



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 05:07 AM UTC

PDB ID : 8RK3 / pdb_00008rk3
EMDB ID : EMD-19256
Title : Bacteriophage JBD30 baseplate - composite structure
Authors : Valentova, L.; Fuzik, T.; Plevka, P.
Deposited on : 2023-12-23
Resolution : 4.46 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

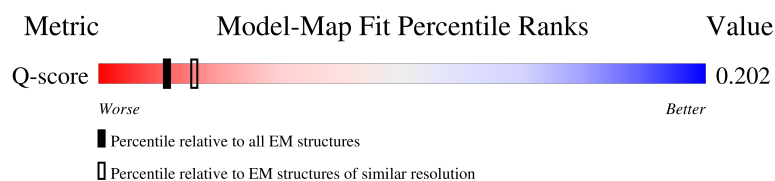
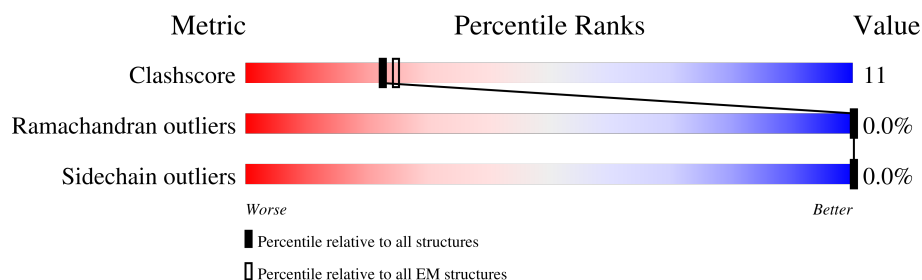
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.46 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.



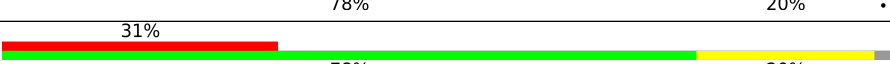
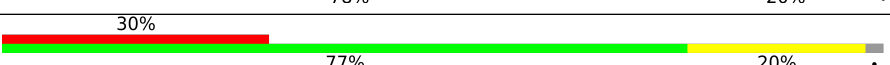
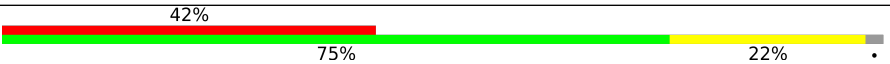
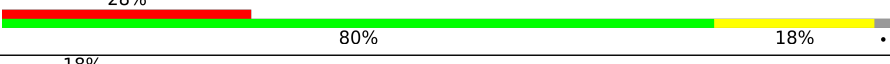
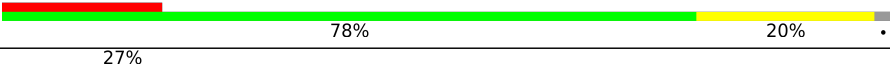
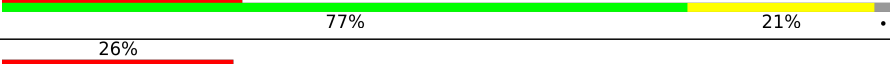
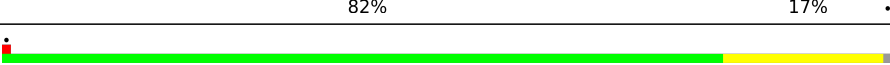
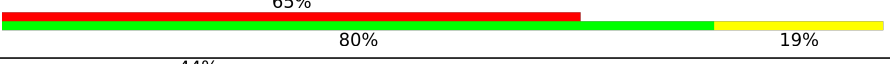
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3001 (3.96 - 4.96)

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	A	1158	97%
1	B	1158	97%
1	C	1158	97%
2	O	273	75% 25%

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Mol	Chain	Length	Quality of chain
2	P	273	
2	g	273	
3	D	567	
3	U	567	
3	r	567	
4	E	382	
4	F	382	
4	I	382	
4	J	382	
4	M	382	
4	N	382	
4	W	382	
4	a	382	
4	e	382	
5	b	735	
5	d	735	
5	o	735	
6	K	318	
6	L	318	
6	Q	318	
6	R	318	
6	T	318	
6	V	318	
6	c	318	
6	i	318	

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Mol	Chain	Length	Quality of chain
6	k	318	
7	G	307	
7	H	307	
7	S	307	
7	X	307	
7	Y	307	
7	Z	307	
7	m	307	
7	n	307	
7	p	307	
8	f	256	
8	h	256	
8	j	256	
8	l	256	
8	q	256	
8	s	256	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 116259 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 Tape measure protein N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	32	Total	C	N	O	S	0	0
			256	161	47	46	2		
1	B	32	Total	C	N	O	S	0	0
			256	161	47	46	2		
1	C	32	Total	C	N	O	S	0	0
			256	161	47	46	2		

- Molecule 2 is a protein called DUF2163 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	g	272	Total	C	N	O	S	0	0
			2099	1311	360	417	11		
2	O	272	Total	C	N	O	S	0	0
			2099	1311	360	417	11		
2	P	272	Total	C	N	O	S	0	0
			2099	1311	360	417	11		

- Molecule 3 is a protein called Virion structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	U	554	Total	C	N	O	S	0	0
			4278	2692	760	813	13		
3	r	554	Total	C	N	O	S	0	0
			4278	2692	760	813	13		
3	D	554	Total	C	N	O	S	0	0
			4278	2692	760	813	13		

- Molecule 4 is a protein called DUF2793 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	W	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	e	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	I	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	E	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	M	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	J	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	F	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		
4	N	373	Total	C	N	O	S	0	0
			2791	1771	485	521	14		

- Molecule 5 is a protein called Tip attachment protein J domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	o	727	Total	C	N	O	S	0	0
			5581	3515	988	1067	11		
5	b	727	Total	C	N	O	S	0	0
			5581	3515	988	1067	11		
5	d	727	Total	C	N	O	S	0	0
			5581	3515	988	1067	11		

- Molecule 6 is a protein called Virion structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	c	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	i	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	k	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	K	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	Q	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	T	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	R	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		
6	V	317	Total	C	N	O	S	0	0
			2470	1580	425	459	6		

- Molecule 7 is a protein called Virion structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	Y	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	m	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	n	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	G	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	X	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	p	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	H	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		
7	Z	305	Total	C	N	O	S	0	0
			2338	1479	407	442	10		

- Molecule 8 is a protein called Virion structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	q	252	Total	C	N	O	S	0	0
			1871	1199	309	360	3		
8	s	252	Total	C	N	O	S	0	0
			1871	1199	309	360	3		
8	f	252	Total	C	N	O	S	0	0
			1871	1199	309	360	3		
8	j	252	Total	C	N	O	S	0	0
			1871	1199	309	360	3		
8	h	252	Total	C	N	O	S	0	0
			1871	1199	309	360	3		

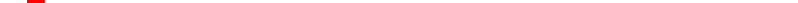
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Mol	Chain	Residues	Atoms					AltConf	Trace
8	1	252	Total	C	N	O	S	0	0
			1871	1199	309	360	3		

[illegible]

- Molecule 1: Tape measure protein N-terminal domain-containing protein

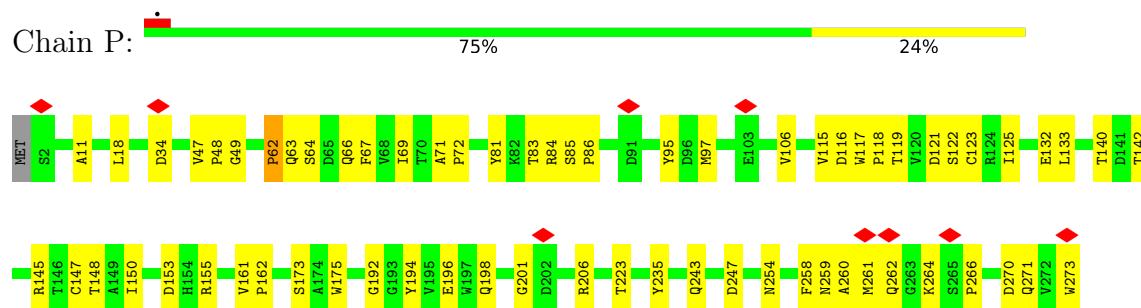
Chain B:  97%

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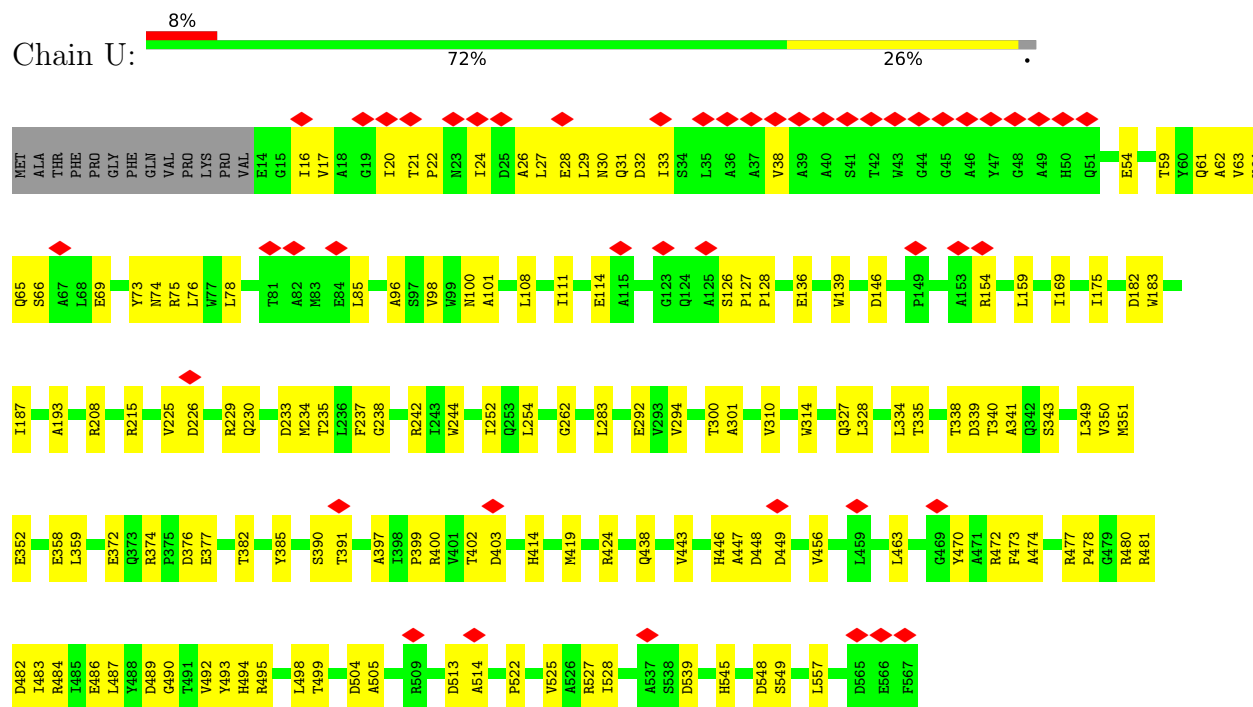
- Molecule 1: Tape measure protein N-terminal domain-containing protein

Chain C: 97%

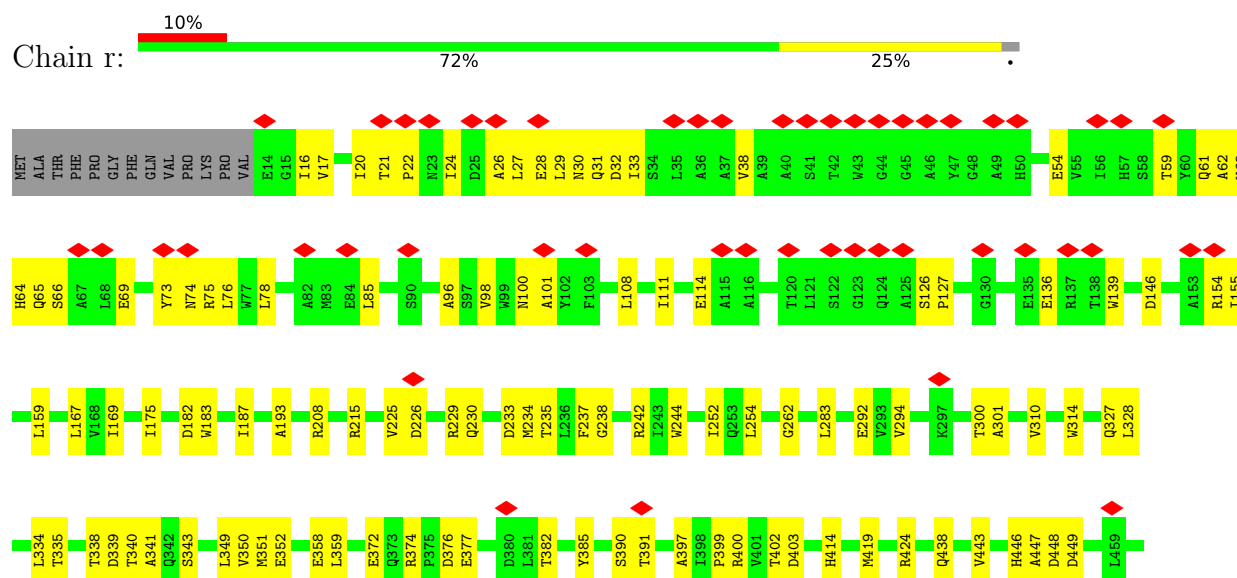
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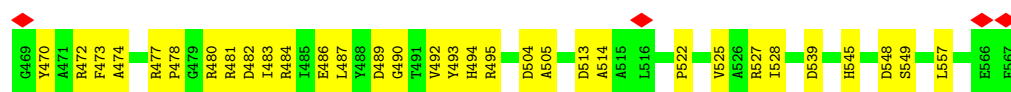


• Molecule 3: Virion structural protein

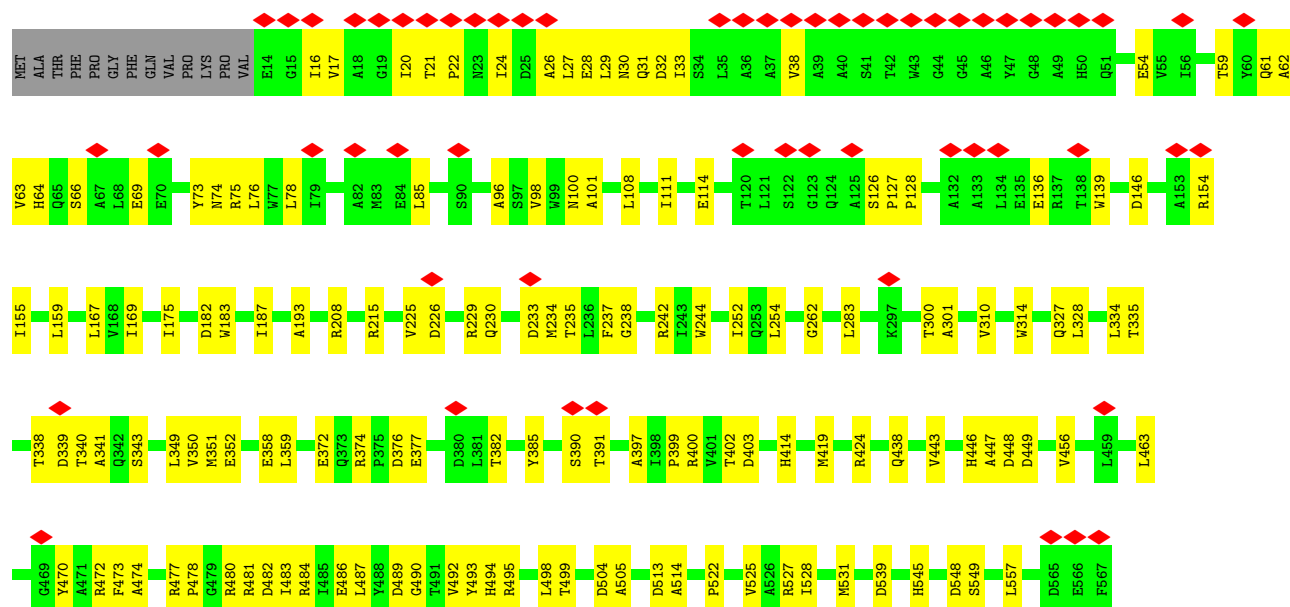


• Molecule 3: Virion structural protein

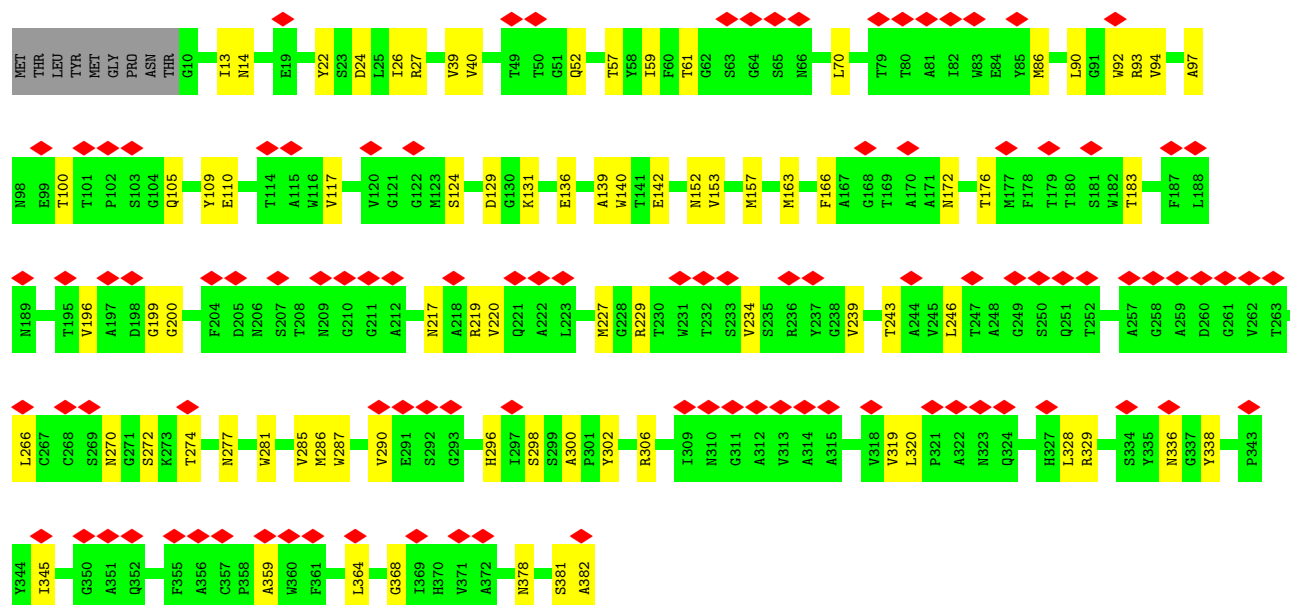
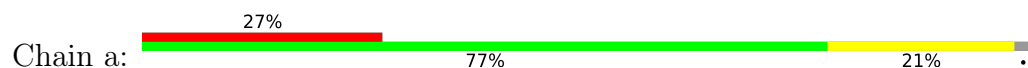




