



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 02:14 AM UTC

PDB ID : 9U4R / pdb_00009u4r
EMDB ID : EMD-63853
Title : Structure of the intial complex in filament assembly at 3.23 angstroms resolution, conformation 2.
Authors : Chen, L.X.; Jiang, W.X.; Cheng, X.Q.; Dong, X.; Xing, Q.
Deposited on : 2025-03-20
Resolution : 3.23 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

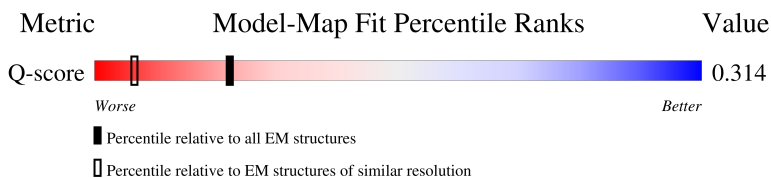
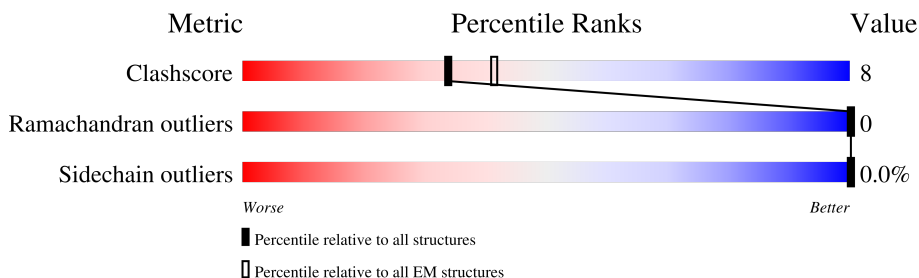
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.23 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	AA	467	<div> <div>52%</div> <div>72%</div> <div>25%</div> <div>.</div> </div>
1	AB	467	<div> <div>45%</div> <div>68%</div> <div>21%</div> <div>11%</div> </div>
1	AD	467	<div> <div>43%</div> <div>64%</div> <div>30%</div> <div>. 5%</div> </div>
1	AE	467	<div> <div>41%</div> <div>67%</div> <div>27%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
2	AC	467	
3	BA	317	
3	BB	317	
3	BC	317	
3	BD	317	
3	BE	317	
3	BG	317	
3	BH	317	
3	BI	317	
3	BJ	317	
3	BK	317	
3	BL	317	
3	BM	317	
3	BN	317	
4	CA	553	
4	CB	553	
4	CC	553	
4	CD	553	
4	CE	553	
4	CF	553	
4	CG	553	
4	CH	553	
4	CI	553	
4	CJ	553	
4	CK	553	



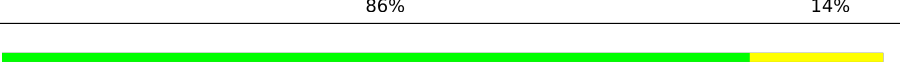
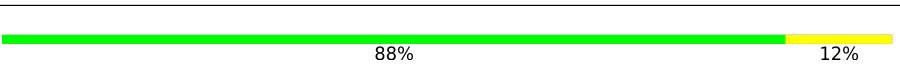


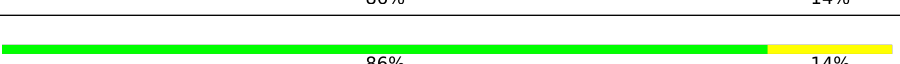

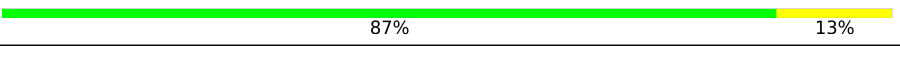




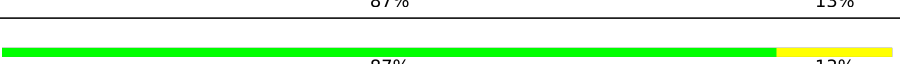





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Mol	Chain	Length	Quality of chain
5	DA	403	 6% 80% 20%
5	DB	403	 1% 79% 20%
5	DC	403	 0% 79% 21%
5	DD	403	 0% 77% 22%
5	DE	403	 0% 83% 17%
5	DF	403	 0% 85% 15%
5	DG	403	 0% 84% 16%
5	DH	403	 0% 86% 14%
5	DI	403	 1% 77% 23%
5	DJ	403	 0% 81% 19%
5	DK	403	 1% 80% 19%
5	EA	403	 0% 86% 13%
5	EB	403	 0% 79% 20%
5	EC	403	 0% 85% 15%
5	ED	403	 0% 80% 20%
5	EE	403	 0% 86% 14%
5	EF	403	 0% 87% 13%
5	EG	403	 0% 82% 18%
5	EH	403	 0% 89% 11%
5	EI	403	 0% 83% 17%
5	EJ	403	 0% 84% 15%
5	EK	403	 0% 86% 14%
5	FA	403	 0% 82% 18%
5	FB	403	 0% 84% 16%
5	FC	403	 0% 87% 13%

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Mol	Chain	Length	Quality of chain
5	FD	403	
5	FE	403	
5	FF	403	
5	FG	403	
5	FH	403	
5	FI	403	
5	FJ	403	
5	FK	403	
5	GA	403	
5	GB	403	
5	GC	403	
5	GD	403	
5	GE	403	
5	GF	403	
5	GG	403	
5	GH	403	
5	GI	403	
5	GJ	403	
5	GK	403	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 219113 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 hook-associated protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	452	Total	C	N	O	S	0	0
			3380	2082	570	722	6		
1	AB	417	Total	C	N	O	S	0	0
			3112	1917	524	666	5		
1	AD	442	Total	C	N	O	S	0	0
			3305	2035	557	707	6		
1	AE	438	Total	C	N	O	S	0	0
			3278	2018	553	701	6		

- Molecule 2 is a protein called Flagellar hook-associated protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AC	447	Total	C	N	O	S	0	0
			3349	2063	565	715	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	47	PHE	TYR	conflict	UNP P16328

- Molecule 3 is a protein called Flagellar hook-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BB	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BC	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BD	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BE	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	BG	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BH	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BI	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BJ	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BK	317	Total	C	N	O	S	0	0
			2391	1463	417	498	13		
3	BL	316	Total	C	N	O	S	0	0
			2384	1459	416	496	13		
3	BM	30	Total	C	N	O	S	0	0
			240	150	40	47	3		
3	BN	30	Total	C	N	O	S	0	0
			240	150	40	47	3		

- Molecule 4 is a protein called Flagellar hook-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CA	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CB	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CC	552	Total	C	N	O	S	0	0
			4149	2548	725	870	6		
4	CD	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CE	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CF	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CG	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CH	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CI	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CJ	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		
4	CK	553	Total	C	N	O	S	0	0
			4157	2553	726	871	7		

- Molecule 5 is a protein called Flagellar hook protein FlgE.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DA	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DB	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DC	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DD	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DE	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DF	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DG	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DH	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DI	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DJ	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	DK	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EA	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EB	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EC	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	ED	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EE	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EF	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EG	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EH	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EI	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	EJ	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	EK	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FA	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FB	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FC	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FD	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FE	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FF	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FG	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FH	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FI	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FJ	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	FK	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GA	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GB	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GC	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GD	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GE	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GF	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GG	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GH	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GI	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		

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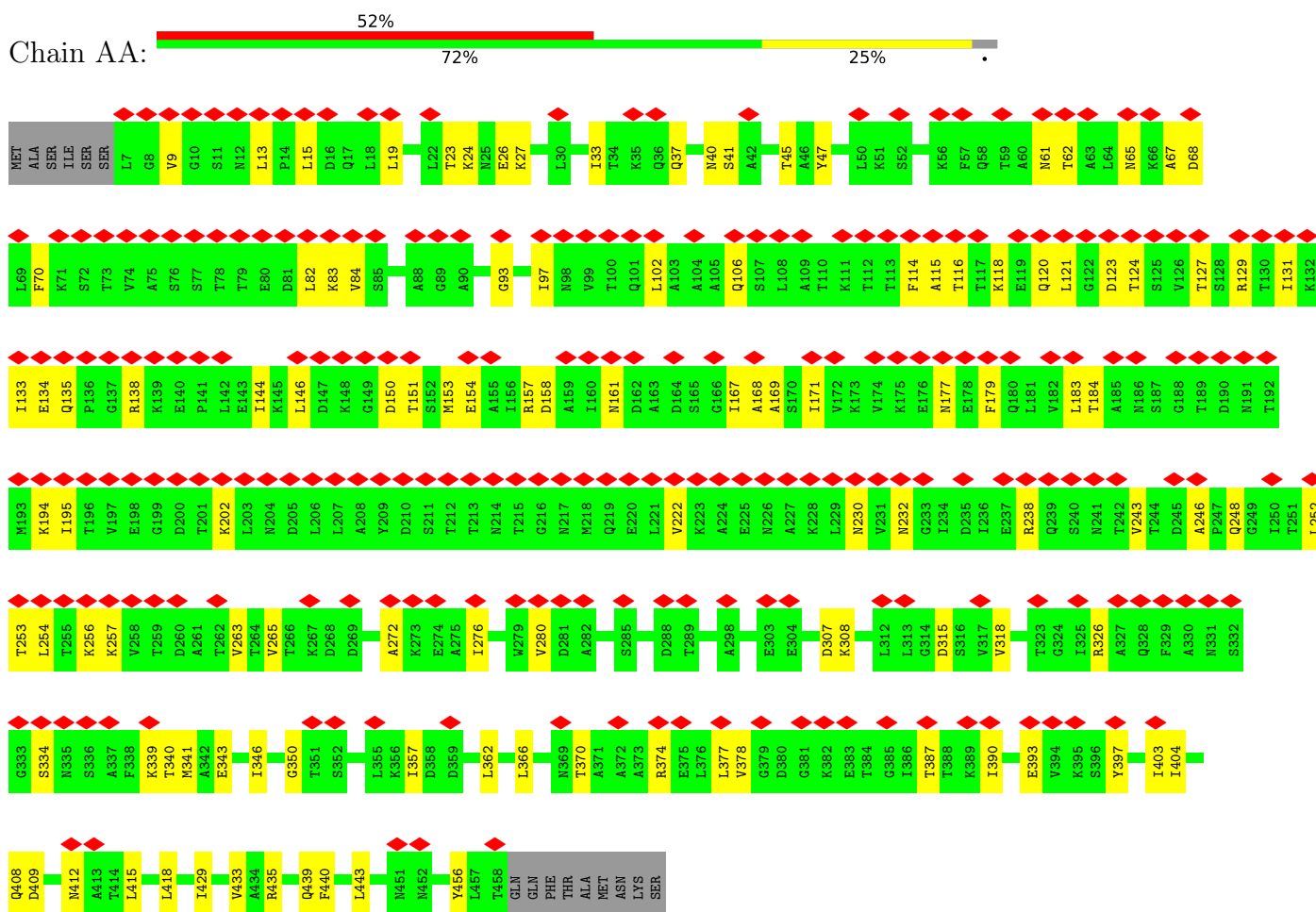
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Mol	Chain	Residues	Atoms					AltConf	Trace
5	GJ	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		
5	GK	402	Total	C	N	O	S	0	0
			2959	1820	511	620	8		

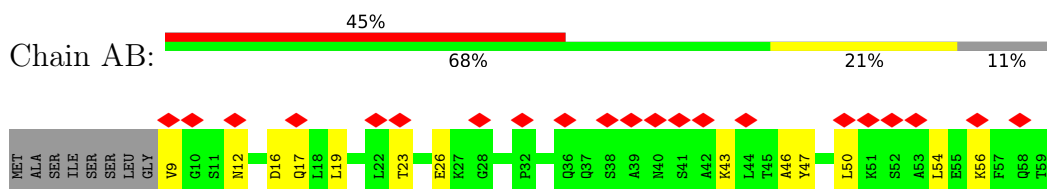
3 Residue-property plots

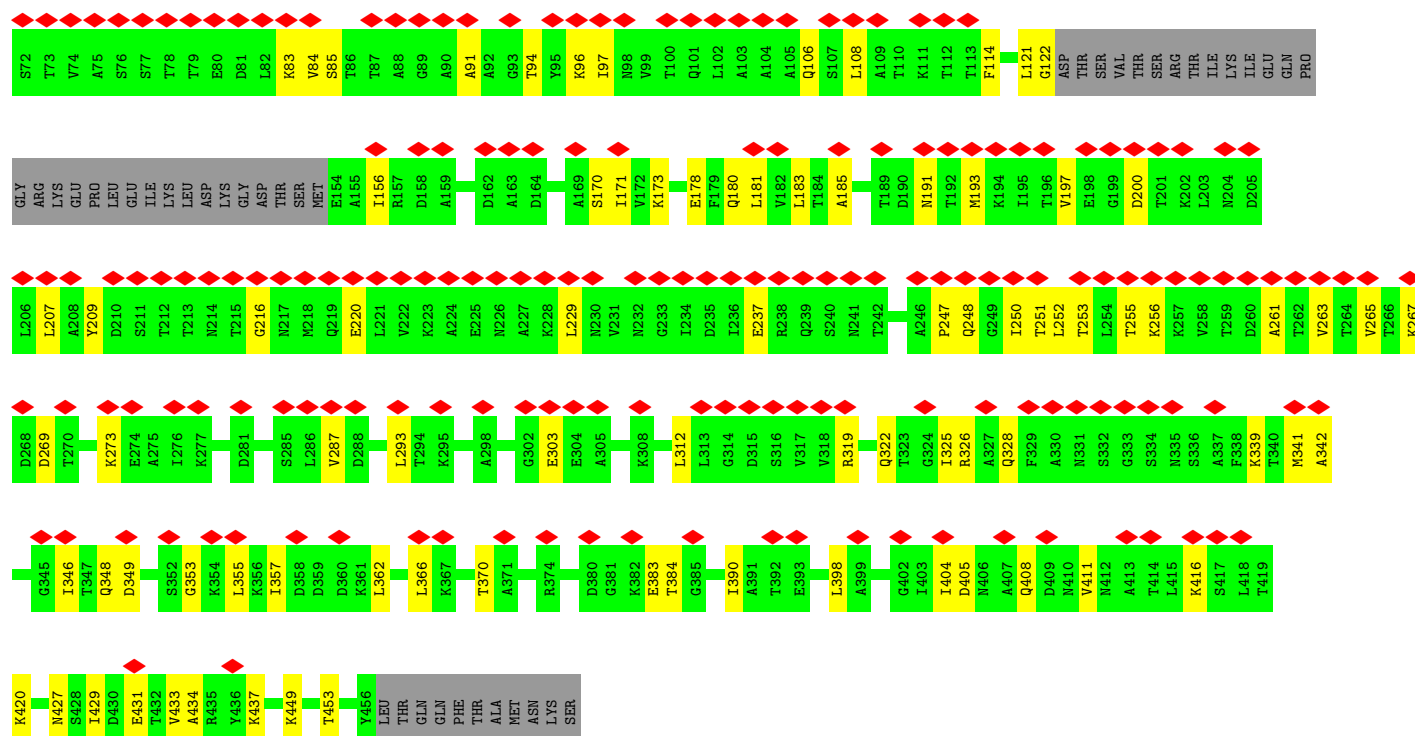
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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 hook-associated protein 2

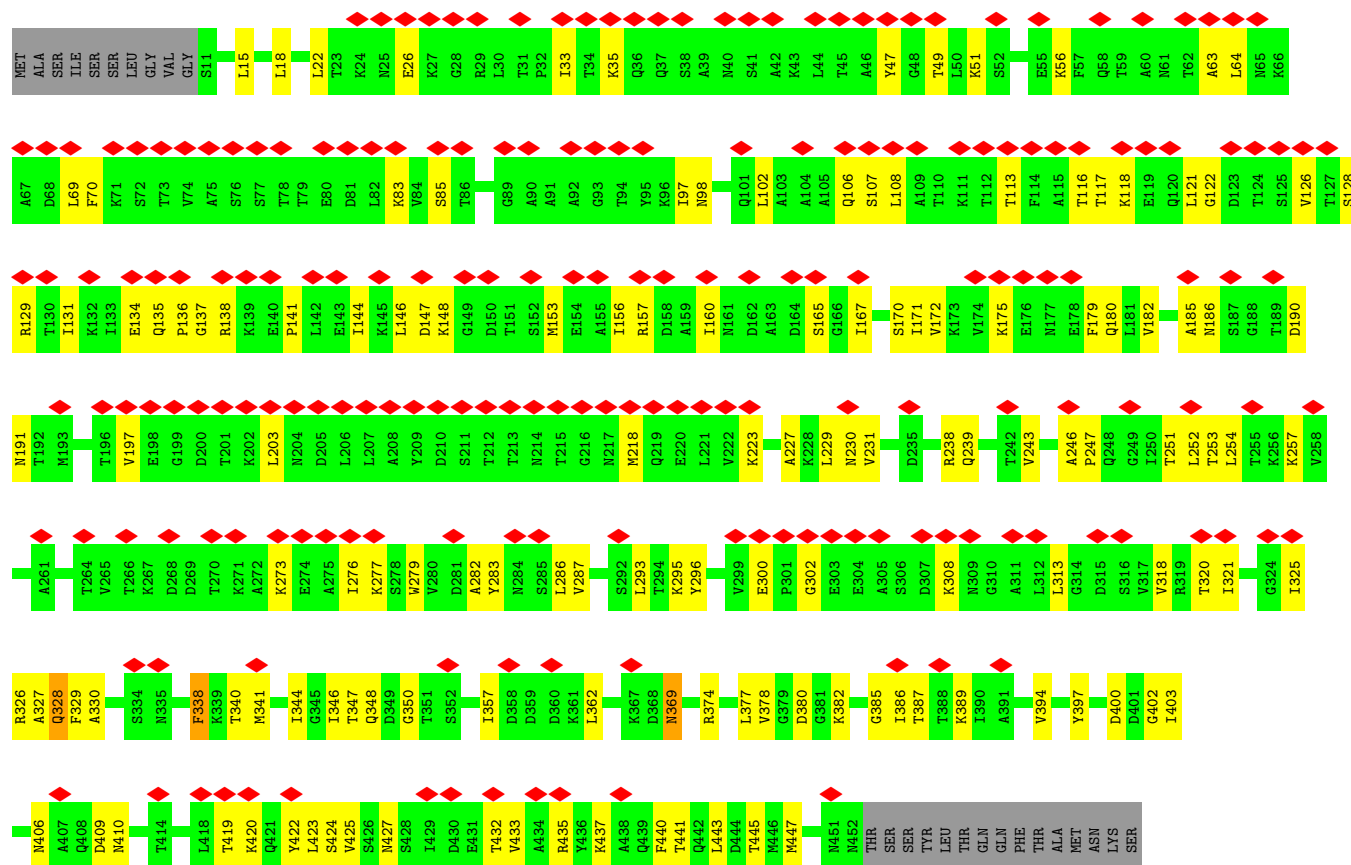
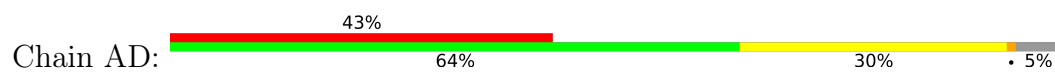


