



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 02:40 AM UTC

PDB ID : 6QVK / pdb_00006qvk
EMDB ID : EMD-4655
Title : The cryo-EM structure of bacteriophage phi29 prohead
Authors : Xu, J.; Gui, M.; Xiang, Y.
Deposited on : 2019-03-03
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

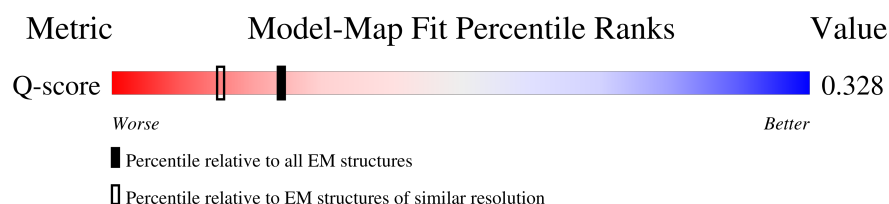
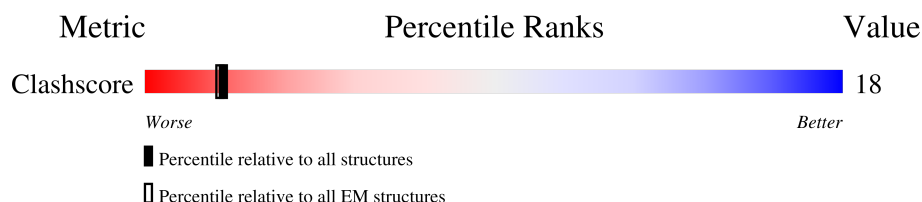
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

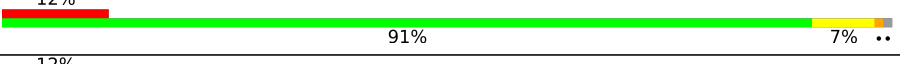
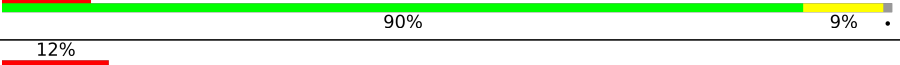
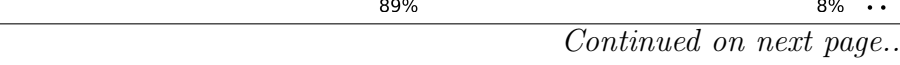
The reported resolution of this entry is 3.60 Å.

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	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	1A	448	
1	1B	448	
1	1C	448	
1	1D	448	
1	1E	448	
1	1F	448	

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Mol	Chain	Length	Quality of chain
1	1G	448	24% 84% 12% .
1	1H	448	12% 90% 8% ..
1	1I	448	11% 88% 11% ..
1	1J	448	10% 90% 9% .
1	1K	448	12% 86% 10% ..
1	1L	448	23% 89% 8% ..
1	1M	448	24% 85% 12% .
1	1N	448	13% 90% 8% ..
1	1O	448	13% 89% 10% ..
1	1P	448	10% 90% 9% .
1	1Q	448	12% 87% 10% ..
1	1R	448	24% 88% 9% ..
1	1S	448	23% 84% 12% .
1	1T	448	12% 90% 8% ..
1	1U	448	11% 88% 11% ..
1	1V	448	10% 90% 9% .
1	1W	448	12% 86% 10% ..
1	1X	448	24% 88% 8% ..
1	1Y	448	24% 85% 11% .
1	1Z	448	12% 90% 8% ..
1	1a	448	12% 88% 11% ..
1	1b	448	9% 90% 9% ..
1	1c	448	13% 86% 10% ..
1	1d	448	24% 88% 8% ..
1	2A	448	12% 89% 9% .

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Mol	Chain	Length	Quality of chain
1	2B	448	12% 88% 10% ..
1	2C	448	14% 90% 9% ..
1	2D	448	14% 92% 7% ..
1	2E	448	13% 85% 13% ..
1	2F	448	12% 89% 8% .
1	2G	448	12% 88% 10% ..
1	2H	448	12% 89% 10% ..
1	2I	448	15% 91% 8% ..
1	2J	448	14% 86% 12% ..
1	2K	448	12% 89% 8% ..
1	2L	448	11% 88% 10% ..
1	2M	448	14% 88% 10% ..
1	2N	448	14% 91% 7% ..
1	2O	448	13% 86% 12% ..
1	2P	448	12% 88% 9% ..
1	2Q	448	10% 87% 12% ..
1	2R	448	13% 88% 11% ..
1	2S	448	14% 91% 8% ..
1	2T	448	13% 86% 12% ..
1	2U	448	11% 89% 8% ..
1	2V	448	12% 88% 10% ..
1	2W	448	14% 89% 10% ..
1	2X	448	15% 91% 7% ..
1	2Y	448	13% 86% 12% ..
1	3A	448	7% 88% 9% .

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Mol	Chain	Length	Quality of chain
1	3B	448	
1	3C	448	
1	3D	448	
1	3E	448	
1	3F	448	
1	3G	448	
1	3H	448	
1	3I	448	
1	3J	448	
1	3K	448	
1	3L	448	
1	3M	448	
1	3N	448	
1	3O	448	
1	3P	448	
1	3Q	448	
1	3R	448	
1	3S	448	
1	3T	448	
1	3U	448	
1	3V	448	
1	3W	448	
1	3X	448	
1	3Y	448	
1	3Z	448	

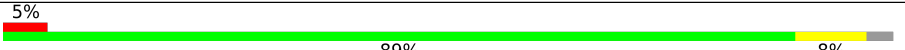
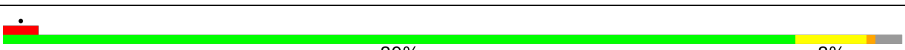
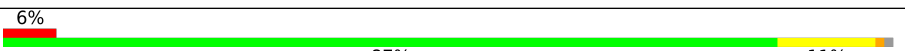
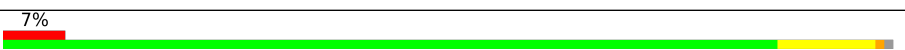
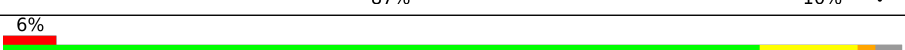
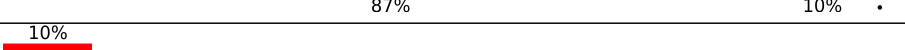
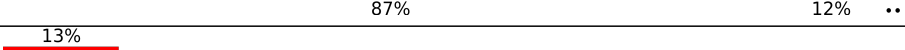
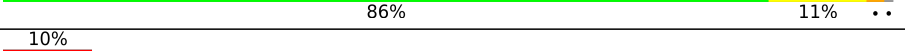
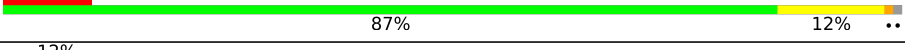
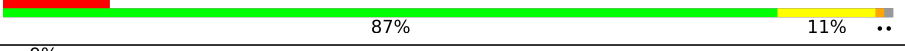
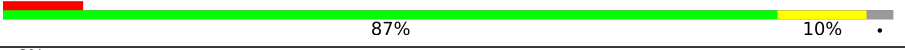
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Mol	Chain	Length	Quality of chain
1	3a	448	
1	3b	448	
1	3c	448	
1	3d	448	
1	4A	448	
1	4B	448	
1	4C	448	
1	4D	448	
1	4E	448	
1	4F	448	
1	4G	448	
1	4H	448	
1	4I	448	
1	4J	448	
1	4K	448	
1	4L	448	
1	4M	448	
1	4N	448	
1	4O	448	
1	4P	448	
1	4Q	448	
1	4R	448	
1	4S	448	
1	4T	448	
1	4U	448	

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Mol	Chain	Length	Quality of chain
1	4V	448	
1	4W	448	
1	4X	448	
1	4Y	448	
1	4Z	448	
1	4a	448	
1	4b	448	
1	4c	448	
1	4d	448	
1	5A	448	
1	5B	448	
1	5C	448	
1	5D	448	
1	5E	448	
1	5F	448	
1	5G	448	
1	5H	448	
1	5I	448	
1	5J	448	
1	5K	448	
1	5L	448	
1	5M	448	
1	5N	448	
1	5O	448	
1	5P	448	

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Mol	Chain	Length	Quality of chain
1	5Q	448	
1	5R	448	
1	5S	448	
1	5T	448	
1	5U	448	
1	5V	448	
1	5W	448	
1	5X	448	
1	5Y	448	
1	5Z	448	
1	5a	448	
1	5b	448	
1	5c	448	
1	5d	448	
1	6A	448	
1	6B	448	
1	6C	448	
1	6D	448	
1	6E	448	
1	6F	448	
1	6G	448	
1	6H	448	
1	6I	448	
1	6J	448	
1	6K	448	

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Mol	Chain	Length	Quality of chain
1	6L	448	
1	6M	448	
1	6N	448	
1	6O	448	
1	6P	448	
1	6Q	448	
1	6R	448	
1	6S	448	
1	6T	448	
1	6U	448	
1	6V	448	
1	6W	448	
1	6X	448	
1	6Y	448	
1	6Z	448	
1	6a	448	
1	6b	448	
1	6c	448	
1	6d	448	
1	7A	448	
1	7B	448	
1	7C	448	
1	7D	448	
1	7E	448	
1	7F	448	

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Mol	Chain	Length	Quality of chain
1	7G	448	27% 92% 7% .
1	7H	448	26% 88% 10% ..
1	7I	448	25% 91% 8% ..
1	7J	448	27% 88% 10% ..
1	7K	448	30% 88% 9% ..
1	7L	448	29% 92% 7% .
1	7M	448	26% 89% 9% ..
1	7N	448	25% 90% 9% ..
1	7O	448	28% 88% 11% ..
1	7P	448	33% 88% 10% ..
1	7Q	448	29% 91% 8% .
1	7R	448	27% 87% 11% ..
1	7S	448	25% 88% 10% ..
1	7T	448	29% 89% 10% ..
1	7U	448	31% 88% 10% ..
1	7V	448	27% 91% 8% .
1	7W	448	27% 88% 10% ..
1	7X	448	25% 90% 9% ..
1	7Y	448	27% 90% 9% ..
1	8A	448	21% 86% 12% ..
1	8B	448	22% 90% 8% ..
1	8C	448	19% 89% 9% ..
1	8D	448	20% 91% 8% .
1	8E	448	20% 90% 9% ..
1	8F	448	22% 88% 10% ..

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Mol	Chain	Length	Quality of chain	
1	8G	448	20%	87% 11% ..
1	8H	448	23%	90% 8% ..
1	8I	448	19%	90% 9% ..
1	8J	448	20%	90% 8% ..
1	8K	448	20%	90% 9% ..
1	8L	448	22%	87% 11% ..
1	8M	448	20%	87% 11% ..
1	8N	448	25%	90% 8% ..
1	8O	448	19%	90% 9% ..
1	8P	448	20%	90% 8% ..
1	8Q	448	21%	90% 9% ..
1	8R	448	22%	88% 11% ..
1	8S	448	20%	86% 12% ..
1	8T	448	24%	91% 8% ..
1	8U	448	20%	89% 9% ..
1	8V	448	19%	90% 8% ..
1	8W	448	20%	90% 9% ..
1	8X	448	22%	88% 10% ..
1	8Y	448	21%	87% 11% ..
1	8Z	448	23%	90% 8% ..
1	8a	448	20%	90% 8% ..
1	8b	448	19%	91% 8% ..
1	8c	448	20%	90% 8% ..
1	8d	448	22%	88% 10% ..
1	9A	448	37%	91% 8% .

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Mol	Chain	Length	Quality of chain
1	9B	448	
1	9C	448	
1	9D	448	
1	9E	448	
2	1e	281	
2	1f	281	
2	1g	281	
2	1h	281	
2	1i	281	
2	1j	281	
2	1k	281	
2	1l	281	
2	1m	281	
2	1n	281	
2	1o	281	
2	1p	281	
2	1q	281	
2	1r	281	
2	1s	281	
2	1t	281	
2	1u	281	
2	1v	281	
2	1w	281	
2	1x	281	
2	2Z	281	

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Mol	Chain	Length	Quality of chain
2	2a	281	91% 71% 28%
2	2b	281	79% 69% 30%
2	2c	281	97% 68% 31%
2	2d	281	81% 65% 34%
2	2e	281	78% 67% 32%
2	2f	281	90% 71% 28%
2	2g	281	78% 69% 30%
2	2h	281	95% 67% 32%
2	2i	281	80% 63% 35%
2	2j	281	79% 67% 32%
2	2k	281	90% 69% 30%
2	2l	281	81% 68% 31%
2	2m	281	96% 68% 31%
2	2n	281	79% 64% 35%
2	2o	281	78% 67% 32%
2	2p	281	89% 70% 29%
2	2q	281	80% 67% 32%
2	2r	281	95% 68% 31%
2	2s	281	81% 64% 35%
2	2t	281	77% 67% 32%
2	2u	281	86% 70% 29%
2	2v	281	82% 69% 30%
2	2w	281	96% 68% 31%
2	2x	281	81% 64% 35%
2	3e	281	84% 62% 37%

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Mol	Chain	Length	Quality of chain
2	3f	281	95% 70% 28%
2	3g	281	81% 59% 40%
2	3h	281	96% 69% 30%
2	3i	281	84% 62% 37%
2	3j	281	94% 70% 28%
2	3k	281	81% 58% 41%
2	3l	281	96% 68% 31%
2	3m	281	83% 62% 37%
2	3n	281	94% 71% 28%
2	3o	281	80% 58% 41%
2	3p	281	94% 68% 31%
2	3q	281	85% 62% 37%
2	3r	281	95% 70% 28%
2	3s	281	77% 58% 41%
2	3t	281	95% 69% 30%
2	3u	281	84% 63% 36%
2	3v	281	95% 70% 28%
2	3w	281	78% 58% 41%
2	3x	281	95% 69% 30%
2	4e	281	84% 71% 28%
2	4f	281	94% 75% 23%
2	4g	281	84% 71% 28%
2	4h	281	93% 75% 23%
2	4i	281	84% 69% 30%
2	4j	281	95% 75% 23%

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Mol	Chain	Length	Quality of chain
2	4k	281	84% 69% 30% .
2	4l	281	94% 75% 23% ..
2	4m	281	84% 70% 28% .
2	4n	281	95% 74% 24% ..
2	5e	281	95% 70% 28% .
2	5f	281	99% 72% 27% .
2	5g	281	96% 70% 29% .
2	5h	281	99% 72% 27% .
2	5i	281	97% 70% 28% .
2	5j	281	98% 71% 28% .
2	5k	281	96% 69% 30% .
2	5l	281	99% 71% 28% .
2	5m	281	95% 70% 29% .
2	5n	281	98% 71% 28% .
2	6e	281	97% 66% 32% ..
2	6f	281	100% 68% 31% .
2	6g	281	96% 62% 37% .
2	6h	281	99% 73% 26% .
2	6i	281	94% 67% 32% ..
2	6j	281	99% 68% 31% .
2	6k	281	97% 61% 38% .
2	6l	281	99% 74% 25% .
2	6m	281	95% 66% 32% ..
2	6n	281	99% 69% 30% .
2	6o	281	97% 60% 38% .

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Mol	Chain	Length	Quality of chain
2	6p	281	99% 74% 25% .
2	6q	281	96% 65% 33% ..
2	6r	281	99% 68% 31% .
2	6s	281	95% 59% 40% .
2	6t	281	99% 73% 26% .
2	6u	281	96% 67% 32% ..
2	6v	281	100% 68% 31% .
2	6w	281	97% 59% 40% .
2	6x	281	99% 72% 27% .
2	7Z	281	94% 68% 31% .
2	7a	281	99% 73% 26% .
2	7b	281	97% 75% 23% .
2	7c	281	99% 64% 35% .
2	7d	281	97% 76% 23% .
2	7e	281	92% 68% 31% .
2	7f	281	98% 73% 26% .
2	7g	281	96% 76% 23% .
2	7h	281	99% 64% 35% .
2	7i	281	96% 77% 22% .
2	7j	281	92% 67% 32% .
2	7k	281	98% 73% 26% .
2	7l	281	95% 77% 22% .
2	7m	281	99% 67% 32% .
2	7n	281	96% 77% 22% .
2	7o	281	94% 66% 33% .

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Mol	Chain	Length	Quality of chain
2	7p	281	98% 71%28%
2	7q	281	97% 75%24%
2	7r	281	100% 66%33%
2	7s	281	97% 77%22%
2	7t	281	94% 67%32%
2	7u	281	98% 72%27%
2	7v	281	98% 75%23%
2	7w	281	99% 65%34%
2	7x	281	98% 77%22%
2	8e	281	97% 58%41%
2	8f	281	99% 78%21%
2	8g	281	98% 65%34%
2	8h	281	98% 74%24%
2	8i	281	98% 71%28%
2	8j	281	99% 65%33%
2	8k	281	98% 60%38%
2	8l	281	100% 78%21%
2	8m	281	98% 65%33%
2	8n	281	98% 74%24%
2	8o	281	97% 70%29%
2	8p	281	98% 64%34%
2	8q	281	98% 59%39%
2	8r	281	99% 78%21%
2	8s	281	98% 65%34%
2	8t	281	99% 75%23%

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Mol	Chain	Length	Quality of chain
2	8u	281	98% 69% 30% .
2	8v	281	98% 64% 34% ..
2	8w	281	98% 58% 40% ..
2	8x	281	99% 79% 20% .
2	8y	281	99% 65% 34% .
2	8z	281	98% 75% 23% ..
2	9F	281	98% 59% 40% .
2	9G	281	99% 59% 40% .
2	9H	281	98% 58% 41% .
2	9I	281	98% 58% 41% .
2	9J	281	98% 58% 41% .
2	9K	281	98% 69% 30% .
2	9L	281	99% 64% 35% ..
2	9M	281	99% 58% 41% ..
2	9N	281	99% 78% 21% .
2	9O	281	98% 65% 33% .
2	9P	281	99% 76% 22% ..
2	9Q	281	98% 70% 29% .
2	9R	281	99% 64% 35% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1161605 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	433	Total	C	N	O	S	0	0
			3397	2146	578	665	8		
1	1B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1E	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	1F	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2A	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3A	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3B	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	4A	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4B	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4C	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4D	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5A	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5B	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5C	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5D	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6A	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6C	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6D	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7A	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7D	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7E	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8A	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8B	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8C	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8D	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8E	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8F	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	9A	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	1G	433	Total 3397	C 2146	N 578	O 665	S 8	0	0
1	1H	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	1I	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	1J	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	1K	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	1L	438	Total 3449	C 2182	N 584	O 675	S 8	0	0
1	2F	438	Total 3430	C 2167	N 583	O 672	S 8	0	0
1	2G	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	2H	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	2I	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	2J	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	3G	435	Total 3426	C 2169	N 579	O 670	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	3H	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3I	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4G	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4H	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4I	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4J	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5G	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5H	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5I	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5J	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6G	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6I	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6J	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	6K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7F	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7G	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7I	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8G	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8H	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8I	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8J	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	9B	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1M	433	Total	C	N	O	S	0	0
			3397	2146	578	665	8		
1	1N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1O	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1P	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1Q	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	1R	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2K	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	2L	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	2M	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	2N	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	2O	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	3M	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	3N	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	3O	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	3P	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	3Q	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	3R	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	4M	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	4N	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	4O	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	4P	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	4Q	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	4R	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	5M	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5N	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5O	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5P	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5Q	445	Total 3487	C 2203	N 592	O 684	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	5R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6M	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6O	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6P	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6Q	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7K	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7L	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7M	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7O	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8M	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8N	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8O	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8P	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8Q	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	9C	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1S	433	Total	C	N	O	S	0	0
			3397	2146	578	665	8		
1	1T	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	1U	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1W	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	1X	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2P	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2Q	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2R	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2S	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2T	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3S	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3T	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3U	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4S	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4T	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4U	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4V	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	5S	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5T	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5U	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5V	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	5W	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	5X	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	6S	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	6T	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	6U	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	6V	435	Total 3426	C 2169	N 579	O 670	S 8	0	0
1	6W	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	6X	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7P	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7Q	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7R	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7S	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	7T	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8S	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8T	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8U	445	Total 3487	C 2203	N 592	O 684	S 8	0	0
1	8V	445	Total 3487	C 2203	N 592	O 684	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	9D	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1Y	433	Total	C	N	O	S	0	0
			3397	2146	578	665	8		
1	1Z	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1a	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1b	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	1c	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	1d	438	Total	C	N	O	S	0	0
			3449	2182	584	675	8		
1	2U	438	Total	C	N	O	S	0	0
			3430	2167	583	672	8		
1	2V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	2Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3Y	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3Z	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	3a	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3b	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3c	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	3d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4Y	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	4Z	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4a	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4b	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	4c	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	4d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5Y	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5Z	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5a	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5b	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	5c	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	5d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6Z	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6a	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6b	435	Total	C	N	O	S	0	0
			3426	2169	579	670	8		
1	6c	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	6d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7U	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7V	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7W	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	7X	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8Y	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8Z	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8a	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8b	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8c	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	8d	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		
1	9E	445	Total	C	N	O	S	0	0
			3487	2203	592	684	8		

- Molecule 2 is a protein called Capsid fiber protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1f	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2Z	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2a	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2b	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2c	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2d	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3e	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	3g	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	3h	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	4e	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	4f	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	5e	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	5f	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	6e	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	6f	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	6g	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	6h	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7Z	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7a	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7b	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7c	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	7d	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8e	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	8f	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8g	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8h	279	Total 2098	C 1312	N 348	O 435	S 3	8	0
2	8i	280	Total 2106	C 1317	N 349	O 436	S 4	8	0
2	8j	279	Total 2098	C 1312	N 348	O 435	S 3	8	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	9F	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1l	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2h	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3i	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3k	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5h	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6i	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6k	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7e	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7f	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7g	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7h	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8k	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8p	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9G	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1p	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	2n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3m	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3o	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5i	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5j	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6m	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6o	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7j	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7l	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7n	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8q	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	8t	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8v	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9H	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1r	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1t	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3q	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3s	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3t	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4l	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5k	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5l	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	6q	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6s	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6t	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7o	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7p	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7r	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7s	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8w	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	8x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8y	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	8z	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9K	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9L	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9I	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1v	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	1w	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	1x	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	2t	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	2u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2w	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	2x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3u	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	3w	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	3x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	4n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	5m	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	5n	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6u	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	6w	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	6x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7t	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7u	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7v	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7w	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	7x	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	9M	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9N	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9O	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9P	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9Q	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		
2	9R	279	Total	C	N	O	S	8	0
			2098	1312	348	435	3		
2	9J	280	Total	C	N	O	S	8	0
			2106	1317	349	436	4		

There are 330 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1e	123	GLU	ASP	conflict	UNP B3VMP4
1e	281	LEU	-	insertion	UNP B3VMP4
1f	123	GLU	ASP	conflict	UNP B3VMP4
1f	281	LEU	-	insertion	UNP B3VMP4
1g	123	GLU	ASP	conflict	UNP B3VMP4
1g	281	LEU	-	insertion	UNP B3VMP4
1h	123	GLU	ASP	conflict	UNP B3VMP4
1h	281	LEU	-	insertion	UNP B3VMP4
2Z	123	GLU	ASP	conflict	UNP B3VMP4
2Z	281	LEU	-	insertion	UNP B3VMP4
2a	123	GLU	ASP	conflict	UNP B3VMP4
2a	281	LEU	-	insertion	UNP B3VMP4
2b	123	GLU	ASP	conflict	UNP B3VMP4
2b	281	LEU	-	insertion	UNP B3VMP4
2c	123	GLU	ASP	conflict	UNP B3VMP4
2c	281	LEU	-	insertion	UNP B3VMP4
2d	123	GLU	ASP	conflict	UNP B3VMP4
2d	281	LEU	-	insertion	UNP B3VMP4
3e	123	GLU	ASP	conflict	UNP B3VMP4
3e	281	LEU	-	insertion	UNP B3VMP4
3f	123	GLU	ASP	conflict	UNP B3VMP4
3f	281	LEU	-	insertion	UNP B3VMP4
3g	123	GLU	ASP	conflict	UNP B3VMP4
3g	281	LEU	-	insertion	UNP B3VMP4
3h	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
3h	281	LEU	-	insertion	UNP B3VMP4
4e	123	GLU	ASP	conflict	UNP B3VMP4
4e	281	LEU	-	insertion	UNP B3VMP4
4f	123	GLU	ASP	conflict	UNP B3VMP4
4f	281	LEU	-	insertion	UNP B3VMP4
5e	123	GLU	ASP	conflict	UNP B3VMP4
5e	281	LEU	-	insertion	UNP B3VMP4
5f	123	GLU	ASP	conflict	UNP B3VMP4
5f	281	LEU	-	insertion	UNP B3VMP4
6e	123	GLU	ASP	conflict	UNP B3VMP4
6e	281	LEU	-	insertion	UNP B3VMP4
6f	123	GLU	ASP	conflict	UNP B3VMP4
6f	281	LEU	-	insertion	UNP B3VMP4
6g	123	GLU	ASP	conflict	UNP B3VMP4
6g	281	LEU	-	insertion	UNP B3VMP4
6h	123	GLU	ASP	conflict	UNP B3VMP4
6h	281	LEU	-	insertion	UNP B3VMP4
7Z	123	GLU	ASP	conflict	UNP B3VMP4
7Z	281	LEU	-	insertion	UNP B3VMP4
7a	123	GLU	ASP	conflict	UNP B3VMP4
7a	281	LEU	-	insertion	UNP B3VMP4
7b	123	GLU	ASP	conflict	UNP B3VMP4
7b	281	LEU	-	insertion	UNP B3VMP4
7c	123	GLU	ASP	conflict	UNP B3VMP4
7c	281	LEU	-	insertion	UNP B3VMP4
7d	123	GLU	ASP	conflict	UNP B3VMP4
7d	281	LEU	-	insertion	UNP B3VMP4
8e	123	GLU	ASP	conflict	UNP B3VMP4
8e	281	LEU	-	insertion	UNP B3VMP4
8f	123	GLU	ASP	conflict	UNP B3VMP4
8f	281	LEU	-	insertion	UNP B3VMP4
8g	123	GLU	ASP	conflict	UNP B3VMP4
8g	281	LEU	-	insertion	UNP B3VMP4
8h	123	GLU	ASP	conflict	UNP B3VMP4
8h	281	LEU	-	insertion	UNP B3VMP4
8i	123	GLU	ASP	conflict	UNP B3VMP4
8i	281	LEU	-	insertion	UNP B3VMP4
8j	123	GLU	ASP	conflict	UNP B3VMP4
8j	281	LEU	-	insertion	UNP B3VMP4
9F	123	GLU	ASP	conflict	UNP B3VMP4
9F	281	LEU	-	insertion	UNP B3VMP4
1i	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
1i	281	LEU	-	insertion	UNP B3VMP4
1j	123	GLU	ASP	conflict	UNP B3VMP4
1j	281	LEU	-	insertion	UNP B3VMP4
1k	123	GLU	ASP	conflict	UNP B3VMP4
1k	281	LEU	-	insertion	UNP B3VMP4
1l	123	GLU	ASP	conflict	UNP B3VMP4
1l	281	LEU	-	insertion	UNP B3VMP4
2e	123	GLU	ASP	conflict	UNP B3VMP4
2e	281	LEU	-	insertion	UNP B3VMP4
2f	123	GLU	ASP	conflict	UNP B3VMP4
2f	281	LEU	-	insertion	UNP B3VMP4
2g	123	GLU	ASP	conflict	UNP B3VMP4
2g	281	LEU	-	insertion	UNP B3VMP4
2h	123	GLU	ASP	conflict	UNP B3VMP4
2h	281	LEU	-	insertion	UNP B3VMP4
2i	123	GLU	ASP	conflict	UNP B3VMP4
2i	281	LEU	-	insertion	UNP B3VMP4
3i	123	GLU	ASP	conflict	UNP B3VMP4
3i	281	LEU	-	insertion	UNP B3VMP4
3j	123	GLU	ASP	conflict	UNP B3VMP4
3j	281	LEU	-	insertion	UNP B3VMP4
3k	123	GLU	ASP	conflict	UNP B3VMP4
3k	281	LEU	-	insertion	UNP B3VMP4
3l	123	GLU	ASP	conflict	UNP B3VMP4
3l	281	LEU	-	insertion	UNP B3VMP4
4g	123	GLU	ASP	conflict	UNP B3VMP4
4g	281	LEU	-	insertion	UNP B3VMP4
4h	123	GLU	ASP	conflict	UNP B3VMP4
4h	281	LEU	-	insertion	UNP B3VMP4
5g	123	GLU	ASP	conflict	UNP B3VMP4
5g	281	LEU	-	insertion	UNP B3VMP4
5h	123	GLU	ASP	conflict	UNP B3VMP4
5h	281	LEU	-	insertion	UNP B3VMP4
6i	123	GLU	ASP	conflict	UNP B3VMP4
6i	281	LEU	-	insertion	UNP B3VMP4
6j	123	GLU	ASP	conflict	UNP B3VMP4
6j	281	LEU	-	insertion	UNP B3VMP4
6k	123	GLU	ASP	conflict	UNP B3VMP4
6k	281	LEU	-	insertion	UNP B3VMP4
6l	123	GLU	ASP	conflict	UNP B3VMP4
6l	281	LEU	-	insertion	UNP B3VMP4
7e	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
7e	281	LEU	-	insertion	UNP B3VMP4
7f	123	GLU	ASP	conflict	UNP B3VMP4
7f	281	LEU	-	insertion	UNP B3VMP4
7g	123	GLU	ASP	conflict	UNP B3VMP4
7g	281	LEU	-	insertion	UNP B3VMP4
7h	123	GLU	ASP	conflict	UNP B3VMP4
7h	281	LEU	-	insertion	UNP B3VMP4
7i	123	GLU	ASP	conflict	UNP B3VMP4
7i	281	LEU	-	insertion	UNP B3VMP4
8k	123	GLU	ASP	conflict	UNP B3VMP4
8k	281	LEU	-	insertion	UNP B3VMP4
8l	123	GLU	ASP	conflict	UNP B3VMP4
8l	281	LEU	-	insertion	UNP B3VMP4
8m	123	GLU	ASP	conflict	UNP B3VMP4
8m	281	LEU	-	insertion	UNP B3VMP4
8n	123	GLU	ASP	conflict	UNP B3VMP4
8n	281	LEU	-	insertion	UNP B3VMP4
8o	123	GLU	ASP	conflict	UNP B3VMP4
8o	281	LEU	-	insertion	UNP B3VMP4
8p	123	GLU	ASP	conflict	UNP B3VMP4
8p	281	LEU	-	insertion	UNP B3VMP4
9G	123	GLU	ASP	conflict	UNP B3VMP4
9G	281	LEU	-	insertion	UNP B3VMP4
1m	123	GLU	ASP	conflict	UNP B3VMP4
1m	281	LEU	-	insertion	UNP B3VMP4
1n	123	GLU	ASP	conflict	UNP B3VMP4
1n	281	LEU	-	insertion	UNP B3VMP4
1o	123	GLU	ASP	conflict	UNP B3VMP4
1o	281	LEU	-	insertion	UNP B3VMP4
1p	123	GLU	ASP	conflict	UNP B3VMP4
1p	281	LEU	-	insertion	UNP B3VMP4
2j	123	GLU	ASP	conflict	UNP B3VMP4
2j	281	LEU	-	insertion	UNP B3VMP4
2k	123	GLU	ASP	conflict	UNP B3VMP4
2k	281	LEU	-	insertion	UNP B3VMP4
2l	123	GLU	ASP	conflict	UNP B3VMP4
2l	281	LEU	-	insertion	UNP B3VMP4
2m	123	GLU	ASP	conflict	UNP B3VMP4
2m	281	LEU	-	insertion	UNP B3VMP4
2n	123	GLU	ASP	conflict	UNP B3VMP4
2n	281	LEU	-	insertion	UNP B3VMP4
3m	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
3m	281	LEU	-	insertion	UNP B3VMP4
3n	123	GLU	ASP	conflict	UNP B3VMP4
3n	281	LEU	-	insertion	UNP B3VMP4
3o	123	GLU	ASP	conflict	UNP B3VMP4
3o	281	LEU	-	insertion	UNP B3VMP4
3p	123	GLU	ASP	conflict	UNP B3VMP4
3p	281	LEU	-	insertion	UNP B3VMP4
4i	123	GLU	ASP	conflict	UNP B3VMP4
4i	281	LEU	-	insertion	UNP B3VMP4
4j	123	GLU	ASP	conflict	UNP B3VMP4
4j	281	LEU	-	insertion	UNP B3VMP4
5i	123	GLU	ASP	conflict	UNP B3VMP4
5i	281	LEU	-	insertion	UNP B3VMP4
5j	123	GLU	ASP	conflict	UNP B3VMP4
5j	281	LEU	-	insertion	UNP B3VMP4
6m	123	GLU	ASP	conflict	UNP B3VMP4
6m	281	LEU	-	insertion	UNP B3VMP4
6n	123	GLU	ASP	conflict	UNP B3VMP4
6n	281	LEU	-	insertion	UNP B3VMP4
6o	123	GLU	ASP	conflict	UNP B3VMP4
6o	281	LEU	-	insertion	UNP B3VMP4
6p	123	GLU	ASP	conflict	UNP B3VMP4
6p	281	LEU	-	insertion	UNP B3VMP4
7j	123	GLU	ASP	conflict	UNP B3VMP4
7j	281	LEU	-	insertion	UNP B3VMP4
7k	123	GLU	ASP	conflict	UNP B3VMP4
7k	281	LEU	-	insertion	UNP B3VMP4
7l	123	GLU	ASP	conflict	UNP B3VMP4
7l	281	LEU	-	insertion	UNP B3VMP4
7m	123	GLU	ASP	conflict	UNP B3VMP4
7m	281	LEU	-	insertion	UNP B3VMP4
7n	123	GLU	ASP	conflict	UNP B3VMP4
7n	281	LEU	-	insertion	UNP B3VMP4
8q	123	GLU	ASP	conflict	UNP B3VMP4
8q	281	LEU	-	insertion	UNP B3VMP4
8r	123	GLU	ASP	conflict	UNP B3VMP4
8r	281	LEU	-	insertion	UNP B3VMP4
8s	123	GLU	ASP	conflict	UNP B3VMP4
8s	281	LEU	-	insertion	UNP B3VMP4
8t	123	GLU	ASP	conflict	UNP B3VMP4
8t	281	LEU	-	insertion	UNP B3VMP4
8u	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
8u	281	LEU	-	insertion	UNP B3VMP4
8v	123	GLU	ASP	conflict	UNP B3VMP4
8v	281	LEU	-	insertion	UNP B3VMP4
9H	123	GLU	ASP	conflict	UNP B3VMP4
9H	281	LEU	-	insertion	UNP B3VMP4
1q	123	GLU	ASP	conflict	UNP B3VMP4
1q	281	LEU	-	insertion	UNP B3VMP4
1r	123	GLU	ASP	conflict	UNP B3VMP4
1r	281	LEU	-	insertion	UNP B3VMP4
1s	123	GLU	ASP	conflict	UNP B3VMP4
1s	281	LEU	-	insertion	UNP B3VMP4
1t	123	GLU	ASP	conflict	UNP B3VMP4
1t	281	LEU	-	insertion	UNP B3VMP4
2o	123	GLU	ASP	conflict	UNP B3VMP4
2o	281	LEU	-	insertion	UNP B3VMP4
2p	123	GLU	ASP	conflict	UNP B3VMP4
2p	281	LEU	-	insertion	UNP B3VMP4
2q	123	GLU	ASP	conflict	UNP B3VMP4
2q	281	LEU	-	insertion	UNP B3VMP4
2r	123	GLU	ASP	conflict	UNP B3VMP4
2r	281	LEU	-	insertion	UNP B3VMP4
2s	123	GLU	ASP	conflict	UNP B3VMP4
2s	281	LEU	-	insertion	UNP B3VMP4
3q	123	GLU	ASP	conflict	UNP B3VMP4
3q	281	LEU	-	insertion	UNP B3VMP4
3r	123	GLU	ASP	conflict	UNP B3VMP4
3r	281	LEU	-	insertion	UNP B3VMP4
3s	123	GLU	ASP	conflict	UNP B3VMP4
3s	281	LEU	-	insertion	UNP B3VMP4
3t	123	GLU	ASP	conflict	UNP B3VMP4
3t	281	LEU	-	insertion	UNP B3VMP4
4k	123	GLU	ASP	conflict	UNP B3VMP4
4k	281	LEU	-	insertion	UNP B3VMP4
4l	123	GLU	ASP	conflict	UNP B3VMP4
4l	281	LEU	-	insertion	UNP B3VMP4
5k	123	GLU	ASP	conflict	UNP B3VMP4
5k	281	LEU	-	insertion	UNP B3VMP4
5l	123	GLU	ASP	conflict	UNP B3VMP4
5l	281	LEU	-	insertion	UNP B3VMP4
6q	123	GLU	ASP	conflict	UNP B3VMP4
6q	281	LEU	-	insertion	UNP B3VMP4
6r	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
6r	281	LEU	-	insertion	UNP B3VMP4
6s	123	GLU	ASP	conflict	UNP B3VMP4
6s	281	LEU	-	insertion	UNP B3VMP4
6t	123	GLU	ASP	conflict	UNP B3VMP4
6t	281	LEU	-	insertion	UNP B3VMP4
7o	123	GLU	ASP	conflict	UNP B3VMP4
7o	281	LEU	-	insertion	UNP B3VMP4
7p	123	GLU	ASP	conflict	UNP B3VMP4
7p	281	LEU	-	insertion	UNP B3VMP4
7q	123	GLU	ASP	conflict	UNP B3VMP4
7q	281	LEU	-	insertion	UNP B3VMP4
7r	123	GLU	ASP	conflict	UNP B3VMP4
7r	281	LEU	-	insertion	UNP B3VMP4
7s	123	GLU	ASP	conflict	UNP B3VMP4
7s	281	LEU	-	insertion	UNP B3VMP4
8w	123	GLU	ASP	conflict	UNP B3VMP4
8w	281	LEU	-	insertion	UNP B3VMP4
8x	123	GLU	ASP	conflict	UNP B3VMP4
8x	281	LEU	-	insertion	UNP B3VMP4
8y	123	GLU	ASP	conflict	UNP B3VMP4
8y	281	LEU	-	insertion	UNP B3VMP4
8z	123	GLU	ASP	conflict	UNP B3VMP4
8z	281	LEU	-	insertion	UNP B3VMP4
9K	123	GLU	ASP	conflict	UNP B3VMP4
9K	281	LEU	-	insertion	UNP B3VMP4
9L	123	GLU	ASP	conflict	UNP B3VMP4
9L	281	LEU	-	insertion	UNP B3VMP4
9I	123	GLU	ASP	conflict	UNP B3VMP4
9I	281	LEU	-	insertion	UNP B3VMP4
1u	123	GLU	ASP	conflict	UNP B3VMP4
1u	281	LEU	-	insertion	UNP B3VMP4
1v	123	GLU	ASP	conflict	UNP B3VMP4
1v	281	LEU	-	insertion	UNP B3VMP4
1w	123	GLU	ASP	conflict	UNP B3VMP4
1w	281	LEU	-	insertion	UNP B3VMP4
1x	123	GLU	ASP	conflict	UNP B3VMP4
1x	281	LEU	-	insertion	UNP B3VMP4
2t	123	GLU	ASP	conflict	UNP B3VMP4
2t	281	LEU	-	insertion	UNP B3VMP4
2u	123	GLU	ASP	conflict	UNP B3VMP4
2u	281	LEU	-	insertion	UNP B3VMP4
2v	123	GLU	ASP	conflict	UNP B3VMP4

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Chain	Residue	Modelled	Actual	Comment	Reference
2v	281	LEU	-	insertion	UNP B3VMP4
2w	123	GLU	ASP	conflict	UNP B3VMP4
2w	281	LEU	-	insertion	UNP B3VMP4
2x	123	GLU	ASP	conflict	UNP B3VMP4
2x	281	LEU	-	insertion	UNP B3VMP4
3u	123	GLU	ASP	conflict	UNP B3VMP4
3u	281	LEU	-	insertion	UNP B3VMP4
3v	123	GLU	ASP	conflict	UNP B3VMP4
3v	281	LEU	-	insertion	UNP B3VMP4
3w	123	GLU	ASP	conflict	UNP B3VMP4
3w	281	LEU	-	insertion	UNP B3VMP4
3x	123	GLU	ASP	conflict	UNP B3VMP4
3x	281	LEU	-	insertion	UNP B3VMP4
4m	123	GLU	ASP	conflict	UNP B3VMP4
4m	281	LEU	-	insertion	UNP B3VMP4
4n	123	GLU	ASP	conflict	UNP B3VMP4
4n	281	LEU	-	insertion	UNP B3VMP4
5m	123	GLU	ASP	conflict	UNP B3VMP4
5m	281	LEU	-	insertion	UNP B3VMP4
5n	123	GLU	ASP	conflict	UNP B3VMP4
5n	281	LEU	-	insertion	UNP B3VMP4
6u	123	GLU	ASP	conflict	UNP B3VMP4
6u	281	LEU	-	insertion	UNP B3VMP4
6v	123	GLU	ASP	conflict	UNP B3VMP4
6v	281	LEU	-	insertion	UNP B3VMP4
6w	123	GLU	ASP	conflict	UNP B3VMP4
6w	281	LEU	-	insertion	UNP B3VMP4
6x	123	GLU	ASP	conflict	UNP B3VMP4
6x	281	LEU	-	insertion	UNP B3VMP4
7t	123	GLU	ASP	conflict	UNP B3VMP4
7t	281	LEU	-	insertion	UNP B3VMP4
7u	123	GLU	ASP	conflict	UNP B3VMP4
7u	281	LEU	-	insertion	UNP B3VMP4
7v	123	GLU	ASP	conflict	UNP B3VMP4
7v	281	LEU	-	insertion	UNP B3VMP4
7w	123	GLU	ASP	conflict	UNP B3VMP4
7w	281	LEU	-	insertion	UNP B3VMP4
7x	123	GLU	ASP	conflict	UNP B3VMP4
7x	281	LEU	-	insertion	UNP B3VMP4
9M	123	GLU	ASP	conflict	UNP B3VMP4
9M	281	LEU	-	insertion	UNP B3VMP4
9N	123	GLU	ASP	conflict	UNP B3VMP4

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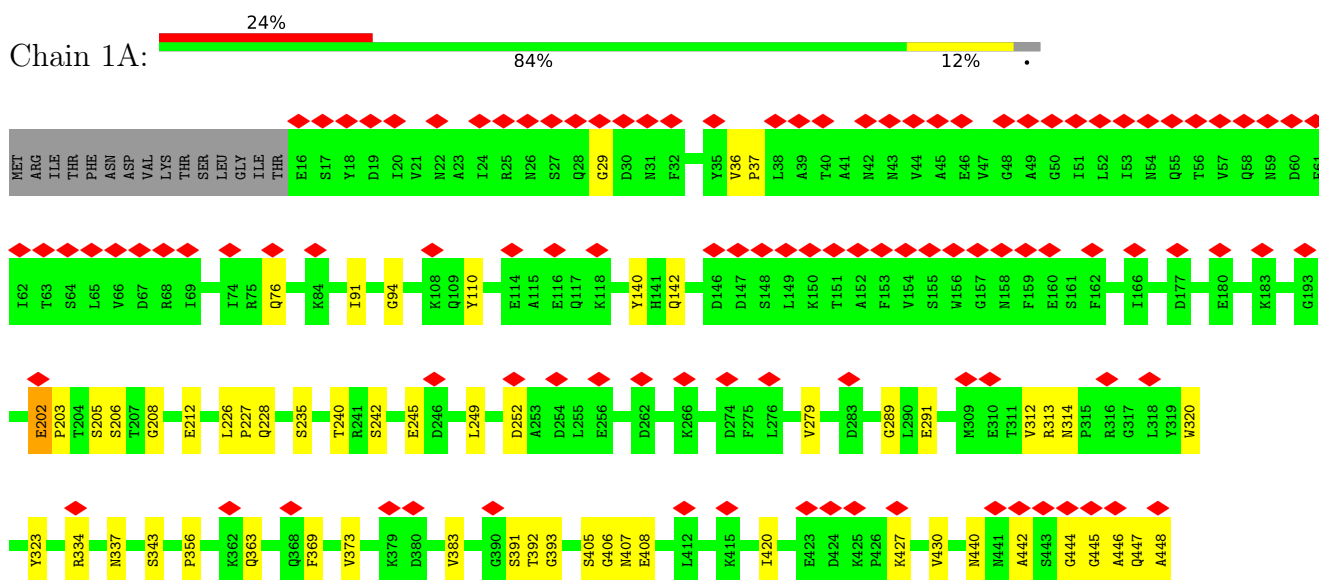
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Chain	Residue	Modelled	Actual	Comment	Reference
9N	281	LEU	-	insertion	UNP B3VMP4
9O	123	GLU	ASP	conflict	UNP B3VMP4
9O	281	LEU	-	insertion	UNP B3VMP4
9P	123	GLU	ASP	conflict	UNP B3VMP4
9P	281	LEU	-	insertion	UNP B3VMP4
9Q	123	GLU	ASP	conflict	UNP B3VMP4
9Q	281	LEU	-	insertion	UNP B3VMP4
9R	123	GLU	ASP	conflict	UNP B3VMP4
9R	281	LEU	-	insertion	UNP B3VMP4
9J	123	GLU	ASP	conflict	UNP B3VMP4
9J	281	LEU	-	insertion	UNP B3VMP4

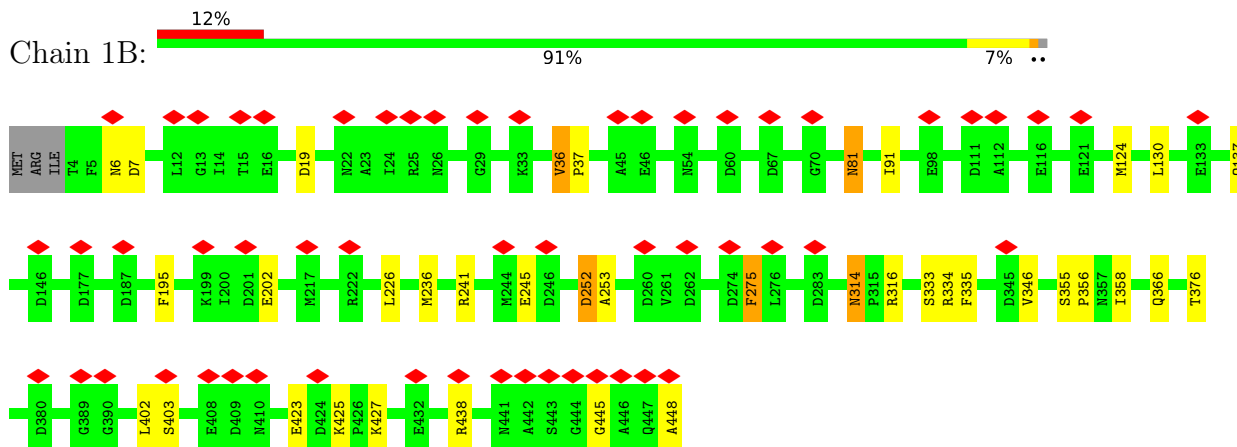
3 Residue-property plots

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.

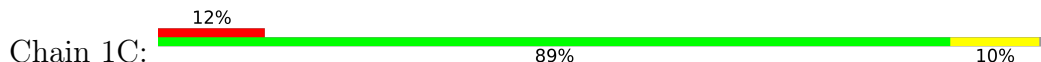
- Molecule 1: Major capsid protein

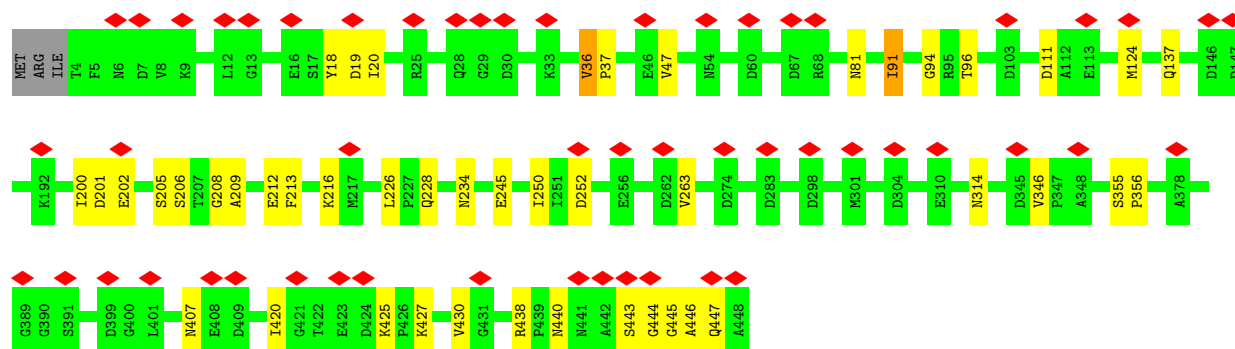


- Molecule 1: Major capsid protein



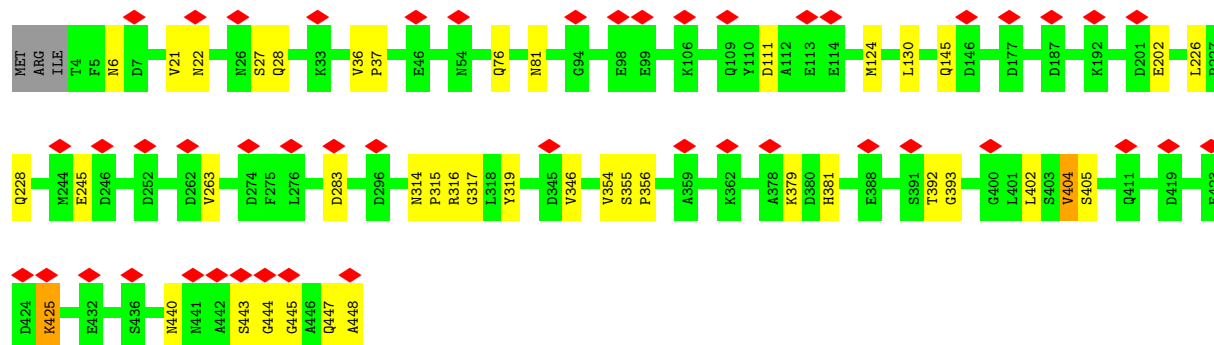
- Molecule 1: Major capsid protein





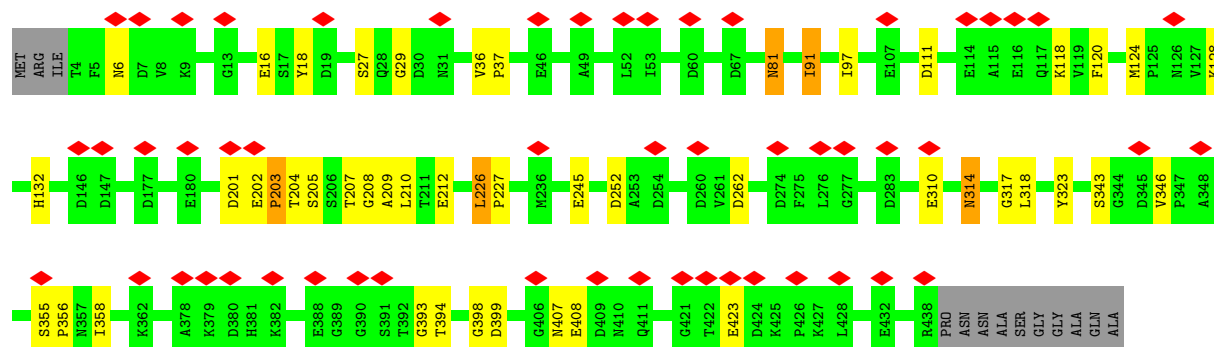
• Molecule 1: Major capsid protein

Chain 1D: 10% 90% 9% .



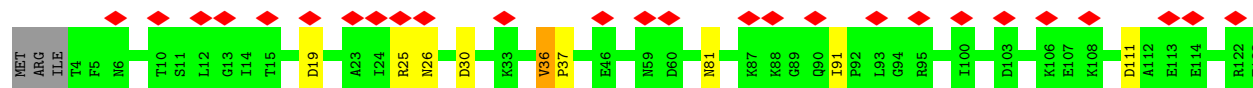
• Molecule 1: Major capsid protein

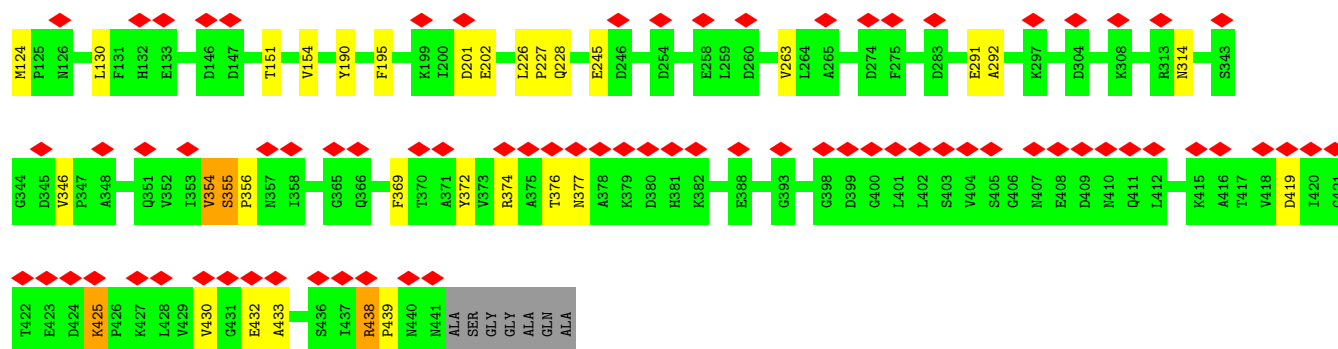
Chain 1E: 12% 86% 10% . .



• Molecule 1: Major capsid protein

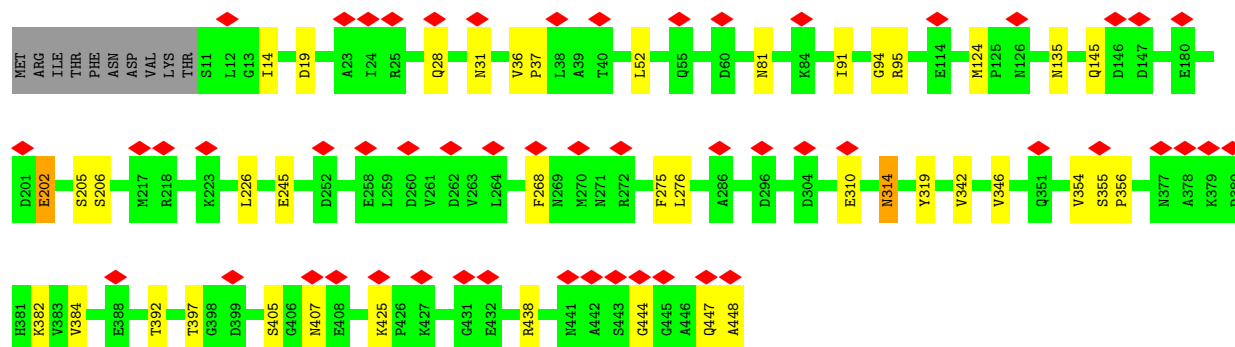
Chain 1F: 23% 89% 8% . .





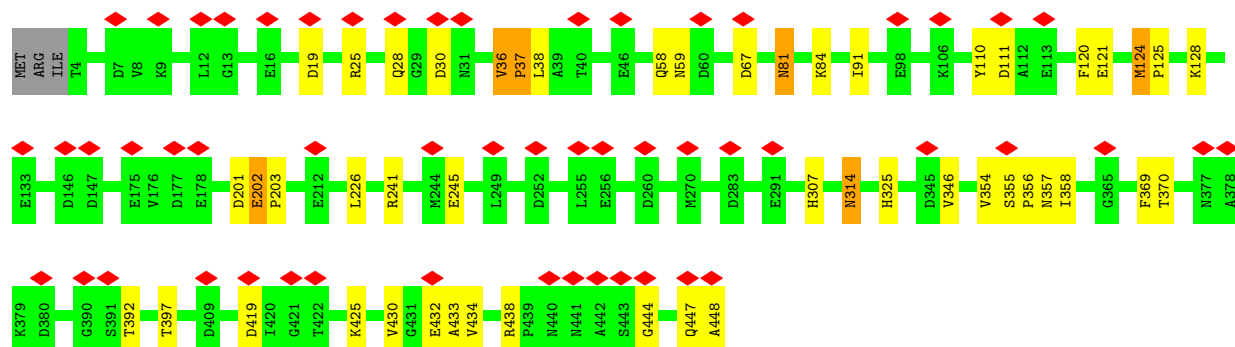
- Molecule 1: Major capsid protein

Chain 2A: 12% 89% 9% .



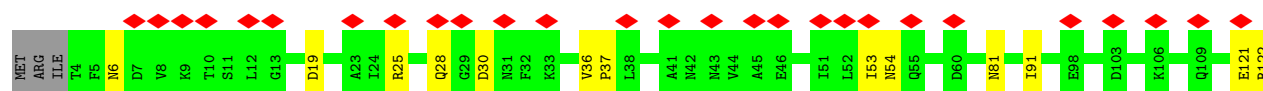
- Molecule 1: Major capsid protein

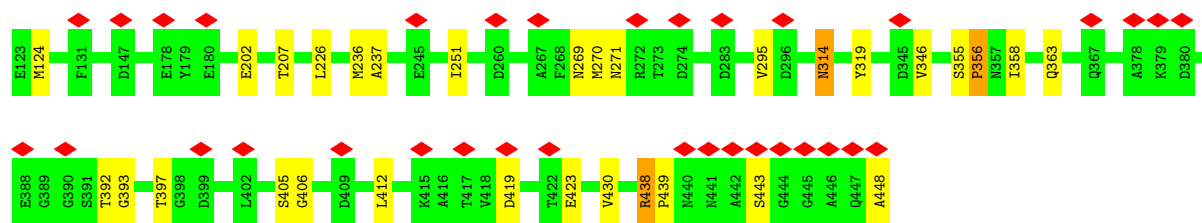
Chain 2B: 12% 88% 10% ..



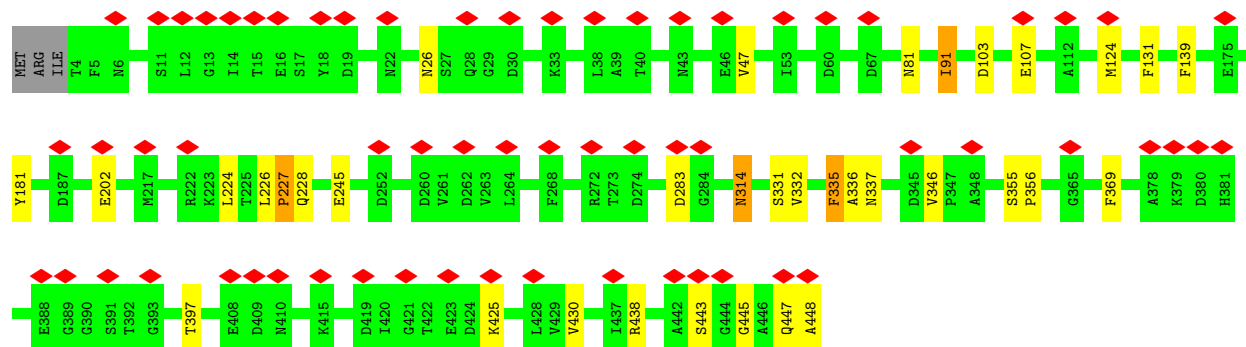
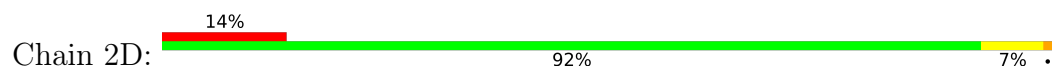
- Molecule 1: Major capsid protein

Chain 2C: 14% 90% 9% ..