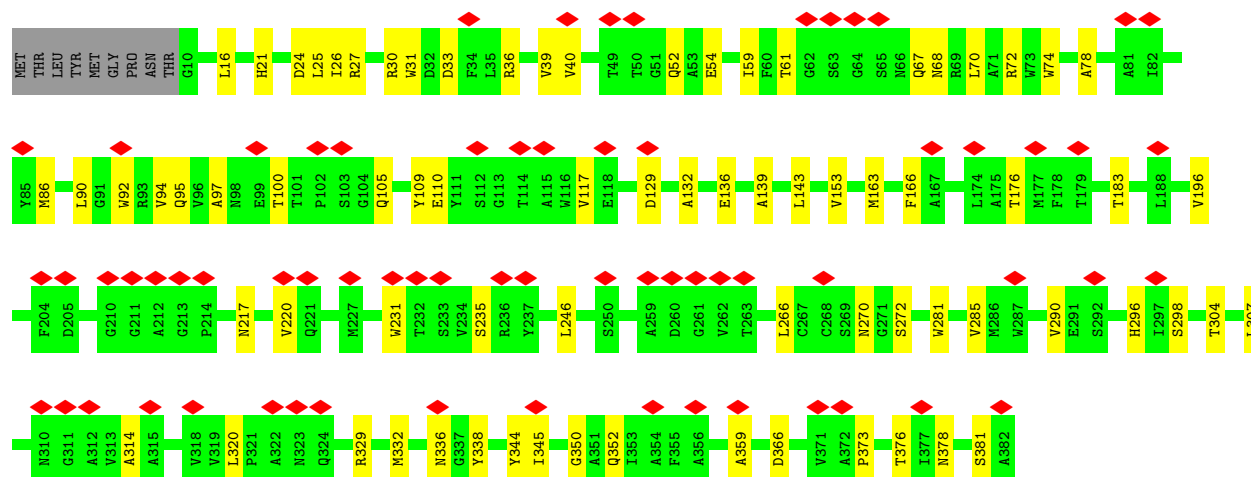
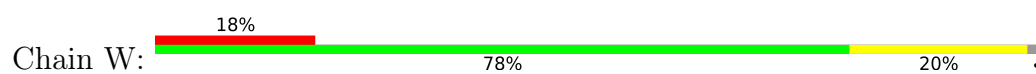
• Molecule 3: Virion structural protein



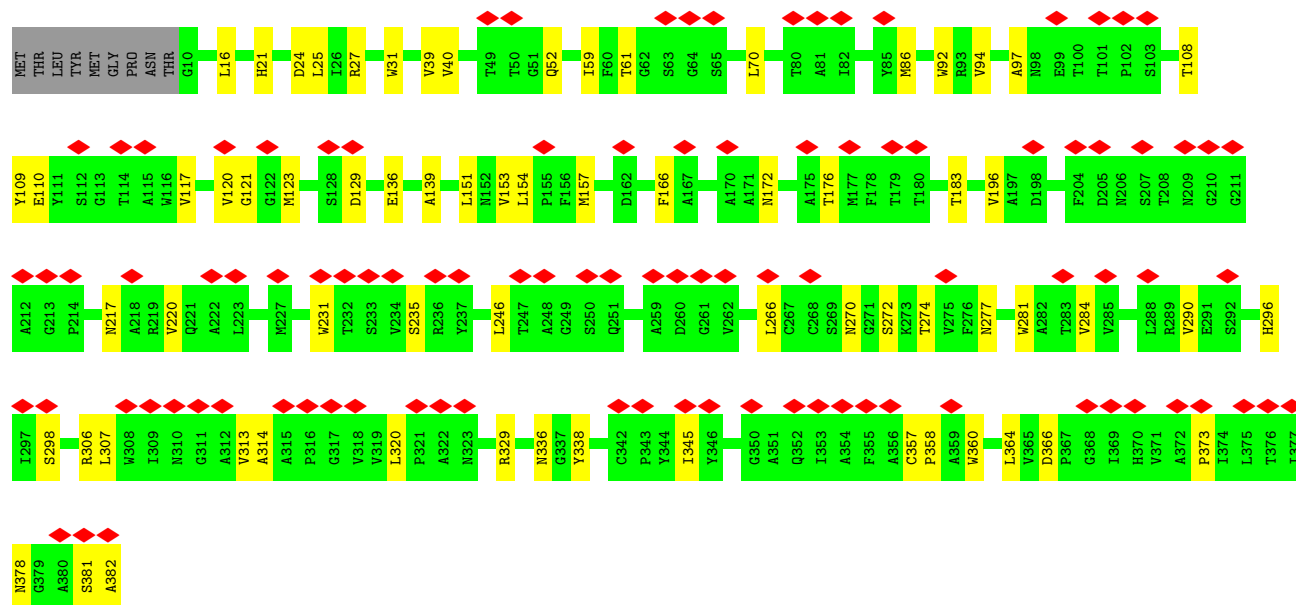
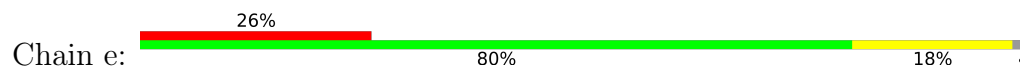
• Molecule 4: DUF2793 domain-containing protein



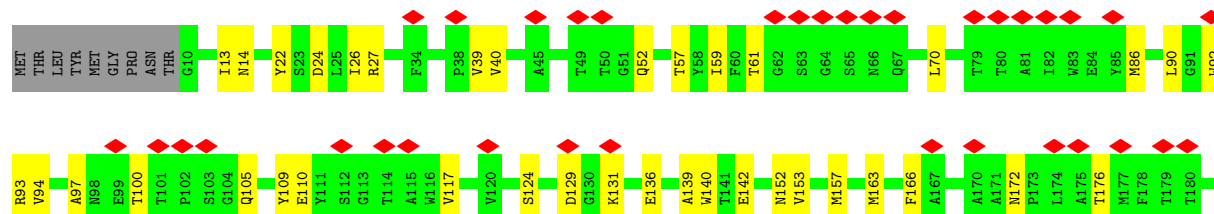
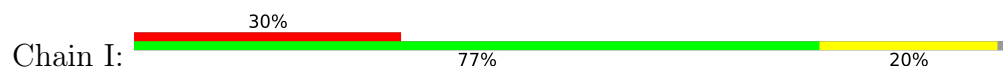
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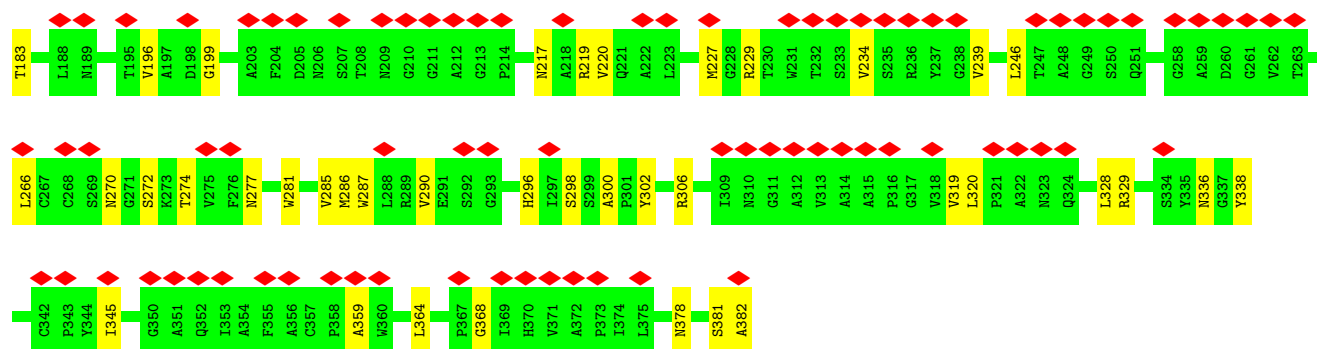


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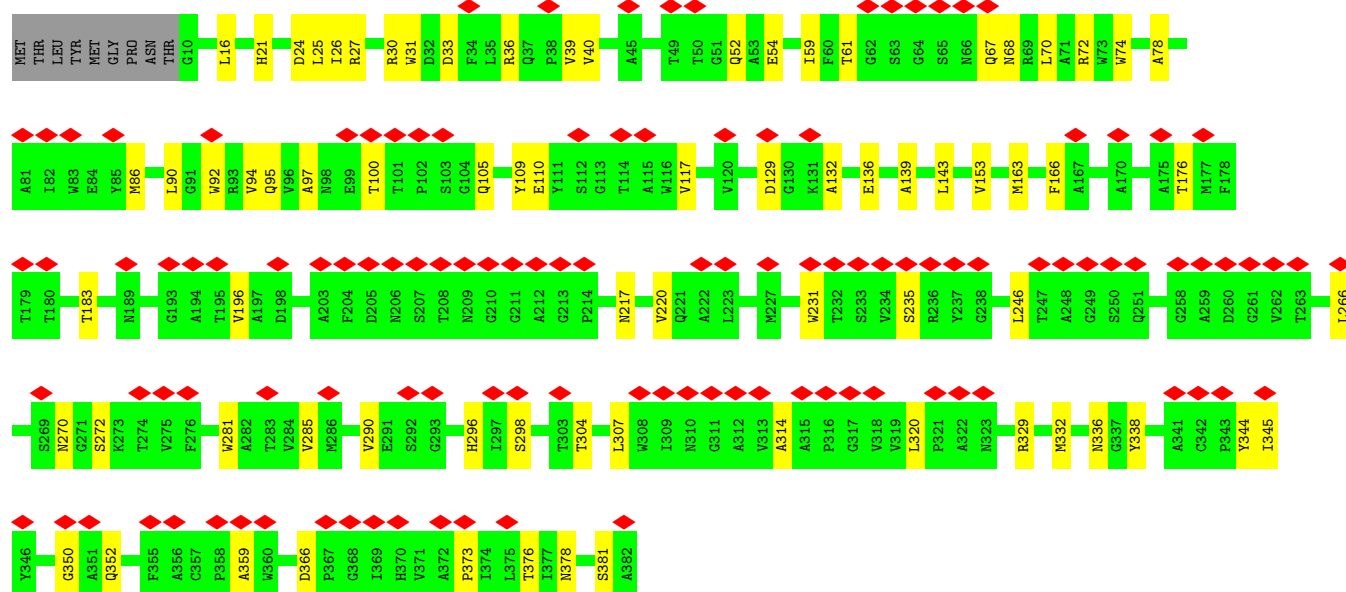
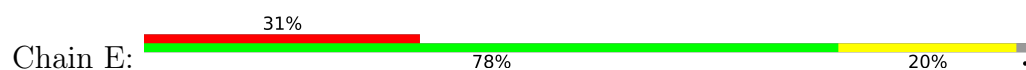


• Molecule 4: DUF2793 domain-containing protein

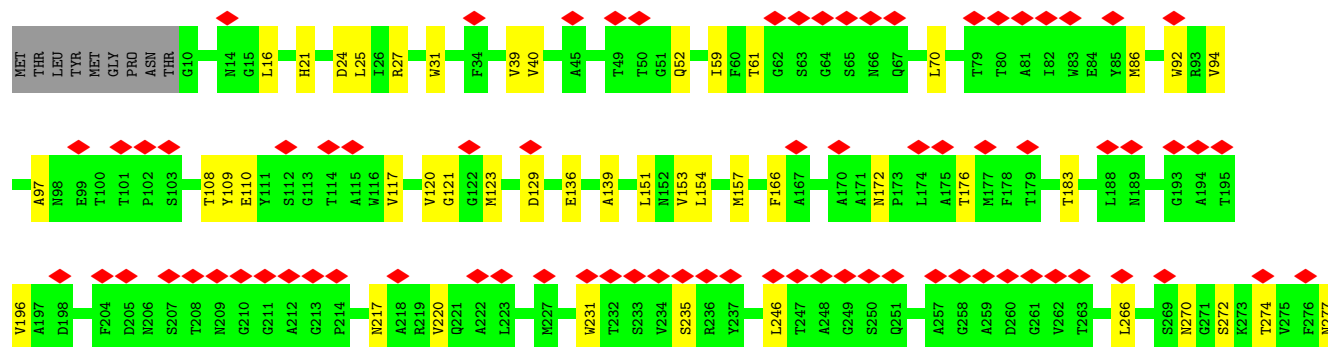
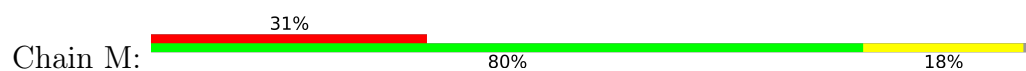


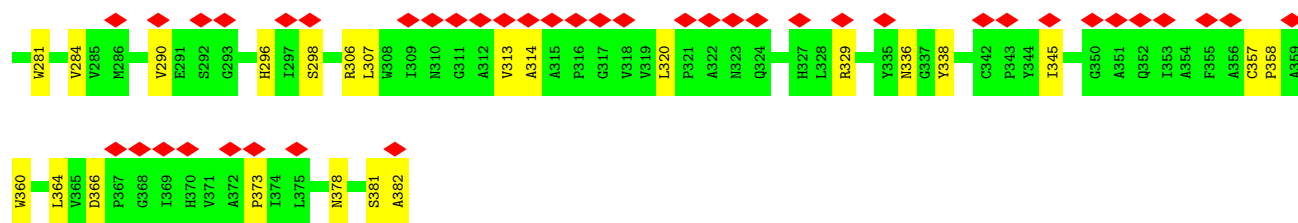


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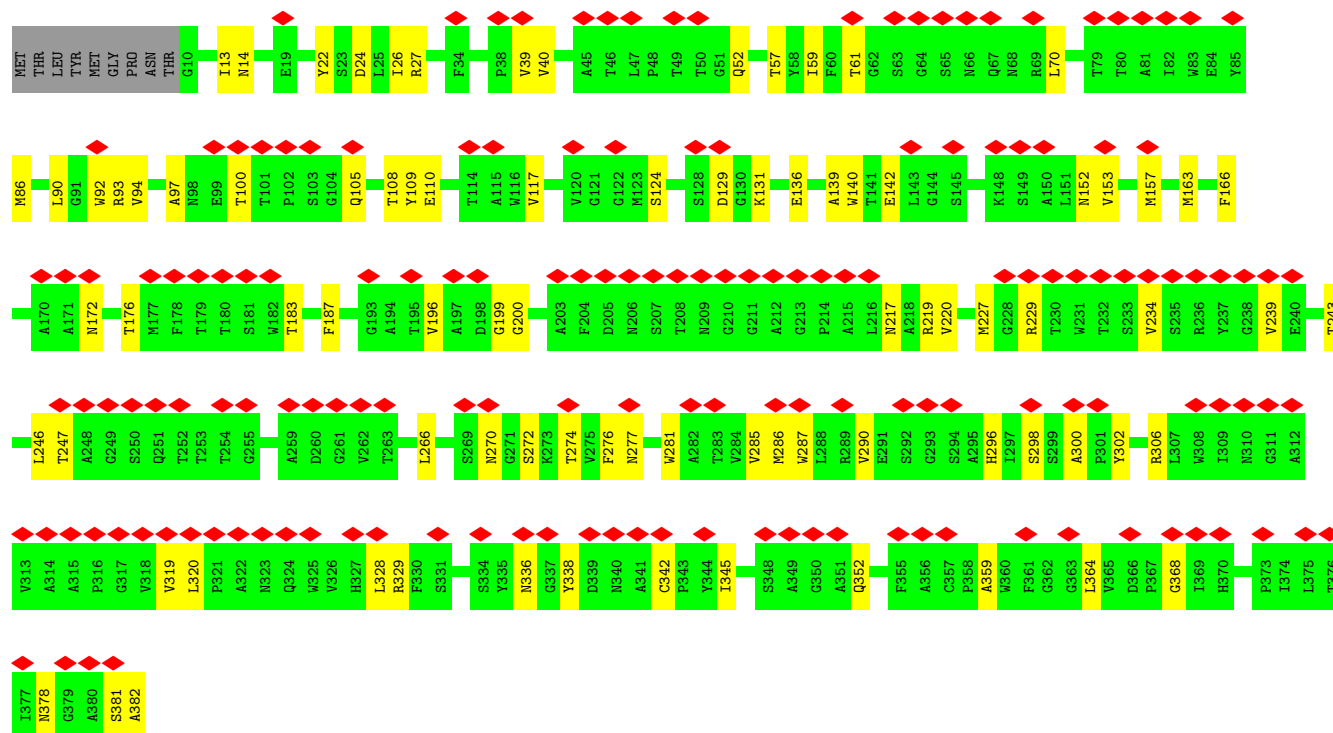
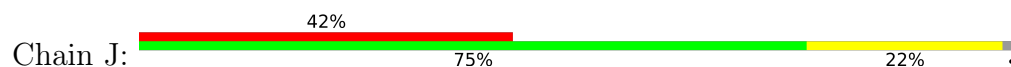


