



## wwPDB EM Validation Summary Report ⓘ

Apr 16, 2025 – 04:26 PM JST

PDB ID : 8ZDS / pdb\_00008zds  
EMDB ID : EMD-60007  
Title : Structure of the Salmonella flagellar MS-ring with C11 symmetry applied  
Authors : Kinoshita, M.; Makino, F.; Miyata, T.; Imada, K.; Minamino, T.; Namba, K.  
Deposited on : 2024-05-03  
Resolution : 3.10 Å(reported)  
Based on initial models : ., 7D84, 7CIK

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

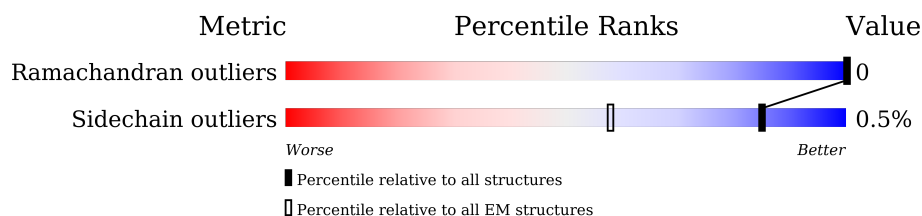
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	A	560	<div> <div>38%</div> <div>46%</div> <div>54%</div> </div>
1	B	560	<div> <div>47%</div> <div>55%</div> <div>45%</div> </div>
1	C	560	<div> <div>38%</div> <div>46%</div> <div>54%</div> </div>
1	D	560	<div> <div>38%</div> <div>45%</div> <div>54%</div> </div>
1	E	560	<div> <div>47%</div> <div>55%</div> <div>45%</div> </div>
1	F	560	<div> <div>37%</div> <div>46%</div> <div>54%</div> </div>
1	G	560	<div> <div>38%</div> <div>46%</div> <div>54%</div> </div>
1	H	560	<div> <div>47%</div> <div>55%</div> <div>45%</div> </div>
1	I	560	<div> <div>37%</div> <div>46%</div> <div>54%</div> </div>

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Mol	Chain	Length	Quality of chain
1	J	560	
1	K	560	
1	L	560	
1	M	560	
1	N	560	
1	O	560	
1	P	560	
1	Q	560	
1	R	560	
1	S	560	
1	T	560	
1	U	560	
1	V	560	
1	W	560	
1	X	560	
1	Y	560	
1	Z	560	
1	a	560	
1	b	560	
1	c	560	
1	d	560	
1	e	560	
1	f	560	
1	g	560	

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 69498 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	A	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	B	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	C	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	D	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	E	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	F	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	G	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	H	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	I	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	J	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	K	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	L	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	M	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	N	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	O	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	P	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	Q	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	S	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	T	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	U	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	V	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	W	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	X	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	Y	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	Z	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	a	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	b	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	c	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	d	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		
1	e	257	Total	C	N	O	S	1	0
			1977	1212	365	396	4		
1	f	309	Total	C	N	O	S	1	0
			2363	1454	437	467	5		
1	g	257	Total	C	N	O	S	1	0
			1978	1213	365	396	4		









GLN	LEU	GLN	GLN	ARG	ALA	ARG	ALA	ASN	ARG	GLN	TRP	LEU	ARG	LEU	VAL	ALA	GLU	VAL	VAL	ASP	GLN	ASP	PRO	ASN	GLN	ASP	PRO	GLN	ARG	GLU	VAL	VAL	ILE	ALA	ARG	LYS	GLU	ASP	GLN	TRP	PHE	SER	ASN	SER	LEU	SER	LEU	D60																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
ASP	GLN	LEU	LEU	GLY	GLY	P401	L402	P403	P404	T405	A406	D407	Q408	M409	K410	Q411	I412	E413	D414	L415	T416	R417	E418	A419	M420	G421	F422	S423	D424	A425	R426	G427	D428	T429	A430	N431	V432	V433	M434	S435	P436	F437	S438	VAL	VAL	ARG	VAL	ASP	ASN	THR	GLY	GLY	GLU	VAL	VAL	ARG	GLN	LEU	PRO	TRP	PHE	GLN	GLN	GLN	SER	SER	LEU	LEU	LEU	ASP	GLN	GLU	LYS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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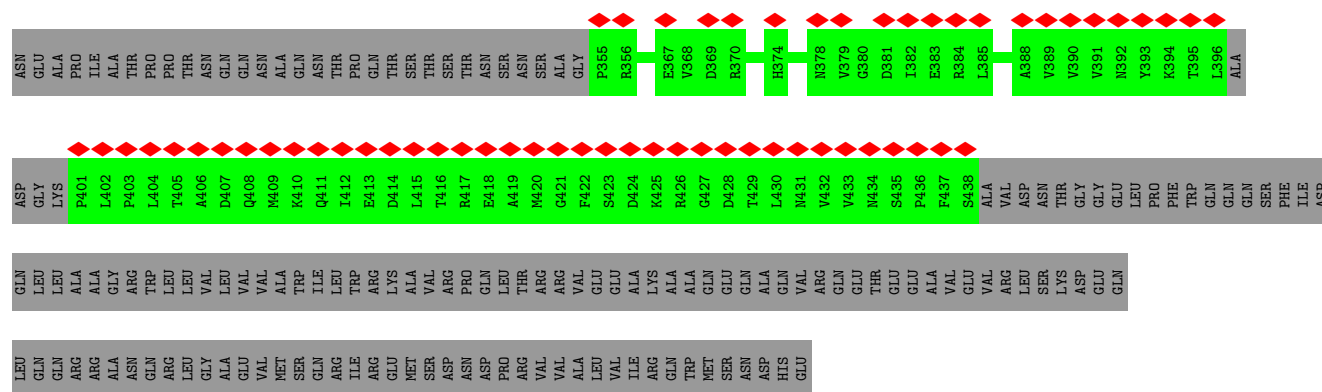
● Molecule 1: Flagellar M-ring protein



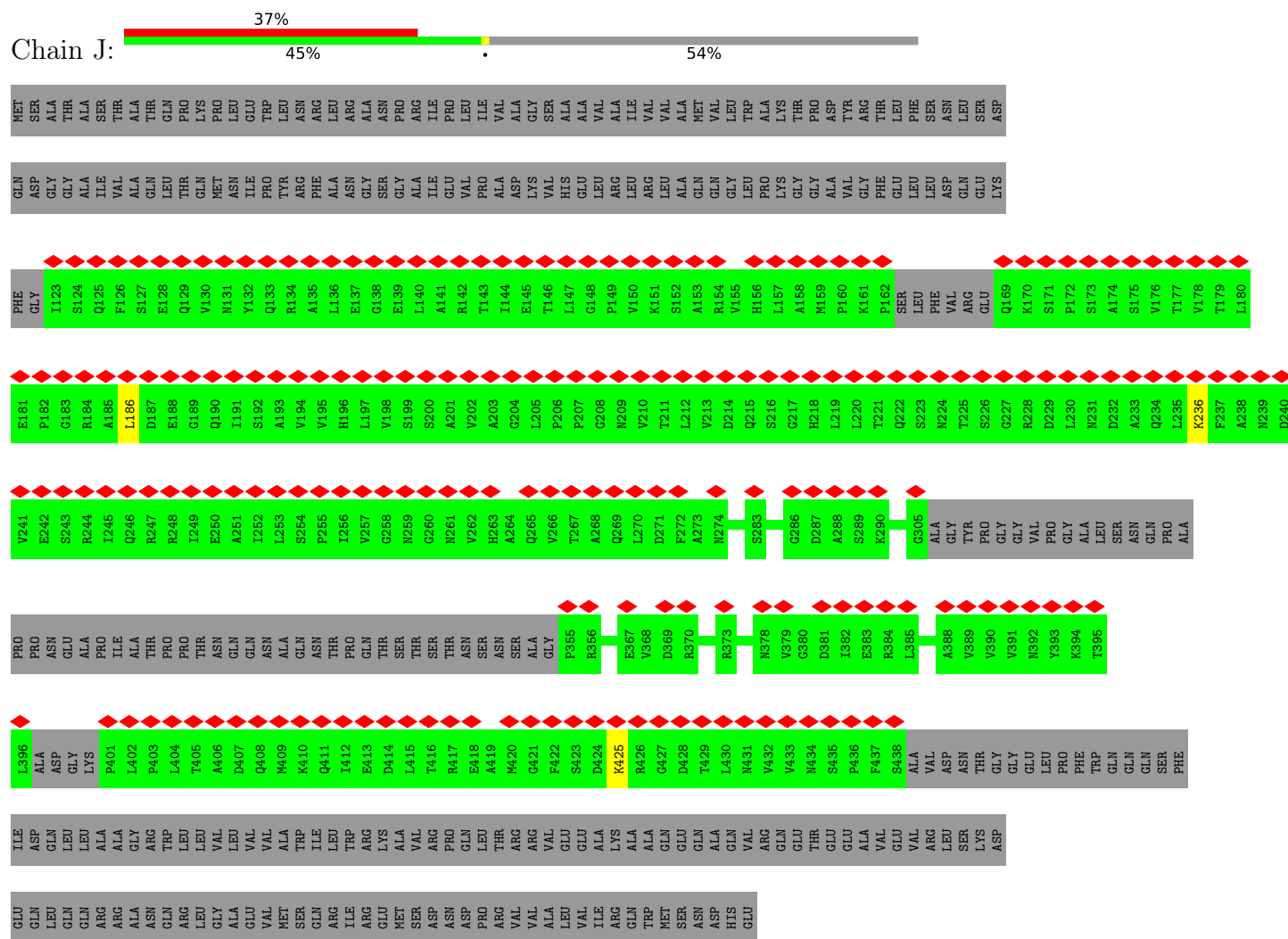
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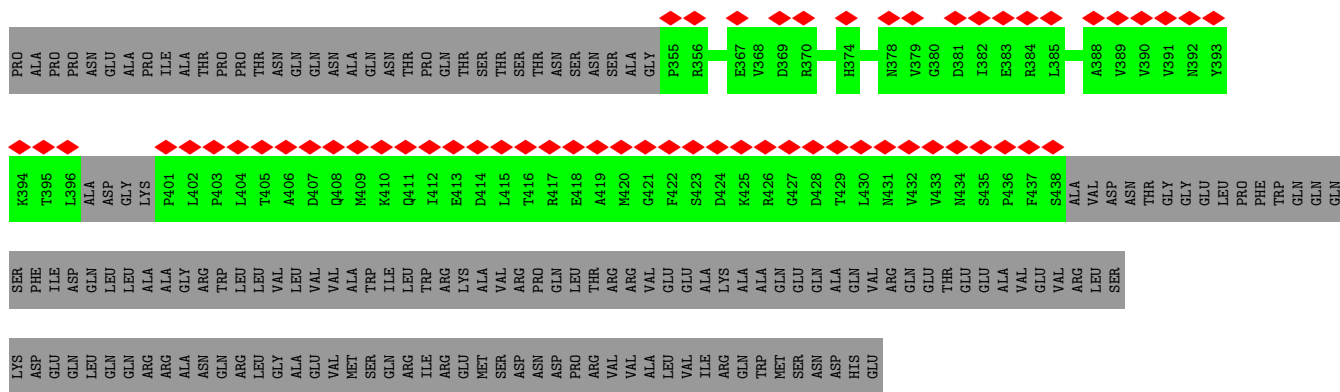
### • Molecule 1: Flagellar M-ring protein



