



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:49 PM UTC

PDB ID : 7E81 / pdb_00007e81
EMDB ID : EMD-31007
Title : Cryo-EM structure of the flagellar MS ring with FlgB-Dc loop and FliE-helix 1 from Salmonella
Authors : Tan, J.X.; Chang, S.H.; Wang, X.F.; Xu, C.H.; Zhou, Y.; Zhang, X.; Zhu, Y.Q.
Deposited on : 2021-02-28
Resolution : 4.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 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

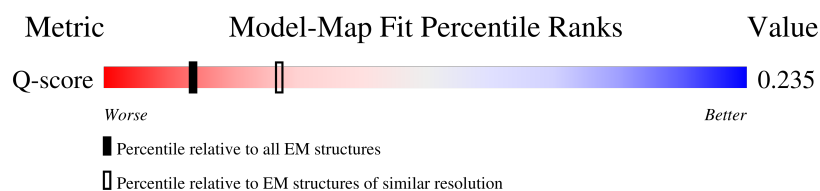
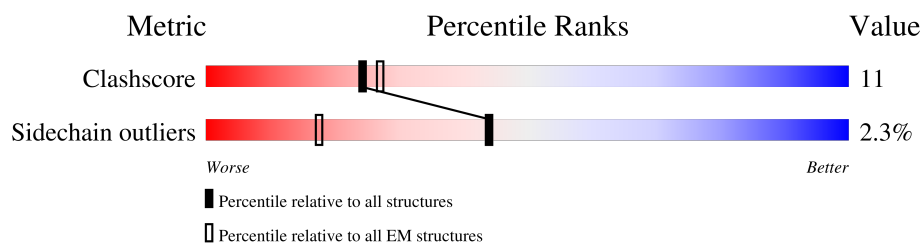
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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.



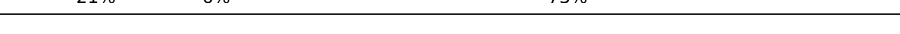
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	Ca	560	
1	Cb	560	
1	Cc	560	
1	Cd	560	
1	Ce	560	

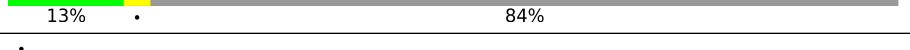
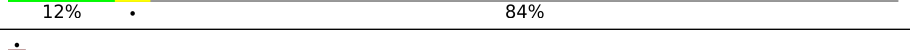
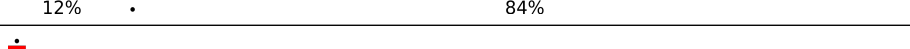
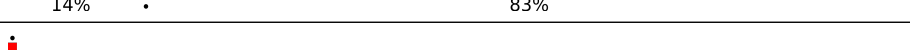
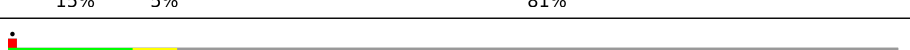
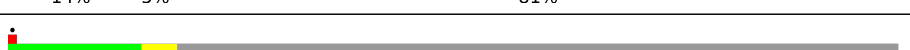
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Mol	Chain	Length	Quality of chain
1	Cf	560	 21% 6% 73%
1	Ch	560	 21% 6% 73%
1	Ci	560	 21% 6% 73%
1	Cj	560	 21% 6% 73%
1	Ck	560	 20% 6% 73%
1	Cl	560	 21% 6% 73%
1	Cm	560	 20% 7% 73%
1	Cn	560	 20% 6% 73%
1	Co	560	 21% 6% 73%
1	Cp	560	 20% 6% 73%
1	Cq	560	 22% 5% 73%
1	Cr	560	 21% 6% 73%
1	Cs	560	 21% 6% 73%
1	Ct	560	 20% 7% 73%
1	Cu	560	 21% 6% 73%
1	Cv	560	 21% 6% 73%
1	Cw	560	 20% 6% 73%
1	Cx	560	 21% 6% 73%
1	Cy	560	 21% 6% 73%
1	Cz	560	 21% 5% 73%
1	Da	560	 15% 5% 81%
1	Db	560	 15% 5% 81%
1	Dc	560	 14% 5% 81%
1	Dd	560	 17% 5% 81%
1	De	560	 14% 5% 82%

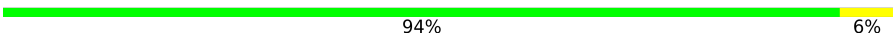
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Mol	Chain	Length	Quality of chain
1	Df	560	 14% 83%
1	Dg	560	 13% 84%
1	Dh	560	 12% 84%
1	Di	560	 12% 84%
1	Dj	560	 12% 84%
1	Dk	560	 12% 84%
1	Di	560	 13% 84%
1	Dm	560	 12% 84%
1	Dn	560	 12% 84%
1	Do	560	 14% 83%
1	Dp	560	 15% 5% 81%
1	Dq	560	 14% 5% 81%
1	Dr	560	 15% 81%
1	Ds	560	 16% 81%
1	Dt	560	 14% 5% 81%
1	Du	560	 15% 81%
1	Dv	560	 14% 5% 81%
1	Dw	560	 15% 81%
1	Ea	560	 20% 6% 73%
1	Eb	560	 21% 5% 73%
1	Ec	560	 21% 6% 73%
1	Ed	560	 20% 6% 73%
1	Ee	560	 21% 6% 73%
1	Ef	560	 21% 6% 73%
1	Eg	560	 21% 6% 73%

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Mol	Chain	Length	Quality of chain
1	Fh	560	
1	cg	560	
2	GA	12	
2	GB	12	
2	GC	12	
2	GD	12	
2	GE	12	
3	GF	18	
3	GG	18	
3	GH	18	
3	GI	18	
3	GJ	18	
3	GK	18	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 57178 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Da	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Db	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Dc	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Dd	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	De	99	Total	C	N	O	S	0	0
			696	432	125	138	1		
1	Df	97	Total	C	N	O	S	0	0
			687	427	123	136	1		
1	Dg	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Dh	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Di	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Dj	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Dk	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Dl	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Dm	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Dn	87	Total	C	N	O	S	0	0
			637	397	113	126	1		
1	Do	97	Total	C	N	O	S	0	0
			687	427	123	136	1		
1	Dp	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Dq	109	Total	C	N	O	S	0	0
			746	462	135	148	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Dr	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Ds	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Dt	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Du	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Dv	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Dw	109	Total	C	N	O	S	0	0
			746	462	135	148	1		
1	Ca	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cb	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cc	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cd	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ce	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cf	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	cg	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ch	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ci	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cj	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ck	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cl	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cm	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cn	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Co	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Cp	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cq	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cr	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cs	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ct	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cu	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cv	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cw	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cx	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cy	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Cz	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ea	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Eb	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ec	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ed	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ee	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Ef	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Eg	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		
1	Fh	150	Total	C	N	O	S	0	0
			1185	722	221	239	3		

- Molecule 2 is a protein called FlgB-Dc loop.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	GA	11	Total	C	N	O	0	0
			55	33	11	11		
2	GC	11	Total	C	N	O	0	0
			55	33	11	11		
2	GE	12	Total	C	N	O	0	0
			60	36	12	12		
2	GD	10	Total	C	N	O	0	0
			50	30	10	10		
2	GB	5	Total	C	N	O	0	0
			25	15	5	5		

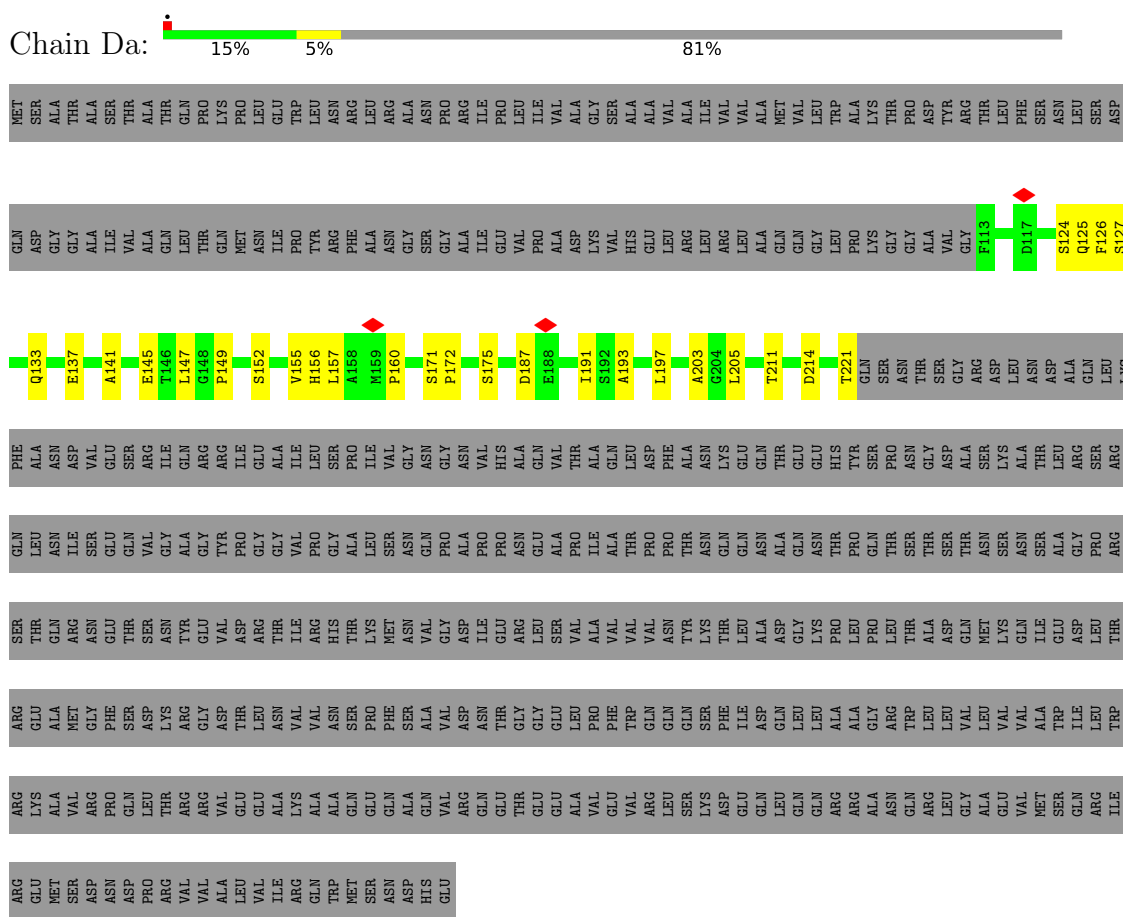
- Molecule 3 is a protein called FliE helix 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	GF	18	Total	C	N	O	0	0
			90	54	18	18		
3	GG	18	Total	C	N	O	0	0
			90	54	18	18		
3	GH	18	Total	C	N	O	0	0
			90	54	18	18		
3	GI	15	Total	C	N	O	0	0
			75	45	15	15		
3	GJ	18	Total	C	N	O	0	0
			90	54	18	18		
3	GK	18	Total	C	N	O	0	0
			90	54	18	18		

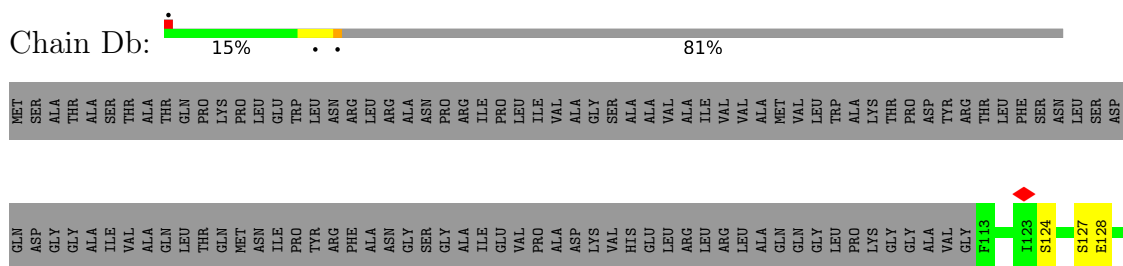
3 Residue-property plots

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.