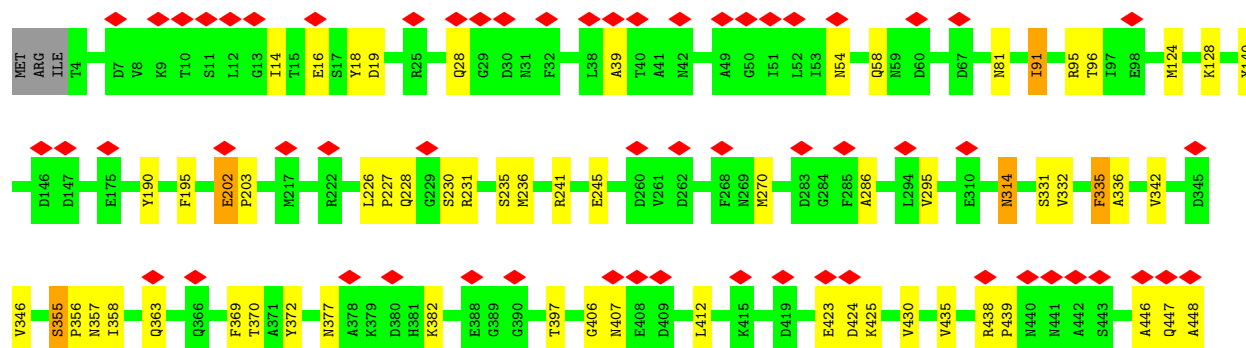
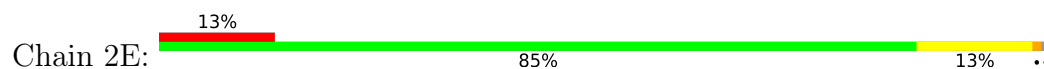




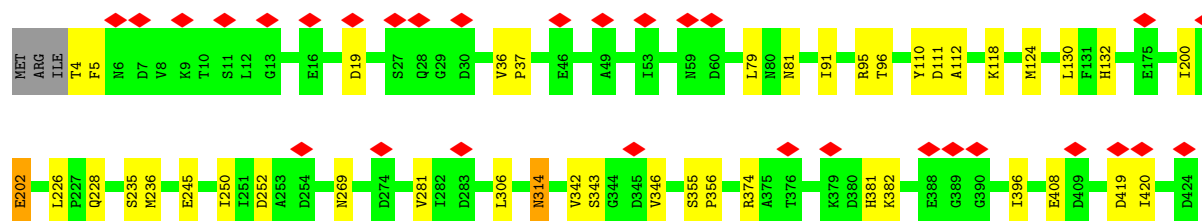
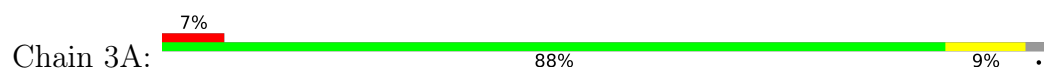
• Molecule 1: Major capsid protein

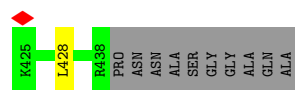


• Molecule 1: Major capsid protein

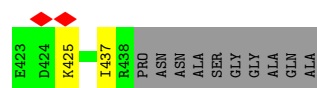
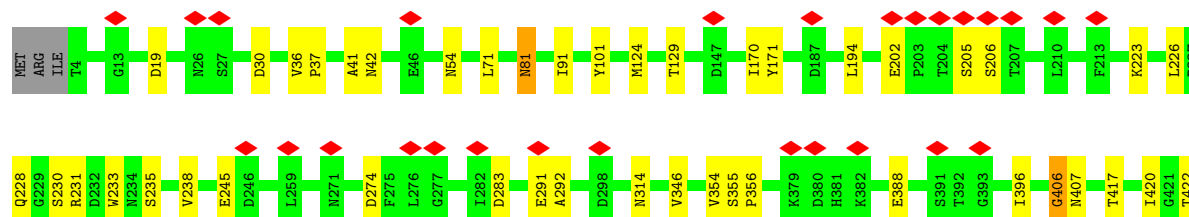
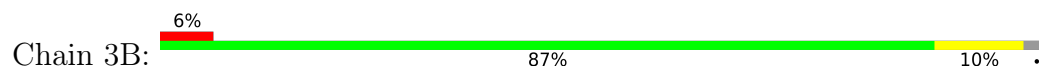


• Molecule 1: Major capsid protein

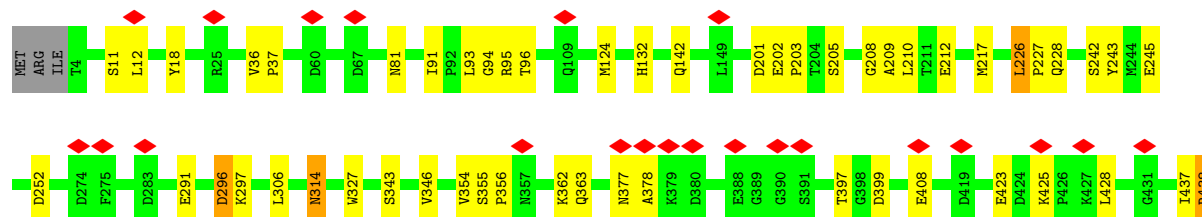
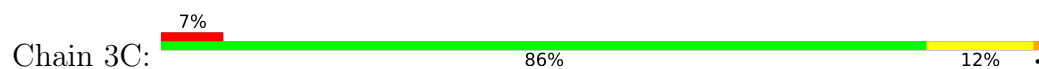




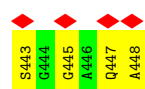
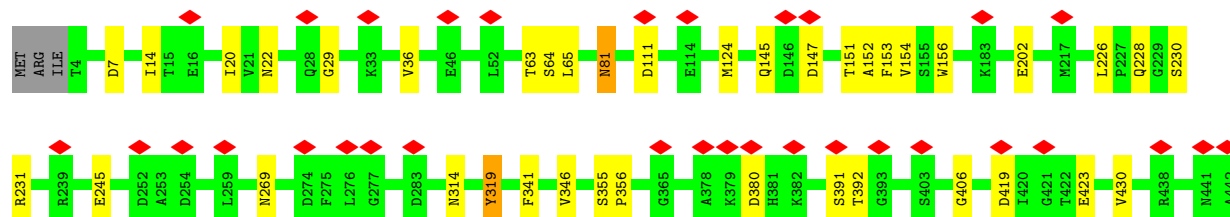
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

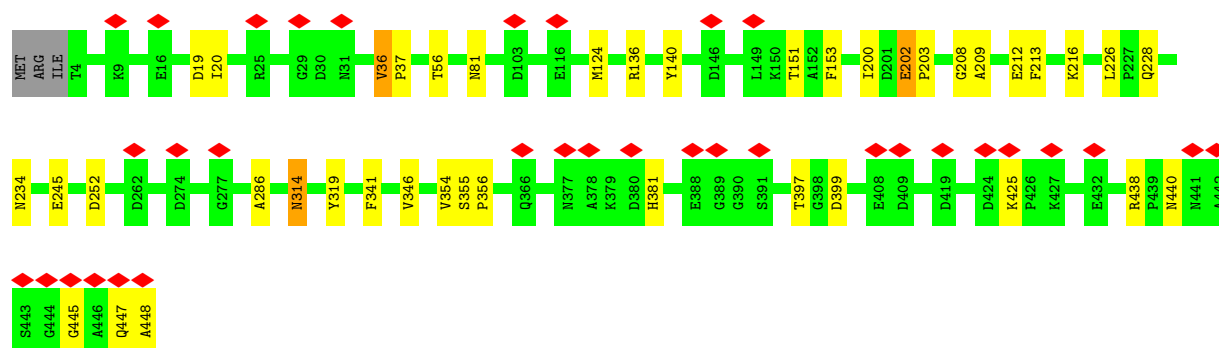


- Molecule 1: Major capsid protein



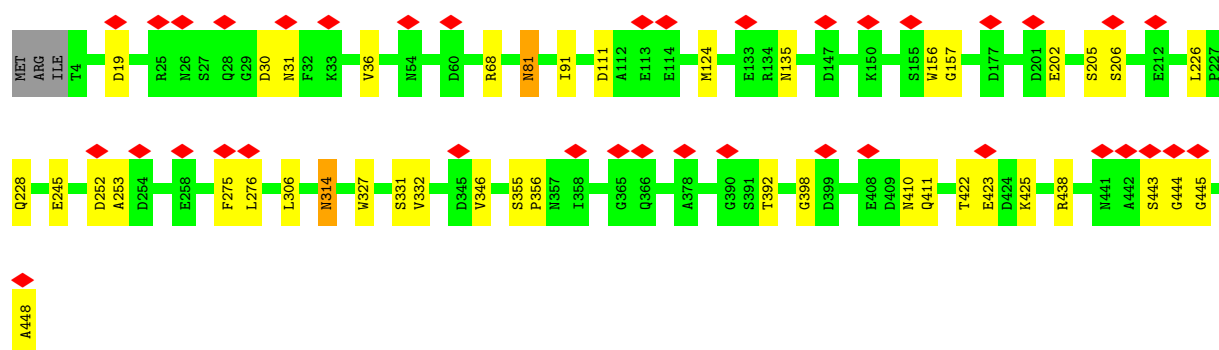
- Molecule 1: Major capsid protein

Chain 3E: 

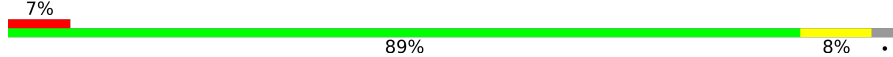


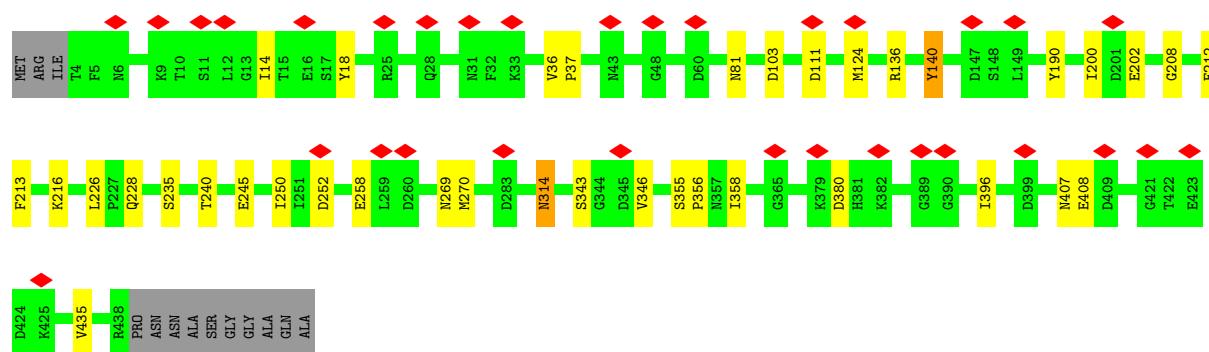
- Molecule 1: Major capsid protein

Chain 3F: 



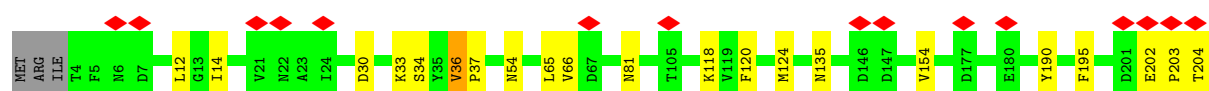
- Molecule 1: Major capsid protein

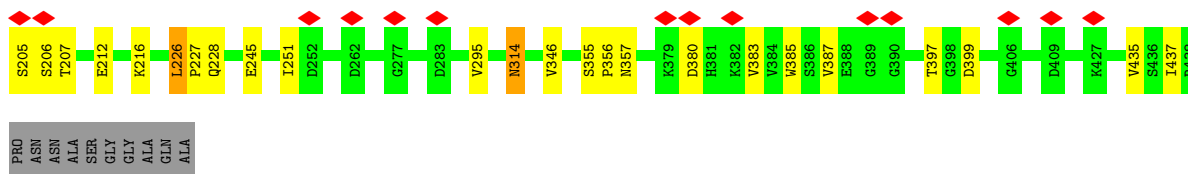
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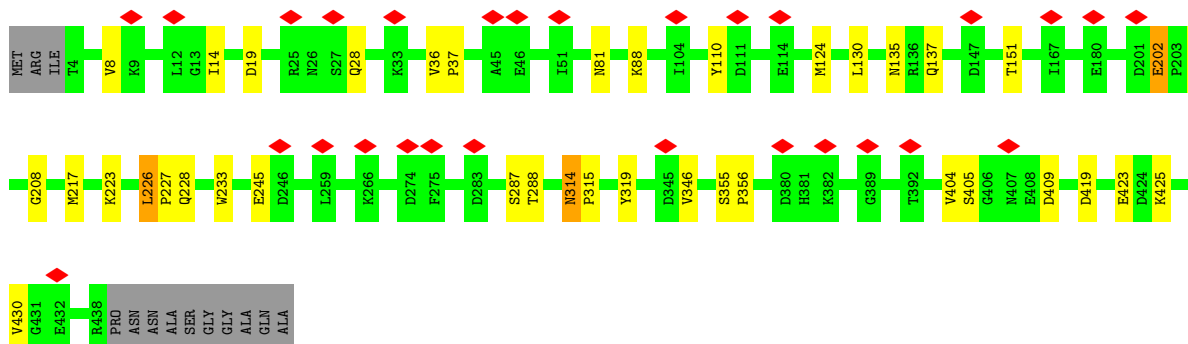
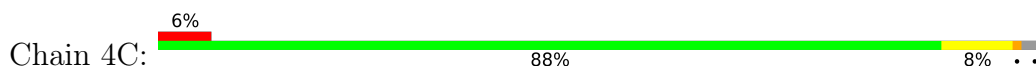
- Molecule 1: Major capsid protein

Chain 4B: 

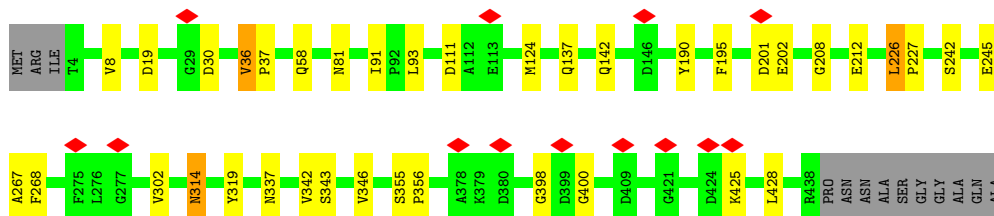
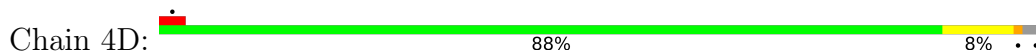




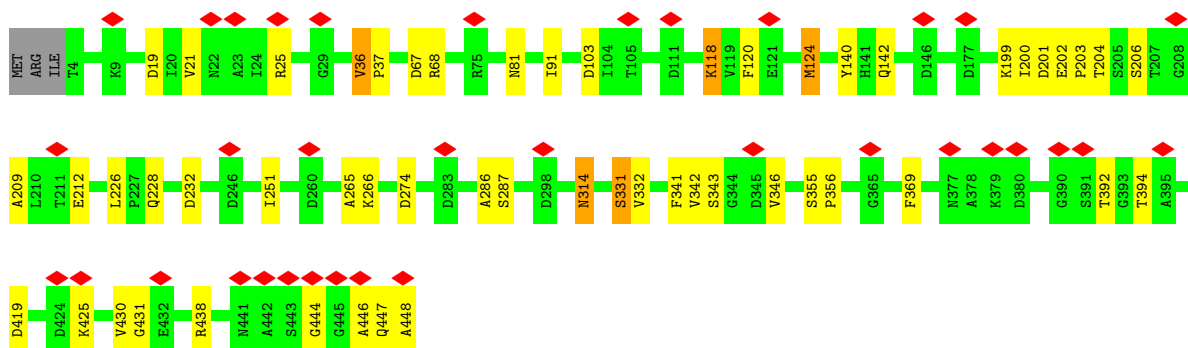
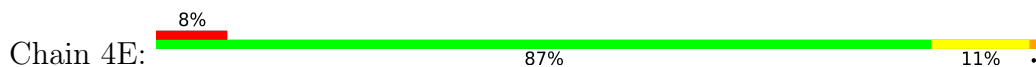
- Molecule 1: Major capsid protein



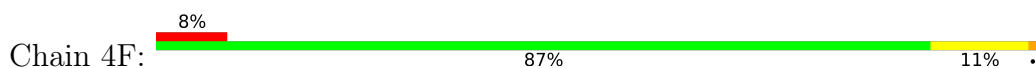
- Molecule 1: Major capsid protein

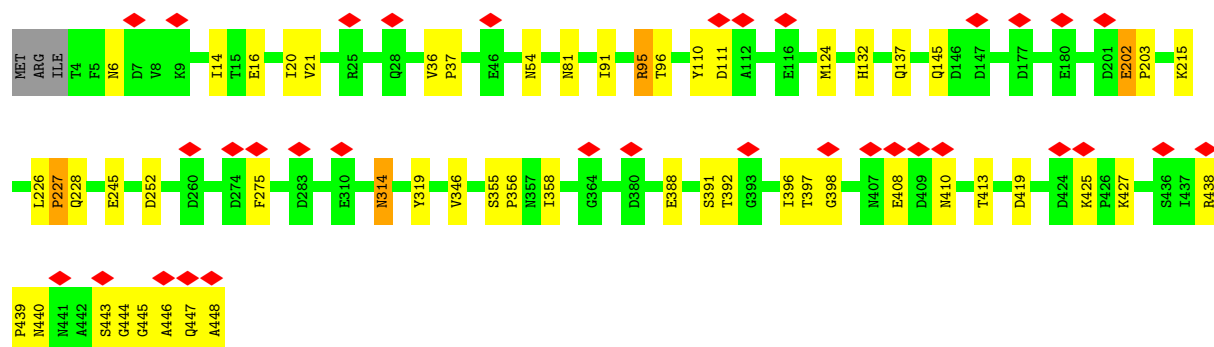


- Molecule 1: Major capsid protein

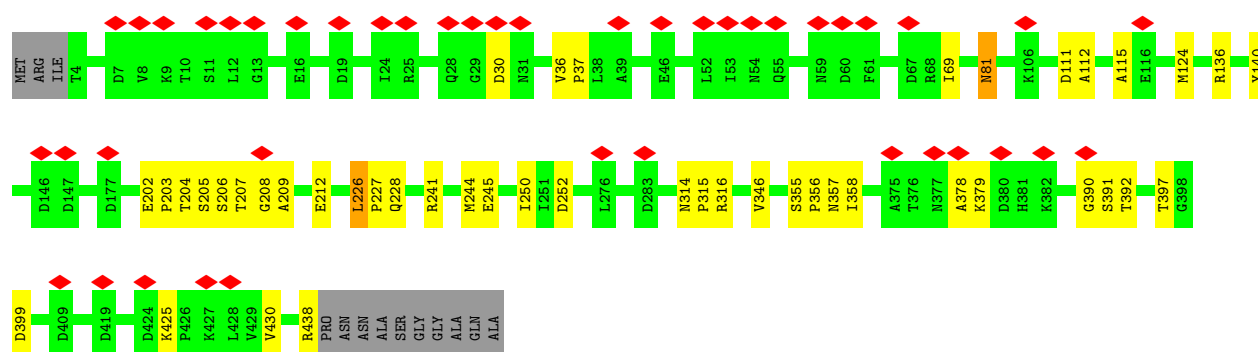


- Molecule 1: Major capsid protein

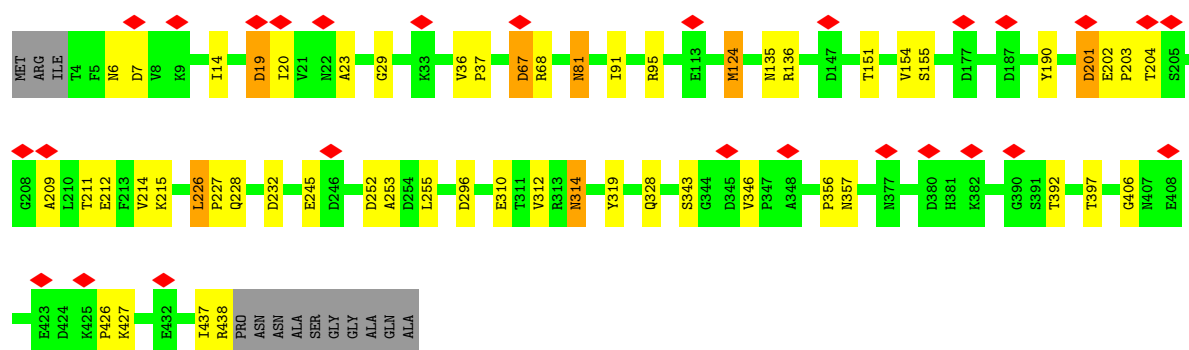
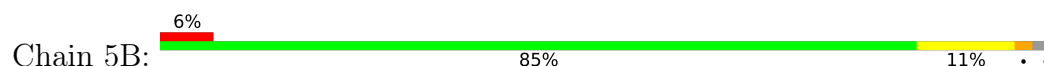




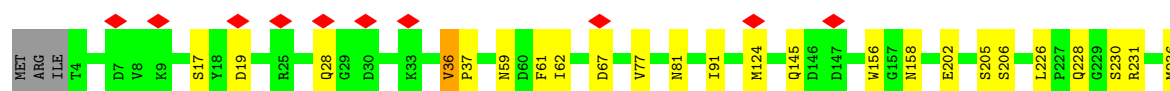
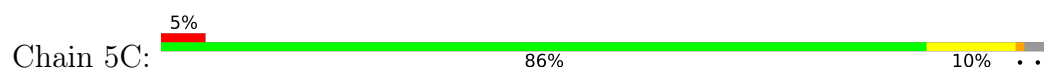
- Molecule 1: Major capsid protein

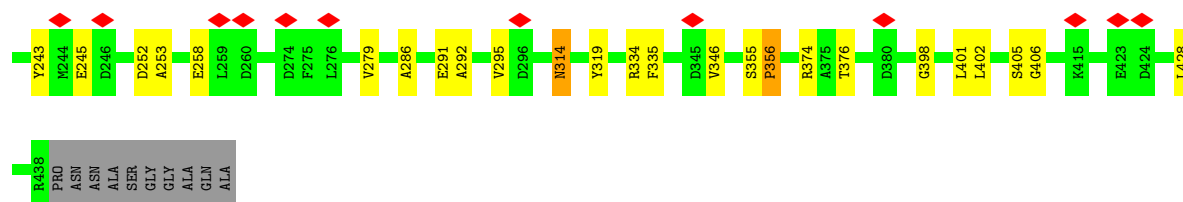


- Molecule 1: Major capsid protein



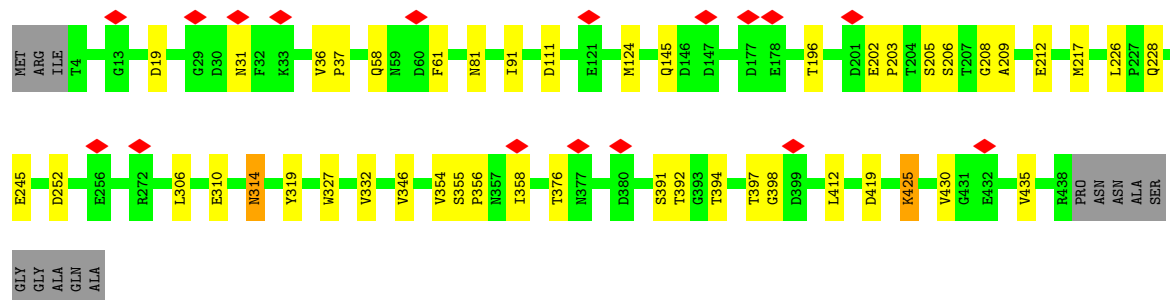
- Molecule 1: Major capsid protein





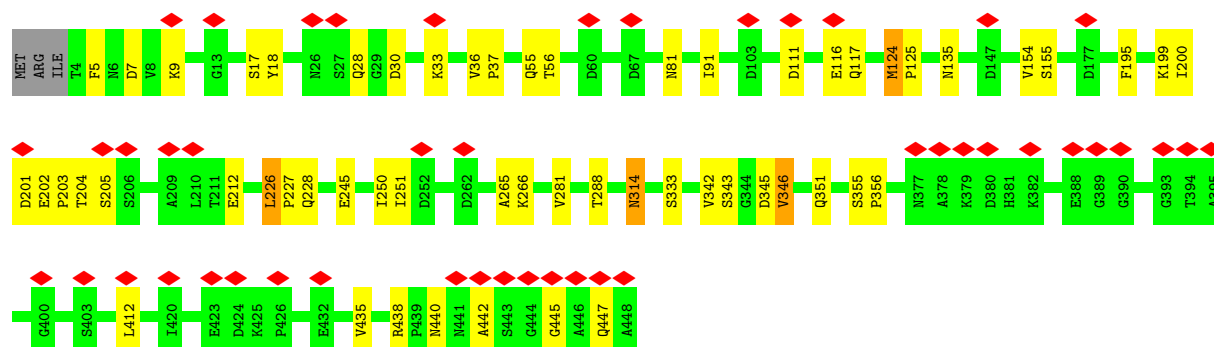
- Molecule 1: Major capsid protein

Chain 5D: 87% 10%



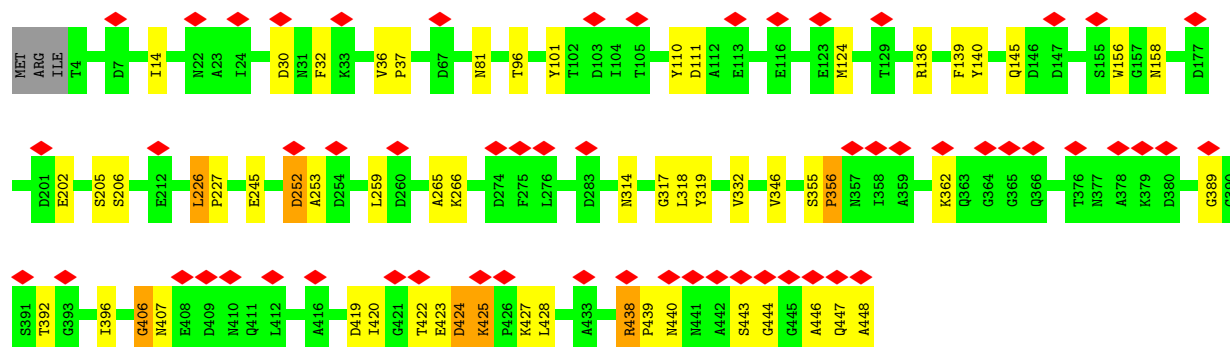
- Molecule 1: Major capsid protein

Chain 5E: 10% 87% 12%

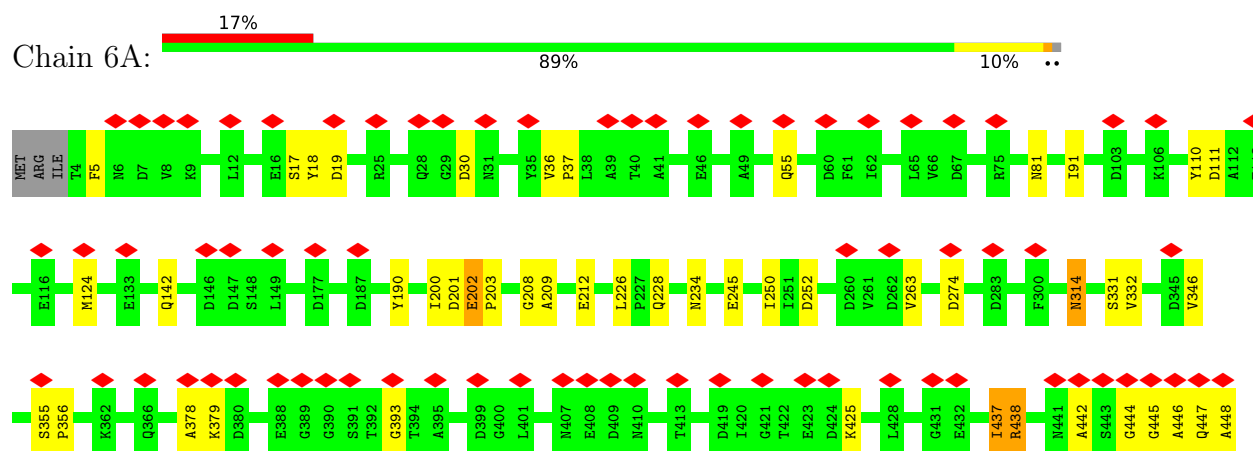


- Molecule 1: Major capsid protein

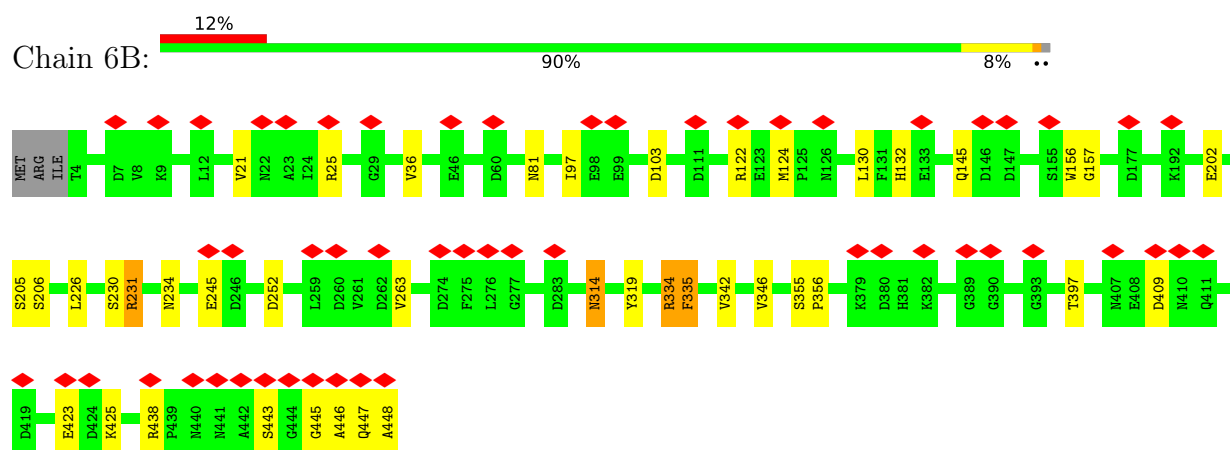
Chain 5F: 13% 86% 11%



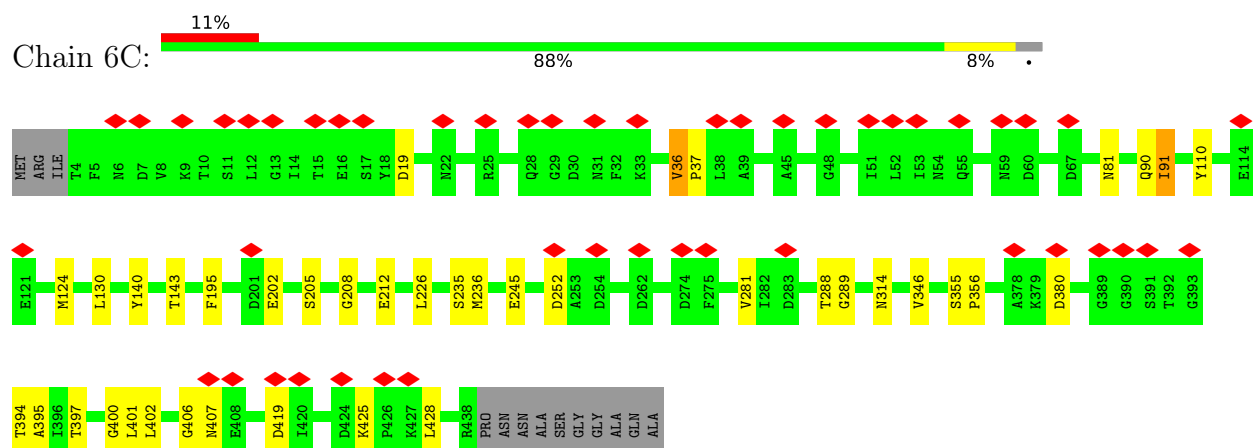
- Molecule 1: Major capsid protein



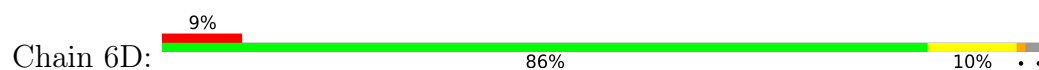
- Molecule 1: Major capsid protein

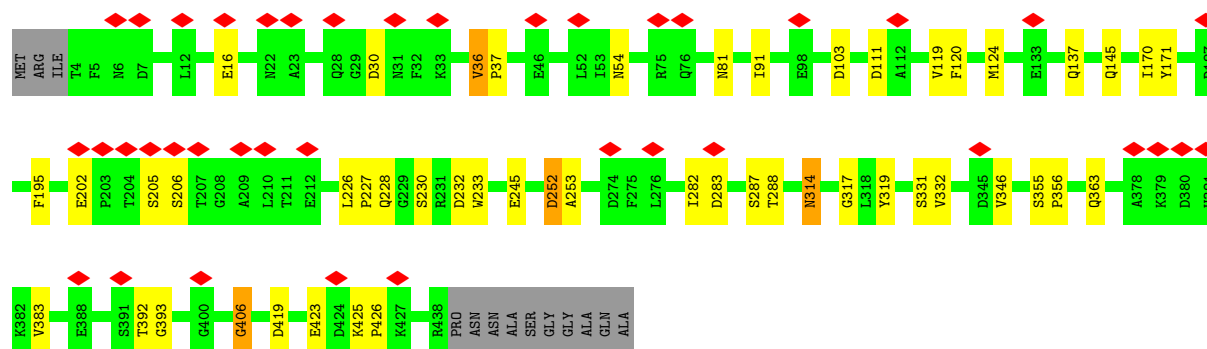


- Molecule 1: Major capsid protein

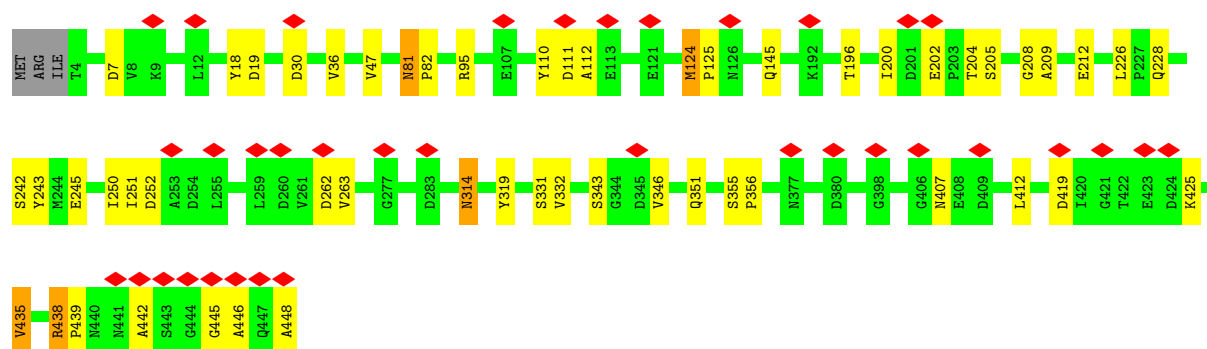


- Molecule 1: Major capsid protein

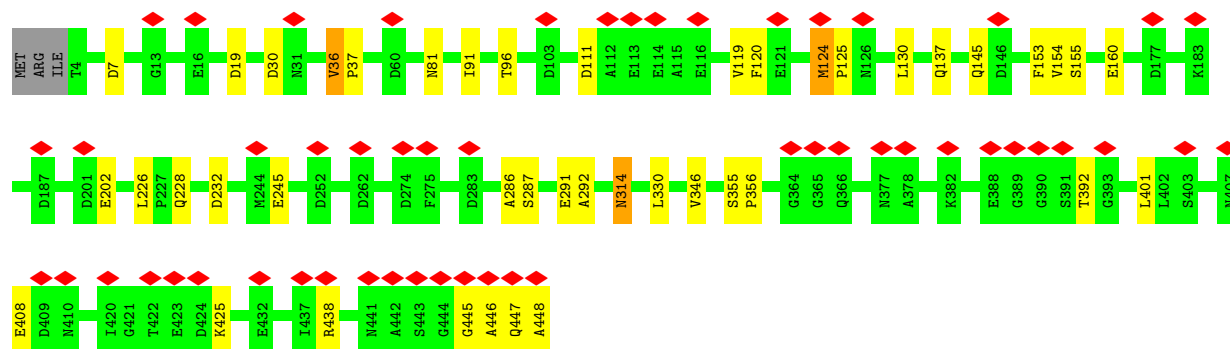
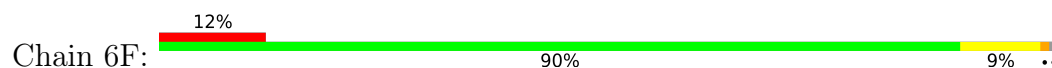




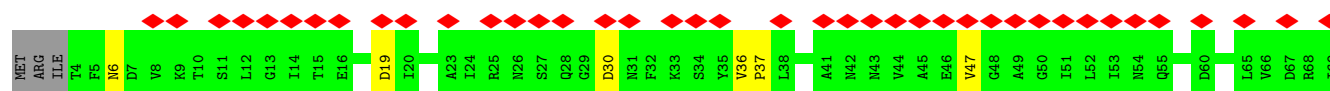
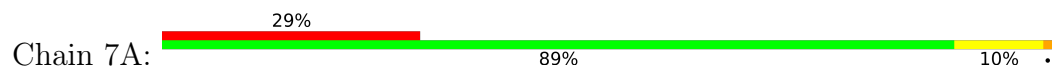
• Molecule 1: Major capsid protein



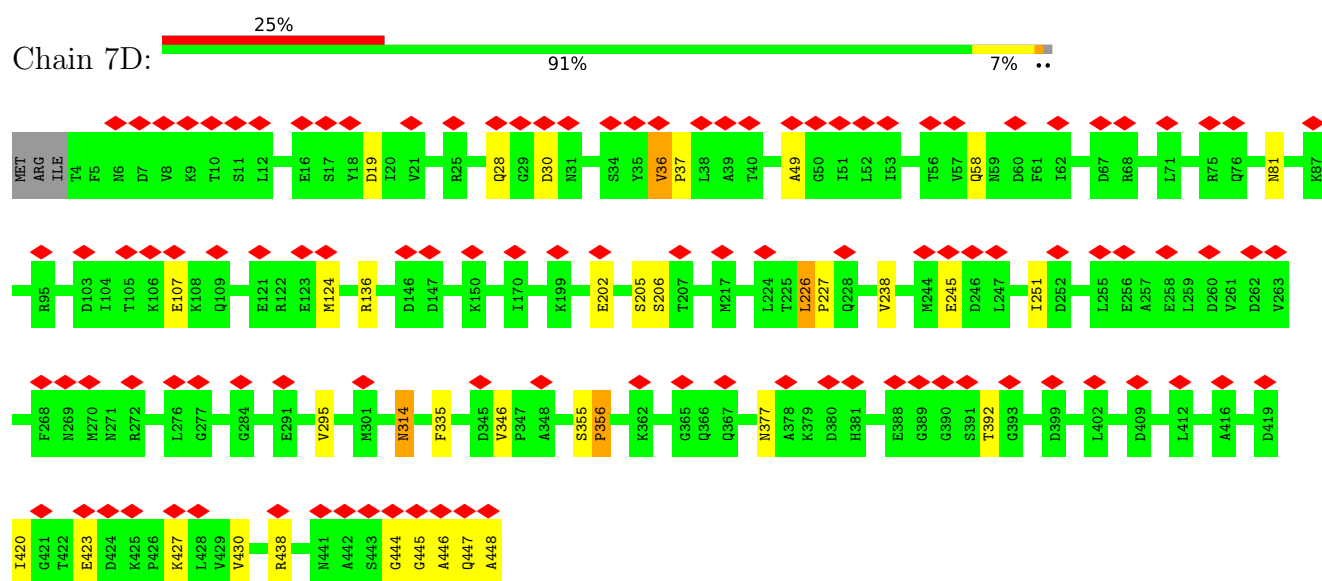
• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein



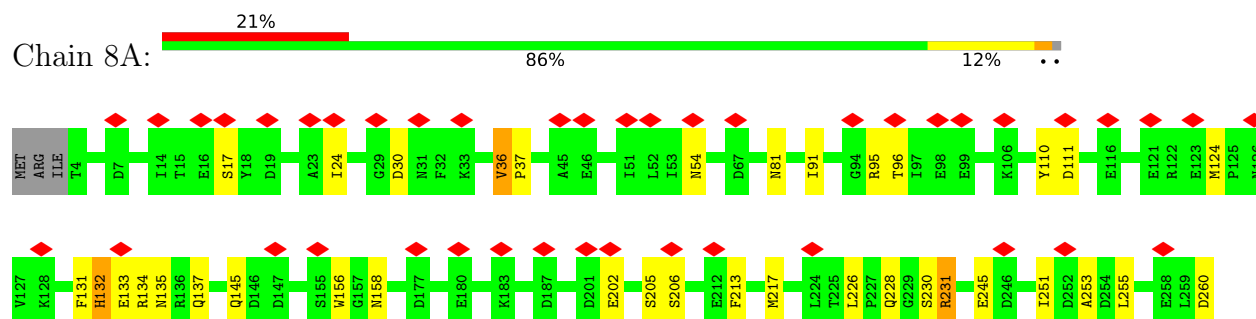


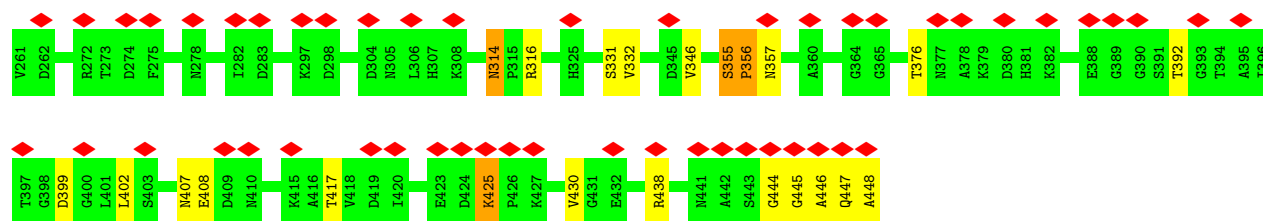


- Molecule 1: Major capsid protein

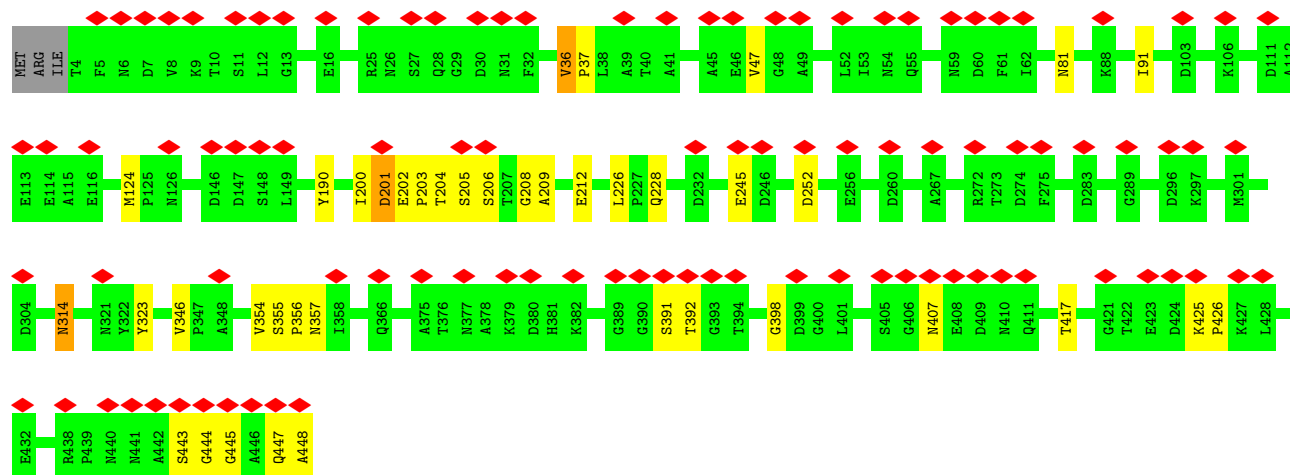
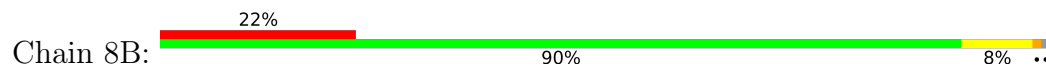


- Molecule 1: Major capsid protein

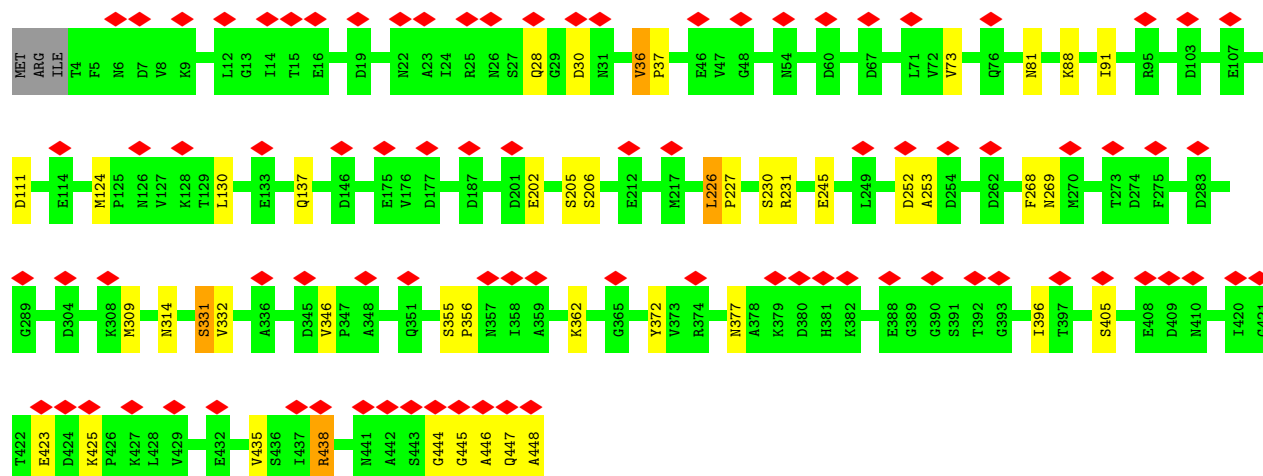




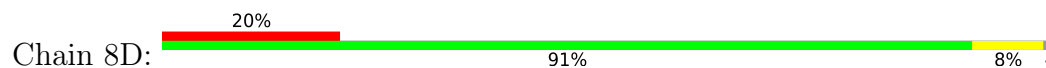
• Molecule 1: Major capsid protein

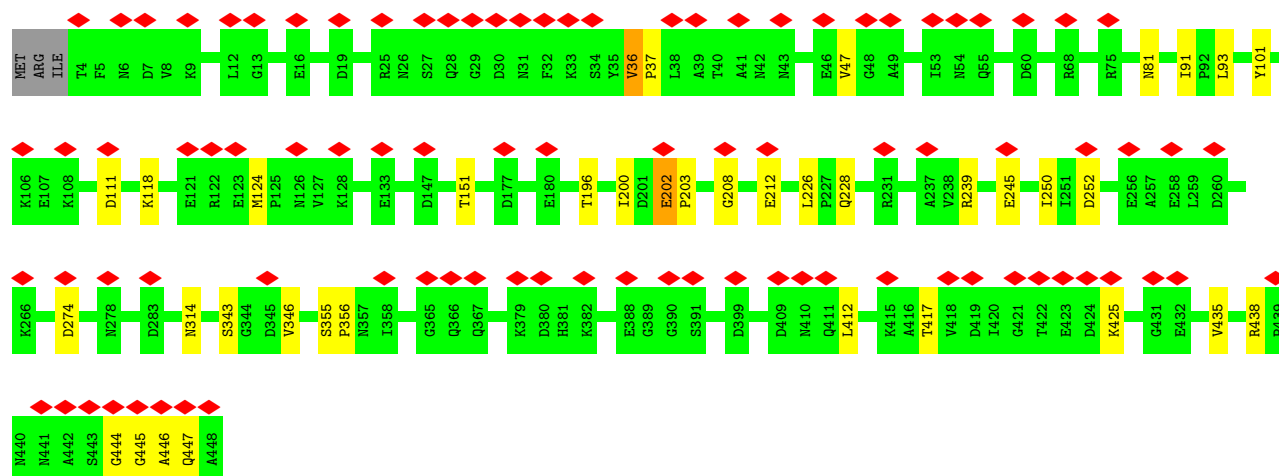


• Molecule 1: Major capsid protein



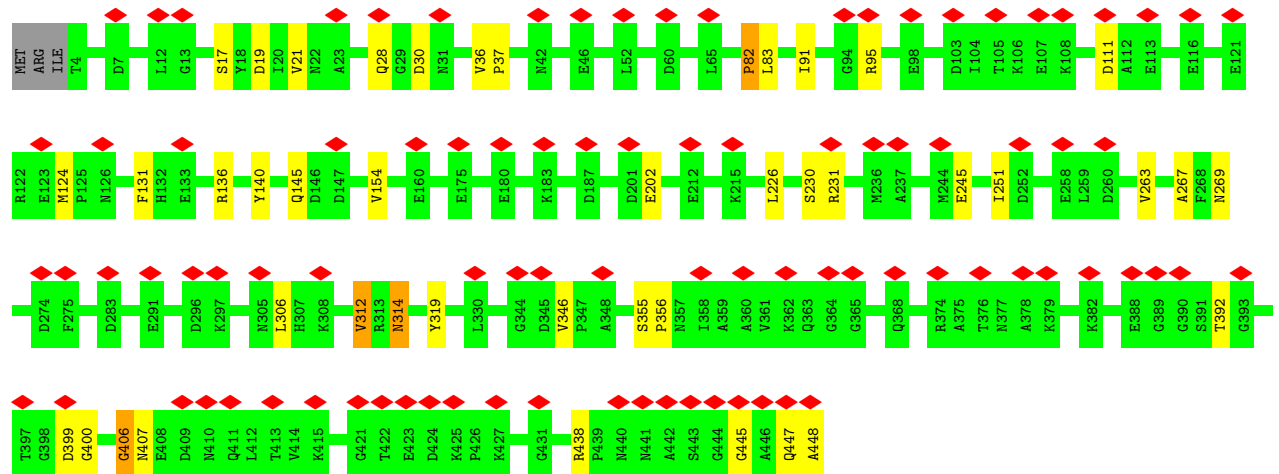
• Molecule 1: Major capsid protein





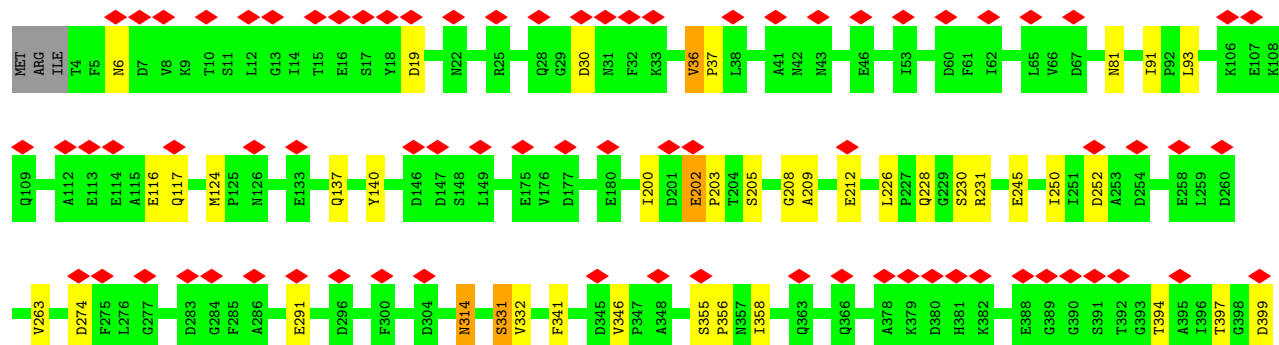
- Molecule 1: Major capsid protein

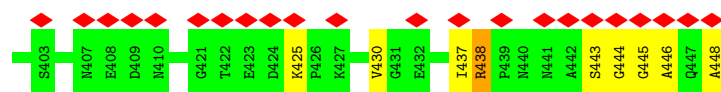
Chain 8E: 20% 90% 9% ..



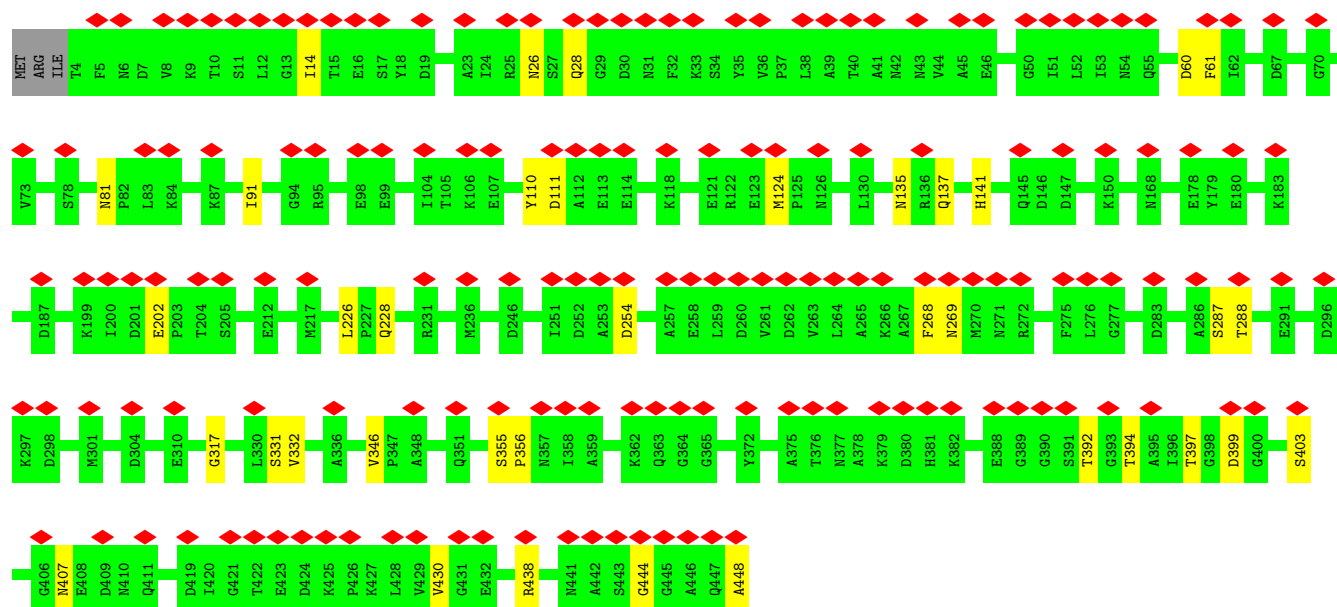
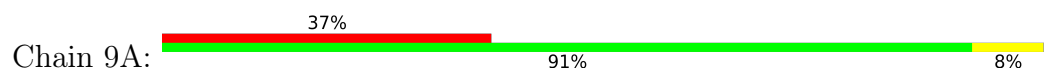
- Molecule 1: Major capsid protein

Chain 8F: 22% 88% 10% ..

