



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:24 PM UTC

PDB ID : 8WLQ / pdb_00008wlq
EMDB ID : EMD-37628
Title : Cryo-EM structure of the whole rod-export apparatus with hook within the flagellar motor-hook complex in the CCW state.
Authors : Tan, J.X.; Zhang, L.; Zhou, Y.; Zhu, Y.Q.
Deposited on : 2023-09-30
Resolution : 3.80 Å(reported)
Based on initial model : .

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:

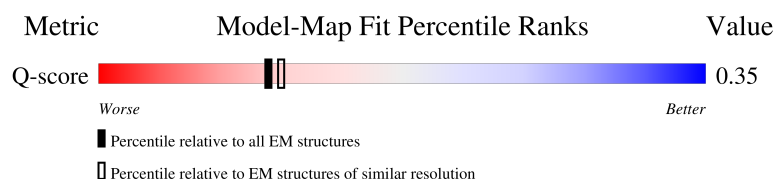
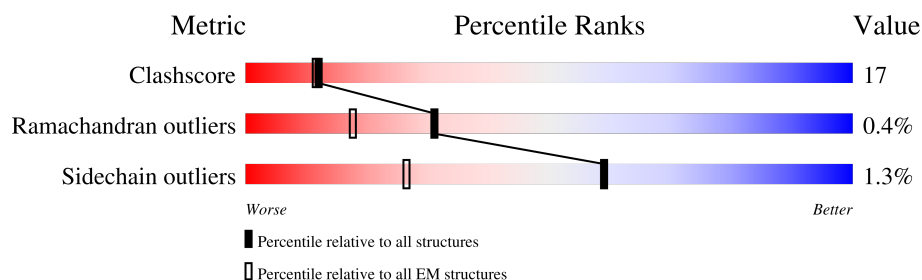
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 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	10198 (3.30 - 4.30)

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	0	260	9% 59% 34% 5%
1	1	260	15% 65% 30% • •
1	2	260	12% 67% 31% •
1	3	260	11% 65% 35% •

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Mol	Chain	Length	Quality of chain
1	4	260	13% 65% 34% .
1	5	260	12% 63% 35% .
1	6	260	8% 66% 33% .
1	7	260	11% 67% 32% .
1	8	260	8% 67% 30% .
1	9	260	13% 71% 28% .
1	ZA	260	12% 65% 33% .
1	ZB	260	13% 67% 31% .
1	ZC	260	8% 68% 31% .
1	ZD	260	11% 63% 35% .
1	ZE	260	13% 69% 29% .
1	r	260	18% 70% 27% ..
1	s	260	10% 56% 40% ..
1	t	260	11% 62% 33% ..
1	u	260	10% 61% 35% ..
1	v	260	12% 62% 33% ..
1	w	260	11% 63% 30% 7%
1	x	260	11% 59% 35% . 5%
1	y	260	11% 59% 33% . 5%
1	z	260	12% 66% 28% . 5%
2	ZF	403	47% 78% 21% .
2	ZG	403	20% 73% 25% .
2	ZH	403	14% 76% 23% .
2	ZI	403	13% 76% 22% .
2	ZJ	403	12% 76% 23%

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Mol	Chain	Length	Quality of chain
2	ZK	403	14% 77% 22%
2	ZL	403	12% 76% 23%
2	ZM	403	13% 72% 27%
2	ZN	403	13% 76% 23%
2	ZO	403	12% 76% 22%
2	ZP	403	12% 69% 30%
2	ZQ	403	13% 71% 29%
2	ZR	403	15% 74% 25%
2	ZS	403	16% 70% 29%
2	ZT	403	16% 73% 26%
2	ZU	403	18% 67% 32%
2	ZV	403	18% 72% 27%
2	ZW	403	23% 72% 26%
2	ZX	403	22% 76% 23%
2	ZY	403	30% 73% 26%
2	ZZ	403	31% 78% 21%
2	Za	403	38% 76% 23%
2	Zb	403	42% 76% 23%
2	Zc	403	44% 75% 24%
2	Zd	403	46% 79% 20%
2	Ze	403	52% 80% 19%
2	Zf	403	54% 75% 24%
2	Zg	403	57% 81% 19%
2	Zh	403	58% 84% 15%
3	A	89	84% 58% 33% 6%

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Mol	Chain	Length	Quality of chain
3	B	89	
3	C	89	
3	D	89	
4	E	264	
5	F	245	
5	G	245	
5	H	245	
5	I	245	
5	J	245	
6	K	104	
6	L	104	
6	M	104	
6	N	104	
6	O	104	
6	P	104	
7	Q	138	
7	R	138	
7	S	138	
7	T	138	
7	U	138	
8	V	134	
8	W	134	
8	X	134	
8	Y	134	
8	Z	134	

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Mol	Chain	Length	Quality of chain
8	a	134	
9	b	560	
9	c	560	
9	d	560	
9	e	560	
9	f	560	
9	g	560	
9	h	560	
9	i	560	
9	j	560	
9	k	560	
9	l	560	
10	m	251	
10	n	251	
10	o	251	
10	p	251	
10	q	251	

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 167758 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 basal-body rod protein FlgG.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	1	252	Total	C	N	O	S	0	0
			1894	1172	331	385	6		
1	2	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	3	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	4	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	5	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	6	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	7	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	8	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	9	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZA	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZB	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZC	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZD	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	ZE	260	Total	C	N	O	S	0	0
			1949	1202	341	400	6		
1	r	254	Total	C	N	O	S	0	0
			1903	1175	334	389	5		
1	s	255	Total	C	N	O	S	0	0
			1911	1181	335	390	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	t	256	Total	C	N	O	S	0	0
			1919	1186	336	391	6		
1	u	254	Total	C	N	O	S	0	0
			1903	1175	334	389	5		
1	v	255	Total	C	N	O	S	0	0
			1911	1181	335	390	5		
1	w	243	Total	C	N	O	S	0	0
			1823	1127	318	373	5		
1	x	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	y	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		
1	z	248	Total	C	N	O	S	0	0
			1866	1154	327	379	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	ZF	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZG	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZH	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZI	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZJ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZK	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZL	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZM	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZN	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZO	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZP	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZQ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	ZR	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZS	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZT	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZU	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZV	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZW	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZX	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZY	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	ZZ	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Za	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zb	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zc	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zd	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Ze	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zf	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zg	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		
2	Zh	401	Total	C	N	O	S	0	0
			2947	1814	507	618	8		

- Molecule 3 is a protein called Flagellar biosynthetic protein FliQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	B	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	89	Total	C	N	O	S	0	0
			670	449	100	114	7		
3	D	89	Total	C	N	O	S	0	0
			670	449	100	114	7		

- Molecule 4 is a protein called Flagellar biosynthetic protein FliR.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	253	Total	C	N	O	S	0	0
			1945	1305	307	318	15		

- Molecule 5 is a protein called Flagellar biosynthetic protein FliP.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	207	Total	C	N	O	S	0	0
			1605	1072	249	272	12		
5	G	209	Total	C	N	O	S	0	0
			1626	1086	252	276	12		
5	H	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
5	I	208	Total	C	N	O	S	0	0
			1614	1077	251	274	12		
5	J	209	Total	C	N	O	S	0	0
			1623	1084	251	276	12		

- Molecule 6 is a protein called Flagellar hook-basal body complex protein FliE.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	40	Total	C	N	O	S	0	0
			300	185	52	57	6		
6	L	72	Total	C	N	O	S	0	0
			543	335	99	103	6		
6	M	74	Total	C	N	O	S	0	0
			557	344	101	106	6		
6	N	74	Total	C	N	O	S	0	0
			557	344	101	106	6		
6	O	74	Total	C	N	O	S	0	0
			557	344	101	106	6		
6	P	73	Total	C	N	O	S	0	0
			550	340	100	104	6		

- Molecule 7 is a protein called Flagellar basal body rod protein FlgB.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	119	Total	C	N	O	S	0	0
			922	565	169	183	5		
7	R	108	Total	C	N	O	S	0	0
			848	523	155	165	5		
7	S	108	Total	C	N	O	S	0	0
			848	523	155	165	5		
7	T	110	Total	C	N	O	S	0	0
			863	531	160	167	5		
7	U	106	Total	C	N	O	S	0	0
			832	514	150	163	5		

- Molecule 8 is a protein called Flagellar basal-body rod protein FlgC.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
8	W	132	Total	C	N	O	S	0	0
			964	601	166	192	5		
8	X	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
8	Y	133	Total	C	N	O	S	0	0
			969	604	167	193	5		
8	Z	131	Total	C	N	O	S	0	0
			956	595	165	191	5		
8	a	133	Total	C	N	O	S	0	0
			969	604	167	193	5		

- Molecule 9 is a protein called Flagellar M-ring protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	b	13	Total	C	N	O	0	0
			81	50	15	16		
9	c	16	Total	C	N	O	0	0
			103	64	19	20		
9	d	20	Total	C	N	O	0	0
			133	83	23	27		
9	e	16	Total	C	N	O	0	0
			103	64	19	20		
9	f	21	Total	C	N	O	0	0
			140	88	24	28		
9	g	16	Total	C	N	O	0	0
			103	64	19	20		
9	h	21	Total	C	N	O	0	0
			140	88	24	28		

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Mol	Chain	Residues	Atoms				AltConf	Trace
9	i	16	Total	C	N	O	0	0
			103	64	19	20		
9	j	20	Total	C	N	O	0	0
			133	83	23	27		
9	k	16	Total	C	N	O	0	0
			103	64	19	20		
9	l	21	Total	C	N	O	0	0
			140	88	24	28		

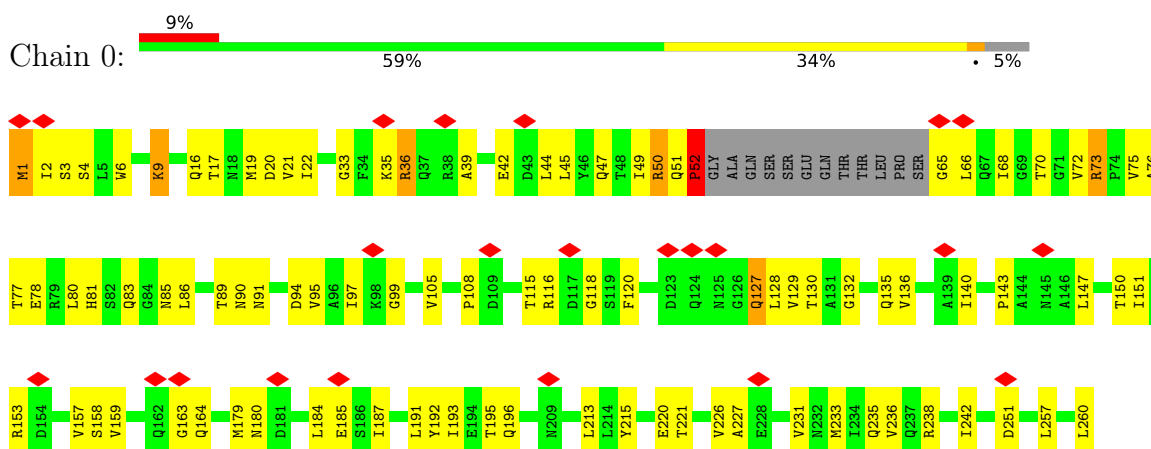
- Molecule 10 is a protein called Flagellar basal-body rod protein FlgF.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	248	Total	C	N	O	S	0	0
			1804	1106	324	367	7		
10	n	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		
10	o	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
10	p	250	Total	C	N	O	S	0	0
			1820	1116	326	369	9		
10	q	249	Total	C	N	O	S	0	0
			1812	1111	325	368	8		

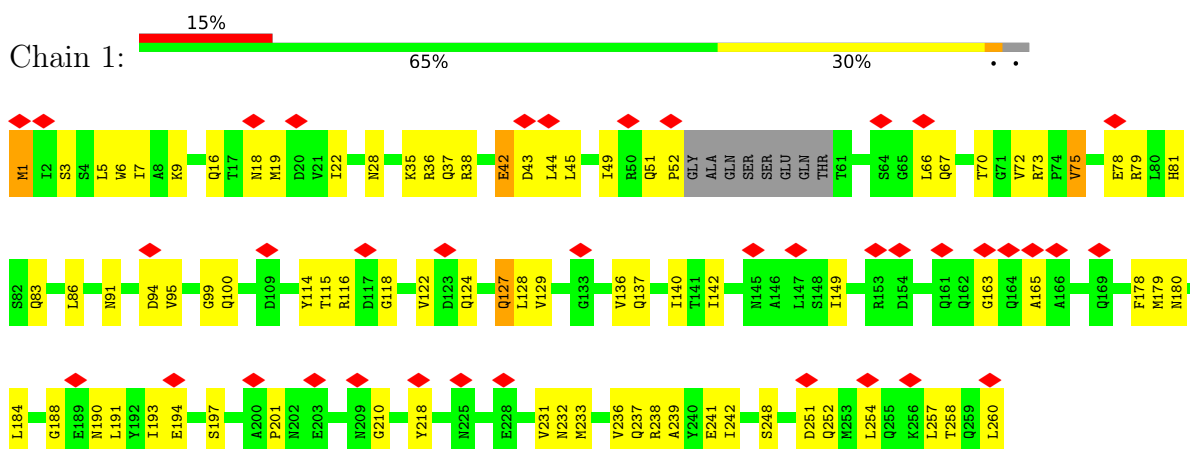
3 Residue-property plots

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.

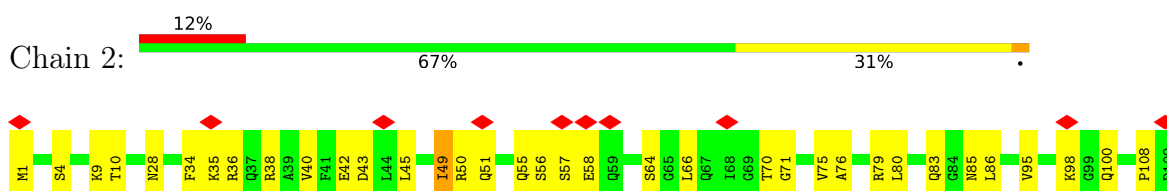
- Molecule 1: Flagellar basal-body rod protein FlgG

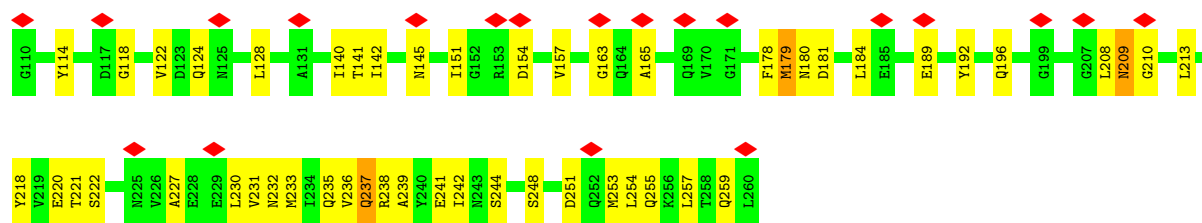


- Molecule 1: Flagellar basal-body rod protein FlgG

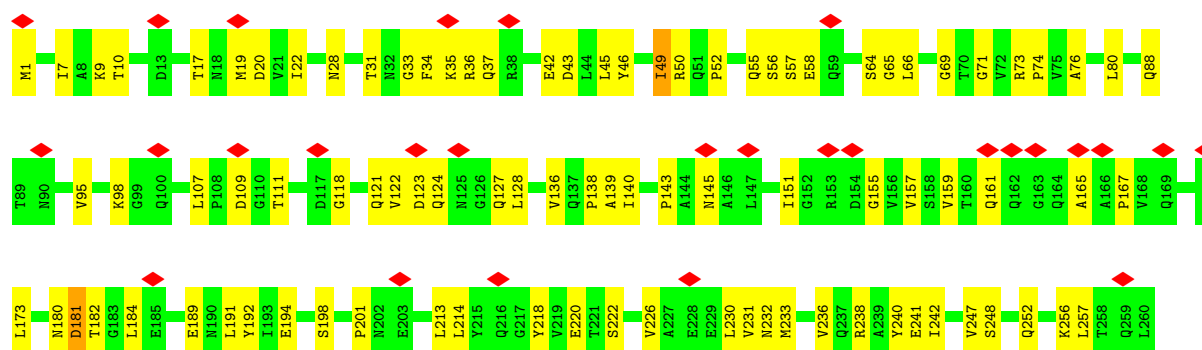


- Molecule 1: Flagellar basal-body rod protein FlgG

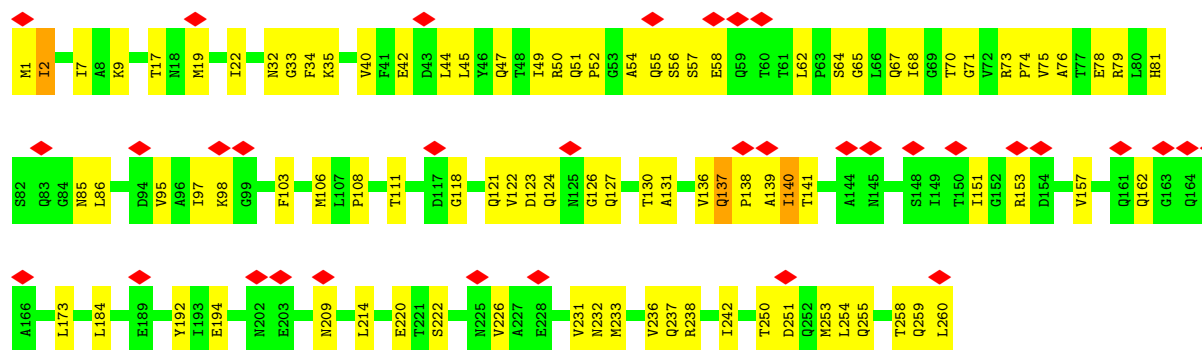




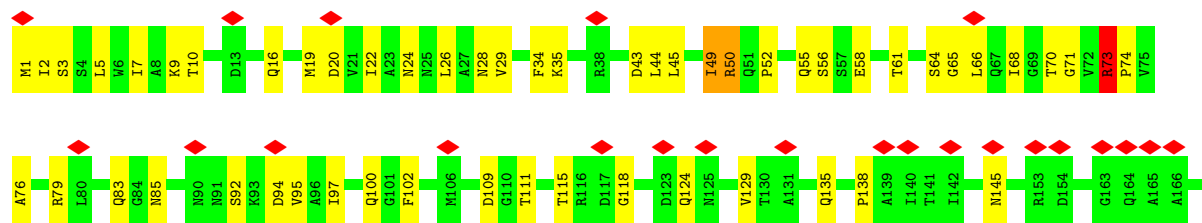
• Molecule 1: Flagellar basal-body rod protein FlgG

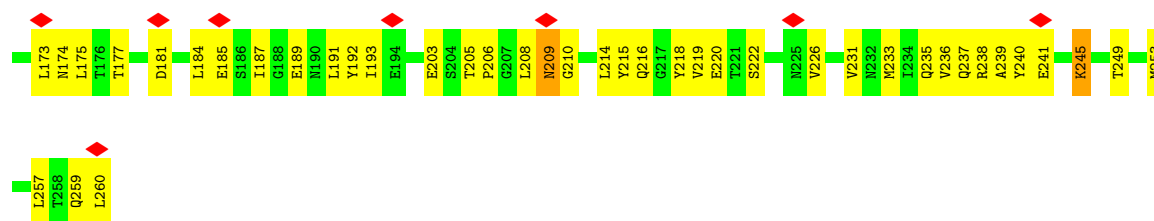


• Molecule 1: Flagellar basal-body rod protein FlgG

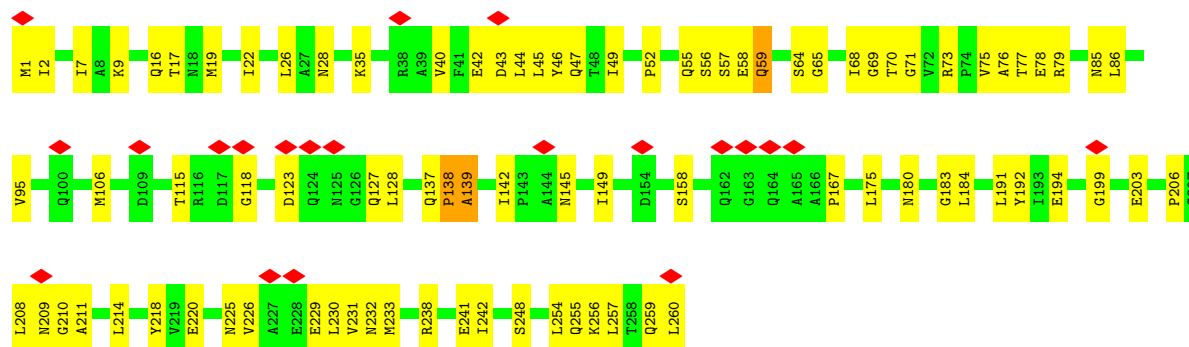


• Molecule 1: Flagellar basal-body rod protein FlgG

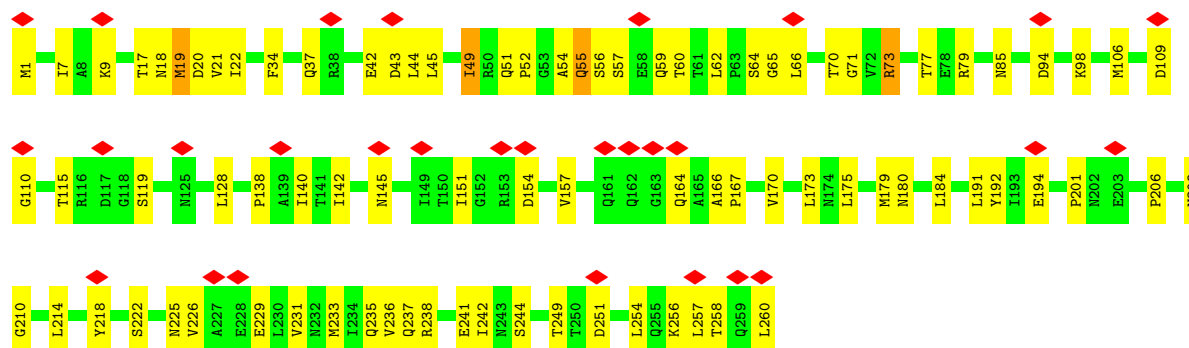




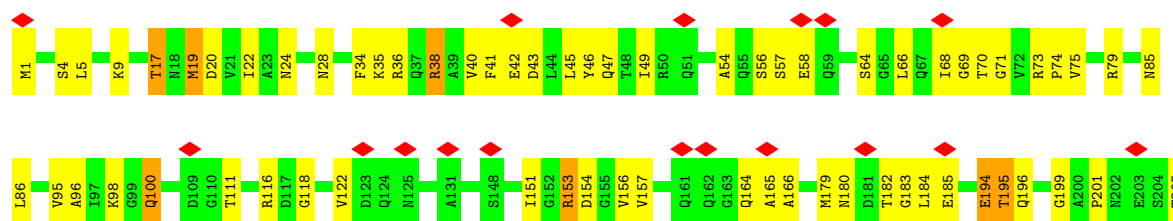
• Molecule 1: Flagellar basal-body rod protein FlgG

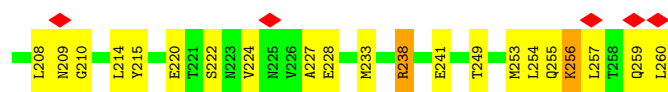


• Molecule 1: Flagellar basal-body rod protein FlgG

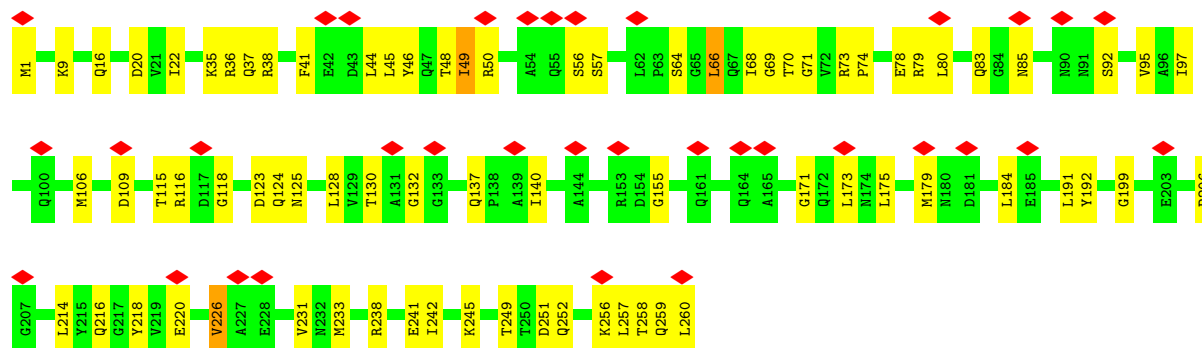


• Molecule 1: Flagellar basal-body rod protein FlgG

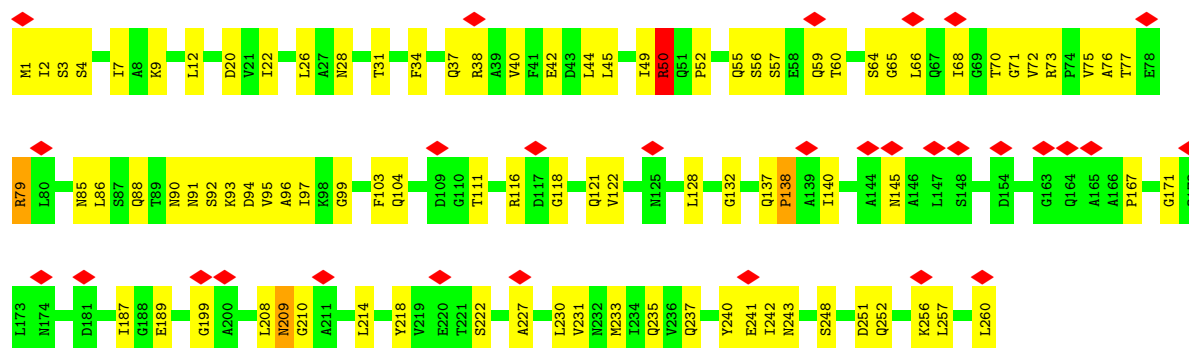




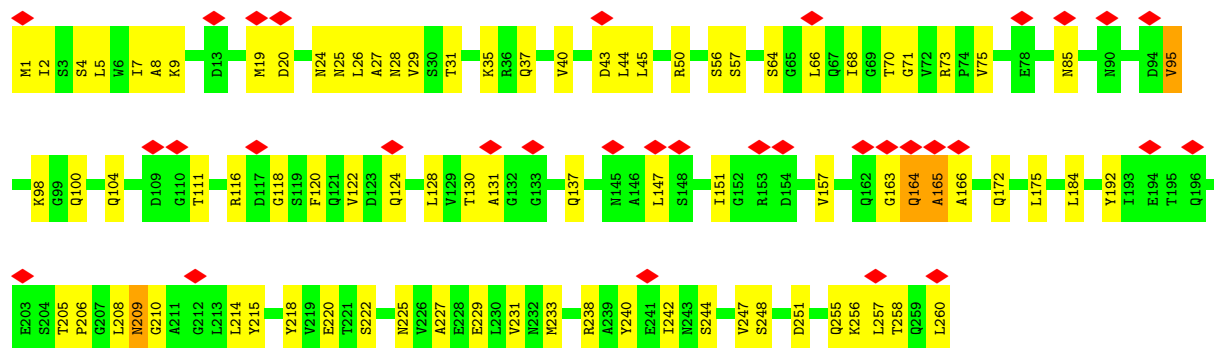
- Molecule 1: Flagellar basal-body rod protein FlgG