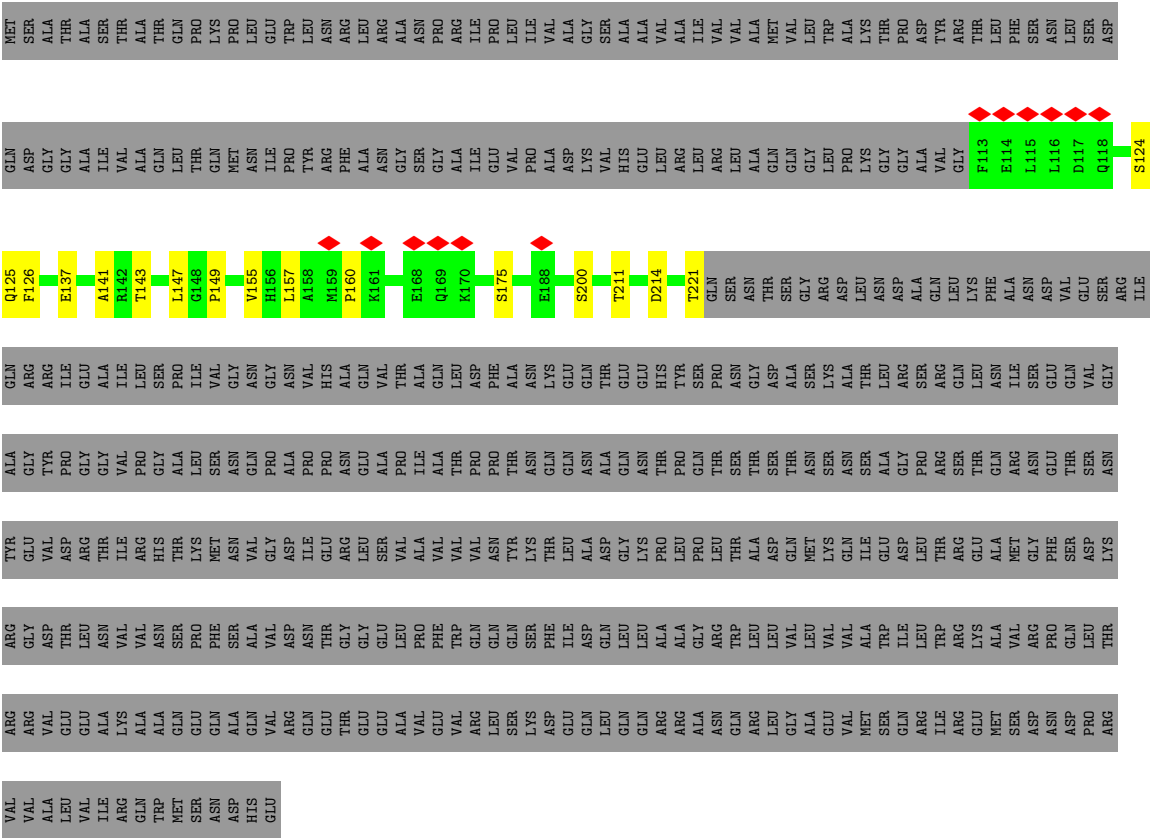
• Molecule 1: Flagellar M-ring protein



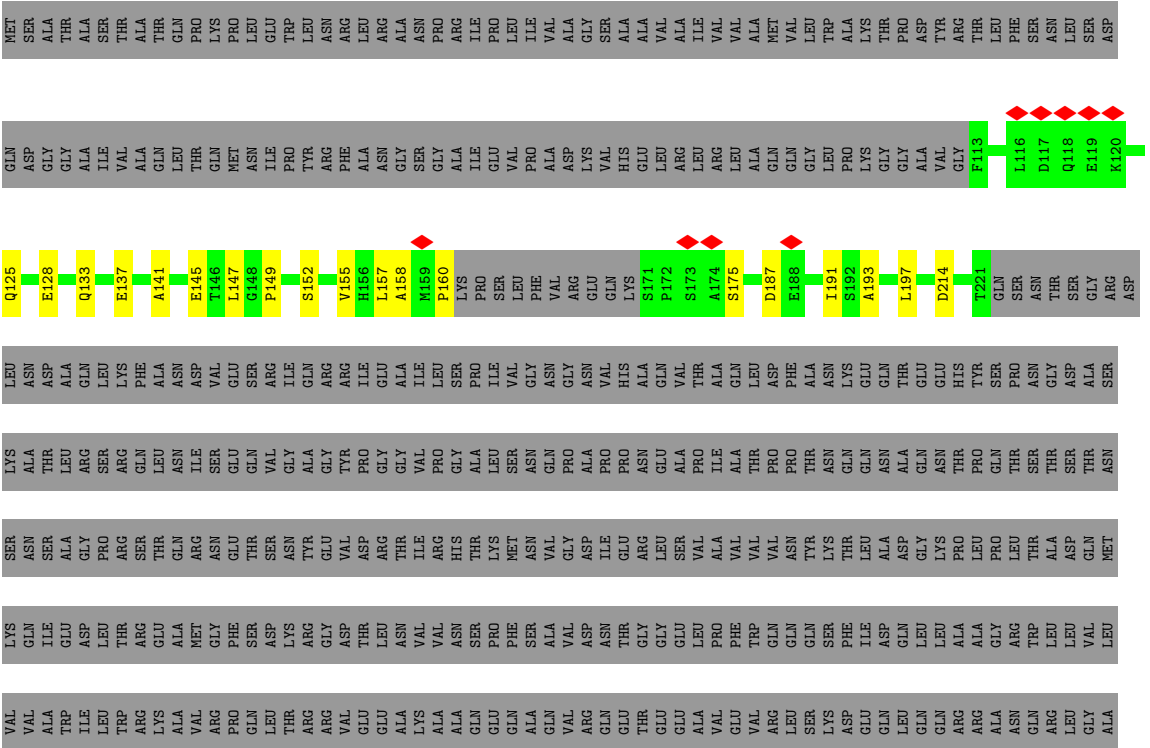
• Molecule 1: Flagellar M-ring protein







• Molecule 1: Flagellar M-ring protein



[illegible]

- Molecule 1: Flagellar M-ring protein

[illegible]

- Molecule 1: Flagellar M-ring protein

[illegible]

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

- Molecule 1: Flagellar M-ring protein



VAL	ARG	GLN	TRP	VAL	THR	LEU	G204	◆	PHE	GLN	MET
ARG	LEU	ASN	GLN	VAL	PRO	ASP	L205	◆	GLY	ASP	ALA
SER	LEU	GLN	TRP	THR	PRO	PHE	P206	◆	ILE	GLY	THR
LYS	THR	LYS	THR	LYS	ASN	ASN	G125	◆	Q125	ALA	SER
ASP	THR	THR	THR	GLN	GLN	GLU	G208	◆	F126	VAL	THR
GLU	GLN	ALA	ASP	ASN	GLN	GLN	N209	◆	S127	ALA	ALA
LEU	GLN	LEU	ASP	ALA	THR	THR	W210	◆	E128	GLN	THR
GLN	GLN	GLY	GLN	GLN	GLU	GLU	T211	◆	E128	LEU	GLN
GLN	LEU	LYS	LEU	ASN	THR	ASN	D214	◆	Q133	THR	PRO
ARG	ALA	PRO	ALA	GLU	HIS	HIS			Q133	LYS	LYS
ARG	ALA	LEU	PRO	THR	TYR	TYR			E137	PRO	PRO
ALA	ALA	PRO	GLN	GLN	GLN	SER	T221	◆	E137	MET	ALA
ASN	ASN	LEU	THR	THR	PRO	PRO	GLN	◆	A141	ASN	GLU
GLN	TRP	THR	THR	SER	ASN	ASN	ASN	◆	R142	PRO	TRP
ARG	ARG	ALA	THR	GLY	GLY	GLY	THR	◆	T143	TYR	LEU
LEU	LEU	LEU	ASP	ASP	SER	ASP	SER	◆	I144	ARG	ASN
GLY	GLY	GLN	GLN	THR	THR	ALA	GLY	◆	E145	PHE	ARG
ALA	LEU	LEU	MET	ASN	ASN	SER	GLY	◆	T146	ALA	LEU
GLU	GLU	VAL	VAL	LYS	SER	ARG	ARG	◆	L147	ASN	ALA
VAL	VAL	VAL	VAL	ASP	ASN	ALA	ASP	◆	G148	GLY	ALA
MET	MET	ALA	ALA	ILE	SER	THR	LEU	◆	P149	SER	ASN
SER	SER	TRP	TRP	ALA	ALA	LEU	ASN	◆		GLY	PRO
GLN	GLN	ILE	ILE	ASP	GLY	ARG	ASP	◆	S152	ALA	ARG
ARG	ARG	TRP	TRP	LEU	PRO	SER	GLN	◆	V155	ILE	ILE
ILE	ILE	TRP	TRP	THR	ARG	ARG	LEU	◆	H156	GLU	PRO
ARG	ARG	ARG	ARG	THR	SER	GLN	GLN	◆	L157	VAL	LEU
GLU	GLU	LYS	LYS	THR	THR	LEU	PHE	◆	A158	PRO	ILE
MET	MET	ALA	ALA	GLN	GLN	ASN	ALA	◆		ALA	ALA
SER	SER	VAL	VAL	ARG	ARG	ILE	ASN	◆	M159	ASP	ALA
ASP	ASP	ARG	ARG	GLY	ASN	SER	ASN	◆		LYS	GLY
ASN	ASN	PRO	PRO	PHE	GLN	GLN	ASP	◆	P160	VAL	GLY
ASP	ASP	GLN	GLN	SER	THR	GLN	VAL	◆		SER	ASN
PRO	PRO	THR	THR	ASP	SER	VAL	GLU	◆		PRO	ALA
ARG	ARG	LYS	LYS	THR	ASN	GLY	GLY	◆		LEU	ALA
VAL	VAL	ARG	ARG	ARG	TYR	ALA	ARG	◆		PHE	VAL
ALA	ALA	GLY	GLY	GLY	GLY	GLY	ILE	◆		LEU	ILE
VAL	VAL	VAL	VAL	ASP	VAL	THR	GLN	◆		VAL	ARG
LEU	LEU	GLU	GLU	THR	ASP	PRO	ARG	◆		LEU	ALA
VAL	VAL	GLU	GLU	LEU	ARG	GLY	ILE	◆		ALA	ALA
ILE	ILE	ALA	ALA	ASN	THR	GLY	GLU	◆		GLN	MET
ARG	ARG	LYS	LYS	VAL	ILE	PRO	ALA	◆	S171	GLN	VAL
GLN	GLN	ALA	ALA	VAL	ARG	PRO	ILE	◆	P172	GLY	LEU
TRP	TRP	ALA	ALA	ASN	HIS	GLY	ILE	◆		LEU	LEU
MET	MET	GLN	GLN	SER	THR	ALA	LEU	◆		PRO	ALA
SER	SER	GLU	GLU	PRO	LYS	LEU	SER	◆	S175	LYS	THR
ASN	ASN	GLN	GLN	PHE	MET	SER	ILE	◆		PRO	LYS
ASP	ASP	SER	SER	SER	ASN	ASN	ILE	◆		GLY	PRO
HIS	HIS	GLN	GLN	ALA	VAL	GLN	VAL	◆	P182	ALA	ASP
GLU	GLU	ALA	ALA	VAL	VAL	PRO	GLY	◆	D187	VAL	TYR
		ARG	ARG	ASP	ASP	ALA	ASN	◆	E188	GLY	GLY
		ASN	ASN	ASN	ILE	PRO	GLY	◆		PHE	THR
		THR	THR	THR	GLU	GLU	ASN	◆		GLU	LEU
		GLY	GLY	GLY	GLY	GLU	HIS	◆	I191	LEU	PHE
		GLU	GLU	GLU	SER	ALA	ALA	◆	S192	LEU	ASN
		ALA	ALA	LEU	VAL	LEU	GLN	◆	A193	GLN	ASN
		VAL	VAL	PRO	VAL	ILE	VAL	◆		GLU	LEU
		PHE	PHE	ALA	VAL	ALA	THR	◆	L197	GLU	SER
				ALA	ALA	ALA	ALA	◆	A201	LYS	ASP

