



wwPDB EM Validation Summary Report ⓘ

Mar 11, 2025 – 03:02 PM JST

PDB ID : 8Z4G
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 ⓘ symbol.

The types of validation reports are described at

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

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

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

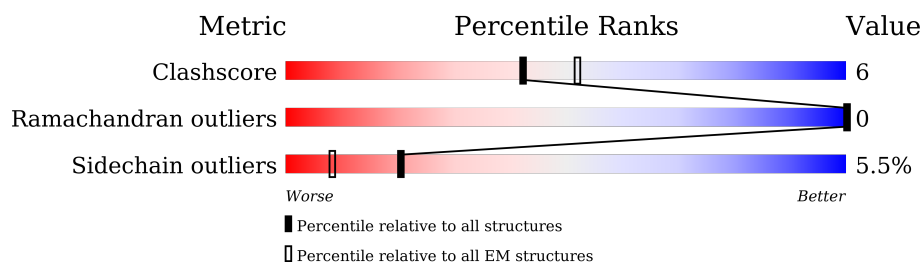
1 Overall quality at a glance

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.








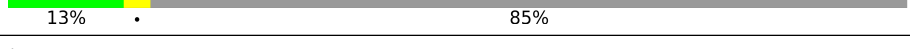

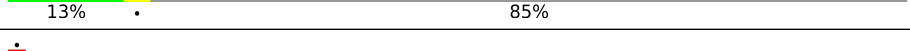
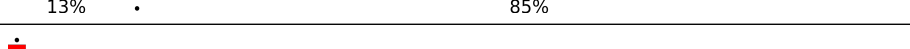
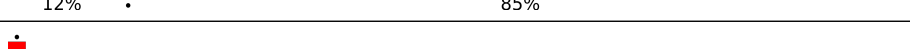















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	1	945	
1	2	945	
1	3	945	
1	4	945	
1	5	945	
1	6	945	
1	7	945	
1	8	945	



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Mol	Chain	Length	Quality of chain
1	9	945	
1	A	945	
1	B	945	
1	C	945	
1	D	945	
1	E	945	
1	F	945	
1	G	945	
1	H	945	
1	I	945	
1	J	945	
1	K	945	
1	L	945	
1	M	945	
1	N	945	
1	O	945	
1	P	945	
1	Q	945	
1	R	945	
1	S	945	
1	T	945	
1	U	945	
1	V	945	
1	W	945	
1	X	945	

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Mol	Chain	Length	Quality of chain
1	Y	945	 13% 85%
1	Z	945	 12% 85%

2 Entry composition

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

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

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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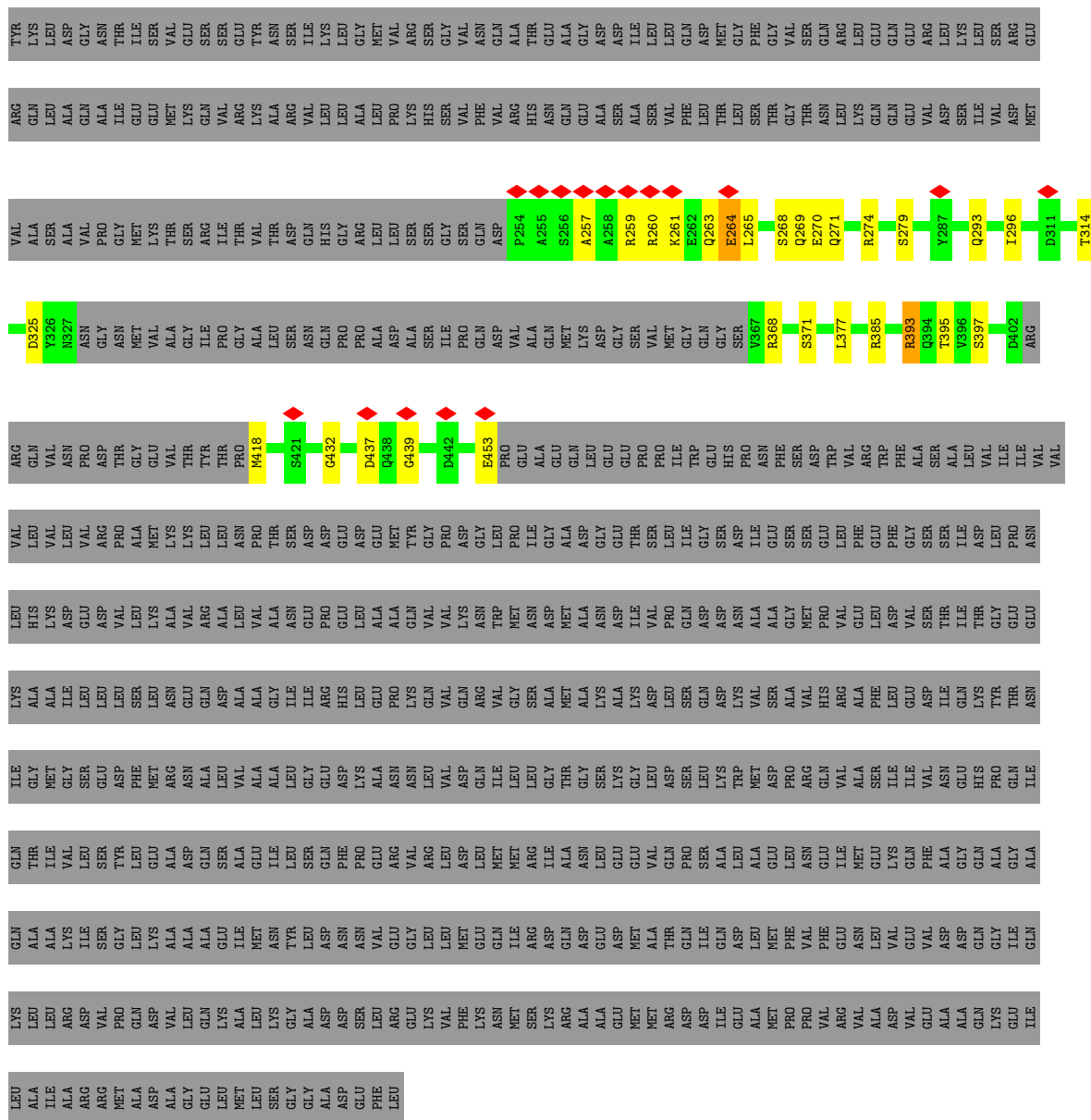
Chain	Residue	Modelled	Actual	Comment	Reference
X	-10	HIS	-	expression tag	UNP Q75N27
X	-9	HIS	-	expression tag	UNP Q75N27
X	-8	HIS	-	expression tag	UNP Q75N27
X	-7	HIS	-	expression tag	UNP Q75N27
X	-6	HIS	-	expression tag	UNP Q75N27
X	-5	HIS	-	expression tag	UNP Q75N27
X	-4	ILE	-	expression tag	UNP 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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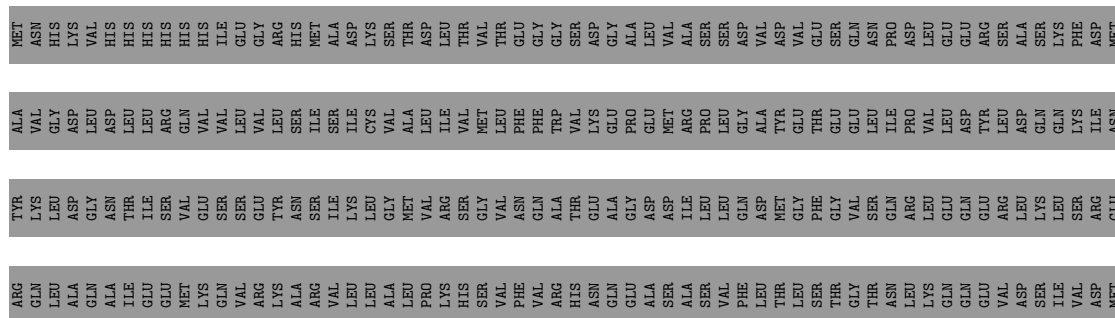
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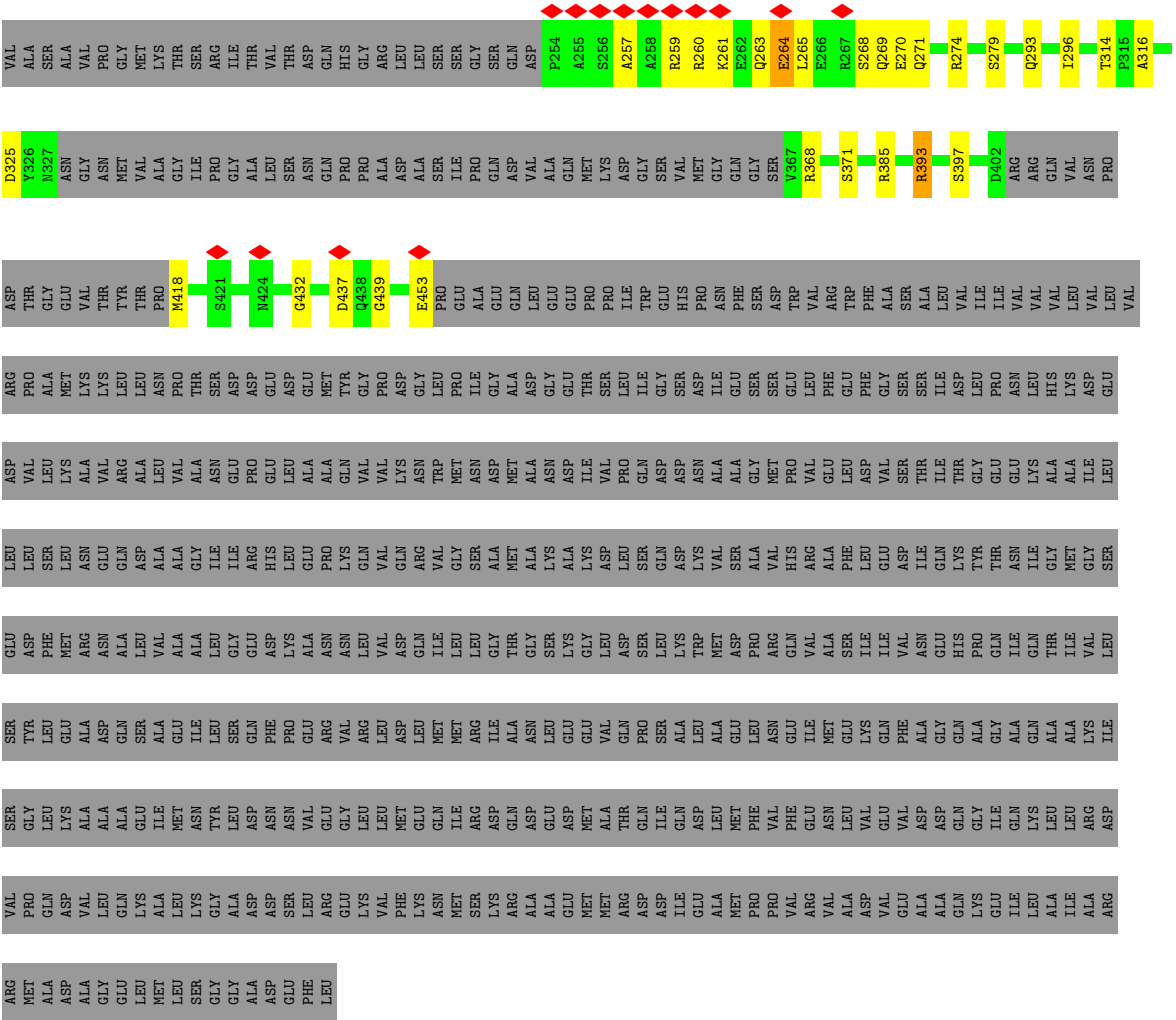
Chain	Residue	Modelled	Actual	Comment	Reference
Z	-2	GLY	-	expression tag	UNP Q75N27
Z	-1	ARG	-	expression tag	UNP Q75N27
Z	0	HIS	-	expression tag	UNP Q75N27
Z	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0