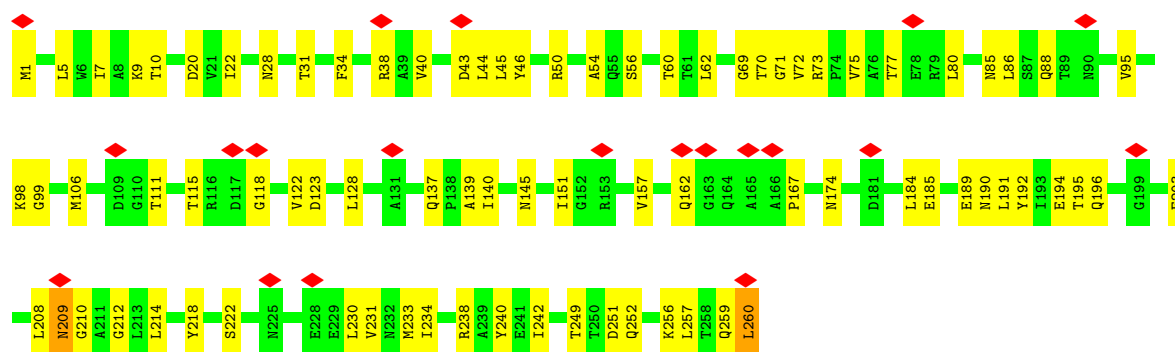
- Molecule 1: Flagellar basal-body rod protein FlgG



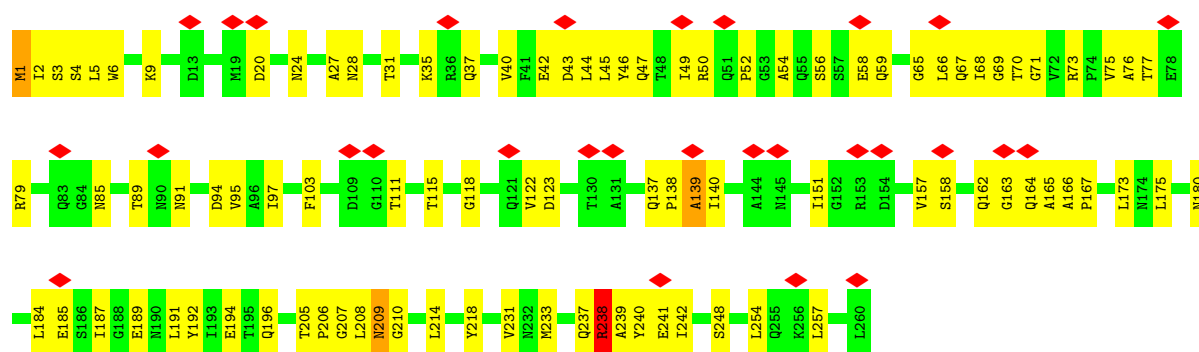
- Molecule 1: Flagellar basal-body rod protein FlgG



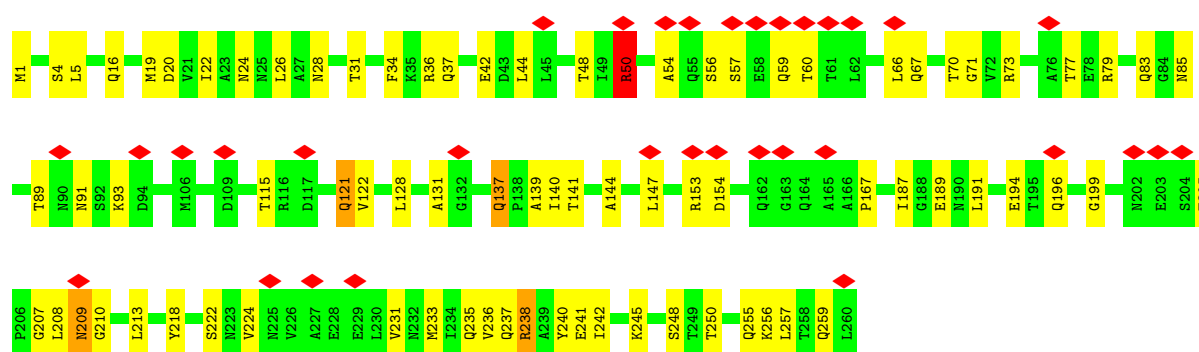
- Molecule 1: Flagellar basal-body rod protein FlgG



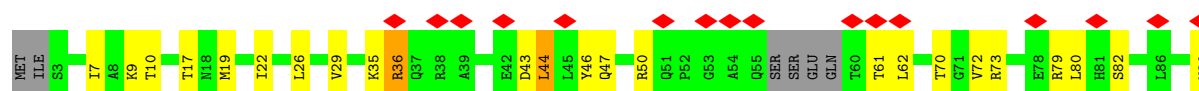
• Molecule 1: Flagellar basal-body rod protein FlgG

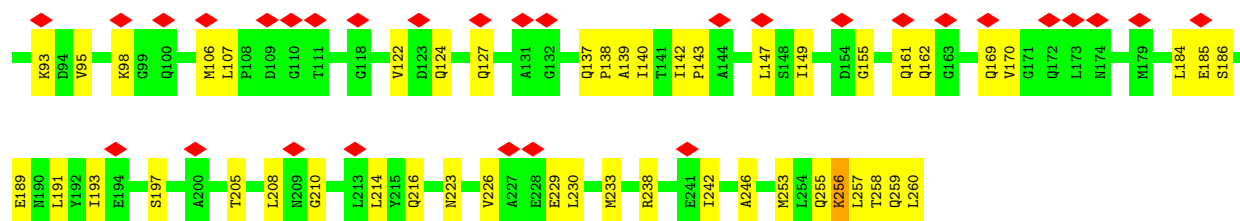


• Molecule 1: Flagellar basal-body rod protein FlgG

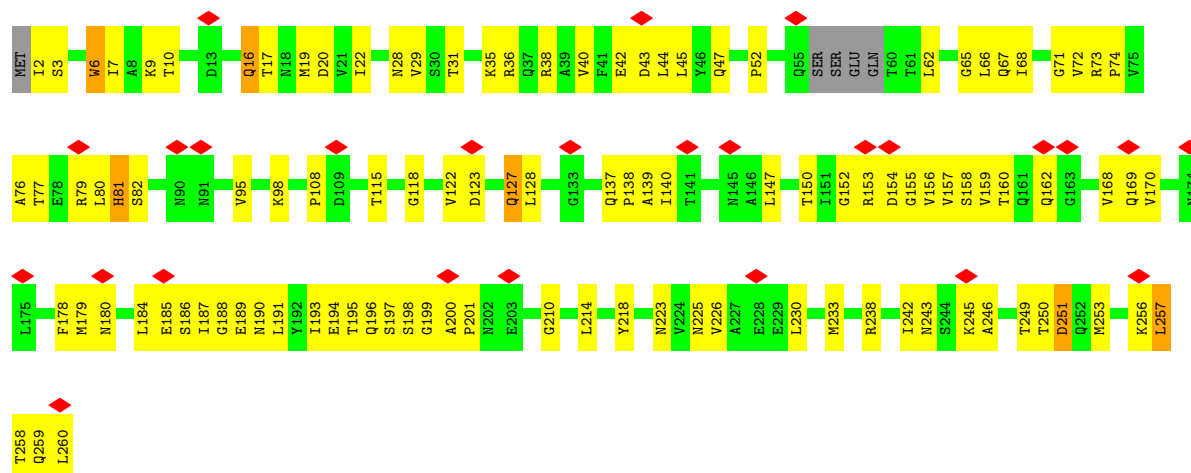


• Molecule 1: Flagellar basal-body rod protein FlgG

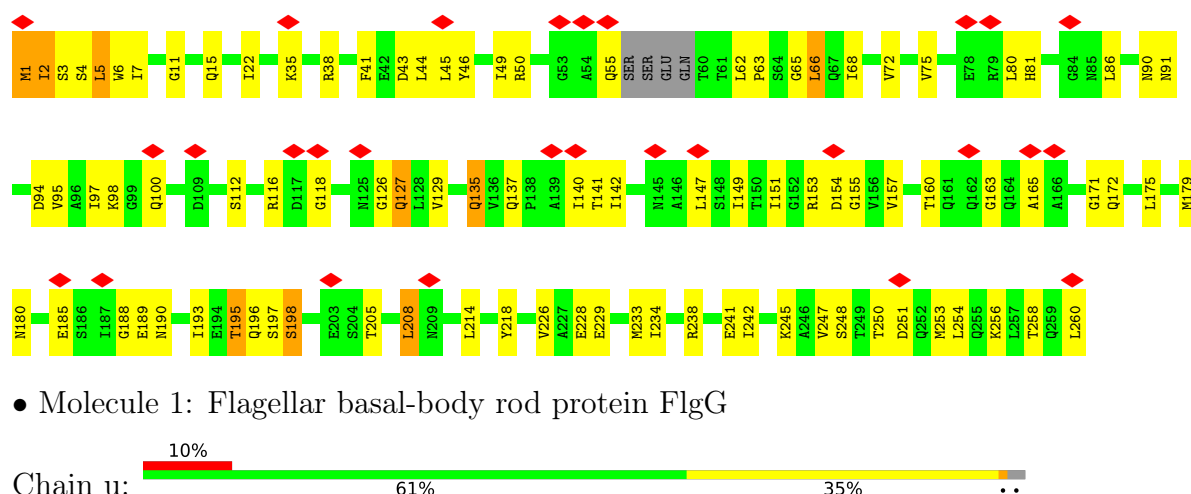




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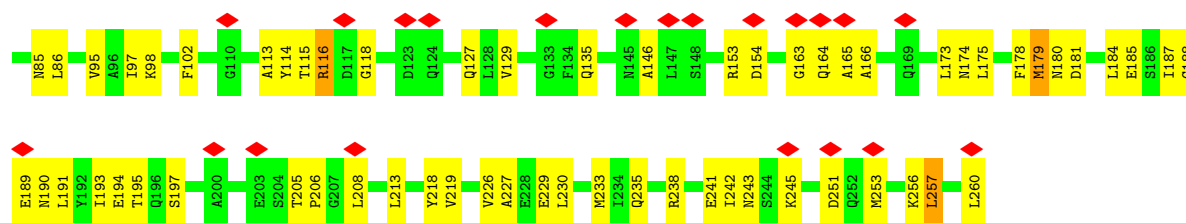


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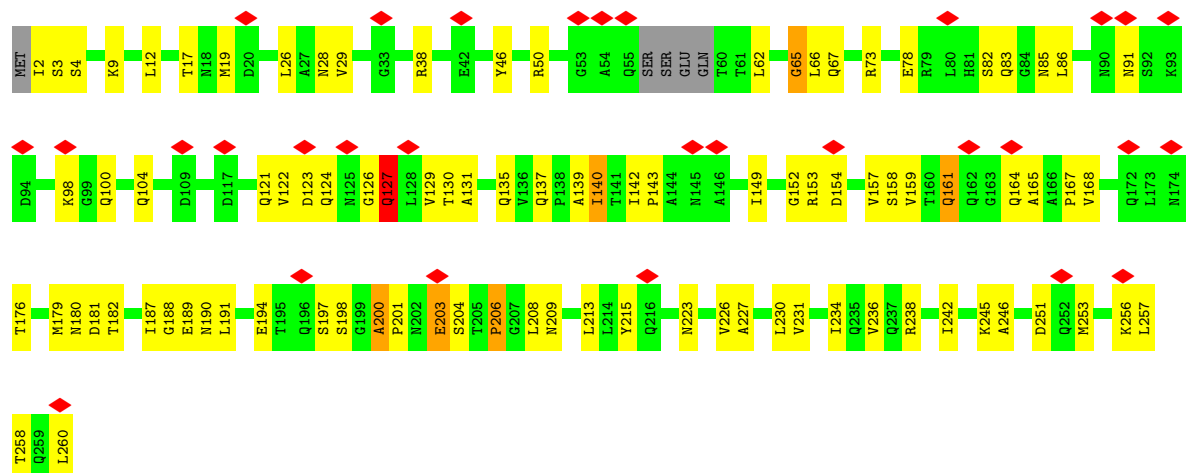


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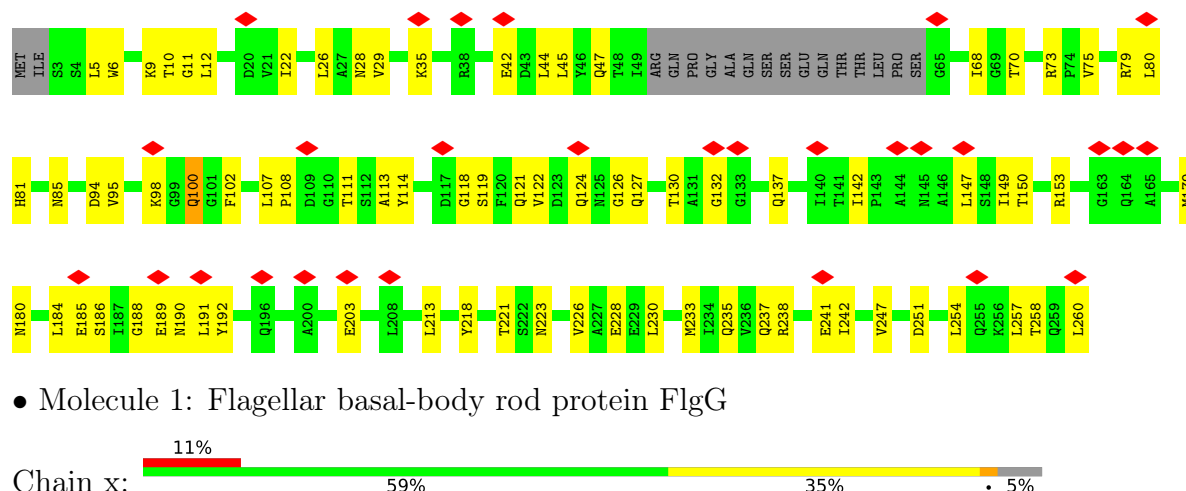




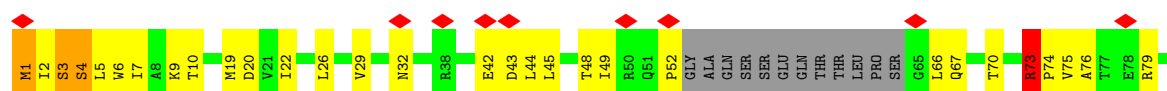
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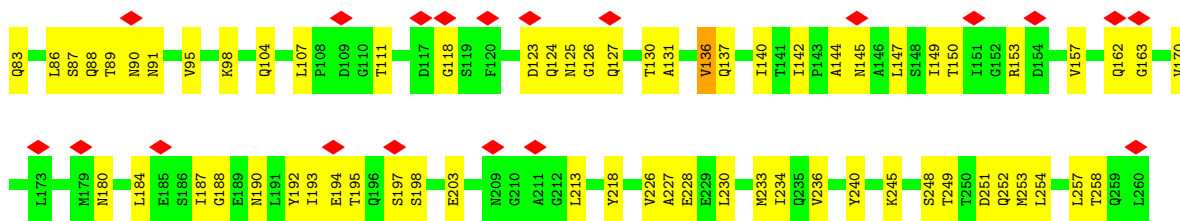


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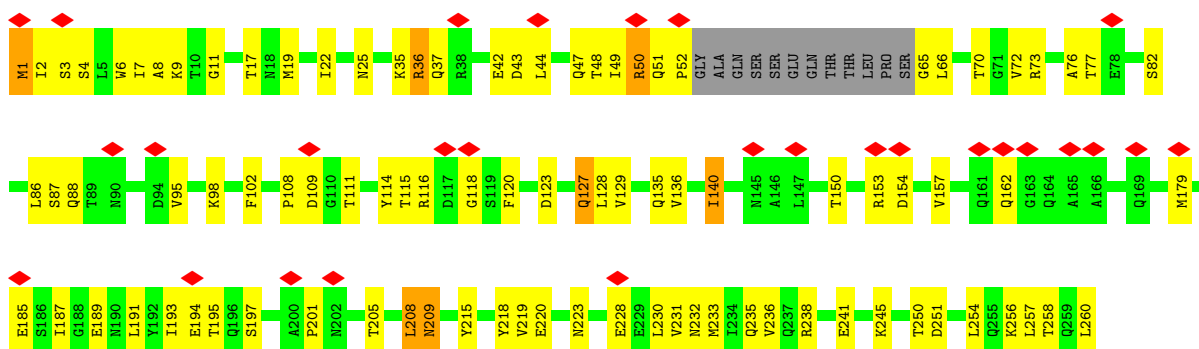


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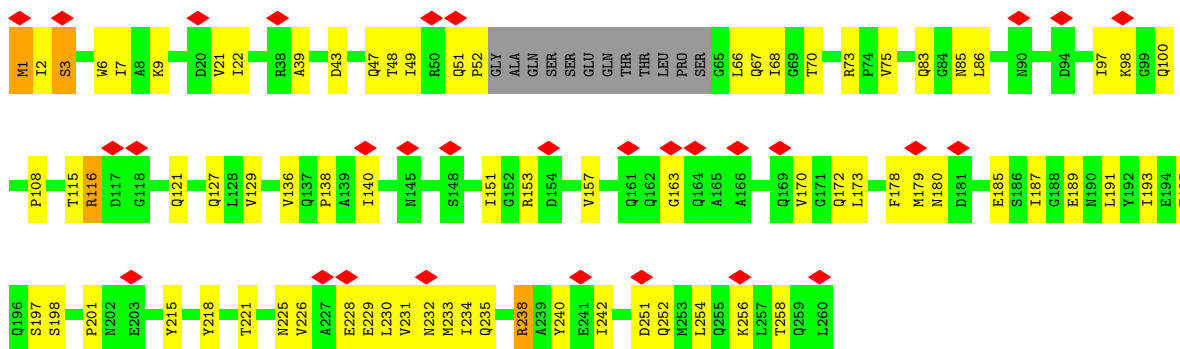




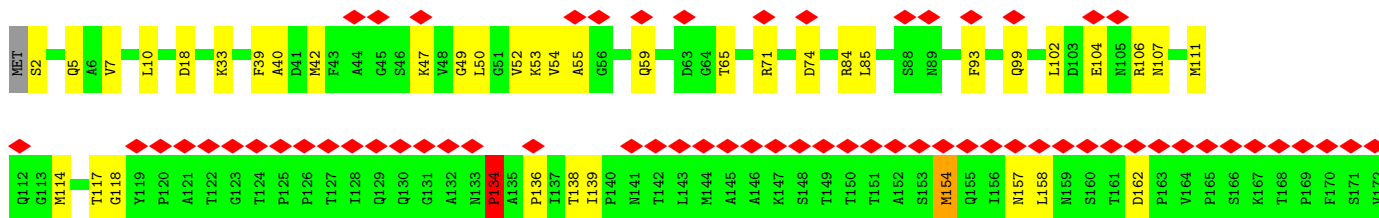
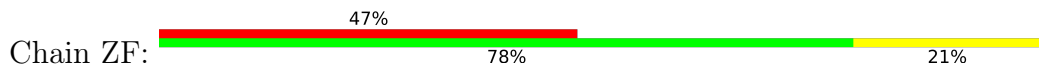
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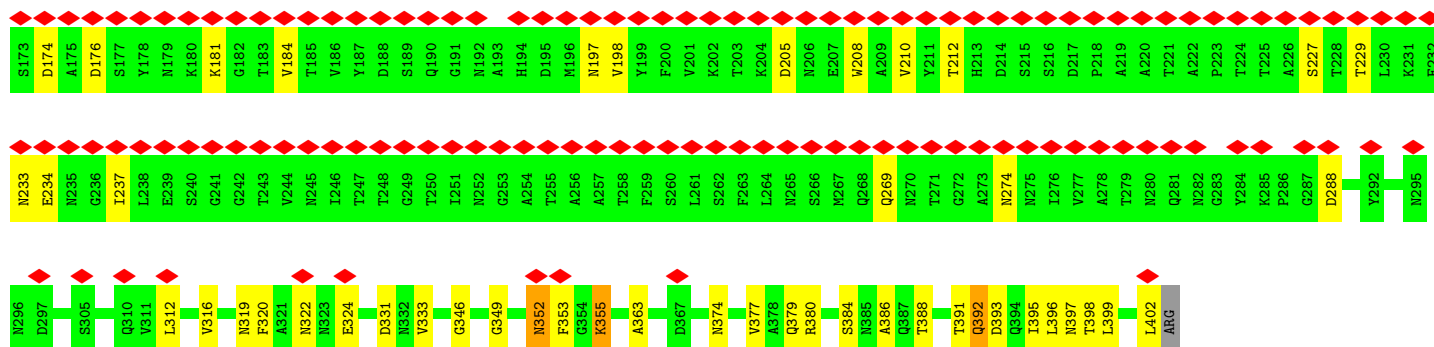


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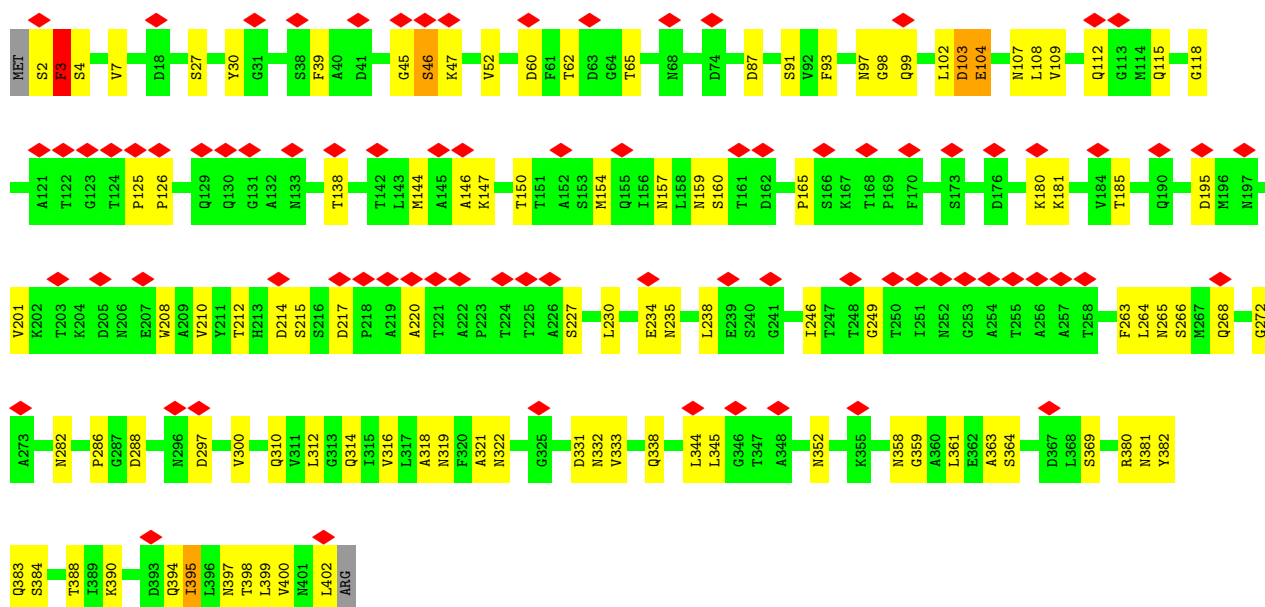
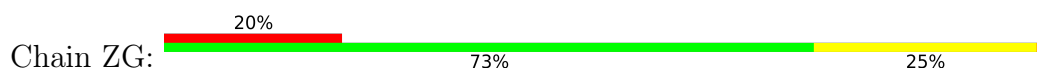


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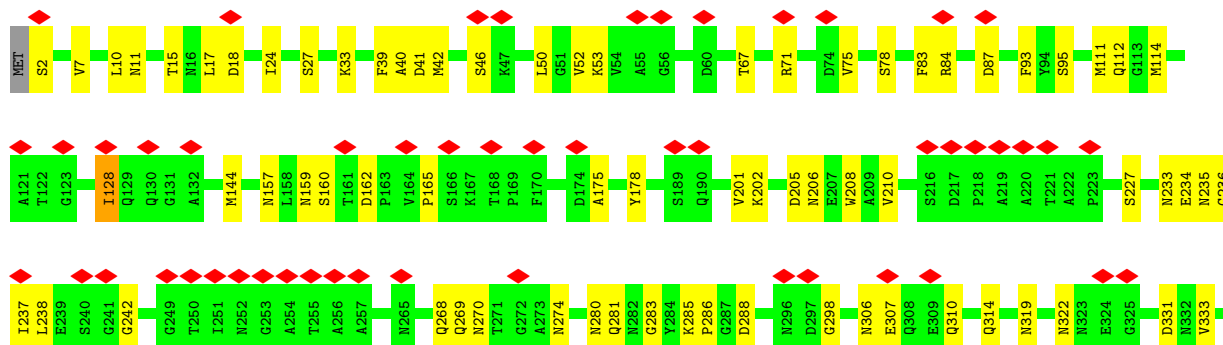
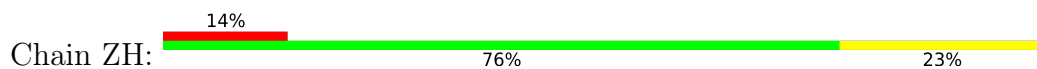