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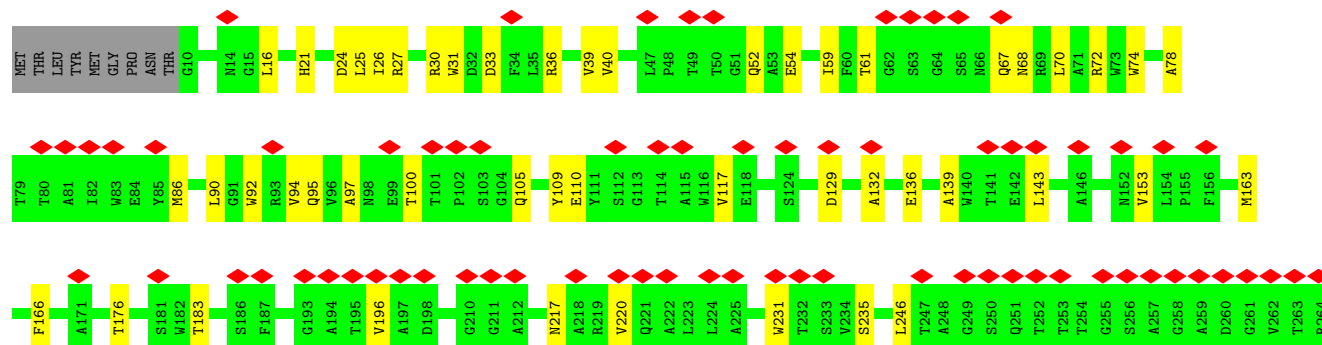
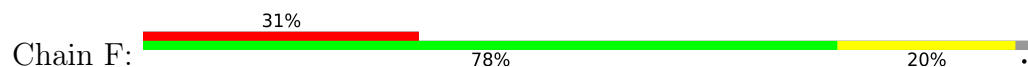


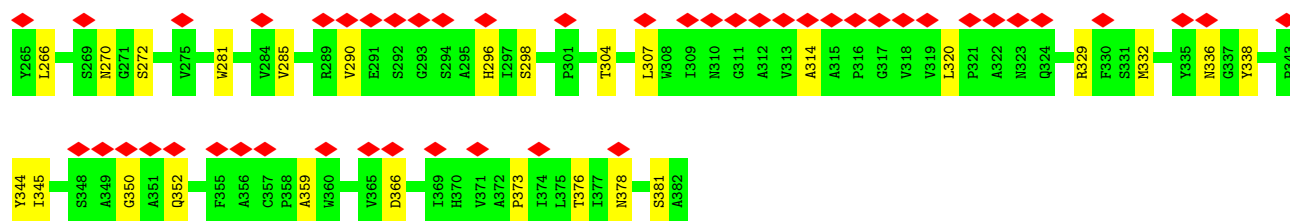


• Molecule 4: DUF2793 domain-containing protein

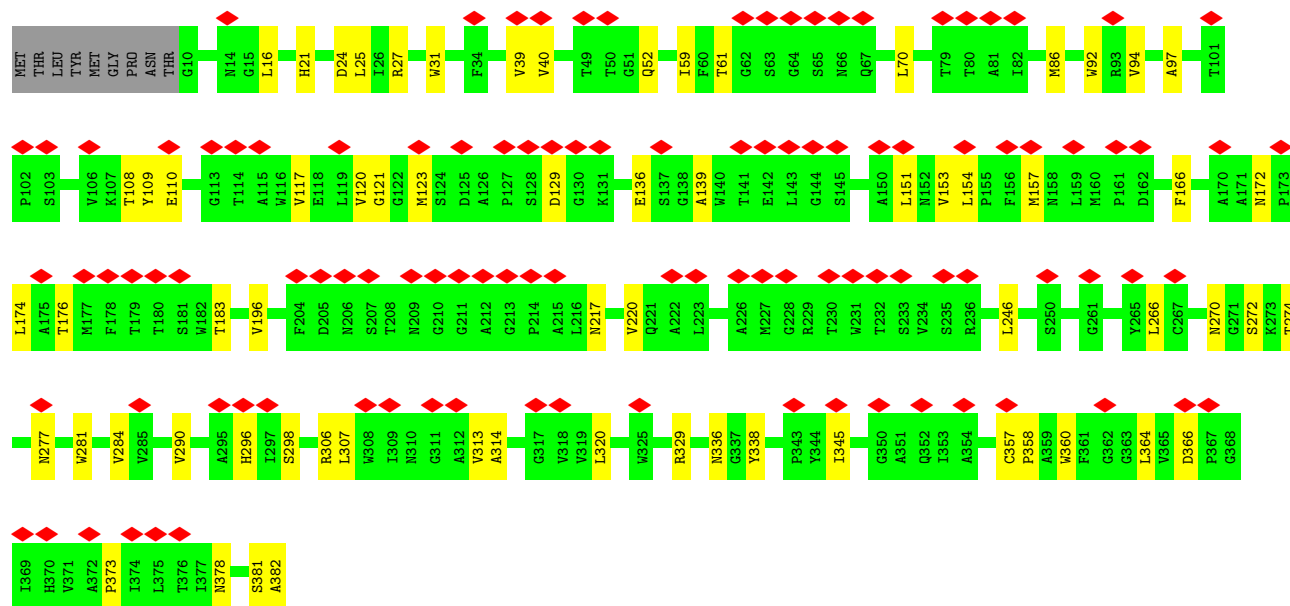
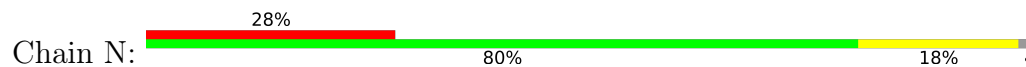


• Molecule 4: DUF2793 domain-containing protein

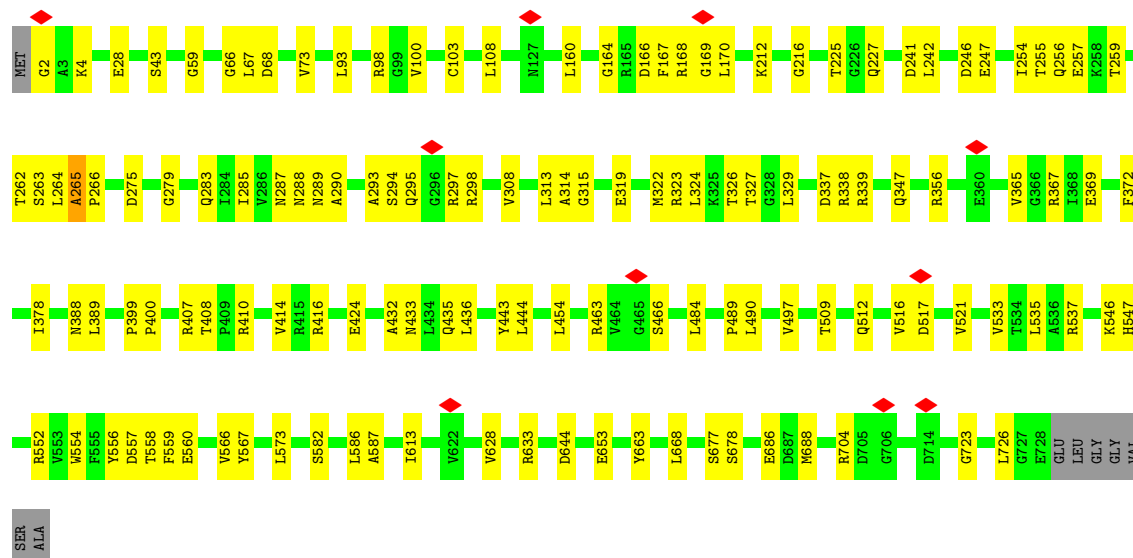
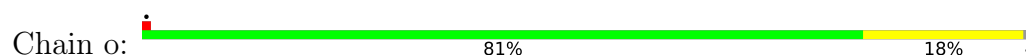




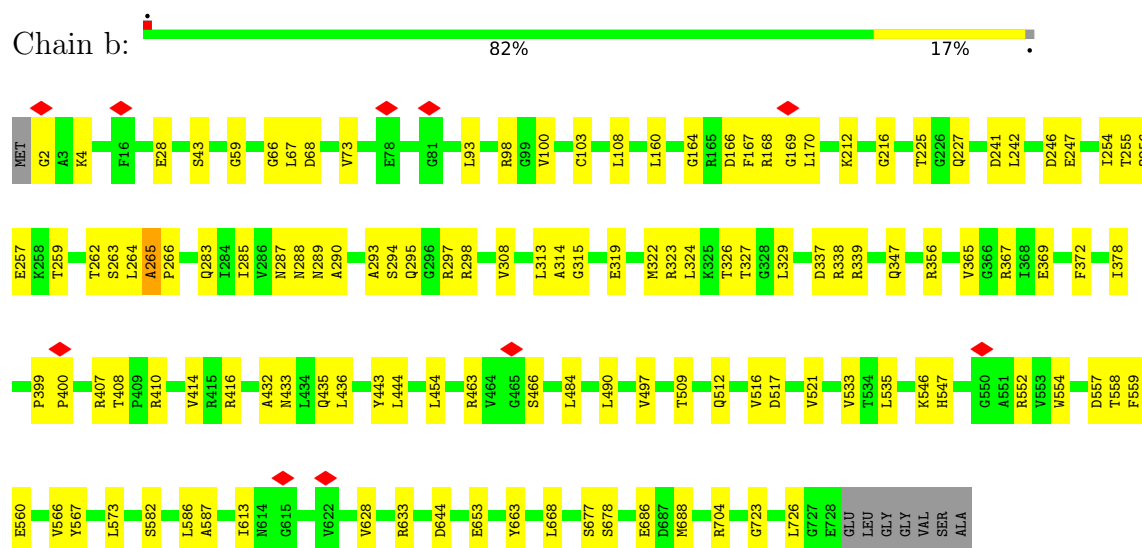
• Molecule 4: DUF2793 domain-containing protein



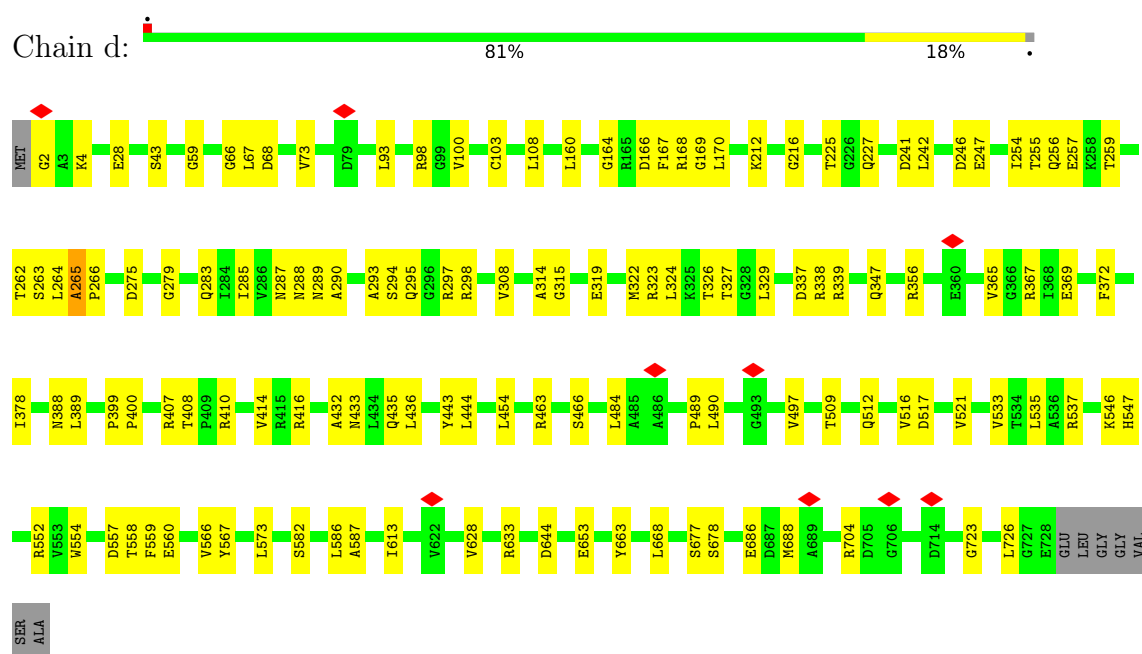
• Molecule 5: Tip attachment protein J domain-containing protein



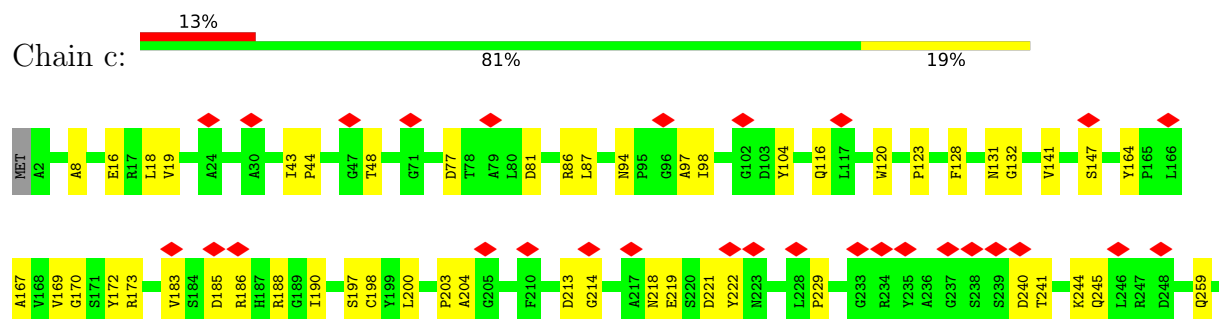
- Molecule 5: Tip attachment protein J domain-containing protein

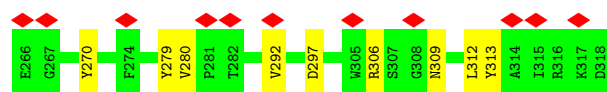


- Molecule 5: Tip attachment protein J domain-containing protein

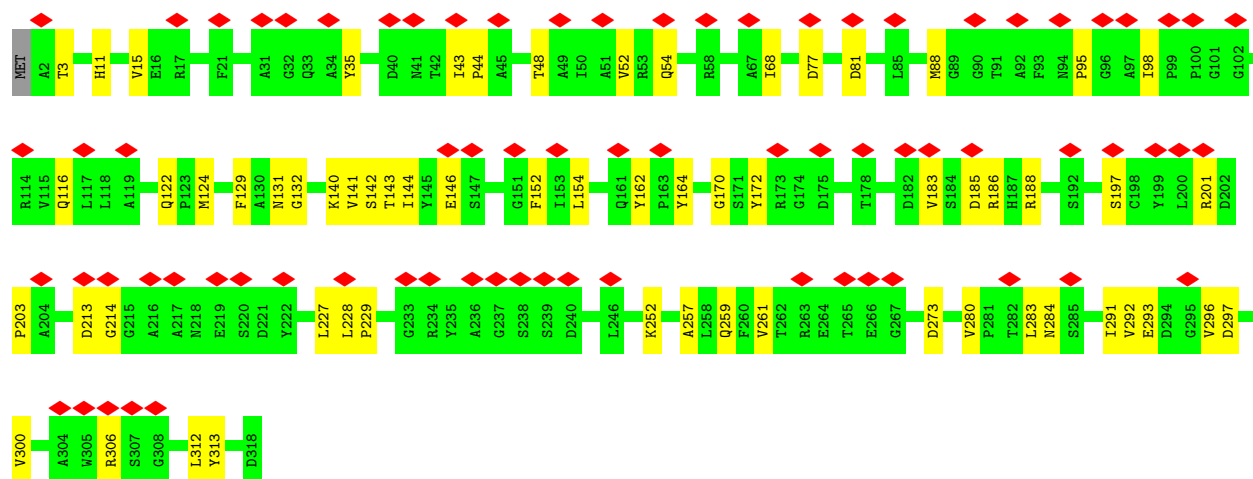
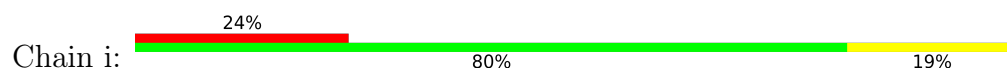


- Molecule 6: Virion structural protein

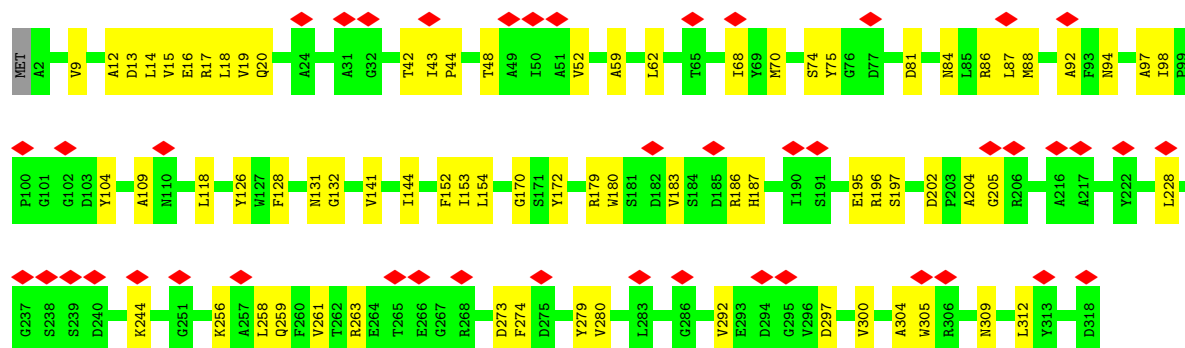
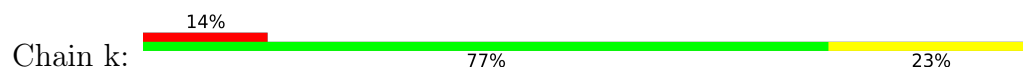




