wwPDB EM Validation Summary Report (i)

Mar 9, 2026 – 12:47 PM UTC

PDB ID	:	8Z4G / pdb_00008z4g
EMDB ID	:	EMD-39763
Title	:	Structure of the S-ring region of the Vibrio flagellar MS-ring protein FliF with 35-fold symmetry applied
Authors	:	Takekawa, N.; Nishikino, T.; Kishikawa, J.; Hirose, M.; Kato, T.; Imada, K.; Homma, M.
Deposited on	:	2024-04-17
Resolution	:	3.23 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 (i) 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 (i)) were used in the production of this report:

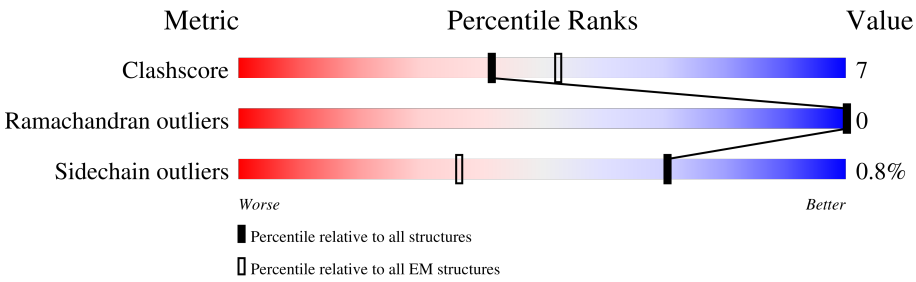
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

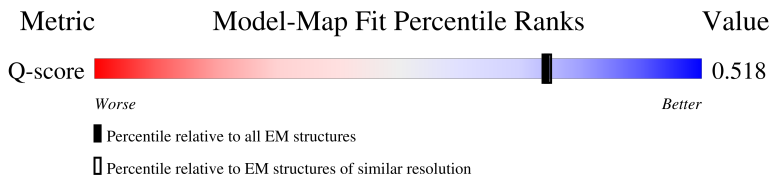
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.23 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14612 (2.73 - 3.73)

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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	945	13% • 85%
1	2	945	13% • 85%
1	3	945	13% • 85%
1	4	945	13% • 85%

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Mol	Chain	Length	Quality of chain
1	5	945	13% 85%
1	6	945	13% 85%
1	7	945	13% 85%
1	8	945	13% 85%
1	9	945	13% 85%
1	A	945	13% 85%
1	B	945	13% 85%
1	C	945	13% 85%
1	D	945	13% 85%
1	E	945	13% 85%
1	F	945	13% 85%
1	G	945	13% 85%
1	H	945	13% 85%
1	I	945	13% 85%
1	J	945	13% 85%
1	K	945	13% 85%
1	L	945	13% 85%
1	M	945	13% 85%
1	N	945	13% 85%
1	O	945	13% 85%
1	P	945	13% 85%
1	Q	945	13% 85%
1	R	945	13% 85%
1	S	945	13% 85%
1	T	945	13% 85%

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Mol	Chain	Length	Quality of chain
1	U	945	13% 85%
1	V	945	13% 85%
1	W	945	13% 85%
1	X	945	13% 85%
1	Y	945	13% 85%
1	Z	945	12% 85%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 40565 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,Flagellar motor switch protein FliG.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1	146	1159	713	210	234	2	0	0
1	2	146	1159	713	210	234	2	0	0
1	3	146	1159	713	210	234	2	0	0
1	4	146	1159	713	210	234	2	0	0
1	5	146	1159	713	210	234	2	0	0
1	6	146	1159	713	210	234	2	0	0
1	7	146	1159	713	210	234	2	0	0
1	8	146	1159	713	210	234	2	0	0
1	9	146	1159	713	210	234	2	0	0
1	A	146	1159	713	210	234	2	0	0
1	B	146	1159	713	210	234	2	0	0
1	C	146	1159	713	210	234	2	0	0
1	D	146	1159	713	210	234	2	0	0
1	E	146	1159	713	210	234	2	0	0
1	F	146	1159	713	210	234	2	0	0
1	G	146	1159	713	210	234	2	0	0
1	H	146	1159	713	210	234	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	I	146	1159	713	210	234	2	0	0
1	J	146	1159	713	210	234	2	0	0
1	K	146	1159	713	210	234	2	0	0
1	L	146	1159	713	210	234	2	0	0
1	M	146	1159	713	210	234	2	0	0
1	N	146	1159	713	210	234	2	0	0
1	O	146	1159	713	210	234	2	0	0
1	P	146	1159	713	210	234	2	0	0
1	Q	146	1159	713	210	234	2	0	0
1	R	146	1159	713	210	234	2	0	0
1	S	146	1159	713	210	234	2	0	0
1	T	146	1159	713	210	234	2	0	0
1	U	146	1159	713	210	234	2	0	0
1	V	146	1159	713	210	234	2	0	0
1	W	146	1159	713	210	234	2	0	0
1	X	146	1159	713	210	234	2	0	0
1	Y	146	1159	713	210	234	2	0	0
1	Z	146	1159	713	210	234	2	0	0

There are 595 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	-15	MET	-	initiating methionine	UNP Q75N27
1	-14	ASN	-	expression tag	UNP Q75N27
1	-13	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
1	-12	LYS	-	expression tag	UNP Q75N27
1	-11	VAL	-	expression tag	UNP Q75N27
1	-10	HIS	-	expression tag	UNP Q75N27
1	-9	HIS	-	expression tag	UNP Q75N27
1	-8	HIS	-	expression tag	UNP Q75N27
1	-7	HIS	-	expression tag	UNP Q75N27
1	-6	HIS	-	expression tag	UNP Q75N27
1	-5	HIS	-	expression tag	UNP Q75N27
1	-4	ILE	-	expression tag	UNP Q75N27
1	-3	GLU	-	expression tag	UNP Q75N27
1	-2	GLY	-	expression tag	UNP Q75N27
1	-1	ARG	-	expression tag	UNP Q75N27
1	0	HIS	-	expression tag	UNP Q75N27
1	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
2	-15	MET	-	initiating methionine	UNP Q75N27
2	-14	ASN	-	expression tag	UNP Q75N27
2	-13	HIS	-	expression tag	UNP Q75N27
2	-12	LYS	-	expression tag	UNP Q75N27
2	-11	VAL	-	expression tag	UNP Q75N27
2	-10	HIS	-	expression tag	UNP Q75N27
2	-9	HIS	-	expression tag	UNP Q75N27
2	-8	HIS	-	expression tag	UNP Q75N27
2	-7	HIS	-	expression tag	UNP Q75N27
2	-6	HIS	-	expression tag	UNP Q75N27
2	-5	HIS	-	expression tag	UNP Q75N27
2	-4	ILE	-	expression tag	UNP Q75N27
2	-3	GLU	-	expression tag	UNP Q75N27
2	-2	GLY	-	expression tag	UNP Q75N27
2	-1	ARG	-	expression tag	UNP Q75N27
2	0	HIS	-	expression tag	UNP Q75N27
2	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
3	-15	MET	-	initiating methionine	UNP Q75N27
3	-14	ASN	-	expression tag	UNP Q75N27
3	-13	HIS	-	expression tag	UNP Q75N27
3	-12	LYS	-	expression tag	UNP Q75N27
3	-11	VAL	-	expression tag	UNP Q75N27
3	-10	HIS	-	expression tag	UNP Q75N27
3	-9	HIS	-	expression tag	UNP Q75N27
3	-8	HIS	-	expression tag	UNP Q75N27
3	-7	HIS	-	expression tag	UNP Q75N27
3	-6	HIS	-	expression tag	UNP Q75N27
3	-5	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
3	-4	ILE	-	expression tag	UNP Q75N27
3	-3	GLU	-	expression tag	UNP Q75N27
3	-2	GLY	-	expression tag	UNP Q75N27
3	-1	ARG	-	expression tag	UNP Q75N27
3	0	HIS	-	expression tag	UNP Q75N27
3	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
4	-15	MET	-	initiating methionine	UNP Q75N27
4	-14	ASN	-	expression tag	UNP Q75N27
4	-13	HIS	-	expression tag	UNP Q75N27
4	-12	LYS	-	expression tag	UNP Q75N27
4	-11	VAL	-	expression tag	UNP Q75N27
4	-10	HIS	-	expression tag	UNP Q75N27
4	-9	HIS	-	expression tag	UNP Q75N27
4	-8	HIS	-	expression tag	UNP Q75N27
4	-7	HIS	-	expression tag	UNP Q75N27
4	-6	HIS	-	expression tag	UNP Q75N27
4	-5	HIS	-	expression tag	UNP Q75N27
4	-4	ILE	-	expression tag	UNP Q75N27
4	-3	GLU	-	expression tag	UNP Q75N27
4	-2	GLY	-	expression tag	UNP Q75N27
4	-1	ARG	-	expression tag	UNP Q75N27
4	0	HIS	-	expression tag	UNP Q75N27
4	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
5	-15	MET	-	initiating methionine	UNP Q75N27
5	-14	ASN	-	expression tag	UNP Q75N27
5	-13	HIS	-	expression tag	UNP Q75N27
5	-12	LYS	-	expression tag	UNP Q75N27
5	-11	VAL	-	expression tag	UNP Q75N27
5	-10	HIS	-	expression tag	UNP Q75N27
5	-9	HIS	-	expression tag	UNP Q75N27
5	-8	HIS	-	expression tag	UNP Q75N27
5	-7	HIS	-	expression tag	UNP Q75N27
5	-6	HIS	-	expression tag	UNP Q75N27
5	-5	HIS	-	expression tag	UNP Q75N27
5	-4	ILE	-	expression tag	UNP Q75N27
5	-3	GLU	-	expression tag	UNP Q75N27
5	-2	GLY	-	expression tag	UNP Q75N27
5	-1	ARG	-	expression tag	UNP Q75N27
5	0	HIS	-	expression tag	UNP Q75N27
5	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
6	-15	MET	-	initiating methionine	UNP Q75N27
6	-14	ASN	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
6	-13	HIS	-	expression tag	UNP Q75N27
6	-12	LYS	-	expression tag	UNP Q75N27
6	-11	VAL	-	expression tag	UNP Q75N27
6	-10	HIS	-	expression tag	UNP Q75N27
6	-9	HIS	-	expression tag	UNP Q75N27
6	-8	HIS	-	expression tag	UNP Q75N27
6	-7	HIS	-	expression tag	UNP Q75N27
6	-6	HIS	-	expression tag	UNP Q75N27
6	-5	HIS	-	expression tag	UNP Q75N27
6	-4	ILE	-	expression tag	UNP Q75N27
6	-3	GLU	-	expression tag	UNP Q75N27
6	-2	GLY	-	expression tag	UNP Q75N27
6	-1	ARG	-	expression tag	UNP Q75N27
6	0	HIS	-	expression tag	UNP Q75N27
6	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
7	-15	MET	-	initiating methionine	UNP Q75N27
7	-14	ASN	-	expression tag	UNP Q75N27
7	-13	HIS	-	expression tag	UNP Q75N27
7	-12	LYS	-	expression tag	UNP Q75N27
7	-11	VAL	-	expression tag	UNP Q75N27
7	-10	HIS	-	expression tag	UNP Q75N27
7	-9	HIS	-	expression tag	UNP Q75N27
7	-8	HIS	-	expression tag	UNP Q75N27
7	-7	HIS	-	expression tag	UNP Q75N27
7	-6	HIS	-	expression tag	UNP Q75N27
7	-5	HIS	-	expression tag	UNP Q75N27
7	-4	ILE	-	expression tag	UNP Q75N27
7	-3	GLU	-	expression tag	UNP Q75N27
7	-2	GLY	-	expression tag	UNP Q75N27
7	-1	ARG	-	expression tag	UNP Q75N27
7	0	HIS	-	expression tag	UNP Q75N27
7	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
8	-15	MET	-	initiating methionine	UNP Q75N27
8	-14	ASN	-	expression tag	UNP Q75N27
8	-13	HIS	-	expression tag	UNP Q75N27
8	-12	LYS	-	expression tag	UNP Q75N27
8	-11	VAL	-	expression tag	UNP Q75N27
8	-10	HIS	-	expression tag	UNP Q75N27
8	-9	HIS	-	expression tag	UNP Q75N27
8	-8	HIS	-	expression tag	UNP Q75N27
8	-7	HIS	-	expression tag	UNP Q75N27
8	-6	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
8	-5	HIS	-	expression tag	UNP Q75N27
8	-4	ILE	-	expression tag	UNP Q75N27
8	-3	GLU	-	expression tag	UNP Q75N27
8	-2	GLY	-	expression tag	UNP Q75N27
8	-1	ARG	-	expression tag	UNP Q75N27
8	0	HIS	-	expression tag	UNP Q75N27
8	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
9	-15	MET	-	initiating methionine	UNP Q75N27
9	-14	ASN	-	expression tag	UNP Q75N27
9	-13	HIS	-	expression tag	UNP Q75N27
9	-12	LYS	-	expression tag	UNP Q75N27
9	-11	VAL	-	expression tag	UNP Q75N27
9	-10	HIS	-	expression tag	UNP Q75N27
9	-9	HIS	-	expression tag	UNP Q75N27
9	-8	HIS	-	expression tag	UNP Q75N27
9	-7	HIS	-	expression tag	UNP Q75N27
9	-6	HIS	-	expression tag	UNP Q75N27
9	-5	HIS	-	expression tag	UNP Q75N27
9	-4	ILE	-	expression tag	UNP Q75N27
9	-3	GLU	-	expression tag	UNP Q75N27
9	-2	GLY	-	expression tag	UNP Q75N27
9	-1	ARG	-	expression tag	UNP Q75N27
9	0	HIS	-	expression tag	UNP Q75N27
9	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
A	-15	MET	-	initiating methionine	UNP Q75N27
A	-14	ASN	-	expression tag	UNP Q75N27
A	-13	HIS	-	expression tag	UNP Q75N27
A	-12	LYS	-	expression tag	UNP Q75N27
A	-11	VAL	-	expression tag	UNP Q75N27
A	-10	HIS	-	expression tag	UNP Q75N27
A	-9	HIS	-	expression tag	UNP Q75N27
A	-8	HIS	-	expression tag	UNP Q75N27
A	-7	HIS	-	expression tag	UNP Q75N27
A	-6	HIS	-	expression tag	UNP Q75N27
A	-5	HIS	-	expression tag	UNP Q75N27
A	-4	ILE	-	expression tag	UNP Q75N27
A	-3	GLU	-	expression tag	UNP Q75N27
A	-2	GLY	-	expression tag	UNP Q75N27
A	-1	ARG	-	expression tag	UNP Q75N27
A	0	HIS	-	expression tag	UNP Q75N27
A	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
B	-15	MET	-	initiating methionine	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	ASN	-	expression tag	UNP Q75N27
B	-13	HIS	-	expression tag	UNP Q75N27
B	-12	LYS	-	expression tag	UNP Q75N27
B	-11	VAL	-	expression tag	UNP Q75N27
B	-10	HIS	-	expression tag	UNP Q75N27
B	-9	HIS	-	expression tag	UNP Q75N27
B	-8	HIS	-	expression tag	UNP Q75N27
B	-7	HIS	-	expression tag	UNP Q75N27
B	-6	HIS	-	expression tag	UNP Q75N27
B	-5	HIS	-	expression tag	UNP Q75N27
B	-4	ILE	-	expression tag	UNP Q75N27
B	-3	GLU	-	expression tag	UNP Q75N27
B	-2	GLY	-	expression tag	UNP Q75N27
B	-1	ARG	-	expression tag	UNP Q75N27
B	0	HIS	-	expression tag	UNP Q75N27
B	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
C	-15	MET	-	initiating methionine	UNP Q75N27
C	-14	ASN	-	expression tag	UNP Q75N27
C	-13	HIS	-	expression tag	UNP Q75N27
C	-12	LYS	-	expression tag	UNP Q75N27
C	-11	VAL	-	expression tag	UNP Q75N27
C	-10	HIS	-	expression tag	UNP Q75N27
C	-9	HIS	-	expression tag	UNP Q75N27
C	-8	HIS	-	expression tag	UNP Q75N27
C	-7	HIS	-	expression tag	UNP Q75N27
C	-6	HIS	-	expression tag	UNP Q75N27
C	-5	HIS	-	expression tag	UNP Q75N27
C	-4	ILE	-	expression tag	UNP Q75N27
C	-3	GLU	-	expression tag	UNP Q75N27
C	-2	GLY	-	expression tag	UNP Q75N27
C	-1	ARG	-	expression tag	UNP Q75N27
C	0	HIS	-	expression tag	UNP Q75N27
C	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
D	-15	MET	-	initiating methionine	UNP Q75N27
D	-14	ASN	-	expression tag	UNP Q75N27
D	-13	HIS	-	expression tag	UNP Q75N27
D	-12	LYS	-	expression tag	UNP Q75N27
D	-11	VAL	-	expression tag	UNP Q75N27
D	-10	HIS	-	expression tag	UNP Q75N27
D	-9	HIS	-	expression tag	UNP Q75N27
D	-8	HIS	-	expression tag	UNP Q75N27
D	-7	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	HIS	-	expression tag	UNP Q75N27
D	-5	HIS	-	expression tag	UNP Q75N27
D	-4	ILE	-	expression tag	UNP Q75N27
D	-3	GLU	-	expression tag	UNP Q75N27
D	-2	GLY	-	expression tag	UNP Q75N27
D	-1	ARG	-	expression tag	UNP Q75N27
D	0	HIS	-	expression tag	UNP Q75N27
D	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
E	-15	MET	-	initiating methionine	UNP Q75N27
E	-14	ASN	-	expression tag	UNP Q75N27
E	-13	HIS	-	expression tag	UNP Q75N27
E	-12	LYS	-	expression tag	UNP Q75N27
E	-11	VAL	-	expression tag	UNP Q75N27
E	-10	HIS	-	expression tag	UNP Q75N27
E	-9	HIS	-	expression tag	UNP Q75N27
E	-8	HIS	-	expression tag	UNP Q75N27
E	-7	HIS	-	expression tag	UNP Q75N27
E	-6	HIS	-	expression tag	UNP Q75N27
E	-5	HIS	-	expression tag	UNP Q75N27
E	-4	ILE	-	expression tag	UNP Q75N27
E	-3	GLU	-	expression tag	UNP Q75N27
E	-2	GLY	-	expression tag	UNP Q75N27
E	-1	ARG	-	expression tag	UNP Q75N27
E	0	HIS	-	expression tag	UNP Q75N27
E	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
F	-15	MET	-	initiating methionine	UNP Q75N27
F	-14	ASN	-	expression tag	UNP Q75N27
F	-13	HIS	-	expression tag	UNP Q75N27
F	-12	LYS	-	expression tag	UNP Q75N27
F	-11	VAL	-	expression tag	UNP Q75N27
F	-10	HIS	-	expression tag	UNP Q75N27
F	-9	HIS	-	expression tag	UNP Q75N27
F	-8	HIS	-	expression tag	UNP Q75N27
F	-7	HIS	-	expression tag	UNP Q75N27
F	-6	HIS	-	expression tag	UNP Q75N27
F	-5	HIS	-	expression tag	UNP Q75N27
F	-4	ILE	-	expression tag	UNP Q75N27
F	-3	GLU	-	expression tag	UNP Q75N27
F	-2	GLY	-	expression tag	UNP Q75N27
F	-1	ARG	-	expression tag	UNP Q75N27
F	0	HIS	-	expression tag	UNP Q75N27
F	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-15	MET	-	initiating methionine	UNP Q75N27
G	-14	ASN	-	expression tag	UNP Q75N27
G	-13	HIS	-	expression tag	UNP Q75N27
G	-12	LYS	-	expression tag	UNP Q75N27
G	-11	VAL	-	expression tag	UNP Q75N27
G	-10	HIS	-	expression tag	UNP Q75N27
G	-9	HIS	-	expression tag	UNP Q75N27
G	-8	HIS	-	expression tag	UNP Q75N27
G	-7	HIS	-	expression tag	UNP Q75N27
G	-6	HIS	-	expression tag	UNP Q75N27
G	-5	HIS	-	expression tag	UNP Q75N27
G	-4	ILE	-	expression tag	UNP Q75N27
G	-3	GLU	-	expression tag	UNP Q75N27
G	-2	GLY	-	expression tag	UNP Q75N27
G	-1	ARG	-	expression tag	UNP Q75N27
G	0	HIS	-	expression tag	UNP Q75N27
G	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
H	-15	MET	-	initiating methionine	UNP Q75N27
H	-14	ASN	-	expression tag	UNP Q75N27
H	-13	HIS	-	expression tag	UNP Q75N27
H	-12	LYS	-	expression tag	UNP Q75N27
H	-11	VAL	-	expression tag	UNP Q75N27
H	-10	HIS	-	expression tag	UNP Q75N27
H	-9	HIS	-	expression tag	UNP Q75N27
H	-8	HIS	-	expression tag	UNP Q75N27
H	-7	HIS	-	expression tag	UNP Q75N27
H	-6	HIS	-	expression tag	UNP Q75N27
H	-5	HIS	-	expression tag	UNP Q75N27
H	-4	ILE	-	expression tag	UNP Q75N27
H	-3	GLU	-	expression tag	UNP Q75N27
H	-2	GLY	-	expression tag	UNP Q75N27
H	-1	ARG	-	expression tag	UNP Q75N27
H	0	HIS	-	expression tag	UNP Q75N27
H	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
I	-15	MET	-	initiating methionine	UNP Q75N27
I	-14	ASN	-	expression tag	UNP Q75N27
I	-13	HIS	-	expression tag	UNP Q75N27
I	-12	LYS	-	expression tag	UNP Q75N27
I	-11	VAL	-	expression tag	UNP Q75N27
I	-10	HIS	-	expression tag	UNP Q75N27
I	-9	HIS	-	expression tag	UNP Q75N27
I	-8	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-7	HIS	-	expression tag	UNP Q75N27
I	-6	HIS	-	expression tag	UNP Q75N27
I	-5	HIS	-	expression tag	UNP Q75N27
I	-4	ILE	-	expression tag	UNP Q75N27
I	-3	GLU	-	expression tag	UNP Q75N27
I	-2	GLY	-	expression tag	UNP Q75N27
I	-1	ARG	-	expression tag	UNP Q75N27
I	0	HIS	-	expression tag	UNP Q75N27
I	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
J	-15	MET	-	initiating methionine	UNP Q75N27
J	-14	ASN	-	expression tag	UNP Q75N27
J	-13	HIS	-	expression tag	UNP Q75N27
J	-12	LYS	-	expression tag	UNP Q75N27
J	-11	VAL	-	expression tag	UNP Q75N27
J	-10	HIS	-	expression tag	UNP Q75N27
J	-9	HIS	-	expression tag	UNP Q75N27
J	-8	HIS	-	expression tag	UNP Q75N27
J	-7	HIS	-	expression tag	UNP Q75N27
J	-6	HIS	-	expression tag	UNP Q75N27
J	-5	HIS	-	expression tag	UNP Q75N27
J	-4	ILE	-	expression tag	UNP Q75N27
J	-3	GLU	-	expression tag	UNP Q75N27
J	-2	GLY	-	expression tag	UNP Q75N27
J	-1	ARG	-	expression tag	UNP Q75N27
J	0	HIS	-	expression tag	UNP Q75N27
J	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
K	-15	MET	-	initiating methionine	UNP Q75N27
K	-14	ASN	-	expression tag	UNP Q75N27
K	-13	HIS	-	expression tag	UNP Q75N27
K	-12	LYS	-	expression tag	UNP Q75N27
K	-11	VAL	-	expression tag	UNP Q75N27
K	-10	HIS	-	expression tag	UNP Q75N27
K	-9	HIS	-	expression tag	UNP Q75N27
K	-8	HIS	-	expression tag	UNP Q75N27
K	-7	HIS	-	expression tag	UNP Q75N27
K	-6	HIS	-	expression tag	UNP Q75N27
K	-5	HIS	-	expression tag	UNP Q75N27
K	-4	ILE	-	expression tag	UNP Q75N27
K	-3	GLU	-	expression tag	UNP Q75N27
K	-2	GLY	-	expression tag	UNP Q75N27
K	-1	ARG	-	expression tag	UNP Q75N27
K	0	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
K	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
L	-15	MET	-	initiating methionine	UNP Q75N27
L	-14	ASN	-	expression tag	UNP Q75N27
L	-13	HIS	-	expression tag	UNP Q75N27
L	-12	LYS	-	expression tag	UNP Q75N27
L	-11	VAL	-	expression tag	UNP Q75N27
L	-10	HIS	-	expression tag	UNP Q75N27
L	-9	HIS	-	expression tag	UNP Q75N27
L	-8	HIS	-	expression tag	UNP Q75N27
L	-7	HIS	-	expression tag	UNP Q75N27
L	-6	HIS	-	expression tag	UNP Q75N27
L	-5	HIS	-	expression tag	UNP Q75N27
L	-4	ILE	-	expression tag	UNP Q75N27
L	-3	GLU	-	expression tag	UNP Q75N27
L	-2	GLY	-	expression tag	UNP Q75N27
L	-1	ARG	-	expression tag	UNP Q75N27
L	0	HIS	-	expression tag	UNP Q75N27
L	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
M	-15	MET	-	initiating methionine	UNP Q75N27
M	-14	ASN	-	expression tag	UNP Q75N27
M	-13	HIS	-	expression tag	UNP Q75N27
M	-12	LYS	-	expression tag	UNP Q75N27
M	-11	VAL	-	expression tag	UNP Q75N27
M	-10	HIS	-	expression tag	UNP Q75N27
M	-9	HIS	-	expression tag	UNP Q75N27
M	-8	HIS	-	expression tag	UNP Q75N27
M	-7	HIS	-	expression tag	UNP Q75N27
M	-6	HIS	-	expression tag	UNP Q75N27
M	-5	HIS	-	expression tag	UNP Q75N27
M	-4	ILE	-	expression tag	UNP Q75N27
M	-3	GLU	-	expression tag	UNP Q75N27
M	-2	GLY	-	expression tag	UNP Q75N27
M	-1	ARG	-	expression tag	UNP Q75N27
M	0	HIS	-	expression tag	UNP Q75N27
M	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
N	-15	MET	-	initiating methionine	UNP Q75N27
N	-14	ASN	-	expression tag	UNP Q75N27
N	-13	HIS	-	expression tag	UNP Q75N27
N	-12	LYS	-	expression tag	UNP Q75N27
N	-11	VAL	-	expression tag	UNP Q75N27
N	-10	HIS	-	expression tag	UNP Q75N27
N	-9	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
N	-8	HIS	-	expression tag	UNP Q75N27
N	-7	HIS	-	expression tag	UNP Q75N27
N	-6	HIS	-	expression tag	UNP Q75N27
N	-5	HIS	-	expression tag	UNP Q75N27
N	-4	ILE	-	expression tag	UNP Q75N27
N	-3	GLU	-	expression tag	UNP Q75N27
N	-2	GLY	-	expression tag	UNP Q75N27
N	-1	ARG	-	expression tag	UNP Q75N27
N	0	HIS	-	expression tag	UNP Q75N27
N	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
O	-15	MET	-	initiating methionine	UNP Q75N27
O	-14	ASN	-	expression tag	UNP Q75N27
O	-13	HIS	-	expression tag	UNP Q75N27
O	-12	LYS	-	expression tag	UNP Q75N27
O	-11	VAL	-	expression tag	UNP Q75N27
O	-10	HIS	-	expression tag	UNP Q75N27
O	-9	HIS	-	expression tag	UNP Q75N27
O	-8	HIS	-	expression tag	UNP Q75N27
O	-7	HIS	-	expression tag	UNP Q75N27
O	-6	HIS	-	expression tag	UNP Q75N27
O	-5	HIS	-	expression tag	UNP Q75N27
O	-4	ILE	-	expression tag	UNP Q75N27
O	-3	GLU	-	expression tag	UNP Q75N27
O	-2	GLY	-	expression tag	UNP Q75N27
O	-1	ARG	-	expression tag	UNP Q75N27
O	0	HIS	-	expression tag	UNP Q75N27
O	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
P	-15	MET	-	initiating methionine	UNP Q75N27
P	-14	ASN	-	expression tag	UNP Q75N27
P	-13	HIS	-	expression tag	UNP Q75N27
P	-12	LYS	-	expression tag	UNP Q75N27
P	-11	VAL	-	expression tag	UNP Q75N27
P	-10	HIS	-	expression tag	UNP Q75N27
P	-9	HIS	-	expression tag	UNP Q75N27
P	-8	HIS	-	expression tag	UNP Q75N27
P	-7	HIS	-	expression tag	UNP Q75N27
P	-6	HIS	-	expression tag	UNP Q75N27
P	-5	HIS	-	expression tag	UNP Q75N27
P	-4	ILE	-	expression tag	UNP Q75N27
P	-3	GLU	-	expression tag	UNP Q75N27
P	-2	GLY	-	expression tag	UNP Q75N27
P	-1	ARG	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
P	0	HIS	-	expression tag	UNP Q75N27
P	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
Q	-15	MET	-	initiating methionine	UNP Q75N27
Q	-14	ASN	-	expression tag	UNP Q75N27
Q	-13	HIS	-	expression tag	UNP Q75N27
Q	-12	LYS	-	expression tag	UNP Q75N27
Q	-11	VAL	-	expression tag	UNP Q75N27
Q	-10	HIS	-	expression tag	UNP Q75N27
Q	-9	HIS	-	expression tag	UNP Q75N27
Q	-8	HIS	-	expression tag	UNP Q75N27
Q	-7	HIS	-	expression tag	UNP Q75N27
Q	-6	HIS	-	expression tag	UNP Q75N27
Q	-5	HIS	-	expression tag	UNP Q75N27
Q	-4	ILE	-	expression tag	UNP Q75N27
Q	-3	GLU	-	expression tag	UNP Q75N27
Q	-2	GLY	-	expression tag	UNP Q75N27
Q	-1	ARG	-	expression tag	UNP Q75N27
Q	0	HIS	-	expression tag	UNP Q75N27
Q	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
R	-15	MET	-	initiating methionine	UNP Q75N27
R	-14	ASN	-	expression tag	UNP Q75N27
R	-13	HIS	-	expression tag	UNP Q75N27
R	-12	LYS	-	expression tag	UNP Q75N27
R	-11	VAL	-	expression tag	UNP Q75N27
R	-10	HIS	-	expression tag	UNP Q75N27
R	-9	HIS	-	expression tag	UNP Q75N27
R	-8	HIS	-	expression tag	UNP Q75N27
R	-7	HIS	-	expression tag	UNP Q75N27
R	-6	HIS	-	expression tag	UNP Q75N27
R	-5	HIS	-	expression tag	UNP Q75N27
R	-4	ILE	-	expression tag	UNP Q75N27
R	-3	GLU	-	expression tag	UNP Q75N27
R	-2	GLY	-	expression tag	UNP Q75N27
R	-1	ARG	-	expression tag	UNP Q75N27
R	0	HIS	-	expression tag	UNP Q75N27
R	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
S	-15	MET	-	initiating methionine	UNP Q75N27
S	-14	ASN	-	expression tag	UNP Q75N27
S	-13	HIS	-	expression tag	UNP Q75N27
S	-12	LYS	-	expression tag	UNP Q75N27
S	-11	VAL	-	expression tag	UNP Q75N27
S	-10	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
S	-9	HIS	-	expression tag	UNP Q75N27
S	-8	HIS	-	expression tag	UNP Q75N27
S	-7	HIS	-	expression tag	UNP Q75N27
S	-6	HIS	-	expression tag	UNP Q75N27
S	-5	HIS	-	expression tag	UNP Q75N27
S	-4	ILE	-	expression tag	UNP Q75N27
S	-3	GLU	-	expression tag	UNP Q75N27
S	-2	GLY	-	expression tag	UNP Q75N27
S	-1	ARG	-	expression tag	UNP Q75N27
S	0	HIS	-	expression tag	UNP Q75N27
S	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
T	-15	MET	-	initiating methionine	UNP Q75N27
T	-14	ASN	-	expression tag	UNP Q75N27
T	-13	HIS	-	expression tag	UNP Q75N27
T	-12	LYS	-	expression tag	UNP Q75N27
T	-11	VAL	-	expression tag	UNP Q75N27
T	-10	HIS	-	expression tag	UNP Q75N27
T	-9	HIS	-	expression tag	UNP Q75N27
T	-8	HIS	-	expression tag	UNP Q75N27
T	-7	HIS	-	expression tag	UNP Q75N27
T	-6	HIS	-	expression tag	UNP Q75N27
T	-5	HIS	-	expression tag	UNP Q75N27
T	-4	ILE	-	expression tag	UNP Q75N27
T	-3	GLU	-	expression tag	UNP Q75N27
T	-2	GLY	-	expression tag	UNP Q75N27
T	-1	ARG	-	expression tag	UNP Q75N27
T	0	HIS	-	expression tag	UNP Q75N27
T	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
U	-15	MET	-	initiating methionine	UNP Q75N27
U	-14	ASN	-	expression tag	UNP Q75N27
U	-13	HIS	-	expression tag	UNP Q75N27
U	-12	LYS	-	expression tag	UNP Q75N27
U	-11	VAL	-	expression tag	UNP Q75N27
U	-10	HIS	-	expression tag	UNP Q75N27
U	-9	HIS	-	expression tag	UNP Q75N27
U	-8	HIS	-	expression tag	UNP Q75N27
U	-7	HIS	-	expression tag	UNP Q75N27
U	-6	HIS	-	expression tag	UNP Q75N27
U	-5	HIS	-	expression tag	UNP Q75N27
U	-4	ILE	-	expression tag	UNP Q75N27
U	-3	GLU	-	expression tag	UNP Q75N27
U	-2	GLY	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
U	-1	ARG	-	expression tag	UNP Q75N27
U	0	HIS	-	expression tag	UNP Q75N27
U	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
V	-15	MET	-	initiating methionine	UNP Q75N27
V	-14	ASN	-	expression tag	UNP Q75N27
V	-13	HIS	-	expression tag	UNP Q75N27
V	-12	LYS	-	expression tag	UNP Q75N27
V	-11	VAL	-	expression tag	UNP Q75N27
V	-10	HIS	-	expression tag	UNP Q75N27
V	-9	HIS	-	expression tag	UNP Q75N27
V	-8	HIS	-	expression tag	UNP Q75N27
V	-7	HIS	-	expression tag	UNP Q75N27
V	-6	HIS	-	expression tag	UNP Q75N27
V	-5	HIS	-	expression tag	UNP Q75N27
V	-4	ILE	-	expression tag	UNP Q75N27
V	-3	GLU	-	expression tag	UNP Q75N27
V	-2	GLY	-	expression tag	UNP Q75N27
V	-1	ARG	-	expression tag	UNP Q75N27
V	0	HIS	-	expression tag	UNP Q75N27
V	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
W	-15	MET	-	initiating methionine	UNP Q75N27
W	-14	ASN	-	expression tag	UNP Q75N27
W	-13	HIS	-	expression tag	UNP Q75N27
W	-12	LYS	-	expression tag	UNP Q75N27
W	-11	VAL	-	expression tag	UNP Q75N27
W	-10	HIS	-	expression tag	UNP Q75N27
W	-9	HIS	-	expression tag	UNP Q75N27
W	-8	HIS	-	expression tag	UNP Q75N27
W	-7	HIS	-	expression tag	UNP Q75N27
W	-6	HIS	-	expression tag	UNP Q75N27
W	-5	HIS	-	expression tag	UNP Q75N27
W	-4	ILE	-	expression tag	UNP Q75N27
W	-3	GLU	-	expression tag	UNP Q75N27
W	-2	GLY	-	expression tag	UNP Q75N27
W	-1	ARG	-	expression tag	UNP Q75N27
W	0	HIS	-	expression tag	UNP Q75N27
W	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
X	-15	MET	-	initiating methionine	UNP Q75N27
X	-14	ASN	-	expression tag	UNP Q75N27
X	-13	HIS	-	expression tag	UNP Q75N27
X	-12	LYS	-	expression tag	UNP Q75N27
X	-11	VAL	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
X	-10	HIS	-	expression tag	UNP Q75N27
X	-9	HIS	-	expression tag	UNP Q75N27
X	-8	HIS	-	expression tag	UNP Q75N27
X	-7	HIS	-	expression tag	UNP Q75N27
X	-6	HIS	-	expression tag	UNP Q75N27
X	-5	HIS	-	expression tag	UNP Q75N27
X	-4	ILE	-	expression tag	UNP Q75N27
X	-3	GLU	-	expression tag	UNP Q75N27
X	-2	GLY	-	expression tag	UNP Q75N27
X	-1	ARG	-	expression tag	UNP Q75N27
X	0	HIS	-	expression tag	UNP Q75N27
X	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
Y	-15	MET	-	initiating methionine	UNP Q75N27
Y	-14	ASN	-	expression tag	UNP Q75N27
Y	-13	HIS	-	expression tag	UNP Q75N27
Y	-12	LYS	-	expression tag	UNP Q75N27
Y	-11	VAL	-	expression tag	UNP Q75N27
Y	-10	HIS	-	expression tag	UNP Q75N27
Y	-9	HIS	-	expression tag	UNP Q75N27
Y	-8	HIS	-	expression tag	UNP Q75N27
Y	-7	HIS	-	expression tag	UNP Q75N27
Y	-6	HIS	-	expression tag	UNP Q75N27
Y	-5	HIS	-	expression tag	UNP Q75N27
Y	-4	ILE	-	expression tag	UNP Q75N27
Y	-3	GLU	-	expression tag	UNP Q75N27
Y	-2	GLY	-	expression tag	UNP Q75N27
Y	-1	ARG	-	expression tag	UNP Q75N27
Y	0	HIS	-	expression tag	UNP Q75N27
Y	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
Z	-15	MET	-	initiating methionine	UNP Q75N27
Z	-14	ASN	-	expression tag	UNP Q75N27
Z	-13	HIS	-	expression tag	UNP Q75N27
Z	-12	LYS	-	expression tag	UNP Q75N27
Z	-11	VAL	-	expression tag	UNP Q75N27
Z	-10	HIS	-	expression tag	UNP Q75N27
Z	-9	HIS	-	expression tag	UNP Q75N27
Z	-8	HIS	-	expression tag	UNP Q75N27
Z	-7	HIS	-	expression tag	UNP Q75N27
Z	-6	HIS	-	expression tag	UNP Q75N27
Z	-5	HIS	-	expression tag	UNP Q75N27
Z	-4	ILE	-	expression tag	UNP Q75N27
Z	-3	GLU	-	expression tag	UNP Q75N27