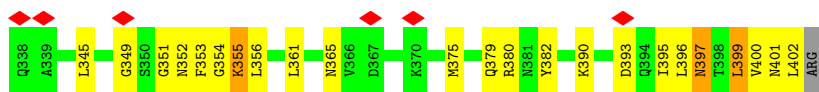


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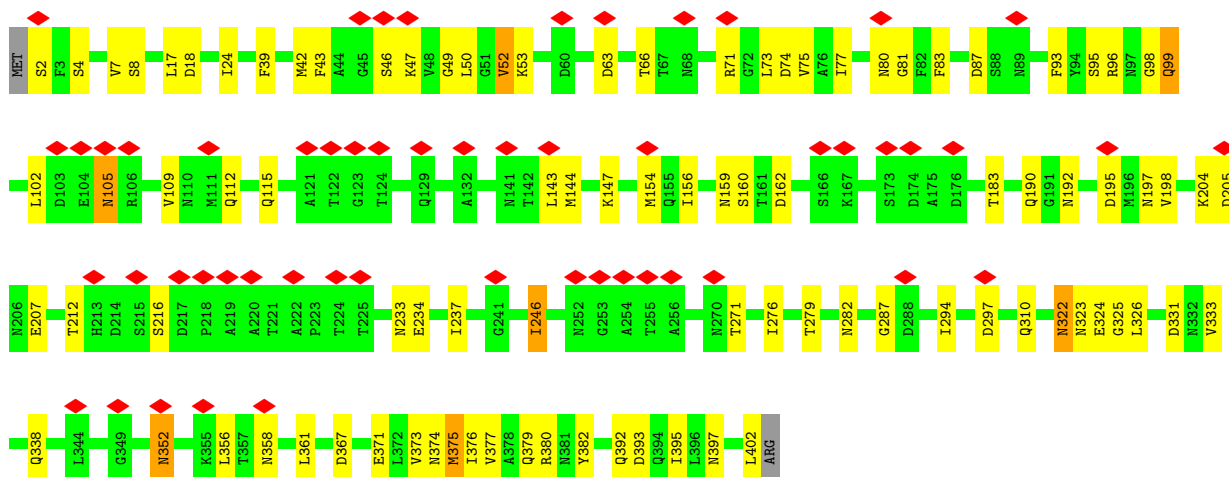
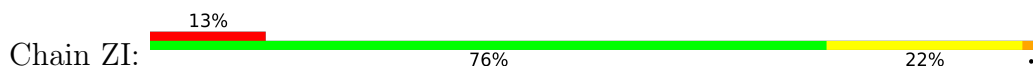


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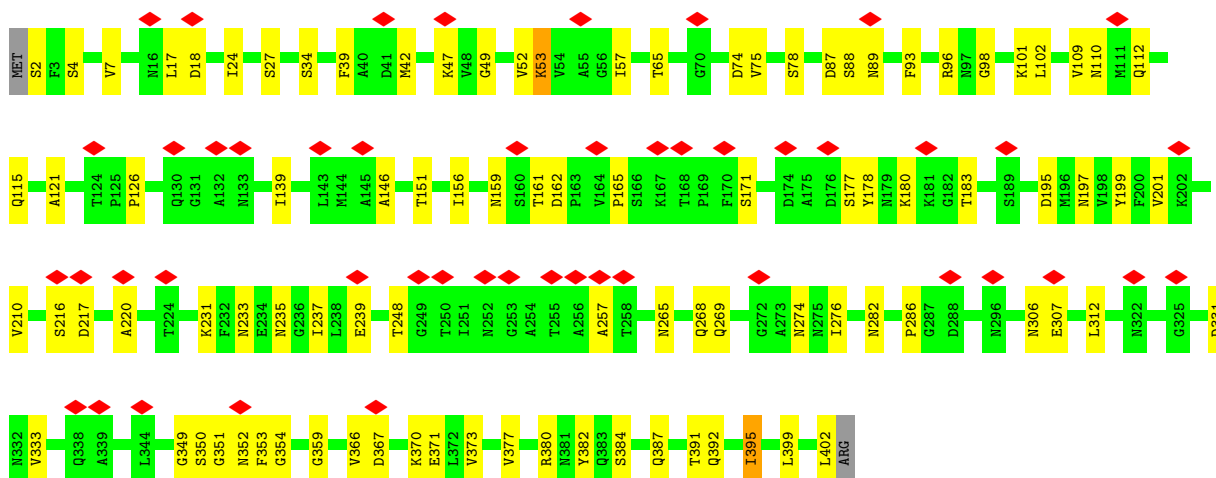
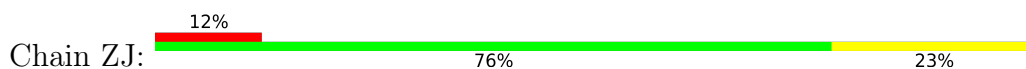




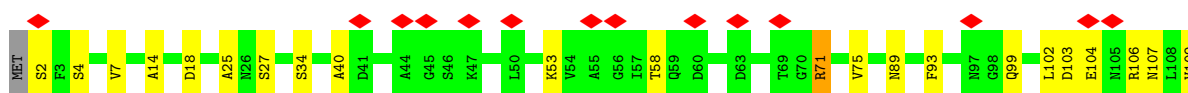
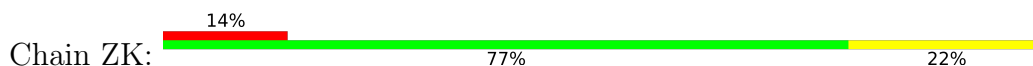
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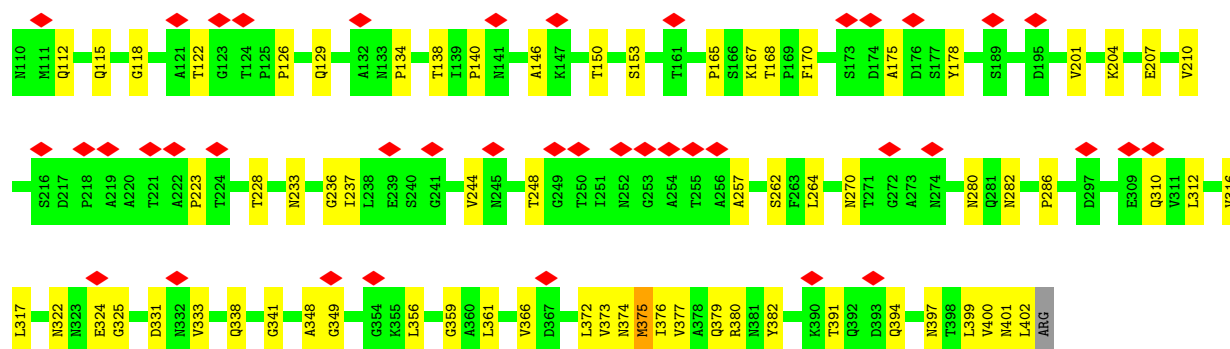


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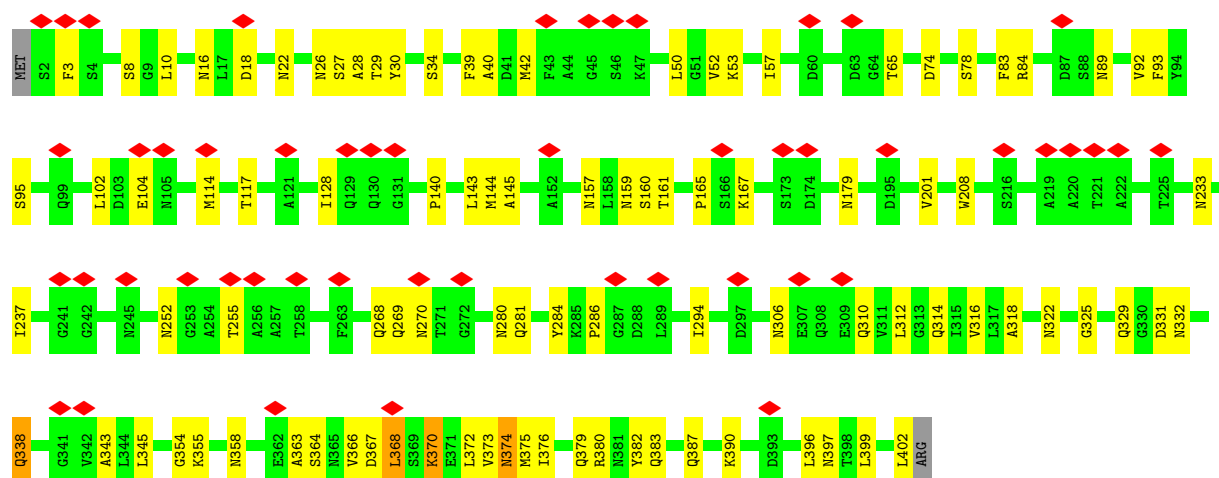
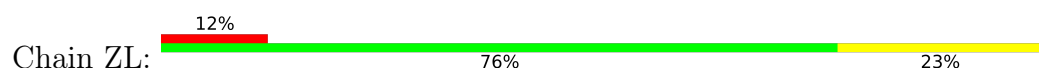


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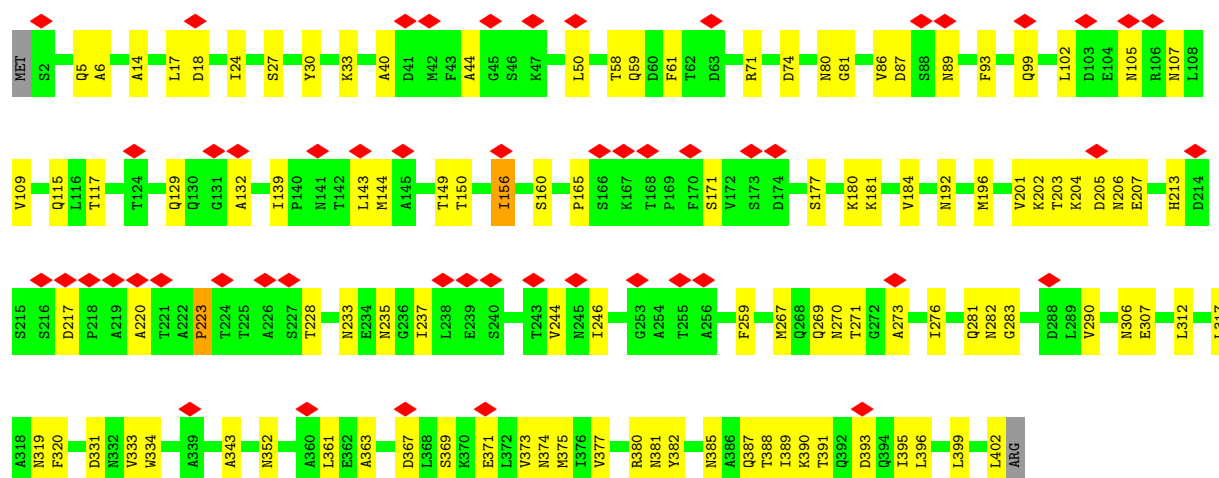
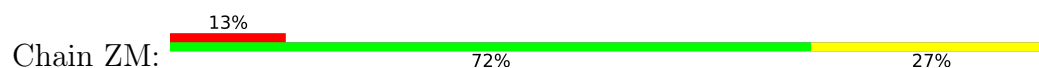




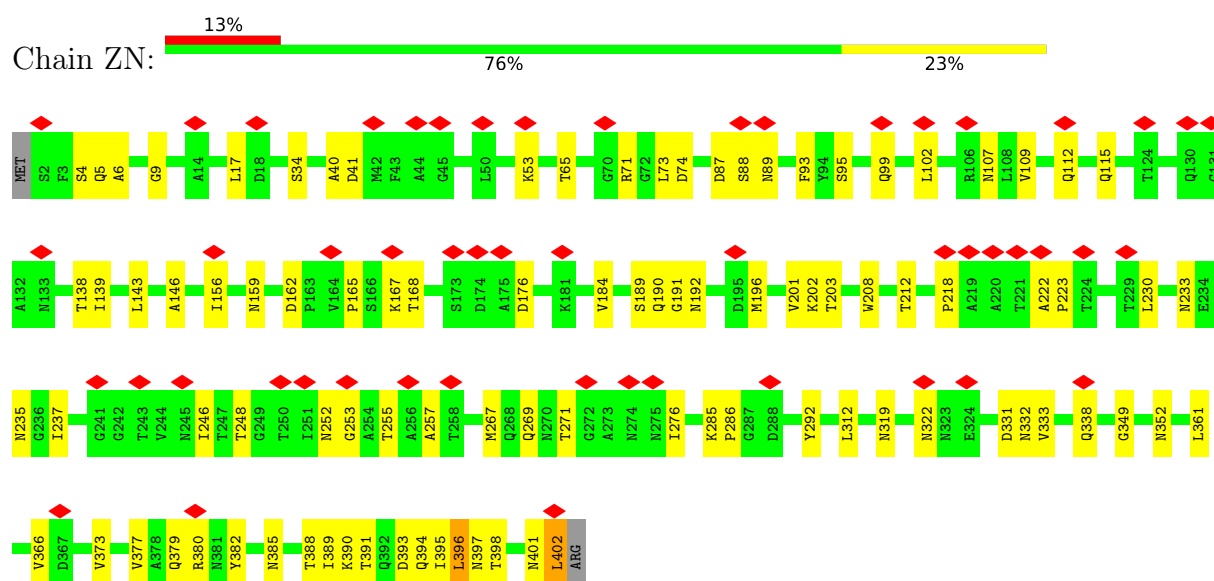
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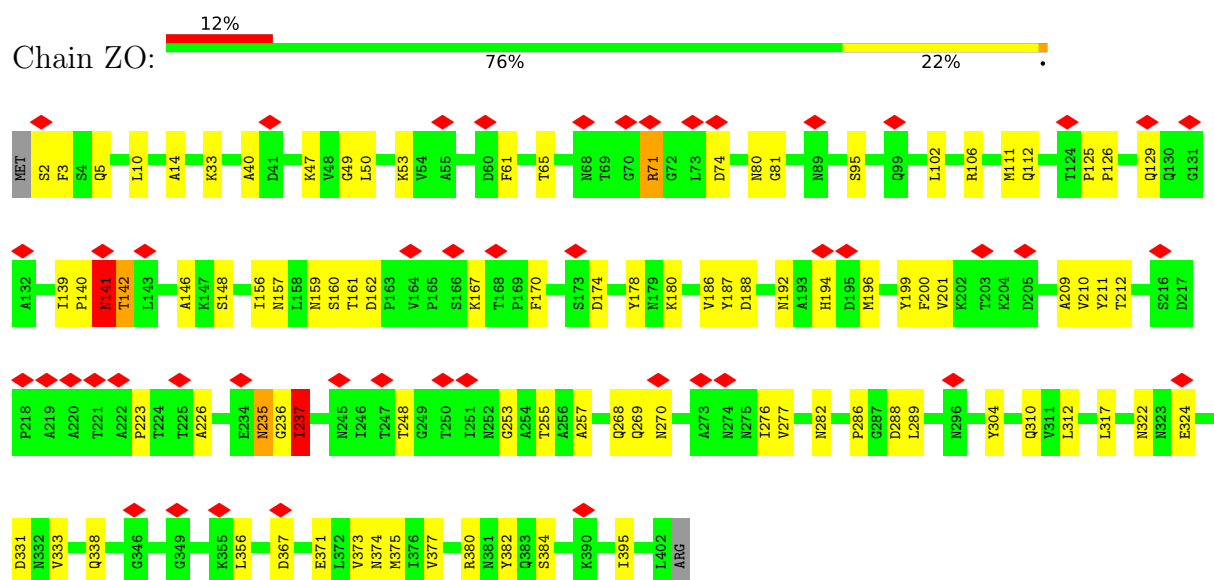
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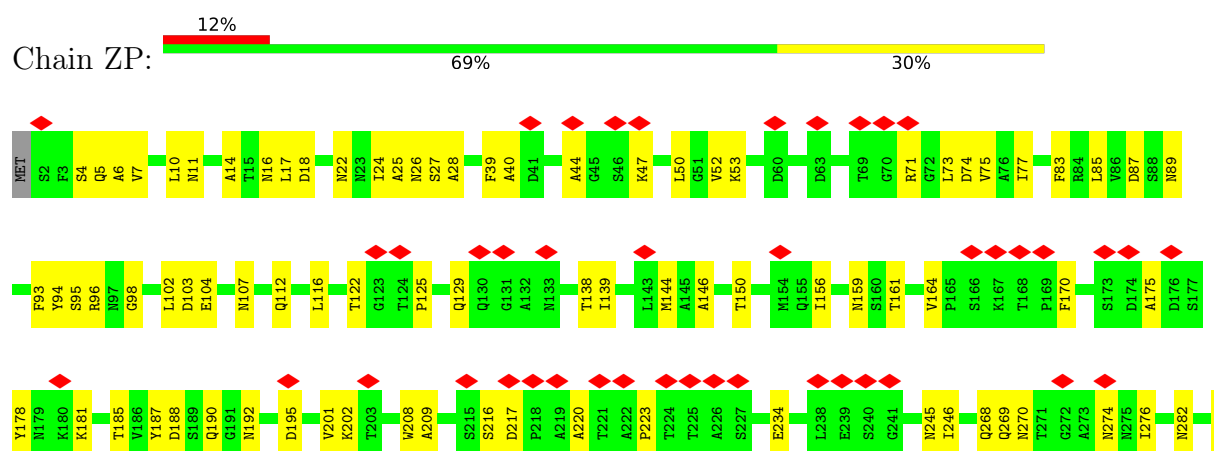
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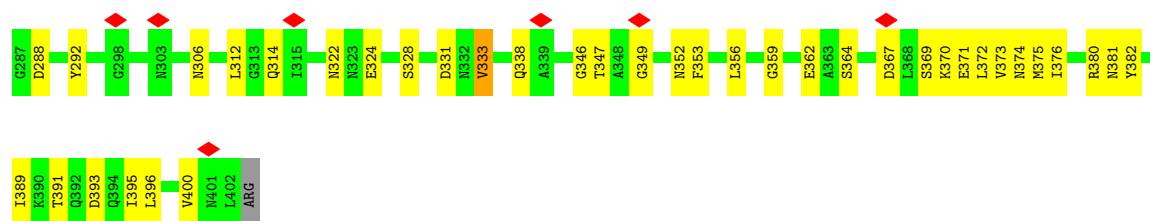


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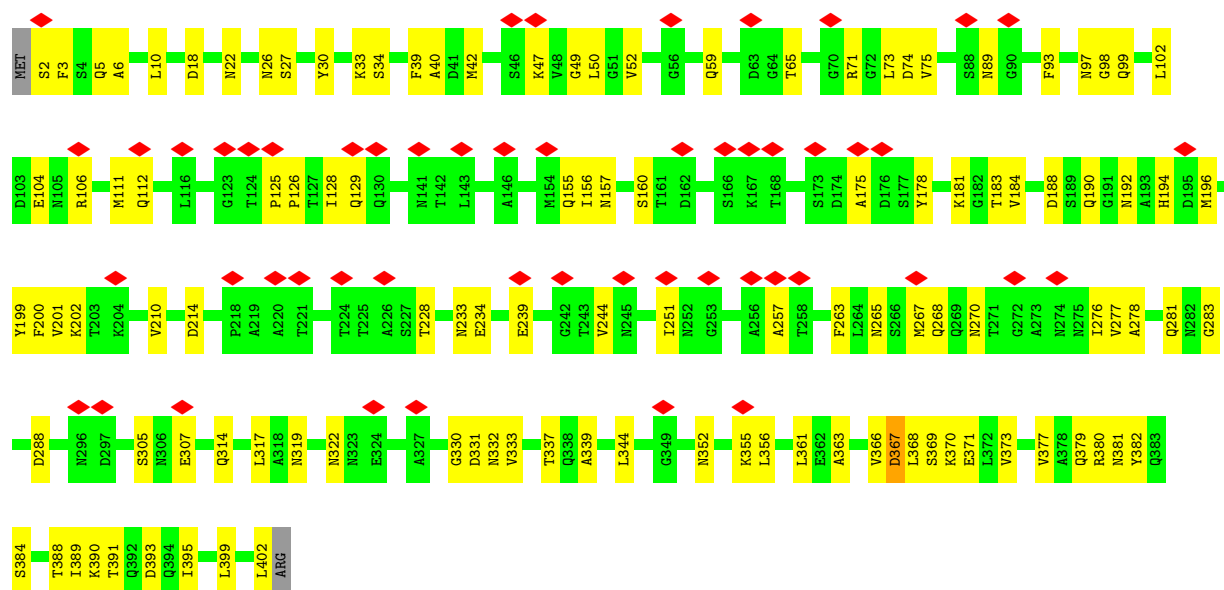
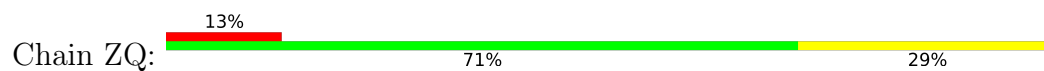


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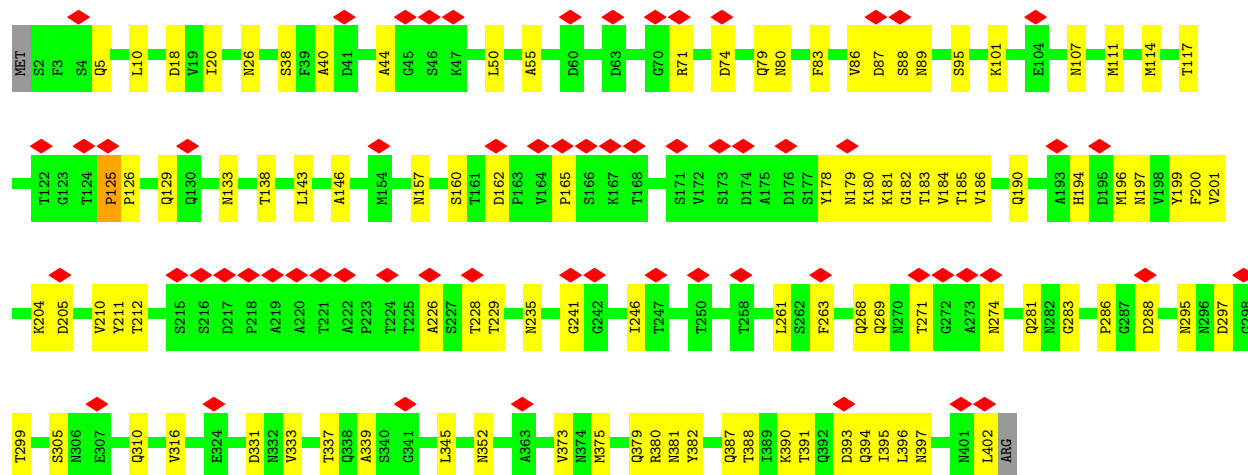
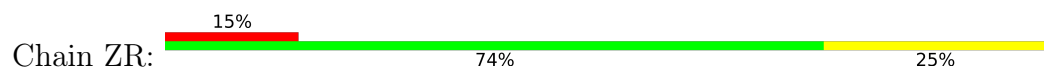