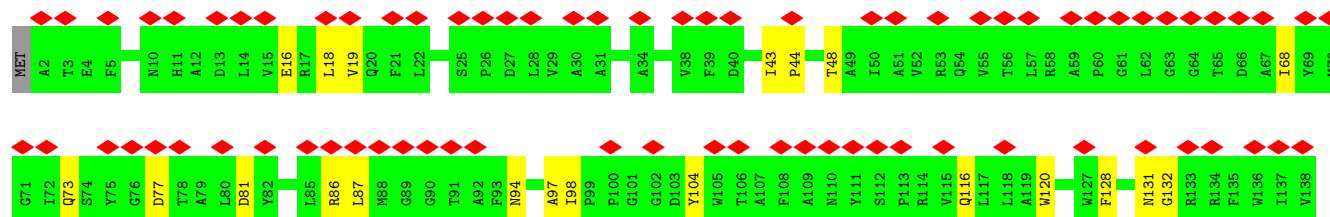
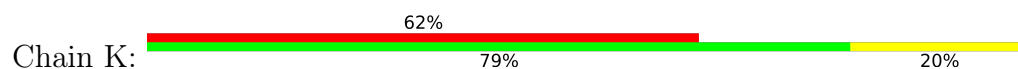
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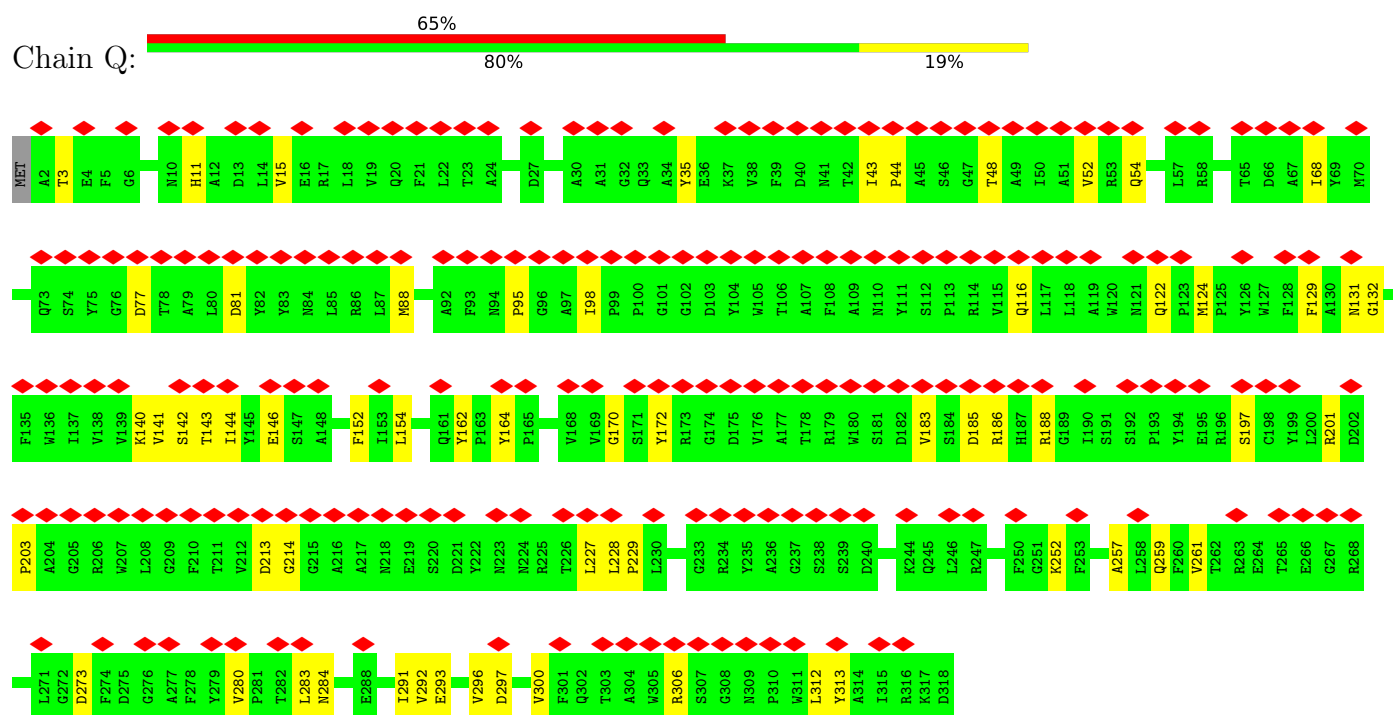


• Molecule 6: Virion structural protein

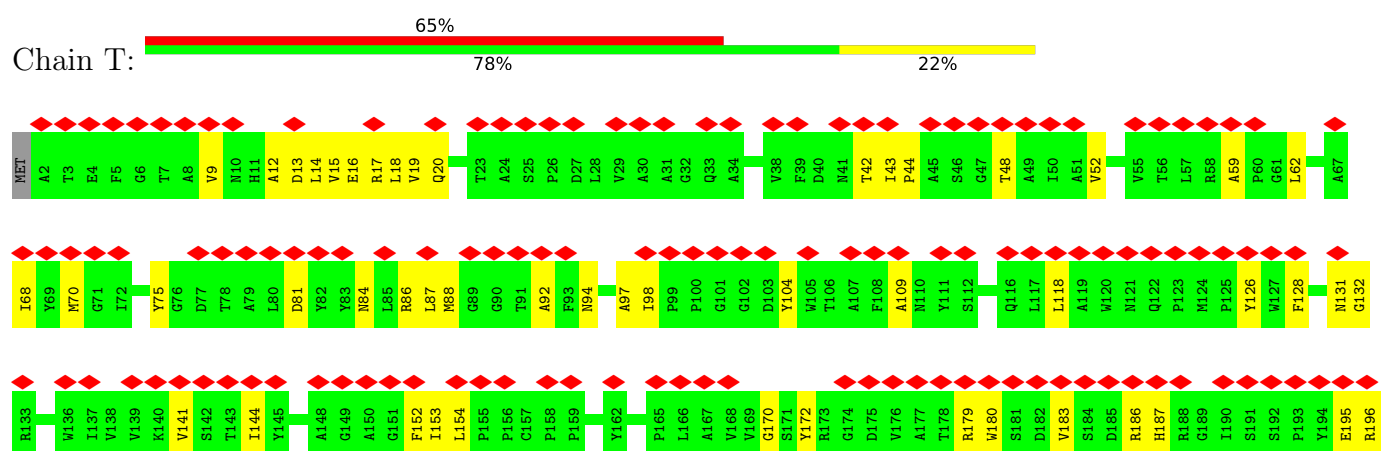


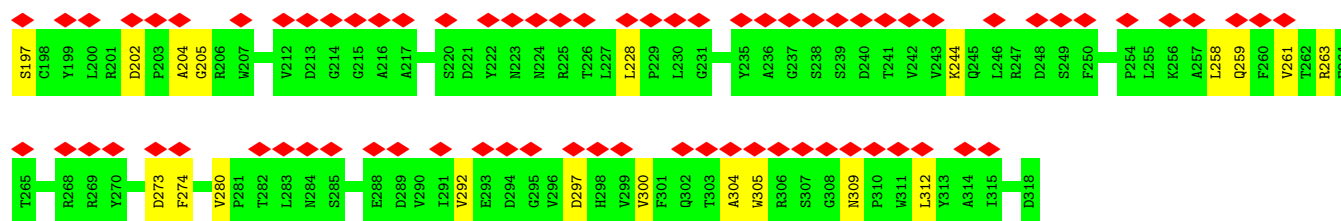


• Molecule 6: Virion structural protein

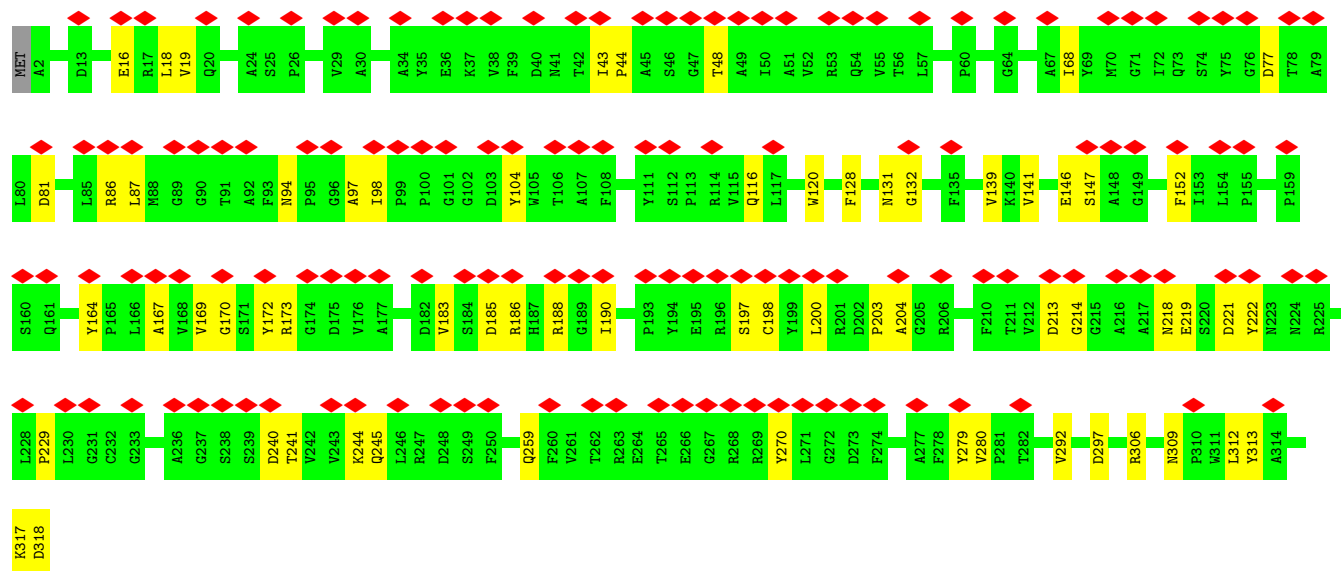
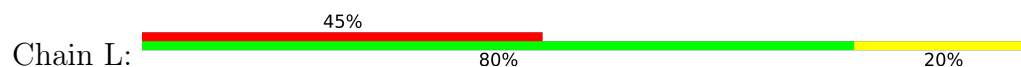


• Molecule 6: Virion structural protein

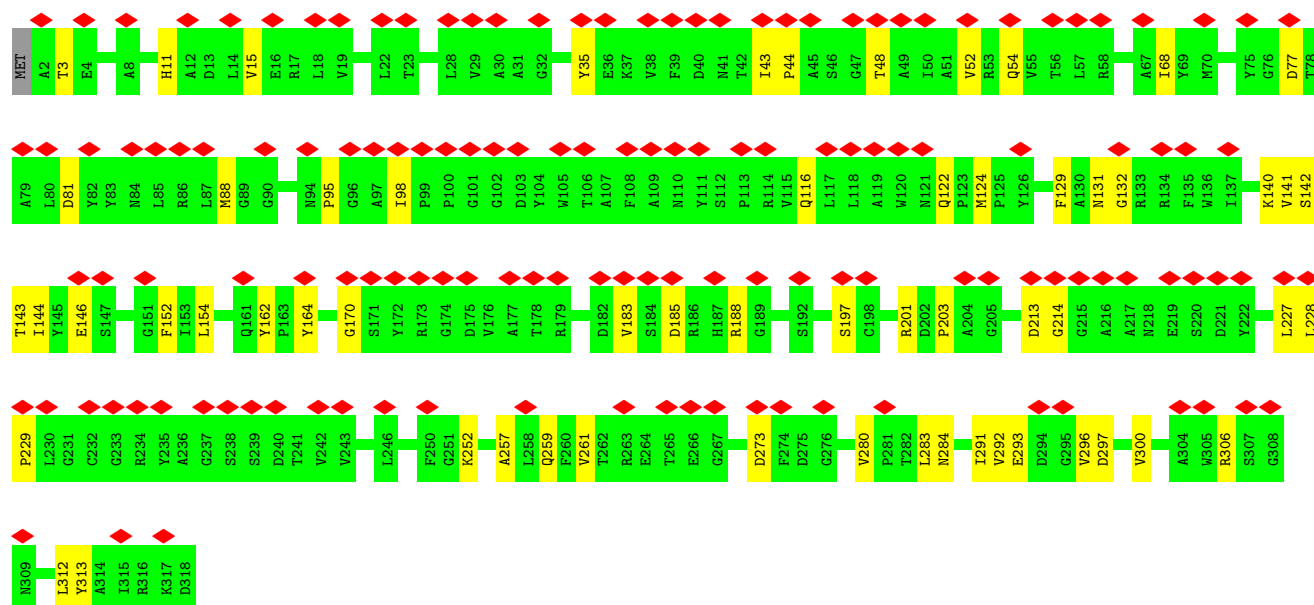
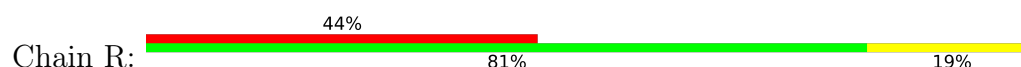