• Molecule 1: Flagellar hook-associated protein 2

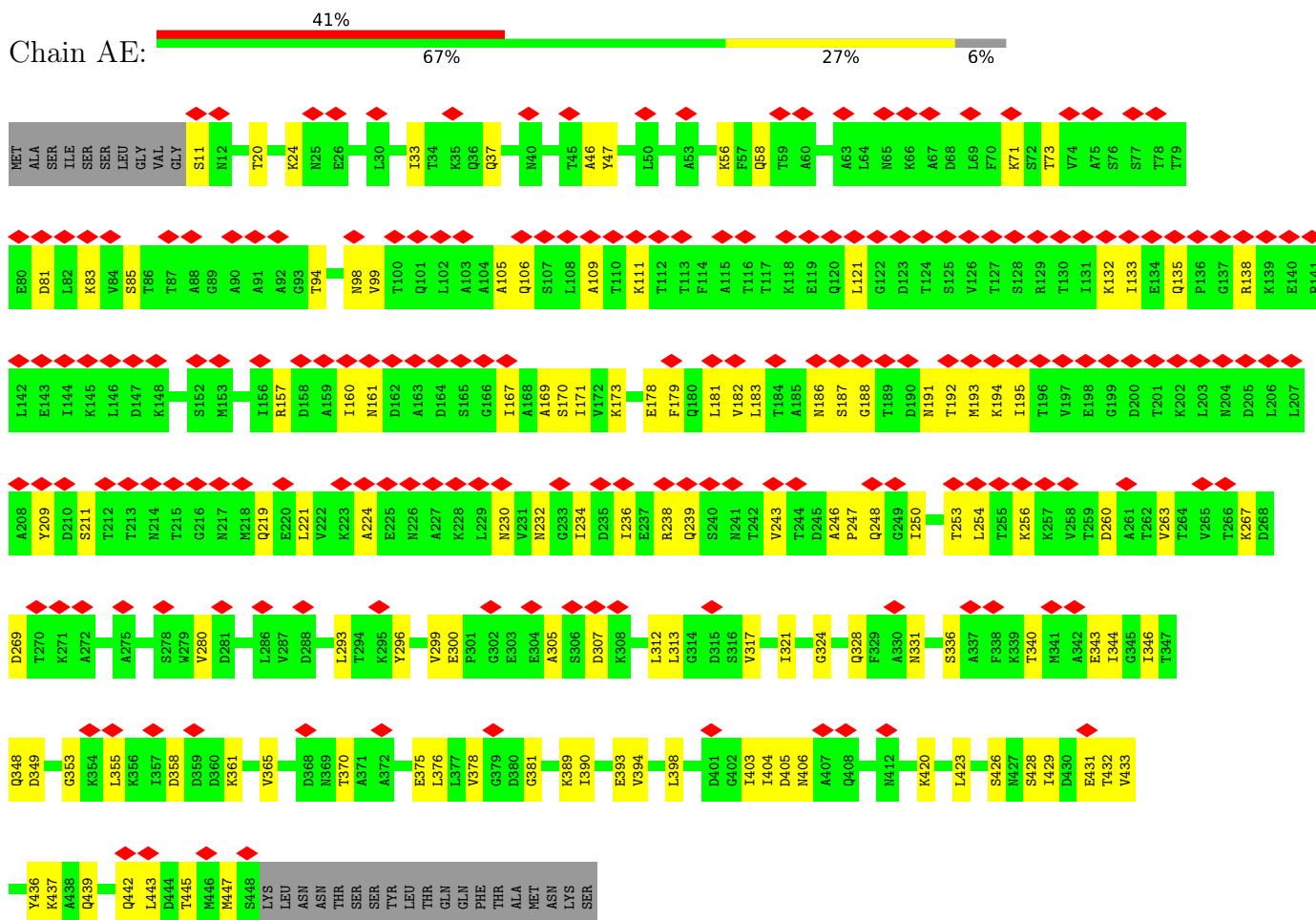




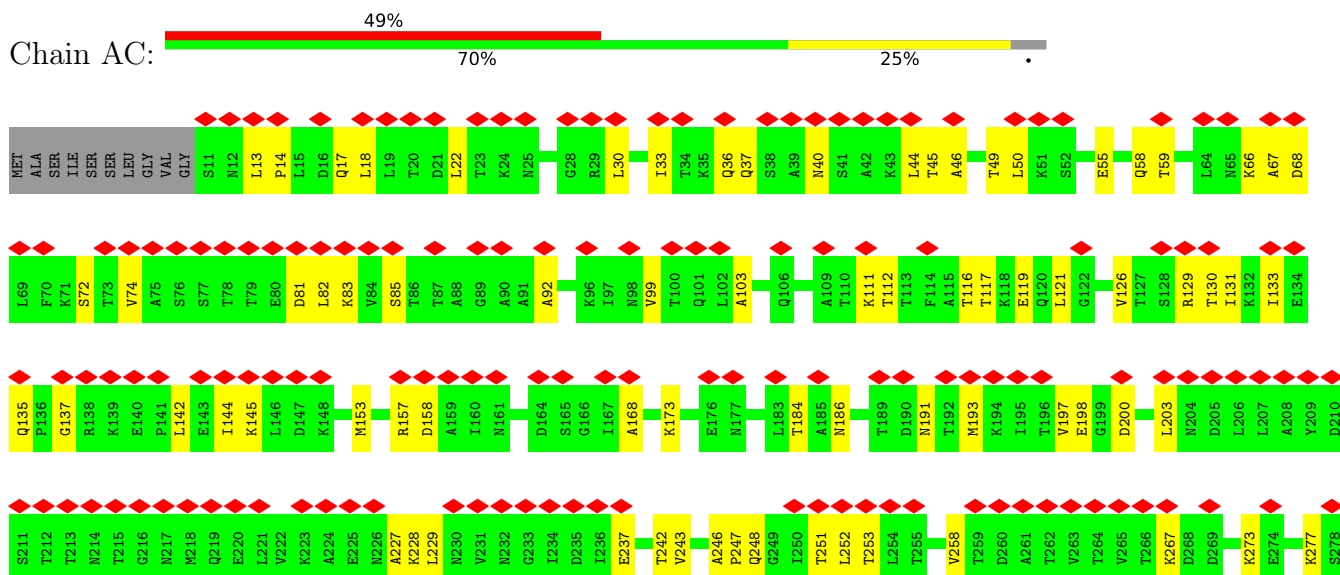
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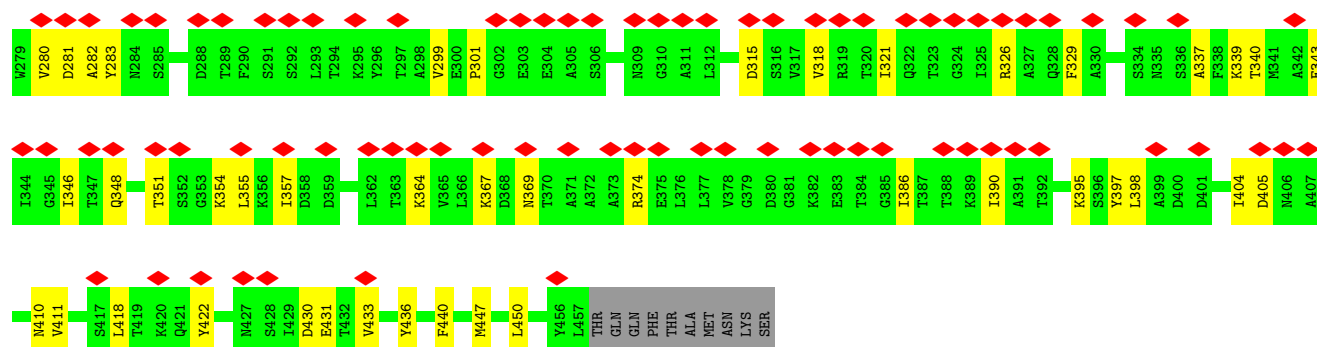


- Molecule 1: Flagellar hook-associated protein 2

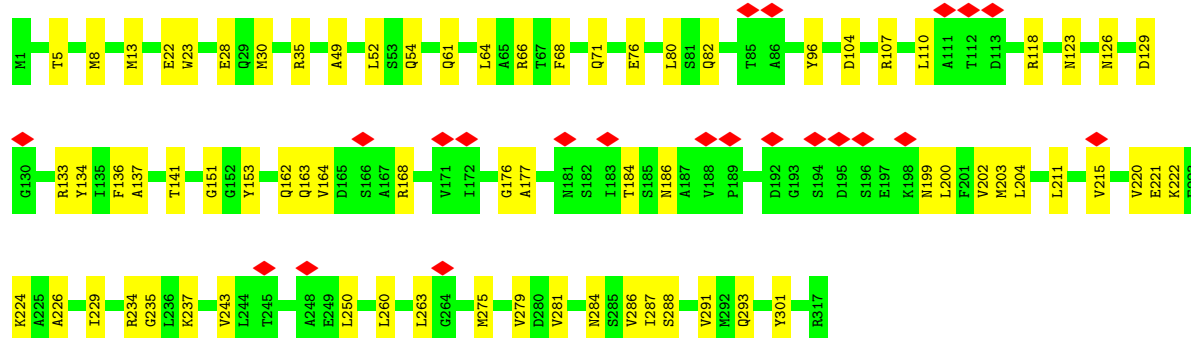
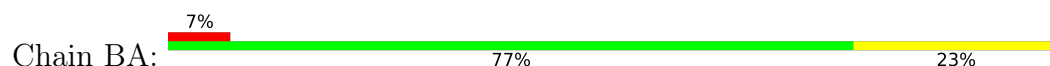


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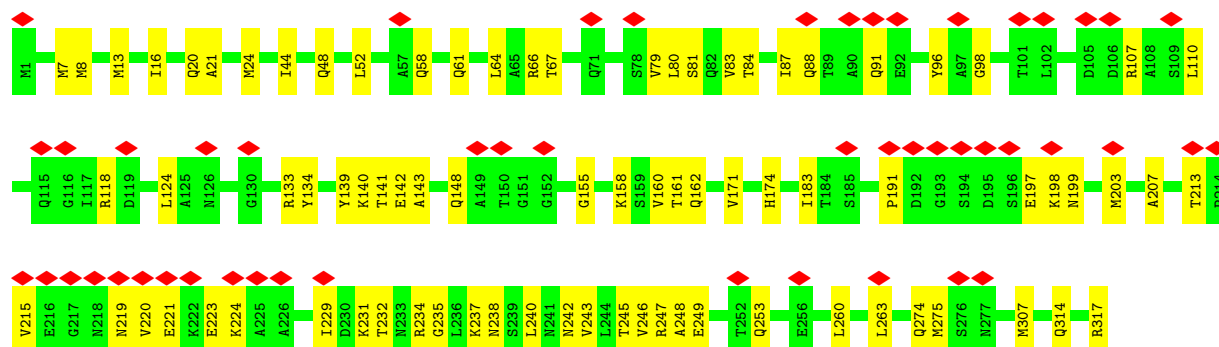
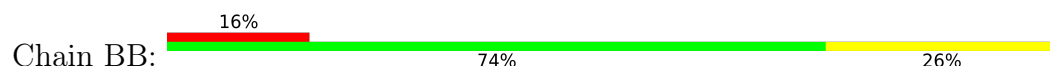




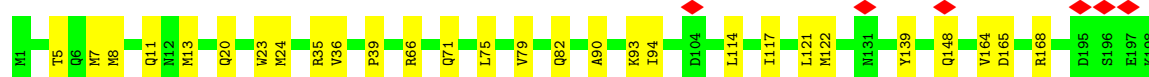
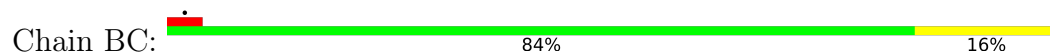
• Molecule 3: Flagellar hook-associated protein 3



• Molecule 3: Flagellar hook-associated protein 3

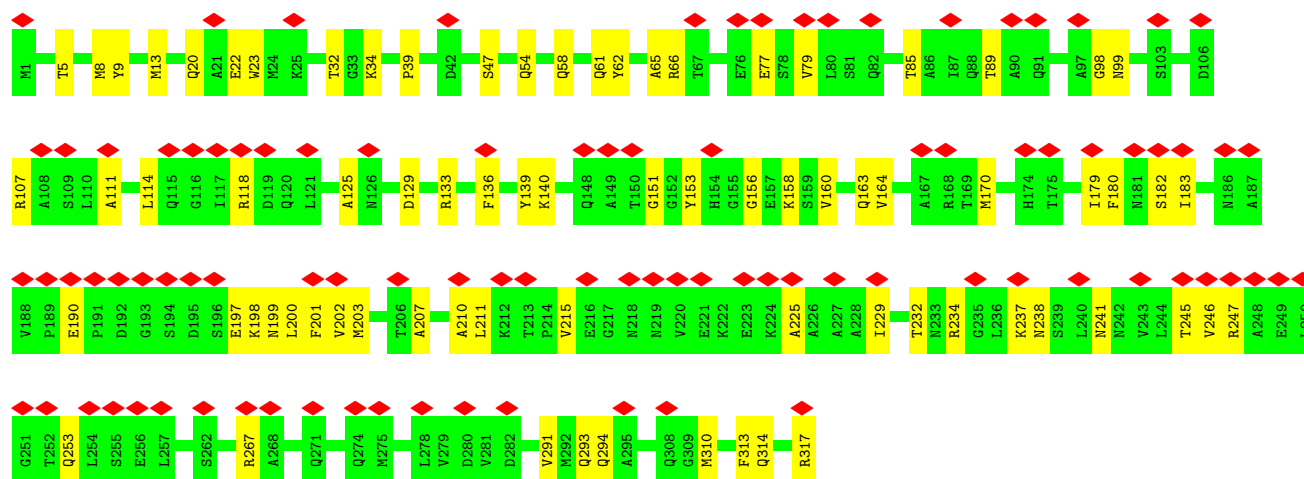
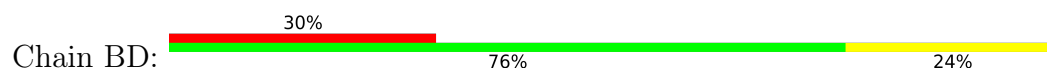


• Molecule 3: Flagellar hook-associated protein 3

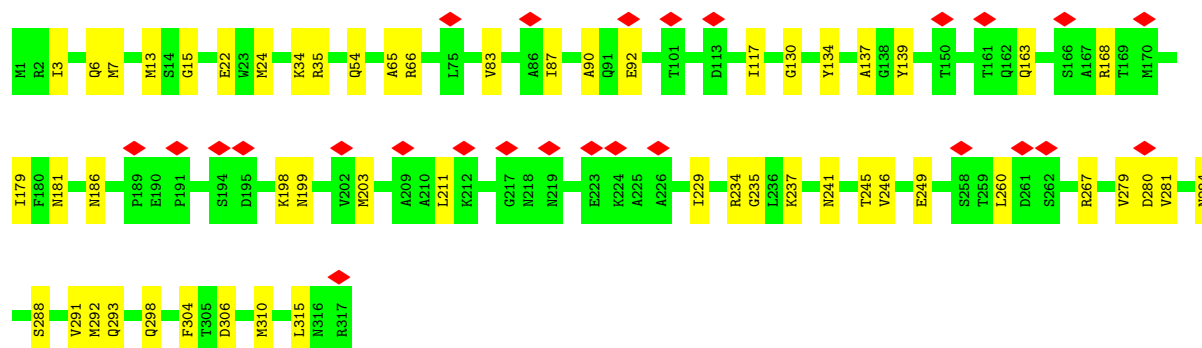
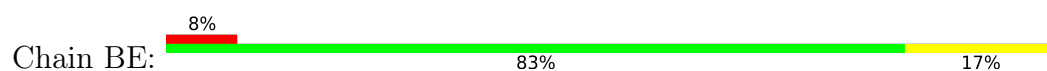




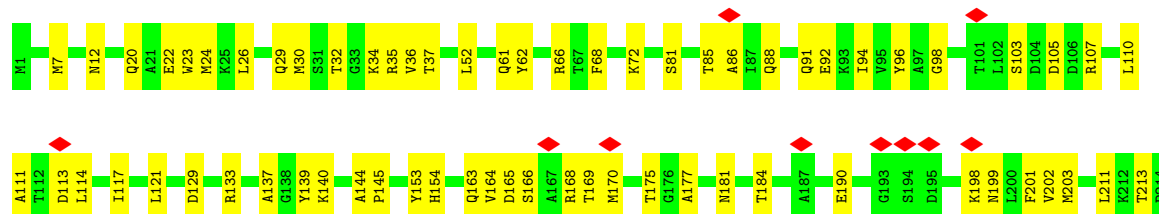
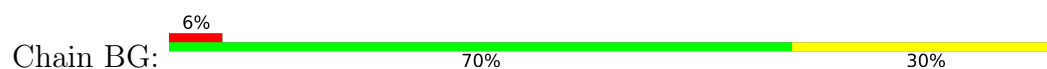
• Molecule 3: Flagellar hook-associated protein 3

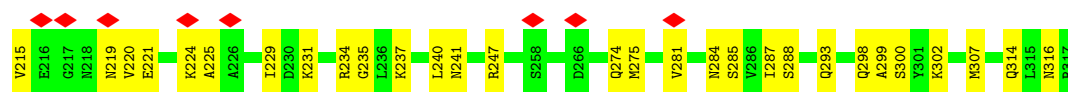


• Molecule 3: Flagellar hook-associated protein 3

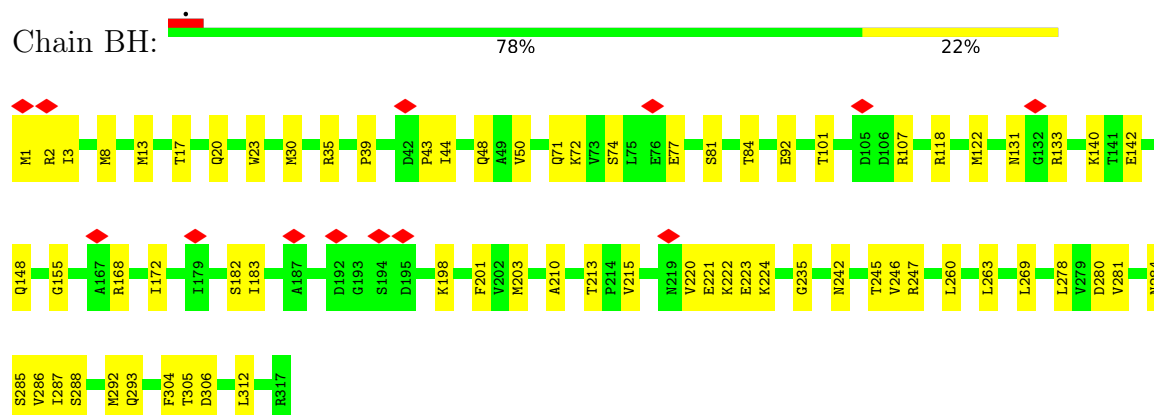


• Molecule 3: Flagellar hook-associated protein 3

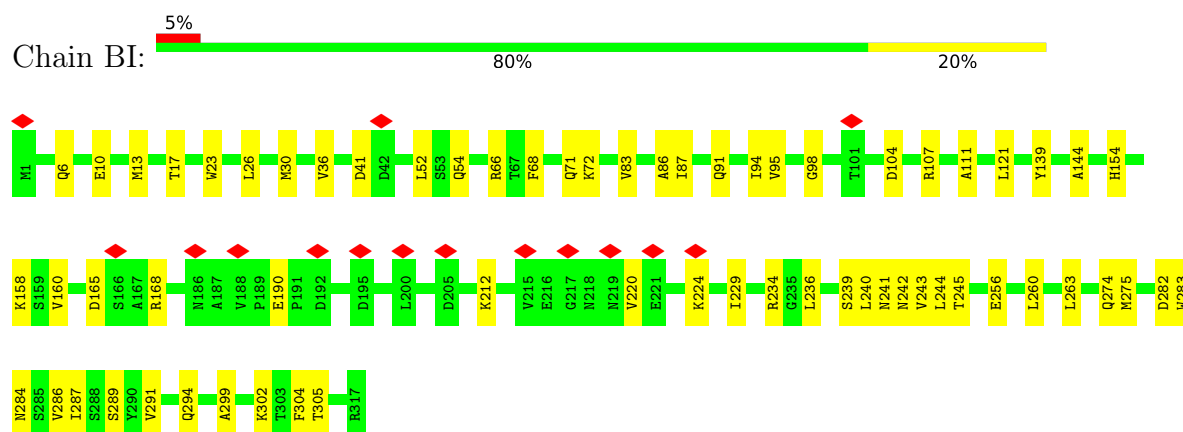




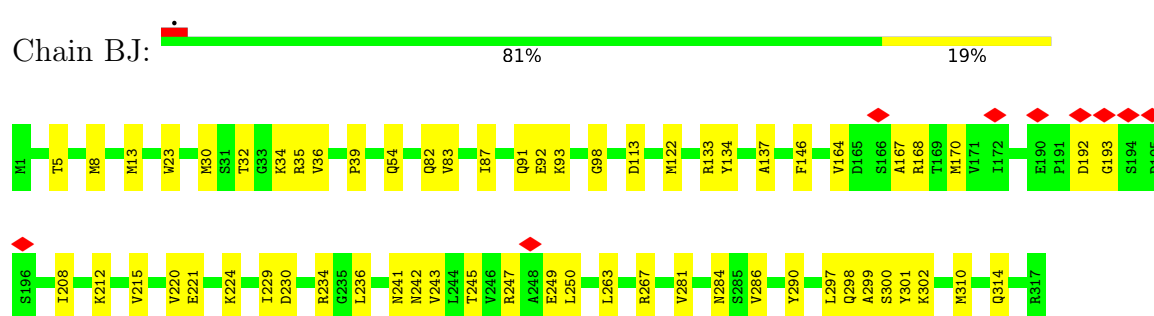
• Molecule 3: Flagellar hook-associated protein 3