[illegible]

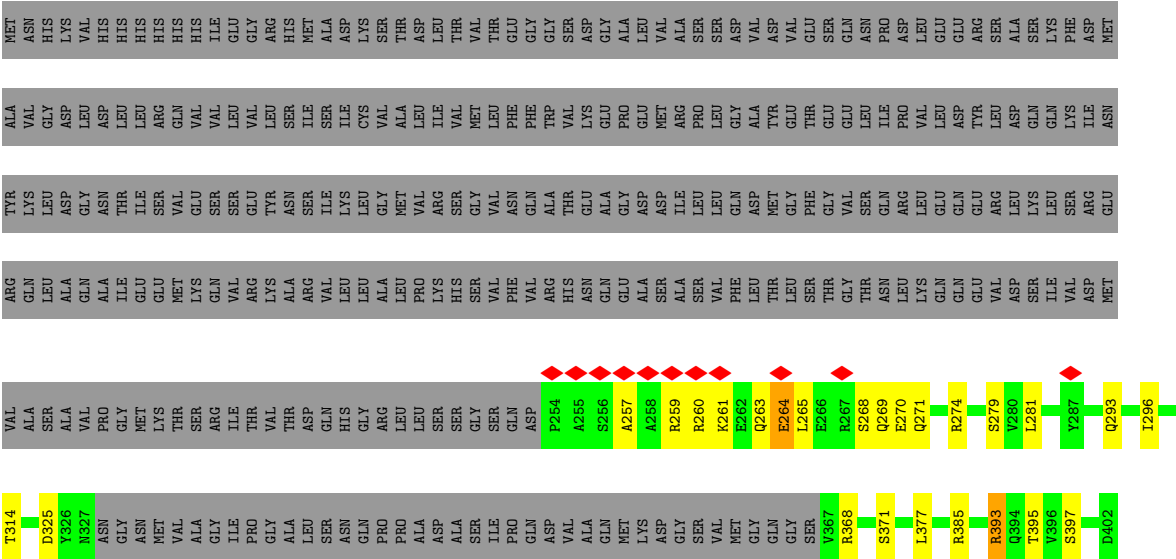


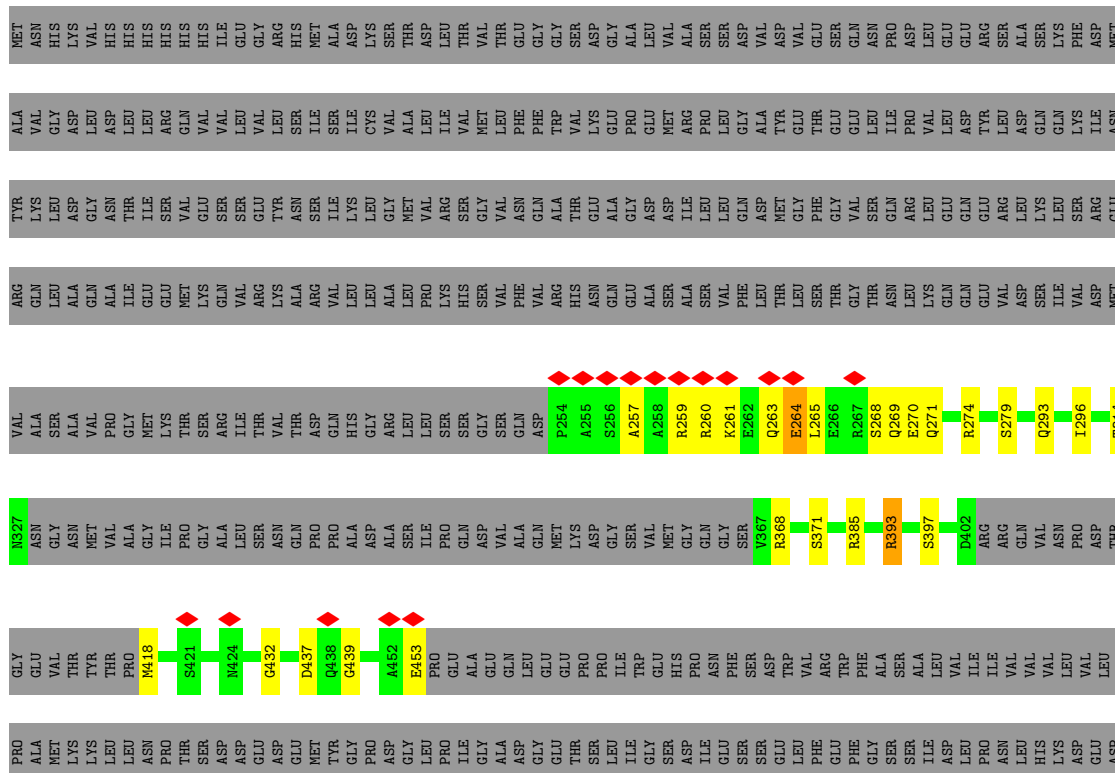
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG





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





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

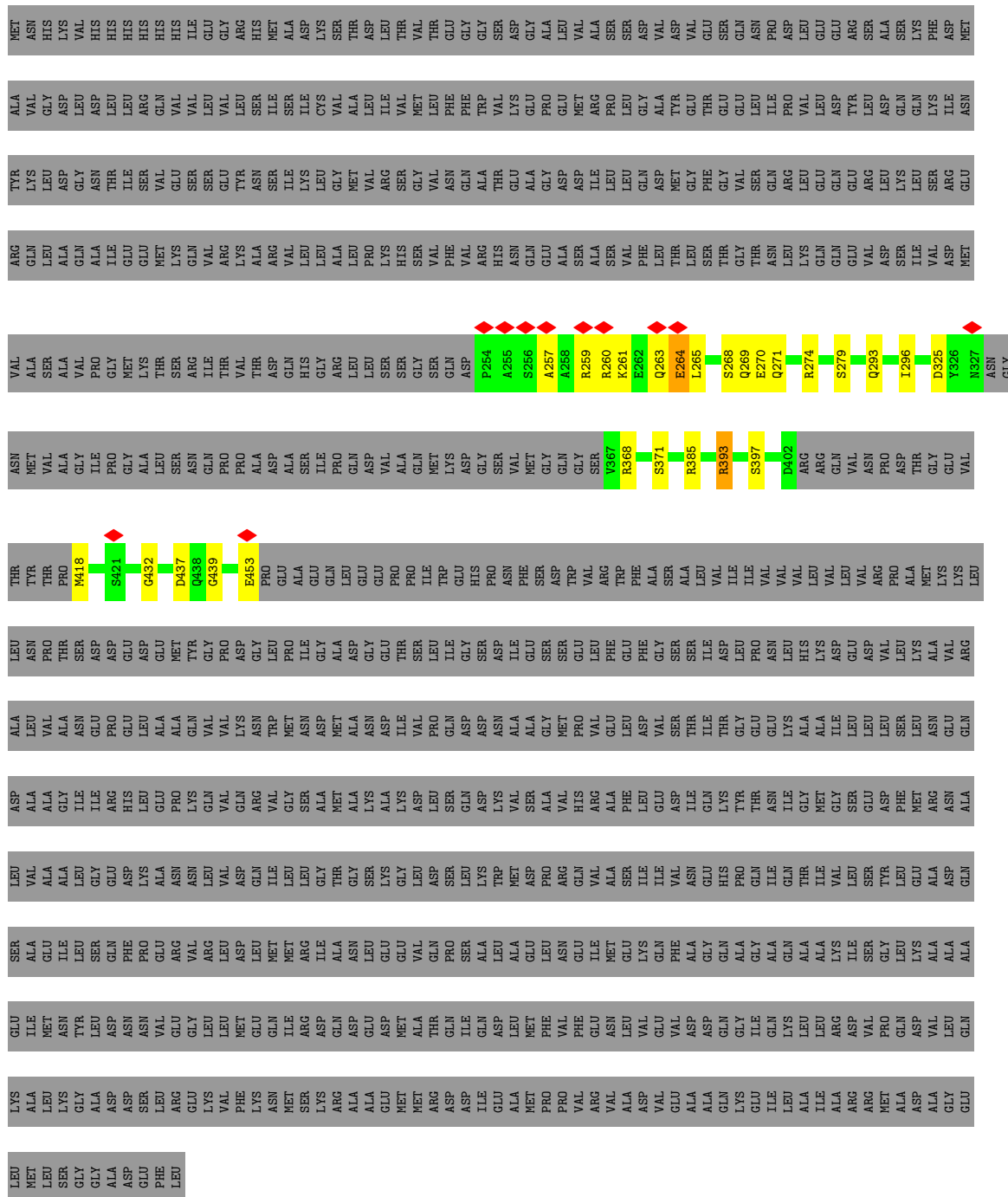
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG