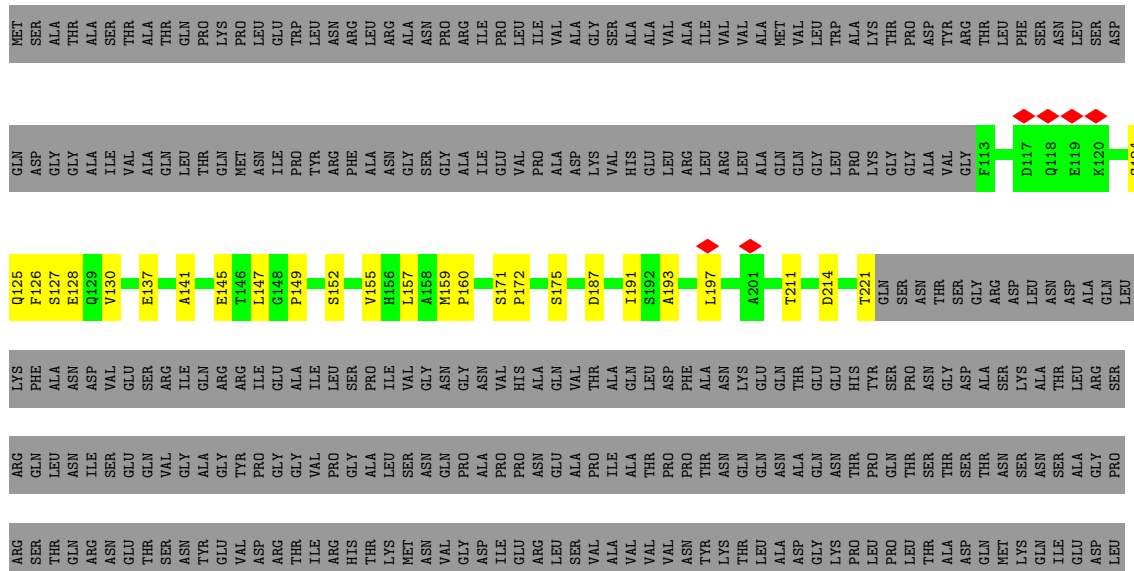
- Molecule 1: Flagellar M-ring protein

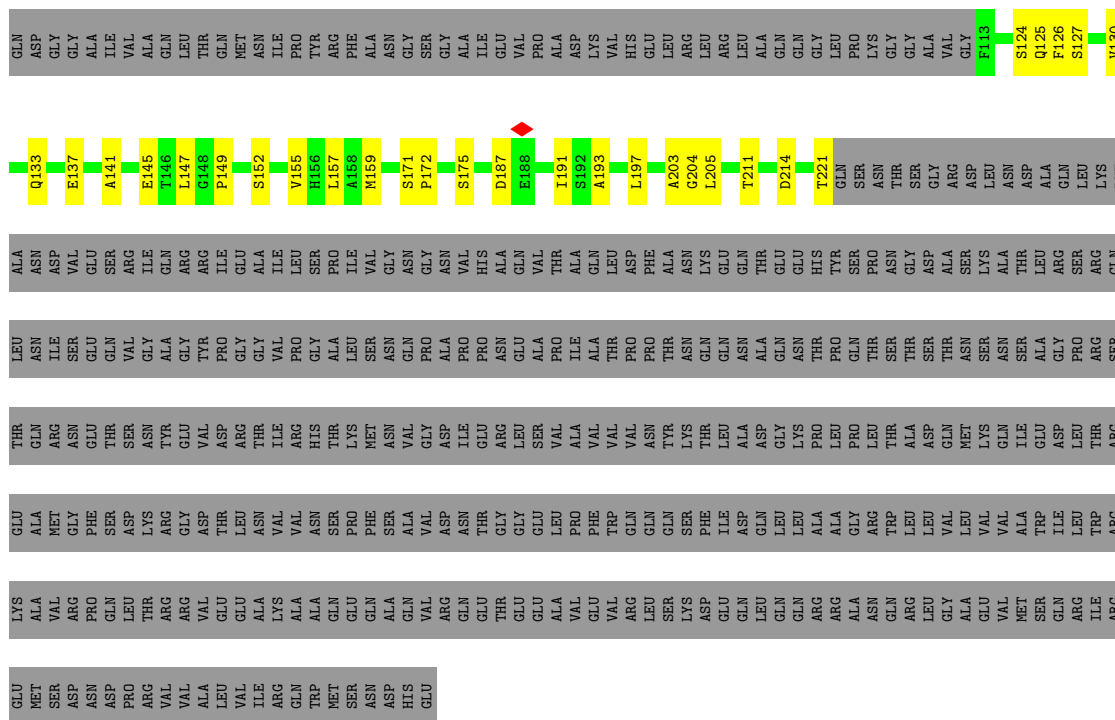
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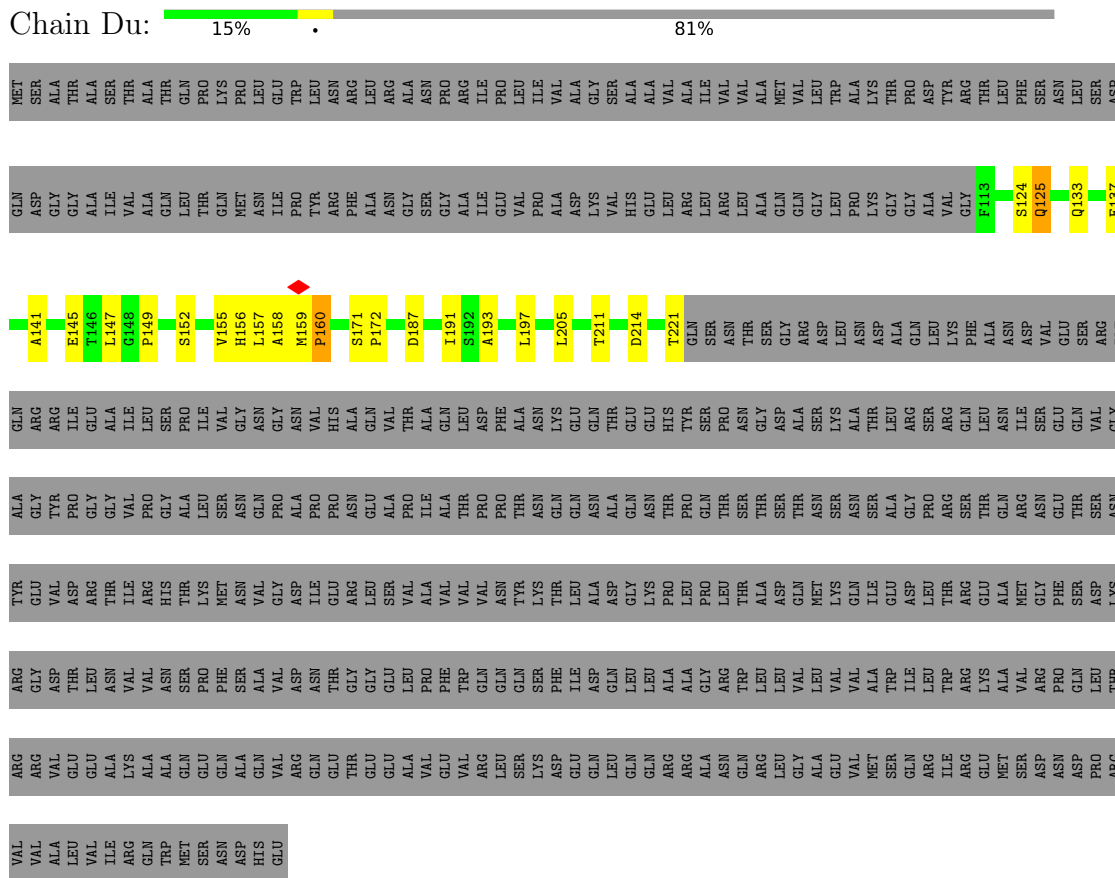


Chain Do: 14% . 83%





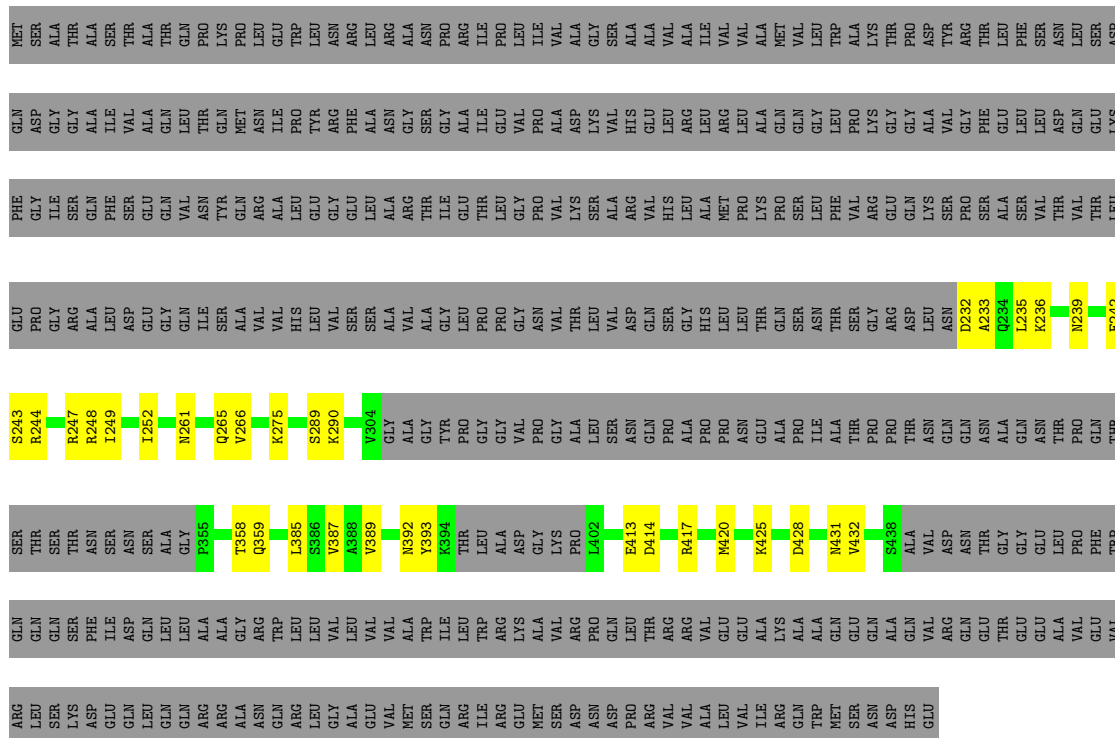
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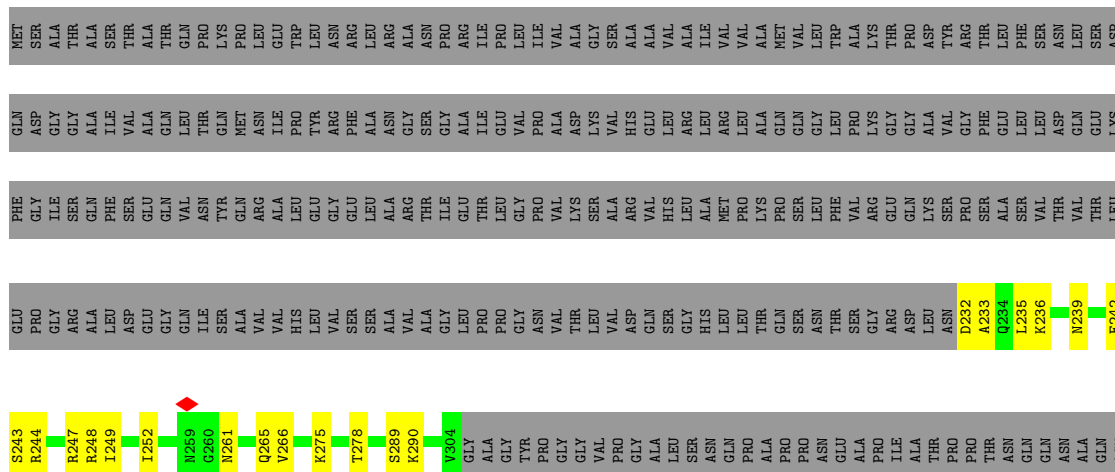
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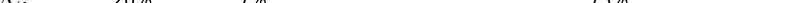
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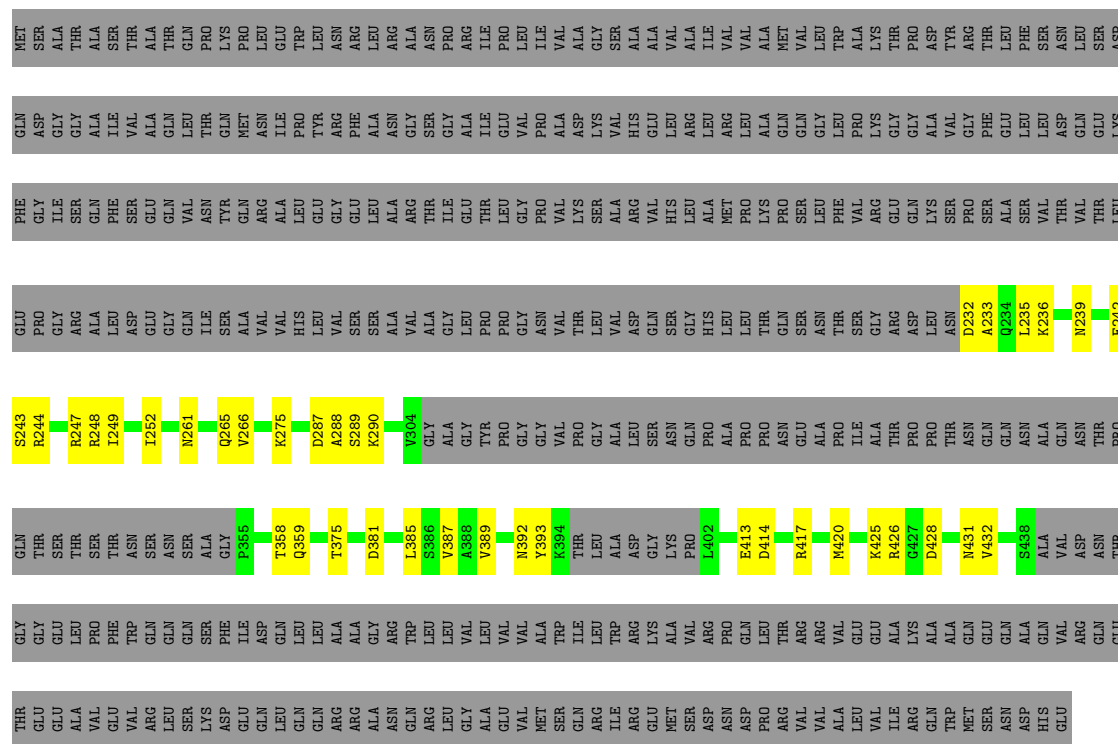


- Molecule 1: Flagellar M-ring protein

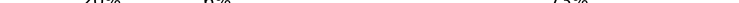


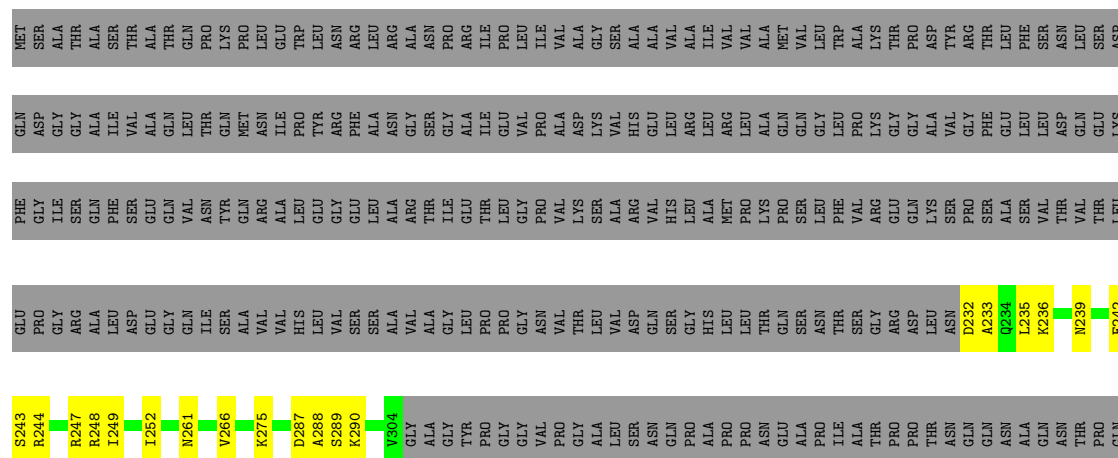
- Molecule 1: Flagellar M-ring protein

Chain Cc:  20% 7% 73%

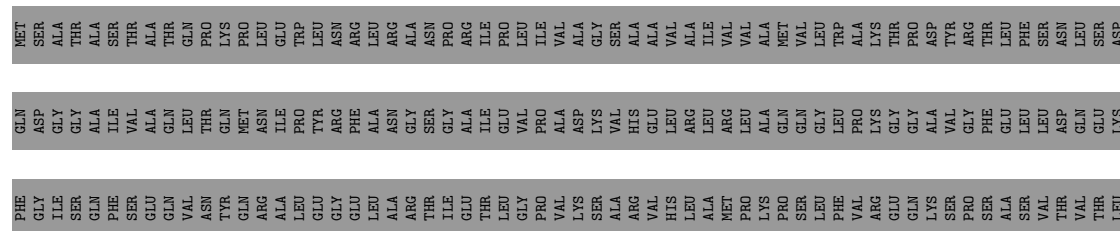


- Molecule 1: Flagellar M-ring protein

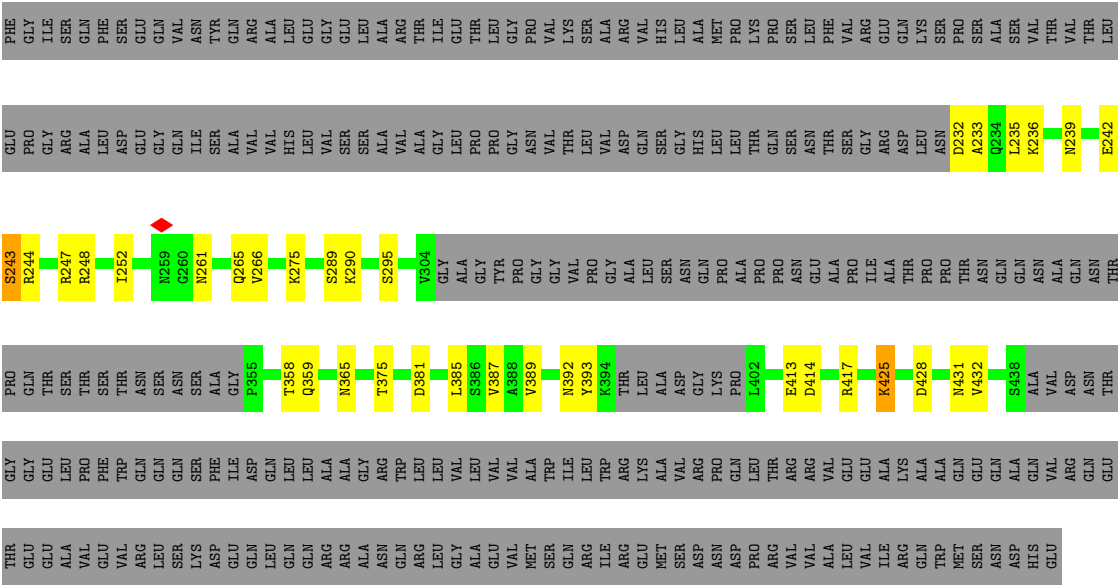
Chain Cd: 