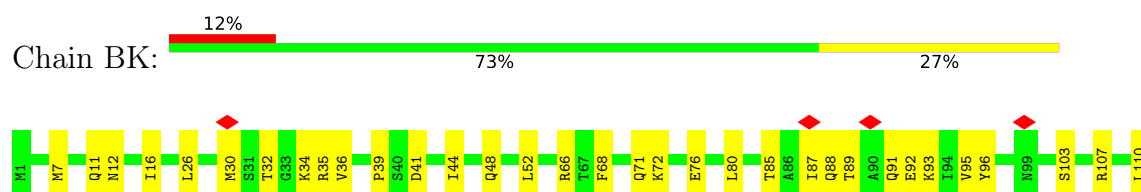
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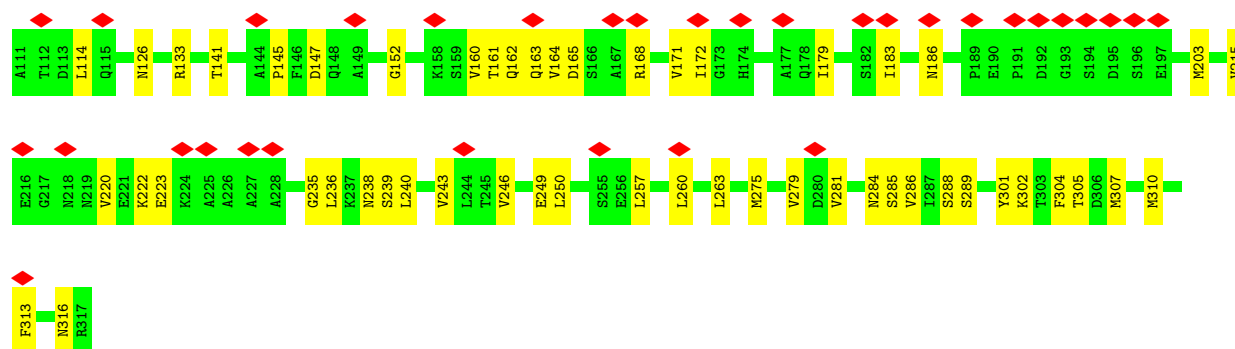


• Molecule 3: Flagellar hook-associated protein 3

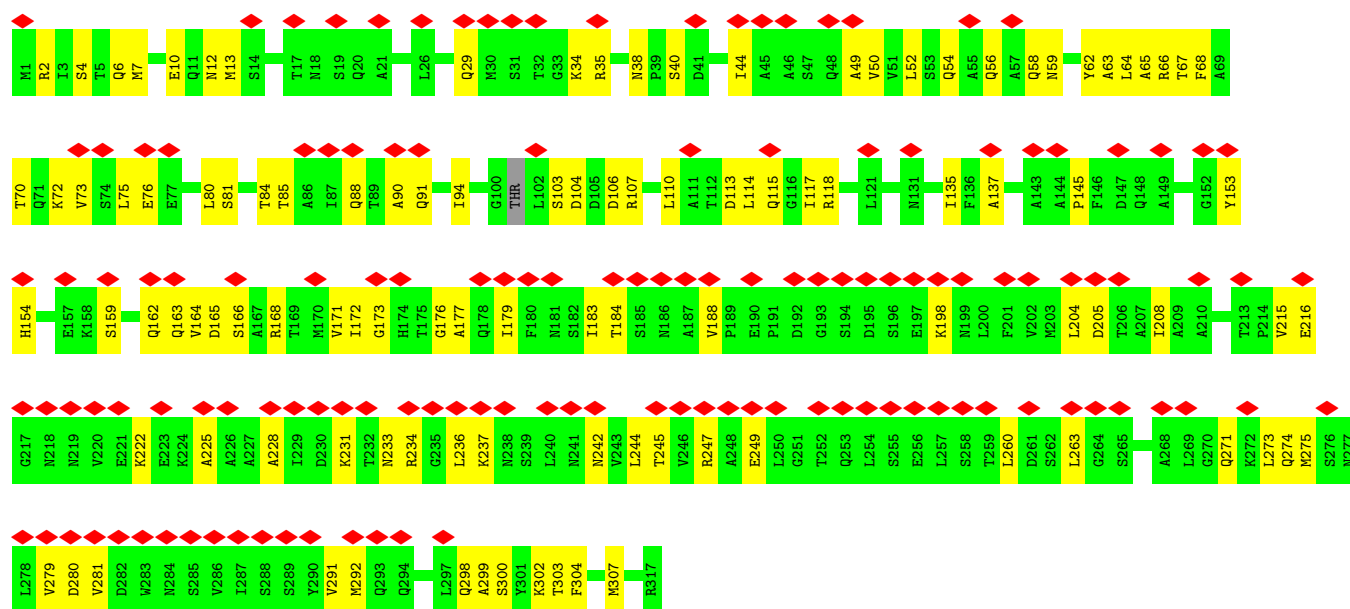
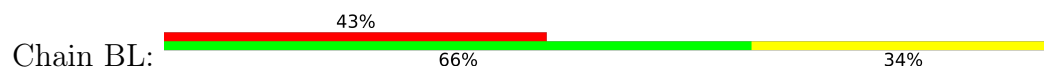


• Molecule 3: Flagellar hook-associated protein 3

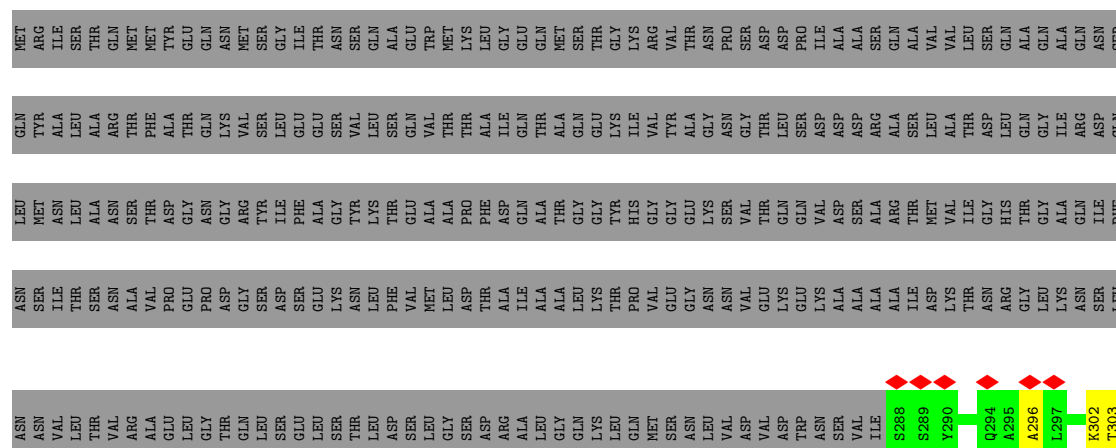




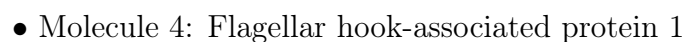
• Molecule 3: Flagellar hook-associated protein 3



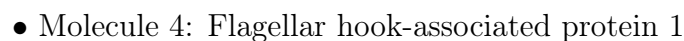
• Molecule 3: Flagellar hook-associated protein 3



Frequency	Percentage
Daily	77%
Weekly	23%
Monthly	0%

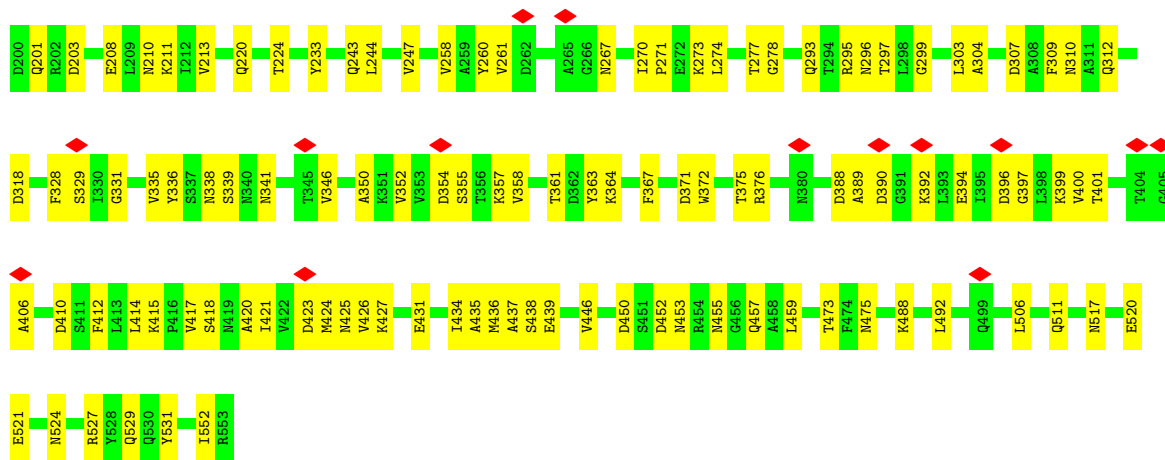


Response	Percentage
Yes	5%
No	77%
Don't know	23%

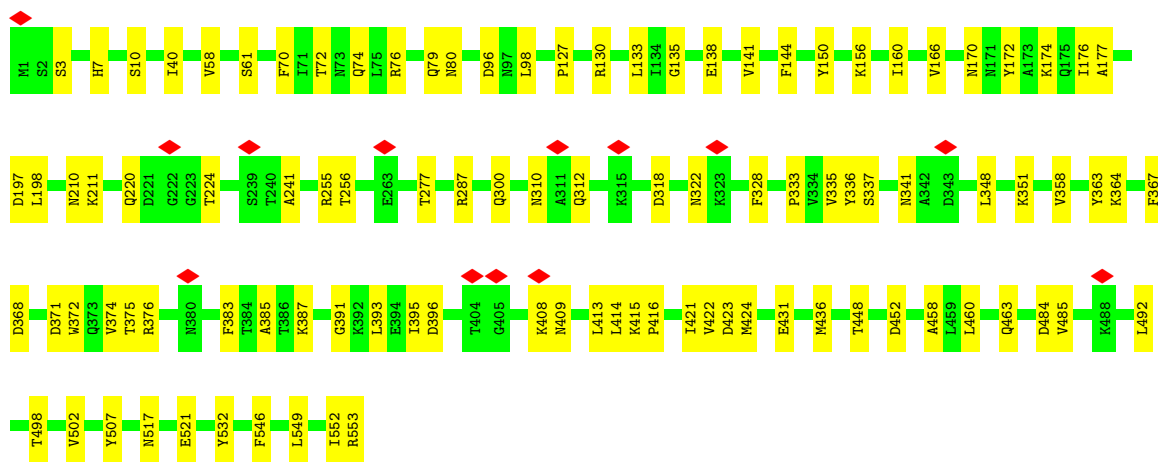
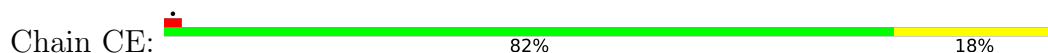


Frequency	Percentage
Daily	74%
Not daily	26%

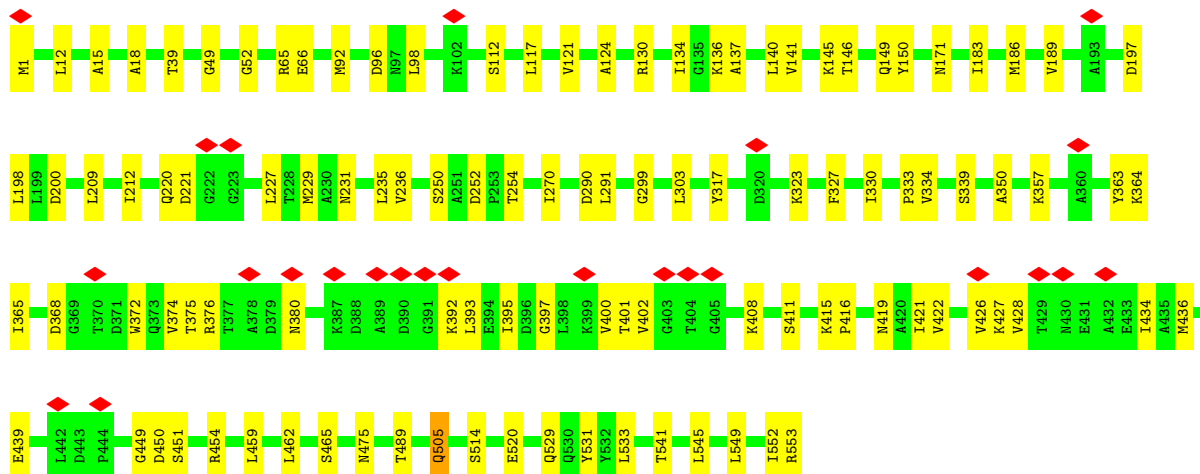
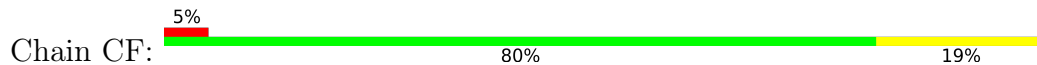


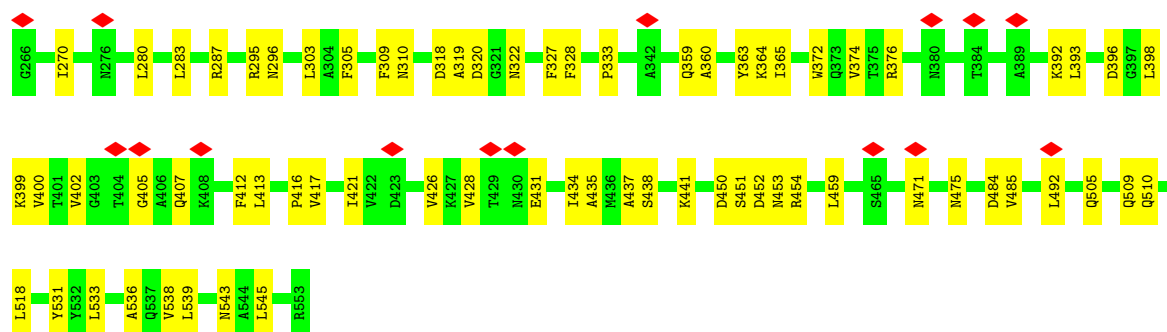


• Molecule 4: Flagellar hook-associated protein 1

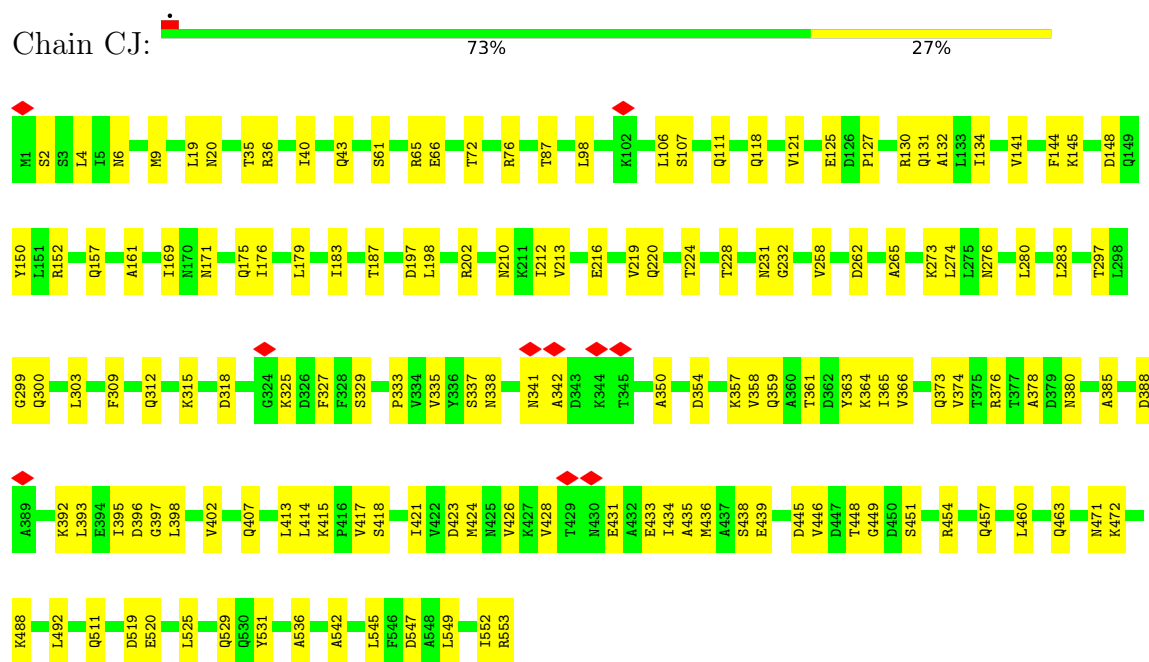


• Molecule 4: Flagellar hook-associated protein 1

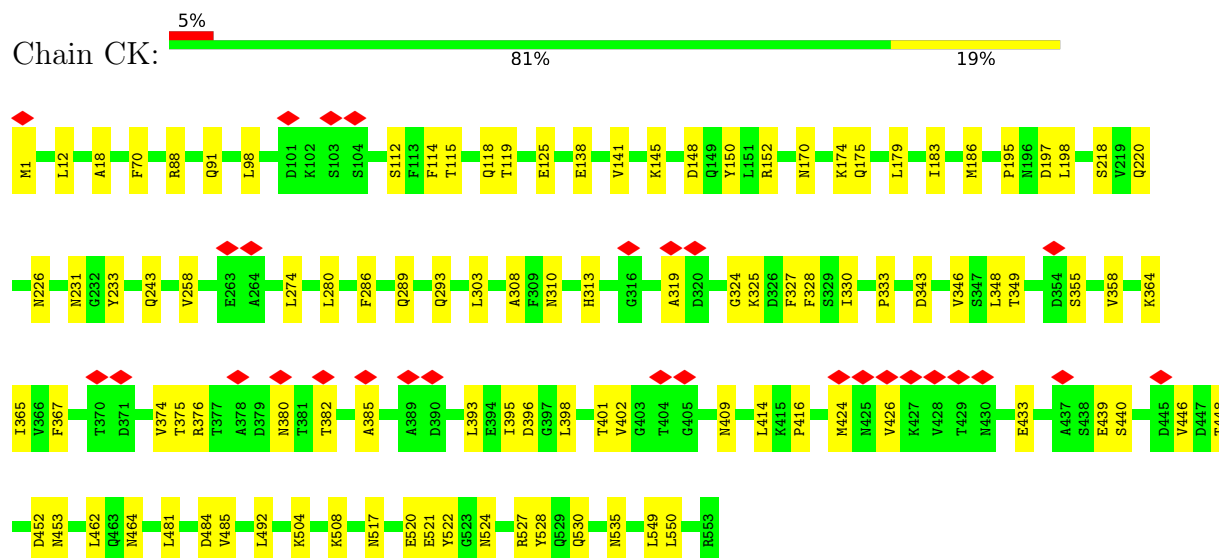




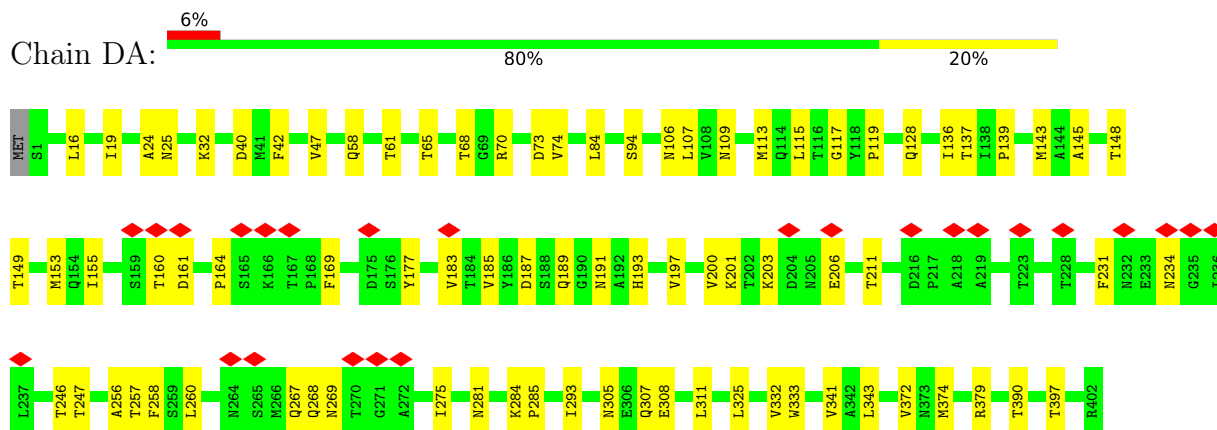
• Molecule 4: Flagellar hook-associated protein 1



