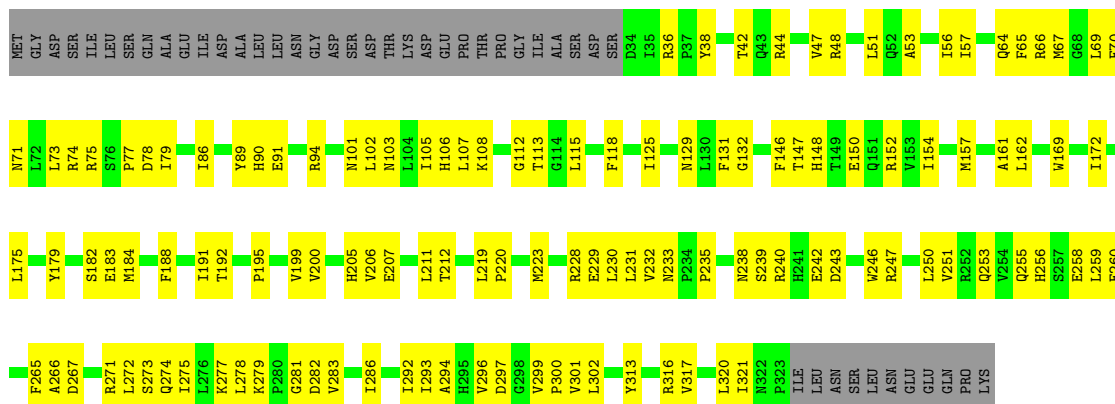
• Molecule 3: Flagellar motor switch protein FlIM

Chain C1: 52% 35% 13%



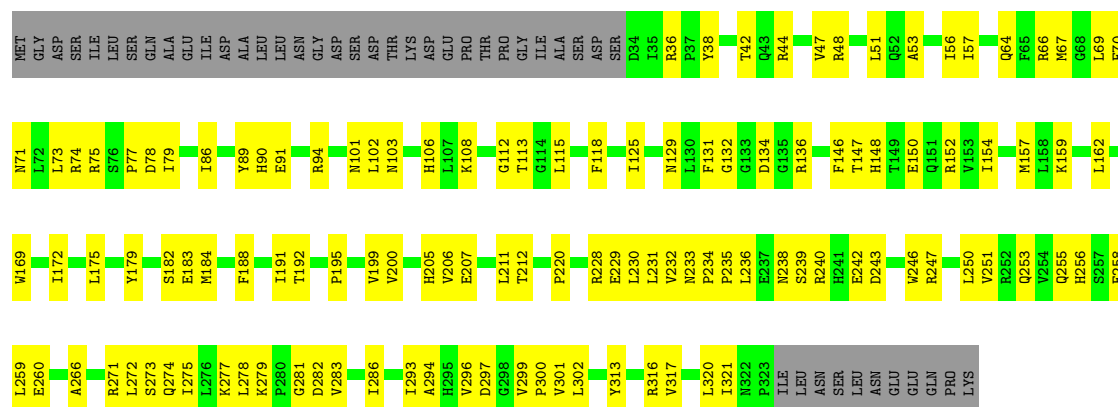
• Molecule 3: Flagellar motor switch protein FlIM

Chain C2: 50% 37% 13%



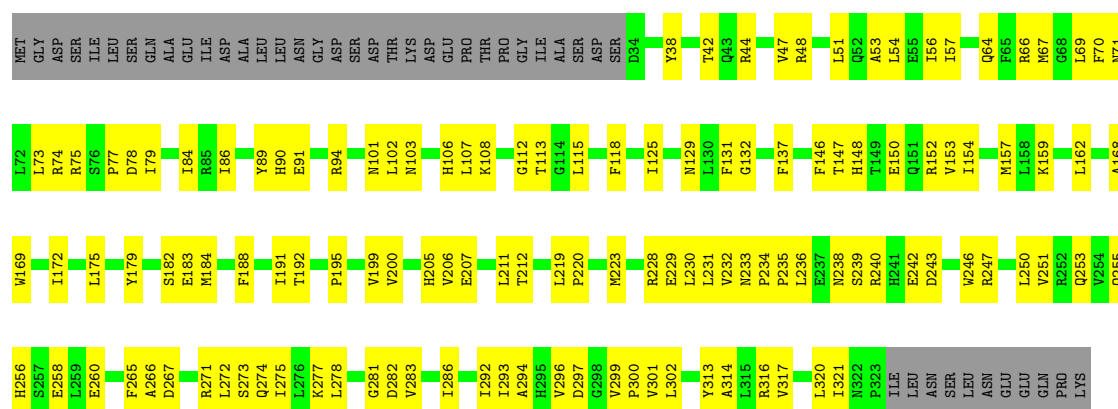
• Molecule 3: Flagellar motor switch protein FlIM

Chain C3: 51% 36% 13%



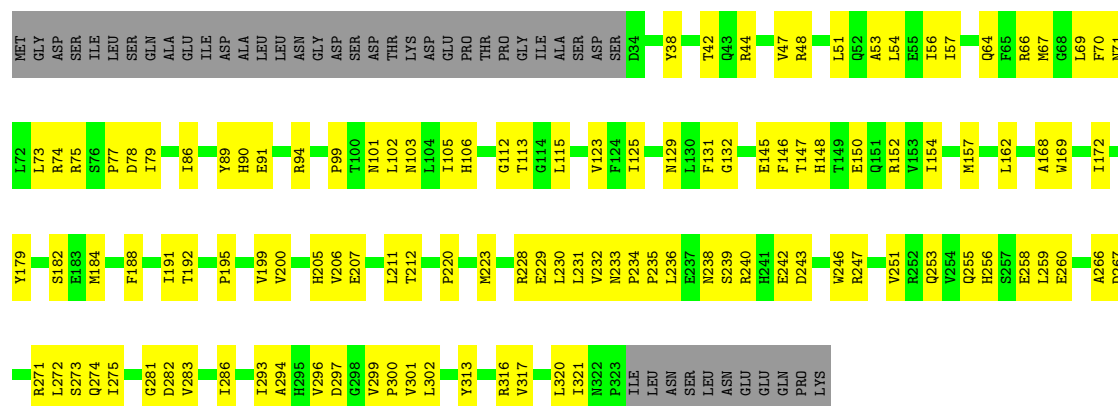
• Molecule 3: Flagellar motor switch protein FlIM

Chain C4: 49% 38% 13%



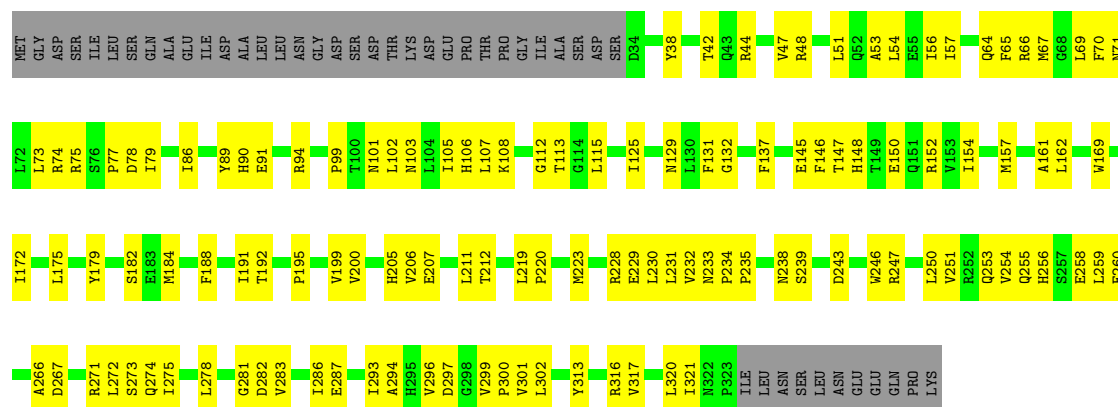
• Molecule 3: Flagellar motor switch protein FlIM

Chain C5: 52% 35% 13%



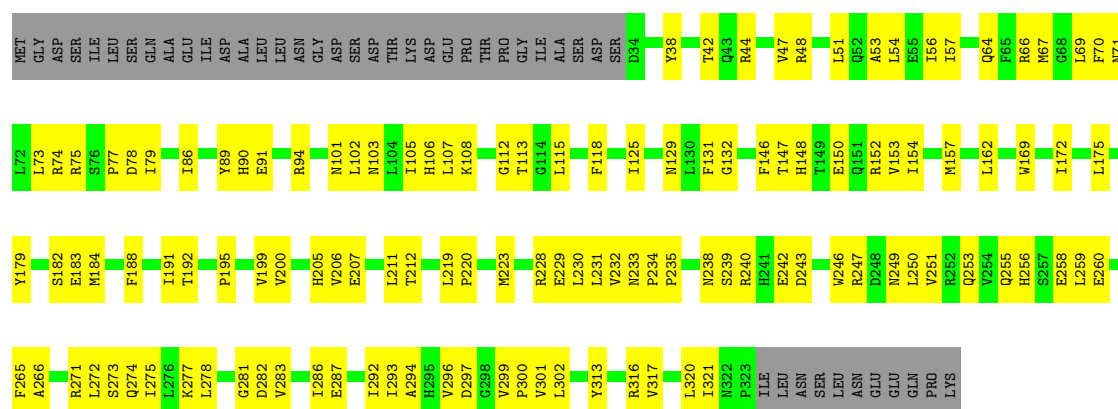
• Molecule 3: Flagellar motor switch protein FlIM

Chain C6: 50% 37% 13%



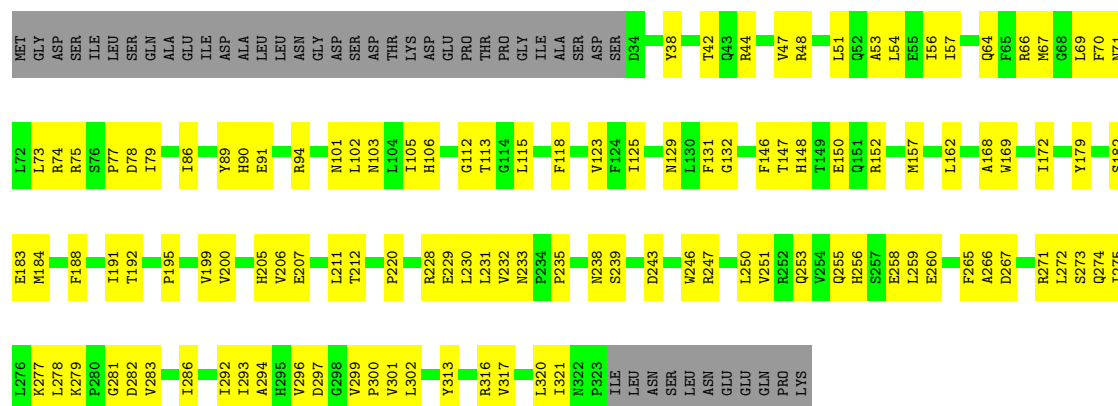
• Molecule 3: Flagellar motor switch protein FliM

Chain C7: 50% 37% 13%



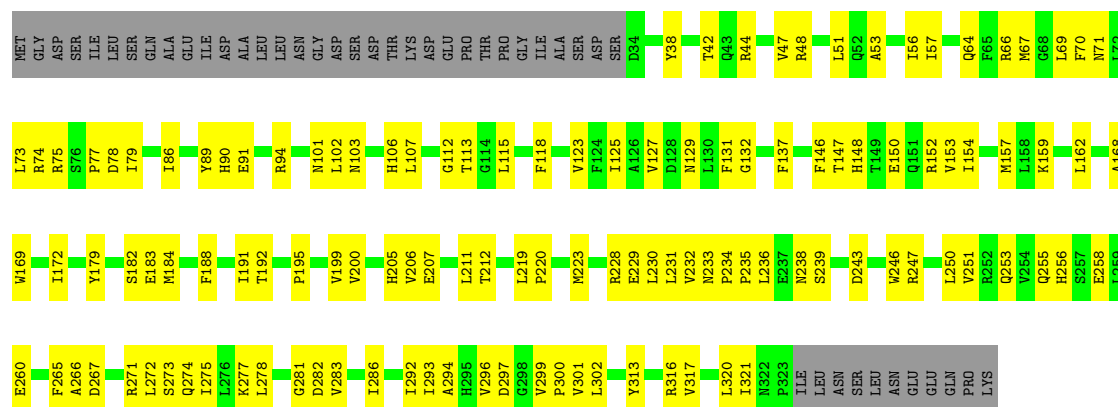
• Molecule 3: Flagellar motor switch protein FliM

Chain C8: 52% 35% 13%



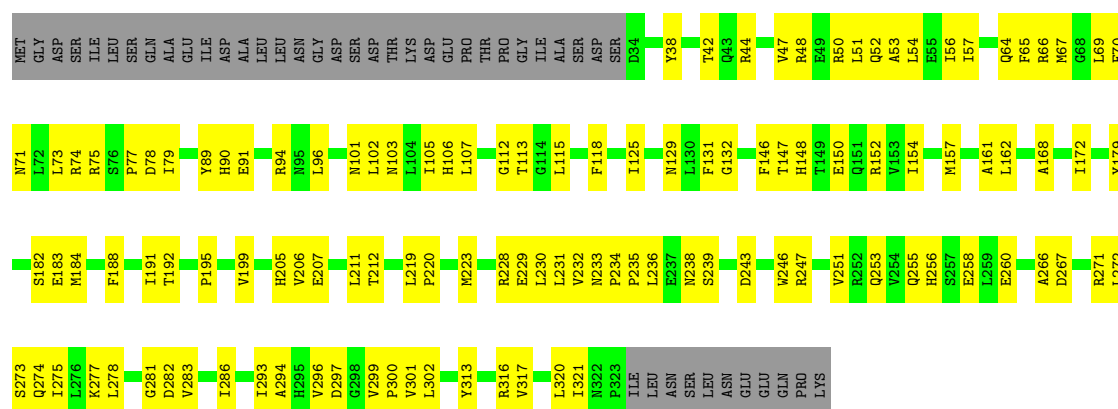
• Molecule 3: Flagellar motor switch protein FliM

Chain C9: 50% 37% 13%



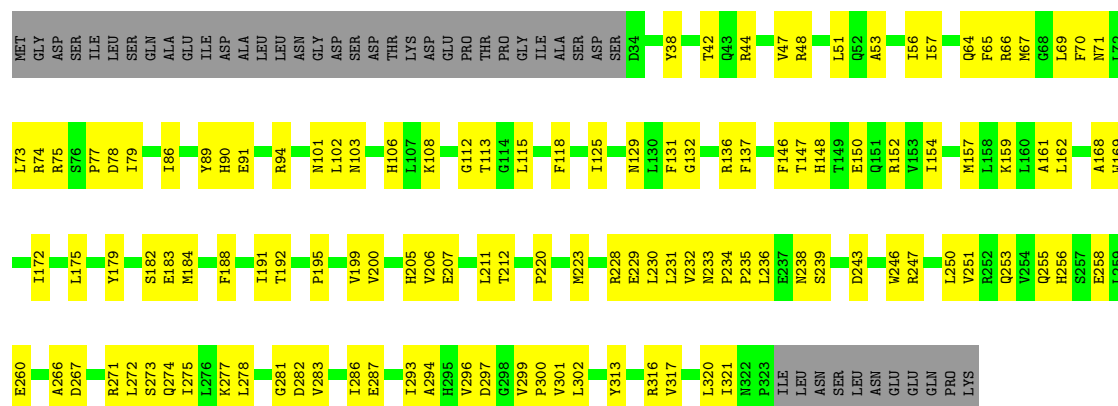
• Molecule 3: Flagellar motor switch protein FlIM

Chain CA: 51% 35% 13%



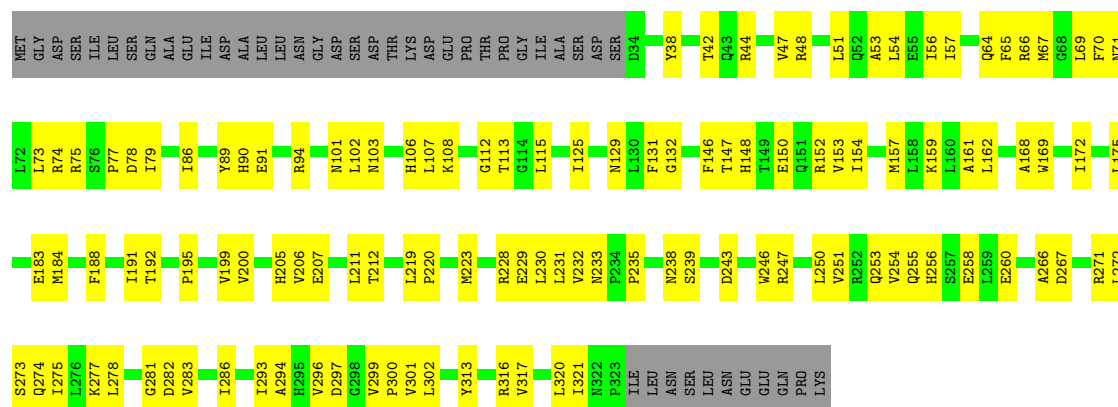
• Molecule 3: Flagellar motor switch protein FlIM

Chain CB: 51% 36% 13%



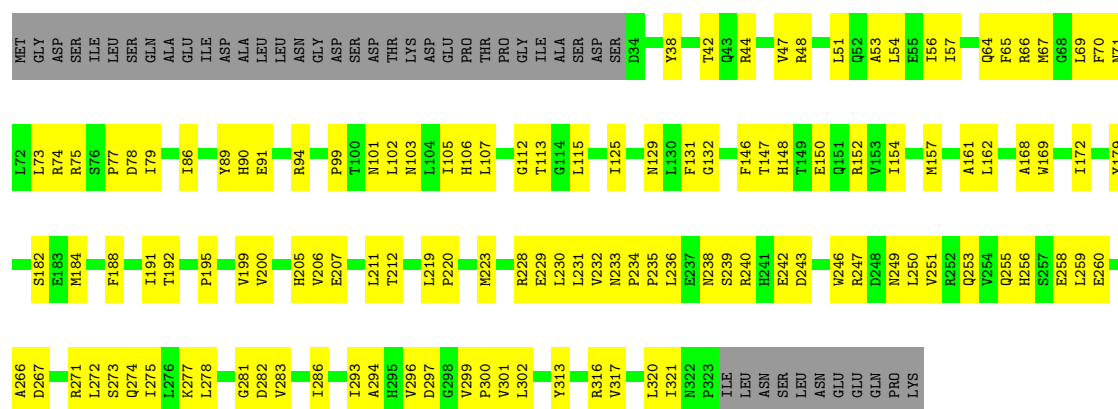
• Molecule 3: Flagellar motor switch protein FlIM

Chain CC: 51% 35% 13%



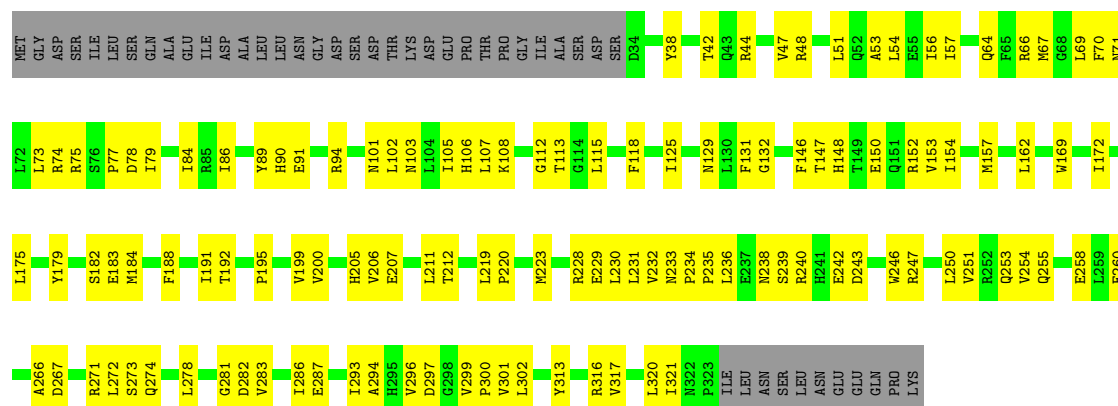
• Molecule 3: Flagellar motor switch protein FlIM