PHE	SER	LEU	ALA	GLU	ASN	VAL	ARG	THR	ALA	MET
ARG	ASN	ALA	MET	VAL	GLY	ALA	GLN	LYS	VAL	ASN
ASN	LEU	ALA	LYS	THR	ASN	SER	SER	LEU	GLY	HIS
ALA	GLN	ARG	LEU	THR	VAL	VAL	GLN	GLN	ASP	VAL
LEU	ASP	ALA	LEU	PRO	ALA	PRO	ILE	THR	LEU	HIS
VAL	ALA	LEU	ASN	ILE	GLY	GLY	ILE	ILE	THR	LEU
ALA	GLY	VAL	THR	GLY	PRO	MET	GLU	GLU	LEU	HIS
ALA	ILE	ASN	SER	GLY	GLY	THR	MET	VAL	GLN	HIS
GLY	ILE	GLU	ASP	ALA	ALA	SER	LYS	GLY	VAL	GLY
GLY	ARG	PRO	ASP	ILE	LEU	ARG	GLN	SER	VAL	ILE
ASP	HIS	GLU	GLU	G432	SER	ILE	VAL	SER	VAL	GLU
LYS	LEU	LEU	ASP	GLY	ASN	THR	ARG	GLU	VAL	GLY
ALA	GLU	ALA	GLU	D437	GLN	VAL	LYS	THR	VAL	LEU
ASN	PRO	ALA	MET	Q438	PRO	THR	ALA	ASN	LEU	LEU
ASN	LYS	GLN	THR	Q439	PRO	ASP	ARG	SER	ILE	MET
LEU	GLN	VAL	GLY	GLY	ALA	GLN	VAL	ILE	SER	ALA
VAL	VAL	VAL	PRO	A452	ASP	HIS	LEU	LYS	ILE	ASP
ASP	GLN	LYS	ASP	E453	ALA	GLY	LEU	CYS	VAL	LYS
GLN	ARG	GLY	LEU	THR	SER	ARG	ALA	GLY	ALA	SER
ILE	VAL	TRP	ASP	PRO	ILE	LEU	LEU	MET	ALA	THR
LEU	GLY	MET	PRO	GLU	PRO	LEU	PRO	VAL	LEU	ASP
ASN	ASN	ASN	ILE	ALA	GLN	SER	LYS	ARG	ILE	LEU
LEU	SER	ASN	GLY	GLU	ASP	SER	HIS	SER	VAL	THR
ALA	ALA	MET	GLY	GLU	VAL	GLY	VAL	GLY	MET	VAL
THR	MET	MET	ALA	GLN	ALA	SER	VAL	VAL	LEU	THR
GLY	ALA	LEU	GLY	ALA	GLN	GLN	PHE	ASN	PHE	GLY
LYS	ALA	ASP	GLY	GLU	MET	ASP	VAL	GLN	PHE	GLY
GLY	LYS	ILE	THR	PRO	LYS	P254	ARG	ALA	TRP	GLY
LEU	ASP	VAL	SER	PRO	ASP	A255	HIS	THR	VAL	SER
ASP	PRO	PRO	ILE	ILE	GLY	S256	ASN	GLY	LYS	ASP
LEU	GLN	GLN	GLY	THR	VAL	R257	GLN	ALA	GLY	ALA
LEU	ASP	ASP	GLY	VAL	VAL	A258	GLU	ASP	PRO	LEU
LYS	ASP	ASN	SER	HIS	MET	GLY	ALA	ASP	GLU	LEU
TRP	LYS	ASN	ASP	PRO	GLY	R259	SER	ASP	MET	VAL
MET	VAL	ALA	ILE	ASN	GLN	R260	ALA	ILE	ARG	ALA
ASP	SER	ALA	GLU	PHE	GLY	K261	SER	LEU	PRO	ALA
PRO	ALA	GLY	SER	SER	SER	Q262	VAL	LEU	LEU	SER
ARG	VAL	MET	SER	ASP	V367	R263	PHE	GLN	GLY	ASP
GLN	HIS	PRO	GLU	THR	R368	Q263	LEU	ASP	ALA	VAL
VAL	ARG	VAL	LEU	VAL	GLY	E264	THR	MET	ALA	ASP
ALA	ALA	GLU	PHE	ARG	ILE	L265	LEU	GLY	TYR	VAL
SER	PHE	LEU	GLU	THR	GLY	Q268	SER	PHE	GLU	VAL
ILE	LEU	ASP	PHE	PHE	R385	Q269	GLY	VAL	GLU	SER
VAL	ASP	VAL	GLY	ALA	Q270	E271	THR	SER	LEU	ASN
ASN	ILE	SER	SER	SER	R393	Q271	ASN	GLN	ILE	PRO
GLU	THR	THR	SER	ALA	S397	R274	LEU	ARG	PRO	ASP
GLY	GLN	ILE	ILE	LEU	GLY	R279	GLN	LEU	VAL	GLU
HIS	LYS	THR	ASP	VAL	D402	ARG	GLN	GLY	LEU	GLY
PRO	THR	GLY	PRO	ILE	THR	ASN	GLY	THR	ASP	ARG
THR	ASN	GLU	ASN	VAL	GLN	Q293	VAL	GLY	LEU	SER
ILE	ILE	LYS	LEU	VAL	VAL	L296	ASP	VAL	THR	ALA
THR	GLY	ALA	HIS	LEU	VAL	T314	ILE	GLN	ASP	ALA
ILE	MET	ILE	LYS	LEU	ASN	Q314	SER	GLN	GLN	ALA
VAL	GLY	ILE	ASP	VAL	PRO	T314	VAL	LYS	GLN	VAL
LEU	SER	LEU	GLU	LEU	ASP	R325	VAL	SER	LYS	PHE
LEU	ASP	LEU	VAL	VAL	GLY	R325	MET	THR	ILE	ASN
SER	ASN	THR	VAL	THR	THR	R325	ASN	THR	ASN	MET

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

Chain B:  13% 85%



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

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

● Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FlhG

Chain G:  13%  85%

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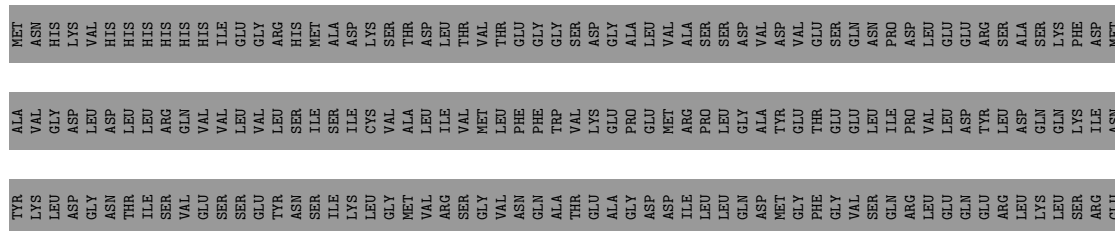
GLU	GLN	ALA	GLN	ALA	GLN	ARG	GLN	ALA	ARG
GLU	GLN	GLU	GLN	GLU	GLN	GLN	GLN	LEU	ASP
MET	ALA	ILE	ALA	ILE	ALA	VAL	VAL	ALA	ALA
LEU	LEU	MET	GLU	MET	GLU	GLU	GLU	ALA	ALA
SER	LYS	ASN	ILE	SER	ILE	LEU	GLY	ILE	ASN
GLY	GLY	TYR	LEU	GLY	GLY	GLY	GLY	ILE	GLU
ALA	ALA	LEU	SER	LEU	GLY	GLY	GLY	ILE	PRO
ASP	ASP	ASP	GLN	ASP	GLN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

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

Chain H: 13% 85%

[illegible]

Chain L: 13% 85%





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

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

Chain P: 12% 85%

LEU	LYS	ALA	ASP	ASN	GLY	THR	ASP	ASN	VAL	ARG	THR	ALA	MET
LYS	ALA	LYS	GLY	ASN	GLY	THR	THR	ASN	ALA	GLN	LYS	VAL	ASN
VAL	ARG	LEU	GLU	MET	VAL	VAL	VAL	VAL	ALA	ALA	GLY	ASP	LYS
ALA	LEU	LEU	THR	ALA	GLY	THR	THR	PRO	PRO	ILE	ASN	ASP	HIS
LEU	ASN	ASN	THR	ILE	ILE	THR	THR	PRO	GLY	ILE	THR	LEU	HIS
VAL	ALA	THR	THR	THR	THR	THR	THR	PRO	MET	GLN	VAL	LEU	HIS
ASN	ASN	THR	M418	ALA	GLY	THR	THR	PRO	THR	MET	GLN	LEU	HIS
GLU	GLU	ASP	GLY	ALA	SER	THR	THR	ASP	ARG	GLN	VAL	VAL	HIS
GLU	GLU	ASP	S421	LEU	SER	ILE	THR	ILE	ARG	GLN	SER	LEU	GLY
LEU	LEU	ASP	G432	ASN	GLN	THR	THR	VAL	ARG	GLY	SER	VAL	GLY
ALA	ALA	GLU	GLY	PRO	GLN	VAL	THR	VAL	ARG	THR	TYR	LEU	ARG
GLN	GLN	THR	D437	PRO	PRO	THR	THR	ASP	ALA	ALA	ASN	SER	HIS
VAL	VAL	GLY	Q438	ALA	ALA	GLN	THR	GLN	VAL	VAL	ILE	SER	ASP
VAL	VAL	PRO	G439	ASP	ASP	HIS	THR	GLN	THR	VAL	ILE	SER	ALA
LYS	ASN	ASP	E453	ALA	ALA	GLY	THR	GLY	LEU	LEU	LYS	ILE	ASP
ASN	ASN	GLY	PRO	SER	SER	ARG	THR	ARG	ALA	ALA	CYS	VAL	LYS
LEU	TRP	LEU	GLU	ILE	ILE	LEU	LEU	LEU	ALA	GLY	GLY	VAL	THR
MET	PRO	ILE	ALA	PRO	GLU	LEU	SER	SER	PRO	VAL	ARG	ILE	ASP
ASN	ASN	ILE	ALA	GLN	GLN	SER	SER	SER	LYS	HIS	THR	VAL	LEU
ASP	ASP	GLY	GLU	ASP	VAL	GLY	GLY	GLY	VAL	VAL	SER	VAL	THR
ALA	ALA	ASP	GLU	ALA	ALA	SER	SER	SER	VAL	VAL	GLY	MET	LEU
GLY	GLY	GLY	GLU	GLN	GLY	GLN	GLN	ASP	PHE	ASN	PHE	GLY	GLY
ASP	ASP	THR	GLU	MET	MET	ASP	ASP	ALA	ARG	ALA	TRP	VAL	SER
ILE	ILE	THR	PRO	LYS	LYS	PRO	P254	ALA	HIS	THR	THR	VAL	GLY
VAL	VAL	SER	ILE	ASP	ASP	ILE	A295	ASN	ASN	GLY	GLY	LYS	ASP
PRO	PRO	ILE	TRP	GLY	GLY	TRP	S256	GLN	GLN	ALA	ALA	GLY	GLY
GLN	GLN	ILE	GLU	SER	SER	ILE	A257	GLY	GLY	GLY	PRO	ALA	ALA
ASP	ASP	SER	HIS	MET	MET	SER	A258	VAL	ALA	ASP	GLY	LEU	LEU
ASN	ASN	ASP	PRO	GLY	GLY	ASN	R259	GLN	ALA	ASP	MET	VAL	ALA
ALA	ALA	ILE	PHE	ASN	PHE	ASN	R260	VAL	VAL	LEU	ARG	ARG	VAL
GLY	GLY	GLU	SER	GLY	SER	SER	K261	SER	SER	LEU	GLY	PRO	ASP
GLY	GLY	SER	SER	SER	SER	SER	K261	PHE	PHE	GLN	GLY	ASP	SER
MET	MET	SER	ASP	ASP	ASP	ASP	E262	LEU	LEU	ASP	ALA	VAL	VAL
PRO	PRO	GLU	TRP	V367	R368	TRP	Q263	THR	THR	MET	TYR	GLU	ASP
VAL	VAL	LEU	VAL	K369	K369	ARG	E264	LEU	LEU	GLY	GLY	GLU	VAL
GLU	GLU	PHE	THR	E370	E370	THR	L265	SER	SER	PHE	THR	GLU	GLN
LEU	LEU	GLU	PHE	S371	S371	GLY		THR	THR	GLY	VAL	GLU	ASN
ASP	ASP	GLY	ALA	R385	R385	ALA		GLY	GLY	VAL	ILE	LEU	PRO
VAL	VAL	SER	SER	ALA	ALA	SER		THR	THR	ASN	GLN	ILE	ASN
THR	THR	SER	THR	R393	R393	LEU		ALA	ALA	ARG	PRO	PRO	ASP
ILE	ILE	ILE	ILE	Q394	Q394	THR		LYS	LYS	LEU	VAL	VAL	GLY
THR	THR	GLY	VAL	T395	T395	ILE		GLN	GLN	GLU	ASP	GLU	GLY
GLU	GLU	PRO	ILE	V396	V396	ILE		GLY	GLY	TYR	TYR	GLU	GLY
GLU	GLU	ASN	VAL	S397	S397	VAL		VAL	VAL	ARG	LEU	LEU	SER
LYS	LYS	LEU	VAL	D402	D402	GLY		ASP	ASP	LEU	ASP	ASP	ALA
ALA	ALA	HIS	LEU	ARG	ARG	ILE		GLY	GLY	GLN	LYS	GLN	ALA
ILE	ILE	ASP	VAL	GLN	GLN	VAL		ILE	ILE	VAL	LYS	GLN	LYS
LEU	LEU	GLU	LEU	VAL	VAL	GLY		VAL	VAL	SER	THR	GLY	PHE
LEU	LEU	VAL	VAL	ASN	VAL	VAL		ASP	ASP	ARG	ILE	ILE	ASN
VAL	VAL	VAL	ARG	ASN	ASN	VAL		MET	MET	GLY	GLY	GLY	MET

[illegible]