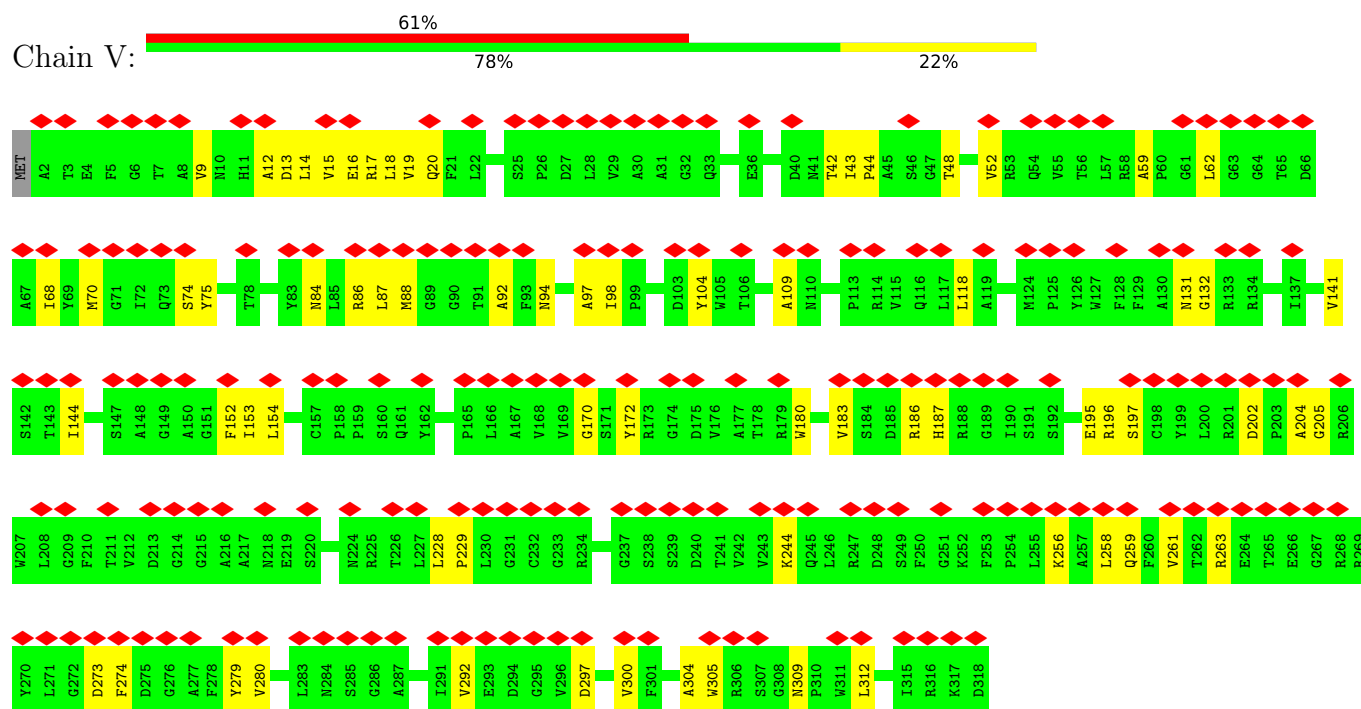
• Molecule 6: Virion structural protein



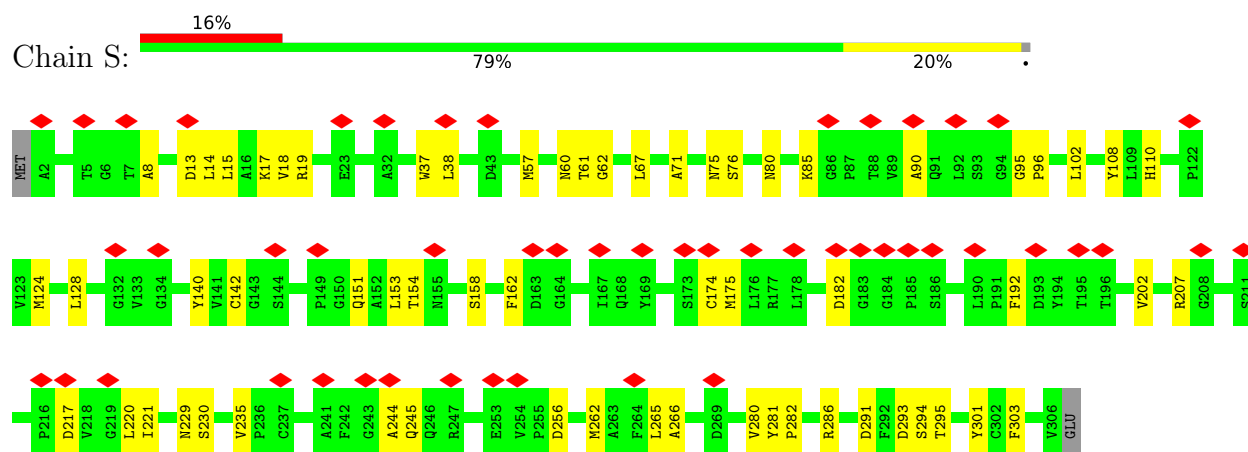
• Molecule 6: Virion structural protein



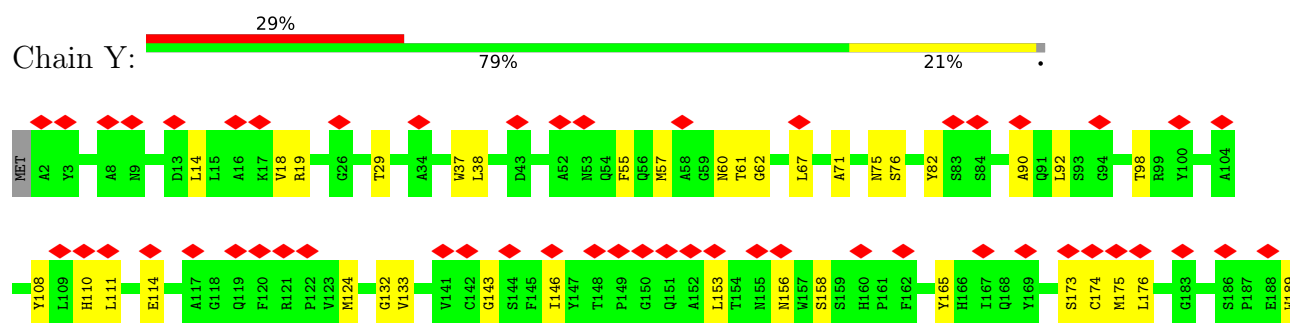
- Molecule 6: Virion structural protein

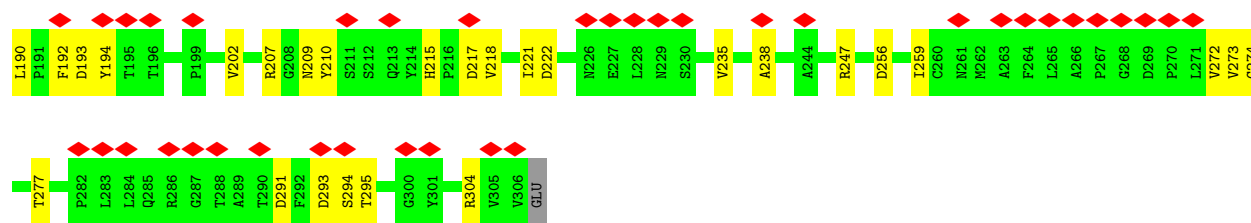


- Molecule 7: Virion structural protein

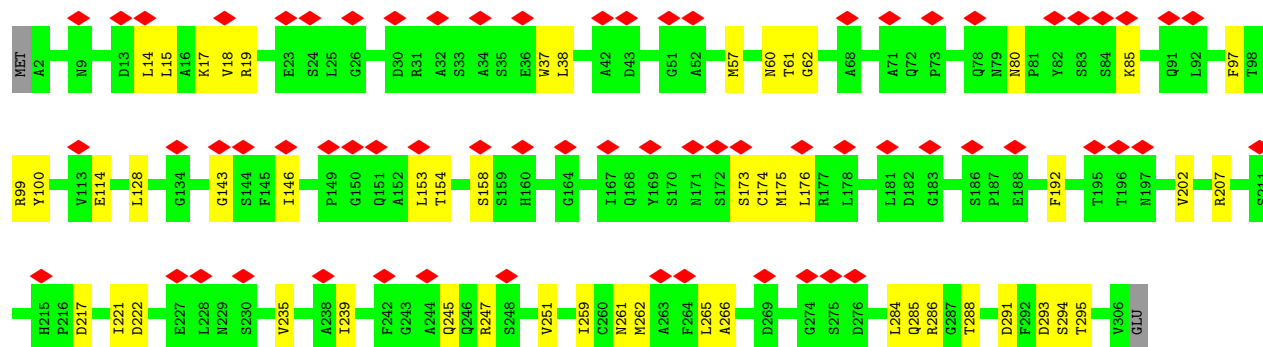
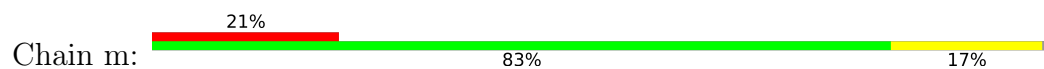


- Molecule 7: Virion structural protein

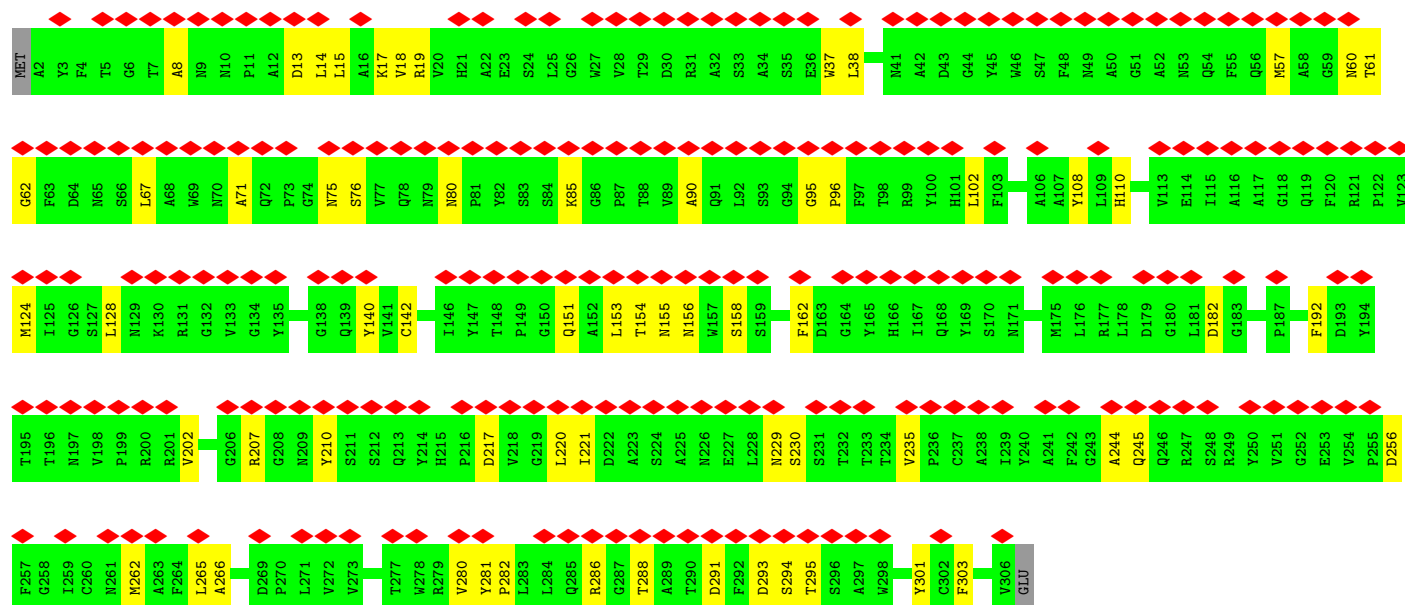
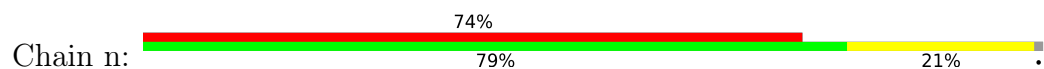




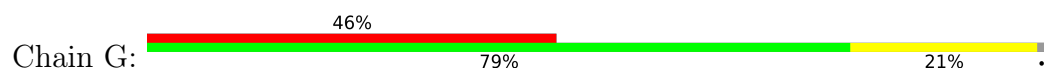
• Molecule 7: Virion structural protein

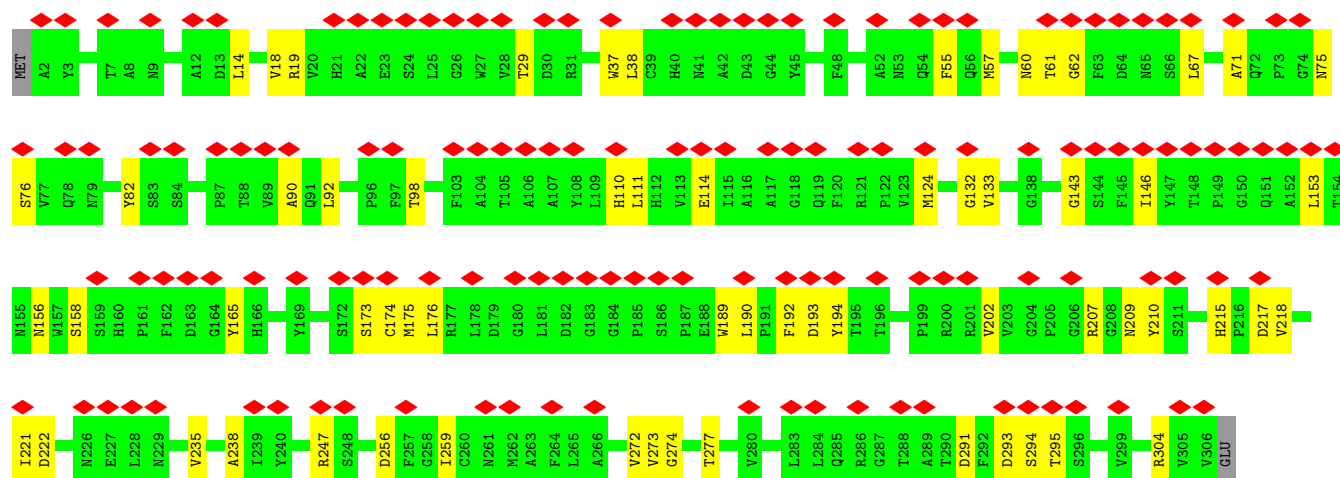


• Molecule 7: Virion structural protein

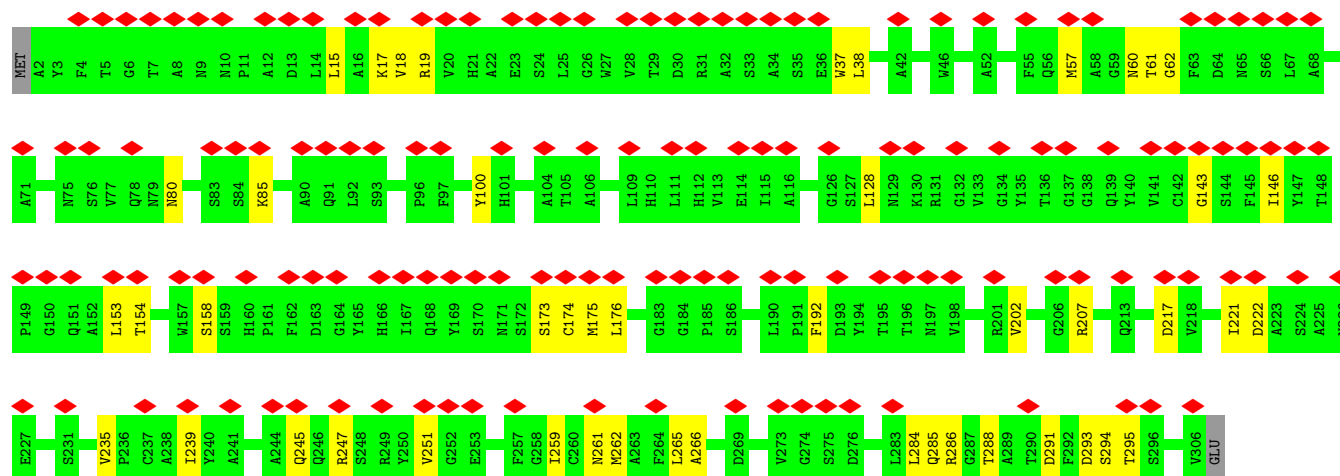
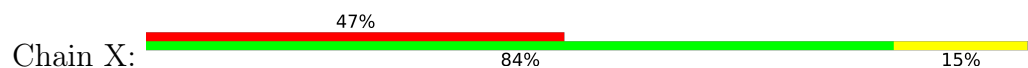


• Molecule 7: Virion structural protein

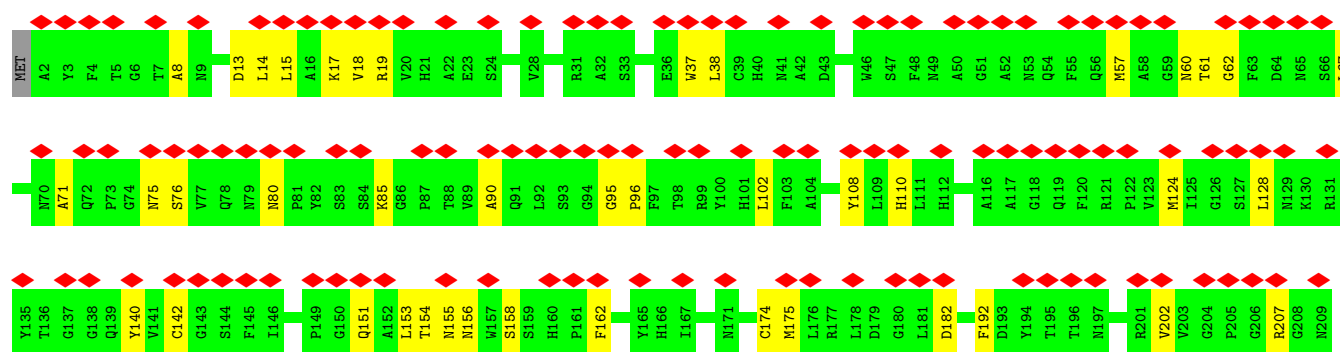
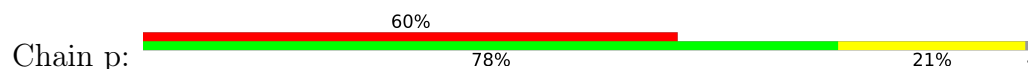


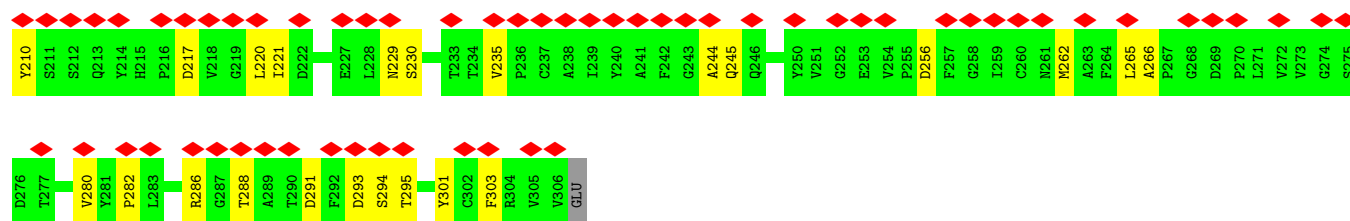


• Molecule 7: Virion structural protein

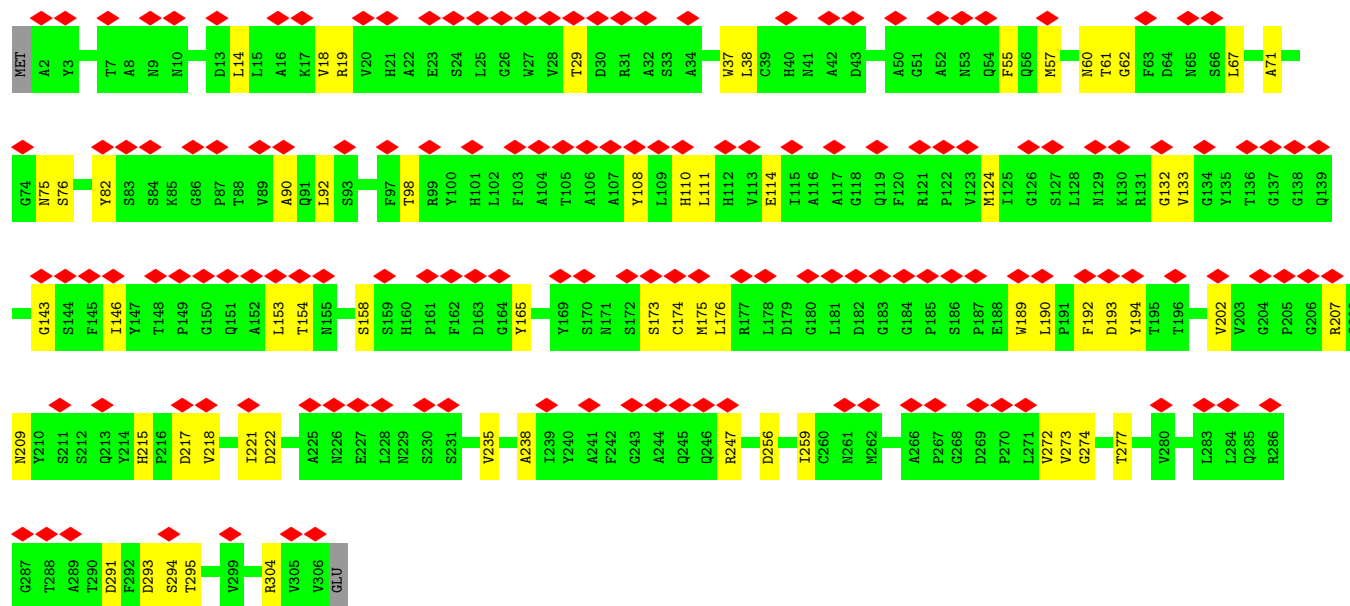
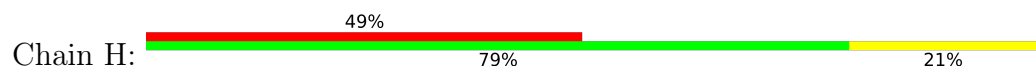