Chain CD: 50% 37% 13%



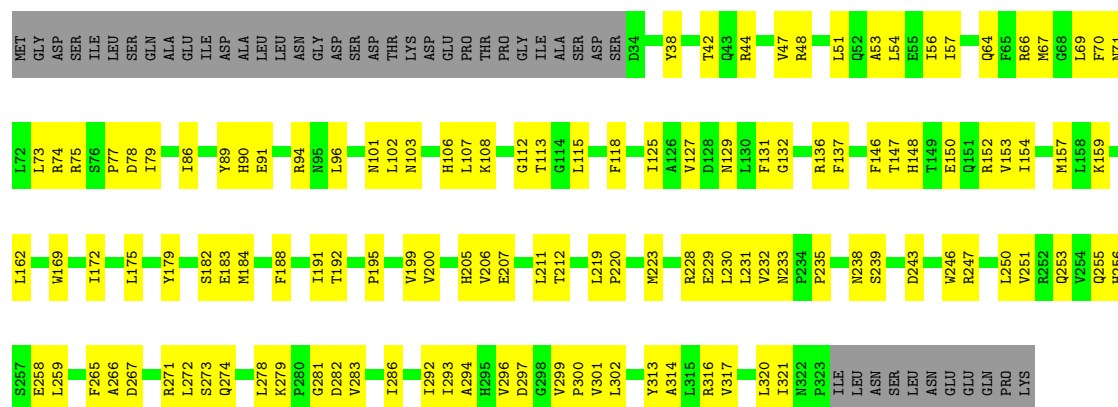
• Molecule 3: Flagellar motor switch protein FlIM

Chain CE: 51% 36% 13%



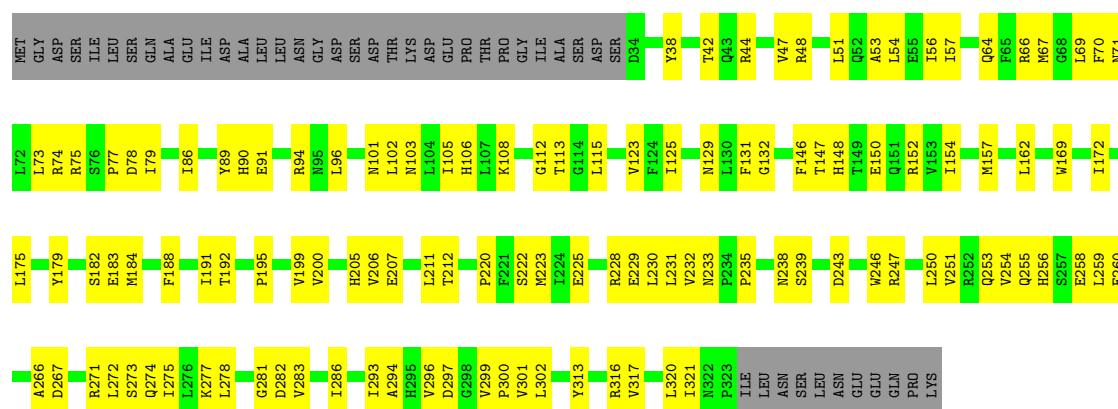
• Molecule 3: Flagellar motor switch protein FlIM

Chain CF: 50% 37% 13%



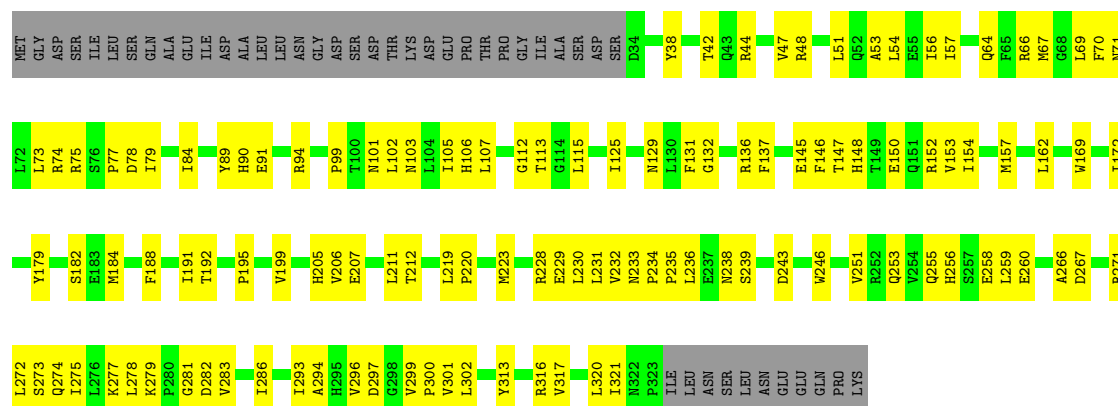
• Molecule 3: Flagellar motor switch protein FlIM

Chain CG: 51% 36% 13%



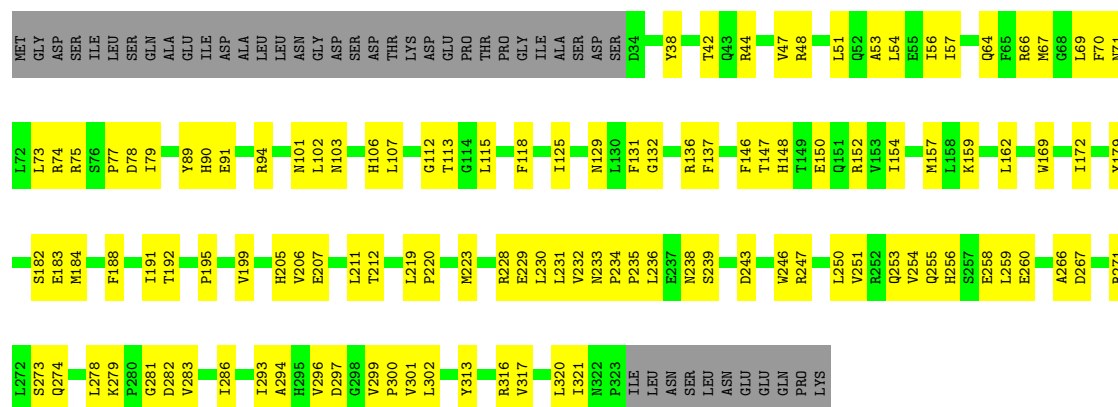
• Molecule 3: Flagellar motor switch protein FlIM

Chain CH: 51% 35% 13%



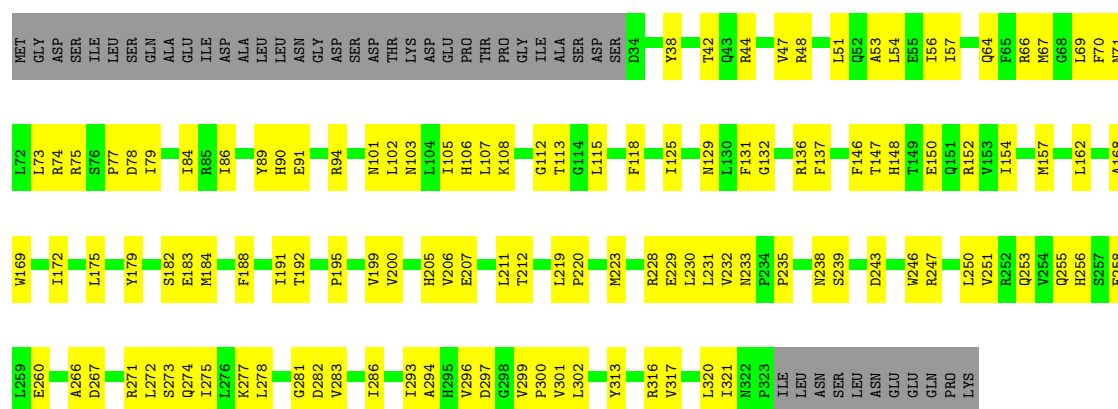
• Molecule 3: Flagellar motor switch protein FlIM

Chain CI: 52% 35% 13%



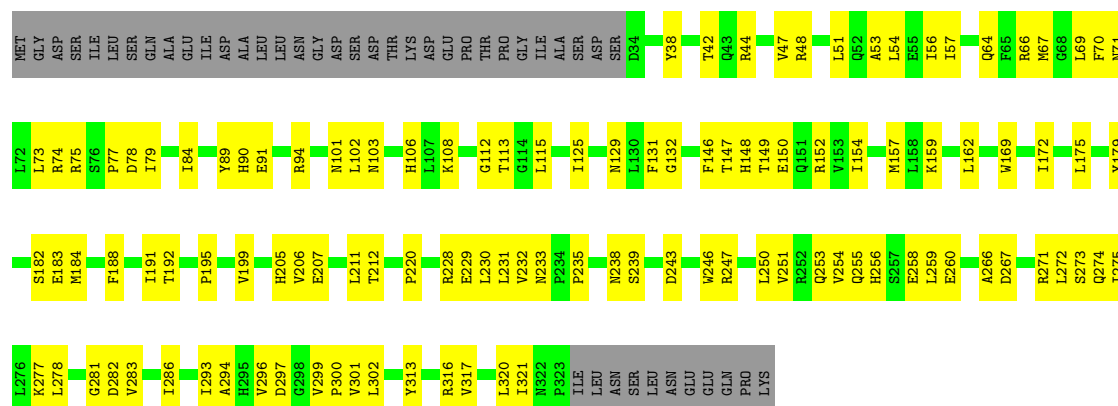
• Molecule 3: Flagellar motor switch protein FlIM

Chain CJ: 51% 36% 13%



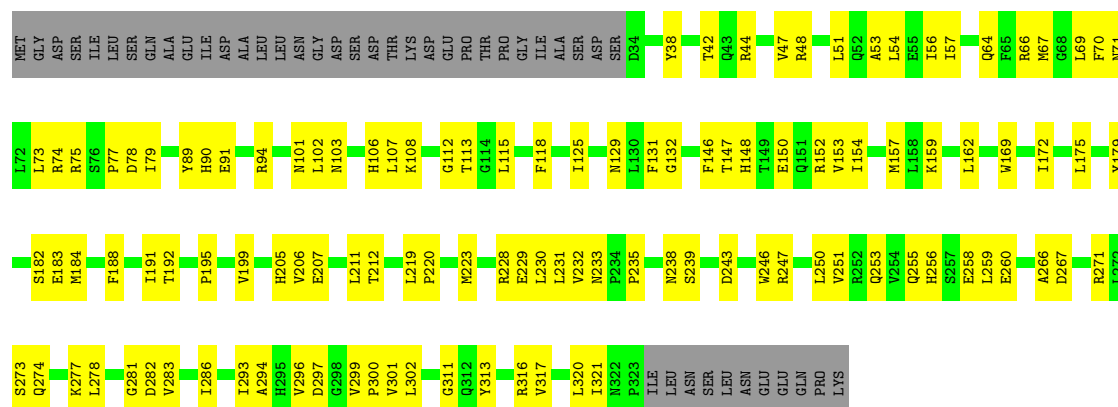
• Molecule 3: Flagellar motor switch protein FlIM

Chain CK: 53% 34% 13%

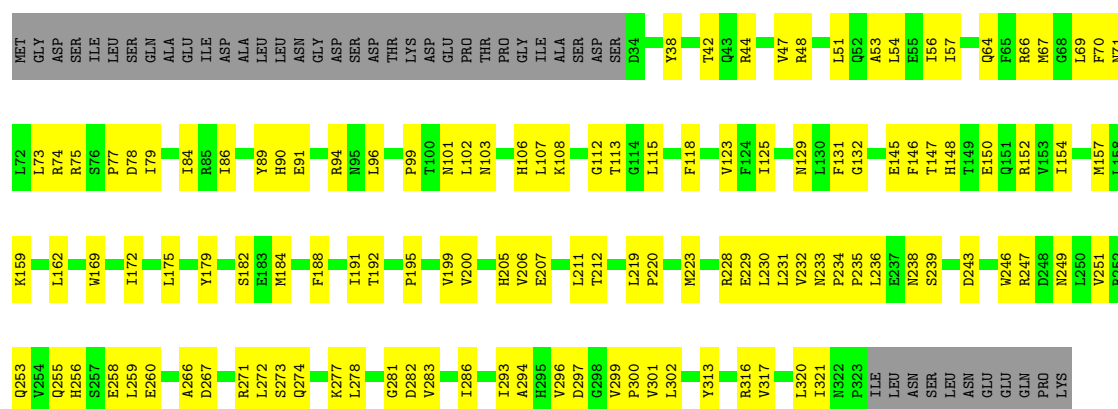


• Molecule 3: Flagellar motor switch protein FlIM

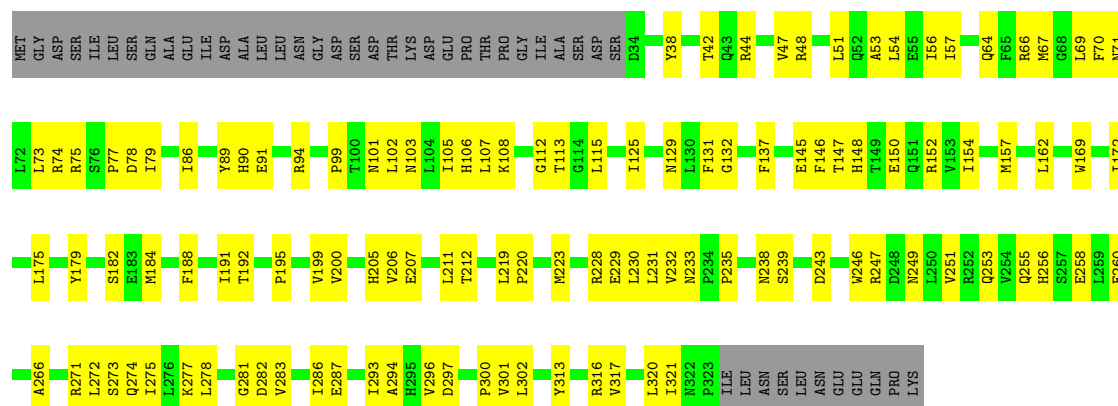
Chain CL: 52% 34% 13%



• Molecule 3: Flagellar motor switch protein FlIM

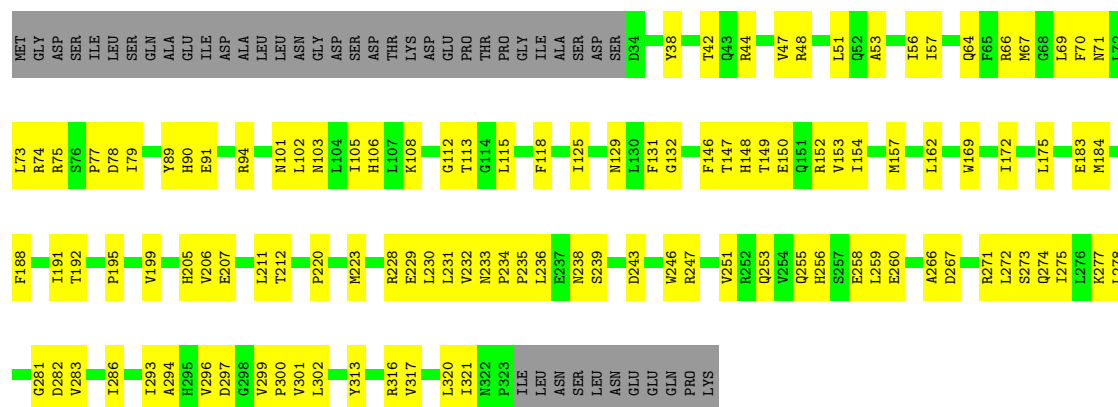


• Molecule 3: Flagellar motor switch protein FlIM



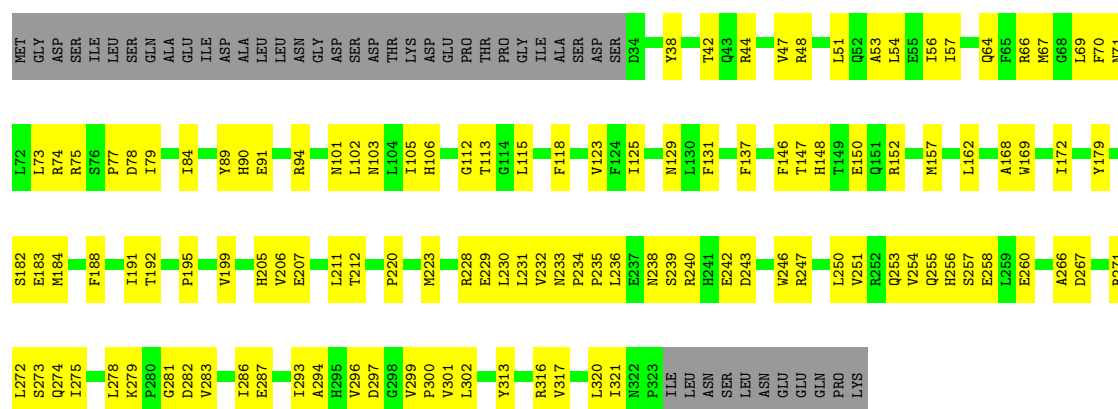
• Molecule 3: Flagellar motor switch protein FlIM





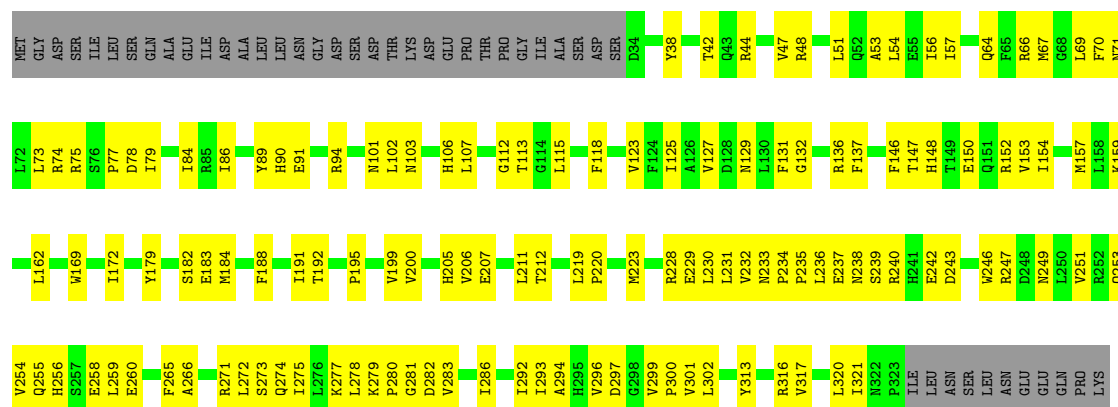
• Molecule 3: Flagellar motor switch protein FlIM

Chain CP: 51% 36% 13%



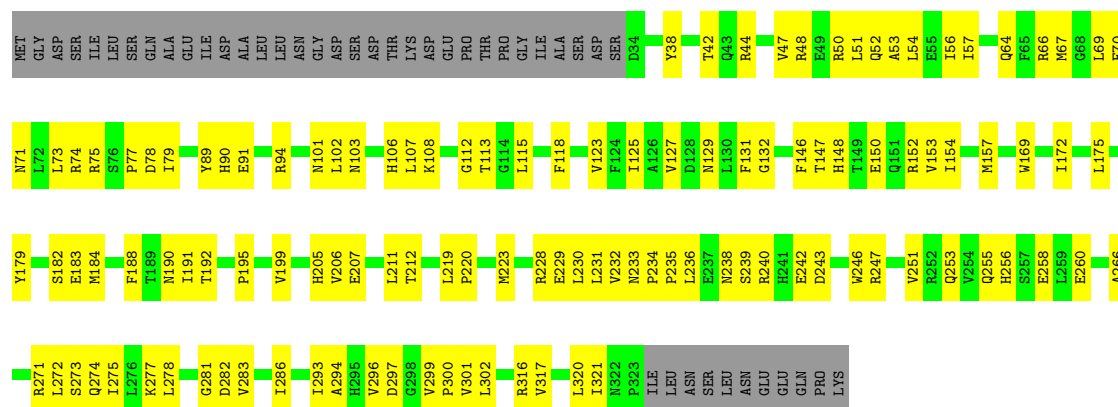
• Molecule 3: Flagellar motor switch protein FlIM

Chain CQ: 48% 39% 13%



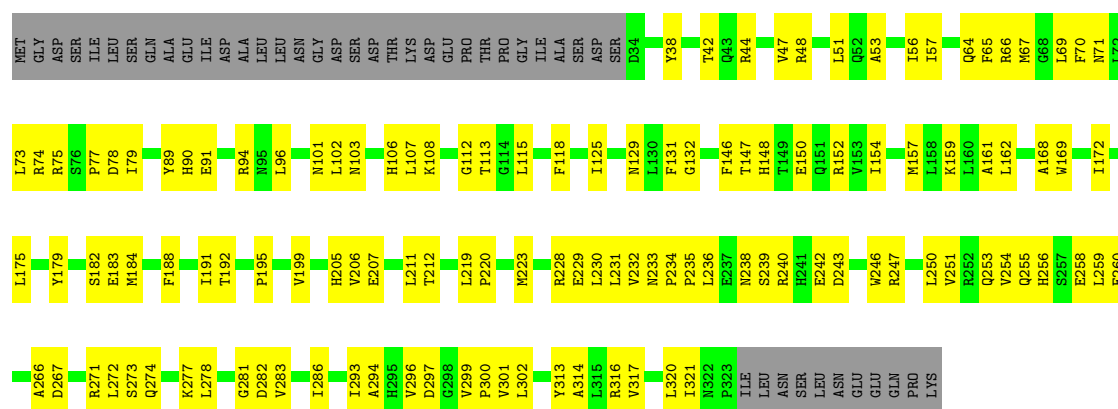
• Molecule 3: Flagellar motor switch protein FlIM