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



Tyr	Asp	Leu	Val	Pro	Asp	D325	Val	Arg	Tyr	Ala	Met
Phe	Met	Ser	Leu	Leu	Thr	H326	Ala	Gln	Lys	Val	Asn
Leu	Arg	Asn	Lys	Met	Glu	H327	Ser	Leu	Leu	Gly	His
Asp	Asn	Glu	Val	Lys	Val	Asn	Ala	Gln	Asp	Val	Lys
Gln	Ala	Gln	Arg	Leu	Thr	Asn	Pro	Ala	Asn	Pro	His
Ser	Leu	Asp	Ala	Leu	Tyr	Met	Gly	Ile	Thr	Leu	His
Ala	Val	Ala	Val	Ala	Thr	Ala	Met	Glu	Ile	Leu	His
Glu	Ala	Gly	Ala	Pro	M418	Ala	Lys	Met	Ser	Gln	His
Leu	Leu	Ile	Asn	Ser	S421	Ile	Ser	Lys	Glu	Val	His
Ser	Gly	Ile	Glu	Asp	S422	Pro	Arg	Gln	Ser	Val	His
Gln	Glu	Arg	Pro	Asp	G432	Gly	Ile	Val	Ser	Leu	Glu
Phe	Asp	His	Glu	Glu	G433	Ala	Thr	Arg	Glu	Val	Gly
Pro	Lys	Leu	Leu	Asp	D437	Leu	Val	Lys	Tyr	Val	Arg
Ala	Ala	Glu	Ala	Glu	D438	Ser	Thr	Ala	Asn	Ser	Met
Asn	Asn	Pro	Ala	Met	G439	Asn	Asp	Arg	Ala	Ser	His
Leu	Leu	Lys	Gln	Tyr	G439	Gln	Gln	Val	Ile	Ser	Ala
Arg	Asn	Gln	Val	Gly	A452	Pro	His	Leu	Lys	Ile	Asp
Leu	Val	Val	Val	Pro	E453	Pro	Gly	Leu	Leu	Cys	Lys
Asp	Asp	Gln	Lys	Asp	E453	Ala	Arg	Ala	Gly	Val	Ser
Gln	Gln	Arg	Asn	Gly	Pro	Leu	Leu	Pro	Val	Ile	Asp
Ile	Ile	Val	Trp	Leu	Ala	Ala	Leu	Lys	Arg	Leu	Leu
Met	Met	Gly	Met	Pro	Glu	Ser	Ser	His	Ser	Val	Thr
Leu	Leu	Ser	Asn	Ile	Ala	Ile	Ser	Lys	His	Met	Thr
Arg	Leu	Ala	Asp	Gly	Gln	Pro	Gly	Val	Gly	Val	Leu
Ile	Gly	Ala	Met	Gly	Glu	Pro	Ser	Phe	Asn	Phe	Glu
Thr	Thr	Met	Ala	Ala	Leu	Gln	Asp	Val	Gln	Phe	Gly
Gly	Gly	Ala	Ala	Asp	Glu	Val	Ala	Val	Gln	Ala	Gly
Lys	Lys	Lys	Asn	Gly	Lys	Val	Asp	Val	Gln	Ala	Gly
Ala	Lys	Ala	Asp	Glu	Glu	Ala	P254	Arg	Ala	Trp	Gly
Lys	Lys	Ile	Ile	Thr	Pro	Gln	A255	His	Thr	Val	Ser
Leu	Leu	Ser	Met	Ser	Pro	Met	A255	Asn	Glu	Lys	Asp
Pro	Asp	Leu	Pro	Ile	Ile	Lys	S256	Gln	Ala	Gly	Gly
Ser	Ser	Ser	Gln	Ile	Trp	Ala	A257	Glu	Gly	Pro	Ala
Leu	Leu	Gln	Glu	Gly	Glu	Gly	A258	Ala	Asp	Glu	Leu
Asp	Asp	Asp	Asp	Ser	His	Ser	A258	Ser	Asp	Met	Val
Trp	Trp	Lys	Asn	Asp	Pro	Val	R259	Ala	Ile	Arg	Val
Ala	Met	Val	Ala	Ile	Asn	Val	R260	Ala	Leu	Pro	Arg
Ser	Asp	Ser	Ala	Glu	Phe	Gly	K261	Val	Leu	Ser	Leu
Pro	Pro	Ala	Gly	Ser	Ser	Gln	E262	Phe	Gln	Gly	Asp
Arg	Arg	Val	Met	Ser	Asp	Gly	E262	Leu	Asp	Ala	Val
Gln	Gln	His	Pro	Glu	Trp	Ser	E263	Thr	Met	Tyr	Asp
Val	Val	Arg	Val	Leu	Val	Ser	E264	Leu	Gly	Glu	Val
Ala	Ala	Ala	Glu	Phe	Arg	H367	L265	Ser	Phe	Thr	Glu
Phe	Ser	Phe	Leu	Thr	Trp	R368	E266	Thr	Gly	Glu	Gln
Leu	Ile	Leu	Asp	Phe	Phe	S371	R267	Val	Val	Glu	Asn
Gly	Val	Val	Val	Gly	Ala	S371	Q268	Thr	Ser	Leu	Leu
Asp	Ser	Ser	Ser	Ser	Ser	R385	Q269	Asn	Gln	Ile	Pro
Ile	Thr	Thr	Thr	Ser	Ala	R393	E270	Leu	Leu	Pro	Asp
Gln	His	Gln	Ile	Ile	Val	S393	Q271	Lys	Leu	Val	Leu
Ala	Pro	Tyr	Gly	Asp	Val	S397	R274	Gln	Glu	Asp	Glu
Gly	Gln	Thr	Glu	Pro	Ile	S397	R274	Glu	Tyr	Tyr	Arg
Ala	Ile	Asn	Glu	Asn	Val	H462	S279	Val	Arg	Leu	Ser
Gln	Gln	Lys	Lys	Leu	Val	Arg	E280	Asp	Asp	Asp	Ala
Ala	Ala	Ala	Ala	His	Val	Arg	L281	Ser	Lys	Gln	Lys
Ile	Ile	Met	Ala	Lys	Val	Gln	Q293	Ile	Lys	Lys	Phe
Val	Val	Gly	Ile	Asp	Leu	Val	Q293	Val	Ser	Gln	Lys
Leu	Leu	Ile	Leu	Leu	Val	Asn	T296	Met	Arg	Ile	Met
Ser	Ser	Gln	Leu	Pro	Val	Pro	T296	Met	Gln	Asn	Met



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



ALA	VAL	GLY	GLU	GLU	GLY	ALA	ASP	GLY	GLY	ALA	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
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● Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG



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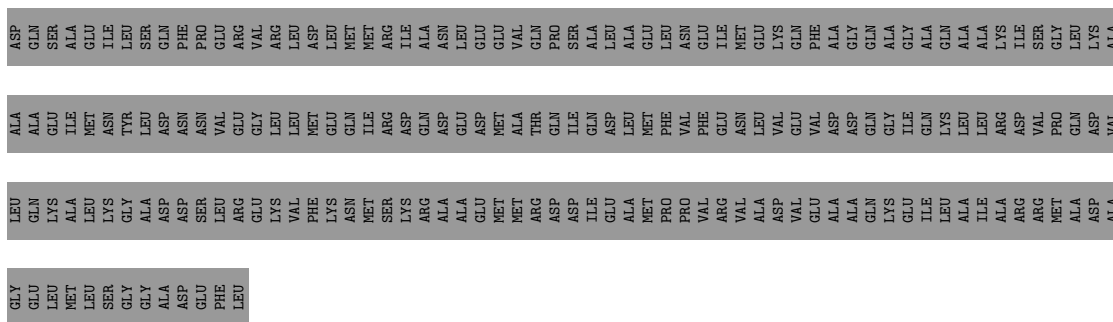


GLU	GLN	ALA	GLN	ALA	GLN	ARG	LEU
LEU	LYS	GLU	SER	LEU	ASP	ASP	LEU
MET	ALA	ILE	ALA	VAL	ALA	ASP	LEU
LEU	LEU	MET	GLU	ALA	VAL	VAL	PRO
SER	LYS	ASN	ILE	ALA	GLY	ASN	SER
GLY	GLY	TYR	LEU	LEU	ILE	GLU	ASP
ALA	ALA	LEU	SER	GLY	ILE	GLU	ASP
ASP	ASP	ASP	GLN	GLU	ARG	PRO	ASP
GLU	SER	ASN	PHE	ASP	HIS	GLU	GLU
GLU	ASP	ASN	GLU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

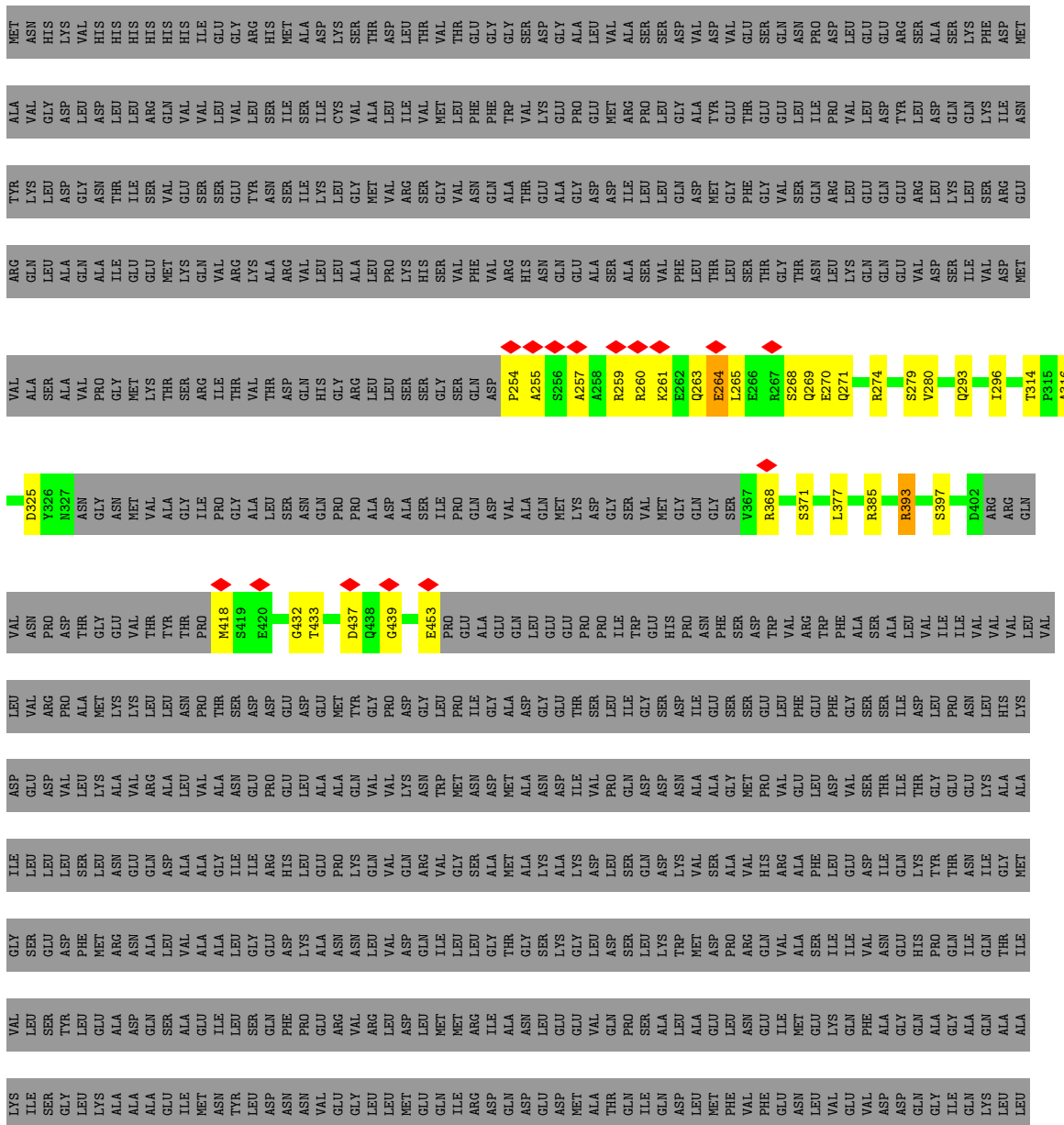
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG

Chain X: 13% 85%

[illegible]



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



ARG
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4 Experimental information

