



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:50 PM UTC

PDB ID : 8Z4D / pdb_00008z4d
EMDB ID : EMD-39761
Title : Structure of the S-ring region of the Vibrio flagellar MS-ring protein FliF with 34-fold symmetry applied
Authors : Takekawa, N.; Nishikino, T.; Kishikawa, J.; Hirose, M.; Kato, T.; Imada, K.; Homma, M.
Deposited on : 2024-04-17
Resolution : 3.33 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

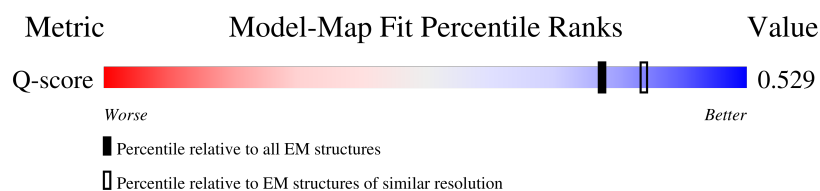
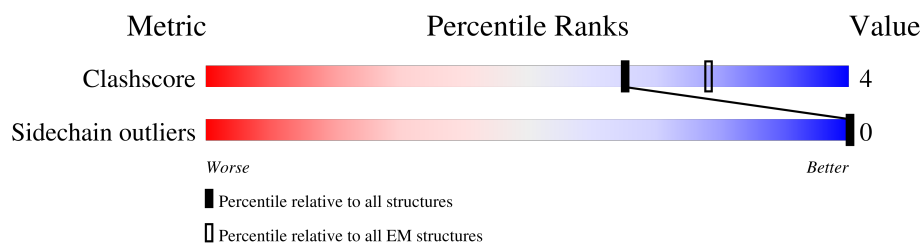
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.33 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.



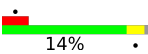
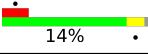
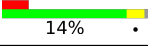
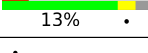
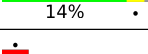
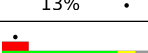
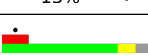
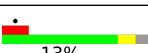
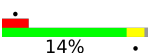
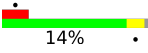
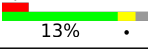
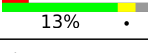
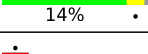
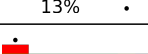
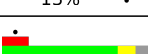
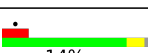
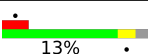
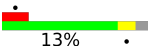
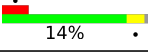
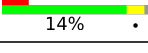
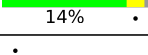
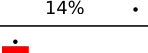
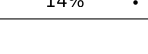
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14484 (2.83 - 3.83)

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	

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

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Mol	Chain	Length	Quality of chain
1	V	945	14% . 85%
1	W	945	14% . 85%
1	X	945	13% . 85%
1	Y	945	14% . 85%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 38862 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	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	2	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	3	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	4	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	5	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	6	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	7	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	8	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	9	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	A	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	B	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	C	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	D	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	E	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	F	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	G	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	H	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	I	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	J	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	K	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	L	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	M	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	N	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	O	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	P	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	Q	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	R	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	S	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	T	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	U	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	V	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	W	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	X	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		
1	Y	144	Total	C	N	O	S	0	0
			1143	703	208	230	2		

There are 578 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
1	-12	LYS	-	expression tag	UNP Q75N27
1	-11	VAL	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
3	-4	ILE	-	expression tag	UNP Q75N27
3	-3	GLU	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
6	-13	HIS	-	expression tag	UNP Q75N27
6	-12	LYS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
8	-5	HIS	-	expression tag	UNP Q75N27
8	-4	ILE	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
B	-14	ASN	-	expression tag	UNP Q75N27
B	-13	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
D	-6	HIS	-	expression tag	UNP Q75N27
D	-5	HIS	-	expression tag	UNP Q75N27

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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
I	-7	HIS	-	expression tag	UNP Q75N27
I	-6	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
K	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0
L	-15	MET	-	initiating methionine	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
N	-8	HIS	-	expression tag	UNP Q75N27
N	-7	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
P	0	HIS	-	expression tag	UNP Q75N27
P	792	SER	GLY	engineered mutation	UNP A0A0T7EAG0

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Chain	Residue	Modelled	Actual	Comment	Reference
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
S	-9	HIS	-	expression tag	UNP Q75N27
S	-8	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
U	-1	ARG	-	expression tag	UNP Q75N27
U	0	HIS	-	expression tag	UNP Q75N27

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Chain	Residue	Modelled	Actual	Comment	Reference
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
X	-10	HIS	-	expression tag	UNP Q75N27
X	-9	HIS	-	expression tag	UNP Q75N27

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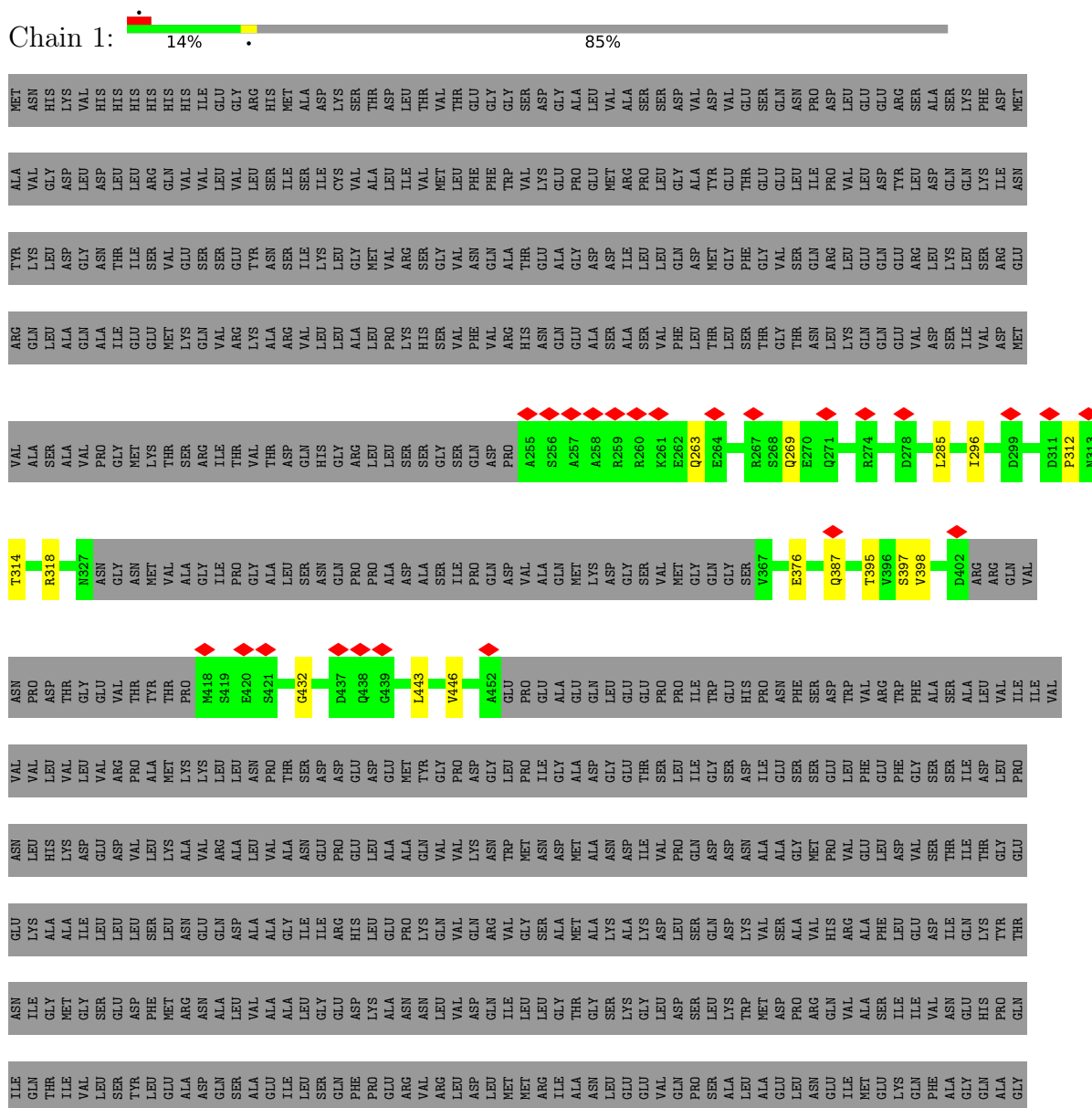
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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

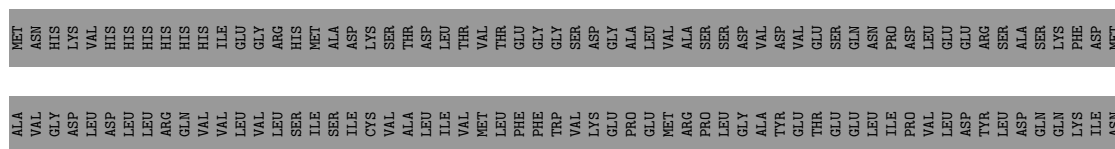
3 Residue-property plots

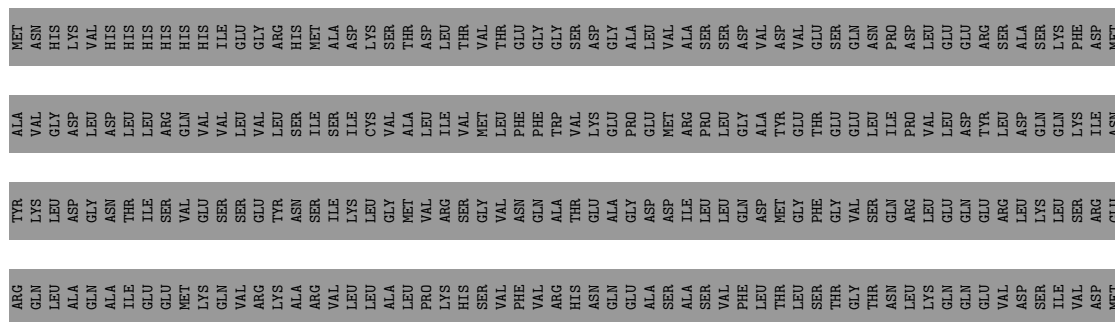
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

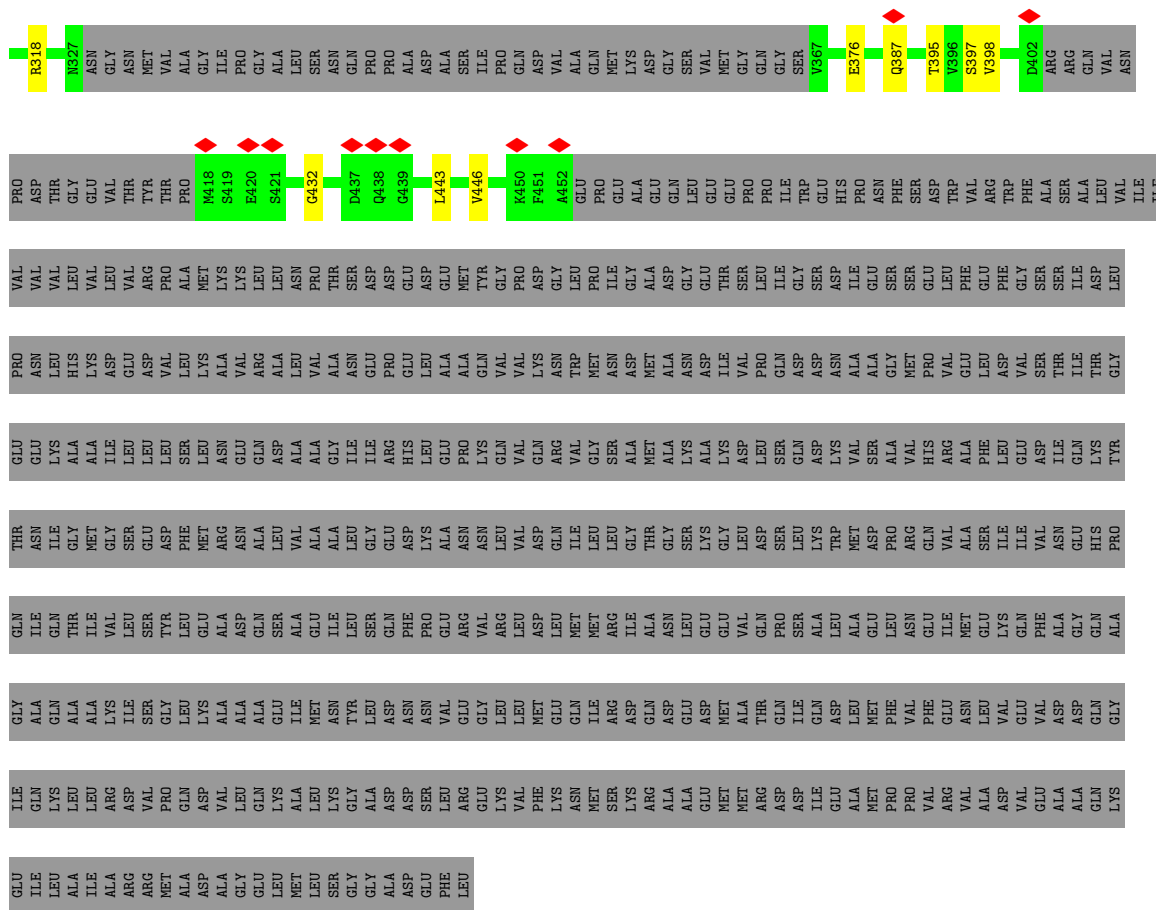
- Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FlgG