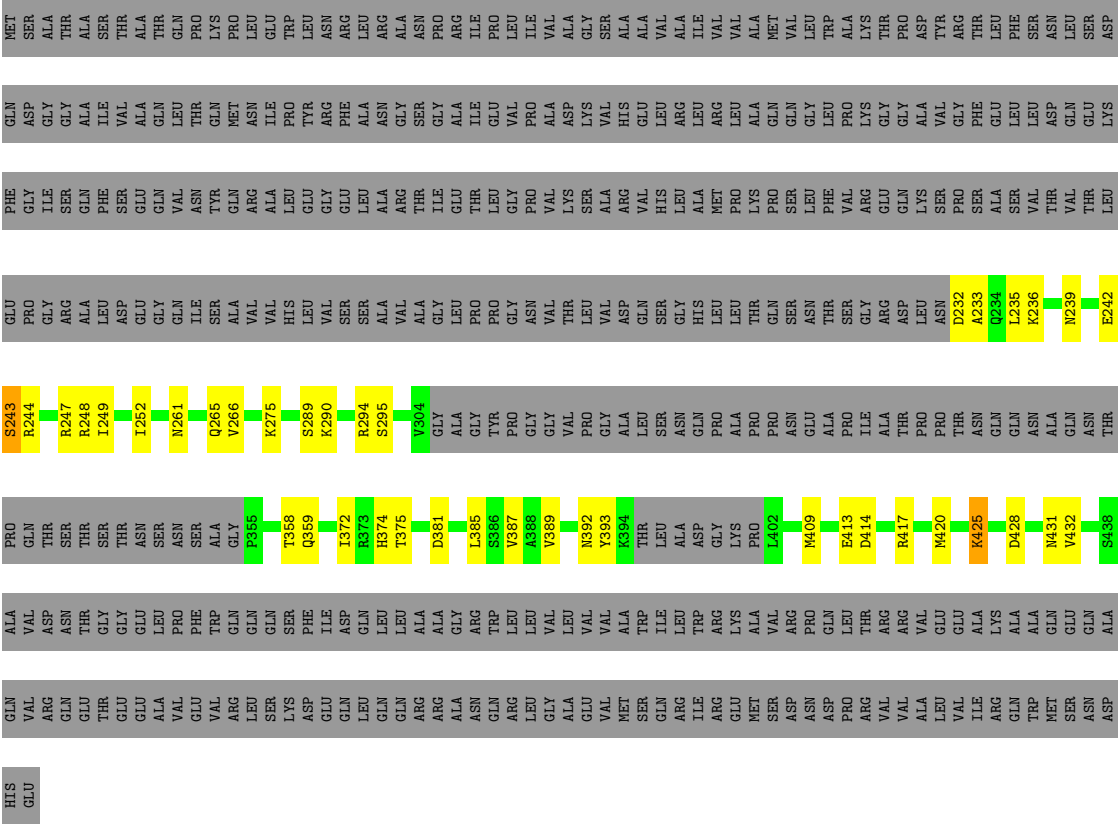








● Molecule 1: Flagellar M-ring protein



● Molecule 1: Flagellar M-ring protein



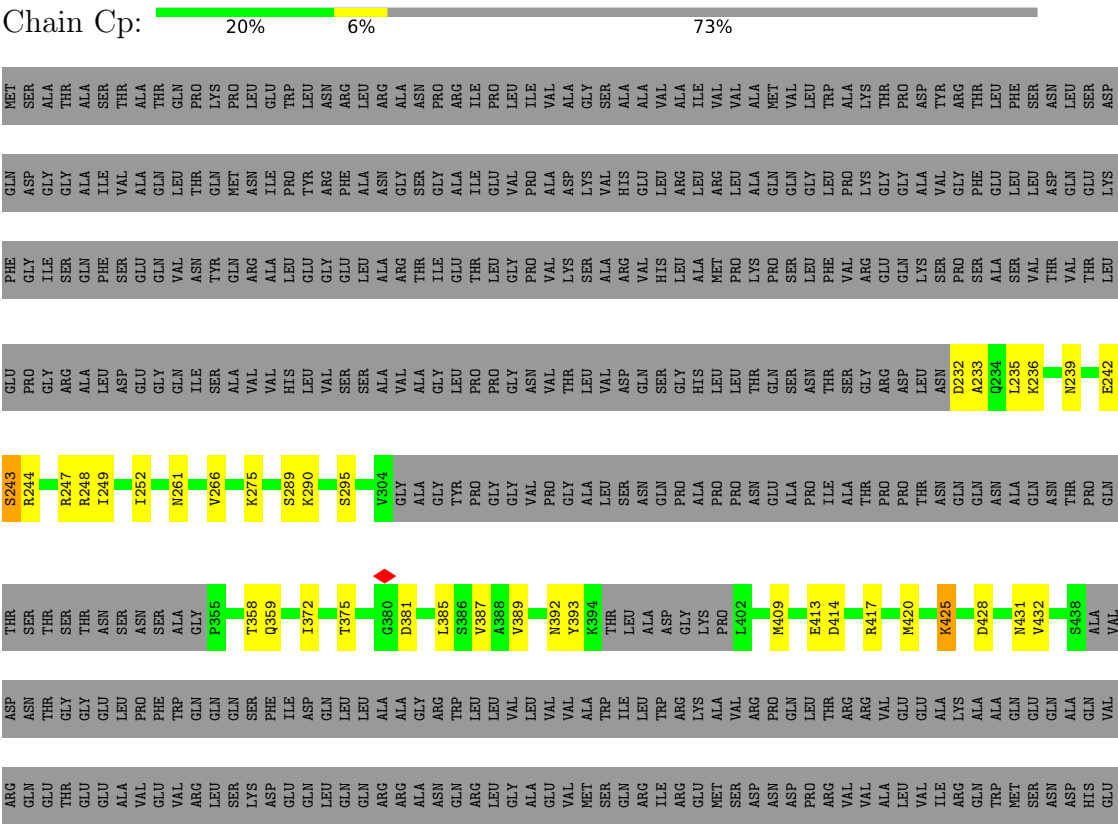
THR	GLU	GLY	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN	THR	GLY	THR	GLN
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● Molecule 1: Flagellar M-ring protein

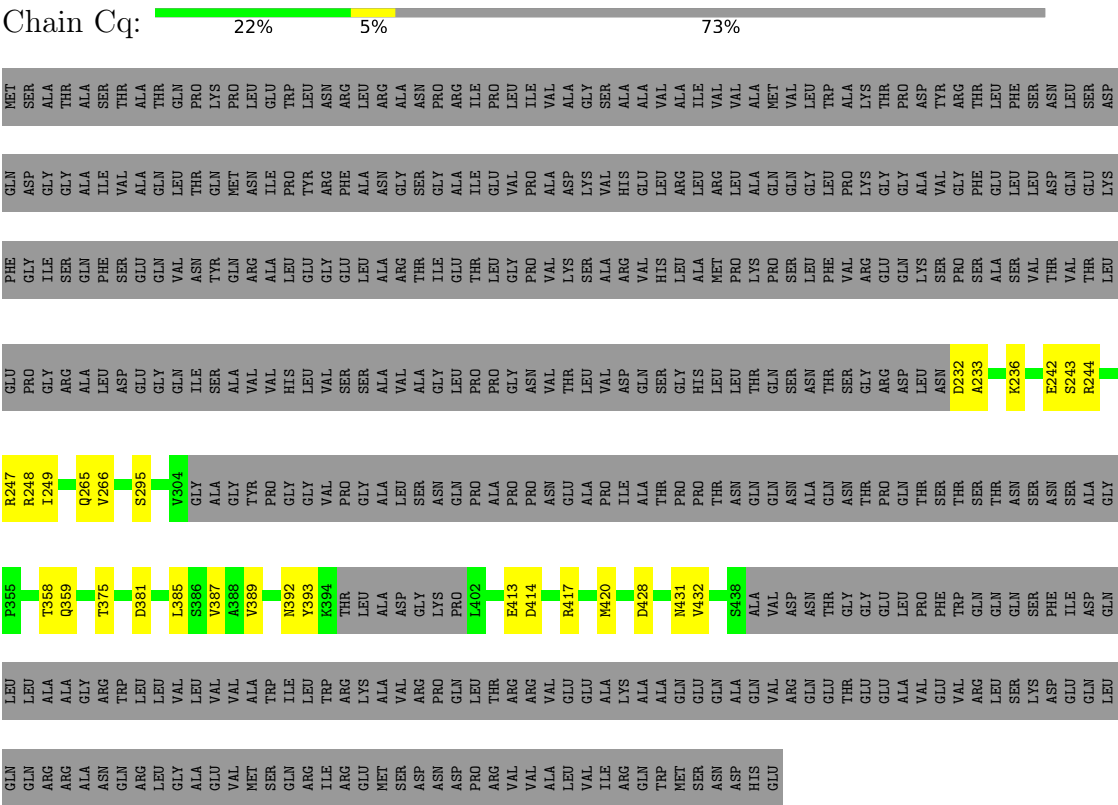


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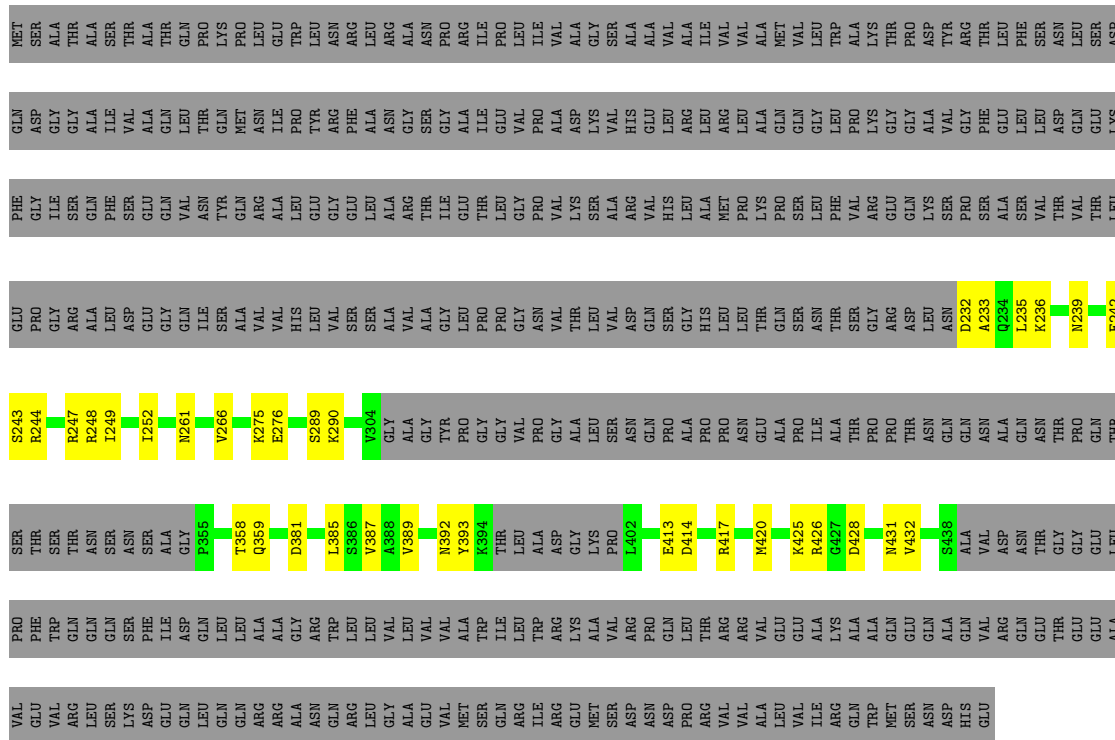
● Molecule 1: Flagellar M-ring protein



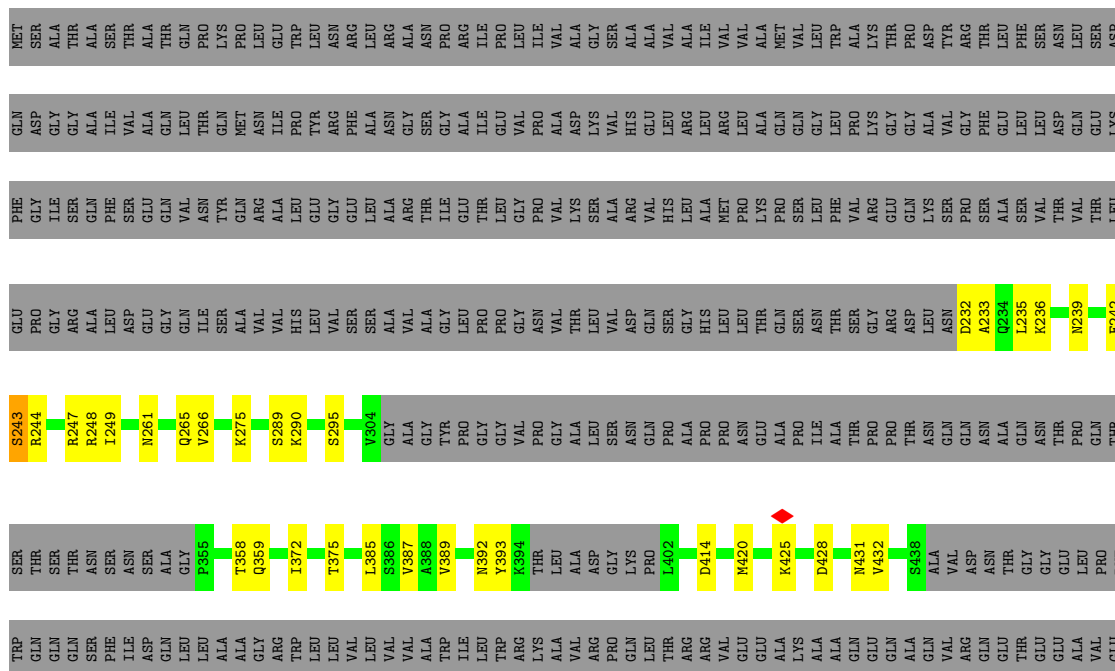
● Molecule 1: Flagellar M-ring protein



Chain Cr: 21% 6% 73%



Chain Cs: 21% 6% 73%



ALA	VAL	GLU	VAL	ARG	SER	LYS	ASP	GLN	LEU	GLN	GLN	ARG	ALA	ALA	GLY	GLY	ALA	GLY	GLN	ARG	ASN	GLN	ARG	LEU	ARG	LEU	ASP	HIS	GLU
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● Molecule 1: Flagellar M-ring protein