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 ($e^-/\text{\AA}^2$)	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 (\AA)	684.0, 684.0, 684.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	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	0.26	0/1170	0.54	0/1573
1	2	0.27	0/1170	0.55	0/1573
1	3	0.27	0/1170	0.54	0/1573
1	4	0.27	0/1170	0.54	0/1573
1	5	0.27	0/1170	0.55	0/1573
1	6	0.27	0/1170	0.55	0/1573
1	7	0.27	0/1170	0.54	0/1573
1	8	0.27	0/1170	0.54	0/1573
1	9	0.27	0/1170	0.54	0/1573
1	A	0.26	0/1170	0.54	0/1573
1	B	0.27	0/1170	0.54	0/1573
1	C	0.27	0/1170	0.54	0/1573
1	D	0.27	0/1170	0.54	0/1573
1	E	0.27	0/1170	0.54	0/1573
1	F	0.26	0/1170	0.54	0/1573
1	G	0.27	0/1170	0.55	0/1573
1	H	0.27	0/1170	0.54	0/1573
1	I	0.27	0/1170	0.54	0/1573
1	J	0.27	0/1170	0.55	0/1573
1	K	0.27	0/1170	0.54	0/1573
1	L	0.27	0/1170	0.54	0/1573
1	M	0.26	0/1170	0.54	0/1573
1	N	0.27	0/1170	0.54	0/1573
1	O	0.26	0/1170	0.54	0/1573
1	P	0.27	0/1170	0.55	0/1573
1	Q	0.26	0/1170	0.55	0/1573
1	R	0.27	0/1170	0.55	0/1573
1	S	0.27	0/1170	0.54	0/1573
1	T	0.27	0/1170	0.54	0/1573
1	U	0.27	0/1170	0.54	0/1573
1	V	0.27	0/1170	0.54	0/1573
1	W	0.27	0/1170	0.54	0/1573
1	X	0.26	0/1170	0.54	0/1573
1	Y	0.27	0/1170	0.54	0/1573

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Z	0.26	0/1170	0.55	0/1573
All	All	0.27	0/40950	0.54	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

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	21	0
1	2	1159	0	1149	15	0
1	3	1159	0	1149	17	0
1	4	1159	0	1149	21	0
1	5	1159	0	1149	20	0
1	6	1159	0	1149	20	0
1	7	1159	0	1149	22	0
1	8	1159	0	1149	19	0
1	9	1159	0	1149	19	0
1	A	1159	0	1149	20	0
1	B	1159	0	1149	18	0
1	C	1159	0	1149	19	0
1	D	1159	0	1149	19	0
1	E	1159	0	1149	18	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	20	0
1	N	1159	0	1149	21	0
1	O	1159	0	1149	19	0
1	P	1159	0	1149	19	0
1	Q	1159	0	1149	20	0
1	R	1159	0	1149	19	0
1	S	1159	0	1149	18	0
1	T	1159	0	1149	17	0
1	U	1159	0	1149	18	0
1	V	1159	0	1149	17	0
1	W	1159	0	1149	17	0
1	X	1159	0	1149	17	0
1	Y	1159	0	1149	17	0
1	Z	1159	0	1149	24	0
All	All	40565	0	40215	523	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 6.

The worst 5 of 523 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

5.3.1 Protein backbone

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 ⓘ

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%)	120 (94%)	7 (6%)	18	48
1	2	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	3	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	4	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	5	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	6	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	7	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	8	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	9	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	A	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	B	127/802 (16%)	120 (94%)	7 (6%)	18	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	D	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	E	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	F	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	G	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	H	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	I	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	J	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	K	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	L	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	M	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	N	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	O	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	P	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	Q	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	R	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	S	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	T	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	U	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	V	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	W	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	X	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	Y	127/802 (16%)	120 (94%)	7 (6%)	18	48
1	Z	127/802 (16%)	120 (94%)	7 (6%)	18	48
All	All	4445/28070 (16%)	4200 (94%)	245 (6%)	20	48

5 of 245 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	371	SER
1	W	385	ARG
1	L	371	SER
1	W	279	SER
1	Y	393	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	263	GLN
1	U	263	GLN
1	X	263	GLN
1	D	263	GLN
1	C	263	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.

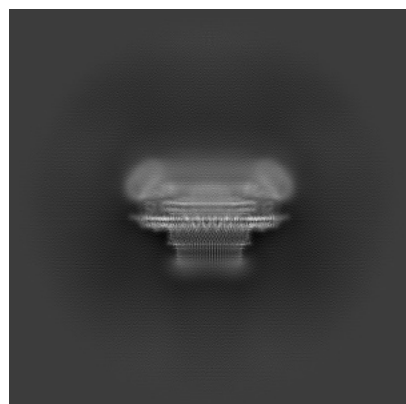
6 Map visualisation [i](#)

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.

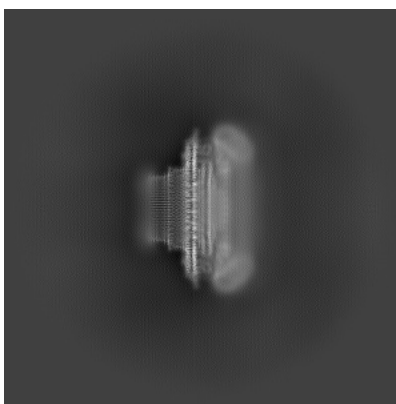
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

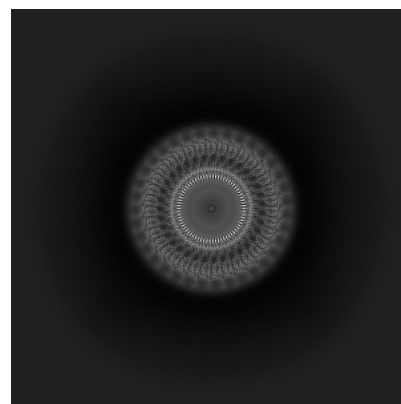
6.1.1 Primary map



X

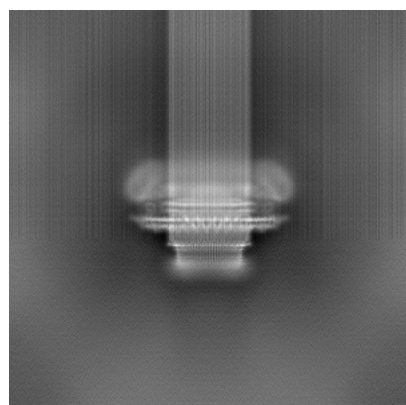


Y

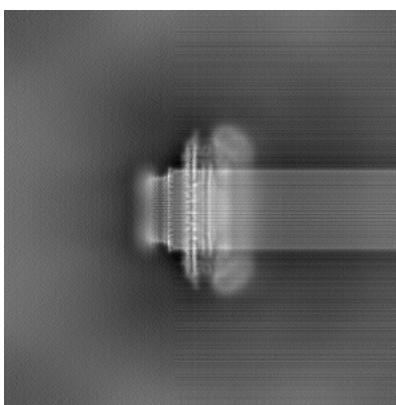


Z

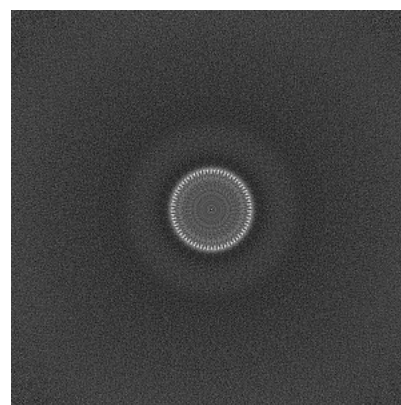
6.1.2 Raw map



X



Y

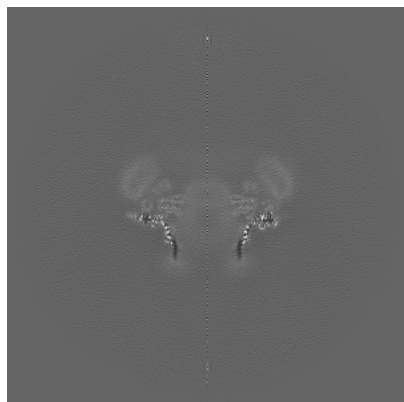


Z

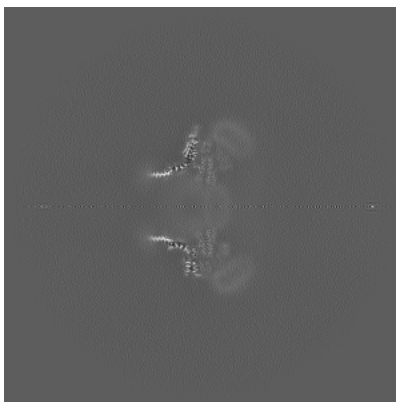
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

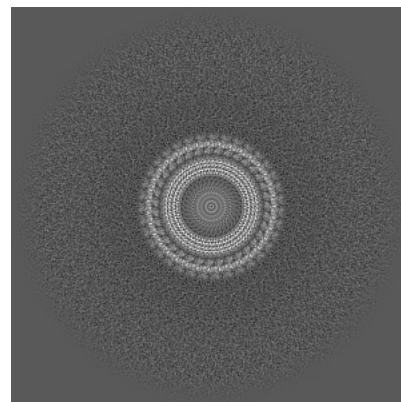
6.2.1 Primary map



X Index: 300

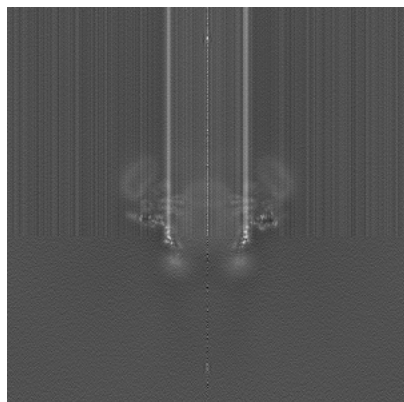


Y Index: 300

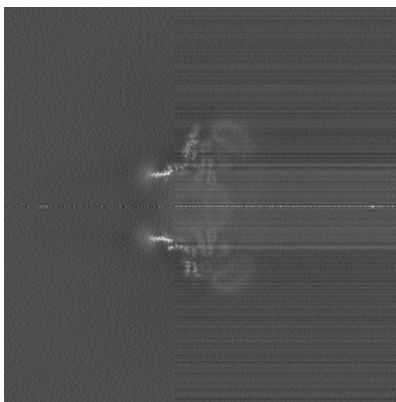


Z Index: 300

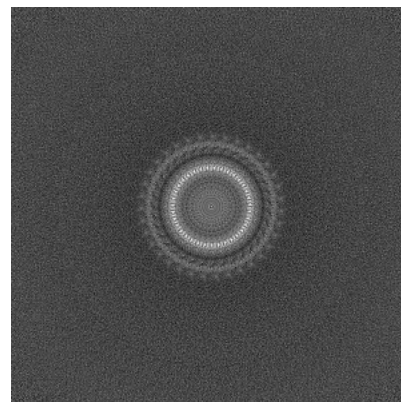
6.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

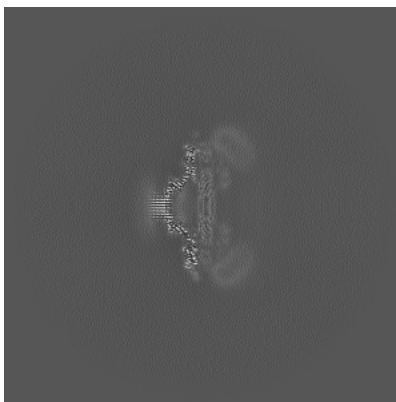
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