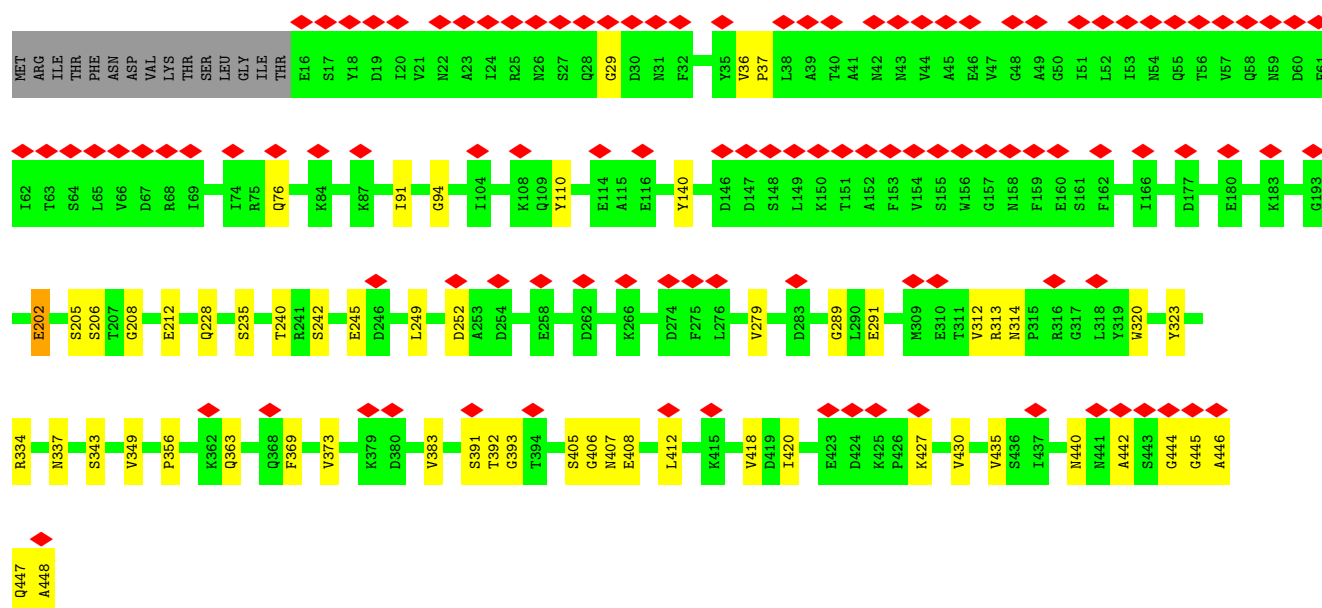
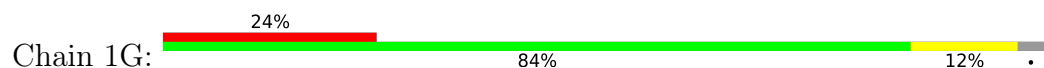




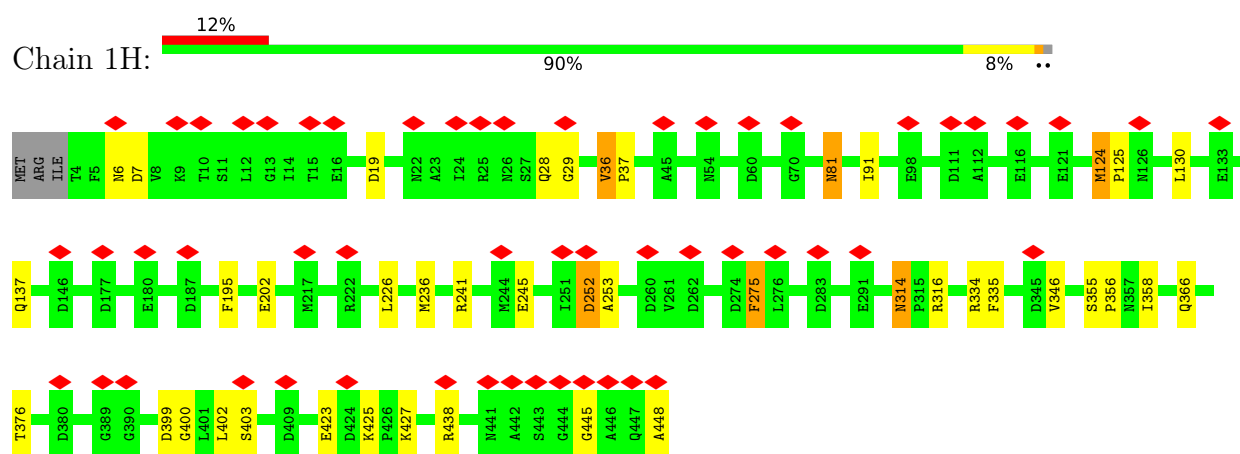
- Molecule 1: Major capsid protein



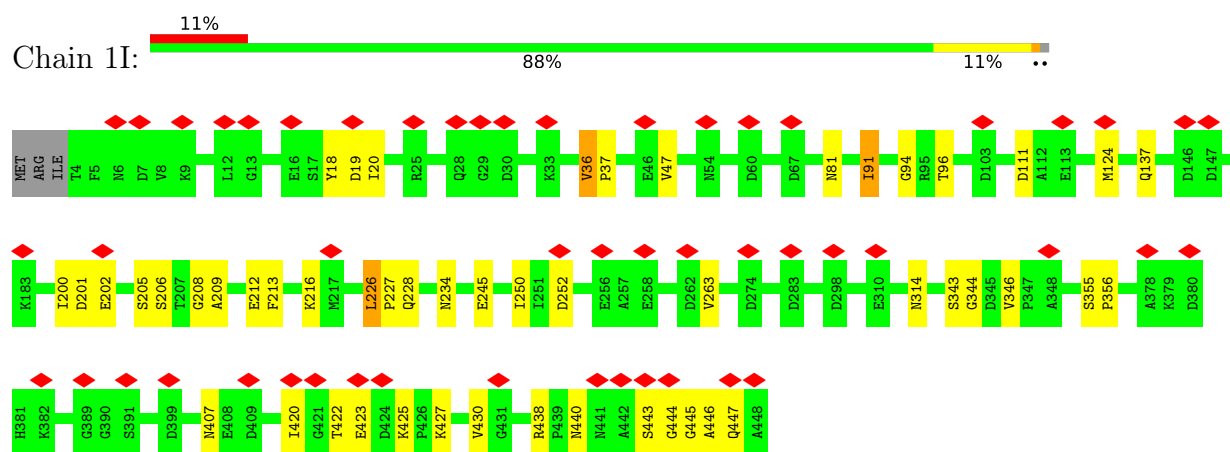
- Molecule 1: Major capsid protein



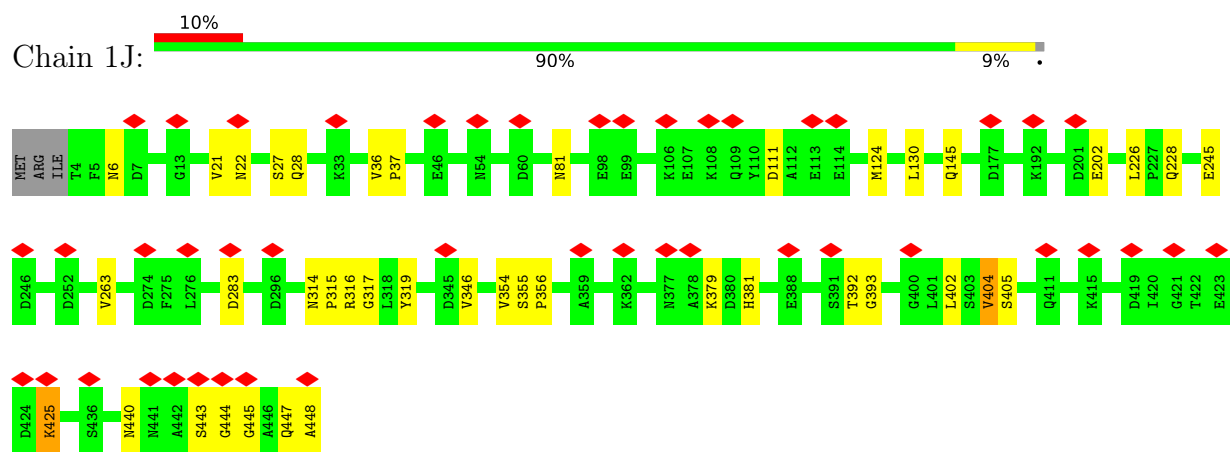
- Molecule 1: Major capsid protein



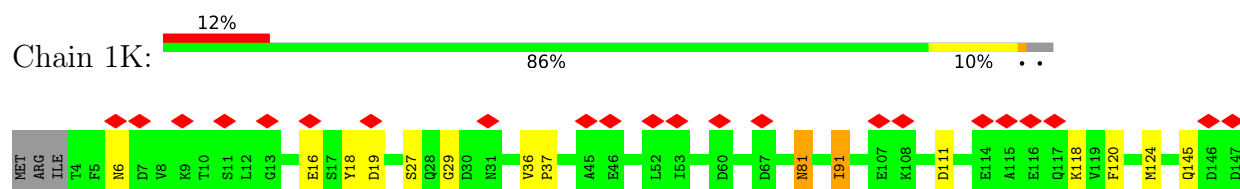
- Molecule 1: Major capsid protein

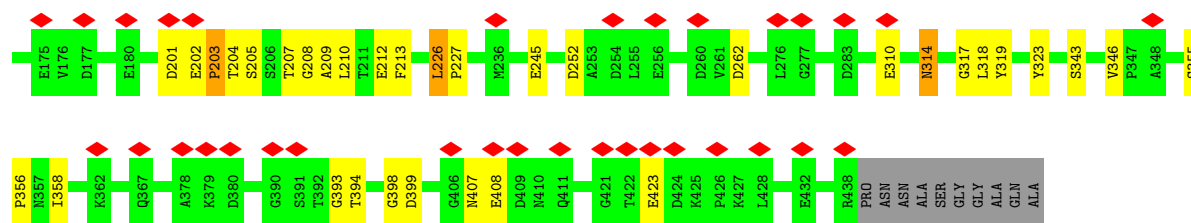


- Molecule 1: Major capsid protein

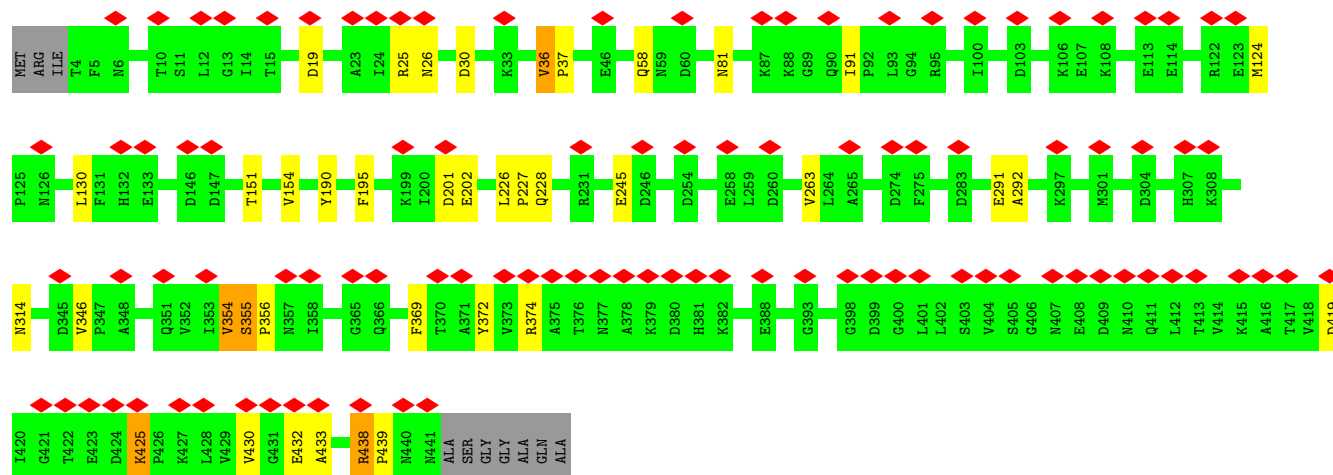
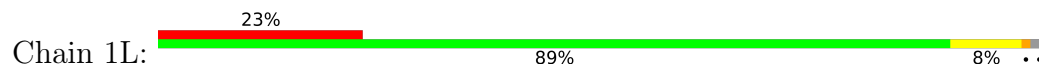


- Molecule 1: Major capsid protein

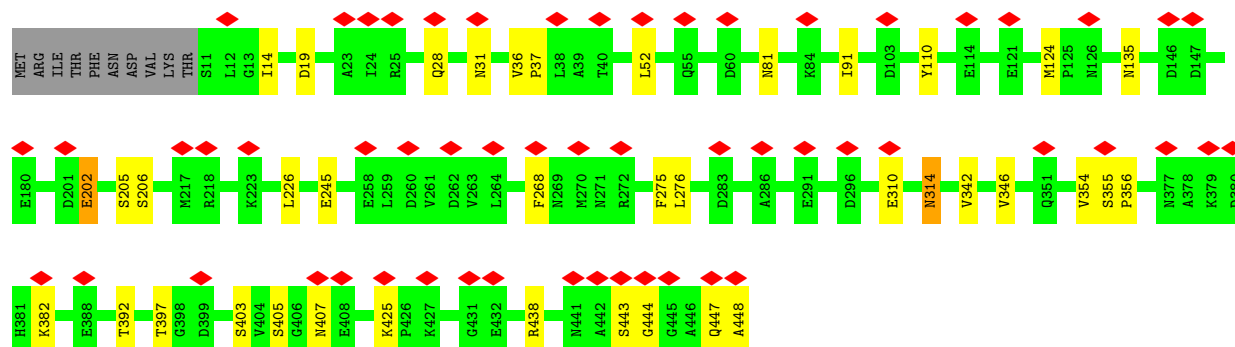
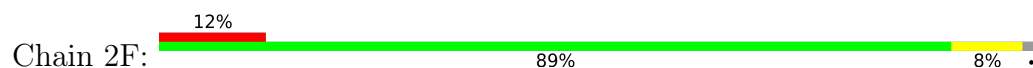




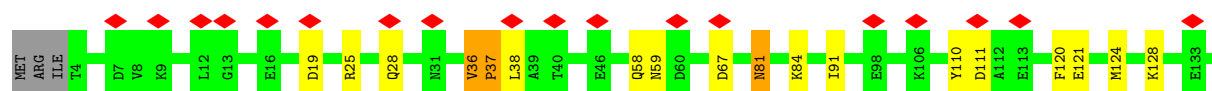
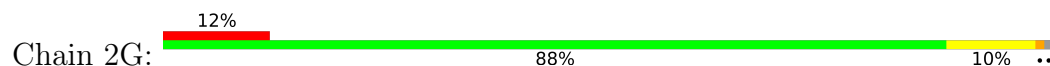
• Molecule 1: Major capsid protein

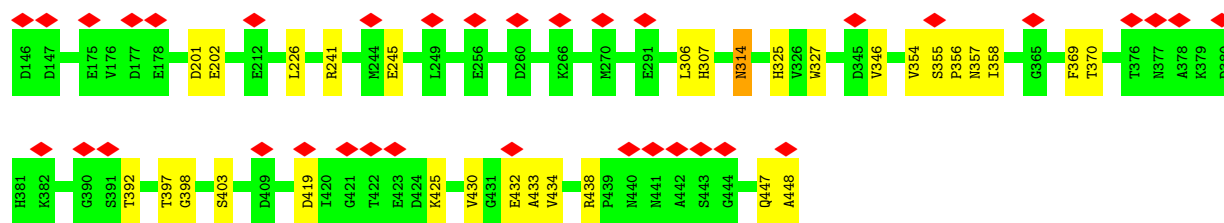


• Molecule 1: Major capsid protein

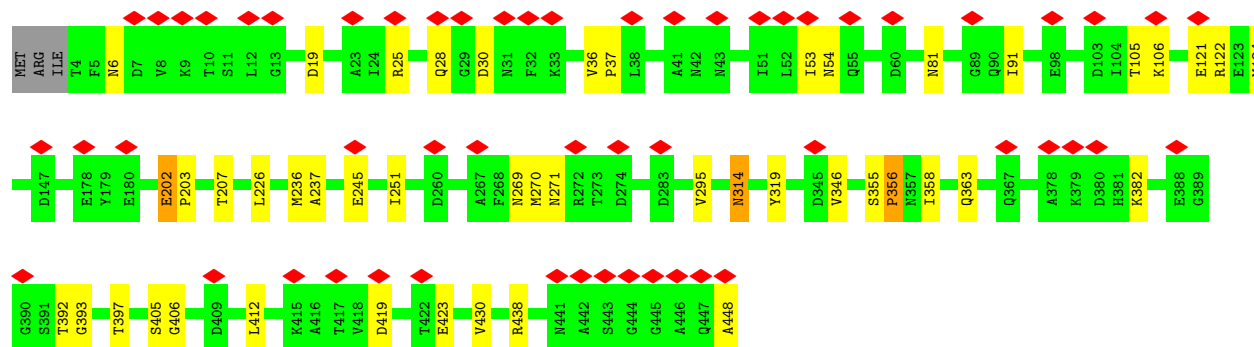
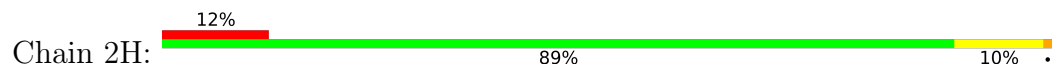


• Molecule 1: Major capsid protein

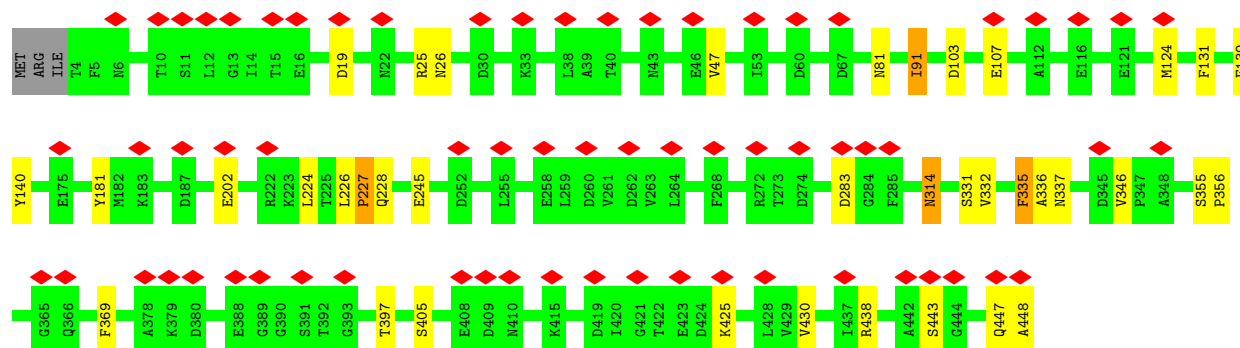
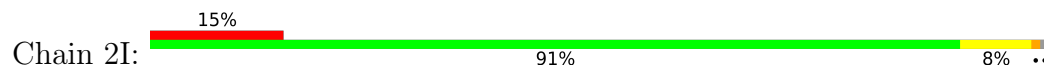




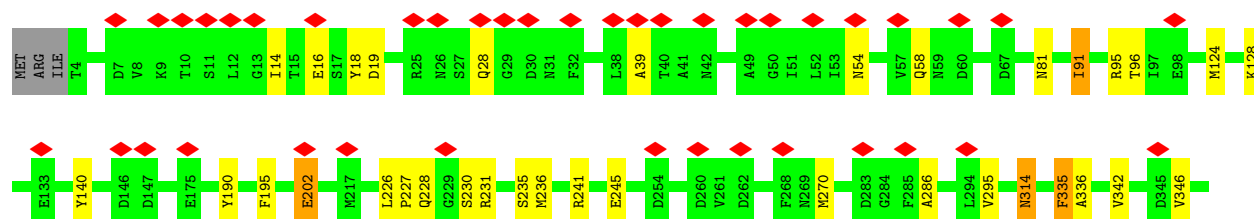
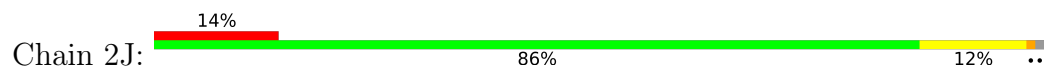
• Molecule 1: Major capsid protein

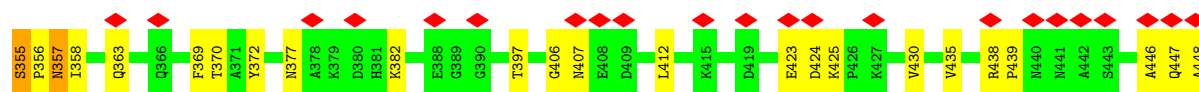


• Molecule 1: Major capsid protein



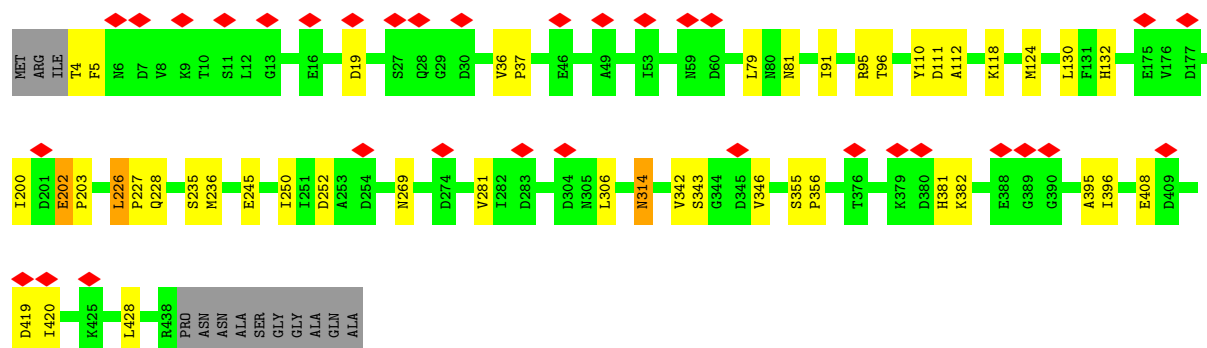
• Molecule 1: Major capsid protein





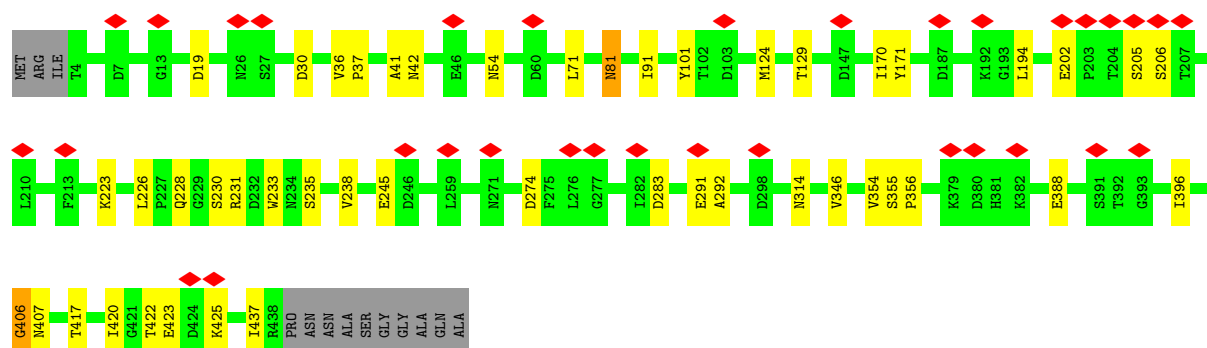
- Molecule 1: Major capsid protein

Chain 3G: 7% 87% 9% ..



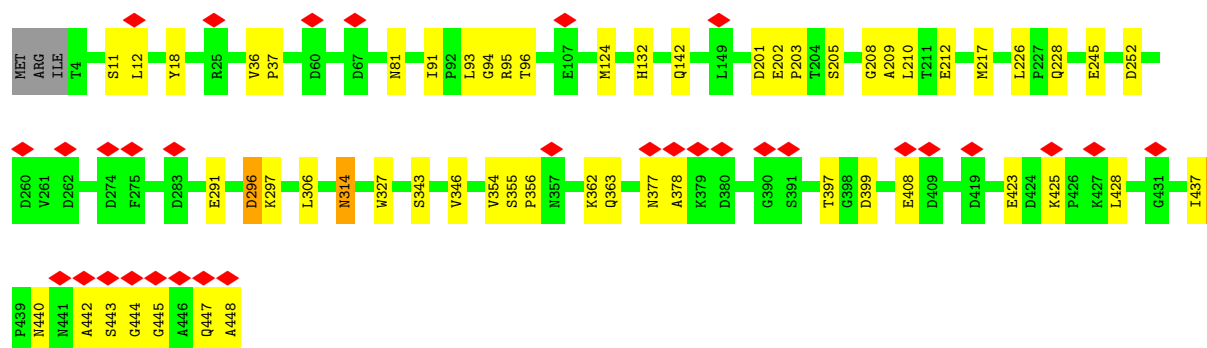
- Molecule 1: Major capsid protein

Chain 3H: 7% 87% 10% .

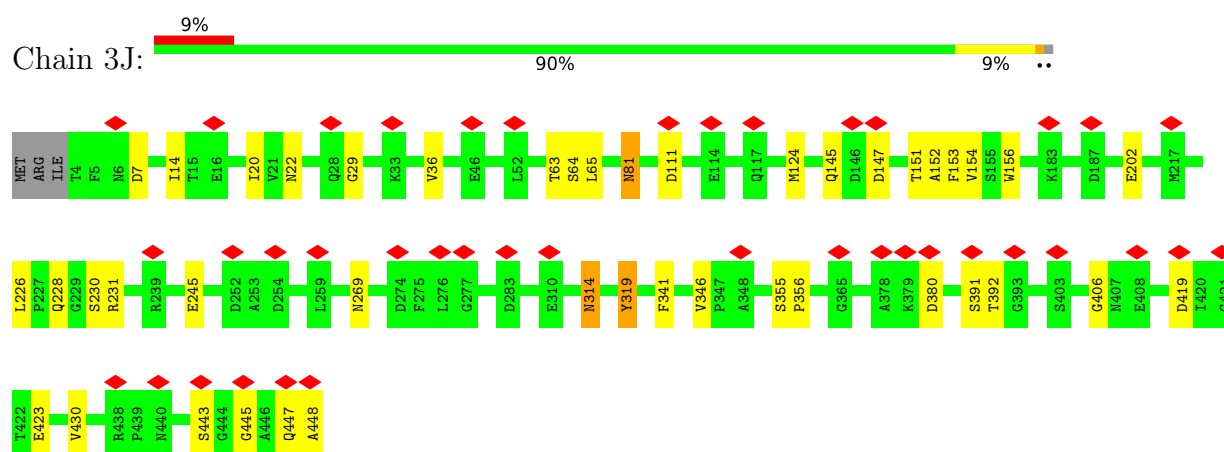


- Molecule 1: Major capsid protein

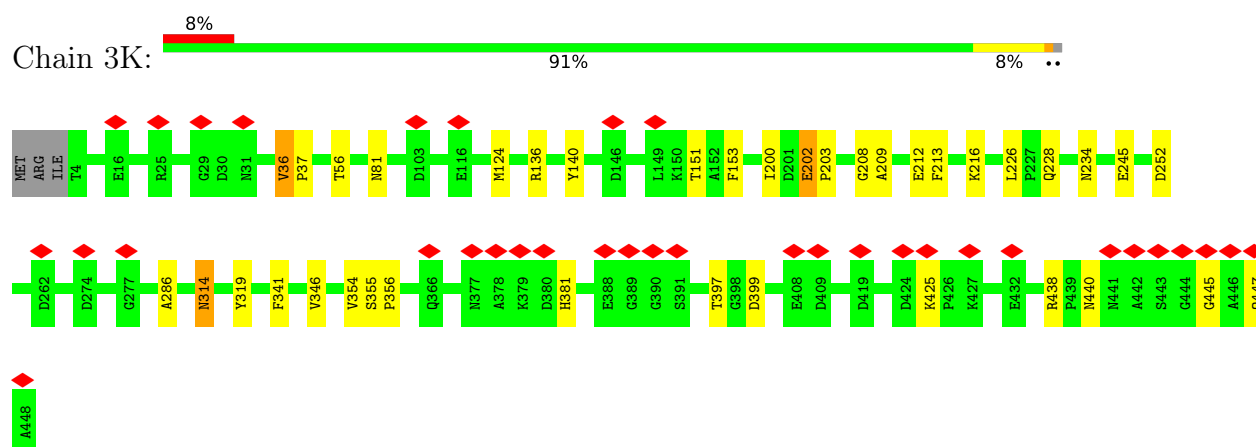
Chain 3I: 7% 87% 12% ..



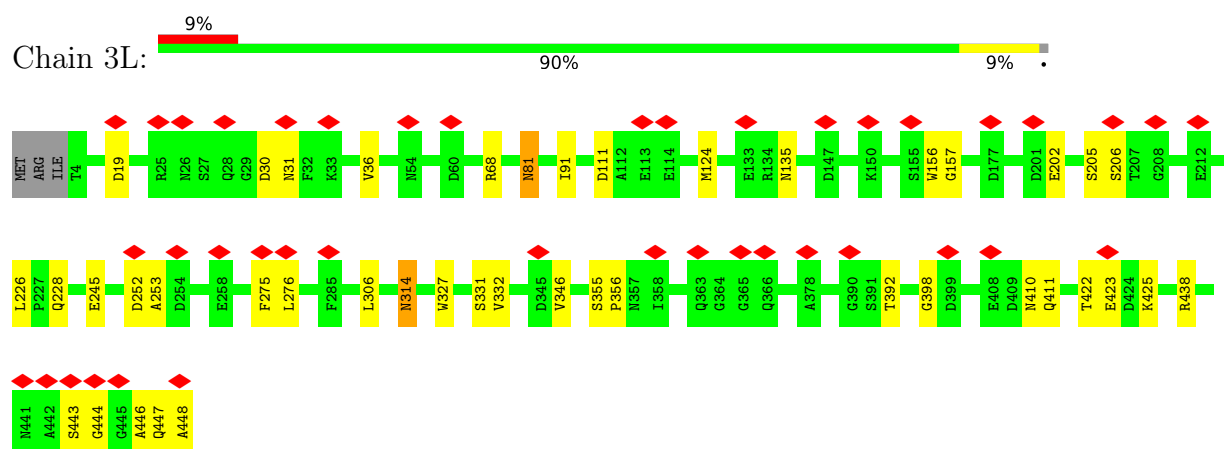
- Molecule 1: Major capsid protein



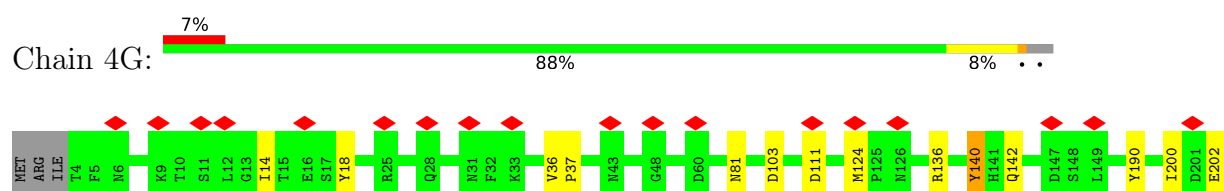
- Molecule 1: Major capsid protein

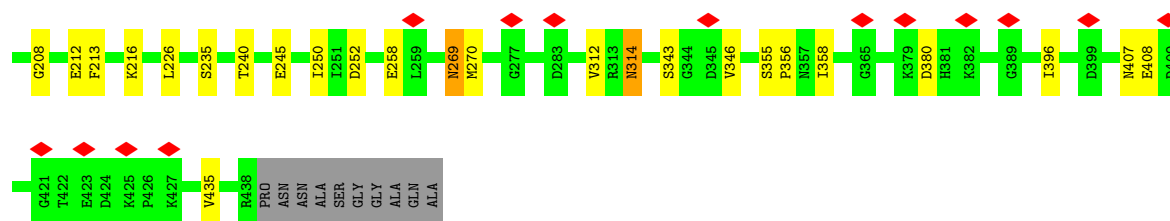


- Molecule 1: Major capsid protein

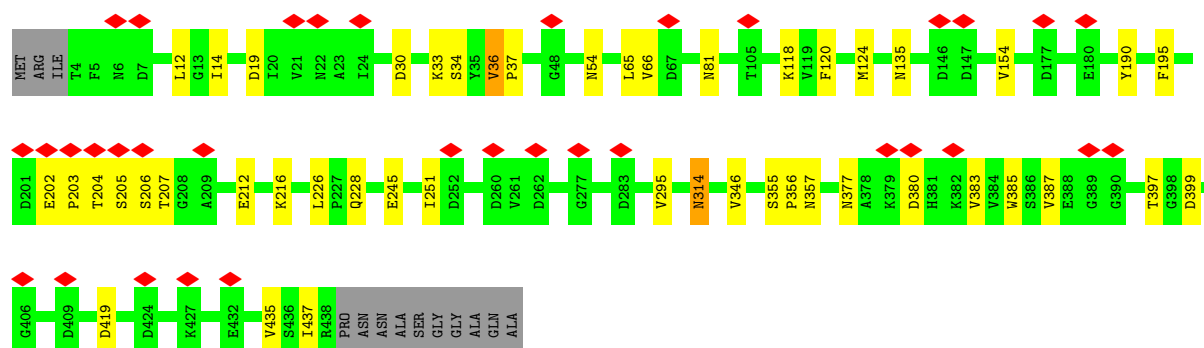
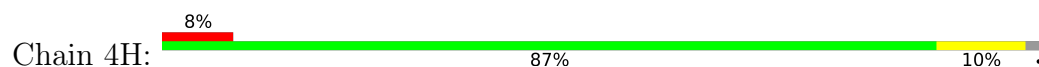


- Molecule 1: Major capsid protein

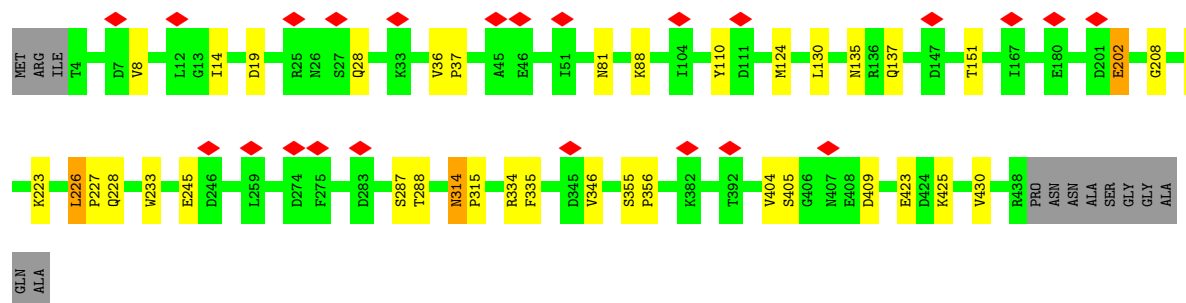
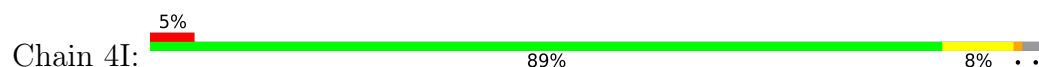




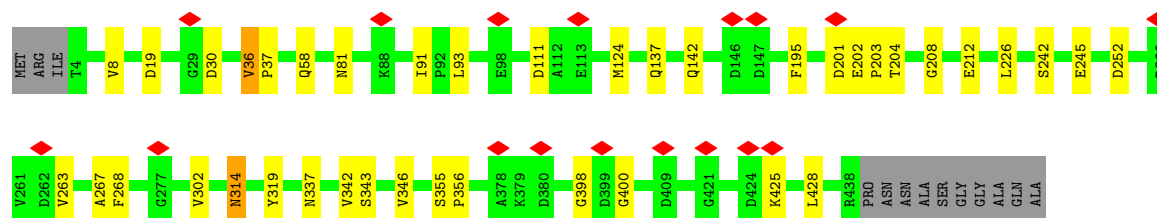
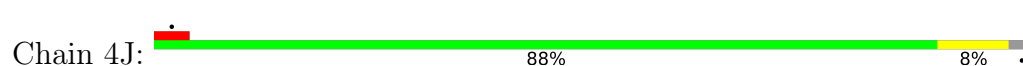
• Molecule 1: Major capsid protein



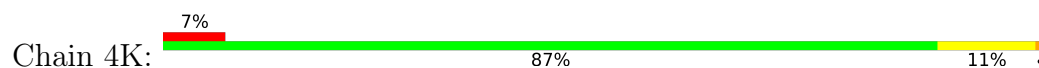
• Molecule 1: Major capsid protein

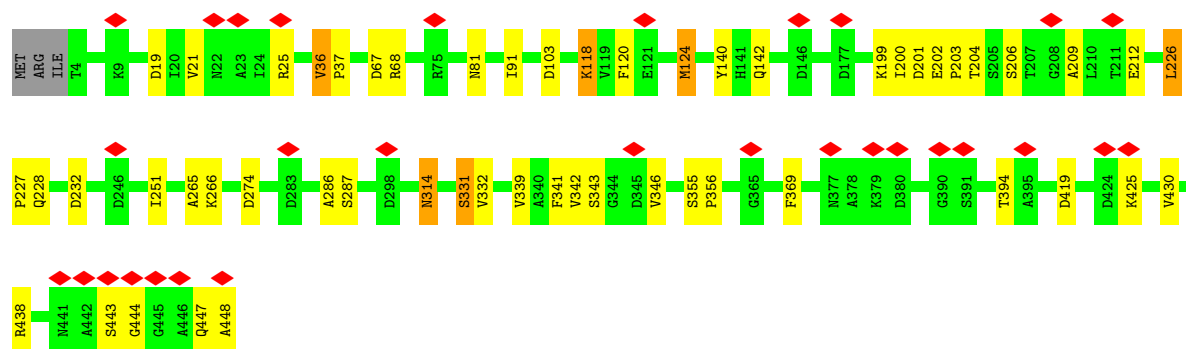


• Molecule 1: Major capsid protein



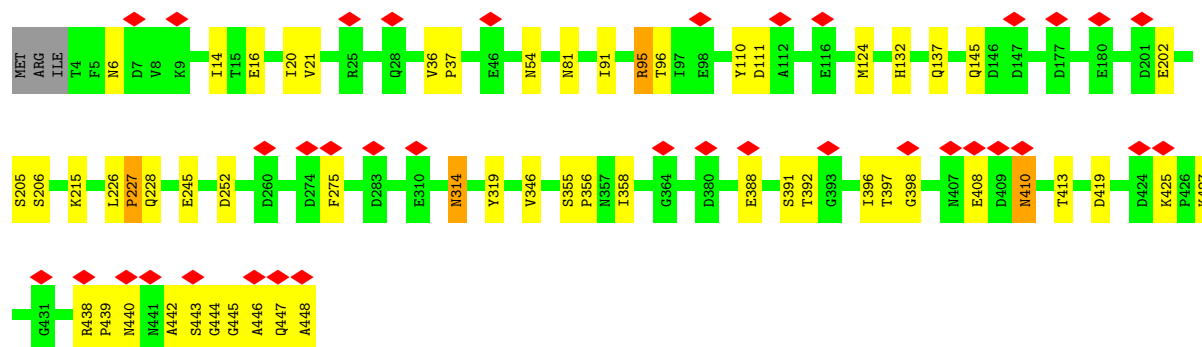
• Molecule 1: Major capsid protein





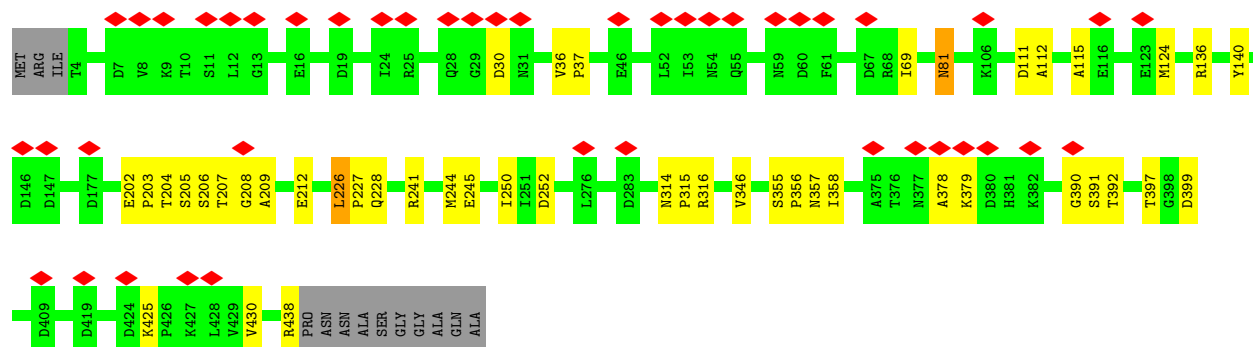
- Molecule 1: Major capsid protein

Chain 4L: 8% 87% 12% ..



- Molecule 1: Major capsid protein

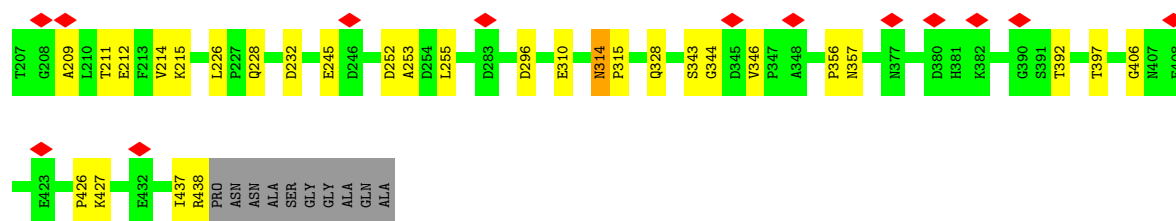
Chain 5G: 10% 87% 10% .



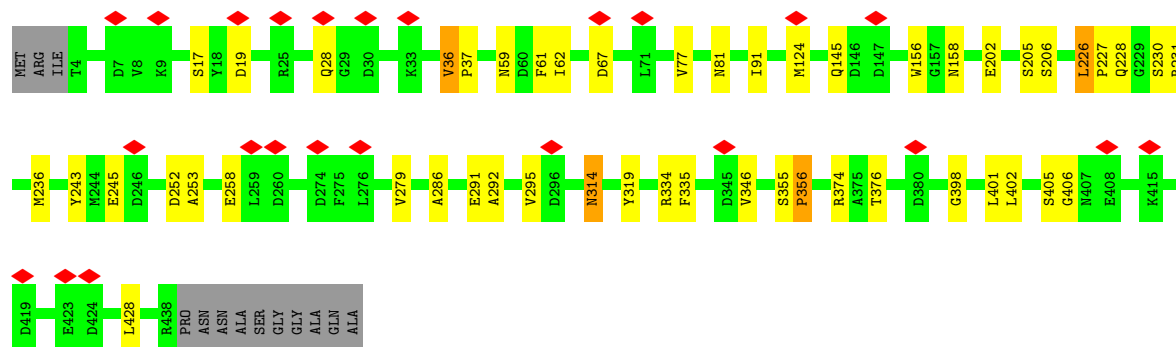
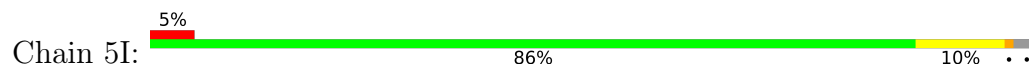
- Molecule 1: Major capsid protein

Chain 5H: 6% 85% 10% . .

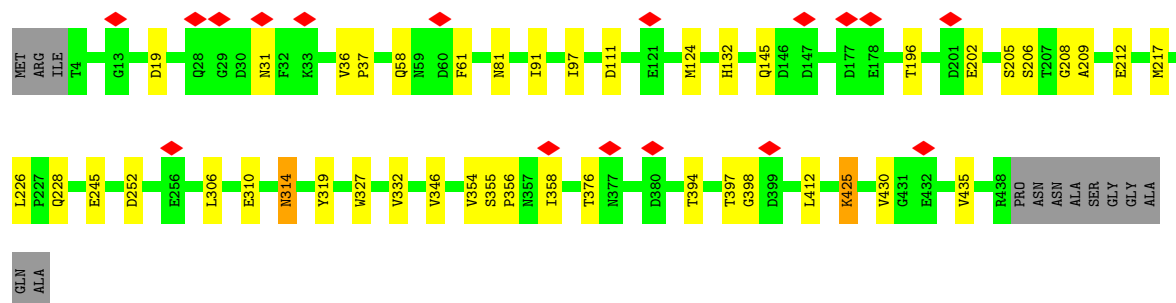
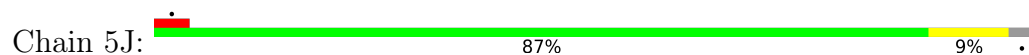




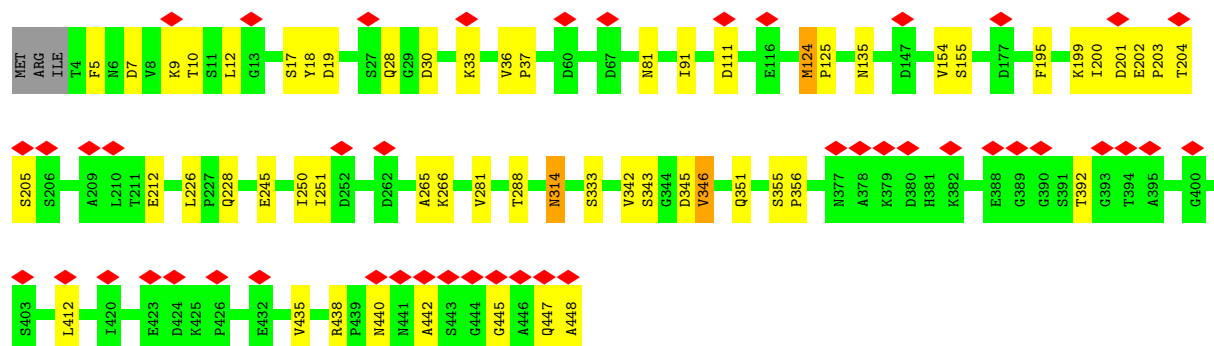
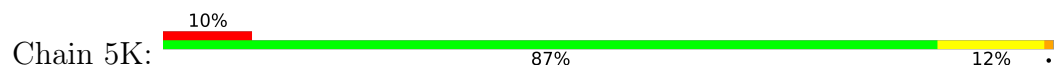
- Molecule 1: Major capsid protein



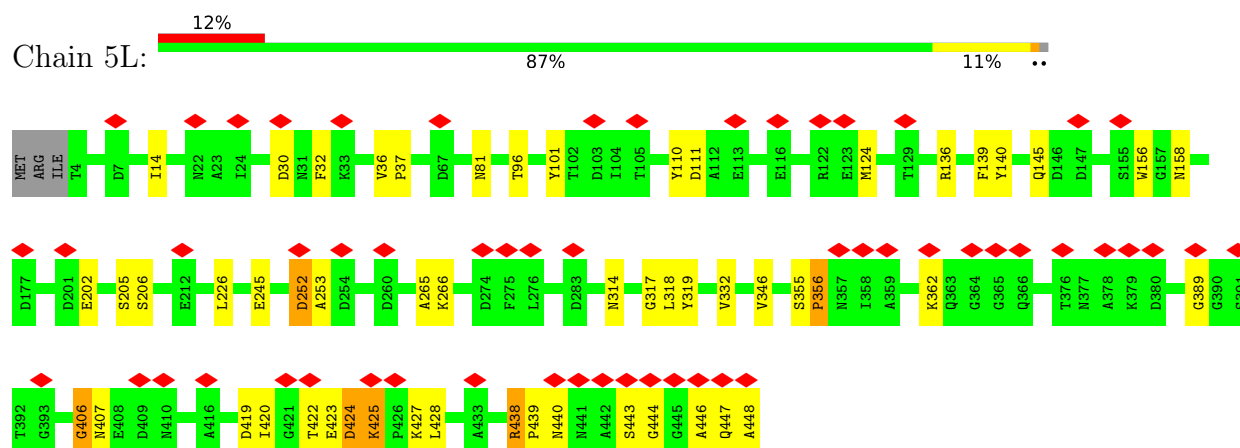
- Molecule 1: Major capsid protein



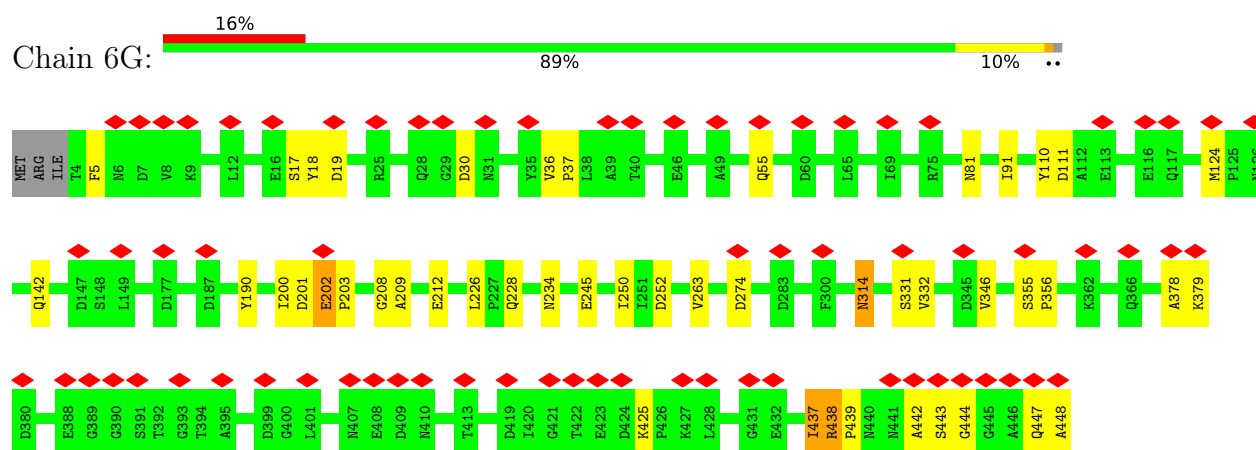
- Molecule 1: Major capsid protein



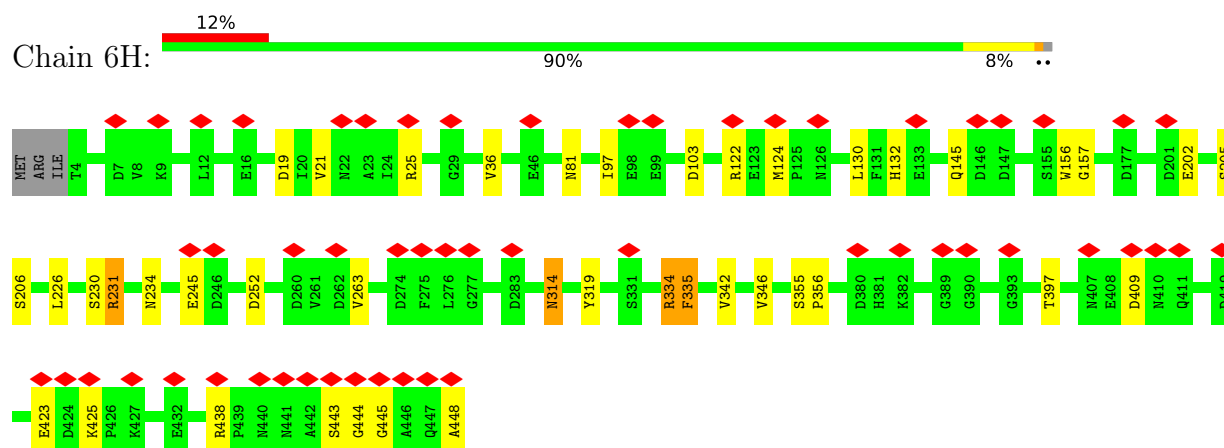
- Molecule 1: Major capsid protein



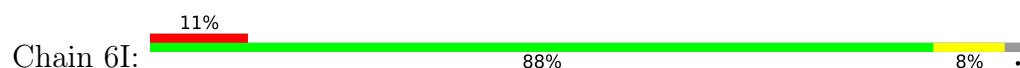
- Molecule 1: Major capsid protein

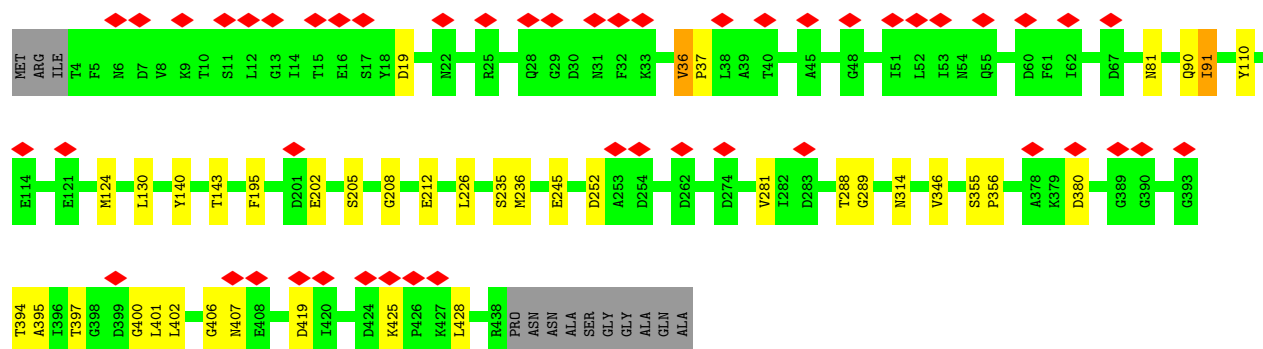


- Molecule 1: Major capsid protein

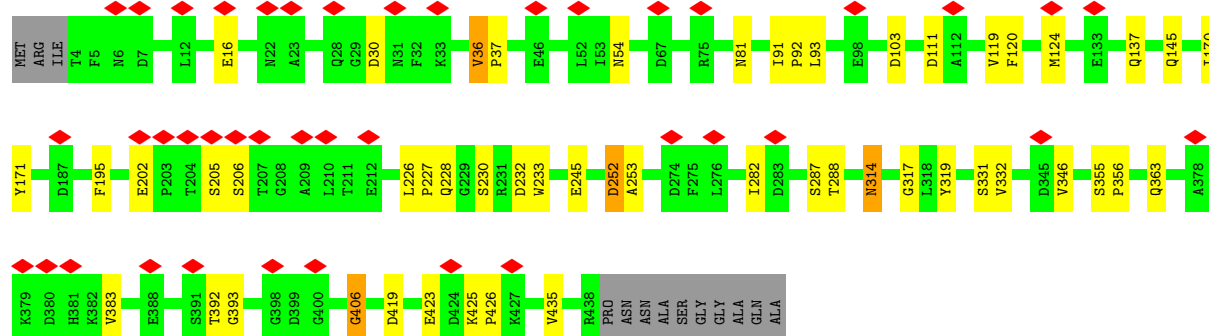
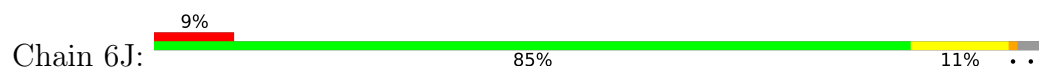


- Molecule 1: Major capsid protein

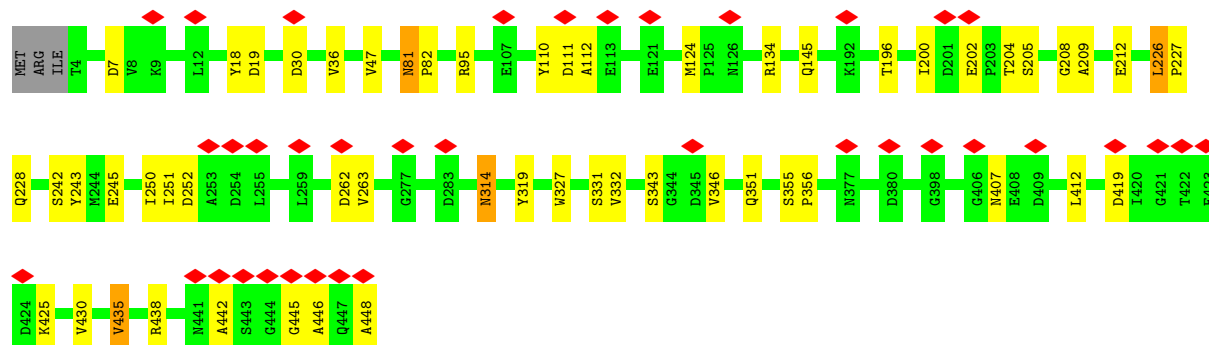
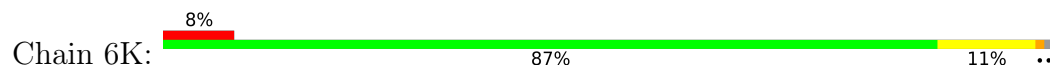




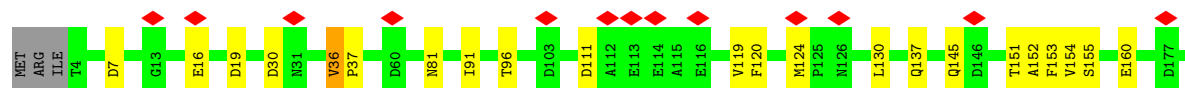
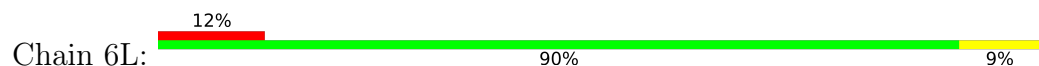
• Molecule 1: Major capsid protein

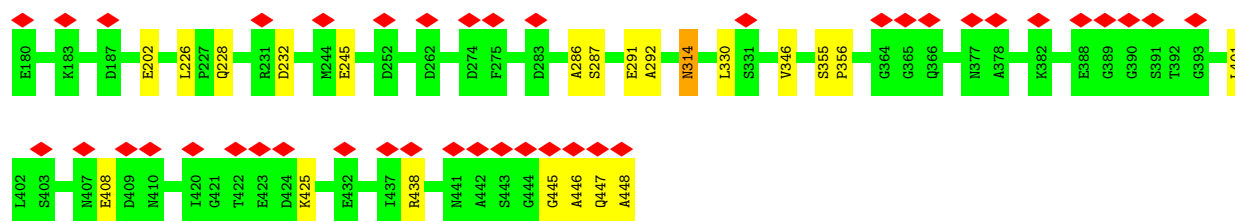


• Molecule 1: Major capsid protein

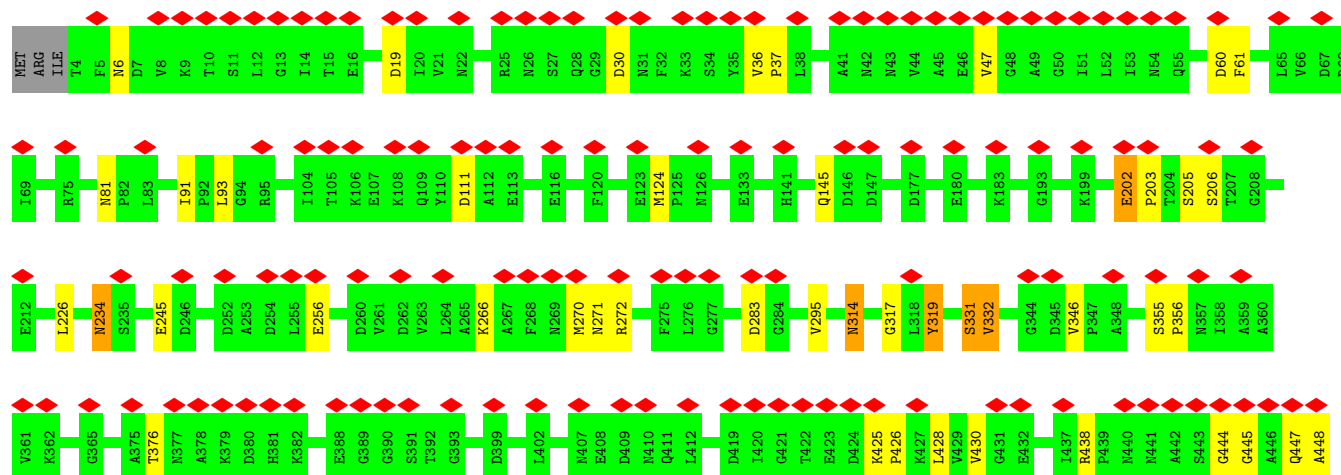
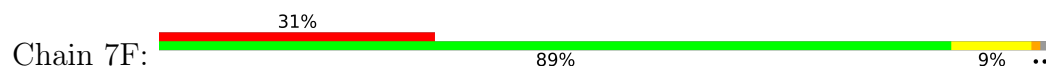


• Molecule 1: Major capsid protein

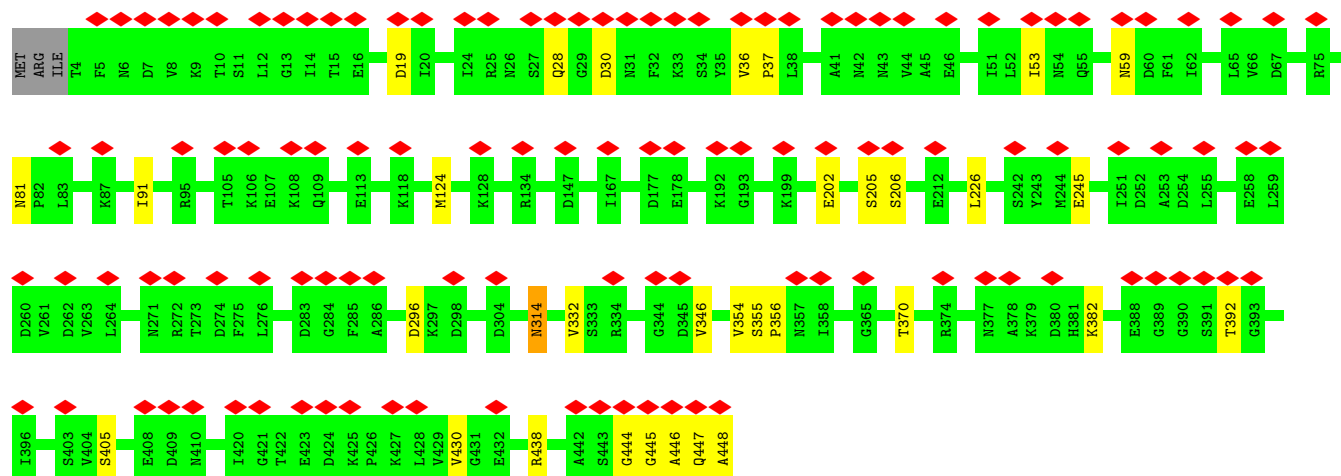




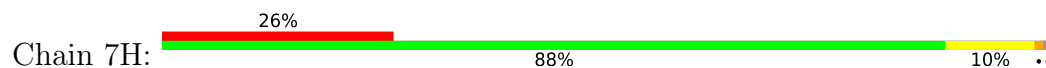
• Molecule 1: Major capsid protein

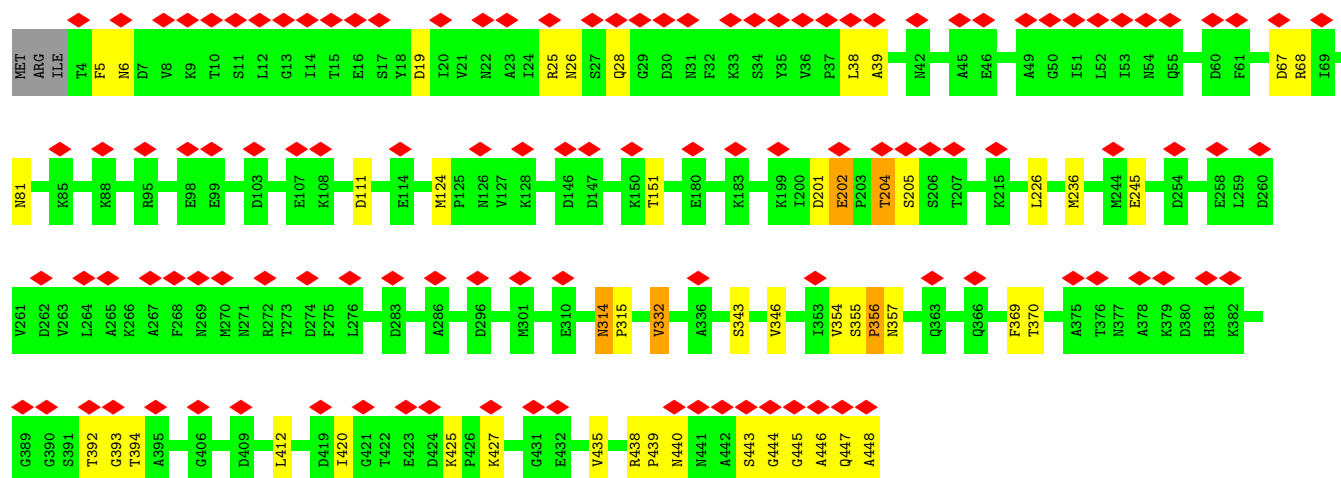


• Molecule 1: Major capsid protein

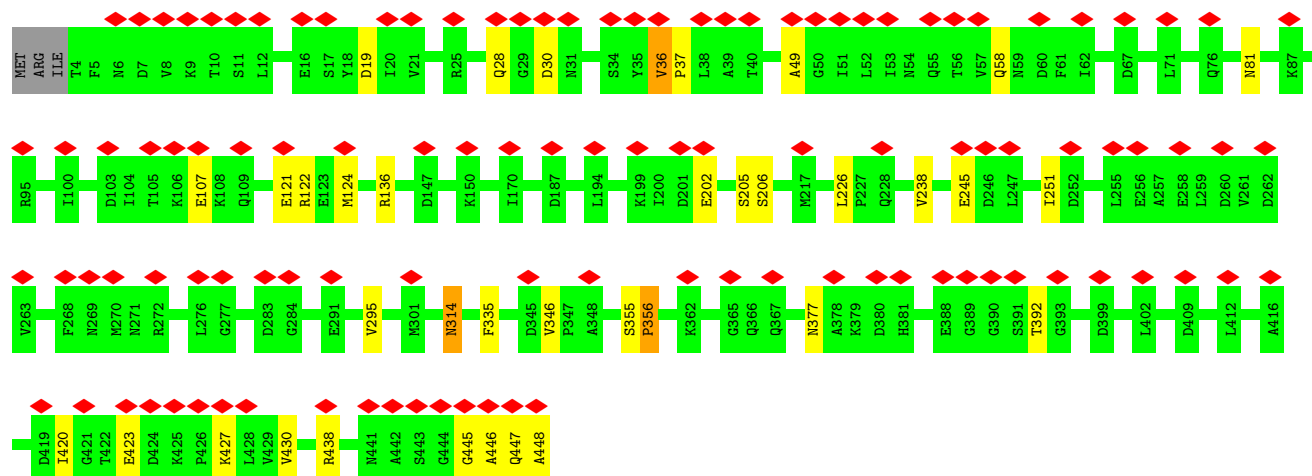


• Molecule 1: Major capsid protein

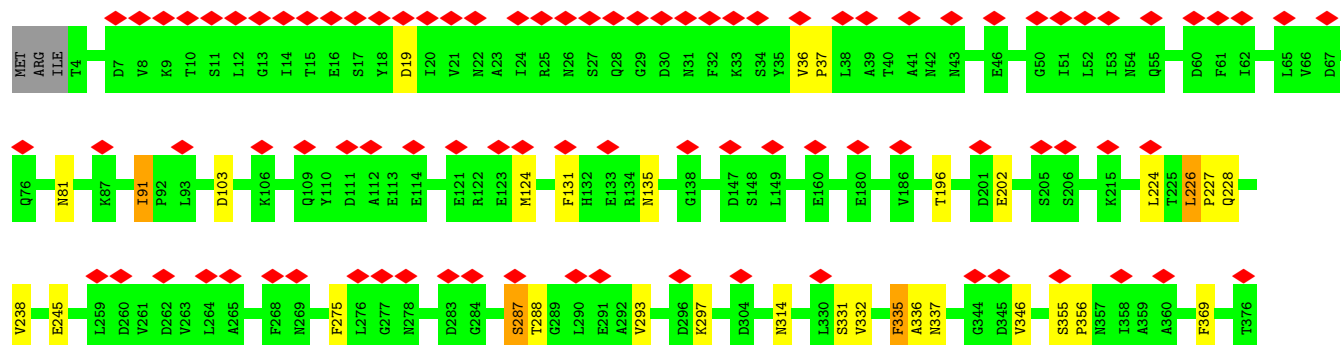
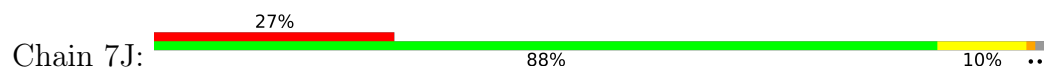