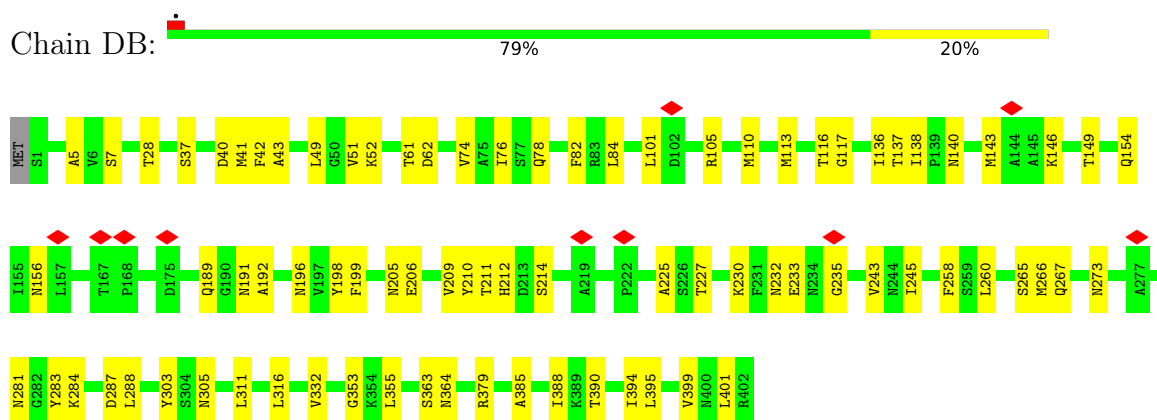
• Molecule 4: Flagellar hook-associated protein 1



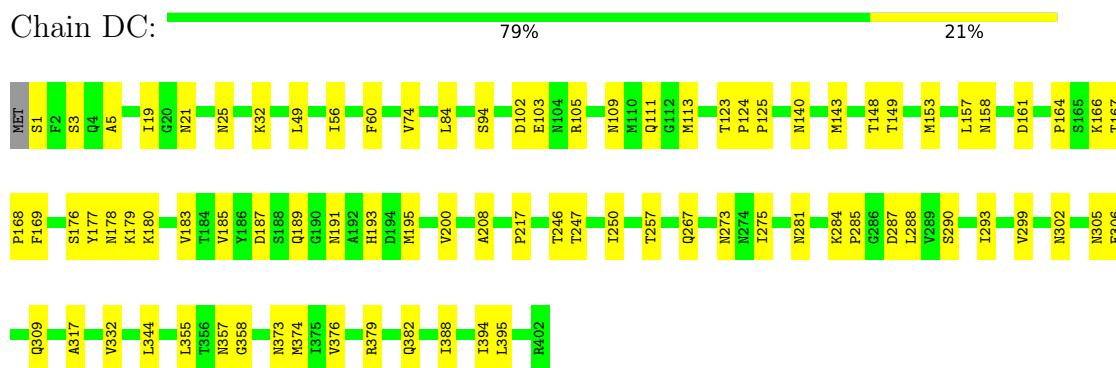
• Molecule 5: Flagellar hook protein FlgE



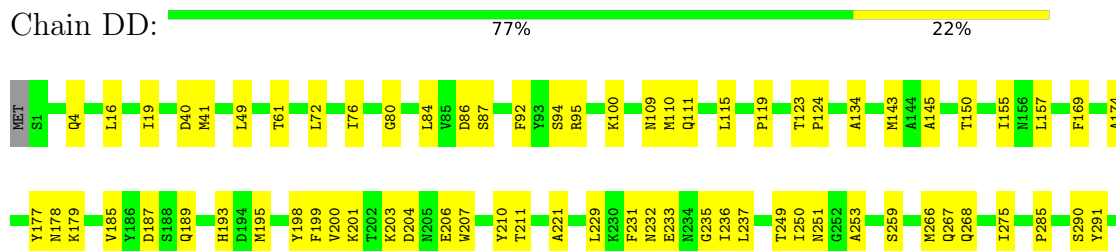
• Molecule 5: Flagellar hook protein FlgE



• Molecule 5: Flagellar hook protein FlgE



• Molecule 5: Flagellar hook protein FlgE





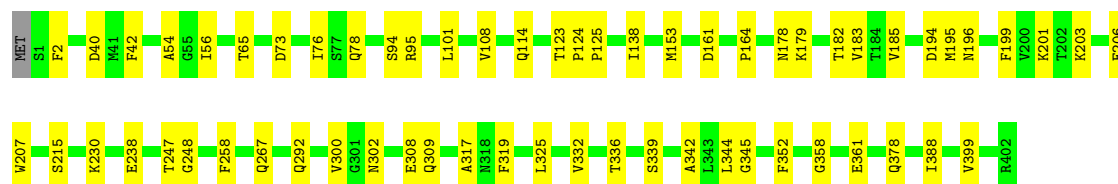
- Molecule 5: Flagellar hook protein FlgE

Chain DE: 83% 17%



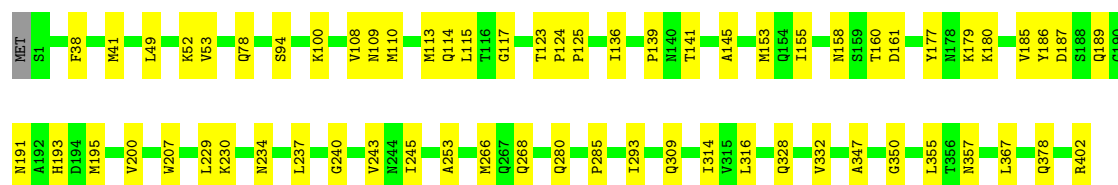
- Molecule 5: Flagellar hook protein FlgE

Chain DF: 85% 15%



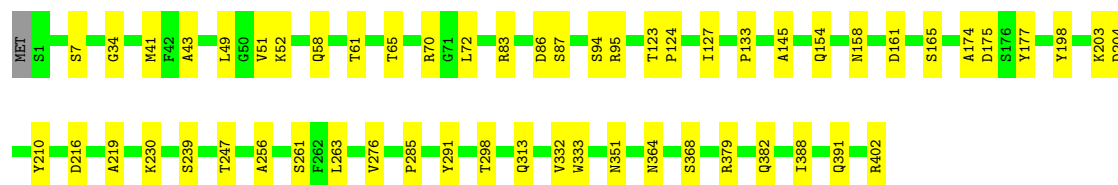
- Molecule 5: Flagellar hook protein FlgE

Chain DG: 84% 16%

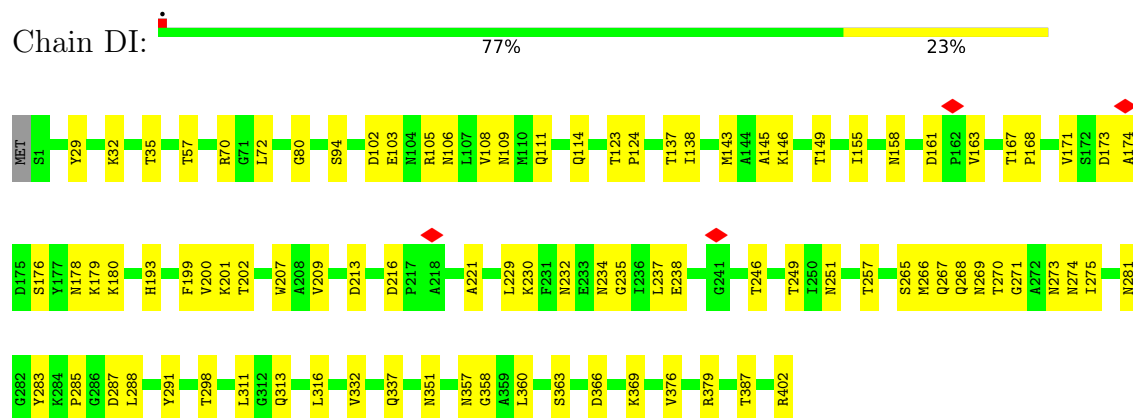


- Molecule 5: Flagellar hook protein FlgE

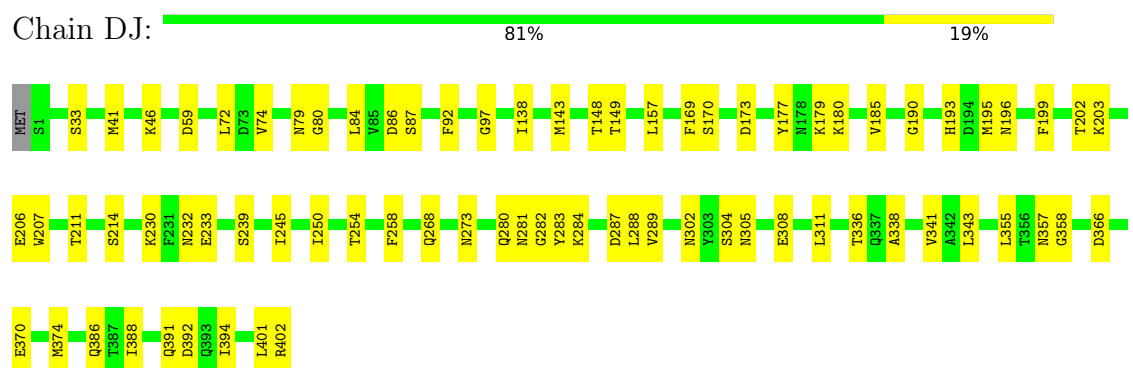
Chain DH: 86% 14%



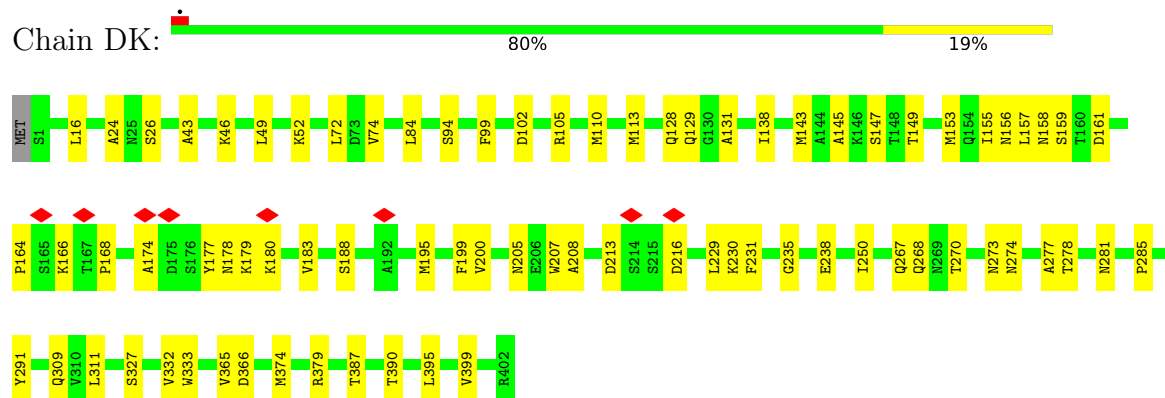
- Molecule 5: Flagellar hook protein FlgE



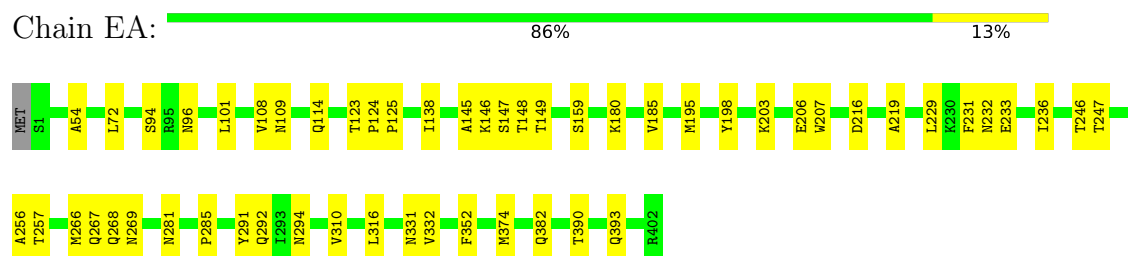
• Molecule 5: Flagellar hook protein FlgE



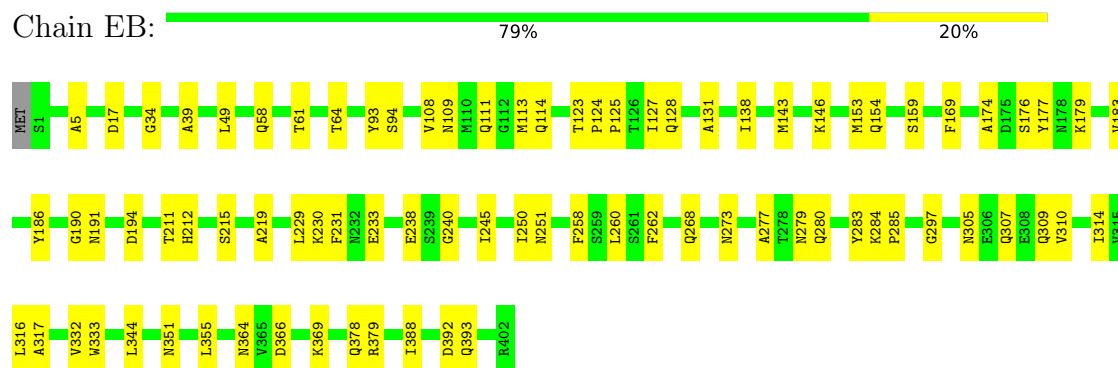
• Molecule 5: Flagellar hook protein FlgE



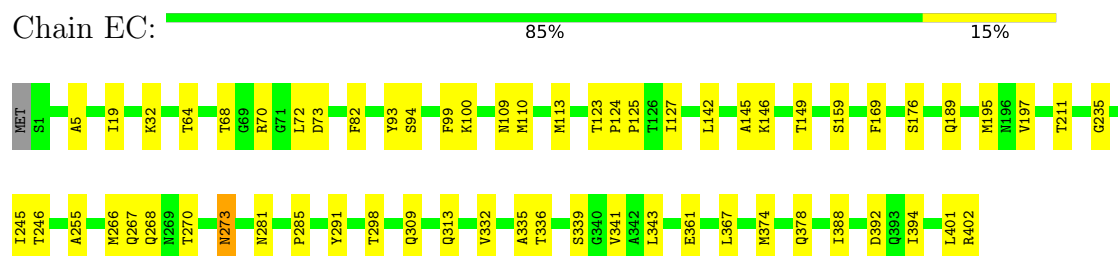
• Molecule 5: Flagellar hook protein FlgE



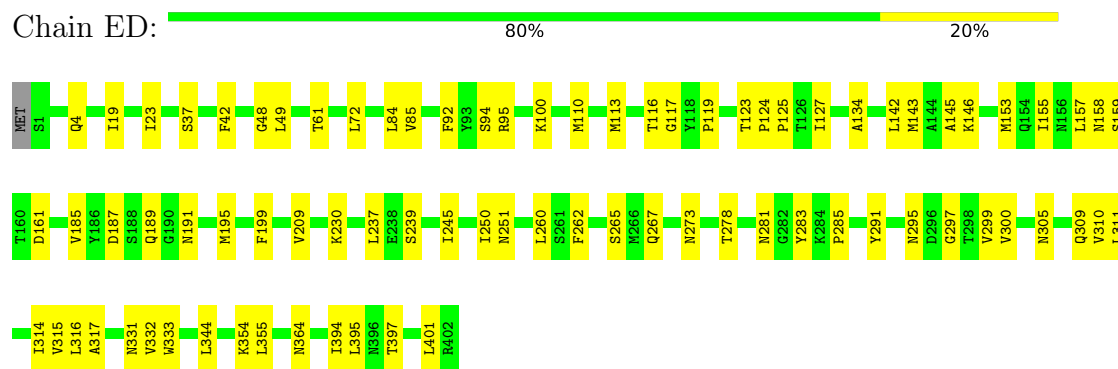
- Molecule 5: Flagellar hook protein FlgE



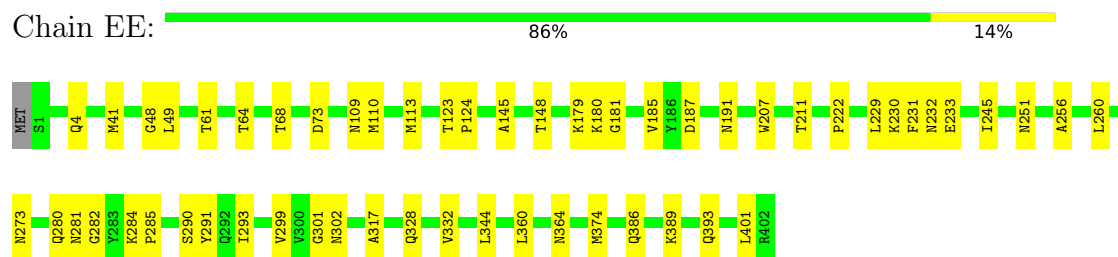
- Molecule 5: Flagellar hook protein FlgE



- Molecule 5: Flagellar hook protein FlgE

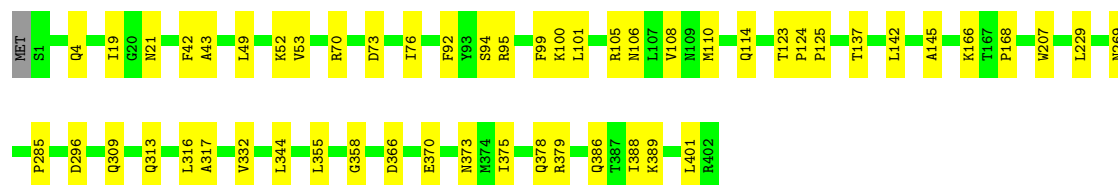


- Molecule 5: Flagellar hook protein FlgE



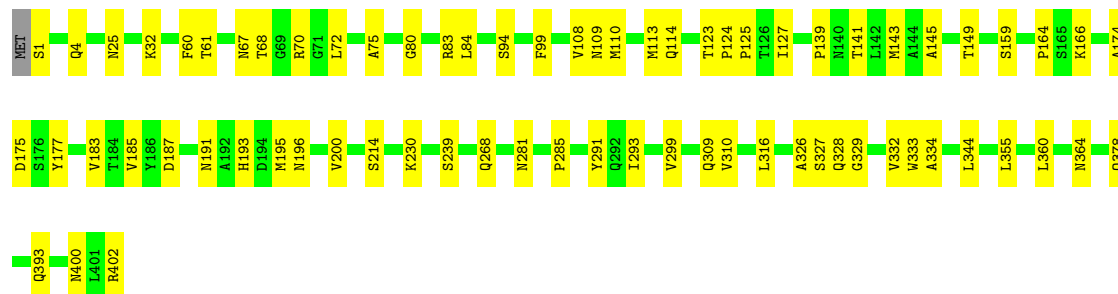
- Molecule 5: Flagellar hook protein FlgE





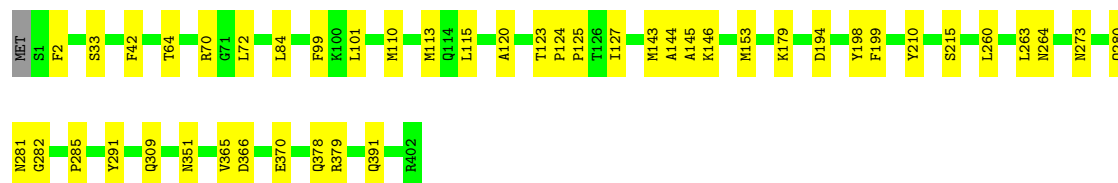
• Molecule 5: Flagellar hook protein FlgE