• Molecule 7: Virion structural protein

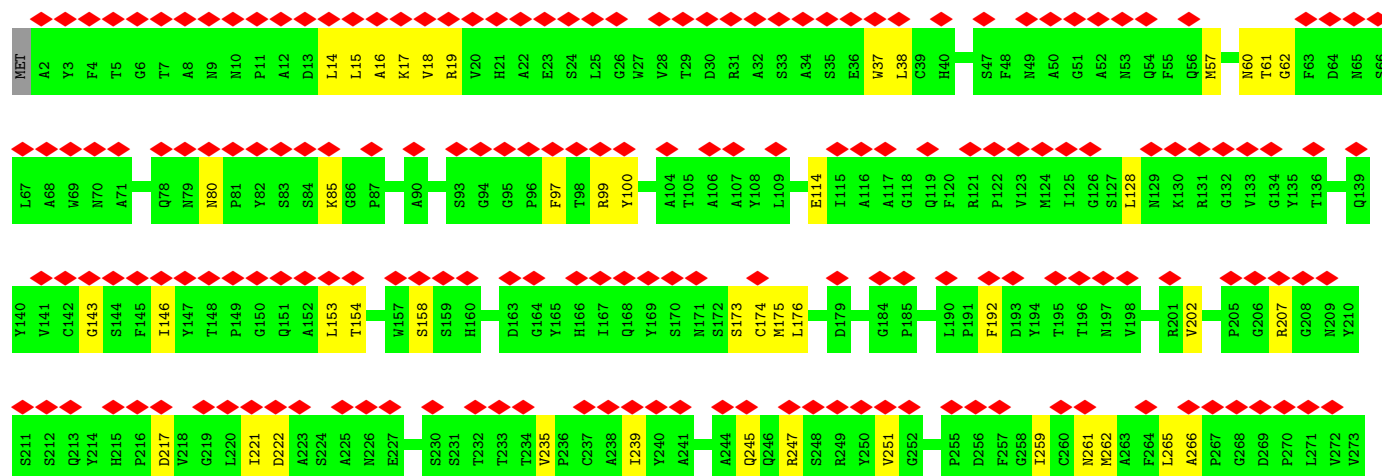
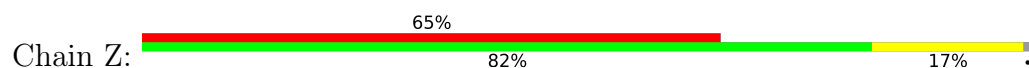


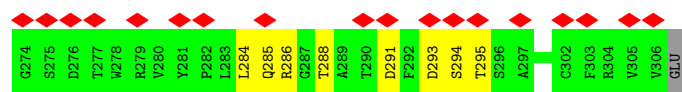


• Molecule 7: Virion structural protein

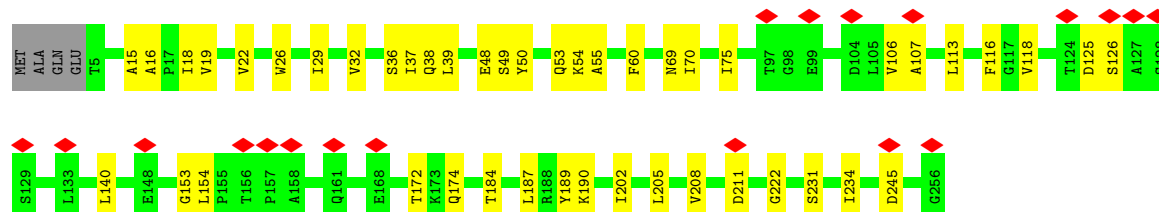
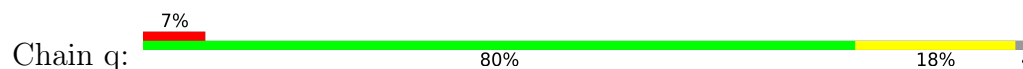


• Molecule 7: Virion structural protein

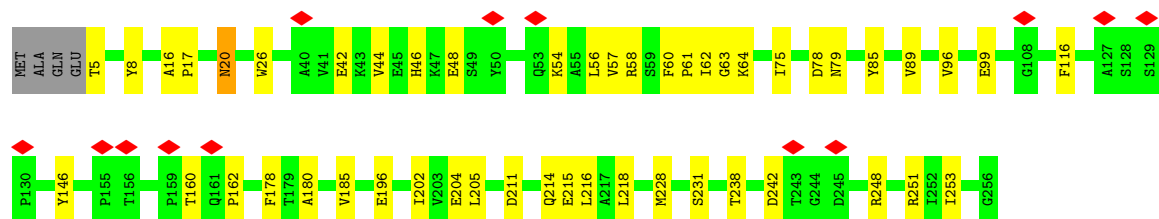
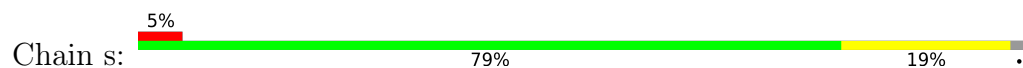




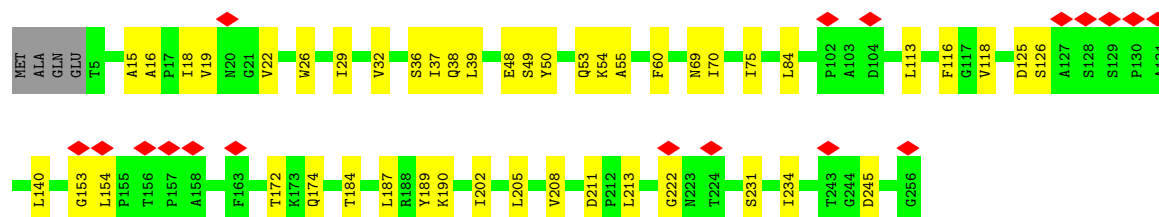
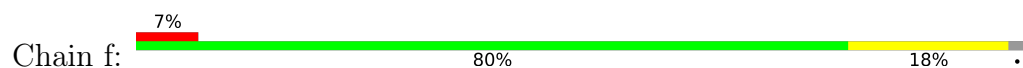
• Molecule 8: Virion structural protein



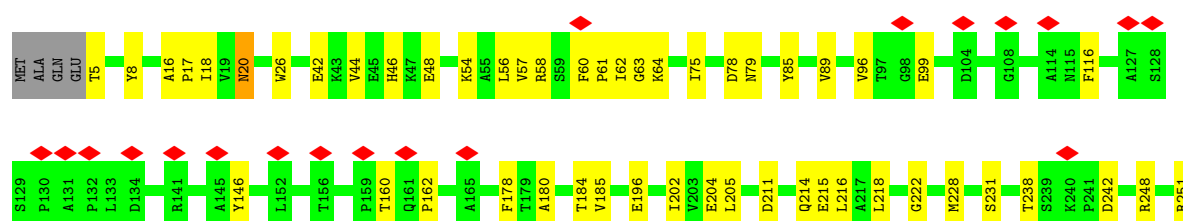
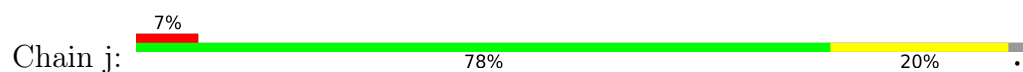
• Molecule 8: Virion structural protein



• Molecule 8: Virion structural protein

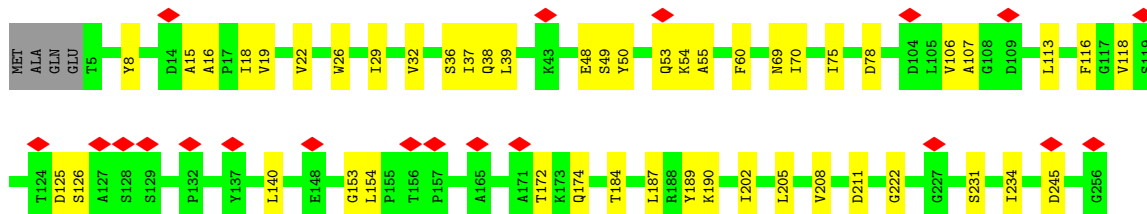
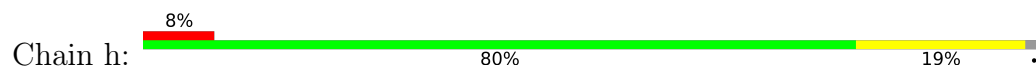


• Molecule 8: Virion structural protein

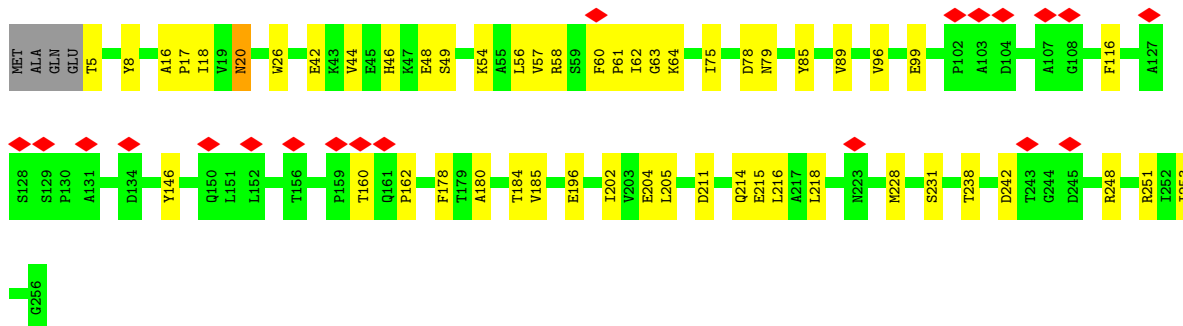
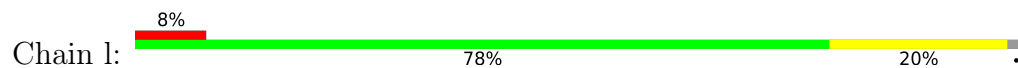




- Molecule 8: Virion structural protein



- Molecule 8: Virion structural protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	1780	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	34	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	36.304	Depositor
Minimum map value	-16.154	Depositor
Average map value	0.060	Depositor
Map value standard deviation	1.061	Depositor
Recommended contour level	5	Depositor
Map size ($\text{\AA}$)	450.14398, 450.14398, 450.14398	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8336, 0.8336, 0.8336	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.16	0/261	0.36	0/350
1	B	0.16	0/261	0.36	0/350
1	C	0.15	0/261	0.36	0/350
2	O	0.56	2/2151 (0.1%)	0.69	5/2934 (0.2%)
2	P	0.56	2/2151 (0.1%)	0.69	5/2934 (0.2%)
2	g	0.56	2/2151 (0.1%)	0.69	5/2934 (0.2%)
3	D	0.10	0/4370	0.30	0/5972
3	U	0.10	0/4370	0.30	0/5972
3	r	0.10	0/4370	0.30	0/5972
4	E	0.09	0/2873	0.24	0/3929
4	F	0.09	0/2873	0.24	0/3929
4	I	0.09	0/2873	0.25	0/3929
4	J	0.09	0/2873	0.25	0/3929
4	M	0.09	0/2873	0.24	0/3929
4	N	0.09	0/2873	0.24	0/3929
4	W	0.09	0/2873	0.24	0/3929
4	a	0.08	0/2873	0.25	0/3929
4	e	0.08	0/2873	0.24	0/3929
5	b	0.12	0/5701	0.24	1/7762 (0.0%)
5	d	0.12	0/5701	0.24	1/7762 (0.0%)
5	o	0.12	0/5701	0.24	1/7762 (0.0%)
6	K	0.10	0/2544	0.28	0/3473
6	L	0.10	0/2544	0.28	0/3473
6	Q	0.10	0/2544	0.26	0/3473
6	R	0.10	0/2544	0.26	0/3473
6	T	0.10	0/2544	0.29	0/3473
6	V	0.10	0/2544	0.28	0/3473
6	c	0.10	0/2544	0.28	0/3473
6	i	0.10	0/2544	0.26	0/3473
6	k	0.10	0/2544	0.29	0/3473
7	G	0.09	0/2412	0.25	0/3299
7	H	0.09	0/2412	0.25	0/3299
7	S	0.11	0/2412	0.27	0/3299
7	X	0.09	0/2412	0.24	0/3299

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	Y	0.09	0/2412	0.25	0/3299
7	Z	0.09	0/2412	0.24	0/3299
7	m	0.09	0/2412	0.24	0/3299
7	n	0.11	0/2412	0.27	0/3299
7	p	0.11	0/2412	0.27	0/3299
8	f	0.10	0/1909	0.26	0/2603
8	h	0.10	0/1909	0.26	0/2603
8	j	0.10	0/1909	0.27	0/2603
8	l	0.10	0/1909	0.28	0/2603
8	q	0.10	0/1909	0.26	0/2603
8	s	0.10	0/1909	0.27	0/2603
All	All	0.16	6/119364 (0.0%)	0.30	18/162981 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	62	PRO	CB-CG	20.81	2.53	1.49
2	g	62	PRO	CB-CG	20.81	2.53	1.49
2	P	62	PRO	CB-CG	20.81	2.53	1.49
2	O	62	PRO	CG-CD	-14.83	1.00	1.50
2	g	62	PRO	CG-CD	-14.83	1.00	1.50

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	62	PRO	CB-CG-CD	-27.41	18.40	106.10
2	O	62	PRO	CB-CG-CD	-27.41	18.41	106.10
2	g	62	PRO	CB-CG-CD	-27.39	18.44	106.10
2	P	62	PRO	CA-N-CD	-16.05	89.54	112.00
2	O	62	PRO	CA-N-CD	-16.04	89.54	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	256	0	246	18	0
1	B	256	0	246	26	0
1	C	256	0	246	21	0
2	O	2099	0	1958	122	0
2	P	2099	0	1957	120	0
2	g	2099	0	1958	122	0
3	D	4278	0	4229	214	0
3	U	4278	0	4229	215	0
3	r	4278	0	4229	218	0
4	E	2791	0	2669	61	0
4	F	2791	0	2669	62	0
4	I	2791	0	2669	56	0
4	J	2791	0	2669	62	0
4	M	2791	0	2669	56	0
4	N	2791	0	2669	56	0
4	W	2791	0	2669	61	0
4	a	2791	0	2669	61	0
4	e	2791	0	2669	56	0
5	b	5581	0	5518	189	0
5	d	5581	0	5518	191	0
5	o	5581	0	5518	195	0
6	K	2470	0	2361	43	0
6	L	2470	0	2361	42	0
6	Q	2470	0	2361	57	0
6	R	2470	0	2361	55	0
6	T	2470	0	2361	50	0
6	V	2470	0	2361	49	0
6	c	2470	0	2361	41	0
6	i	2470	0	2361	57	0
6	k	2470	0	2361	52	0
7	G	2338	0	2174	48	0
7	H	2338	0	2174	48	0
7	S	2338	0	2172	44	0
7	X	2338	0	2174	31	0
7	Y	2338	0	2174	48	0
7	Z	2338	0	2174	34	0
7	m	2338	0	2174	33	0
7	n	2338	0	2172	48	0
7	p	2338	0	2172	48	0
8	f	1871	0	1889	87	0
8	h	1871	0	1889	92	0
8	j	1871	0	1893	85	0
8	l	1871	0	1893	84	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	q	1871	0	1889	87	0
8	s	1871	0	1893	81	0
All	All	116259	0	112028	2587	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 2587 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)
8:q:53:GLN:HB3	8:l:64:LYS:CD	1.38	1.52
8:j:64:LYS:CD	8:h:53:GLN:HB3	1.38	1.51
8:s:64:LYS:CD	8:f:53:GLN:HB3	1.38	1.49
2:O:140:THR:HG21	5:d:298:ARG:NH1	1.21	1.49
2:g:140:THR:HG21	5:b:298:ARG:NH1	1.21	1.48