• Molecule 1: Major capsid protein

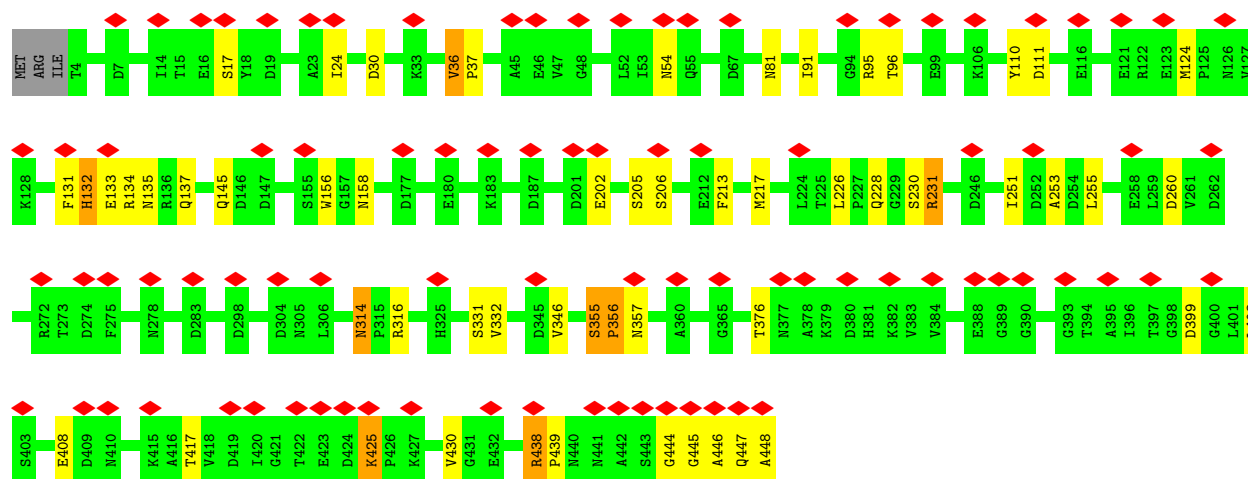
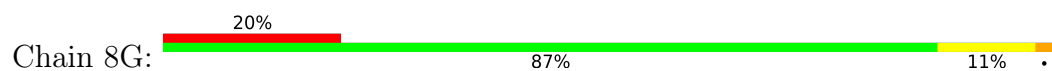


• Molecule 1: Major capsid protein

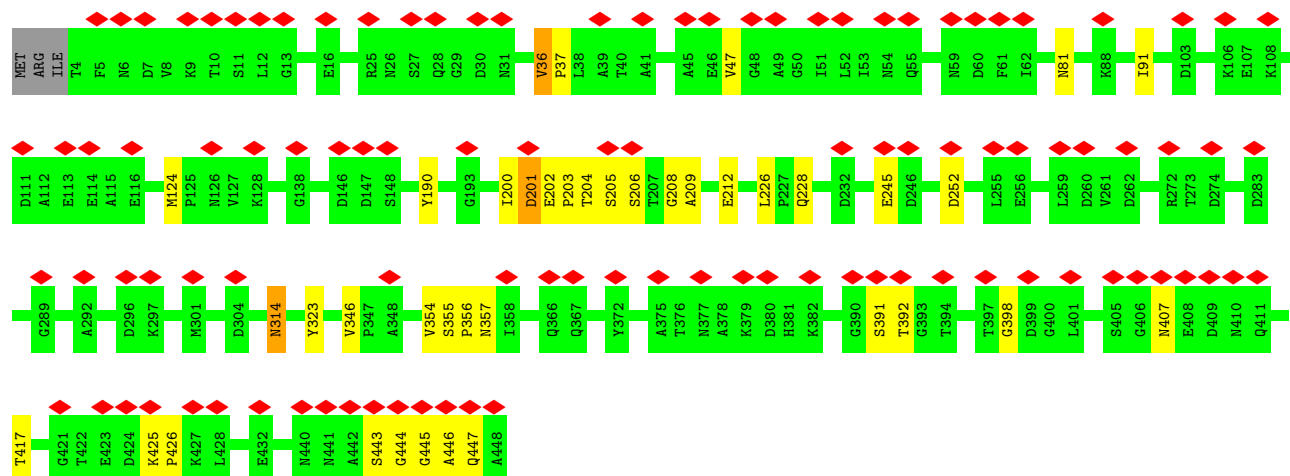
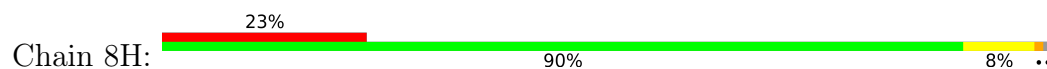




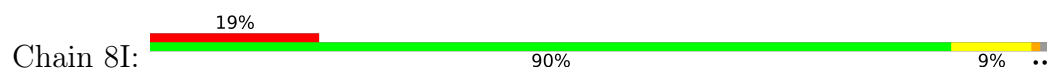
• Molecule 1: Major capsid protein

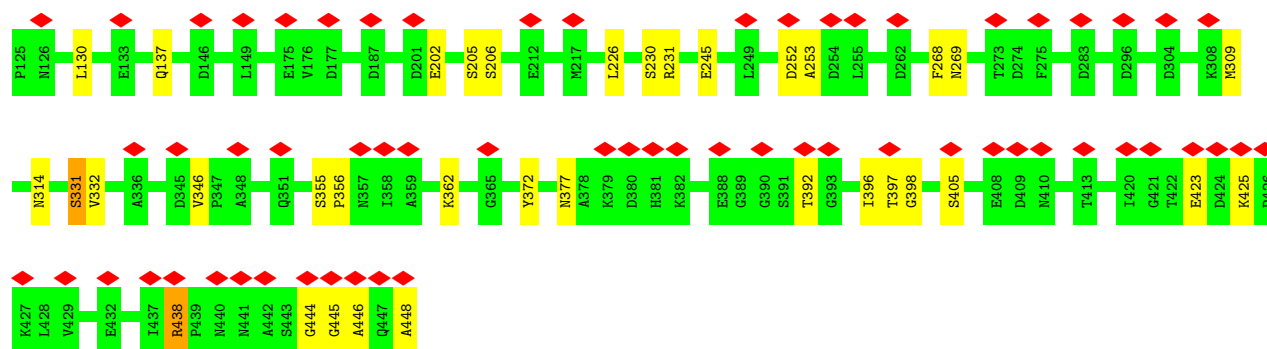


• Molecule 1: Major capsid protein

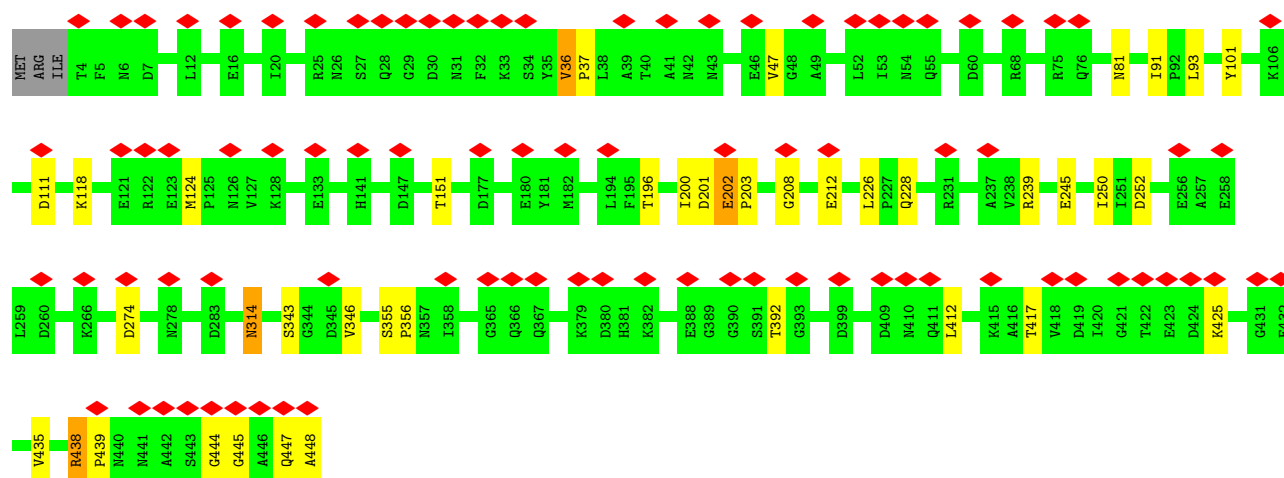
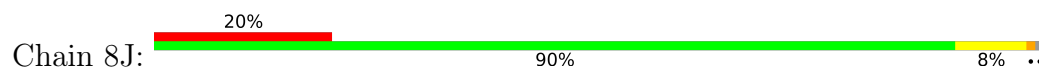


• Molecule 1: Major capsid protein

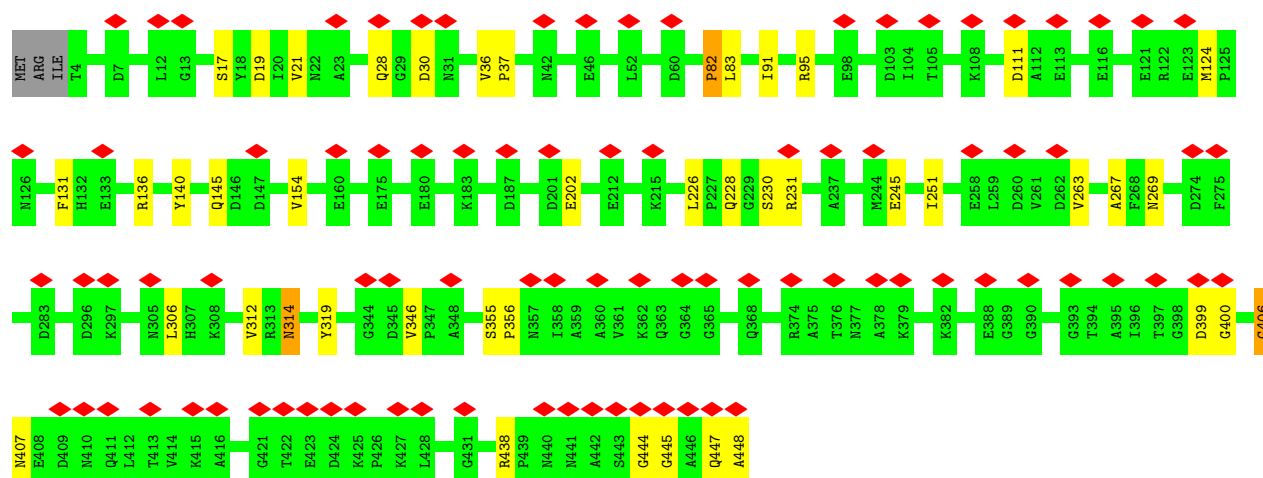
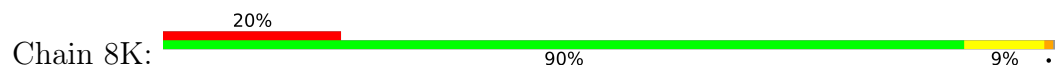




- Molecule 1: Major capsid protein

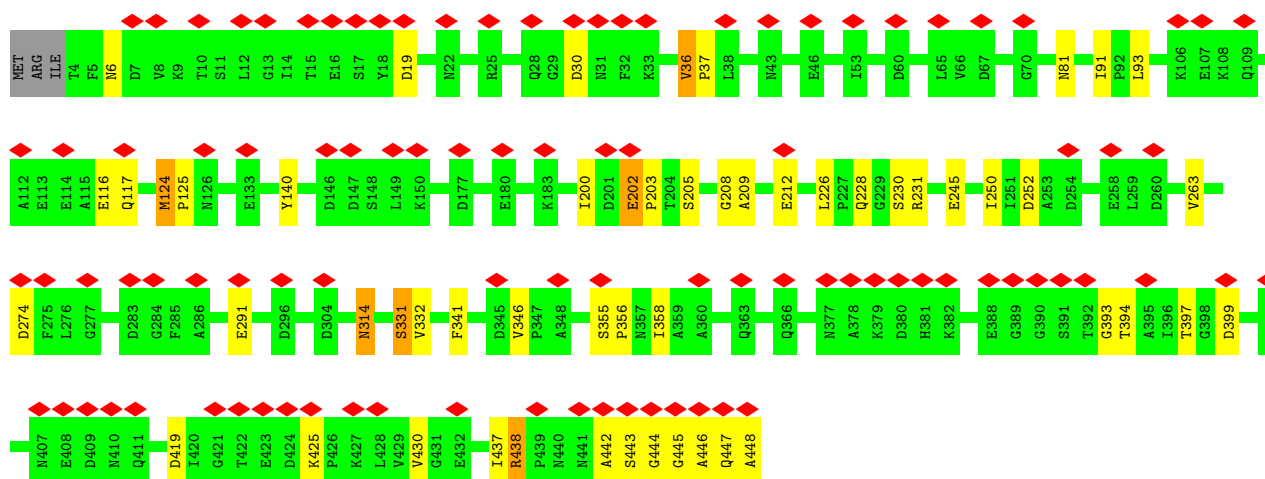


- Molecule 1: Major capsid protein



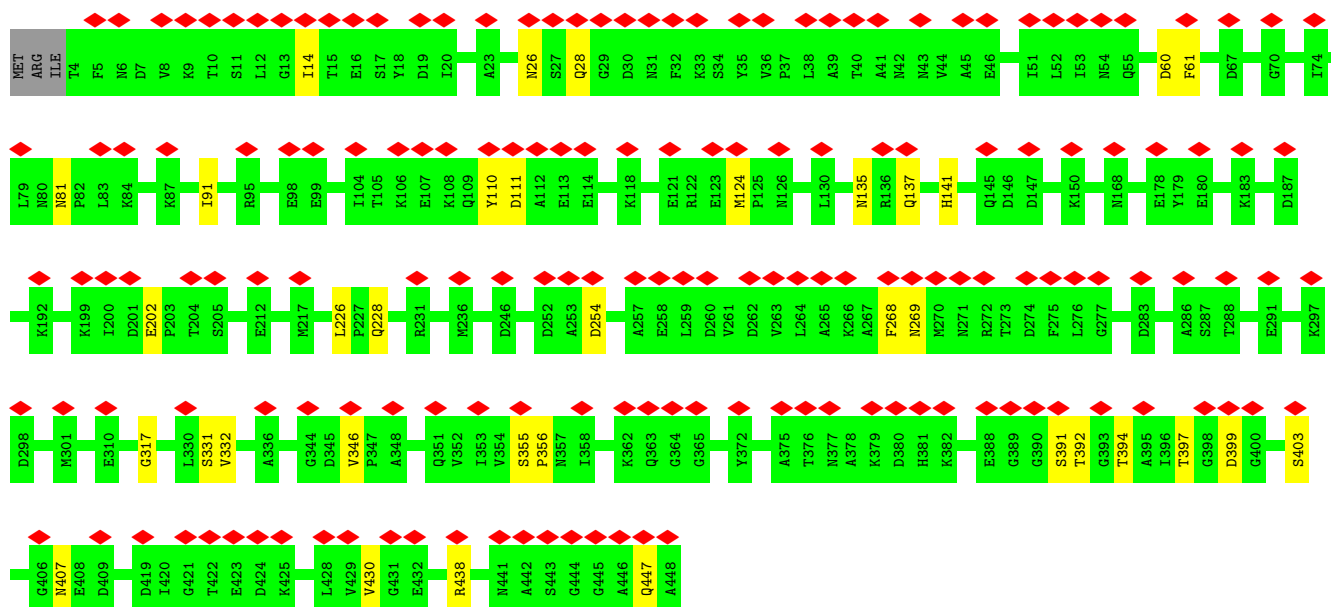
- Molecule 1: Major capsid protein

Chain 8L: 22% 87% 11% ..



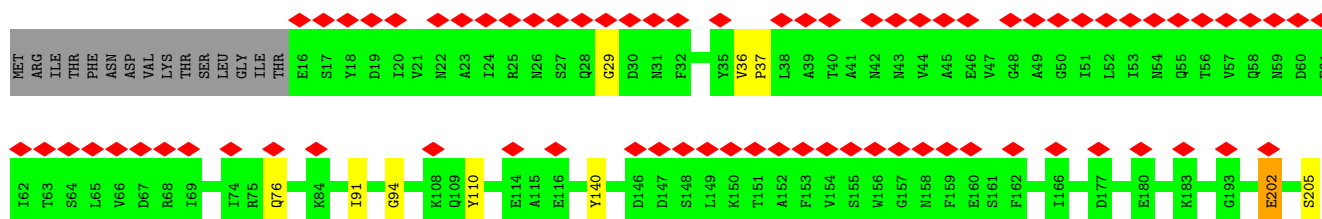
• Molecule 1: Major capsid protein

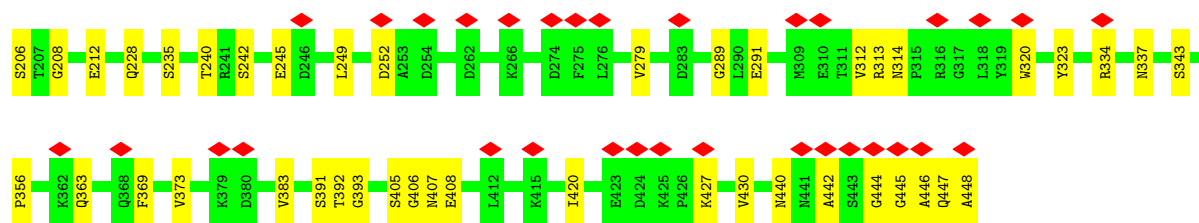
Chain 9B: 37% 92% 8% .



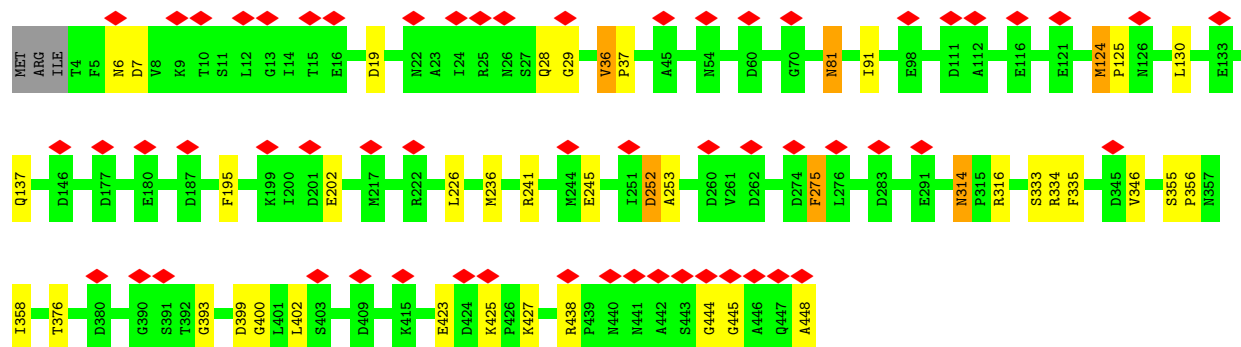
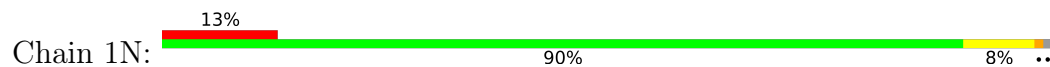
• Molecule 1: Major capsid protein

Chain 1M: 24% 85% 12% .

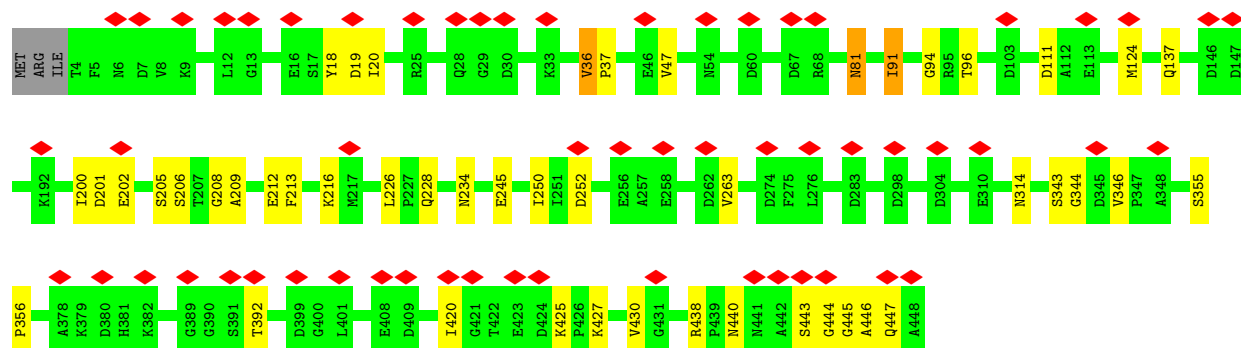
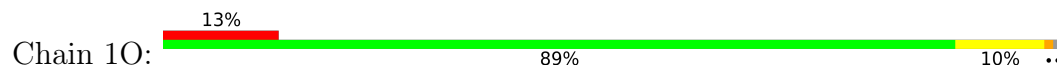




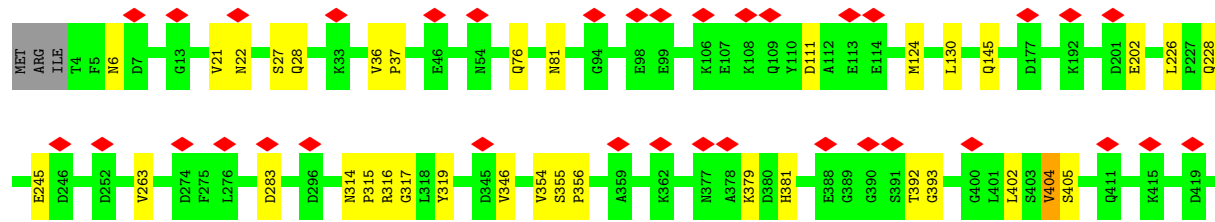
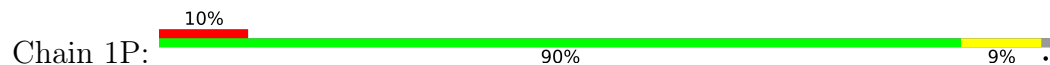
• Molecule 1: Major capsid protein

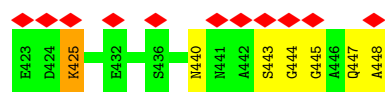


• Molecule 1: Major capsid protein

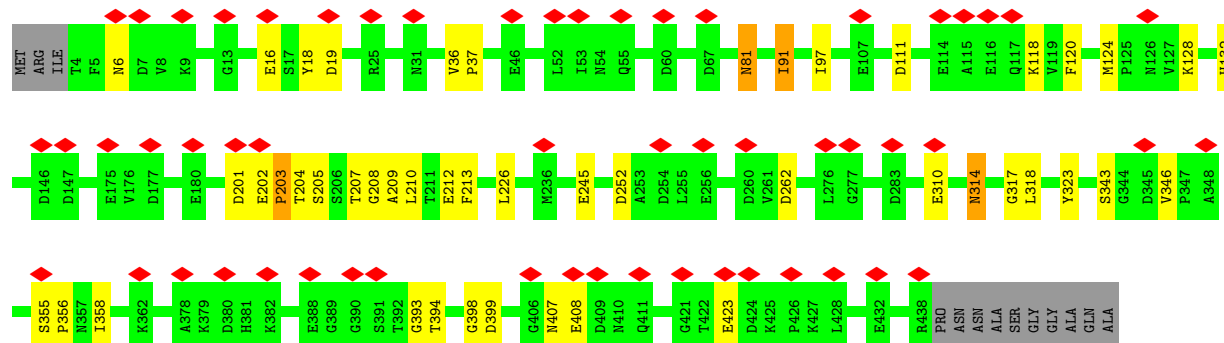
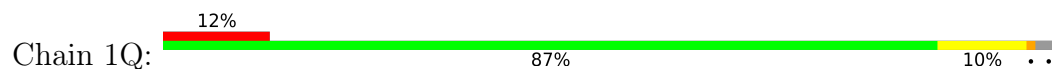


• Molecule 1: Major capsid protein

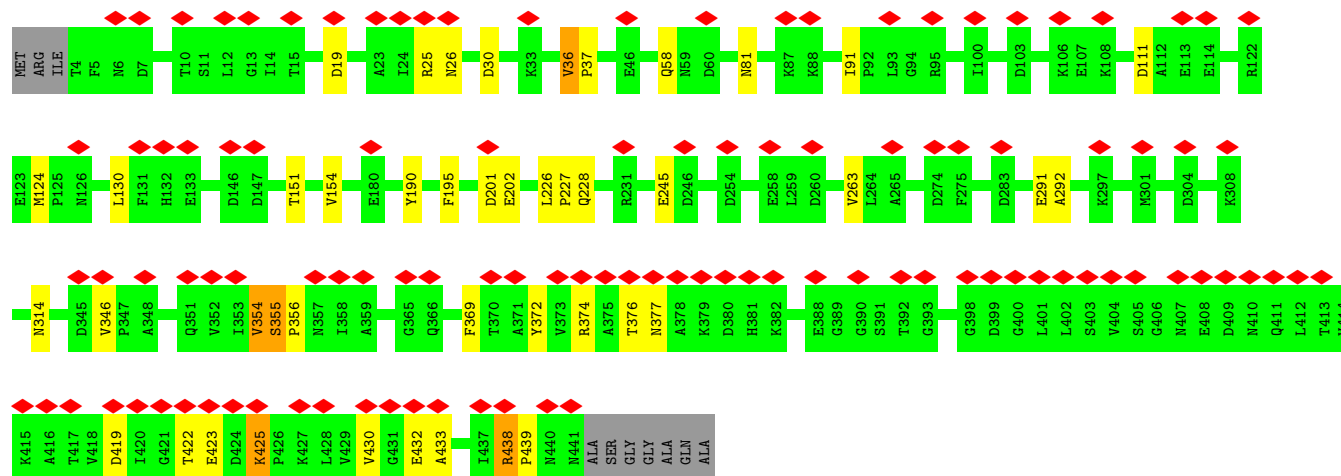
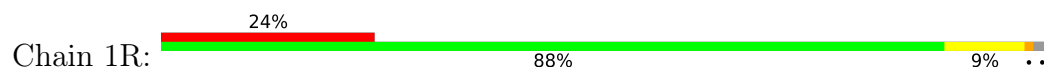




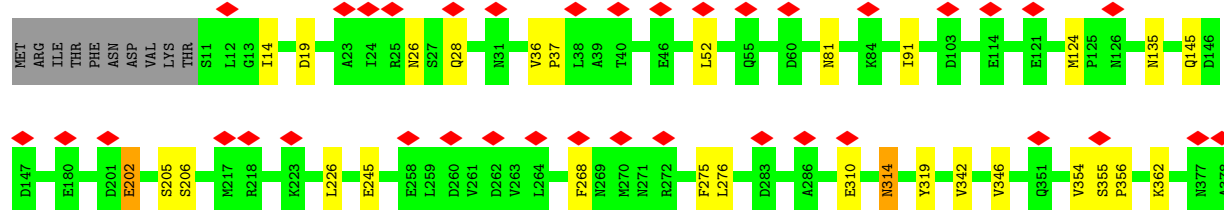
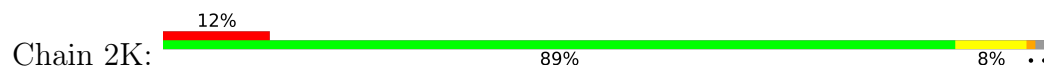
• Molecule 1: Major capsid protein

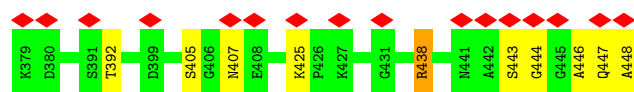


• Molecule 1: Major capsid protein



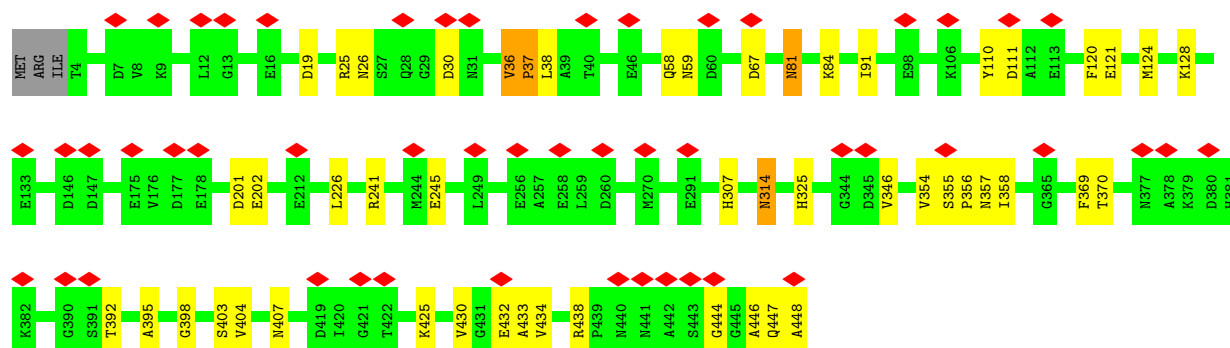
• Molecule 1: Major capsid protein





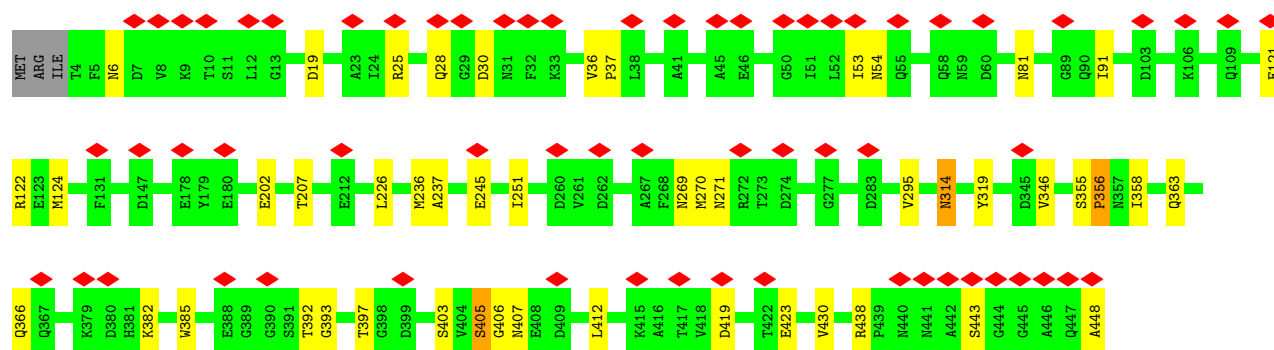
- Molecule 1: Major capsid protein

Chain 2L: 11% 88% 10% ..



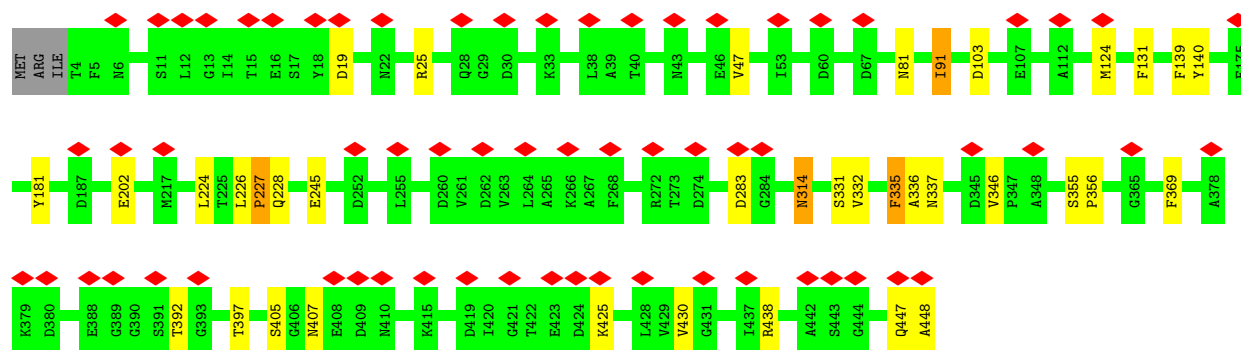
- Molecule 1: Major capsid protein

Chain 2M: 14% 88% 10% ..



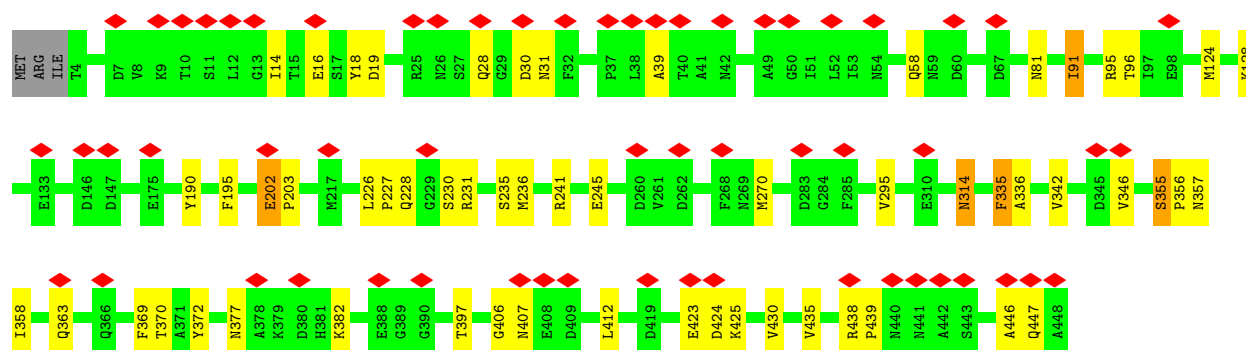
- Molecule 1: Major capsid protein

Chain 2N: 14% 91% 7% ..



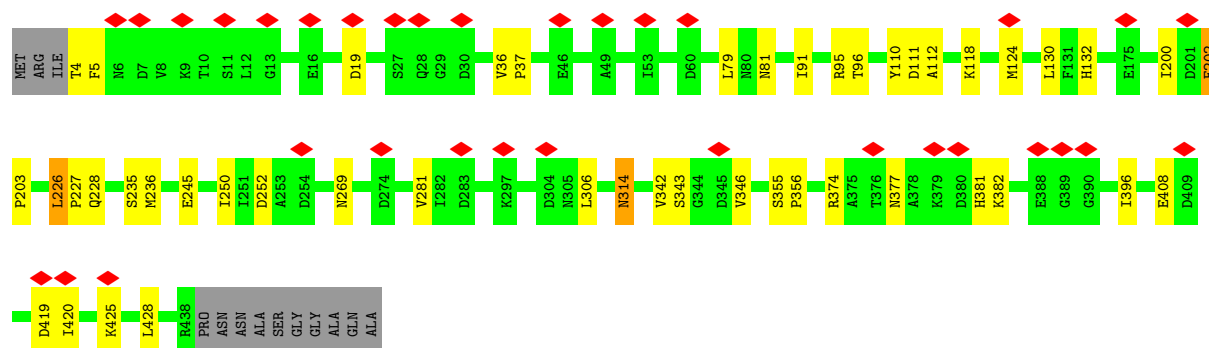
- Molecule 1: Major capsid protein

Chain 2O: 



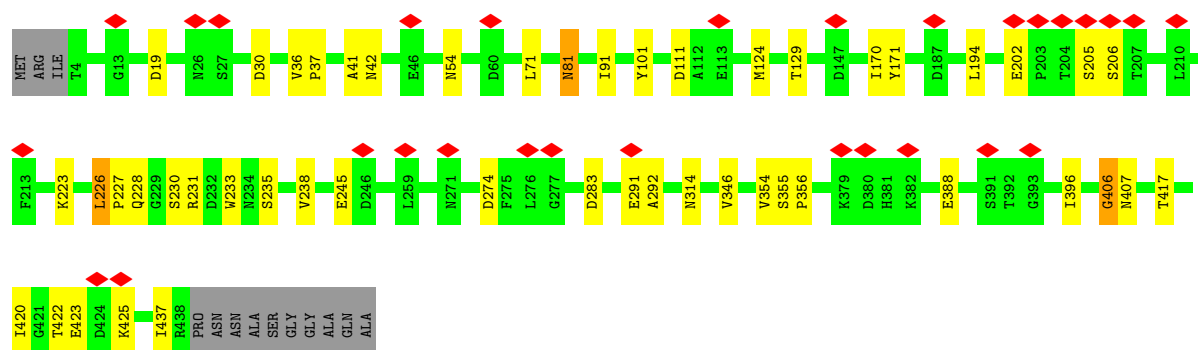
• Molecule 1: Major capsid protein

Chain 3M: 



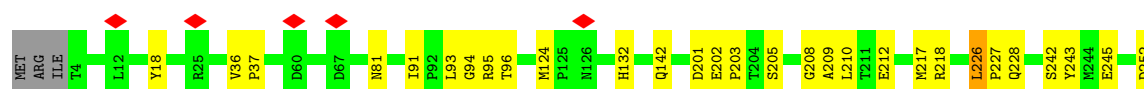
• Molecule 1: Major capsid protein

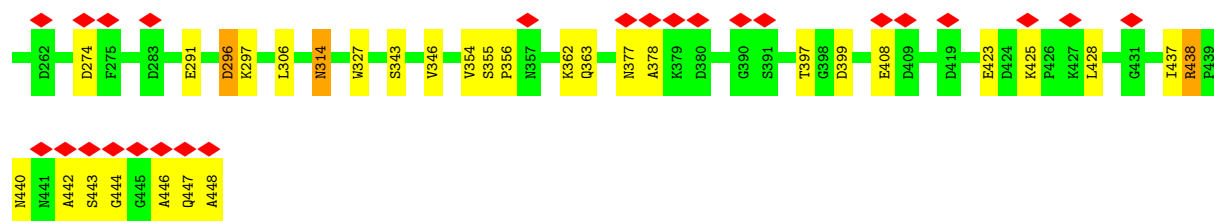
Chain 3N: 



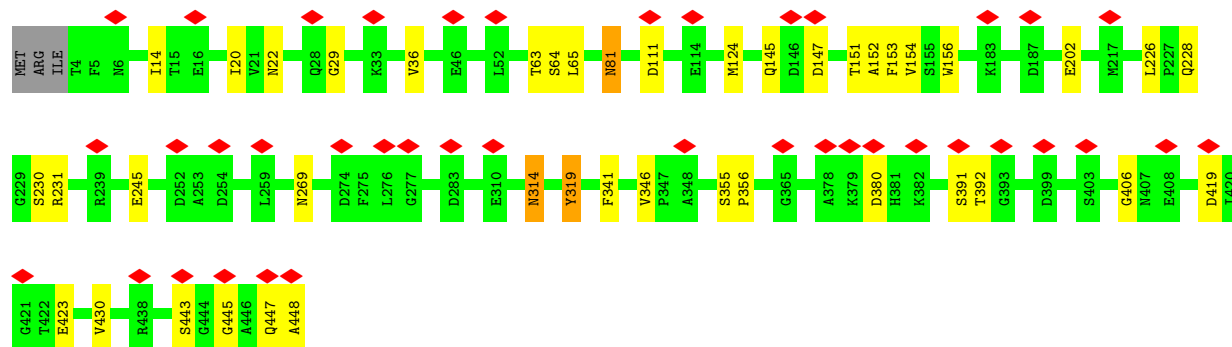
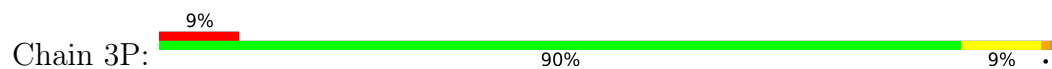
• Molecule 1: Major capsid protein

Chain 3O: 

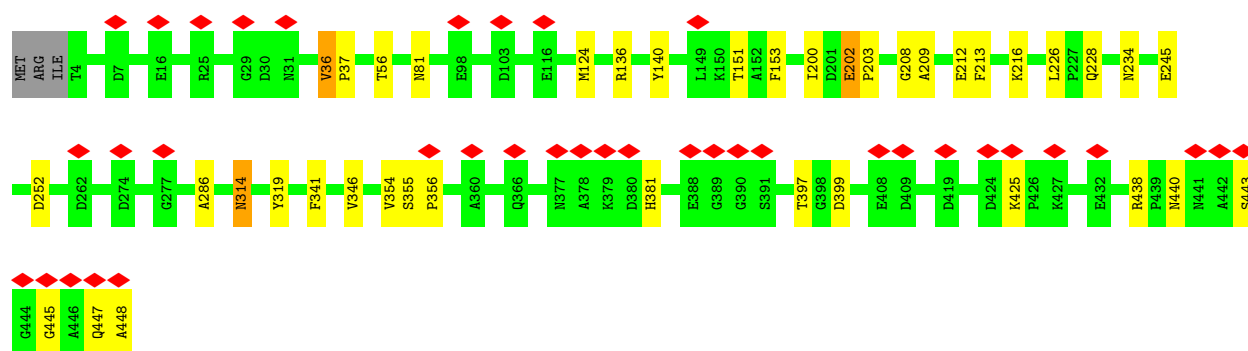
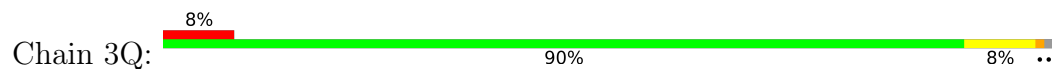




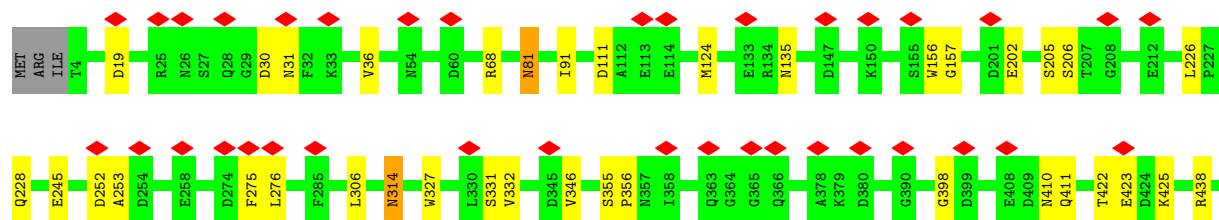
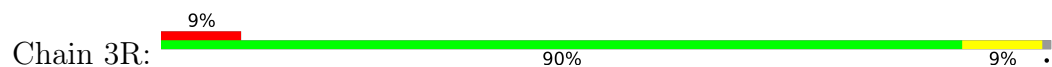
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

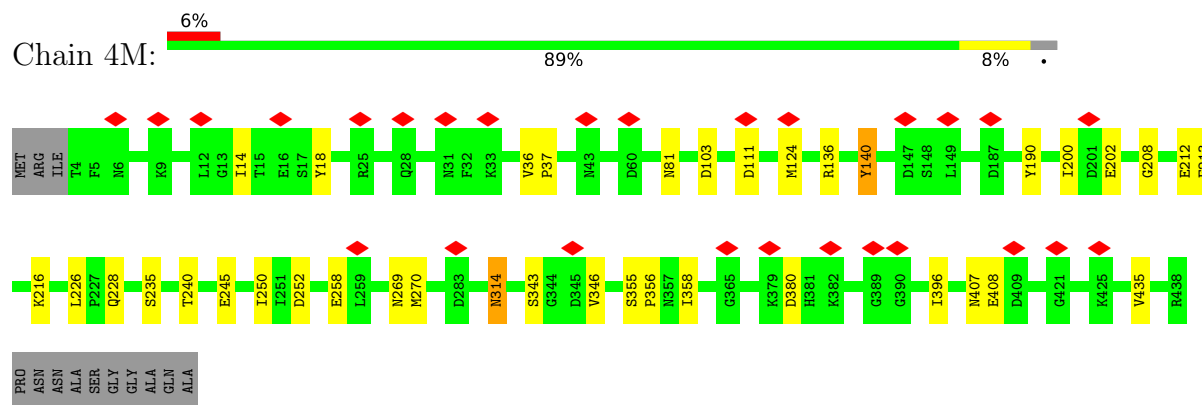


- Molecule 1: Major capsid protein

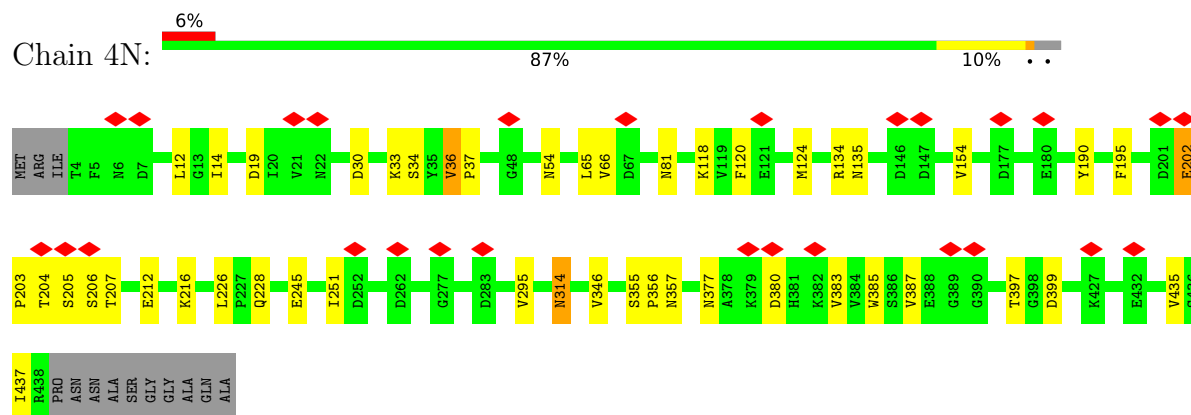




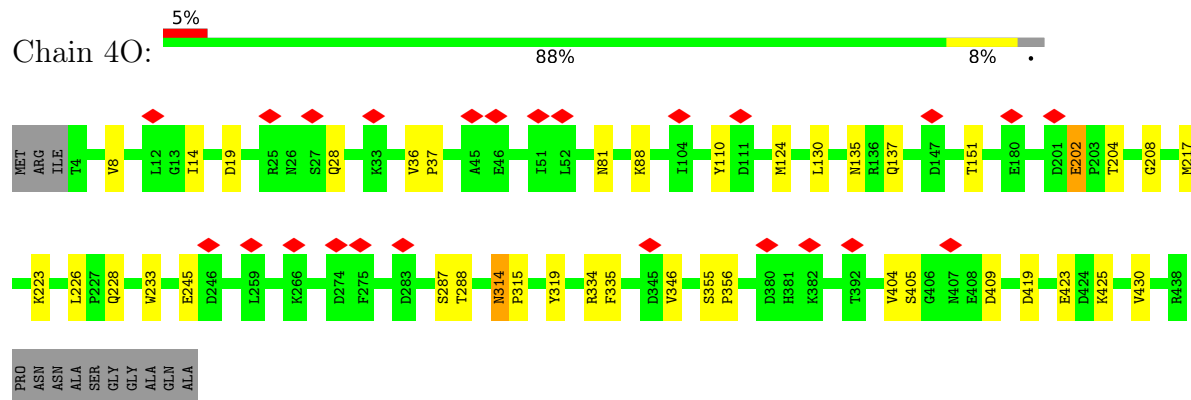
- Molecule 1: Major capsid protein



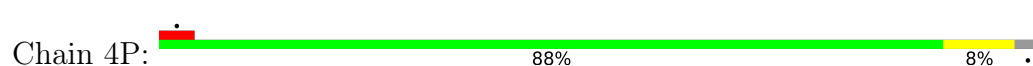
- Molecule 1: Major capsid protein

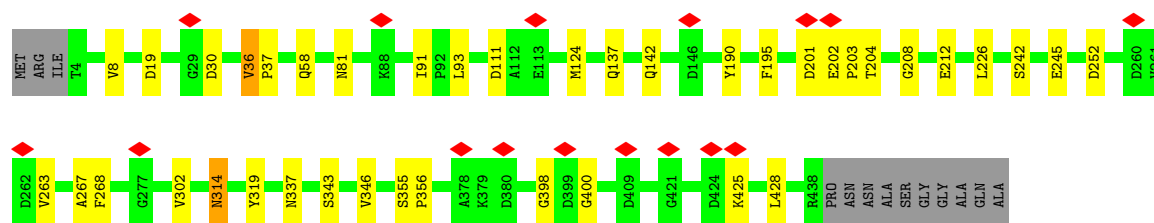


- Molecule 1: Major capsid protein

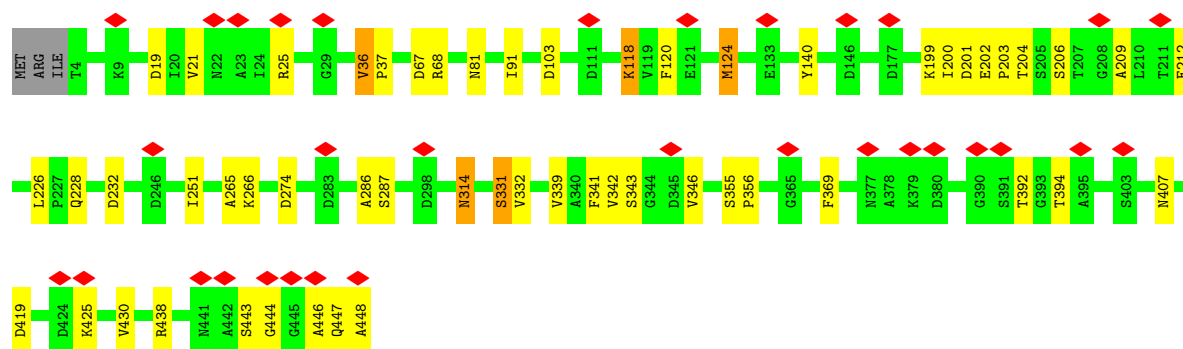
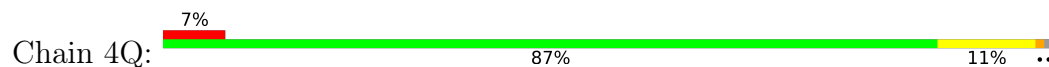


- Molecule 1: Major capsid protein

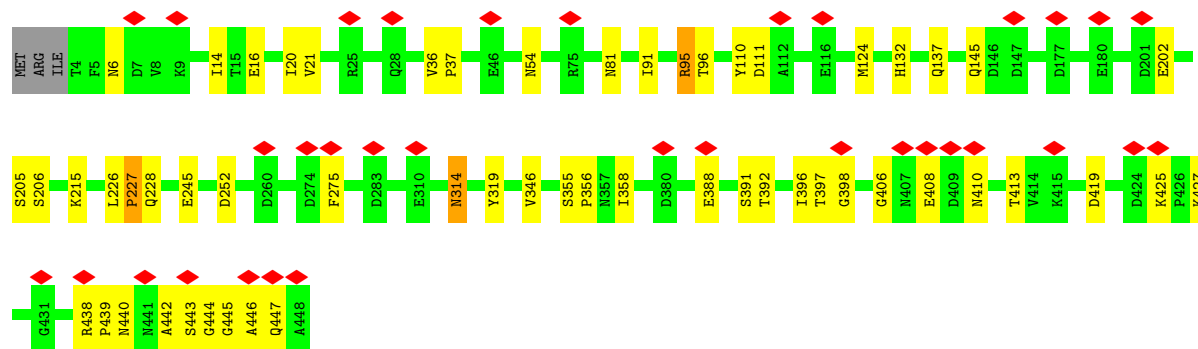
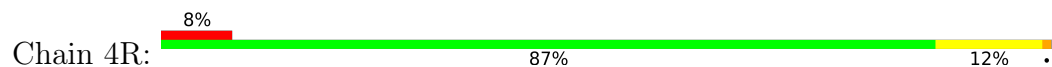




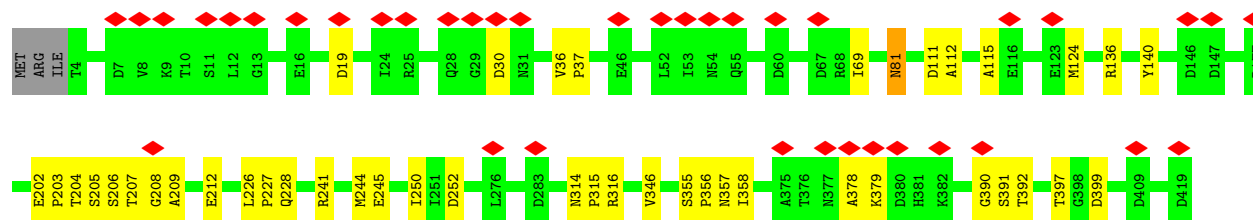
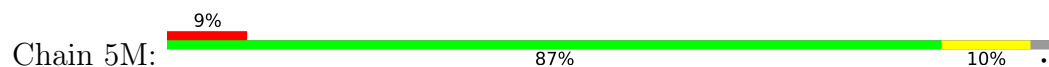
• Molecule 1: Major capsid protein

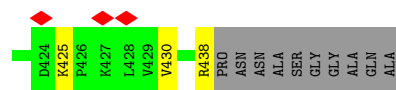


• Molecule 1: Major capsid protein

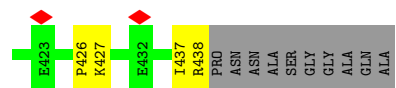
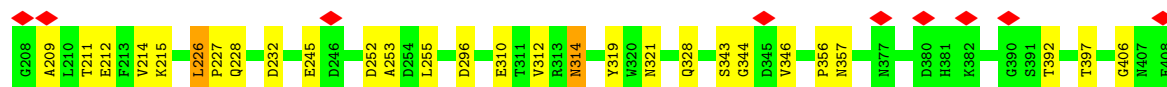
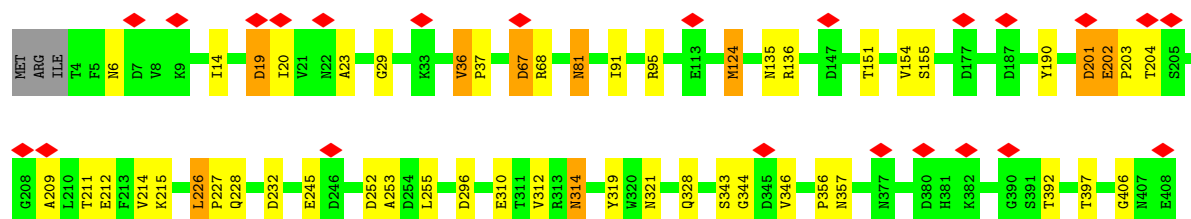
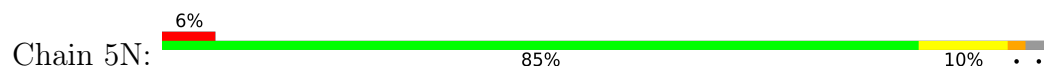


• Molecule 1: Major capsid protein

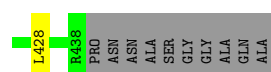
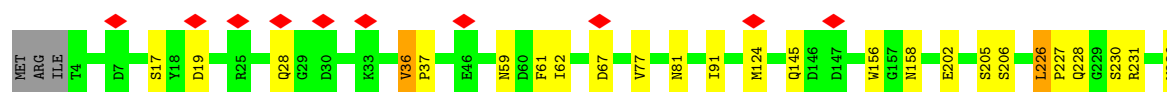
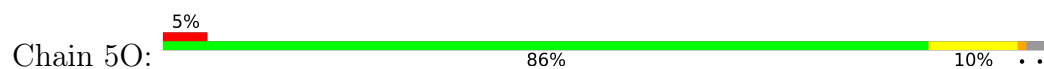




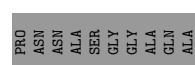
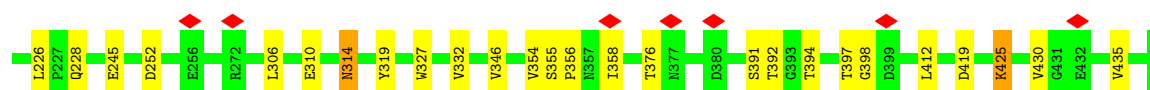
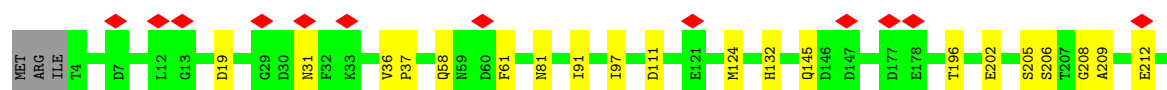
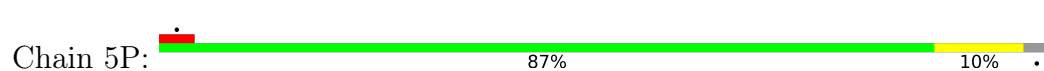
- Molecule 1: Major capsid protein