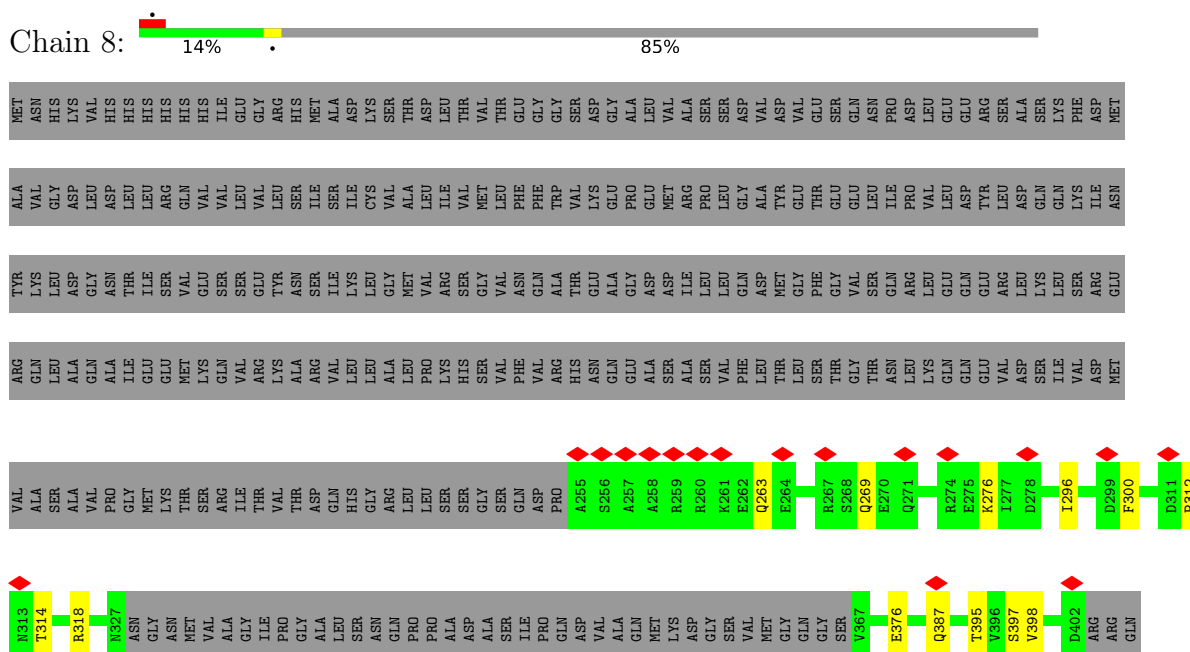


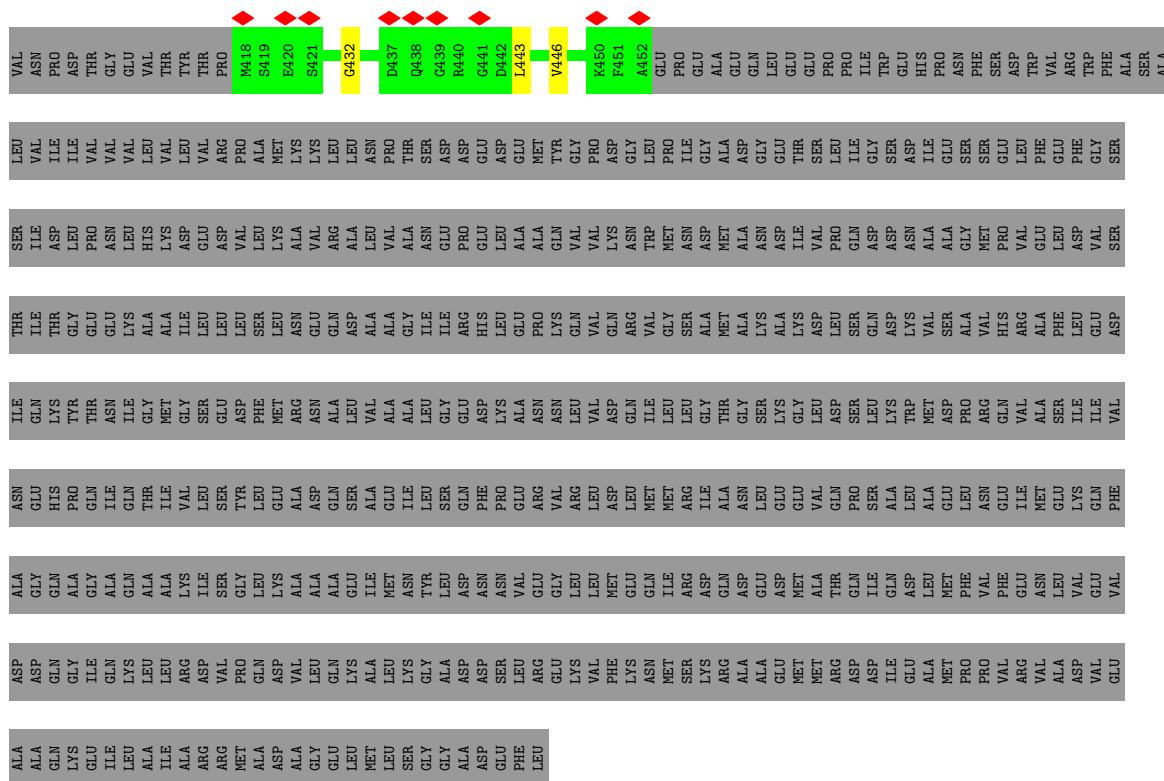






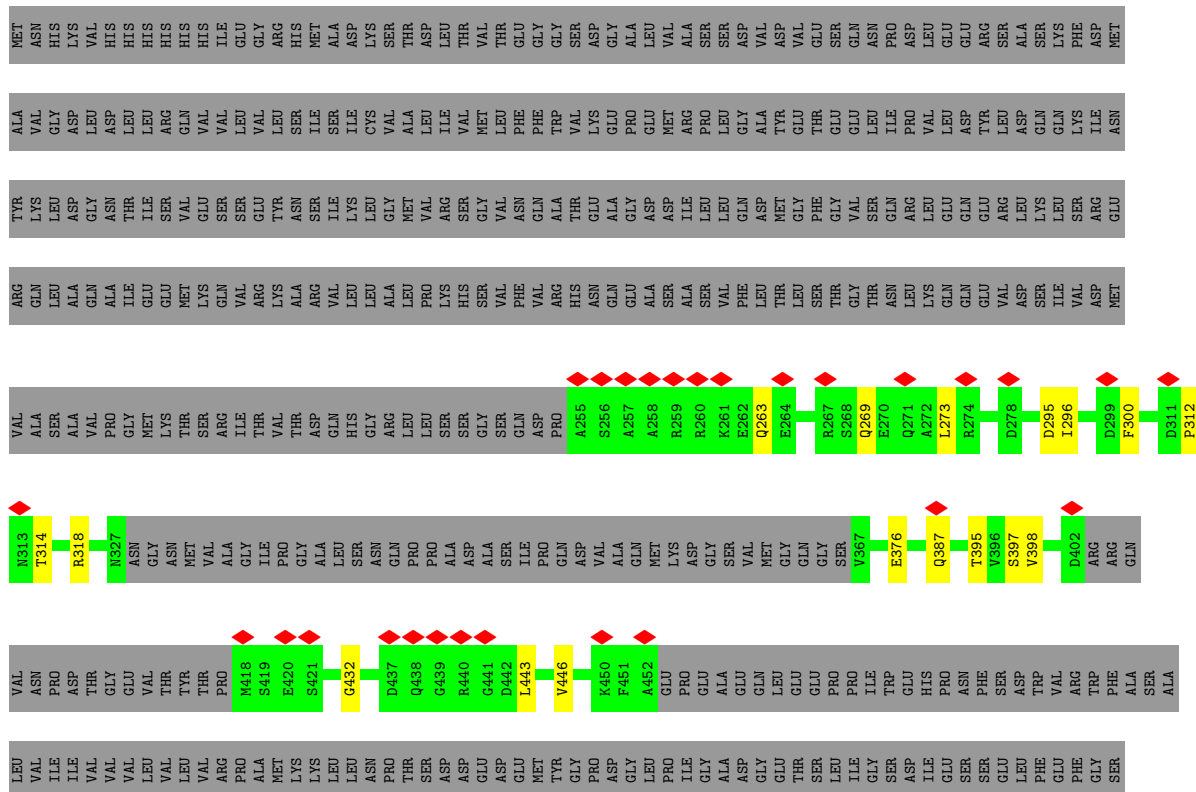
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG





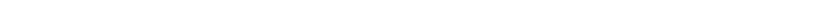
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG

Chain 9: 13% . 85%



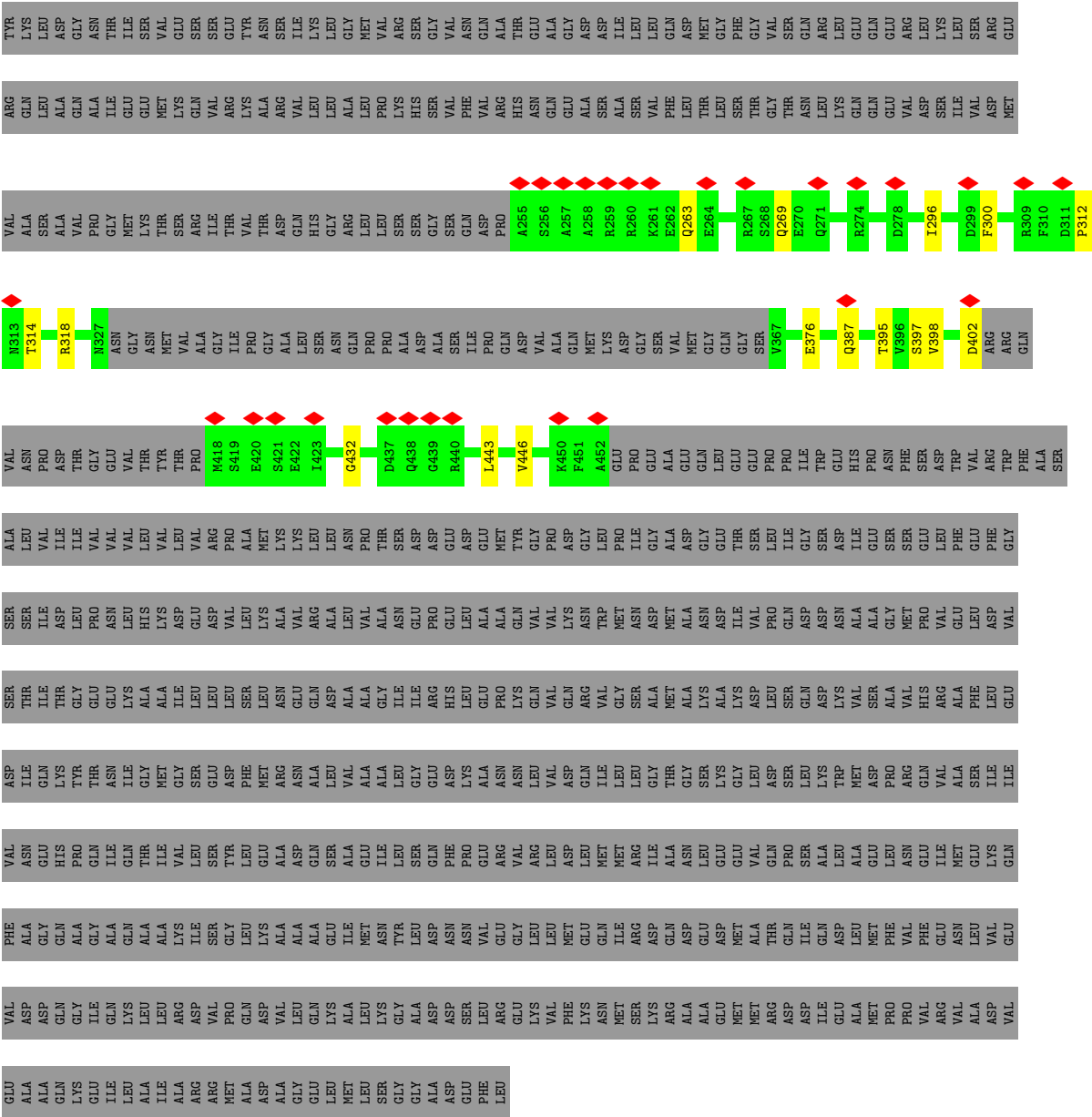
[illegible]

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

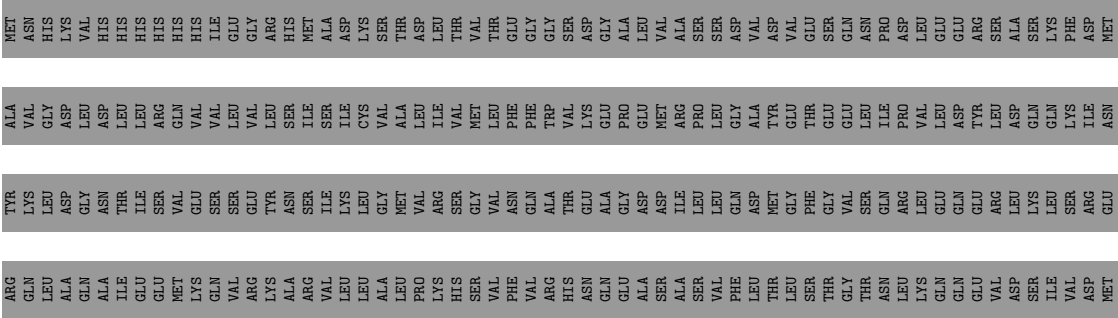
Chain A:  14% 85%

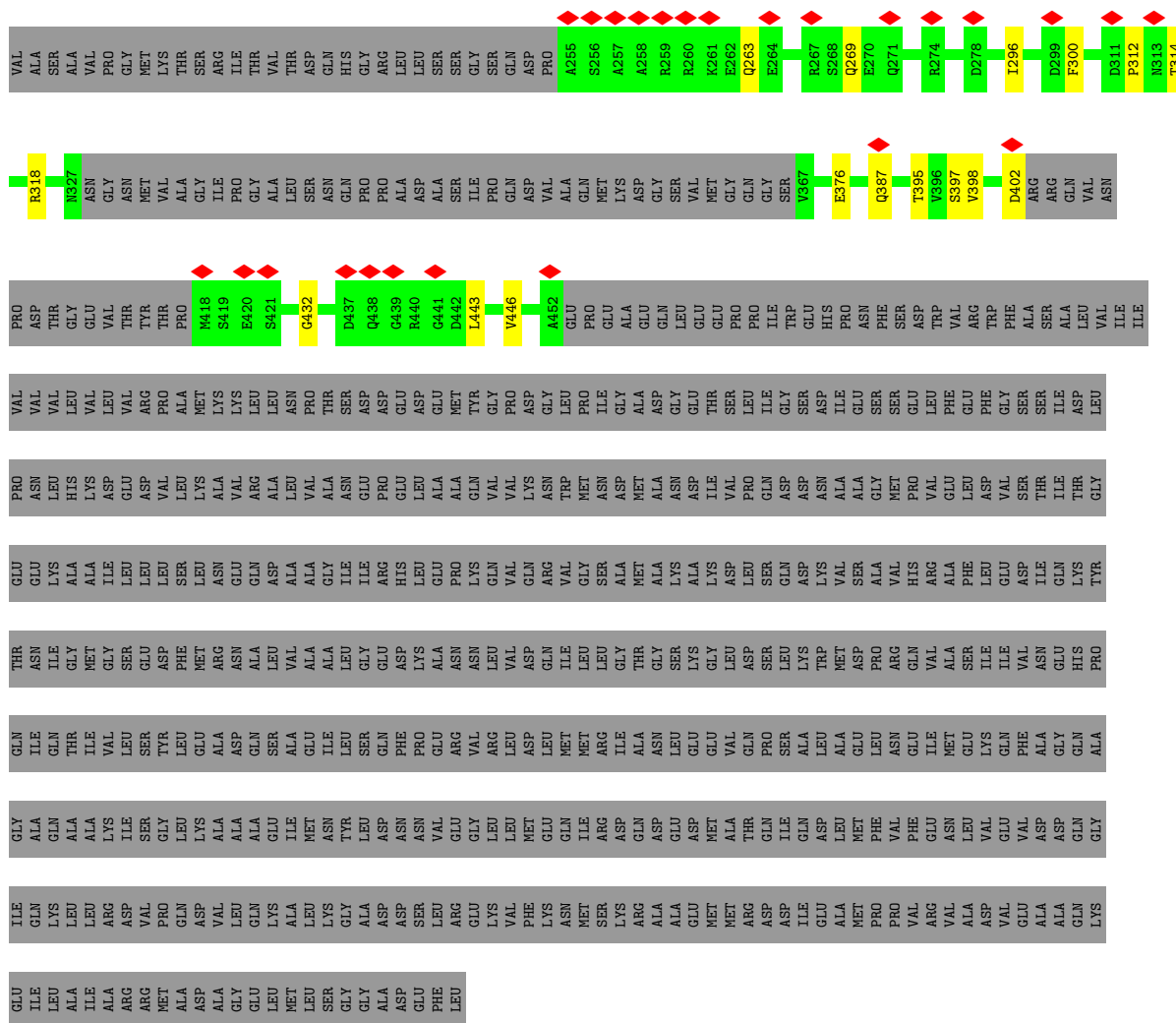
[illegible]