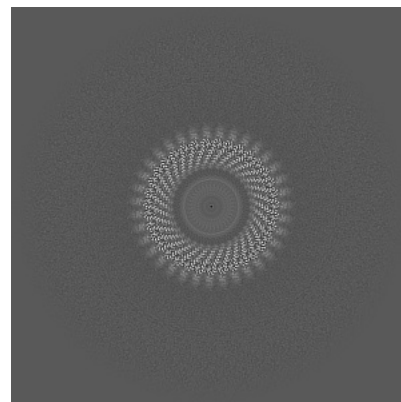
6.3.1 Primary map



X Index: 349

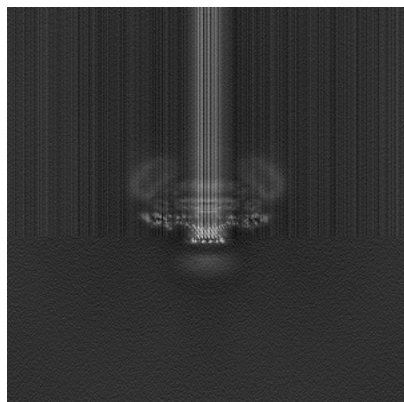


Y Index: 348

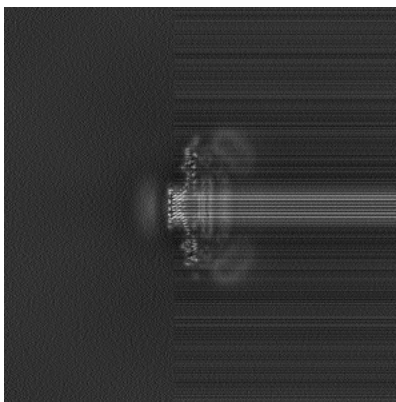


Z Index: 285

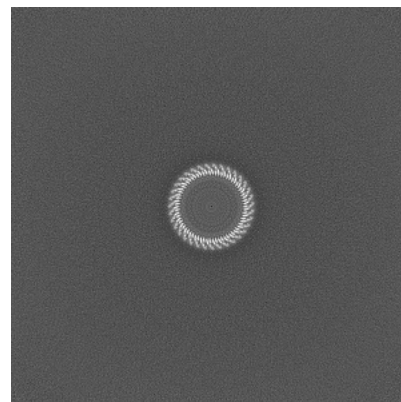
6.3.2 Raw map



X Index: 242



Y Index: 243

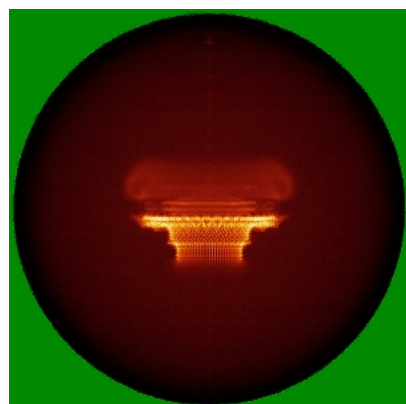


Z Index: 247

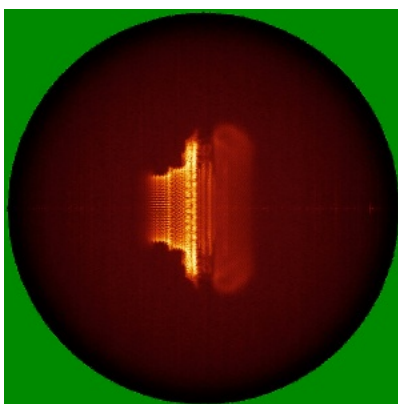
The images above show the largest variance slices of the map in three orthogonal directions.

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

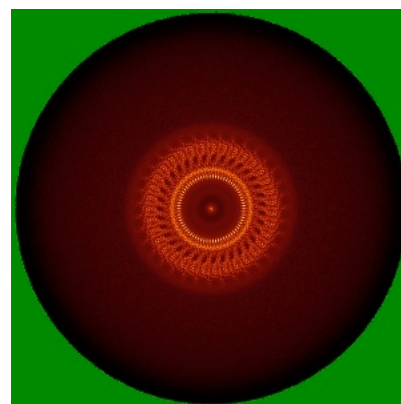
6.4.1 Primary map



X

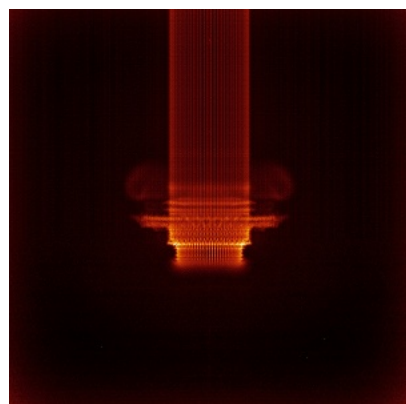


Y

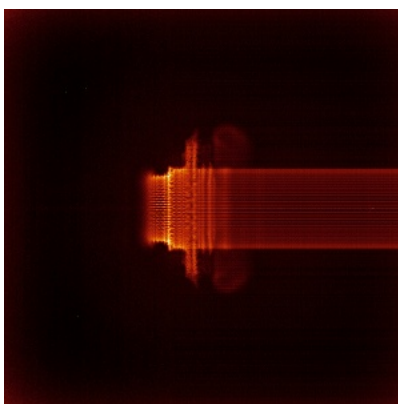


Z

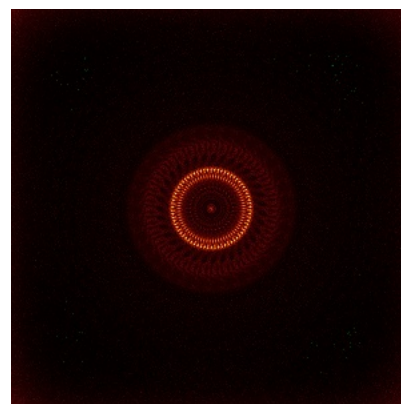
6.4.2 Raw map



X



Y

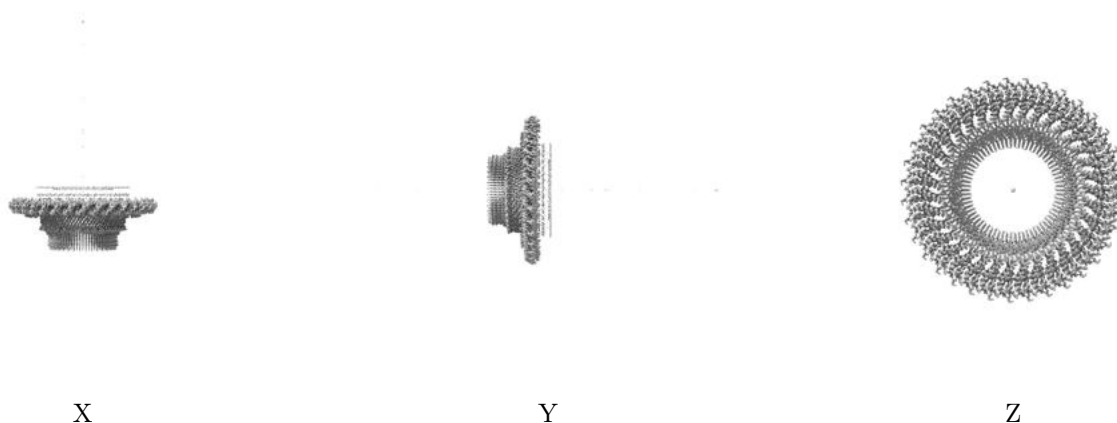


Z

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.

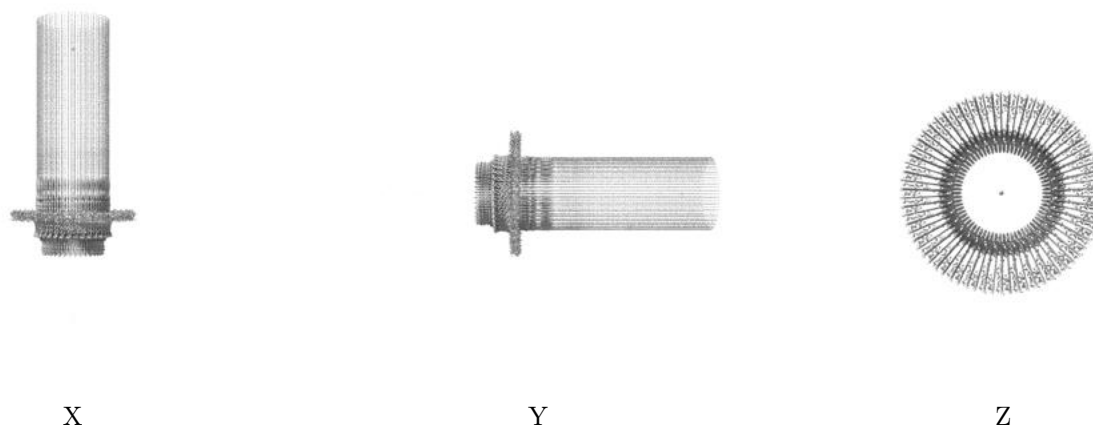
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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



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.

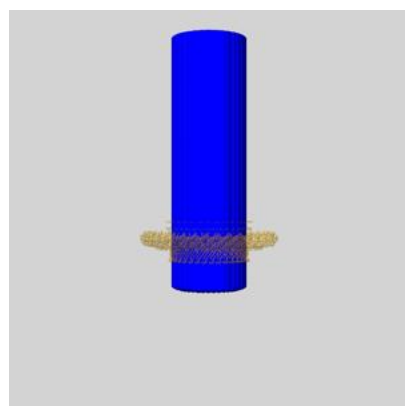
6.6 Mask visualisation [i](#)

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

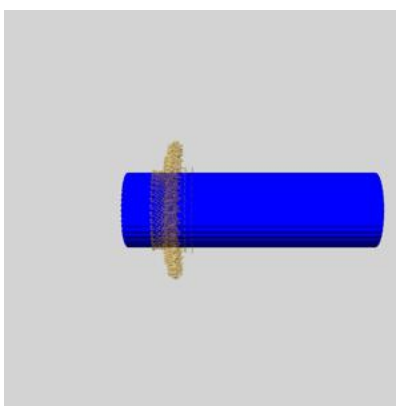
A mask typically either:

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

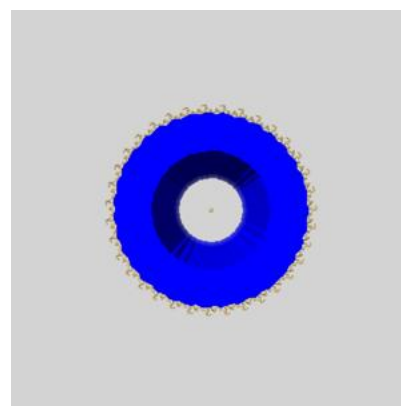
6.6.1 emd_39763_msk_1.map [i](#)