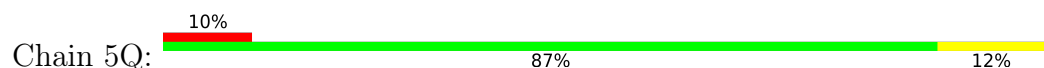
- Molecule 1: Major capsid protein

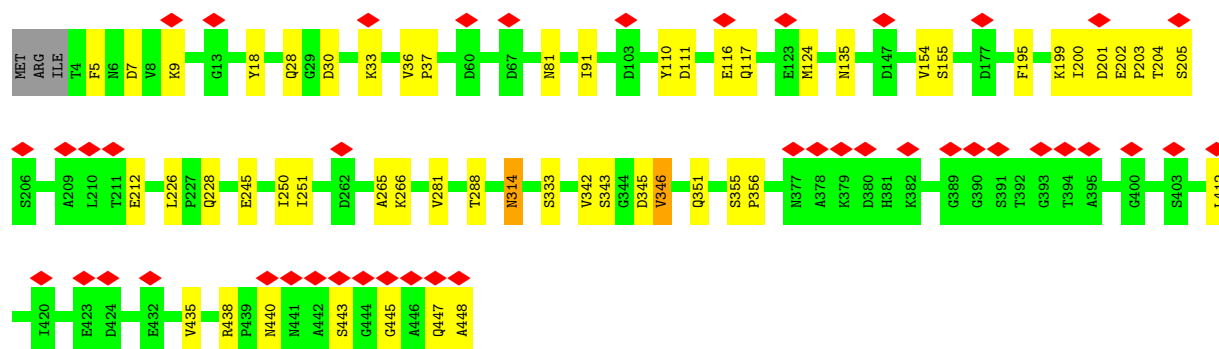


- Molecule 1: Major capsid protein

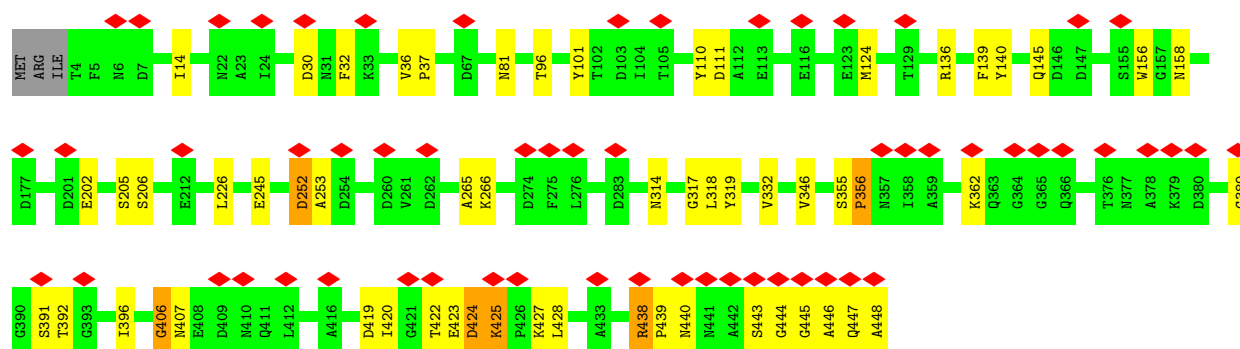
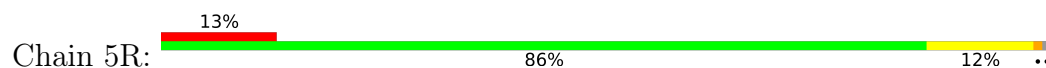


- Molecule 1: Major capsid protein

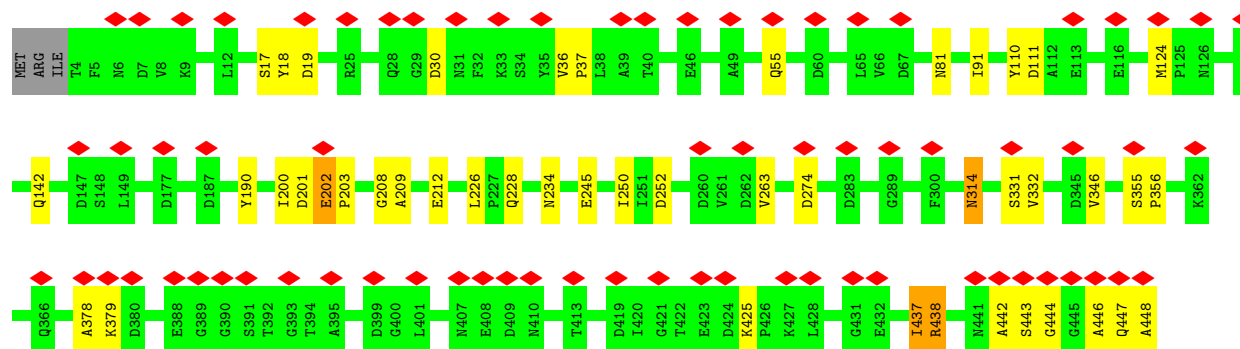
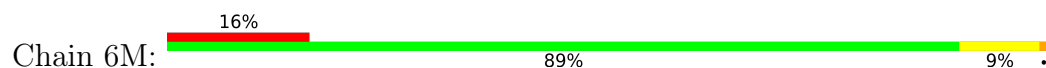




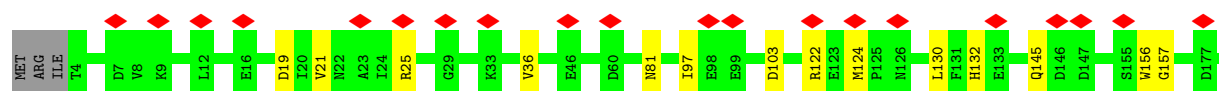
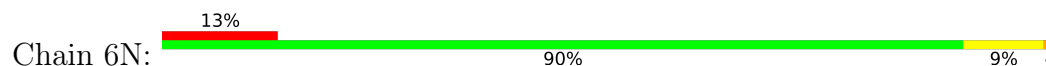
- Molecule 1: Major capsid protein

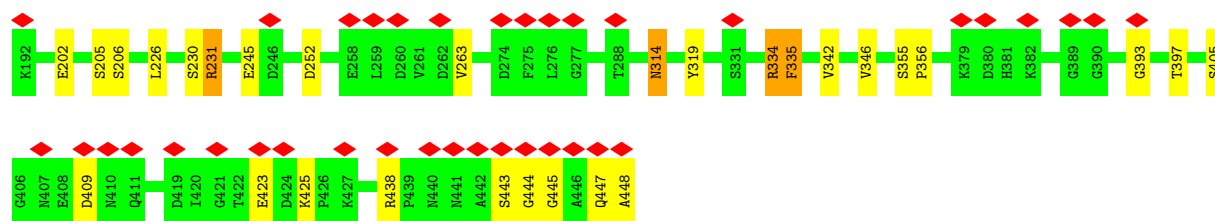


- Molecule 1: Major capsid protein

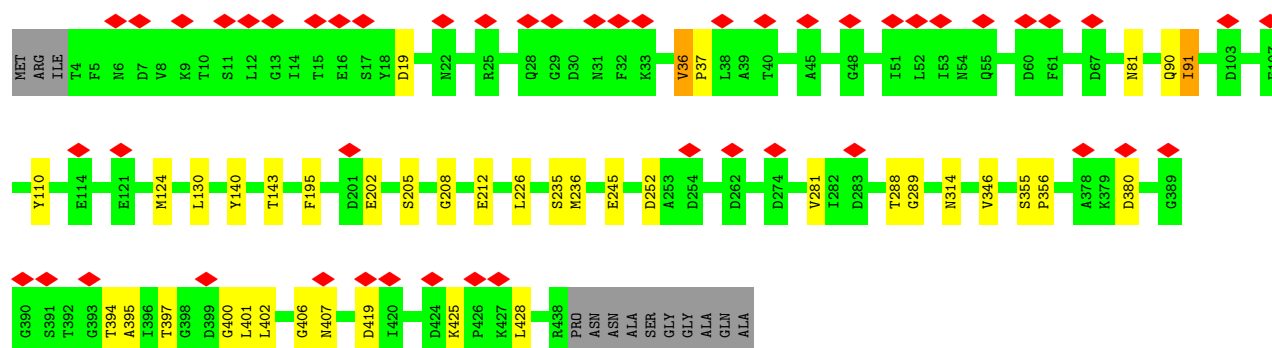
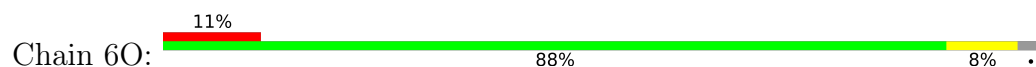


- Molecule 1: Major capsid protein

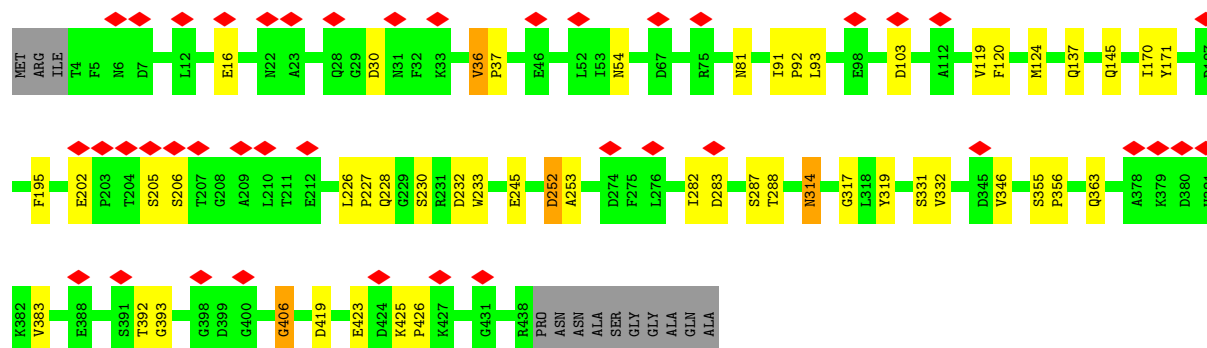
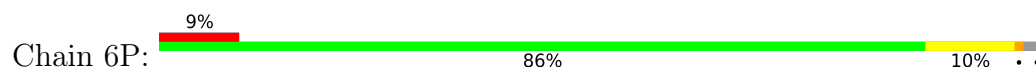




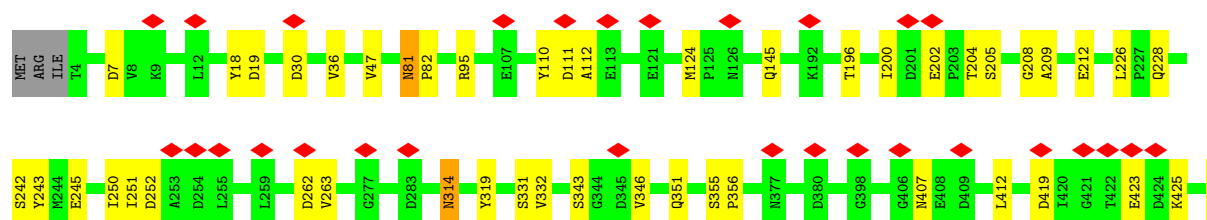
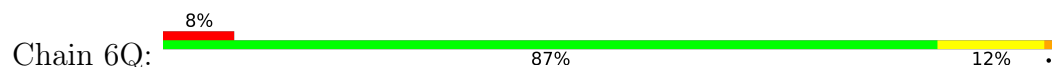
• Molecule 1: Major capsid protein



• Molecule 1: Major capsid protein

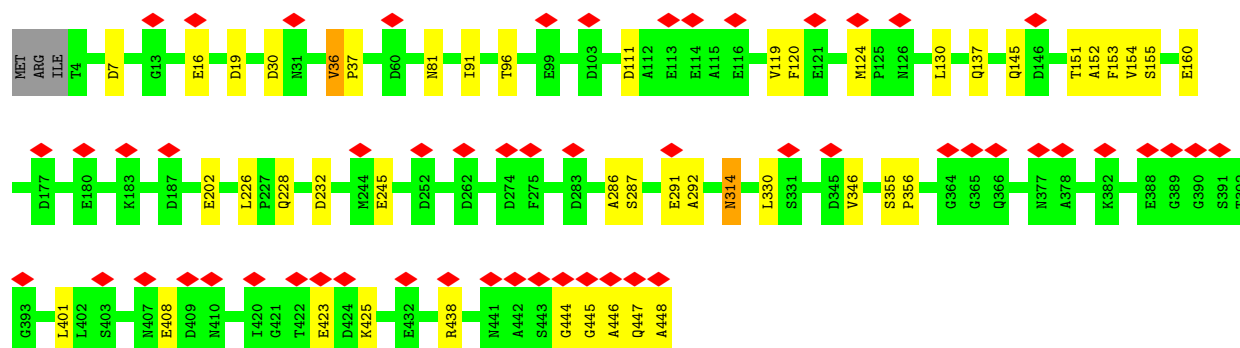
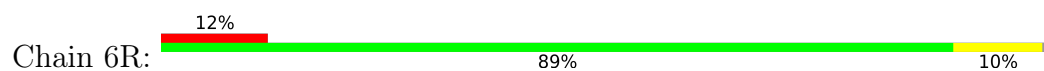


• Molecule 1: Major capsid protein

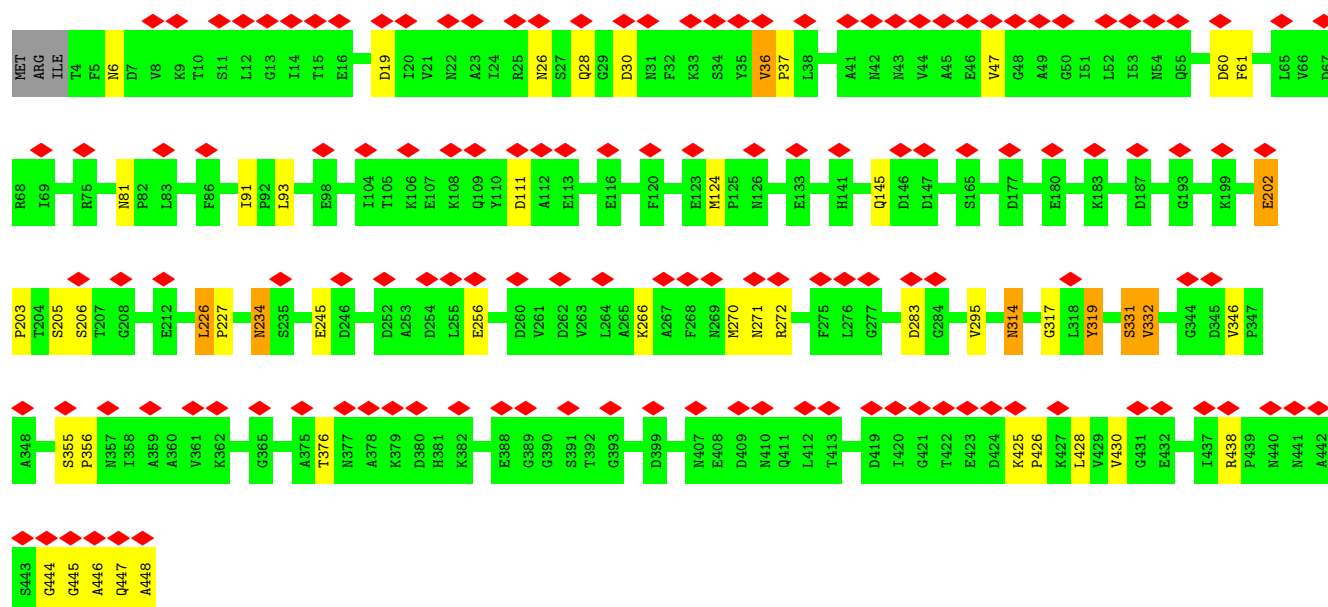
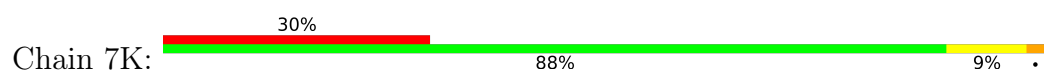




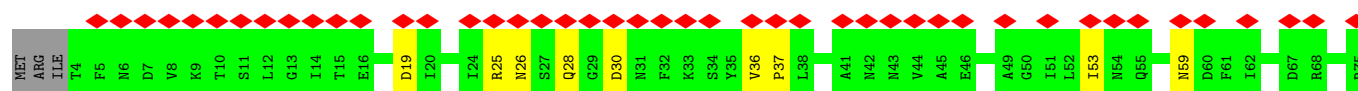
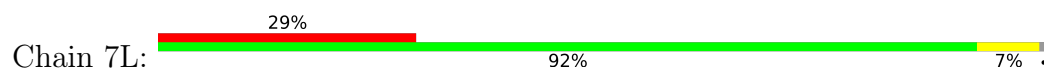
• Molecule 1: Major capsid protein

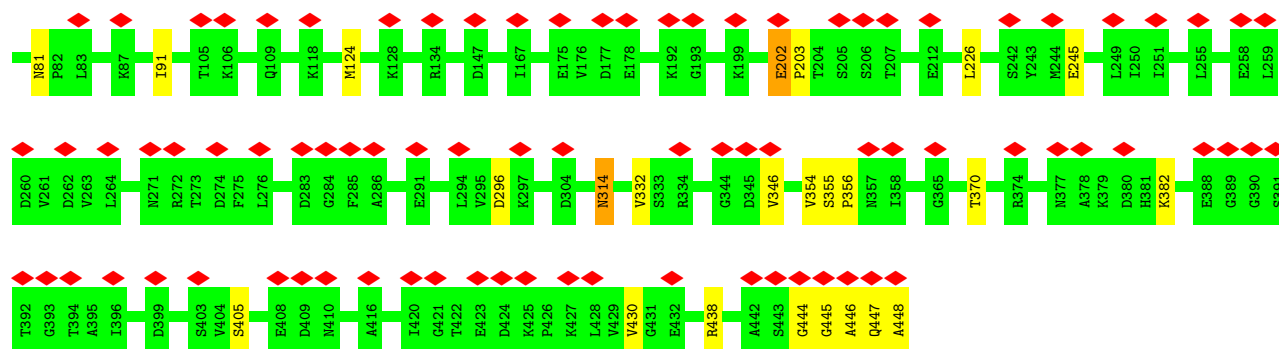


• Molecule 1: Major capsid protein



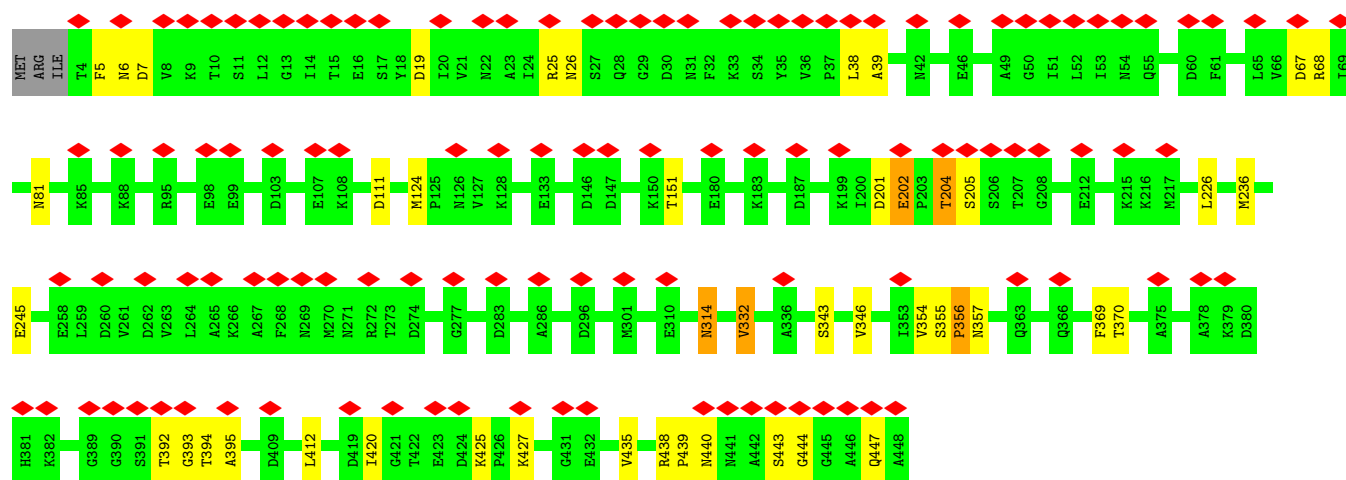
• Molecule 1: Major capsid protein





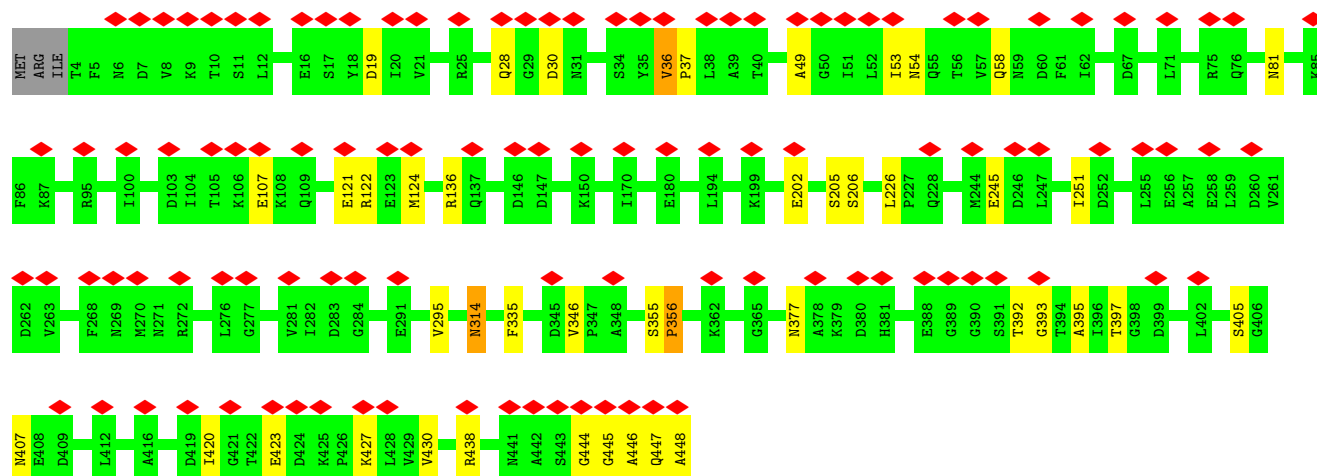
- Molecule 1: Major capsid protein

Chain 7M: 26% 89% 9% ..

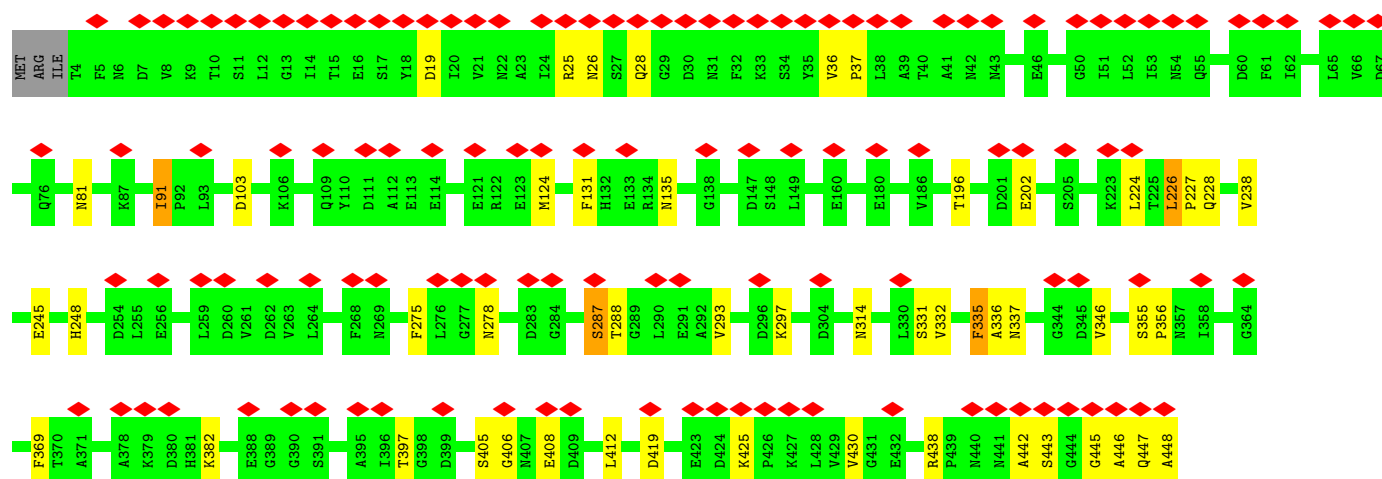
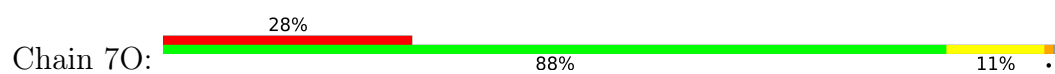


- Molecule 1: Major capsid protein

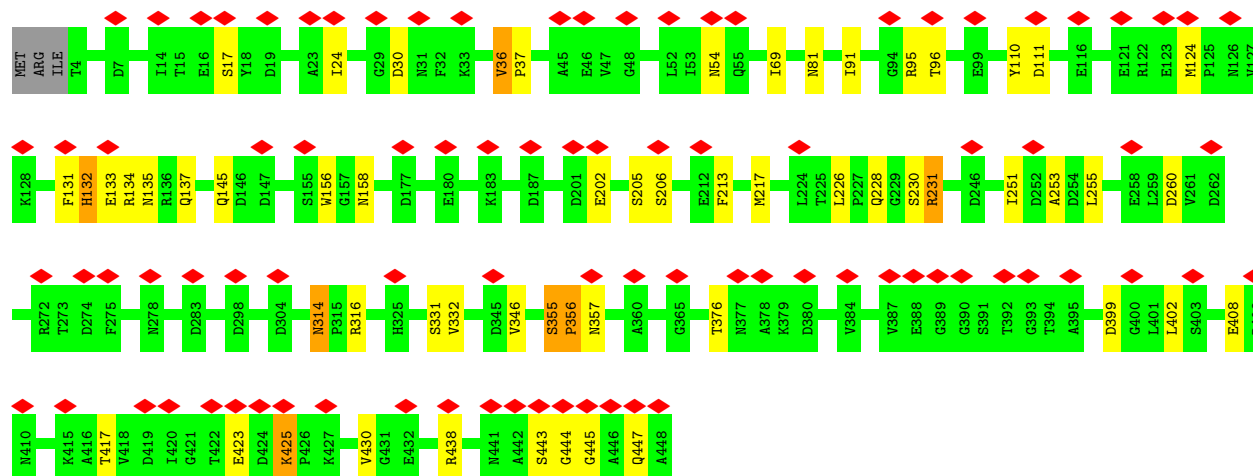
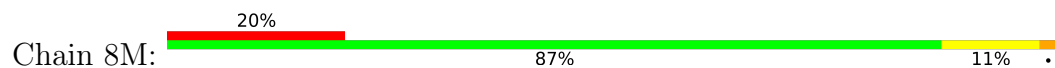
Chain 7N: 25% 90% 9% ..



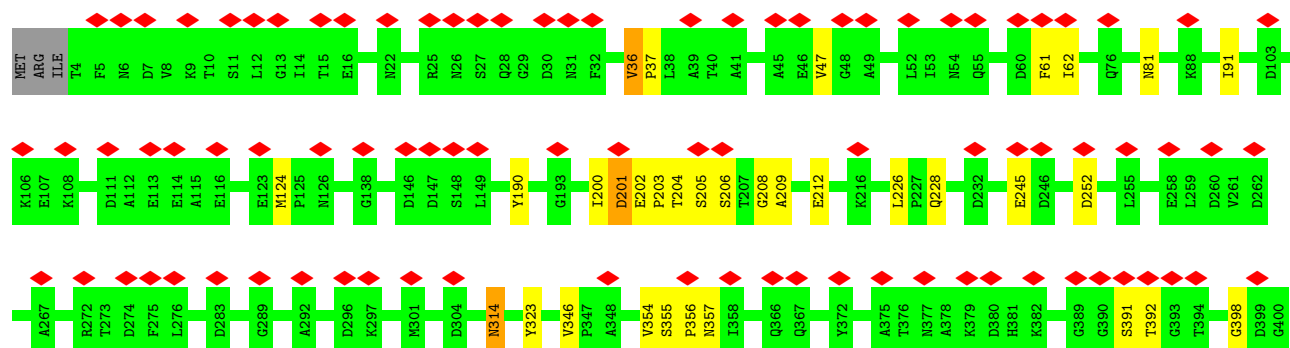
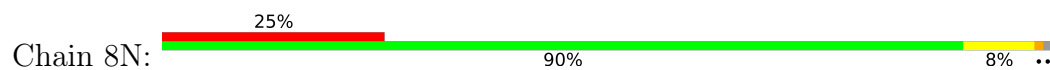
- Molecule 1: Major capsid protein

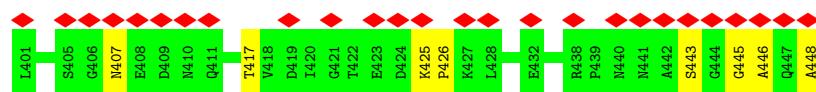


• Molecule 1: Major capsid protein

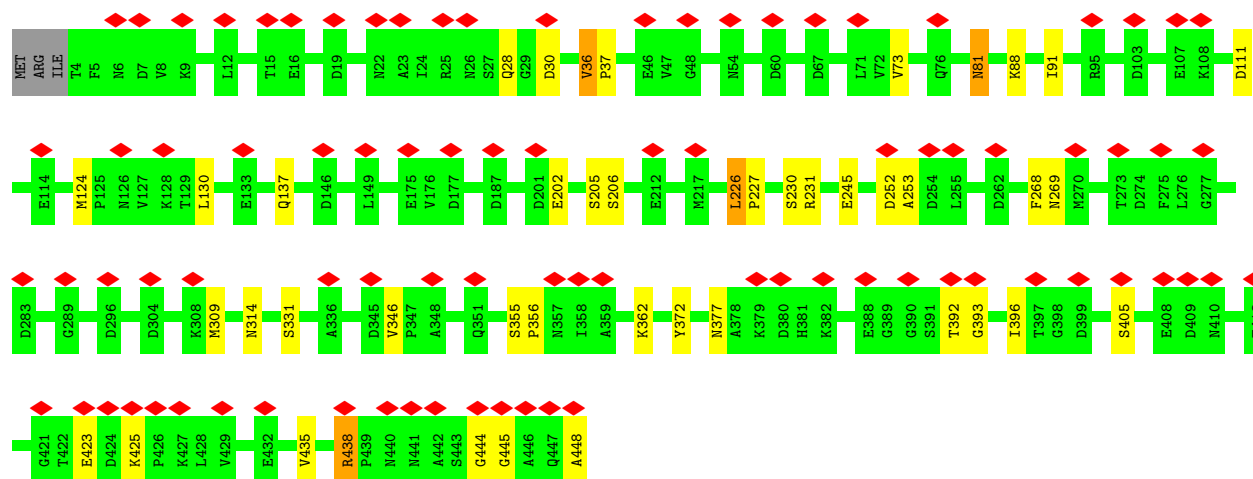
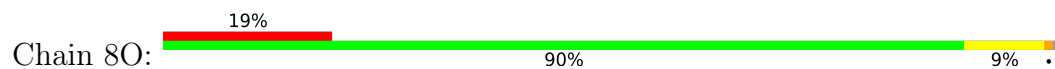


• Molecule 1: Major capsid protein

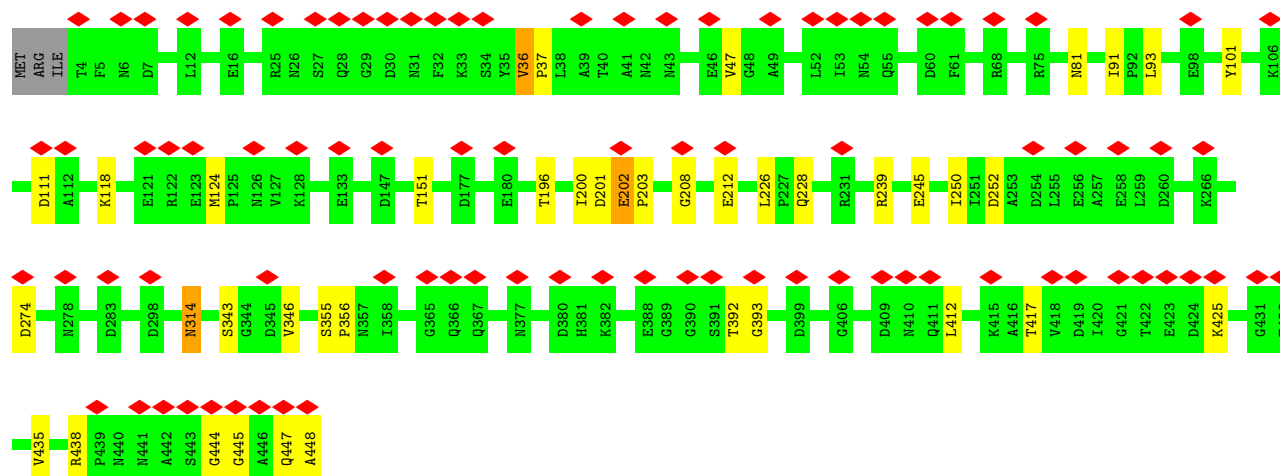
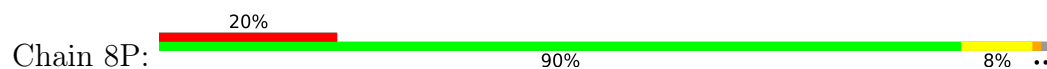




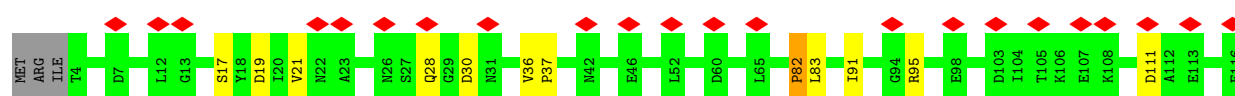
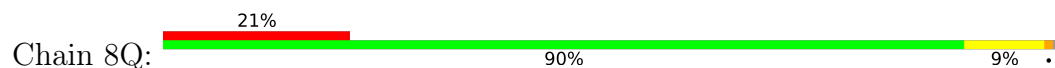
• Molecule 1: Major capsid protein

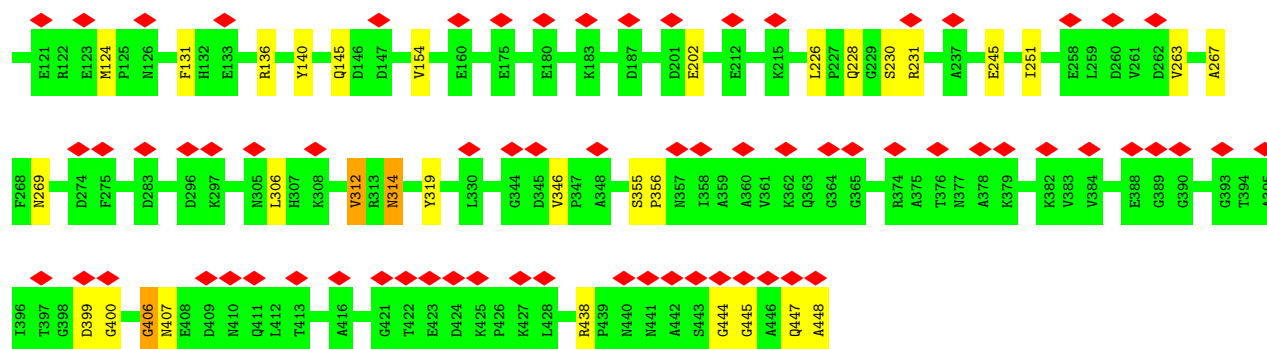


• Molecule 1: Major capsid protein

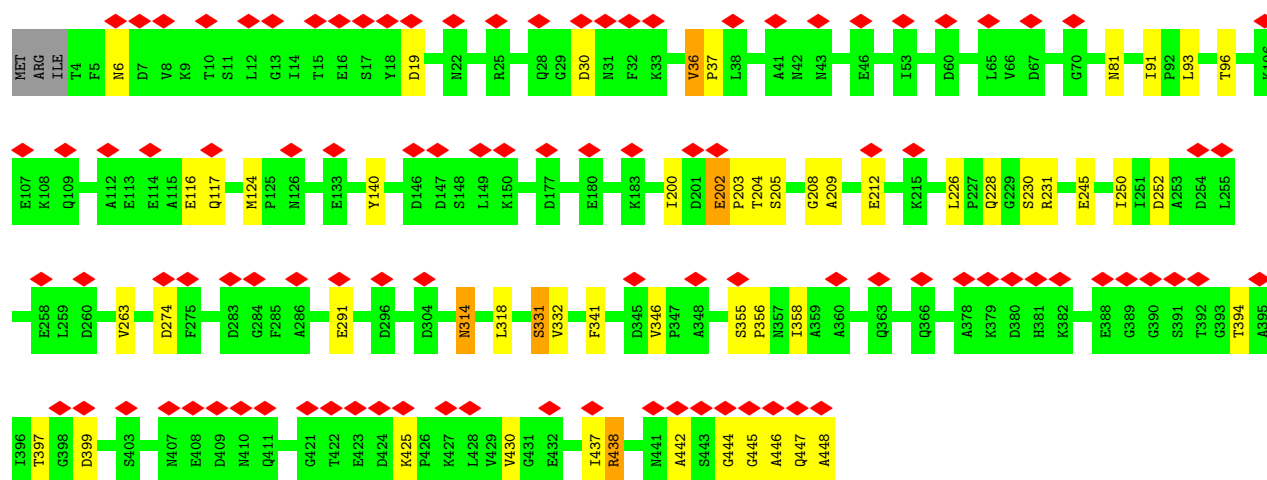
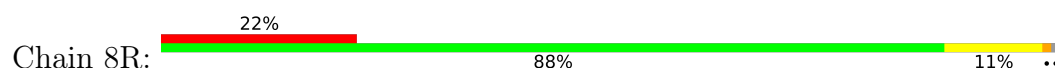


• Molecule 1: Major capsid protein

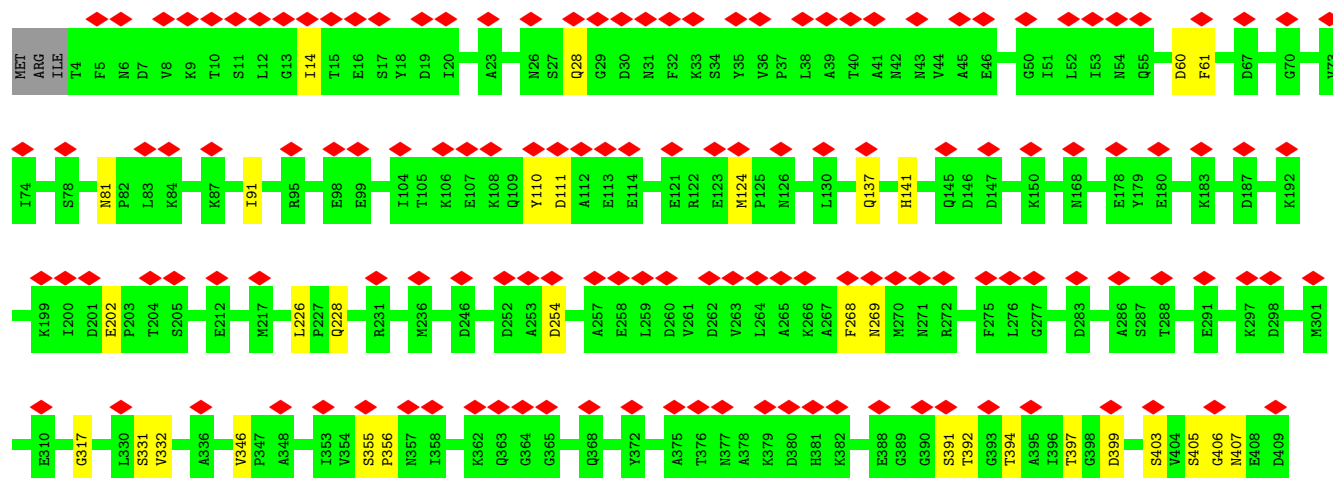


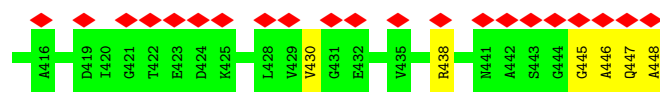


• Molecule 1: Major capsid protein

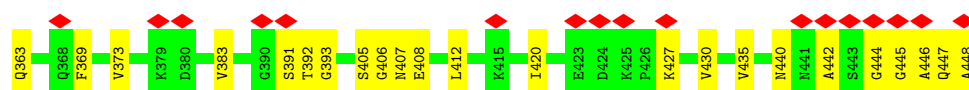
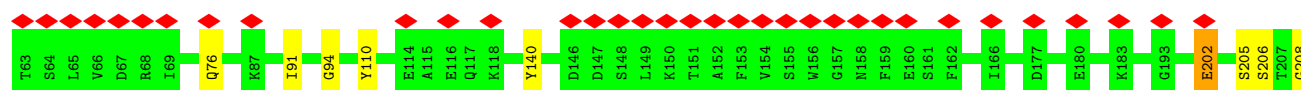
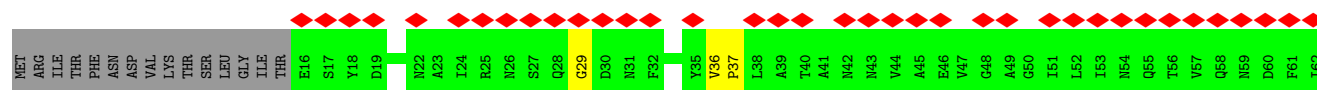
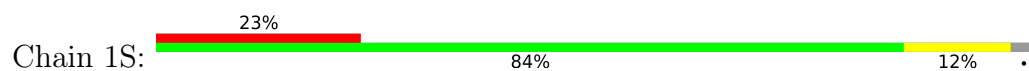


• Molecule 1: Major capsid protein

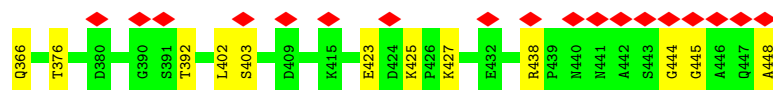
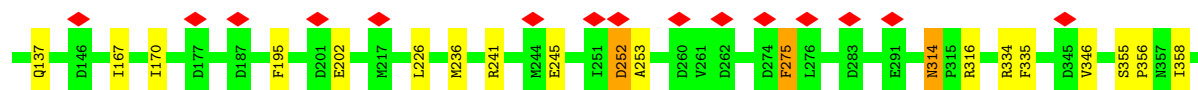
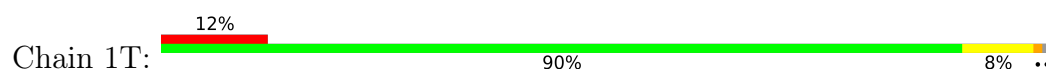




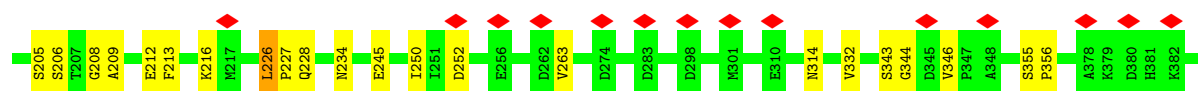
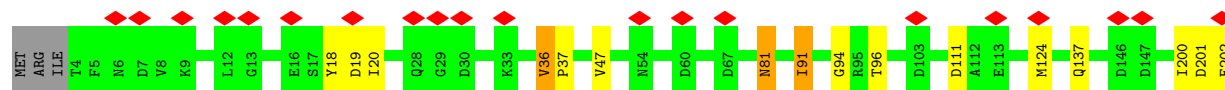
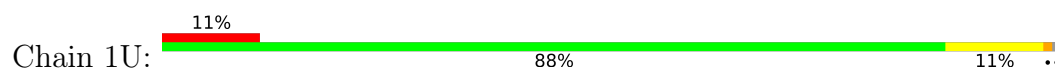
• Molecule 1: Major capsid protein

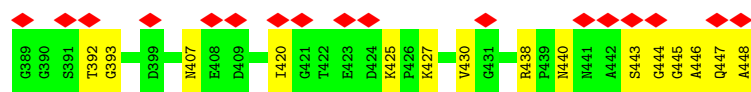


• Molecule 1: Major capsid protein

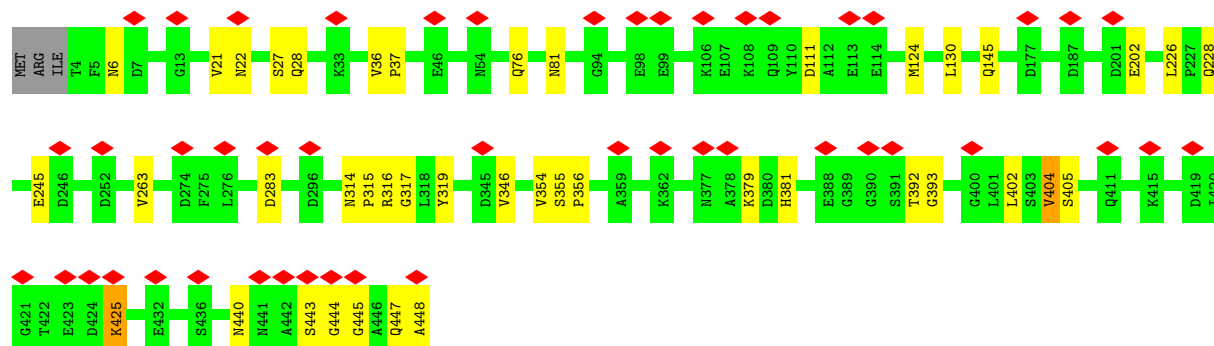
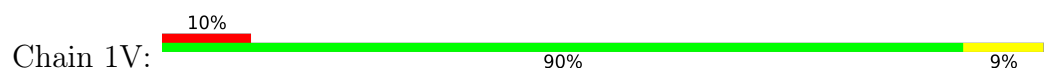


• Molecule 1: Major capsid protein

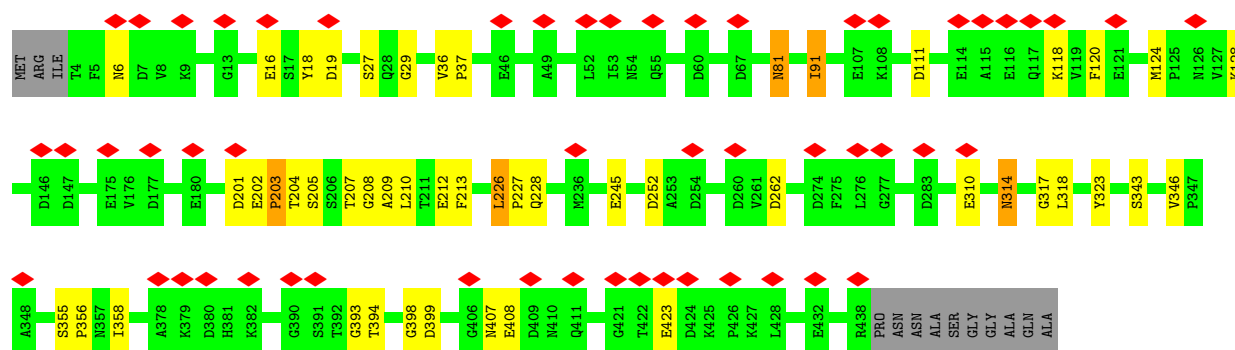
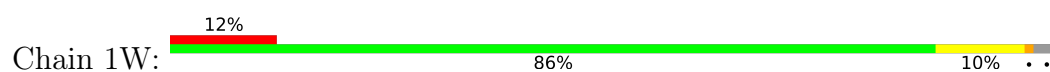




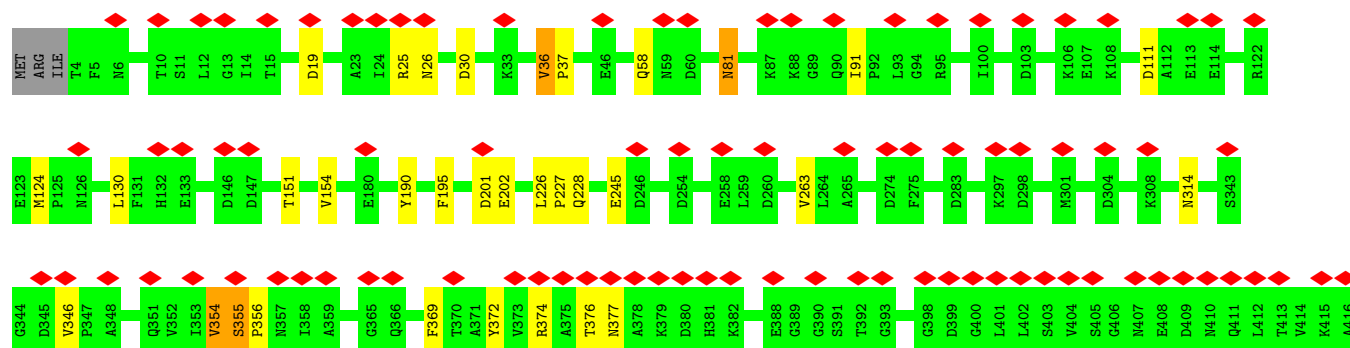
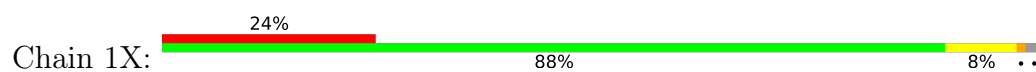
• Molecule 1: Major capsid protein

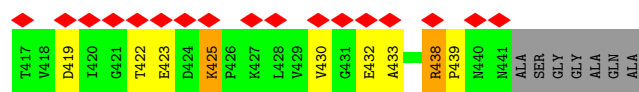


• Molecule 1: Major capsid protein



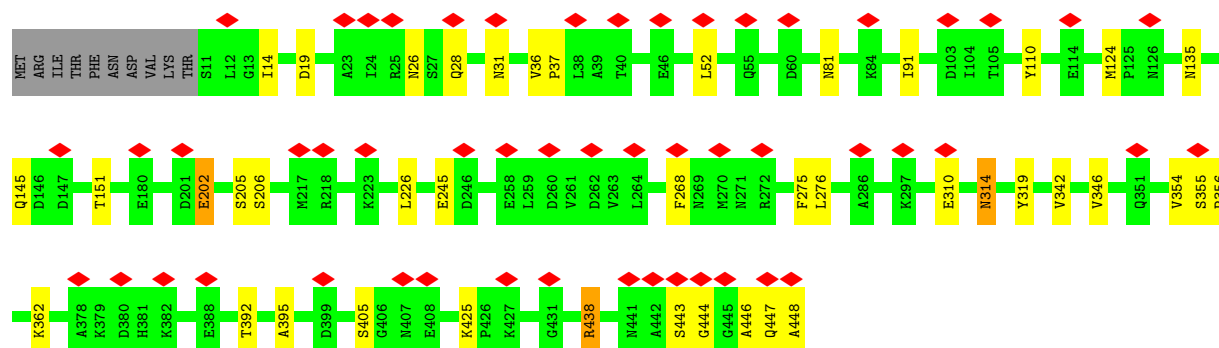
• Molecule 1: Major capsid protein





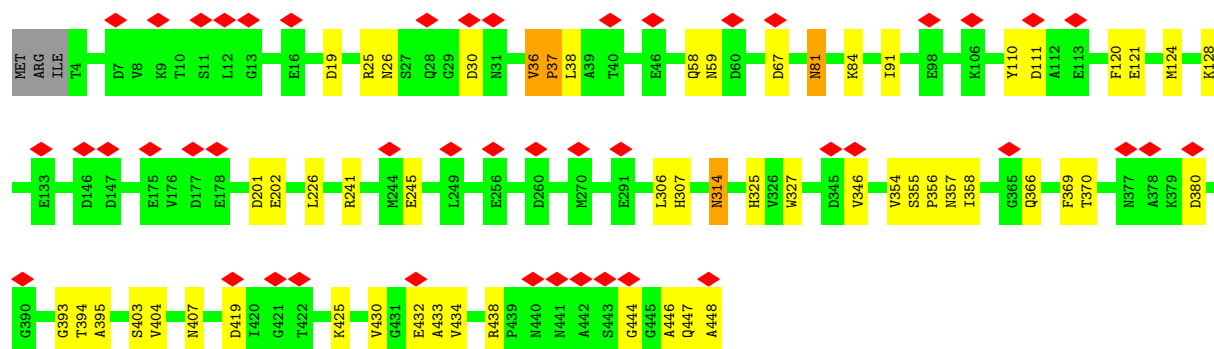
- Molecule 1: Major capsid protein

Chain 2P: 12% 88% 9% ..



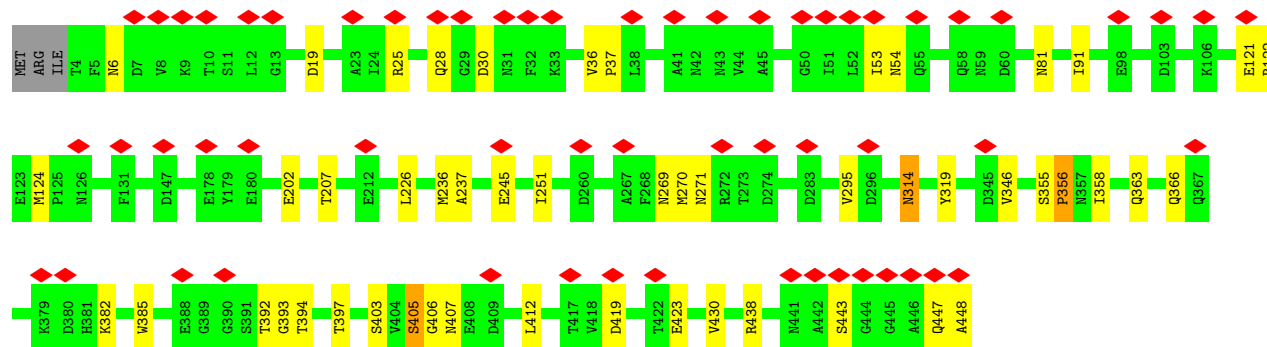
- Molecule 1: Major capsid protein

Chain 2Q: 10% 87% 12% ..

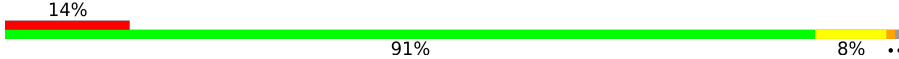


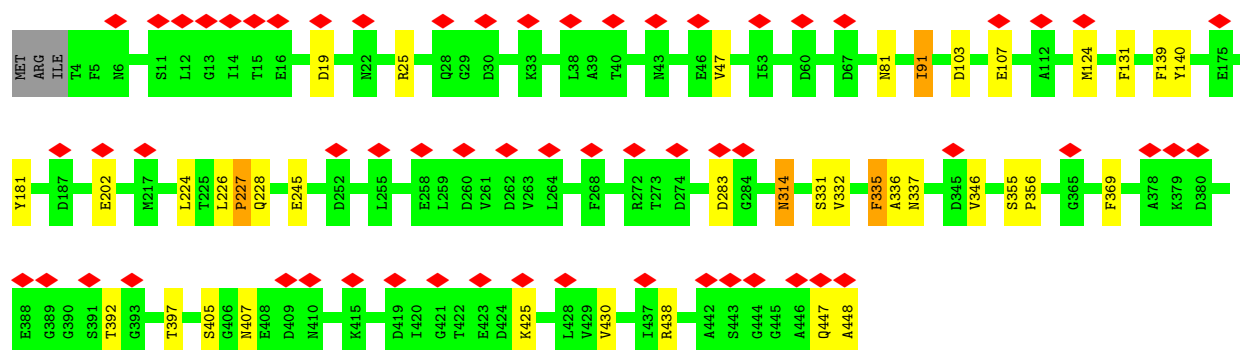
- Molecule 1: Major capsid protein

Chain 2R: 13% 88% 11% ..



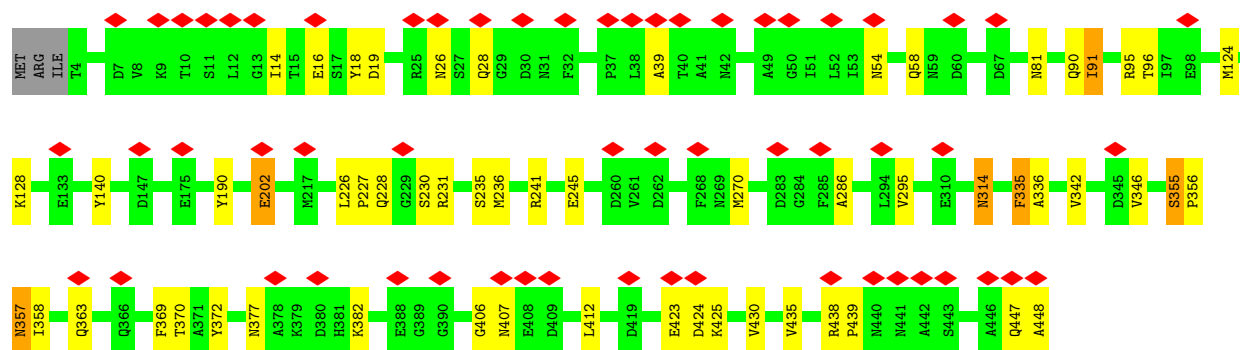
- Molecule 1: Major capsid protein

Chain 2S:  14% 91% 8% ..



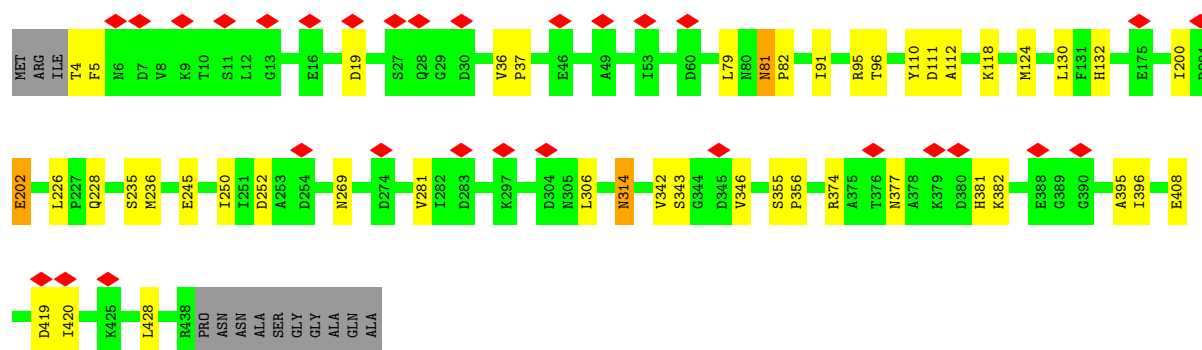
• Molecule 1: Major capsid protein

Chain 2T:  13% 86% 12% ..



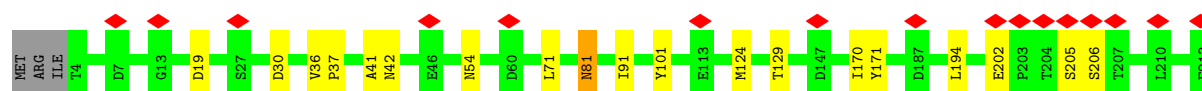
• Molecule 1: Major capsid protein

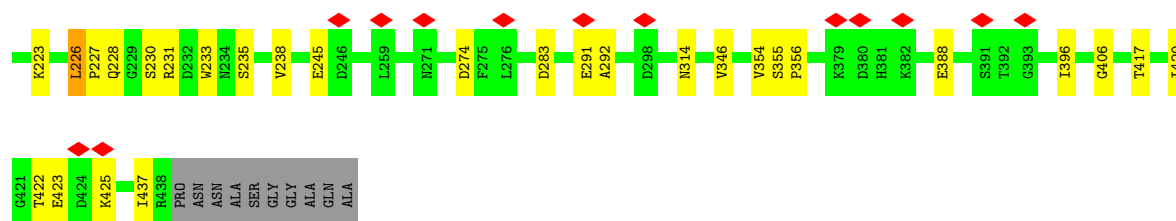
Chain 3S:  7% 87% 10% ..