Chain EG: 82% 18%



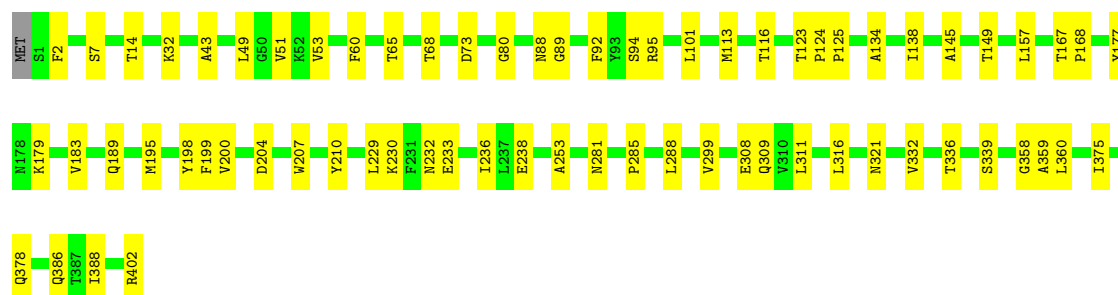
• Molecule 5: Flagellar hook protein FlgE

Chain EH: 89% 11%



• Molecule 5: Flagellar hook protein FlgE

Chain EI: 83% 17%



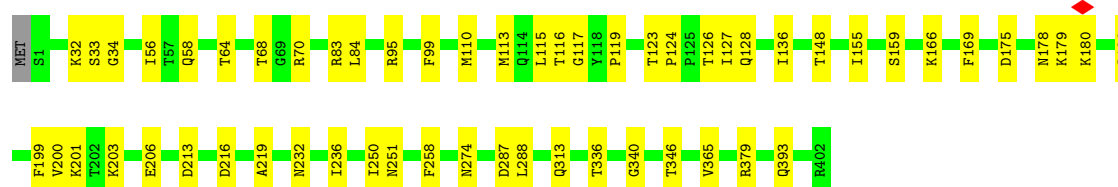
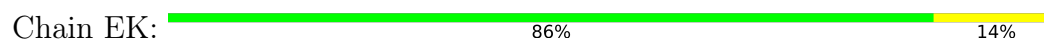
• Molecule 5: Flagellar hook protein FlgE

Chain EJ: 84% 15%

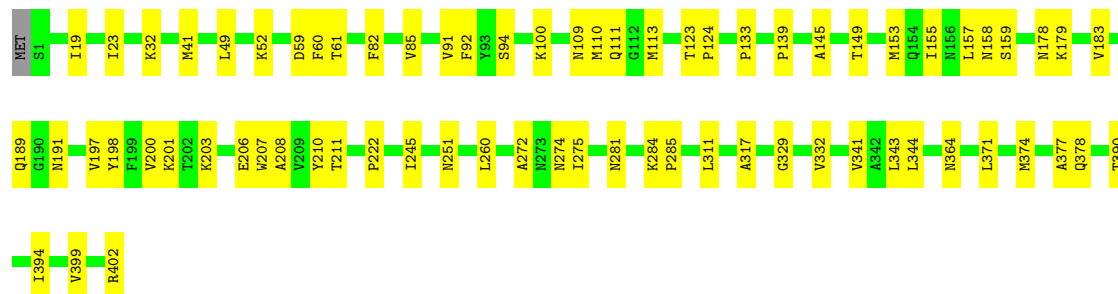
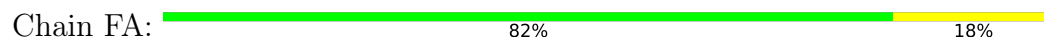




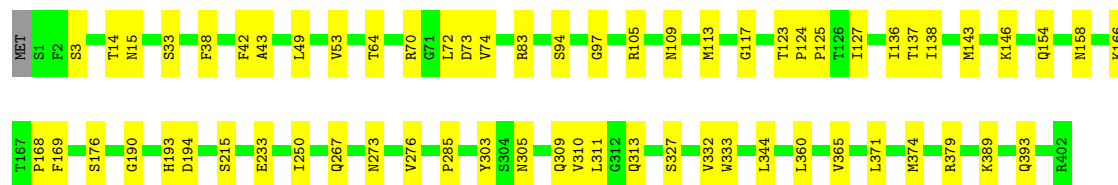
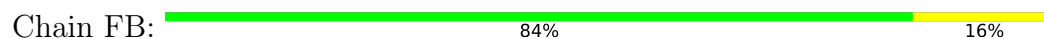
- Molecule 5: Flagellar hook protein FlgE



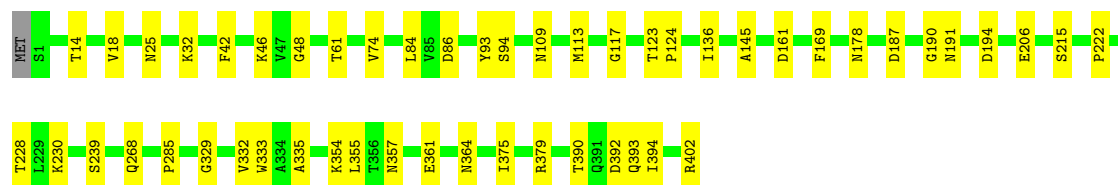
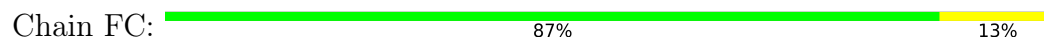
- Molecule 5: Flagellar hook protein FlgE




- Molecule 5: Flagellar hook protein FlgE

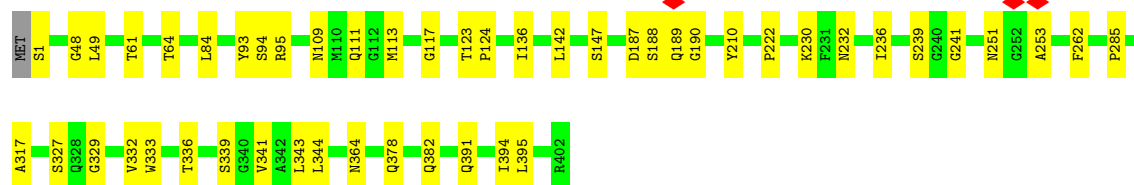


- Molecule 5: Flagellar hook protein FlgE




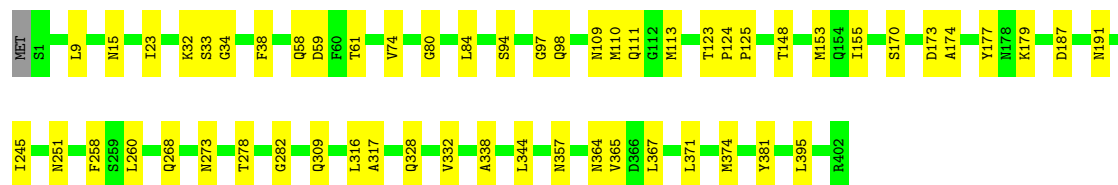
- Molecule 5: Flagellar hook protein FlgE

Chain FD:  88% 12%




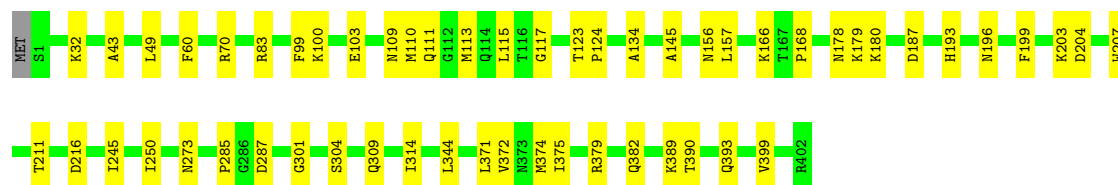
- Molecule 5: Flagellar hook protein FlgE

Chain FE:  86% 14%




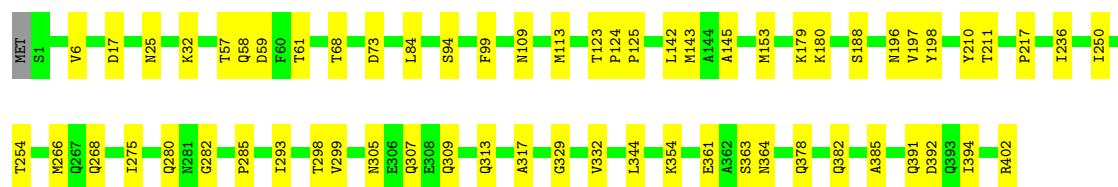
- Molecule 5: Flagellar hook protein FlgE

Chain FF:  86% 14%




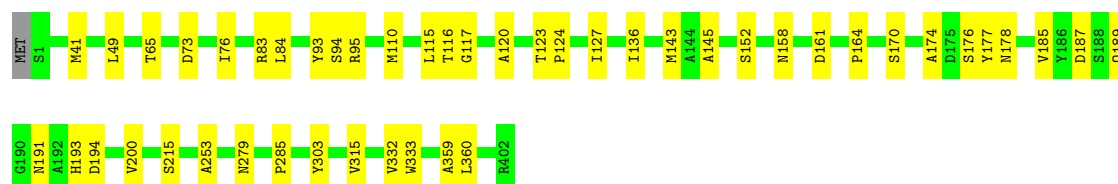
- Molecule 5: Flagellar hook protein FlgE

Chain FG:  84% 15%




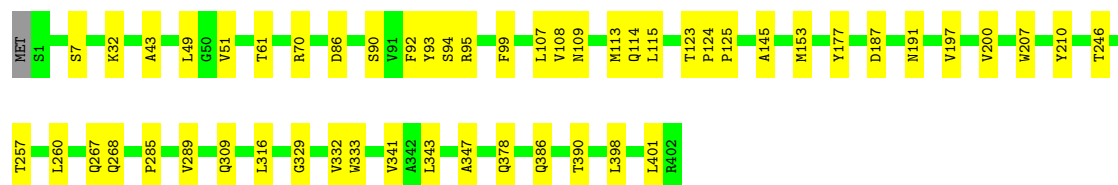
- Molecule 5: Flagellar hook protein FlgE

Chain FH:  88% 12%




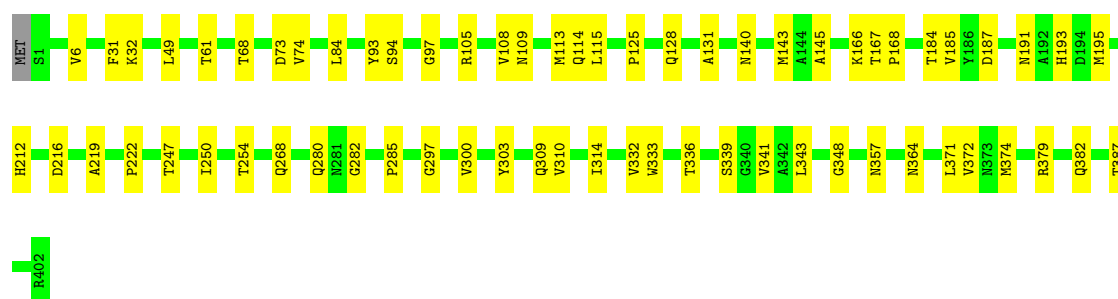
- Molecule 5: Flagellar hook protein FlgE

Chain FI:  87% 13%




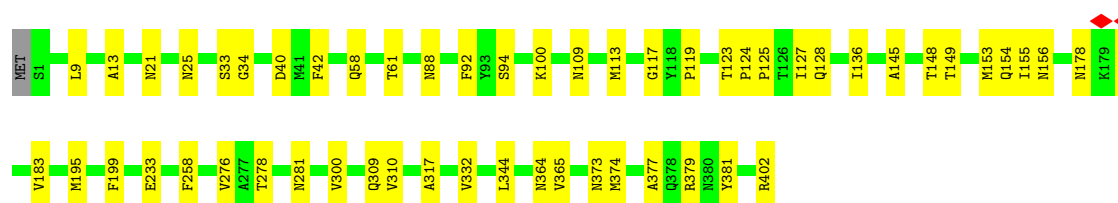
- Molecule 5: Flagellar hook protein FlgE

Chain FJ:  84% 16%




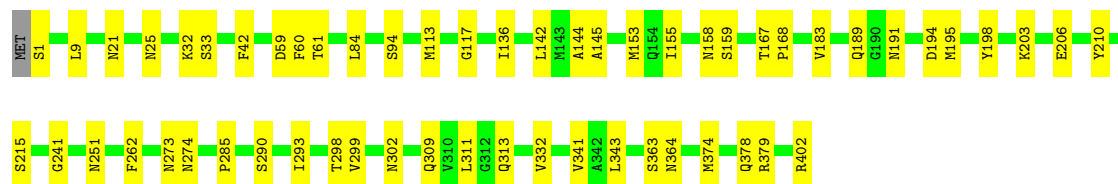
- Molecule 5: Flagellar hook protein FlgE

Chain FK:  86% 14%




- Molecule 5: Flagellar hook protein FlgE

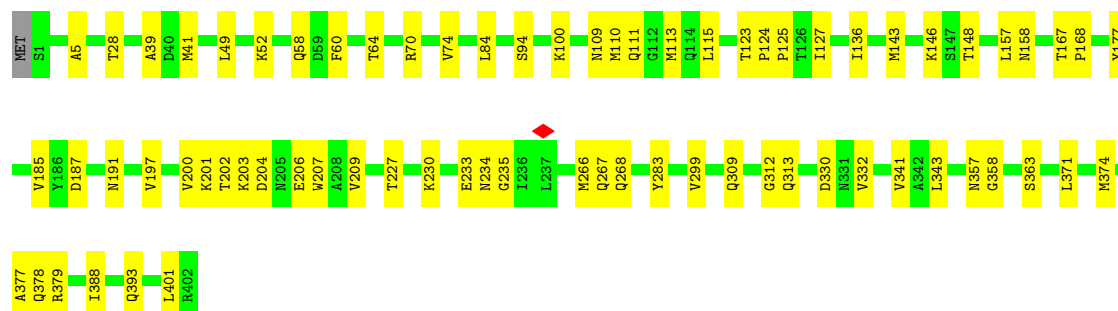
Chain GA:  86% 14%



- Molecule 5: Flagellar hook protein FlgE

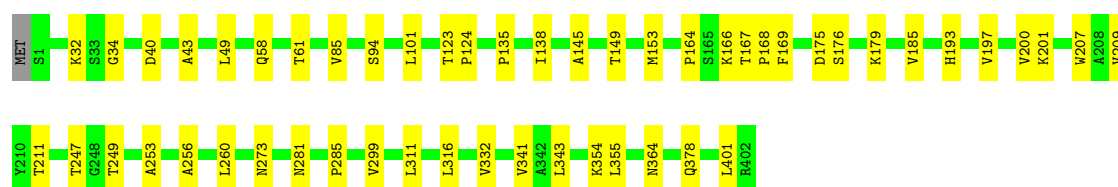
Chain GB:  82% 18%





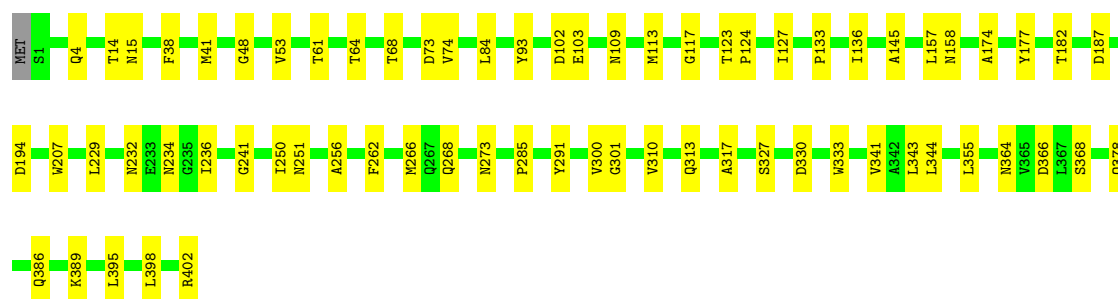
- Molecule 5: Flagellar hook protein FlgE

Chain GC: 87% 13%



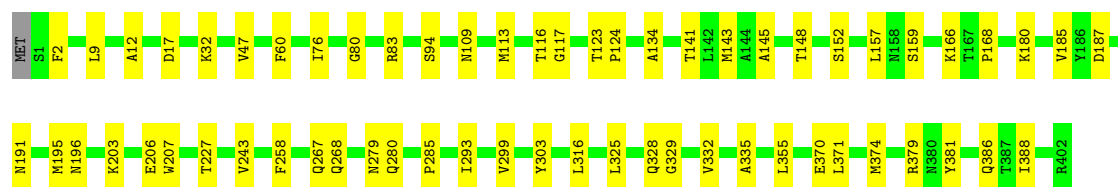
- Molecule 5: Flagellar hook protein FlgE

Chain GD: 83% 17%



- Molecule 5: Flagellar hook protein FlgE

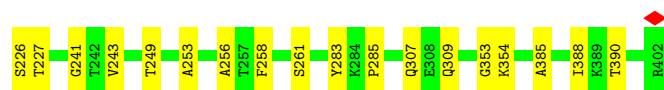
Chain GE: 85% 15%



- Molecule 5: Flagellar hook protein FlgE

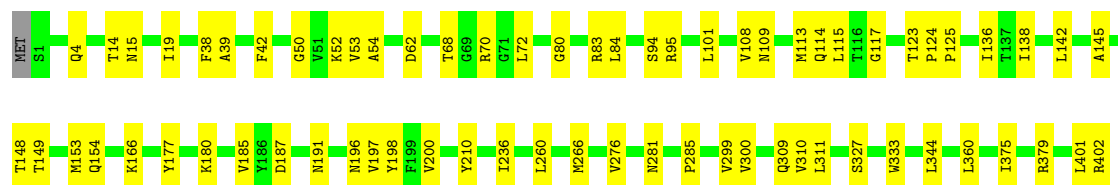
Chain GF: 87% 12%





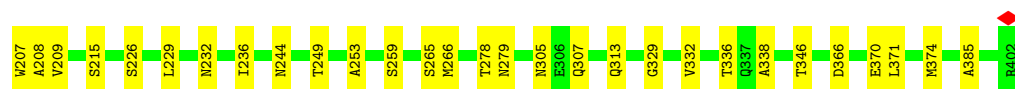
• Molecule 5: Flagellar hook protein FlgE

Chain GG: 83% 17%



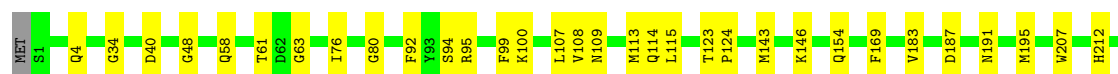
• Molecule 5: Flagellar hook protein FlgE

Chain GH: 84% 15%



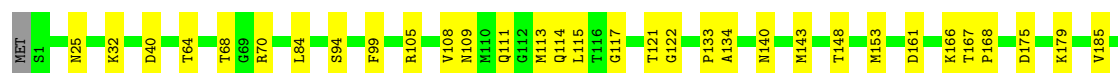
• Molecule 5: Flagellar hook protein FlgE

Chain GI: 87% 13%



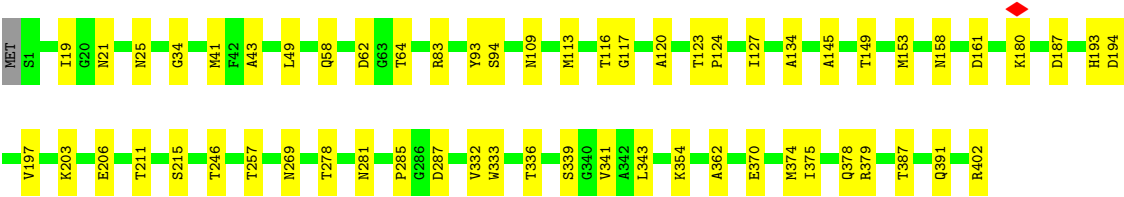
• Molecule 5: Flagellar hook protein FlgE