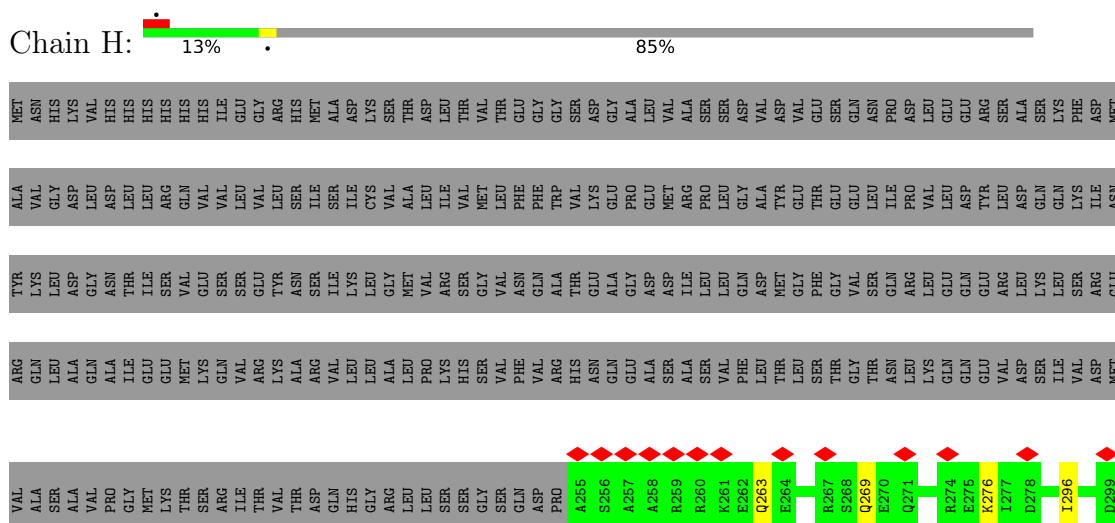


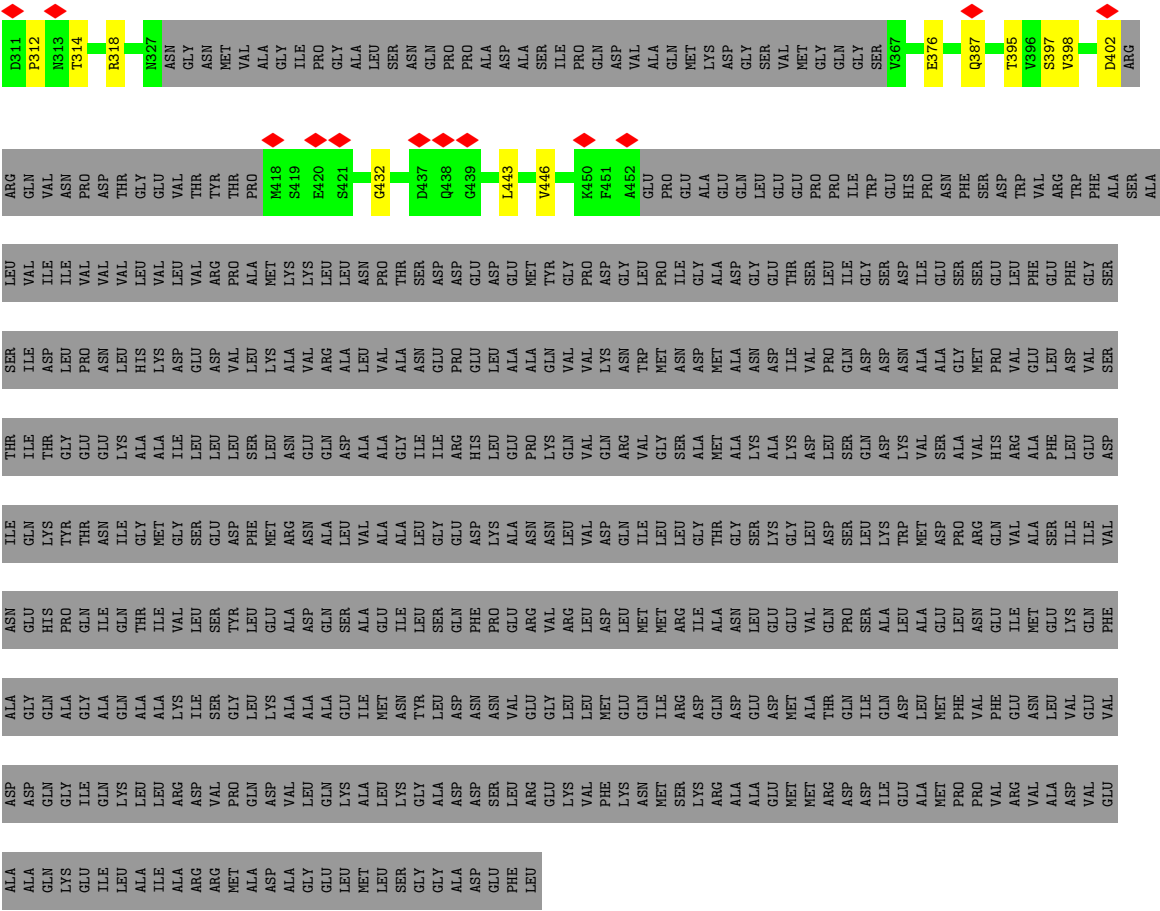
● Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG





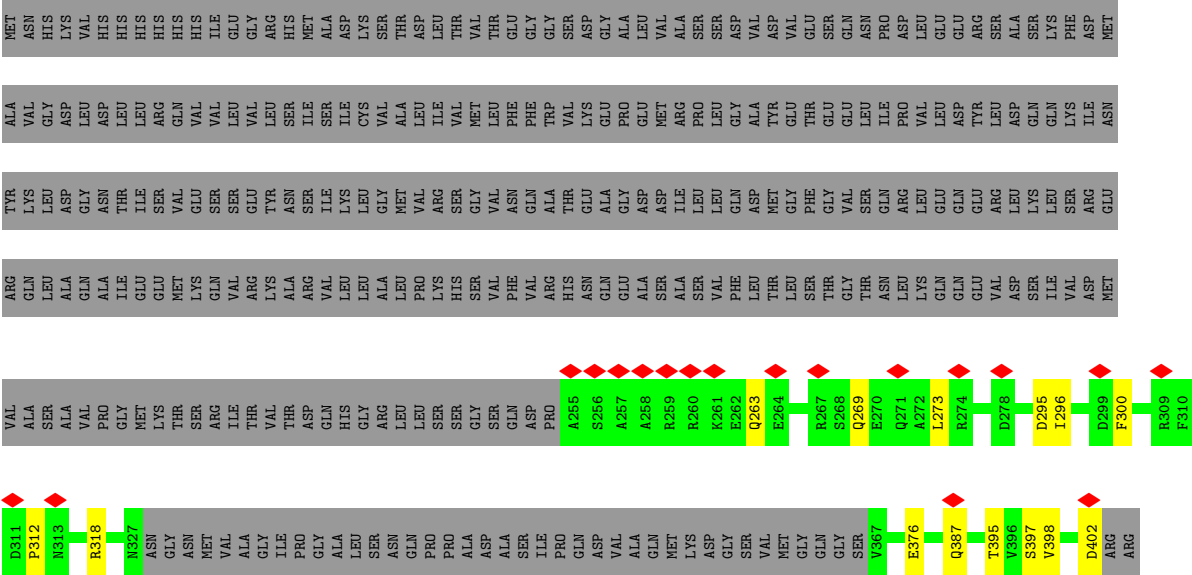
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG





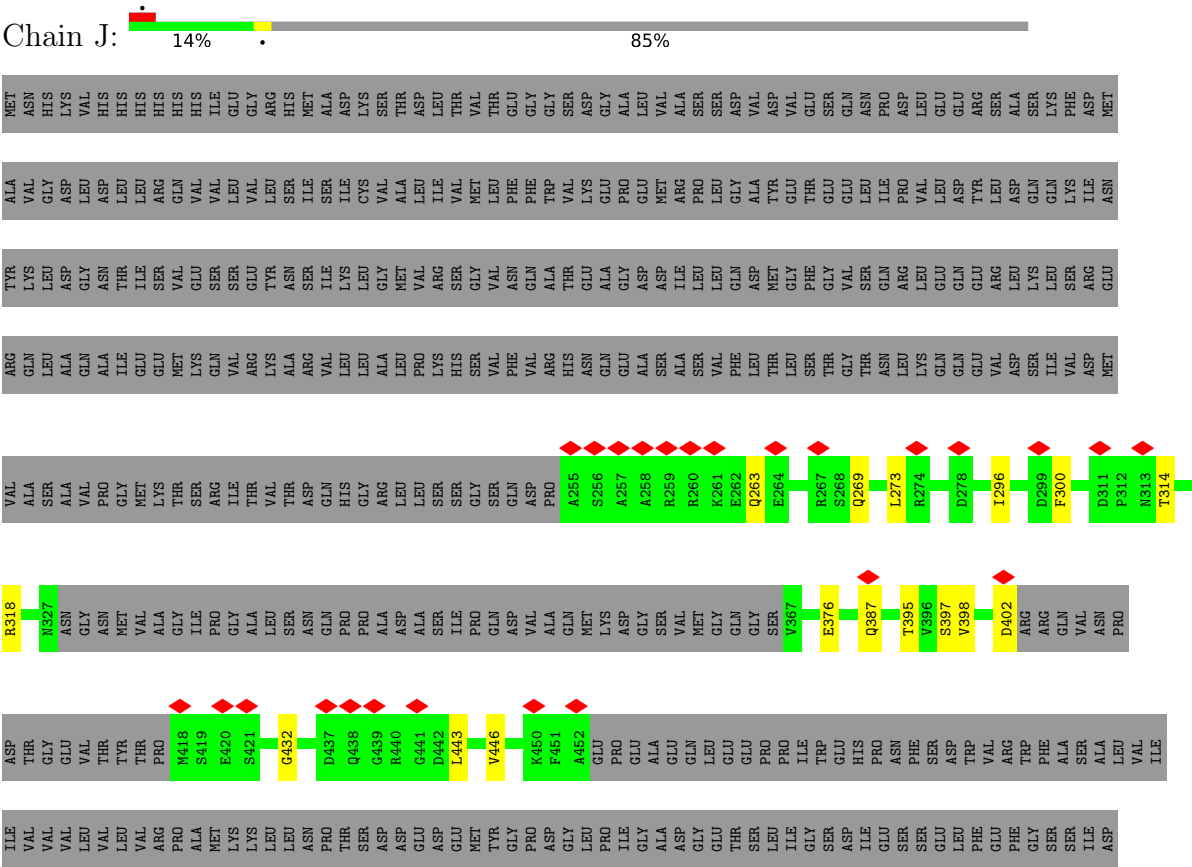
● Molecule 1: Flagellar M-ring protein,Flagellar motor switch protein FliG

Chain I: 13% 85%





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



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

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

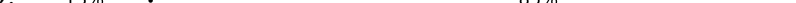
Chain K: 13% 85%

[illegible]

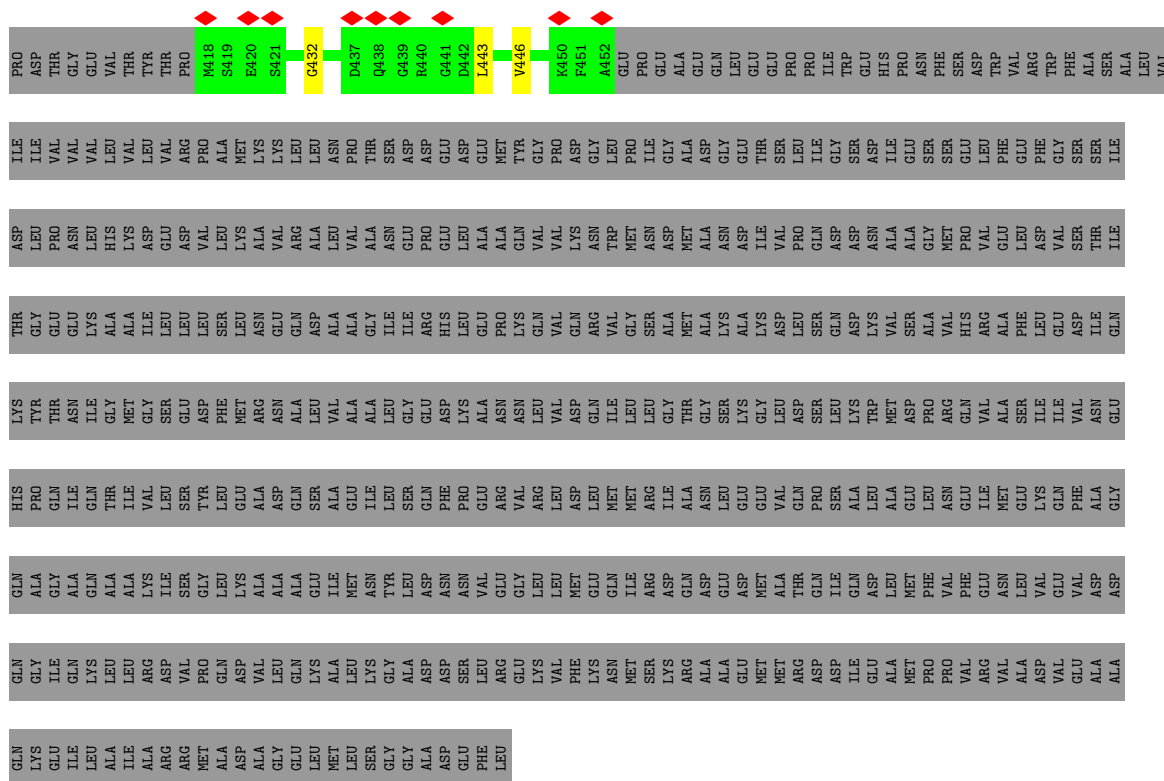


Chain N: 14% . 85%

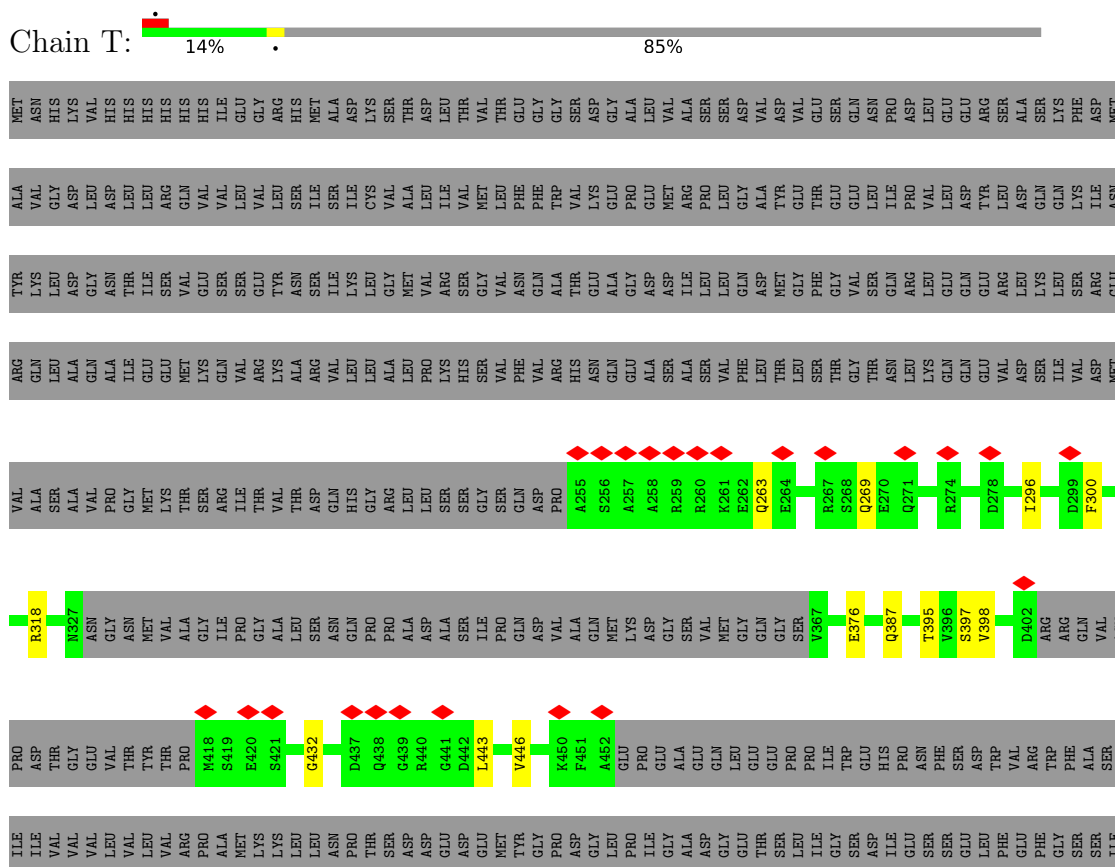


Chain 0:  13% 85%

[illegible]