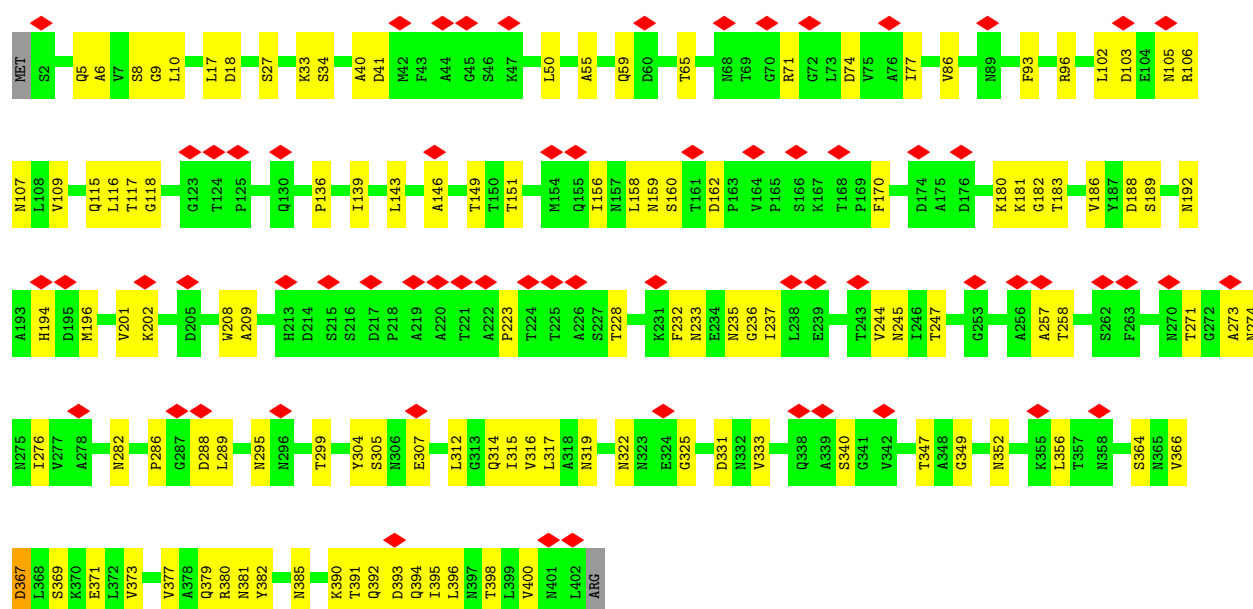
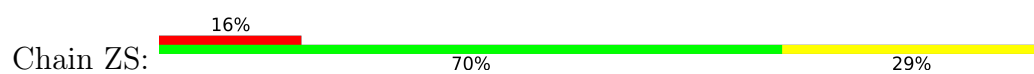
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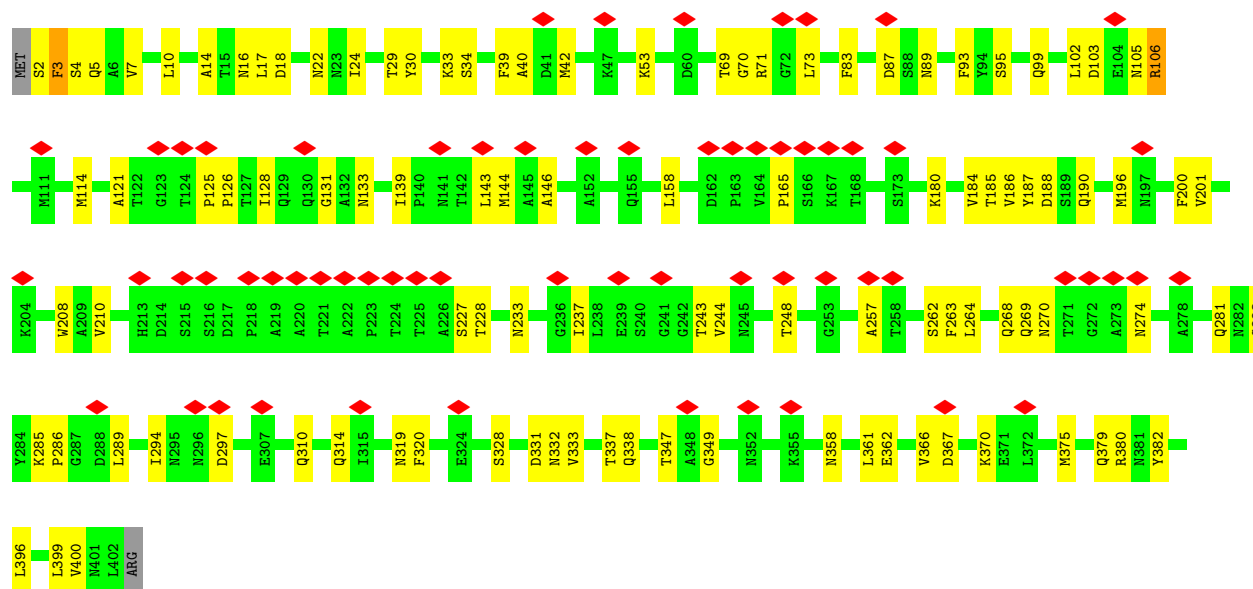
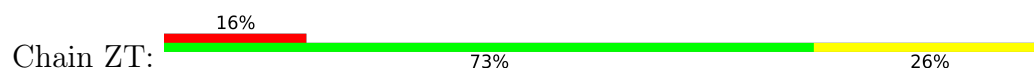
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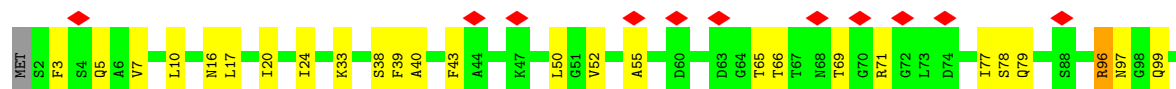
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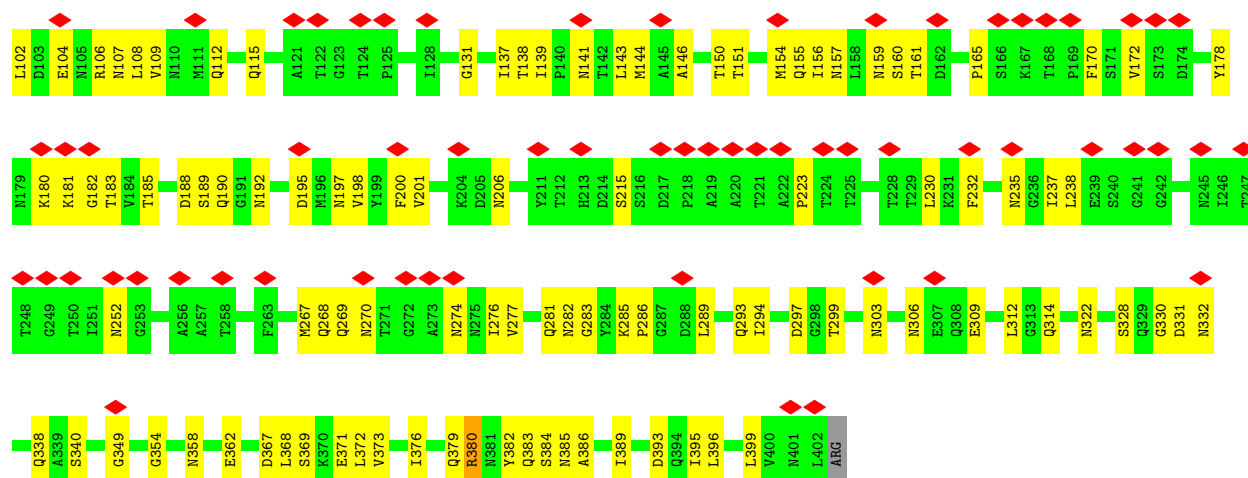


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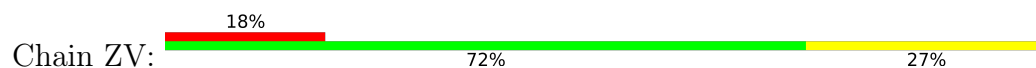


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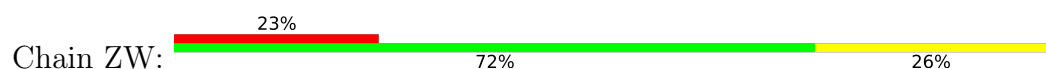


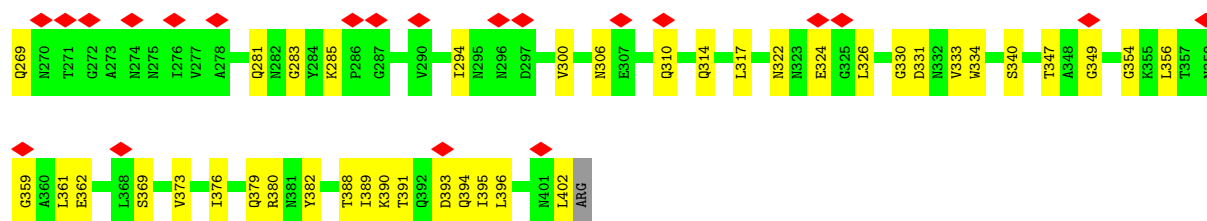


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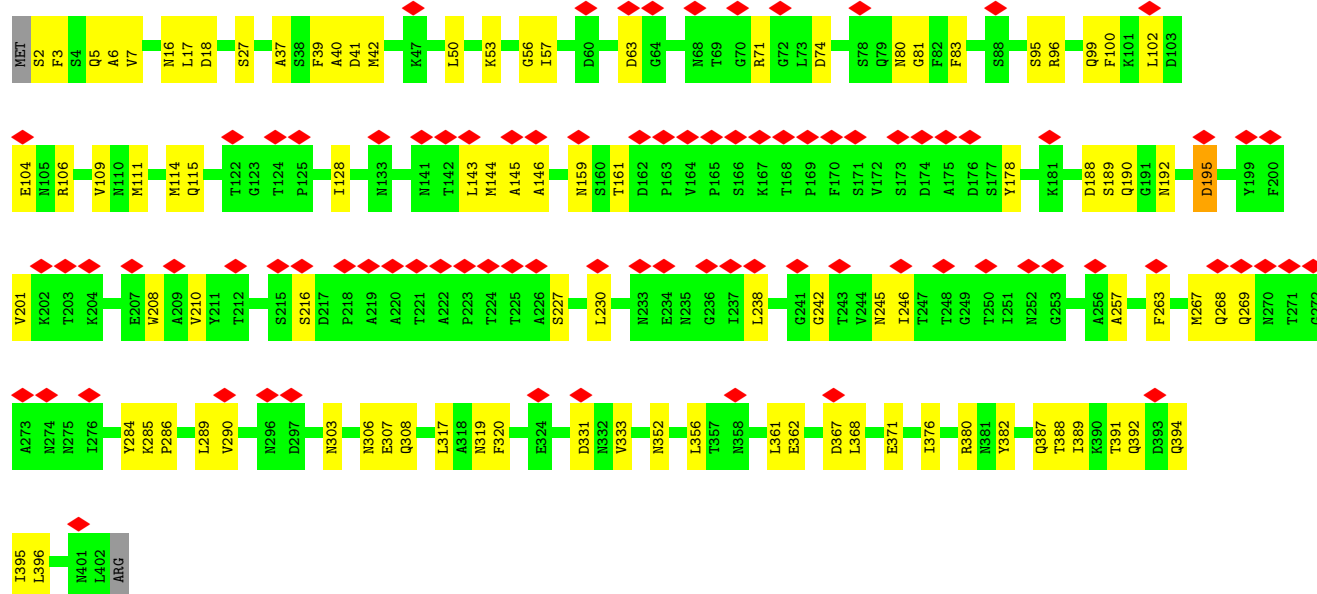
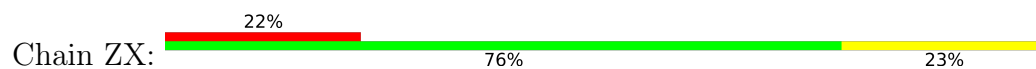


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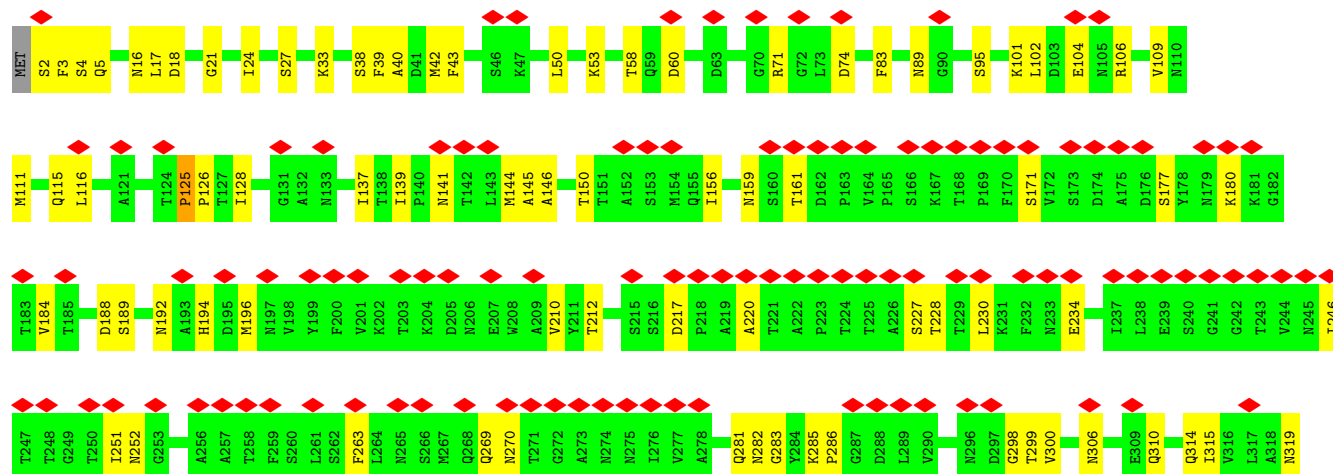
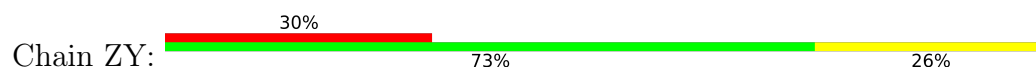


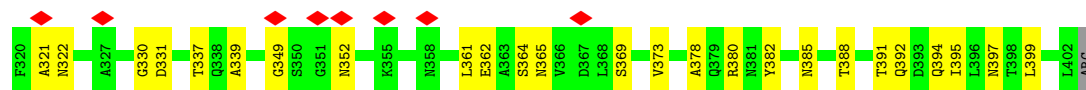


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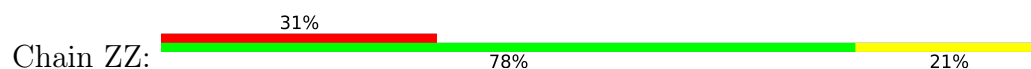


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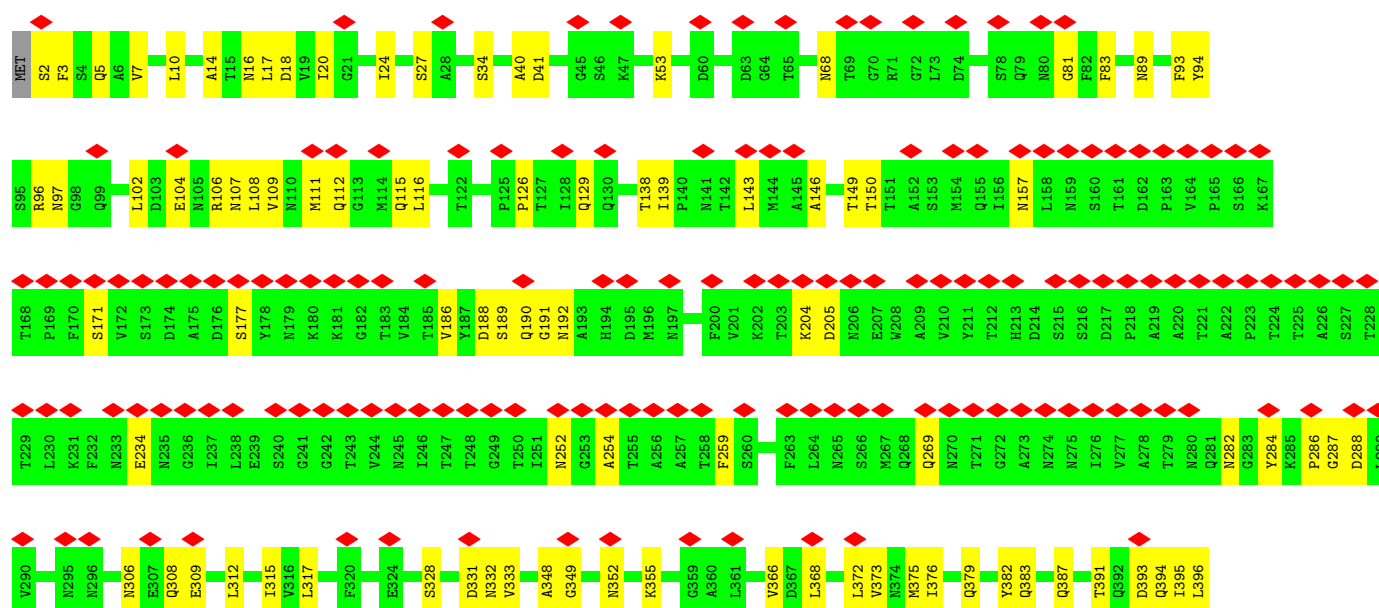
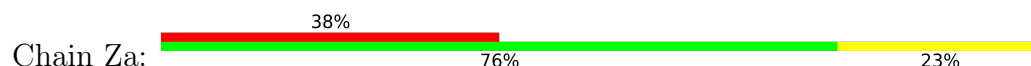




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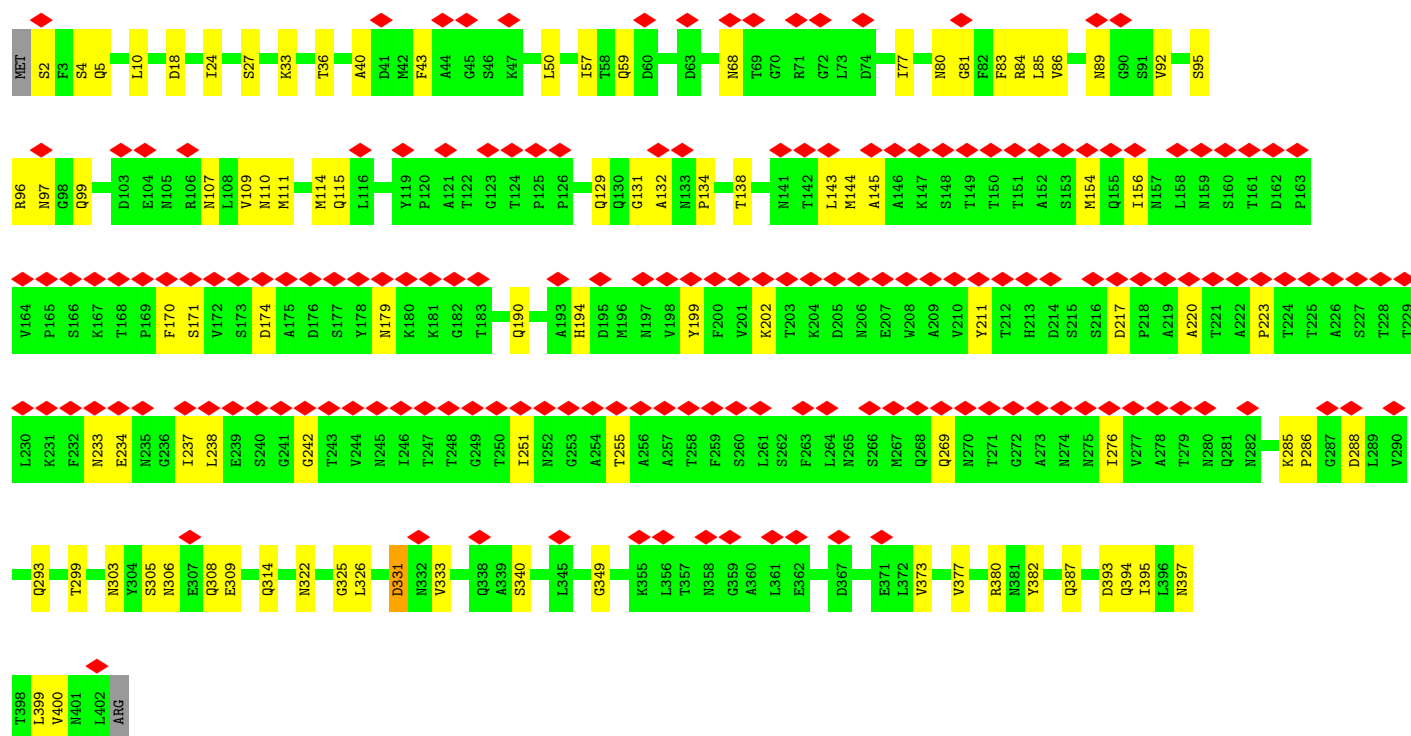
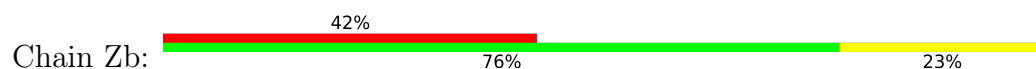


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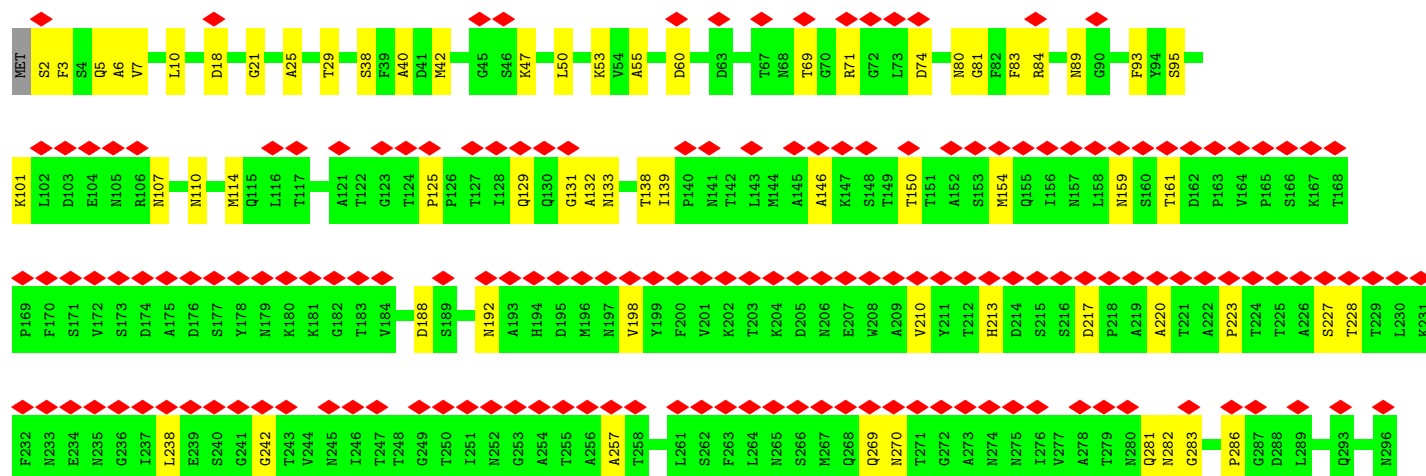
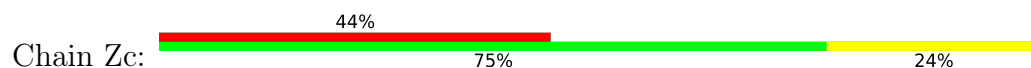


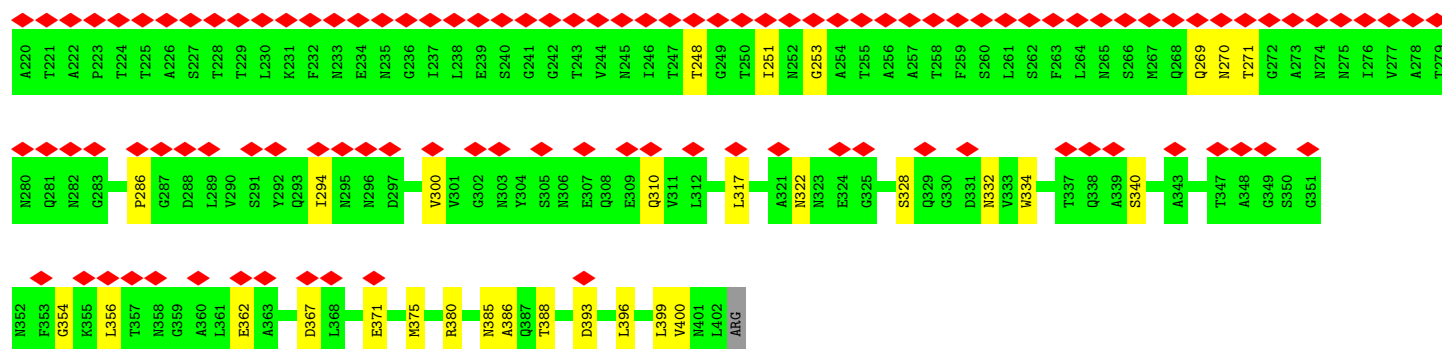


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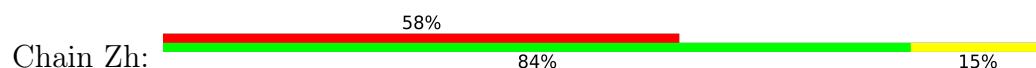


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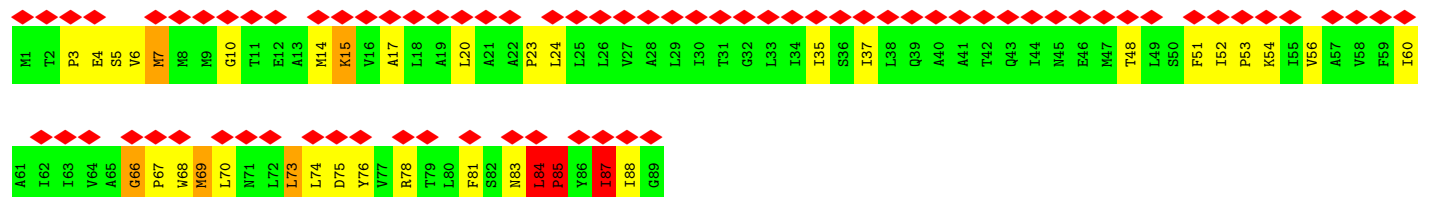
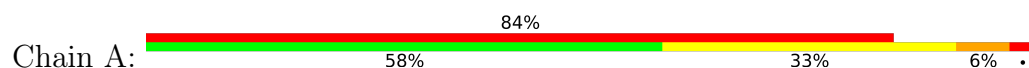




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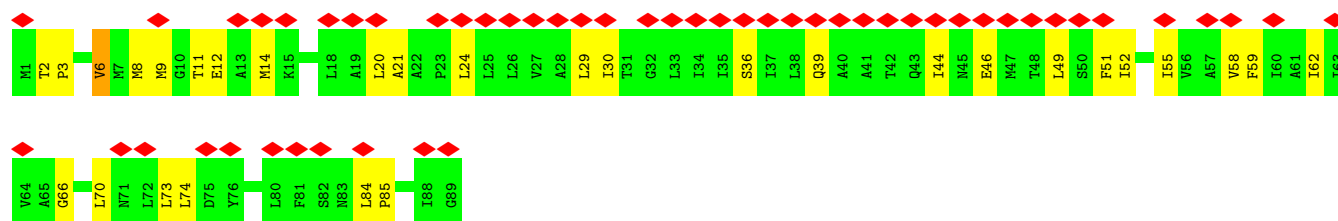


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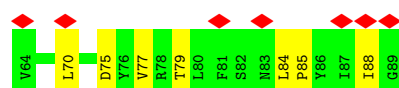
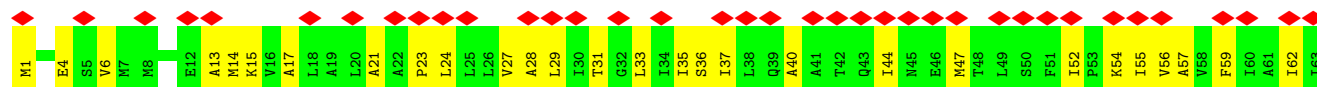


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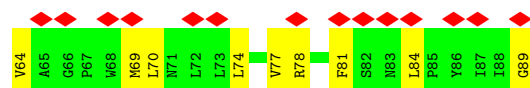
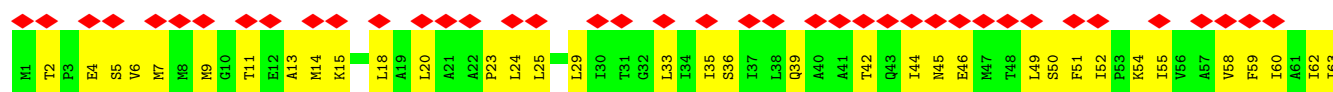