MET	SER	ALA	THR	ALA	SER	THR	ALA	THR	PRO	GLN	LYS	PRO	GLN	LEU	ARG	THR	PRO	TYR	GLY	ARG	ASN	GLN	LEU	ARG	LEU	ASP	THR	ASP
GLN	ASP	GLY	THR	ALA	ILE	GLN	VAL	THR	GLN	THR	MET	ASN	ILE	PRO	TYR	GLY	ARG	PHE	ALA	ASN	GLY	ALA	ARG	GLY	VAL	ASP	GLY	LYS
PHE	GLY	ILE	SER	GLN	PHE	SER	GLU	VAL	GLN	VAL	TYR	ARG	ALA	VAL	GLY	THR	ILE	GLY	ALA	THR	ILE	GLY	LEU	THR	LEU	THR	THR	LEU
GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	ILE	SER	ALA	VAL	VAL	HIS	GLY	VAL	SER	GLY	ALA	VAL	GLY	THR	LEU	THR	LEU	THR	THR	LEU
S243	R244	R247	R261	Q265	V266	K275	T278	S289	K290	S295	V304	GLY	ALA	GLY	TYR	PRO	GLY	PRO	GLY	VAL	ASN	PRO	GLY	VAL	THR	LEU	LEU	THR
SER	THR	SER	THR	ASN	SER	ASN	SER	ALA	P355	T358	Q359	T375	L385	S386	V387	N392	Y393	K394	THR	LEU	ALA	ASP	GLY	VAL	GLY	PRO	ALA	THR
GLN	GLN	SER	PHE	ILE	GLN	ASP	GLN	LEU	ALA	GLY	TRP	LEU	VAL	VAL	VAL	ILE	TRP	ILE	TRP	ARG	LYS	VAL	VAL	GLY	VAL	GLY	GLY	ARG
LEU	SER	LYS	ASP	GLN	LEU	GLN	GLN	ARG	ALA	ALA	ASN	GLN	ARG	GLY	VAL	GLY	ALA	GLY	ILE	ARG	GLY	VAL	GLY	VAL	VAL	VAL	VAL	GLY
MET	SER	ALA	THR	ALA	SER	THR	ALA	THR	PRO	LYS	PRO	LEU	LEU	ARG	THR	PRO	ILE	ILE	ILE	ILE	ALA	ASP	ALA	GLY	GLY	GLY	THR	ASP
GLN	ASP	GLY	THR	ILE	GLN	VAL	GLN	THR	GLN	MET	ASN	GLN	GLY	PHE	ALA	ASN	GLY	ALA	THR	PRO	GLY	ARG	GLY	VAL	VAL	VAL	VAL	GLY
PHE	GLY	ILE	SER	PHE	SER	GLU	VAL	GLN	ASN	GLN	ARG	ALA	GLY	GLY	LEU	ALA	ASN	GLY	THR	ILE	GLY	VAL	GLY	VAL	VAL	VAL	VAL	GLY
GLU	PRO	GLY	ARG	LEU	ASP	GLY	GLU	GLY	ILE	SER	ALA	VAL	VAL	HIS	LEU	SER	GLY	VAL	PRO	GLY	THR	GLY	VAL	VAL	VAL	VAL	VAL	GLY
S243	R244	R248	I249	I252	N261	V266	K275	S289	K290	S295	V304	GLY	ALA	GLY	TYR	PRO	GLY	GLY	PRO	GLY	VAL	ASN	PRO	GLY	VAL	THR	LEU	THR
SER	THR	SER	THR	ASN	SER	ALA	T358	Q359	N365	T375	D381	L385	S386	V387	A388	V389	N392	Y393	K394	THR	LEU	ALA	ASP	GLY	VAL	THR	THR	GLY
GLY	GLY	GLU	PRO	PHE	GLN	GLY	PHE	ILE	ASP	GLN	ARG	THR	THR	LEU	VAL	VAL	VAL	ALA	ILE	ILE	LEU	THR	THR	THR	THR	THR	THR	GLY

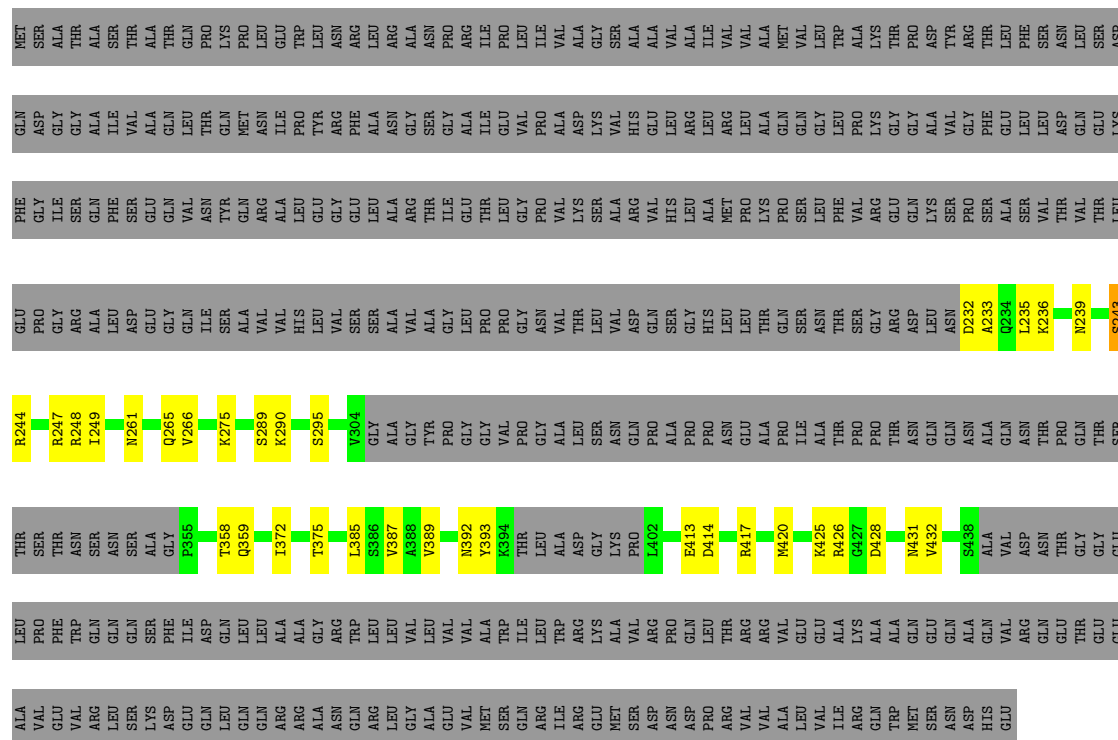
● Molecule 1: Flagellar M-ring protein



MET	SER	ALA	THR	ALA	SER	THR	ALA	THR	PRO	LYS	PRO	LEU	LEU	ARG	THR	PRO	ILE	ILE	ILE	ILE	ALA	ASP	ALA	GLY	GLY	GLY	THR	ASP
GLN	ASP	GLY	THR	ALA	ILE	GLN	VAL	GLN	THR	GLN	MET	ASN	ILE	PRO	TYR	GLY	ARG	PHE	ALA	ASN	GLY	VAL	GLY	VAL	VAL	VAL	VAL	GLY
PHE	GLY	ILE	SER	PHE	SER	GLU	VAL	GLN	ASN	GLN	ARG	ALA	GLY	GLY	GLY	LEU	ALA	ASN	GLY	THR	ILE	GLY	VAL	VAL	VAL	VAL	VAL	GLY
GLU	PRO	GLY	ARG	LEU	ASP	GLY	GLU	GLY	ILE	SER	ALA	VAL	VAL	HIS	LEU	SER	GLY	VAL	PRO	GLY	THR	GLY	VAL	VAL	VAL	VAL	VAL	GLY
S243	R244	R248	I249	I252	N261	V266	K275	S289	K290	S295	V304	GLY	ALA	GLY	TYR	PRO	GLY	GLY	PRO	GLY	VAL	ASN	PRO	GLY	VAL	THR	LEU	THR
SER	THR	SER	THR	ASN	SER	ALA	T358	Q359	N365	T375	D381	L385	S386	V387	A388	V389	N392	Y393	K394	THR	LEU	ALA	ASP	GLY	VAL	THR	THR	GLY
GLY	GLY	GLU	PRO	PHE	GLN	GLY	PHE	ILE	ASP	GLN	ARG	THR	THR	LEU	VAL	VAL	VAL	ALA	ILE	ILE	LEU	THR	THR	THR	THR	THR	THR	GLY

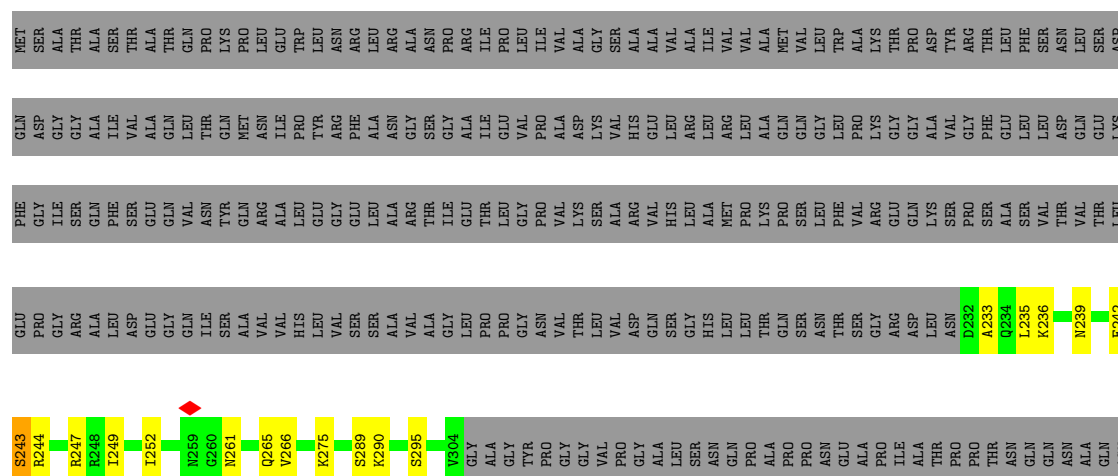
- Molecule 1: Flagellar M-ring protein

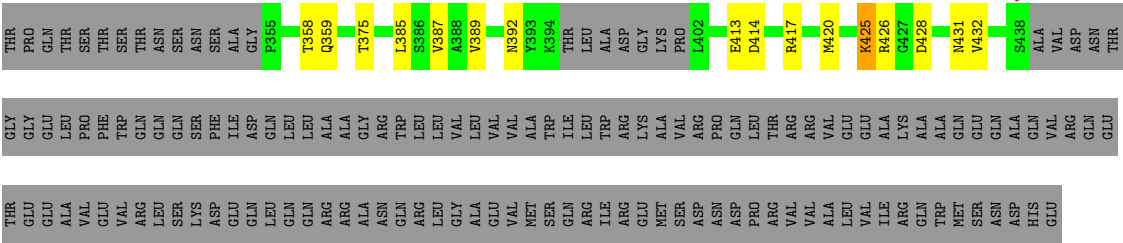
Chain Ef:



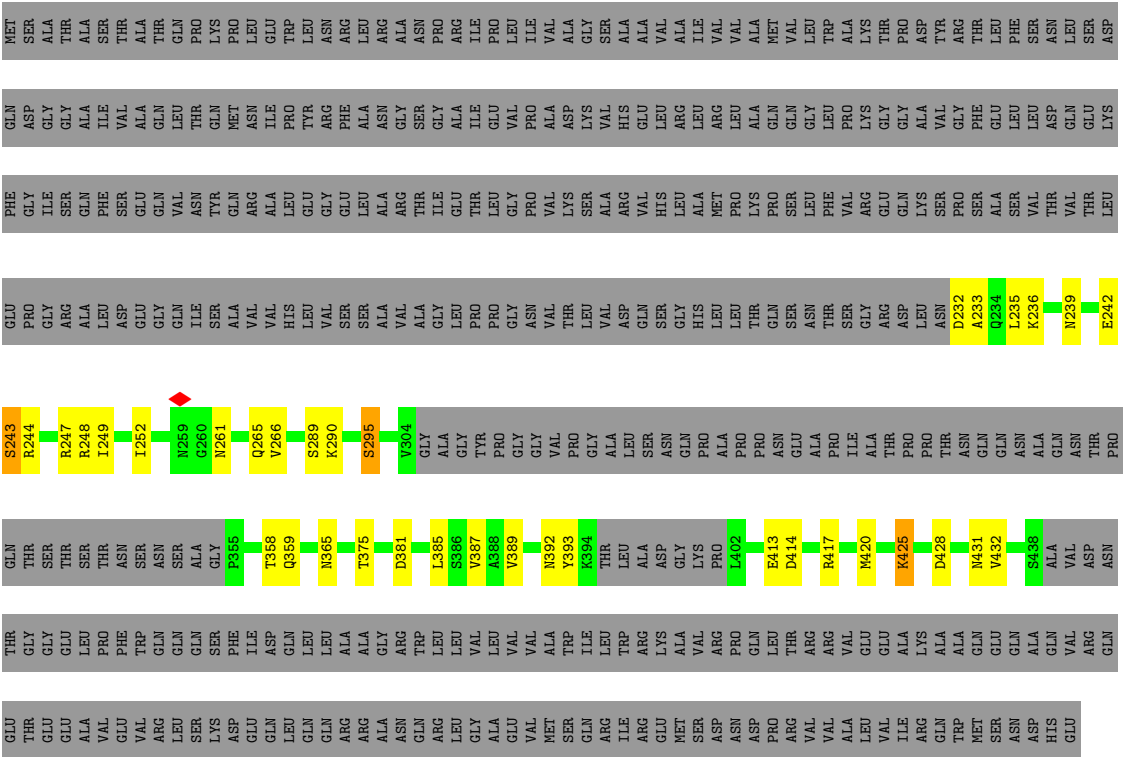
- Molecule 1: Flagellar M-ring protein

Chain Eg:

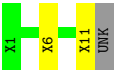
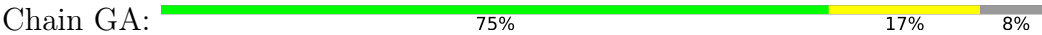




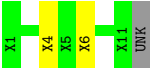
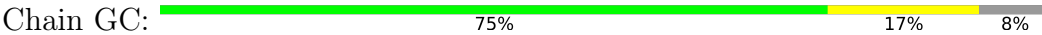
• Molecule 1: Flagellar M-ring protein



• Molecule 2: FlgB-Dc loop



• Molecule 2: FlgB-Dc loop



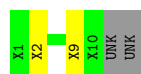
• Molecule 2: FlgB-Dc loop

Chain GE:  67% 33%



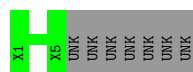
- Molecule 2: FlgB-Dc loop

Chain GD:  67% 17% 17%



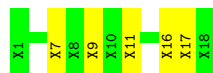
- Molecule 2: FlgB-Dc loop

Chain GB:  42% 58%



- Molecule 3: FliE helix 1

Chain GF:  72% 28%



- Molecule 3: FliE helix 1

Chain GG:  94% 6%



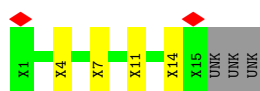
- Molecule 3: FliE helix 1

Chain GH:  78% 22%



- Molecule 3: FliE helix 1

Chain GI:  11% 61% 22% 17%



- Molecule 3: FliE helix 1

Chain GJ:  83% 17%



- Molecule 3: FliE helix 1

Chain GK: 6% 89% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52714	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.123	Depositor
Minimum map value	-0.372	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.238	Depositor
Map size ($\text{\AA}$)	669.184, 669.184, 669.184	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.307, 1.307, 1.307	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	Ca	0.25	0/1197	0.41	0/1613
1	Cb	0.25	0/1197	0.41	0/1613
1	Cc	0.25	0/1197	0.41	0/1613
1	Cd	0.25	0/1197	0.41	0/1613
1	Ce	0.25	0/1197	0.41	0/1613
1	Cf	0.25	0/1197	0.41	0/1613
1	Ch	0.25	0/1197	0.41	0/1613
1	Ci	0.25	0/1197	0.41	0/1613
1	Cj	0.25	0/1197	0.41	0/1613
1	Ck	0.25	0/1197	0.41	0/1613
1	Cl	0.25	0/1197	0.41	0/1613
1	Cm	0.25	0/1197	0.41	0/1613
1	Cn	0.25	0/1197	0.41	0/1613
1	Co	0.25	0/1197	0.41	0/1613
1	Cp	0.25	0/1197	0.41	0/1613
1	Cq	0.25	0/1197	0.41	0/1613
1	Cr	0.25	0/1197	0.41	0/1613
1	Cs	0.25	0/1197	0.41	0/1613
1	Ct	0.25	0/1197	0.41	0/1613
1	Cu	0.25	0/1197	0.41	0/1613
1	Cv	0.25	0/1197	0.41	0/1613
1	Cw	0.25	0/1197	0.41	0/1613
1	Cx	0.25	0/1197	0.41	0/1613
1	Cy	0.25	0/1197	0.41	0/1613
1	Cz	0.25	0/1197	0.41	0/1613
1	Da	0.55	0/756	0.79	0/1036
1	Db	0.91	3/756 (0.4%)	1.26	5/1036 (0.5%)
1	Dc	0.59	0/756	0.76	0/1036
1	Dd	0.58	0/756	0.86	2/1036 (0.2%)
1	De	0.44	0/705	0.57	0/963
1	Df	0.90	3/697 (0.4%)	1.24	5/954 (0.5%)
1	Dg	0.37	0/646	0.50	0/881
1	Dh	0.37	0/646	0.50	0/881
1	Di	0.37	0/646	0.50	0/881

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Dj	0.37	0/646	0.50	0/881
1	Dk	0.38	0/646	0.50	0/881
1	DI	0.37	0/646	0.50	0/881
1	Dm	0.37	0/646	0.50	0/881
1	Dn	0.37	0/646	0.50	0/881
1	Do	0.44	0/697	0.59	1/954 (0.1%)
1	Dp	0.56	0/756	0.82	0/1036
1	Dq	0.62	0/756	0.99	4/1036 (0.4%)
1	Dr	0.76	1/756 (0.1%)	1.02	2/1036 (0.2%)
1	Ds	0.77	1/756 (0.1%)	1.15	4/1036 (0.4%)
1	Dt	0.56	0/756	0.80	0/1036
1	Du	0.60	0/756	0.94	5/1036 (0.5%)
1	Dv	0.59	0/756	0.80	0/1036
1	Dw	0.60	0/756	0.88	1/1036 (0.1%)
1	Ea	0.25	0/1197	0.41	0/1613
1	Eb	0.25	0/1197	0.41	0/1613
1	Ec	0.25	0/1197	0.41	0/1613
1	Ed	0.25	0/1197	0.41	0/1613
1	Ee	0.25	0/1197	0.41	0/1613
1	Ef	0.25	0/1197	0.41	0/1613
1	Eg	0.25	0/1197	0.41	0/1613
1	Fh	0.25	0/1197	0.41	0/1613
1	cg	0.25	0/1197	0.41	0/1613
All	All	0.37	8/57037 (0.0%)	0.56	29/77193 (0.0%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Db	160	PRO	N-CA	17.48	1.69	1.47
1	Df	160	PRO	N-CA	17.46	1.69	1.47
1	Dr	171	SER	C-N	13.99	1.50	1.33
1	Ds	171	SER	C-N	13.59	1.50	1.33
1	Df	171	SER	C-N	7.39	1.51	1.33

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ds	171	SER	CA-C-N	17.94	138.28	120.52
1	Ds	171	SER	C-N-CA	17.94	138.28	120.52
1	Db	159	MET	CA-C-N	17.44	141.63	119.84
1	Db	159	MET	C-N-CA	17.44	141.63	119.84
1	Df	159	MET	CA-C-N	17.10	141.21	119.84

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	Ca	1185	0	1167	27	0
1	Cb	1185	0	1167	28	0
1	Cc	1185	0	1167	29	0
1	Cd	1185	0	1167	30	0
1	Ce	1185	0	1167	27	0
1	Cf	1185	0	1167	30	0
1	Ch	1185	0	1167	27	0
1	Ci	1185	0	1167	24	0
1	Cj	1185	0	1167	24	0
1	Ck	1185	0	1167	28	0
1	Cl	1185	0	1167	30	0
1	Cm	1185	0	1167	35	0
1	Cn	1185	0	1167	34	0
1	Co	1185	0	1167	28	0
1	Cp	1185	0	1167	29	0
1	Cq	1185	0	1167	21	0
1	Cr	1185	0	1167	25	0
1	Cs	1185	0	1167	27	0
1	Ct	1185	0	1167	32	0
1	Cu	1185	0	1167	32	0
1	Cv	1185	0	1167	26	0
1	Cw	1185	0	1167	25	0
1	Cx	1185	0	1167	26	0
1	Cy	1185	0	1167	28	0
1	Cz	1185	0	1167	28	0
1	Da	746	0	689	22	0
1	Db	746	0	689	21	0
1	Dc	746	0	689	26	0
1	Dd	746	0	689	15	0
1	De	696	0	669	12	0
1	Df	687	0	664	23	0
1	Dg	637	0	644	10	0
1	Dh	637	0	644	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Di	637	0	644	13	0
1	Dj	637	0	644	18	0
1	Dk	637	0	644	13	0
1	Dl	637	0	644	9	0
1	Dm	637	0	644	13	0
1	Dn	637	0	644	15	0
1	Do	687	0	664	14	0
1	Dp	746	0	689	16	0
1	Dq	746	0	689	26	0
1	Dr	746	0	689	15	0
1	Ds	746	0	689	17	0
1	Dt	746	0	689	35	0
1	Du	746	0	689	21	0
1	Dv	746	0	689	30	0
1	Dw	746	0	689	23	0
1	Ea	1185	0	1167	32	0
1	Eb	1185	0	1167	22	0
1	Ec	1185	0	1167	28	0
1	Ed	1185	0	1167	29	0
1	Ee	1185	0	1167	26	0
1	Ef	1185	0	1167	24	0
1	Eg	1185	0	1167	23	0
1	Fh	1185	0	1167	31	0
1	cg	1185	0	1167	26	0
2	GA	55	0	14	4	0
2	GB	25	0	7	0	0
2	GC	55	0	14	2	0
2	GD	50	0	12	3	0
2	GE	60	0	15	4	0
3	GF	90	0	20	9	0
3	GG	90	0	20	1	0
3	GH	90	0	20	10	0
3	GI	75	0	17	7	0
3	GJ	90	0	20	4	0
3	GK	90	0	20	2	0
All	All	57178	0	55274	1135	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 11.

The worst 5 of 1135 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:Db:160:PRO:N	1:Db:160:PRO:CA	1.69	1.41
1:Df:160:PRO:N	1:Df:160:PRO:CA	1.69	1.31
3:GH:8:UNK:CB	1:Ct:372:ILE:HG21	1.86	1.06
3:GH:15:UNK:CB	1:Cs:372:ILE:HG21	1.85	1.05
1:Db:124:SER:CB	1:Db:127:SER:HB3	1.90	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Cf	15/467 (3%)	14 (93%)	1 (7%)	15	37
1	Ch	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Ci	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cj	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Ck	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cl	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cm	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cn	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Co	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cp	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cq	72/467 (15%)	70 (97%)	2 (3%)	38	59
1	Cs	36/467 (8%)	34 (94%)	2 (6%)	19	41
1	Cx	74/467 (16%)	73 (99%)	1 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Cy	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Cz	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Dr	15/467 (3%)	15 (100%)	0	100	100
1	Ea	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Eb	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Ec	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Ed	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Ee	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Ef	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Eg	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	Fh	133/467 (28%)	130 (98%)	3 (2%)	44	63
1	cg	111/467 (24%)	109 (98%)	2 (2%)	51	67
All	All	2850/11675 (24%)	2785 (98%)	65 (2%)	44	63

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Ef	295	SER
1	Eg	243	SER
1	Co	243	SER
1	Cn	425	LYS
1	Eg	295	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	Ee	281	HIS
1	Ee	361	ASN
1	Eg	365	ASN
1	Cn	361	ASN
1	Cn	281	HIS

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.

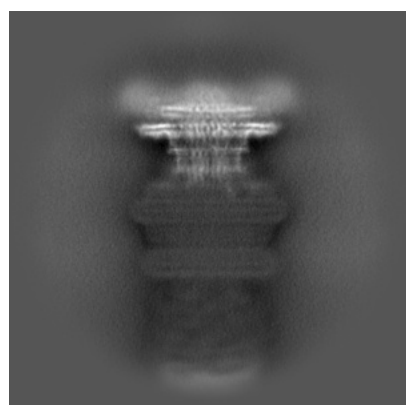
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31007. These allow visual inspection of the internal detail of the map and identification of artifacts.

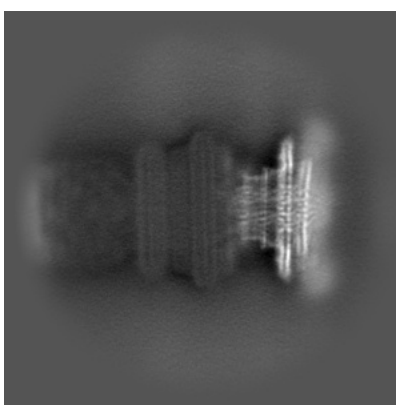
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

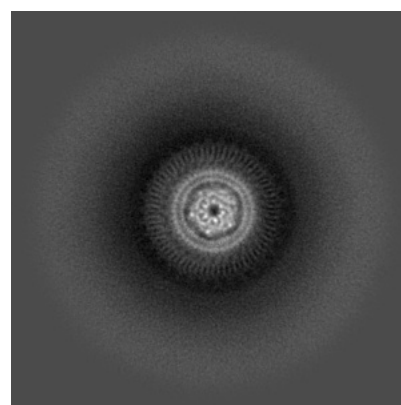
6.1.1 Primary map



X



Y

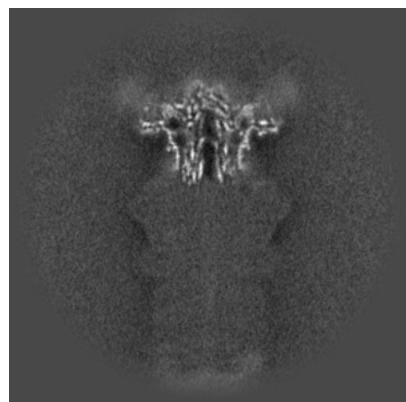


Z

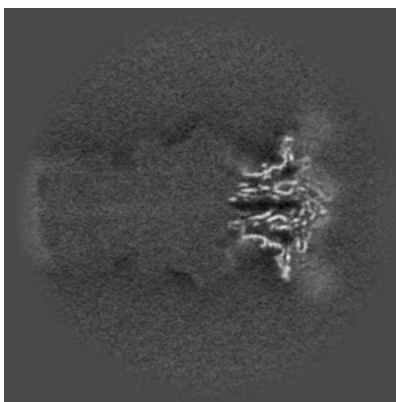
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