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



[illegible]

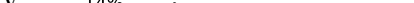
- Molecule 1: Flagellar M-ring protein, Flagellar motor switch protein FliG

Chain U: 14% 85%

[illegible]

[illegible]

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

Chain V:  14% 85%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C34	Depositor
Number of particles used	43546	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	1.398	Depositor
Minimum map value	-0.702	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.45	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	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	0.10	0/1153	0.25	0/1550
1	2	0.10	0/1153	0.25	0/1550
1	3	0.10	0/1153	0.25	0/1550
1	4	0.10	0/1153	0.25	0/1550
1	5	0.10	0/1153	0.25	0/1550
1	6	0.10	0/1153	0.25	0/1550
1	7	0.10	0/1153	0.25	0/1550
1	8	0.10	0/1153	0.25	0/1550
1	9	0.10	0/1153	0.25	0/1550
1	A	0.10	0/1153	0.25	0/1550
1	B	0.10	0/1153	0.25	0/1550
1	C	0.10	0/1153	0.25	0/1550
1	D	0.10	0/1153	0.25	0/1550
1	E	0.10	0/1153	0.25	0/1550
1	F	0.10	0/1153	0.25	0/1550
1	G	0.10	0/1153	0.25	0/1550
1	H	0.10	0/1153	0.25	0/1550
1	I	0.10	0/1153	0.25	0/1550
1	J	0.10	0/1153	0.25	0/1550
1	K	0.10	0/1153	0.25	0/1550
1	L	0.10	0/1153	0.25	0/1550
1	M	0.10	0/1153	0.25	0/1550
1	N	0.10	0/1153	0.25	0/1550
1	O	0.10	0/1153	0.25	0/1550
1	P	0.10	0/1153	0.25	0/1550
1	Q	0.10	0/1153	0.25	0/1550
1	R	0.10	0/1153	0.25	0/1550
1	S	0.10	0/1153	0.25	0/1550
1	T	0.10	0/1153	0.25	0/1550
1	U	0.10	0/1153	0.25	0/1550
1	V	0.10	0/1153	0.25	0/1550
1	W	0.10	0/1153	0.25	0/1550
1	X	0.10	0/1153	0.25	0/1550
1	Y	0.10	0/1153	0.25	0/1550

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.10	0/39202	0.25	0/52700

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1143	0	1135	12	0
1	2	1143	0	1135	12	0
1	3	1143	0	1135	12	0
1	4	1143	0	1135	13	0
1	5	1143	0	1135	13	0
1	6	1143	0	1135	13	0
1	7	1143	0	1135	13	0
1	8	1143	0	1135	13	0
1	9	1143	0	1135	14	0
1	A	1143	0	1135	13	0
1	B	1143	0	1135	13	0
1	C	1143	0	1135	14	0
1	D	1143	0	1135	14	0
1	E	1143	0	1135	14	0
1	F	1143	0	1135	13	0
1	G	1143	0	1135	13	0
1	H	1143	0	1135	14	0
1	I	1143	0	1135	14	0
1	J	1143	0	1135	13	0
1	K	1143	0	1135	14	0
1	L	1143	0	1135	14	0
1	M	1143	0	1135	14	0
1	N	1143	0	1135	13	0
1	O	1143	0	1135	14	0
1	P	1143	0	1135	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	1143	0	1135	13	0
1	R	1143	0	1135	12	0
1	S	1143	0	1135	12	0
1	T	1143	0	1135	12	0
1	U	1143	0	1135	13	0
1	V	1143	0	1135	13	0
1	W	1143	0	1135	12	0
1	X	1143	0	1135	14	0
1	Y	1143	0	1135	12	0
All	All	38862	0	38590	309	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 4.