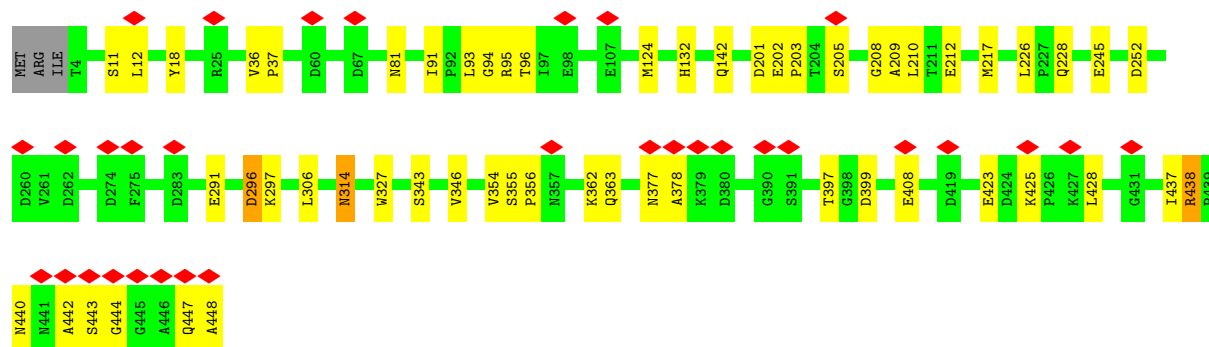
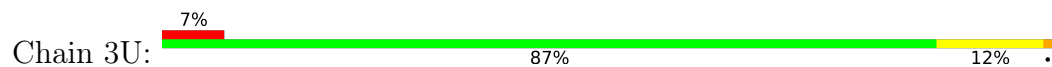
• Molecule 1: Major capsid protein

Chain 3T:  6% 87% 10% .

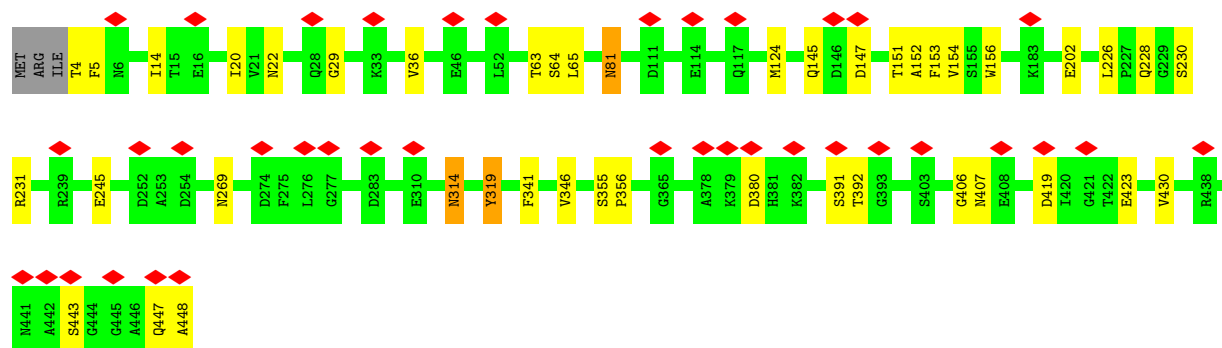
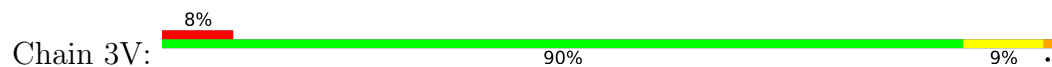




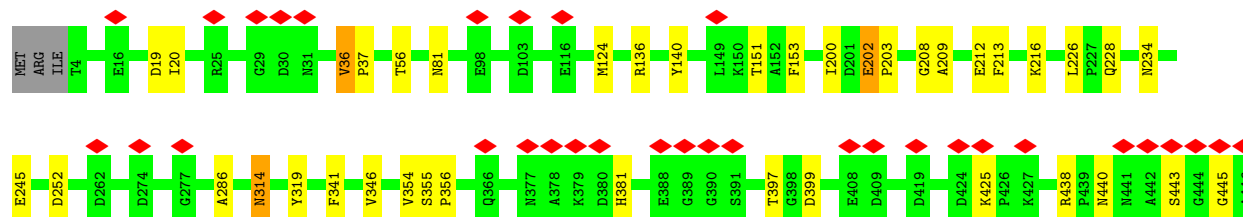
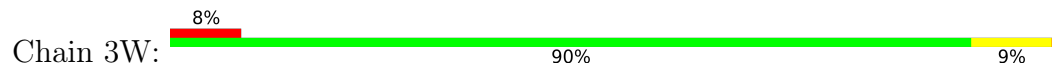
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

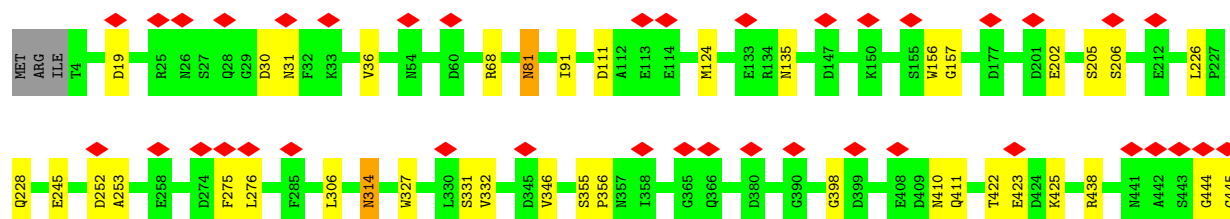
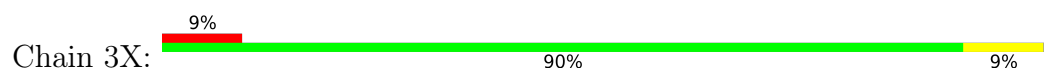


- Molecule 1: Major capsid protein

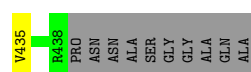
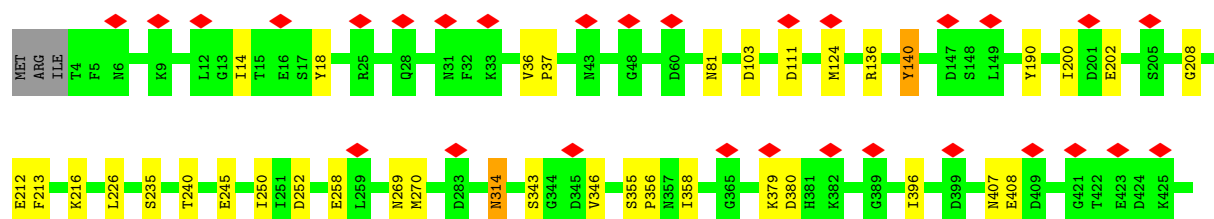
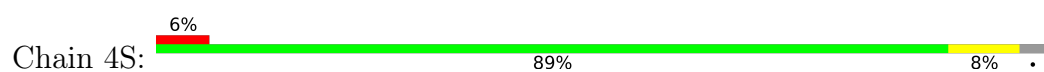




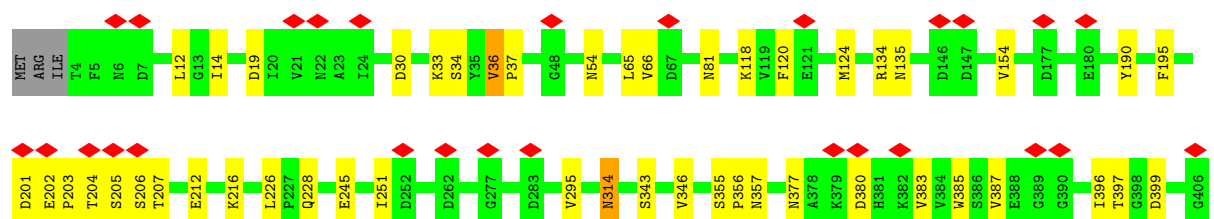
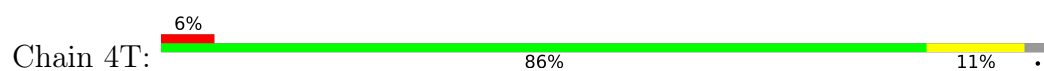
- Molecule 1: Major capsid protein



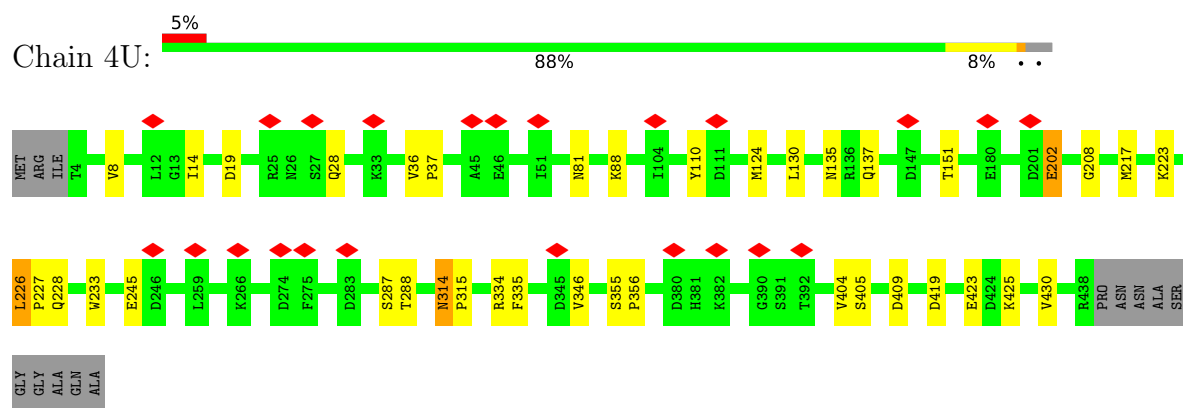
- Molecule 1: Major capsid protein



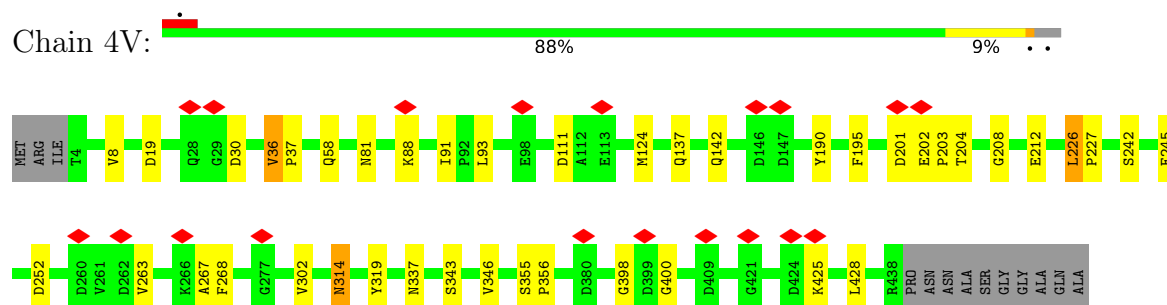
- Molecule 1: Major capsid protein



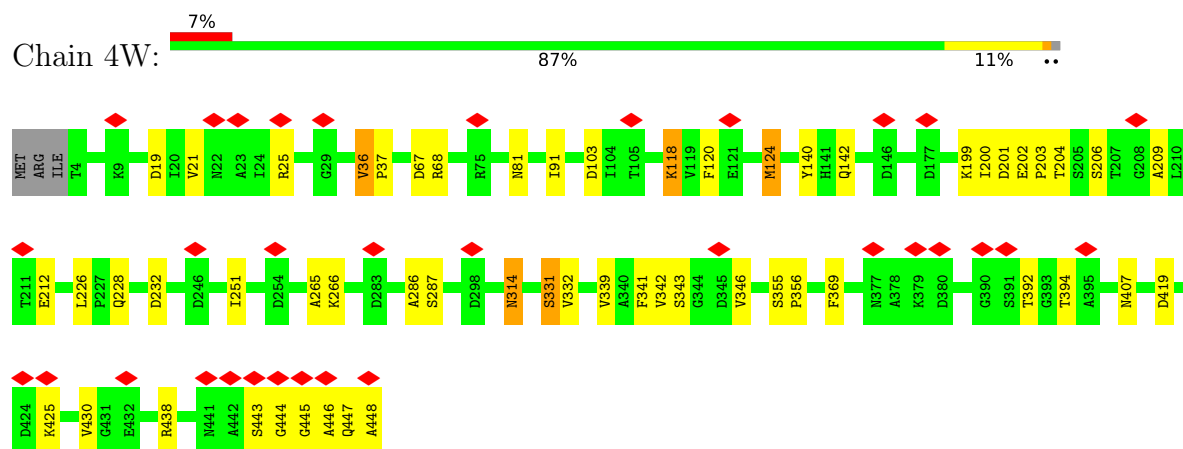
- Molecule 1: Major capsid protein



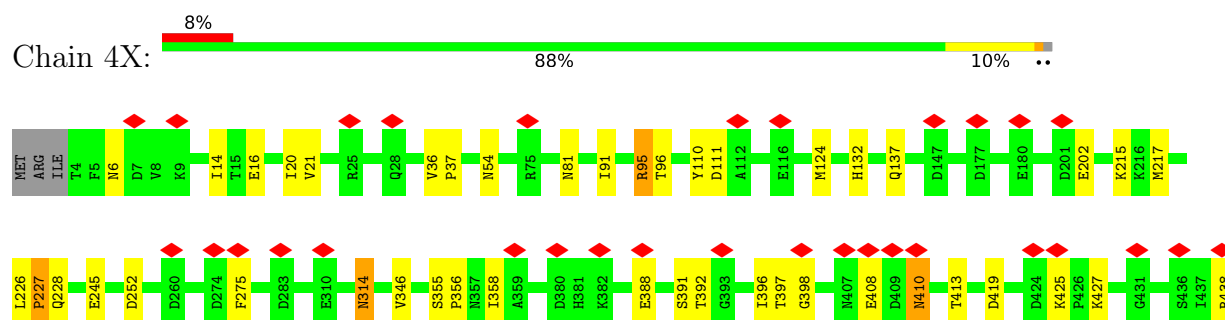
- Molecule 1: Major capsid protein

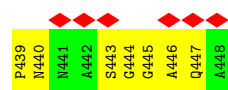


- Molecule 1: Major capsid protein

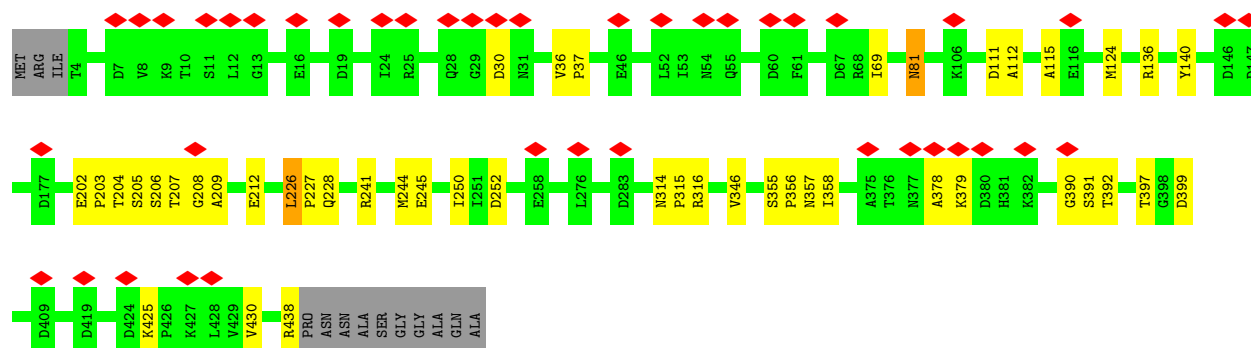
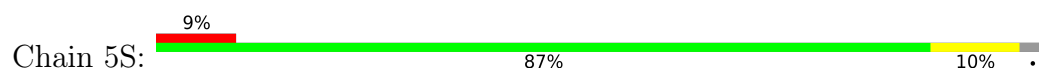


- Molecule 1: Major capsid protein

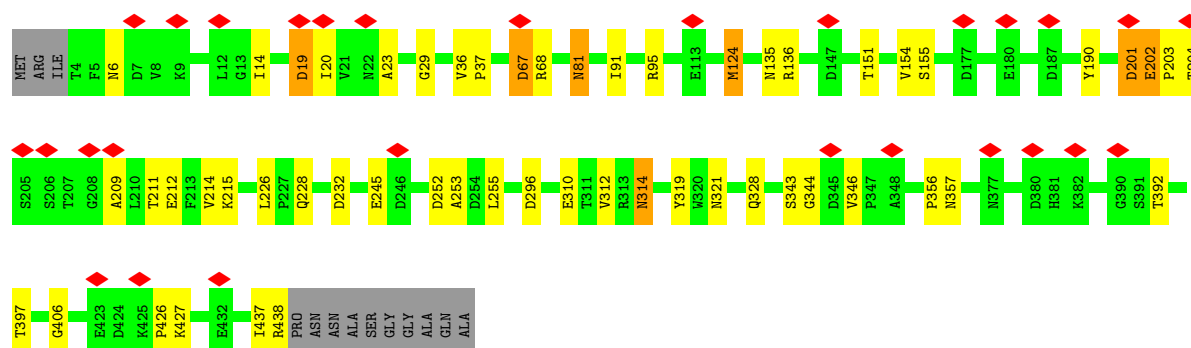
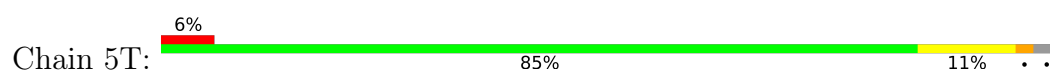




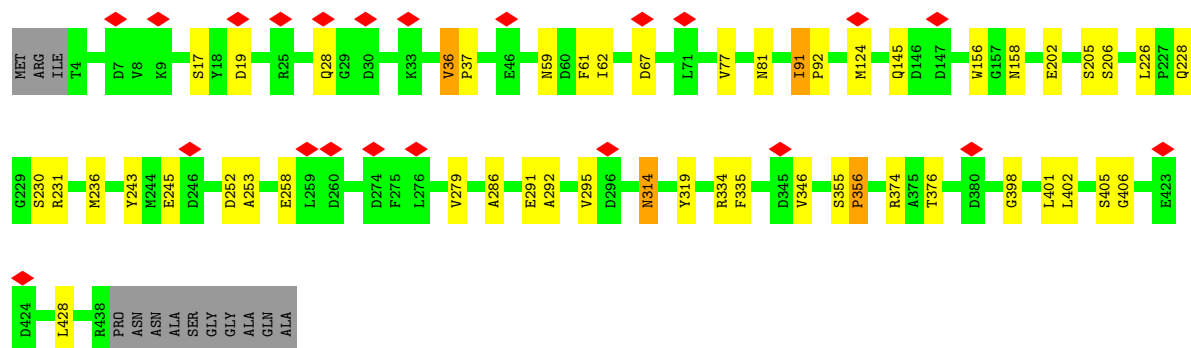
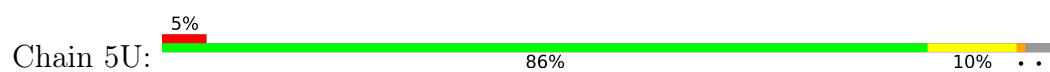
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

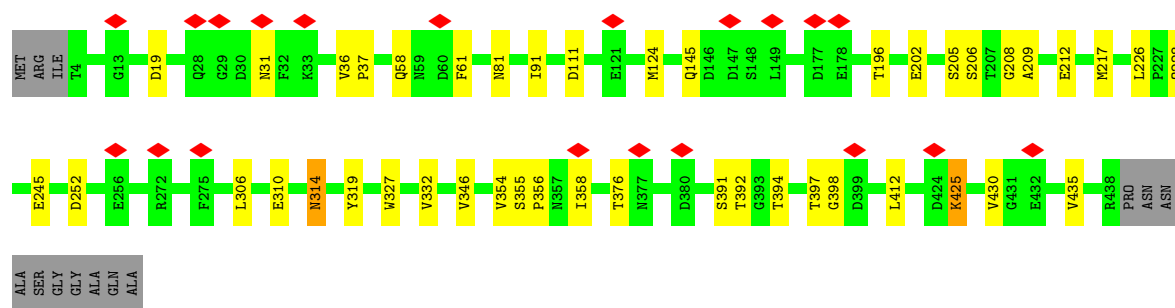


- Molecule 1: Major capsid protein



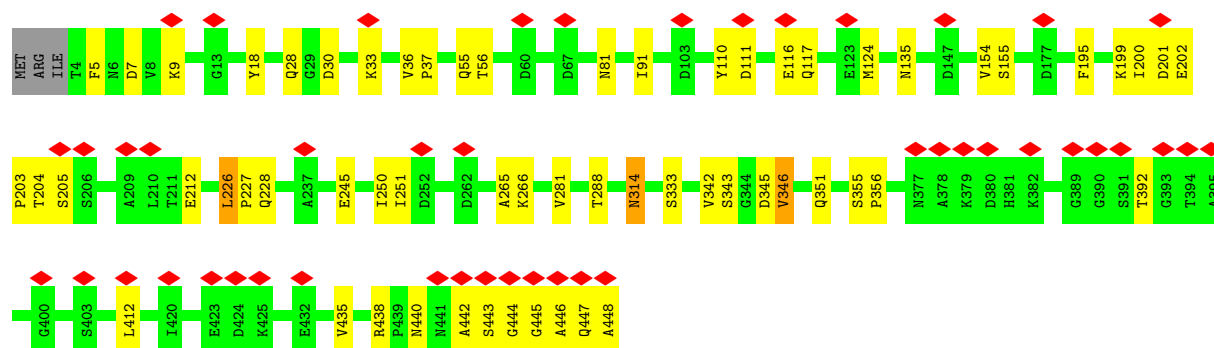
- Molecule 1: Major capsid protein

Chain 5V:  87% 9%



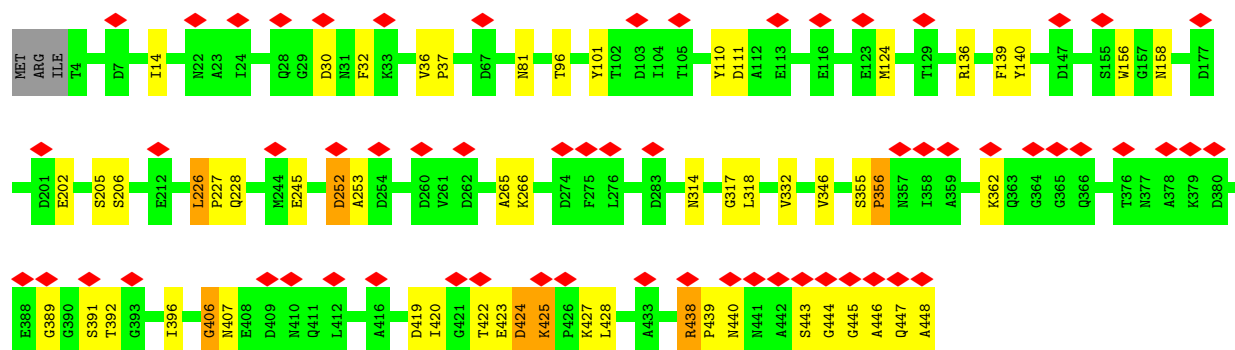
• Molecule 1: Major capsid protein

Chain 5W:  86% 13%



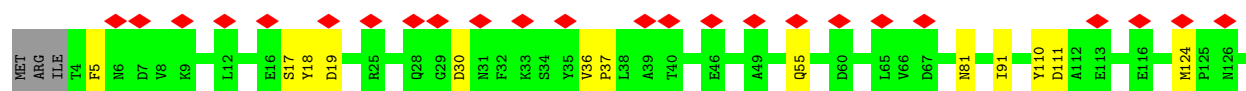
• Molecule 1: Major capsid protein

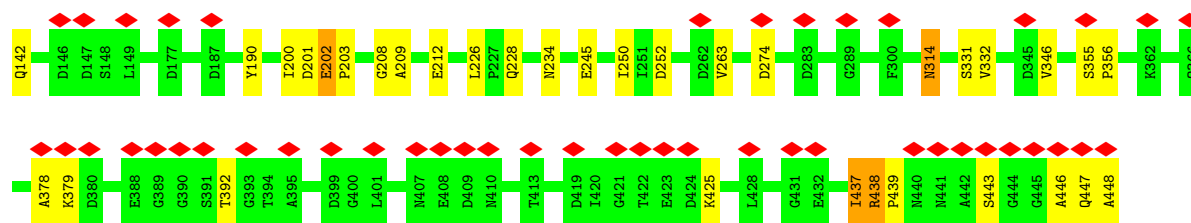
Chain 5X:  86% 11%



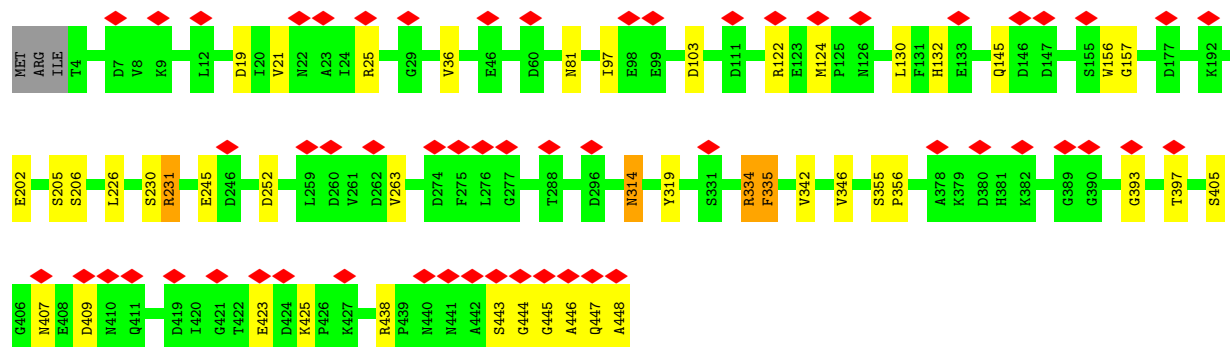
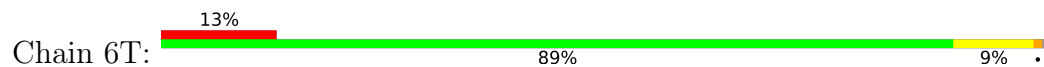
• Molecule 1: Major capsid protein

Chain 6S:  89% 10%

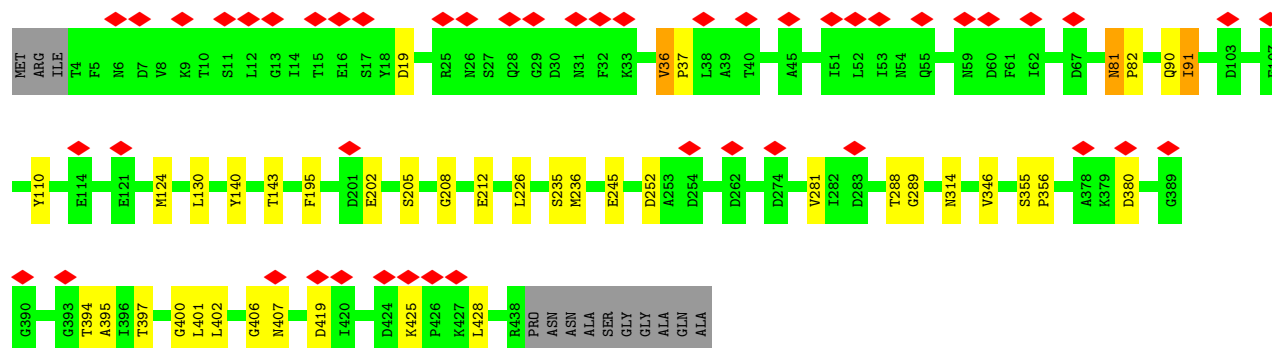
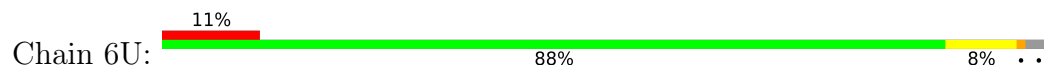




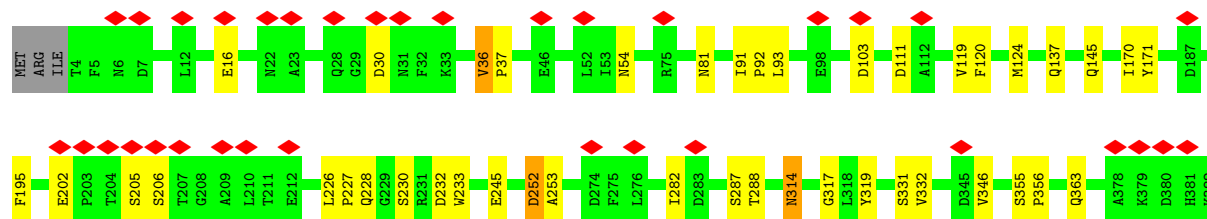
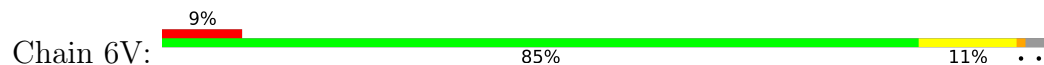
• Molecule 1: Major capsid protein

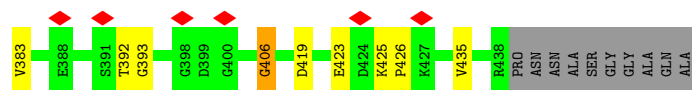


• Molecule 1: Major capsid protein

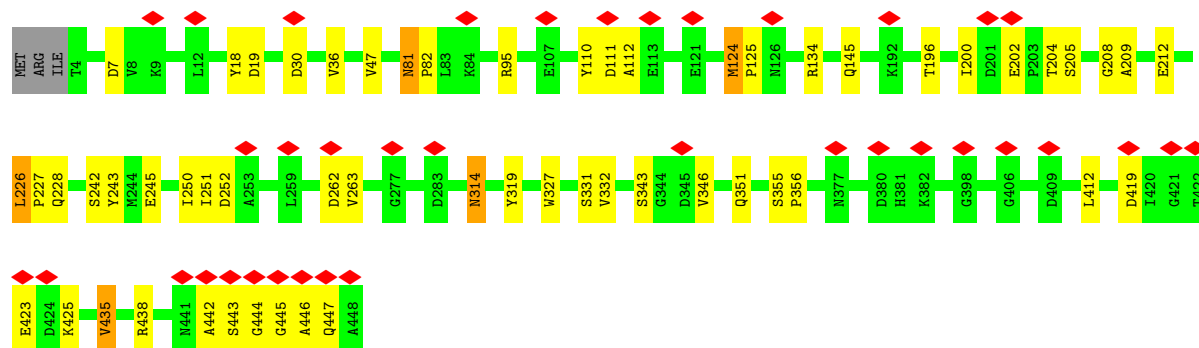
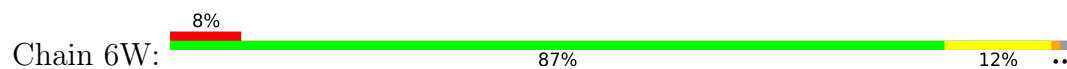


• Molecule 1: Major capsid protein

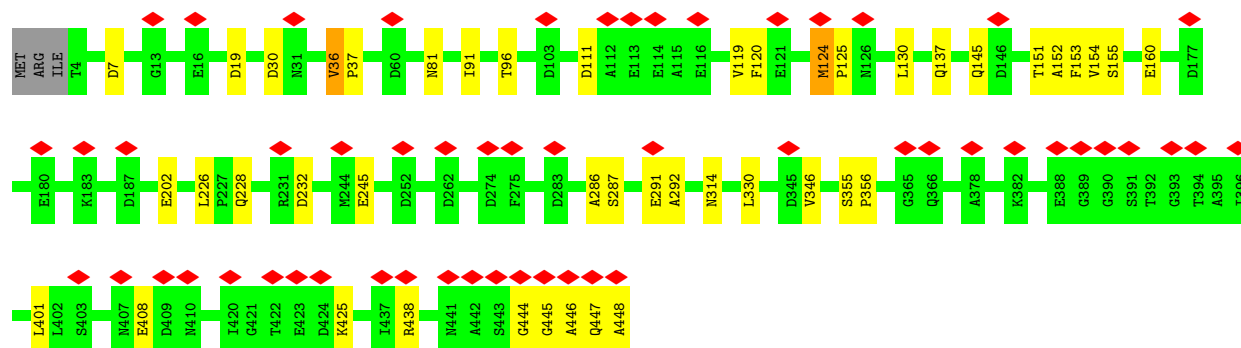
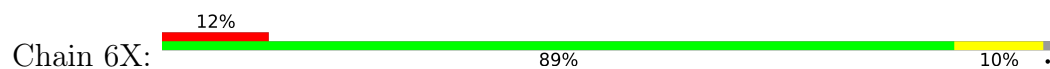




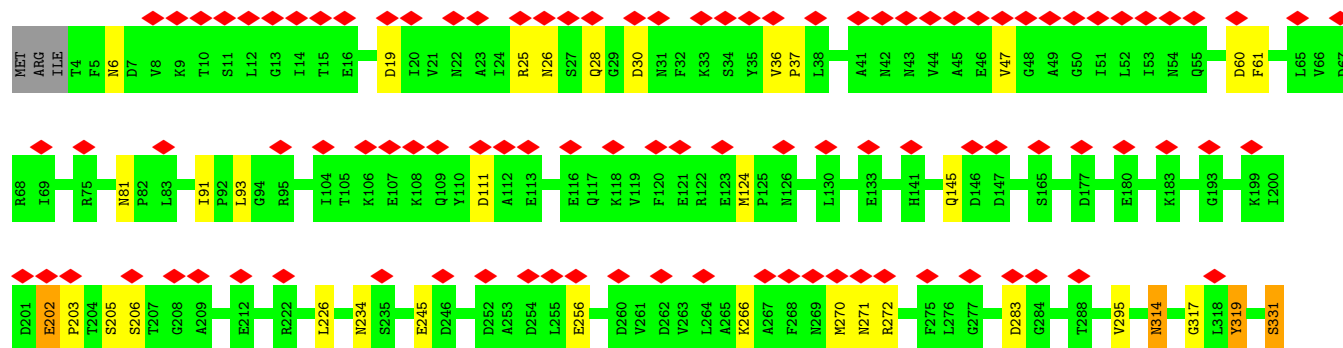
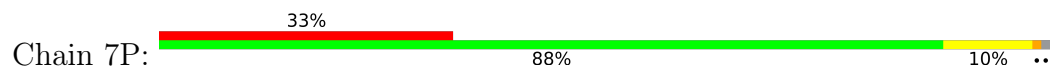
- Molecule 1: Major capsid protein



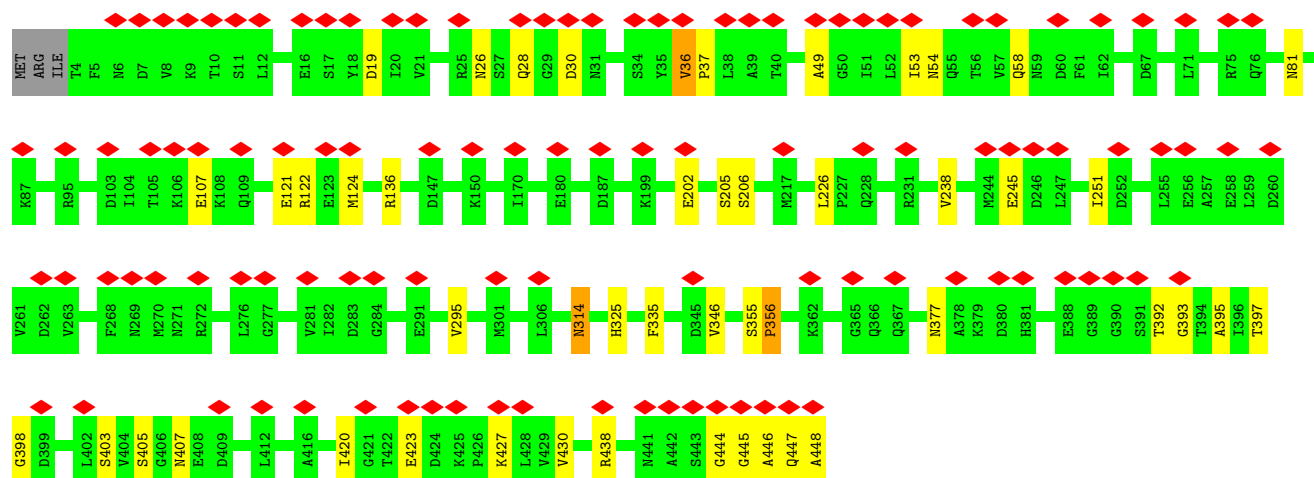
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

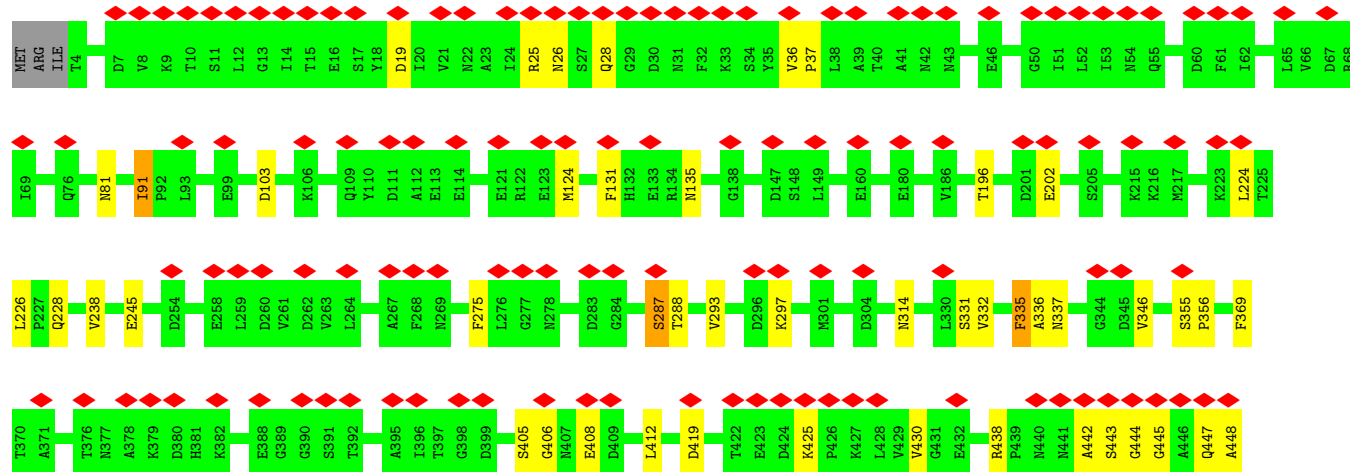






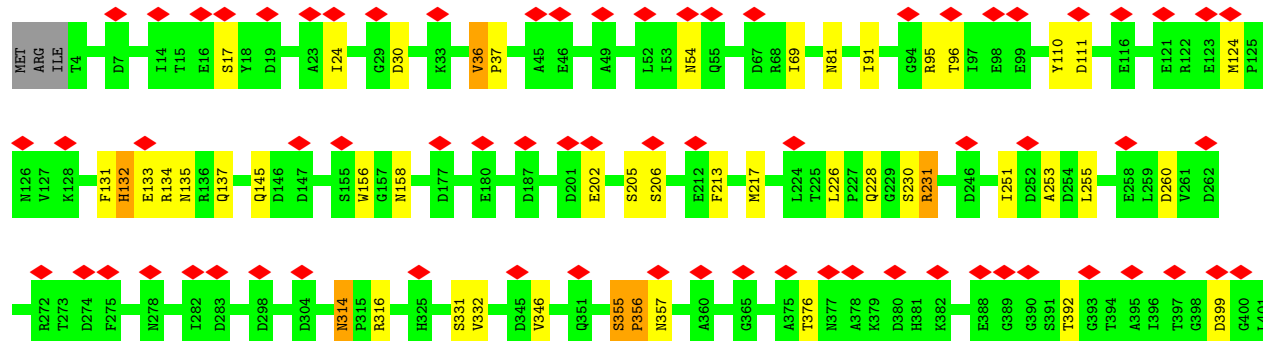
• Molecule 1: Major capsid protein

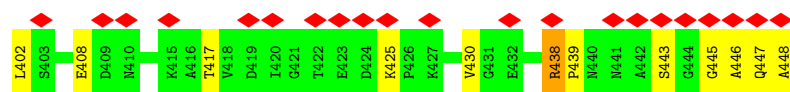
Chain 7T: 29% 89% 10% ..



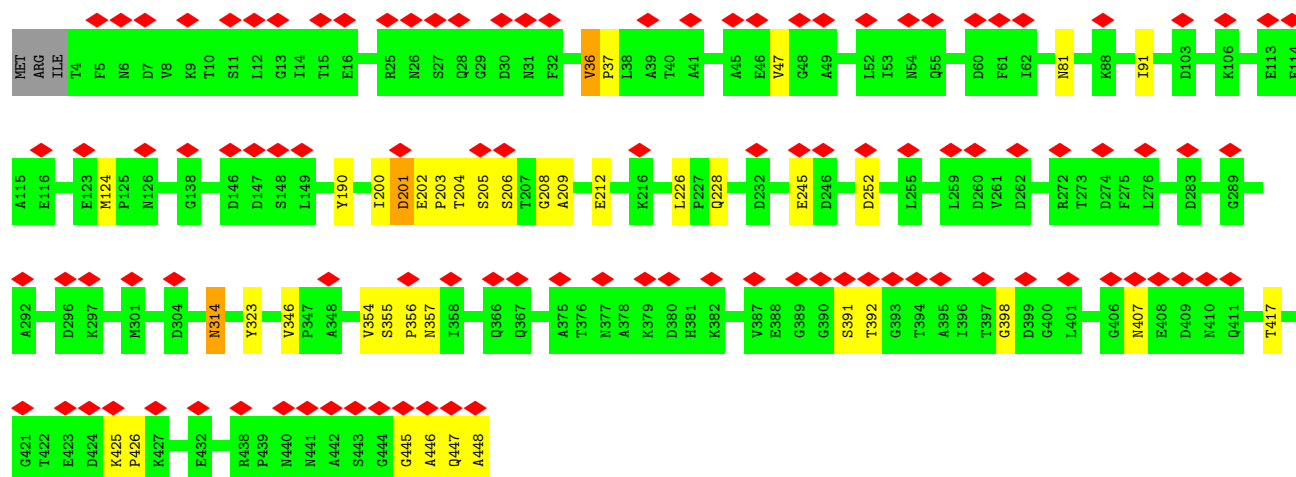
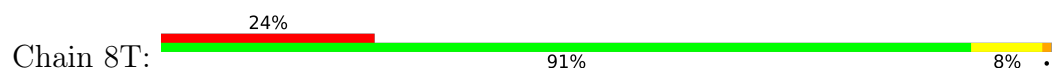
• Molecule 1: Major capsid protein

Chain 8S: 20% 86% 12% ..

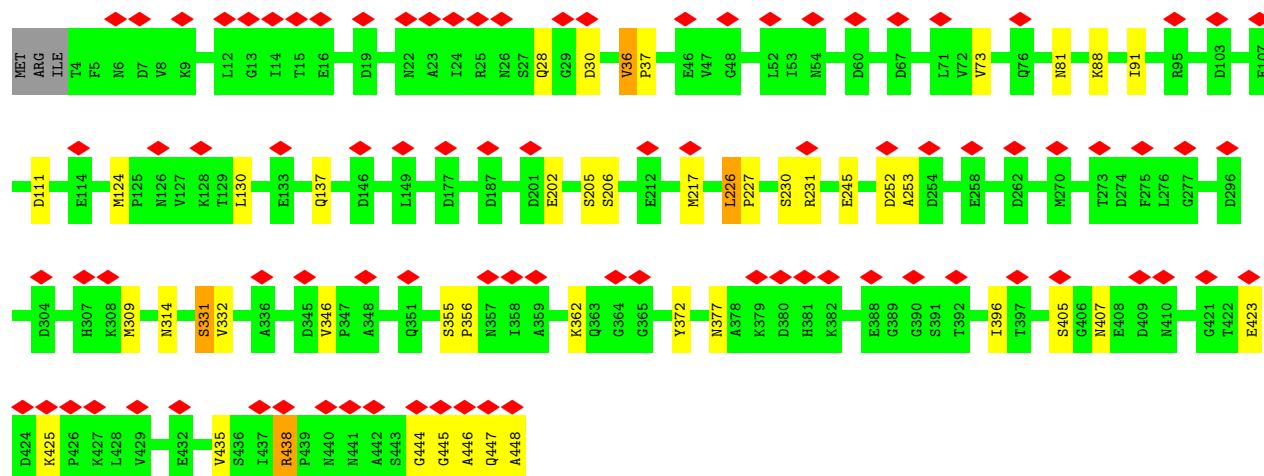
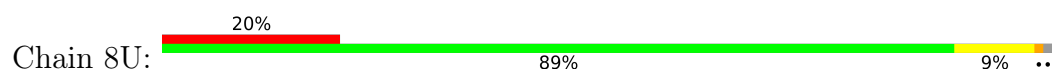




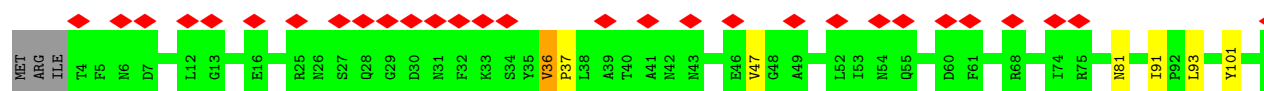
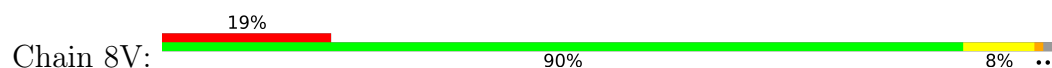
• Molecule 1: Major capsid protein

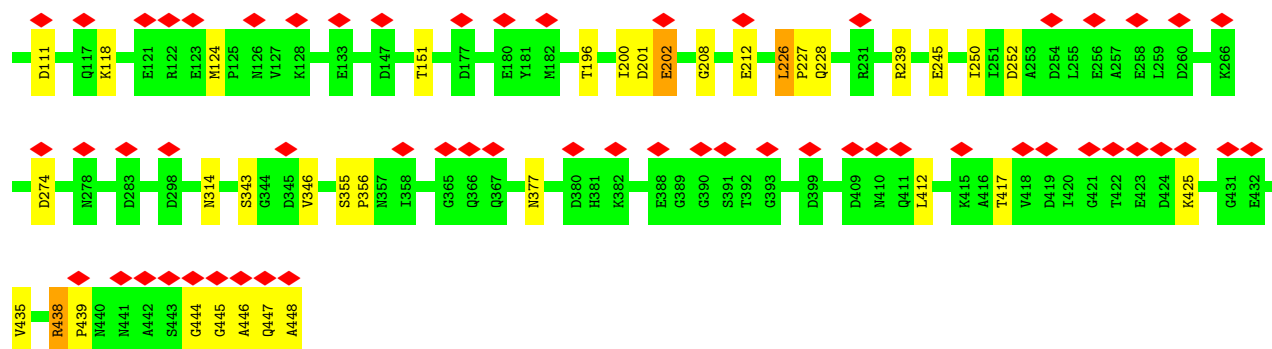


• Molecule 1: Major capsid protein

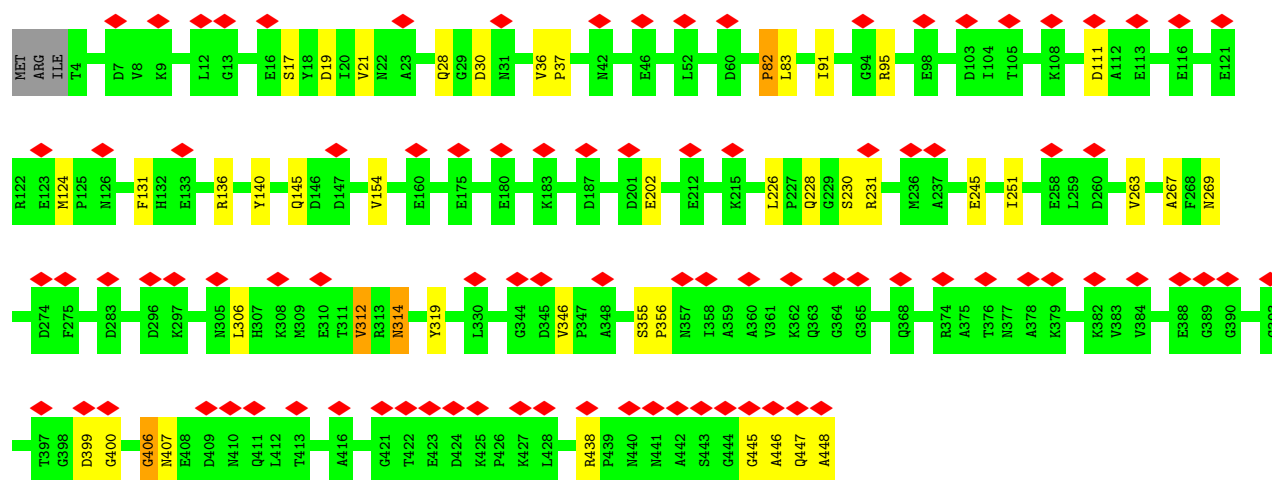
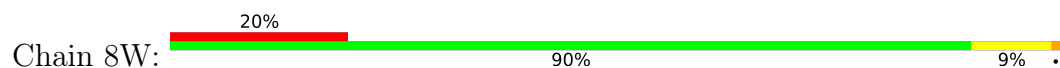


• Molecule 1: Major capsid protein

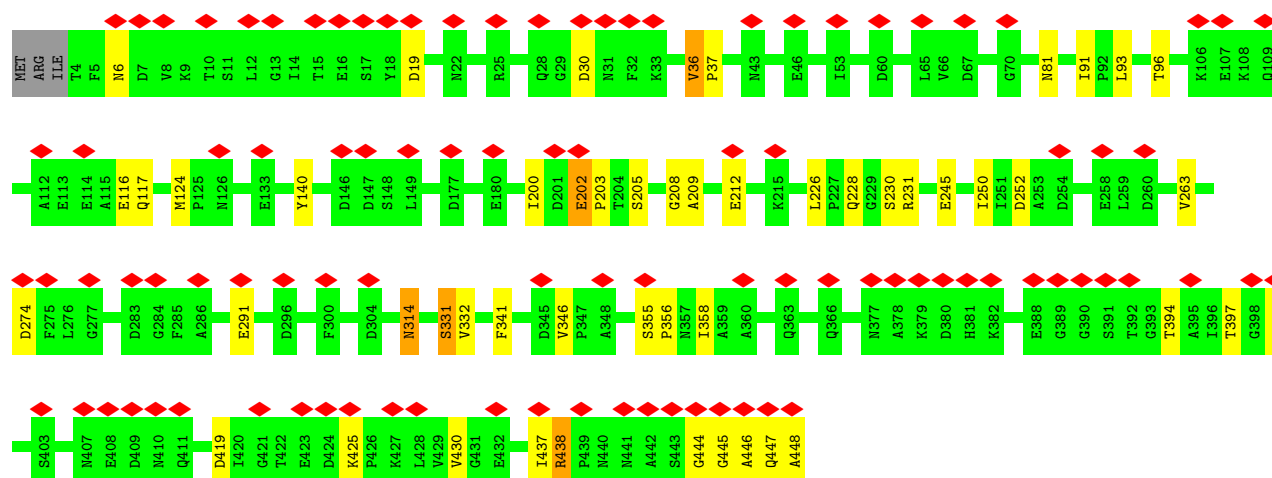
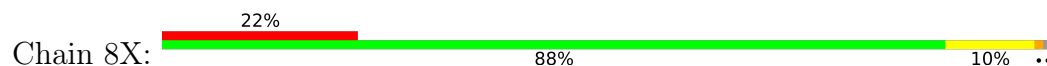




• Molecule 1: Major capsid protein

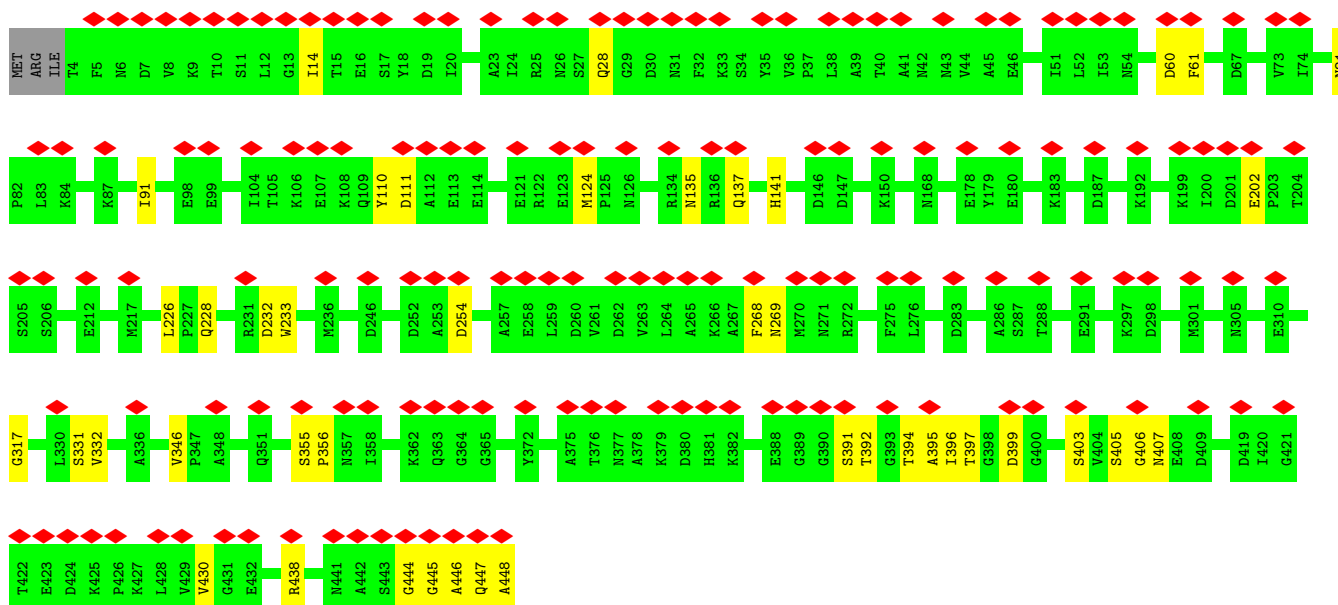


• Molecule 1: Major capsid protein



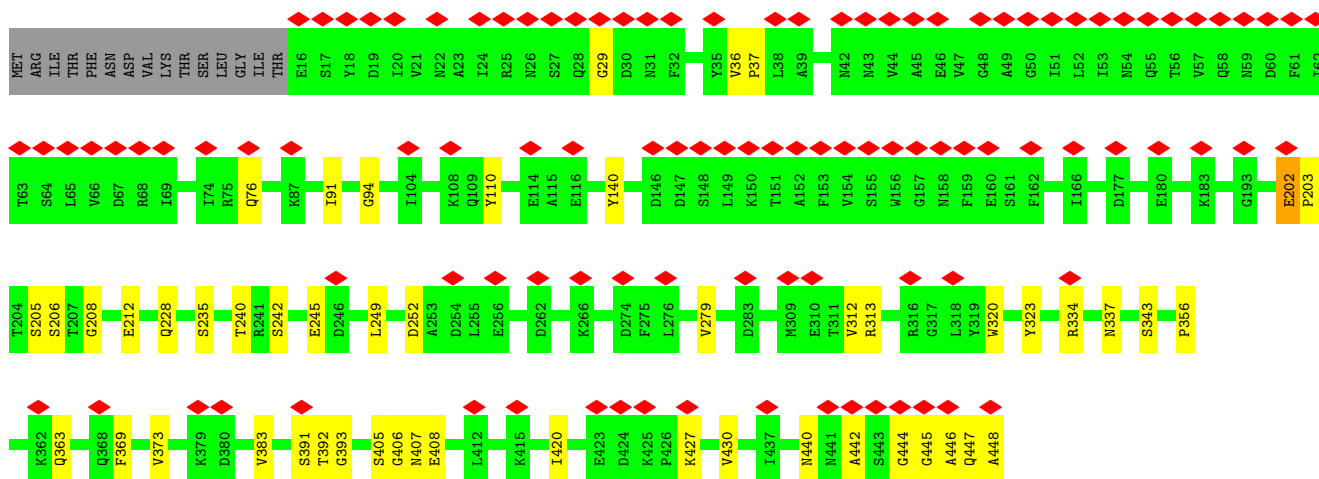
• Molecule 1: Major capsid protein

Chain 9D: 



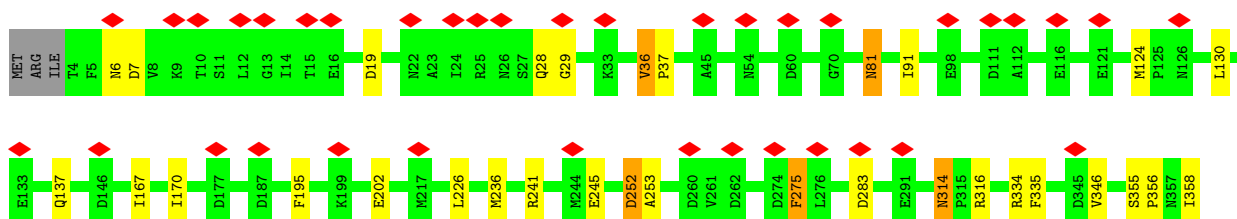
• Molecule 1: Major capsid protein

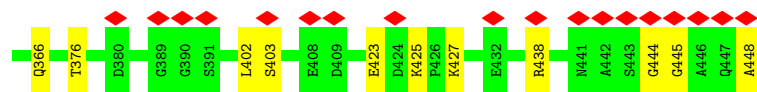
Chain 1Y: 



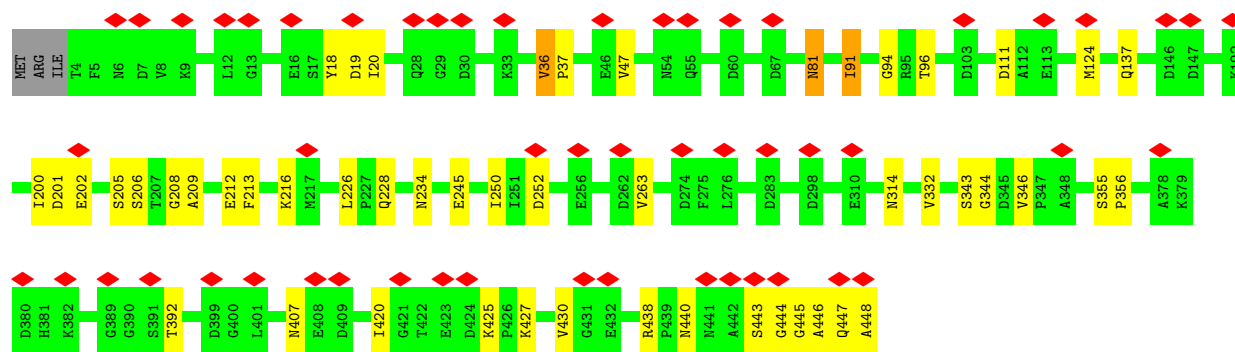
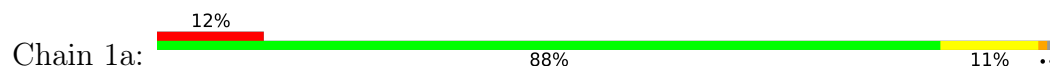
• Molecule 1: Major capsid protein

Chain 1Z: 

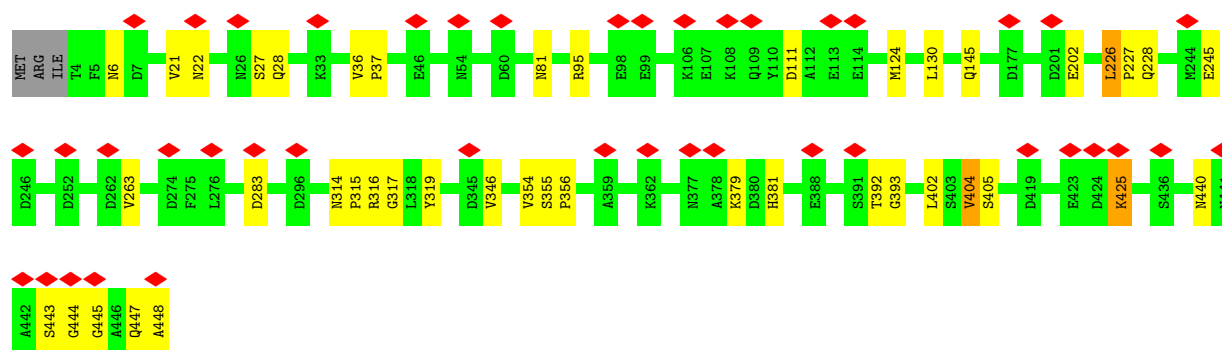
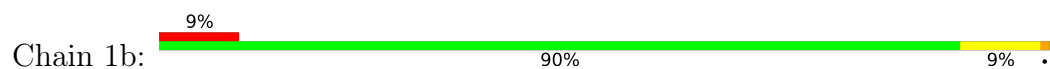