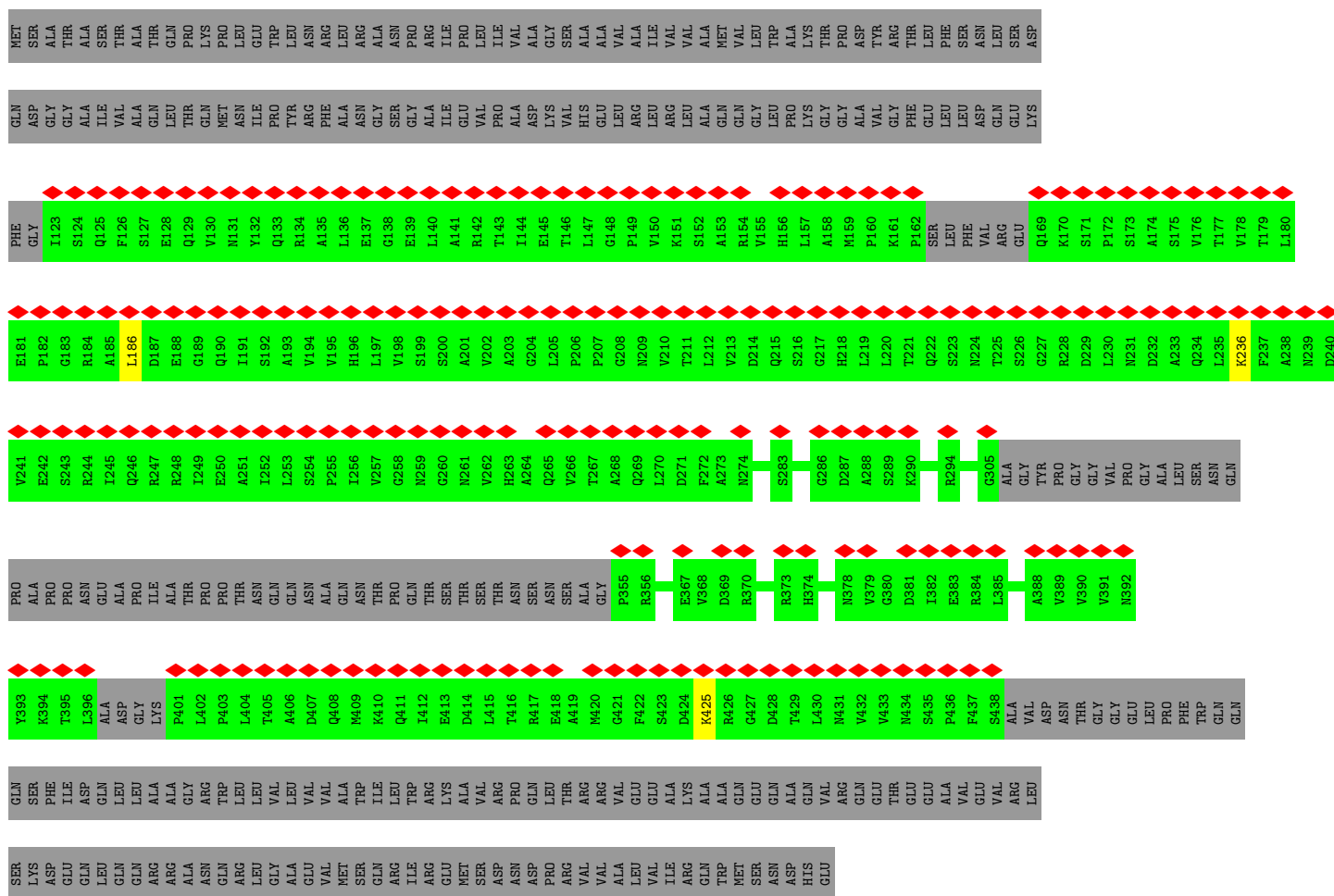
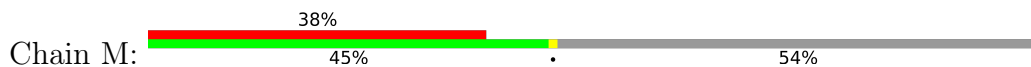
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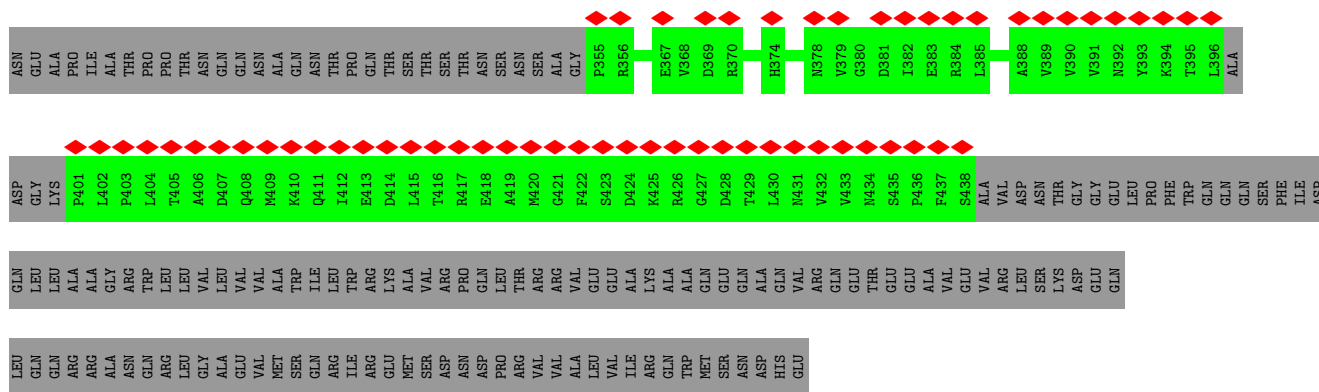
- Molecule 1: Flagellar M-ring protein