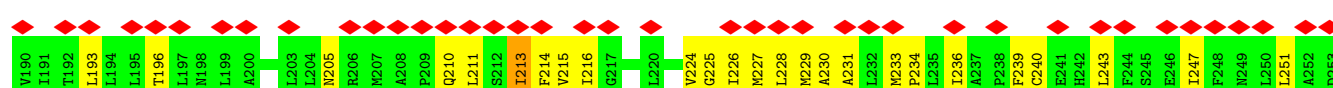
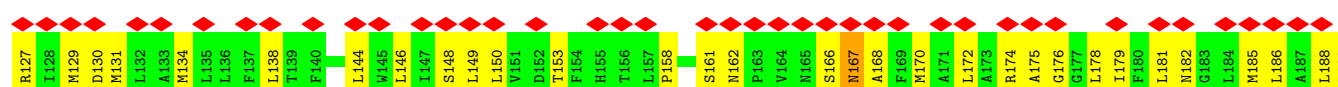
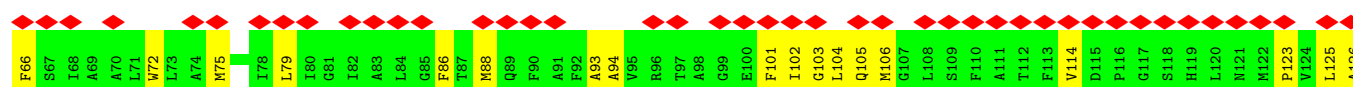
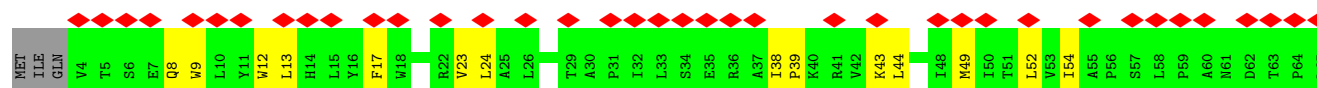
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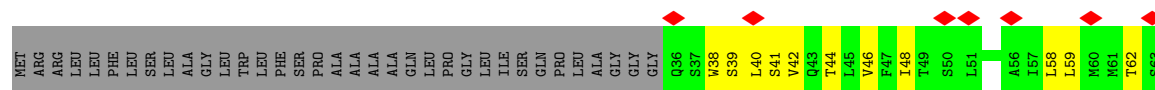


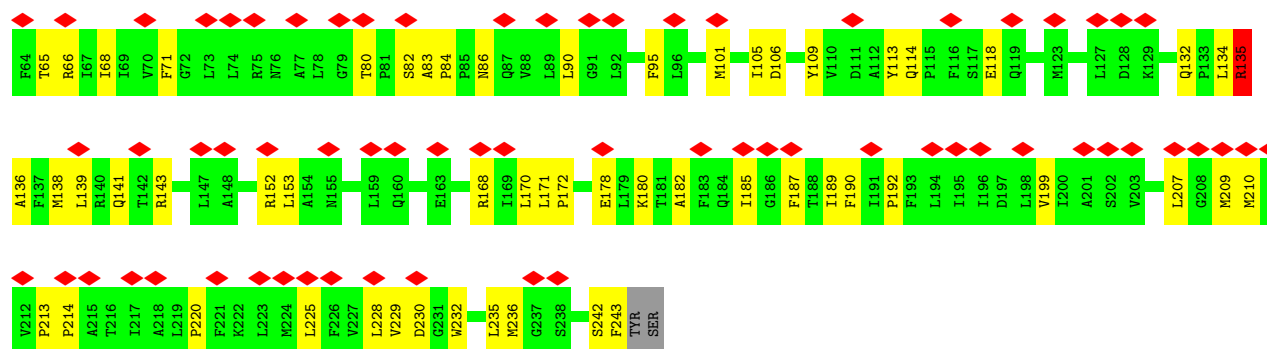
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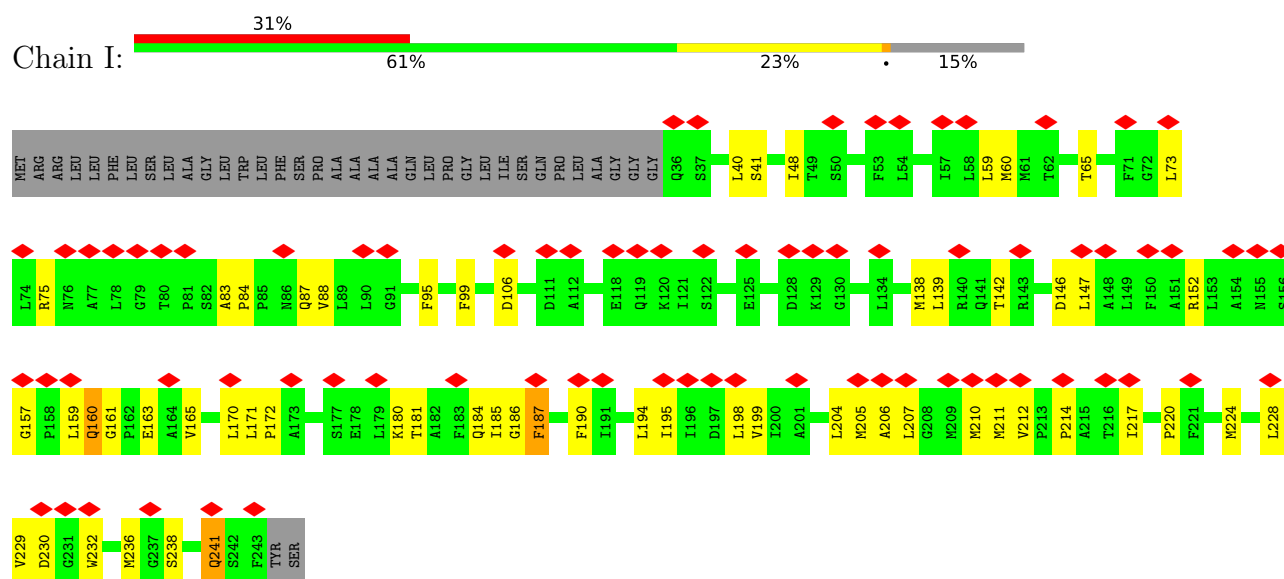
• Molecule 4: Flagellar biosynthetic protein FliR



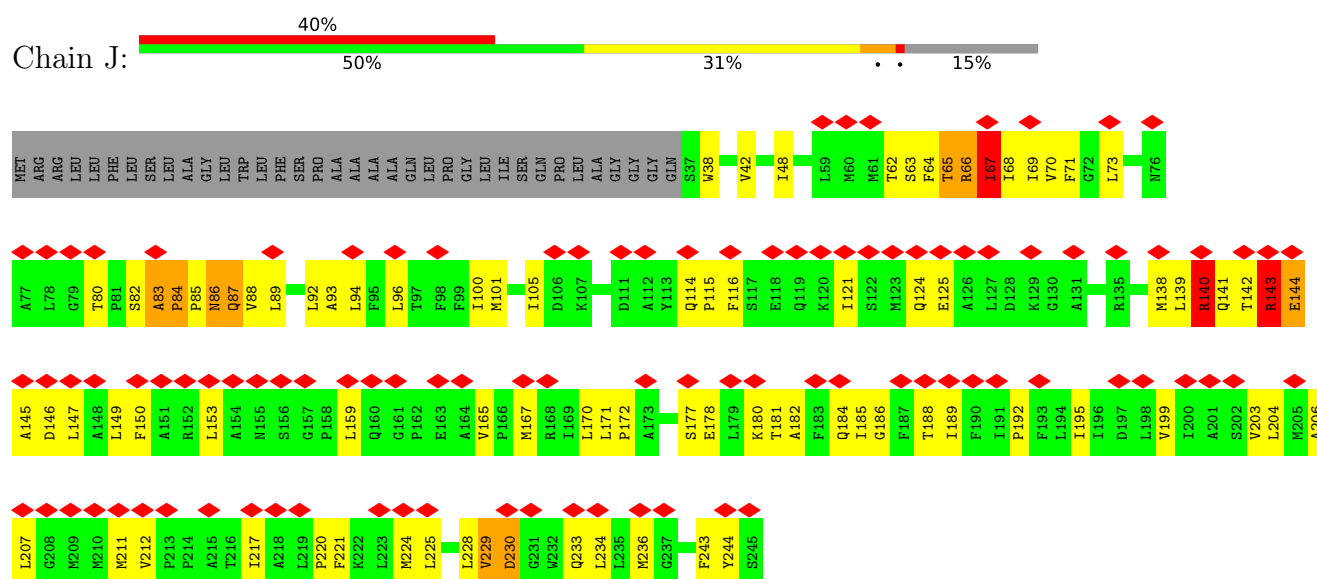




• Molecule 5: Flagellar biosynthetic protein Flp



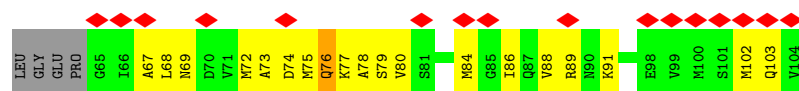
• Molecule 5: Flagellar biosynthetic protein Flp



• Molecule 6: Flagellar hook-basal body complex protein FliE



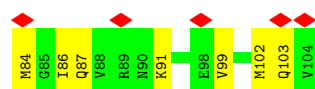
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- Molecule 6: Flagellar hook-basal body complex protein FliE



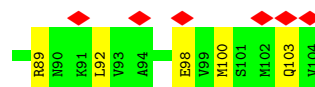
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- Molecule 6: Flagellar hook-basal body complex protein FliE



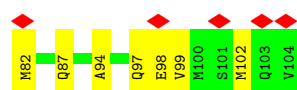
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- Molecule 6: Flagellar hook-basal body complex protein FliE



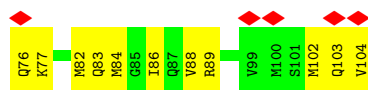
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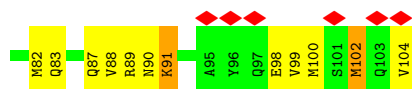
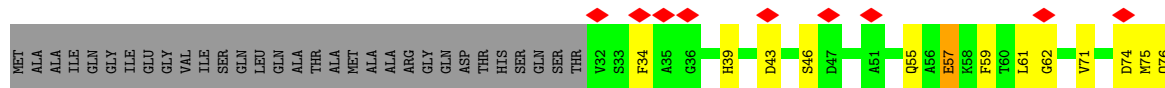
- Molecule 6: Flagellar hook-basal body complex protein FliE



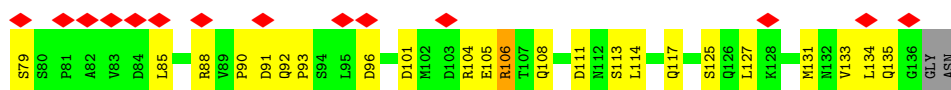
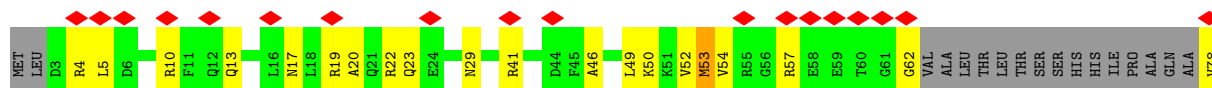
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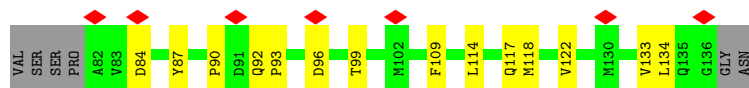
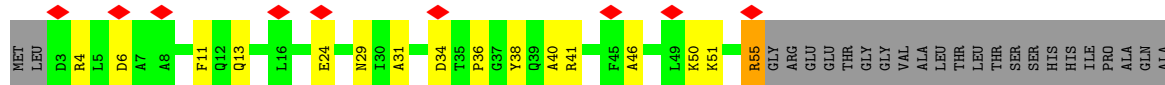
- Molecule 6: Flagellar hook-basal body complex protein FliE



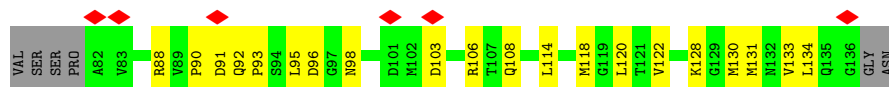
- Molecule 7: Flagellar basal body rod protein FlgB



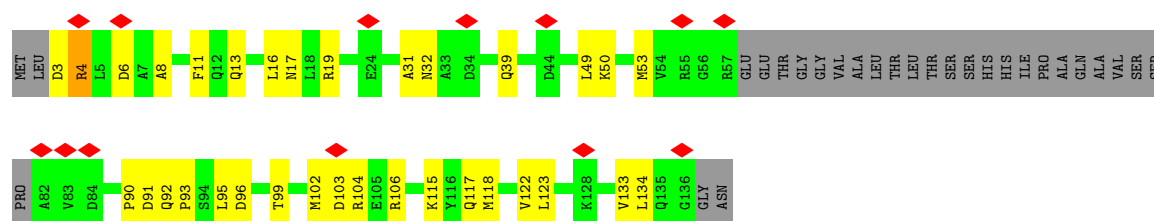
- Molecule 7: Flagellar basal body rod protein FlgB



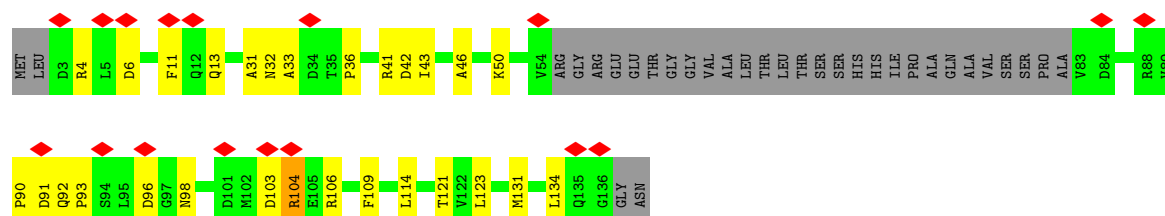
- Molecule 7: Flagellar basal body rod protein FlgB



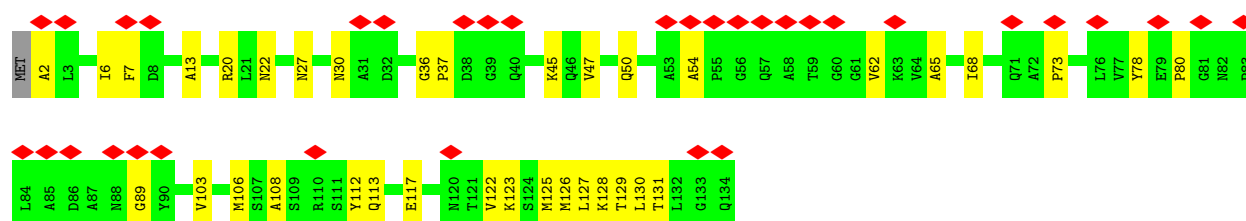
- Molecule 7: Flagellar basal body rod protein FlgB



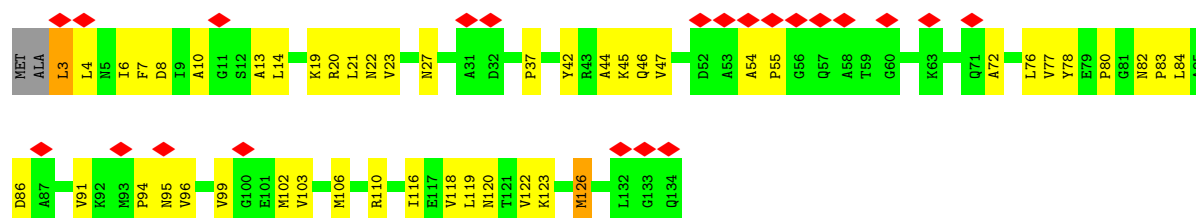
• Molecule 7: Flagellar basal body rod protein FlgB



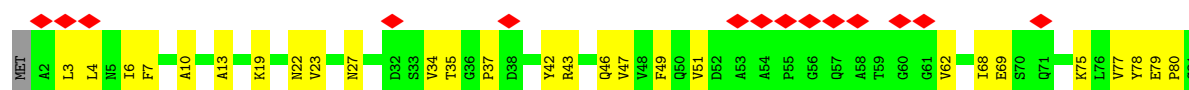
• Molecule 8: Flagellar basal-body rod protein FlgC



• Molecule 8: Flagellar basal-body rod protein FlgC

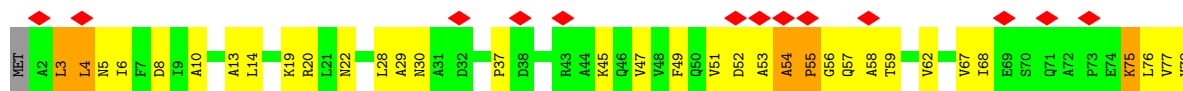


• Molecule 8: Flagellar basal-body rod protein FlgC

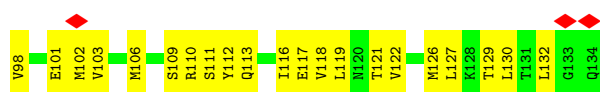
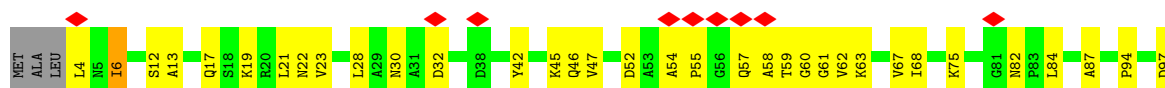




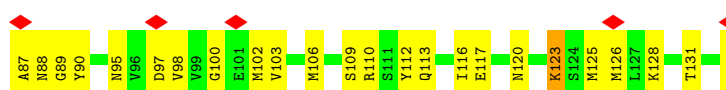
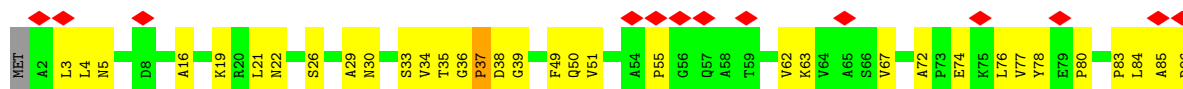
• Molecule 8: Flagellar basal-body rod protein FlgC



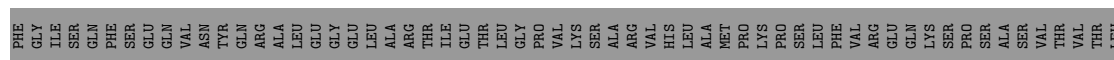
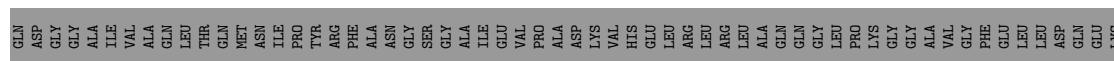
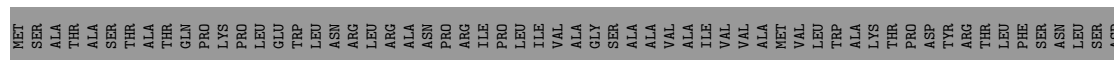
• Molecule 8: Flagellar basal-body rod protein FlgC



• Molecule 8: Flagellar basal-body rod protein FlgC



• Molecule 9: Flagellar M-ring protein





[illegible]

- Molecule 9: Flagellar M-ring protein

Chain f: 96%

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

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

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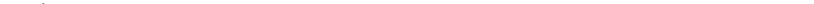
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VAL	ASN	SER	PRO	PRO	PHE	SER	ALA	VAL	ASP	ASN	THR	GLY	GLY	LEU	LEU	PRO	PHE	TRP	GLN	GLN	GLN	SER	PHE	ILE	ASP	GLN	LEU	LEU	ALA	ALA	GLY	ARG	TRP	LEU	LEU	VAL	LEU	VAL	VAL	ALA	ALA	TRP	TRP	ILE	LEU	TRP	ARG	LYS	ALA	VAL	VAL	GLN	PRO	GLN	THR	LEU	ARG	ARG	VAL	GLU	GLU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

- Molecule 9: Flagellar M-ring protein

Chain g:  97%

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

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

GLU	PRO	GLY	ARG	ALA	LEU	ASP	GLU	GLY	GLN	ILE	SER	ALA	VAL	VAL	HIS	LEU	VAL	SER	SER	ALA	VAL	ALA	ALA	GLY	LEU	PRO	PRO	GLY	ASN	ASN	VAL	THR	THR	LEU	THR	GLN	SER	ASN	THR	THR	SER	GLY	ARG	ASP	LEU	ASN	ASN	ALA	ALA	ASN	ASP
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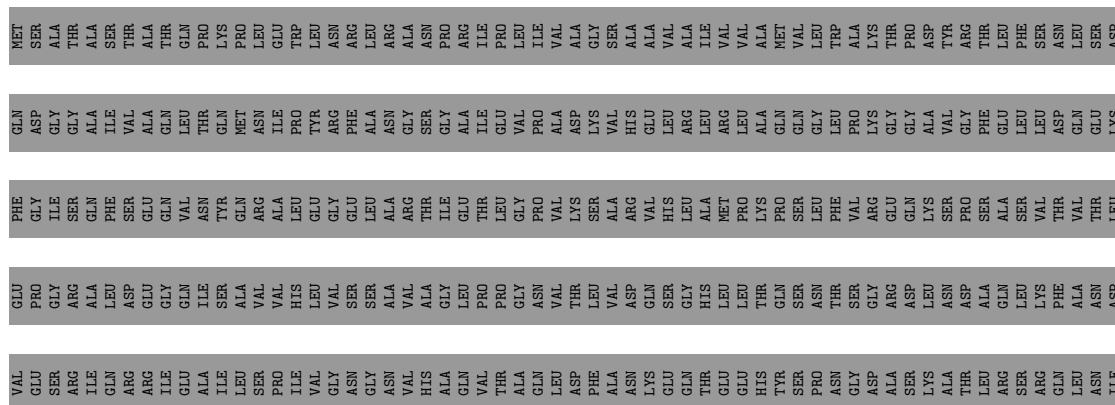
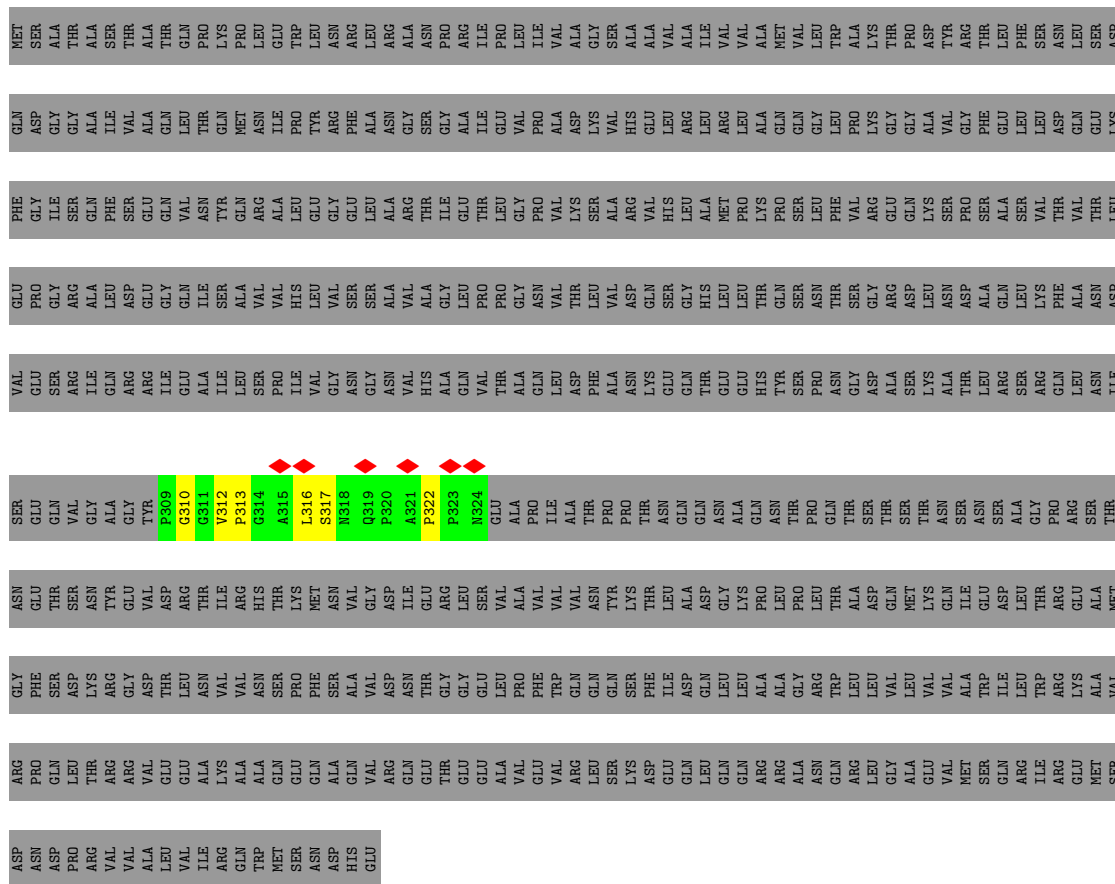
VAL	GLU	SER	ARG	ILE	GLN	ARG	ARG	ILE	GLU	ALA	ALA	ILE	LEU	SER	PRO	ILE	VAL	GLY	ASN	GLY	VAL	THR	ALA	ALA	GLN	LEU	ASP	PHE	ALA	ASN	LYS	ASN	ASP	GLY	GLU	GLN	THR	GLU	GLY	THR	TYR	SER	PRO	ASN	GLY	GLY	THR	ALA	ALA	LEU	ARG	SER	GLN	LEU	ASN	ILE
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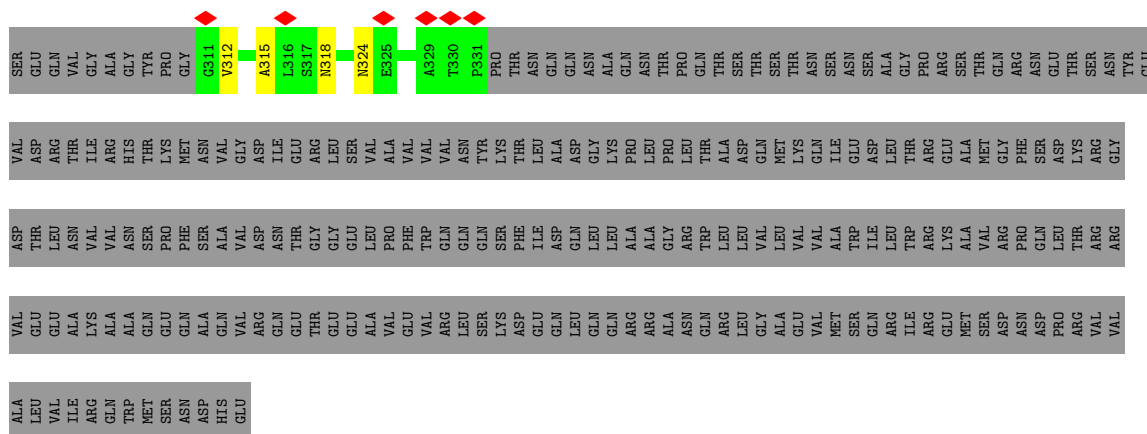
[illegible]