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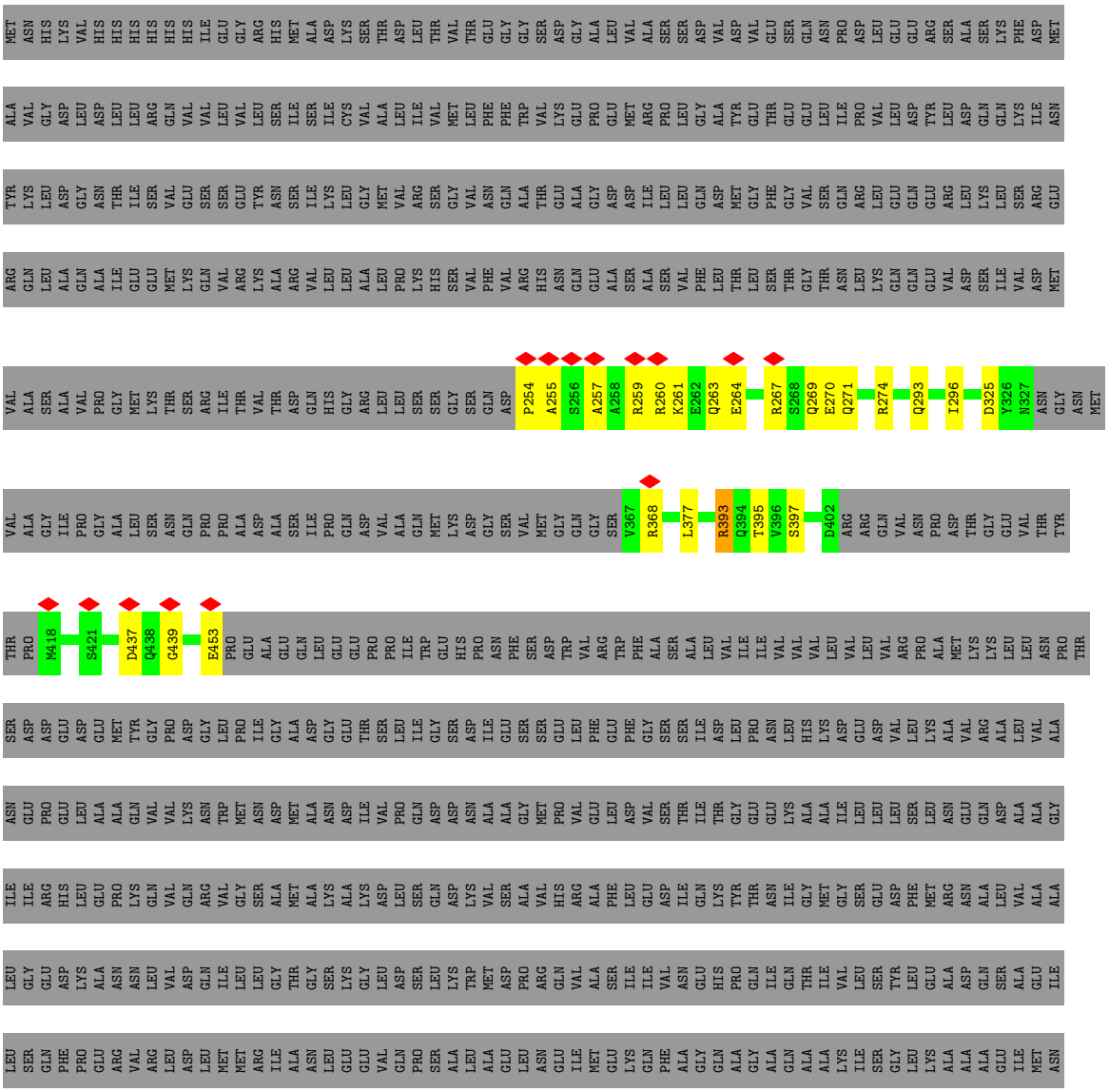
Chain	Residue	Modelled	Actual	Comment	Reference
Z	-2	GLY	-	expression tag	UNP Q75N27
Z	-1	ARG	-	expression tag	UNP Q75N27
Z	0	HIS	-	expression tag	UNP Q75N27
Z	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0

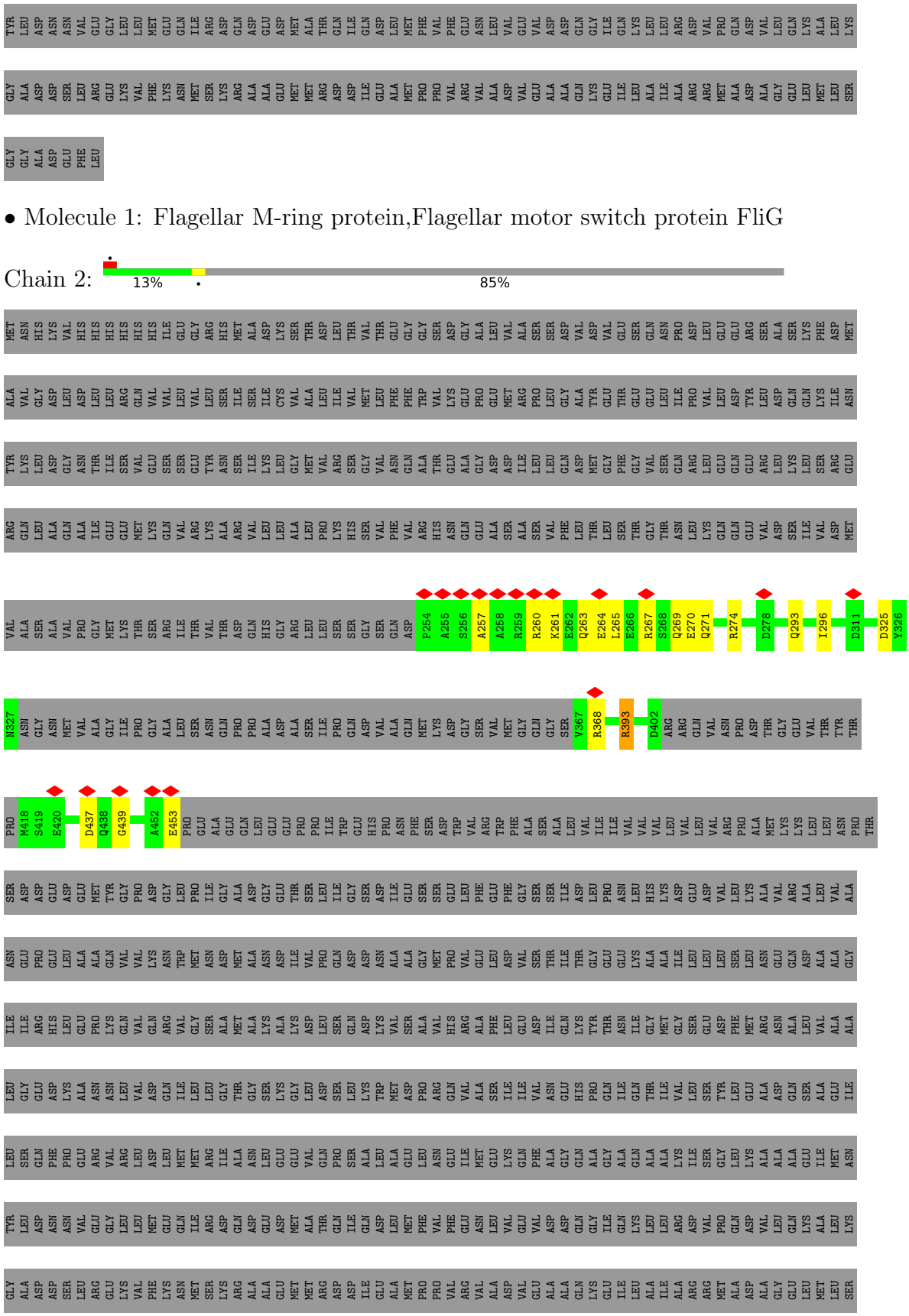
3 Residue-property plots (i)

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

- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

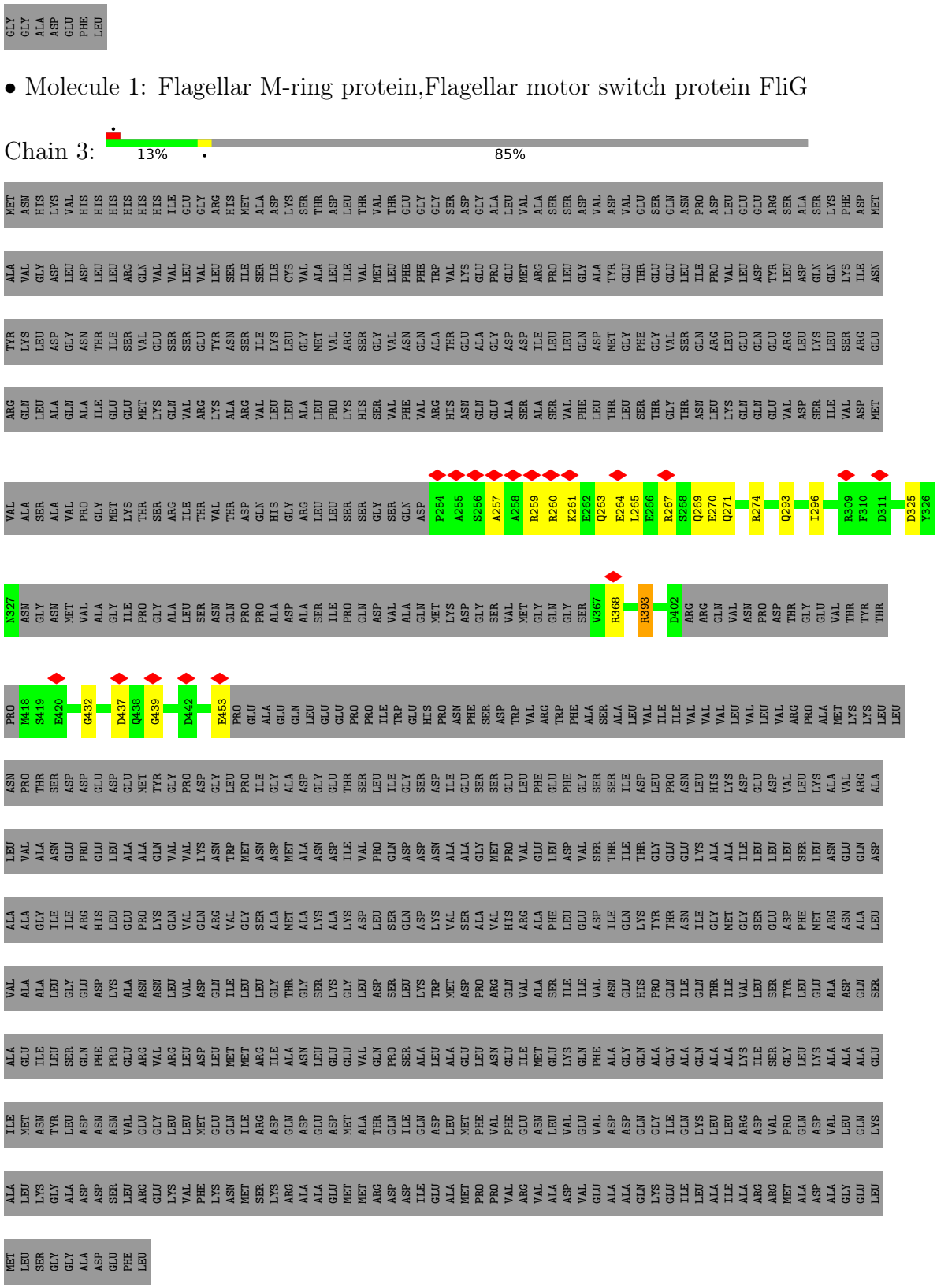
Chain 1:

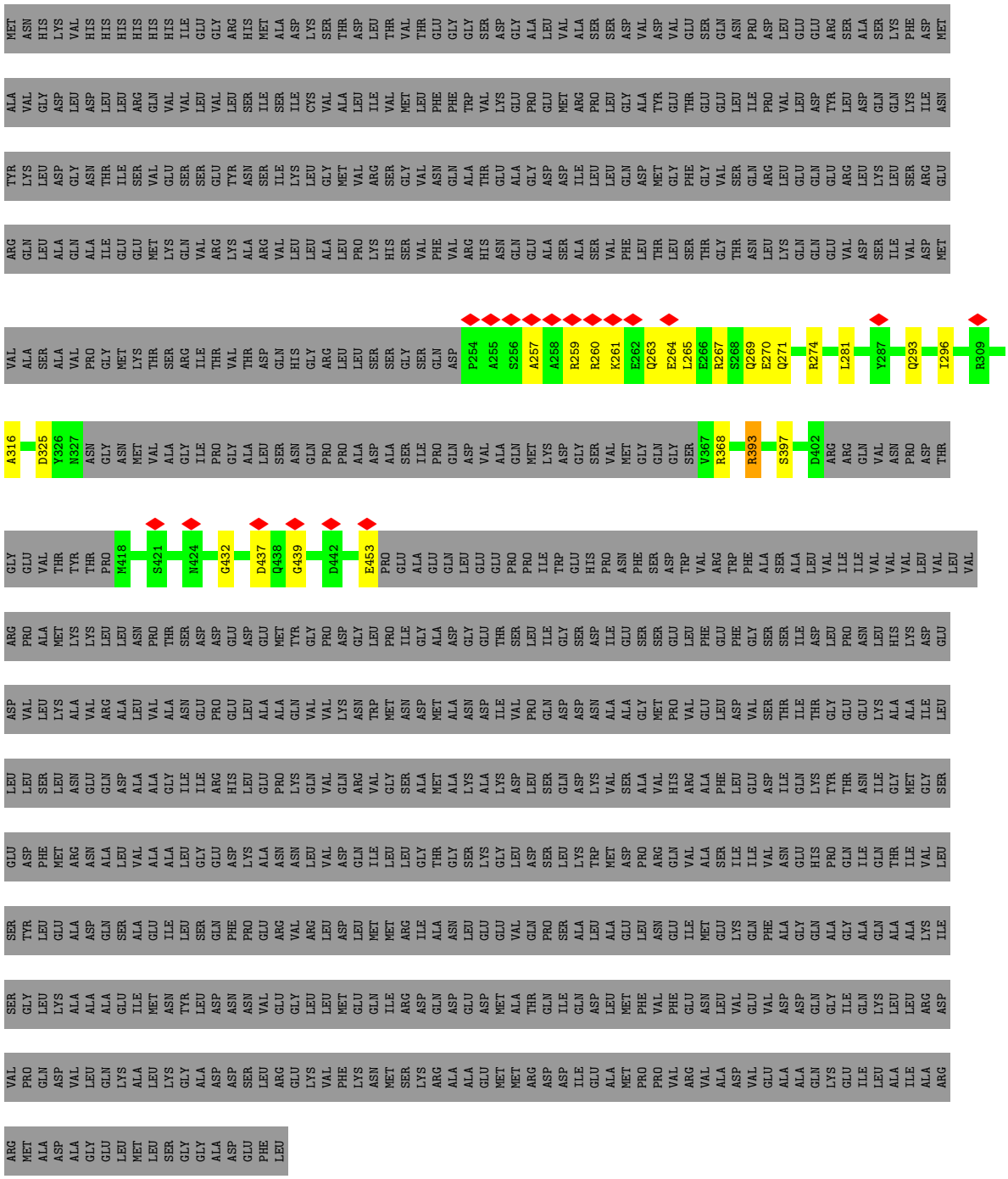




• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

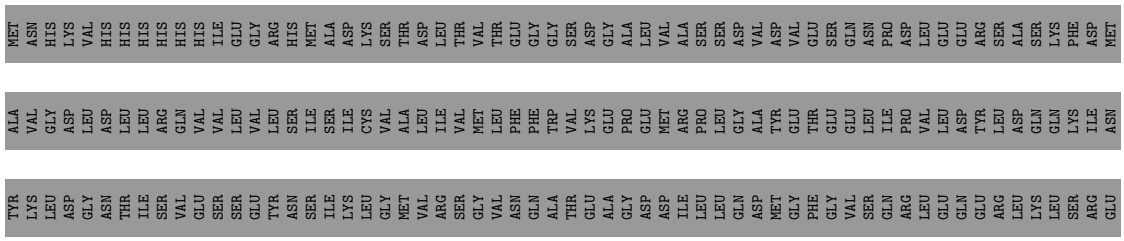
Chain 2: 13% 85%

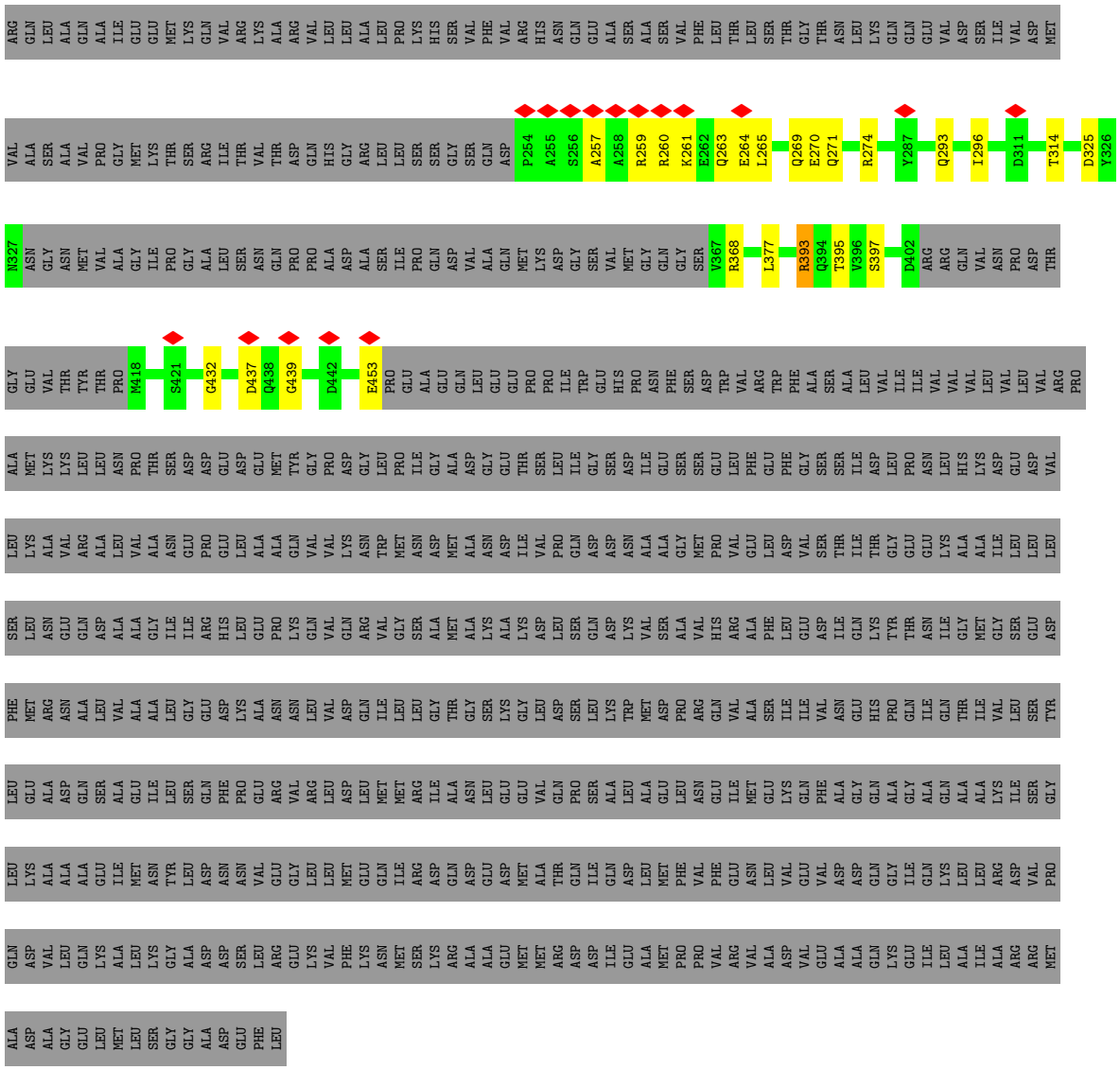

GLY GLY ALA ASP GLU PHE LEU
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG
Chain 3:
13%
85%
MET ASN HIS LYS VAL HIS HIS HIS HIS HIS ILE GLU GLY ARG HIS MET ALA ASP LYS SER THR ASP LEU THR VAL THR GLU GLY GLY SER ASP GLY ALA LEU VAL ALA SER SER ASP VAL ASP VAL GLU SER GLN ASN PRO ASP LEU GLU GLU ARG SER ALA SER LYS PHE ASP MET
ALA VAL GLY ASP LEU ASP LEU LEU ARG GLN VAL VAL LEU VAL LEU SER ILE SER ILE LYS VAL ALA LEU ILE VAL MET LEU PHE PHE TRP VAL LYS GLU PRO GLU MET ARG PRO LEU GLY ALA TYR GLU THR GLU GLU LEU ILE PRO VAL LEU ASP TYR LEU ASP GLN GLN LYS ILE ASN
TYR LYS LEU ASP GLY ASN THR ILE SER VAL GLU SER SER GLU TYR ASN SER ILE LYS LEU GLY MET VAL ARG SER GLY VAL ASN GLN ALA THR GLU ALA GLY ASP ASP ILE LEU LEU GLN ASP MET GLY PHE GLY VAL SER GLN ARG LEU GLU GLN GLU ARG LEU LYS LEU SER ARG GLU
ARG GLN LEU ALA GLN ALA ILE GLU GLU MET LYS GLN VAL ARG LYS ALA ARG VAL LEU LEU ALA LEU PRO LYS HIS SER VAL PHE VAL ARG HIS ASN GLN GLU ALA SER ALA SER VAL PHE LEU THR LEU SER THR GLY THR ASN LEU LYS GLN GLN GLU VAL ASP SER ILE VAL ASP MET
VAL ALA SER ALA VAL PRO GLY MET LYS THR SER ARG ILE THR VAL THR ASP GLN HIS GLY ARG LEU LEU SER SER GLY SER GLN ASP P254 A255 S256 A257 A258 R259 R260 K261 E262 Q263 E264 L265 E266 R267 S268 Q269 E270 Q271 R274 Q293 I296 R309 F310 D311 D325 Y326
N327 ASN GLY ASN MET VAL ALA GLY ILE PRO GLY ALA LEU SER ASN GLN PRO PRO ALA ASP ALA SER ILE PRO GLN ASP VAL ALA GLN MET LYS ASP GLY SER VAL MET GLY GLN GLY SER V367 R368 R393 D402 ARG ARG GLN VAL ASN PRO ASP THR GLY GLU VAL THR TYR THR
PRO M418 S419 E420 G432 D437 G438 G439 D442 E453 PRO GLU ALA GLU GLN LEU GLU GLU PRO PRO ILE TRP GLU HIS PRO ASN PHE SER ASP TRP VAL ARG TRP PHE ALA SER ALA LEU VAL ILE ILE VAL VAL VAL LEU VAL LEU VAL ARG PRO ALA MET LYS LYS LEU LEU
ASN PRO THR SER ASP ASP GLU ASP GLU MET TYR GLY PRO ASP GLY LEU PRO ILE GLY ALA ASP GLY GLU THR SER LEU ILE GLY SER ASP ILE GLU SER SER GLU LEU PHE GLU PHE GLY SER SER ILE ASP LEU PRO ASN LEU HIS LYS ASP GLU ASP VAL LEU LYS ALA VAL ARG ALA
LEU VAL ALA ASN GLU PRO GLU GLU LEU ALA ALA GLN VAL VAL LYS ASN TRP MET ASN ASP MET ALA ASN ASP ILE VAL PRO GLN ASP ASP ASN ALA ALA GLY MET PRO VAL GLU LEU PHE GLU PHE GLY SER THR ILE THR GLY GLU GLU LYS ALA ALA ILE LEU LEU LEU SER LEU ASN GLU GLN ASP
ALA ALA GLY ILE ILE ARG HIS LEU GLU PRO LYS GLN VAL GLN ARG VAL GLY SER ALA MET ALA LYS ASP LEU SER GLN ASP LYS VAL SER ALA VAL HIS ARG ALA PHE LEU GLU ASP ILE GLN LYS TYR THR ASN ILE GLY MET GLY SER GLU ASP PHE MET ARG ASN ALA LEU
VAL ALA ALA LEU GLY GLU ASP LYS ASN ALA ASN LEU VAL ASP GLN ILE LEU LEU GLY THR GLY SER LYS GLY LEU ASP SER LEU LYS TRP MET ASP PRO ARG GLN VAL ALA SER ILE ILE VAL ASN GLU HIS PRO GLN ILE GLN THR ILE VAL LEU SER TYR LEU GLU ALA ASP GLN SER
ALA GLU ILE LEU SER GLN PHE PRO GLU ARG VAL ARG LEU ASP LEU MET MET ARG ILE ALA ASN LEU GLU GLU VAL GLN PRO SER ALA LEU ALA GLU LEU ASN GLU ILE MET GLU LYS GLN PHE ALA GLY GLN ALA GLY ALA ALA GLN ALA ALA LYS ILE SER GLY LEU LYS ALA ALA ALA GLU
ILE MET ASN TYR LEU ASP ASN ASN VAL GLU GLY LEU LEU MET GLU GLN ILE ARG ASP GLN ASP GLU ASP MET ALA THR GLN ILE GLN ASP LEU MET PHE VAL PHE GLU ASN LEU VAL GLU VAL ASP ASP GLN GLY ILE GLN LYS LEU LEU ALA LEU ARG ASP VAL PRO GLN ASP VAL LEU GLN LYS
ALA LEU LYS GLY ALA ASP ASP SER LEU ARG GLU LYS VAL PHE LYS ASN MET SER LYS ARG ALA ALA GLU MET MET ARG ASP ASP ILE GLU ALA MET PRO PRO VAL ARG VAL ALA ASP VAL GLU ALA ALA GLN LYS GLU ILE LEU ALA ILE ALA ARG ARG MET ALA ASP ALA GLY GLU LEU
MET LEU SER GLY GLY ALA ASP GLU PHE LEU
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG
Chain 4:
13%
85%



- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

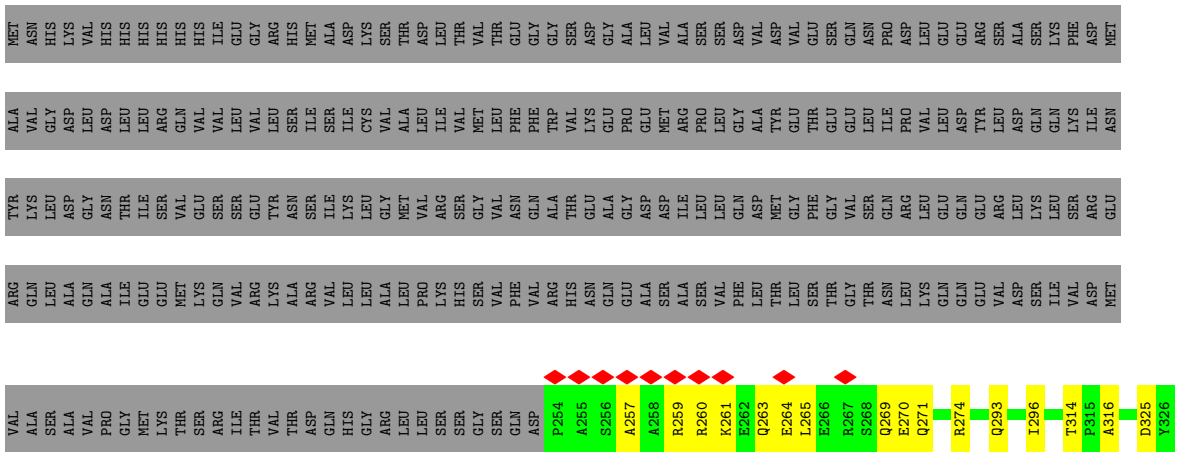
Chain 5:

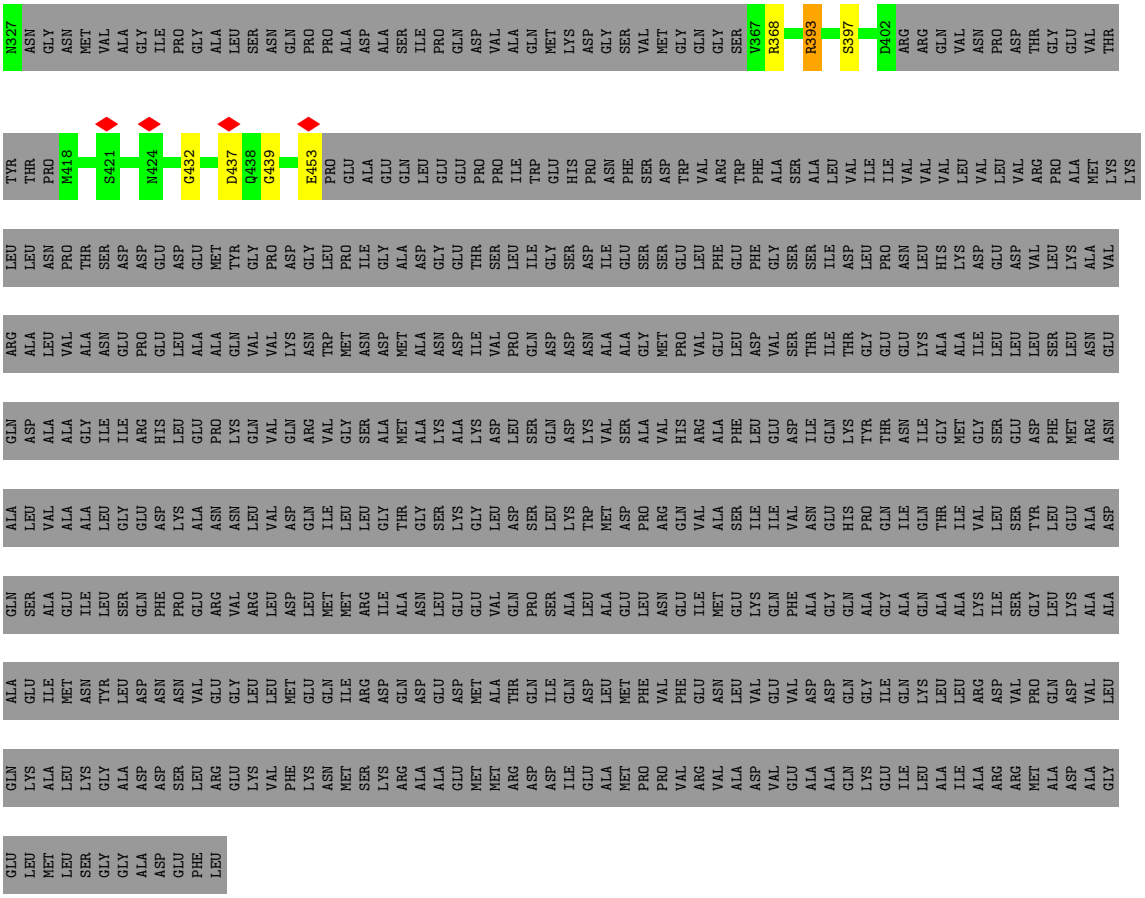




• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

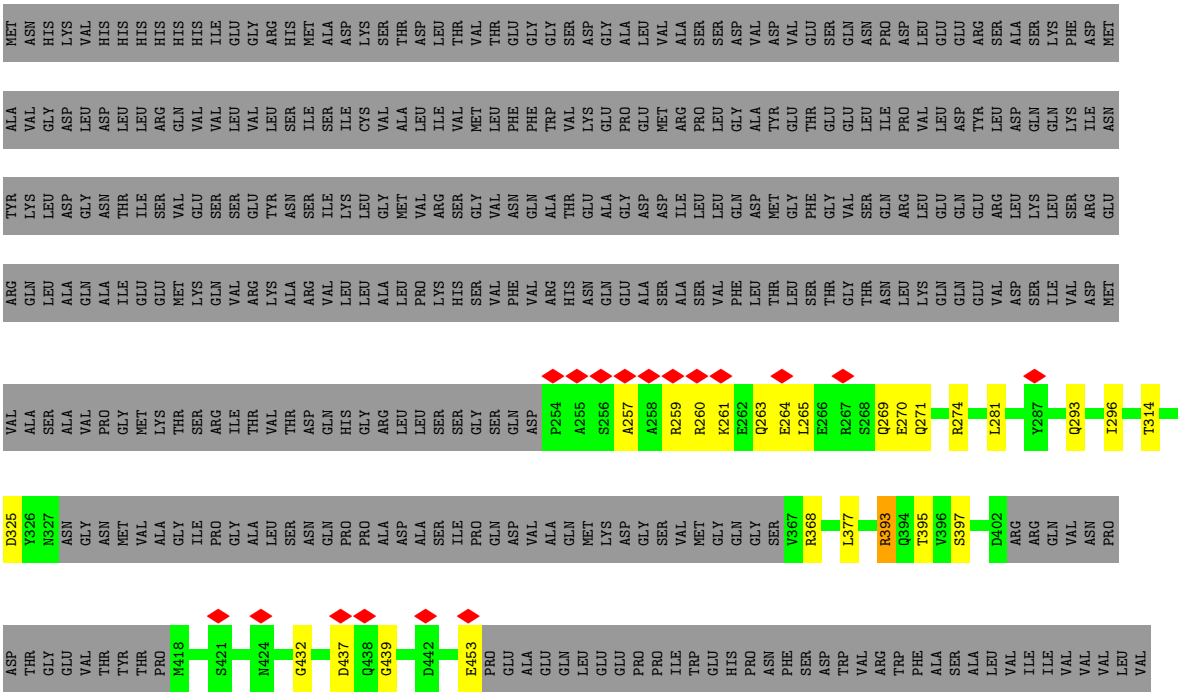
Chain 6:

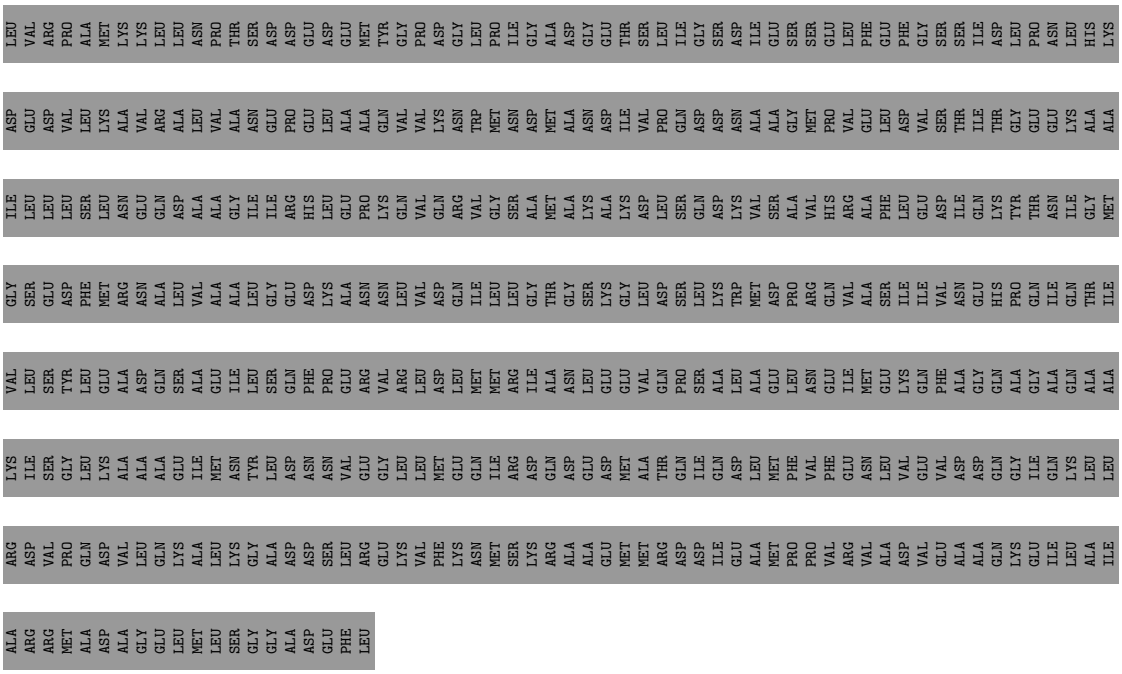




• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

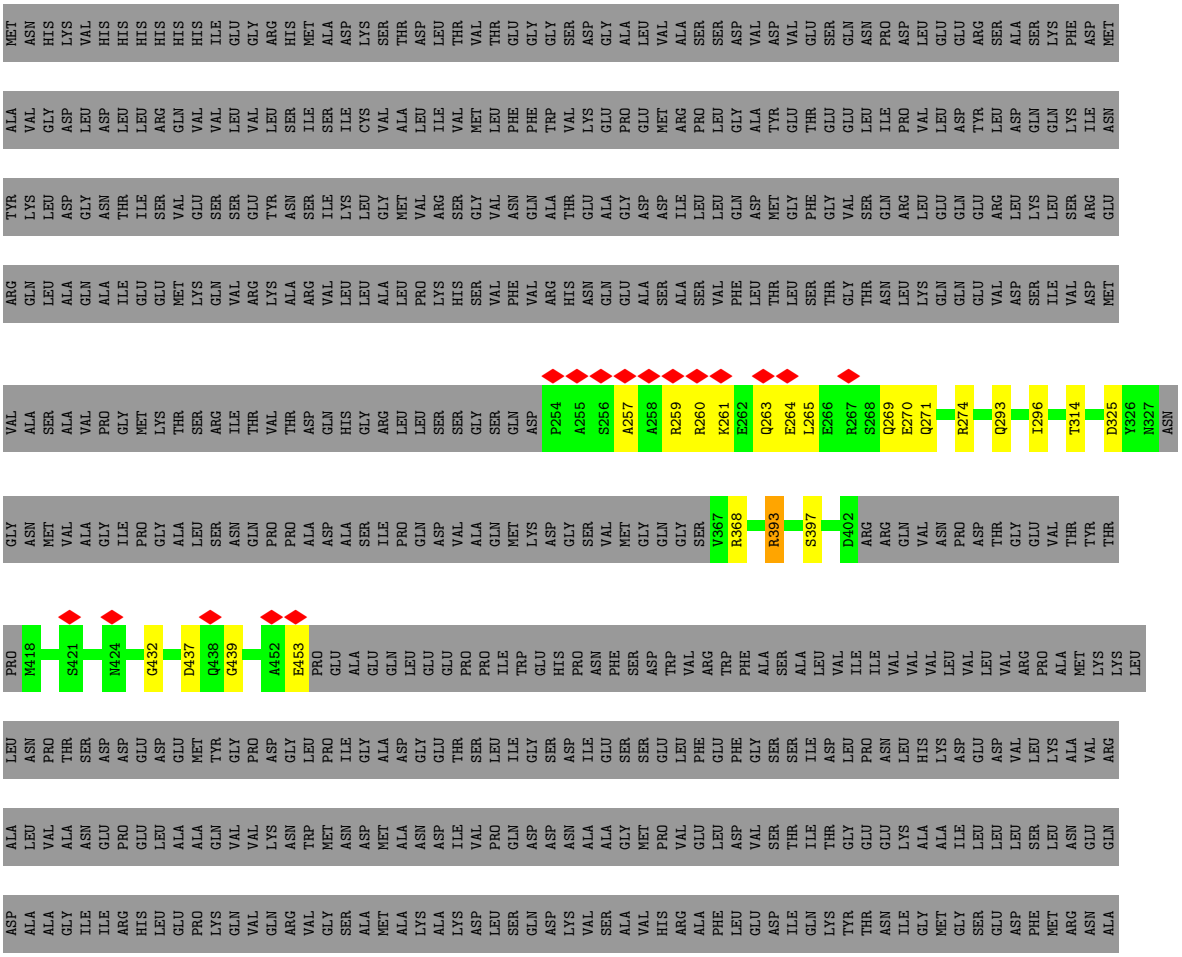
Chain 7: 13% 85%

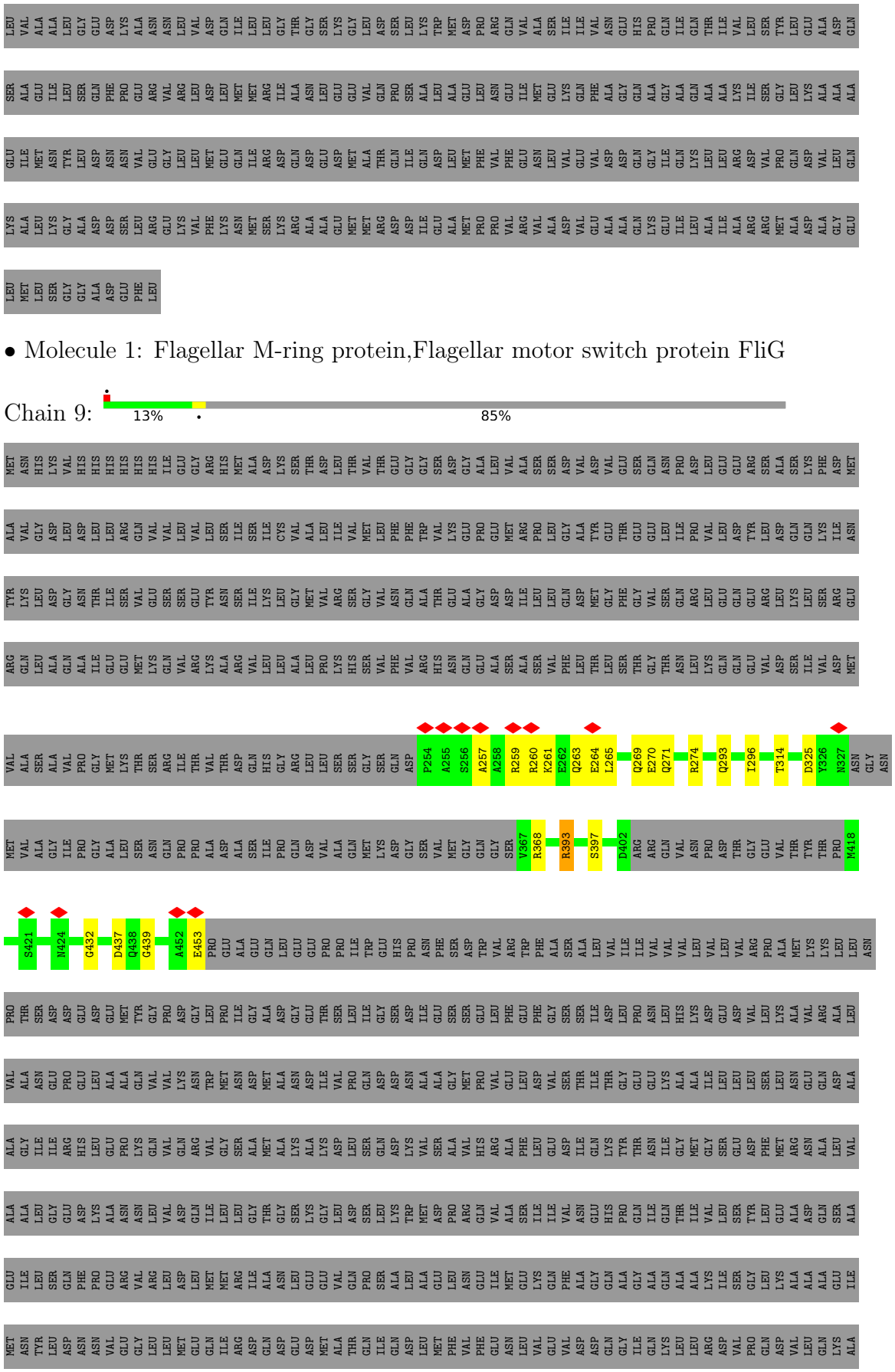




- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

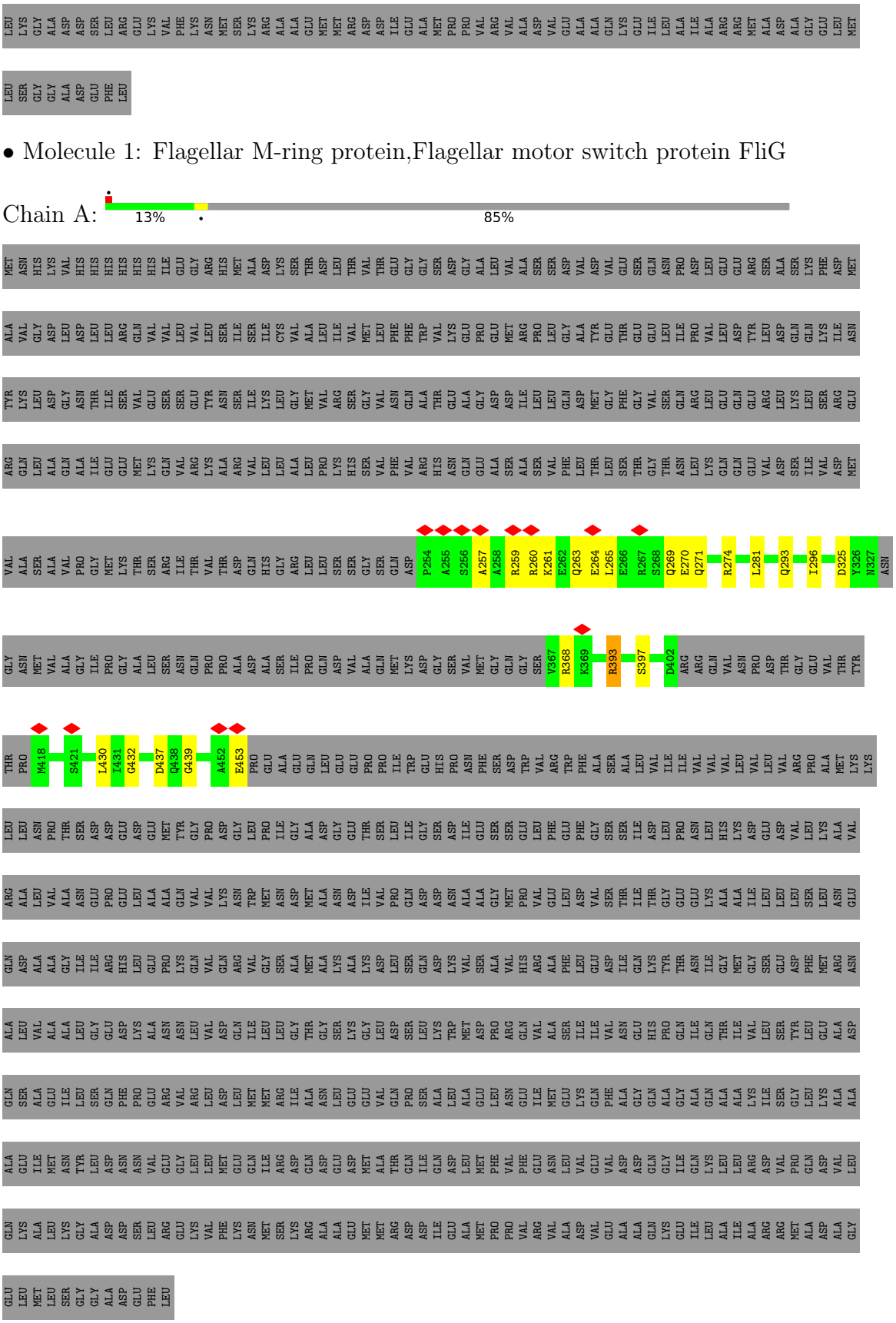
Chain 8:





• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain 9:



• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain A: 13% 85%

• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain B: 13% 85%

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

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

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

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

VAL ALA SER ALA VAL PRO GLY MET LYS THR SER ARG ILE THR VAL THR ASP GLN HIS GLY ARG LEU LEU SER SER GLY SER GLN ASP P254 A255 S256 A257 A258 R259 R260 K261 E262 Q263 E264 L265 Q269 E270 Q271 R274 Q293 I296 D325 Y326 N327 ASN GLY ASN MET VAL

ALA GLY ILE PRO GLY ALA LEU SER ASN GLN PRO PRO ALA ASP ALA SER ILE PRO GLN ASP VAL ALA GLN MET LYS ASP GLY SER VAL MET GLY GLN GLY SER V367 R368 R393 S397 D402 ARG ARG GLN VAL ASN PRO ASP THR GLY GLU VAL THR TYR THR PRO M418 S421

G432 D437 Q438 G439 E453 PRO GLU ALA GLU GLN LEU GLU GLU PRO PRO ILE TRP GLU HIS PRO ASN PHE SER ASP TRP VAL ARG TRP PHE ALA SER ALA LEU VAL ILE ILE VAL VAL VAL LEU VAL LEU VAL ARG PRO ALA MET LYS LYS LEU LEU ASN PRO THR SER ASP ASP

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

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

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

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

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

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

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

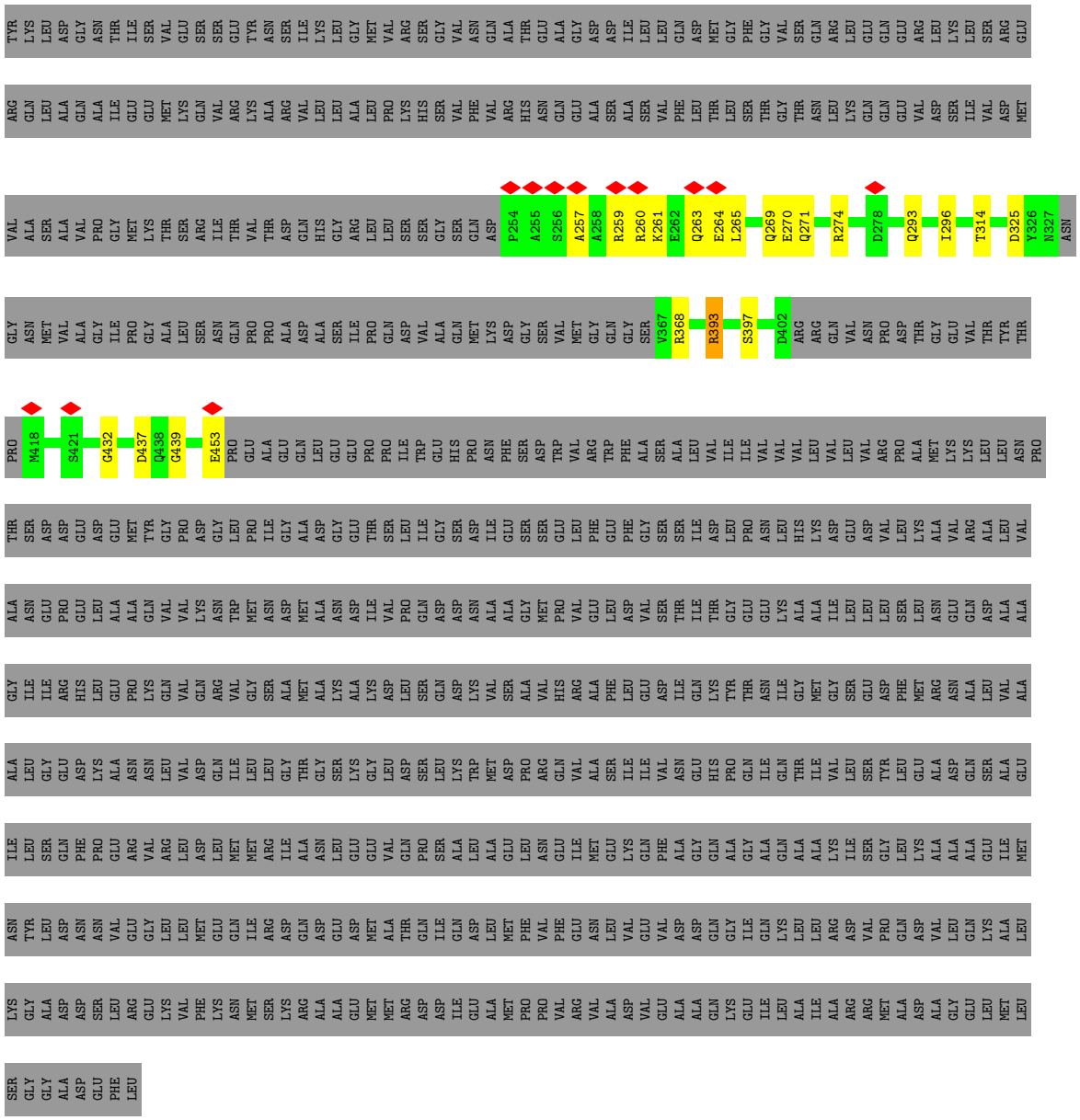
ASP GLU PHE LEU

- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain C: 13% 85%

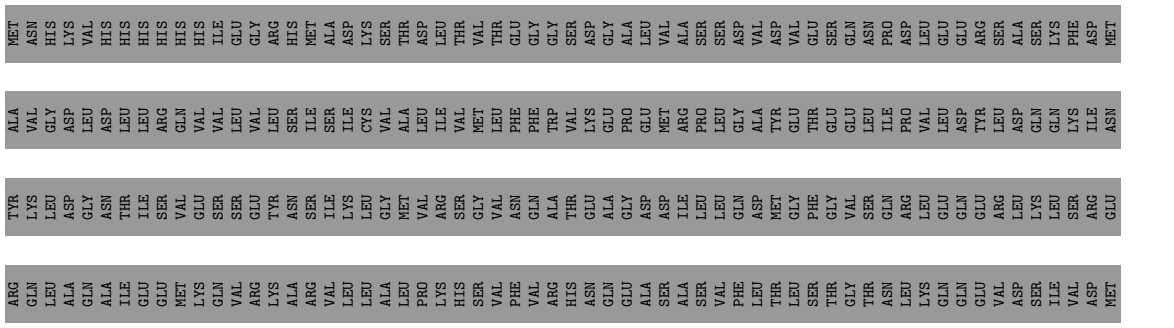
MET ASN HIS LYS VAL HIS HIS HIS HIS HIS ILE GLU GLY ARG HIS MET ALA ASP LYS SER THR ASP LEU THR VAL THR GLU GLY GLY SER ASP GLY ALA LEU VAL ALA SER SER ASP VAL ASP VAL GLU SER GLN ASN PRO ASP LEU GLU GLU ARG SER ALA SER LYS PHE ASP MET

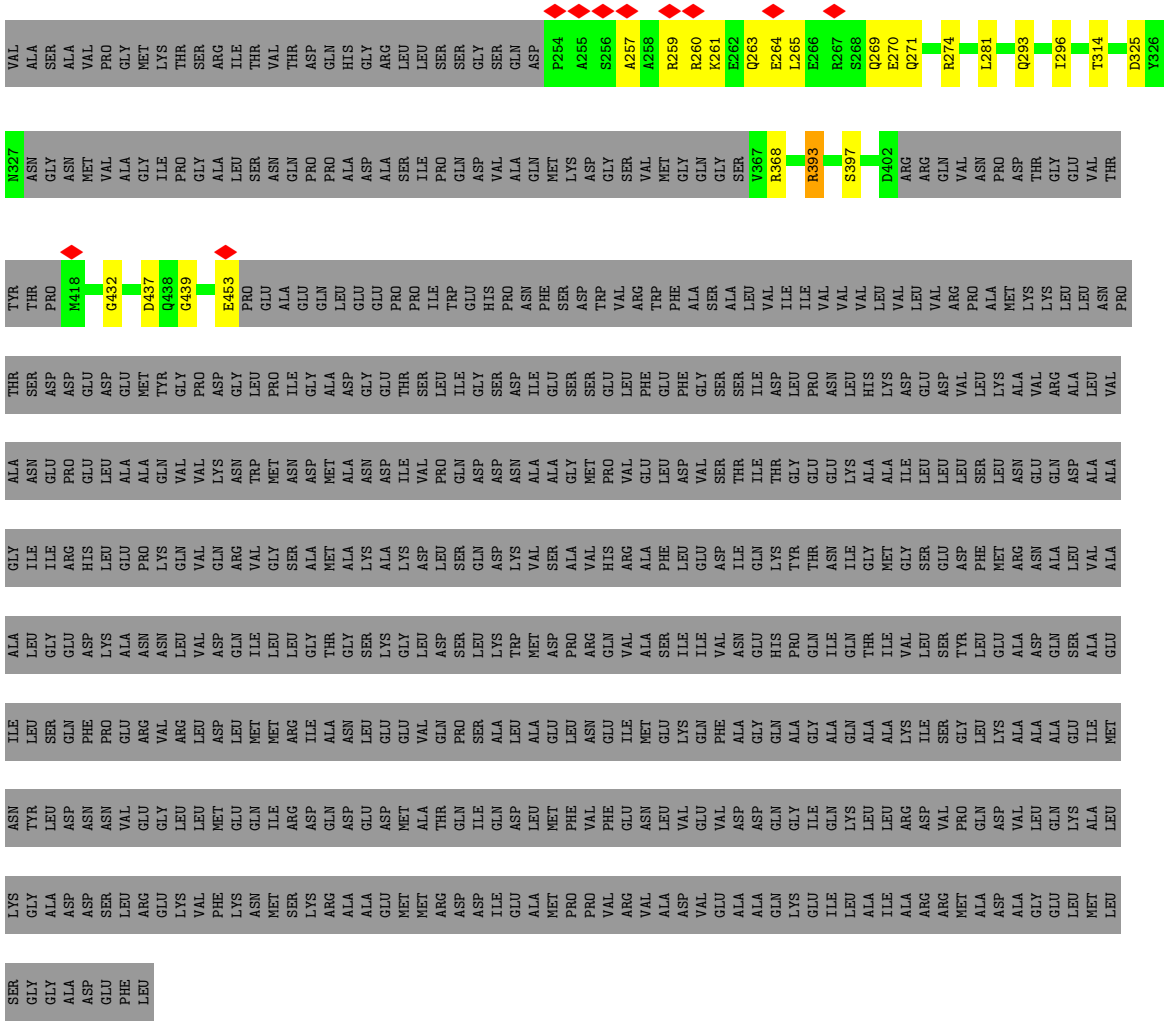
ALA VAL GLY ASP LEU ASP LEU LEU ARG GLN VAL VAL VAL LEU VAL LEU SER ILE SER ILE LYS CYS VAL ALA LEU ILE VAL MET LEU PHE PHE TRP VAL LYS GLU PRO GLU MET ARG PRO LEU GLY ALA TYR GLU THR GLU GLU LEU ILE PRO VAL LEU ASP TYR LEU ASP GLN GLN LYS ILE ASN



- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

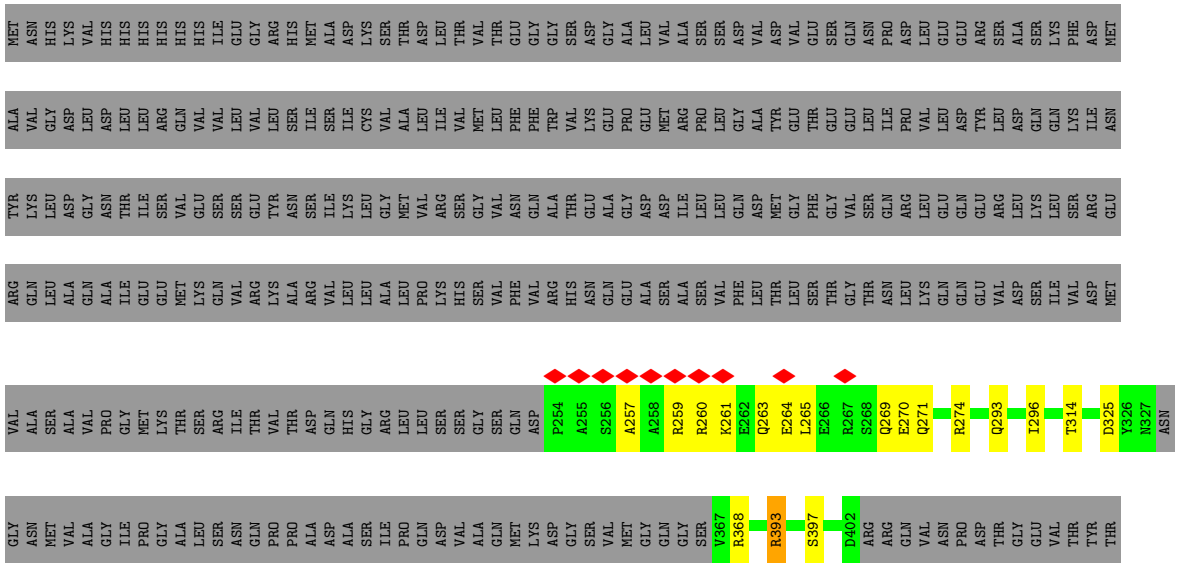
Chain D: 13% 85%





• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain E:

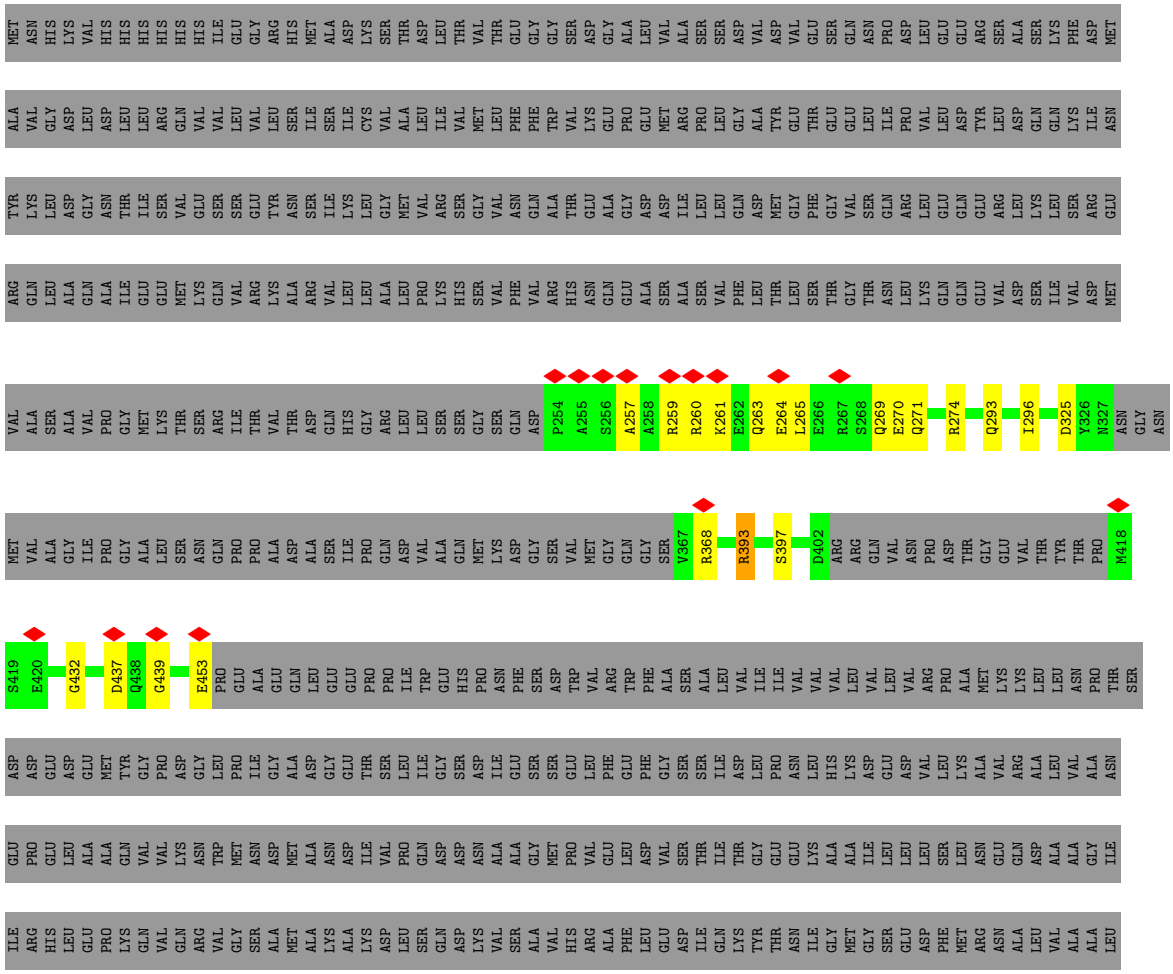


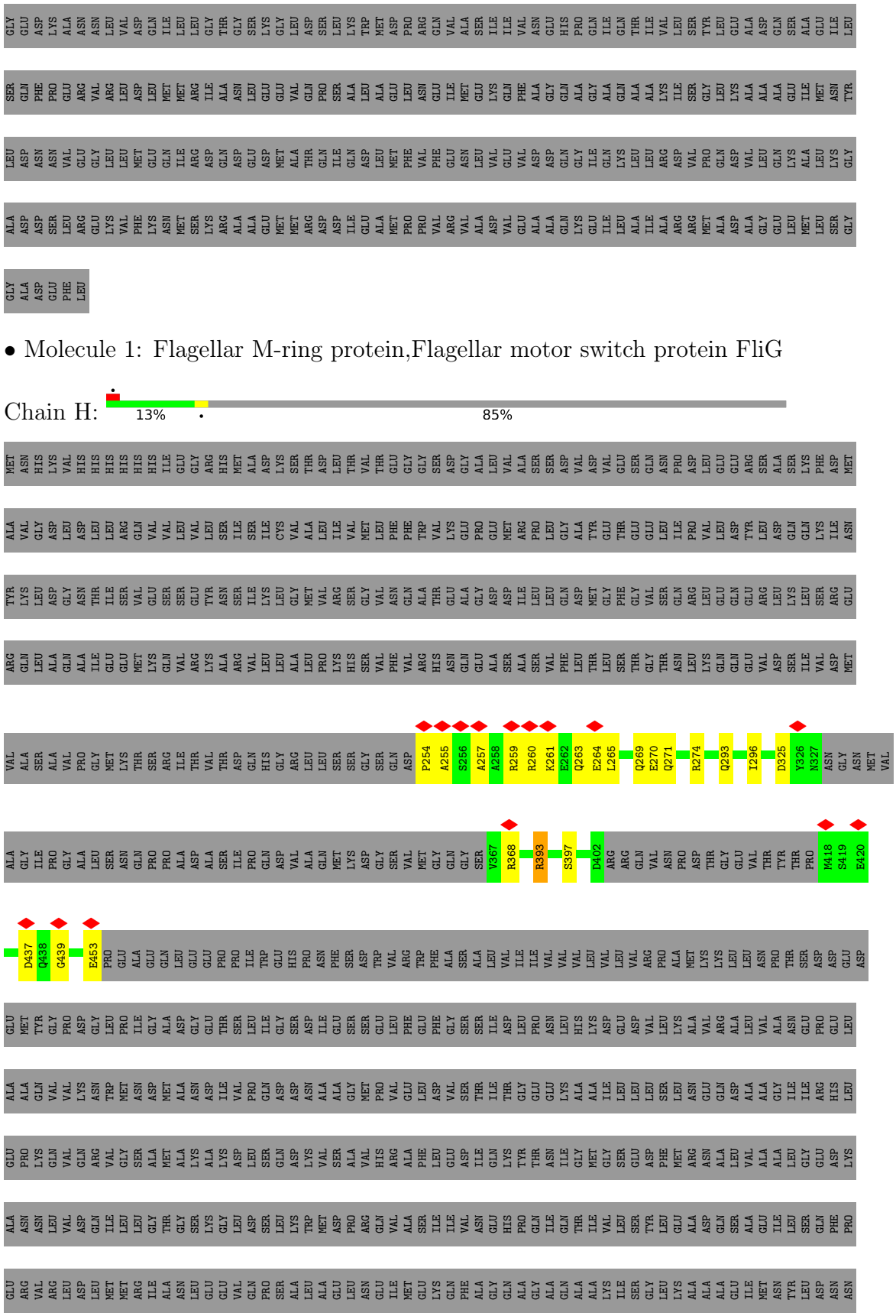
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain F: 13% 85%

• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

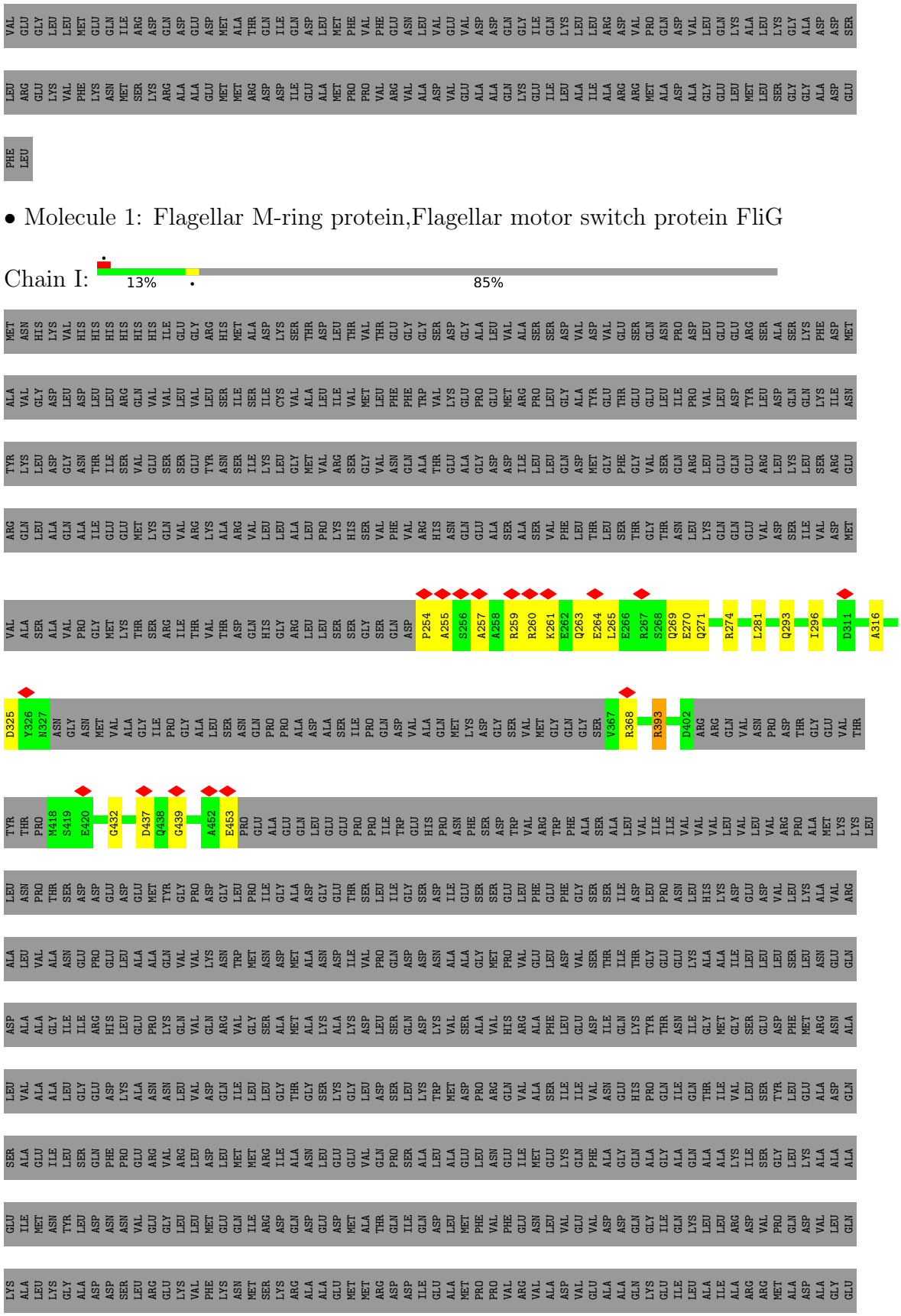
Chain G:





• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain H: 13% 85%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LEU ARG GLU LYS VAL PHE LYS ASN MET SER LYS ARG ALA ALA GLU MET MET ARG ASP ASP ILE GLU ALA MET PRO VAL ARG VAL ALA ASP VAL GLU ALA ALA GLN LYS GLU ILE LEU ALA ILE ALA ARG ARG MET ALA ASP ALA GLY GLU LEU MET LEU SER GLY GLY ALA ASP GLU
PHE LEU
Chain I:
13%
85%
MET ASN HIS LYS VAL HIS HIS HIS HIS HIS ILE GLU GLY ARG HIS MET ALA ASP LYS SER THR ASP LEU THR VAL THR GLU GLY GLY SER ASP GLY ALA LEU VAL ALA SER SER ASP VAL ASP VAL GLU SER GLN ASN PRO ASP LEU GLU GLU ARG SER ALA SER LYS PHE ASP MET
ALA VAL GLY ASP LEU ASP LEU LEU ARG GLN VAL VAL LEU VAL LEU SER ILE SER ILE CYS VAL ALA LEU ILE VAL MET LEU PHE PHE TRP VAL LYS GLU PRO GLU MET ARG PRO LEU GLY ALA TYR GLU THR GLU GLU LEU ILE PRO VAL LEU ASP TYR LEU ASP GLN GLN LYS ILE ASN
TYR LYS LEU ASP GLY ASN THR ILE SER VAL GLU SER SER GLU TYR ASN SER ILE LYS LEU GLY MET VAL VAL ARG SER GLY VAL ASN ASN GLN ALA THR GLU ALA GLY ASP ASP ILE LEU LEU GLN ASP MET GLY PHE GLY VAL SER GLN ARG LEU GLU GLN GLN GLU ARG LEU LYS LEU SER ARG GLU
ARG GLN LEU ALA GLN ALA ILE GLU GLU MET LYS GLN VAL ARG LYS ALA ARG VAL LEU LEU ALA LEU PRO LYS HIS SER VAL PHE VAL ARG HIS ASN GLN GLU ALA SER ALA SER VAL PHE LEU THR LEU SER THR GLY THR ASN LEU LYS GLN GLN GLU VAL ASP SER ILE VAL ASP MET
VAL ALA SER ALA VAL PRO GLY MET LYS THR SER ARG ILE THR VAL THR ASP GLN HIS GLY ARG LEU LEU SER SER GLY SER GLN ASP P254 A255 S256 A257 A258 R259 R260 K261 E262 Q263 E264 L265 E266 R267 S268 Q269 E270 Q271 R274 L281 Q293 I296 D311 A316
D325 Y326 N327 ASN GLY ASN MET VAL ALA GLY ILE PRO GLY ALA LEU SER ASN GLN PRO PRO ALA ASP ALA SER ILE PRO GLN ASP VAL ALA GLN MET LYS ASP GLY SER VAL MET GLY GLN GLY SER V367 R368 R393 D402 ARG ARG GLN VAL ASN PRO ASP THR GLY GLU VAL THR
TYR THR PRO M418 S419 E420 G432 D437 Q438 G439 A452 E453 PRO GLU ALA GLU GLN LEU GLU GLU PRO PRO ILE TRP GLU HIS PRO ASN PHE SER ASP TRP VAL ARG TRP PHE ALA SER ALA LEU VAL ILE ILE VAL VAL LEU VAL LEU VAL VAL ARG PRO ALA MET LYS LYS LEU
LEU ASN PRO THR SER ASP ASP GLU ASP GLU MET TYR GLY PRO ASP GLY LEU PRO ILE GLY ALA ASP GLY GLU THR SER LEU ILE GLY SER ASP ILE GLU SER SER GLU LEU PHE GLU PHE GLY SER SER ILE ASP LEU PRO ASN LEU HIS LYS ASP GLU ASP VAL LEU LYS ALA VAL ARG
ALA LEU VAL ALA ASN GLU PRO GLU LEU ALA ALA GLN VAL VAL LYS ASN TRP MET ASN ASP MET ALA ASN ASP ILE VAL PRO GLN ASP ASP ASN ALA GLY MET PRO VAL GLU LEU ASP VAL SER THR ILE THR GLY GLU GLU LYS ALA ALA ILE LEU LEU LEU SER LEU ASN GLU GLN
ASP ALA ALA GLY ILE ILE ARG HIS LEU GLU PRO LYS GLN VAL GLN ARG VAL GLY SER ALA MET ALA LYS ALA LYS ASP LEU SER GLN ASP LYS VAL SER ALA MET VAL HIS ARG ALA PHE LEU GLU ASP ILE GLN LYS TYR THR ASN ILE GLY MET GLY SER GLU ASP PHE MET ARG ASN ALA
LEU VAL ALA ALA LEU GLY GLU ASP LYS ALA ASN ASN LEU VAL ASP GLN ILE LEU LEU GLY GLU ASP LYS GLY LEU ASP SER LEU LYS TRP MET ASP PRO ARG GLN VAL ALA ILE ASN GLU HIS PRO GLN ILE GLN THR ILE VAL LEU SER TYR LEU GLU ALA ASP GLN
SER ALA GLU ILE LEU SER GLN PHE PRO GLU GLU ARG VAL ARG LEU ASP LEU MET MET ARG ILE ALA ASN LEU GLU GLU VAL GLN PRO SER ALA LEU ALA GLU LEU ASN GLU ILE MET GLU LYS GLN PHE ALA GLY GLN ALA GLY ALA GLN ALA ALA LYS ILE SER GLY LEU LYS ALA ALA ALA
GLU ILE MET ASN TYR LEU ASP ASN ASN VAL GLU GLY LEU LEU MET GLU GLN ILE ARG ASP GLN ASP GLU ASP MET ALA THR GLN ILE GLN ASP LEU MET PHE VAL PHE GLU ASN LEU VAL GLU VAL ASP ASP GLN GLY ILE GLN LYS LEU LEU ARG ASP VAL PRO GLN ASP VAL LEU GLN
LYS ALA LEU LYS GLY ALA ASP ASP SER LEU ARG GLU LYS VAL PHE LYS ASN MET SER LYS ARG ALA ALA GLU MET MET ARG ASP ASP ILE GLU ALA MET PRO VAL ARG VAL ALA ASP VAL GLU ALA ALA GLN LYS GLU ILE LEU ALA ILE ALA ARG ARG MET ALA ASP ALA GLY GLU

LEU MET LEU SER GLY GLY ALA ASP GLU PHE LEU

• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain J: 13% 85%

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

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

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

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

VAL ALA SER ALA VAL PRO GLY MET LYS THR SER ARG ILE THR VAL THR ASP GLN HIS GLY ARG LEU LEU SER SER GLY SER GLN ASP P254 A255 S256 A257 A258 R259 R260 K261 E262 Q263 E264 L265 E266 R267 S268 Q269 E270 Q271 R274 D278 Q293 I296 R309 F310 D311

D325 Y326 N327 ASN GLY ASN MET VAL ALA GLY ILE PRO GLY ALA LEU SER ASN GLN PRO PRO ALA ASP ALA SER ILE PRO GLN ASP VAL ALA GLN MET LYS ASP GLY SER VAL MET MET GLY GLN GLY SER V367 R368 L377 R393 S397 D402 ARG ARG GLN VAL ASN PRO ASP THR

GLY GLU VAL THR TYR THR PRO M418 S419 E420 G432 D437 Q438 G439 E453 PRO GLU ALA GLU GLN LEU GLU GLU PRO PRO ILE TRP GLU HIS PRO ASN PHE SER ASP TRP VAL ARG TRP PHE ALA SER ALA LEU VAL ILE ILE VAL VAL VAL LEU VAL LEU VAL ARG PRO ALA MET

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

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

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

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

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

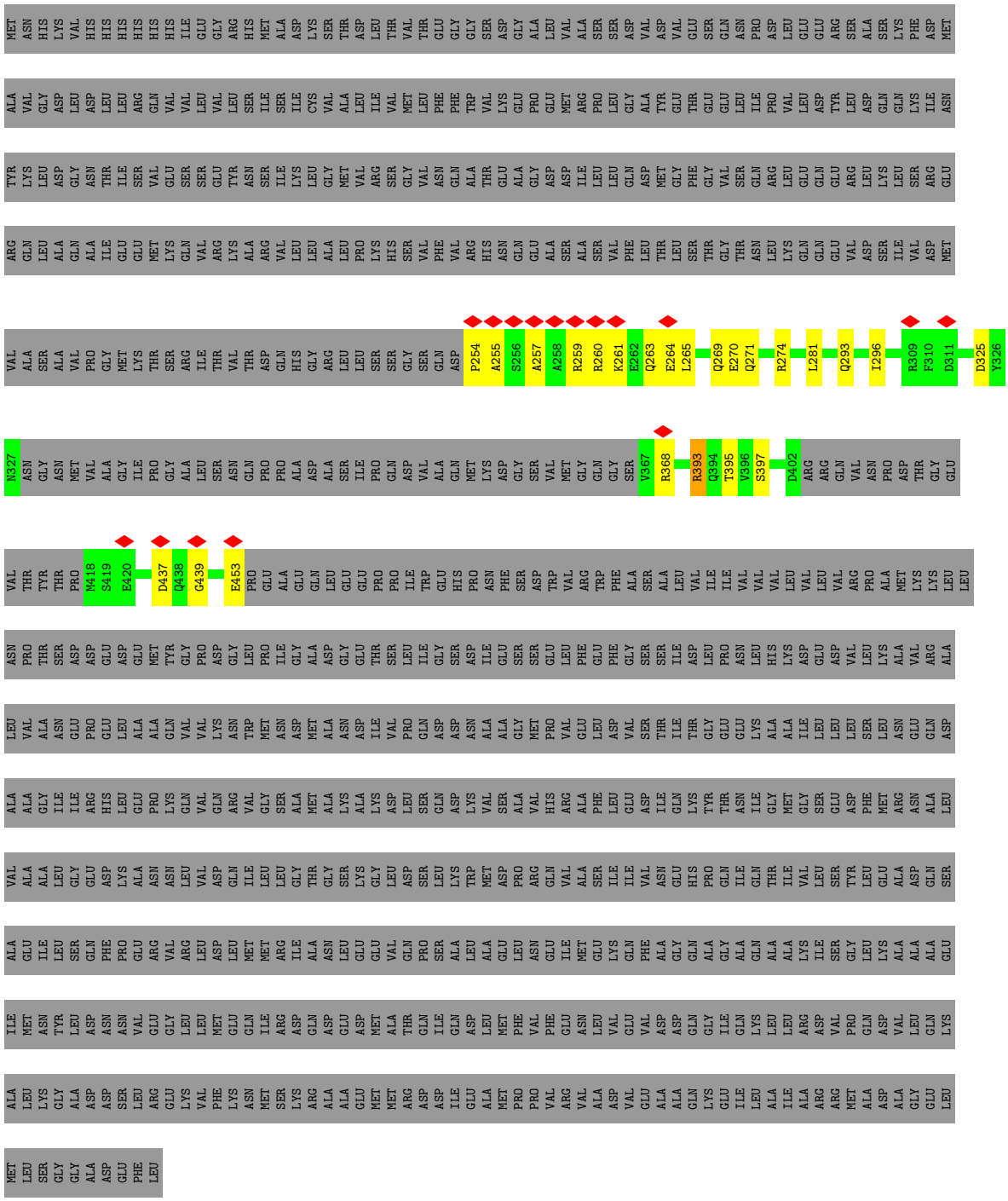
ALA ALA ALA GLU ILE MET ASN TYR LEU ASP ASN ASN VAL GLU GLY LEU LEU MET GLU GLN ILE ARG ASP GLN ASP GLU ASP MET ALA THR GLN ILE GLN ASP LEU ALA MET PHE VAL PHE GLU ASN LEU VAL GLU VAL ASP ASP GLN GLY ILE GLN LYS LEU LEU ARG ASP VAL PRO GLN ASP

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

ALA GLY GLU LEU MET LEU SER GLY GLY ALA ASP GLU PHE LEU

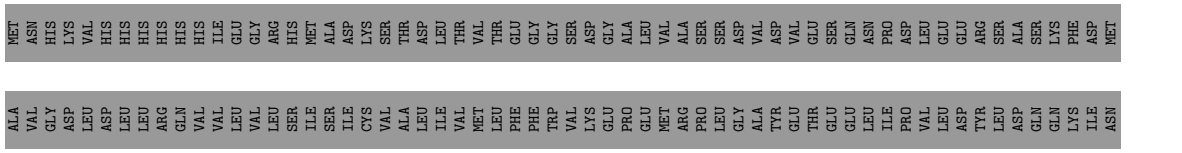
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

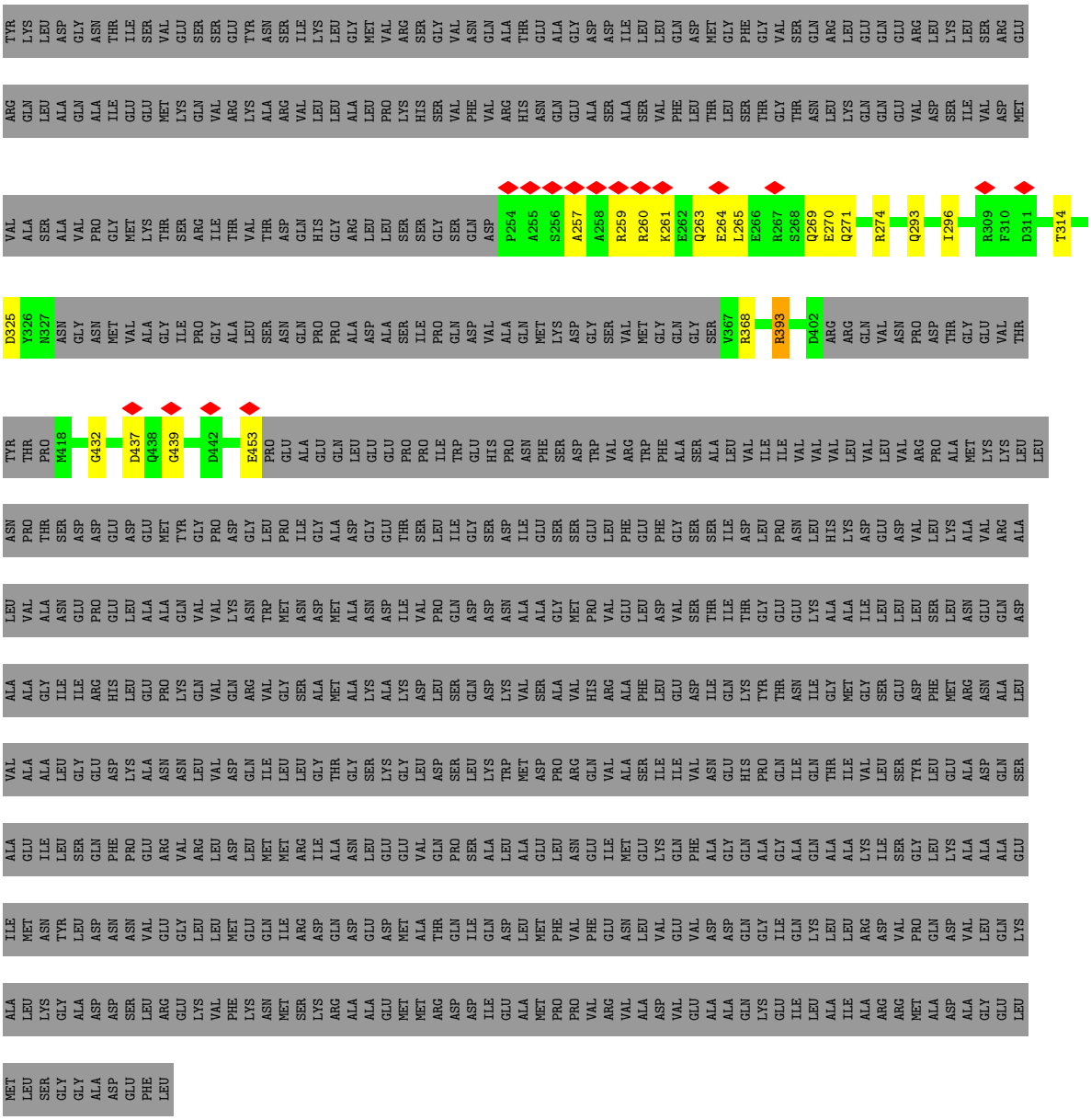
Chain K: 13% 85%



• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

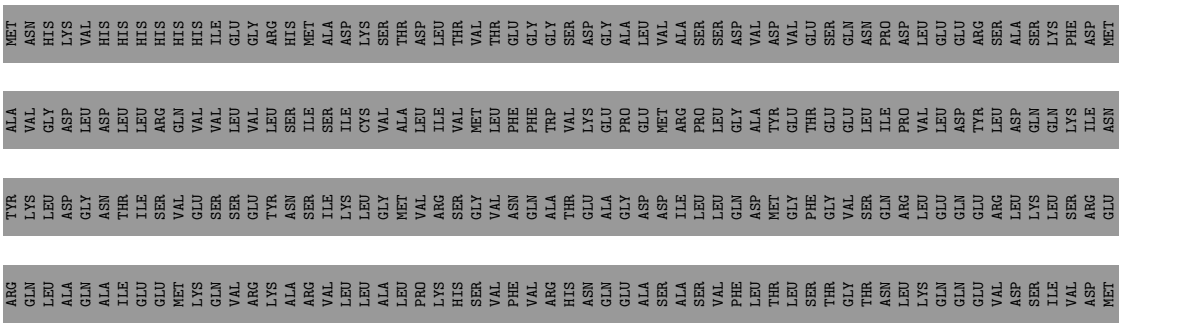
Chain L:

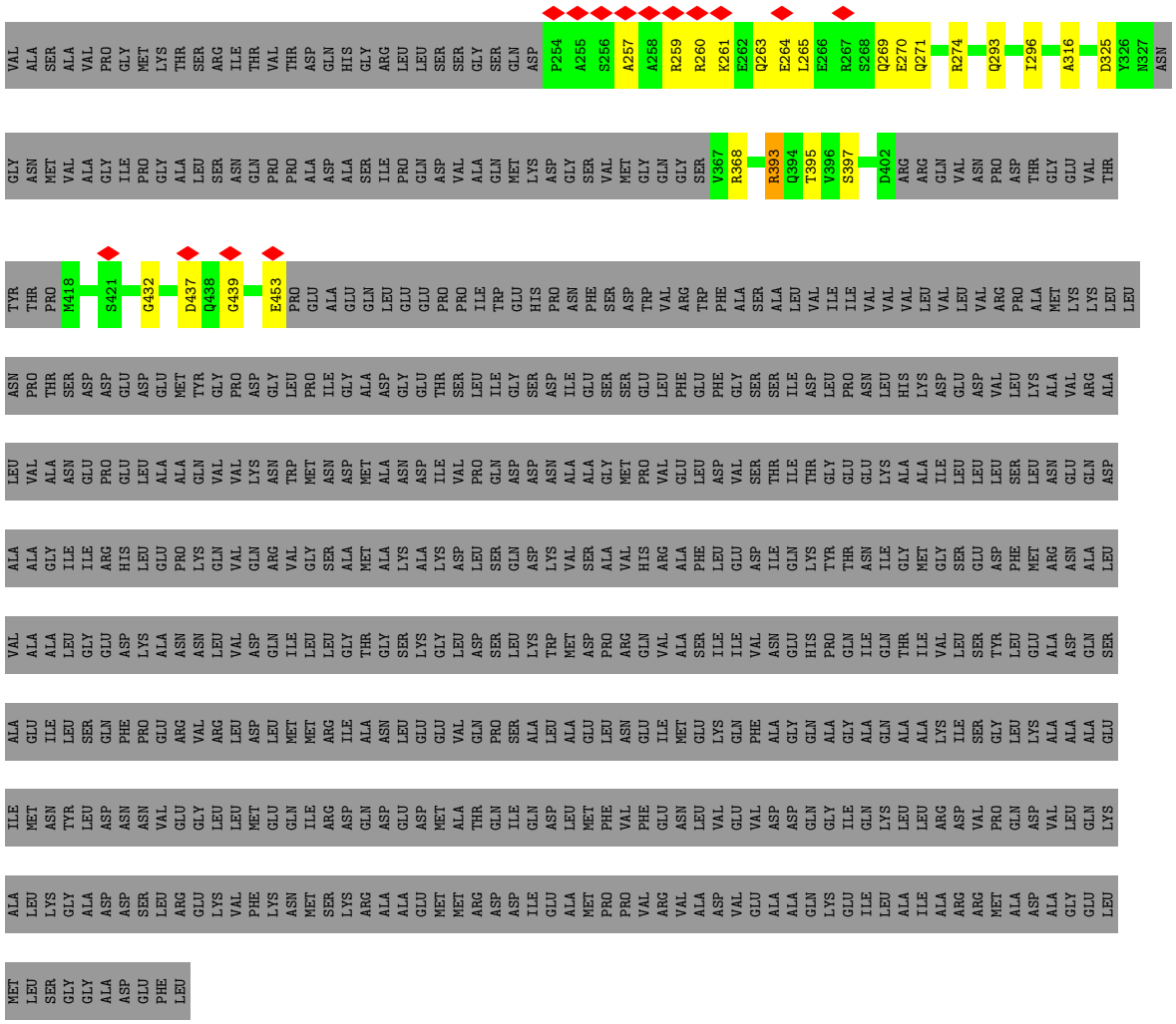




• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

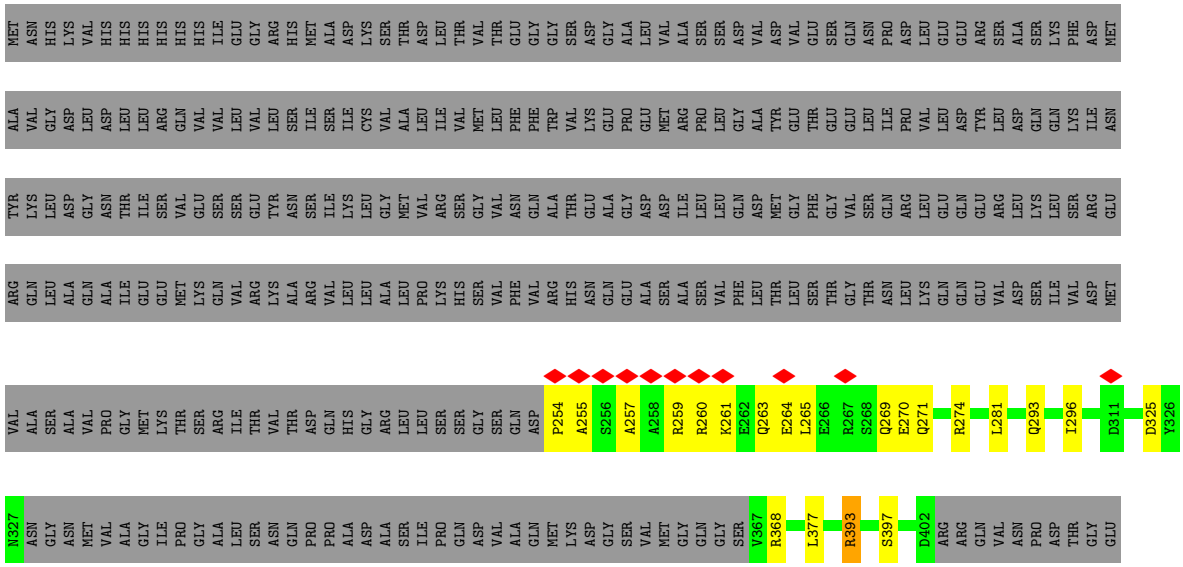
Chain M: 13% 85%





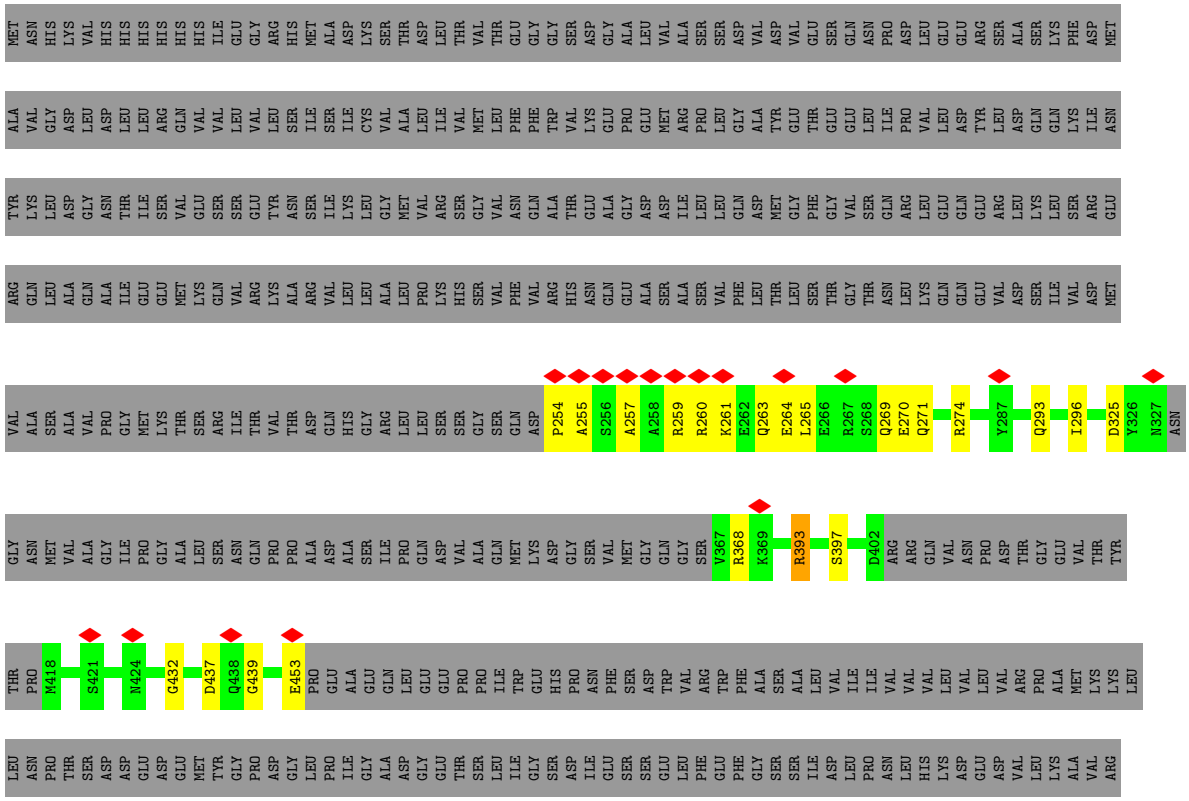
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain N:



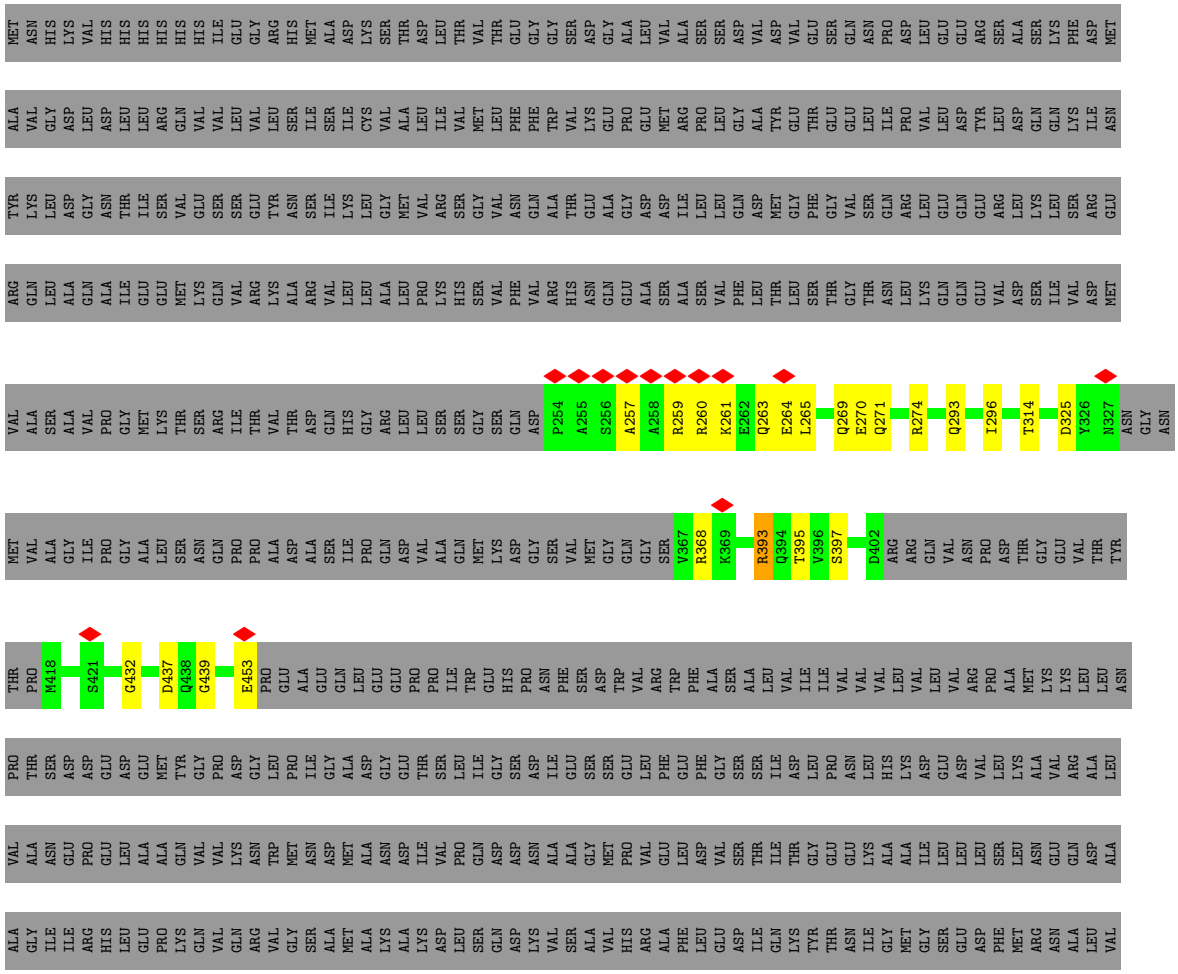
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