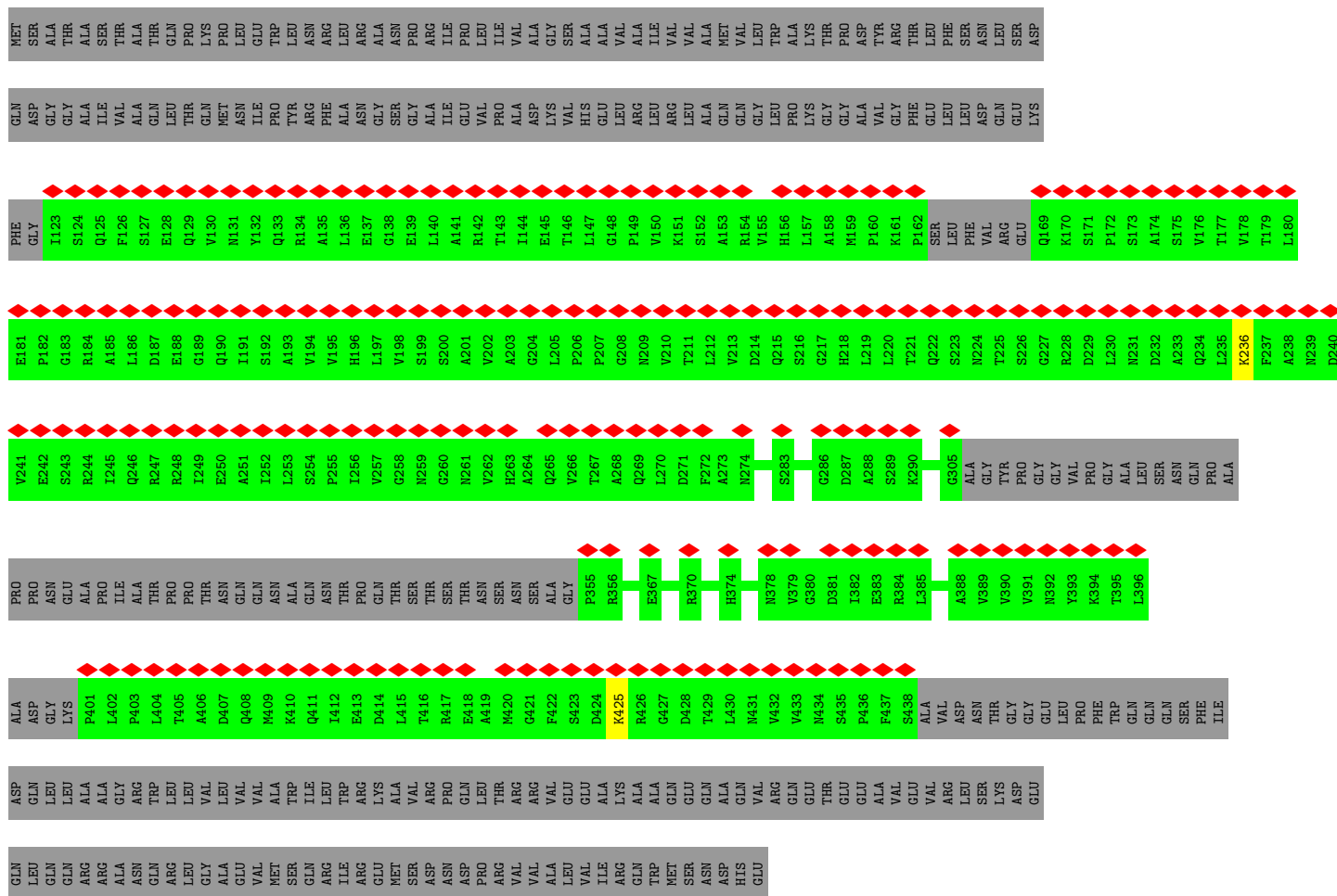
- Molecule 1: Flagellar M-ring protein







- Molecule 1: Flagellar M-ring protein

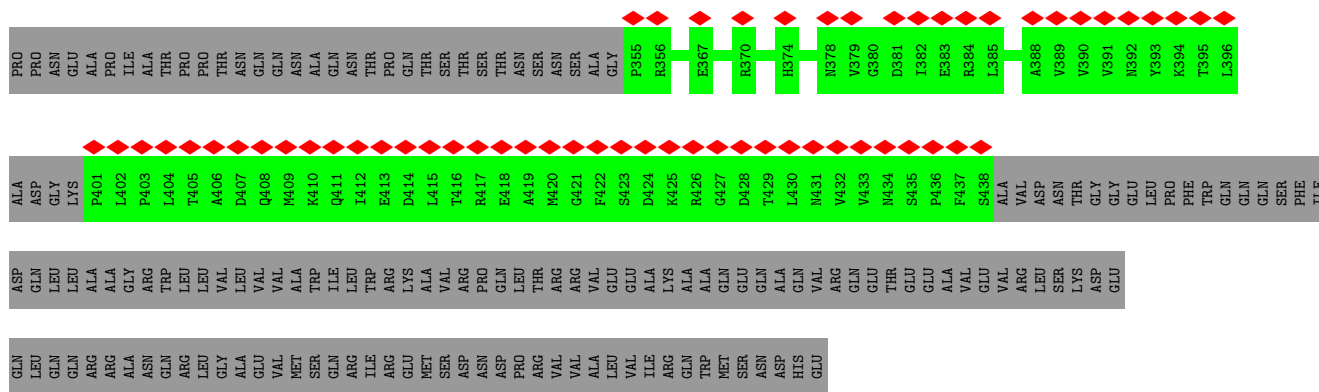


- Molecule 1: Flagellar M-ring protein

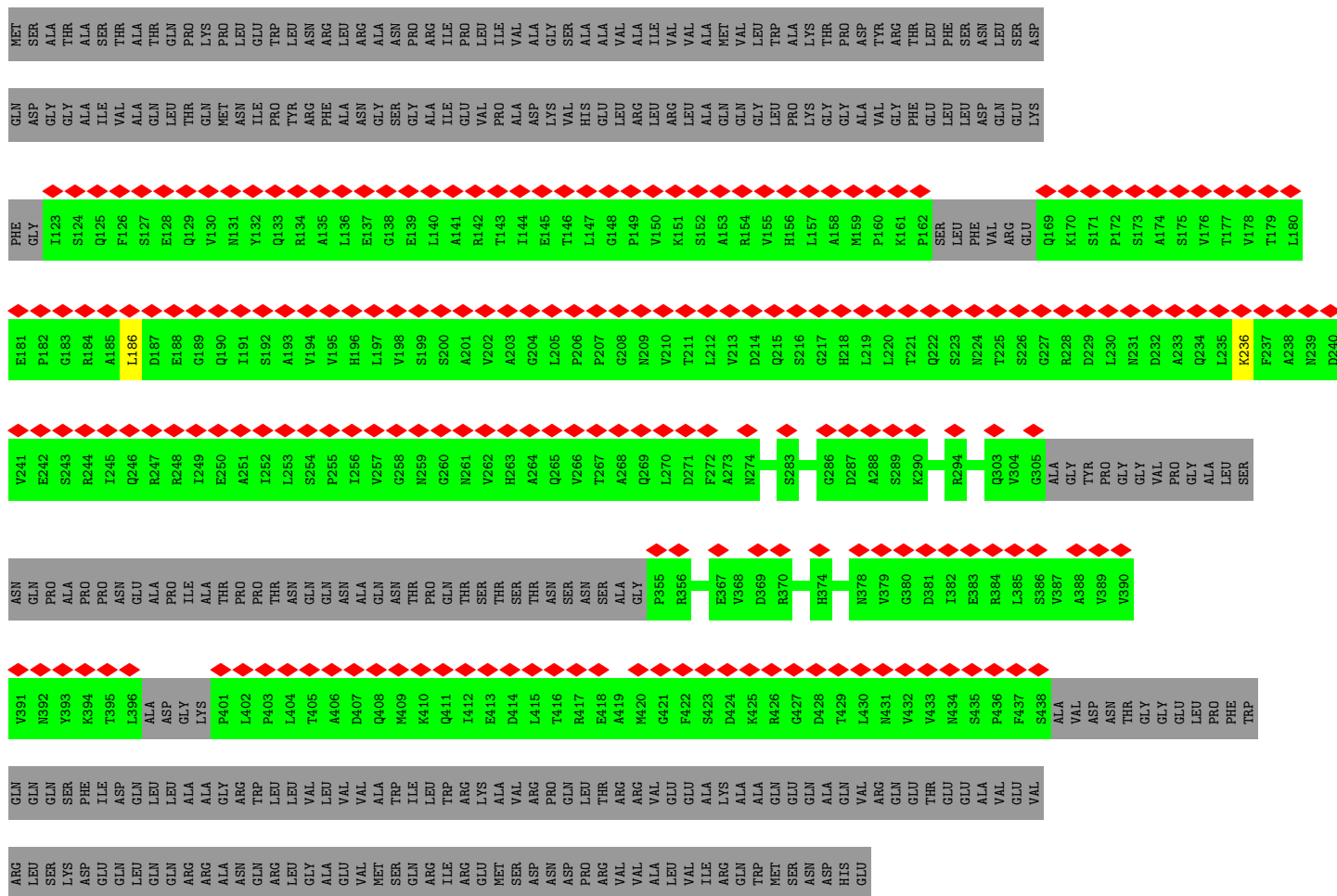








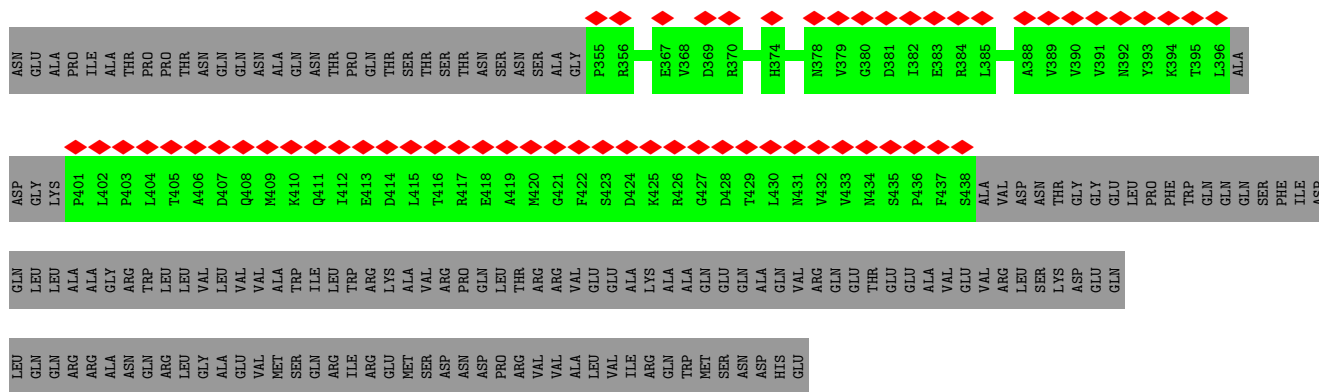
- Molecule 1: Flagellar M-ring protein



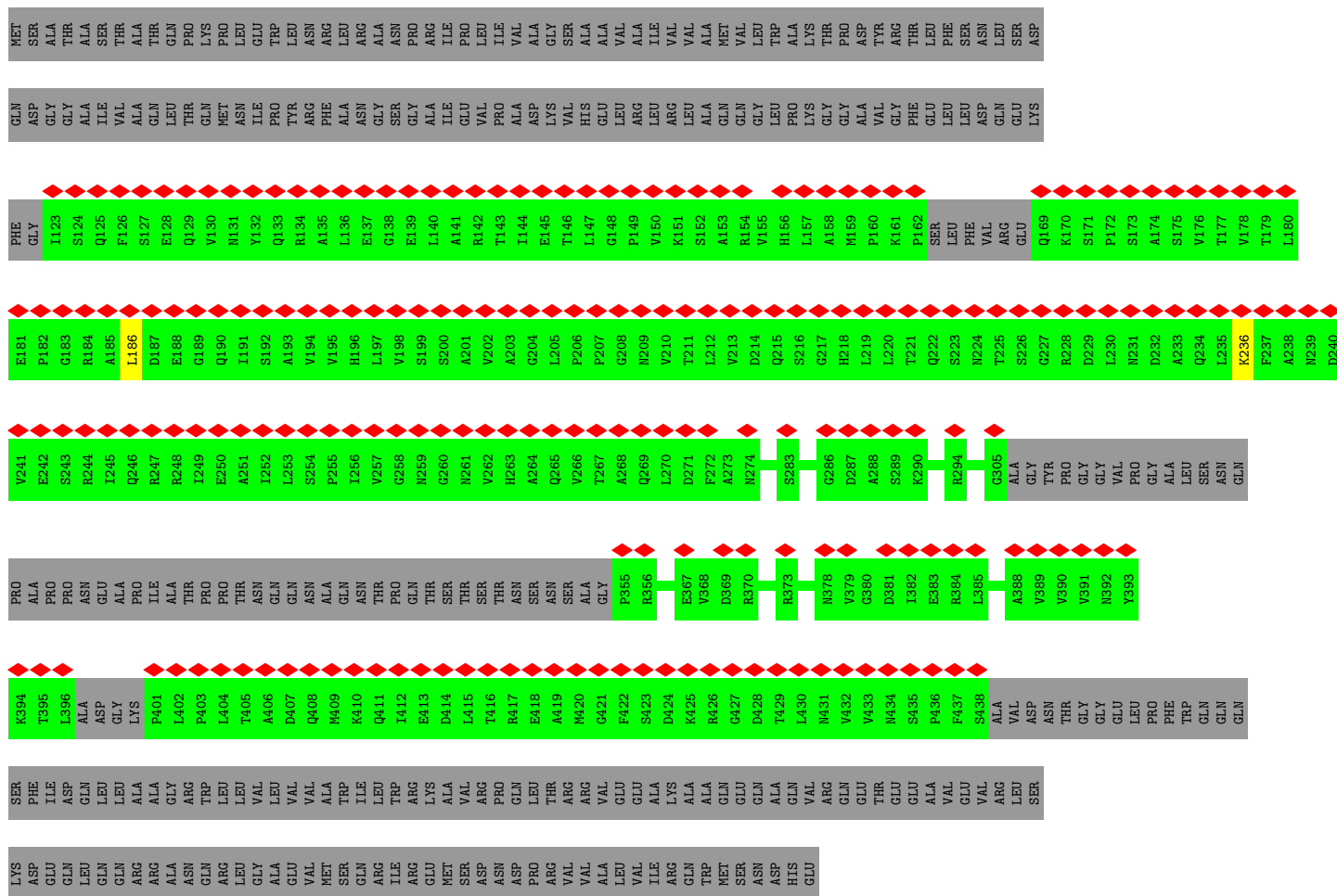
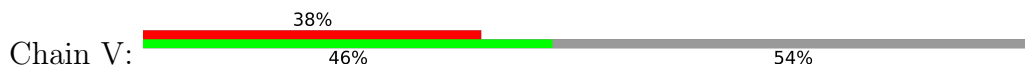
- Molecule 1: Flagellar M-ring protein