Chain CR: 51% 36% 13%



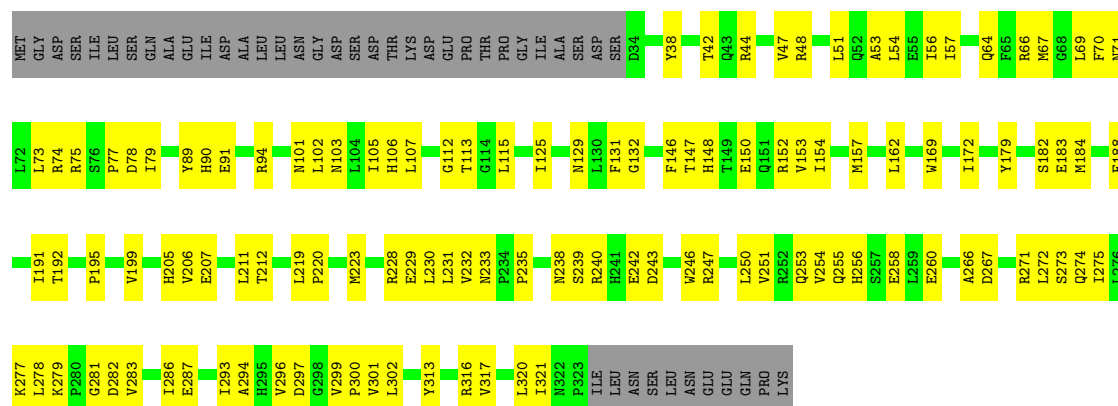
• Molecule 3: Flagellar motor switch protein FlIM

Chain CS: 50% 37% 13%



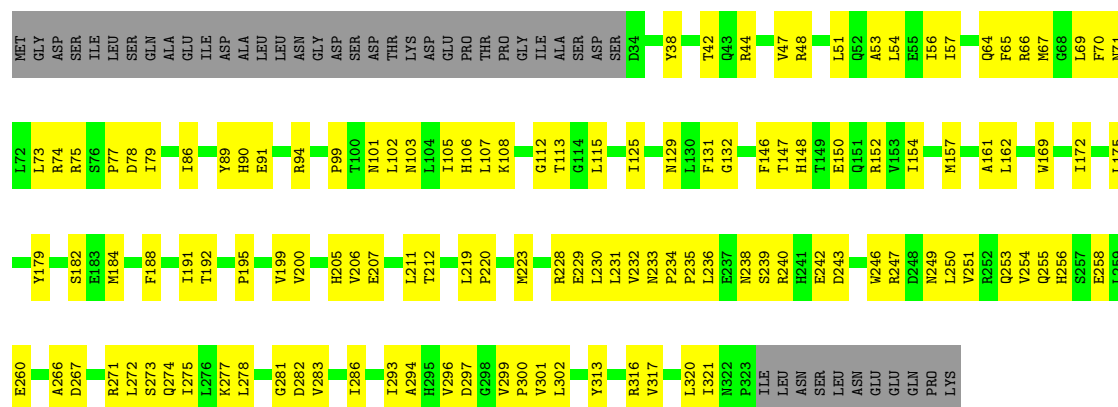
• Molecule 3: Flagellar motor switch protein FlIM

Chain CT: 52% 35% 13%



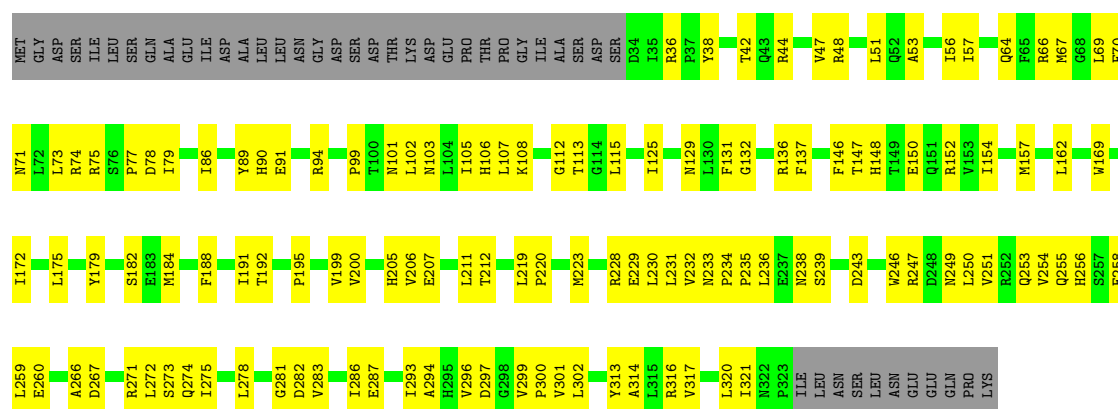
• Molecule 3: Flagellar motor switch protein FlIM

Chain CU: 50% 37% 13%



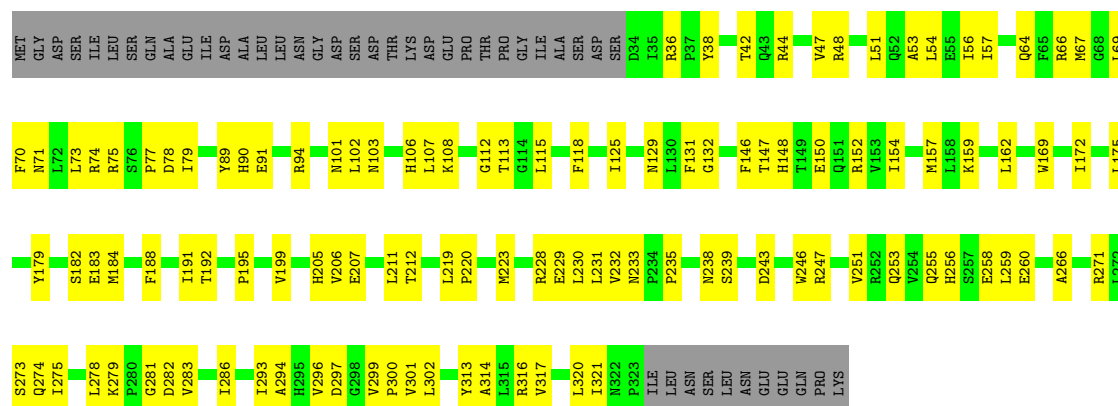
• Molecule 3: Flagellar motor switch protein FlIM

Chain CV: 50% 37% 13%



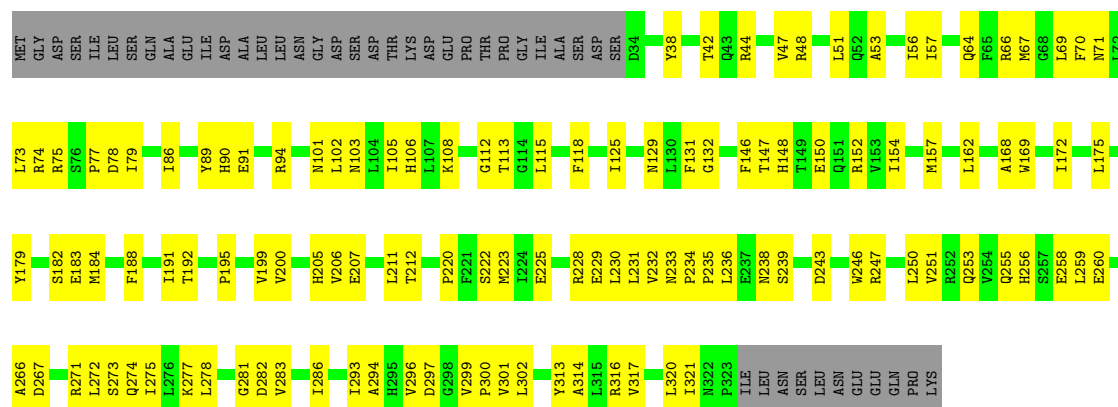
• Molecule 3: Flagellar motor switch protein FlIM

Chain CW: 53% 34% 13%



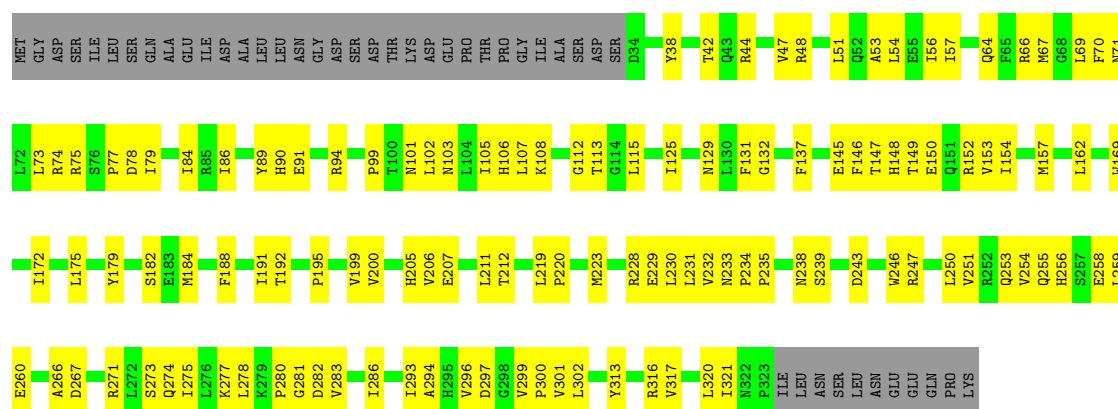
• Molecule 3: Flagellar motor switch protein FlIM

Chain CX: 51% 36% 13%



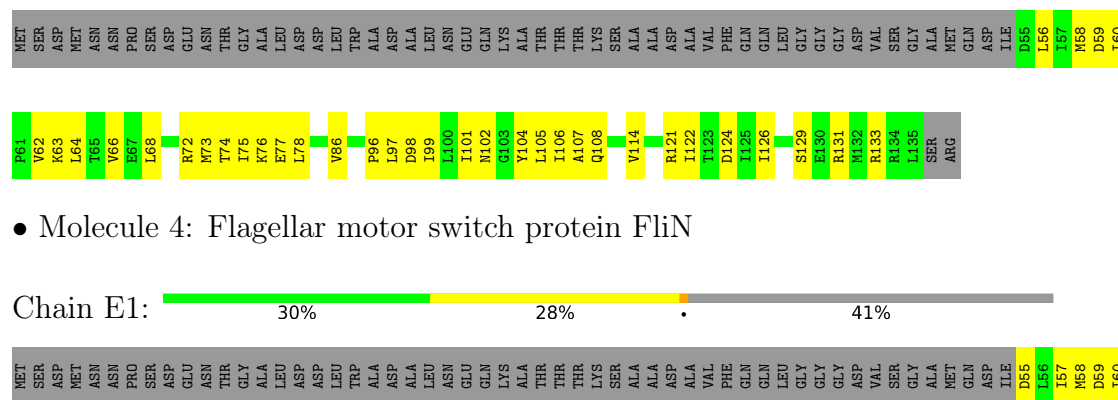
• Molecule 3: Flagellar motor switch protein FliM

Chain CY: 50% 37% 13%



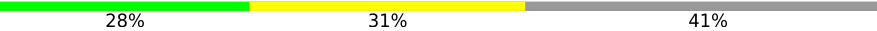
• Molecule 4: Flagellar motor switch protein FliN

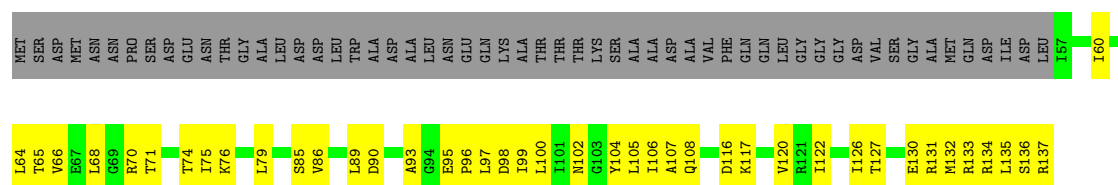
Chain D1: 33% 26% 41%



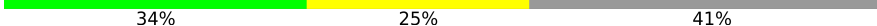
• Molecule 4: Flagellar motor switch protein FliN

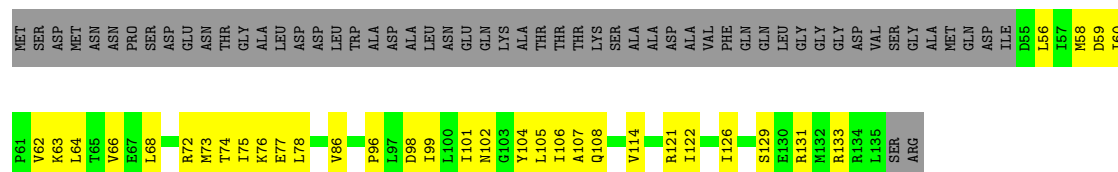


Chain F1:  28% 31% 41%

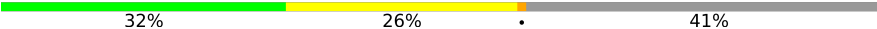


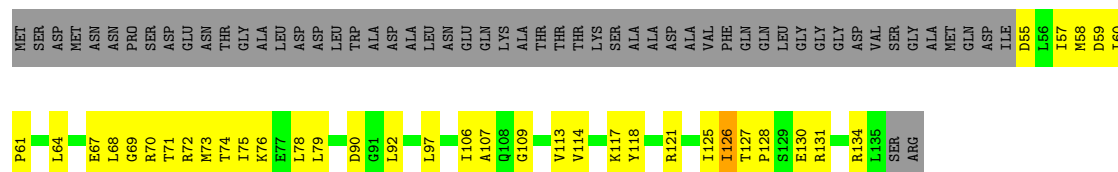
• Molecule 4: Flagellar motor switch protein FliN

Chain D2:  34% 25% 41%

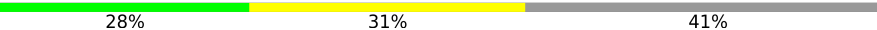


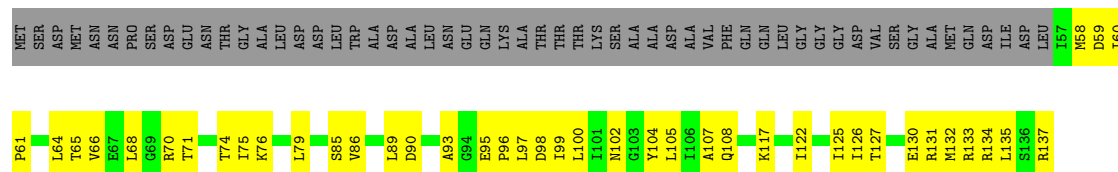
• Molecule 4: Flagellar motor switch protein FliN

Chain E2:  32% 26% 41%

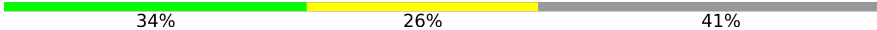


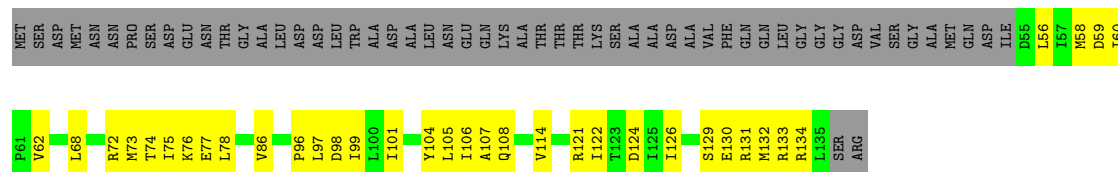
• Molecule 4: Flagellar motor switch protein FliN

Chain F2:  28% 31% 41%

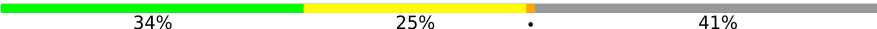


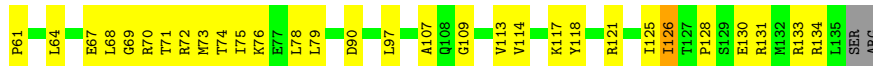
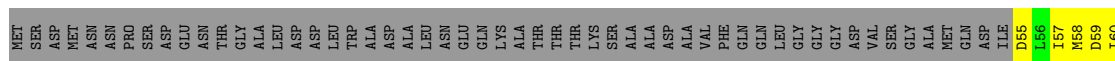
• Molecule 4: Flagellar motor switch protein FliN

Chain D3:  34% 26% 41%

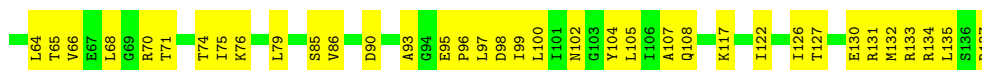
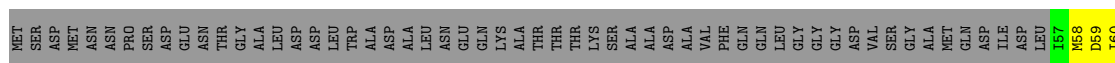
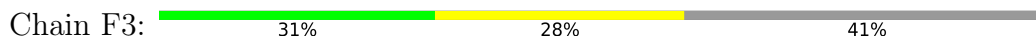


• Molecule 4: Flagellar motor switch protein FliN

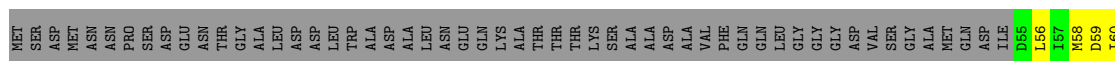
Chain E3:  34% 25% 41%



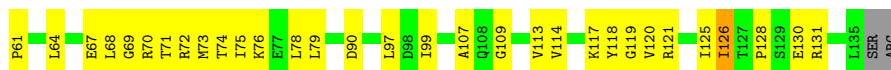
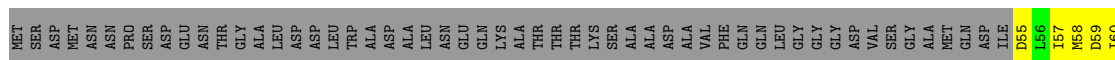
• Molecule 4: Flagellar motor switch protein FliN



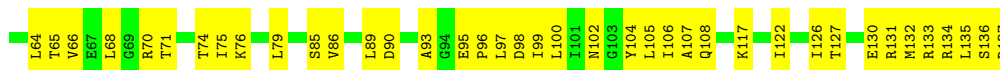
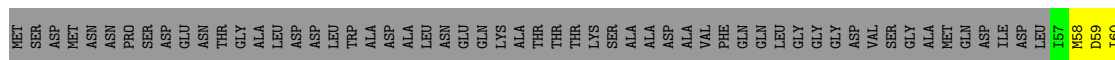
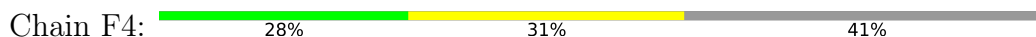
• Molecule 4: Flagellar motor switch protein FliN



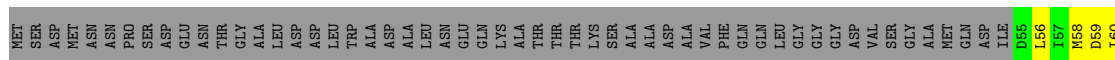
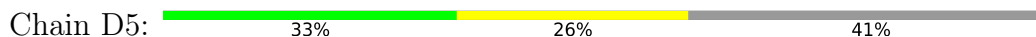
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN



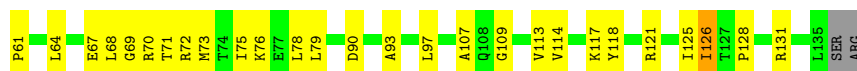
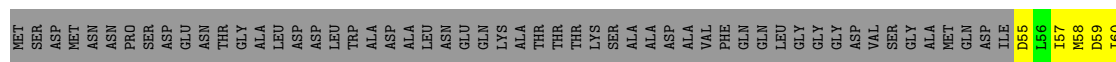
• Molecule 4: Flagellar motor switch protein FliN