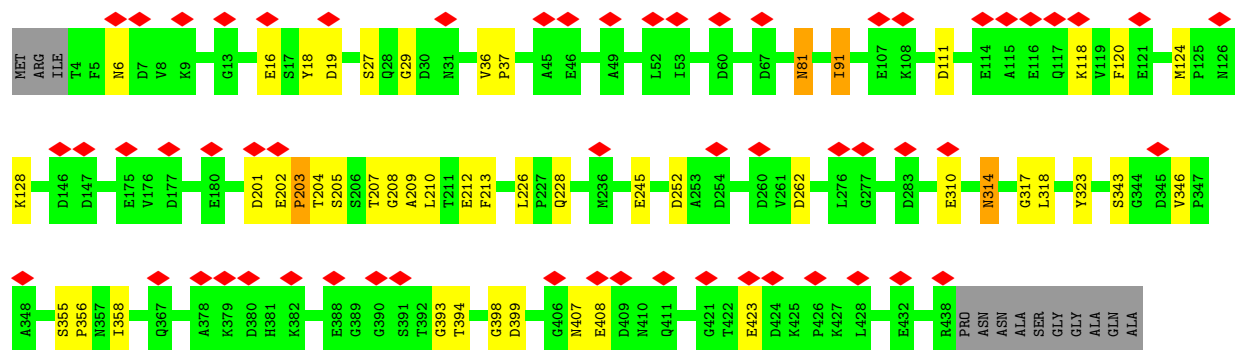
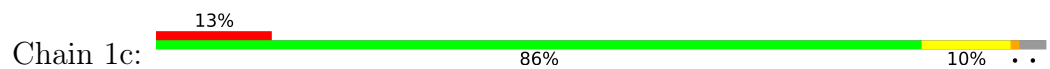
• Molecule 1: Major capsid protein



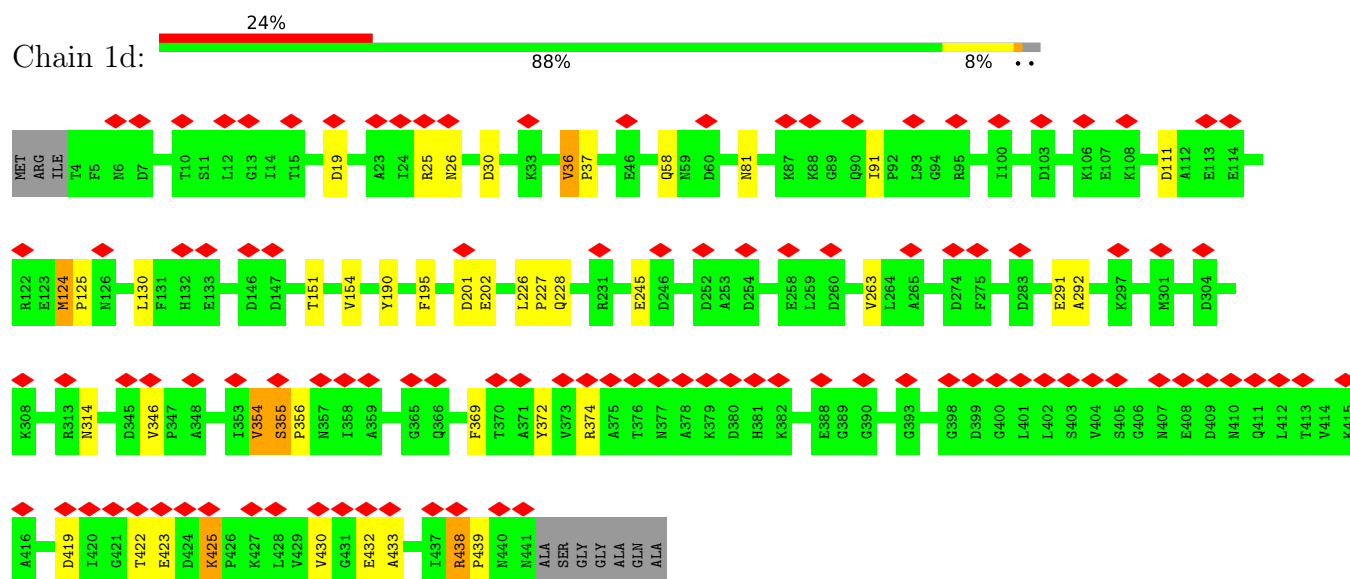
• Molecule 1: Major capsid protein



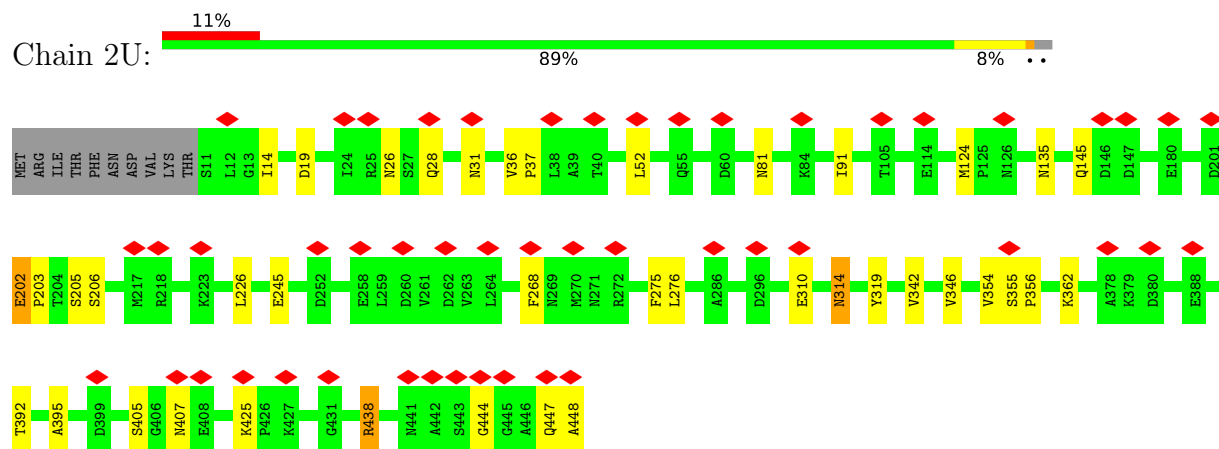
• Molecule 1: Major capsid protein



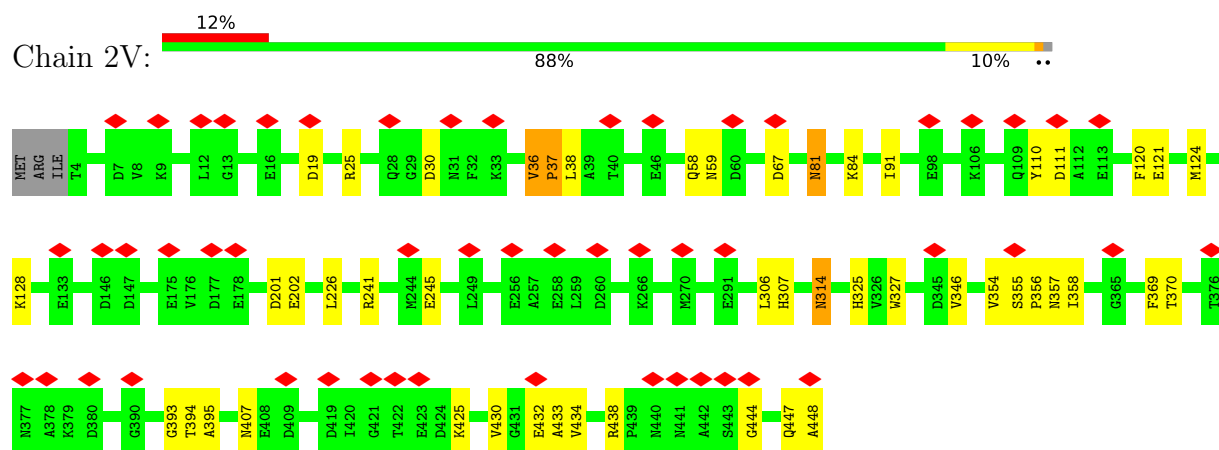
• Molecule 1: Major capsid protein



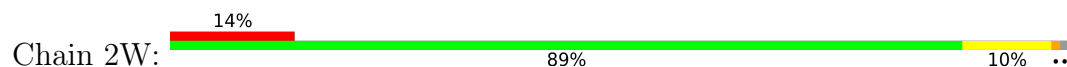
• Molecule 1: Major capsid protein

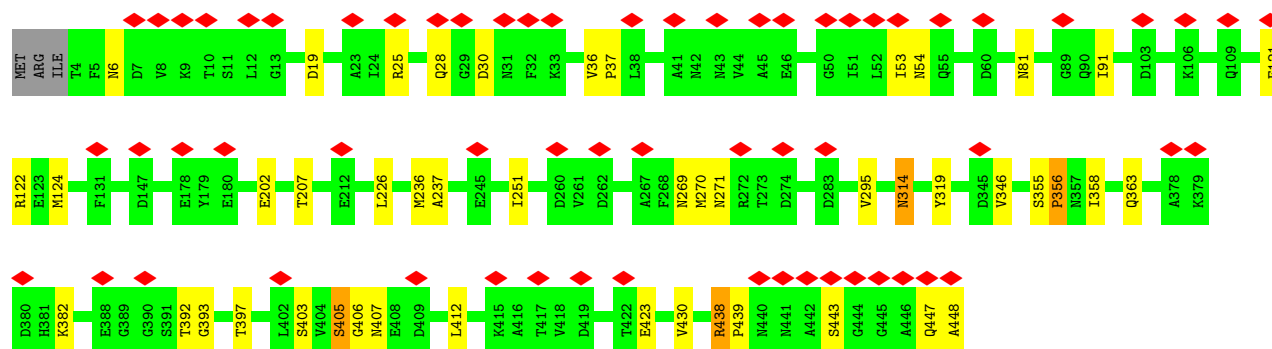


• Molecule 1: Major capsid protein

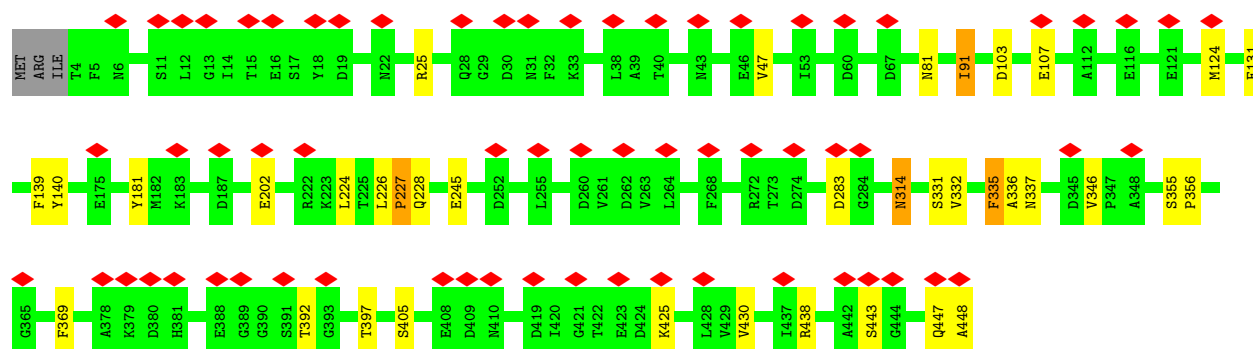


• Molecule 1: Major capsid protein

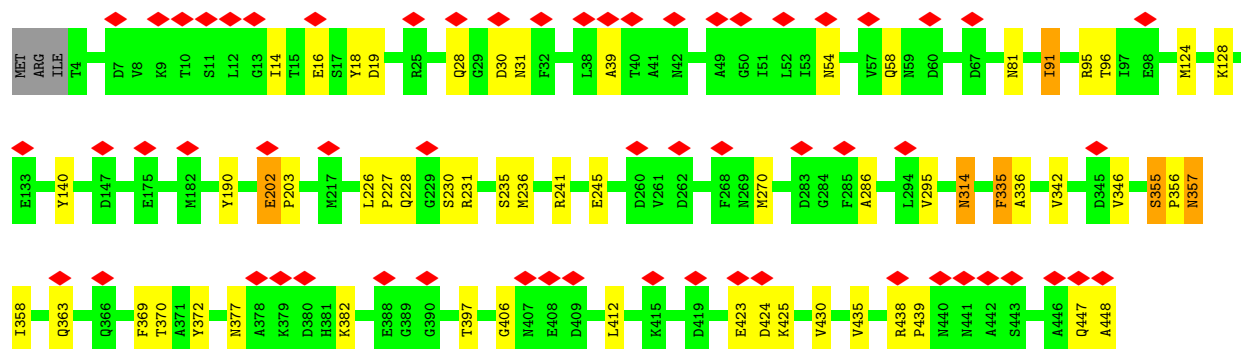
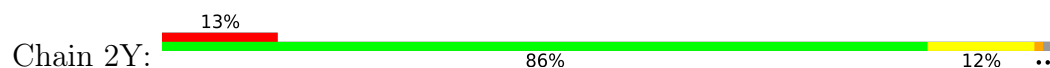




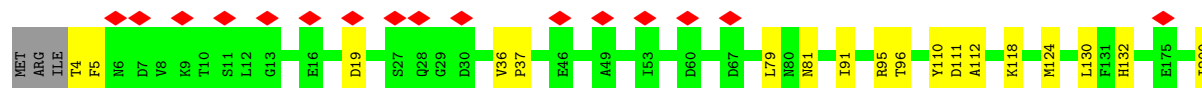
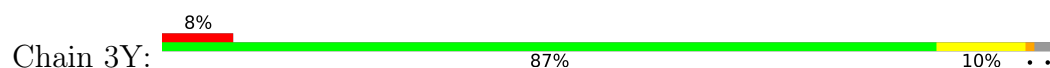
• Molecule 1: Major capsid protein

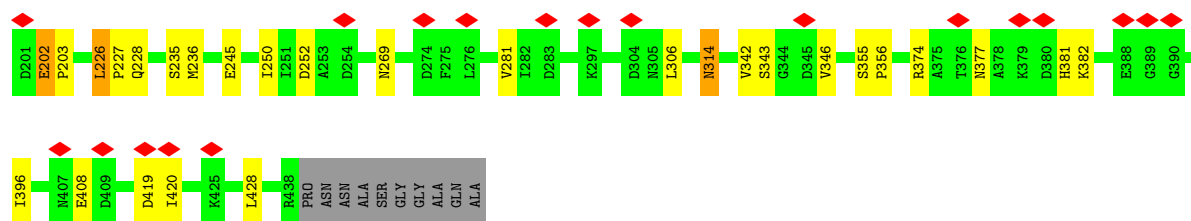


• Molecule 1: Major capsid protein

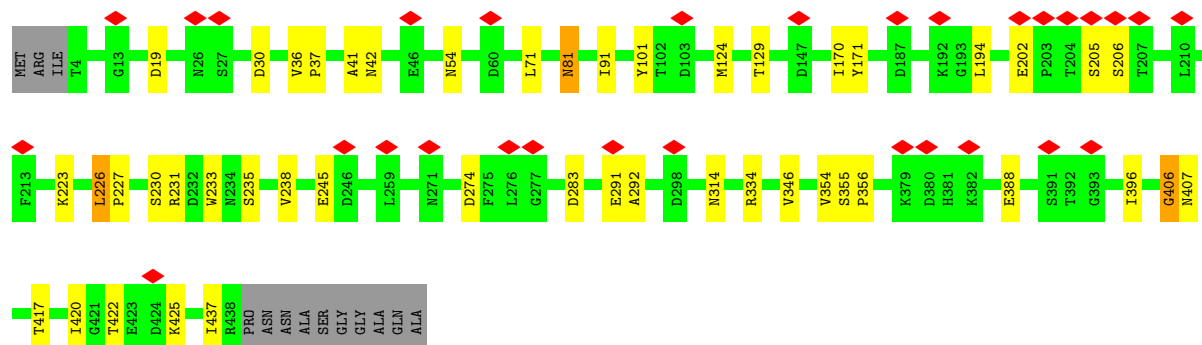
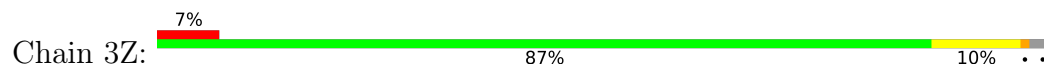


• Molecule 1: Major capsid protein

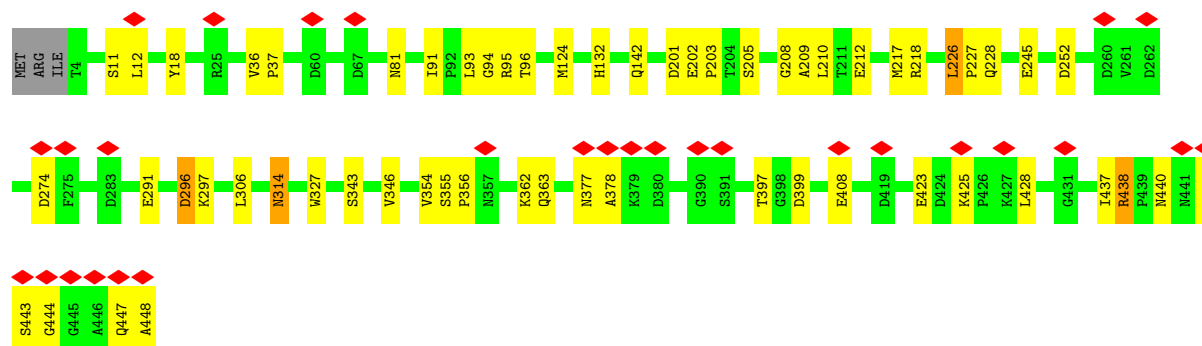
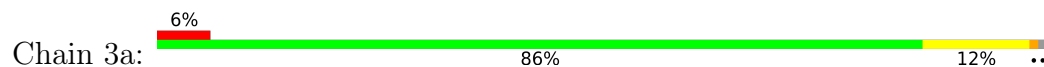




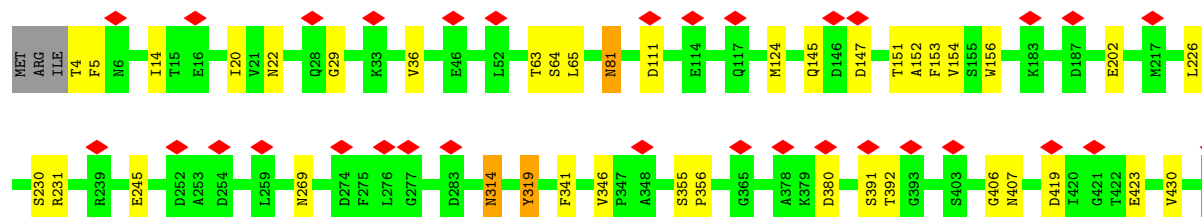
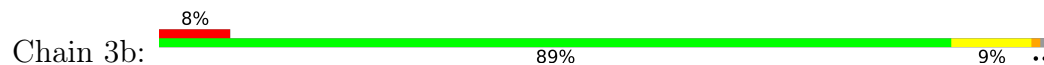
- Molecule 1: Major capsid protein

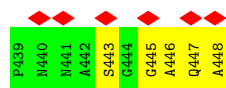


- Molecule 1: Major capsid protein

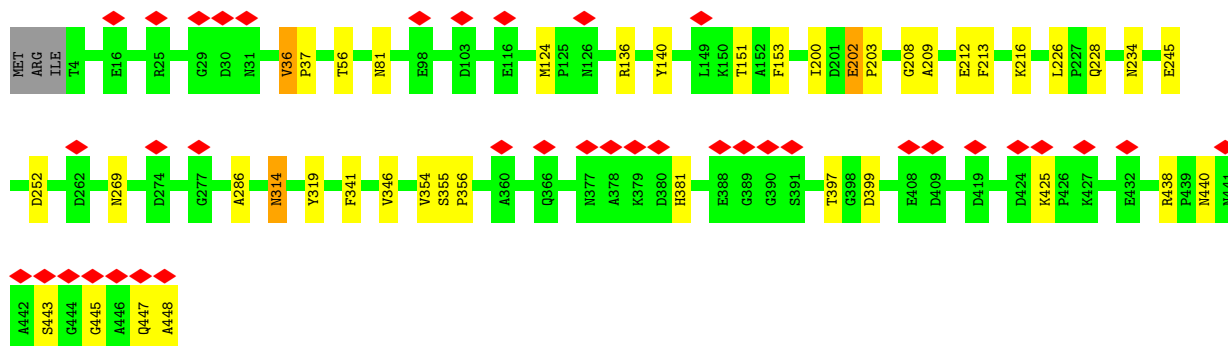
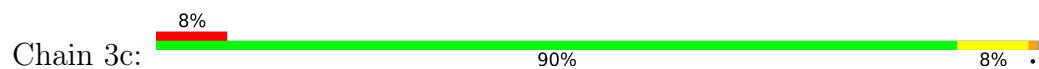


- Molecule 1: Major capsid protein

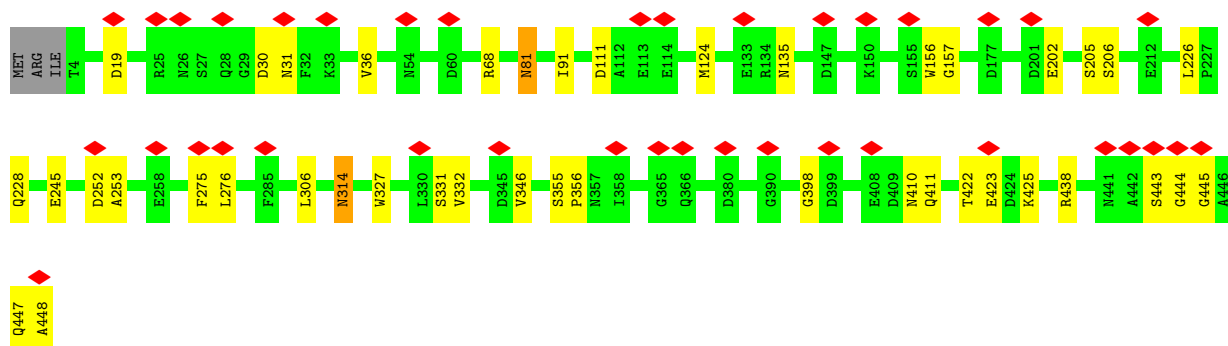
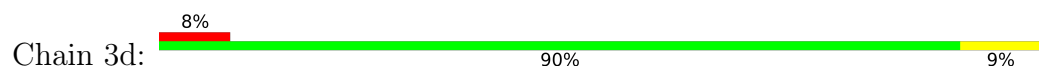




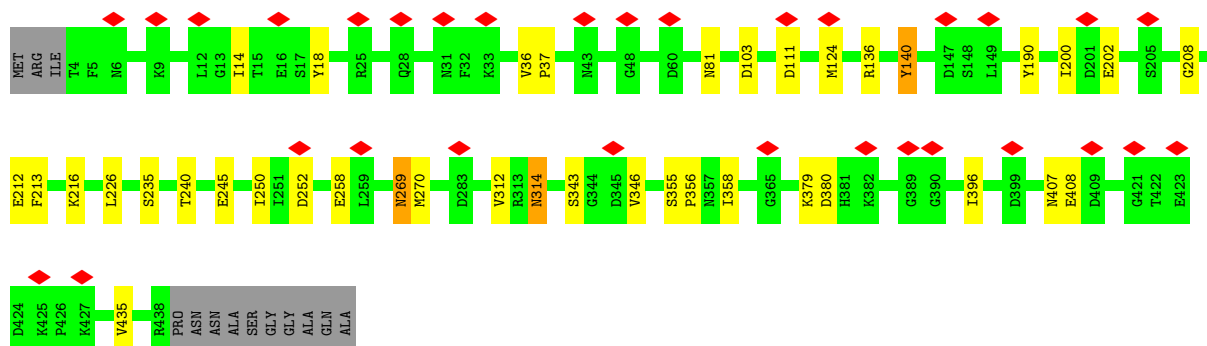
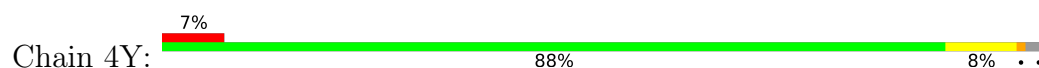
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

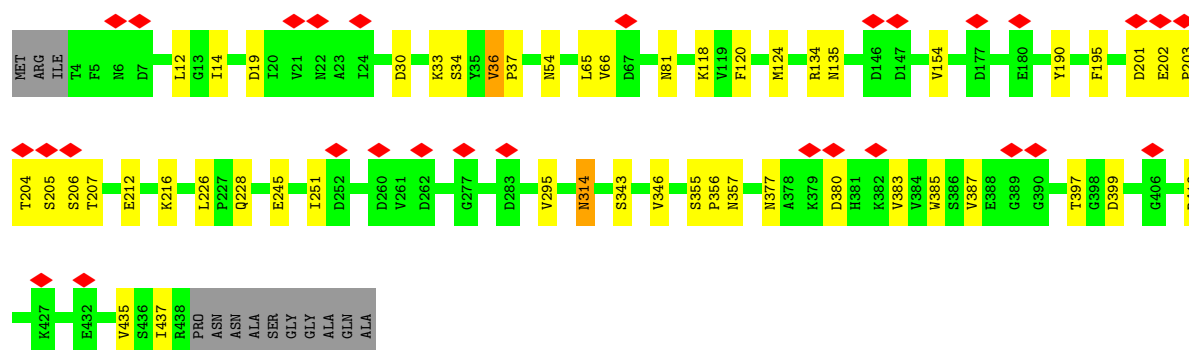


- Molecule 1: Major capsid protein



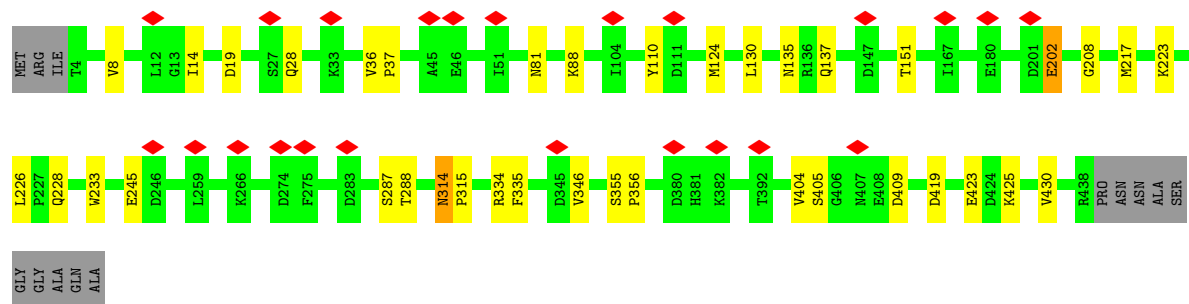
- Molecule 1: Major capsid protein

Chain 4Z: 



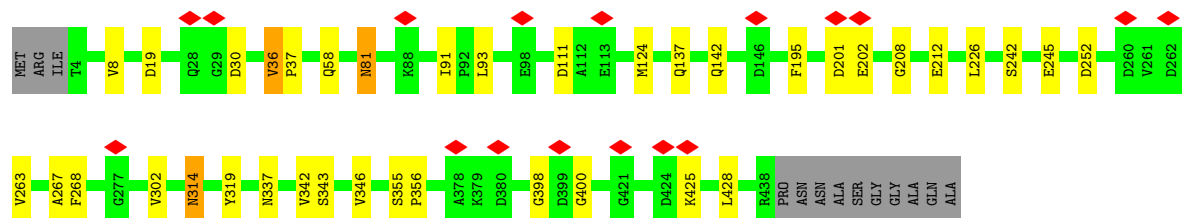
• Molecule 1: Major capsid protein

Chain 4a: 



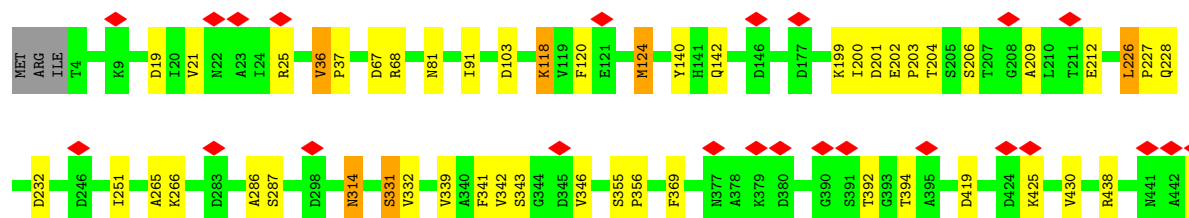
• Molecule 1: Major capsid protein

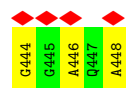
Chain 4b: 



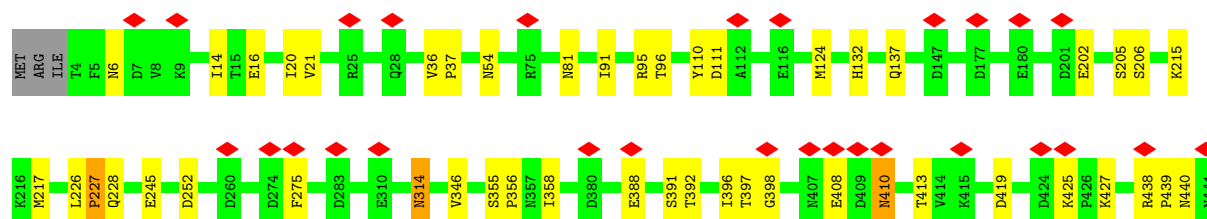
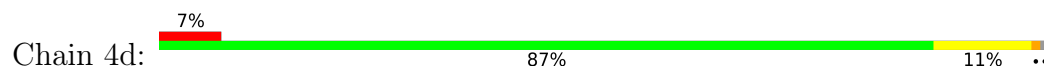
• Molecule 1: Major capsid protein

Chain 4c: 

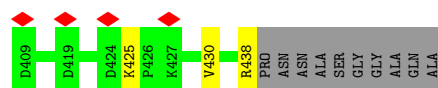
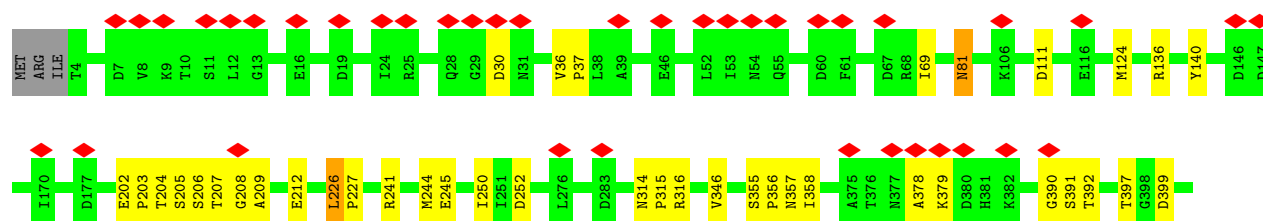
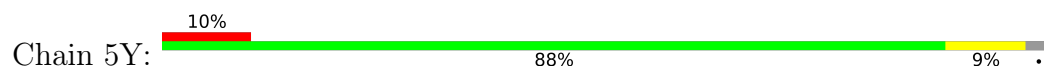




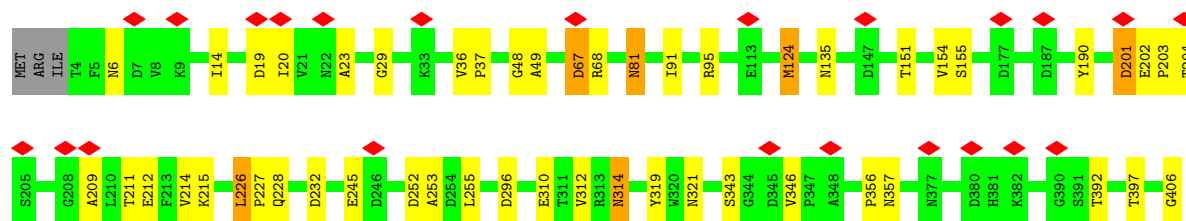
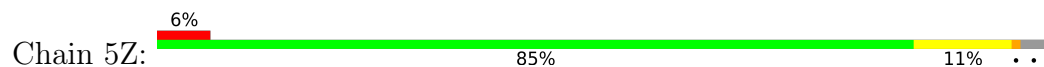
- Molecule 1: Major capsid protein



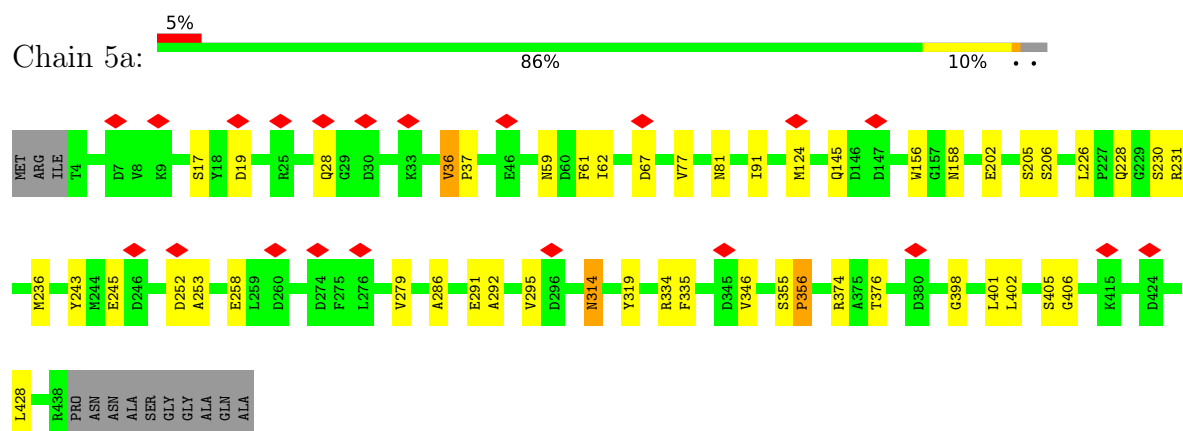
- Molecule 1: Major capsid protein



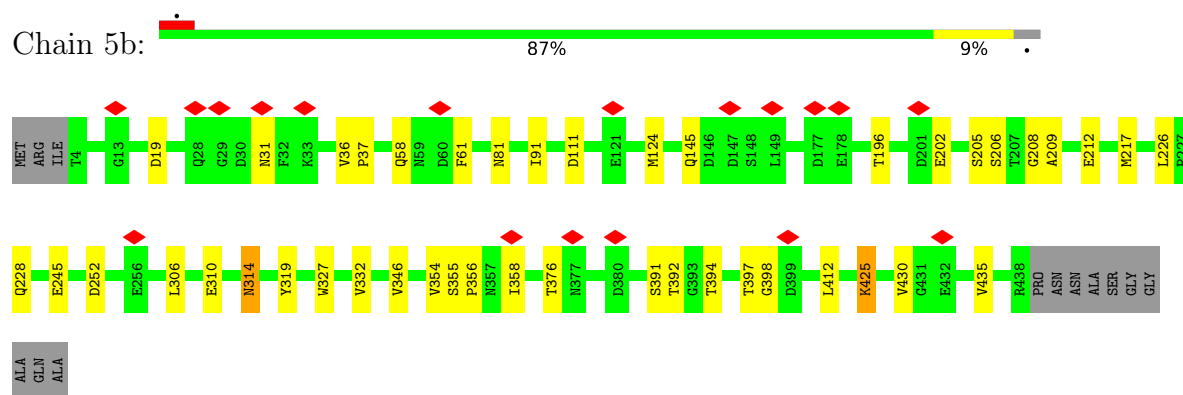
- Molecule 1: Major capsid protein



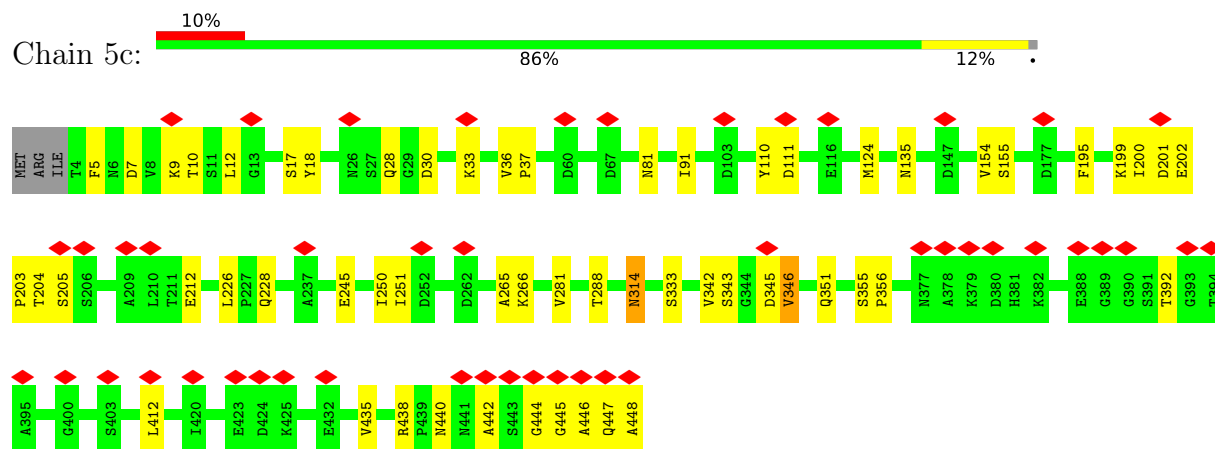
- Molecule 1: Major capsid protein



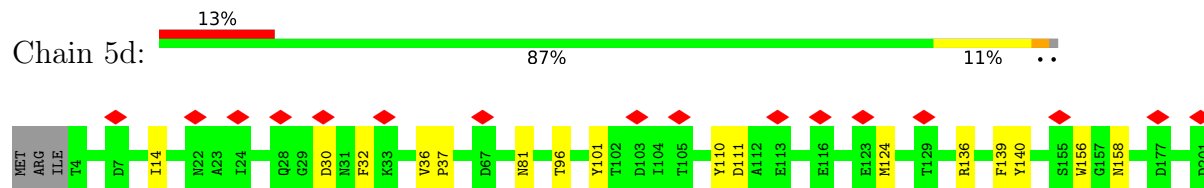
- Molecule 1: Major capsid protein

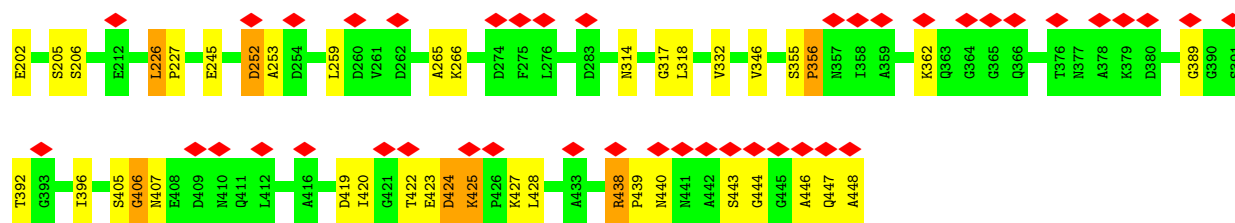


- Molecule 1: Major capsid protein

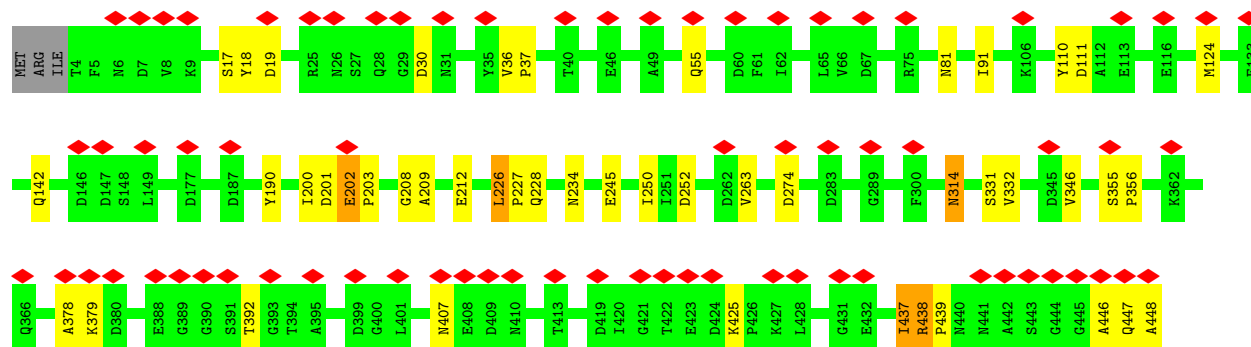
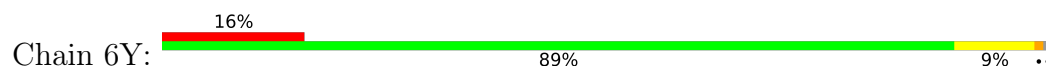


- Molecule 1: Major capsid protein

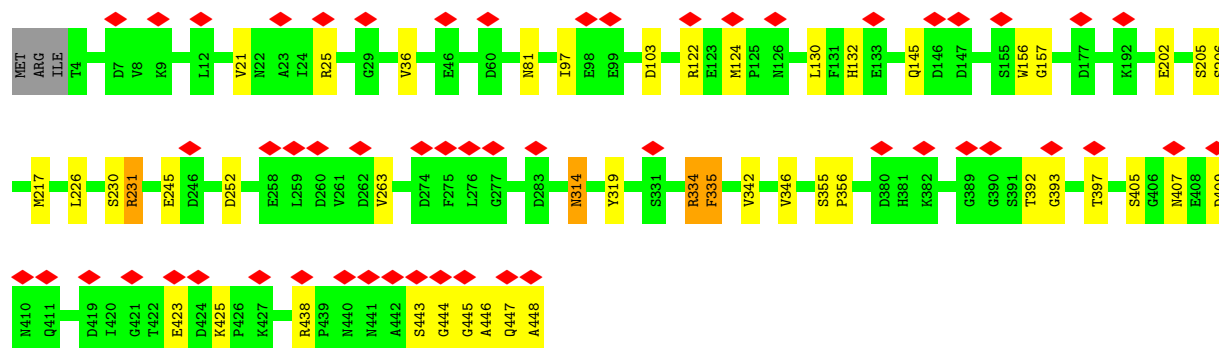
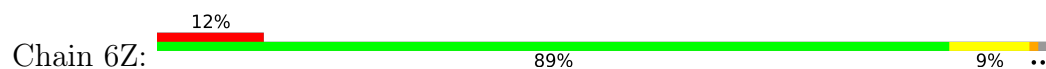




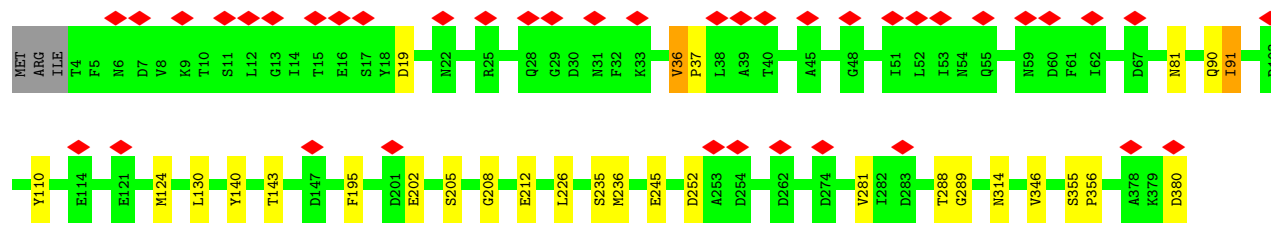
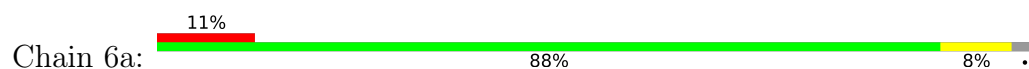
• Molecule 1: Major capsid protein

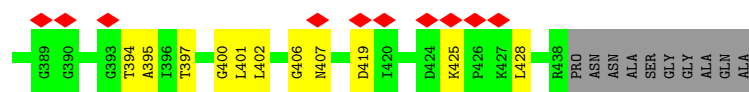


• Molecule 1: Major capsid protein

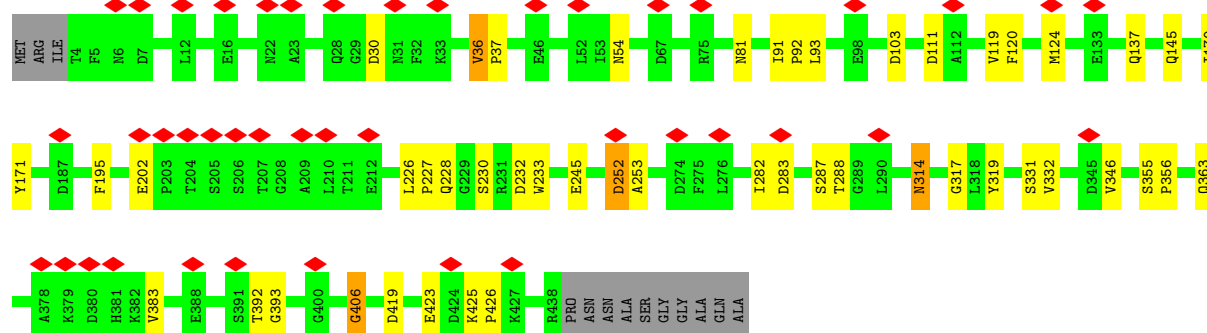
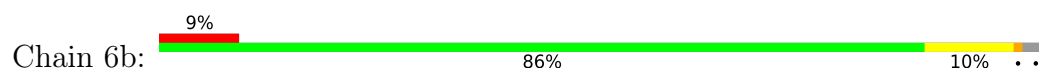


• Molecule 1: Major capsid protein

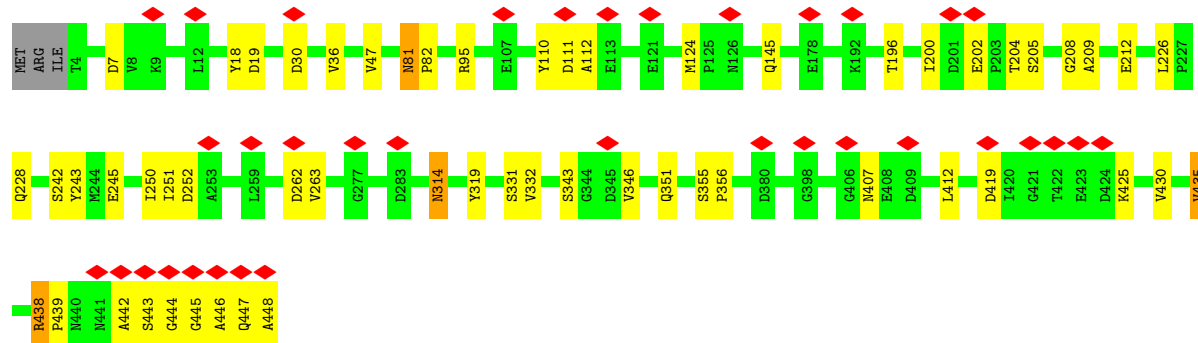
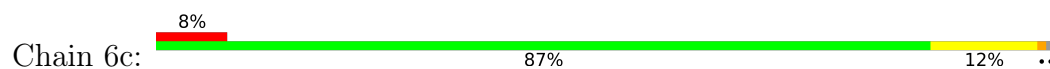




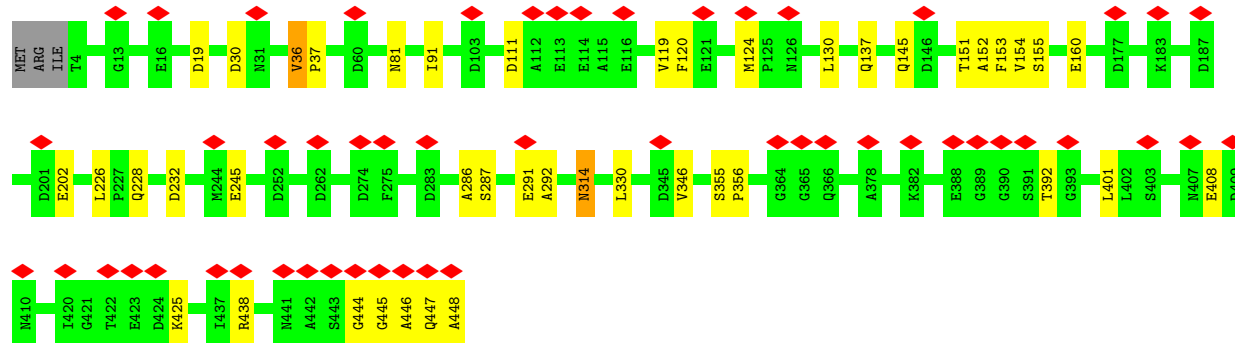
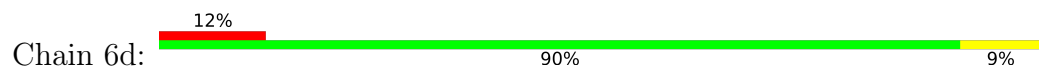
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

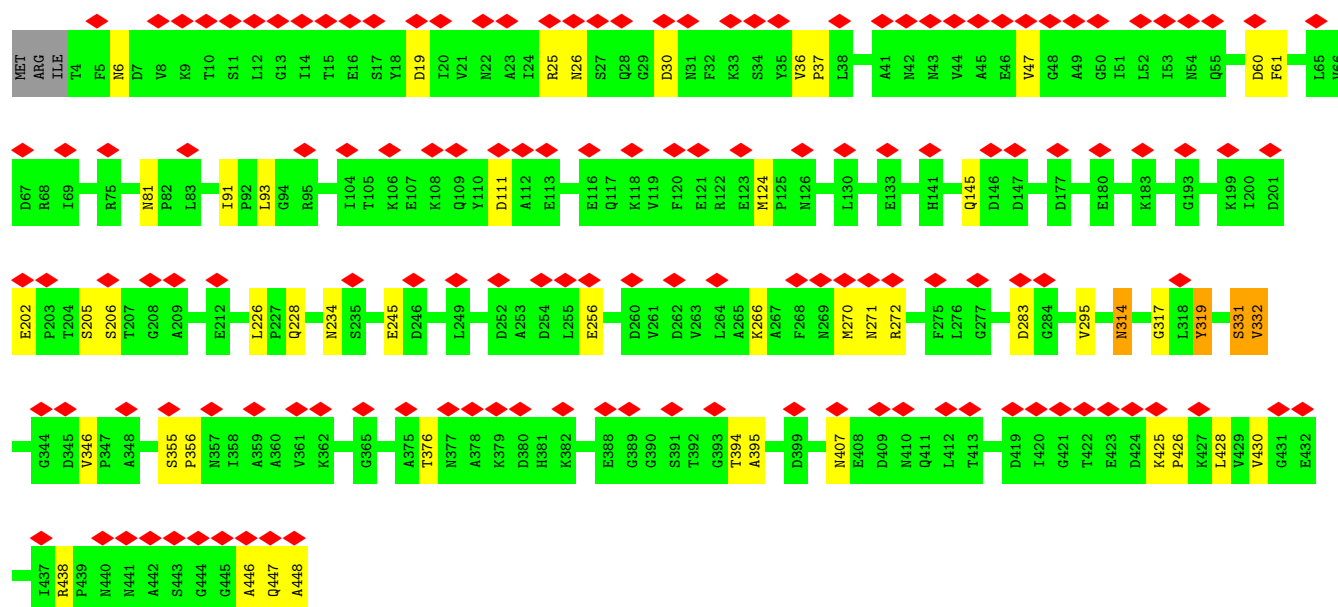


- Molecule 1: Major capsid protein

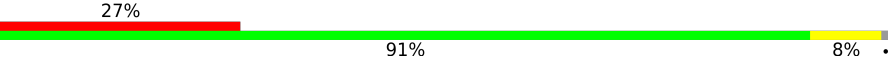


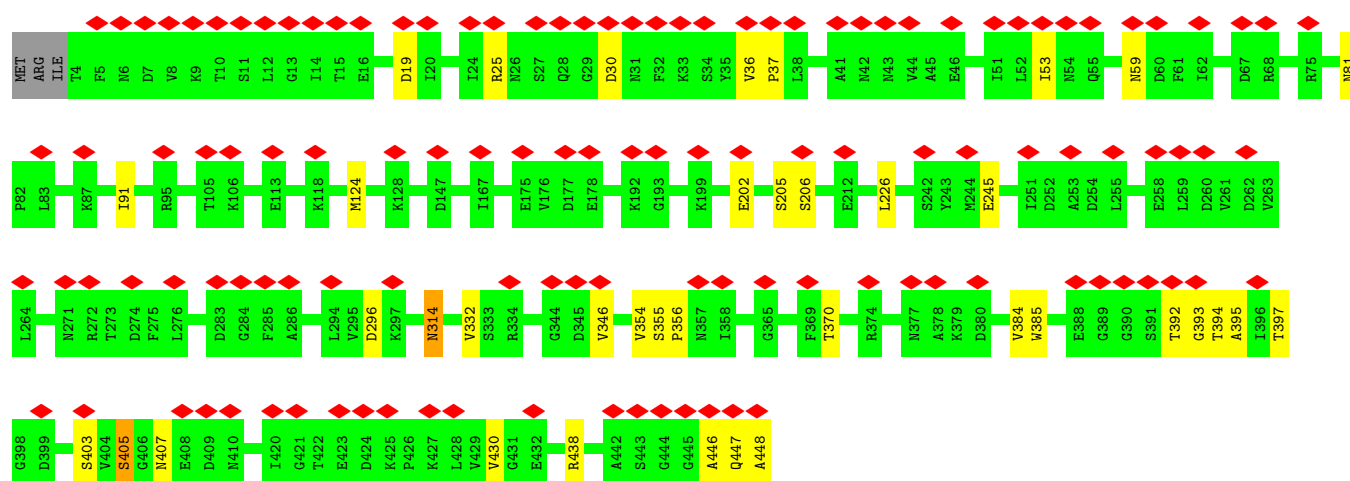
- Molecule 1: Major capsid protein

Chain 7U: 



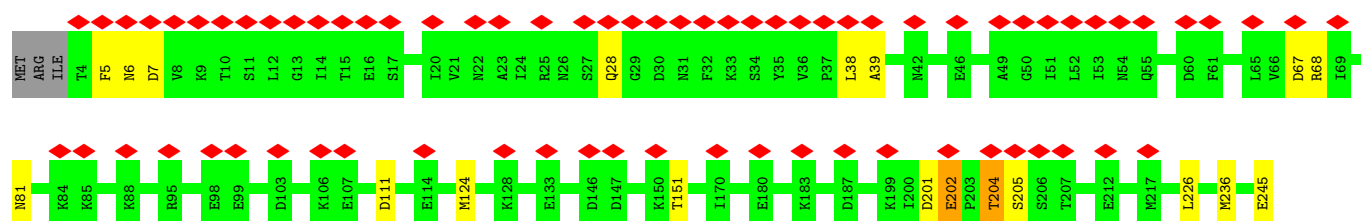
- Molecule 1: Major capsid protein

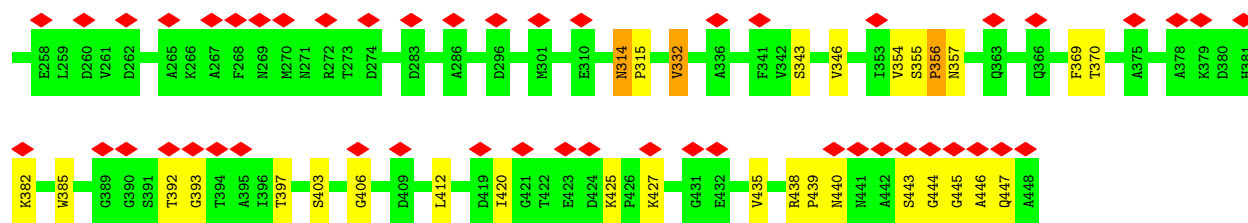
Chain 7V: 



- Molecule 1: Major capsid protein

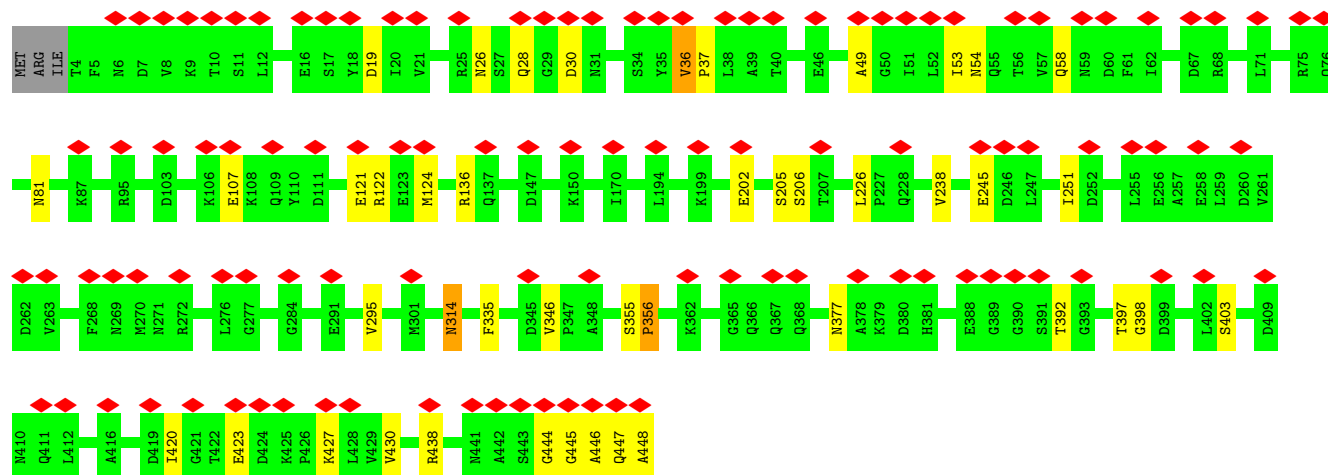
Chain 7W: 





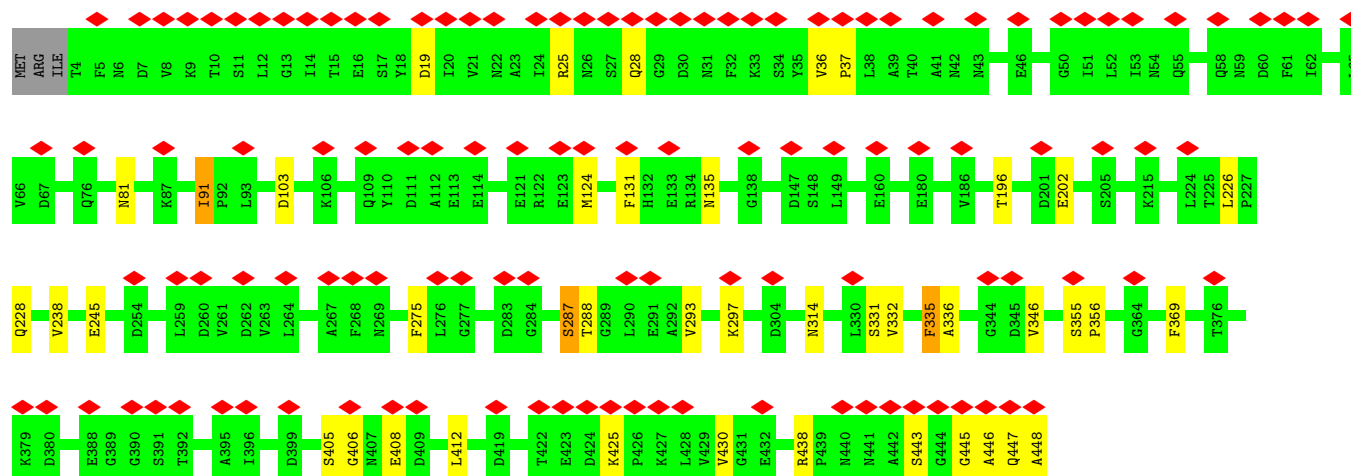
- Molecule 1: Major capsid protein

Chain 7X: 25% 90% 9% ..