- Molecule 1: Flagellar M-ring protein

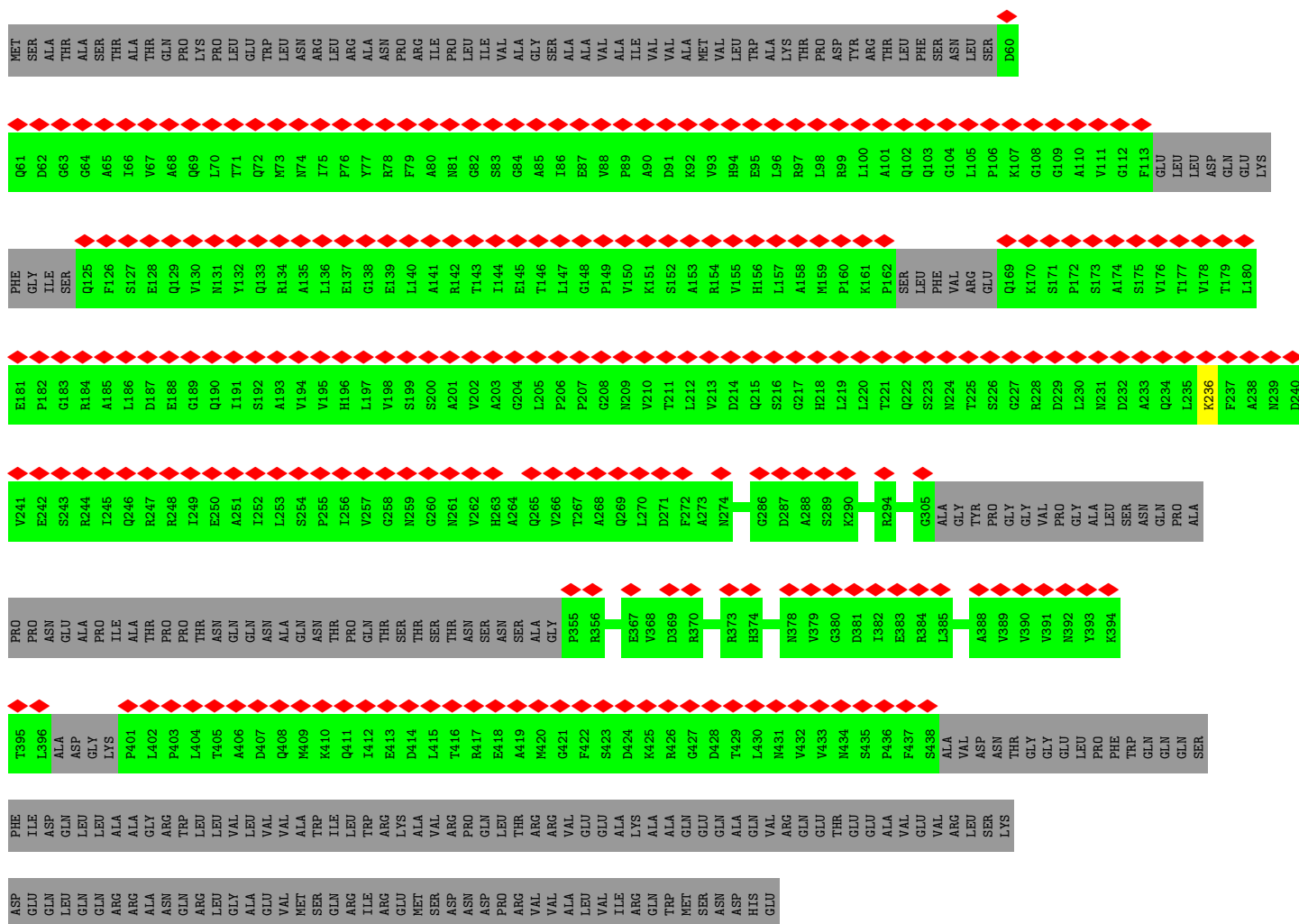


- Molecule 1: Flagellar M-ring protein

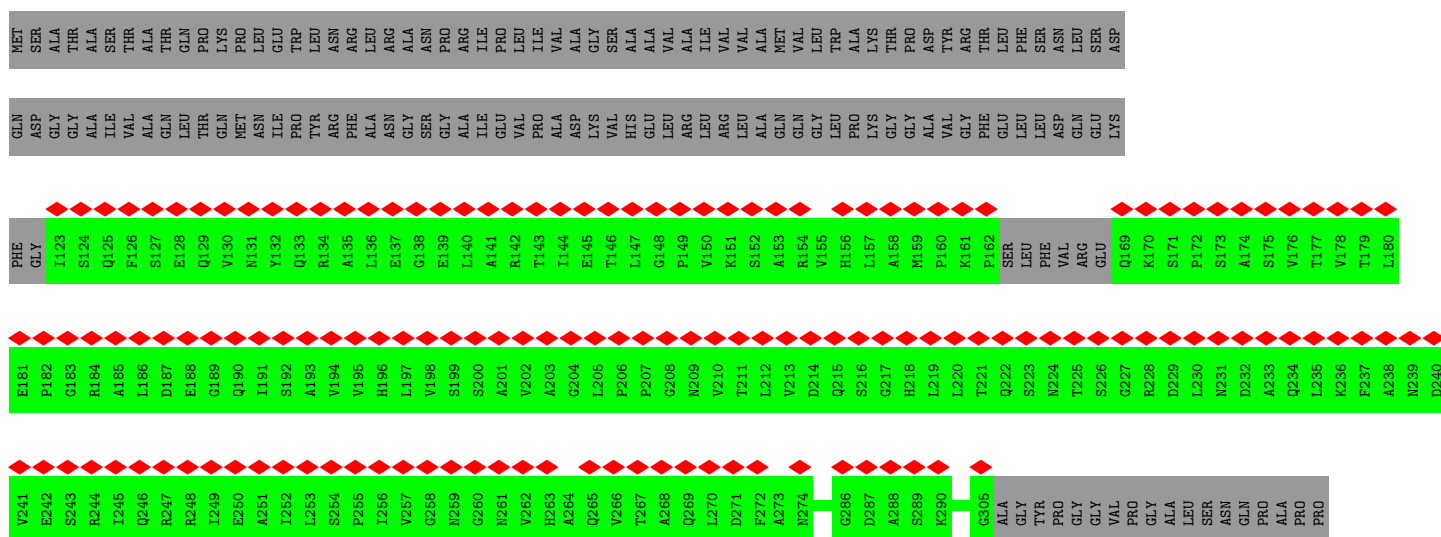


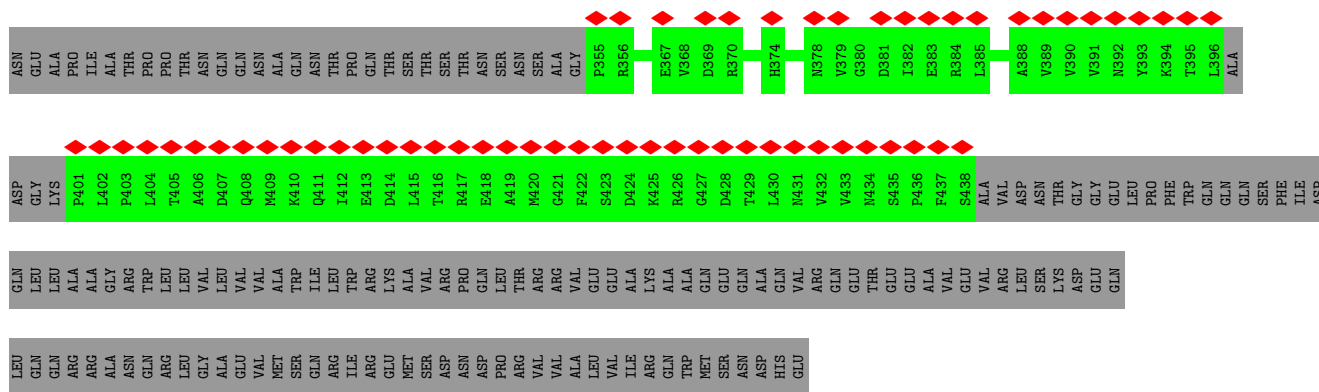




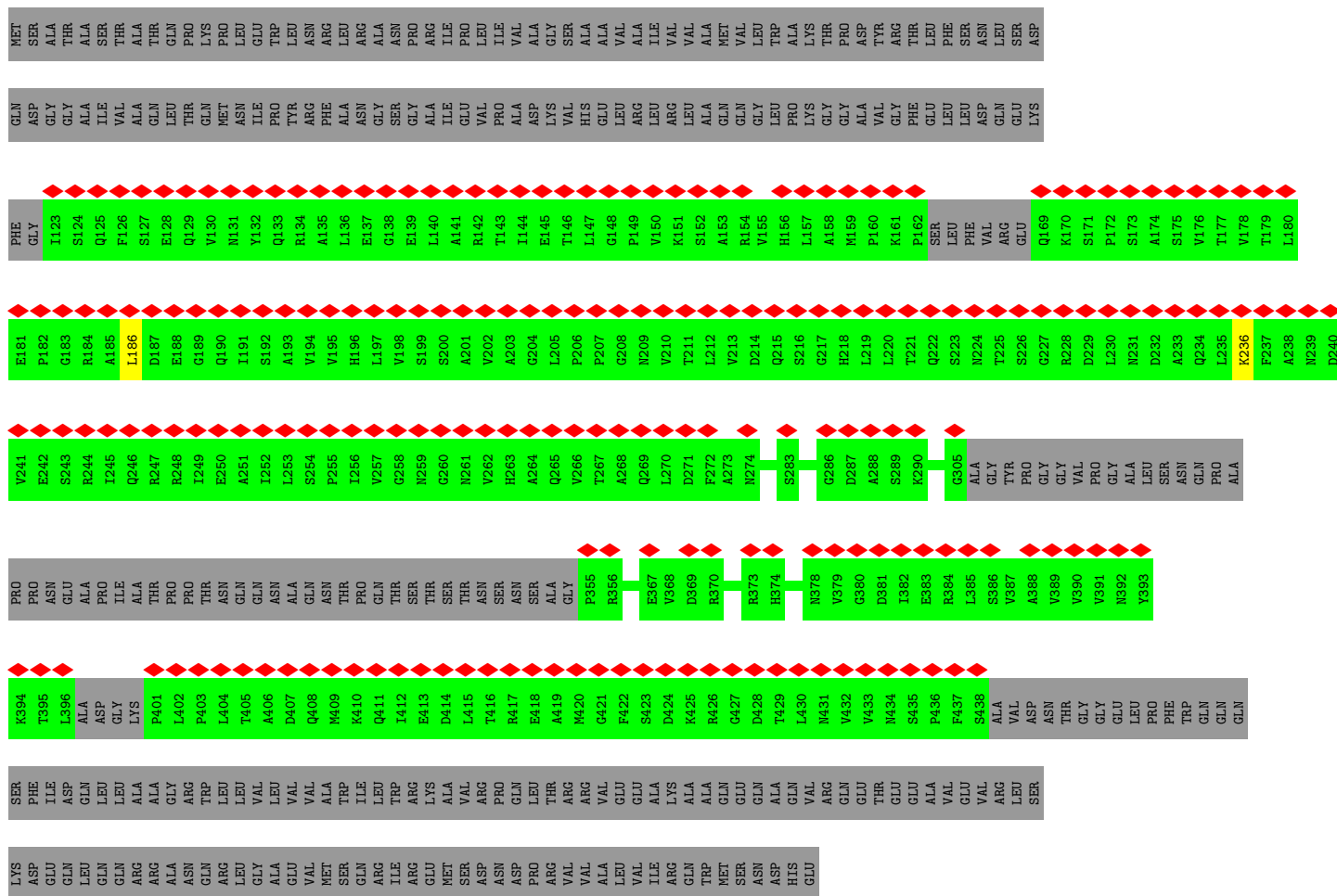
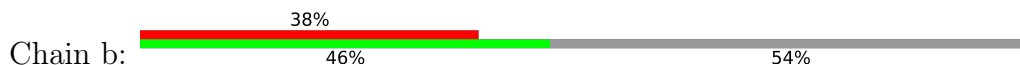


- Molecule 1: Flagellar M-ring protein





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- Molecule 1: Flagellar M-ring protein





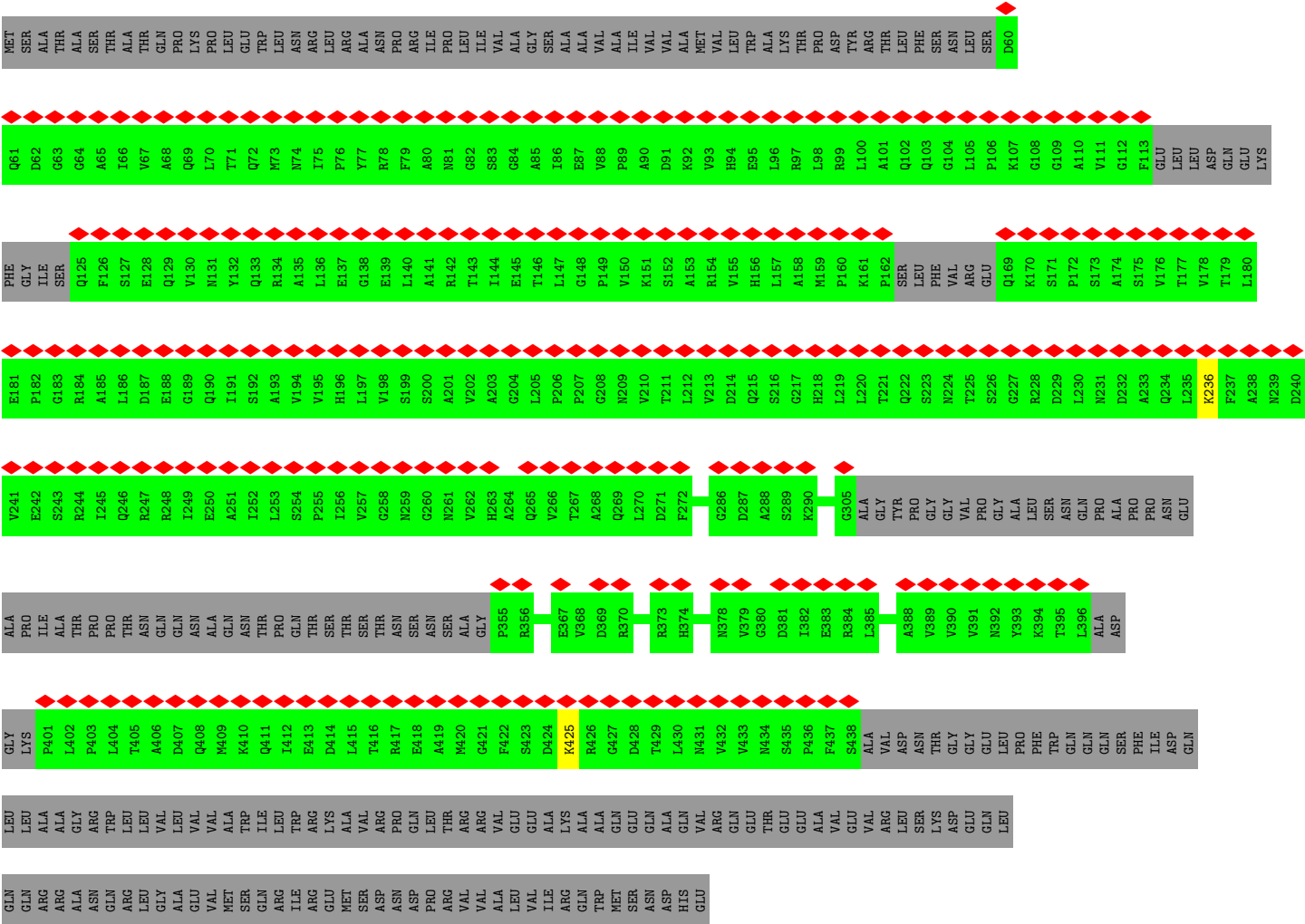
ASP	GLU	GLN	LEU	GLN	GLN	ARG	ALA	ALA	ASN	GLN	ARG	TRP	PRO	LEU	GLY	VAL	LEU	VAL	VAL	ALA	MET	SER	GLN	ILE	ARG	VAL	VAL	ALA	GLU	GLN	GLN	ASP	HIS	GLU
PHE	ILE	ASP	GLN	LEU	LEU	ALA	ALA	GLY	ALA	ARG	TRP	PRO	PRO	LEU	GLY	VAL	LEU	VAL	VAL	ALA	VAL	GLU	GLN	TRP	ARG	VAL	VAL	ALA	GLU	GLN	GLN	VAL	GLN	GLU
T395	L396	ASP	GLY	LYS	P401	L402	P403	L404	T405	A406	D407	Q408	M409	K410	Q411	I412	E413	D414	L415	T416	R417	E418	A419	M420	C421	F422	S423	D424	K425	R426	C427	D428	T429	L430
ALA	VAL	VAL	VAL	VAL	ALA	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
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● Molecule 1: Flagellar M-ring protein