Chain GJ: 87% 13%



• Molecule 5: Flagellar hook protein FlgE

Chain GK: 85% 15%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	254124	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.924	Depositor
Minimum map value	-0.519	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	510.0, 510.0, 510.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	AA	0.13	0/3404	0.31	0/4609
1	AB	0.12	0/3133	0.30	0/4243
1	AD	0.15	0/3328	0.40	0/4506
1	AE	0.14	0/3301	0.37	1/4469 (0.0%)
2	AC	0.15	0/3373	0.37	0/4566
3	BA	0.14	0/2417	0.33	0/3268
3	BB	0.16	0/2417	0.35	0/3268
3	BC	0.14	0/2417	0.30	0/3268
3	BD	0.14	0/2417	0.32	0/3268
3	BE	0.15	0/2417	0.33	0/3268
3	BG	0.15	0/2417	0.34	0/3268
3	BH	0.16	0/2417	0.38	0/3268
3	BI	0.14	0/2417	0.32	0/3268
3	BJ	0.15	0/2417	0.33	0/3268
3	BK	0.14	0/2417	0.29	0/3268
3	BL	0.15	0/2409	0.38	0/3255
3	BM	0.15	0/243	0.56	0/323
3	BN	0.15	0/243	0.47	0/323
4	CA	0.15	0/4203	0.35	0/5706
4	CB	0.13	0/4203	0.30	0/5706
4	CC	0.13	0/4195	0.30	0/5696
4	CD	0.15	0/4203	0.33	0/5706
4	CE	0.13	0/4203	0.30	0/5706
4	CF	0.13	0/4203	0.32	0/5706
4	CG	0.13	0/4203	0.31	0/5706
4	CH	0.13	0/4203	0.30	0/5706
4	CI	0.13	0/4203	0.31	0/5706
4	CJ	0.15	0/4203	0.33	0/5706
4	CK	0.14	0/4203	0.32	0/5706
5	DA	0.13	0/3003	0.36	0/4090
5	DB	0.12	0/3003	0.33	0/4090
5	DC	0.14	0/3003	0.35	2/4090 (0.0%)
5	DD	0.12	0/3003	0.33	0/4090
5	DE	0.10	0/3003	0.30	0/4090

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	DF	0.11	0/3003	0.31	0/4090
5	DG	0.12	0/3003	0.35	0/4090
5	DH	0.11	0/3003	0.31	0/4090
5	DI	0.12	0/3003	0.35	2/4090 (0.0%)
5	DJ	0.12	0/3003	0.34	0/4090
5	DK	0.12	0/3003	0.33	0/4090
5	EA	0.11	0/3003	0.30	0/4090
5	EB	0.11	0/3003	0.30	0/4090
5	EC	0.10	0/3003	0.28	0/4090
5	ED	0.12	0/3003	0.31	0/4090
5	EE	0.10	0/3003	0.29	0/4090
5	EF	0.11	0/3003	0.28	0/4090
5	EG	0.11	0/3003	0.30	0/4090
5	EH	0.10	0/3003	0.28	0/4090
5	EI	0.10	0/3003	0.29	0/4090
5	EJ	0.11	0/3003	0.30	0/4090
5	EK	0.11	0/3003	0.34	0/4090
5	FA	0.09	0/3003	0.27	0/4090
5	FB	0.12	0/3003	0.31	0/4090
5	FC	0.10	0/3003	0.26	0/4090
5	FD	0.10	0/3003	0.28	0/4090
5	FE	0.10	0/3003	0.27	0/4090
5	FF	0.10	0/3003	0.26	0/4090
5	FG	0.10	0/3003	0.26	0/4090
5	FH	0.11	0/3003	0.27	0/4090
5	FI	0.09	0/3003	0.27	0/4090
5	FJ	0.09	0/3003	0.28	0/4090
5	FK	0.10	0/3003	0.30	0/4090
5	GA	0.10	0/3003	0.29	0/4090
5	GB	0.11	0/3003	0.33	0/4090
5	GC	0.10	0/3003	0.25	0/4090
5	GD	0.10	0/3003	0.27	1/4090 (0.0%)
5	GE	0.09	0/3003	0.28	0/4090
5	GF	0.09	0/3003	0.26	0/4090
5	GG	0.10	0/3003	0.27	0/4090
5	GH	0.10	0/3003	0.27	0/4090
5	GI	0.09	0/3003	0.27	0/4090
5	GJ	0.10	0/3003	0.27	0/4090
5	GK	0.11	0/3003	0.28	0/4090
All	All	0.12	0/221961	0.31	6/301690 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AD	0	2

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AE	307	ASP	N-CA-C	-5.97	104.12	112.25
5	DC	217	PRO	CA-N-CD	-5.71	104.00	112.00
5	DI	363	SER	CA-C-N	5.40	135.66	125.66
5	DI	363	SER	C-N-CA	5.40	135.66	125.66
5	GD	330	ASP	CB-CA-C	-5.30	110.44	116.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AD	328	GLN	Peptide
1	AD	338	PHE	Peptide

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	AA	3380	0	3435	78	0
1	AB	3112	0	3150	73	0
1	AD	3305	0	3354	121	0
1	AE	3278	0	3329	98	0
2	AC	3349	0	3402	79	0
3	BA	2391	0	2350	51	0
3	BB	2391	0	2350	72	0
3	BC	2391	0	2350	44	0
3	BD	2391	0	2350	71	0
3	BE	2391	0	2350	40	0
3	BG	2391	0	2350	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	BH	2391	0	2350	57	0
3	BI	2391	0	2350	51	0
3	BJ	2391	0	2350	40	0
3	BK	2391	0	2350	64	0
3	BL	2384	0	2342	86	0
3	BM	240	0	232	8	0
3	BN	240	0	232	9	0
4	CA	4157	0	4071	116	0
4	CB	4157	0	4071	90	0
4	CC	4149	0	4059	91	0
4	CD	4157	0	4071	107	0
4	CE	4157	0	4071	71	0
4	CF	4157	0	4071	82	0
4	CG	4157	0	4071	101	0
4	CH	4157	0	4071	69	0
4	CI	4157	0	4071	92	0
4	CJ	4157	0	4071	109	0
4	CK	4157	0	4071	84	0
5	DA	2959	0	2855	53	0
5	DB	2959	0	2855	54	0
5	DC	2959	0	2855	55	0
5	DD	2959	0	2855	65	0
5	DE	2959	0	2855	49	0
5	DF	2959	0	2855	40	0
5	DG	2959	0	2855	43	0
5	DH	2959	0	2855	37	0
5	DI	2959	0	2855	61	0
5	DJ	2959	0	2855	53	0
5	DK	2959	0	2855	60	0
5	EA	2959	0	2855	33	0
5	EB	2959	0	2855	59	0
5	EC	2959	0	2855	45	0
5	ED	2959	0	2855	52	0
5	EE	2959	0	2855	41	0
5	EF	2959	0	2855	34	0
5	EG	2959	0	2855	47	0
5	EH	2959	0	2855	28	0
5	EI	2959	0	2855	45	0
5	EJ	2959	0	2855	46	0
5	EK	2959	0	2855	43	0
5	FA	2959	0	2855	52	0
5	FB	2959	0	2855	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	FC	2959	0	2855	33	0
5	FD	2959	0	2855	36	0
5	FE	2959	0	2855	35	0
5	FF	2959	0	2855	37	0
5	FG	2959	0	2855	42	0
5	FH	2959	0	2855	26	0
5	FI	2959	0	2855	31	0
5	FJ	2959	0	2855	41	0
5	FK	2959	0	2855	41	0
5	GA	2959	0	2855	37	0
5	GB	2959	0	2855	53	0
5	GC	2959	0	2855	31	0
5	GD	2959	0	2855	42	0
5	GE	2959	0	2855	37	0
5	GF	2959	0	2855	29	0
5	GG	2959	0	2855	41	0
5	GH	2959	0	2855	38	0
5	GI	2959	0	2855	35	0
5	GJ	2959	0	2855	31	0
5	GK	2959	0	2855	35	0
All	All	219113	0	213365	3546	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 8.

The worst 5 of 3546 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)
5:DK:183:VAL:HB	5:DK:195:MET:HB2	1.50	0.91
4:CG:125:GLU:HG2	4:CG:450:ASP:HB3	1.54	0.88
4:CJ:363:TYR:HB2	4:CJ:414:LEU:O	1.73	0.88
2:AC:348:GLN:HA	2:AC:355:LEU:HB3	1.58	0.85
1:AD:443:LEU:O	1:AD:447:MET:HB2	1.77	0.84

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	450/467 (96%)	440 (98%)	10 (2%)	0	100	100
1	AB	413/467 (88%)	405 (98%)	8 (2%)	0	100	100
1	AD	440/467 (94%)	429 (98%)	11 (2%)	0	100	100
1	AE	436/467 (93%)	427 (98%)	9 (2%)	0	100	100
2	AC	445/467 (95%)	427 (96%)	18 (4%)	0	100	100
3	BA	315/317 (99%)	312 (99%)	3 (1%)	0	100	100
3	BB	315/317 (99%)	311 (99%)	4 (1%)	0	100	100
3	BC	315/317 (99%)	310 (98%)	5 (2%)	0	100	100
3	BD	315/317 (99%)	308 (98%)	7 (2%)	0	100	100
3	BE	315/317 (99%)	311 (99%)	4 (1%)	0	100	100
3	BG	315/317 (99%)	310 (98%)	5 (2%)	0	100	100
3	BH	315/317 (99%)	308 (98%)	7 (2%)	0	100	100
3	BI	315/317 (99%)	309 (98%)	6 (2%)	0	100	100
3	BJ	315/317 (99%)	307 (98%)	8 (2%)	0	100	100
3	BK	315/317 (99%)	309 (98%)	6 (2%)	0	100	100
3	BL	312/317 (98%)	305 (98%)	7 (2%)	0	100	100
3	BM	28/317 (9%)	26 (93%)	2 (7%)	0	100	100
3	BN	28/317 (9%)	26 (93%)	2 (7%)	0	100	100
4	CA	551/553 (100%)	545 (99%)	6 (1%)	0	100	100
4	CB	551/553 (100%)	545 (99%)	6 (1%)	0	100	100
4	CC	550/553 (100%)	542 (98%)	8 (2%)	0	100	100
4	CD	551/553 (100%)	547 (99%)	4 (1%)	0	100	100
4	CE	551/553 (100%)	546 (99%)	5 (1%)	0	100	100
4	CF	551/553 (100%)	541 (98%)	10 (2%)	0	100	100
4	CG	551/553 (100%)	542 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	CH	551/553 (100%)	545 (99%)	6 (1%)	0	100	100
4	CI	551/553 (100%)	541 (98%)	10 (2%)	0	100	100
4	CJ	551/553 (100%)	546 (99%)	5 (1%)	0	100	100
4	CK	551/553 (100%)	545 (99%)	6 (1%)	0	100	100
5	DA	400/403 (99%)	390 (98%)	10 (2%)	0	100	100
5	DB	400/403 (99%)	383 (96%)	17 (4%)	0	100	100
5	DC	400/403 (99%)	390 (98%)	10 (2%)	0	100	100
5	DD	400/403 (99%)	391 (98%)	9 (2%)	0	100	100
5	DE	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	DF	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	DG	400/403 (99%)	391 (98%)	9 (2%)	0	100	100
5	DH	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	DI	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	DJ	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	DK	400/403 (99%)	393 (98%)	7 (2%)	0	100	100
5	EA	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	EB	400/403 (99%)	389 (97%)	11 (3%)	0	100	100
5	EC	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	ED	400/403 (99%)	388 (97%)	12 (3%)	0	100	100
5	EE	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	EF	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	EG	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	EH	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	EI	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	EJ	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	EK	400/403 (99%)	396 (99%)	4 (1%)	0	100	100
5	FA	400/403 (99%)	396 (99%)	4 (1%)	0	100	100
5	FB	400/403 (99%)	393 (98%)	7 (2%)	0	100	100
5	FC	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	FD	400/403 (99%)	391 (98%)	9 (2%)	0	100	100
5	FE	400/403 (99%)	394 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	FF	400/403 (99%)	393 (98%)	7 (2%)	0	100	100
5	FG	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	FH	400/403 (99%)	396 (99%)	4 (1%)	0	100	100
5	FI	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	FJ	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	FK	400/403 (99%)	391 (98%)	9 (2%)	0	100	100
5	GA	400/403 (99%)	396 (99%)	4 (1%)	0	100	100
5	GB	400/403 (99%)	388 (97%)	12 (3%)	0	100	100
5	GC	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	GD	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	GE	400/403 (99%)	396 (99%)	4 (1%)	0	100	100
5	GF	400/403 (99%)	393 (98%)	7 (2%)	0	100	100
5	GG	400/403 (99%)	392 (98%)	8 (2%)	0	100	100
5	GH	400/403 (99%)	394 (98%)	6 (2%)	0	100	100
5	GI	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	GJ	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
5	GK	400/403 (99%)	389 (97%)	11 (3%)	0	100	100
All	All	29362/30271 (97%)	28843 (98%)	519 (2%)	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	AA	378/391 (97%)	378 (100%)	0	100	100
1	AB	346/391 (88%)	346 (100%)	0	100	100
1	AD	369/391 (94%)	368 (100%)	1 (0%)	86	87
1	AE	366/391 (94%)	366 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AC	375/391 (96%)	375 (100%)	0	100	100
3	BA	261/261 (100%)	261 (100%)	0	100	100
3	BB	261/261 (100%)	261 (100%)	0	100	100
3	BC	261/261 (100%)	261 (100%)	0	100	100
3	BD	261/261 (100%)	260 (100%)	1 (0%)	84	85
3	BE	261/261 (100%)	261 (100%)	0	100	100
3	BG	261/261 (100%)	261 (100%)	0	100	100
3	BH	261/261 (100%)	261 (100%)	0	100	100
3	BI	261/261 (100%)	261 (100%)	0	100	100
3	BJ	261/261 (100%)	261 (100%)	0	100	100
3	BK	261/261 (100%)	261 (100%)	0	100	100
3	BL	260/261 (100%)	260 (100%)	0	100	100
3	BM	26/261 (10%)	26 (100%)	0	100	100
3	BN	26/261 (10%)	26 (100%)	0	100	100
4	CA	453/453 (100%)	453 (100%)	0	100	100
4	CB	453/453 (100%)	453 (100%)	0	100	100
4	CC	452/453 (100%)	452 (100%)	0	100	100
4	CD	453/453 (100%)	453 (100%)	0	100	100
4	CE	453/453 (100%)	453 (100%)	0	100	100
4	CF	453/453 (100%)	452 (100%)	1 (0%)	87	88
4	CG	453/453 (100%)	452 (100%)	1 (0%)	87	88
4	CH	453/453 (100%)	453 (100%)	0	100	100
4	CI	453/453 (100%)	453 (100%)	0	100	100
4	CJ	453/453 (100%)	453 (100%)	0	100	100
4	CK	453/453 (100%)	453 (100%)	0	100	100
5	DA	322/323 (100%)	322 (100%)	0	100	100
5	DB	322/323 (100%)	322 (100%)	0	100	100
5	DC	322/323 (100%)	322 (100%)	0	100	100
5	DD	322/323 (100%)	322 (100%)	0	100	100
5	DE	322/323 (100%)	322 (100%)	0	100	100
5	DF	322/323 (100%)	322 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	DG	322/323 (100%)	322 (100%)	0	100	100
5	DH	322/323 (100%)	322 (100%)	0	100	100
5	DI	322/323 (100%)	322 (100%)	0	100	100
5	DJ	322/323 (100%)	322 (100%)	0	100	100
5	DK	322/323 (100%)	322 (100%)	0	100	100
5	EA	322/323 (100%)	322 (100%)	0	100	100
5	EB	322/323 (100%)	322 (100%)	0	100	100
5	EC	322/323 (100%)	321 (100%)	1 (0%)	86	87
5	ED	322/323 (100%)	322 (100%)	0	100	100
5	EE	322/323 (100%)	322 (100%)	0	100	100
5	EF	322/323 (100%)	322 (100%)	0	100	100
5	EG	322/323 (100%)	322 (100%)	0	100	100
5	EH	322/323 (100%)	322 (100%)	0	100	100
5	EI	322/323 (100%)	322 (100%)	0	100	100
5	EJ	322/323 (100%)	322 (100%)	0	100	100
5	EK	322/323 (100%)	322 (100%)	0	100	100
5	FA	322/323 (100%)	322 (100%)	0	100	100
5	FB	322/323 (100%)	322 (100%)	0	100	100
5	FC	322/323 (100%)	322 (100%)	0	100	100
5	FD	322/323 (100%)	322 (100%)	0	100	100
5	FE	322/323 (100%)	322 (100%)	0	100	100
5	FF	322/323 (100%)	322 (100%)	0	100	100
5	FG	322/323 (100%)	322 (100%)	0	100	100
5	FH	322/323 (100%)	322 (100%)	0	100	100
5	FI	322/323 (100%)	322 (100%)	0	100	100
5	FJ	322/323 (100%)	322 (100%)	0	100	100
5	FK	322/323 (100%)	322 (100%)	0	100	100
5	GA	322/323 (100%)	322 (100%)	0	100	100
5	GB	322/323 (100%)	322 (100%)	0	100	100
5	GC	322/323 (100%)	322 (100%)	0	100	100
5	GD	322/323 (100%)	322 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	GE	322/323 (100%)	322 (100%)	0	100	100
5	GF	322/323 (100%)	322 (100%)	0	100	100
5	GG	322/323 (100%)	322 (100%)	0	100	100
5	GH	322/323 (100%)	322 (100%)	0	100	100
5	GI	322/323 (100%)	322 (100%)	0	100	100
5	GJ	322/323 (100%)	322 (100%)	0	100	100
5	GK	322/323 (100%)	322 (100%)	0	100	100
All	All	23906/24543 (97%)	23901 (100%)	5 (0%)	100	100

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AD	369	ASN
3	BD	163	GLN
4	CF	505	GLN
4	CG	466	ASN
5	EC	273	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 423 such sidechains are listed below:

Mol	Chain	Res	Type
5	EB	267	GLN
5	FB	267	GLN
5	GI	212	HIS
5	ED	98	GLN
5	EH	191	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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.

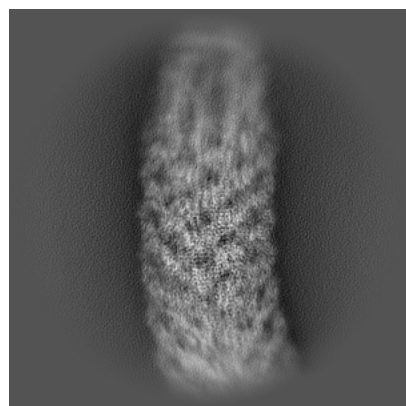
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63853. These allow visual inspection of the internal detail of the map and identification of artifacts.