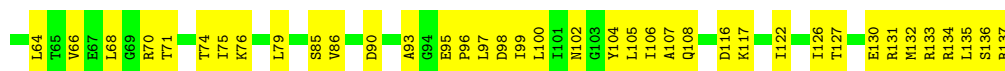
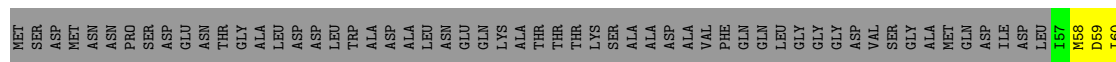
• Molecule 4: Flagellar motor switch protein FliN

Chain E5: 36% 23% 41%



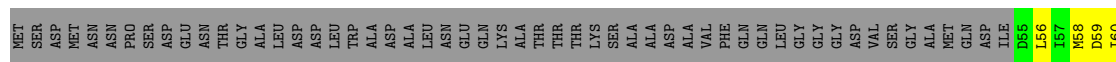
• Molecule 4: Flagellar motor switch protein FliN

Chain F5: 29% 30% 41%



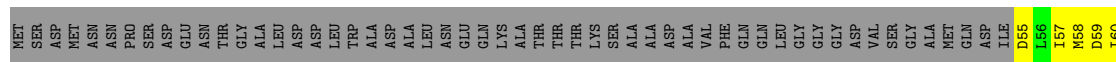
• Molecule 4: Flagellar motor switch protein FliN

Chain D6: 31% 28% 41%



• Molecule 4: Flagellar motor switch protein FliN

Chain E6: 29% 29% 41%

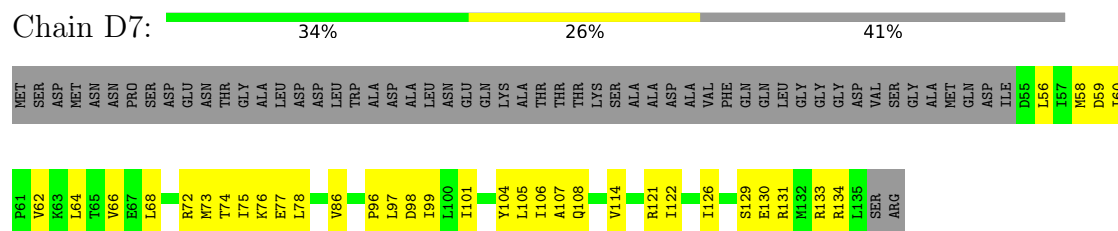


• Molecule 4: Flagellar motor switch protein FliN

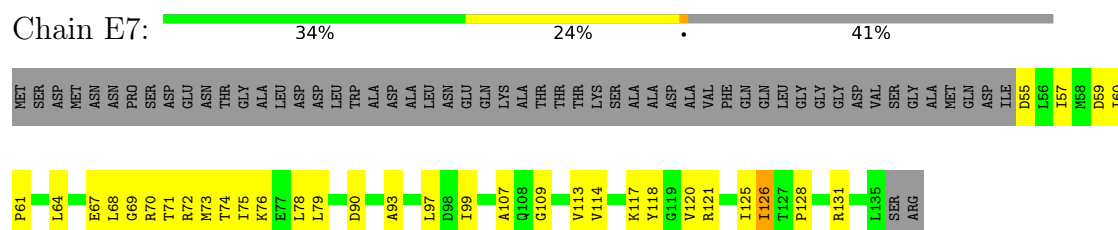
Chain F6: 29% 30% 41%



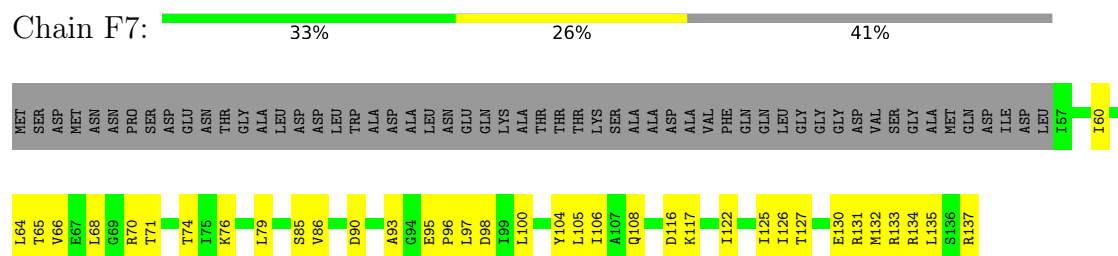
- Molecule 4: Flagellar motor switch protein FliN



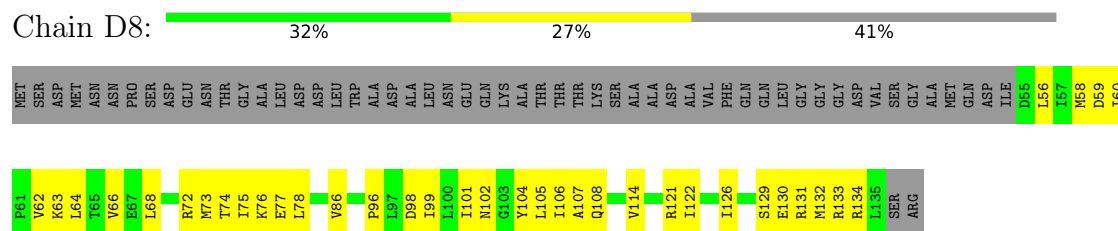
- Molecule 4: Flagellar motor switch protein FliN



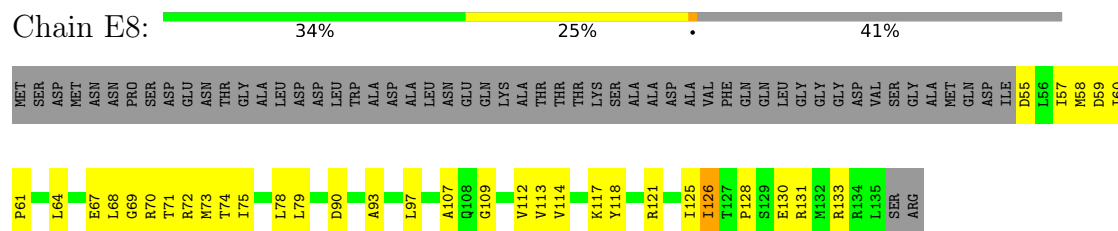
- Molecule 4: Flagellar motor switch protein FliN



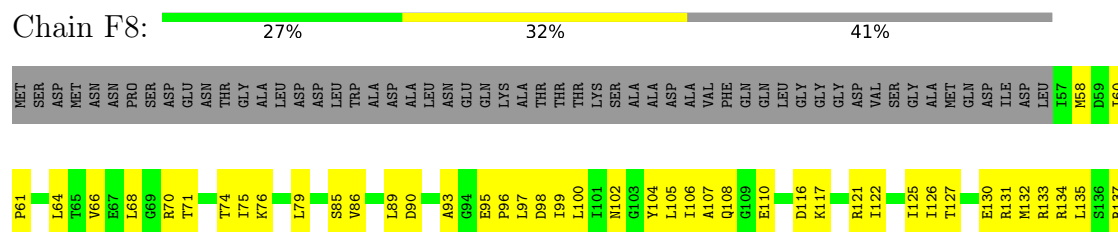
- Molecule 4: Flagellar motor switch protein FliN



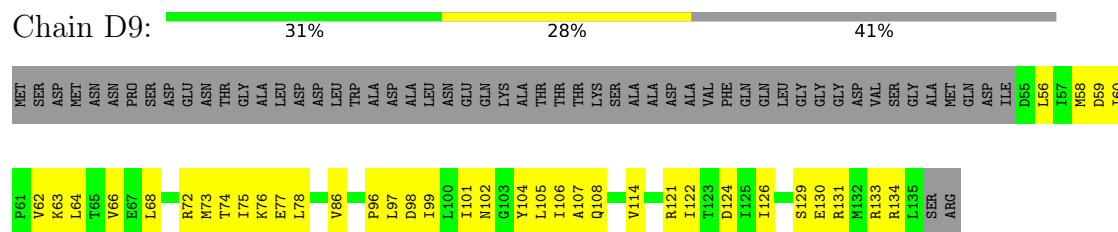
- Molecule 4: Flagellar motor switch protein FliN



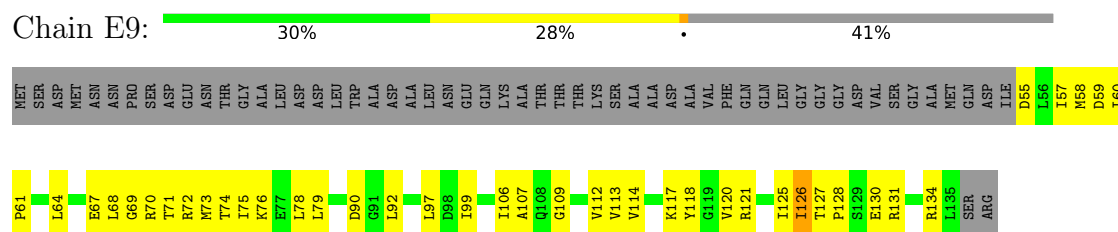
- Molecule 4: Flagellar motor switch protein FliN



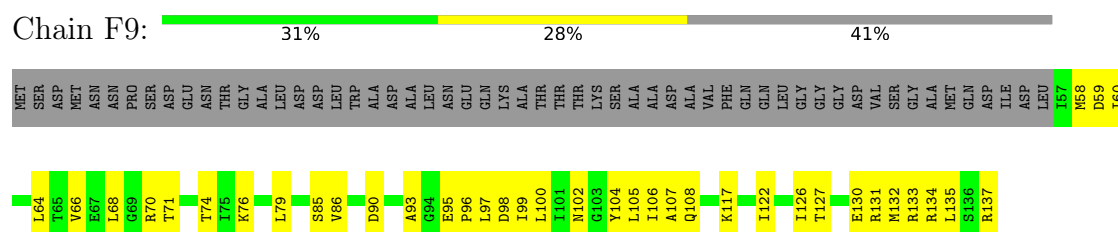
• Molecule 4: Flagellar motor switch protein FliN



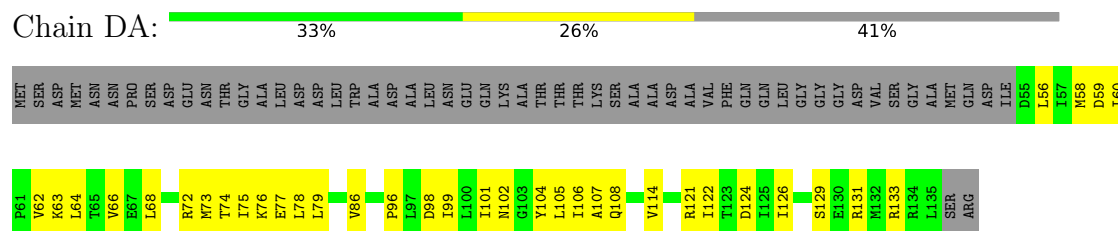
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN

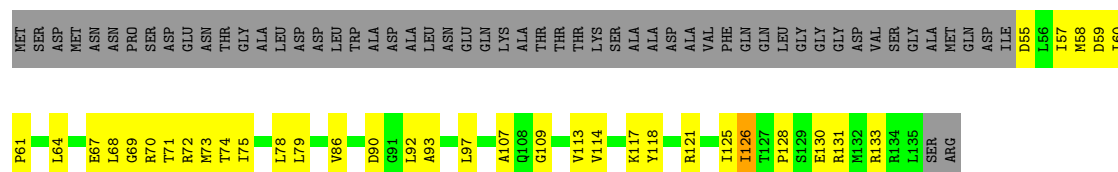


• Molecule 4: Flagellar motor switch protein FliN

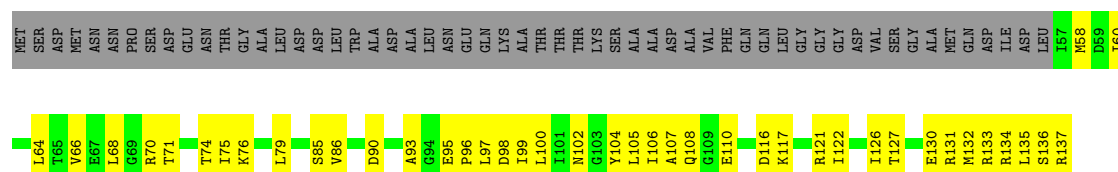
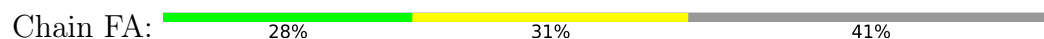


• Molecule 4: Flagellar motor switch protein FliN

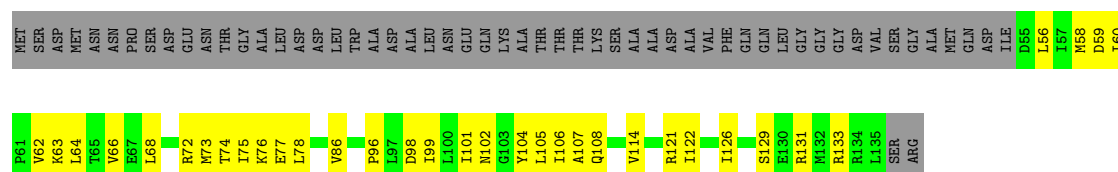




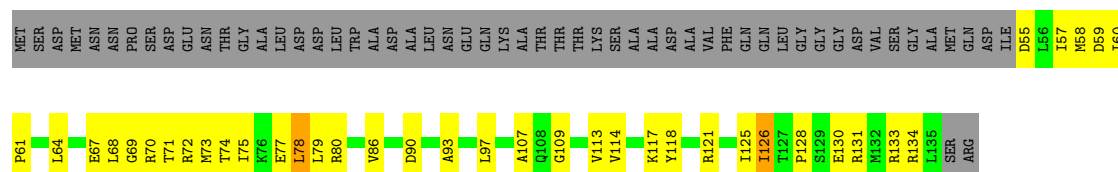
• Molecule 4: Flagellar motor switch protein FliN



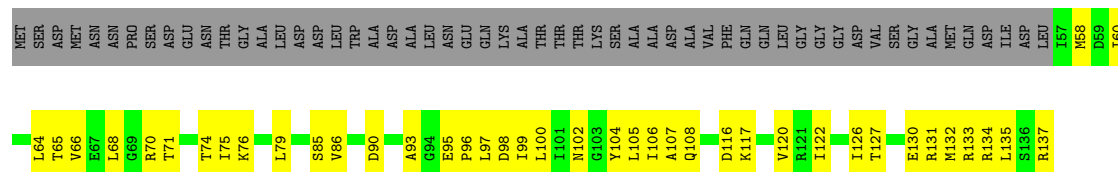
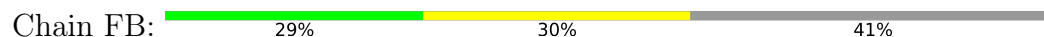
• Molecule 4: Flagellar motor switch protein FliN



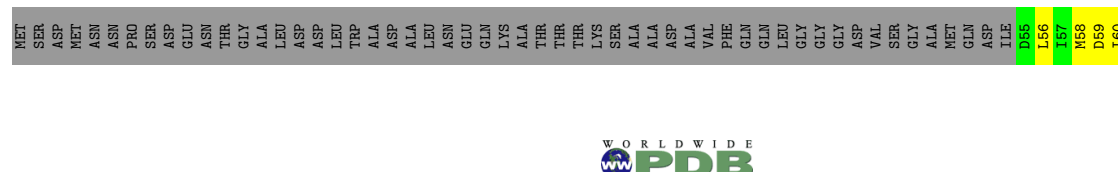
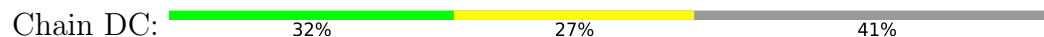
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN



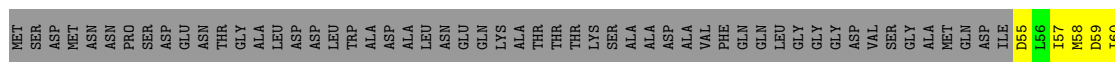
• Molecule 4: Flagellar motor switch protein FliN





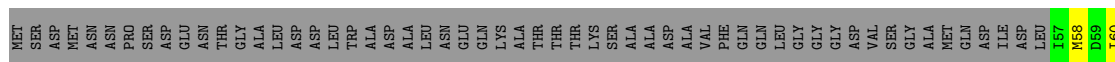
• Molecule 4: Flagellar motor switch protein FliN

Chain EC: 33% 26% 41%



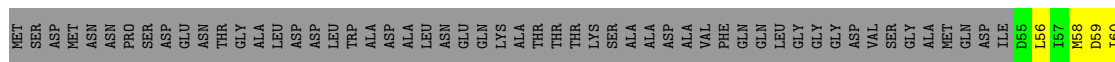
• Molecule 4: Flagellar motor switch protein FliN

Chain FC: 29% 30% 41%



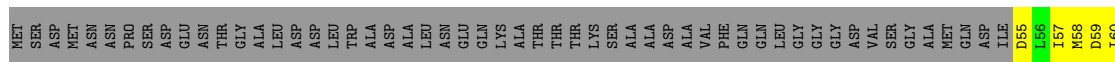
• Molecule 4: Flagellar motor switch protein FliN

Chain DD: 31% 28% 41%



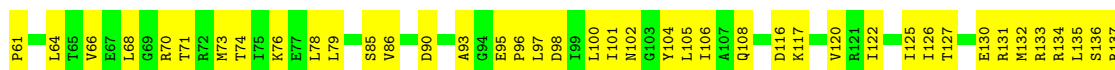
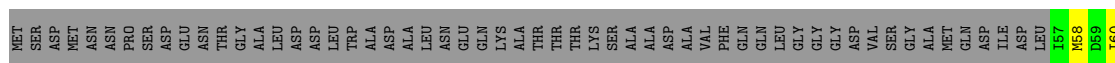
• Molecule 4: Flagellar motor switch protein FliN

Chain ED: 31% 27% 41%

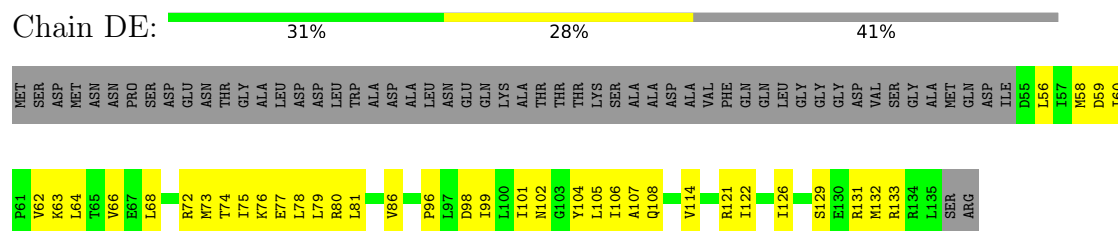


• Molecule 4: Flagellar motor switch protein FliN

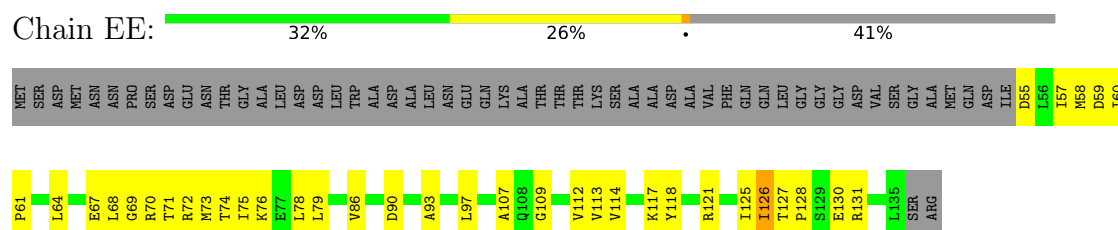
Chain FD: 28% 31% 41%



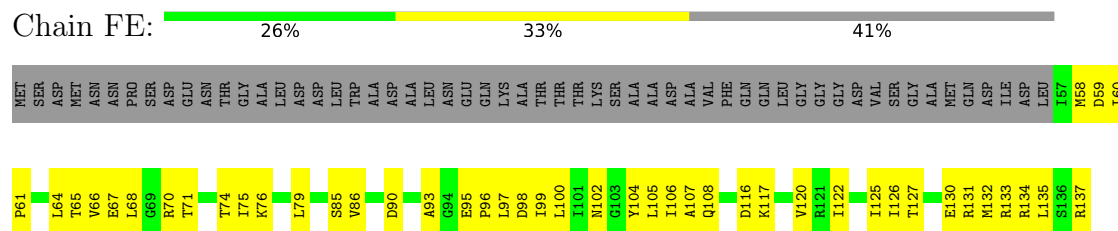
- Molecule 4: Flagellar motor switch protein FliN