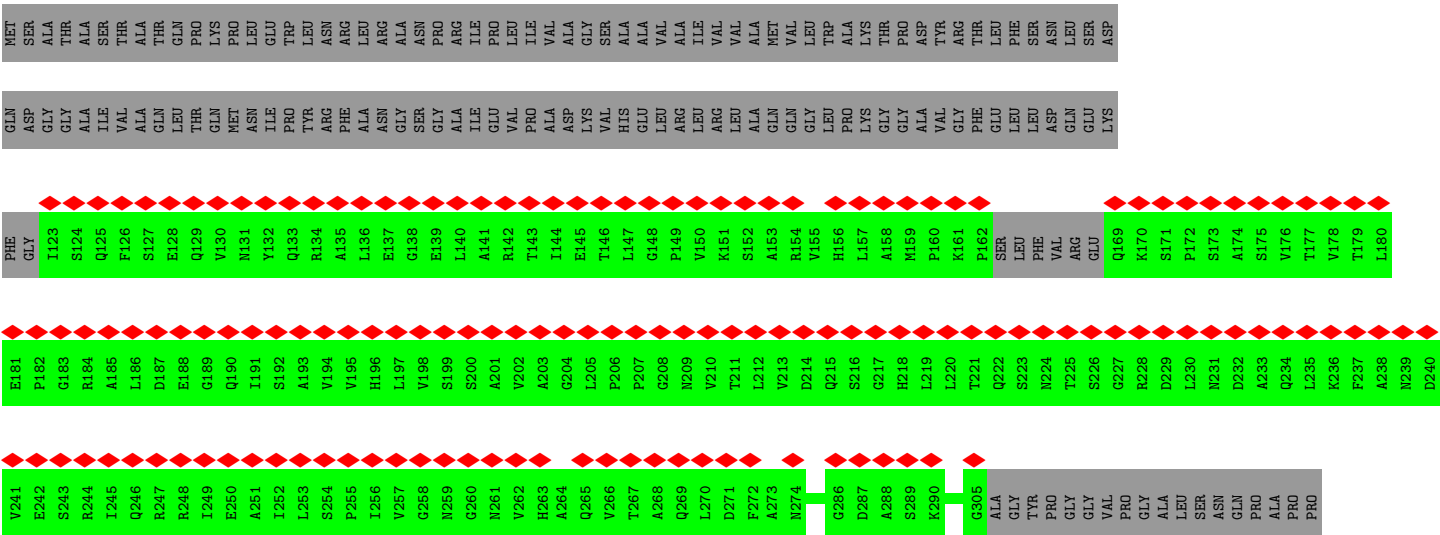


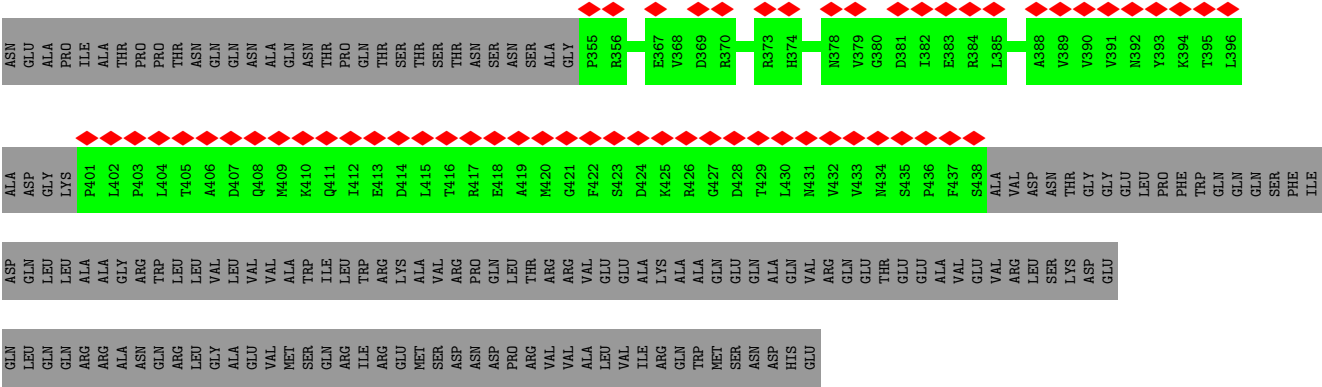
V241	E242	S243	R244	T245	Q246	R247	R248	L249	E250	A251	L253	S254	P255	T256	V257	G258	N259	G260	N261	V262	H263	A264	Q265	V266	T267	A268	Q269	L270	D271	F272	A273	N274											G286	D287	A288	S289	K290	G305	ALA	GLY	TYR	PRO	GLY	GLY	VAL	PRO	GLY	ALA	LEU	ASN	GLN	PRO	ALA	PRO																																						
E181	P182	G183	R184	A185	L186	D187	E188	G189	Q190	I191	S192	A193	V194	V195	H196	L197	V198	S199	S200	A201	V202	A203	G204	L205	P206	P207	G208	N209	V210	T211	L212	V213	D214	Q215	S216	G217	H218	L219	L220	T221	Q222	S223	N224	T225	S226	G227	R228	D229	L230	N231	D232	A233	Q234	L235	K236	F237	A238	N239	D240																																											
																																				E123	S124	Q125	F126	S127	E128	Q129	V130	M131	Y132	Q133	R134	A135	L136	E137	G138	E139	L140	A141	R142	T143	I144	E145	T146	L147	G148	P149	V150	K151	S152	A153	R154	V155	H156	L157	A158	M159	P160	K161	P162											SER	LEU	PHE	VAL	ARG	GLU	Q169	K170	S171	P172	S173	A174	S175	V176	T177	V178	L180
																																				GLN	ASP	GLY	GLY	ALA	VAL	GLN	LEU	THR	GLN	PRO	TYR	ASN	ARG	ALA	GLY	SER	ASN	GLY	ASN	ALA	LEU	ARG	ALA	LEU	LEU	VAL	PRO	ILE	GLU	GLY	VAL	PRO	GLN	GLN	GLY	LEU	TRP	ALA	LYS	THR	PRO	ASP	TYR	ARG	THR	LEU	PHE	SER	ASN	LEU	SER	ASP	GLN	GLU	SER	ASP										





● Molecule 1: Flagellar M-ring protein





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C11	Depositor
Number of particles used	70250	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	50000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	400.0, 400.0, 400.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	A	0.28	0/2005	0.52	0/2713
1	B	0.27	0/2397	0.51	0/3242
1	C	0.28	0/2006	0.54	0/2715
1	D	0.28	0/2005	0.53	0/2713
1	E	0.27	0/2397	0.51	0/3242
1	F	0.29	0/2006	0.53	0/2715
1	G	0.28	0/2005	0.53	0/2713
1	H	0.27	0/2397	0.52	0/3242
1	I	0.28	0/2006	0.54	0/2715
1	J	0.28	0/2005	0.51	0/2713
1	K	0.27	0/2397	0.51	0/3242
1	L	0.28	0/2006	0.53	0/2715
1	M	0.28	0/2005	0.54	0/2713
1	N	0.27	0/2397	0.51	0/3242
1	O	0.28	0/2006	0.52	0/2715
1	P	0.28	0/2005	0.52	0/2713
1	Q	0.27	0/2397	0.53	0/3242
1	R	0.28	0/2006	0.52	0/2715
1	S	0.27	0/2005	0.52	0/2713
1	T	0.27	0/2397	0.51	0/3242
1	U	0.28	0/2006	0.53	0/2715
1	V	0.28	0/2005	0.54	0/2713
1	W	0.27	0/2397	0.51	0/3242
1	X	0.28	0/2006	0.53	0/2715
1	Y	0.28	0/2005	0.54	0/2713
1	Z	0.27	0/2397	0.51	0/3242
1	a	0.28	0/2006	0.54	0/2715
1	b	0.28	0/2005	0.52	0/2713
1	c	0.27	0/2397	0.51	0/3242
1	d	0.28	0/2006	0.53	0/2715
1	e	0.28	0/2005	0.52	0/2713
1	f	0.27	0/2397	0.52	0/3242
1	g	0.28	0/2006	0.53	0/2715
All	All	0.28	0/70488	0.52	0/95370

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	B	300/560 (54%)	284 (95%)	16 (5%)	0	100	100
1	C	250/560 (45%)	241 (96%)	9 (4%)	0	100	100
1	D	250/560 (45%)	239 (96%)	11 (4%)	0	100	100
1	E	300/560 (54%)	284 (95%)	16 (5%)	0	100	100
1	F	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	G	250/560 (45%)	239 (96%)	11 (4%)	0	100	100
1	H	300/560 (54%)	285 (95%)	15 (5%)	0	100	100
1	I	250/560 (45%)	239 (96%)	11 (4%)	0	100	100
1	J	250/560 (45%)	238 (95%)	12 (5%)	0	100	100
1	K	300/560 (54%)	282 (94%)	18 (6%)	0	100	100
1	L	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	M	250/560 (45%)	235 (94%)	15 (6%)	0	100	100
1	N	300/560 (54%)	283 (94%)	17 (6%)	0	100	100
1	O	250/560 (45%)	241 (96%)	9 (4%)	0	100	100
1	P	250/560 (45%)	241 (96%)	9 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	300/560 (54%)	284 (95%)	16 (5%)	0	100	100
1	R	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	S	250/560 (45%)	241 (96%)	9 (4%)	0	100	100
1	T	300/560 (54%)	285 (95%)	15 (5%)	0	100	100
1	U	250/560 (45%)	241 (96%)	9 (4%)	0	100	100
1	V	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	W	300/560 (54%)	285 (95%)	15 (5%)	0	100	100
1	X	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	Y	250/560 (45%)	239 (96%)	11 (4%)	0	100	100
1	Z	300/560 (54%)	285 (95%)	15 (5%)	0	100	100
1	a	250/560 (45%)	240 (96%)	10 (4%)	0	100	100
1	b	250/560 (45%)	239 (96%)	11 (4%)	0	100	100
1	c	300/560 (54%)	286 (95%)	14 (5%)	0	100	100
1	d	250/560 (45%)	242 (97%)	8 (3%)	0	100	100
1	e	250/560 (45%)	241 (96%)	9 (4%)	0	100	100
1	f	300/560 (54%)	284 (95%)	16 (5%)	0	100	100
1	g	250/560 (45%)	239 (96%)	11 (4%)	0	100	100
All	All	8800/18480 (48%)	8402 (96%)	398 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	223/467 (48%)	221 (99%)	2 (1%)	75	88
1	B	260/467 (56%)	258 (99%)	2 (1%)	79	89
1	C	223/467 (48%)	223 (100%)	0	100	100
1	D	223/467 (48%)	220 (99%)	3 (1%)	65	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	F	223/467 (48%)	222 (100%)	1 (0%)	89	94
1	G	222/467 (48%)	221 (100%)	1 (0%)	86	92
1	H	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	I	223/467 (48%)	223 (100%)	0	100	100
1	J	223/467 (48%)	220 (99%)	3 (1%)	65	82
1	K	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	L	223/467 (48%)	223 (100%)	0	100	100
1	M	223/467 (48%)	220 (99%)	3 (1%)	65	82
1	N	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	O	223/467 (48%)	223 (100%)	0	100	100
1	P	222/467 (48%)	220 (99%)	2 (1%)	75	88
1	Q	260/467 (56%)	258 (99%)	2 (1%)	79	89
1	R	223/467 (48%)	223 (100%)	0	100	100
1	S	223/467 (48%)	221 (99%)	2 (1%)	75	88
1	T	260/467 (56%)	258 (99%)	2 (1%)	79	89
1	U	223/467 (48%)	223 (100%)	0	100	100
1	V	223/467 (48%)	221 (99%)	2 (1%)	75	88
1	W	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	X	223/467 (48%)	223 (100%)	0	100	100
1	Y	223/467 (48%)	221 (99%)	2 (1%)	75	88
1	Z	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	a	223/467 (48%)	223 (100%)	0	100	100
1	b	223/467 (48%)	221 (99%)	2 (1%)	75	88
1	c	260/467 (56%)	259 (100%)	1 (0%)	89	94
1	d	223/467 (48%)	223 (100%)	0	100	100
1	e	223/467 (48%)	220 (99%)	3 (1%)	65	82
1	f	260/467 (56%)	258 (99%)	2 (1%)	79	89
1	g	223/467 (48%)	223 (100%)	0	100	100
All	All	7764/15411 (50%)	7723 (100%)	41 (0%)	85	92

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	V	236	LYS
1	c	236	LYS
1	W	236	LYS
1	Z	236	LYS
1	e	236	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	133	GLN
1	Q	103	GLN
1	Z	196	HIS
1	Y	133	GLN
1	Z	103	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

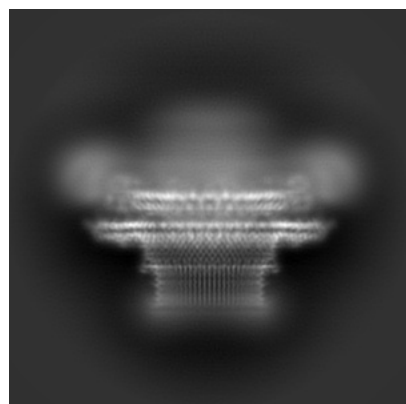
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60007. These allow visual inspection of the internal detail of the map and identification of artifacts.

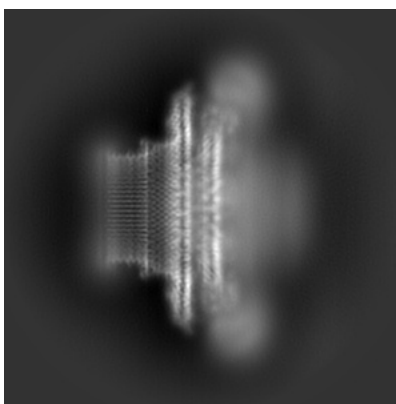
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

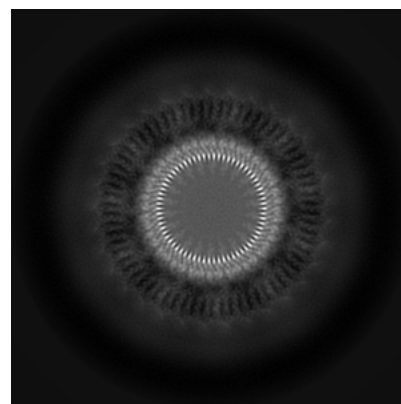
#### 6.1.1 Primary map



X

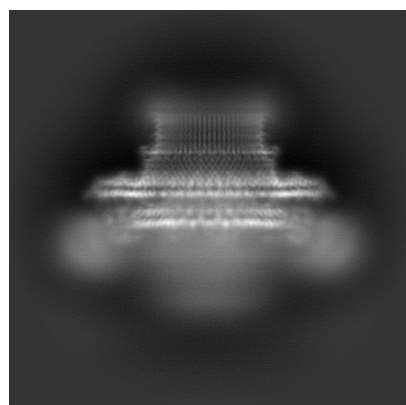


Y

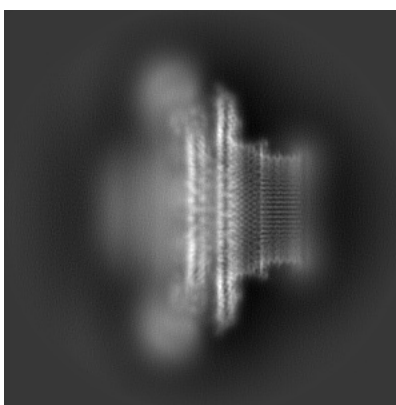


Z

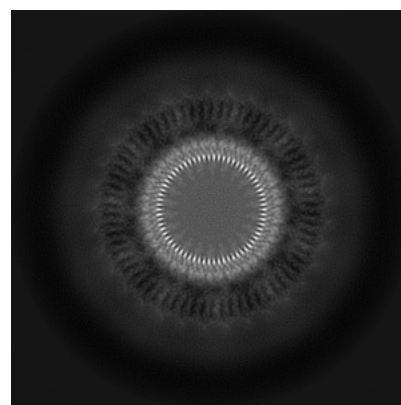
#### 6.1.2 Raw map



X



Y

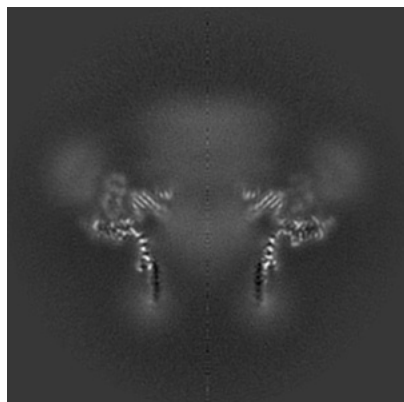


Z

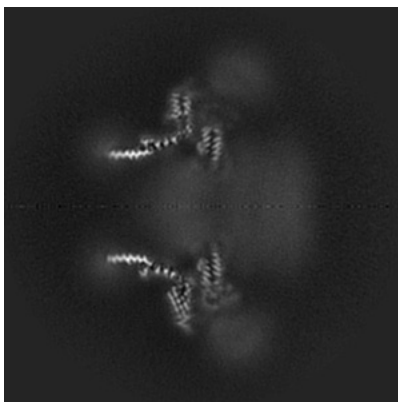
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