- Molecule 9: Flagellar M-ring protein

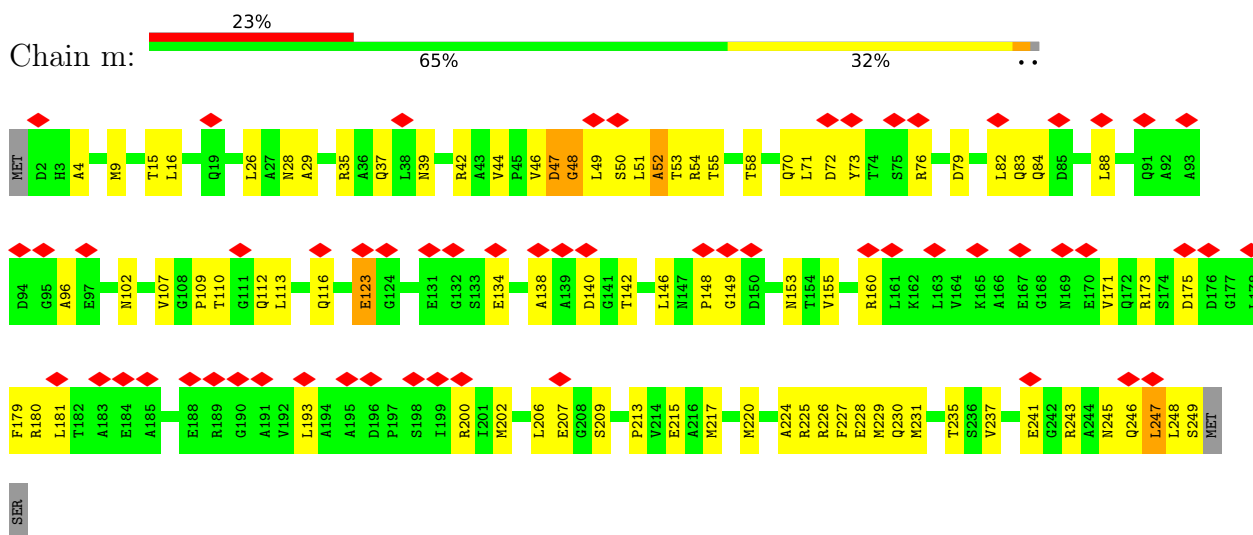
Chain j: .. 96%

[illegible]

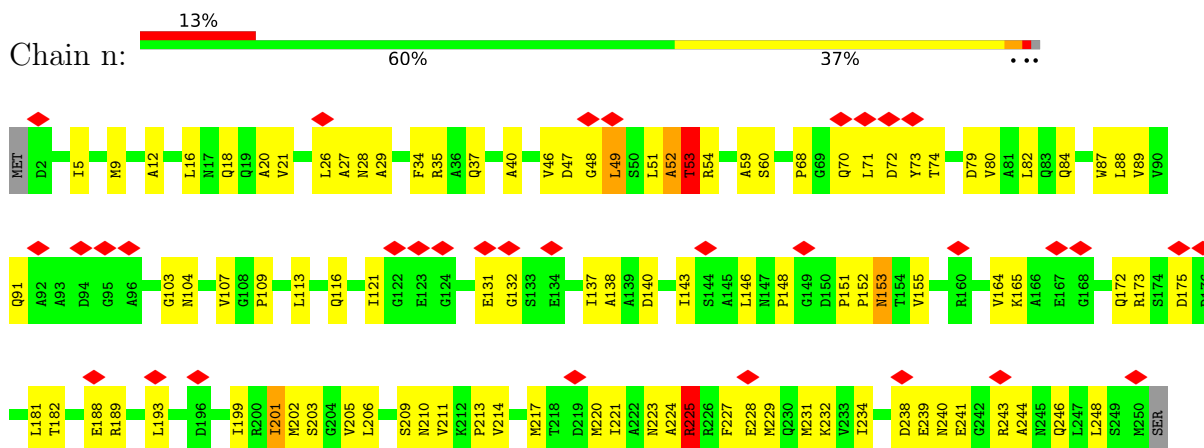




- Molecule 10: Flagellar basal-body rod protein FlgF

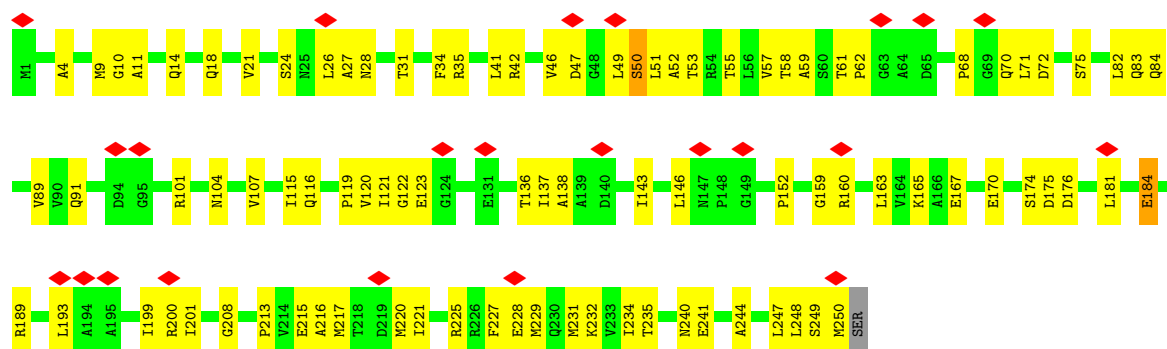


- Molecule 10: Flagellar basal-body rod protein FlgF

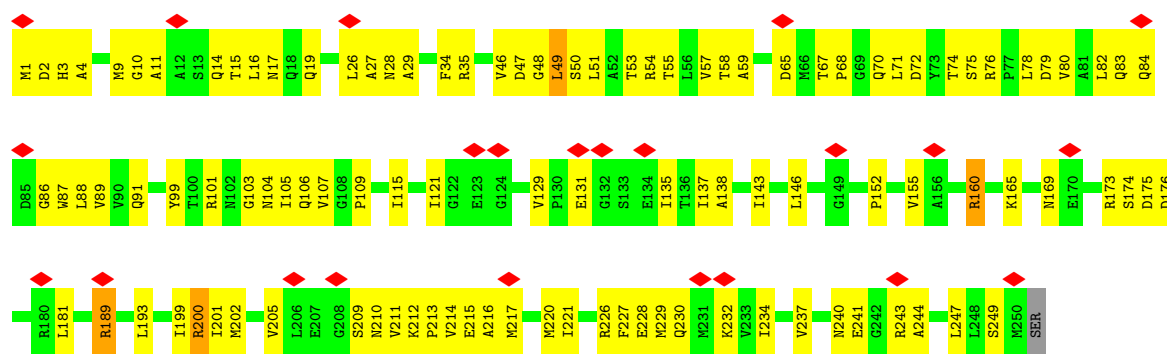


- Molecule 10: Flagellar basal-body rod protein FlgF

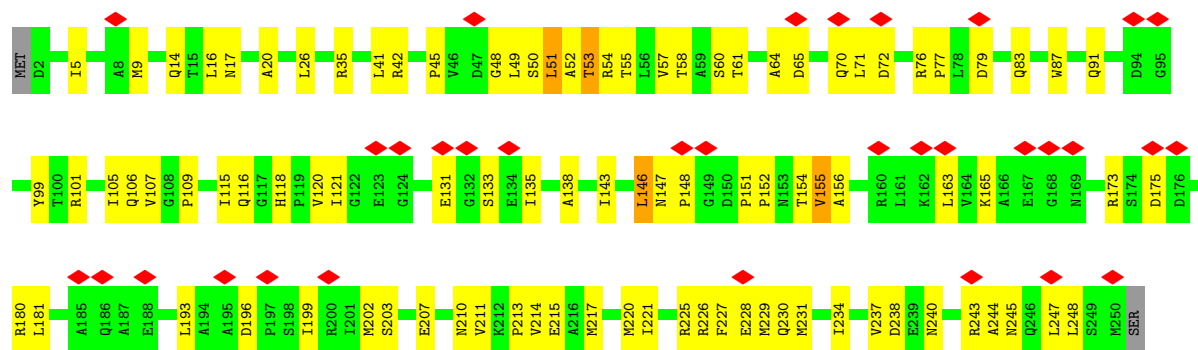




- Molecule 10: Flagellar basal-body rod protein FlgF



- Molecule 10: Flagellar basal-body rod protein FlgF



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	11858	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.384	Depositor
Minimum map value	-1.313	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.124	Depositor
Recommended contour level	0.65	Depositor
Map size ($\text{\AA}$)	681.984, 681.984, 681.984	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.332, 1.332, 1.332	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	0	0.34	0/1888	0.61	3/2564 (0.1%)
1	1	0.29	0/1917	0.54	0/2605
1	2	0.25	0/1973	0.53	1/2682 (0.0%)
1	3	0.22	0/1973	0.50	0/2682
1	4	0.22	0/1973	0.47	0/2682
1	5	0.36	0/1973	0.59	0/2682
1	6	0.34	0/1973	0.65	0/2682
1	7	0.33	0/1973	0.59	2/2682 (0.1%)
1	8	0.35	0/1973	0.68	3/2682 (0.1%)
1	9	0.29	0/1973	0.54	0/2682
1	ZA	0.32	0/1973	0.57	0/2682
1	ZB	0.26	0/1973	0.49	0/2682
1	ZC	0.40	0/1973	0.67	0/2682
1	ZD	0.33	0/1973	0.61	0/2682
1	ZE	0.29	0/1973	0.54	0/2682
1	r	0.39	0/1926	0.64	0/2618
1	s	0.46	0/1934	0.77	3/2629 (0.1%)
1	t	0.48	0/1942	0.73	3/2639 (0.1%)
1	u	0.38	0/1926	0.67	3/2618 (0.1%)
1	v	0.41	0/1934	0.65	1/2629 (0.0%)
1	w	0.36	0/1844	0.63	0/2505
1	x	0.36	0/1888	0.59	0/2564
1	y	0.36	0/1888	0.66	2/2564 (0.1%)
1	z	0.30	0/1888	0.55	1/2564 (0.0%)
2	ZF	0.23	0/2991	0.46	1/4076 (0.0%)
2	ZG	0.35	1/2991 (0.0%)	0.59	4/4076 (0.1%)
2	ZH	0.26	0/2991	0.49	1/4076 (0.0%)
2	ZI	0.29	0/2991	0.51	1/4076 (0.0%)
2	ZJ	0.27	0/2991	0.48	0/4076
2	ZK	0.27	0/2991	0.51	0/4076
2	ZL	0.25	0/2991	0.47	0/4076
2	ZM	0.22	0/2991	0.48	1/4076 (0.0%)
2	ZN	0.21	0/2991	0.46	1/4076 (0.0%)
2	ZO	0.27	0/2991	0.50	1/4076 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	ZP	0.20	0/2991	0.43	1/4076 (0.0%)
2	ZQ	0.23	0/2991	0.48	0/4076
2	ZR	0.22	1/2991 (0.0%)	0.47	2/4076 (0.0%)
2	ZS	0.22	0/2991	0.44	0/4076
2	ZT	0.24	0/2991	0.46	1/4076 (0.0%)
2	ZU	0.23	0/2991	0.45	0/4076
2	ZV	0.48	4/2991 (0.1%)	0.65	7/4076 (0.2%)
2	ZW	0.19	0/2991	0.43	0/4076
2	ZX	0.19	0/2991	0.41	0/4076
2	ZY	0.24	1/2991 (0.0%)	0.47	2/4076 (0.0%)
2	ZZ	0.15	0/2991	0.37	0/4076
2	Za	0.21	0/2991	0.43	1/4076 (0.0%)
2	Zb	0.28	0/2991	0.49	1/4076 (0.0%)
2	Zc	0.23	0/2991	0.49	3/4076 (0.1%)
2	Zd	0.27	0/2991	0.51	1/4076 (0.0%)
2	Ze	0.25	0/2991	0.48	0/4076
2	Zf	0.21	0/2991	0.45	0/4076
2	Zg	0.23	0/2991	0.46	0/4076
2	Zh	0.21	0/2991	0.42	1/4076 (0.0%)
3	A	0.62	0/681	1.02	4/930 (0.4%)
3	B	0.33	0/681	0.60	0/930
3	C	0.24	0/681	0.54	1/930 (0.1%)
3	D	0.19	0/681	0.45	0/930
4	E	0.29	0/1994	0.52	0/2724
5	F	0.32	0/1643	0.64	5/2237 (0.2%)
5	G	0.27	0/1665	0.46	2/2267 (0.1%)
5	H	0.24	0/1652	0.48	3/2249 (0.1%)
5	I	0.24	0/1652	0.45	1/2249 (0.0%)
5	J	0.36	0/1662	0.62	4/2263 (0.2%)
6	K	0.24	0/300	0.63	2/400 (0.5%)
6	L	0.12	0/547	0.25	0/733
6	M	0.18	0/561	0.30	0/753
6	N	0.14	0/561	0.27	0/753
6	O	0.15	0/561	0.31	0/753
6	P	0.28	0/554	0.41	0/743
7	Q	0.24	0/930	0.56	2/1251 (0.2%)
7	R	0.18	0/855	0.40	0/1150
7	S	0.21	0/855	0.41	0/1150
7	T	0.20	0/870	0.36	0/1169
7	U	0.19	0/839	0.35	0/1129
8	V	0.22	0/981	0.42	0/1334
8	W	0.24	0/976	0.47	0/1327
8	X	0.35	0/981	0.55	0/1334

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	Y	0.32	0/981	0.65	1/1334 (0.1%)
8	Z	0.24	0/968	0.43	0/1316
8	a	0.40	0/981	0.55	1/1334 (0.1%)
9	b	0.59	0/83	1.23	2/114 (1.8%)
9	c	0.17	0/107	0.37	0/148
9	d	0.27	0/137	0.51	0/191
9	e	0.22	0/107	0.45	0/148
9	f	0.48	0/145	0.69	0/203
9	g	0.23	0/107	0.57	0/148
9	h	0.14	0/145	0.29	0/203
9	i	0.15	0/107	0.42	0/148
9	j	0.35	0/137	0.93	0/191
9	k	0.17	0/107	0.30	0/148
9	l	0.27	0/145	0.44	0/203
10	m	0.33	0/1828	0.57	2/2492 (0.1%)
10	n	0.36	0/1836	0.62	1/2502 (0.0%)
10	o	0.42	0/1844	0.62	0/2512
10	p	0.36	0/1844	0.63	0/2512
10	q	0.35	0/1836	0.57	0/2502
All	All	0.29	7/170171 (0.0%)	0.53	83/231606 (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	0	0	2
1	1	0	1
1	5	0	2
1	7	0	1
1	8	0	2
1	ZA	0	2
1	ZD	0	1
1	ZE	0	3
1	r	0	1
1	u	0	1
1	w	0	1
1	x	0	1
1	y	0	2
1	z	0	3
2	ZI	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	ZK	0	1
2	ZO	0	1
2	ZT	0	1
2	ZU	0	1
2	ZW	0	1
2	ZZ	0	1
2	Zd	0	1
2	Ze	0	1
5	H	0	2
5	J	0	2
7	Q	0	1
7	R	0	1
7	T	0	1
7	U	0	1
8	Y	0	1
8	a	0	1
10	m	0	1
10	n	0	2
10	p	0	1
All	All	0	46

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	ZV	140	PRO	CG-CD	-15.67	0.97	1.50
2	ZV	125	PRO	CG-CD	-12.77	1.17	1.51
2	ZV	140	PRO	N-CD	8.37	1.59	1.47
2	ZY	125	PRO	CG-CD	-7.04	1.32	1.51
2	ZR	125	PRO	CG-CD	-6.62	1.33	1.51

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	ZV	140	PRO	N-CD-CG	-17.34	77.19	103.20
2	ZV	125	PRO	N-CD-CG	-14.57	86.32	103.80
2	ZR	125	PRO	CA-N-CD	-13.94	91.98	111.50
2	ZY	125	PRO	CA-N-CD	-13.33	92.84	111.50
2	ZV	125	PRO	CA-N-CD	-13.25	92.95	111.50

There are no chirality outliers.

5 of 46 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	36	ARG	Sidechain
1	0	50	ARG	Sidechain
1	1	36	ARG	Sidechain
1	5	50	ARG	Sidechain
1	5	73	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1866	0	1848	134	0
1	1	1894	0	1878	129	0
1	2	1949	0	1926	104	0
1	3	1949	0	1926	91	0
1	4	1949	0	1926	114	0
1	5	1949	0	1926	118	0
1	6	1949	0	1926	105	0
1	7	1949	0	1926	88	0
1	8	1949	0	1926	106	0
1	9	1949	0	1926	92	0
1	ZA	1949	0	1926	147	0
1	ZB	1949	0	1926	117	0
1	ZC	1949	0	1926	100	0
1	ZD	1949	0	1926	124	0
1	ZE	1949	0	1926	102	0
1	r	1903	0	1878	134	0
1	s	1911	0	1889	177	0
1	t	1919	0	1901	144	0
1	u	1903	0	1878	160	0
1	v	1911	0	1889	177	0
1	w	1823	0	1797	127	0
1	x	1866	0	1848	148	0
1	y	1866	0	1848	154	0
1	z	1866	0	1848	105	0
2	ZF	2947	0	2839	103	0
2	ZG	2947	0	2839	104	0
2	ZH	2947	0	2839	132	0
2	ZI	2947	0	2839	122	0
2	ZJ	2947	0	2839	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	ZK	2947	0	2839	80	0
2	ZL	2947	0	2839	97	0
2	ZM	2947	0	2839	91	0
2	ZN	2947	0	2839	101	0
2	ZO	2947	0	2839	89	0
2	ZP	2947	0	2839	118	0
2	ZQ	2947	0	2839	136	0
2	ZR	2947	0	2839	100	0
2	ZS	2947	0	2839	117	0
2	ZT	2947	0	2839	109	0
2	ZU	2947	0	2839	148	0
2	ZV	2947	0	2839	118	0
2	ZW	2947	0	2839	111	0
2	ZX	2947	0	2839	93	0
2	ZY	2947	0	2839	109	0
2	ZZ	2947	0	2839	90	0
2	Za	2947	0	2839	104	0
2	Zb	2947	0	2839	97	0
2	Zc	2947	0	2839	97	0
2	Zd	2947	0	2839	84	0
2	Ze	2947	0	2839	55	0
2	Zf	2947	0	2839	111	0
2	Zg	2947	0	2839	67	0
2	Zh	2947	0	2839	68	0
3	A	670	0	739	51	0
3	B	670	0	739	37	0
3	C	670	0	739	49	0
3	D	670	0	739	87	0
4	E	1945	0	2063	100	0
5	F	1605	0	1701	69	0
5	G	1626	0	1718	82	0
5	H	1614	0	1709	69	0
5	I	1614	0	1709	68	0
5	J	1623	0	1715	113	0
6	K	300	0	311	32	0
6	L	543	0	550	18	0
6	M	557	0	566	30	0
6	N	557	0	566	20	0
6	O	557	0	566	31	0
6	P	550	0	559	32	0
7	Q	922	0	914	46	0
7	R	848	0	847	69	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	S	848	0	847	55	0
7	T	863	0	863	51	0
7	U	832	0	829	39	0
8	V	969	0	981	51	0
8	W	964	0	976	98	0
8	X	969	0	981	76	0
8	Y	969	0	981	81	0
8	Z	956	0	965	84	0
8	a	969	0	981	106	0
9	b	81	0	78	11	0
9	c	103	0	99	5	0
9	d	133	0	129	5	0
9	e	103	0	99	3	0
9	f	140	0	136	5	0
9	g	103	0	99	11	0
9	h	140	0	136	11	0
9	i	103	0	99	15	0
9	j	133	0	129	3	0
9	k	103	0	99	9	0
9	l	140	0	136	3	0
10	m	1804	0	1791	187	0
10	n	1812	0	1800	226	0
10	o	1820	0	1812	167	0
10	p	1820	0	1812	208	0
10	q	1812	0	1800	232	0
All	All	167758	0	164979	5760	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 17.

The worst 5 of 5760 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:w:258:THR:HG21	10:q:228:GLU:CB	1.27	1.63
1:y:73:ARG:CD	10:n:202:MET:HE1	1.40	1.49
1:u:38:ARG:NH1	10:p:74:THR:HG21	1.18	1.48
1:6:56:SER:HA	10:q:138:ALA:CB	1.40	1.48
1:v:257:LEU:CA	10:q:231:MET:HE3	1.40	1.48

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	0	244/260 (94%)	236 (97%)	5 (2%)	3 (1%)	10	40
1	1	248/260 (95%)	238 (96%)	9 (4%)	1 (0%)	30	62
1	2	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	48
1	3	258/260 (99%)	247 (96%)	9 (4%)	2 (1%)	16	48
1	4	258/260 (99%)	245 (95%)	11 (4%)	2 (1%)	16	48
1	5	258/260 (99%)	240 (93%)	15 (6%)	3 (1%)	10	40
1	6	258/260 (99%)	244 (95%)	10 (4%)	4 (2%)	7	35
1	7	258/260 (99%)	244 (95%)	11 (4%)	3 (1%)	10	40
1	8	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	10	40
1	9	258/260 (99%)	244 (95%)	13 (5%)	1 (0%)	30	62
1	ZA	258/260 (99%)	242 (94%)	13 (5%)	3 (1%)	10	40
1	ZB	258/260 (99%)	243 (94%)	12 (5%)	3 (1%)	10	40
1	ZC	258/260 (99%)	242 (94%)	14 (5%)	2 (1%)	16	48
1	ZD	258/260 (99%)	237 (92%)	18 (7%)	3 (1%)	10	40
1	ZE	258/260 (99%)	242 (94%)	15 (6%)	1 (0%)	30	62
1	r	250/260 (96%)	238 (95%)	11 (4%)	1 (0%)	30	62
1	s	251/260 (96%)	234 (93%)	14 (6%)	3 (1%)	10	40
1	t	252/260 (97%)	234 (93%)	16 (6%)	2 (1%)	16	48
1	u	250/260 (96%)	239 (96%)	9 (4%)	2 (1%)	16	48
1	v	251/260 (96%)	235 (94%)	10 (4%)	6 (2%)	4	29
1	w	239/260 (92%)	231 (97%)	7 (3%)	1 (0%)	30	62
1	x	244/260 (94%)	229 (94%)	10 (4%)	5 (2%)	6	32
1	y	244/260 (94%)	234 (96%)	9 (4%)	1 (0%)	30	62
1	z	244/260 (94%)	239 (98%)	4 (2%)	1 (0%)	30	62
2	ZF	399/403 (99%)	387 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	ZG	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	36	67
2	ZH	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
2	ZI	399/403 (99%)	387 (97%)	10 (2%)	2 (0%)	24	57
2	ZJ	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
2	ZK	399/403 (99%)	387 (97%)	11 (3%)	1 (0%)	36	67
2	ZL	399/403 (99%)	389 (98%)	9 (2%)	1 (0%)	36	67
2	ZM	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
2	ZN	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
2	ZO	399/403 (99%)	381 (96%)	15 (4%)	3 (1%)	16	48
2	ZP	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	36	67
2	ZQ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
2	ZR	399/403 (99%)	391 (98%)	8 (2%)	0	100	100
2	ZS	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
2	ZT	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
2	ZU	399/403 (99%)	387 (97%)	12 (3%)	0	100	100
2	ZV	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
2	ZW	399/403 (99%)	380 (95%)	18 (4%)	1 (0%)	36	67
2	ZX	399/403 (99%)	388 (97%)	11 (3%)	0	100	100
2	ZY	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
2	ZZ	399/403 (99%)	389 (98%)	10 (2%)	0	100	100
2	Za	399/403 (99%)	386 (97%)	12 (3%)	1 (0%)	36	67
2	Zb	399/403 (99%)	392 (98%)	7 (2%)	0	100	100
2	Zc	399/403 (99%)	390 (98%)	9 (2%)	0	100	100
2	Zd	399/403 (99%)	385 (96%)	14 (4%)	0	100	100
2	Ze	399/403 (99%)	385 (96%)	13 (3%)	1 (0%)	36	67
2	Zf	399/403 (99%)	386 (97%)	13 (3%)	0	100	100
2	Zg	399/403 (99%)	383 (96%)	16 (4%)	0	100	100
2	Zh	399/403 (99%)	391 (98%)	8 (2%)	0	100	100
3	A	87/89 (98%)	81 (93%)	4 (5%)	2 (2%)	5	30
3	B	87/89 (98%)	86 (99%)	1 (1%)	0	100	100
3	C	87/89 (98%)	86 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
4	E	251/264 (95%)	234 (93%)	15 (6%)	2 (1%)	16	48
5	F	205/245 (84%)	197 (96%)	8 (4%)	0	100	100
5	G	207/245 (84%)	199 (96%)	6 (3%)	2 (1%)	12	43
5	H	206/245 (84%)	201 (98%)	5 (2%)	0	100	100
5	I	206/245 (84%)	199 (97%)	6 (3%)	1 (0%)	24	57
5	J	207/245 (84%)	192 (93%)	10 (5%)	5 (2%)	4	29
6	K	38/104 (36%)	35 (92%)	3 (8%)	0	100	100
6	L	70/104 (67%)	70 (100%)	0	0	100	100
6	M	72/104 (69%)	70 (97%)	2 (3%)	0	100	100
6	N	72/104 (69%)	72 (100%)	0	0	100	100
6	O	72/104 (69%)	72 (100%)	0	0	100	100
6	P	71/104 (68%)	71 (100%)	0	0	100	100
7	Q	115/138 (83%)	114 (99%)	1 (1%)	0	100	100
7	R	104/138 (75%)	103 (99%)	1 (1%)	0	100	100
7	S	104/138 (75%)	103 (99%)	1 (1%)	0	100	100
7	T	106/138 (77%)	104 (98%)	2 (2%)	0	100	100
7	U	102/138 (74%)	101 (99%)	1 (1%)	0	100	100
8	V	131/134 (98%)	122 (93%)	9 (7%)	0	100	100
8	W	130/134 (97%)	123 (95%)	7 (5%)	0	100	100
8	X	131/134 (98%)	124 (95%)	7 (5%)	0	100	100
8	Y	131/134 (98%)	121 (92%)	7 (5%)	3 (2%)	5	30
8	Z	129/134 (96%)	123 (95%)	5 (4%)	1 (1%)	16	48
8	a	131/134 (98%)	124 (95%)	7 (5%)	0	100	100
9	b	11/560 (2%)	9 (82%)	2 (18%)	0	100	100
9	c	14/560 (2%)	12 (86%)	2 (14%)	0	100	100
9	d	18/560 (3%)	18 (100%)	0	0	100	100
9	e	14/560 (2%)	14 (100%)	0	0	100	100
9	f	19/560 (3%)	18 (95%)	1 (5%)	0	100	100
9	g	14/560 (2%)	13 (93%)	1 (7%)	0	100	100
9	h	19/560 (3%)	19 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	i	14/560 (2%)	14 (100%)	0	0	100	100
9	j	18/560 (3%)	18 (100%)	0	0	100	100
9	k	14/560 (2%)	14 (100%)	0	0	100	100
9	l	19/560 (3%)	19 (100%)	0	0	100	100
10	m	246/251 (98%)	238 (97%)	7 (3%)	1 (0%)	30	62
10	n	247/251 (98%)	242 (98%)	4 (2%)	1 (0%)	30	62
10	o	248/251 (99%)	233 (94%)	13 (5%)	2 (1%)	16	48
10	p	248/251 (99%)	235 (95%)	13 (5%)	0	100	100
10	q	247/251 (98%)	236 (96%)	9 (4%)	2 (1%)	16	48
All	All	22391/29305 (76%)	21536 (96%)	763 (3%)	92 (0%)	31	62