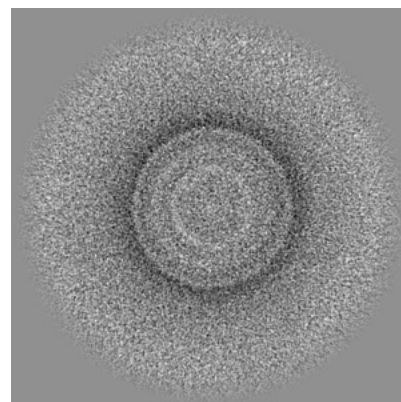
6.2.1 Primary map



X Index: 256



Y Index: 256

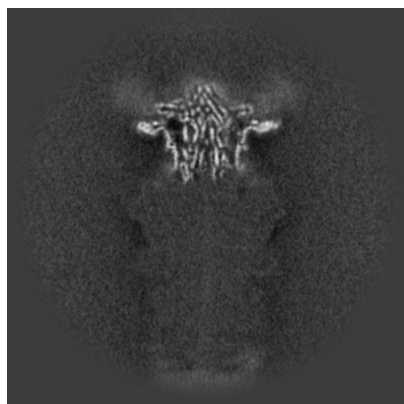


Z Index: 256

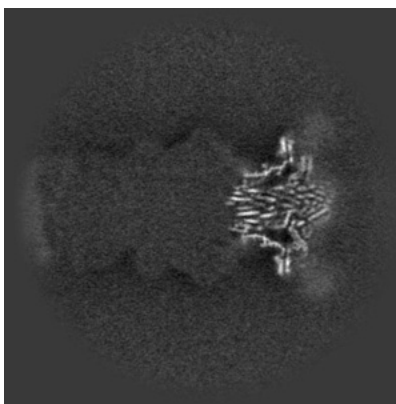
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

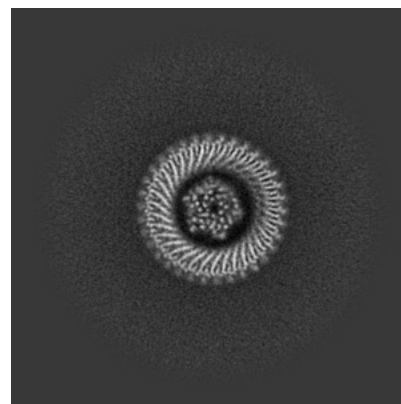
6.3.1 Primary map



X Index: 251



Y Index: 247

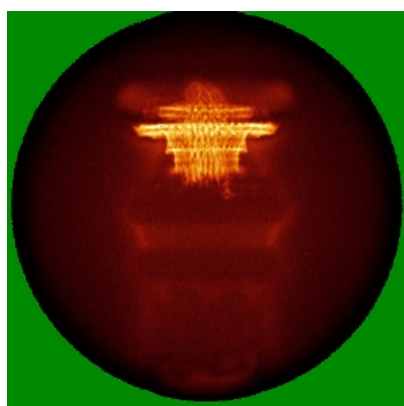


Z Index: 364

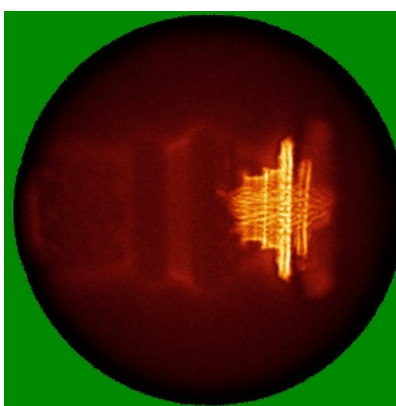
The images above show the largest variance slices of the map in three orthogonal directions.

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

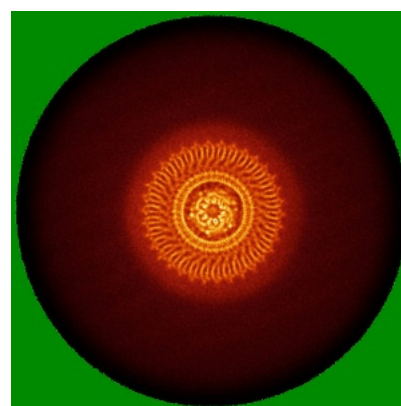
6.4.1 Primary map



X



Y

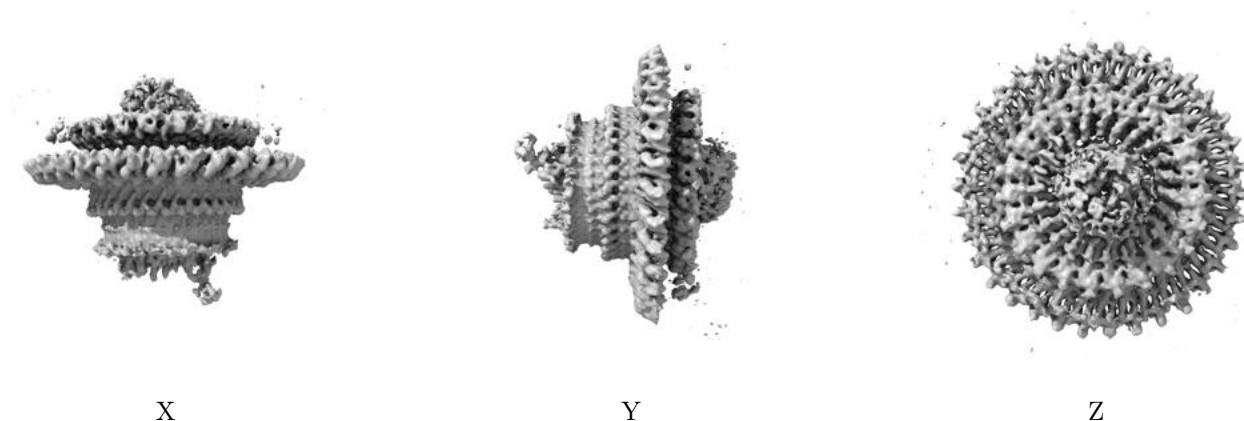


Z

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 0.238. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

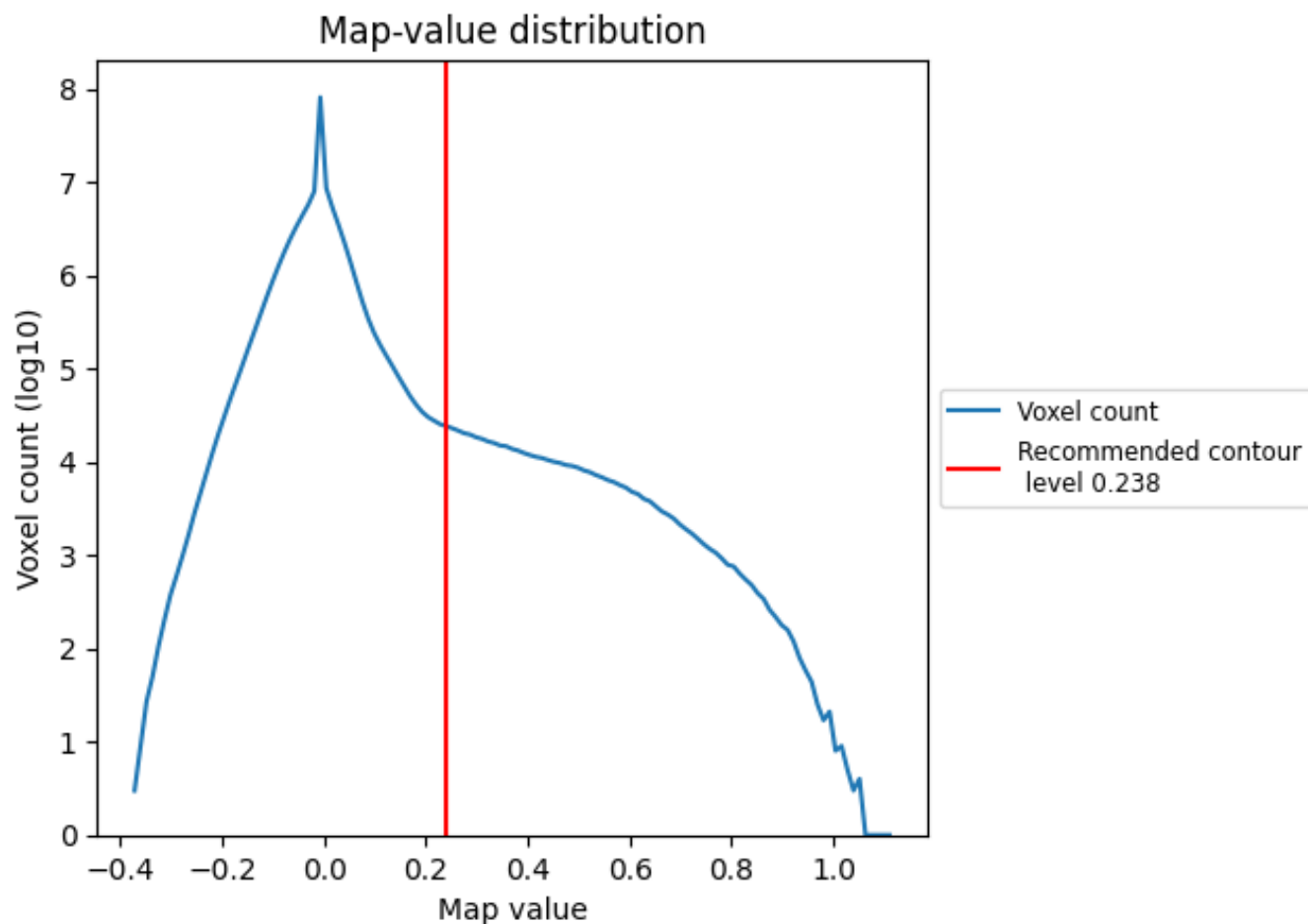
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

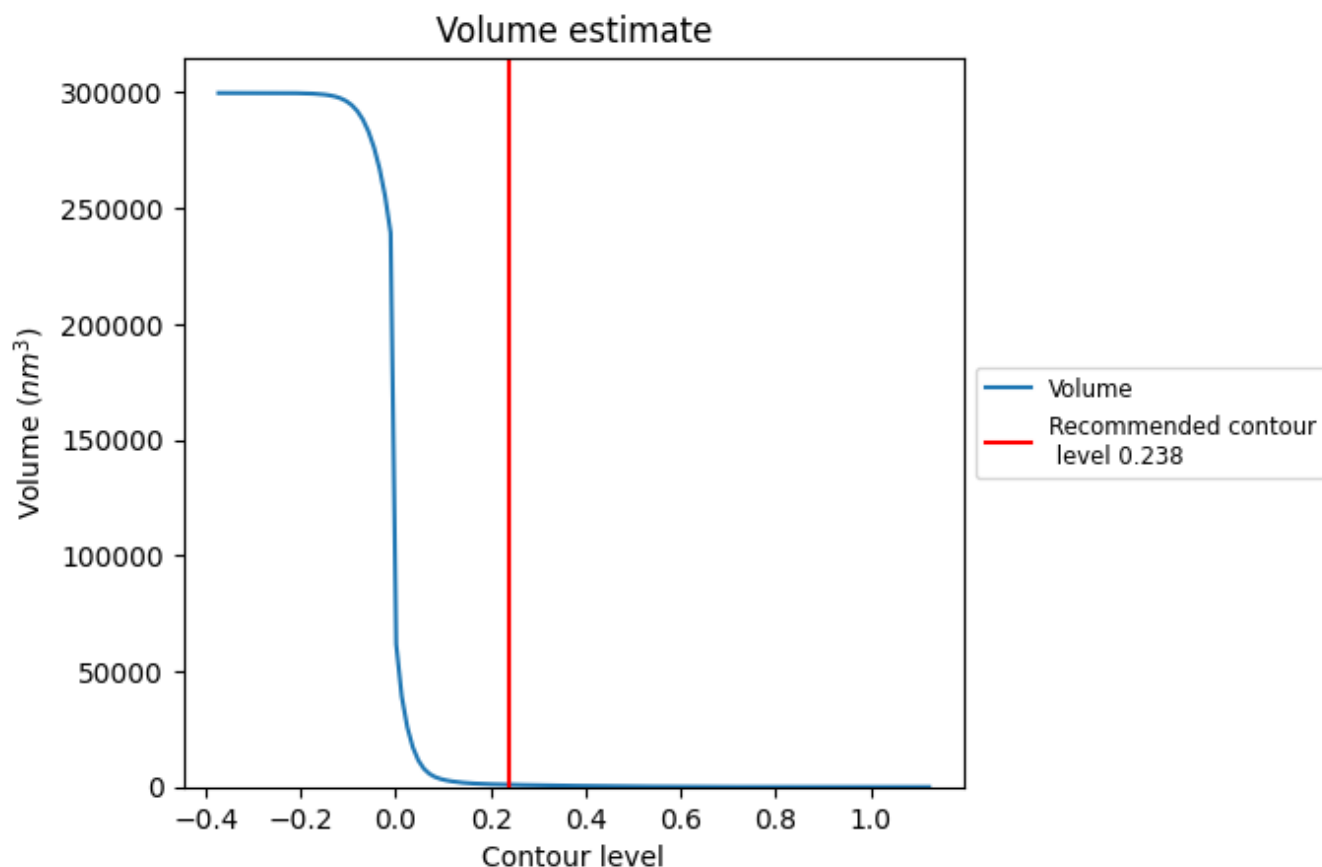
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