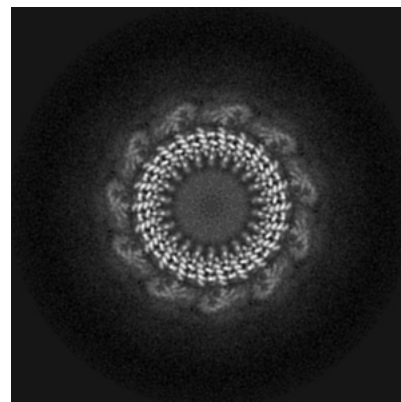
### 6.2.1 Primary map



X Index: 200

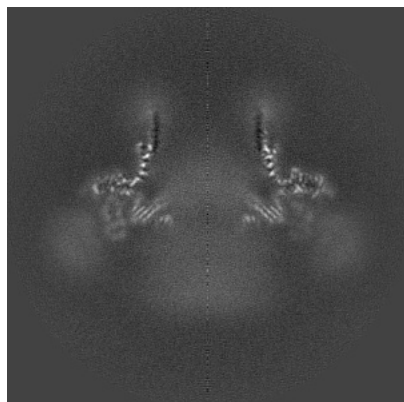


Y Index: 200

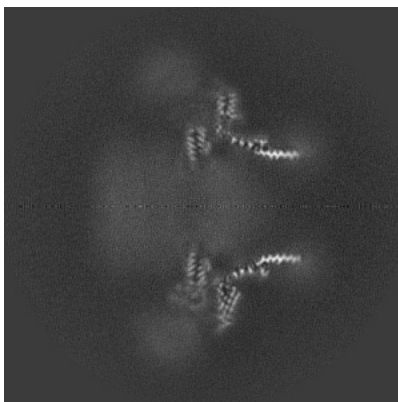


Z Index: 200

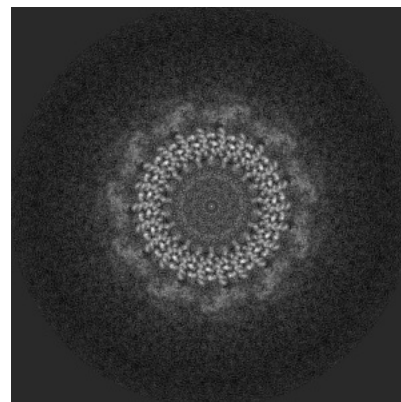
### 6.2.2 Raw map



X Index: 200



Y Index: 200

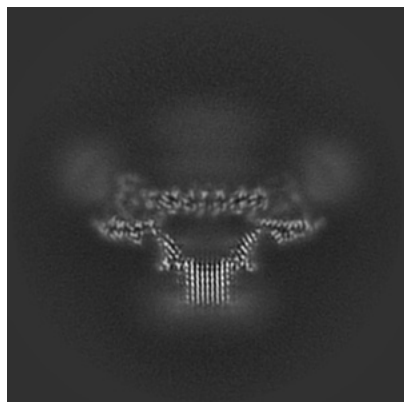


Z Index: 200

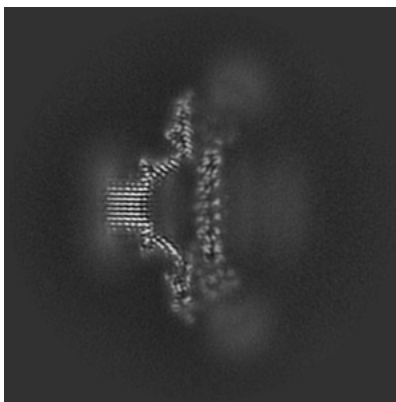
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

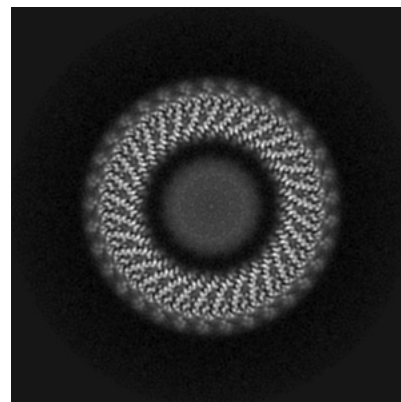
### 6.3.1 Primary map



X Index: 149

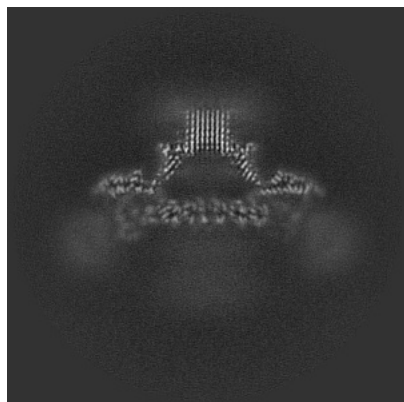


Y Index: 251

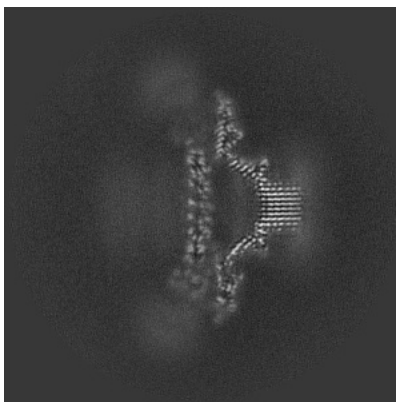


Z Index: 183

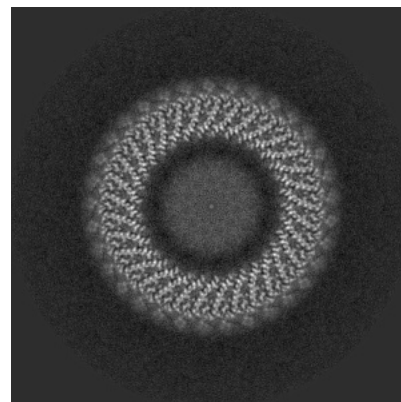
### 6.3.2 Raw map



X Index: 149



Y Index: 251

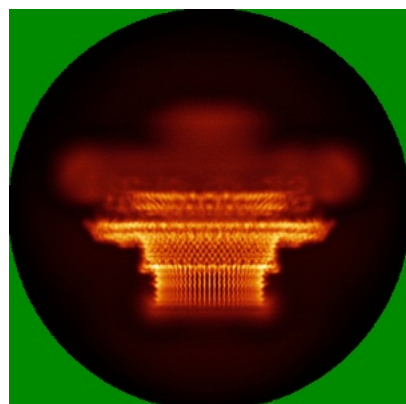


Z Index: 216

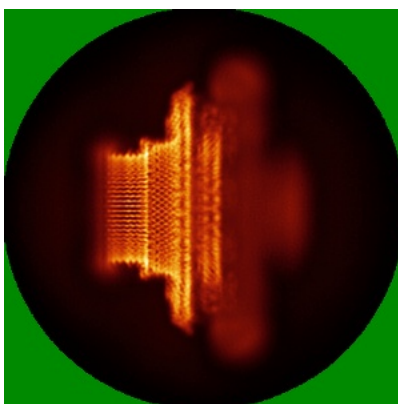
The images above show the largest variance slices of the map in three orthogonal directions.

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

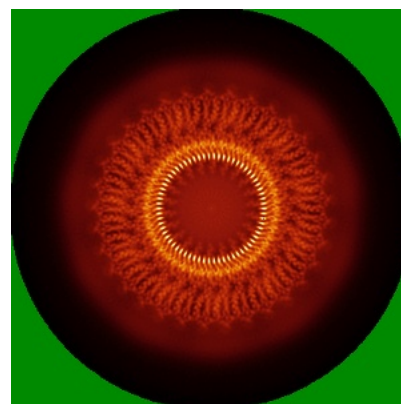
### 6.4.1 Primary map



X

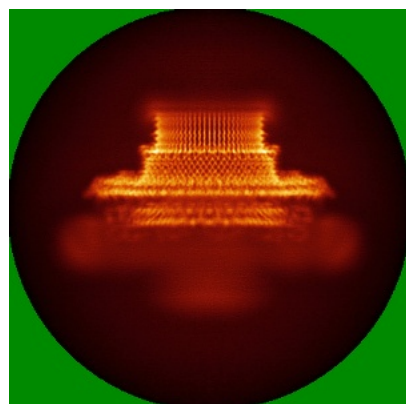


Y

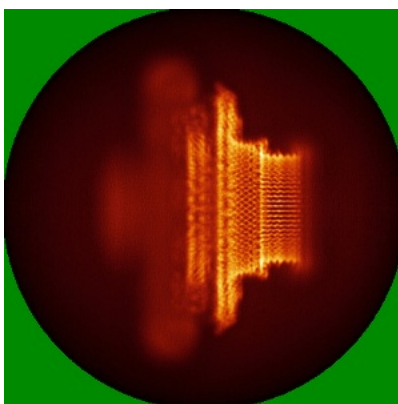


Z

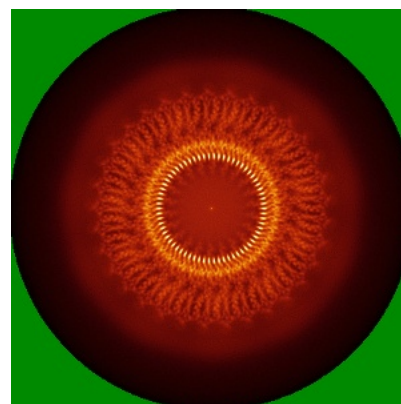
### 6.4.2 Raw map



X



Y



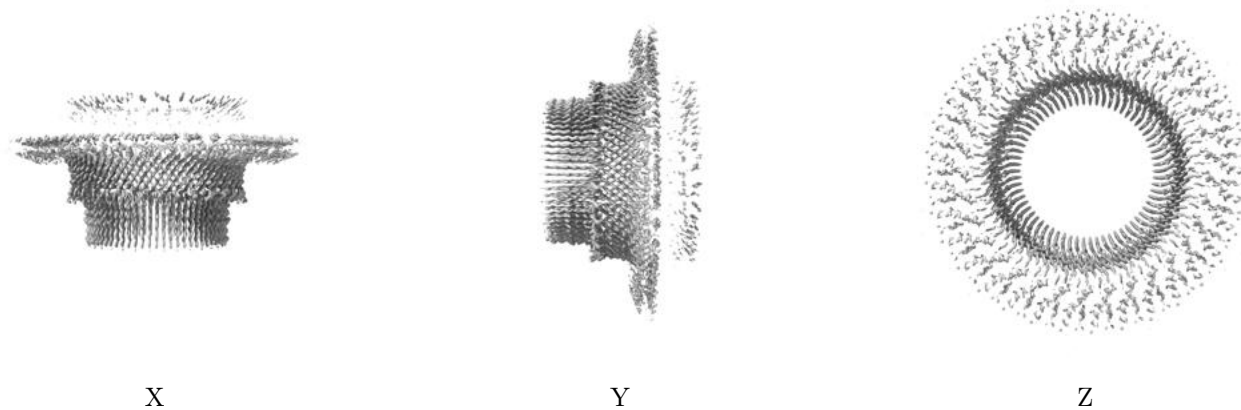
Z

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.



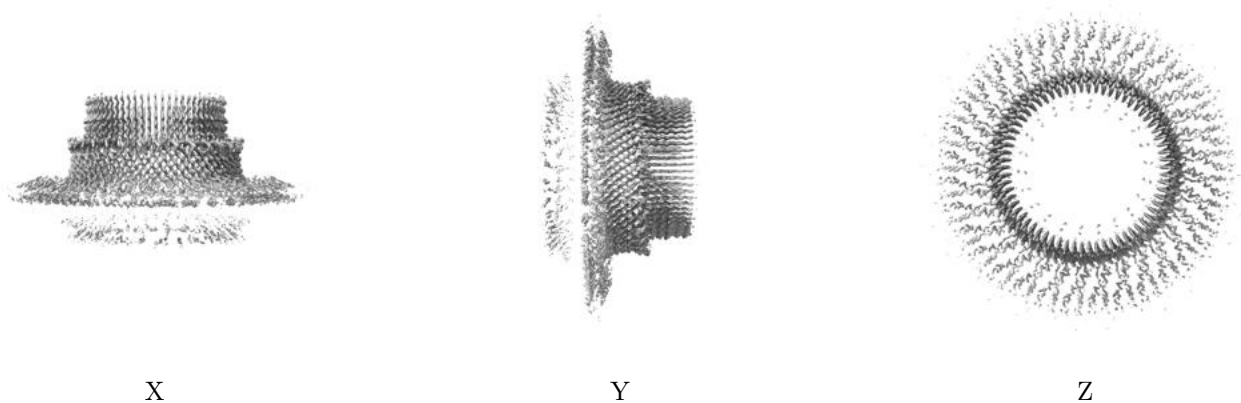
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. 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.