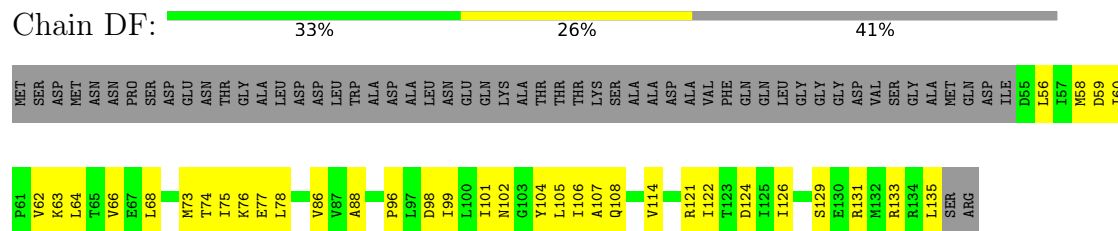
- Molecule 4: Flagellar motor switch protein FliN



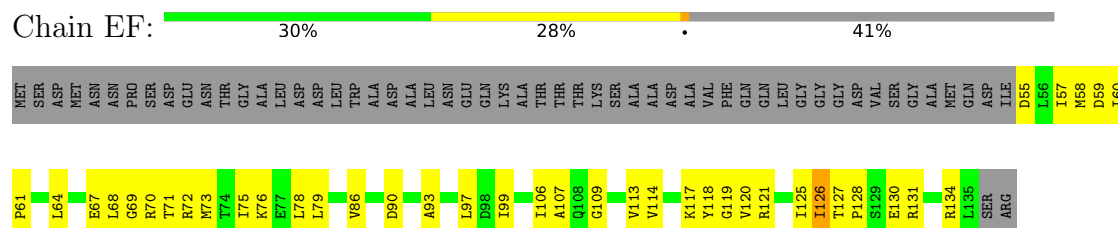
- Molecule 4: Flagellar motor switch protein FliN



- Molecule 4: Flagellar motor switch protein FliN

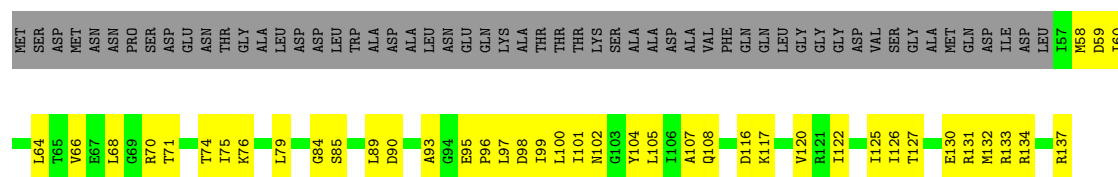


- Molecule 4: Flagellar motor switch protein FliN



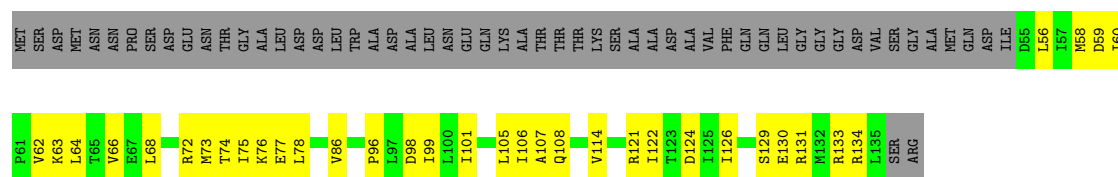
- Molecule 4: Flagellar motor switch protein FliN

Chain FF: 28% 31% 41%



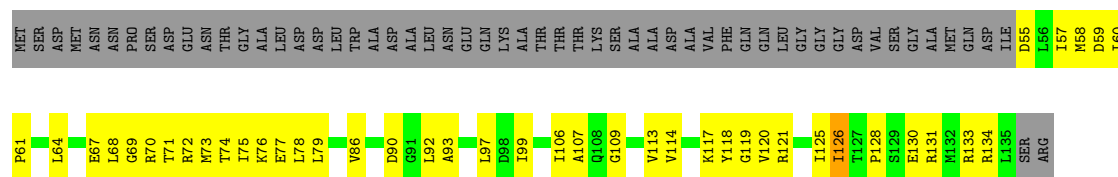
• Molecule 4: Flagellar motor switch protein FliN

Chain DG: 34% 26% 41%



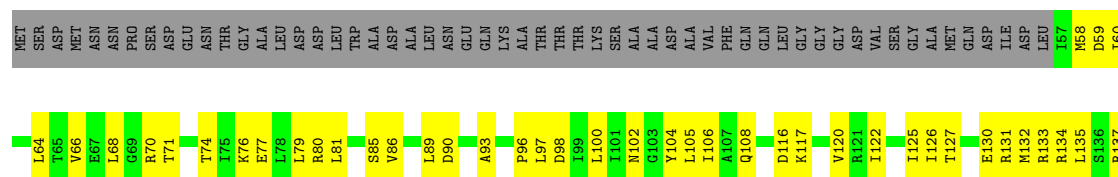
• Molecule 4: Flagellar motor switch protein FliN

Chain EG: 28% 31% 41%



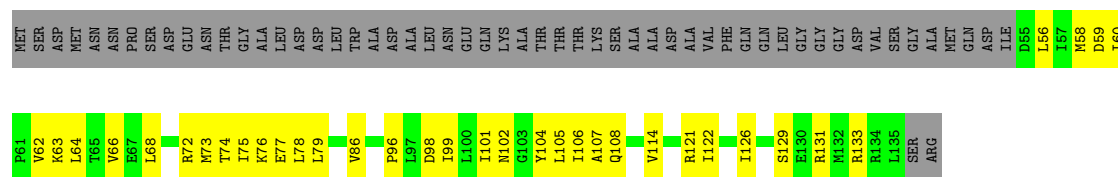
• Molecule 4: Flagellar motor switch protein FliN

Chain FG: 28% 31% 41%



• Molecule 4: Flagellar motor switch protein FliN

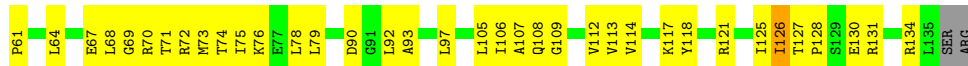
Chain DH: 34% 26% 41%



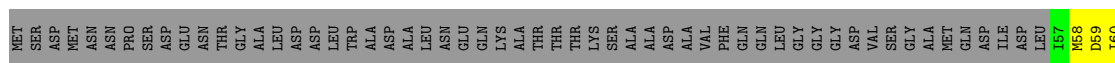
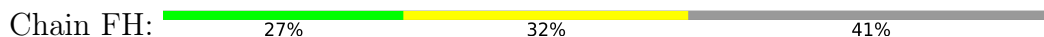
• Molecule 4: Flagellar motor switch protein FliN

Chain EH: 29% 29% 41%

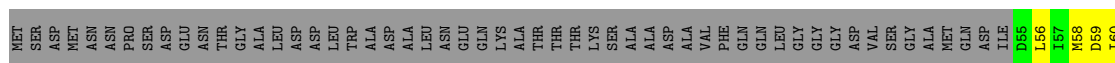




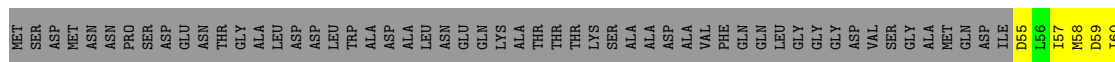
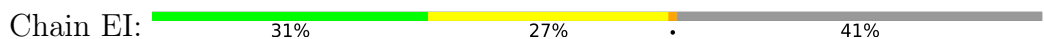
- Molecule 4: Flagellar motor switch protein FliN



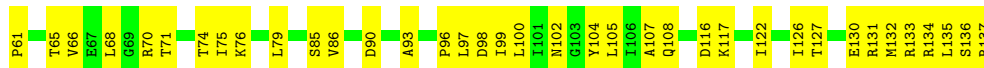
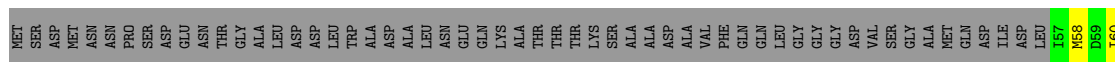
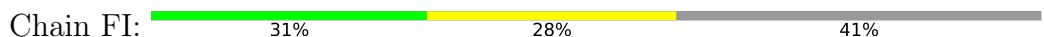
- Molecule 4: Flagellar motor switch protein FliN



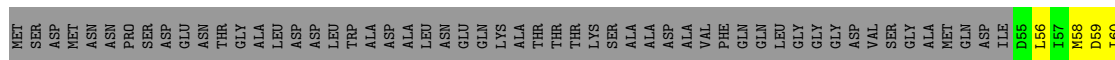
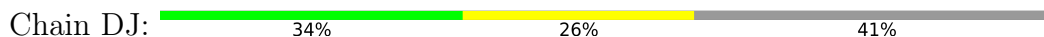
- Molecule 4: Flagellar motor switch protein FliN



- Molecule 4: Flagellar motor switch protein FliN



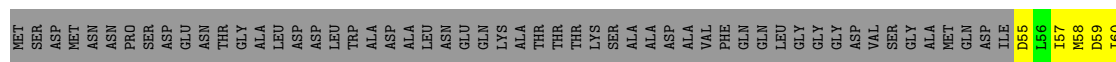
- Molecule 4: Flagellar motor switch protein FliN





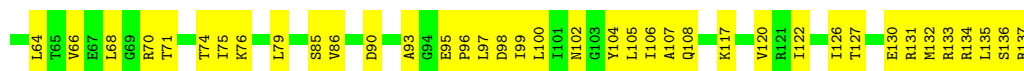
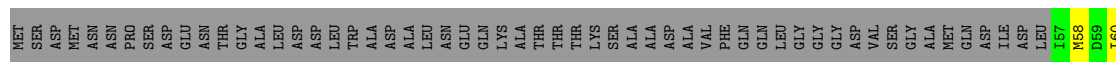
• Molecule 4: Flagellar motor switch protein FliN

Chain EJ: 34% 25% 41%



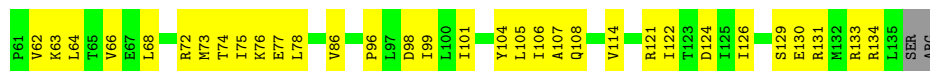
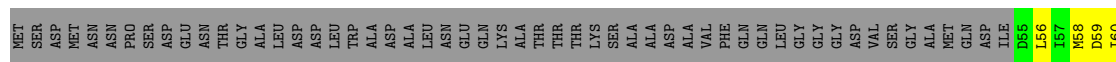
• Molecule 4: Flagellar motor switch protein FliN

Chain FJ: 30% 29% 41%



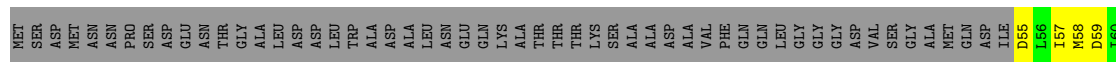
• Molecule 4: Flagellar motor switch protein FliN

Chain DK: 33% 26% 41%



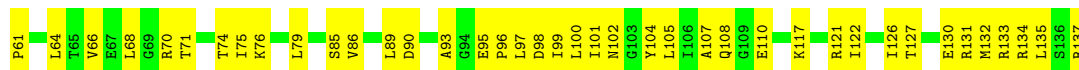
• Molecule 4: Flagellar motor switch protein FliN

Chain EK: 33% 26% 41%

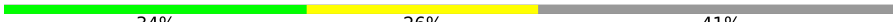


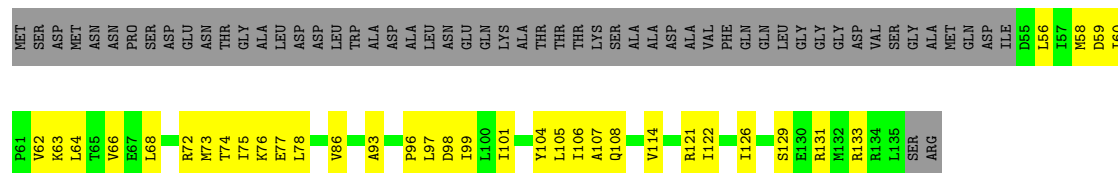
• Molecule 4: Flagellar motor switch protein FliN

Chain FK: 28% 31% 41%

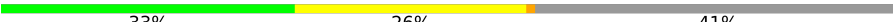


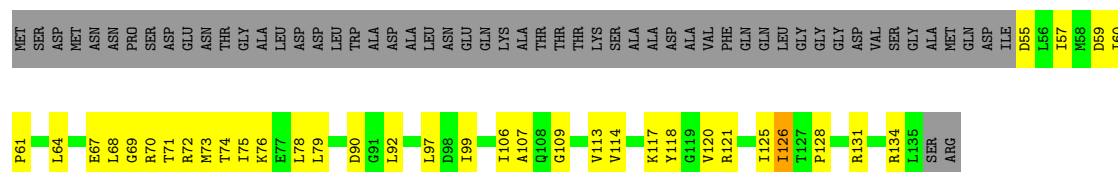
- Molecule 4: Flagellar motor switch protein FliN

Chain DL:  34% 26% 41%

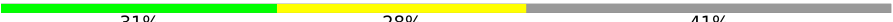


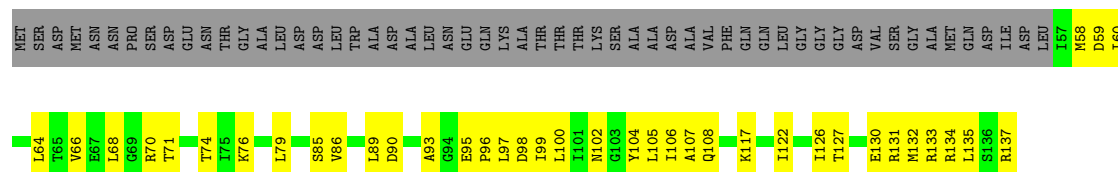
- Molecule 4: Flagellar motor switch protein FliN

Chain EL:  33% 26% 41%



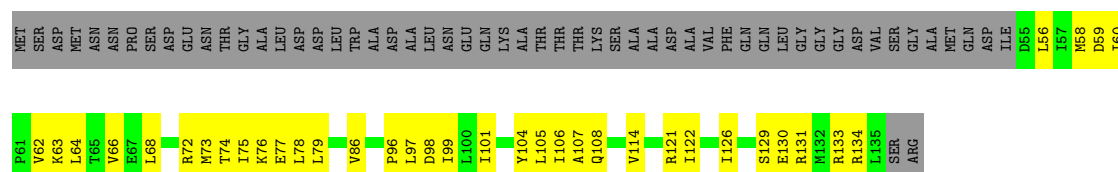
- Molecule 4: Flagellar motor switch protein FliN

Chain FL:  31% 28% 41%



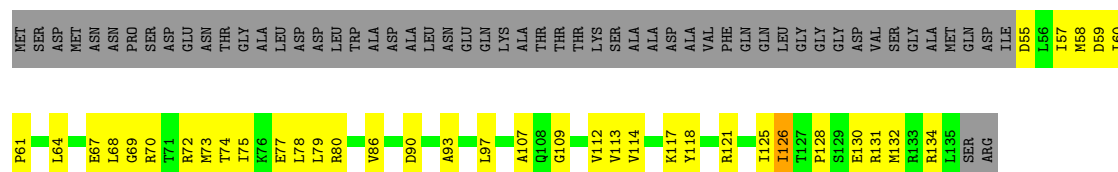
- Molecule 4: Flagellar motor switch protein FliN

Chain DM:  32% 27% 41%

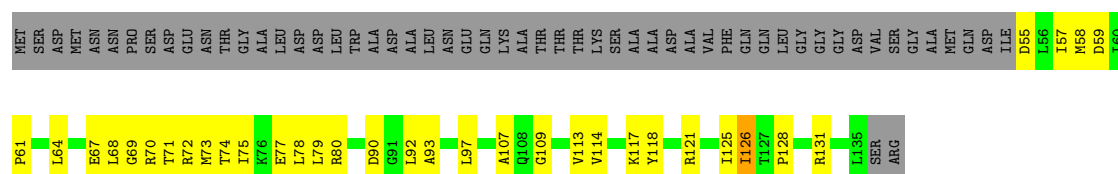


- Molecule 4: Flagellar motor switch protein FliN

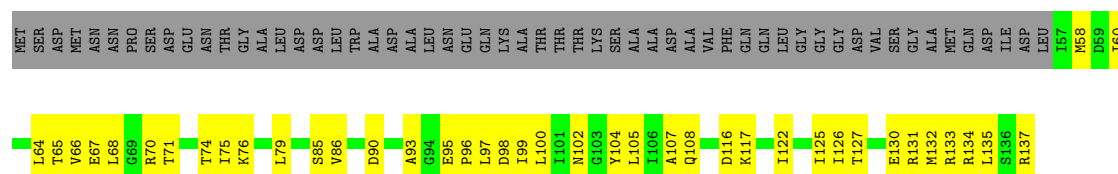
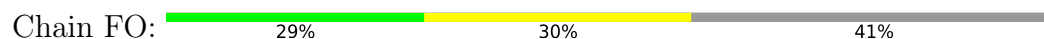
Chain EM:  31% 27% 41%



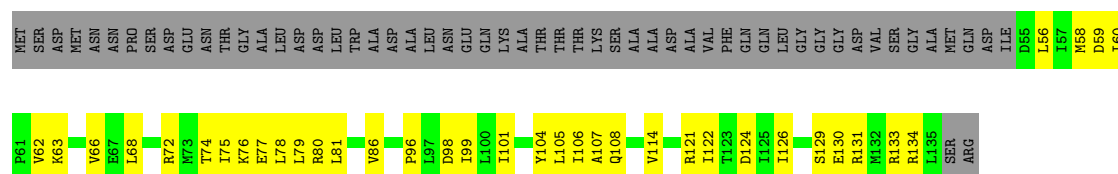
- Molecule 4: Flagellar motor switch protein FliN



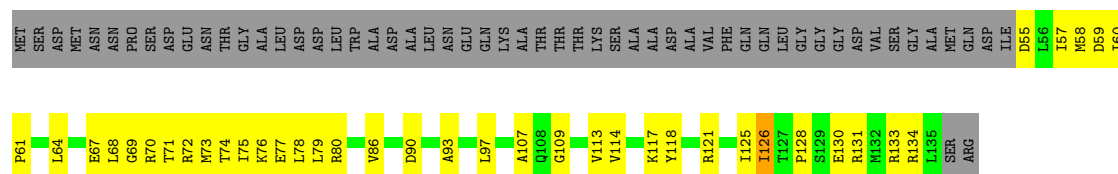
• Molecule 4: Flagellar motor switch protein FliN



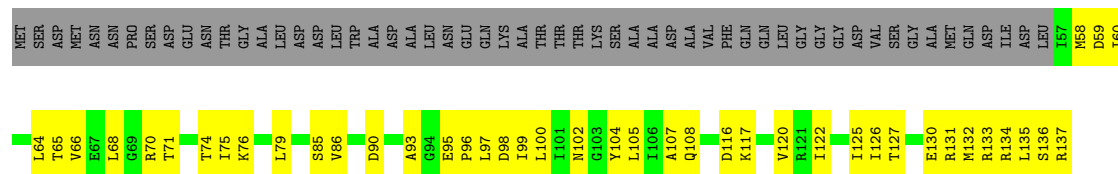
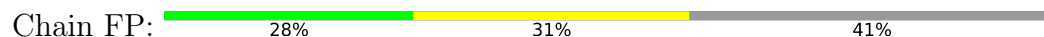
• Molecule 4: Flagellar motor switch protein FliN



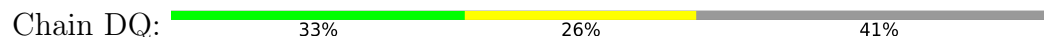
• Molecule 4: Flagellar motor switch protein FliN



• Molecule 4: Flagellar motor switch protein FliN

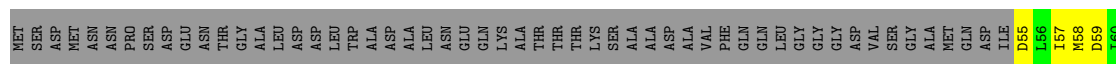


• Molecule 4: Flagellar motor switch protein FliN

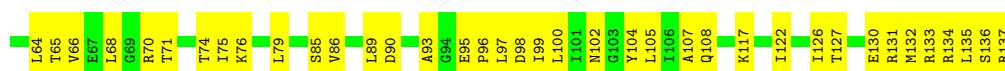
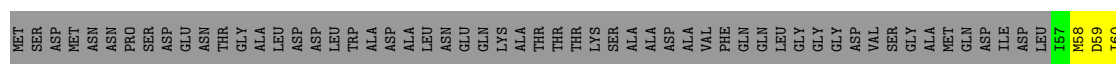
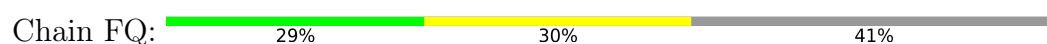