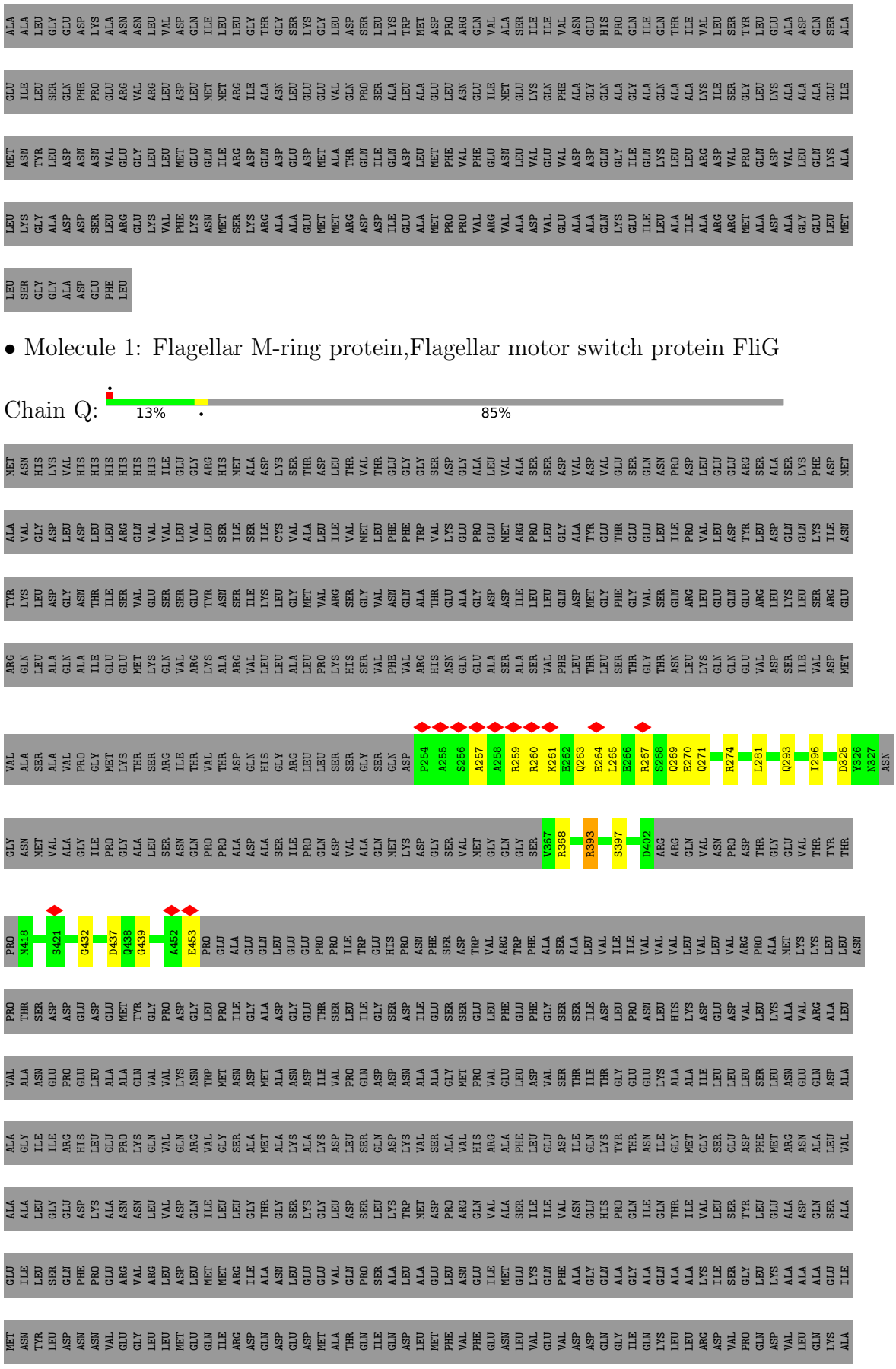
Chain O: 13% 85%



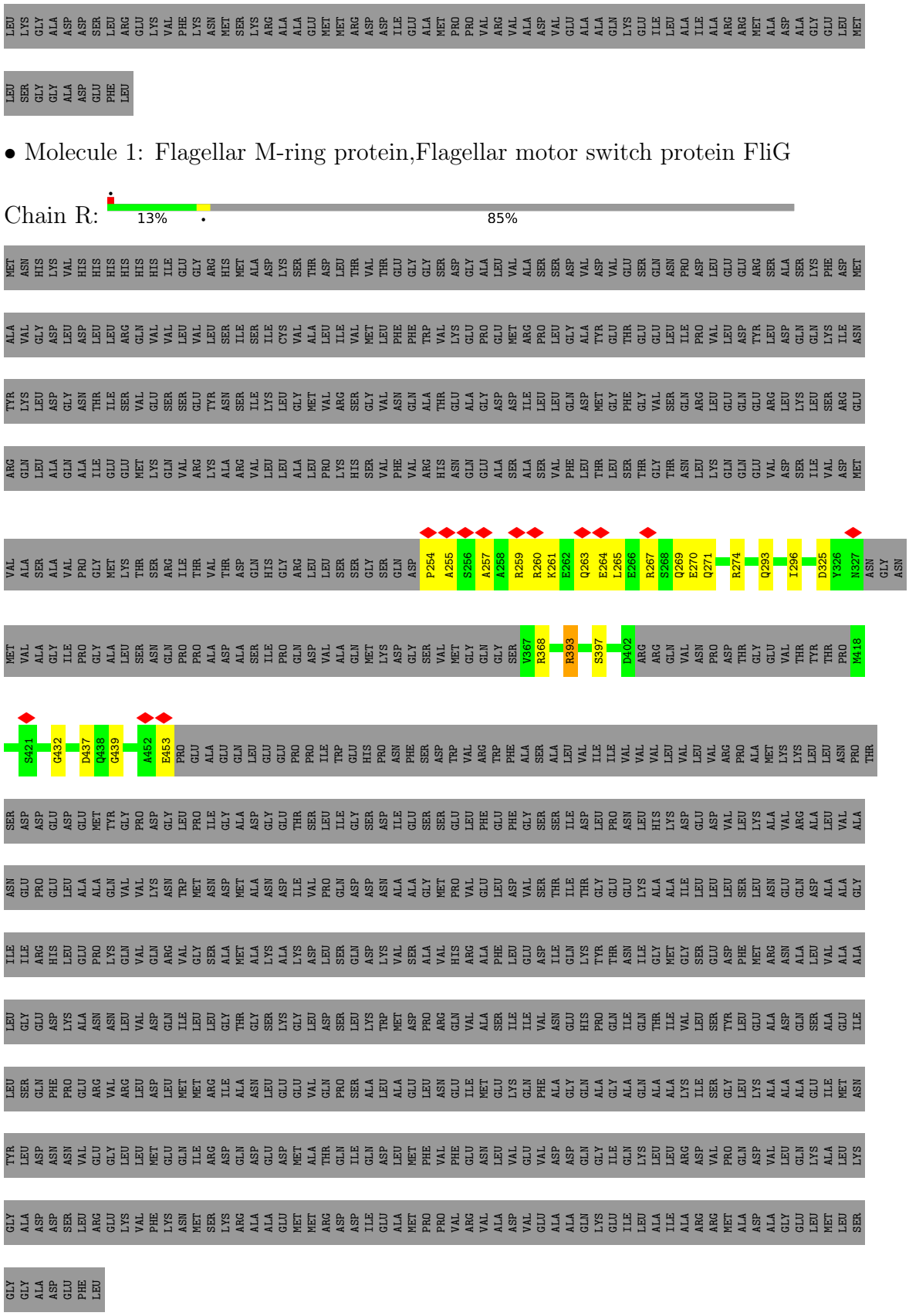
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain P: 13% 85%





• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG



• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain R: 13% 85%

• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain S: 13% 85%

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

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

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

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

VAL ALA SER ALA VAL PRO GLY MET LYS THR SER ARG ILE THR VAL THR ASP GLN HIS GLY ARG LEU LEU SER SER GLY SER GLN ASP P254 A255 S256 A257 A258 R259 R260 K261 E262 Q263 E264 L265 E266 R267 S268 Q269 E270 Q271 R274 D278 Q293 I296 D325 Y326 N327 ASN

GLY ASN MET VAL ALA GLY ILE PRO GLY ALA LEU SER ASN GLN PRO PRO ALA ASP ALA SER ILE PRO GLN ASP VAL ALA GLN MET LYS ASP GLY SER VAL MET GLY GLN GLY SER V367 R368 R393 S397 D402 ARG ARG GLN VAL ASN PRO ASP THR GLY GLU VAL THR TYR THR

PRO M418 S421 G432 D437 Q438 G439 A452 E453 PRO GLU ALA GLU GLN GLN LEU GLU GLU PRO PRO ILE TRP GLU HIS PRO ASN PHE SER ASP TRP VAL ARG TRP PHE ALA SER ALA LEU VAL ILE ILE VAL VAL VAL LEU VAL LEU VAL ARG PRO ALA MET LYS LYS LEU LEU ASN

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

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

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

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

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

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

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

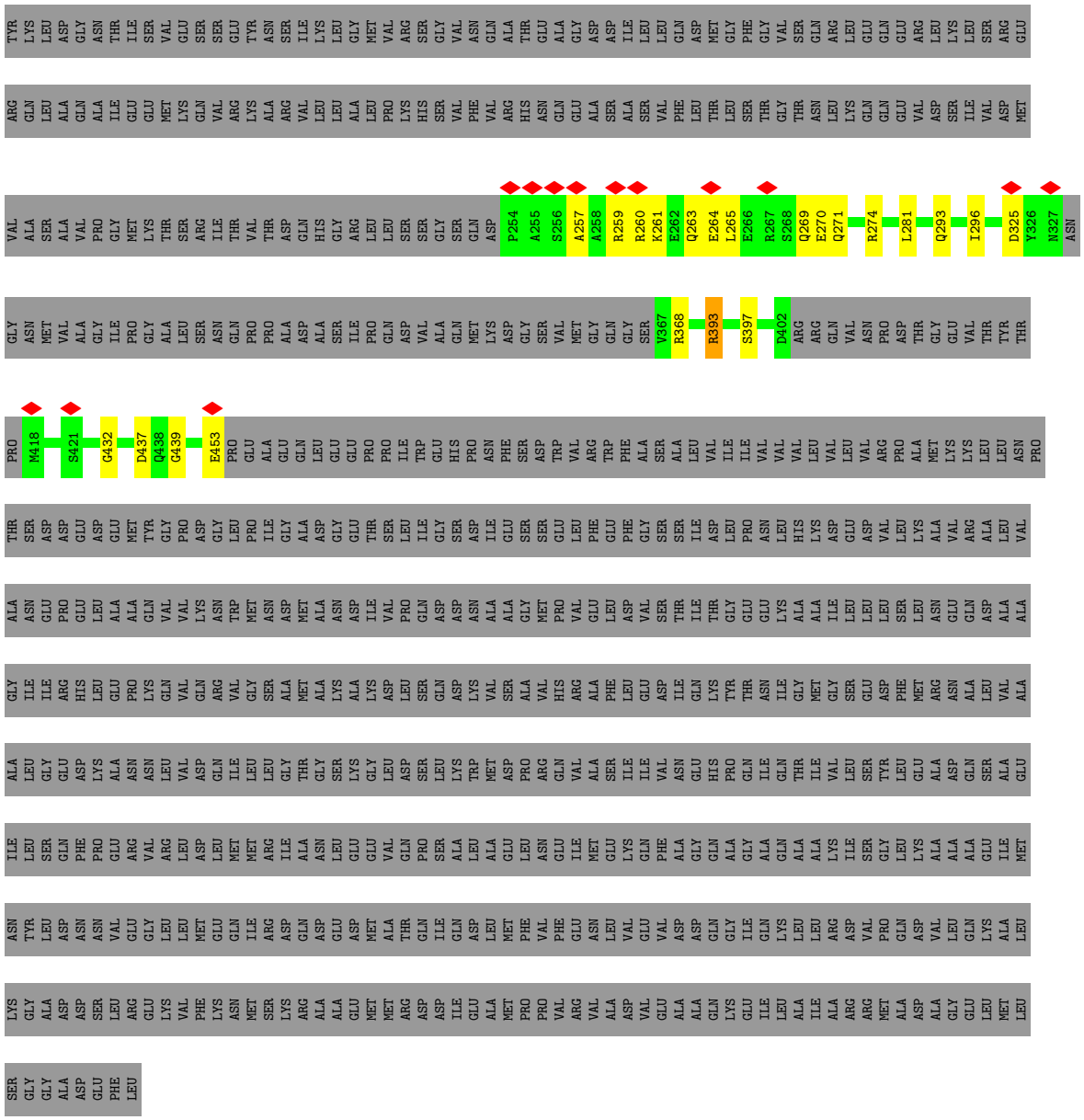
LEU SER GLY GLY ALA ASP GLU PHE LEU

• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain T: 13% 85%

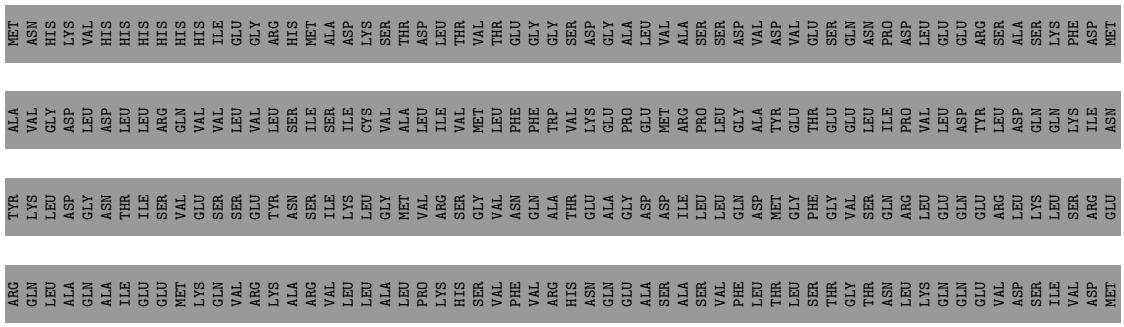
MET ASN HIS LYS VAL HIS HIS HIS HIS HIS ILE GLU GLY ARG HIS MET ALA ASP LYS SER THR ASP LEU THR VAL THR GLU GLY GLY SER ASP GLY ALA LEU VAL ALA SER SER ASP VAL ASP VAL GLU SER GLN ASN PRO ASP LEU GLU GLU ARG SER ALA SER LYS PHE ASP MET

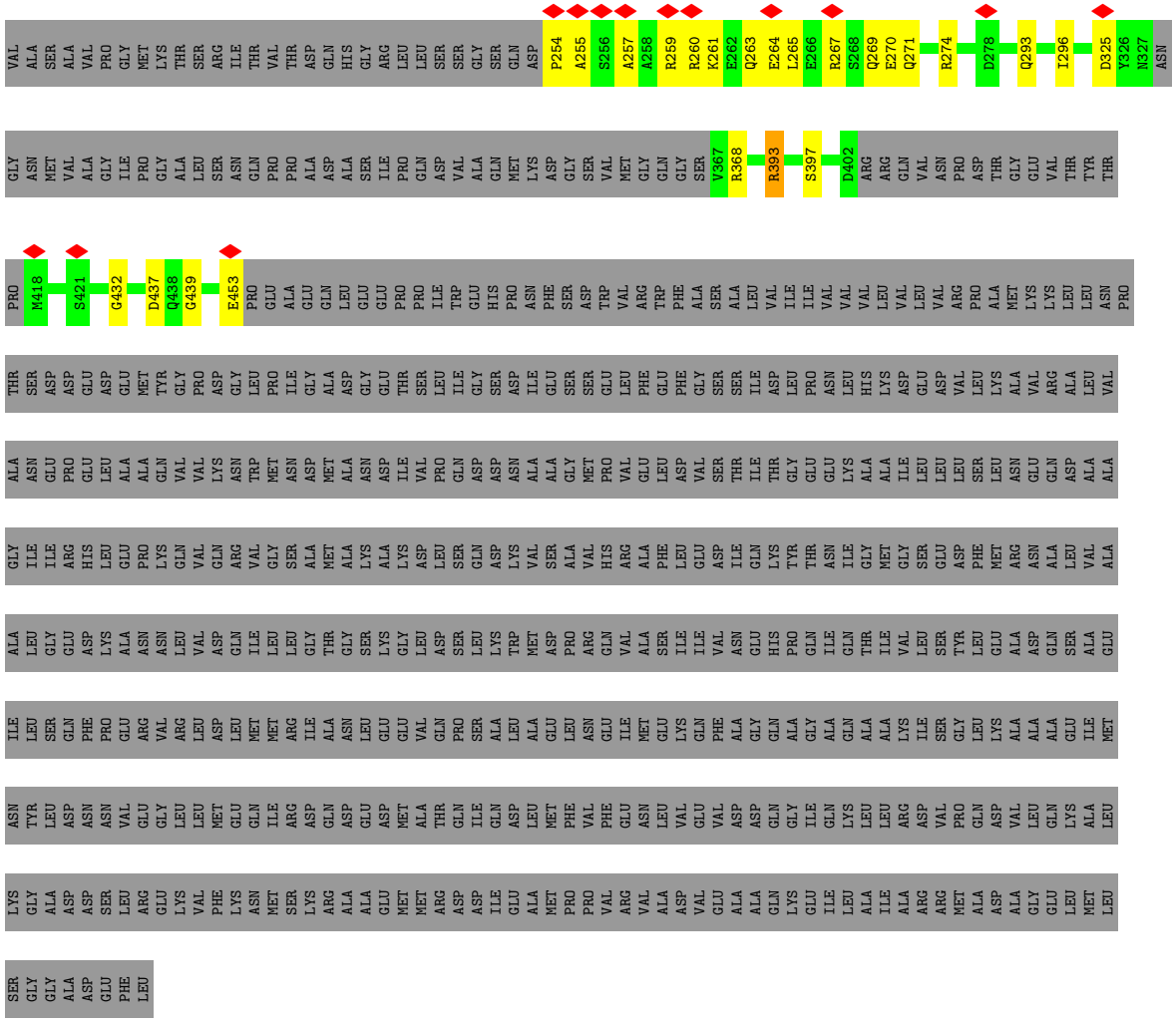
ALA VAL GLY ASP LEU ASP LEU LEU ARG GLN VAL VAL LEU VAL LEU SER ILE SER ILE LYS CYS VAL ALA LEU ILE VAL MET LEU PHE PHE TRP VAL LYS GLU PRO GLU MET ARG PRO LEU GLY ALA TYR GLU THR GLU GLU LEU ILE PRO VAL LEU ASP TYR LEU ASP GLN GLN LYS ILE ASN



- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

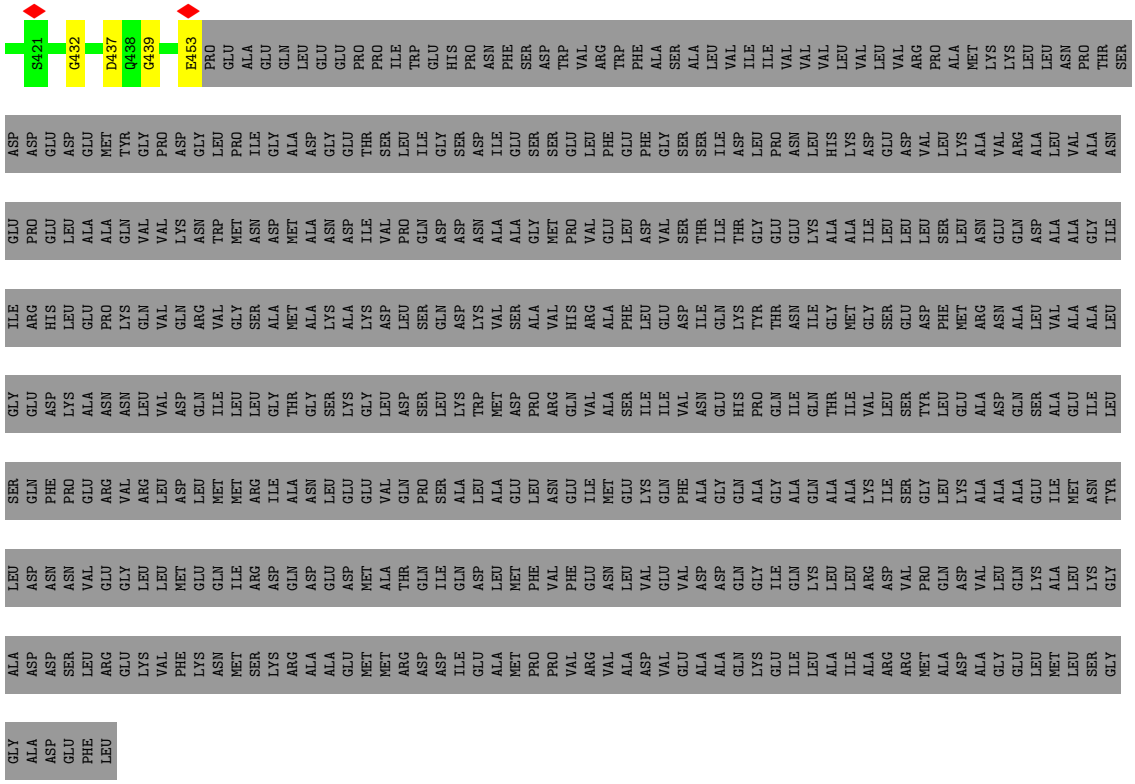
Chain U: 13% 85%





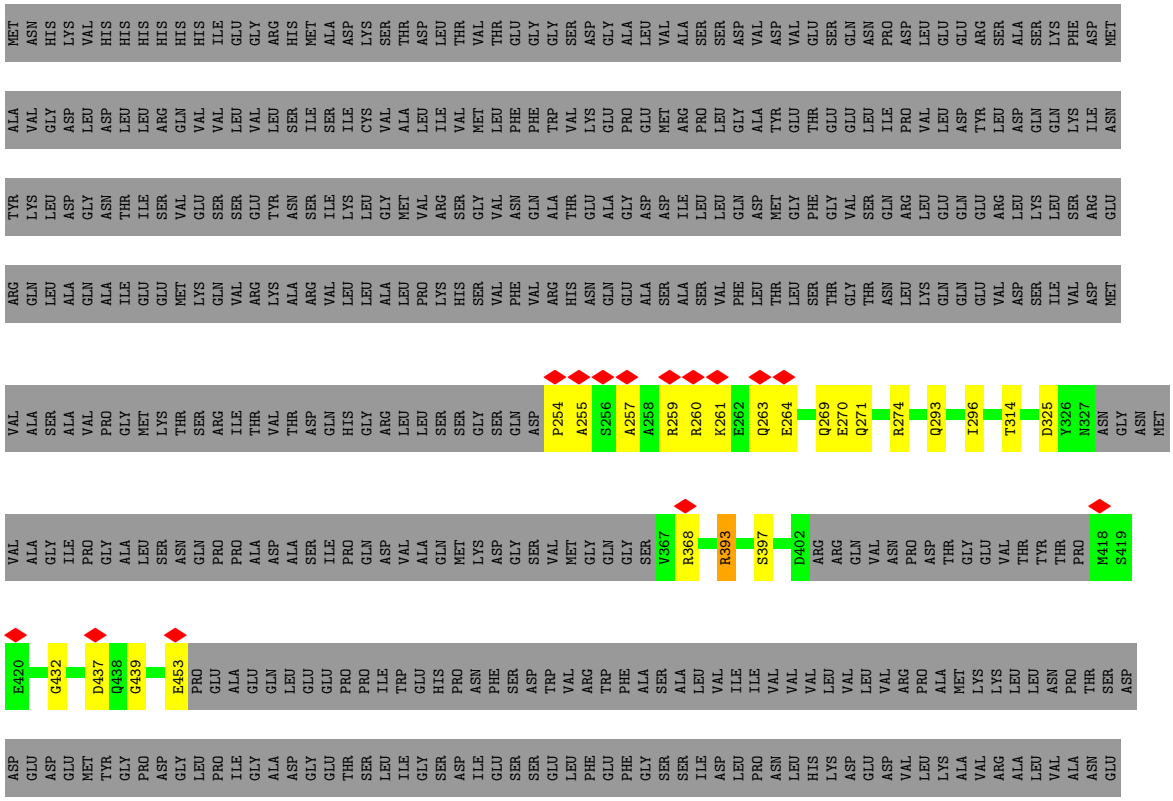
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain V: 13% 85%



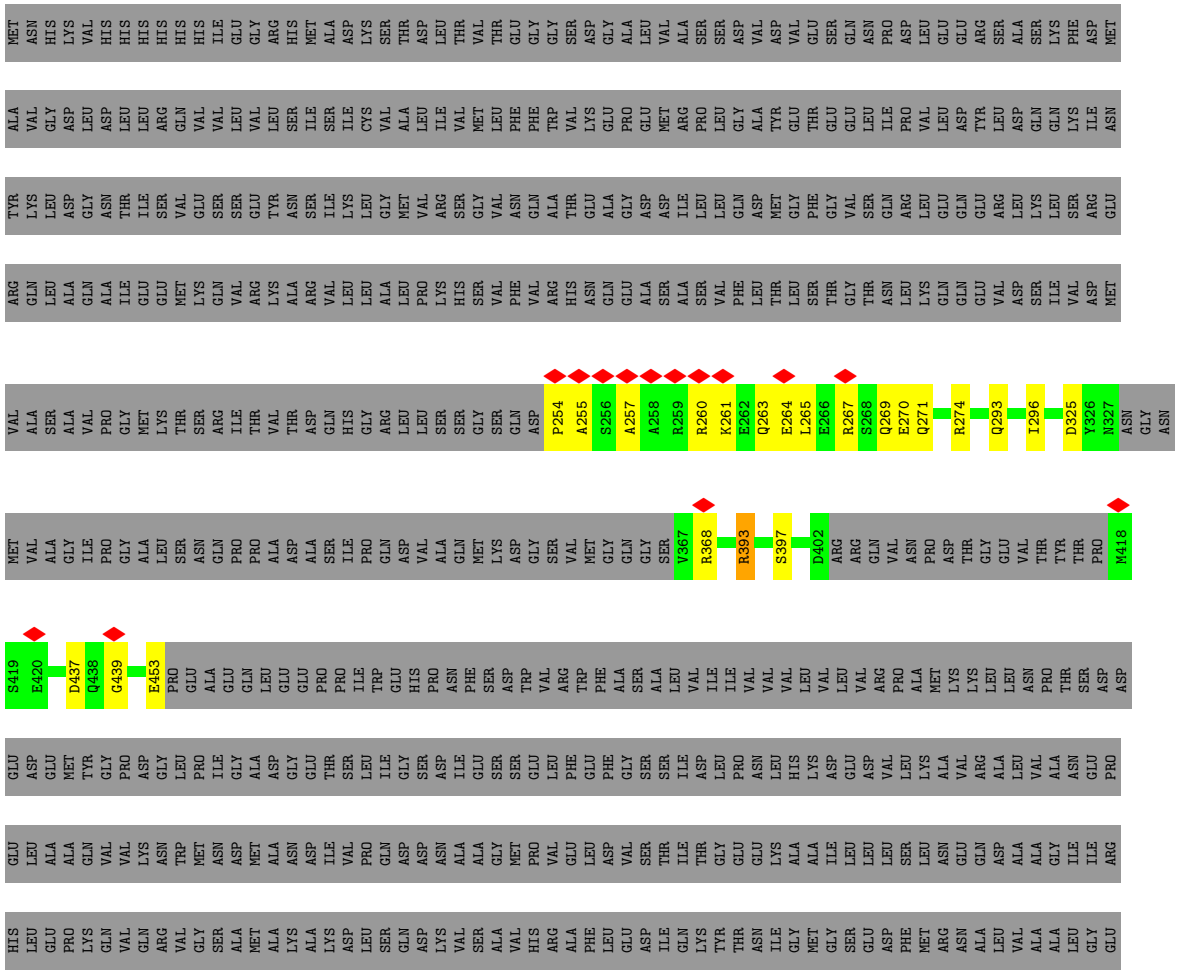
• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