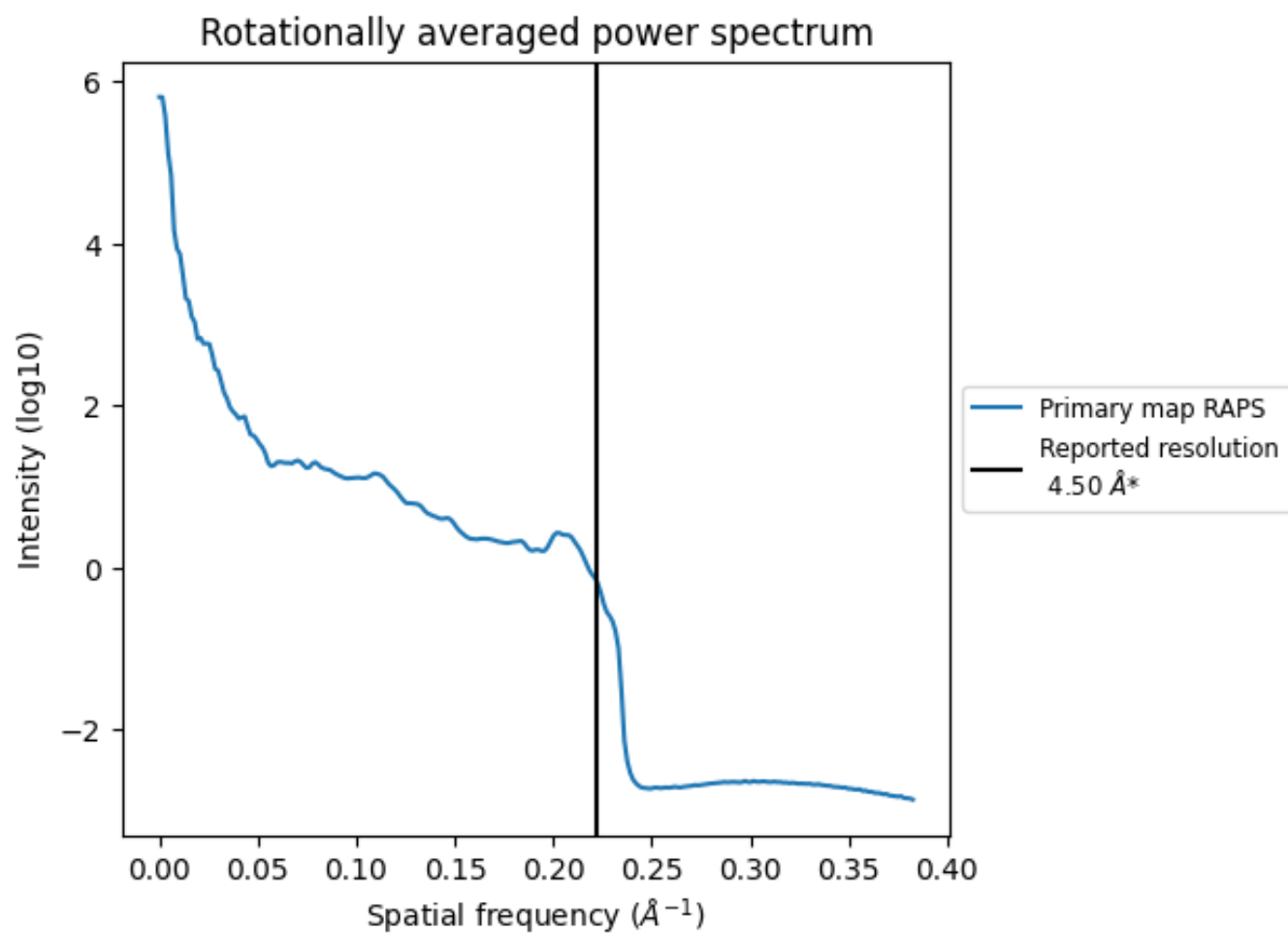
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982 nm³; this corresponds to an approximate mass of 887 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 0.222 $\text{\AA}^{-1}$

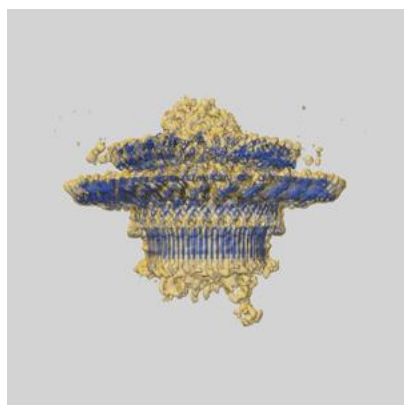
8 Fourier-Shell correlation

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

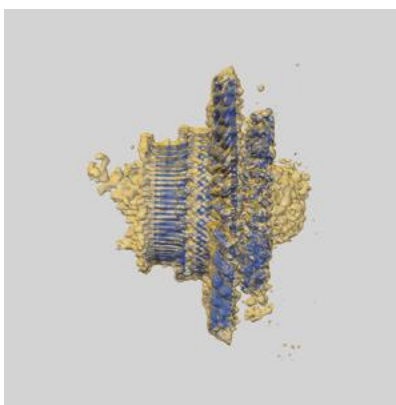
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-31007 and PDB model 7E81. Per-residue inclusion information can be found in section [3](#) on page [10](#).

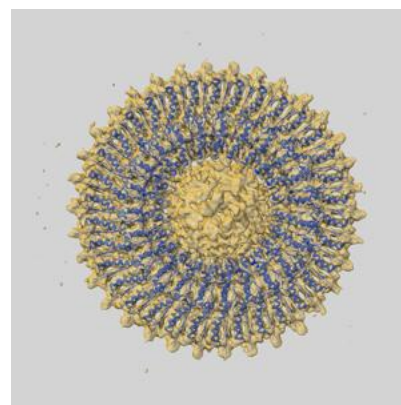
9.1 Map-model overlay [i](#)



X



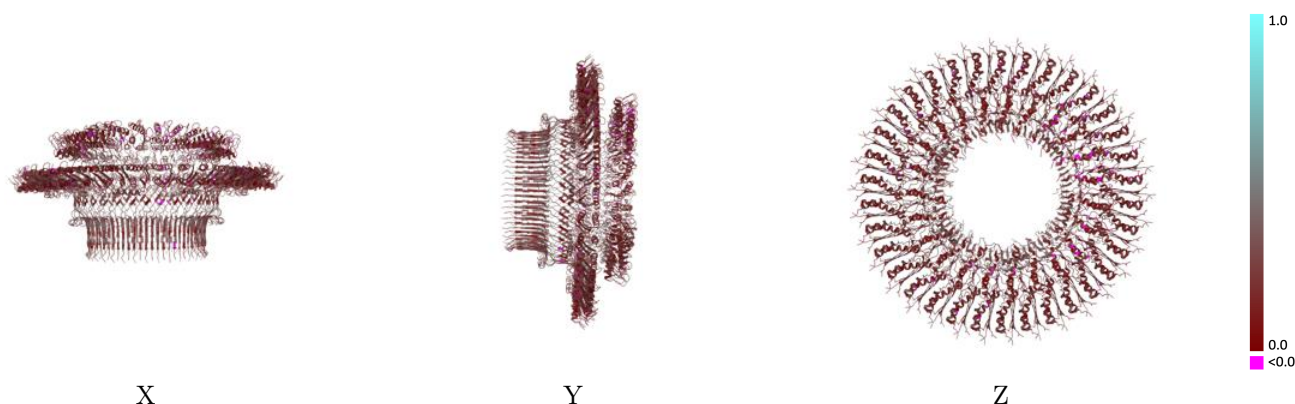
Y



Z

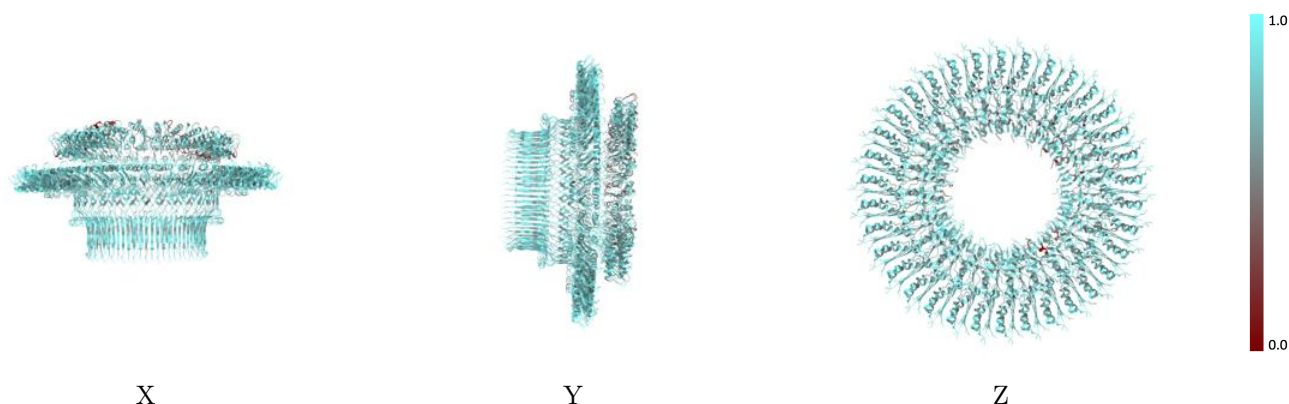
The images above show the 3D surface view of the map at the recommended contour level 0.238 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



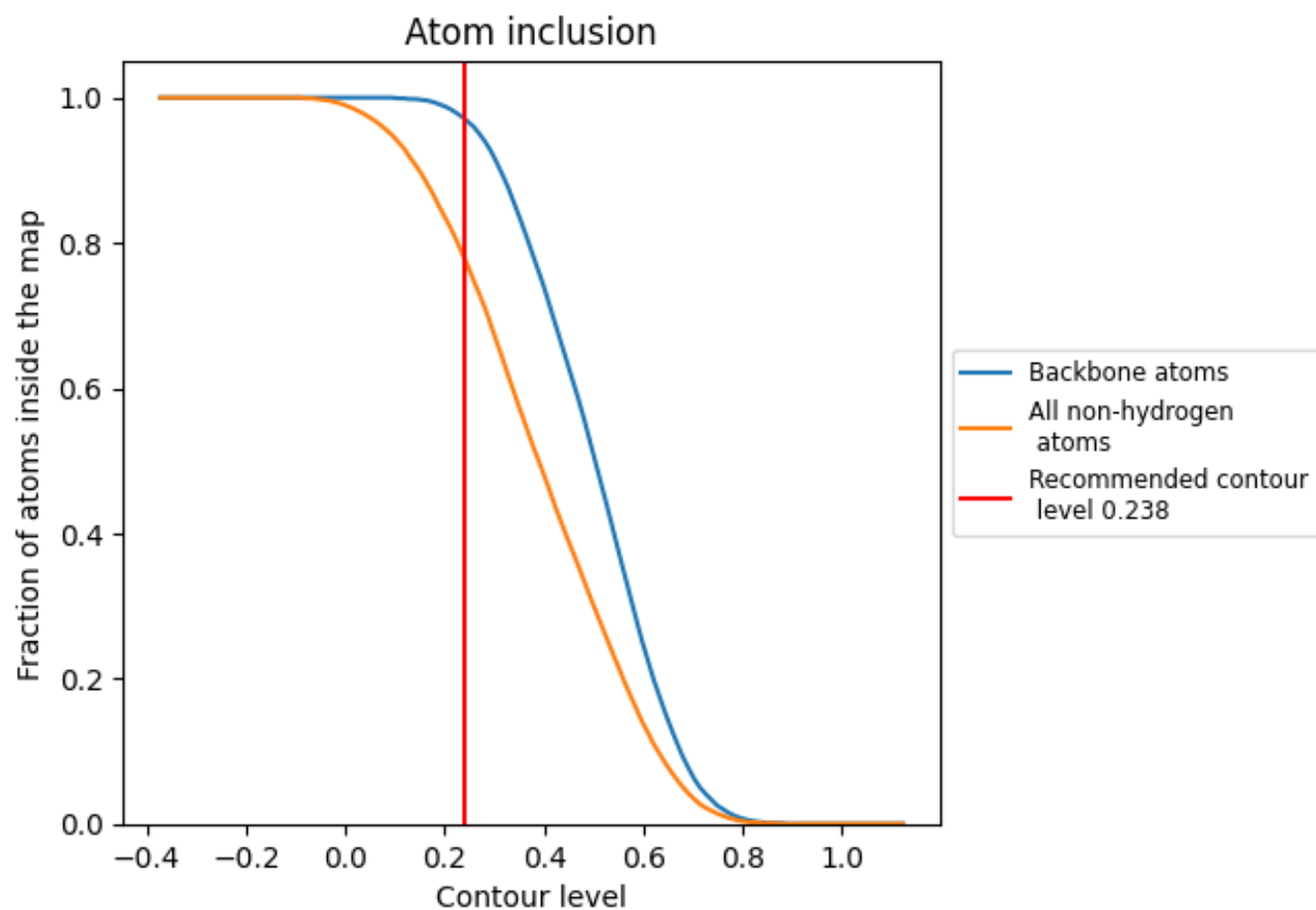
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.238).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 78% 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 (0.238) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7820	 0.2350
Ca	 0.8060	 0.2360
Cb	 0.8030	 0.2450
Cc	 0.8070	 0.2380
Cd	 0.8160	 0.2420
Ce	 0.8070	 0.2310
Cf	 0.8040	 0.2370
Ch	 0.8070	 0.2360
Ci	 0.8030	 0.2450
Cj	 0.8040	 0.2490
Ck	 0.8000	 0.2470
Cl	 0.7980	 0.2440
Cm	 0.7960	 0.2500
Cn	 0.7920	 0.2400
Co	 0.8070	 0.2450
Cp	 0.7880	 0.2390
Cq	 0.7930	 0.2240
Cr	 0.8020	 0.2320
Cs	 0.7890	 0.2310
Ct	 0.8070	 0.2370
Cu	 0.8070	 0.2390
Cv	 0.8120	 0.2440
Cw	 0.8070	 0.2480
Cx	 0.8070	 0.2460
Cy	 0.8030	 0.2410
Cz	 0.8190	 0.2530
Da	 0.7650	 0.2190
Db	 0.7680	 0.2250
Dc	 0.7460	 0.2260
Dd	 0.7100	 0.2090
De	 0.7020	 0.2110
Df	 0.7270	 0.1850
Dg	 0.7330	 0.1780
Dh	 0.6880	 0.1570
Di	 0.6320	 0.1730



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Chain	Atom inclusion	Q-score
Dj	 0.6230	 0.1630
Dk	 0.6500	 0.1750
Dl	 0.6310	 0.1630
Dm	 0.6130	 0.1790
Dn	 0.6720	 0.1880
Do	 0.6890	 0.2070
Dp	 0.7450	 0.2260
Dq	 0.7570	 0.2460
Dr	 0.7450	 0.2330
Ds	 0.7560	 0.2490
Dt	 0.7900	 0.2440
Du	 0.7790	 0.2500
Dv	 0.7690	 0.2300
Dw	 0.7800	 0.2340
Ea	 0.8190	 0.2600
Eb	 0.8140	 0.2520
Ec	 0.8110	 0.2520
Ed	 0.8100	 0.2520
Ee	 0.8000	 0.2590
Ef	 0.8170	 0.2570
Eg	 0.8020	 0.2540
Fh	 0.8030	 0.2460
GA	 0.9090	 0.4060
GB	 0.9200	 0.4010
GC	 0.8910	 0.3930
GD	 0.8800	 0.3640
GE	 0.9330	 0.4570
GF	 0.8670	 0.3010
GG	 0.8780	 0.3500
GH	 0.8560	 0.3180
GI	 0.7470	 0.2920
GJ	 0.9330	 0.2640
GK	 0.8560	 0.3030
cg	 0.8020	 0.2340