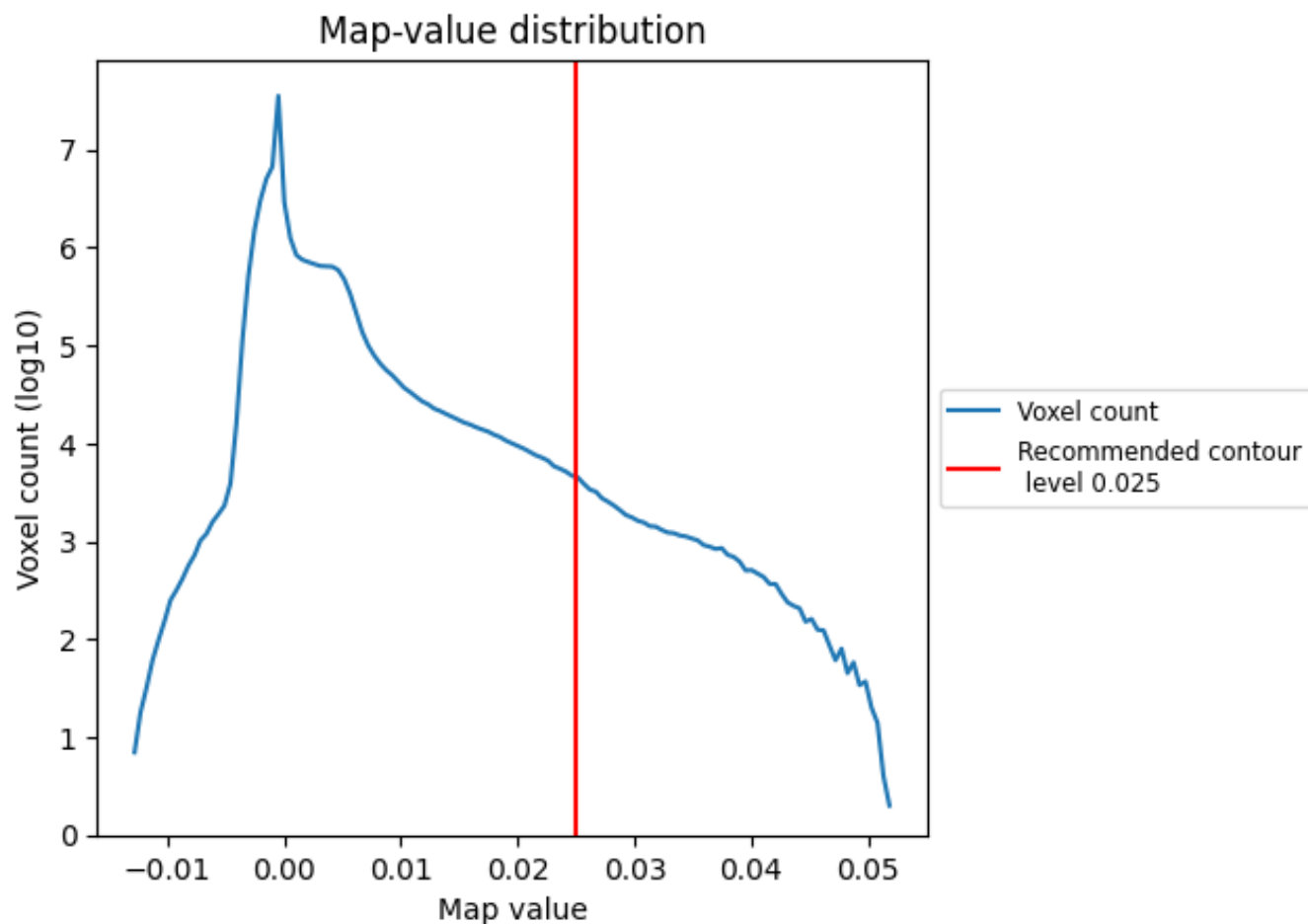
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

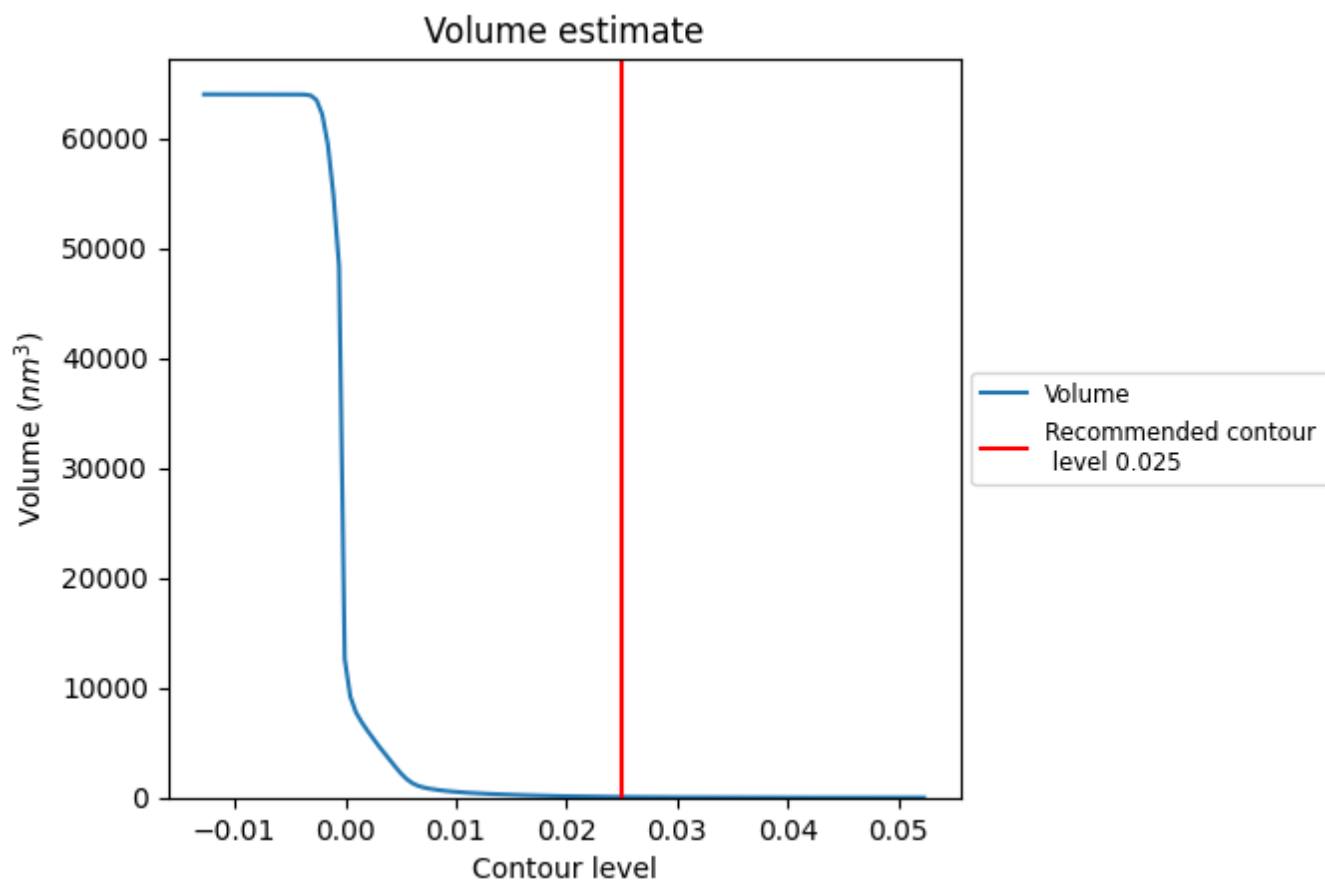
### 7.1 Map-value distribution [i](#)



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.



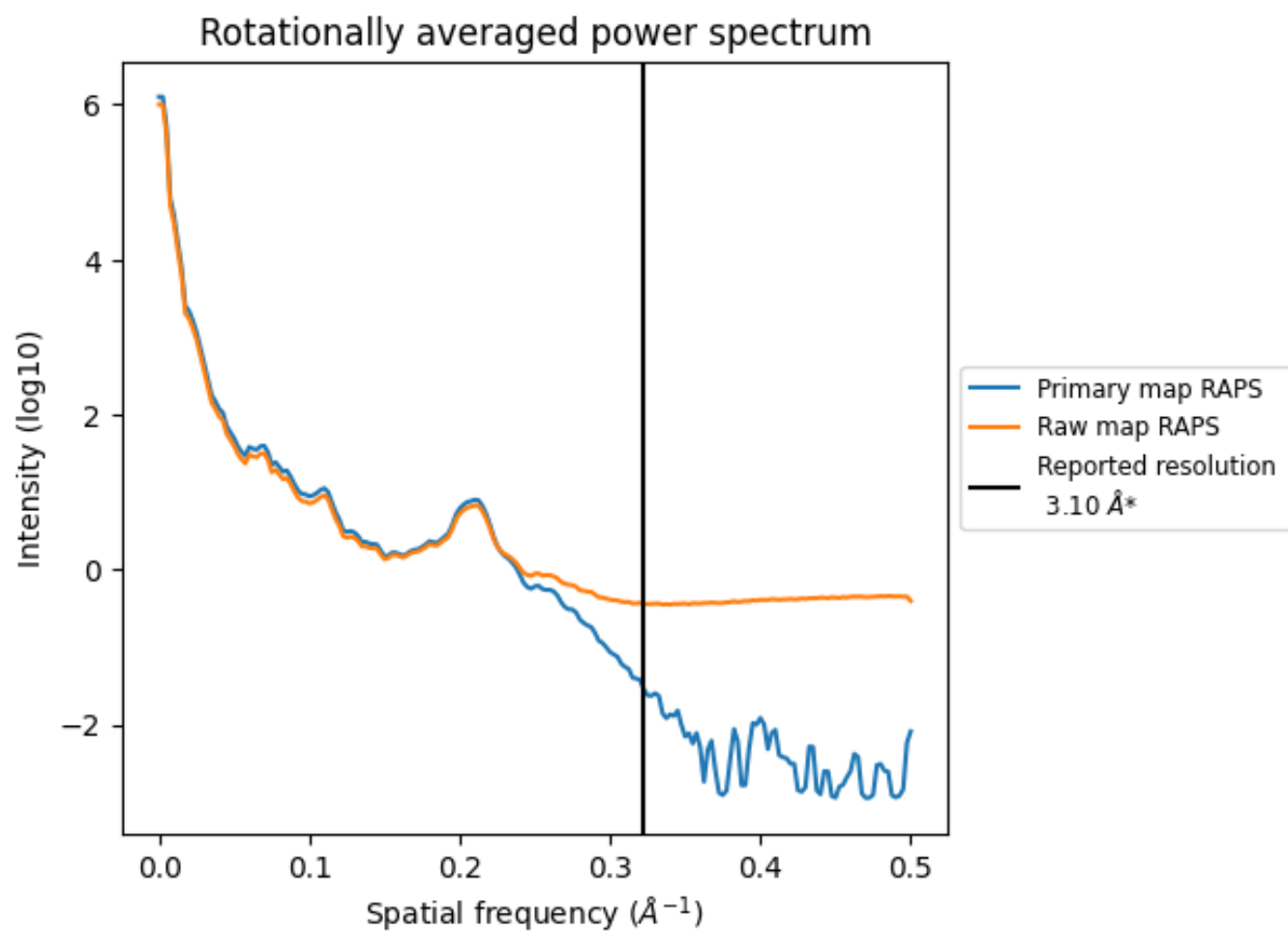
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm<sup>3</sup>; this corresponds to an approximate mass of 49 kDa.