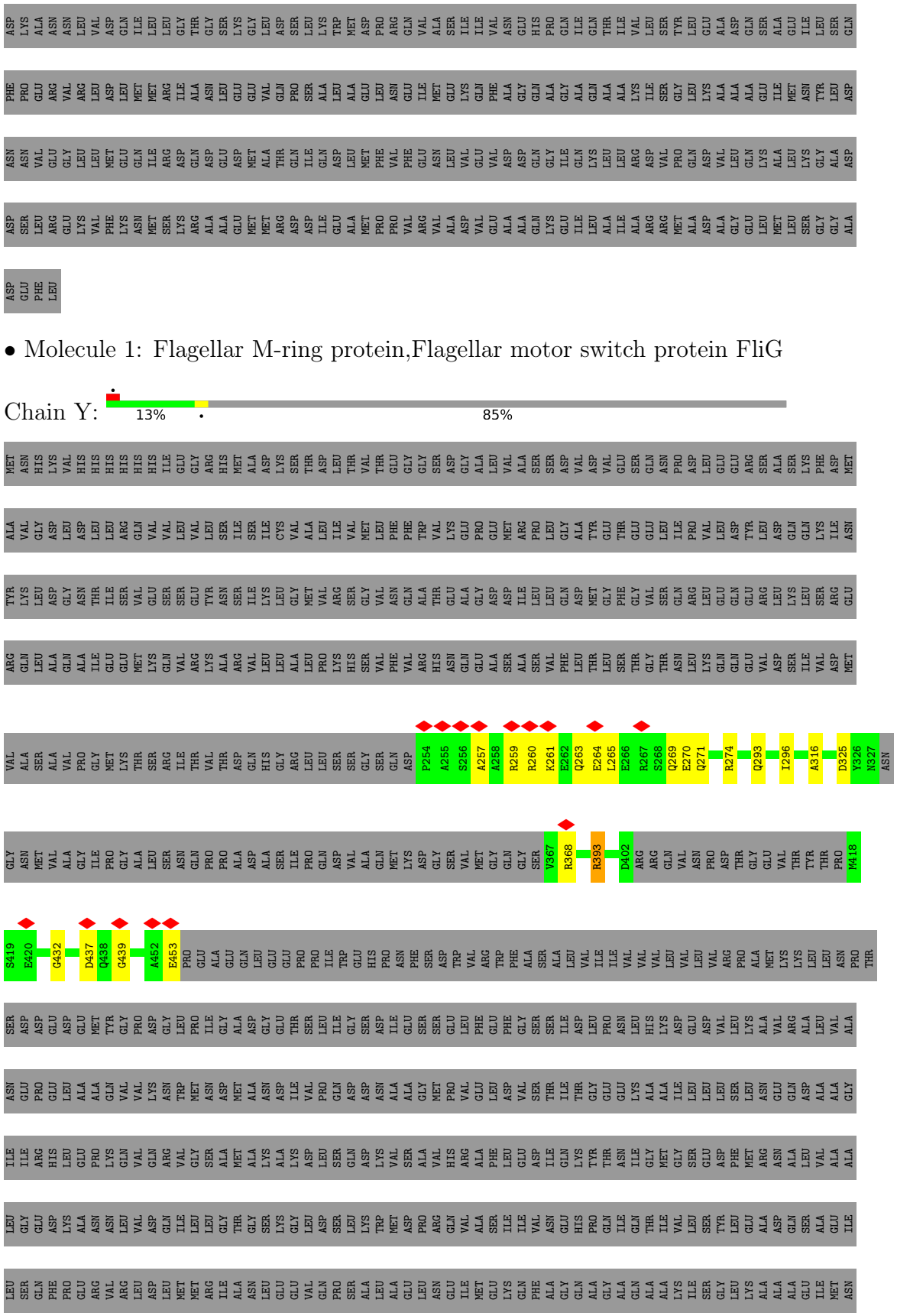
Chain W:



• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

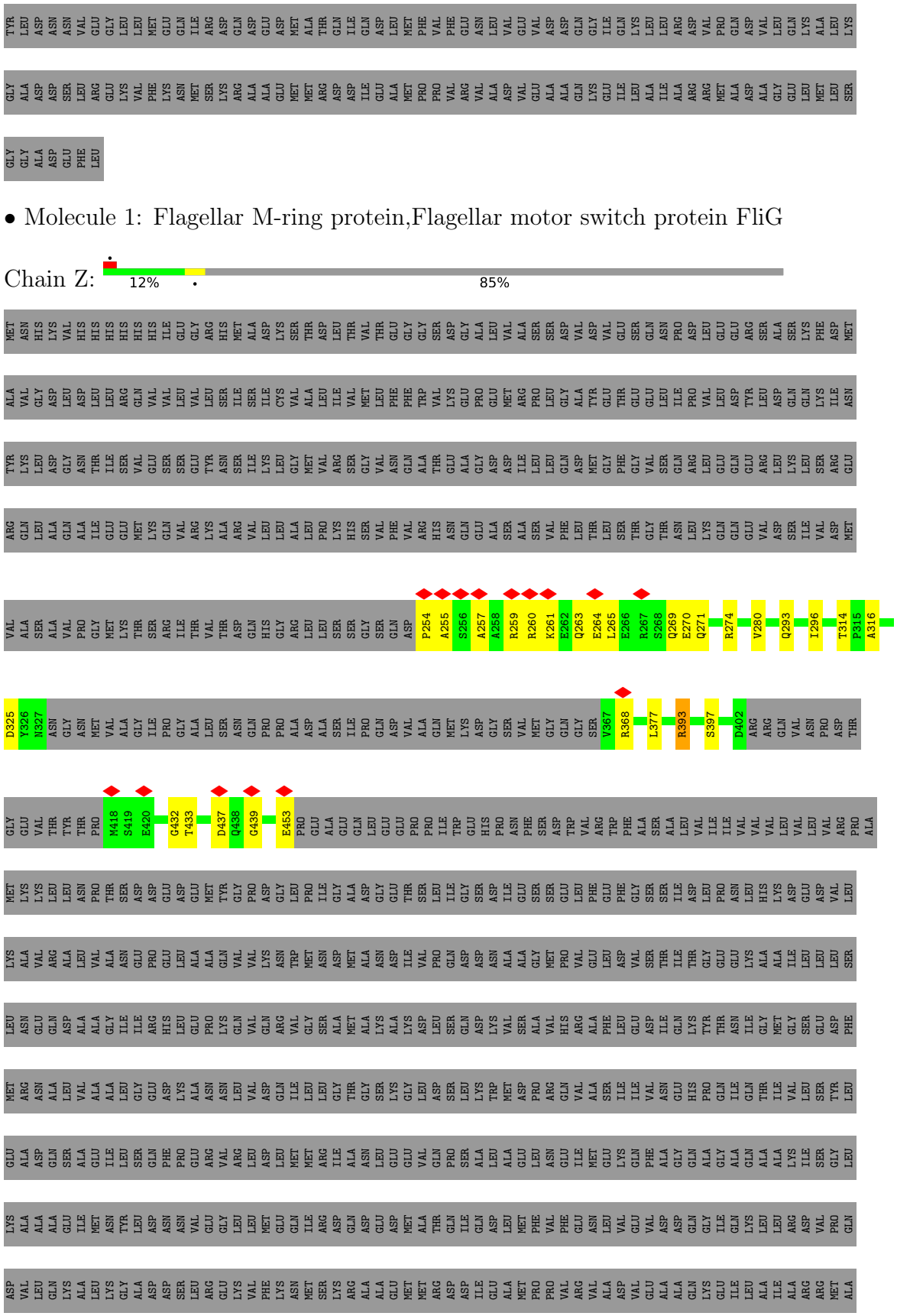
Chain X:





• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain Y: 13% 85%



• Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain Z: 12% 85%

ASP
ALA
GLY
GLU
LEU
MET
LEU
SER
GLY
GLY
ALA
ASP
GLU
PHE
LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C35	Depositor
Number of particles used	184915	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	49.7	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	1.682	Depositor
Minimum map value	-0.966	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	684.0, 684.0, 684.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.14, 1.14, 1.14	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	1	0.19	0/1170	0.36	0/1573
1	2	0.19	0/1170	0.36	0/1573
1	3	0.19	0/1170	0.36	0/1573
1	4	0.19	0/1170	0.36	0/1573
1	5	0.19	0/1170	0.36	0/1573
1	6	0.19	0/1170	0.36	0/1573
1	7	0.19	0/1170	0.36	0/1573
1	8	0.19	0/1170	0.36	0/1573
1	9	0.19	0/1170	0.36	0/1573
1	A	0.19	0/1170	0.36	0/1573
1	B	0.19	0/1170	0.36	0/1573
1	C	0.19	0/1170	0.36	0/1573
1	D	0.19	0/1170	0.36	0/1573
1	E	0.19	0/1170	0.36	0/1573
1	F	0.19	0/1170	0.36	0/1573
1	G	0.19	0/1170	0.36	0/1573
1	H	0.19	0/1170	0.36	0/1573
1	I	0.19	0/1170	0.36	0/1573
1	J	0.19	0/1170	0.36	0/1573
1	K	0.19	0/1170	0.36	0/1573
1	L	0.19	0/1170	0.36	0/1573
1	M	0.19	0/1170	0.36	0/1573
1	N	0.19	0/1170	0.36	0/1573
1	O	0.19	0/1170	0.36	0/1573
1	P	0.19	0/1170	0.36	0/1573
1	Q	0.19	0/1170	0.36	0/1573
1	R	0.19	0/1170	0.36	0/1573
1	S	0.19	0/1170	0.36	0/1573
1	T	0.19	0/1170	0.36	0/1573
1	U	0.19	0/1170	0.36	0/1573
1	V	0.19	0/1170	0.36	0/1573
1	W	0.19	0/1170	0.36	0/1573
1	X	0.19	0/1170	0.36	0/1573
1	Y	0.19	0/1170	0.36	0/1573

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	Z	0.19	0/1170	0.36	0/1573
All	All	0.19	0/40950	0.36	0/55055

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	1
1	2	0	1
1	3	0	1
1	4	0	1
1	5	0	1
1	6	0	1
1	7	0	1
1	8	0	1
1	9	0	1
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	Y	0	1
1	Z	0	1
All	All	0	35

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	393	ARG	Sidechain
1	2	393	ARG	Sidechain
1	3	393	ARG	Sidechain
1	4	393	ARG	Sidechain
1	5	393	ARG	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1159	0	1149	22	0
1	2	1159	0	1149	16	0
1	3	1159	0	1149	18	0
1	4	1159	0	1149	21	0
1	5	1159	0	1149	20	0
1	6	1159	0	1149	21	0
1	7	1159	0	1149	23	0
1	8	1159	0	1149	20	0
1	9	1159	0	1149	20	0
1	A	1159	0	1149	20	0
1	B	1159	0	1149	19	0
1	C	1159	0	1149	20	0
1	D	1159	0	1149	20	0
1	E	1159	0	1149	19	0
1	F	1159	0	1149	20	0
1	G	1159	0	1149	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1159	0	1149	18	0
1	I	1159	0	1149	20	0
1	J	1159	0	1149	22	0
1	K	1159	0	1149	20	0
1	L	1159	0	1149	19	0
1	M	1159	0	1149	19	0
1	N	1159	0	1149	21	0
1	O	1159	0	1149	20	0
1	P	1159	0	1149	20	0
1	Q	1159	0	1149	20	0
1	R	1159	0	1149	20	0
1	S	1159	0	1149	19	0
1	T	1159	0	1149	18	0
1	U	1159	0	1149	19	0
1	V	1159	0	1149	18	0
1	W	1159	0	1149	18	0
1	X	1159	0	1149	18	0
1	Y	1159	0	1149	18	0
1	Z	1159	0	1149	25	0
All	All	40565	0	40215	545	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 7.

The worst 5 of 545 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)
1:1:263:GLN:NE2	1:Z:269:GLN:HE21	1.71	0.87
1:2:269:GLN:HE21	1:3:263:GLN:NE2	1.72	0.87
1:L:269:GLN:HE21	1:M:263:GLN:NE2	1.73	0.86
1:5:269:GLN:HE21	1:6:263:GLN:NE2	1.74	0.85
1:K:269:GLN:HE21	1:L:263:GLN:NE2	1.76	0.83

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	1	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	2	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	3	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	4	140/945 (15%)	140 (100%)	0	0	100	100
1	5	140/945 (15%)	140 (100%)	0	0	100	100
1	6	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	7	140/945 (15%)	140 (100%)	0	0	100	100
1	8	140/945 (15%)	140 (100%)	0	0	100	100
1	9	140/945 (15%)	140 (100%)	0	0	100	100
1	A	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	B	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	C	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	D	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	E	140/945 (15%)	140 (100%)	0	0	100	100
1	F	140/945 (15%)	140 (100%)	0	0	100	100
1	G	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	H	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	I	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	J	140/945 (15%)	140 (100%)	0	0	100	100
1	K	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	L	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	M	140/945 (15%)	140 (100%)	0	0	100	100
1	N	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	O	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	P	140/945 (15%)	140 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	140/945 (15%)	140 (100%)	0	0	100	100
1	R	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	S	140/945 (15%)	140 (100%)	0	0	100	100
1	T	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	U	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	V	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	W	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	X	140/945 (15%)	140 (100%)	0	0	100	100
1	Y	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
1	Z	140/945 (15%)	139 (99%)	1 (1%)	0	100	100
All	All	4900/33075 (15%)	4878 (100%)	22 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	1	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	2	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	3	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	4	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	5	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	6	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	7	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	8	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	9	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	A	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	B	127/802 (16%)	126 (99%)	1 (1%)	73	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	D	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	E	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	F	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	G	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	H	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	I	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	J	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	K	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	L	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	M	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	N	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	O	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	P	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	Q	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	R	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	S	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	T	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	U	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	V	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	W	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	X	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	Y	127/802 (16%)	126 (99%)	1 (1%)	73	80
1	Z	127/802 (16%)	126 (99%)	1 (1%)	73	80
All	All	4445/28070 (16%)	4410 (99%)	35 (1%)	70	80

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T	393	ARG
1	U	393	ARG
1	X	393	ARG
1	D	393	ARG
1	C	393	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 140 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	394	GLN
1	U	394	GLN
1	X	383	HIS
1	D	263	GLN
1	C	394	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

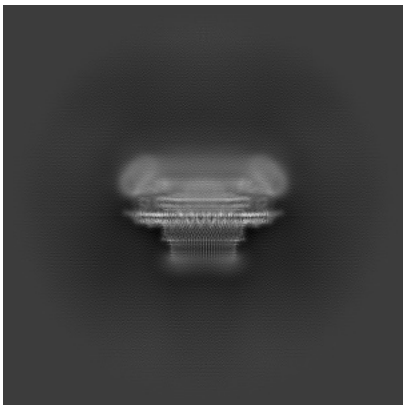
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-39763. These allow visual inspection of the internal detail of the map and identification of artifacts.

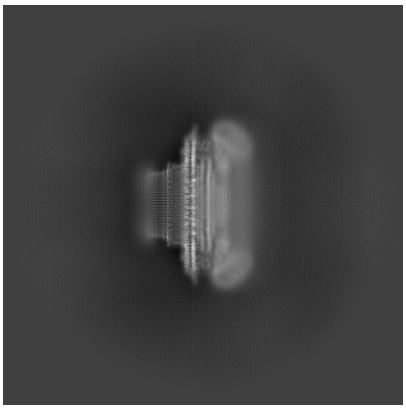
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

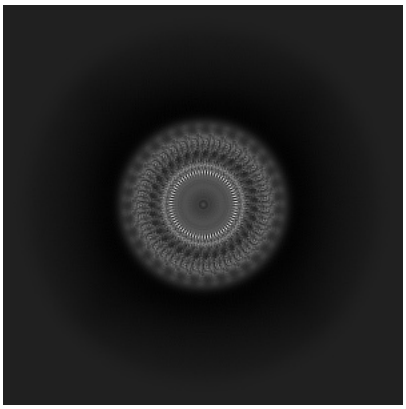
6.1.1 Primary map



X

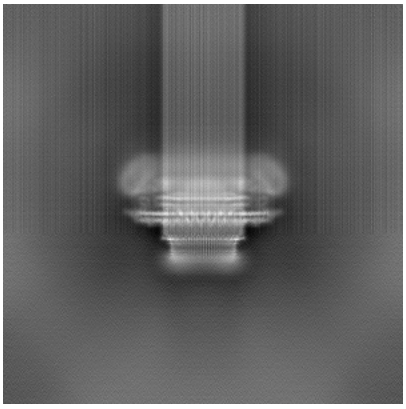


Y

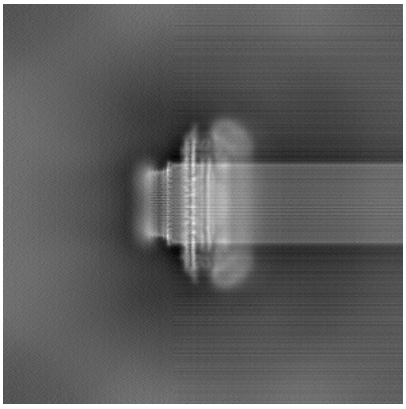


Z

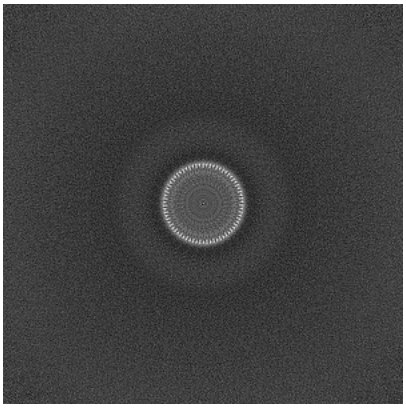
6.1.2 Raw map



X



Y

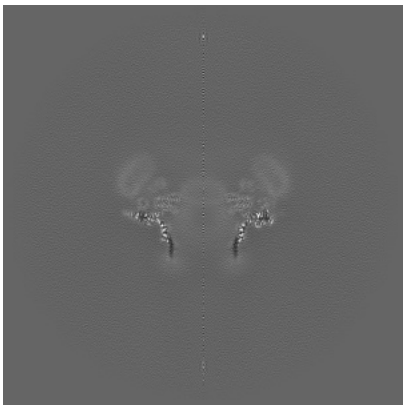


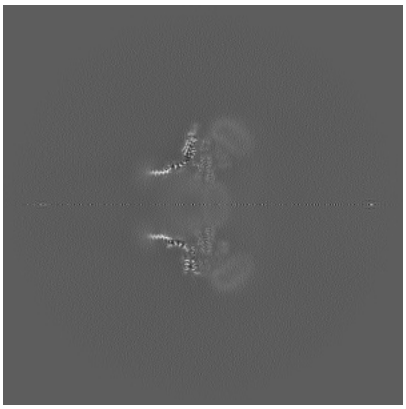
Z

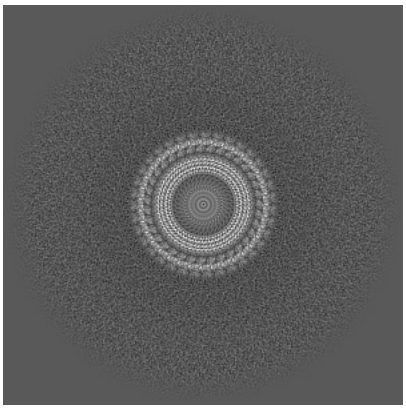
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

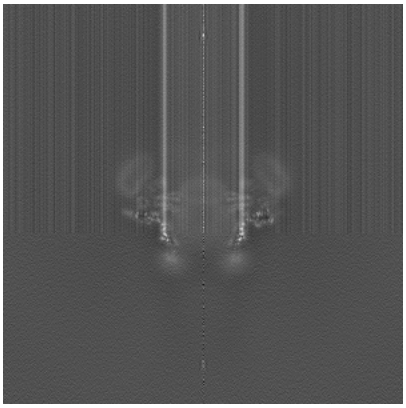
6.2.1 Primary map

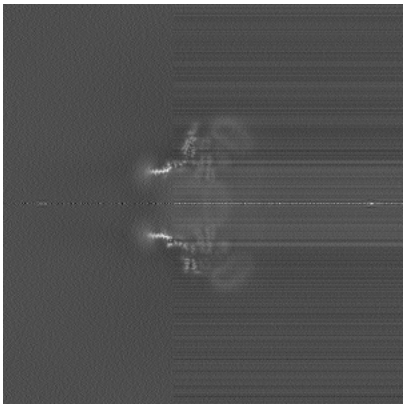

X Index: 300

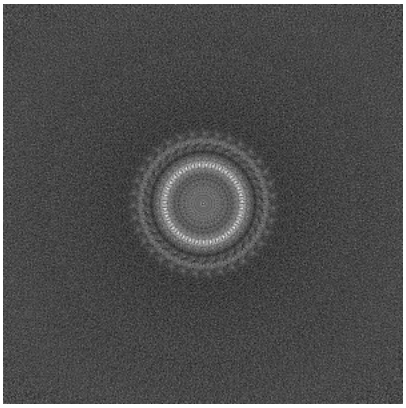

Y Index: 300


Z Index: 300

6.2.2 Raw map


X Index: 300


Y Index: 300

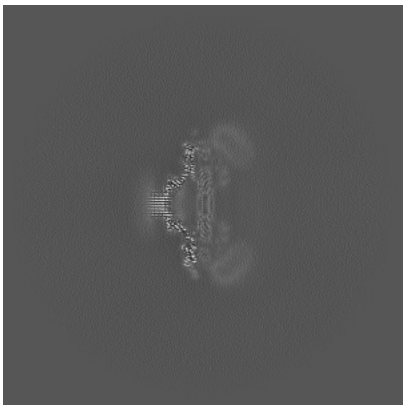

Z Index: 300

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

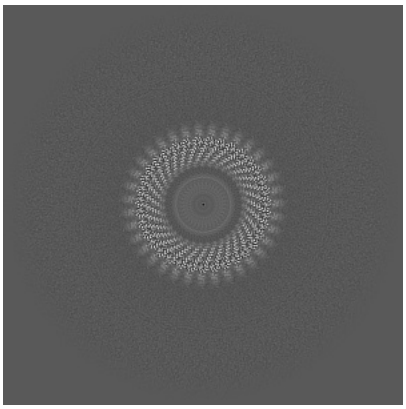
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 349

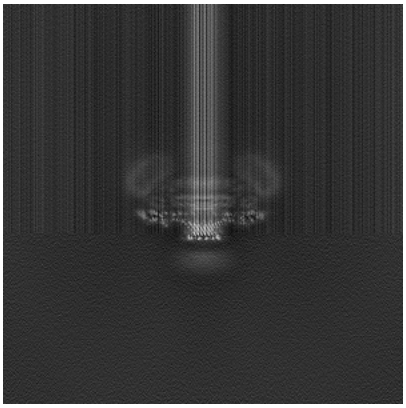


Y Index: 348

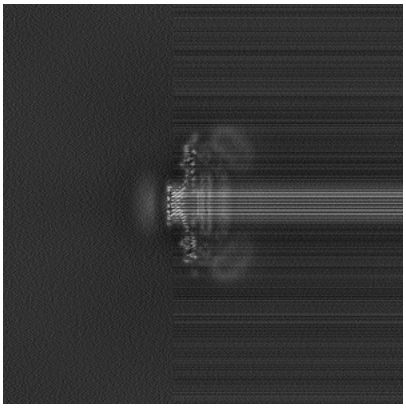


Z Index: 285

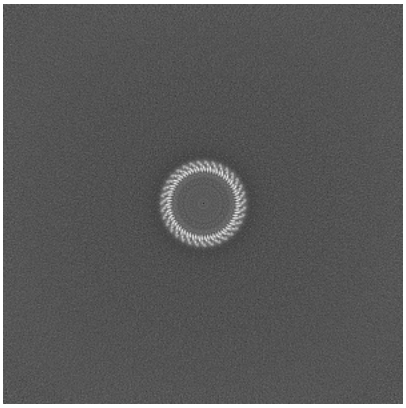
6.3.2 Raw map



X Index: 242



Y Index: 243

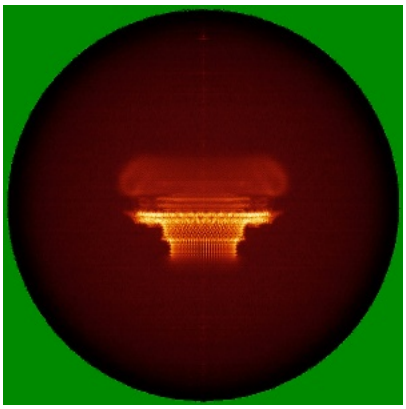


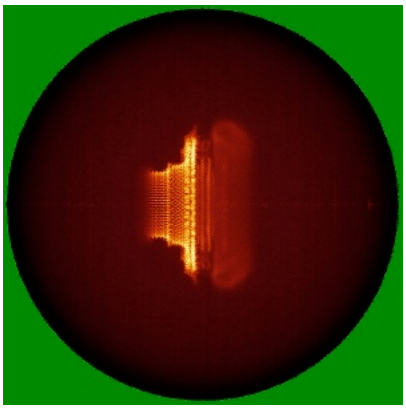
Z Index: 247

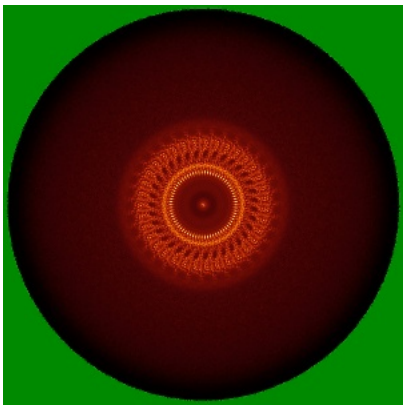
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

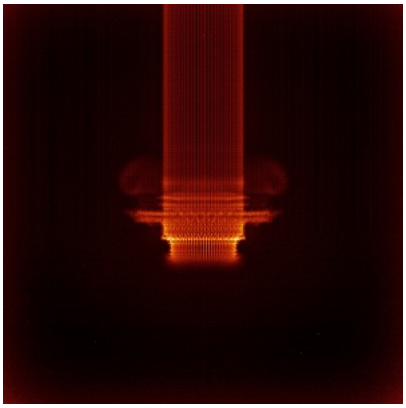
6.4.1 Primary map

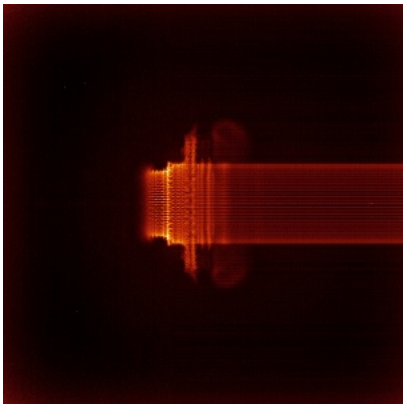

X

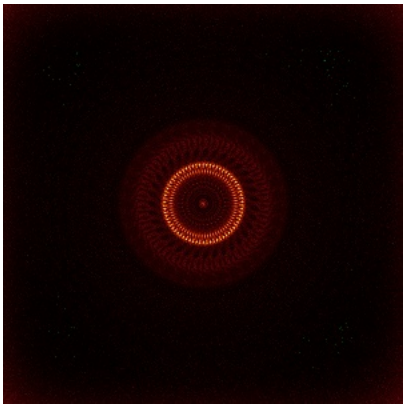

Y


Z

6.4.2 Raw map


X

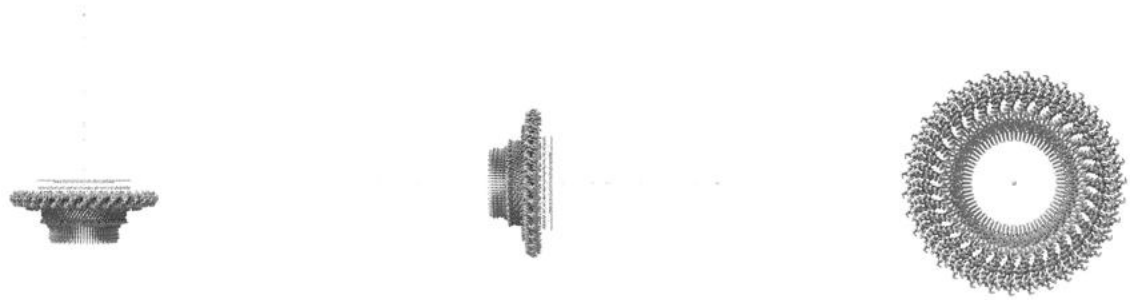

Y


Z

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

6.5 Orthogonal surface views (i)

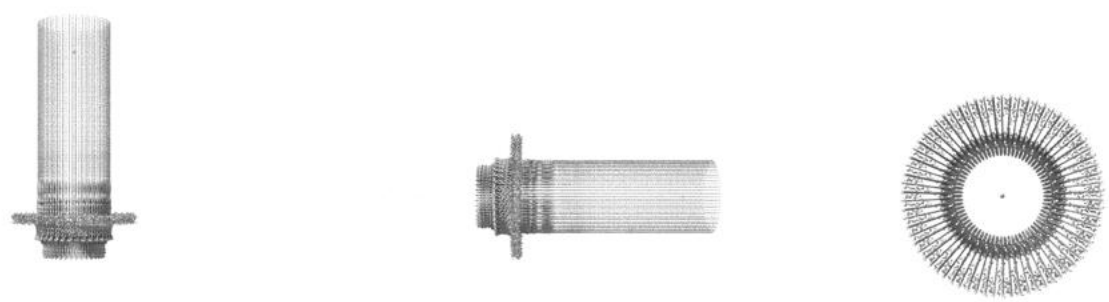
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