All (309) 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)
1:4:395:THR:HG22	1:4:443:LEU:HB3	1.83	0.61
1:2:395:THR:HG22	1:2:443:LEU:HB3	1.83	0.61
1:8:395:THR:HG22	1:8:443:LEU:HB3	1.83	0.61
1:1:395:THR:HG22	1:1:443:LEU:HB3	1.83	0.61
1:5:395:THR:HG22	1:5:443:LEU:HB3	1.83	0.61
1:6:395:THR:HG22	1:6:443:LEU:HB3	1.83	0.61
1:A:395:THR:HG22	1:A:443:LEU:HB3	1.83	0.61
1:Y:395:THR:HG22	1:Y:443:LEU:HB3	1.83	0.61
1:7:395:THR:HG22	1:7:443:LEU:HB3	1.83	0.61
1:9:395:THR:HG22	1:9:443:LEU:HB3	1.83	0.61
1:C:395:THR:HG22	1:C:443:LEU:HB3	1.83	0.61
1:3:395:THR:HG22	1:3:443:LEU:HB3	1.83	0.60
1:W:395:THR:HG22	1:W:443:LEU:HB3	1.83	0.60
1:B:395:THR:HG22	1:B:443:LEU:HB3	1.83	0.60
1:D:395:THR:HG22	1:D:443:LEU:HB3	1.83	0.60
1:U:395:THR:HG22	1:U:443:LEU:HB3	1.83	0.60
1:X:395:THR:HG22	1:X:443:LEU:HB3	1.83	0.60
1:E:395:THR:HG22	1:E:443:LEU:HB3	1.83	0.60
1:F:395:THR:HG22	1:F:443:LEU:HB3	1.83	0.60
1:S:395:THR:HG22	1:S:443:LEU:HB3	1.83	0.60
1:V:395:THR:HG22	1:V:443:LEU:HB3	1.83	0.60
1:H:395:THR:HG22	1:H:443:LEU:HB3	1.83	0.60
1:G:395:THR:HG22	1:G:443:LEU:HB3	1.83	0.60
1:Q:395:THR:HG22	1:Q:443:LEU:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:395:THR:HG22	1:T:443:LEU:HB3	1.83	0.60
1:J:395:THR:HG22	1:J:443:LEU:HB3	1.83	0.59
1:R:395:THR:HG22	1:R:443:LEU:HB3	1.83	0.59
1:N:395:THR:HG22	1:N:443:LEU:HB3	1.83	0.59
1:I:395:THR:HG22	1:I:443:LEU:HB3	1.83	0.59
1:O:395:THR:HG22	1:O:443:LEU:HB3	1.83	0.59
1:P:395:THR:HG22	1:P:443:LEU:HB3	1.83	0.59
1:L:395:THR:HG22	1:L:443:LEU:HB3	1.83	0.59
1:M:395:THR:HG22	1:M:443:LEU:HB3	1.83	0.59
1:K:395:THR:HG22	1:K:443:LEU:HB3	1.83	0.59
1:S:269:GLN:NE2	1:T:263:GLN:OE1	2.37	0.54
1:Q:269:GLN:NE2	1:R:263:GLN:OE1	2.37	0.54
1:N:269:GLN:NE2	1:O:263:GLN:OE1	2.37	0.53
1:T:269:GLN:NE2	1:U:263:GLN:OE1	2.38	0.53
1:O:269:GLN:NE2	1:P:263:GLN:OE1	2.38	0.52
1:R:269:GLN:NE2	1:S:263:GLN:OE1	2.37	0.52
1:U:269:GLN:NE2	1:V:263:GLN:OE1	2.37	0.52
1:M:269:GLN:NE2	1:N:263:GLN:OE1	2.39	0.52
1:X:269:GLN:NE2	1:Y:263:GLN:OE1	2.37	0.52
1:J:269:GLN:NE2	1:K:263:GLN:OE1	2.37	0.52
1:V:269:GLN:NE2	1:W:263:GLN:OE1	2.39	0.52
1:L:269:GLN:NE2	1:M:263:GLN:OE1	2.38	0.52
1:P:269:GLN:NE2	1:Q:263:GLN:OE1	2.39	0.52
1:I:269:GLN:NE2	1:2:263:GLN:OE1	2.37	0.51
1:K:269:GLN:NE2	1:L:263:GLN:OE1	2.39	0.51
1:I:269:GLN:NE2	1:J:263:GLN:OE1	2.38	0.51
1:W:269:GLN:NE2	1:X:263:GLN:OE1	2.39	0.50
1:G:269:GLN:NE2	1:H:263:GLN:OE1	2.38	0.50
1:2:269:GLN:NE2	1:3:263:GLN:OE1	2.38	0.50
1:H:269:GLN:NE2	1:I:263:GLN:OE1	2.39	0.50
1:3:269:GLN:NE2	1:4:263:GLN:OE1	2.39	0.49
1:F:269:GLN:NE2	1:G:263:GLN:OE1	2.39	0.49
1:X:276:LYS:NZ	1:Y:295:ASP:OD1	2.36	0.49
1:E:269:GLN:NE2	1:F:263:GLN:OE1	2.38	0.49
1:4:269:GLN:NE2	1:5:263:GLN:OE1	2.38	0.49
1:I:269:GLN:HB3	1:I:296:ILE:HD13	1.95	0.48
1:D:269:GLN:NE2	1:E:263:GLN:OE1	2.38	0.48
1:O:269:GLN:HB3	1:O:296:ILE:HD13	1.95	0.48
1:4:269:GLN:HB3	1:4:296:ILE:HD13	1.95	0.48
1:B:269:GLN:NE2	1:C:263:GLN:OE1	2.38	0.48
1:J:269:GLN:HB3	1:J:296:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:269:GLN:HB3	1:L:296:ILE:HD13	1.95	0.48
1:W:269:GLN:HB3	1:W:296:ILE:HD13	1.95	0.48
1:G:269:GLN:HB3	1:G:296:ILE:HD13	1.95	0.48
1:R:269:GLN:HB3	1:R:296:ILE:HD13	1.96	0.48
1:7:269:GLN:HB3	1:7:296:ILE:HD13	1.95	0.48
1:I:269:GLN:HB3	1:I:296:ILE:HD13	1.95	0.48
1:M:269:GLN:HB3	1:M:296:ILE:HD13	1.95	0.48
1:U:269:GLN:HB3	1:U:296:ILE:HD13	1.95	0.48
1:3:269:GLN:HB3	1:3:296:ILE:HD13	1.96	0.48
1:6:269:GLN:HB3	1:6:296:ILE:HD13	1.95	0.48
1:T:269:GLN:HB3	1:T:296:ILE:HD13	1.95	0.48
1:7:269:GLN:NE2	1:8:263:GLN:OE1	2.38	0.48
1:A:269:GLN:HB3	1:A:296:ILE:HD13	1.95	0.48
1:D:269:GLN:HB3	1:D:296:ILE:HD13	1.96	0.48
1:F:269:GLN:HB3	1:F:296:ILE:HD13	1.95	0.48
1:Y:269:GLN:HB3	1:Y:296:ILE:HD13	1.95	0.48
1:9:269:GLN:HB3	1:9:296:ILE:HD13	1.96	0.48
1:C:269:GLN:HB3	1:C:296:ILE:HD13	1.95	0.48
1:M:432:GLY:HA3	1:N:397:SER:HB3	1.96	0.48
1:T:432:GLY:HA3	1:U:397:SER:HB3	1.96	0.48
1:6:269:GLN:NE2	1:7:263:GLN:OE1	2.38	0.48
1:Q:269:GLN:HB3	1:Q:296:ILE:HD13	1.95	0.48
1:X:269:GLN:HB3	1:X:296:ILE:HD13	1.95	0.48
1:9:269:GLN:NE2	1:A:263:GLN:OE1	2.38	0.48
1:9:432:GLY:HA3	1:A:397:SER:HB3	1.95	0.48
1:P:269:GLN:HB3	1:P:296:ILE:HD13	1.95	0.48
1:A:269:GLN:NE2	1:B:263:GLN:OE1	2.38	0.47
1:2:269:GLN:HB3	1:2:296:ILE:HD13	1.95	0.47
1:5:269:GLN:NE2	1:6:263:GLN:OE1	2.39	0.47
1:G:432:GLY:HA3	1:H:397:SER:HB3	1.96	0.47
1:Q:432:GLY:HA3	1:R:397:SER:HB3	1.96	0.47
1:N:269:GLN:HB3	1:N:296:ILE:HD13	1.95	0.47
1:H:269:GLN:HB3	1:H:296:ILE:HD13	1.95	0.47
1:S:432:GLY:HA3	1:T:397:SER:HB3	1.96	0.47
1:U:276:LYS:NZ	1:V:295:ASP:OD1	2.37	0.47
1:V:269:GLN:HB3	1:V:296:ILE:HD13	1.96	0.47
1:I:432:GLY:HA3	1:J:397:SER:HB3	1.96	0.47
1:5:269:GLN:HB3	1:5:296:ILE:HD13	1.95	0.47
1:B:432:GLY:HA3	1:C:397:SER:HB3	1.96	0.47
1:V:432:GLY:HA3	1:W:397:SER:HB3	1.97	0.47
1:3:432:GLY:HA3	1:4:397:SER:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:GLN:HB3	1:B:296:ILE:HD13	1.95	0.47
1:C:269:GLN:NE2	1:D:263:GLN:OE1	2.39	0.47
1:E:269:GLN:HB3	1:E:296:ILE:HD13	1.95	0.47
1:F:432:GLY:HA3	1:G:397:SER:HB3	1.96	0.47
1:K:269:GLN:HB3	1:K:296:ILE:HD13	1.96	0.47
1:S:269:GLN:HB3	1:S:296:ILE:HD13	1.95	0.47
1:5:276:LYS:NZ	1:6:295:ASP:OD1	2.37	0.47
1:8:269:GLN:HB3	1:8:296:ILE:HD13	1.95	0.47
1:8:269:GLN:NE2	1:9:263:GLN:OE1	2.39	0.47
1:K:432:GLY:HA3	1:L:397:SER:HB3	1.97	0.47
1:W:432:GLY:HA3	1:X:397:SER:HB3	1.97	0.47
1:1:397:SER:HB3	1:Y:432:GLY:HA3	1.97	0.47
1:O:432:GLY:HA3	1:P:397:SER:HB3	1.96	0.47
1:P:432:GLY:HA3	1:Q:397:SER:HB3	1.97	0.47
1:C:432:GLY:HA3	1:D:397:SER:HB3	1.96	0.47
1:E:432:GLY:HA3	1:F:397:SER:HB3	1.97	0.47
1:J:432:GLY:HA3	1:K:397:SER:HB3	1.97	0.46
1:5:432:GLY:HA3	1:6:397:SER:HB3	1.96	0.46
1:K:398:VAL:HB	1:K:446:VAL:HG22	1.98	0.46
1:N:398:VAL:HB	1:N:446:VAL:HG22	1.98	0.46
1:N:432:GLY:HA3	1:O:397:SER:HB3	1.98	0.46
1:P:398:VAL:HB	1:P:446:VAL:HG22	1.98	0.46
1:I:398:VAL:HB	1:I:446:VAL:HG22	1.98	0.46
1:J:398:VAL:HB	1:J:446:VAL:HG22	1.98	0.46
1:M:398:VAL:HB	1:M:446:VAL:HG22	1.98	0.46
1:R:398:VAL:HB	1:R:446:VAL:HG22	1.98	0.46
1:S:398:VAL:HB	1:S:446:VAL:HG22	1.98	0.46
1:T:398:VAL:HB	1:T:446:VAL:HG22	1.98	0.46
1:G:398:VAL:HB	1:G:446:VAL:HG22	1.98	0.46
1:H:398:VAL:HB	1:H:446:VAL:HG22	1.98	0.46
1:H:432:GLY:HA3	1:I:397:SER:HB3	1.98	0.46
1:L:398:VAL:HB	1:L:446:VAL:HG22	1.98	0.46
1:O:398:VAL:HB	1:O:446:VAL:HG22	1.98	0.46
1:Q:398:VAL:HB	1:Q:446:VAL:HG22	1.98	0.46
1:U:398:VAL:HB	1:U:446:VAL:HG22	1.98	0.46
1:V:398:VAL:HB	1:V:446:VAL:HG22	1.98	0.46
1:X:432:GLY:HA3	1:Y:397:SER:HB3	1.96	0.46
1:D:432:GLY:HA3	1:E:397:SER:HB3	1.97	0.46
1:F:398:VAL:HB	1:F:446:VAL:HG22	1.98	0.46
1:W:398:VAL:HB	1:W:446:VAL:HG22	1.98	0.46
1:6:398:VAL:HB	1:6:446:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:8:398:VAL:HB	1:8:446:VAL:HG22	1.98	0.46
1:B:398:VAL:HB	1:B:446:VAL:HG22	1.98	0.46
1:C:398:VAL:HB	1:C:446:VAL:HG22	1.98	0.46
1:E:398:VAL:HB	1:E:446:VAL:HG22	1.98	0.46
1:X:398:VAL:HB	1:X:446:VAL:HG22	1.98	0.46
1:8:432:GLY:HA3	1:9:397:SER:HB3	1.97	0.46
1:A:398:VAL:HB	1:A:446:VAL:HG22	1.98	0.46
1:Y:398:VAL:HB	1:Y:446:VAL:HG22	1.98	0.46
1:1:398:VAL:HB	1:1:446:VAL:HG22	1.98	0.46
1:2:398:VAL:HB	1:2:446:VAL:HG22	1.98	0.46
1:3:398:VAL:HB	1:3:446:VAL:HG22	1.98	0.46
1:4:398:VAL:HB	1:4:446:VAL:HG22	1.98	0.46
1:5:398:VAL:HB	1:5:446:VAL:HG22	1.98	0.46
1:7:398:VAL:HB	1:7:446:VAL:HG22	1.98	0.46
1:9:398:VAL:HB	1:9:446:VAL:HG22	1.98	0.46
1:D:398:VAL:HB	1:D:446:VAL:HG22	1.98	0.46
1:1:263:GLN:OE1	1:Y:269:GLN:NE2	2.44	0.45
1:6:432:GLY:HA3	1:7:397:SER:HB3	1.97	0.45
1:U:432:GLY:HA3	1:V:397:SER:HB3	1.97	0.45
1:1:432:GLY:HA3	1:2:397:SER:HB3	1.98	0.45
1:L:432:GLY:HA3	1:M:397:SER:HB3	1.98	0.45
1:7:432:GLY:HA3	1:8:397:SER:HB3	1.97	0.45
1:R:432:GLY:HA3	1:S:397:SER:HB3	1.98	0.45
1:2:432:GLY:HA3	1:3:397:SER:HB3	1.97	0.45
1:4:432:GLY:HA3	1:5:397:SER:HB3	1.97	0.45
1:1:387:GLN:HG3	1:2:300:PHE:HB2	1.98	0.45
1:D:273:LEU:HD12	1:D:273:LEU:HA	1.89	0.44
1:A:432:GLY:HA3	1:B:397:SER:HB3	1.98	0.44
1:F:387:GLN:HG3	1:G:300:PHE:HB2	2.00	0.44
1:9:387:GLN:HG3	1:A:300:PHE:HB2	2.00	0.44
1:P:273:LEU:HD12	1:P:273:LEU:HA	1.89	0.44
1:I:273:LEU:HD12	1:I:273:LEU:HA	1.89	0.44
1:M:387:GLN:HG3	1:N:300:PHE:HB2	2.00	0.44
1:G:387:GLN:HG3	1:H:300:PHE:HB2	2.00	0.44
1:Q:387:GLN:HG3	1:R:300:PHE:HB2	2.00	0.44
1:P:276:LYS:NZ	1:Q:295:ASP:OD1	2.35	0.44
1:X:387:GLN:HG3	1:Y:300:PHE:HB2	2.00	0.44
1:4:387:GLN:HG3	1:5:300:PHE:HB2	2.00	0.43
1:4:273:LEU:HD12	1:4:273:LEU:HA	1.89	0.43
1:N:387:GLN:HG3	1:O:300:PHE:HB2	2.00	0.43
1:6:387:GLN:HG3	1:7:300:PHE:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:387:GLN:HG3	1:S:300:PHE:HB2	2.01	0.43
1:T:387:GLN:HG3	1:U:300:PHE:HB2	2.00	0.43
1:B:278:ASP:OD1	1:B:290:TYR:OH	2.35	0.43
1:B:387:GLN:HG3	1:C:300:PHE:HB2	2.01	0.43
1:E:273:LEU:HD12	1:E:273:LEU:HA	1.89	0.43
1:L:387:GLN:HG3	1:M:300:PHE:HB2	2.01	0.43
1:S:387:GLN:HG3	1:T:300:PHE:HB2	2.01	0.43
1:W:387:GLN:HG3	1:X:300:PHE:HB2	2.01	0.43
1:A:387:GLN:HG3	1:B:300:PHE:HB2	2.01	0.43
1:I:387:GLN:HG3	1:J:300:PHE:HB2	2.00	0.43
1:8:387:GLN:HG3	1:9:300:PHE:HB2	2.00	0.43
1:A:314:THR:HG23	1:B:312:PRO:HG3	2.01	0.43
1:3:387:GLN:HG3	1:4:300:PHE:HB2	2.00	0.43
1:5:387:GLN:HG3	1:6:300:PHE:HB2	2.01	0.43
1:C:387:GLN:HG3	1:D:300:PHE:HB2	2.00	0.43
1:J:314:THR:HG23	1:K:312:PRO:HG3	2.01	0.43
1:K:387:GLN:HG3	1:L:300:PHE:HB2	2.01	0.43
1:L:276:LYS:NZ	1:M:295:ASP:OD1	2.36	0.43
1:Q:273:LEU:HD12	1:Q:273:LEU:HA	1.89	0.43
1:J:273:LEU:HD12	1:J:273:LEU:HA	1.89	0.42
1:9:273:LEU:HD12	1:9:273:LEU:HA	1.89	0.42
1:X:273:LEU:HD12	1:X:273:LEU:HA	1.89	0.42
1:Y:318:ARG:NH1	1:Y:376:GLU:OE1	2.52	0.42
1:1:318:ARG:NH1	1:1:376:GLU:OE1	2.52	0.42
1:2:387:GLN:HG3	1:3:300:PHE:HB2	2.00	0.42
1:8:276:LYS:NZ	1:9:295:ASP:OD1	2.35	0.42
1:C:318:ARG:NH1	1:C:376:GLU:OE1	2.52	0.42
1:D:314:THR:HG23	1:E:312:PRO:HG3	2.01	0.42
1:D:387:GLN:HG3	1:E:300:PHE:HB2	2.01	0.42
1:E:387:GLN:HG3	1:F:300:PHE:HB2	2.01	0.42
1:H:387:GLN:HG3	1:I:300:PHE:HB2	2.01	0.42
1:P:387:GLN:HG3	1:Q:300:PHE:HB2	2.00	0.42
1:U:318:ARG:NH1	1:U:376:GLU:OE1	2.52	0.42
1:X:318:ARG:NH1	1:X:376:GLU:OE1	2.52	0.42
1:D:318:ARG:NH1	1:D:376:GLU:OE1	2.52	0.42
1:H:314:THR:HG23	1:I:312:PRO:HG3	2.01	0.42
1:L:314:THR:HG23	1:M:312:PRO:HG3	2.01	0.42
1:O:318:ARG:NH1	1:O:376:GLU:OE1	2.52	0.42
1:P:318:ARG:NH1	1:P:376:GLU:OE1	2.52	0.42
1:S:318:ARG:NH1	1:S:376:GLU:OE1	2.52	0.42
1:T:318:ARG:NH1	1:T:376:GLU:OE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:318:ARG:NH1	1:V:376:GLU:OE1	2.52	0.42
1:W:318:ARG:NH1	1:W:376:GLU:OE1	2.52	0.42
1:6:314:THR:HG23	1:7:312:PRO:HG3	2.01	0.42
1:B:318:ARG:NH1	1:B:376:GLU:OE1	2.52	0.42
1:Q:318:ARG:NH1	1:Q:376:GLU:OE1	2.52	0.42
1:R:318:ARG:NH1	1:R:376:GLU:OE1	2.52	0.42
1:2:318:ARG:NH1	1:2:376:GLU:OE1	2.52	0.42
1:A:318:ARG:NH1	1:A:376:GLU:OE1	2.52	0.42
1:E:318:ARG:NH1	1:E:376:GLU:OE1	2.52	0.42
1:F:318:ARG:NH1	1:F:376:GLU:OE1	2.52	0.42
1:J:387:GLN:HG3	1:K:300:PHE:HB2	2.01	0.42
1:N:318:ARG:NH1	1:N:376:GLU:OE1	2.52	0.42
1:V:387:GLN:HG3	1:W:300:PHE:HB2	2.01	0.42
1:E:314:THR:HG23	1:F:312:PRO:HG3	2.02	0.42
1:O:387:GLN:HG3	1:P:300:PHE:HB2	2.01	0.42
1:4:314:THR:HG23	1:5:312:PRO:HG3	2.01	0.42
1:8:314:THR:HG23	1:9:312:PRO:HG3	2.01	0.42
1:9:318:ARG:NH1	1:9:376:GLU:OE1	2.52	0.42
1:G:318:ARG:NH1	1:G:376:GLU:OE1	2.52	0.42
1:H:318:ARG:NH1	1:H:376:GLU:OE1	2.52	0.42
1:M:318:ARG:NH1	1:M:376:GLU:OE1	2.52	0.42
1:3:318:ARG:NH1	1:3:376:GLU:OE1	2.52	0.42
1:8:318:ARG:NH1	1:8:376:GLU:OE1	2.52	0.42
1:I:318:ARG:NH1	1:I:376:GLU:OE1	2.52	0.42
1:K:314:THR:HG23	1:L:312:PRO:HG3	2.02	0.42
1:U:314:THR:HG23	1:V:312:PRO:HG3	2.01	0.42
1:7:318:ARG:NH1	1:7:376:GLU:OE1	2.52	0.41
1:J:318:ARG:NH1	1:J:376:GLU:OE1	2.52	0.41
1:L:318:ARG:NH1	1:L:376:GLU:OE1	2.52	0.41
1:O:314:THR:HG23	1:P:312:PRO:HG3	2.01	0.41
1:4:318:ARG:NH1	1:4:376:GLU:OE1	2.52	0.41
1:6:318:ARG:NH1	1:6:376:GLU:OE1	2.52	0.41
1:2:314:THR:HG23	1:3:312:PRO:HG3	2.01	0.41
1:5:318:ARG:NH1	1:5:376:GLU:OE1	2.52	0.41
1:K:273:LEU:HD12	1:K:273:LEU:HA	1.89	0.41
1:V:314:THR:HG23	1:W:312:PRO:HG3	2.02	0.41
1:D:402:ASP:OD1	1:D:402:ASP:N	2.54	0.41
1:F:314:THR:HG23	1:G:312:PRO:HG3	2.03	0.41
1:G:314:THR:HG23	1:H:312:PRO:HG3	2.02	0.41
1:H:276:LYS:NZ	1:I:295:ASP:OD1	2.36	0.41
1:H:402:ASP:OD1	1:H:402:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:318:ARG:NH1	1:K:376:GLU:OE1	2.52	0.41
1:R:314:THR:HG23	1:S:312:PRO:HG3	2.01	0.41
1:1:312:PRO:HG3	1:Y:314:THR:HG23	2.01	0.41
1:C:402:ASP:OD1	1:C:402:ASP:N	2.54	0.41
1:E:402:ASP:OD1	1:E:402:ASP:N	2.54	0.41
1:F:402:ASP:OD1	1:F:402:ASP:N	2.54	0.41
1:G:402:ASP:OD1	1:G:402:ASP:N	2.54	0.41
1:I:402:ASP:OD1	1:I:402:ASP:N	2.54	0.41
1:J:402:ASP:OD1	1:J:402:ASP:N	2.54	0.41
1:N:314:THR:HG23	1:O:312:PRO:HG3	2.01	0.41
1:7:387:GLN:HG3	1:8:300:PHE:HB2	2.01	0.41
1:K:402:ASP:OD1	1:K:402:ASP:N	2.54	0.41
1:L:402:ASP:OD1	1:L:402:ASP:N	2.54	0.41
1:N:285:LEU:HD23	1:N:285:LEU:HA	1.94	0.41
1:P:314:THR:HG23	1:Q:312:PRO:HG3	2.01	0.41
1:U:387:GLN:HG3	1:V:300:PHE:HB2	2.01	0.41
1:M:402:ASP:OD1	1:M:402:ASP:N	2.54	0.41
1:X:314:THR:HG23	1:Y:312:PRO:HG3	2.02	0.41
1:B:314:THR:HG23	1:C:312:PRO:HG3	2.02	0.41
1:N:402:ASP:OD1	1:N:402:ASP:N	2.54	0.41
1:5:285:LEU:HD23	1:5:285:LEU:HA	1.94	0.41
1:M:285:LEU:HD23	1:M:285:LEU:HA	1.94	0.41
1:O:402:ASP:OD1	1:O:402:ASP:N	2.54	0.41
1:S:314:THR:HG23	1:T:312:PRO:HG3	2.02	0.41
1:W:314:THR:HG23	1:X:312:PRO:HG3	2.02	0.41
1:7:285:LEU:HD23	1:7:285:LEU:HA	1.94	0.41
1:R:273:LEU:HD12	1:R:273:LEU:HA	1.89	0.41
1:3:285:LEU:HD23	1:3:285:LEU:HA	1.94	0.40
1:7:314:THR:HG23	1:8:312:PRO:HG3	2.01	0.40
1:C:314:THR:HG23	1:D:312:PRO:HG3	2.02	0.40
1:T:314:THR:HG23	1:U:312:PRO:HG3	2.02	0.40
1:4:285:LEU:HD23	1:4:285:LEU:HA	1.94	0.40
1:6:273:LEU:HD12	1:6:273:LEU:HA	1.89	0.40
1:9:314:THR:HG23	1:A:312:PRO:HG3	2.03	0.40
1:1:285:LEU:HD23	1:1:285:LEU:HA	1.94	0.40
1:1:314:THR:HG23	1:2:312:PRO:HG3	2.02	0.40
1:C:276:LYS:HB2	1:C:276:LYS:HE2	1.98	0.40
1:O:273:LEU:HD12	1:O:273:LEU:HA	1.89	0.40
1:A:285:LEU:HD23	1:A:285:LEU:HA	1.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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	125/802 (16%)	125 (100%)	0	100	100
1	2	125/802 (16%)	125 (100%)	0	100	100
1	3	125/802 (16%)	125 (100%)	0	100	100
1	4	125/802 (16%)	125 (100%)	0	100	100
1	5	125/802 (16%)	125 (100%)	0	100	100
1	6	125/802 (16%)	125 (100%)	0	100	100
1	7	125/802 (16%)	125 (100%)	0	100	100
1	8	125/802 (16%)	125 (100%)	0	100	100
1	9	125/802 (16%)	125 (100%)	0	100	100
1	A	125/802 (16%)	125 (100%)	0	100	100
1	B	125/802 (16%)	125 (100%)	0	100	100
1	C	125/802 (16%)	125 (100%)	0	100	100
1	D	125/802 (16%)	125 (100%)	0	100	100
1	E	125/802 (16%)	125 (100%)	0	100	100
1	F	125/802 (16%)	125 (100%)	0	100	100
1	G	125/802 (16%)	125 (100%)	0	100	100
1	H	125/802 (16%)	125 (100%)	0	100	100
1	I	125/802 (16%)	125 (100%)	0	100	100
1	J	125/802 (16%)	125 (100%)	0	100	100
1	K	125/802 (16%)	125 (100%)	0	100	100
1	L	125/802 (16%)	125 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	125/802 (16%)	125 (100%)	0	100	100
1	N	125/802 (16%)	125 (100%)	0	100	100
1	O	125/802 (16%)	125 (100%)	0	100	100
1	P	125/802 (16%)	125 (100%)	0	100	100
1	Q	125/802 (16%)	125 (100%)	0	100	100
1	R	125/802 (16%)	125 (100%)	0	100	100
1	S	125/802 (16%)	125 (100%)	0	100	100
1	T	125/802 (16%)	125 (100%)	0	100	100
1	U	125/802 (16%)	125 (100%)	0	100	100
1	V	125/802 (16%)	125 (100%)	0	100	100
1	W	125/802 (16%)	125 (100%)	0	100	100
1	X	125/802 (16%)	125 (100%)	0	100	100
1	Y	125/802 (16%)	125 (100%)	0	100	100
All	All	4250/27268 (16%)	4250 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (97) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	327	ASN
1	1	383	HIS
1	1	394	GLN
1	2	327	ASN
1	2	383	HIS
1	2	394	GLN
1	3	327	ASN
1	3	383	HIS
1	3	394	GLN
1	4	327	ASN
1	4	383	HIS
1	4	394	GLN
1	5	327	ASN
1	5	383	HIS
1	5	394	GLN
1	6	327	ASN
1	6	383	HIS