X



Y

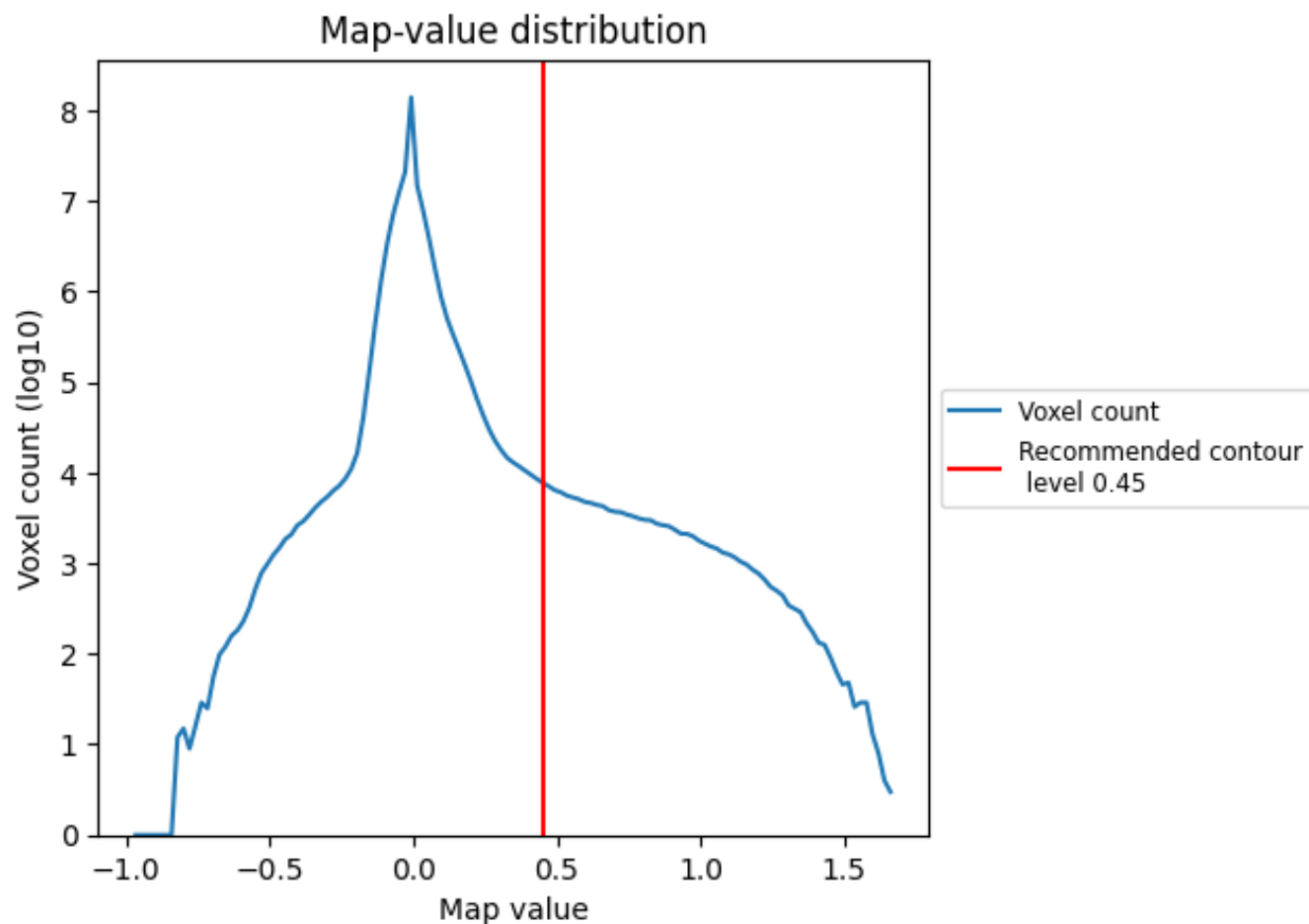


Z

7 Map analysis [i](#)

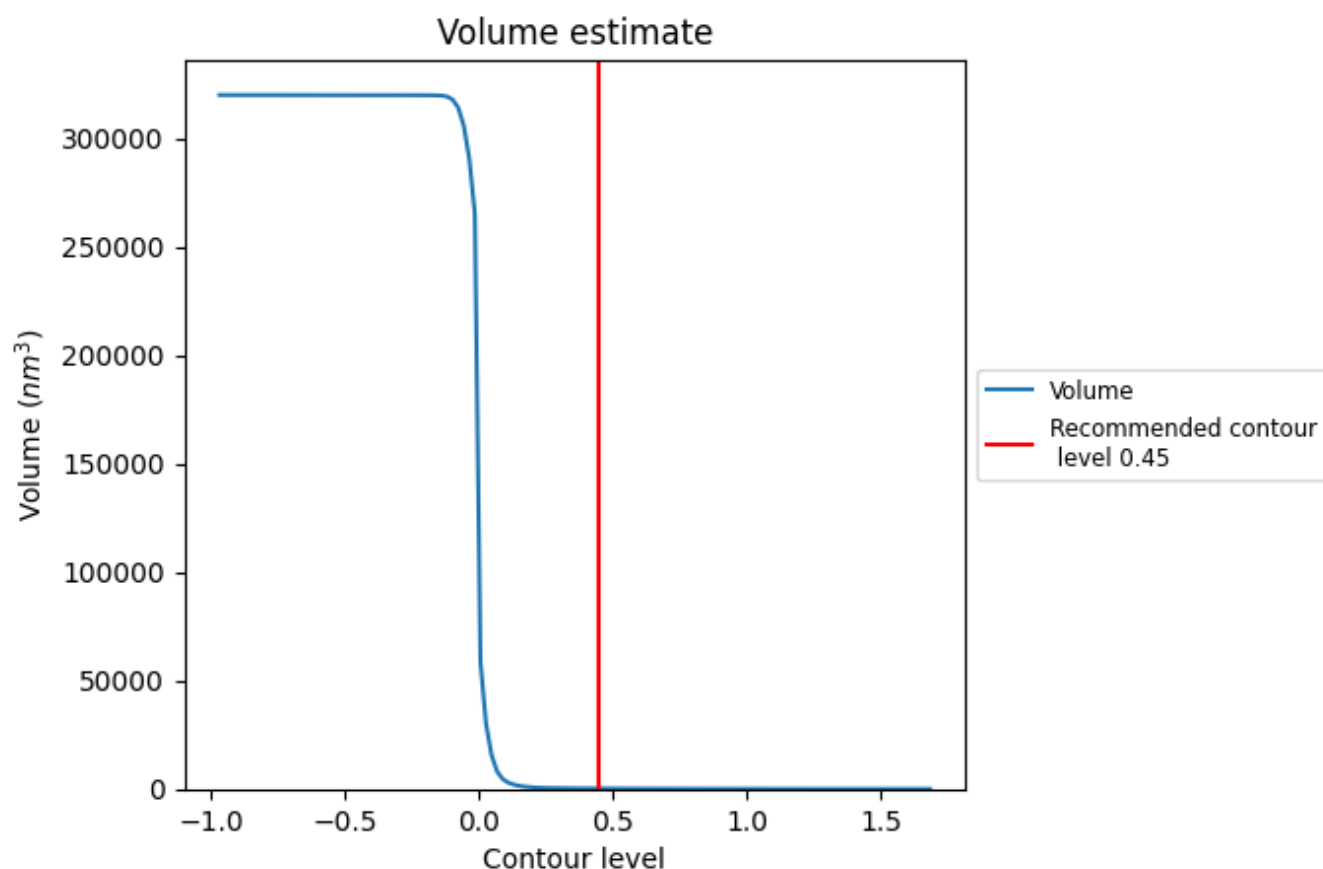
This section contains the results of statistical analysis of the map.

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.

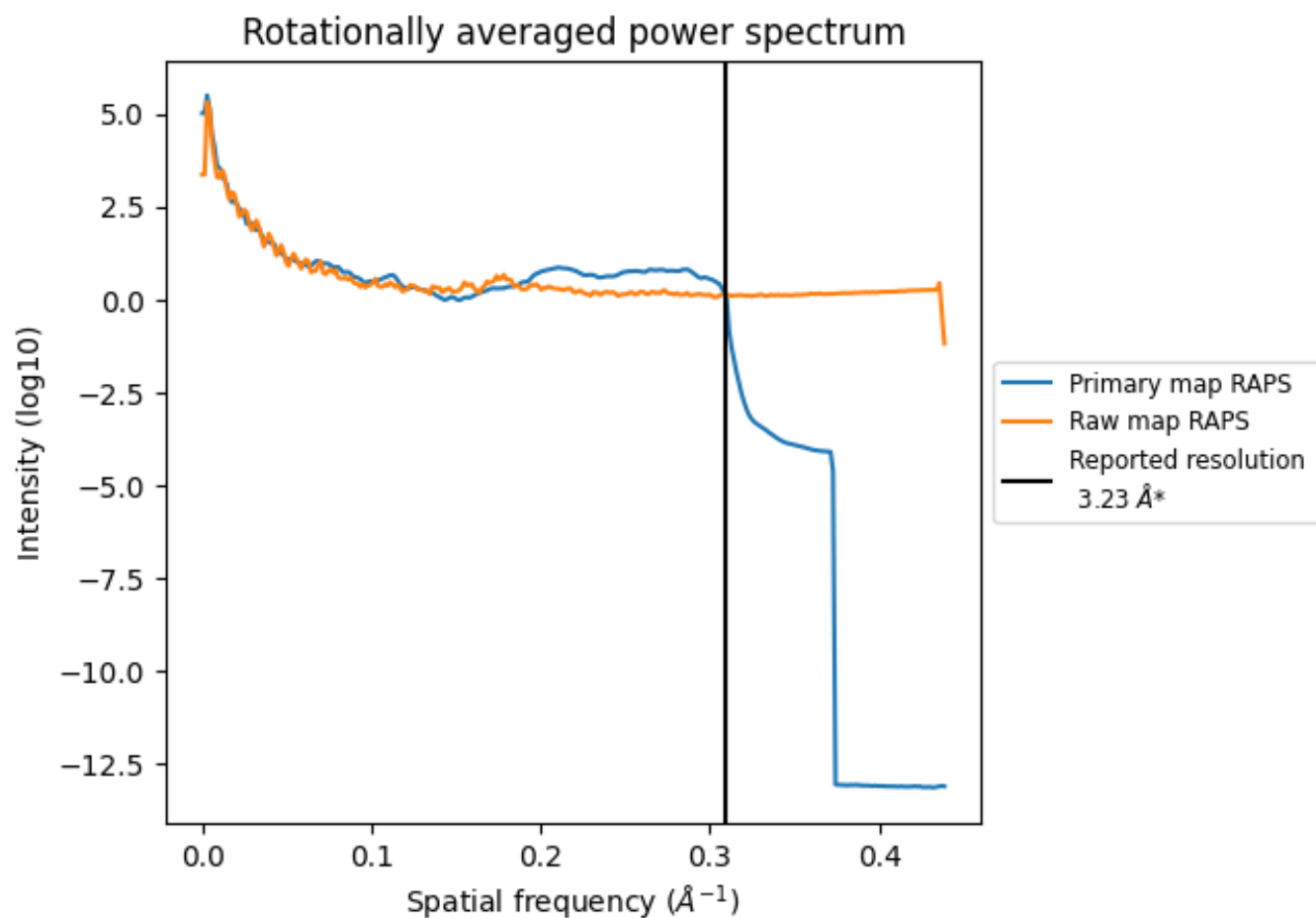
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 183 nm³; 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 ⓘ