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

### 7.3 Rotationally averaged power spectrum [i](#)

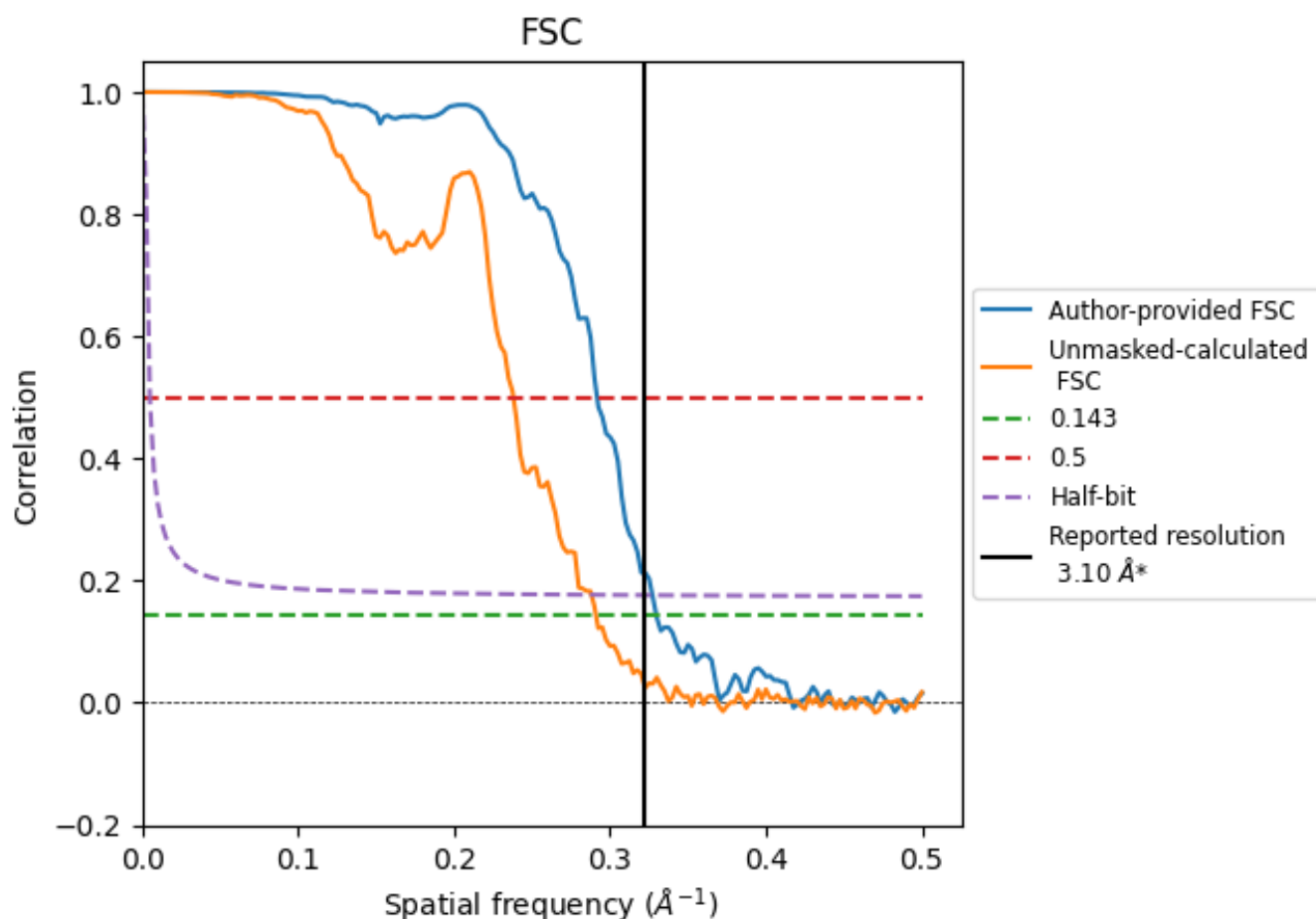


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 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 0.323  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

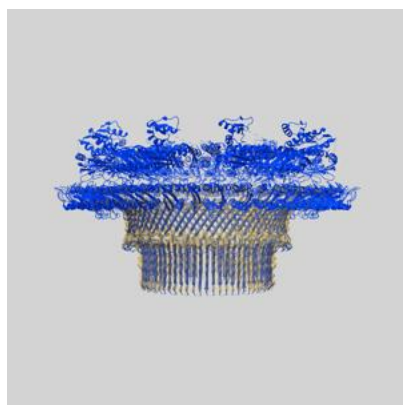
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.03	3.43	3.06
Unmasked-calculated*	3.44	4.20	3.47

\*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 3.44 differs from the reported value 3.1 by more than 10 %

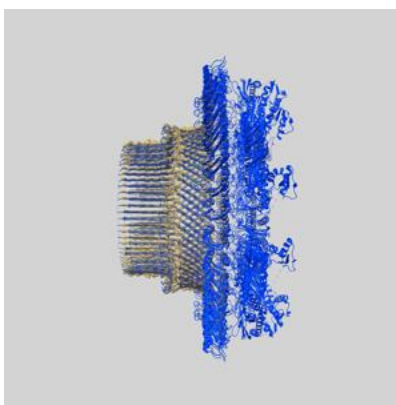
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60007 and PDB model 8ZDS. Per-residue inclusion information can be found in section [3](#) on page [6](#).

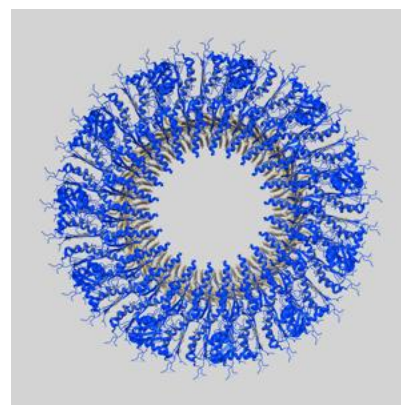
### 9.1 Map-model overlay [i](#)



X



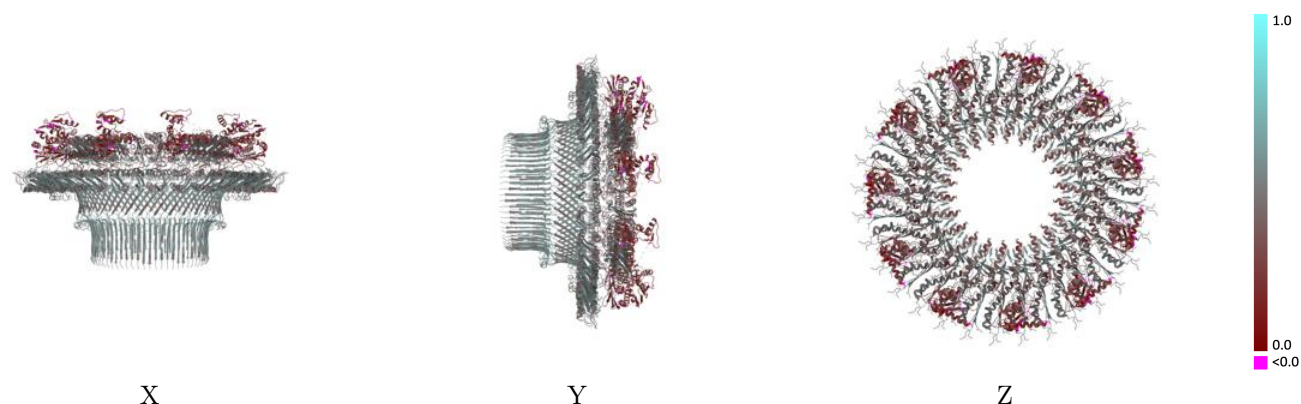
Y



Z

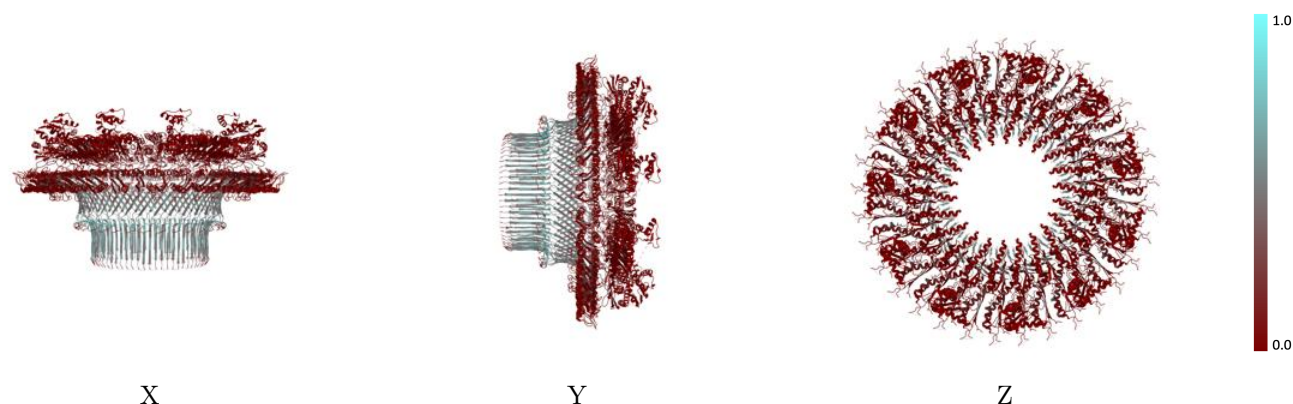
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



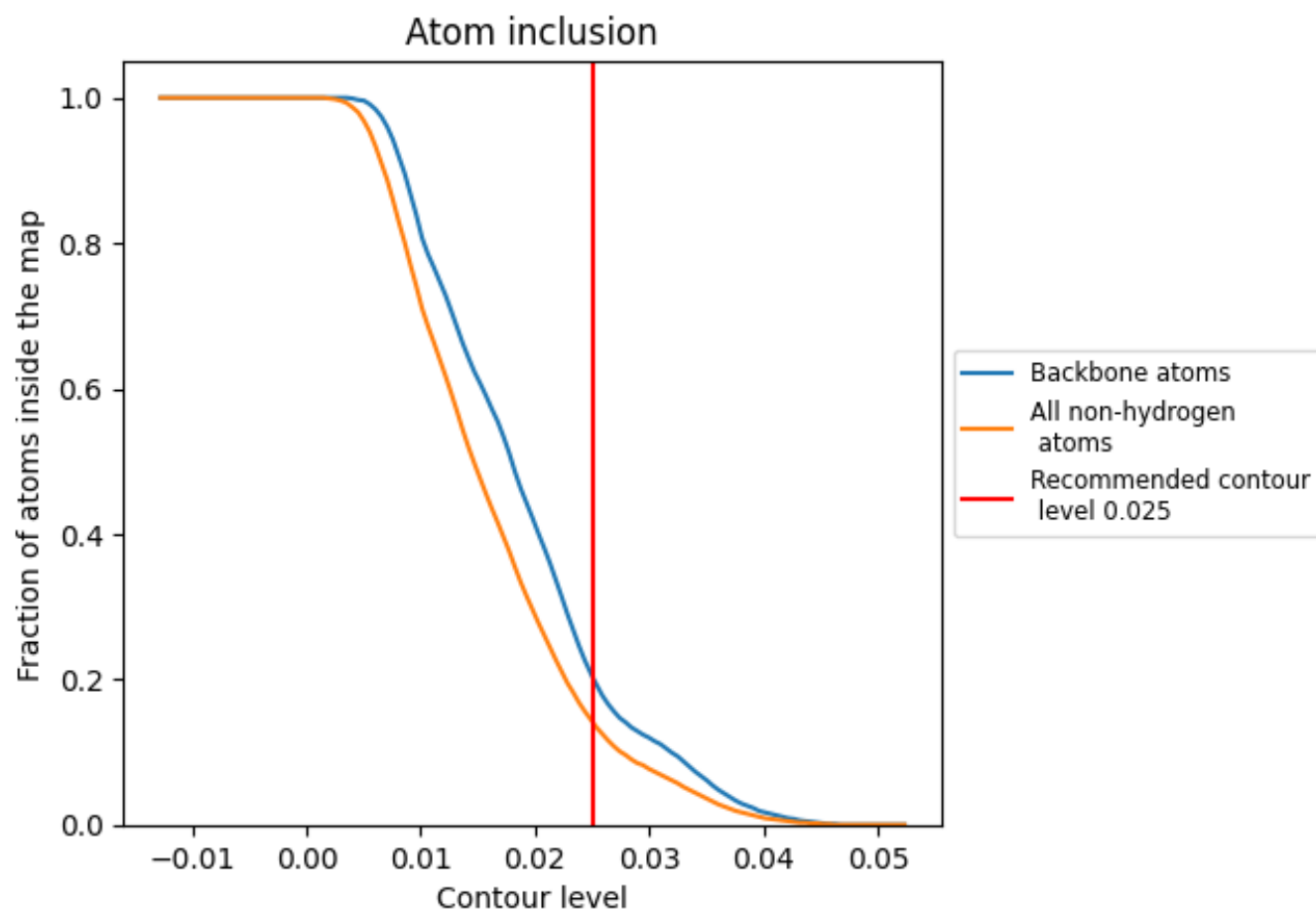
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).





































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 20% of all backbone atoms, 14% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.1420	 0.4300
A	 0.1580	 0.4660
B	 0.1260	 0.3720
C	 0.1510	 0.4630
D	 0.1510	 0.4650
E	 0.1260	 0.3710
F	 0.1500	 0.4640
G	 0.1500	 0.4650
H	 0.1260	 0.3720
I	 0.1540	 0.4610
J	 0.1570	 0.4670
K	 0.1270	 0.3710
L	 0.1520	 0.4620
M	 0.1510	 0.4630
N	 0.1260	 0.3720
O	 0.1530	 0.4620
P	 0.1540	 0.4660
Q	 0.1240	 0.3750
R	 0.1510	 0.4640
S	 0.1490	 0.4670
T	 0.1230	 0.3760
U	 0.1460	 0.4630
V	 0.1490	 0.4660
W	 0.1240	 0.3780
X	 0.1500	 0.4650
Y	 0.1490	 0.4660
Z	 0.1240	 0.3730
a	 0.1520	 0.4630
b	 0.1530	 0.4670
c	 0.1260	 0.3750
d	 0.1530	 0.4640
e	 0.1520	 0.4650
f	 0.1240	 0.3720
g	 0.1540	 0.4640