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Mol	Chain	Res	Type
1	6	394	GLN
1	7	327	ASN
1	7	383	HIS
1	8	327	ASN
1	8	383	HIS
1	8	394	GLN
1	9	327	ASN
1	9	383	HIS
1	9	394	GLN
1	A	327	ASN
1	A	383	HIS
1	A	394	GLN
1	B	327	ASN
1	B	383	HIS
1	B	394	GLN
1	C	327	ASN
1	C	383	HIS
1	C	394	GLN
1	D	327	ASN
1	D	383	HIS
1	D	394	GLN
1	E	327	ASN
1	E	383	HIS
1	E	394	GLN
1	F	327	ASN
1	F	383	HIS
1	F	394	GLN
1	G	327	ASN
1	G	383	HIS
1	G	394	GLN
1	H	327	ASN
1	H	383	HIS
1	I	327	ASN
1	I	383	HIS
1	I	394	GLN
1	J	327	ASN
1	J	383	HIS
1	J	394	GLN
1	K	327	ASN
1	K	383	HIS
1	L	327	ASN
1	L	383	HIS

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Mol	Chain	Res	Type
1	M	327	ASN
1	M	383	HIS
1	M	394	GLN
1	N	327	ASN
1	N	383	HIS
1	O	327	ASN
1	O	383	HIS
1	O	394	GLN
1	P	327	ASN
1	P	383	HIS
1	P	394	GLN
1	Q	327	ASN
1	Q	383	HIS
1	Q	394	GLN
1	R	327	ASN
1	R	383	HIS
1	R	394	GLN
1	S	327	ASN
1	S	383	HIS
1	S	394	GLN
1	T	327	ASN
1	T	383	HIS
1	T	394	GLN
1	U	327	ASN
1	U	383	HIS
1	U	394	GLN
1	V	327	ASN
1	V	383	HIS
1	V	394	GLN
1	W	327	ASN
1	W	383	HIS
1	W	394	GLN
1	X	327	ASN
1	X	383	HIS
1	X	394	GLN
1	Y	327	ASN
1	Y	383	HIS
1	Y	394	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

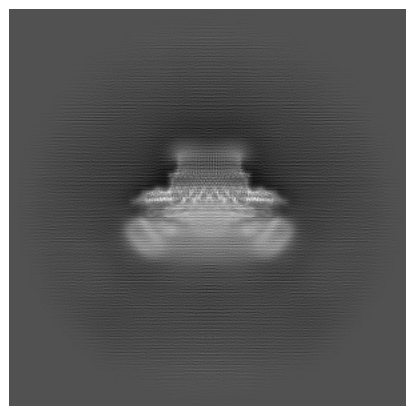
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39761. These allow visual inspection of the internal detail of the map and identification of artifacts.

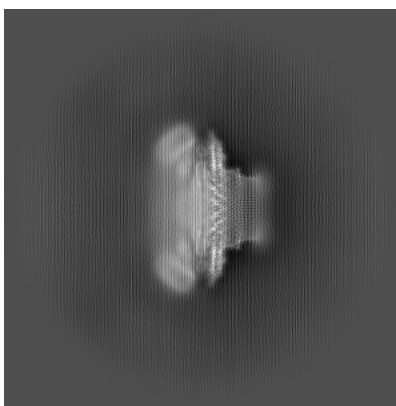
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

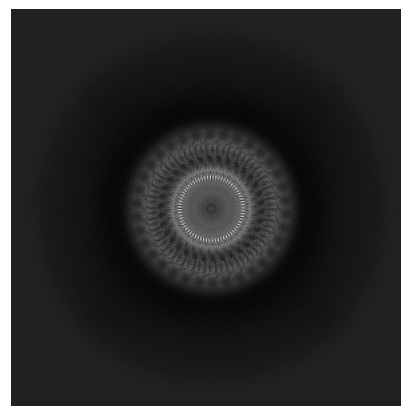
6.1.1 Primary map



X

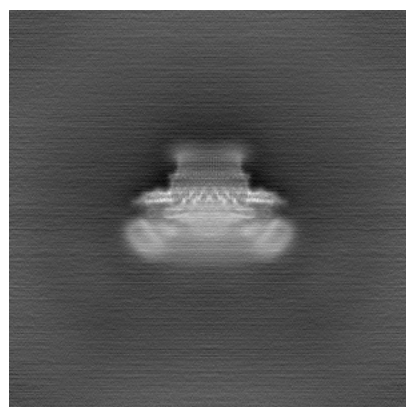


Y

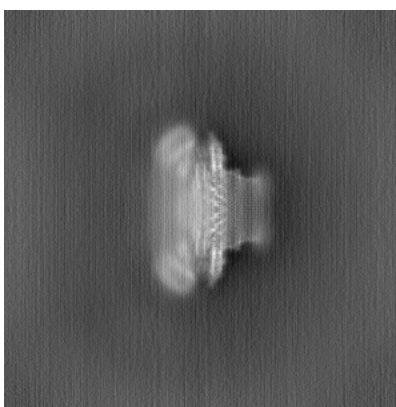


Z

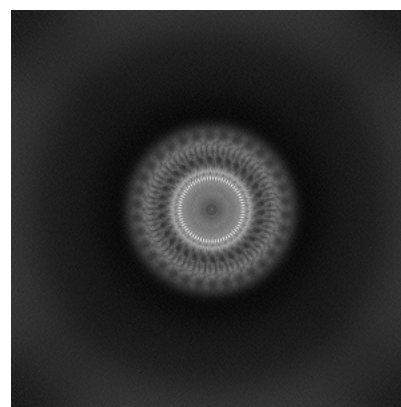
6.1.2 Raw map



X



Y

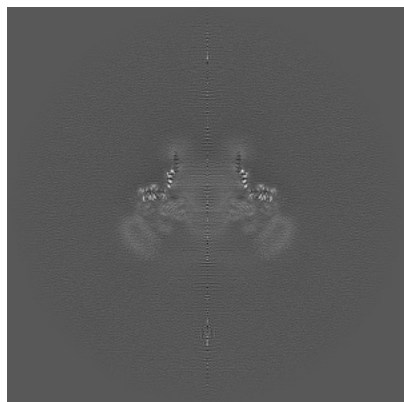


Z

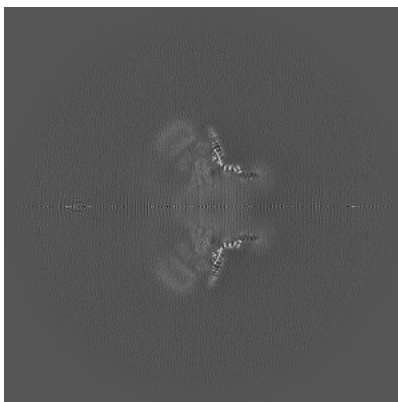
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

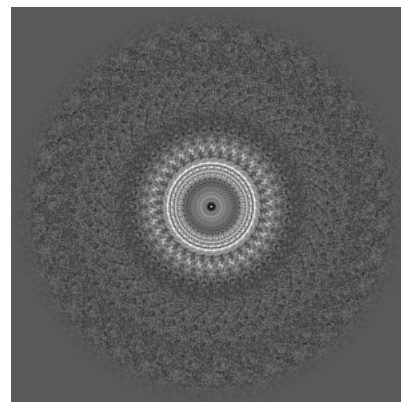
6.2.1 Primary map



X Index: 300

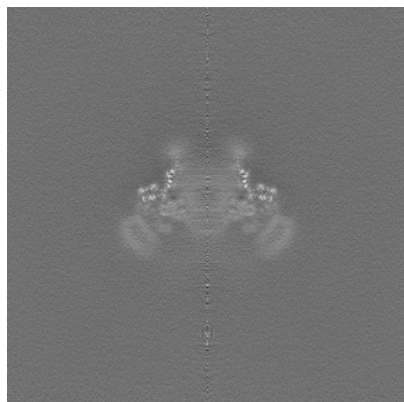


Y Index: 300

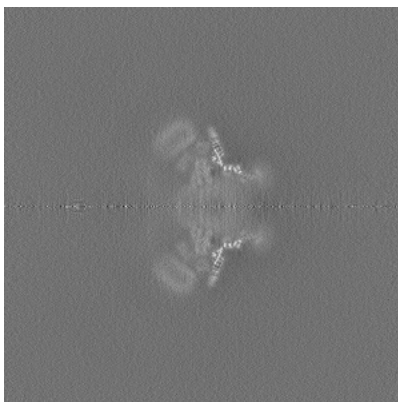


Z Index: 300

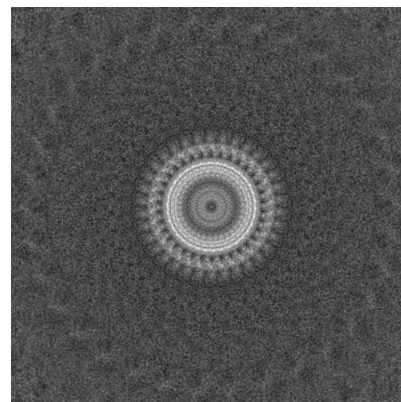
6.2.2 Raw map



X Index: 300



Y Index: 300

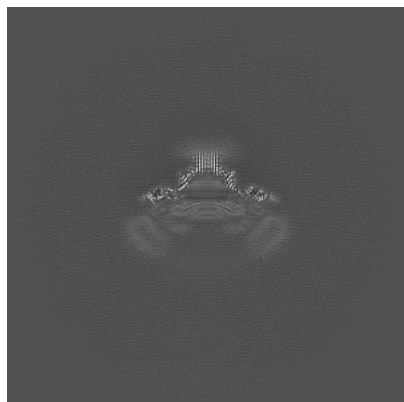


Z Index: 300

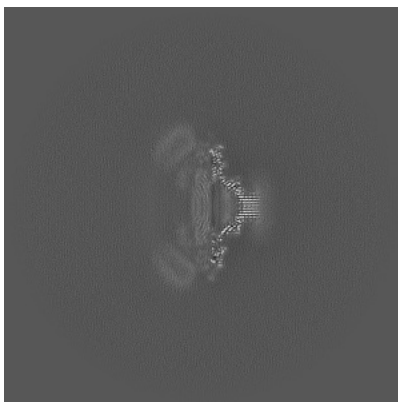
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

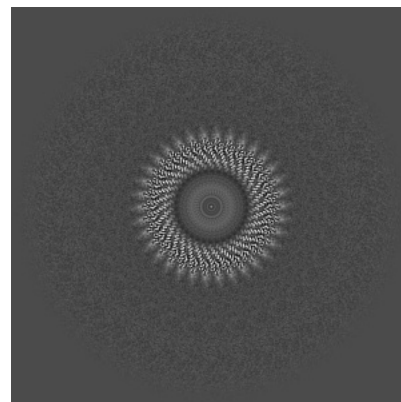
6.3.1 Primary map



X Index: 346

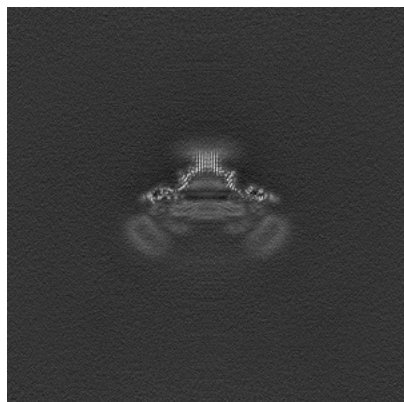


Y Index: 254

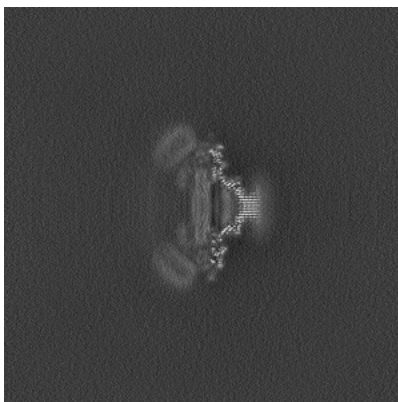


Z Index: 315

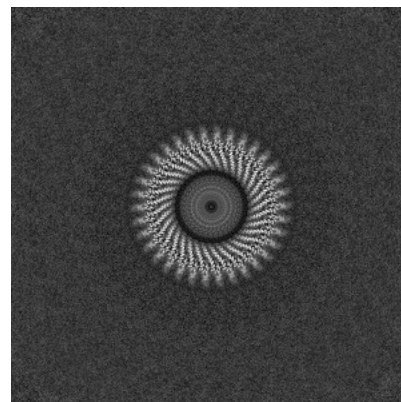
6.3.2 Raw map



X Index: 346



Y Index: 254

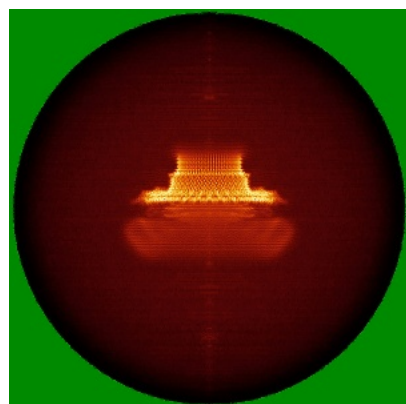


Z Index: 314

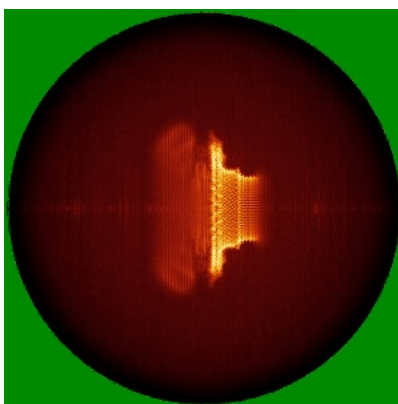
The images above show the largest variance slices of the map in three orthogonal directions.