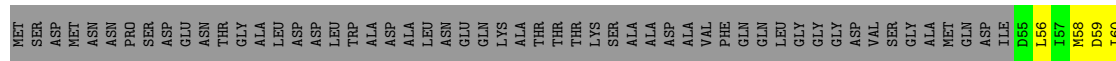
• Molecule 4: Flagellar motor switch protein FliN



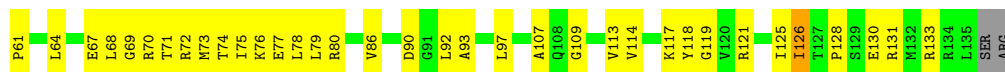
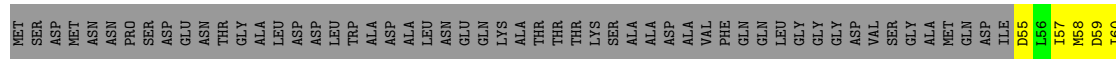
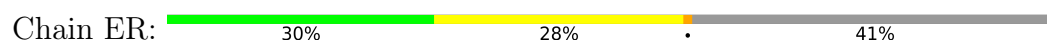
• Molecule 4: Flagellar motor switch protein FliN



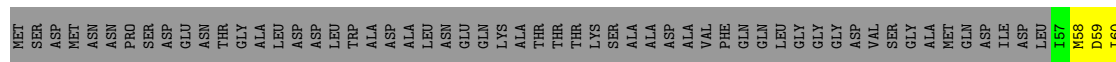
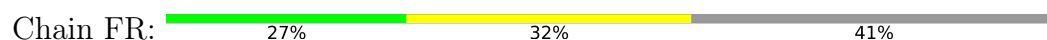
• Molecule 4: Flagellar motor switch protein FliN



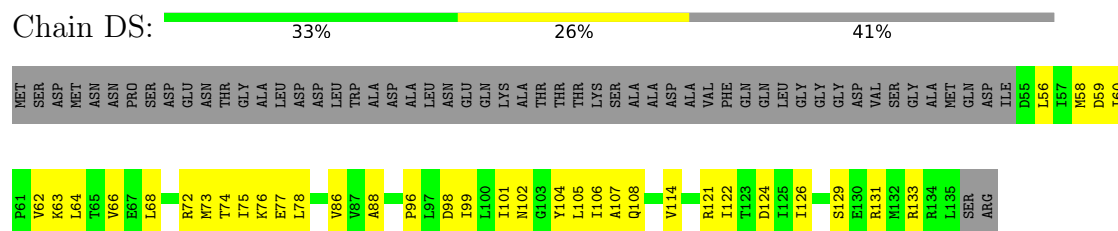
• Molecule 4: Flagellar motor switch protein FliN



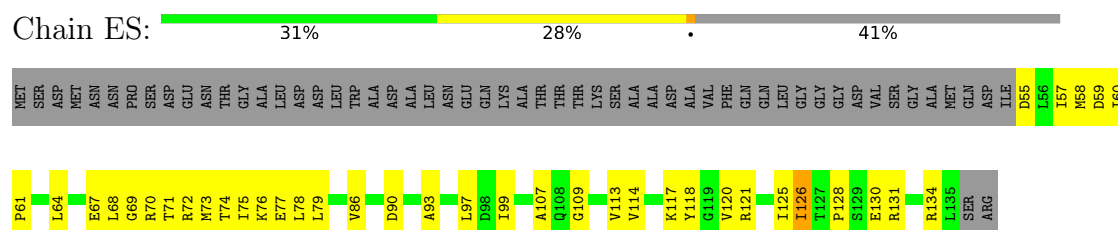
• Molecule 4: Flagellar motor switch protein FliN



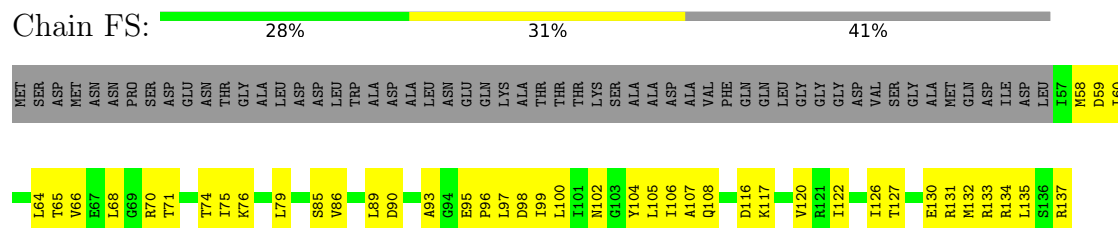
- Molecule 4: Flagellar motor switch protein FliN



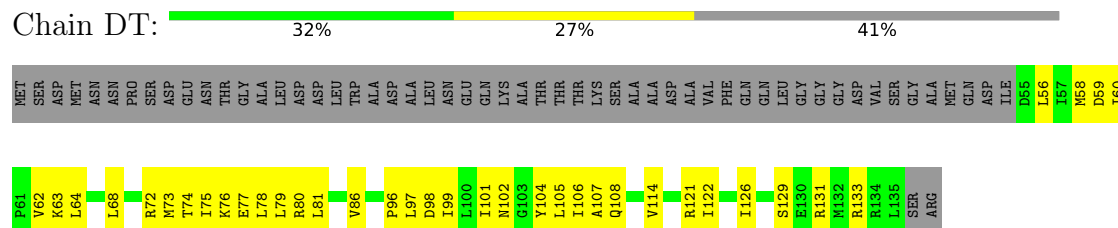
- Molecule 4: Flagellar motor switch protein FliN



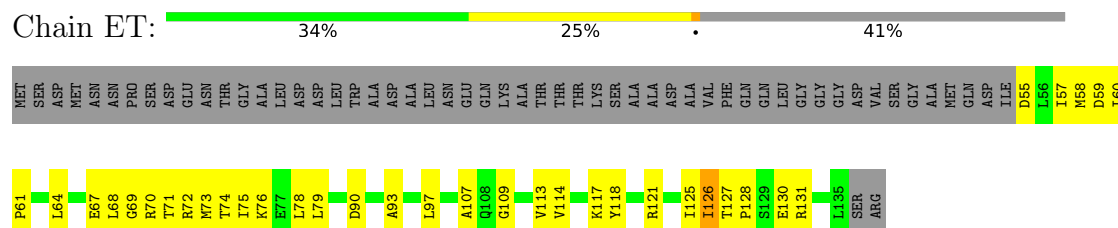
- Molecule 4: Flagellar motor switch protein FliN



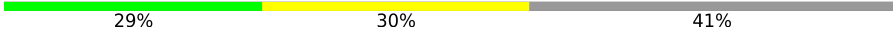
- Molecule 4: Flagellar motor switch protein FliN

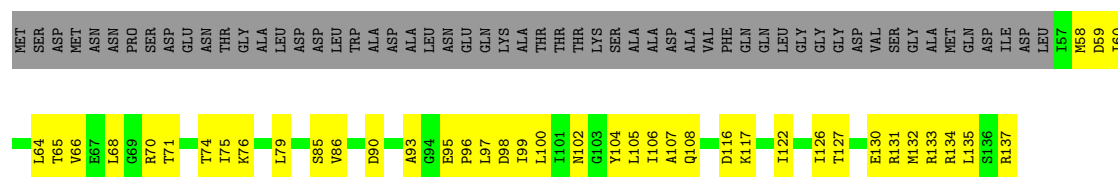


- Molecule 4: Flagellar motor switch protein FliN

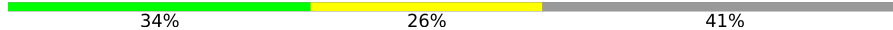


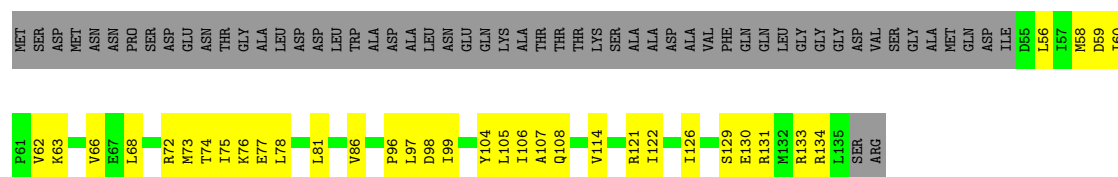
- Molecule 4: Flagellar motor switch protein FliN

Chain FT:  29% 30% 41%

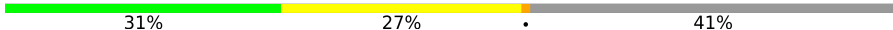


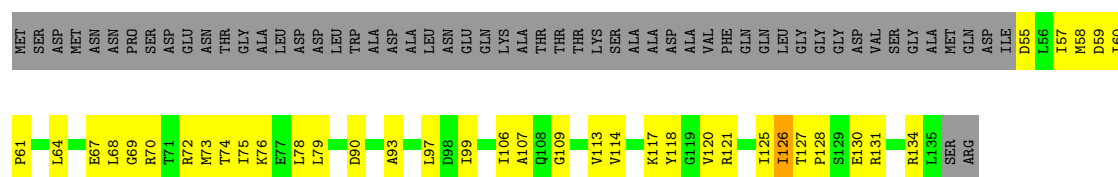
• Molecule 4: Flagellar motor switch protein FliN

Chain DU:  34% 26% 41%

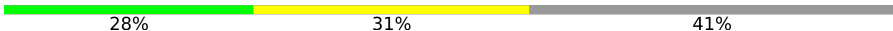


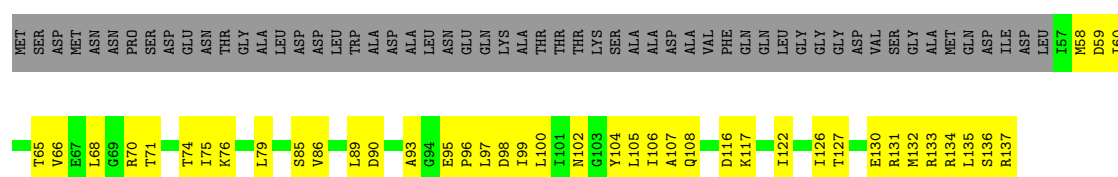
• Molecule 4: Flagellar motor switch protein FliN

Chain EU:  31% 27% 41%

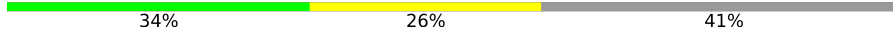


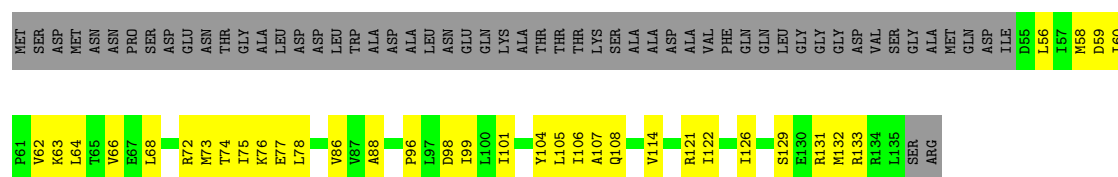
• Molecule 4: Flagellar motor switch protein FliN

Chain FU:  28% 31% 41%

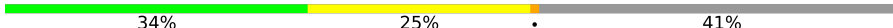


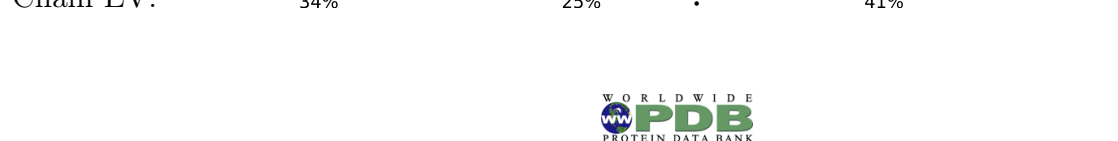
• Molecule 4: Flagellar motor switch protein FliN

Chain DV:  34% 26% 41%

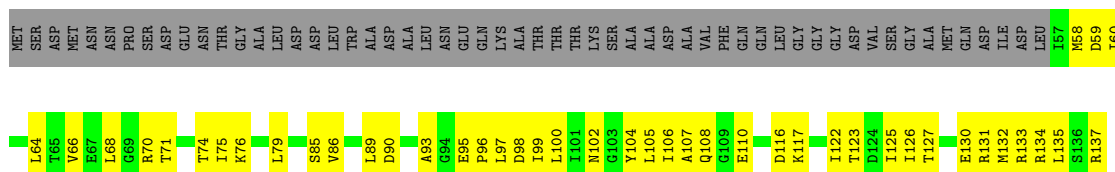
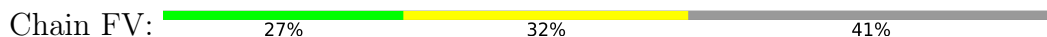


• Molecule 4: Flagellar motor switch protein FliN

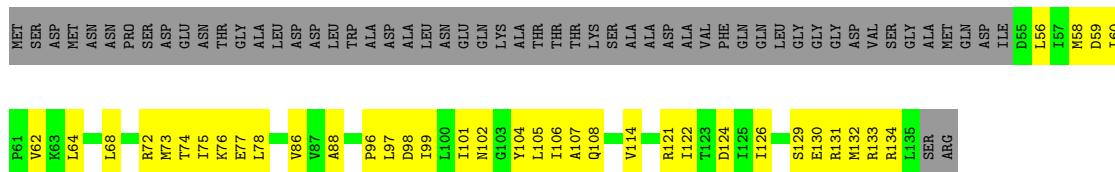
Chain EV:  34% 25% 41%



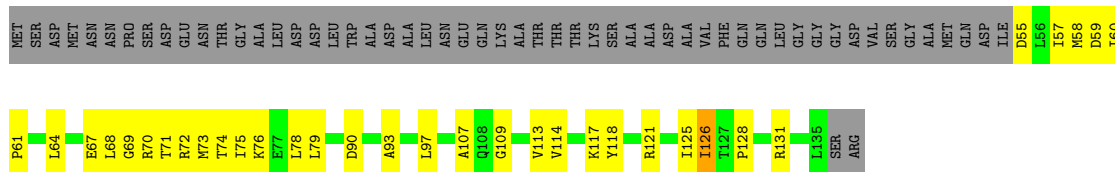
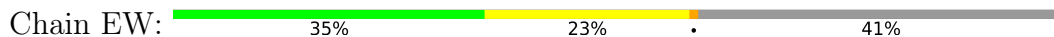
- Molecule 4: Flagellar motor switch protein FliN



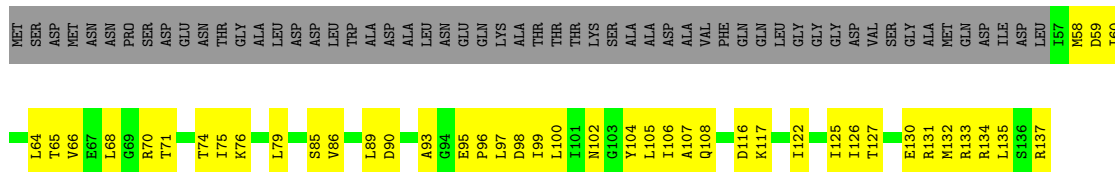
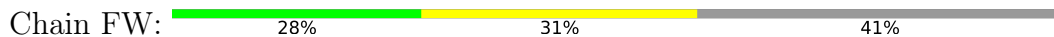
- Molecule 4: Flagellar motor switch protein FliN



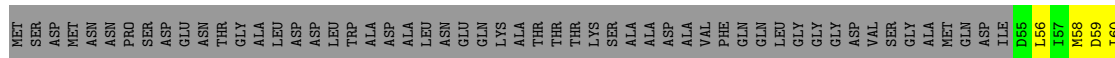
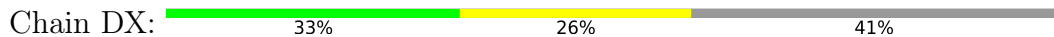
- Molecule 4: Flagellar motor switch protein FliN



- Molecule 4: Flagellar motor switch protein FliN



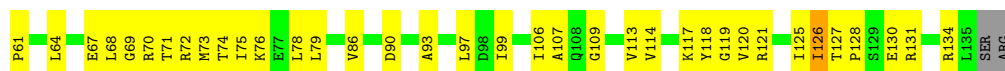
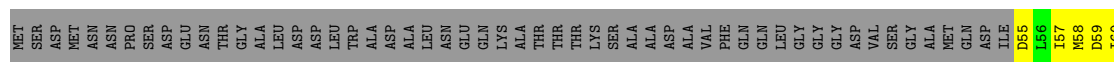
- Molecule 4: Flagellar motor switch protein FliN





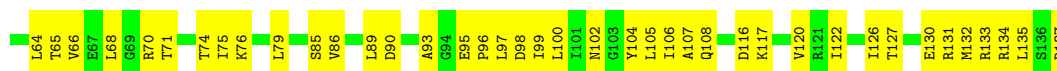
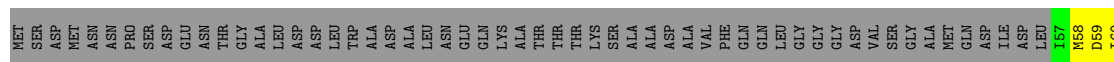
- Molecule 4: Flagellar motor switch protein FliN

Chain EX: 29% 29% 41%



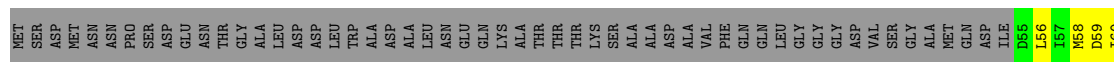
- Molecule 4: Flagellar motor switch protein FliN

Chain FX: 28% 31% 41%



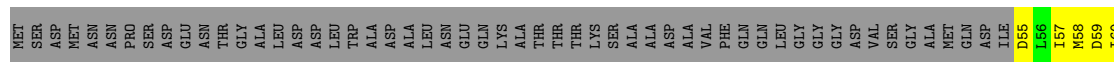
- Molecule 4: Flagellar motor switch protein FliN

Chain DY: 29% 30% 41%



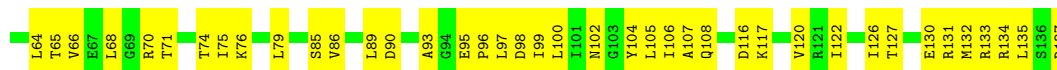
- Molecule 4: Flagellar motor switch protein FliN

Chain EY: 31% 27% 41%



- Molecule 4: Flagellar motor switch protein FliN

Chain FY: 28% 31% 41%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15952	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 ($e^-/\text{\AA}^2$)	58.5	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A1	0.16	0/396	0.39	0/528
1	A2	0.14	0/396	0.43	0/528
1	A3	0.18	0/396	0.40	0/528
1	A4	0.16	0/396	0.43	0/528
1	A5	0.16	0/396	0.45	0/528
1	A6	0.15	0/396	0.46	0/528
1	A7	0.15	0/396	0.42	0/528
1	A8	0.16	0/396	0.46	0/528
1	A9	0.15	0/396	0.42	0/528
1	AA	0.15	0/396	0.42	0/528
1	AB	0.14	0/396	0.43	0/528
1	AC	0.15	0/396	0.41	0/528
1	AD	0.14	0/396	0.40	0/528
1	AE	0.16	0/396	0.42	0/528
1	AF	0.14	0/396	0.41	0/528
1	AG	0.15	0/396	0.42	0/528
1	AH	0.15	0/396	0.43	0/528
1	AI	0.16	0/396	0.43	0/528
1	AJ	0.15	0/396	0.45	0/528
1	AK	0.15	0/396	0.43	0/528
1	AL	0.16	0/396	0.44	0/528
1	AM	0.15	0/396	0.47	0/528
1	AN	0.14	0/396	0.41	0/528
1	AO	0.15	0/396	0.44	0/528
1	AP	0.15	0/396	0.44	0/528
1	AQ	0.18	0/396	0.41	0/528
1	AR	0.15	0/396	0.46	0/528
1	AS	0.14	0/396	0.44	0/528
1	AT	0.14	0/396	0.44	0/528
1	AU	0.14	0/396	0.41	0/528
1	AV	0.21	0/396	0.45	0/528
1	AW	0.14	0/396	0.43	0/528
1	AX	0.14	0/396	0.40	0/528
1	AY	0.19	0/396	0.46	0/528