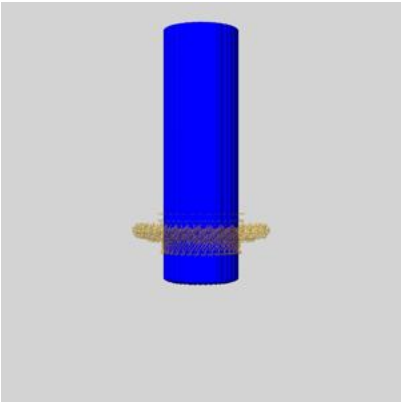
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

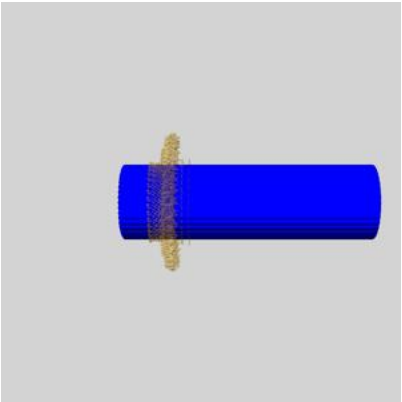
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

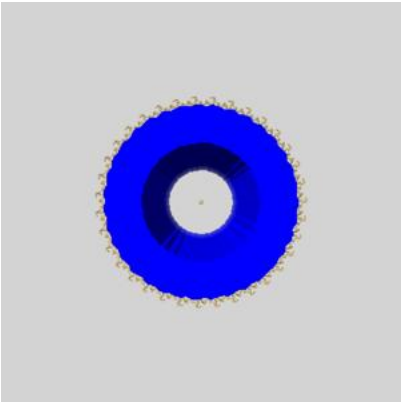
6.6.1 emd_39763_msk_1.map (i)



X



Y

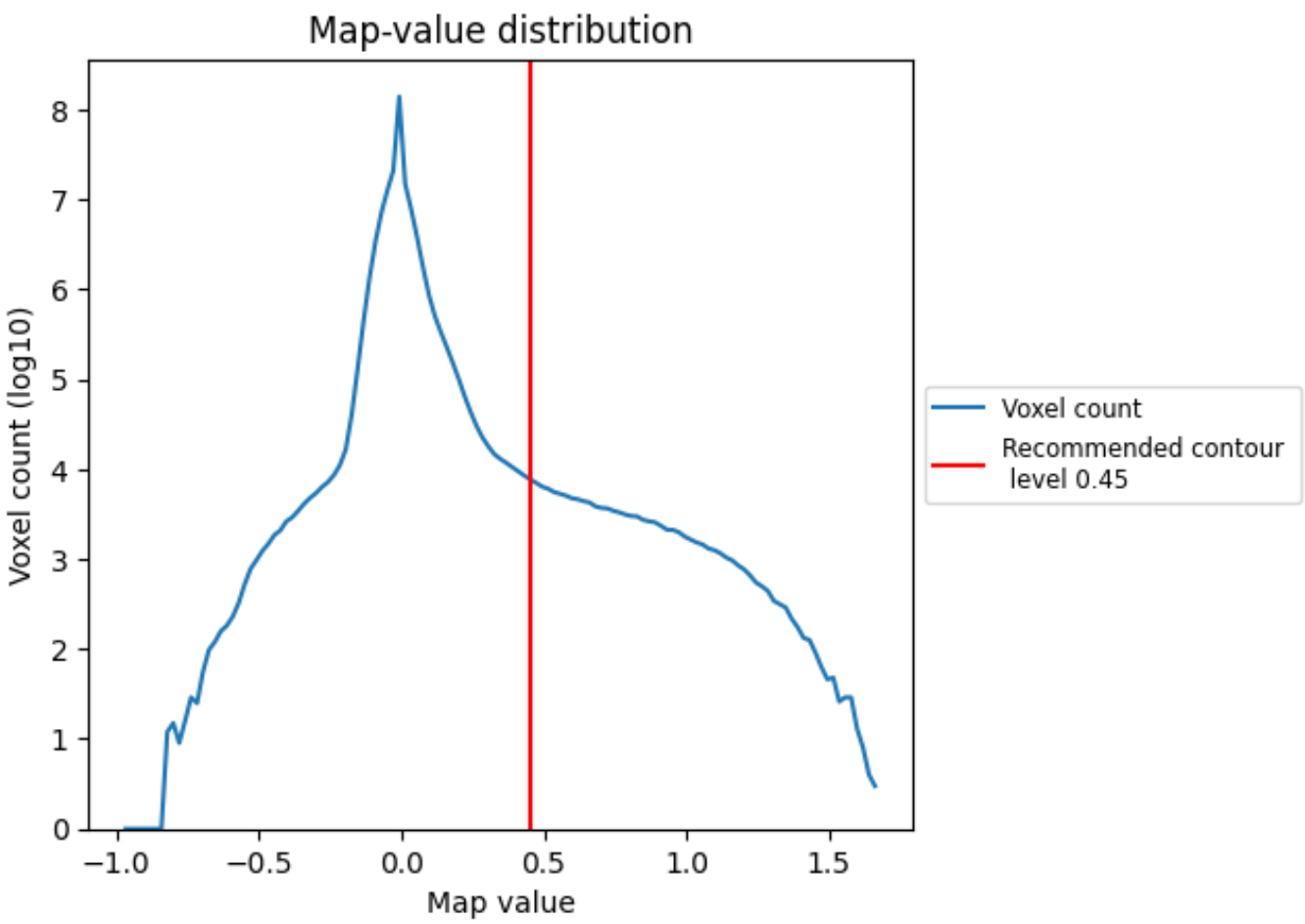


Z

7 Map analysis (i)

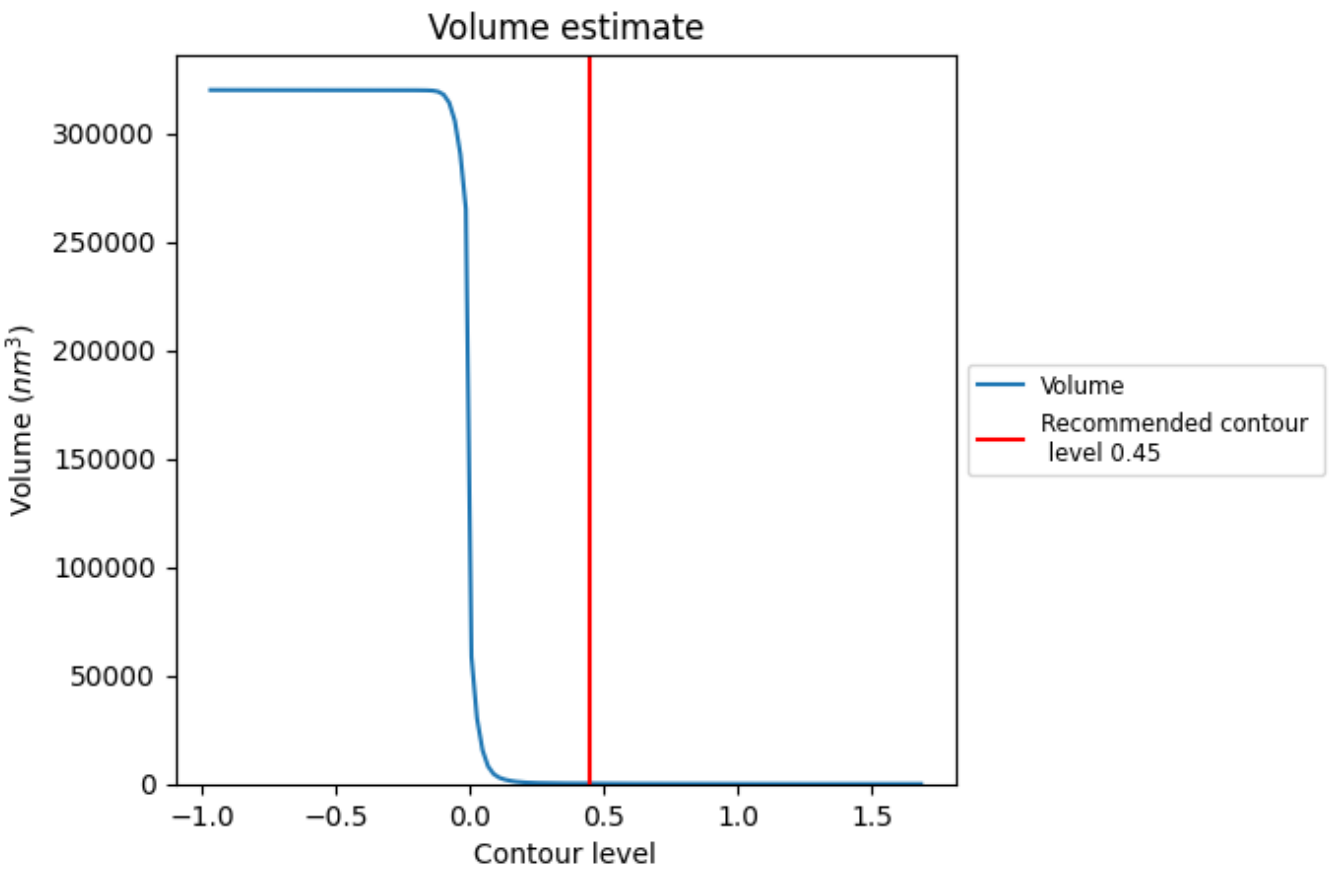
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

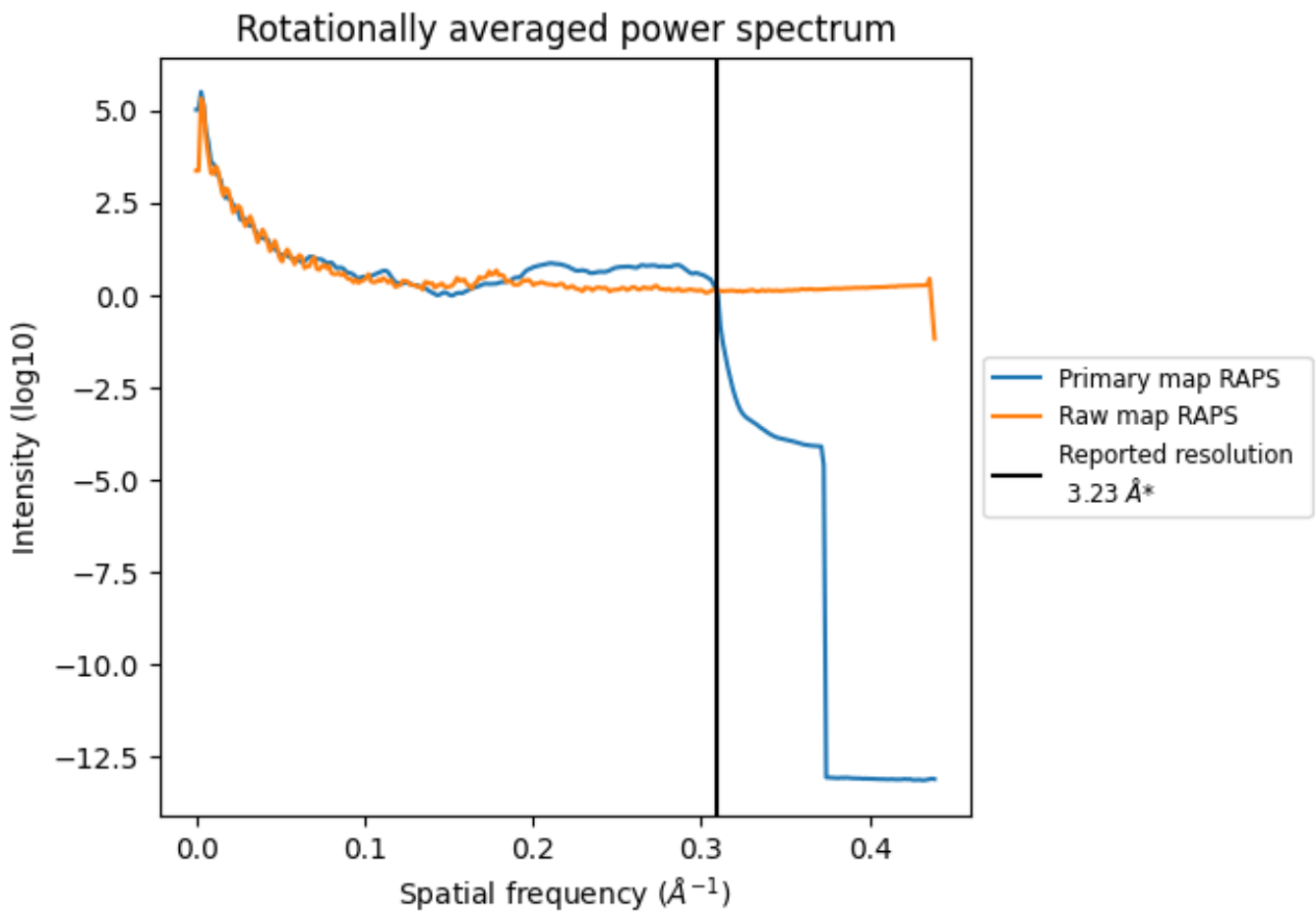
7.2 Volume estimate (i)



The volume at the recommended contour level is 183 nm^3; this corresponds to an approximate mass of 165 kDa.

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

7.3 Rotationally averaged power spectrum (i)

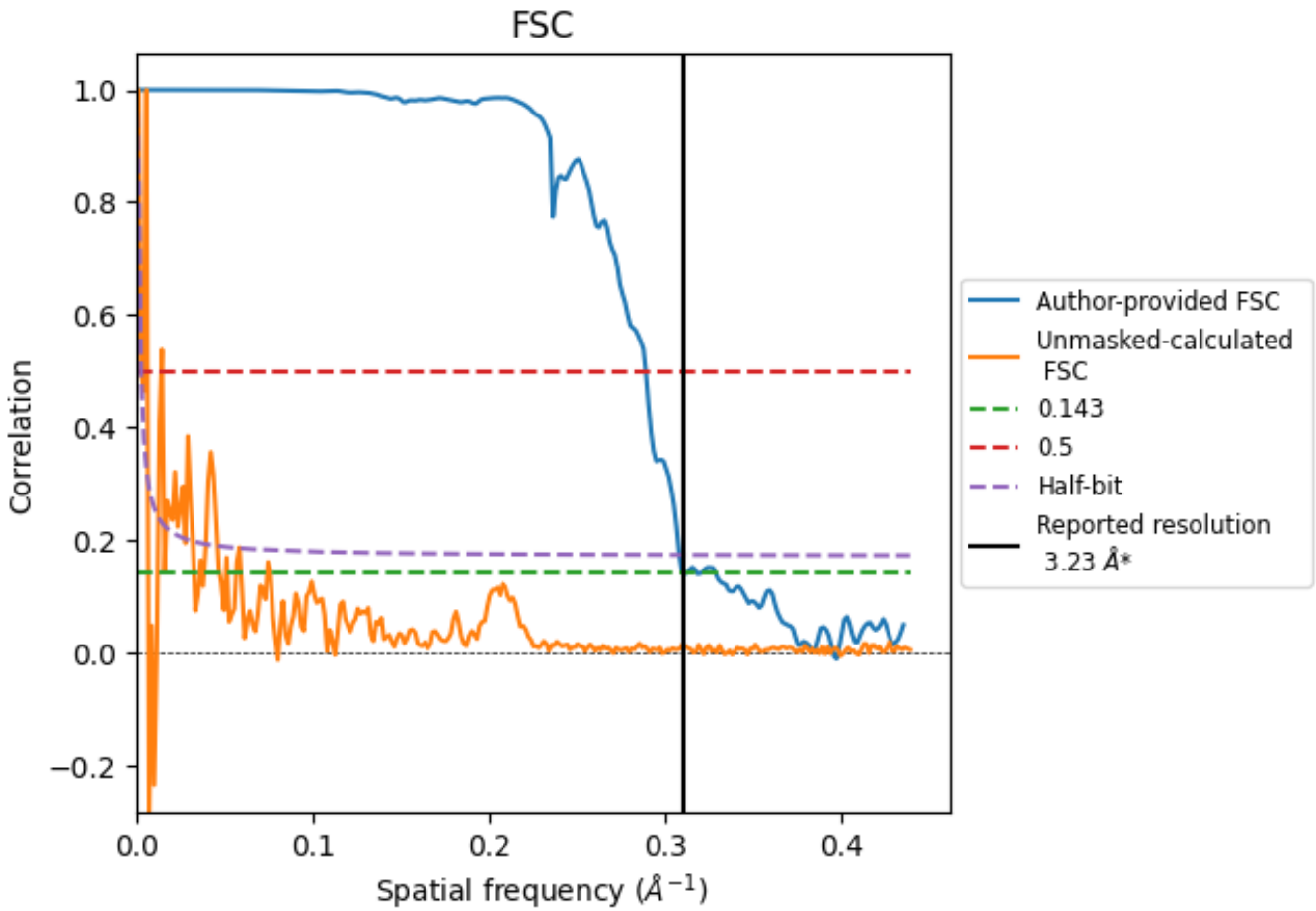


*Reported resolution corresponds to spatial frequency of 0.310 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.310 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	3.23	3.46	3.25
Unmasked-calculated*	147.06	344.83	151.52

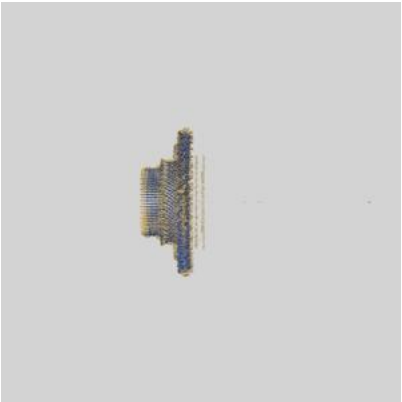
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 147.06 differs from the reported value 3.23 by more than 10 %

9 Map-model fit (i)

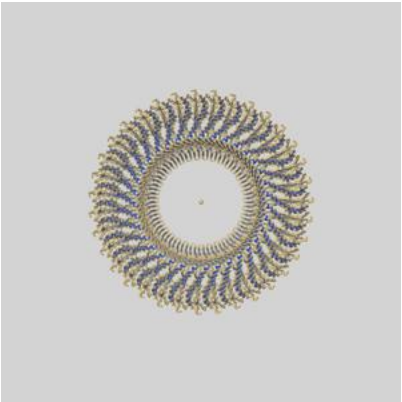
This section contains information regarding the fit between EMDB map EMD-39763 and PDB model 8Z4G. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay (i)

X



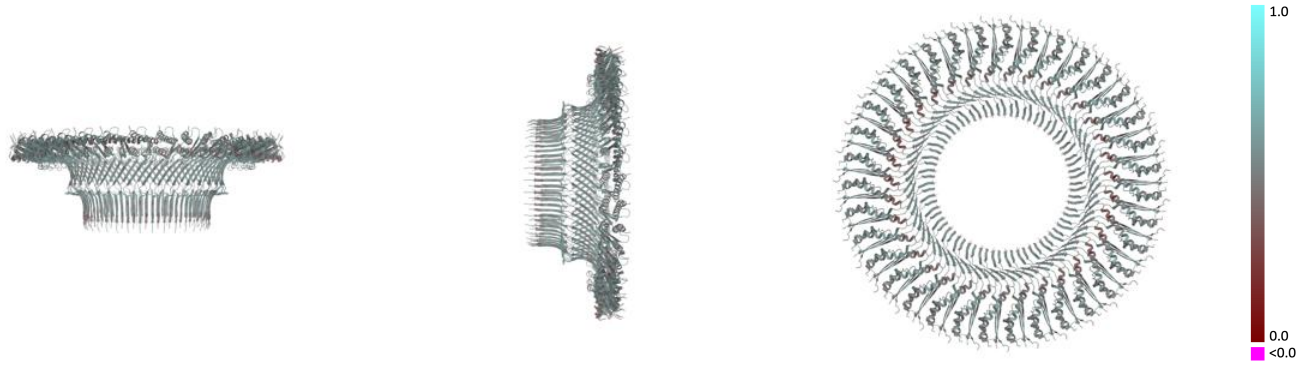
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

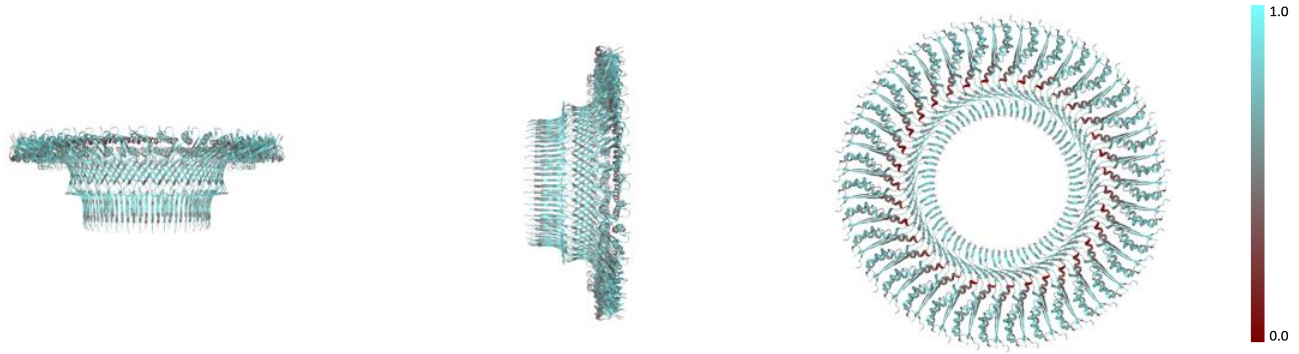
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

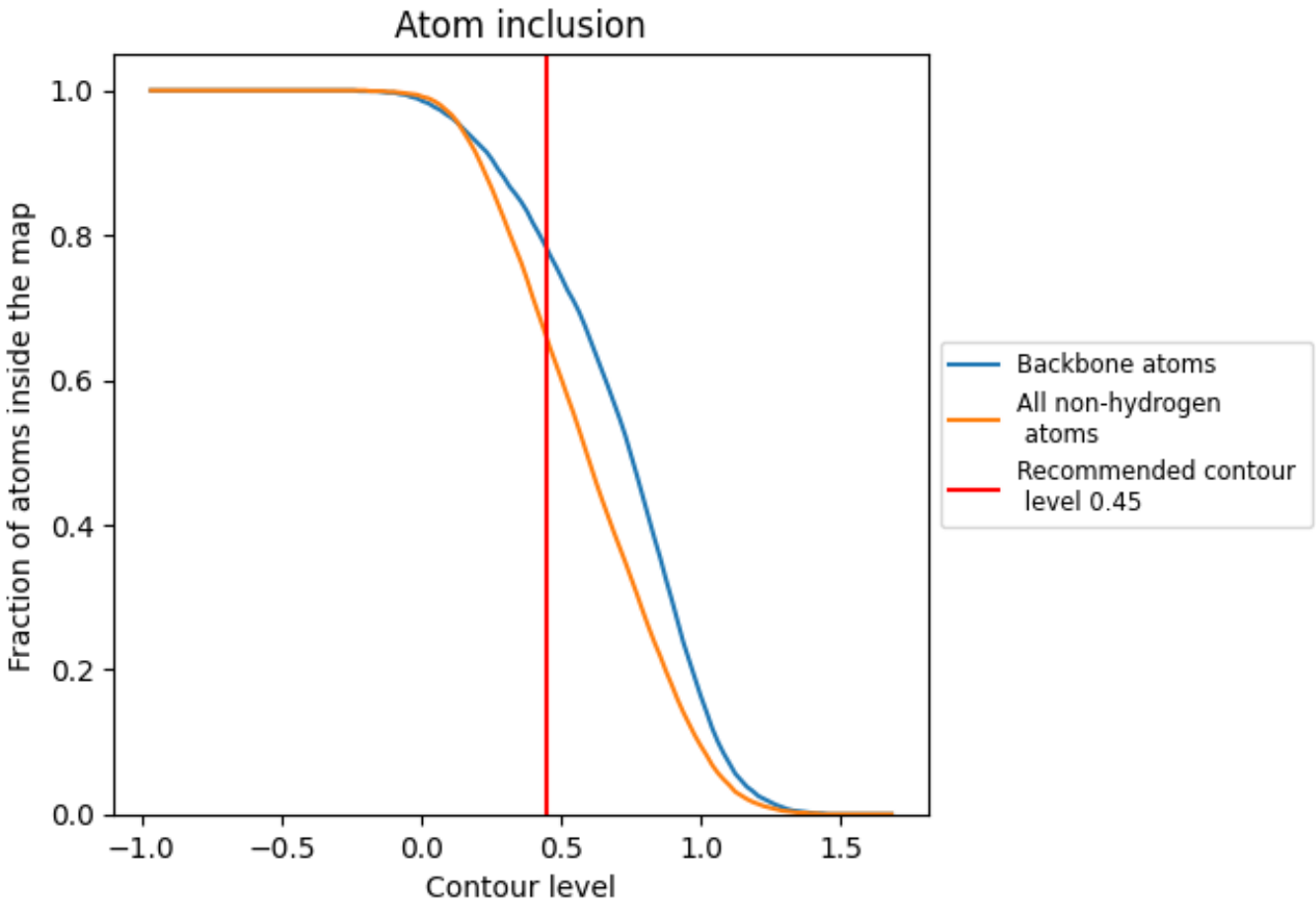
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.45).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 66% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6570	0.5180
1	0.6580	0.5320
2	0.6520	0.5130
3	0.6470	0.5120
4	0.6510	0.5130
5	0.6500	0.5190
6	0.6540	0.5120
7	0.6530	0.5120
8	0.6510	0.5140
9	0.6620	0.5170
A	0.6670	0.5240
B	0.6680	0.5220
C	0.6660	0.5280
D	0.6650	0.5290
E	0.6550	0.5260
F	0.6620	0.5260
G	0.6640	0.5220
H	0.6540	0.5260
I	0.6510	0.5160
J	0.6470	0.5140
K	0.6490	0.5190
L	0.6490	0.5150
M	0.6550	0.5130
N	0.6550	0.5140
O	0.6480	0.5110
P	0.6560	0.5110
Q	0.6620	0.5100
R	0.6610	0.5110
S	0.6610	0.5140
T	0.6560	0.5180
U	0.6700	0.5190
V	0.6650	0.5200
W	0.6660	0.5180
X	0.6560	0.5170
Y	0.6580	0.5190
Z	0.6540	0.5170