5 of 92 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2	209	ASN
1	4	140	ILE
1	5	209	ASN
1	6	139	ALA
1	8	209	ASN

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	0	205/215 (95%)	199 (97%)	6 (3%)	37	58
1	1	209/215 (97%)	206 (99%)	3 (1%)	59	70
1	2	215/215 (100%)	214 (100%)	1 (0%)	81	81
1	3	215/215 (100%)	214 (100%)	1 (0%)	81	81
1	4	215/215 (100%)	212 (99%)	3 (1%)	59	70
1	5	215/215 (100%)	211 (98%)	4 (2%)	50	66
1	6	215/215 (100%)	212 (99%)	3 (1%)	59	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	7	215/215 (100%)	214 (100%)	1 (0%)	81	81
1	8	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	9	215/215 (100%)	213 (99%)	2 (1%)	70	74
1	ZA	215/215 (100%)	214 (100%)	1 (0%)	81	81
1	ZB	215/215 (100%)	213 (99%)	2 (1%)	70	74
1	ZC	215/215 (100%)	212 (99%)	3 (1%)	59	70
1	ZD	215/215 (100%)	209 (97%)	6 (3%)	38	58
1	ZE	215/215 (100%)	210 (98%)	5 (2%)	44	63
1	r	209/215 (97%)	205 (98%)	4 (2%)	50	66
1	s	210/215 (98%)	202 (96%)	8 (4%)	29	53
1	t	211/215 (98%)	204 (97%)	7 (3%)	33	56
1	u	209/215 (97%)	202 (97%)	7 (3%)	33	56
1	v	210/215 (98%)	204 (97%)	6 (3%)	37	58
1	w	200/215 (93%)	196 (98%)	4 (2%)	48	65
1	x	205/215 (95%)	202 (98%)	3 (2%)	57	69
1	y	205/215 (95%)	200 (98%)	5 (2%)	43	62
1	z	205/215 (95%)	201 (98%)	4 (2%)	48	65
2	ZF	321/323 (99%)	315 (98%)	6 (2%)	50	66
2	ZG	321/323 (99%)	315 (98%)	6 (2%)	50	66
2	ZH	321/323 (99%)	316 (98%)	5 (2%)	55	68
2	ZI	321/323 (99%)	316 (98%)	5 (2%)	55	68
2	ZJ	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	ZK	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	ZL	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	ZM	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	ZN	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	ZO	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	ZP	321/323 (99%)	317 (99%)	4 (1%)	63	72
2	ZQ	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	ZR	321/323 (99%)	321 (100%)	0	100	100
2	ZS	321/323 (99%)	320 (100%)	1 (0%)	86	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	ZT	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	ZU	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	ZV	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	ZW	321/323 (99%)	320 (100%)	1 (0%)	86	84
2	ZX	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	ZY	321/323 (99%)	321 (100%)	0	100	100
2	ZZ	321/323 (99%)	321 (100%)	0	100	100
2	Za	321/323 (99%)	320 (100%)	1 (0%)	86	84
2	Zb	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	Zc	321/323 (99%)	318 (99%)	3 (1%)	70	74
2	Zd	321/323 (99%)	320 (100%)	1 (0%)	86	84
2	Ze	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	Zf	321/323 (99%)	319 (99%)	2 (1%)	78	79
2	Zg	321/323 (99%)	320 (100%)	1 (0%)	86	84
2	Zh	321/323 (99%)	321 (100%)	0	100	100
3	A	74/74 (100%)	67 (90%)	7 (10%)	8	30
3	B	74/74 (100%)	72 (97%)	2 (3%)	39	59
3	C	74/74 (100%)	74 (100%)	0	100	100
3	D	74/74 (100%)	74 (100%)	0	100	100
4	E	210/221 (95%)	210 (100%)	0	100	100
5	F	177/204 (87%)	174 (98%)	3 (2%)	53	67
5	G	179/204 (88%)	175 (98%)	4 (2%)	45	63
5	H	178/204 (87%)	176 (99%)	2 (1%)	65	73
5	I	178/204 (87%)	175 (98%)	3 (2%)	53	67
5	J	179/204 (88%)	174 (97%)	5 (3%)	38	58
6	K	33/79 (42%)	33 (100%)	0	100	100
6	L	56/79 (71%)	56 (100%)	0	100	100
6	M	58/79 (73%)	58 (100%)	0	100	100
6	N	58/79 (73%)	57 (98%)	1 (2%)	53	67
6	O	58/79 (73%)	58 (100%)	0	100	100
6	P	57/79 (72%)	54 (95%)	3 (5%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	Q	98/113 (87%)	95 (97%)	3 (3%)	35	57
7	R	90/113 (80%)	90 (100%)	0	100	100
7	S	90/113 (80%)	90 (100%)	0	100	100
7	T	91/113 (80%)	91 (100%)	0	100	100
7	U	89/113 (79%)	88 (99%)	1 (1%)	65	73
8	V	104/105 (99%)	104 (100%)	0	100	100
8	W	104/105 (99%)	101 (97%)	3 (3%)	37	58
8	X	104/105 (99%)	102 (98%)	2 (2%)	50	66
8	Y	104/105 (99%)	100 (96%)	4 (4%)	29	53
8	Z	103/105 (98%)	101 (98%)	2 (2%)	50	66
8	a	104/105 (99%)	102 (98%)	2 (2%)	50	66
9	b	8/467 (2%)	7 (88%)	1 (12%)	4	21
9	c	11/467 (2%)	11 (100%)	0	100	100
9	d	14/467 (3%)	12 (86%)	2 (14%)	3	17
9	e	11/467 (2%)	11 (100%)	0	100	100
9	f	15/467 (3%)	15 (100%)	0	100	100
9	g	11/467 (2%)	11 (100%)	0	100	100
9	h	15/467 (3%)	15 (100%)	0	100	100
9	i	11/467 (2%)	11 (100%)	0	100	100
9	j	14/467 (3%)	13 (93%)	1 (7%)	13	39
9	k	11/467 (2%)	11 (100%)	0	100	100
9	l	15/467 (3%)	14 (93%)	1 (7%)	15	41
10	m	190/193 (98%)	186 (98%)	4 (2%)	47	64
10	n	191/193 (99%)	186 (97%)	5 (3%)	40	60
10	o	192/193 (100%)	190 (99%)	2 (1%)	68	74
10	p	192/193 (100%)	188 (98%)	4 (2%)	47	64
10	q	191/193 (99%)	187 (98%)	4 (2%)	47	64
All	All	18272/23835 (77%)	18039 (99%)	233 (1%)	59	71

5 of 233 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	r	44	LEU

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Mol	Chain	Res	Type
10	n	201	ILE
1	v	161	GLN
10	n	53	THR
8	X	119	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 652 such sidechains are listed below:

Mol	Chain	Res	Type
2	Zh	385	ASN
6	O	83	GLN
1	s	88	GLN
2	Zh	383	GLN
1	x	47	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.

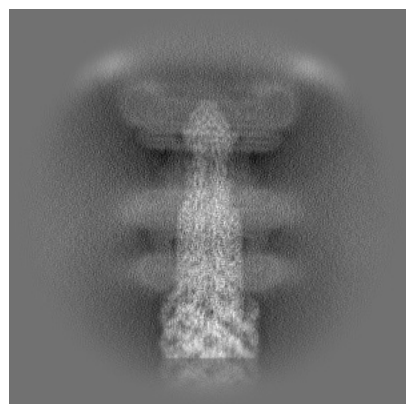
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37628. These allow visual inspection of the internal detail of the map and identification of artifacts.

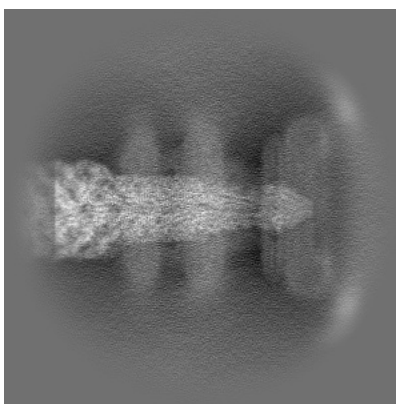
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

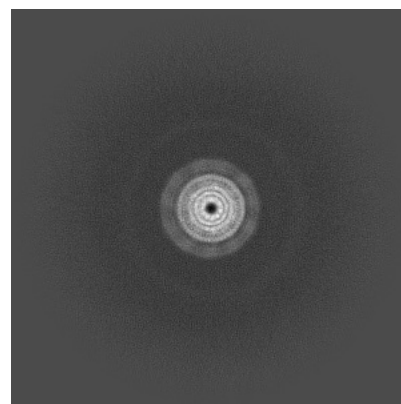
6.1.1 Primary map



X

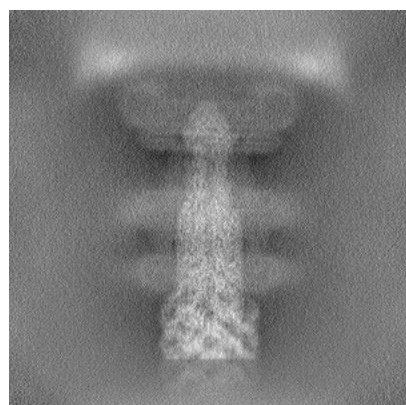


Y

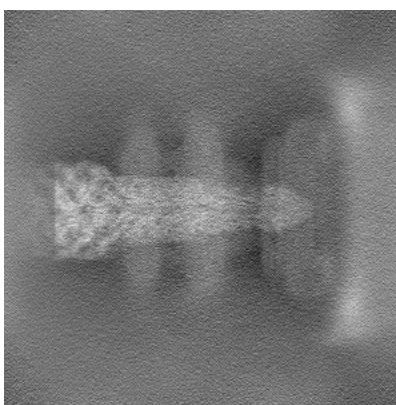


Z

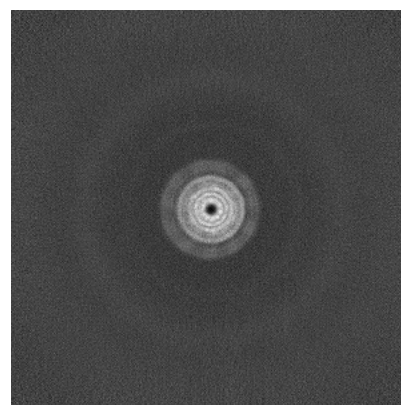
6.1.2 Raw map



X



Y

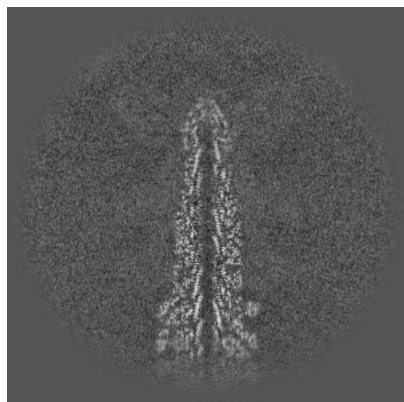


Z

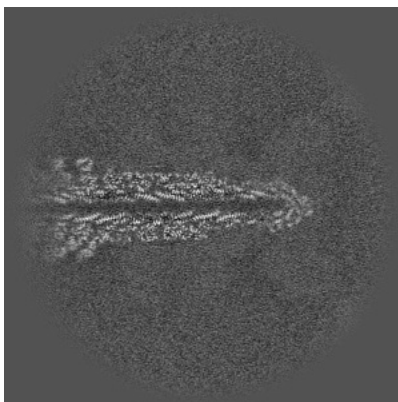
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

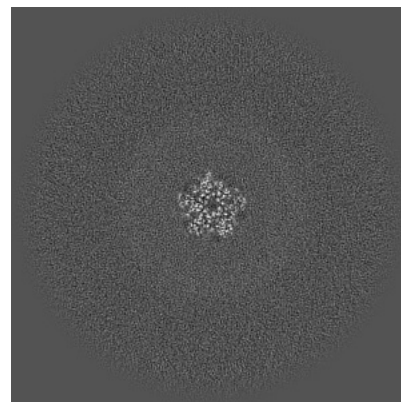
6.2.1 Primary map



X Index: 256

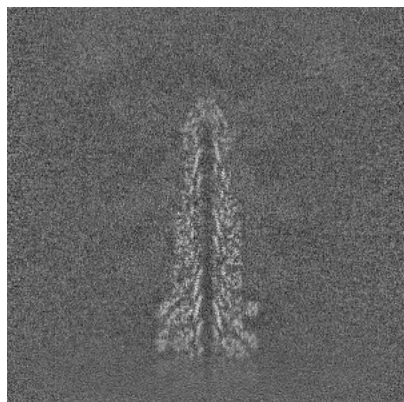


Y Index: 256

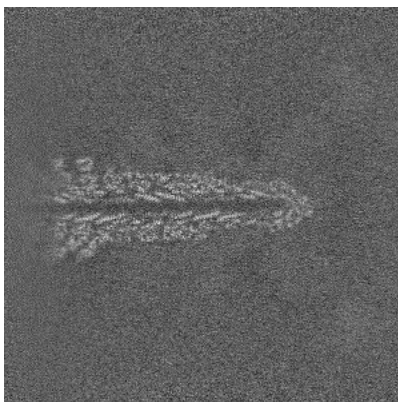


Z Index: 256

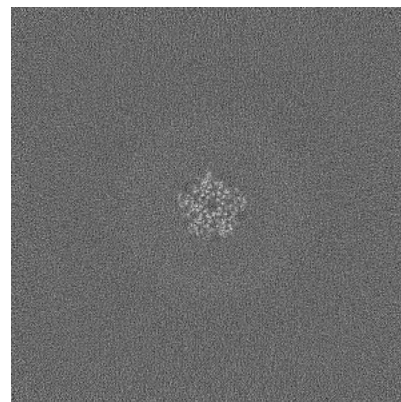
6.2.2 Raw map



X Index: 256



Y Index: 256

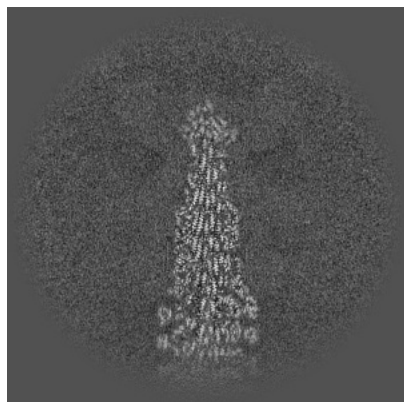


Z Index: 256

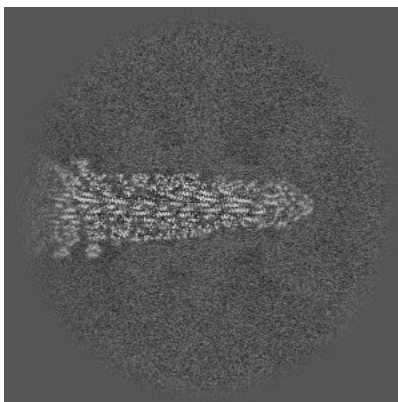
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

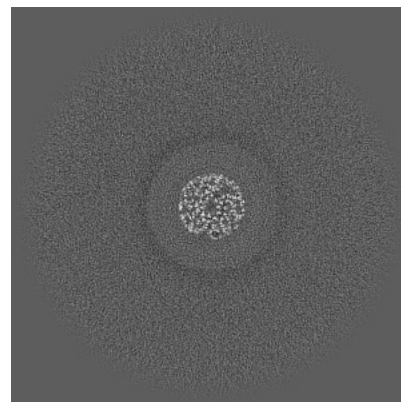
6.3.1 Primary map



X Index: 245

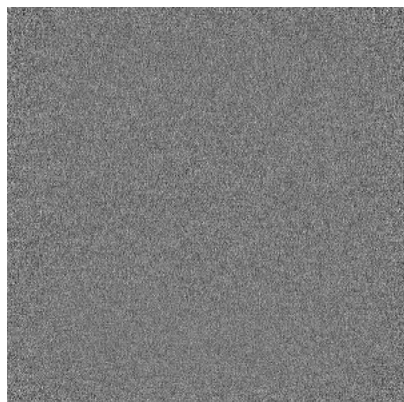


Y Index: 246

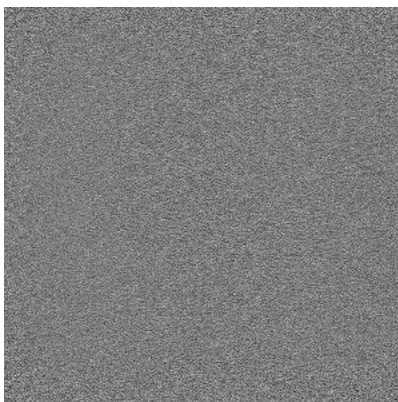


Z Index: 229

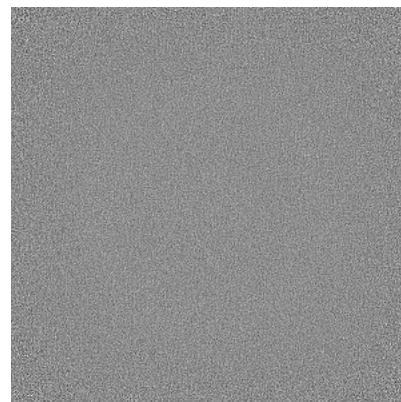
6.3.2 Raw map



X Index: 0



Y Index: 0

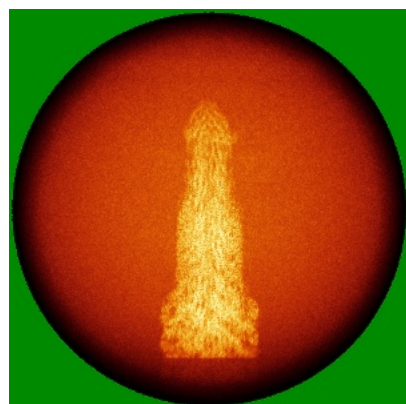


Z Index: 511

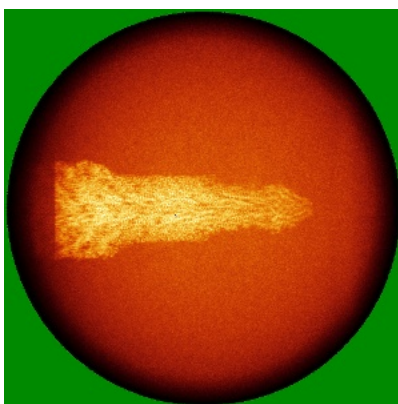
The images above show the largest variance slices of the map in three orthogonal directions.

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

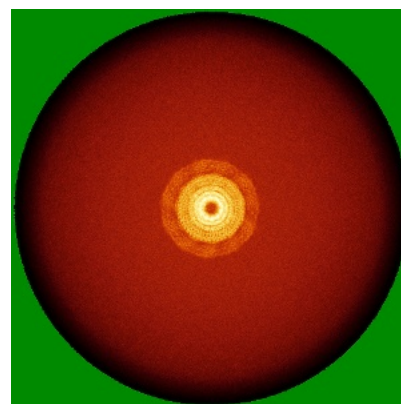
6.4.1 Primary map



X

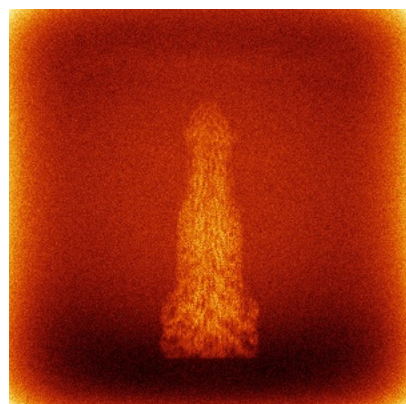


Y

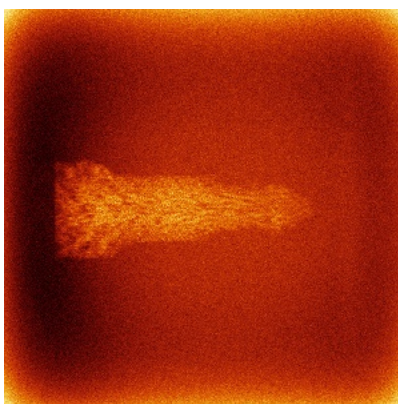


Z

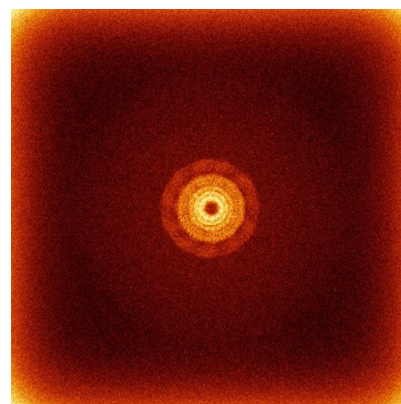
6.4.2 Raw map



X



Y

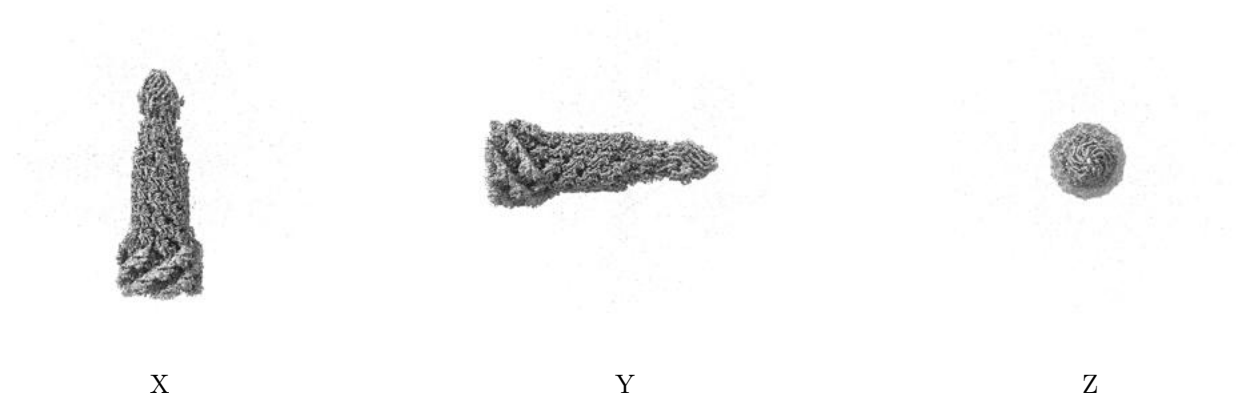


Z

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.

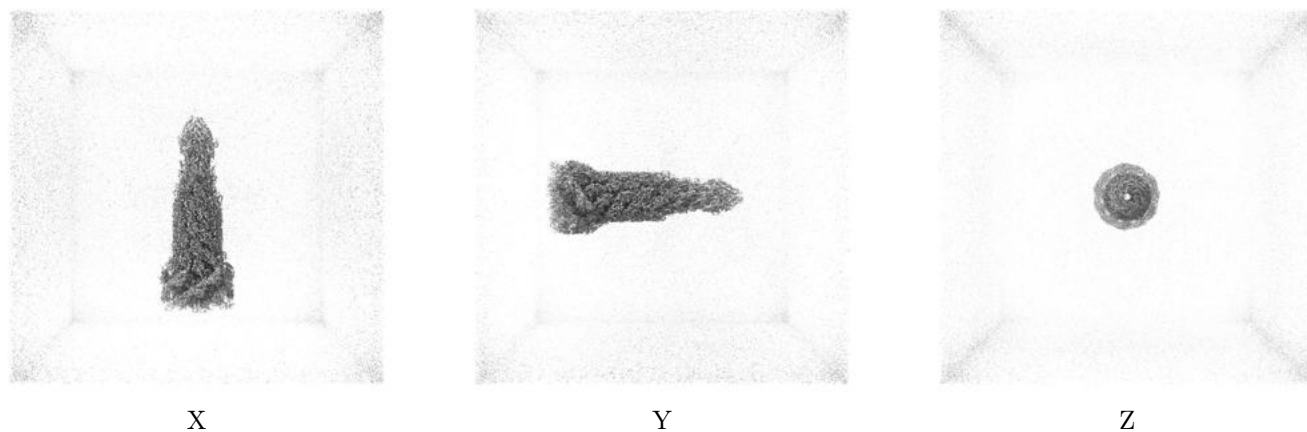
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.65. 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.