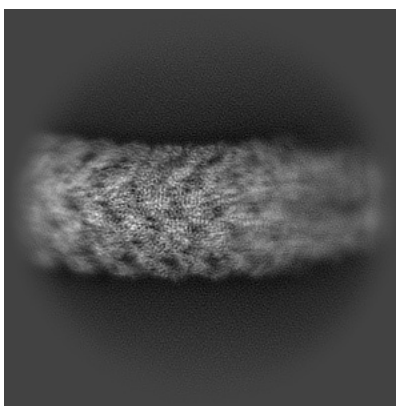
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

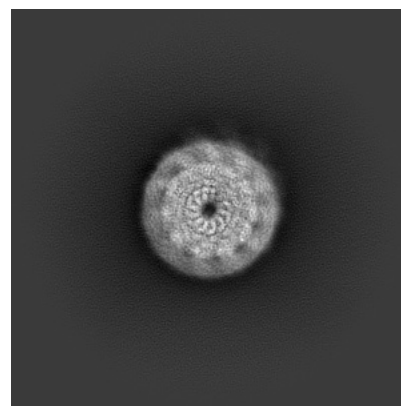
6.1.1 Primary map



X

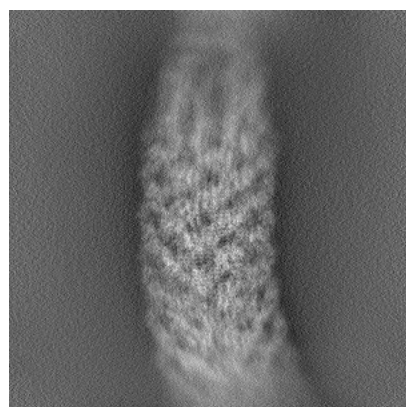


Y

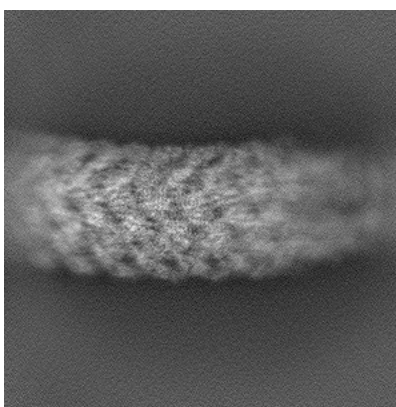


Z

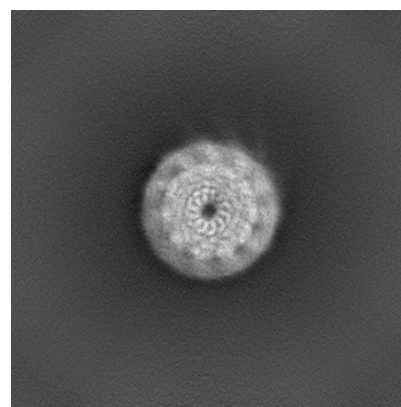
6.1.2 Raw map



X



Y

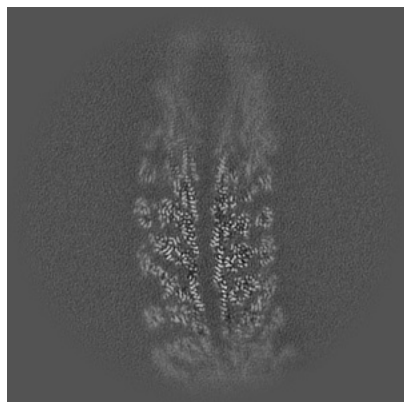


Z

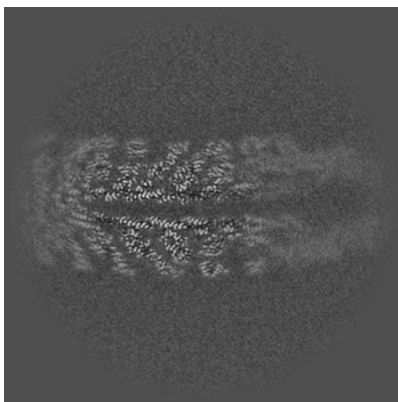
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

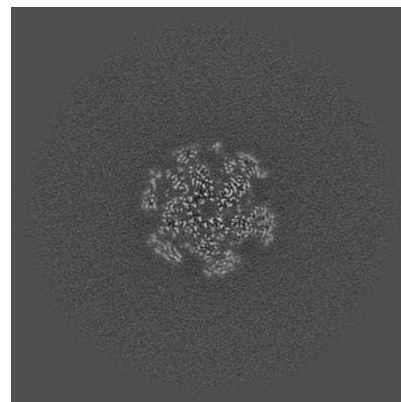
6.2.1 Primary map



X Index: 300

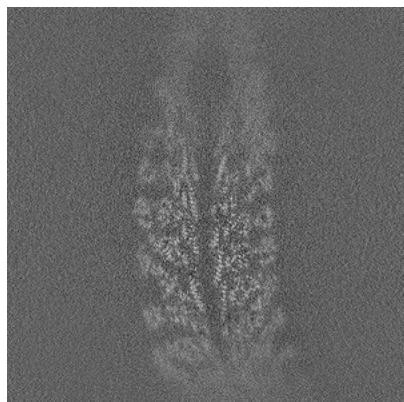


Y Index: 300

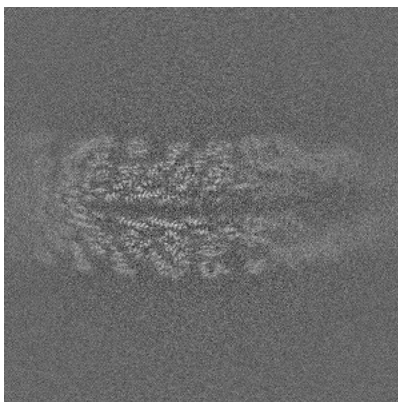


Z Index: 300

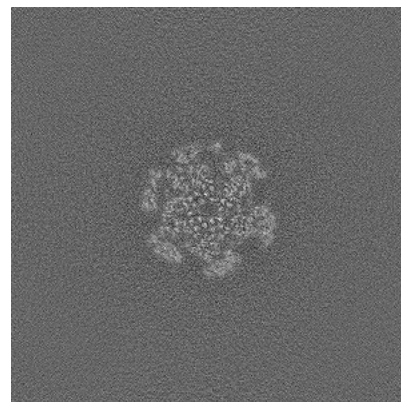
6.2.2 Raw map



X Index: 300



Y Index: 300

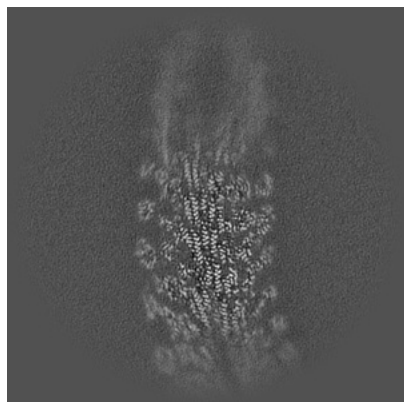


Z Index: 300

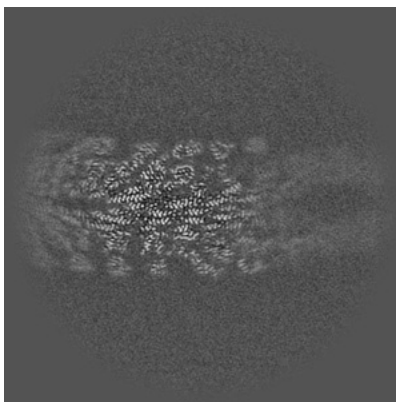
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

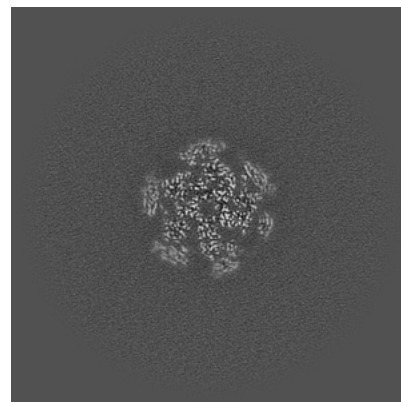
6.3.1 Primary map



X Index: 314

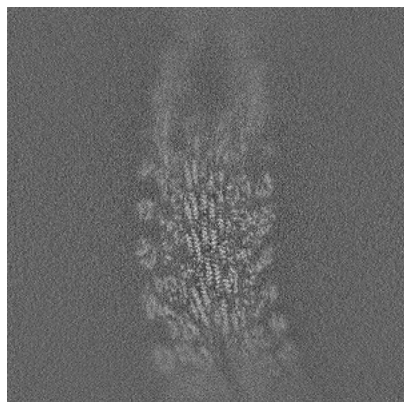


Y Index: 315

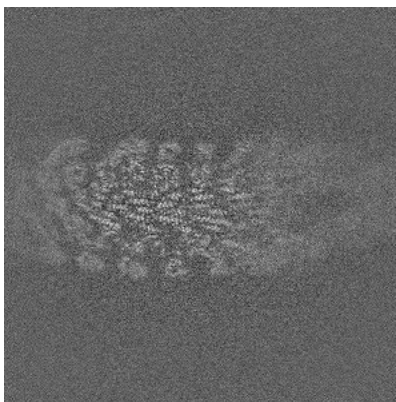


Z Index: 235

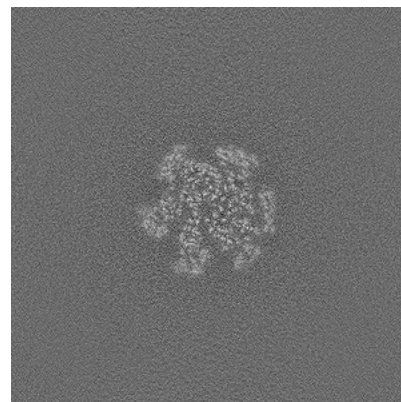
6.3.2 Raw map



X Index: 315



Y Index: 281

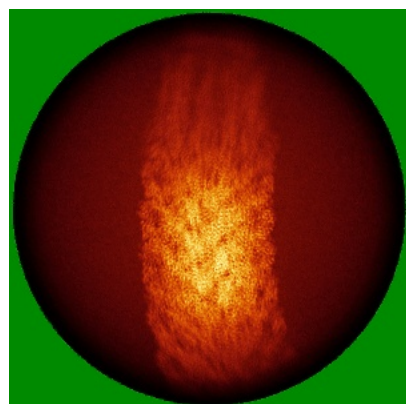


Z Index: 261

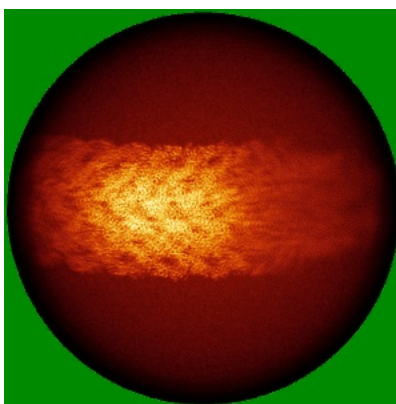
The images above show the largest variance slices of the map in three orthogonal directions.

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

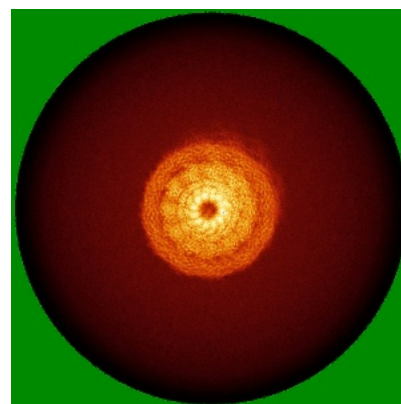
6.4.1 Primary map



X

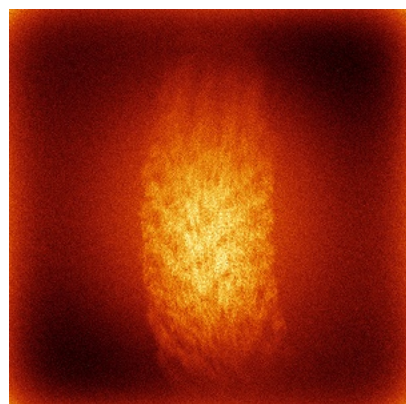


Y

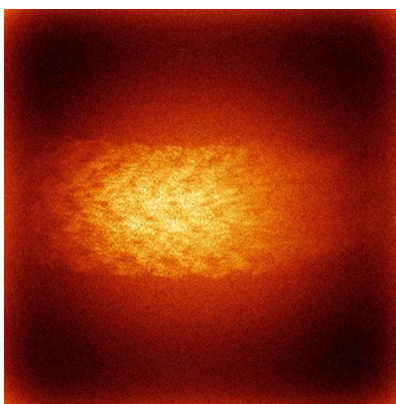


Z

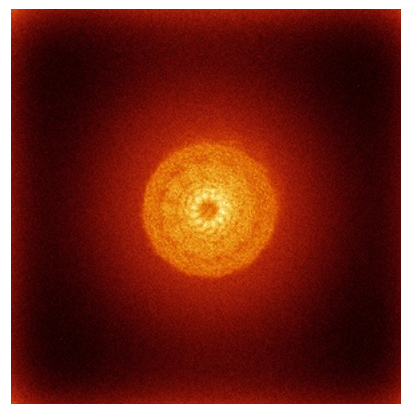
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

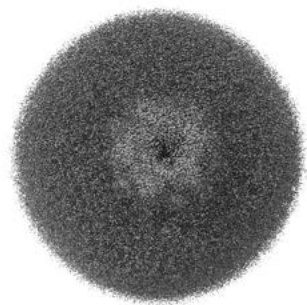
6.5.1 Primary map



X



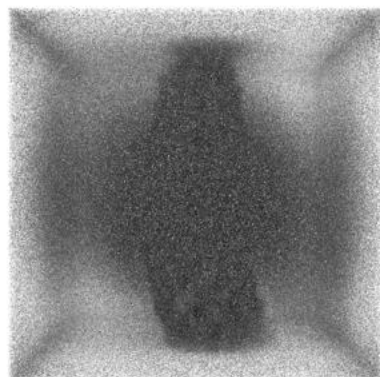
Y



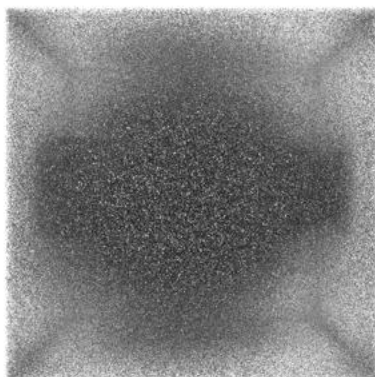
Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

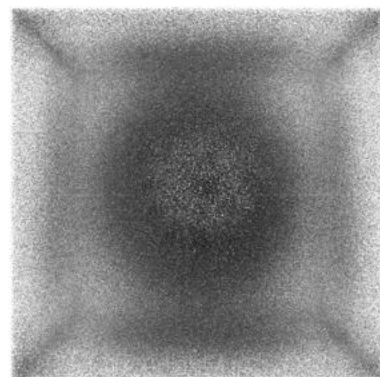
6.5.2 Raw map



X



Y



Z

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

6.6 Mask visualisation [i](#)

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

A mask typically either:

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

6.6.1 emd_63853_msk_1.map [i](#)



X



Y

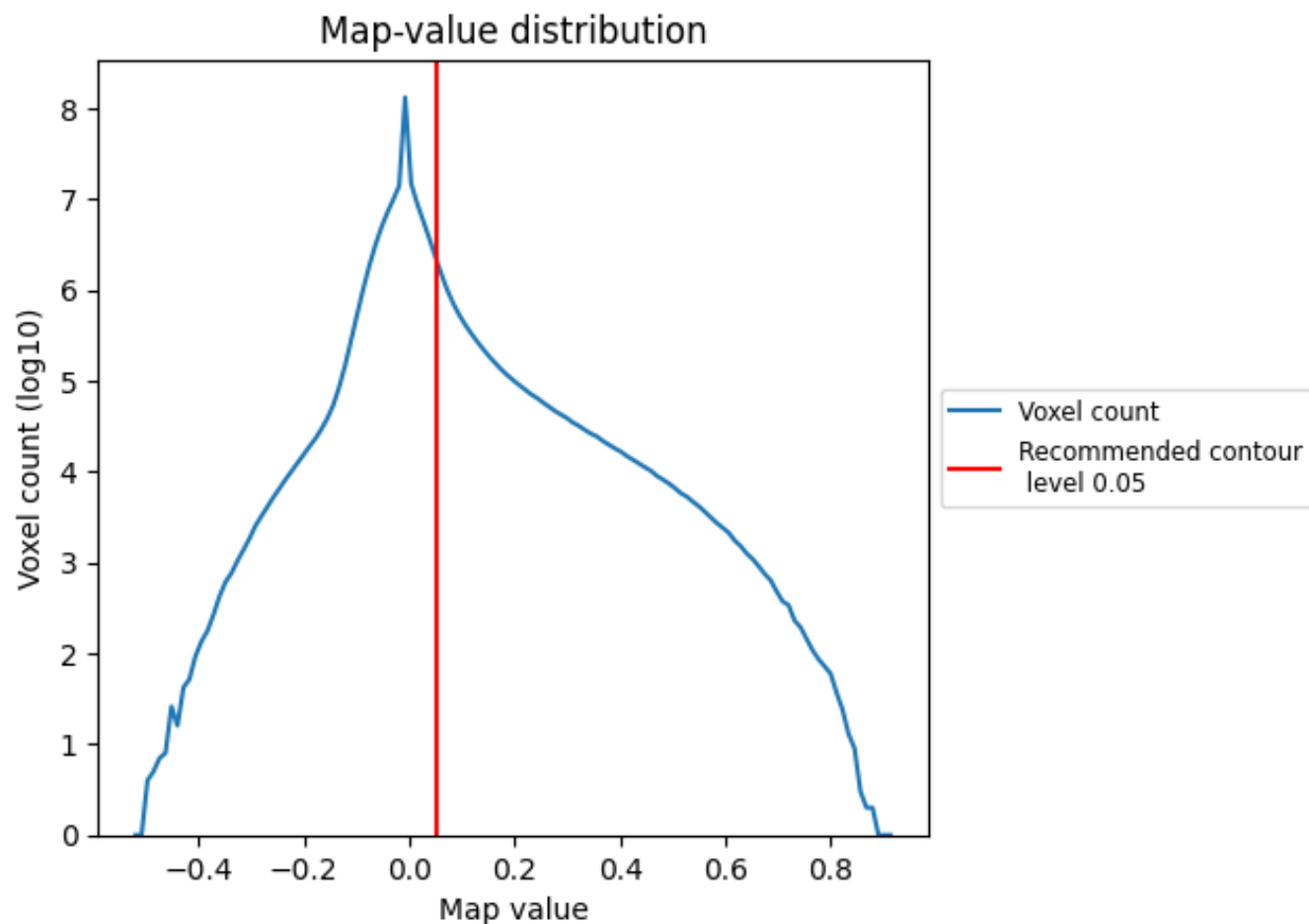


Z

7 Map analysis [i](#)

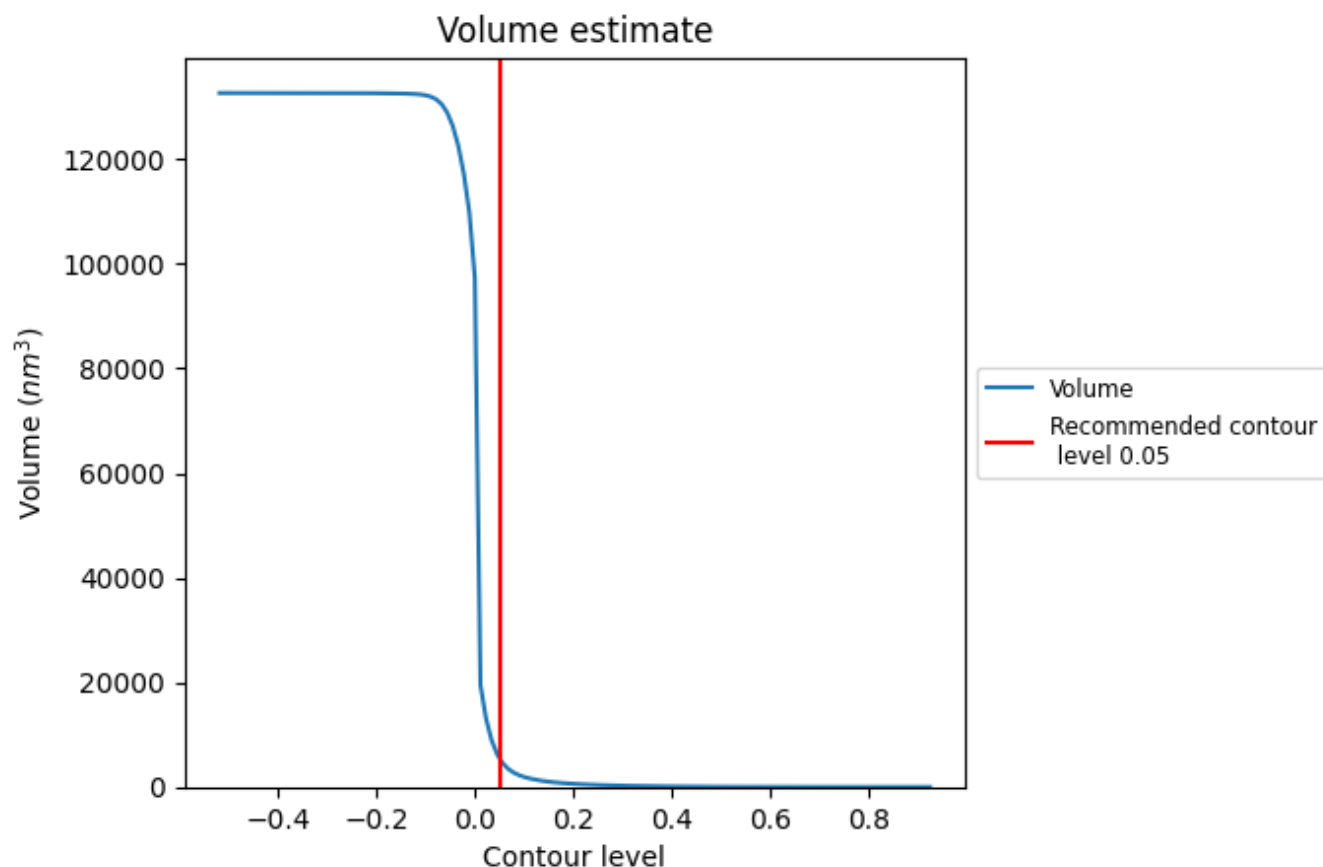
This section contains the results of statistical analysis of the map.