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	B1	0.16	0/2604	0.42	2/3511 (0.1%)
2	B2	0.15	0/2604	0.40	2/3511 (0.1%)
2	B3	0.16	0/2604	0.41	0/3511
2	B4	0.16	0/2604	0.41	2/3511 (0.1%)
2	B5	0.16	0/2604	0.42	2/3511 (0.1%)
2	B6	0.16	0/2604	0.42	2/3511 (0.1%)
2	B7	0.16	0/2604	0.42	2/3511 (0.1%)
2	B8	0.15	0/2604	0.42	2/3511 (0.1%)
2	B9	0.16	0/2604	0.41	2/3511 (0.1%)
2	BA	0.15	0/2604	0.40	2/3511 (0.1%)
2	BB	0.17	0/2604	0.43	2/3511 (0.1%)
2	BC	0.16	0/2604	0.43	2/3511 (0.1%)
2	BD	0.16	0/2604	0.42	2/3511 (0.1%)
2	BE	0.16	0/2604	0.43	2/3511 (0.1%)
2	BF	0.16	0/2604	0.41	2/3511 (0.1%)
2	BG	0.16	0/2604	0.41	2/3511 (0.1%)
2	BH	0.16	0/2604	0.43	2/3511 (0.1%)
2	BI	0.16	0/2604	0.42	2/3511 (0.1%)
2	BJ	0.17	0/2604	0.43	2/3511 (0.1%)
2	BK	0.16	0/2604	0.43	2/3511 (0.1%)
2	BL	0.16	0/2604	0.42	2/3511 (0.1%)
2	BM	0.16	0/2604	0.42	2/3511 (0.1%)
2	BN	0.16	0/2604	0.41	2/3511 (0.1%)
2	BO	0.16	0/2604	0.41	2/3511 (0.1%)
2	BP	0.16	0/2604	0.43	2/3511 (0.1%)
2	BQ	0.17	0/2604	0.43	2/3511 (0.1%)
2	BR	0.17	0/2604	0.43	2/3511 (0.1%)
2	BS	0.17	0/2604	0.43	2/3511 (0.1%)
2	BT	0.15	0/2604	0.41	2/3511 (0.1%)
2	BU	0.16	0/2604	0.41	2/3511 (0.1%)
2	BV	0.16	0/2604	0.41	2/3511 (0.1%)
2	BW	0.16	0/2604	0.41	2/3511 (0.1%)
2	BX	0.16	0/2604	0.40	2/3511 (0.1%)
2	BY	0.16	0/2604	0.42	2/3511 (0.1%)
3	C1	0.15	0/2401	0.32	0/3267
3	C2	0.16	0/2401	0.34	0/3267
3	C3	0.16	0/2401	0.34	0/3267
3	C4	0.15	0/2401	0.33	0/3267
3	C5	0.16	0/2401	0.33	0/3267
3	C6	0.16	0/2401	0.34	0/3267
3	C7	0.16	0/2401	0.34	0/3267
3	C8	0.15	0/2401	0.32	0/3267
3	C9	0.15	0/2401	0.32	0/3267

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
3	CA	0.16	0/2401	0.34	0/3267
3	CB	0.16	0/2401	0.34	0/3267
3	CC	0.16	0/2401	0.33	0/3267
3	CD	0.16	0/2401	0.34	0/3267
3	CE	0.16	0/2401	0.34	0/3267
3	CF	0.16	0/2401	0.32	0/3267
3	CG	0.15	0/2401	0.33	0/3267
3	CH	0.15	0/2401	0.33	0/3267
3	CI	0.15	0/2401	0.32	0/3267
3	CJ	0.16	0/2401	0.34	0/3267
3	CK	0.15	0/2401	0.34	0/3267
3	CL	0.15	0/2401	0.33	0/3267
3	CM	0.15	0/2401	0.33	0/3267
3	CN	0.16	0/2401	0.33	0/3267
3	CO	0.16	0/2401	0.34	0/3267
3	CP	0.16	0/2401	0.33	0/3267
3	CQ	0.15	0/2401	0.33	0/3267
3	CR	0.15	0/2401	0.33	0/3267
3	CS	0.16	0/2401	0.34	0/3267
3	CT	0.16	0/2401	0.34	0/3267
3	CU	0.16	0/2401	0.34	0/3267
3	CV	0.16	0/2401	0.33	0/3267
3	CW	0.15	0/2401	0.32	0/3267
3	CX	0.15	0/2401	0.33	0/3267
3	CY	0.15	0/2401	0.33	0/3267
4	D1	0.15	0/629	0.40	0/851
4	D2	0.15	0/629	0.40	0/851
4	D3	0.15	0/629	0.40	0/851
4	D4	0.15	0/629	0.42	0/851
4	D5	0.16	0/629	0.42	0/851
4	D6	0.15	0/629	0.40	0/851
4	D7	0.15	0/629	0.41	0/851
4	D8	0.14	0/629	0.42	0/851
4	D9	0.15	0/629	0.41	0/851
4	DA	0.15	0/629	0.40	0/851
4	DB	0.15	0/629	0.40	0/851
4	DC	0.15	0/629	0.41	0/851
4	DD	0.15	0/629	0.41	0/851
4	DE	0.16	0/629	0.42	0/851
4	DF	0.14	0/629	0.41	0/851
4	DG	0.16	0/629	0.44	0/851
4	DH	0.14	0/629	0.40	0/851
4	DI	0.15	0/629	0.42	0/851

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	DJ	0.15	0/629	0.41	0/851
4	DK	0.14	0/629	0.40	0/851
4	DL	0.15	0/629	0.41	0/851
4	DM	0.15	0/629	0.41	0/851
4	DN	0.15	0/629	0.40	0/851
4	DO	0.15	0/629	0.41	0/851
4	DP	0.15	0/629	0.42	0/851
4	DQ	0.20	0/629	0.46	0/851
4	DR	0.14	0/629	0.42	0/851
4	DS	0.16	0/629	0.41	0/851
4	DT	0.15	0/629	0.41	0/851
4	DU	0.15	0/629	0.41	0/851
4	DV	0.15	0/629	0.41	0/851
4	DW	0.14	0/629	0.41	0/851
4	DX	0.15	0/629	0.43	0/851
4	DY	0.20	0/629	0.45	0/851
4	E1	0.17	0/629	0.49	0/851
4	E2	0.18	0/629	0.50	0/851
4	E3	0.17	0/629	0.49	0/851
4	E4	0.17	0/629	0.49	0/851
4	E5	0.17	0/629	0.49	0/851
4	E6	0.19	0/629	0.53	0/851
4	E7	0.17	0/629	0.50	0/851
4	E8	0.17	0/629	0.50	0/851
4	E9	0.17	0/629	0.51	1/851 (0.1%)
4	EA	0.17	0/629	0.50	0/851
4	EB	0.21	0/629	0.58	1/851 (0.1%)
4	EC	0.16	0/629	0.48	0/851
4	ED	0.23	0/629	0.49	0/851
4	EE	0.18	0/629	0.50	0/851
4	EF	0.18	0/629	0.50	0/851
4	EG	0.19	0/629	0.51	0/851
4	EH	0.17	0/629	0.50	0/851
4	EI	0.19	0/629	0.53	0/851
4	EJ	0.17	0/629	0.49	0/851
4	EK	0.19	0/629	0.51	0/851
4	EL	0.18	0/629	0.49	0/851
4	EM	0.20	0/629	0.53	0/851
4	EN	0.20	0/629	0.55	0/851
4	EO	0.20	0/629	0.56	0/851
4	EP	0.21	0/629	0.51	0/851
4	EQ	0.17	0/629	0.50	0/851
4	ER	0.21	0/629	0.53	0/851

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
4	ES	0.17	0/629	0.50	0/851
4	ET	0.17	0/629	0.50	0/851
4	EU	0.18	0/629	0.51	0/851
4	EV	0.17	0/629	0.49	0/851
4	EW	0.17	0/629	0.51	0/851
4	EX	0.18	0/629	0.51	0/851
4	EY	0.18	0/629	0.50	0/851
4	F1	0.17	0/631	0.48	0/851
4	F2	0.17	0/631	0.48	0/851
4	F3	0.17	0/631	0.49	0/851
4	F4	0.17	0/631	0.48	0/851
4	F5	0.18	0/631	0.51	0/851
4	F6	0.19	0/631	0.52	0/851
4	F7	0.19	0/631	0.51	0/851
4	F8	0.19	0/631	0.53	0/851
4	F9	0.18	0/631	0.48	0/851
4	FA	0.18	0/631	0.48	0/851
4	FB	0.18	0/631	0.51	0/851
4	FC	0.18	0/631	0.48	0/851
4	FD	0.18	0/631	0.48	0/851
4	FE	0.19	0/631	0.51	0/851
4	FF	0.18	0/631	0.48	0/851
4	FG	0.19	0/631	0.50	0/851
4	FH	0.18	0/631	0.49	0/851
4	FI	0.18	0/631	0.50	0/851
4	FJ	0.17	0/631	0.46	0/851
4	FK	0.19	0/631	0.50	0/851
4	FL	0.16	0/631	0.45	0/851
4	FM	0.18	0/631	0.48	0/851
4	FN	0.18	0/631	0.47	0/851
4	FO	0.19	0/631	0.51	0/851
4	FP	0.18	0/631	0.49	0/851
4	FQ	0.17	0/631	0.47	0/851
4	FR	0.18	0/631	0.48	0/851
4	FS	0.18	0/631	0.50	0/851
4	FT	0.20	0/631	0.51	0/851
4	FU	0.18	0/631	0.50	0/851
4	FV	0.18	0/631	0.48	0/851
4	FW	0.19	0/631	0.51	0/851
4	FX	0.19	0/631	0.52	0/851
4	FY	0.19	0/631	0.52	0/851
All	All	0.16	0/247860	0.41	68/335206 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BM	242	VAL	CA-C-N	5.91	132.83	121.54
2	BM	242	VAL	C-N-CA	5.91	132.83	121.54
2	BJ	242	VAL	CA-C-N	5.87	132.75	121.54
2	BJ	242	VAL	C-N-CA	5.87	132.75	121.54
2	BN	242	VAL	CA-C-N	5.77	132.56	121.54

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	A1	393	0	384	26	0
1	A2	393	0	384	22	0
1	A3	393	0	384	23	0
1	A4	393	0	384	27	0
1	A5	393	0	384	26	0
1	A6	393	0	384	29	0
1	A7	393	0	384	25	0
1	A8	393	0	384	23	0
1	A9	393	0	384	26	0
1	AA	393	0	384	25	0
1	AB	393	0	384	23	0
1	AC	393	0	384	26	0
1	AD	393	0	384	23	0
1	AE	393	0	384	25	0
1	AF	393	0	384	26	0
1	AG	393	0	384	23	0
1	AH	393	0	384	27	0
1	AI	393	0	384	27	0
1	AJ	393	0	384	25	0
1	AK	393	0	384	22	0
1	AL	393	0	384	23	0
1	AM	393	0	384	24	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AN	393	0	384	24	0
1	AO	393	0	384	27	0
1	AP	393	0	384	20	0
1	AQ	393	0	384	25	0
1	AR	393	0	384	22	0
1	AS	393	0	384	22	0
1	AT	393	0	384	25	0
1	AU	393	0	384	25	0
1	AV	393	0	384	22	0
1	AW	393	0	384	23	0
1	AX	393	0	384	21	0
1	AY	393	0	384	27	0
2	B1	2583	0	2632	123	0
2	B2	2583	0	2632	120	0
2	B3	2583	0	2632	122	0
2	B4	2583	0	2632	120	0
2	B5	2583	0	2632	114	0
2	B6	2583	0	2632	131	0
2	B7	2583	0	2632	123	0
2	B8	2583	0	2632	126	0
2	B9	2583	0	2632	120	0
2	BA	2583	0	2632	119	0
2	BB	2583	0	2632	135	0
2	BC	2583	0	2632	132	0
2	BD	2583	0	2632	123	0
2	BE	2583	0	2632	119	0
2	BF	2583	0	2632	118	0
2	BG	2583	0	2632	135	0
2	BH	2583	0	2632	129	0
2	BI	2583	0	2632	124	0
2	BJ	2583	0	2632	119	0
2	BK	2583	0	2632	126	0
2	BL	2583	0	2632	119	0
2	BM	2583	0	2632	103	0
2	BN	2583	0	2632	122	0
2	BO	2583	0	2632	120	0
2	BP	2583	0	2632	128	0
2	BQ	2583	0	2632	129	0
2	BR	2583	0	2632	127	0
2	BS	2583	0	2632	136	0
2	BT	2583	0	2632	136	0
2	BU	2583	0	2632	122	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BV	2583	0	2632	118	0
2	BW	2583	0	2632	117	0
2	BX	2583	0	2632	115	0
2	BY	2583	0	2632	130	0
3	C1	2348	0	2376	95	0
3	C2	2348	0	2376	100	0
3	C3	2348	0	2376	99	0
3	C4	2348	0	2376	106	0
3	C5	2348	0	2376	98	0
3	C6	2348	0	2376	104	0
3	C7	2348	0	2376	103	0
3	C8	2348	0	2376	100	0
3	C9	2348	0	2376	101	0
3	CA	2348	0	2376	97	0
3	CB	2348	0	2376	106	0
3	CC	2348	0	2376	101	0
3	CD	2348	0	2376	101	0
3	CE	2348	0	2376	102	0
3	CF	2348	0	2376	103	0
3	CG	2348	0	2376	101	0
3	CH	2348	0	2376	99	0
3	CI	2348	0	2376	95	0
3	CJ	2348	0	2376	103	0
3	CK	2348	0	2376	97	0
3	CL	2348	0	2376	97	0
3	CM	2348	0	2376	104	0
3	CN	2348	0	2376	96	0
3	CO	2348	0	2376	96	0
3	CP	2348	0	2376	100	0
3	CQ	2348	0	2376	105	0
3	CR	2348	0	2376	98	0
3	CS	2348	0	2376	102	0
3	CT	2348	0	2376	103	0
3	CU	2348	0	2376	103	0
3	CV	2348	0	2376	106	0
3	CW	2348	0	2376	97	0
3	CX	2348	0	2376	102	0
3	CY	2348	0	2376	103	0
4	D1	625	0	676	39	0
4	D2	625	0	676	37	0
4	D3	625	0	676	35	0
4	D4	625	0	676	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D5	625	0	676	37	0
4	D6	625	0	676	37	0
4	D7	625	0	676	38	0
4	D8	625	0	676	38	0
4	D9	625	0	676	37	0
4	DA	625	0	676	38	0
4	DB	625	0	676	37	0
4	DC	625	0	676	40	0
4	DD	625	0	676	38	0
4	DE	625	0	676	41	0
4	DF	625	0	676	37	0
4	DG	625	0	676	37	0
4	DH	625	0	676	38	0
4	DI	625	0	676	37	0
4	DJ	625	0	676	39	0
4	DK	625	0	676	37	0
4	DL	625	0	676	37	0
4	DM	625	0	676	39	0
4	DN	625	0	676	34	0
4	DO	625	0	676	34	0
4	DP	625	0	676	40	0
4	DQ	625	0	676	36	0
4	DR	625	0	676	38	0
4	DS	625	0	676	38	0
4	DT	625	0	676	40	0
4	DU	625	0	676	36	0
4	DV	625	0	676	39	0
4	DW	625	0	676	39	0
4	DX	625	0	676	37	0
4	DY	625	0	676	42	0
4	E1	625	0	676	43	0
4	E2	625	0	676	44	0
4	E3	625	0	676	40	0
4	E4	625	0	676	39	0
4	E5	625	0	676	40	0
4	E6	625	0	676	39	0
4	E7	625	0	676	41	0
4	E8	625	0	676	43	0
4	E9	625	0	676	43	0
4	EA	625	0	676	41	0
4	EB	625	0	676	46	0
4	EC	625	0	676	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	ED	625	0	676	43	0
4	EE	625	0	676	41	0
4	EF	625	0	676	43	0
4	EG	625	0	676	48	0
4	EH	625	0	676	46	0
4	EI	625	0	676	37	0
4	EJ	625	0	676	43	0
4	EK	625	0	676	39	0
4	EL	625	0	676	42	0
4	EM	625	0	676	47	0
4	EN	625	0	676	44	0
4	EO	625	0	676	38	0
4	EP	625	0	676	50	0
4	EQ	625	0	676	37	0
4	ER	625	0	676	51	0
4	ES	625	0	676	45	0
4	ET	625	0	676	41	0
4	EU	625	0	676	43	0
4	EV	625	0	676	42	0
4	EW	625	0	676	40	0
4	EX	625	0	676	45	0
4	EY	625	0	676	43	0
4	F1	627	0	679	47	0
4	F2	627	0	679	48	0
4	F3	627	0	679	44	0
4	F4	627	0	679	46	0
4	F5	627	0	679	46	0
4	F6	627	0	679	46	0
4	F7	627	0	679	44	0
4	F8	627	0	679	48	0
4	F9	627	0	679	46	0
4	FA	627	0	679	46	0
4	FB	627	0	679	49	0
4	FC	627	0	679	52	0
4	FD	627	0	679	52	0
4	FE	627	0	679	53	0
4	FF	627	0	679	43	0
4	FG	627	0	679	53	0
4	FH	627	0	679	49	0
4	FI	627	0	679	43	0
4	FJ	627	0	679	49	0
4	FK	627	0	679	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	FL	627	0	679	47	0
4	FM	627	0	679	47	0
4	FN	627	0	679	49	0
4	FO	627	0	679	48	0
4	FP	627	0	679	48	0
4	FQ	627	0	679	46	0
4	FR	627	0	679	52	0
4	FS	627	0	679	50	0
4	FT	627	0	679	48	0
4	FU	627	0	679	47	0
4	FV	627	0	679	45	0
4	FW	627	0	679	48	0
4	FX	627	0	679	49	0
4	FY	627	0	679	48	0
All	All	244834	0	252382	9884	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 20.