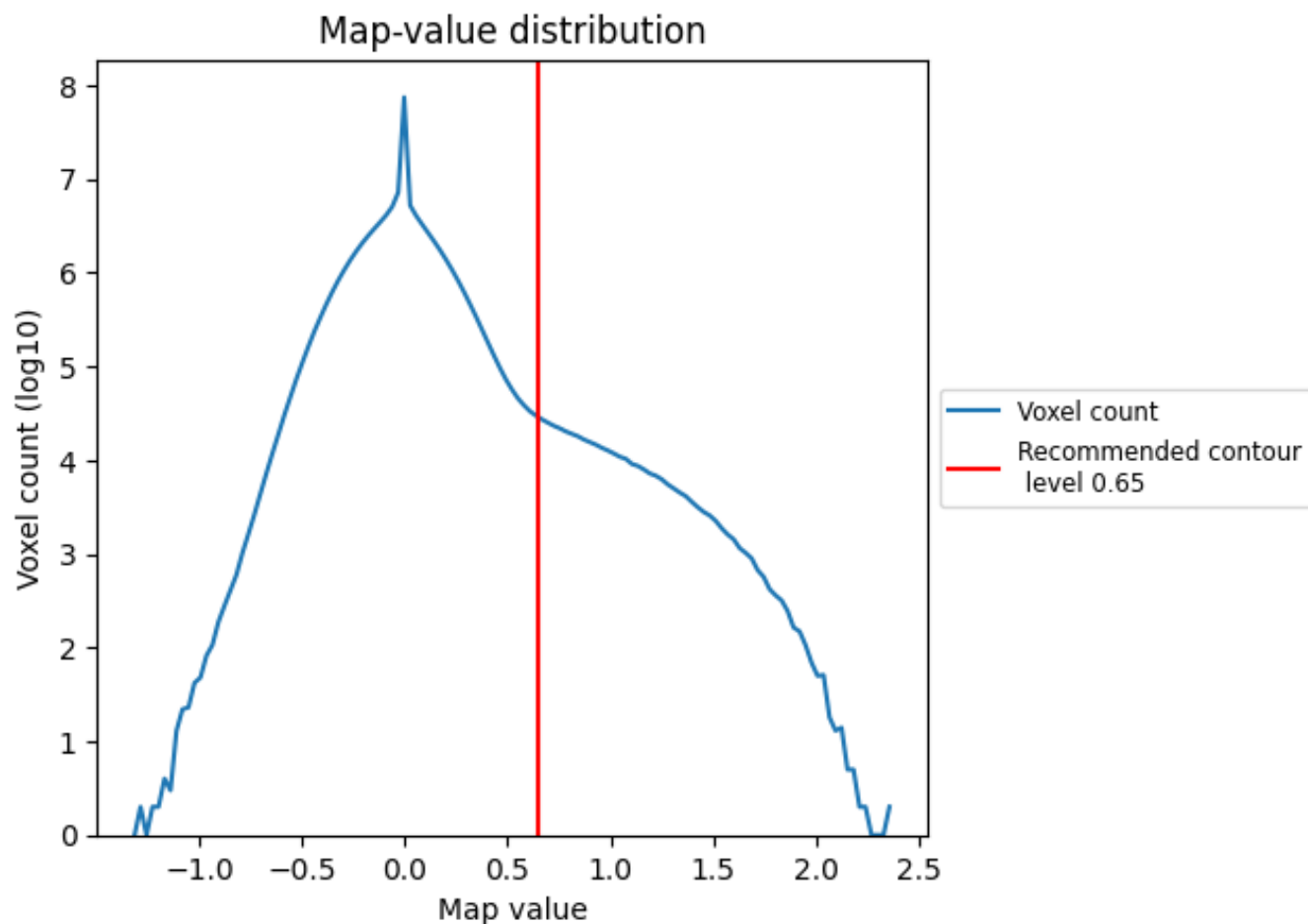
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

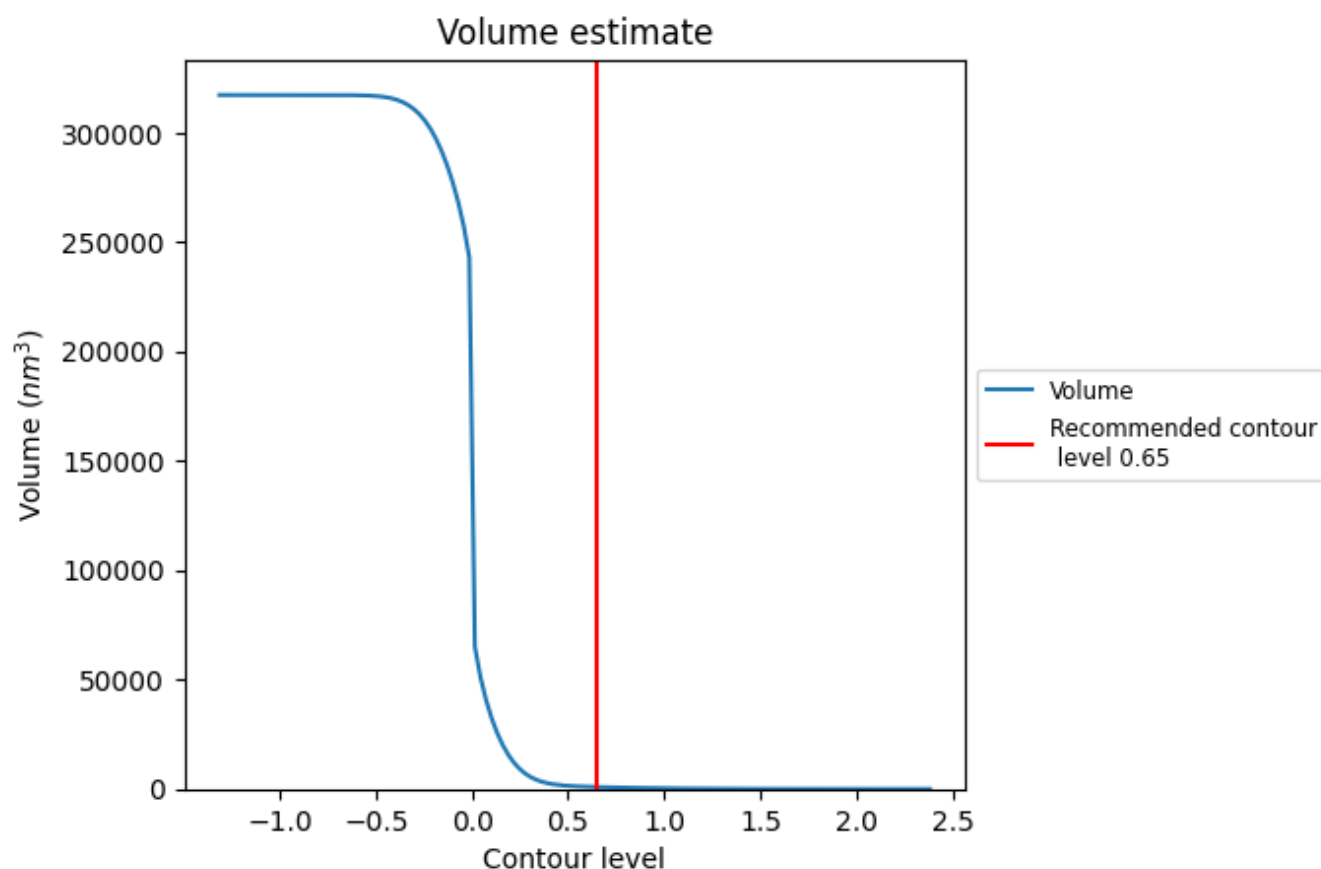
This section contains the results of statistical analysis of the map.

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.

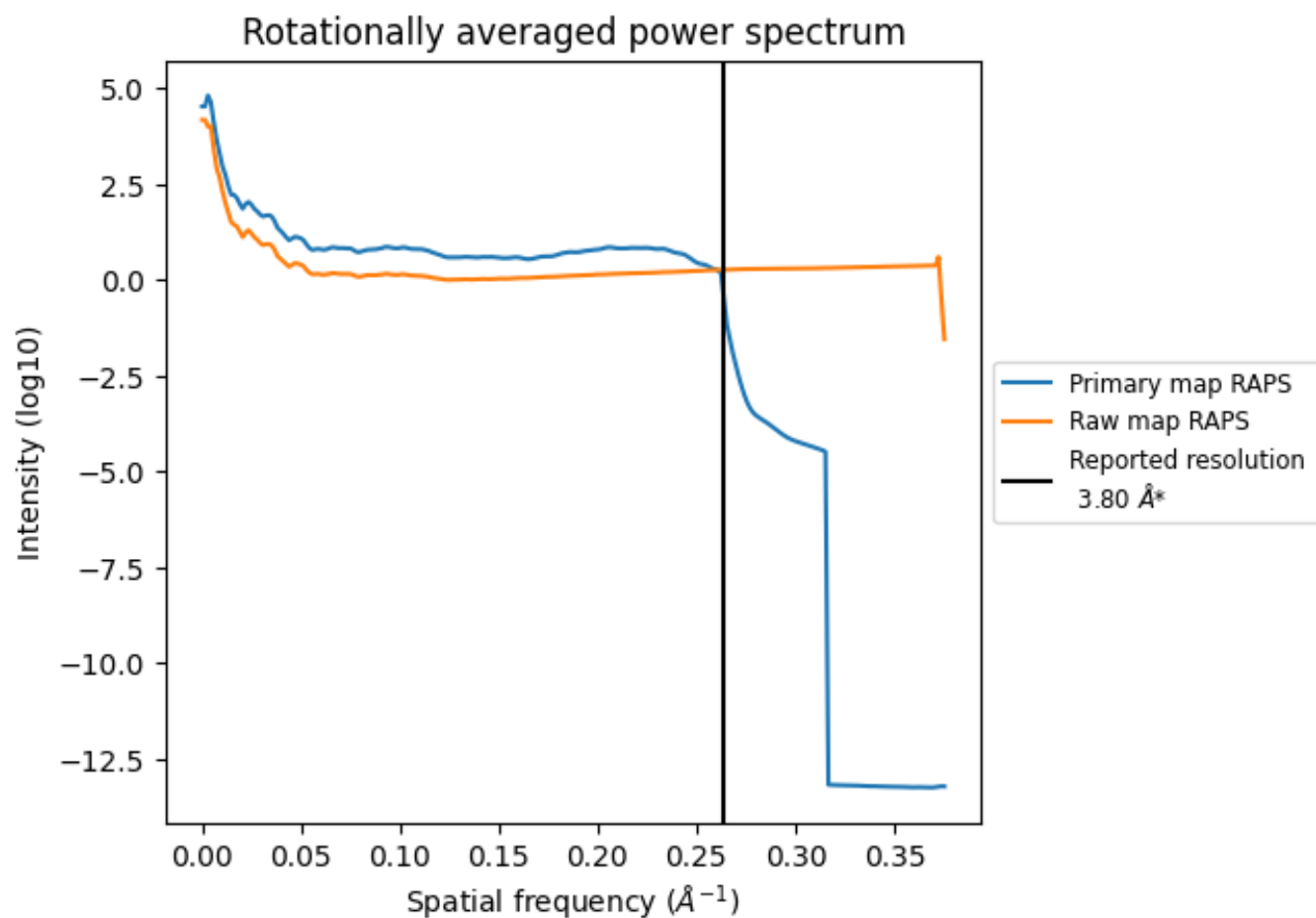
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm³; this corresponds to an approximate mass of 787 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 ⓘ

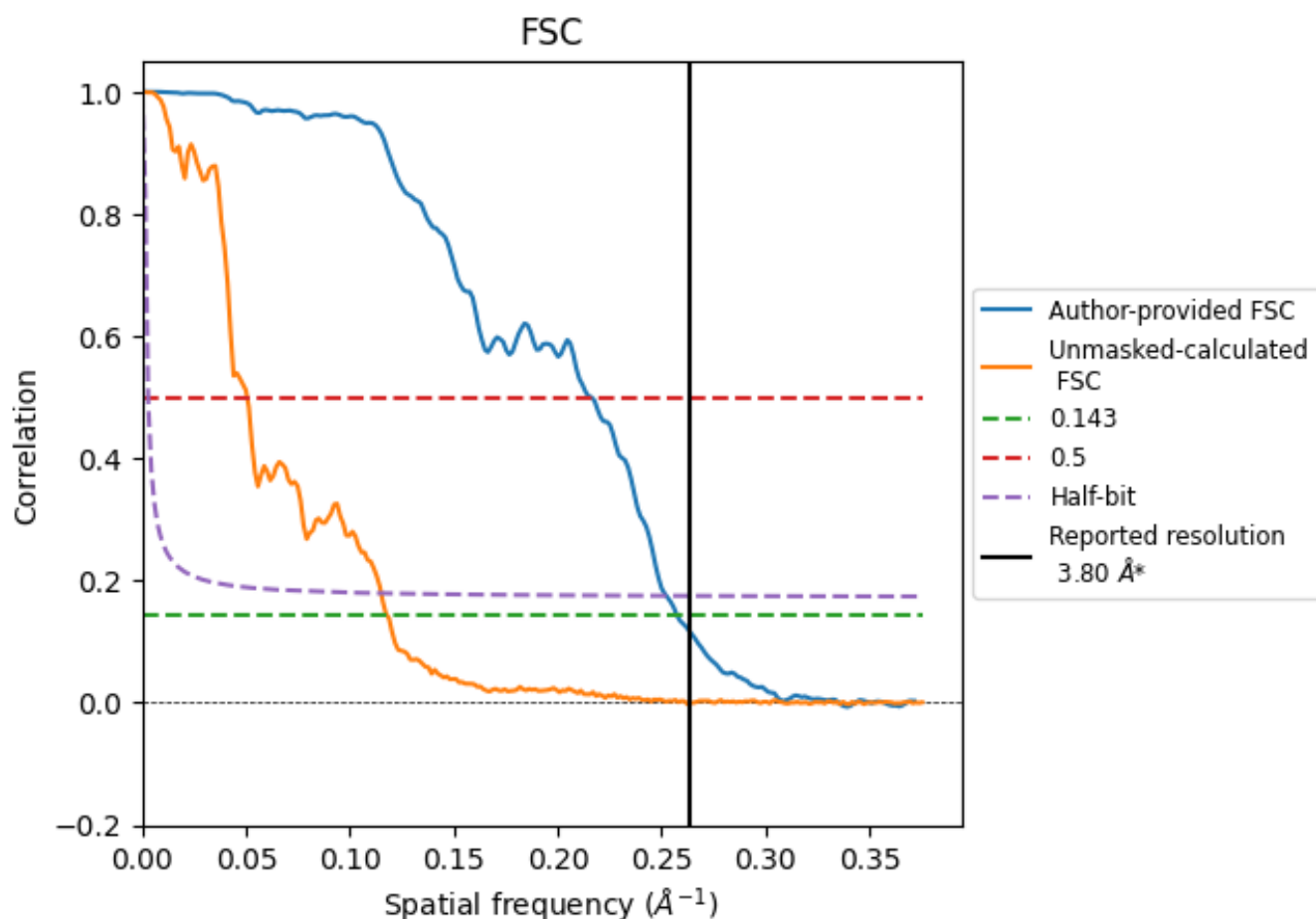


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.263 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

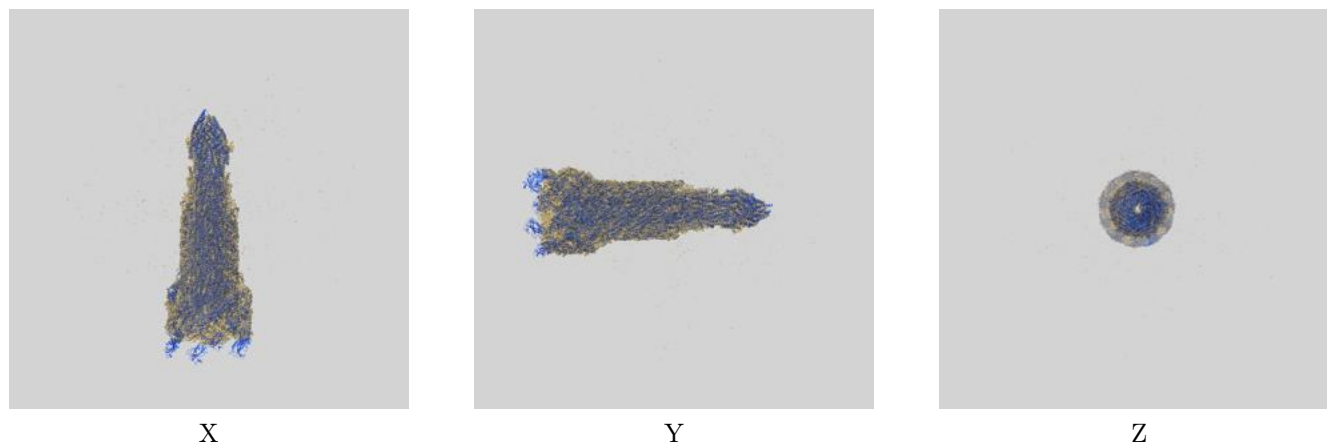
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.89	4.63	3.97
Unmasked-calculated*	8.49	19.80	8.70

*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 8.49 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

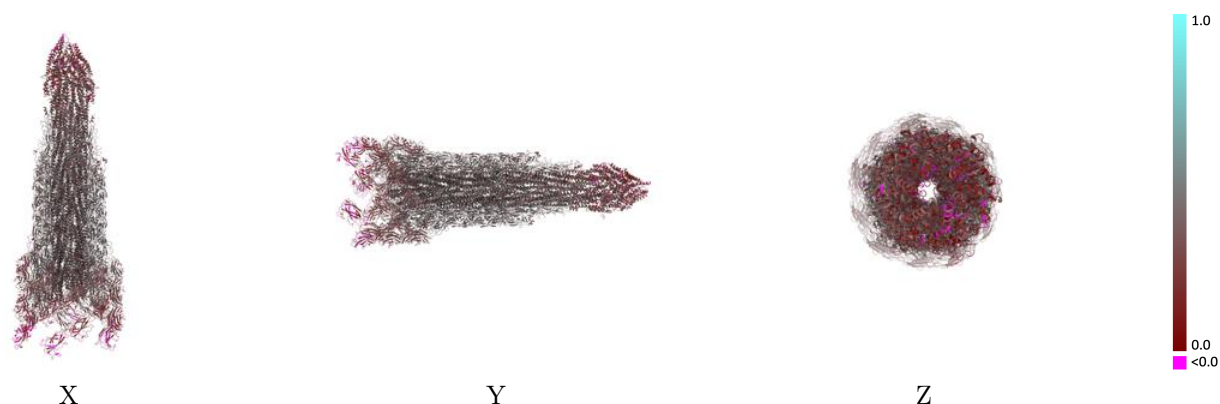
This section contains information regarding the fit between EMDB map EMD-37628 and PDB model 8WLQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



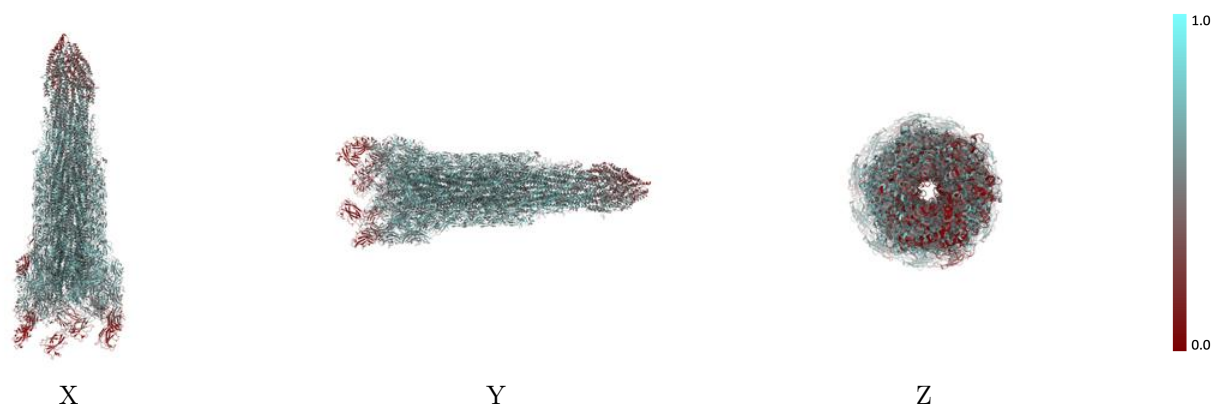
The images above show the 3D surface view of the map at the recommended contour level 0.65 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



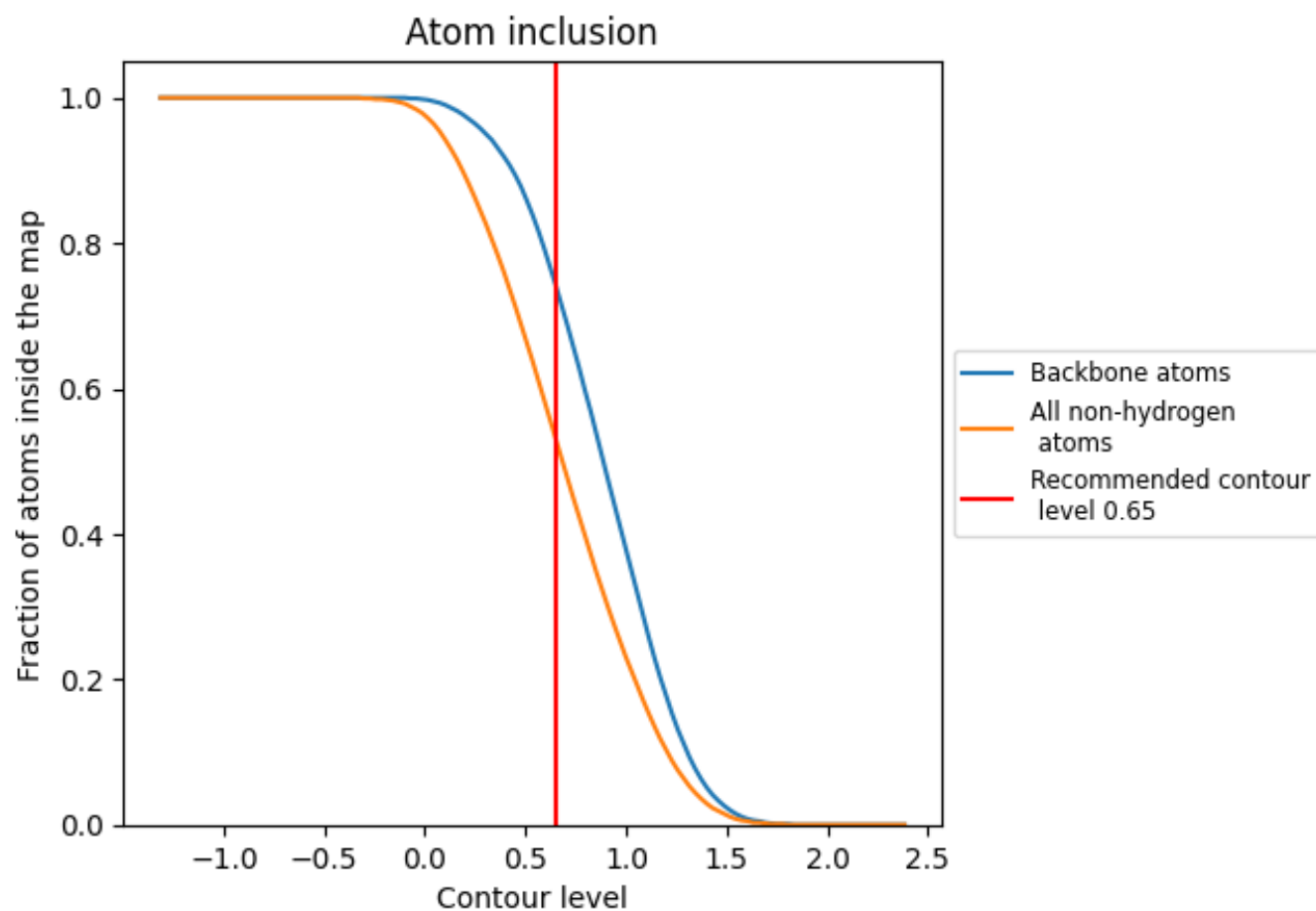
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.65).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 53% 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 (0.65) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5300	 0.3500
0	 0.6070	 0.4090
1	 0.5800	 0.4020
2	 0.5900	 0.4060
3	 0.5980	 0.3990
4	 0.6000	 0.3950
5	 0.5870	 0.4010
6	 0.6040	 0.4060
7	 0.5970	 0.4070
8	 0.5940	 0.4040
9	 0.5740	 0.3940
A	 0.1730	 0.1850
B	 0.3560	 0.2400
C	 0.3900	 0.2320
D	 0.3590	 0.1900
E	 0.3230	 0.2250
F	 0.3730	 0.2390
G	 0.4440	 0.2750
H	 0.4670	 0.2980
I	 0.4650	 0.2870
J	 0.4240	 0.2890
K	 0.4440	 0.2800
L	 0.5070	 0.3100
M	 0.5330	 0.3380
N	 0.5530	 0.3390
O	 0.5200	 0.3260
P	 0.5320	 0.3370
Q	 0.4940	 0.3360
R	 0.5870	 0.3710
S	 0.5930	 0.3730
T	 0.6070	 0.3750
U	 0.5700	 0.3680
V	 0.5200	 0.3610
W	 0.5610	 0.3730
X	 0.5850	 0.4010



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Chain	Atom inclusion	Q-score
Y	 0.5810	 0.4000
Z	 0.6090	 0.3980
ZA	 0.5780	 0.3920
ZB	 0.5910	 0.3970
ZC	 0.6080	 0.4120
ZD	 0.5910	 0.4090
ZE	 0.5700	 0.3960
ZF	 0.3840	 0.3220
ZG	 0.5490	 0.3670
ZH	 0.5850	 0.3690
ZI	 0.6000	 0.3760
ZJ	 0.6020	 0.3740
ZK	 0.5880	 0.3660
ZL	 0.5930	 0.3710
ZM	 0.5910	 0.3750
ZN	 0.6010	 0.3710
ZO	 0.6000	 0.3650
ZP	 0.6030	 0.3630
ZQ	 0.5830	 0.3570
ZR	 0.5800	 0.3520
ZS	 0.5890	 0.3550
ZT	 0.5660	 0.3490
ZU	 0.5590	 0.3420
ZV	 0.5520	 0.3350
ZW	 0.5380	 0.3290
ZX	 0.5310	 0.3240
ZY	 0.5000	 0.3190
ZZ	 0.4900	 0.3060
Za	 0.4610	 0.3080
Zb	 0.4190	 0.2820
Zc	 0.4030	 0.2900
Zd	 0.3780	 0.2790
Ze	 0.3450	 0.2630
Zf	 0.3370	 0.2470
Zg	 0.3130	 0.2380
Zh	 0.2950	 0.2350
a	 0.5650	 0.3790
b	 0.3210	 0.3210
c	 0.4470	 0.3630
d	 0.3990	 0.3370
e	 0.6210	 0.4010
f	 0.5500	 0.3570

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Chain	Atom inclusion	Q-score
g	 0.5240	 0.3350
h	 0.6000	 0.4050
i	 0.5530	 0.3420
j	 0.5870	 0.3990
k	 0.4560	 0.2680
l	 0.4860	 0.3280
m	 0.5430	 0.3860
n	 0.6180	 0.4010
o	 0.6160	 0.4150
p	 0.6110	 0.4030
q	 0.5920	 0.3880
r	 0.5490	 0.3830
s	 0.5910	 0.4050
t	 0.6130	 0.4110
u	 0.5920	 0.4070
v	 0.5820	 0.4080
w	 0.5950	 0.4020
x	 0.5890	 0.3990
y	 0.5950	 0.4080
z	 0.5810	 0.3980