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.

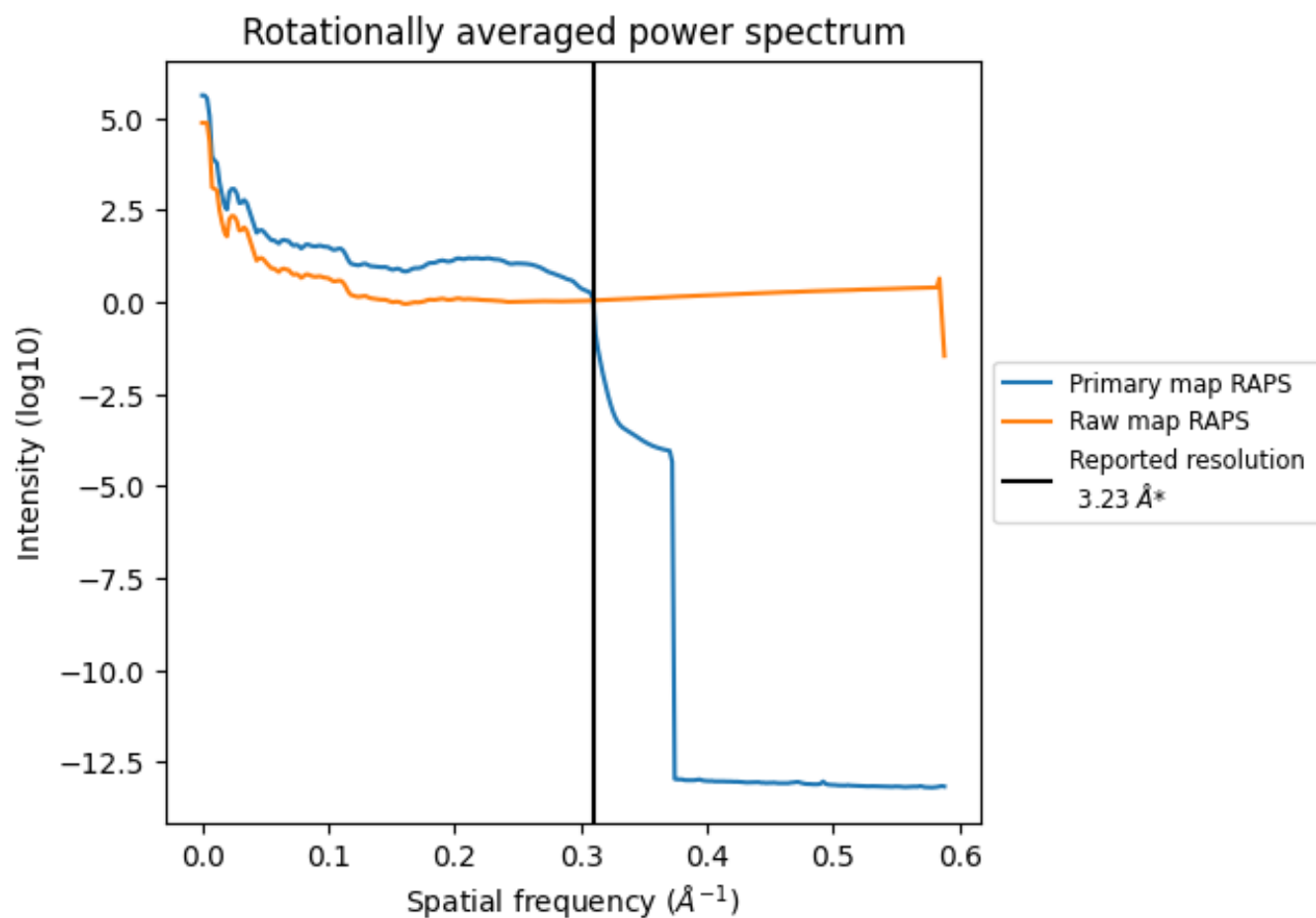
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5481 nm^3 ; this corresponds to an approximate mass of 4951 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

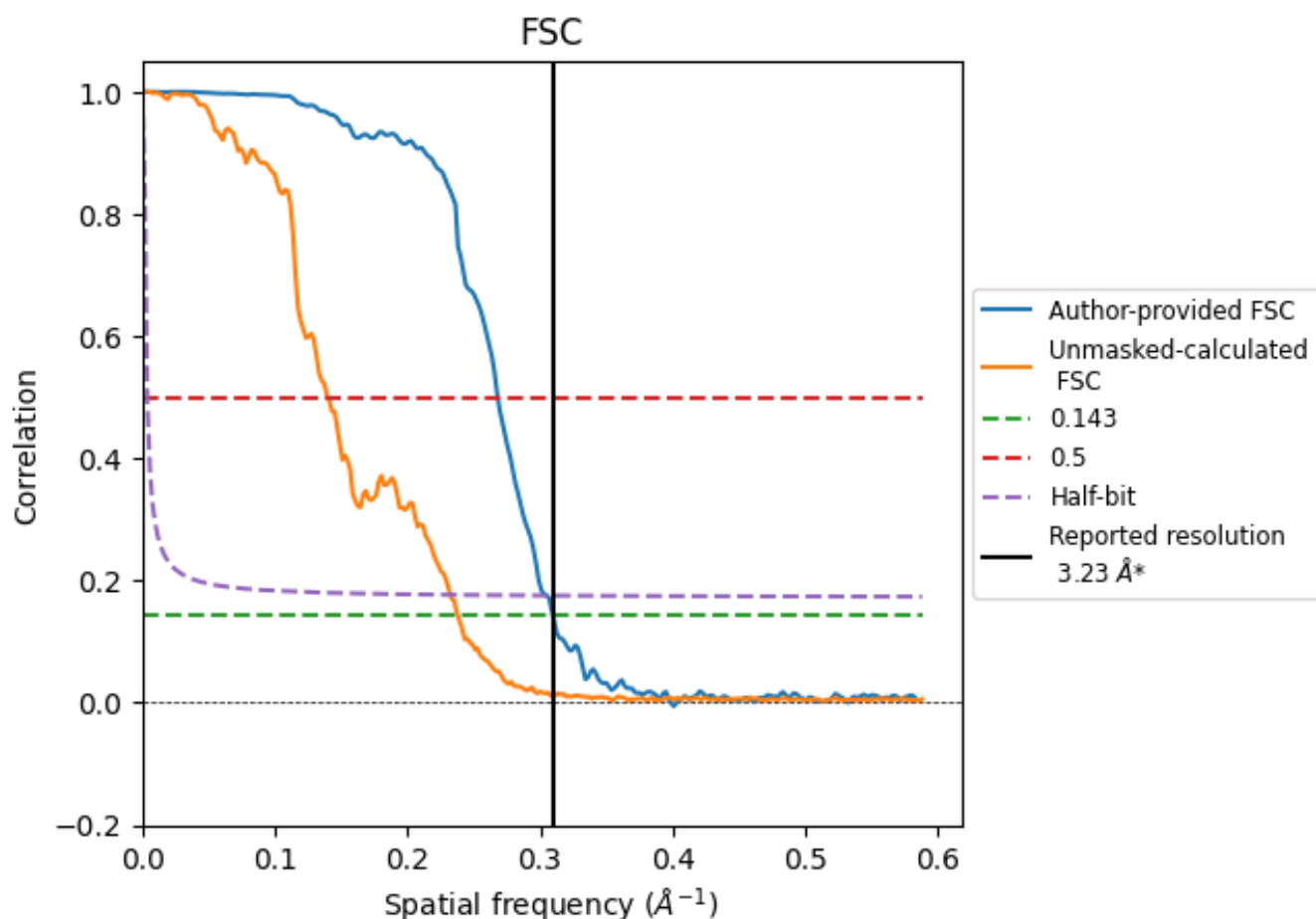


*Reported resolution corresponds to spatial frequency of 0.310 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

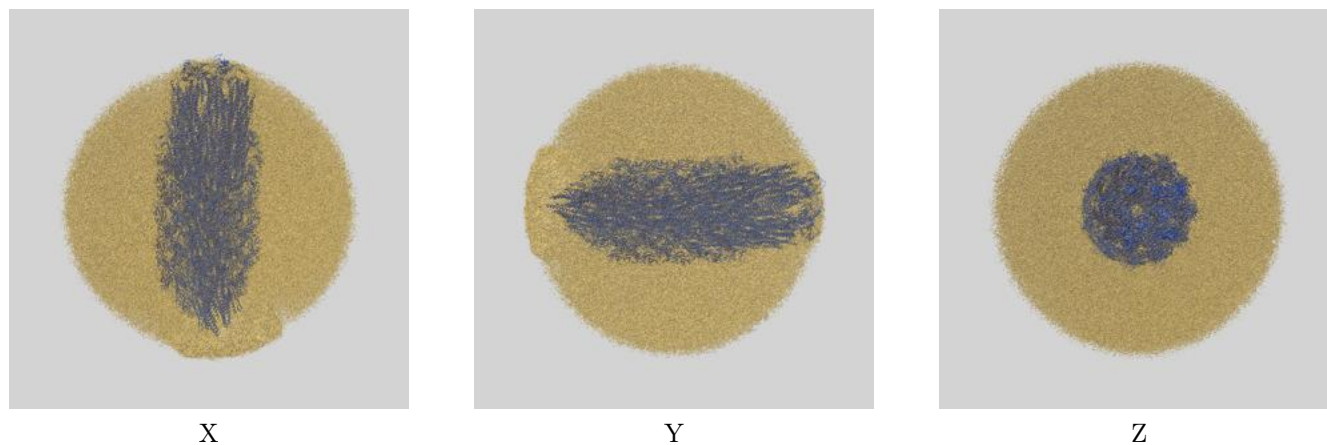
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	3.23	3.73	3.28
Unmasked-calculated*	4.20	7.14	4.30

*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 4.20 differs from the reported value 3.23 by more than 10 %

9 Map-model fit [i](#)

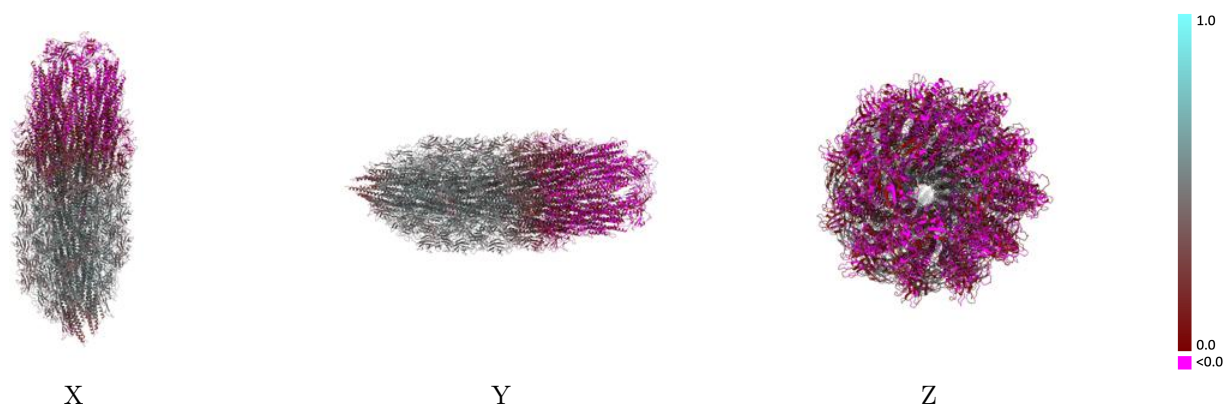
This section contains information regarding the fit between EMDB map EMD-63853 and PDB model 9U4R. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



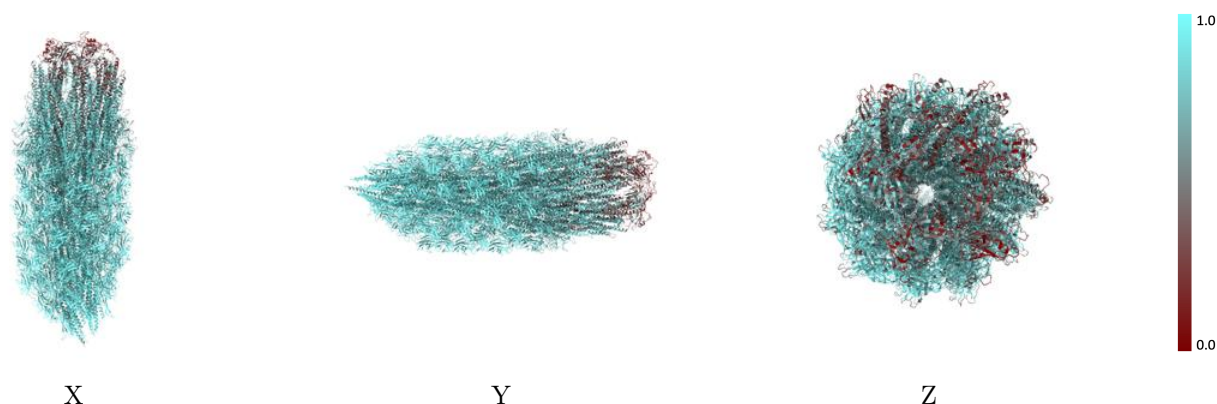
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



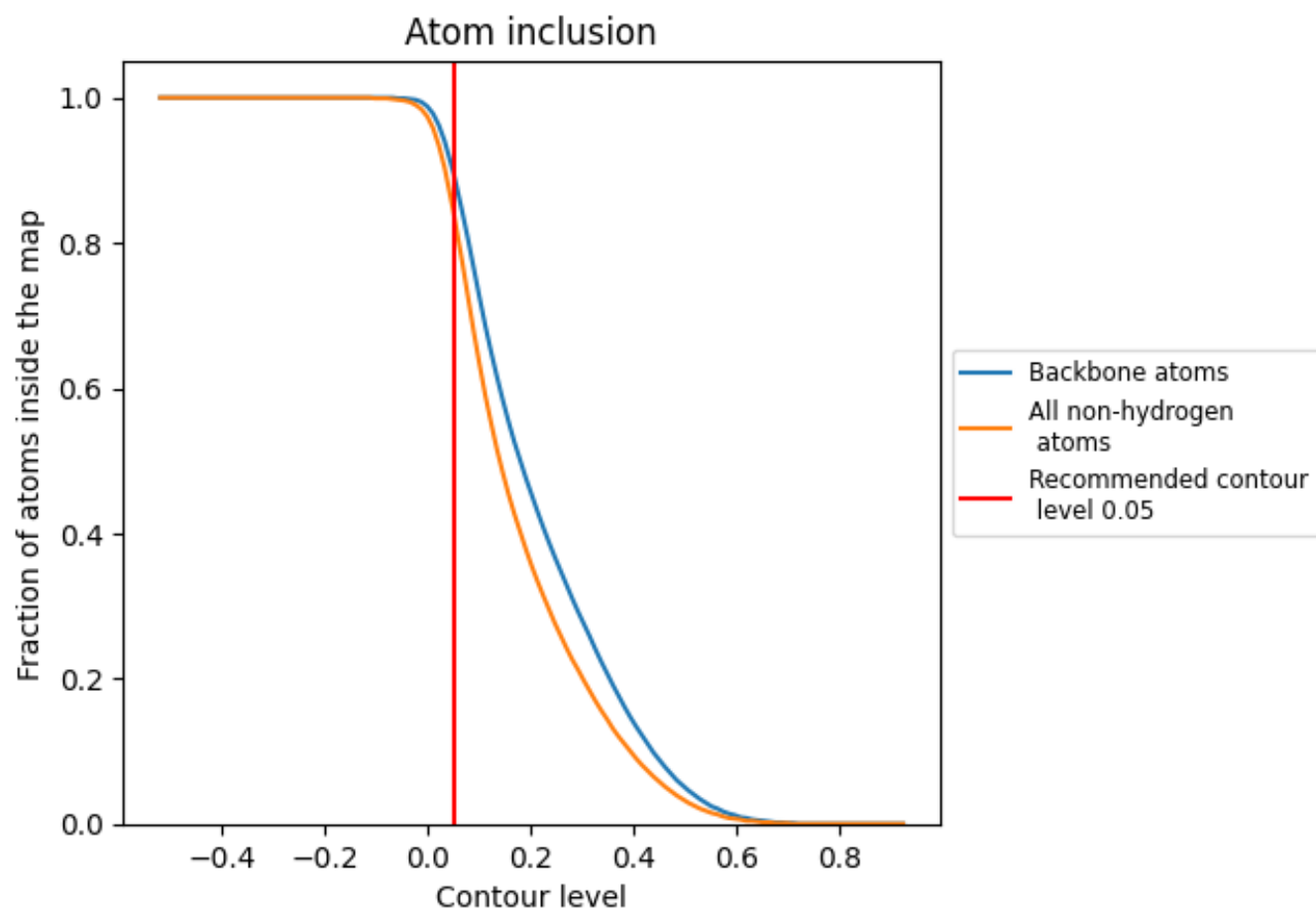
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 84% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8450	 0.3140
AA	 0.3960	 0.0380
AB	 0.4110	 0.0140
AC	 0.4080	 0.0120
AD	 0.4420	 0.0300
AE	 0.4440	 0.0430
BA	 0.7710	 0.1250
BB	 0.6740	 0.0710
BC	 0.7910	 0.0910
BD	 0.5840	 0.0410
BE	 0.7640	 0.0860
BG	 0.7520	 0.1000
BH	 0.8110	 0.1290
BI	 0.7690	 0.1010
BJ	 0.8110	 0.1390
BK	 0.6930	 0.0880
BL	 0.4750	 0.0380
BM	 0.5810	 0.1060
BN	 0.5380	 0.0760
CA	 0.7580	 0.1110
CB	 0.8240	 0.2350
CC	 0.8360	 0.2100
CD	 0.8360	 0.1910
CE	 0.8450	 0.2320
CF	 0.8350	 0.2070
CG	 0.7870	 0.1380
CH	 0.8420	 0.2560
CI	 0.8100	 0.2020
CJ	 0.8490	 0.2160
CK	 0.8060	 0.1750
DA	 0.8200	 0.2810
DB	 0.8640	 0.3150
DC	 0.9340	 0.4280
DD	 0.9240	 0.4070
DE	 0.9370	 0.4040



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Chain	Atom inclusion	Q-score
DF	 0.9370	 0.4410
DG	 0.9270	 0.3730
DH	 0.9410	 0.4210
DI	 0.9020	 0.3700
DJ	 0.9310	 0.4140
DK	 0.8990	 0.3620
EA	 0.9410	 0.4610
EB	 0.9320	 0.4540
EC	 0.9480	 0.4830
ED	 0.9440	 0.4830
EE	 0.9450	 0.4750
EF	 0.9520	 0.4830
EG	 0.9500	 0.4680
EH	 0.9520	 0.4760
EI	 0.9410	 0.4450
EJ	 0.9450	 0.4700
EK	 0.9270	 0.4390
FA	 0.9460	 0.4930
FB	 0.9360	 0.4760
FC	 0.9440	 0.4900
FD	 0.9380	 0.4770
FE	 0.9560	 0.4860
FF	 0.9460	 0.4620
FG	 0.9500	 0.4660
FH	 0.9540	 0.4590
FI	 0.9500	 0.4820
FJ	 0.9530	 0.4890
FK	 0.9310	 0.4690
GA	 0.9410	 0.4680
GB	 0.9280	 0.4510
GC	 0.9280	 0.4390
GD	 0.9290	 0.4320
GE	 0.9350	 0.4060
GF	 0.9240	 0.3460
GG	 0.9460	 0.4200
GH	 0.9430	 0.3840
GI	 0.9490	 0.4370
GJ	 0.9250	 0.3960
GK	 0.9350	 0.4590