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

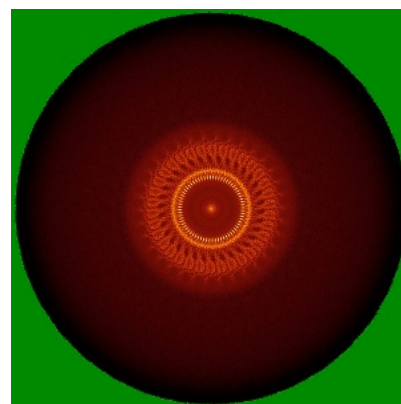
6.4.1 Primary map



X

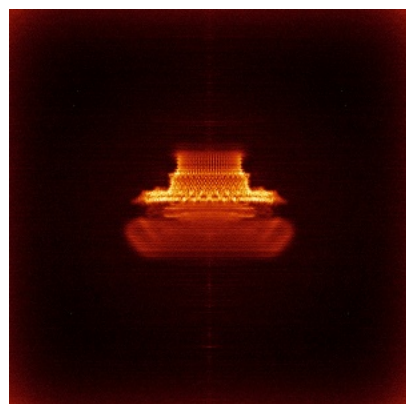


Y

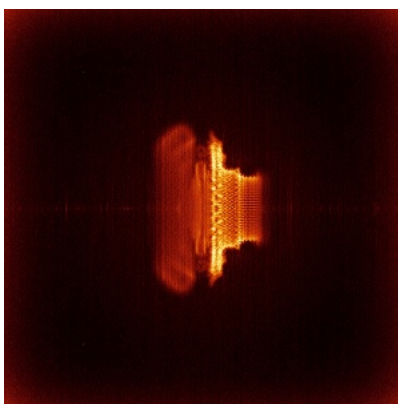


Z

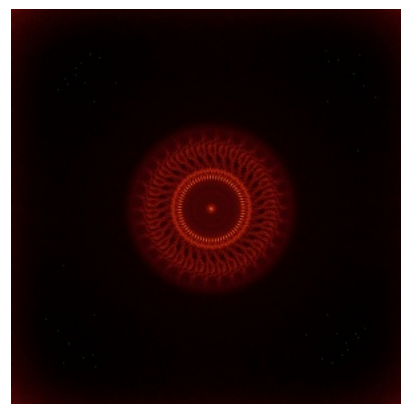
6.4.2 Raw map



X



Y

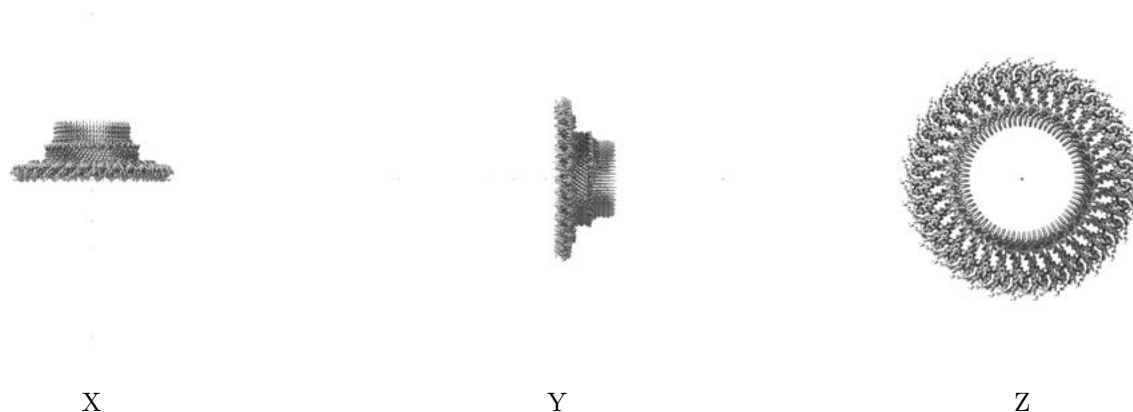


Z

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.

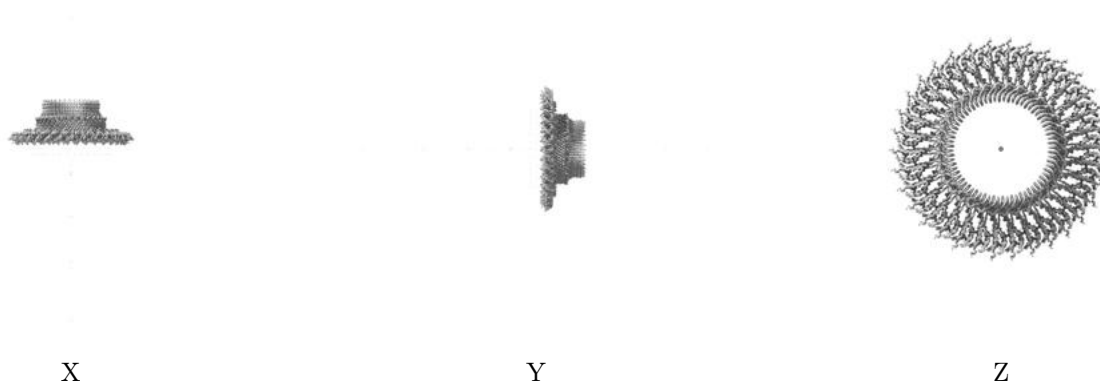
6.5 Orthogonal surface views [i](#)

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

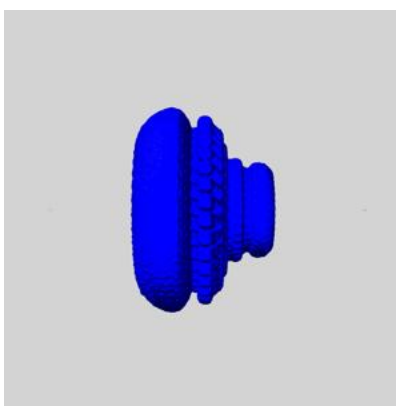
A mask typically either:

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

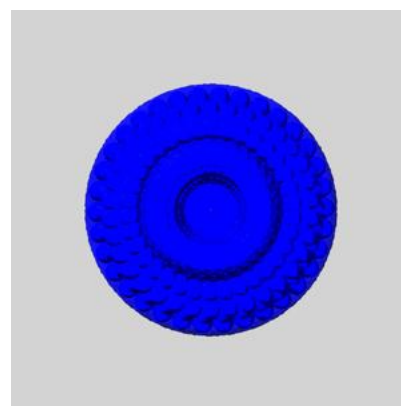
6.6.1 emd_39761_msk_1.map [i](#)



X



Y

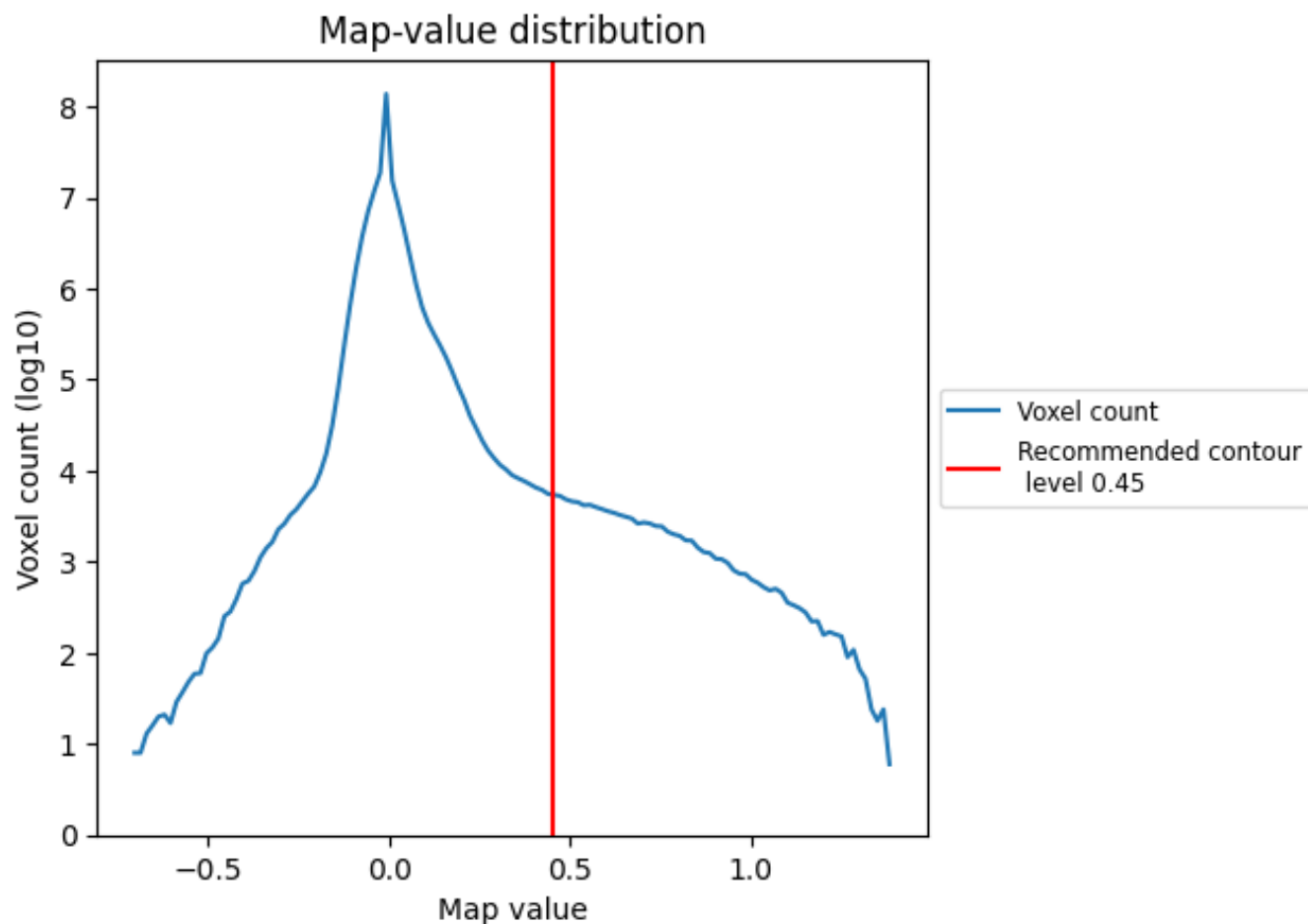


Z

7 Map analysis [i](#)

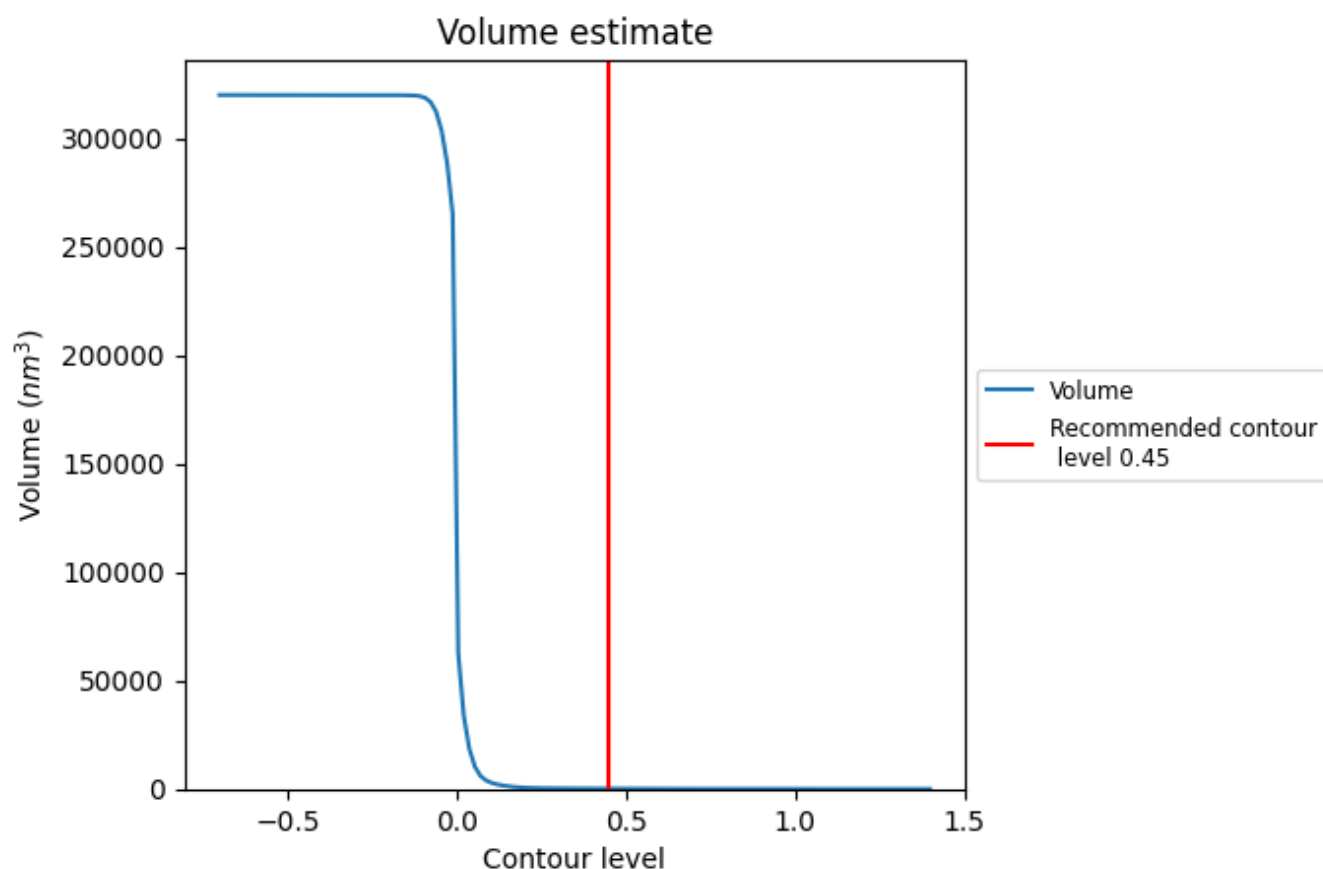
This section contains the results of statistical analysis of the map.

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.

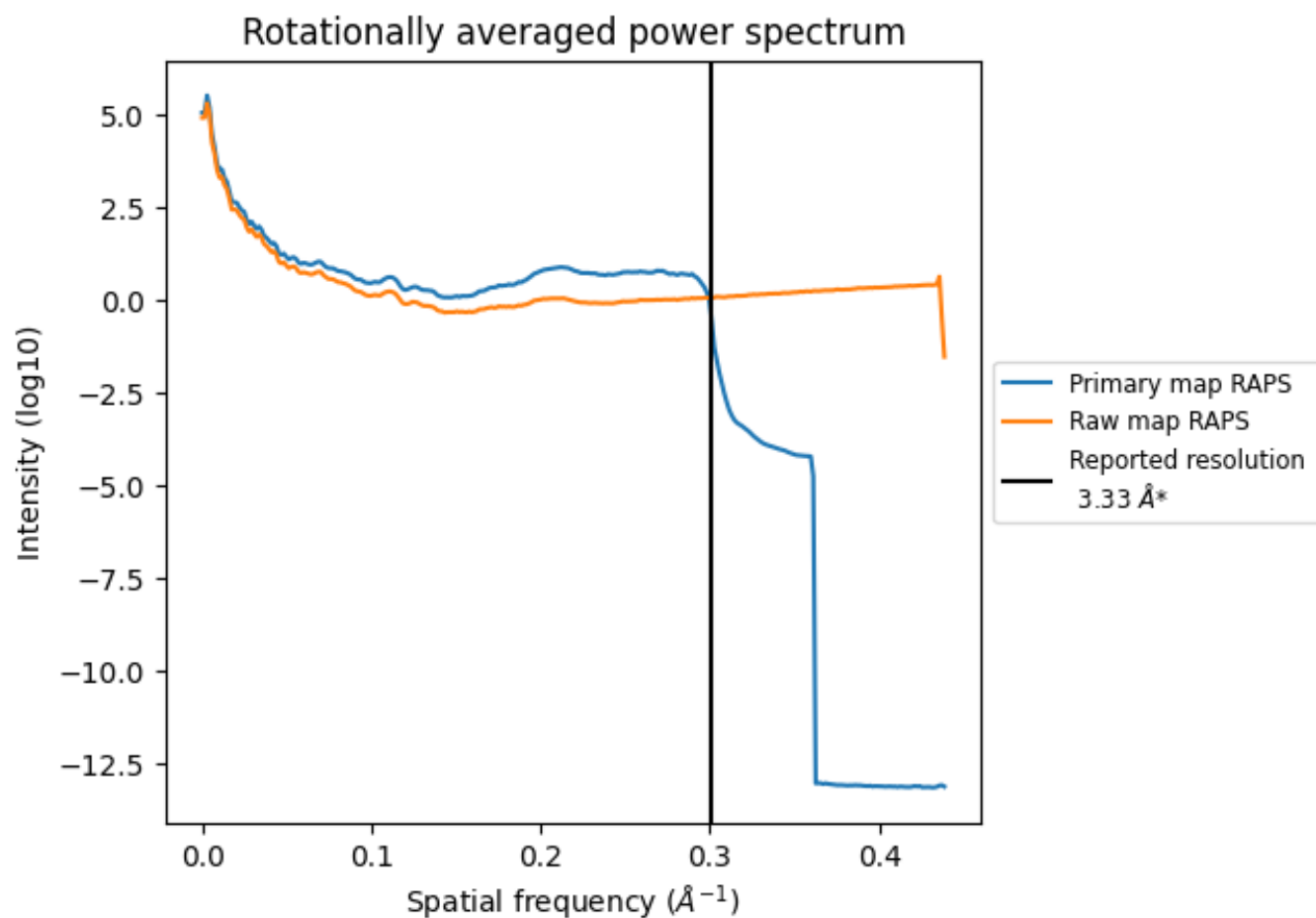
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 144 nm^3 ; this corresponds to an approximate mass of 130 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 ⓘ