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	30/1158 (3%)	29 (97%)	1 (3%)	0	100	100
1	B	30/1158 (3%)	29 (97%)	1 (3%)	0	100	100
1	C	30/1158 (3%)	29 (97%)	1 (3%)	0	100	100
2	O	270/273 (99%)	261 (97%)	9 (3%)	0	100	100
2	P	270/273 (99%)	261 (97%)	9 (3%)	0	100	100
2	g	270/273 (99%)	261 (97%)	9 (3%)	0	100	100
3	D	552/567 (97%)	499 (90%)	52 (9%)	1 (0%)	43	77
3	U	552/567 (97%)	499 (90%)	52 (9%)	1 (0%)	43	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	r	552/567 (97%)	499 (90%)	52 (9%)	1 (0%)	43	77
4	E	371/382 (97%)	353 (95%)	18 (5%)	0	100	100
4	F	371/382 (97%)	352 (95%)	19 (5%)	0	100	100
4	I	371/382 (97%)	352 (95%)	19 (5%)	0	100	100
4	J	371/382 (97%)	352 (95%)	19 (5%)	0	100	100
4	M	371/382 (97%)	357 (96%)	14 (4%)	0	100	100
4	N	371/382 (97%)	357 (96%)	14 (4%)	0	100	100
4	W	371/382 (97%)	353 (95%)	18 (5%)	0	100	100
4	a	371/382 (97%)	352 (95%)	19 (5%)	0	100	100
4	e	371/382 (97%)	357 (96%)	14 (4%)	0	100	100
5	b	725/735 (99%)	696 (96%)	28 (4%)	1 (0%)	48	83
5	d	725/735 (99%)	696 (96%)	28 (4%)	1 (0%)	48	83
5	o	725/735 (99%)	696 (96%)	28 (4%)	1 (0%)	48	83
6	K	315/318 (99%)	305 (97%)	10 (3%)	0	100	100
6	L	315/318 (99%)	305 (97%)	10 (3%)	0	100	100
6	Q	315/318 (99%)	304 (96%)	11 (4%)	0	100	100
6	R	315/318 (99%)	304 (96%)	11 (4%)	0	100	100
6	T	315/318 (99%)	299 (95%)	16 (5%)	0	100	100
6	V	315/318 (99%)	299 (95%)	16 (5%)	0	100	100
6	c	315/318 (99%)	305 (97%)	10 (3%)	0	100	100
6	i	315/318 (99%)	304 (96%)	11 (4%)	0	100	100
6	k	315/318 (99%)	299 (95%)	16 (5%)	0	100	100
7	G	303/307 (99%)	293 (97%)	10 (3%)	0	100	100
7	H	303/307 (99%)	293 (97%)	10 (3%)	0	100	100
7	S	303/307 (99%)	288 (95%)	15 (5%)	0	100	100
7	X	303/307 (99%)	286 (94%)	17 (6%)	0	100	100
7	Y	303/307 (99%)	293 (97%)	10 (3%)	0	100	100
7	Z	303/307 (99%)	286 (94%)	17 (6%)	0	100	100
7	m	303/307 (99%)	286 (94%)	17 (6%)	0	100	100
7	n	303/307 (99%)	288 (95%)	15 (5%)	0	100	100
7	p	303/307 (99%)	288 (95%)	15 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	f	250/256 (98%)	244 (98%)	6 (2%)	0	100	100
8	h	250/256 (98%)	244 (98%)	6 (2%)	0	100	100
8	j	250/256 (98%)	240 (96%)	10 (4%)	0	100	100
8	l	250/256 (98%)	240 (96%)	10 (4%)	0	100	100
8	q	250/256 (98%)	244 (98%)	6 (2%)	0	100	100
8	s	250/256 (98%)	240 (96%)	10 (4%)	0	100	100
All	All	15132/18798 (80%)	14417 (95%)	709 (5%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	U	482	ASP
3	r	482	ASP
3	D	482	ASP
5	o	265	ALA
5	b	265	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	25/834 (3%)	25 (100%)	0	100	100
1	B	25/834 (3%)	25 (100%)	0	100	100
1	C	25/834 (3%)	25 (100%)	0	100	100
2	O	226/227 (100%)	226 (100%)	0	100	100
2	P	226/227 (100%)	226 (100%)	0	100	100
2	g	226/227 (100%)	226 (100%)	0	100	100
3	D	450/461 (98%)	450 (100%)	0	100	100
3	U	450/461 (98%)	450 (100%)	0	100	100
3	r	450/461 (98%)	450 (100%)	0	100	100
4	E	278/286 (97%)	278 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	F	278/286 (97%)	278 (100%)	0	100	100
4	I	278/286 (97%)	278 (100%)	0	100	100
4	J	278/286 (97%)	278 (100%)	0	100	100
4	M	278/286 (97%)	278 (100%)	0	100	100
4	N	278/286 (97%)	278 (100%)	0	100	100
4	W	278/286 (97%)	278 (100%)	0	100	100
4	a	278/286 (97%)	278 (100%)	0	100	100
4	e	278/286 (97%)	278 (100%)	0	100	100
5	b	585/590 (99%)	585 (100%)	0	100	100
5	d	585/590 (99%)	585 (100%)	0	100	100
5	o	585/590 (99%)	585 (100%)	0	100	100
6	K	252/253 (100%)	252 (100%)	0	100	100
6	L	252/253 (100%)	252 (100%)	0	100	100
6	Q	252/253 (100%)	252 (100%)	0	100	100
6	R	252/253 (100%)	252 (100%)	0	100	100
6	T	252/253 (100%)	252 (100%)	0	100	100
6	V	252/253 (100%)	252 (100%)	0	100	100
6	c	252/253 (100%)	252 (100%)	0	100	100
6	i	252/253 (100%)	252 (100%)	0	100	100
6	k	252/253 (100%)	252 (100%)	0	100	100
7	G	243/245 (99%)	243 (100%)	0	100	100
7	H	243/245 (99%)	243 (100%)	0	100	100
7	S	243/245 (99%)	243 (100%)	0	100	100
7	X	243/245 (99%)	243 (100%)	0	100	100
7	Y	243/245 (99%)	243 (100%)	0	100	100
7	Z	243/245 (99%)	243 (100%)	0	100	100
7	m	243/245 (99%)	243 (100%)	0	100	100
7	n	243/245 (99%)	243 (100%)	0	100	100
7	p	243/245 (99%)	243 (100%)	0	100	100
8	f	195/198 (98%)	195 (100%)	0	100	100
8	h	195/198 (98%)	195 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	j	195/198 (98%)	194 (100%)	1 (0%)	81	81
8	l	195/198 (98%)	194 (100%)	1 (0%)	81	81
8	q	195/198 (98%)	195 (100%)	0	100	100
8	s	195/198 (98%)	194 (100%)	1 (0%)	81	81
All	All	11985/14580 (82%)	11982 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	s	20	ASN
8	j	20	ASN
8	l	20	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	271	GLN
7	p	91	GLN
4	J	370	HIS
4	N	209	ASN
6	R	187	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

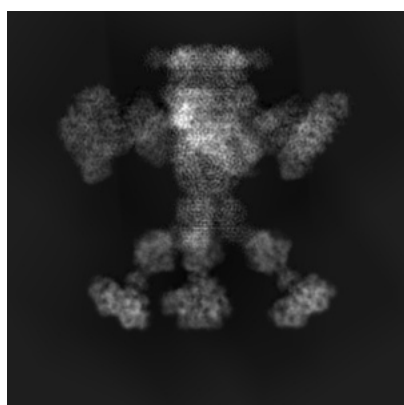
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19256. These allow visual inspection of the internal detail of the map and identification of artifacts.

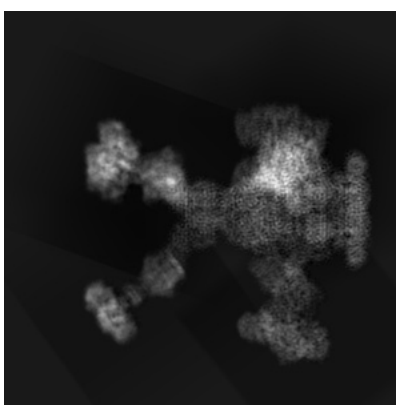
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

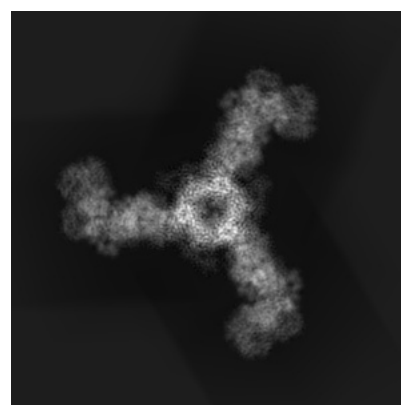
6.1.1 Primary map



X



Y

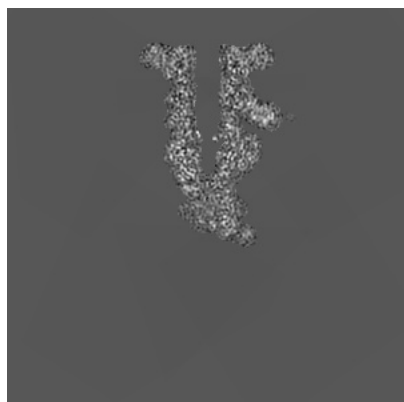


Z

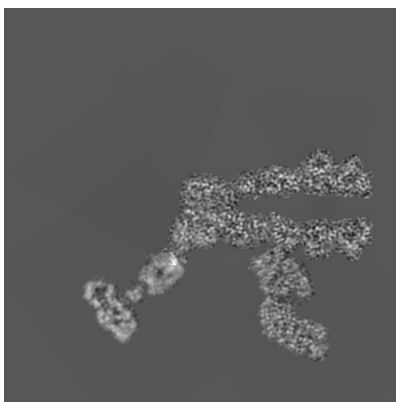
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 270



Y Index: 270

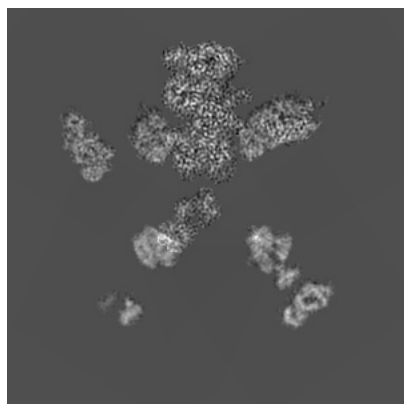


Z Index: 270

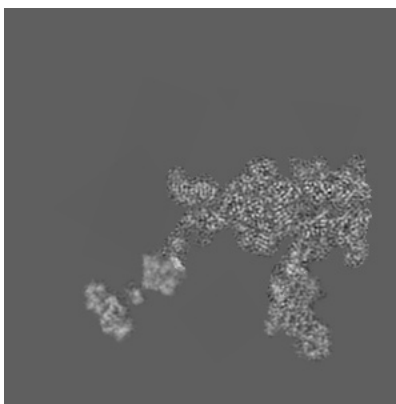
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

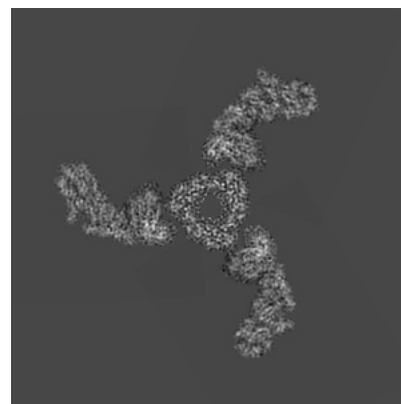
6.3.1 Primary map



X Index: 308



Y Index: 246

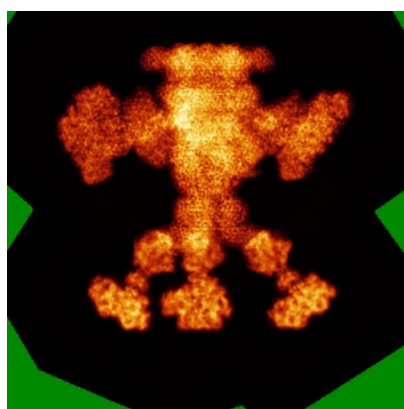


Z Index: 386

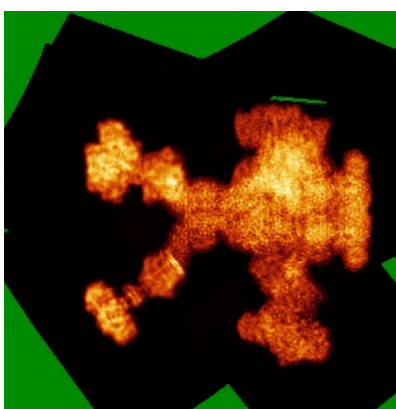
The images above show the largest variance slices of the map in three orthogonal directions.

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

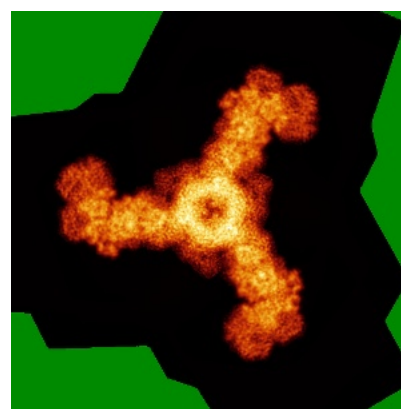
6.4.1 Primary map



X



Y

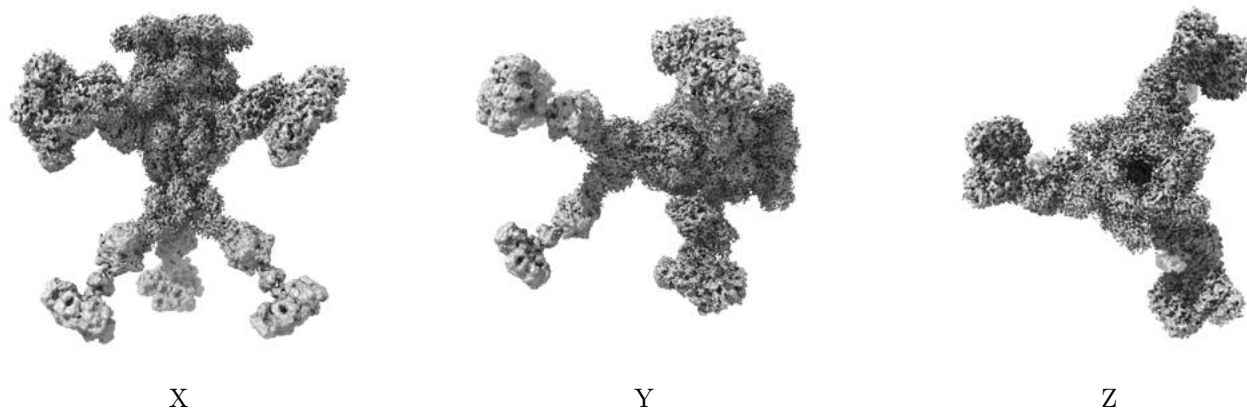


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

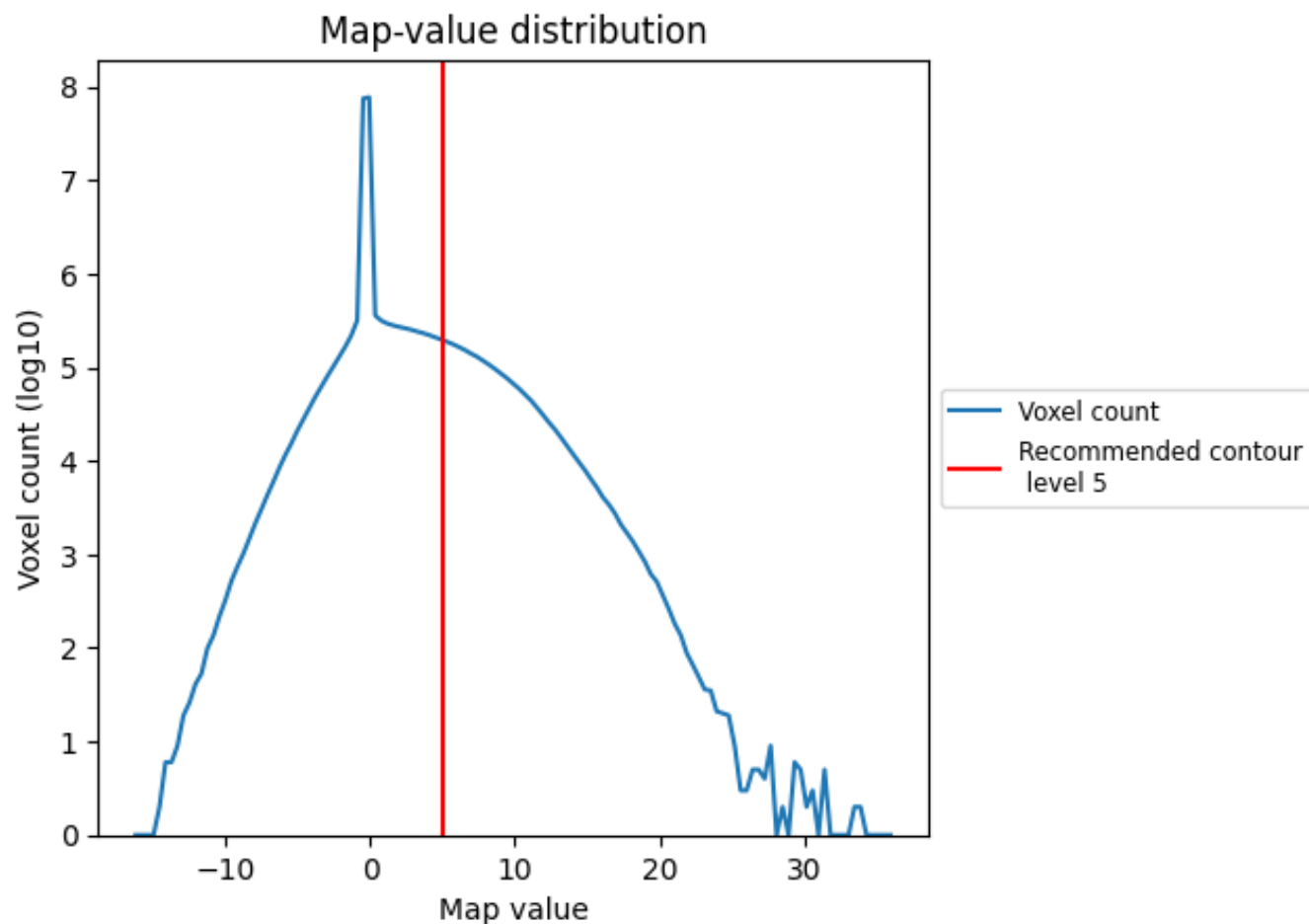
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