The worst 5 of 9884 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BW:251:LEU:HD22	2:BW:278:MET:HG2	1.50	0.94
2:BK:251:LEU:HD22	2:BK:278:MET:HG2	1.49	0.94
2:BF:251:LEU:HD22	2:BF:278:MET:HG2	1.50	0.93
2:B5:251:LEU:HD22	2:B5:278:MET:HG2	1.50	0.93
2:BD:251:LEU:HD22	2:BD:278:MET:HG2	1.49	0.93

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	A1	45/560 (8%)	45 (100%)	0	0	100	100
1	A2	45/560 (8%)	45 (100%)	0	0	100	100
1	A3	45/560 (8%)	45 (100%)	0	0	100	100
1	A4	45/560 (8%)	45 (100%)	0	0	100	100
1	A5	45/560 (8%)	45 (100%)	0	0	100	100
1	A6	45/560 (8%)	45 (100%)	0	0	100	100
1	A7	45/560 (8%)	45 (100%)	0	0	100	100
1	A8	45/560 (8%)	45 (100%)	0	0	100	100
1	A9	45/560 (8%)	45 (100%)	0	0	100	100
1	AA	45/560 (8%)	45 (100%)	0	0	100	100
1	AB	45/560 (8%)	45 (100%)	0	0	100	100
1	AC	45/560 (8%)	45 (100%)	0	0	100	100
1	AD	45/560 (8%)	45 (100%)	0	0	100	100
1	AE	45/560 (8%)	45 (100%)	0	0	100	100
1	AF	45/560 (8%)	45 (100%)	0	0	100	100
1	AG	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	AH	45/560 (8%)	45 (100%)	0	0	100	100
1	AI	45/560 (8%)	45 (100%)	0	0	100	100
1	AJ	45/560 (8%)	45 (100%)	0	0	100	100
1	AK	45/560 (8%)	45 (100%)	0	0	100	100
1	AL	45/560 (8%)	45 (100%)	0	0	100	100
1	AM	45/560 (8%)	45 (100%)	0	0	100	100
1	AN	45/560 (8%)	45 (100%)	0	0	100	100
1	AO	45/560 (8%)	45 (100%)	0	0	100	100
1	AP	45/560 (8%)	45 (100%)	0	0	100	100
1	AQ	45/560 (8%)	45 (100%)	0	0	100	100
1	AR	45/560 (8%)	45 (100%)	0	0	100	100
1	AS	45/560 (8%)	45 (100%)	0	0	100	100
1	AT	45/560 (8%)	45 (100%)	0	0	100	100
1	AU	45/560 (8%)	45 (100%)	0	0	100	100
1	AV	45/560 (8%)	45 (100%)	0	0	100	100
1	AW	45/560 (8%)	45 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AX	45/560 (8%)	44 (98%)	1 (2%)	0	100	100
1	AY	45/560 (8%)	45 (100%)	0	0	100	100
2	B1	329/331 (99%)	315 (96%)	11 (3%)	3 (1%)	14	49
2	B2	329/331 (99%)	312 (95%)	15 (5%)	2 (1%)	21	58
2	B3	329/331 (99%)	315 (96%)	12 (4%)	2 (1%)	21	58
2	B4	329/331 (99%)	312 (95%)	14 (4%)	3 (1%)	14	49
2	B5	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	B6	329/331 (99%)	315 (96%)	11 (3%)	3 (1%)	14	49
2	B7	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49
2	B8	329/331 (99%)	311 (94%)	15 (5%)	3 (1%)	14	49
2	B9	329/331 (99%)	315 (96%)	11 (3%)	3 (1%)	14	49
2	BA	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49
2	BB	329/331 (99%)	312 (95%)	15 (5%)	2 (1%)	21	58
2	BC	329/331 (99%)	315 (96%)	11 (3%)	3 (1%)	14	49
2	BD	329/331 (99%)	315 (96%)	11 (3%)	3 (1%)	14	49
2	BE	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	BF	329/331 (99%)	311 (94%)	15 (5%)	3 (1%)	14	49
2	BG	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49
2	BH	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49
2	BI	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	BJ	329/331 (99%)	312 (95%)	15 (5%)	2 (1%)	21	58
2	BK	329/331 (99%)	311 (94%)	15 (5%)	3 (1%)	14	49
2	BL	329/331 (99%)	315 (96%)	11 (3%)	3 (1%)	14	49
2	BM	329/331 (99%)	310 (94%)	17 (5%)	2 (1%)	21	58
2	BN	329/331 (99%)	314 (95%)	13 (4%)	2 (1%)	21	58
2	BO	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	BP	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49
2	BQ	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	BR	329/331 (99%)	313 (95%)	14 (4%)	2 (1%)	21	58
2	BS	329/331 (99%)	313 (95%)	14 (4%)	2 (1%)	21	58
2	BT	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	BU	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	BV	329/331 (99%)	314 (95%)	12 (4%)	3 (1%)	14	49
2	BW	329/331 (99%)	317 (96%)	9 (3%)	3 (1%)	14	49
2	BX	329/331 (99%)	311 (94%)	15 (5%)	3 (1%)	14	49
2	BY	329/331 (99%)	313 (95%)	13 (4%)	3 (1%)	14	49
3	C1	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	C2	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	C3	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	C4	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	C5	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	C6	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	C7	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	C8	288/334 (86%)	275 (96%)	13 (4%)	0	100	100
3	C9	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CA	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CB	288/334 (86%)	275 (96%)	13 (4%)	0	100	100
3	CC	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CD	288/334 (86%)	279 (97%)	9 (3%)	0	100	100
3	CE	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CF	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CG	288/334 (86%)	275 (96%)	13 (4%)	0	100	100
3	CH	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CI	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	CJ	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CK	288/334 (86%)	276 (96%)	12 (4%)	0	100	100
3	CL	288/334 (86%)	276 (96%)	12 (4%)	0	100	100
3	CM	288/334 (86%)	276 (96%)	12 (4%)	0	100	100
3	CN	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	CO	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CP	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CQ	288/334 (86%)	278 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CR	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	CS	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	CT	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CU	288/334 (86%)	278 (96%)	10 (4%)	0	100	100
3	CV	288/334 (86%)	277 (96%)	11 (4%)	0	100	100
3	CW	288/334 (86%)	275 (96%)	13 (4%)	0	100	100
3	CX	288/334 (86%)	276 (96%)	12 (4%)	0	100	100
3	CY	288/334 (86%)	275 (96%)	13 (4%)	0	100	100
4	D1	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D2	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D3	79/137 (58%)	70 (89%)	9 (11%)	0	100	100
4	D4	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D5	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D6	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D7	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D8	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	D9	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DA	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DB	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DC	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DD	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DE	79/137 (58%)	72 (91%)	7 (9%)	0	100	100
4	DF	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DG	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DH	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DI	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DJ	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DK	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DL	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DM	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DN	79/137 (58%)	70 (89%)	9 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	DO	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DP	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DQ	79/137 (58%)	70 (89%)	9 (11%)	0	100	100
4	DR	79/137 (58%)	70 (89%)	9 (11%)	0	100	100
4	DS	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DT	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DU	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DV	79/137 (58%)	72 (91%)	7 (9%)	0	100	100
4	DW	79/137 (58%)	70 (89%)	9 (11%)	0	100	100
4	DX	79/137 (58%)	71 (90%)	8 (10%)	0	100	100
4	DY	79/137 (58%)	72 (91%)	7 (9%)	0	100	100
4	E1	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E2	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E3	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E4	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E5	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E6	79/137 (58%)	75 (95%)	3 (4%)	1 (1%)	9	41
4	E7	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E8	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	E9	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EA	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EB	79/137 (58%)	75 (95%)	3 (4%)	1 (1%)	9	41
4	EC	79/137 (58%)	75 (95%)	3 (4%)	1 (1%)	9	41
4	ED	79/137 (58%)	77 (98%)	1 (1%)	1 (1%)	9	41
4	EE	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EF	79/137 (58%)	73 (92%)	5 (6%)	1 (1%)	9	41
4	EG	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EH	79/137 (58%)	73 (92%)	5 (6%)	1 (1%)	9	41
4	EI	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EJ	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EK	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	EL	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EM	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EN	79/137 (58%)	75 (95%)	3 (4%)	1 (1%)	9	41
4	EO	79/137 (58%)	73 (92%)	5 (6%)	1 (1%)	9	41
4	EP	79/137 (58%)	75 (95%)	3 (4%)	1 (1%)	9	41
4	EQ	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	ER	79/137 (58%)	76 (96%)	2 (2%)	1 (1%)	9	41
4	ES	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	ET	79/137 (58%)	75 (95%)	3 (4%)	1 (1%)	9	41
4	EU	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EV	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EW	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EX	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	EY	79/137 (58%)	74 (94%)	4 (5%)	1 (1%)	9	41
4	F1	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	F2	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	F3	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	F4	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	F5	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	F6	79/137 (58%)	75 (95%)	4 (5%)	0	100	100
4	F7	79/137 (58%)	75 (95%)	4 (5%)	0	100	100
4	F8	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	F9	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FA	79/137 (58%)	77 (98%)	2 (2%)	0	100	100
4	FB	79/137 (58%)	75 (95%)	4 (5%)	0	100	100
4	FC	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	FD	79/137 (58%)	74 (94%)	5 (6%)	0	100	100
4	FE	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FF	79/137 (58%)	75 (95%)	4 (5%)	0	100	100
4	FG	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FH	79/137 (58%)	77 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	FI	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FJ	79/137 (58%)	75 (95%)	4 (5%)	0	100	100
4	FK	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FL	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FM	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FN	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FO	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FP	79/137 (58%)	75 (95%)	4 (5%)	0	100	100
4	FQ	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FR	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FS	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FT	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FU	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FV	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FW	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FX	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
4	FY	79/137 (58%)	76 (96%)	3 (4%)	0	100	100
All	All	30566/55624 (55%)	29108 (95%)	1330 (4%)	128 (0%)	31	67

5 of 128 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E1	126	ILE
4	E2	126	ILE
4	E3	126	ILE
4	E4	126	ILE
4	E5	126	ILE

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	A1	43/467 (9%)	43 (100%)	0	100	100
1	A2	43/467 (9%)	43 (100%)	0	100	100
1	A3	43/467 (9%)	43 (100%)	0	100	100
1	A4	43/467 (9%)	43 (100%)	0	100	100
1	A5	43/467 (9%)	43 (100%)	0	100	100
1	A6	43/467 (9%)	43 (100%)	0	100	100
1	A7	43/467 (9%)	43 (100%)	0	100	100
1	A8	43/467 (9%)	43 (100%)	0	100	100
1	A9	43/467 (9%)	43 (100%)	0	100	100
1	AA	43/467 (9%)	43 (100%)	0	100	100
1	AB	43/467 (9%)	43 (100%)	0	100	100
1	AC	43/467 (9%)	43 (100%)	0	100	100
1	AD	43/467 (9%)	43 (100%)	0	100	100
1	AE	43/467 (9%)	43 (100%)	0	100	100
1	AF	43/467 (9%)	43 (100%)	0	100	100
1	AG	43/467 (9%)	43 (100%)	0	100	100
1	AH	43/467 (9%)	43 (100%)	0	100	100
1	AI	43/467 (9%)	43 (100%)	0	100	100
1	AJ	43/467 (9%)	43 (100%)	0	100	100
1	AK	43/467 (9%)	43 (100%)	0	100	100
1	AL	43/467 (9%)	43 (100%)	0	100	100
1	AM	43/467 (9%)	43 (100%)	0	100	100
1	AN	43/467 (9%)	43 (100%)	0	100	100
1	AO	43/467 (9%)	43 (100%)	0	100	100
1	AP	43/467 (9%)	43 (100%)	0	100	100
1	AQ	43/467 (9%)	43 (100%)	0	100	100
1	AR	43/467 (9%)	43 (100%)	0	100	100
1	AS	43/467 (9%)	43 (100%)	0	100	100
1	AT	43/467 (9%)	43 (100%)	0	100	100
1	AU	43/467 (9%)	43 (100%)	0	100	100
1	AV	43/467 (9%)	43 (100%)	0	100	100
1	AW	43/467 (9%)	43 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AX	43/467 (9%)	43 (100%)	0	100	100
1	AY	43/467 (9%)	43 (100%)	0	100	100
2	B1	282/282 (100%)	282 (100%)	0	100	100
2	B2	282/282 (100%)	282 (100%)	0	100	100
2	B3	282/282 (100%)	282 (100%)	0	100	100
2	B4	282/282 (100%)	282 (100%)	0	100	100
2	B5	282/282 (100%)	282 (100%)	0	100	100
2	B6	282/282 (100%)	282 (100%)	0	100	100
2	B7	282/282 (100%)	282 (100%)	0	100	100
2	B8	282/282 (100%)	282 (100%)	0	100	100
2	B9	282/282 (100%)	282 (100%)	0	100	100
2	BA	282/282 (100%)	282 (100%)	0	100	100
2	BB	282/282 (100%)	282 (100%)	0	100	100
2	BC	282/282 (100%)	282 (100%)	0	100	100
2	BD	282/282 (100%)	282 (100%)	0	100	100
2	BE	282/282 (100%)	282 (100%)	0	100	100
2	BF	282/282 (100%)	282 (100%)	0	100	100
2	BG	282/282 (100%)	282 (100%)	0	100	100
2	BH	282/282 (100%)	282 (100%)	0	100	100
2	BI	282/282 (100%)	282 (100%)	0	100	100
2	BJ	282/282 (100%)	282 (100%)	0	100	100
2	BK	282/282 (100%)	282 (100%)	0	100	100
2	BL	282/282 (100%)	282 (100%)	0	100	100
2	BM	282/282 (100%)	282 (100%)	0	100	100
2	BN	282/282 (100%)	282 (100%)	0	100	100
2	BO	282/282 (100%)	282 (100%)	0	100	100
2	BP	282/282 (100%)	282 (100%)	0	100	100
2	BQ	282/282 (100%)	282 (100%)	0	100	100
2	BR	282/282 (100%)	282 (100%)	0	100	100
2	BS	282/282 (100%)	282 (100%)	0	100	100
2	BT	282/282 (100%)	282 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	BU	282/282 (100%)	282 (100%)	0	100	100
2	BV	282/282 (100%)	282 (100%)	0	100	100
2	BW	282/282 (100%)	282 (100%)	0	100	100
2	BX	282/282 (100%)	282 (100%)	0	100	100
2	BY	282/282 (100%)	282 (100%)	0	100	100
3	C1	263/301 (87%)	263 (100%)	0	100	100
3	C2	263/301 (87%)	263 (100%)	0	100	100
3	C3	263/301 (87%)	263 (100%)	0	100	100
3	C4	263/301 (87%)	263 (100%)	0	100	100
3	C5	263/301 (87%)	263 (100%)	0	100	100
3	C6	263/301 (87%)	263 (100%)	0	100	100
3	C7	263/301 (87%)	263 (100%)	0	100	100
3	C8	263/301 (87%)	263 (100%)	0	100	100
3	C9	263/301 (87%)	263 (100%)	0	100	100
3	CA	263/301 (87%)	263 (100%)	0	100	100
3	CB	263/301 (87%)	263 (100%)	0	100	100
3	CC	263/301 (87%)	263 (100%)	0	100	100
3	CD	263/301 (87%)	263 (100%)	0	100	100
3	CE	263/301 (87%)	263 (100%)	0	100	100
3	CF	263/301 (87%)	263 (100%)	0	100	100
3	CG	263/301 (87%)	263 (100%)	0	100	100
3	CH	263/301 (87%)	263 (100%)	0	100	100
3	CI	263/301 (87%)	263 (100%)	0	100	100
3	CJ	263/301 (87%)	263 (100%)	0	100	100
3	CK	263/301 (87%)	263 (100%)	0	100	100
3	CL	263/301 (87%)	263 (100%)	0	100	100
3	CM	263/301 (87%)	263 (100%)	0	100	100
3	CN	263/301 (87%)	263 (100%)	0	100	100
3	CO	263/301 (87%)	263 (100%)	0	100	100
3	CP	263/301 (87%)	263 (100%)	0	100	100
3	CQ	263/301 (87%)	263 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CR	263/301 (87%)	263 (100%)	0	100	100
3	CS	263/301 (87%)	263 (100%)	0	100	100
3	CT	263/301 (87%)	263 (100%)	0	100	100
3	CU	263/301 (87%)	263 (100%)	0	100	100
3	CV	263/301 (87%)	263 (100%)	0	100	100
3	CW	263/301 (87%)	263 (100%)	0	100	100
3	CX	263/301 (87%)	263 (100%)	0	100	100
3	CY	263/301 (87%)	263 (100%)	0	100	100
4	D1	70/113 (62%)	70 (100%)	0	100	100
4	D2	70/113 (62%)	70 (100%)	0	100	100
4	D3	70/113 (62%)	70 (100%)	0	100	100
4	D4	70/113 (62%)	70 (100%)	0	100	100
4	D5	70/113 (62%)	70 (100%)	0	100	100
4	D6	70/113 (62%)	70 (100%)	0	100	100
4	D7	70/113 (62%)	70 (100%)	0	100	100
4	D8	70/113 (62%)	70 (100%)	0	100	100
4	D9	70/113 (62%)	70 (100%)	0	100	100
4	DA	70/113 (62%)	70 (100%)	0	100	100
4	DB	70/113 (62%)	70 (100%)	0	100	100
4	DC	70/113 (62%)	70 (100%)	0	100	100
4	DD	70/113 (62%)	70 (100%)	0	100	100
4	DE	70/113 (62%)	70 (100%)	0	100	100
4	DF	70/113 (62%)	70 (100%)	0	100	100
4	DG	70/113 (62%)	70 (100%)	0	100	100
4	DH	70/113 (62%)	70 (100%)	0	100	100
4	DI	70/113 (62%)	70 (100%)	0	100	100
4	DJ	70/113 (62%)	70 (100%)	0	100	100
4	DK	70/113 (62%)	70 (100%)	0	100	100
4	DL	70/113 (62%)	70 (100%)	0	100	100
4	DM	70/113 (62%)	70 (100%)	0	100	100
4	DN	70/113 (62%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	DO	70/113 (62%)	70 (100%)	0	100	100
4	DP	70/113 (62%)	70 (100%)	0	100	100
4	DQ	70/113 (62%)	70 (100%)	0	100	100
4	DR	70/113 (62%)	70 (100%)	0	100	100
4	DS	70/113 (62%)	70 (100%)	0	100	100
4	DT	70/113 (62%)	70 (100%)	0	100	100
4	DU	70/113 (62%)	70 (100%)	0	100	100
4	DV	70/113 (62%)	70 (100%)	0	100	100
4	DW	70/113 (62%)	70 (100%)	0	100	100
4	DX	70/113 (62%)	70 (100%)	0	100	100
4	DY	70/113 (62%)	70 (100%)	0	100	100
4	E1	70/113 (62%)	70 (100%)	0	100	100
4	E2	70/113 (62%)	70 (100%)	0	100	100
4	E3	70/113 (62%)	70 (100%)	0	100	100
4	E4	70/113 (62%)	70 (100%)	0	100	100
4	E5	70/113 (62%)	70 (100%)	0	100	100
4	E6	70/113 (62%)	70 (100%)	0	100	100
4	E7	70/113 (62%)	70 (100%)	0	100	100
4	E8	70/113 (62%)	70 (100%)	0	100	100
4	E9	70/113 (62%)	70 (100%)	0	100	100
4	EA	70/113 (62%)	70 (100%)	0	100	100
4	EB	70/113 (62%)	70 (100%)	0	100	100
4	EC	70/113 (62%)	70 (100%)	0	100	100
4	ED	70/113 (62%)	70 (100%)	0	100	100
4	EE	70/113 (62%)	70 (100%)	0	100	100
4	EF	70/113 (62%)	70 (100%)	0	100	100
4	EG	70/113 (62%)	70 (100%)	0	100	100
4	EH	70/113 (62%)	70 (100%)	0	100	100
4	EI	70/113 (62%)	70 (100%)	0	100	100
4	EJ	70/113 (62%)	70 (100%)	0	100	100
4	EK	70/113 (62%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	EL	70/113 (62%)	70 (100%)	0	100	100
4	EM	70/113 (62%)	70 (100%)	0	100	100
4	EN	70/113 (62%)	70 (100%)	0	100	100
4	EO	70/113 (62%)	70 (100%)	0	100	100
4	EP	70/113 (62%)	70 (100%)	0	100	100
4	EQ	70/113 (62%)	70 (100%)	0	100	100
4	ER	70/113 (62%)	70 (100%)	0	100	100
4	ES	70/113 (62%)	70 (100%)	0	100	100
4	ET	70/113 (62%)	70 (100%)	0	100	100
4	EU	70/113 (62%)	70 (100%)	0	100	100
4	EV	70/113 (62%)	70 (100%)	0	100	100
4	EW	70/113 (62%)	70 (100%)	0	100	100
4	EX	70/113 (62%)	70 (100%)	0	100	100
4	EY	70/113 (62%)	70 (100%)	0	100	100
4	F1	70/113 (62%)	70 (100%)	0	100	100
4	F2	70/113 (62%)	70 (100%)	0	100	100
4	F3	70/113 (62%)	70 (100%)	0	100	100
4	F4	70/113 (62%)	70 (100%)	0	100	100
4	F5	70/113 (62%)	70 (100%)	0	100	100
4	F6	70/113 (62%)	70 (100%)	0	100	100
4	F7	70/113 (62%)	70 (100%)	0	100	100
4	F8	70/113 (62%)	70 (100%)	0	100	100
4	F9	70/113 (62%)	70 (100%)	0	100	100
4	FA	70/113 (62%)	70 (100%)	0	100	100
4	FB	70/113 (62%)	70 (100%)	0	100	100
4	FC	70/113 (62%)	70 (100%)	0	100	100
4	FD	70/113 (62%)	70 (100%)	0	100	100
4	FE	70/113 (62%)	70 (100%)	0	100	100
4	FF	70/113 (62%)	70 (100%)	0	100	100
4	FG	70/113 (62%)	70 (100%)	0	100	100
4	FH	70/113 (62%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	FI	70/113 (62%)	70 (100%)	0	100	100
4	FJ	70/113 (62%)	70 (100%)	0	100	100
4	FK	70/113 (62%)	70 (100%)	0	100	100
4	FL	70/113 (62%)	70 (100%)	0	100	100
4	FM	70/113 (62%)	70 (100%)	0	100	100
4	FN	70/113 (62%)	70 (100%)	0	100	100
4	FO	70/113 (62%)	70 (100%)	0	100	100
4	FP	70/113 (62%)	70 (100%)	0	100	100
4	FQ	70/113 (62%)	70 (100%)	0	100	100
4	FR	70/113 (62%)	70 (100%)	0	100	100
4	FS	70/113 (62%)	70 (100%)	0	100	100
4	FT	70/113 (62%)	70 (100%)	0	100	100
4	FU	70/113 (62%)	70 (100%)	0	100	100
4	FV	70/113 (62%)	70 (100%)	0	100	100
4	FW	70/113 (62%)	70 (100%)	0	100	100
4	FX	70/113 (62%)	70 (100%)	0	100	100
4	FY	70/113 (62%)	70 (100%)	0	100	100
All	All	27132/47226 (58%)	27132 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 438 such sidechains are listed below:

Mol	Chain	Res	Type
2	BI	70	ASN
3	CM	256	HIS
2	BW	51	GLN
3	CI	256	HIS
3	CK	173	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

This section contains visualisations of the EMDB entry EMD-42439. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.