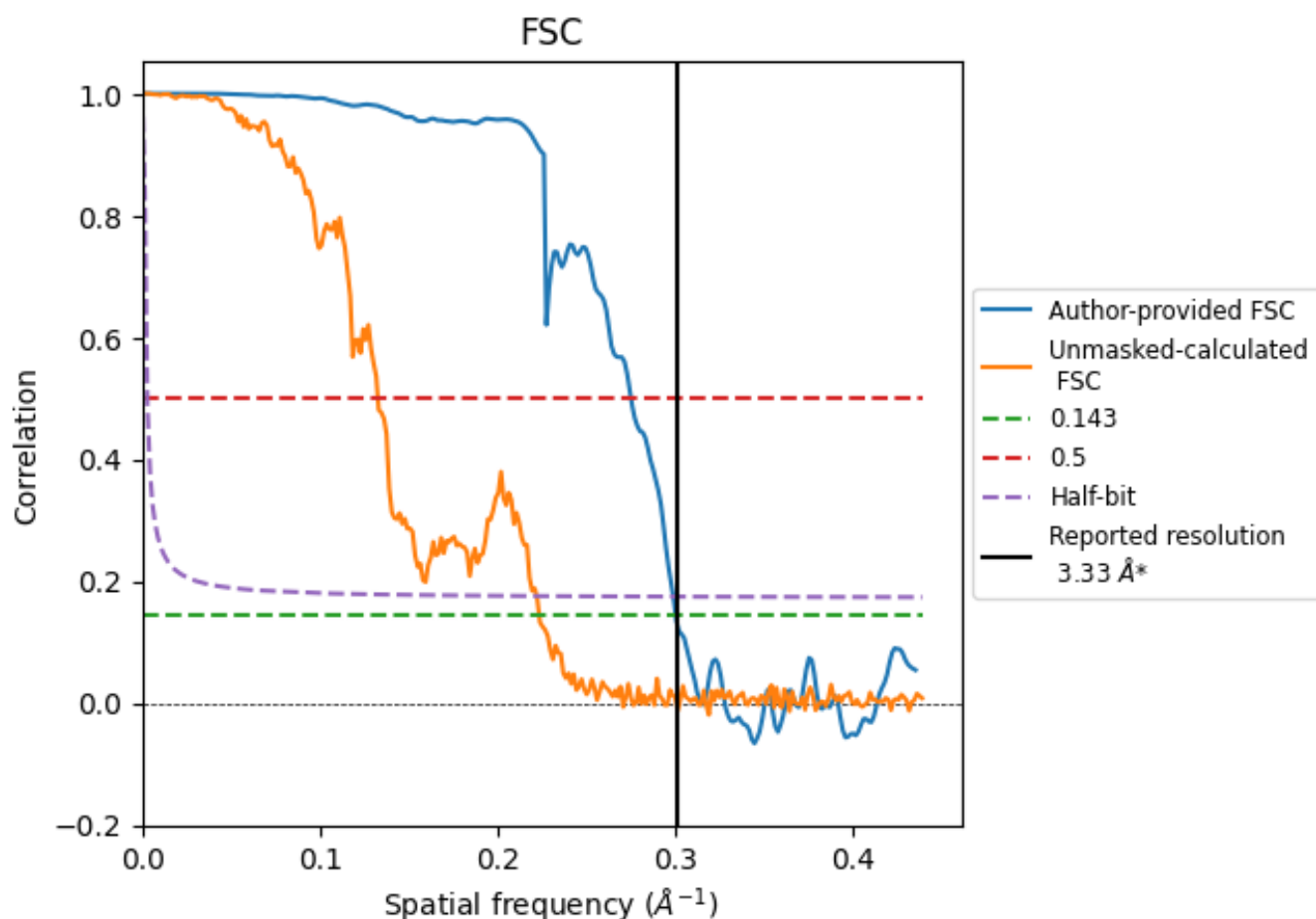


*Reported resolution corresponds to spatial frequency of 0.300 Å⁻¹

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 0.300 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

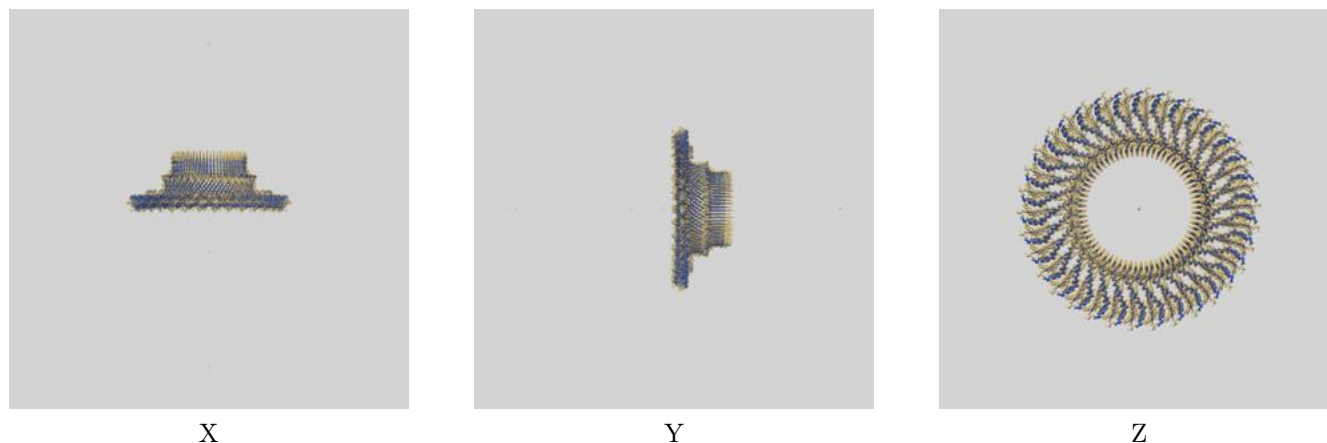
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.33	-	-
Author-provided FSC curve	3.33	3.64	3.35
Unmasked-calculated*	4.48	7.55	4.51

*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 4.48 differs from the reported value 3.33 by more than 10 %

9 Map-model fit [i](#)

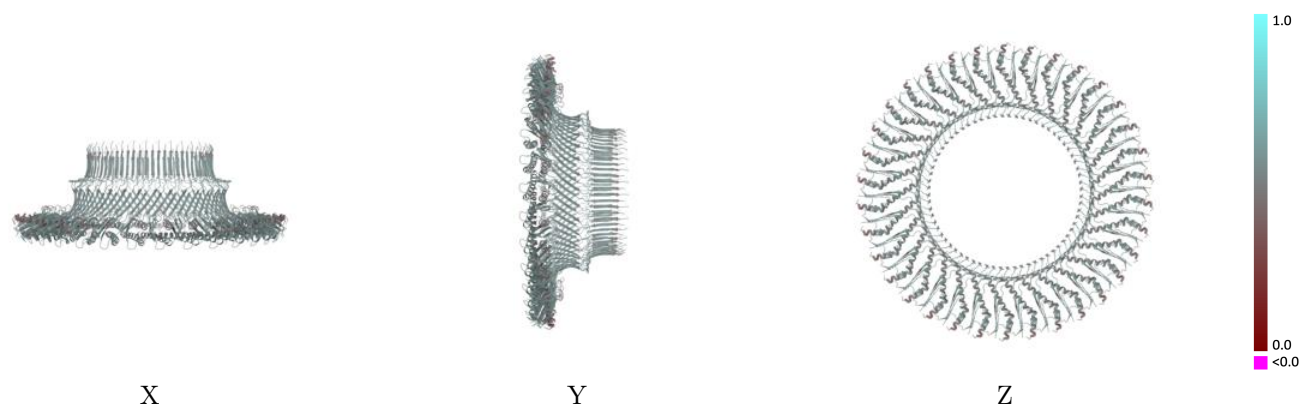
This section contains information regarding the fit between EMDB map EMD-39761 and PDB model 8Z4D. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



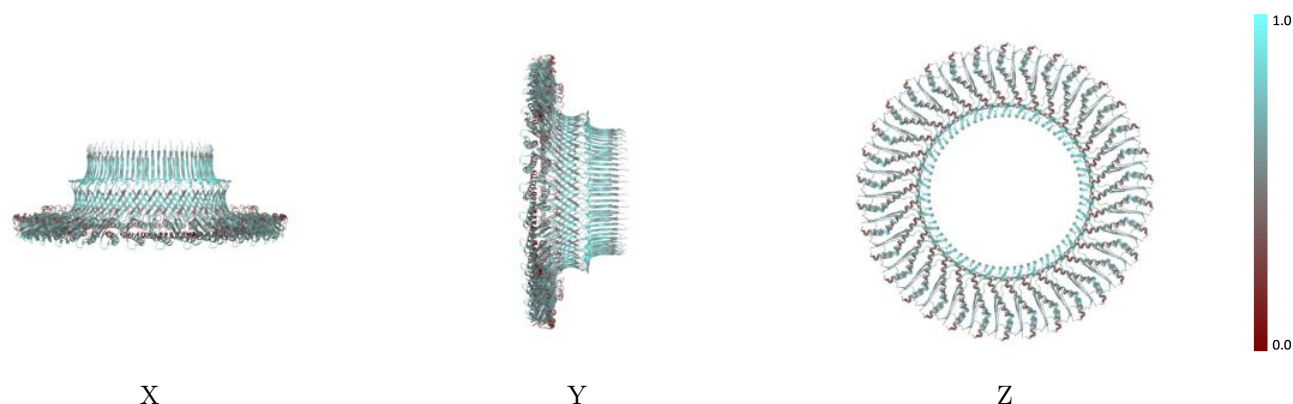
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



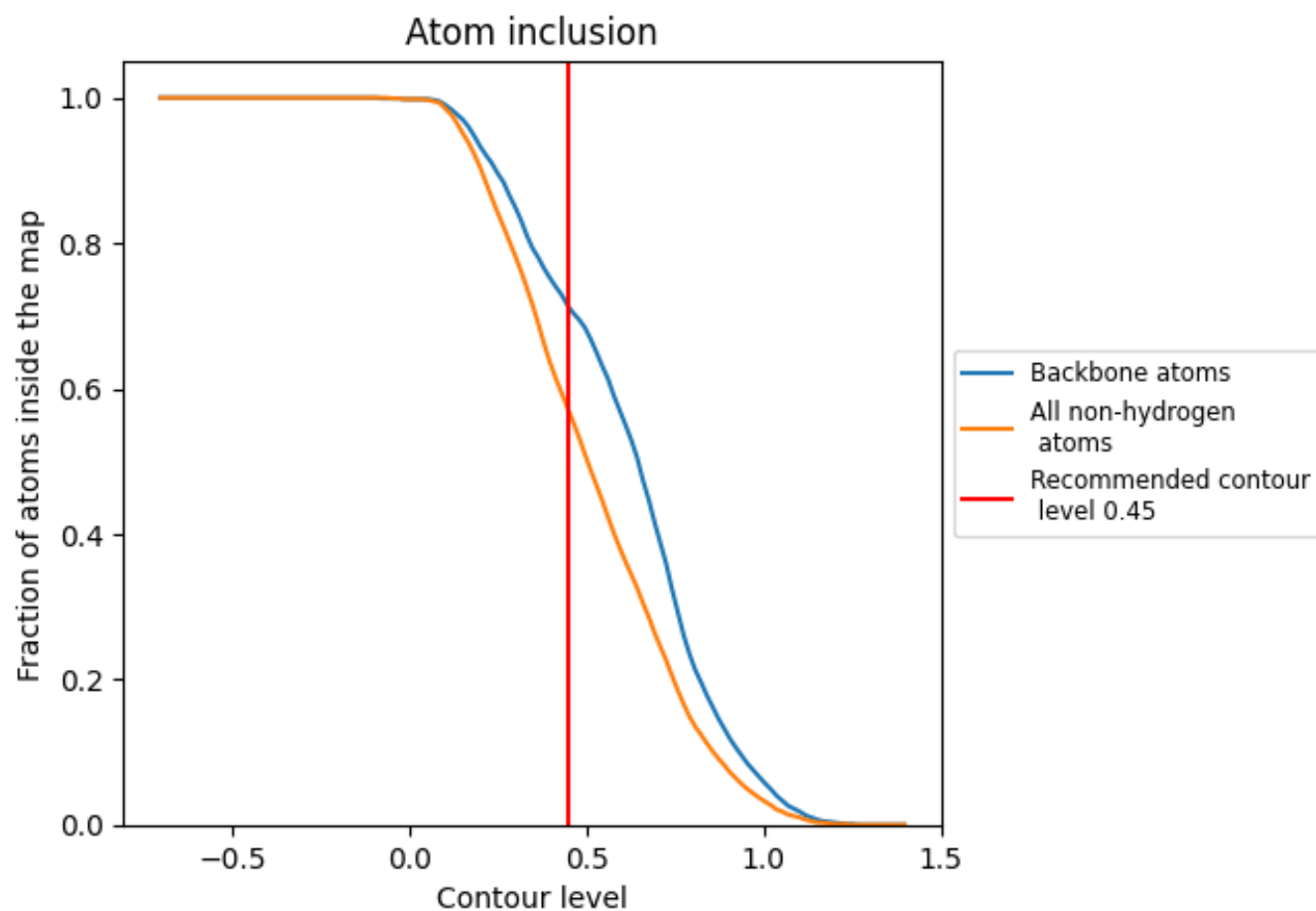
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 57% 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	 0.5690	 0.5290
1	 0.5680	 0.5300
2	 0.5720	 0.5310
3	 0.5630	 0.5300
4	 0.5660	 0.5290
5	 0.5630	 0.5290
6	 0.5680	 0.5290
7	 0.5730	 0.5290
8	 0.5700	 0.5280
9	 0.5700	 0.5250
A	 0.5730	 0.5270
B	 0.5710	 0.5260
C	 0.5730	 0.5270
D	 0.5660	 0.5280
E	 0.5700	 0.5300
F	 0.5710	 0.5290
G	 0.5670	 0.5290
H	 0.5660	 0.5270
I	 0.5720	 0.5280
J	 0.5720	 0.5290
K	 0.5630	 0.5310
L	 0.5640	 0.5290
M	 0.5640	 0.5290
N	 0.5680	 0.5300
O	 0.5750	 0.5300
P	 0.5700	 0.5280
Q	 0.5710	 0.5270
R	 0.5730	 0.5300
S	 0.5720	 0.5290
T	 0.5740	 0.5290
U	 0.5660	 0.5300
V	 0.5690	 0.5300
W	 0.5710	 0.5290
X	 0.5650	 0.5290
Y	 0.5680	 0.5290