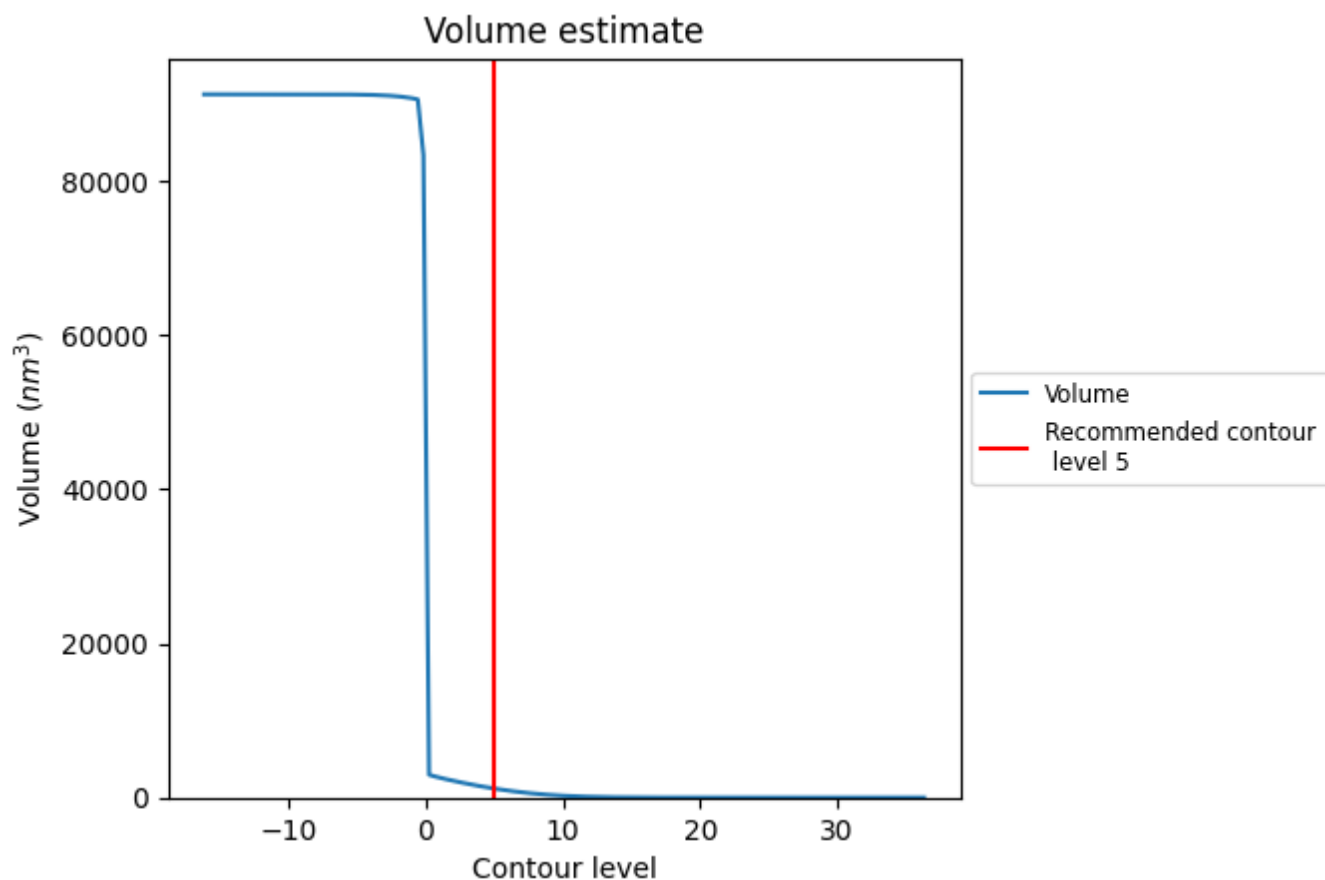
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

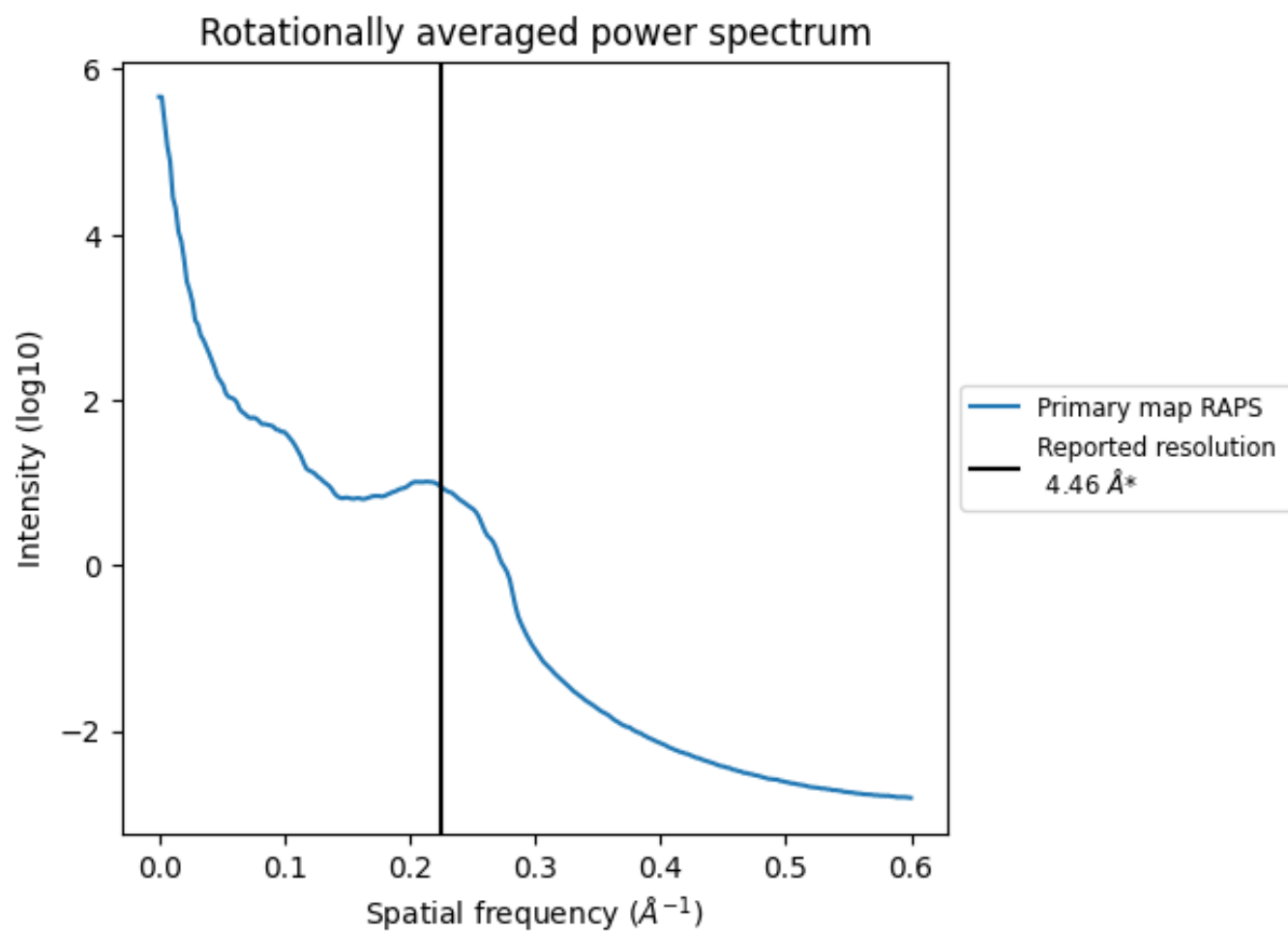
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1167 nm^3 ; this corresponds to an approximate mass of 1054 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 0.224 Å⁻¹

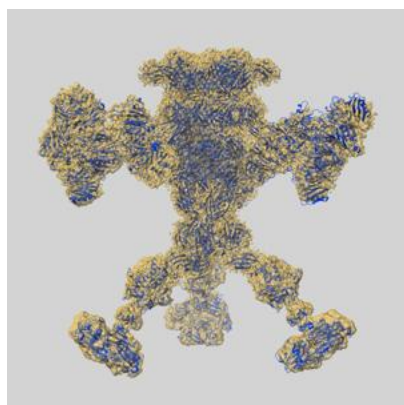
8 Fourier-Shell correlation

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

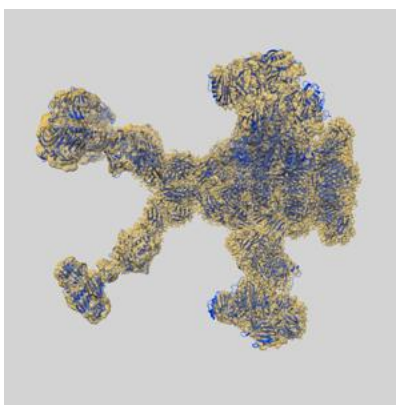
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19256 and PDB model 8RK3. Per-residue inclusion information can be found in section [3](#) on page [9](#).

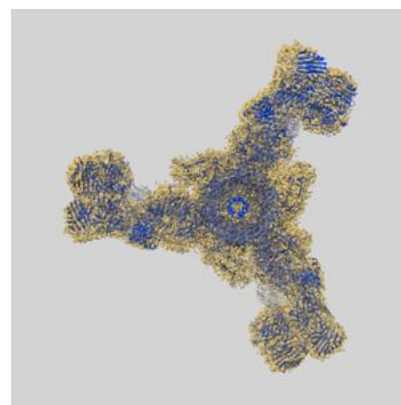
9.1 Map-model overlay [i](#)



X



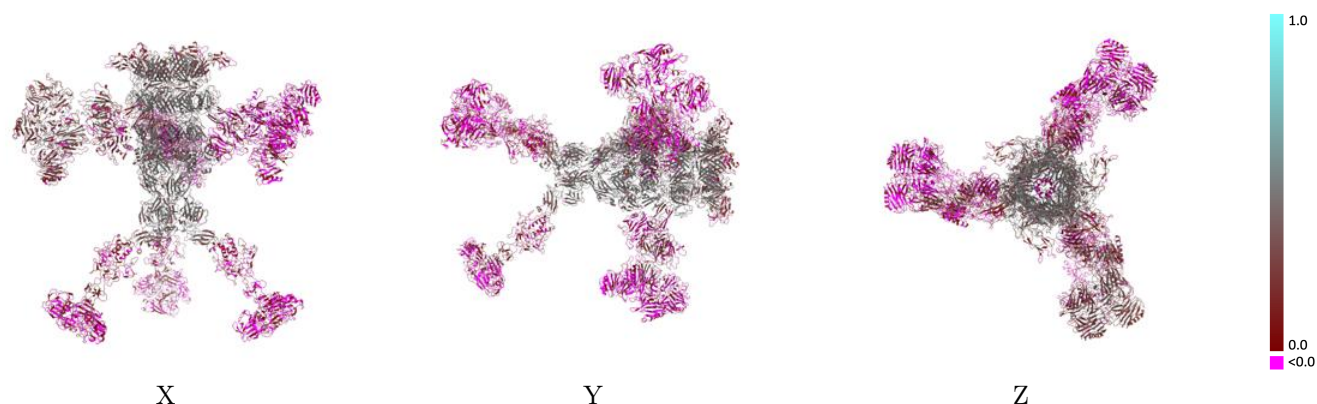
Y



Z

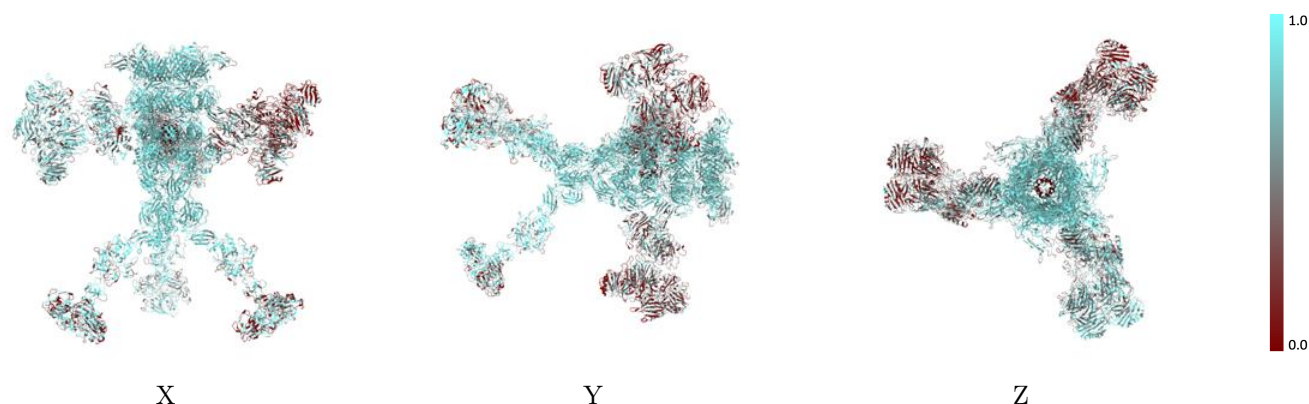
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



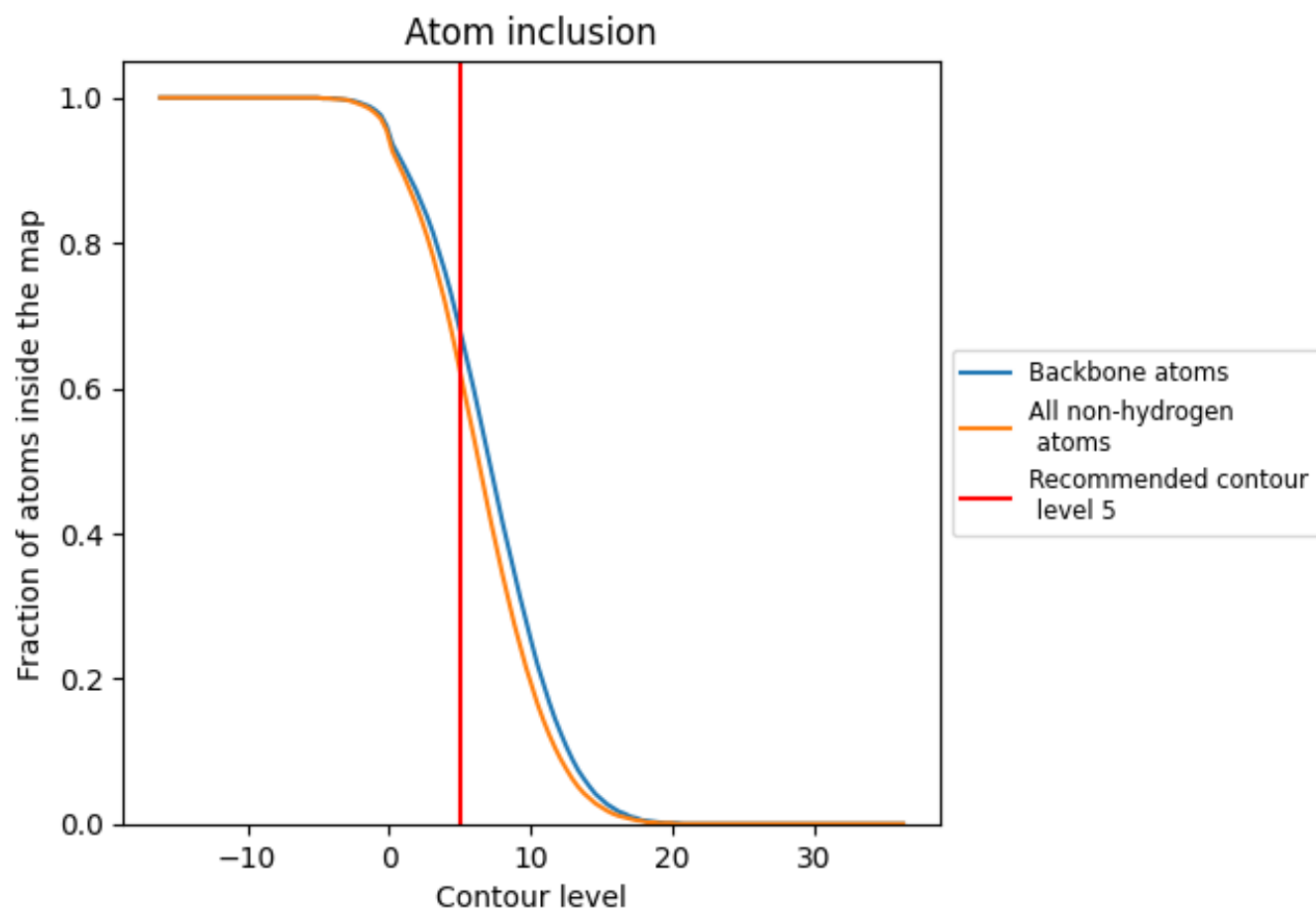
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 62% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6250	 0.2020
A	 0.1670	 0.0240
B	 0.1670	 0.0300
C	 0.1630	 0.0520
D	 0.7290	 0.3320
E	 0.6060	 0.0530
F	 0.6070	 0.0380
G	 0.4370	 0.0630
H	 0.4440	 0.0620
I	 0.6050	 0.0610
J	 0.5200	 0.0260
K	 0.3500	 -0.0010
L	 0.4550	 0.0620
M	 0.6080	 0.0670
N	 0.6190	 0.0430
O	 0.8200	 0.4180
P	 0.8080	 0.4150
Q	 0.3180	 0.0050
R	 0.4830	 0.1380
S	 0.6590	 0.2860
T	 0.3070	 -0.0130
U	 0.7890	 0.3530
V	 0.3560	 0.0030
W	 0.7250	 0.0990
X	 0.4310	 0.0400
Y	 0.5630	 0.1730
Z	 0.3000	 -0.0120
a	 0.6430	 0.0710
b	 0.8290	 0.4100
c	 0.6920	 0.2930
d	 0.8150	 0.4110
e	 0.6380	 0.0750
f	 0.7350	 0.3150
g	 0.8450	 0.4290
h	 0.7410	 0.3210



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Chain	Atom inclusion	Q-score
i	 0.6190	 0.2530
j	 0.6960	 0.3180
k	 0.6680	 0.2540
l	 0.7330	 0.3230
m	 0.6210	 0.2040
n	 0.2260	 -0.0050
o	 0.8480	 0.4240
p	 0.3470	 -0.0060
q	 0.7410	 0.3460
r	 0.7450	 0.3230
s	 0.7780	 0.3400