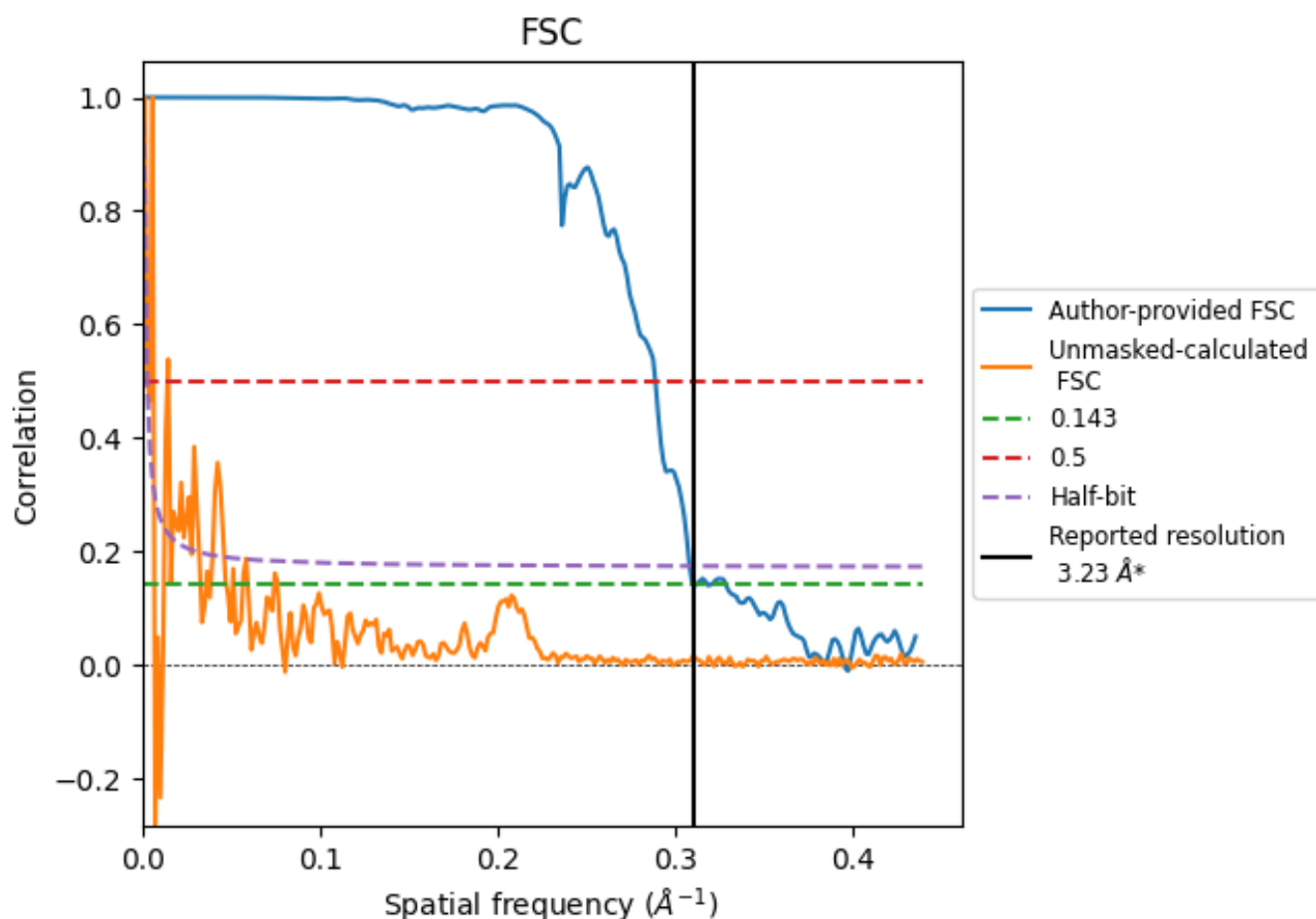


*Reported resolution corresponds to spatial frequency of 0.310 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

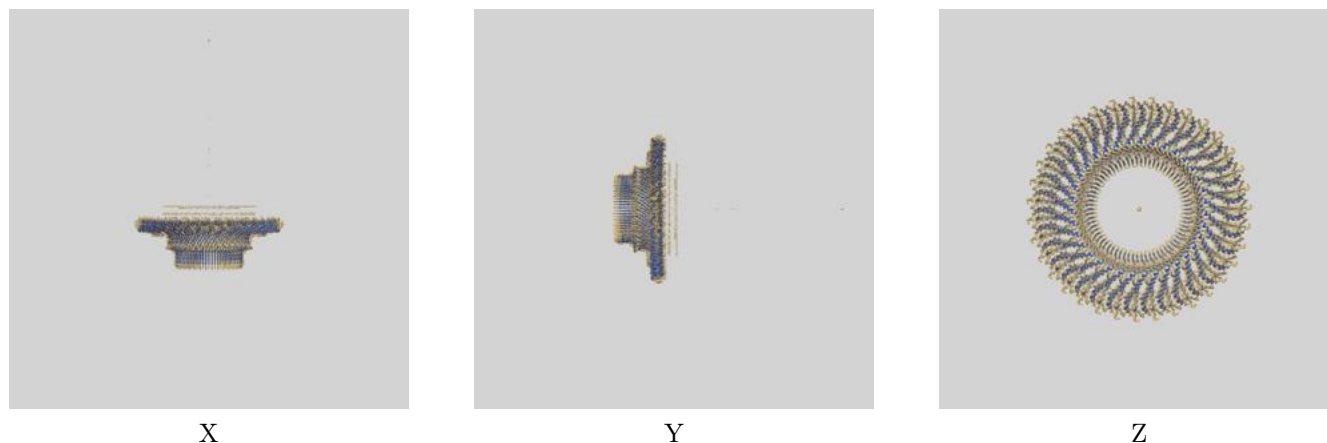
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	3.23	3.46	3.25
Unmasked-calculated*	147.06	344.83	151.52

*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](#)

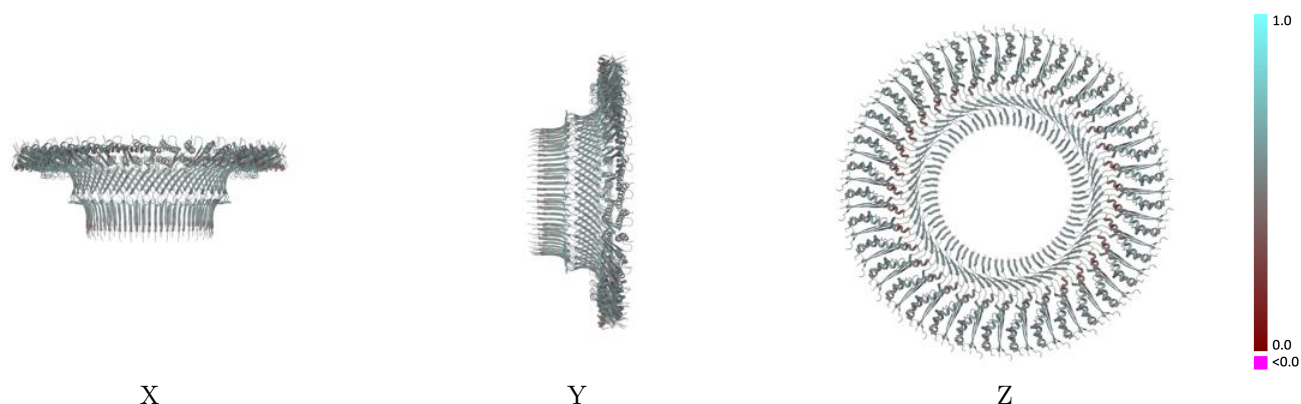
This section contains information regarding the fit between EMDB map EMD-39763 and PDB model 8Z4G. Per-residue inclusion information can be found in section [3](#) on page [22](#).

9.1 Map-model overlay [i](#)



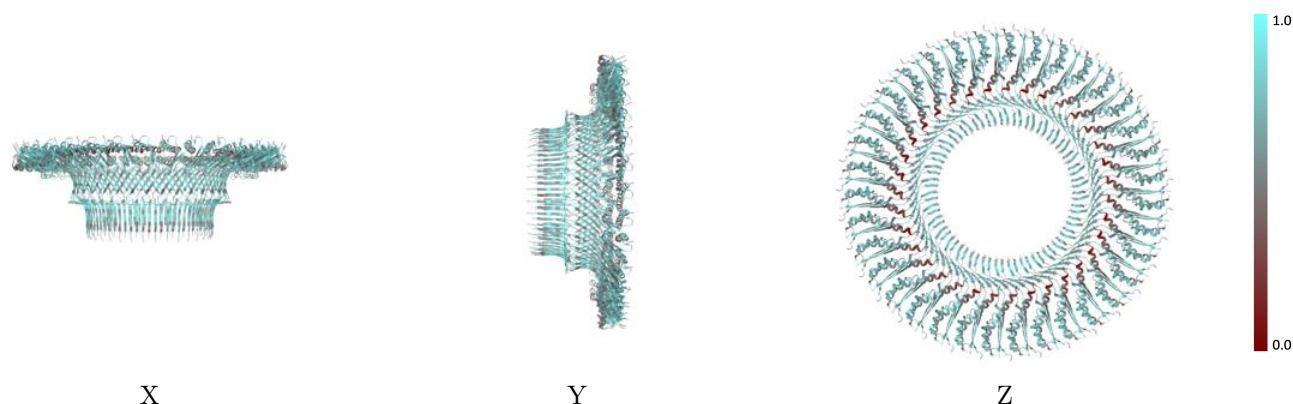
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



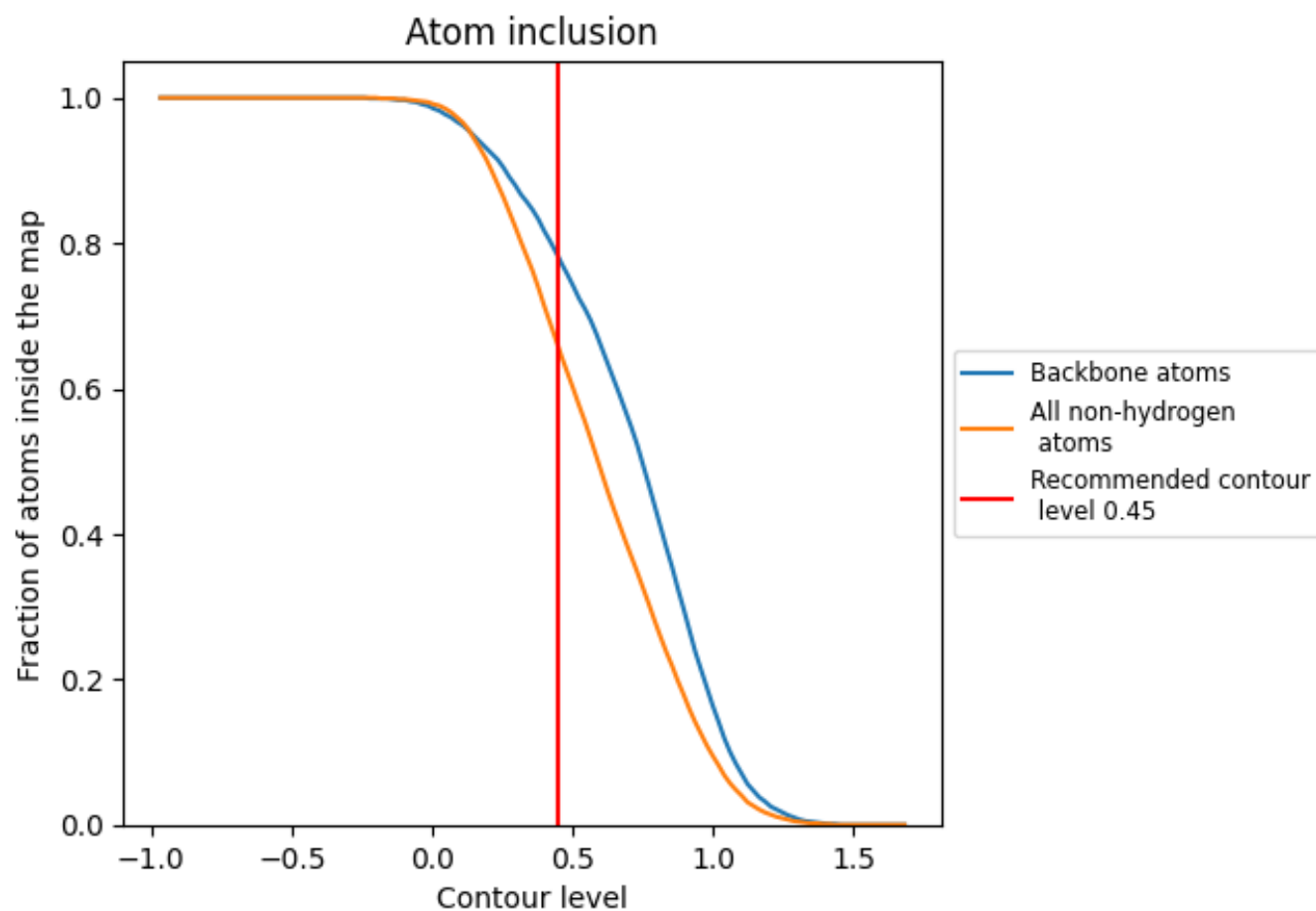
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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









































































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

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