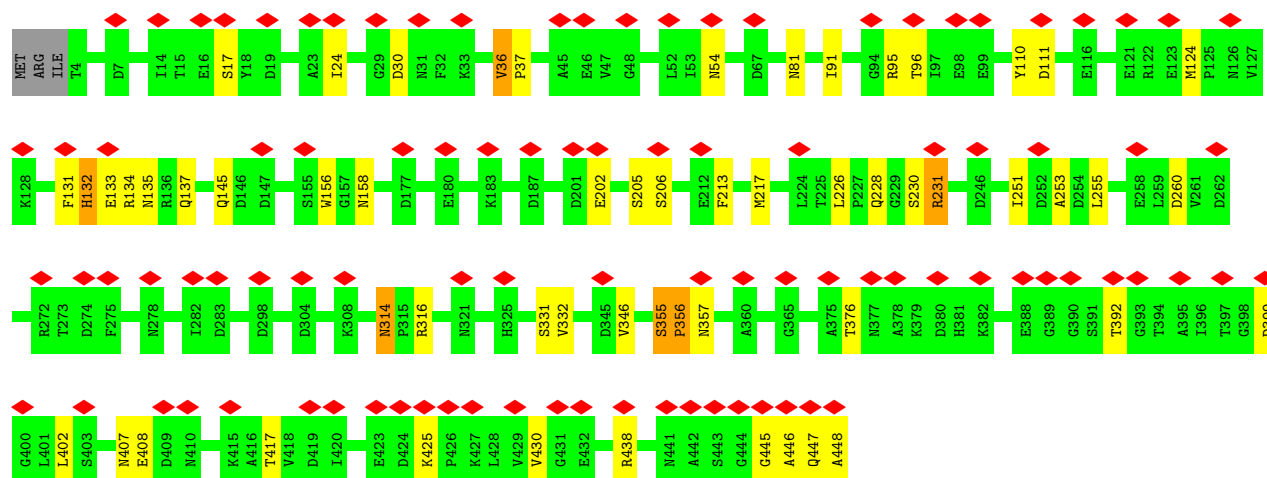
- Molecule 1: Major capsid protein

Chain 7Y: 27% 90% 9% ..

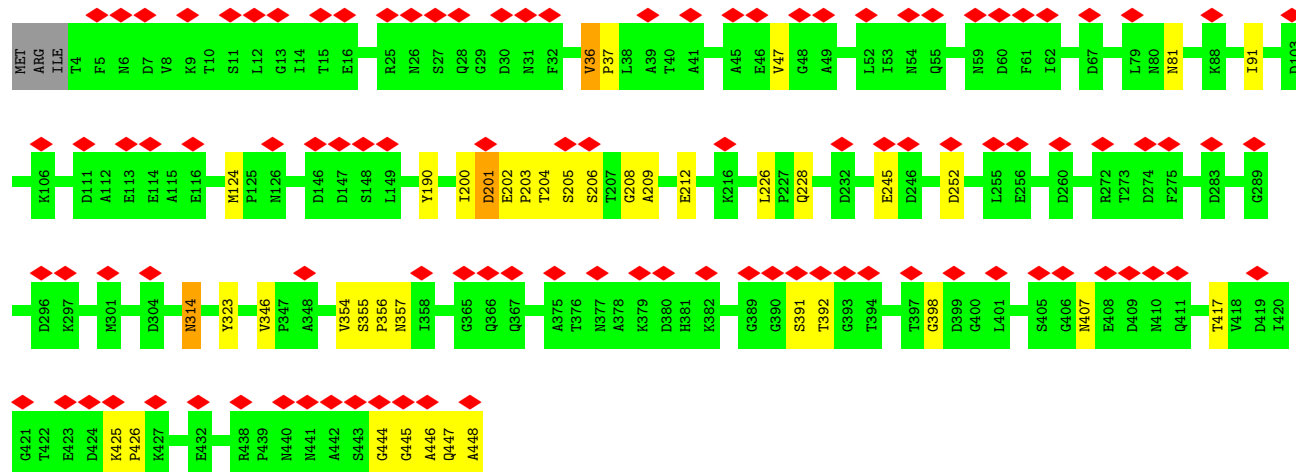
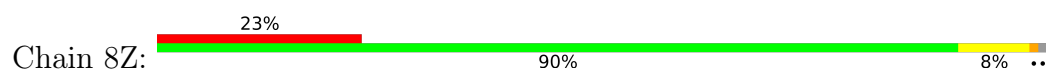


- Molecule 1: Major capsid protein

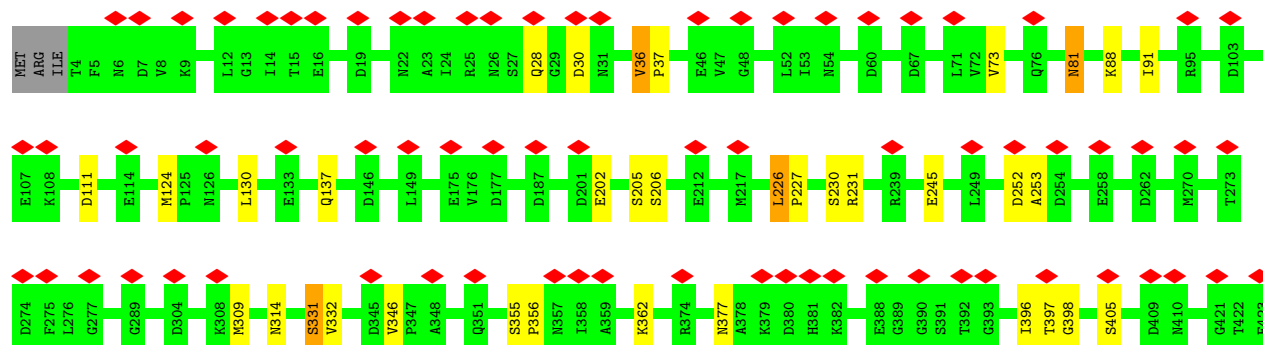
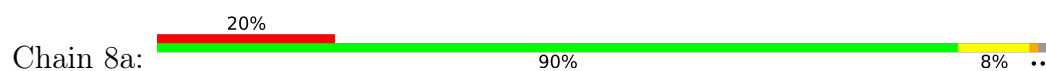
Chain 8Y: 21% 87% 11% ..

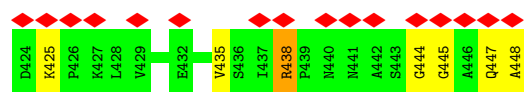


• Molecule 1: Major capsid protein



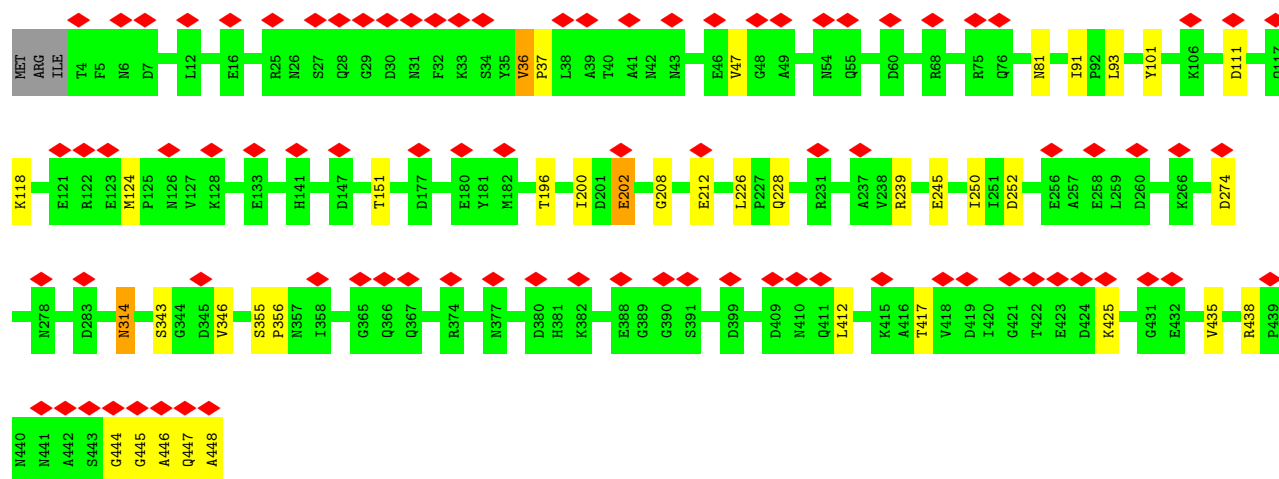
• Molecule 1: Major capsid protein





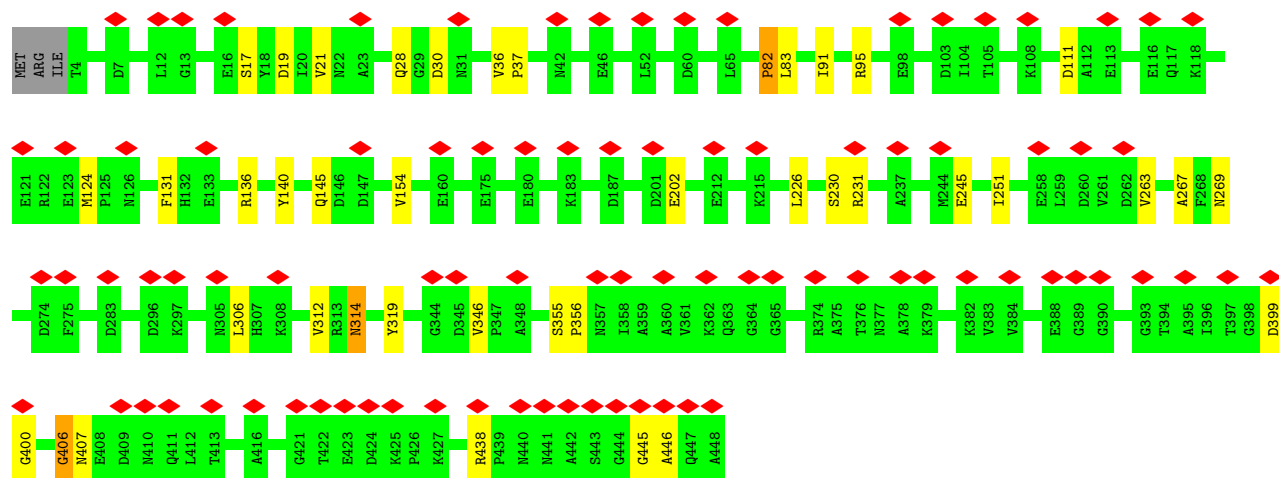
- Molecule 1: Major capsid protein

Chain 8b: 19% 91% 8% ..



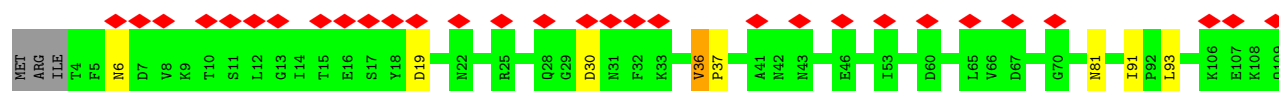
- Molecule 1: Major capsid protein

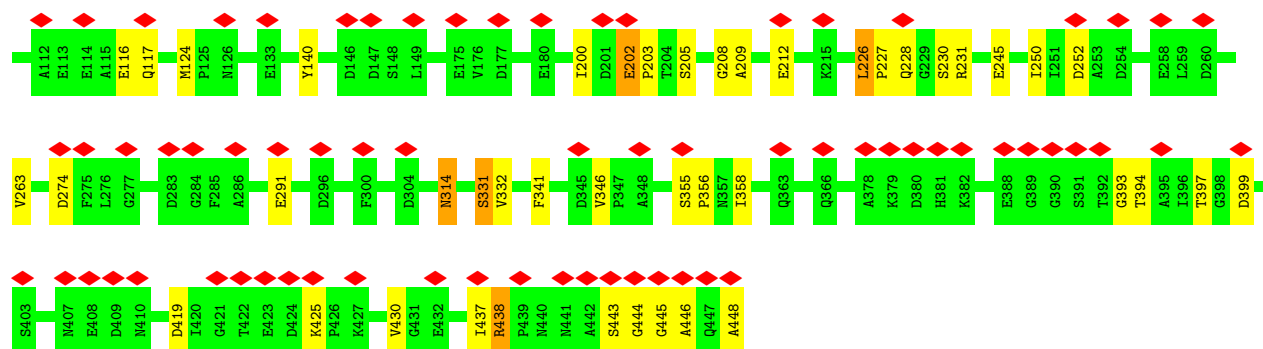
Chain 8c: 20% 90% 8% ..



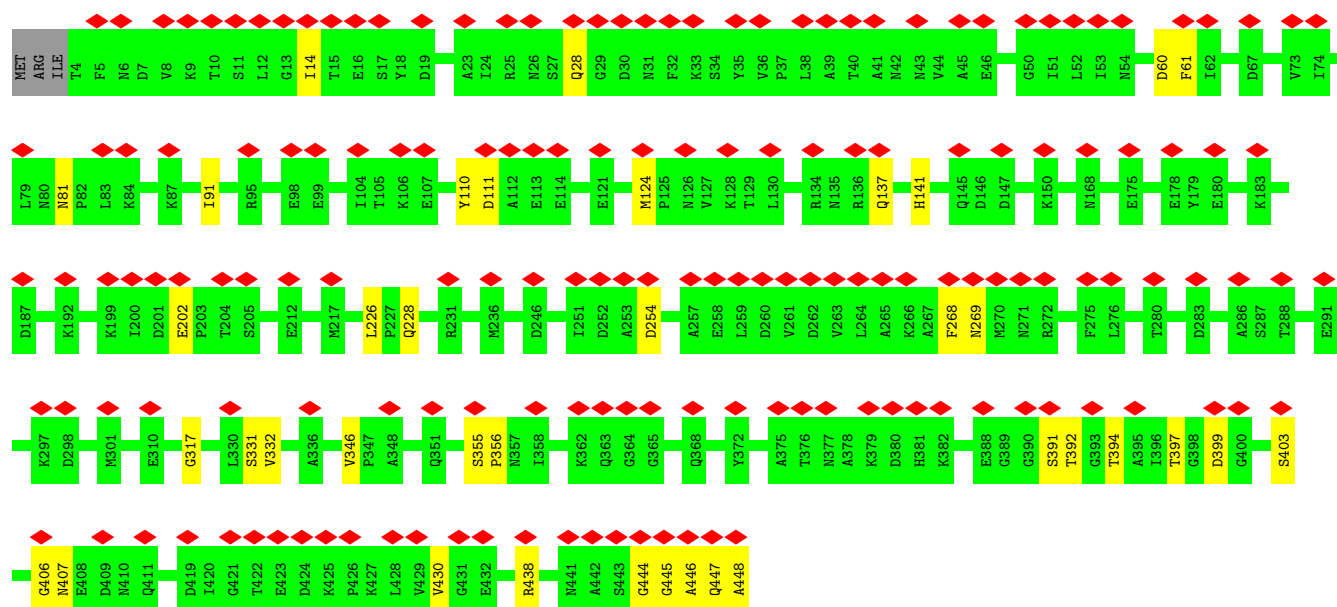
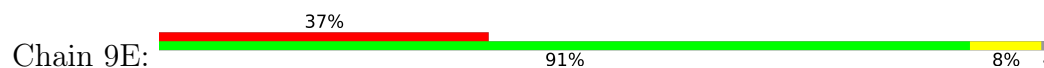
- Molecule 1: Major capsid protein

Chain 8d: 22% 88% 10% ..

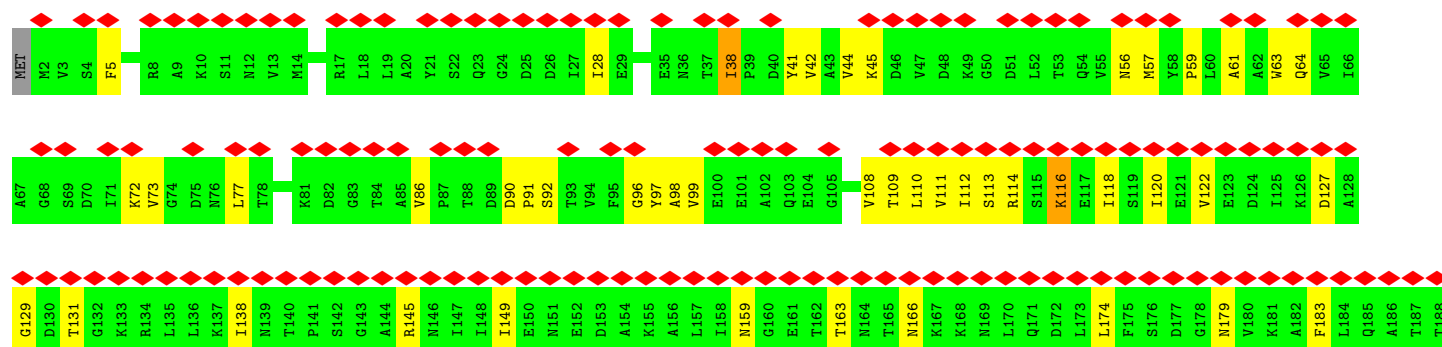
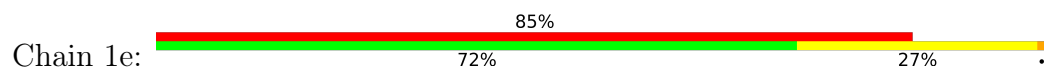




• Molecule 1: Major capsid protein

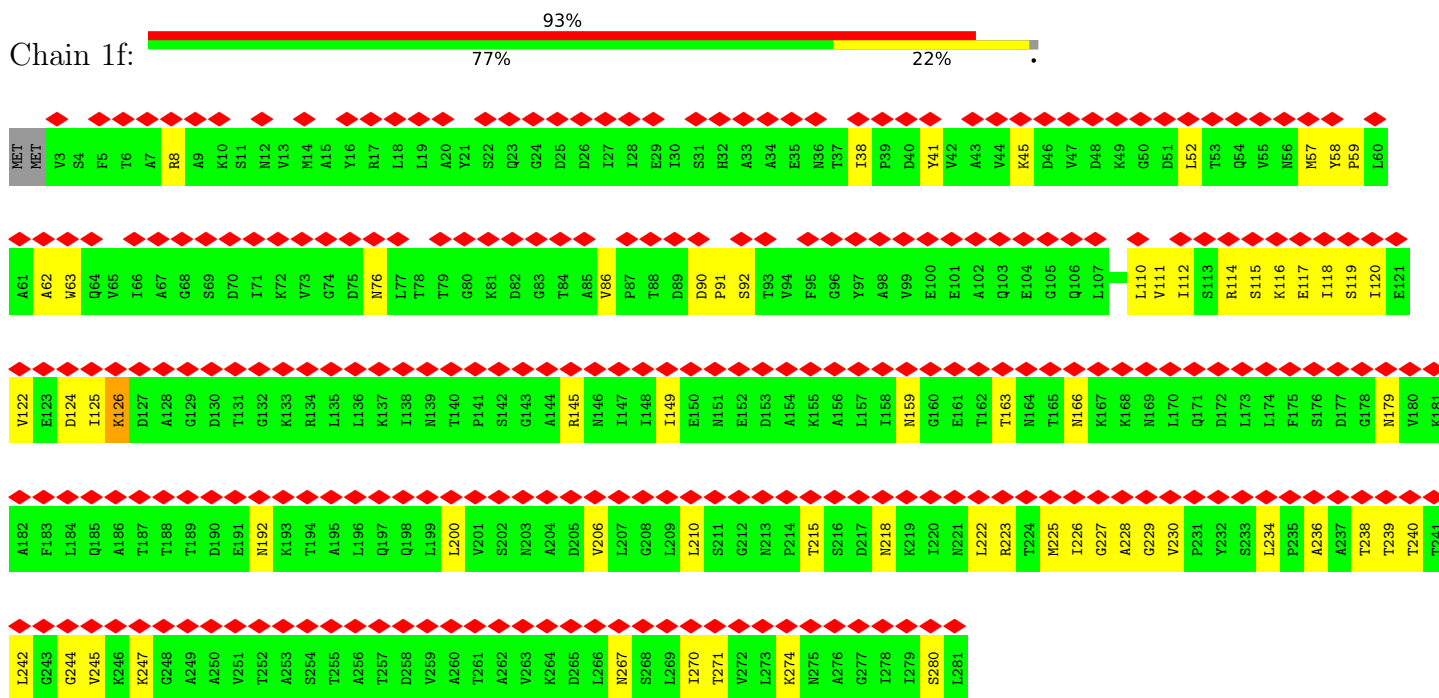


• Molecule 2: Capsid fiber protein

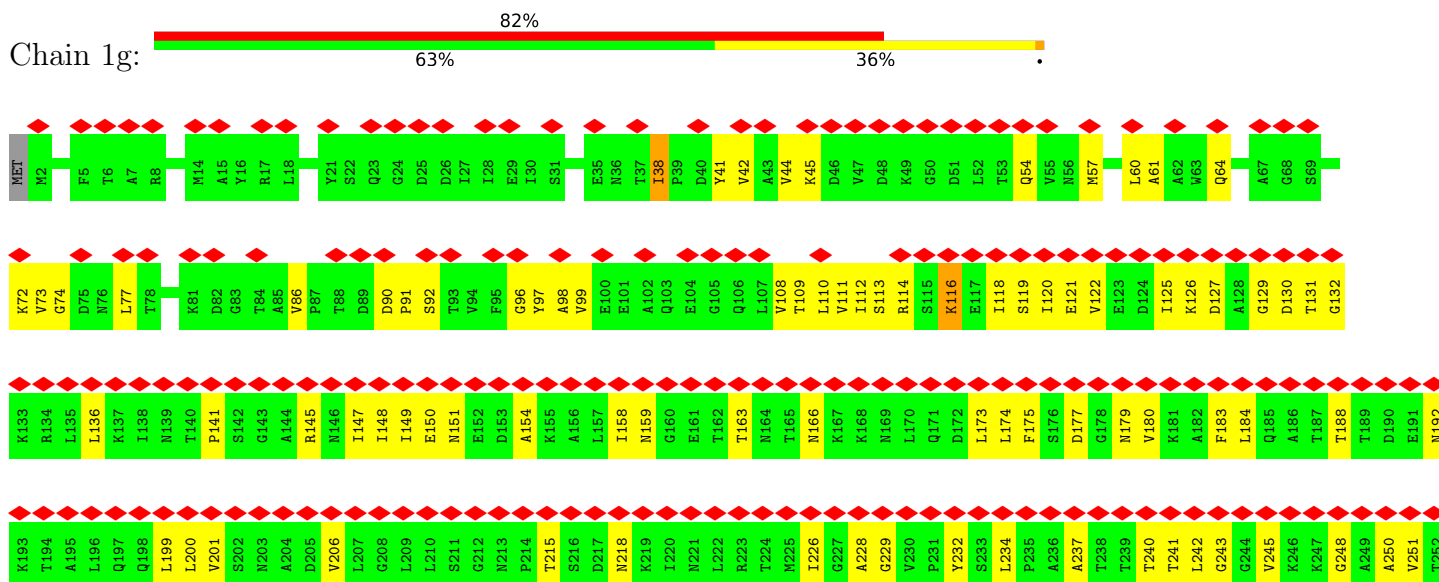




• Molecule 2: Capsid fiber protein

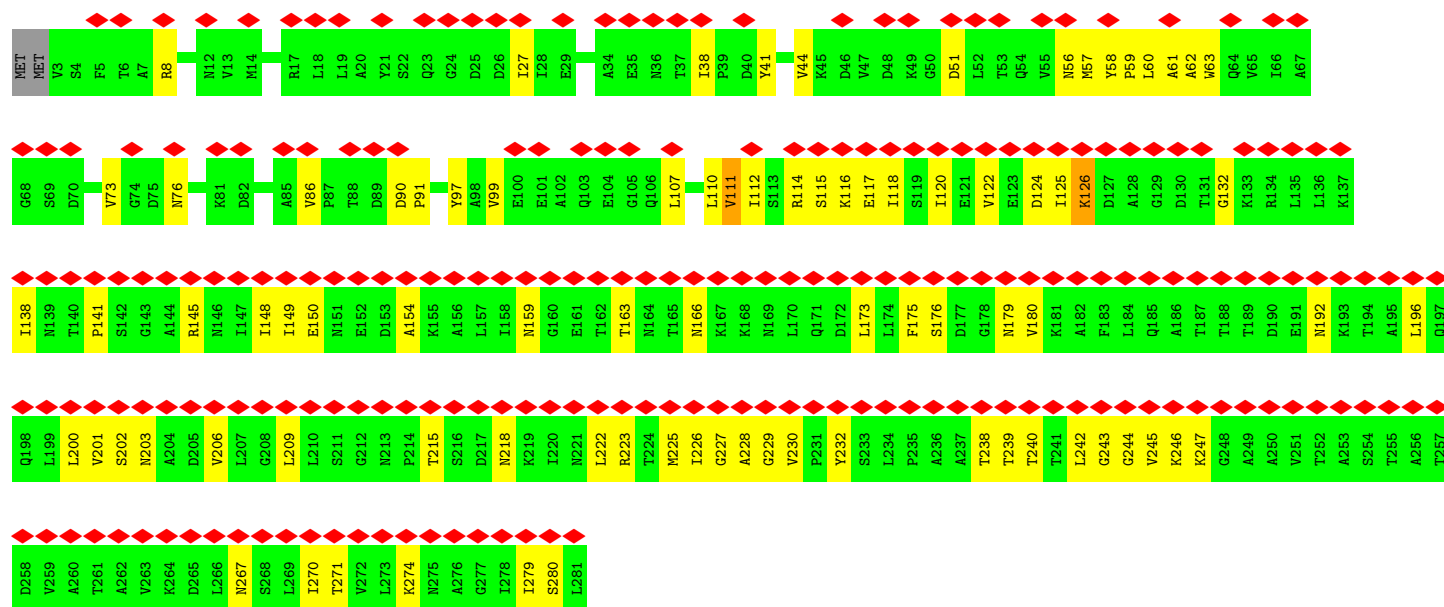
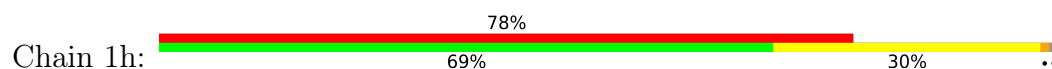


• Molecule 2: Capsid fiber protein

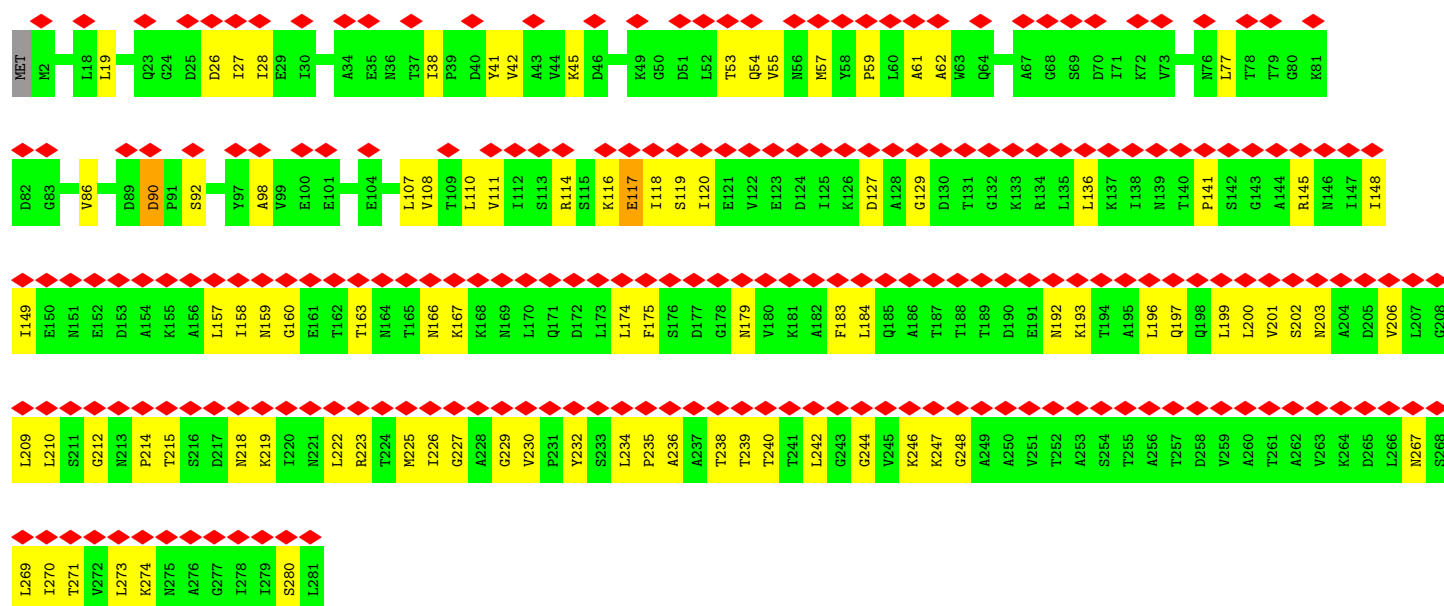
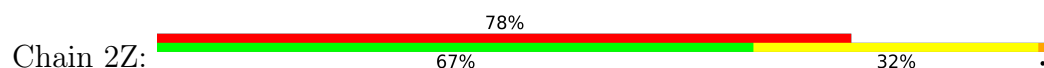




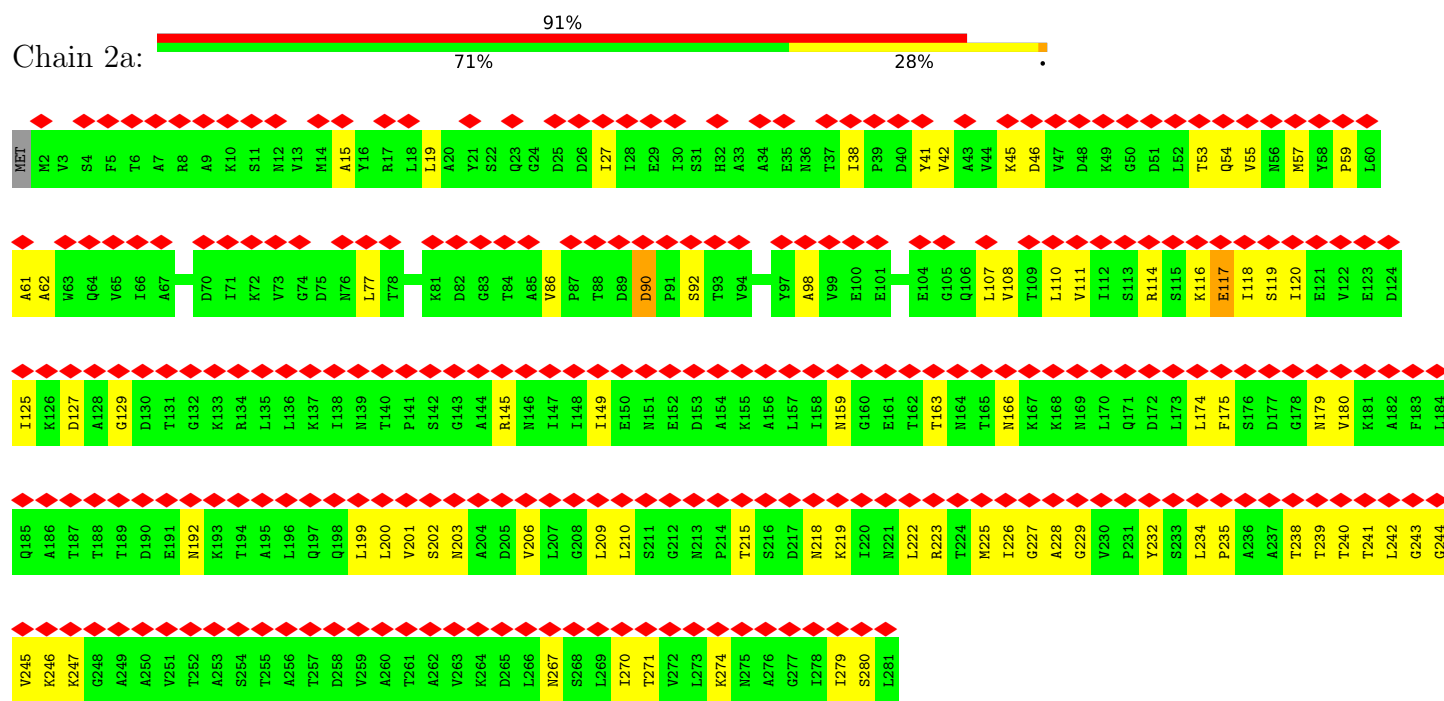
• Molecule 2: Capsid fiber protein



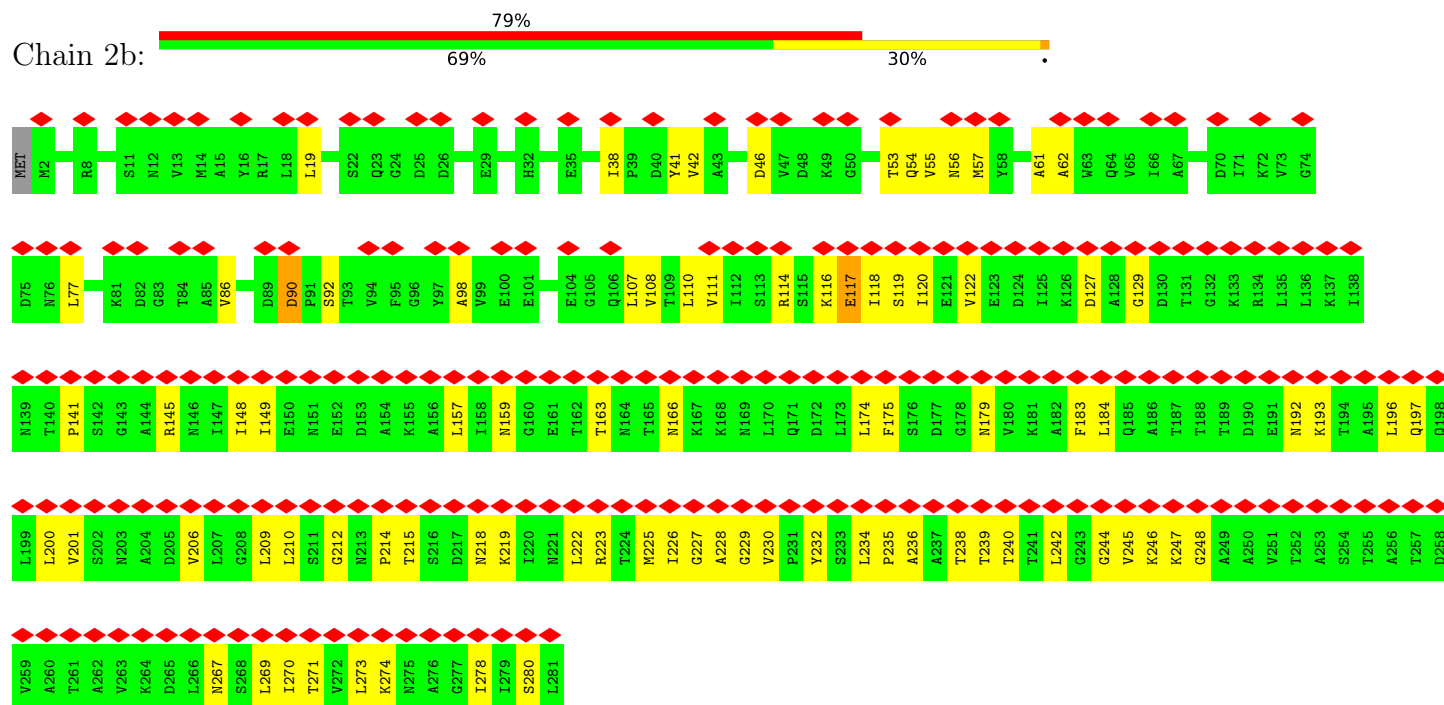
• Molecule 2: Capsid fiber protein



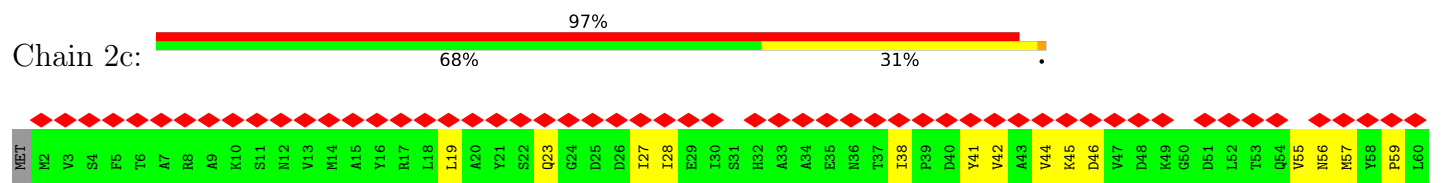
• Molecule 2: Capsid fiber protein

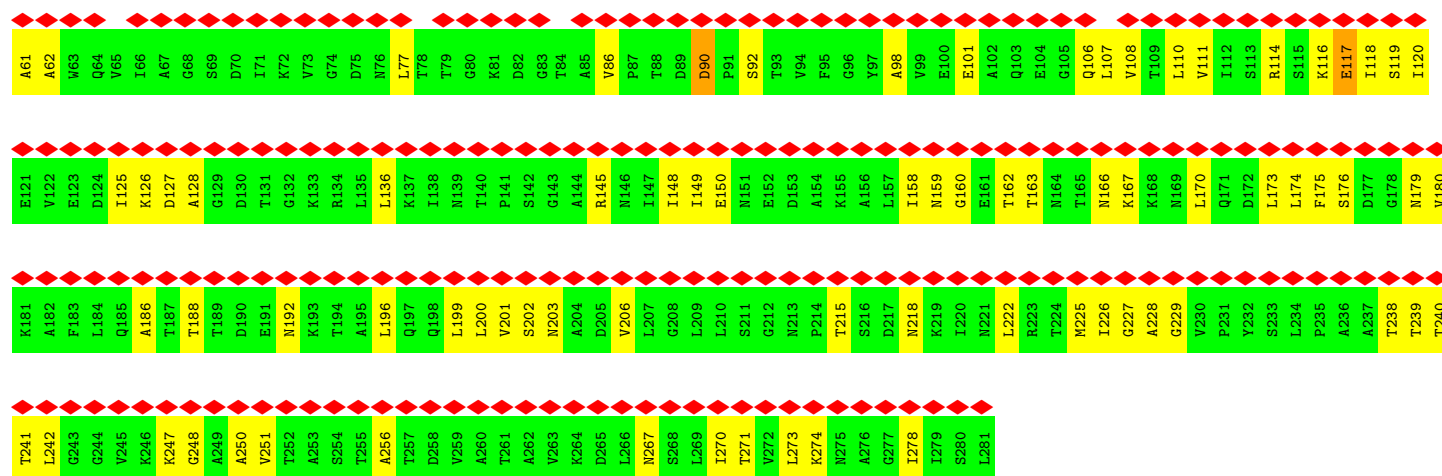


• Molecule 2: Capsid fiber protein

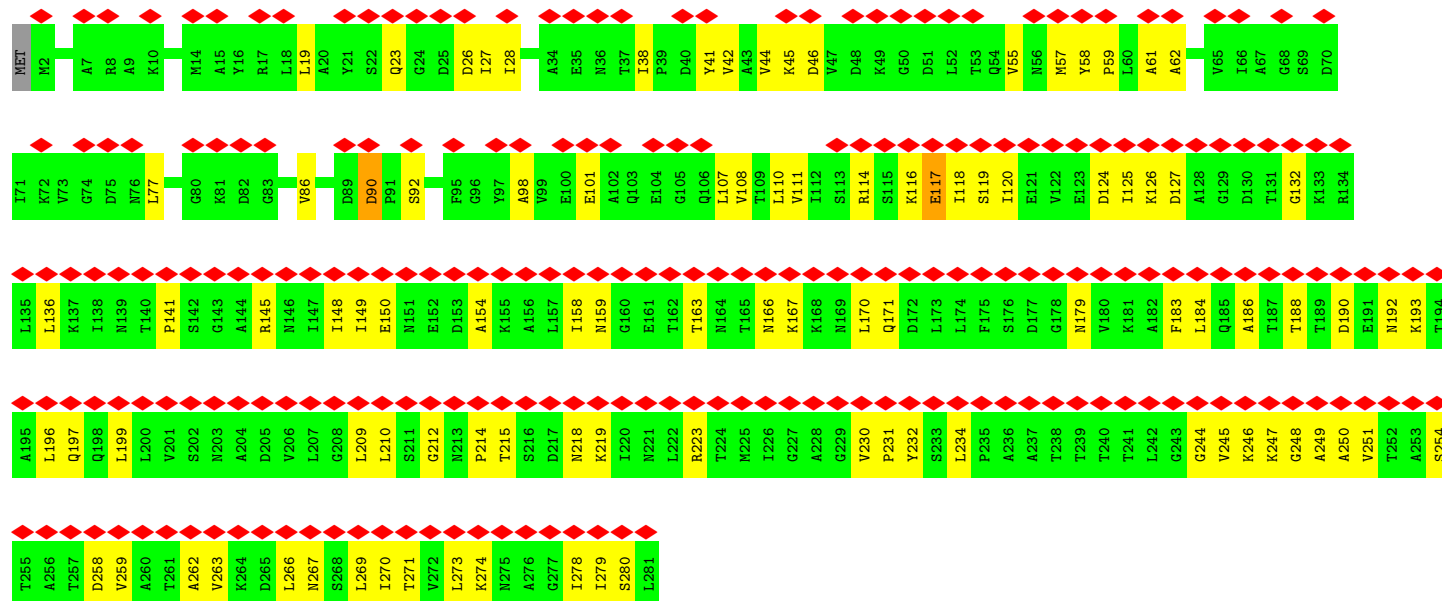
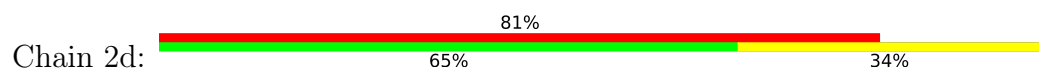


• Molecule 2: Capsid fiber protein

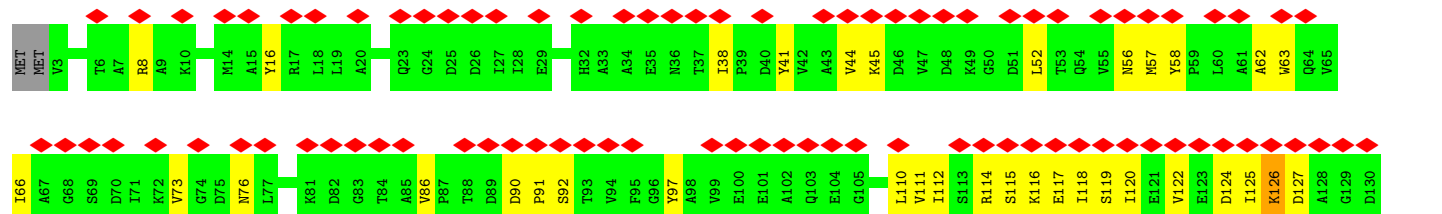
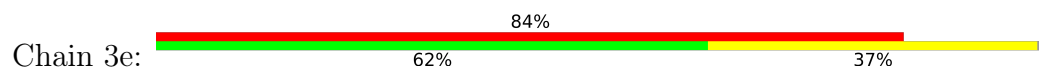




• Molecule 2: Capsid fiber protein



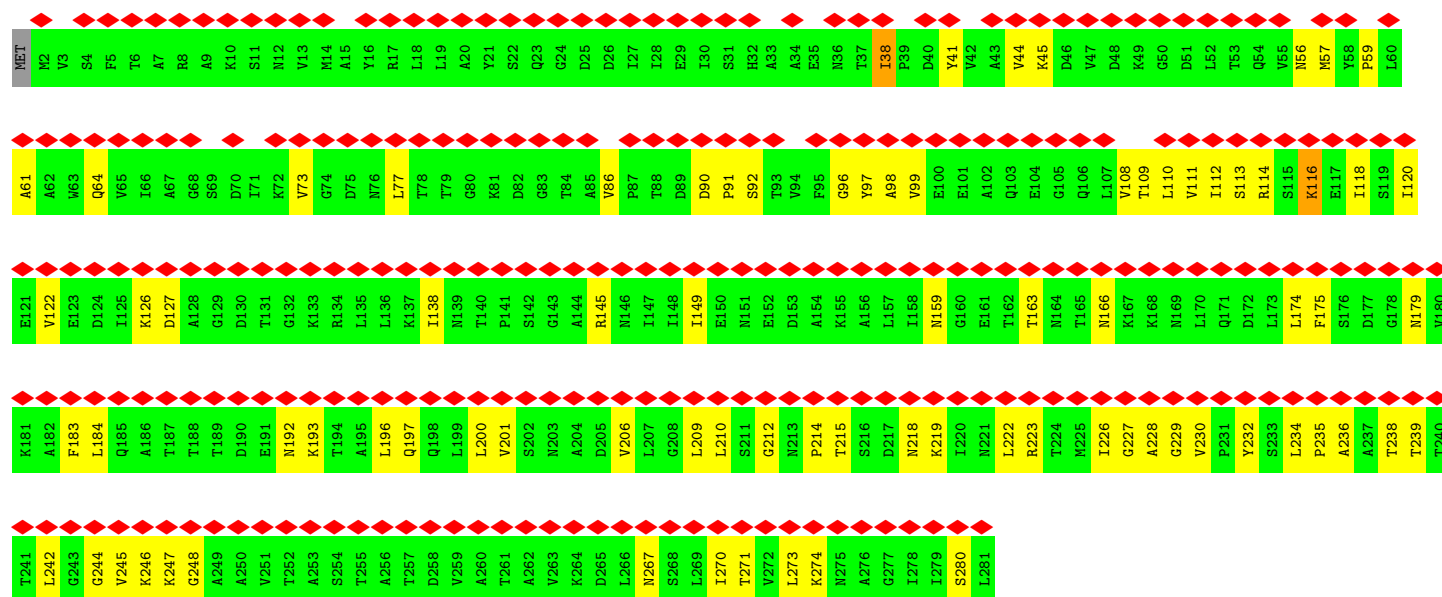
• Molecule 2: Capsid fiber protein





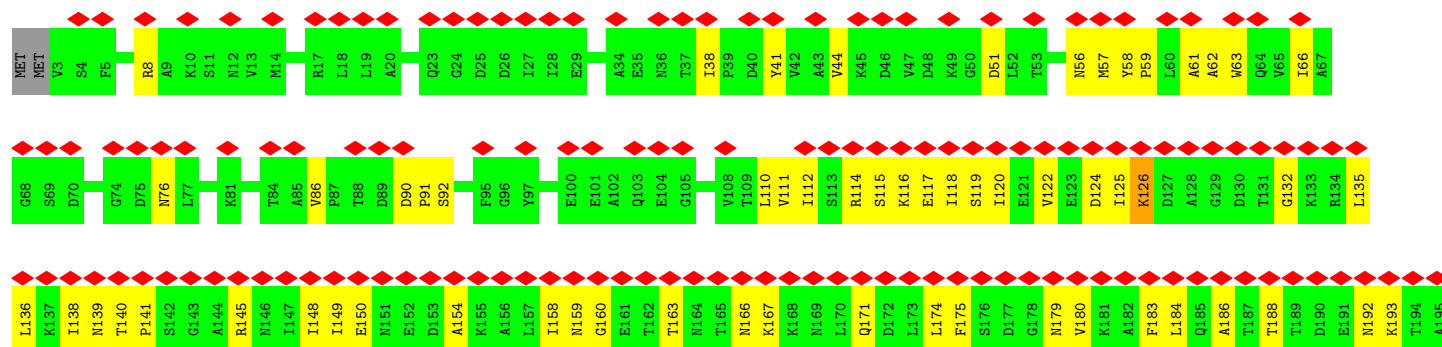
• Molecule 2: Capsid fiber protein

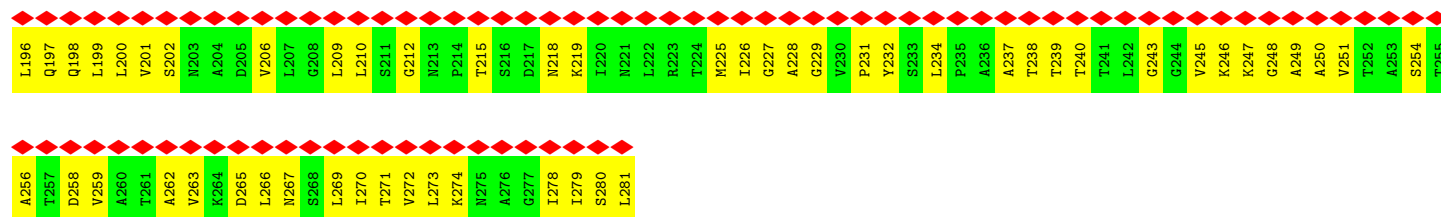
Chain 3f: 70% 95% 28% .



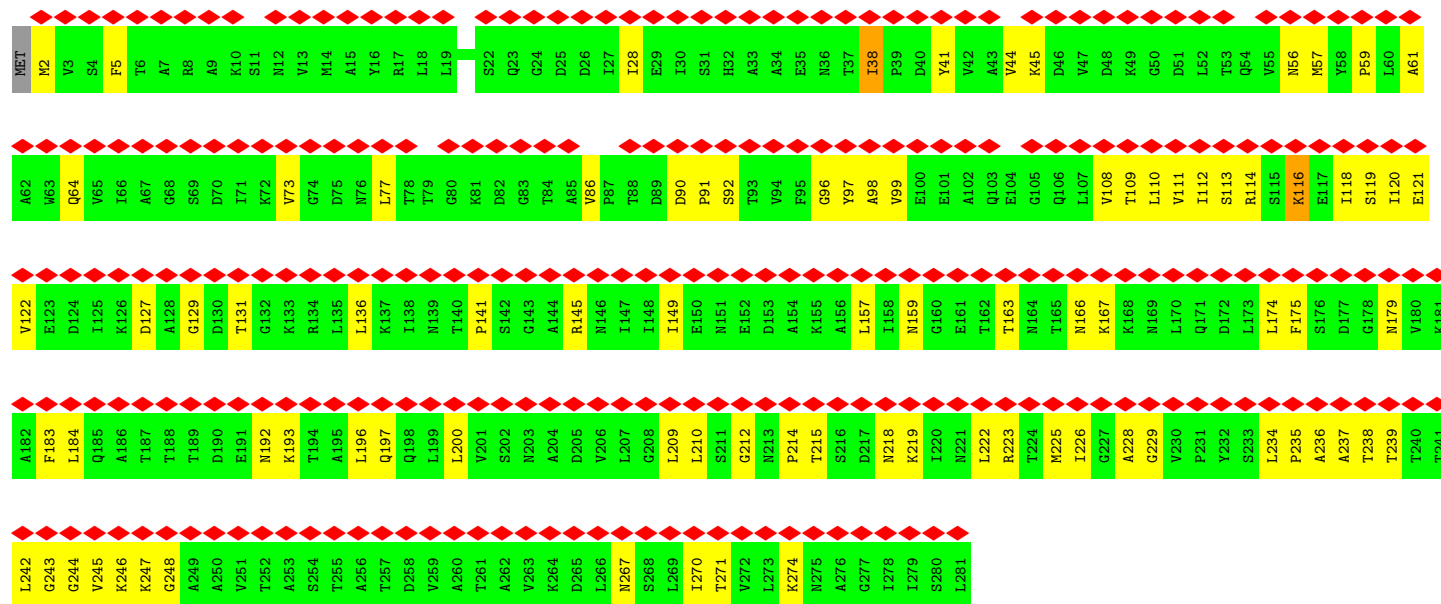
• Molecule 2: Capsid fiber protein

Chain 3g: 59% 81% 40% .

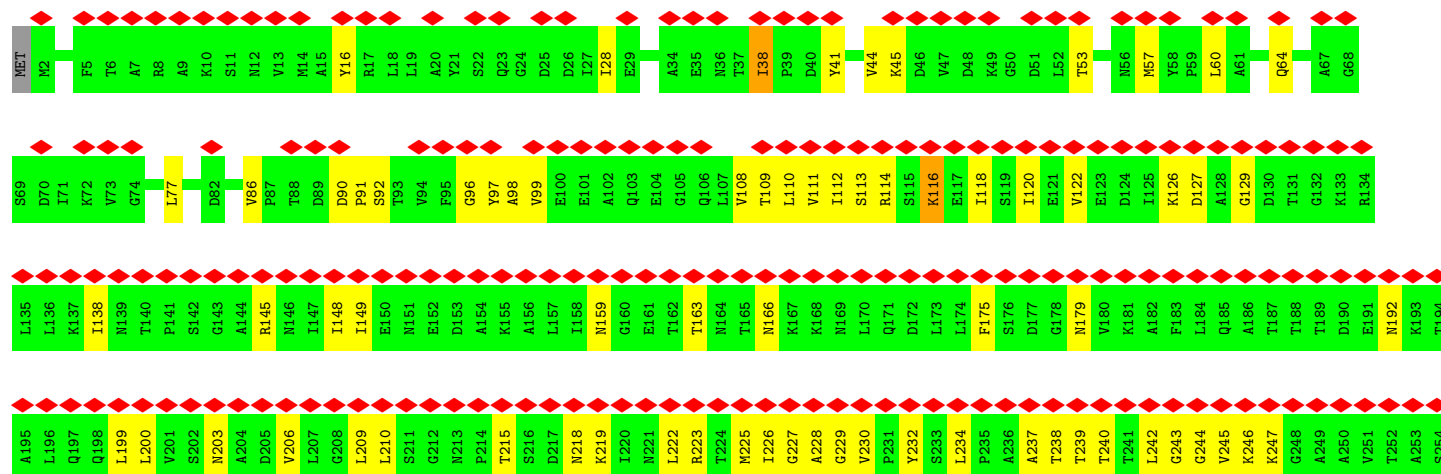
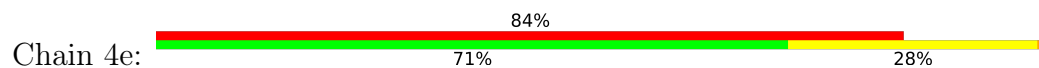




• Molecule 2: Capsid fiber protein

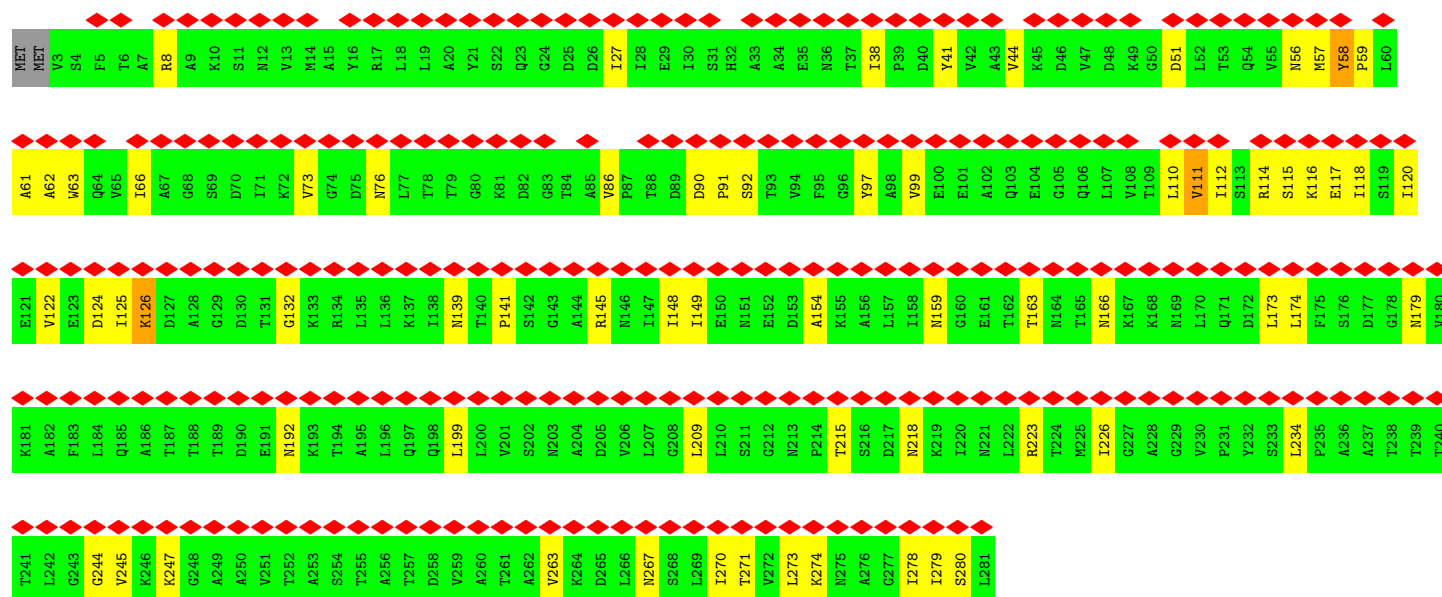
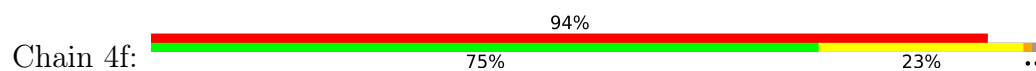


• Molecule 2: Capsid fiber protein

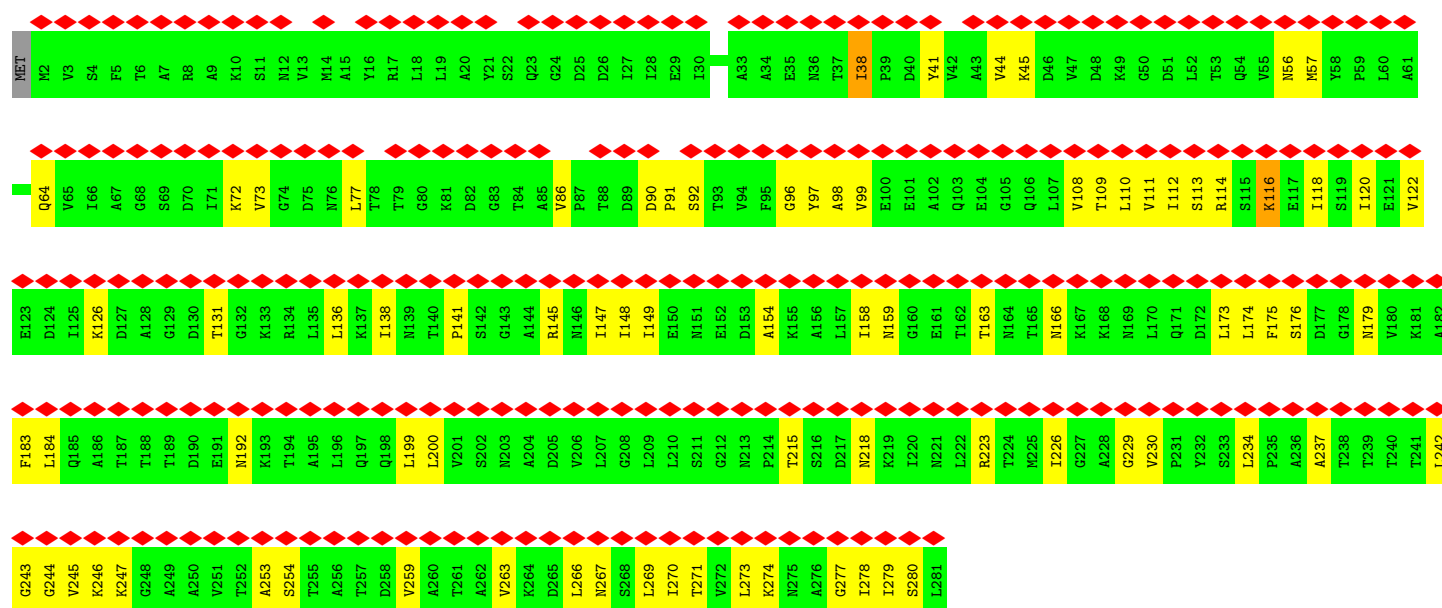
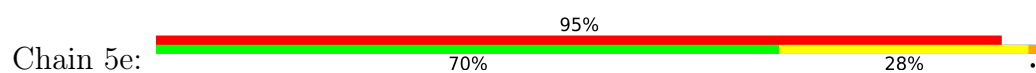




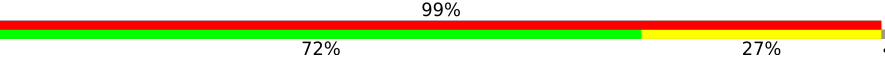
• Molecule 2: Capsid fiber protein

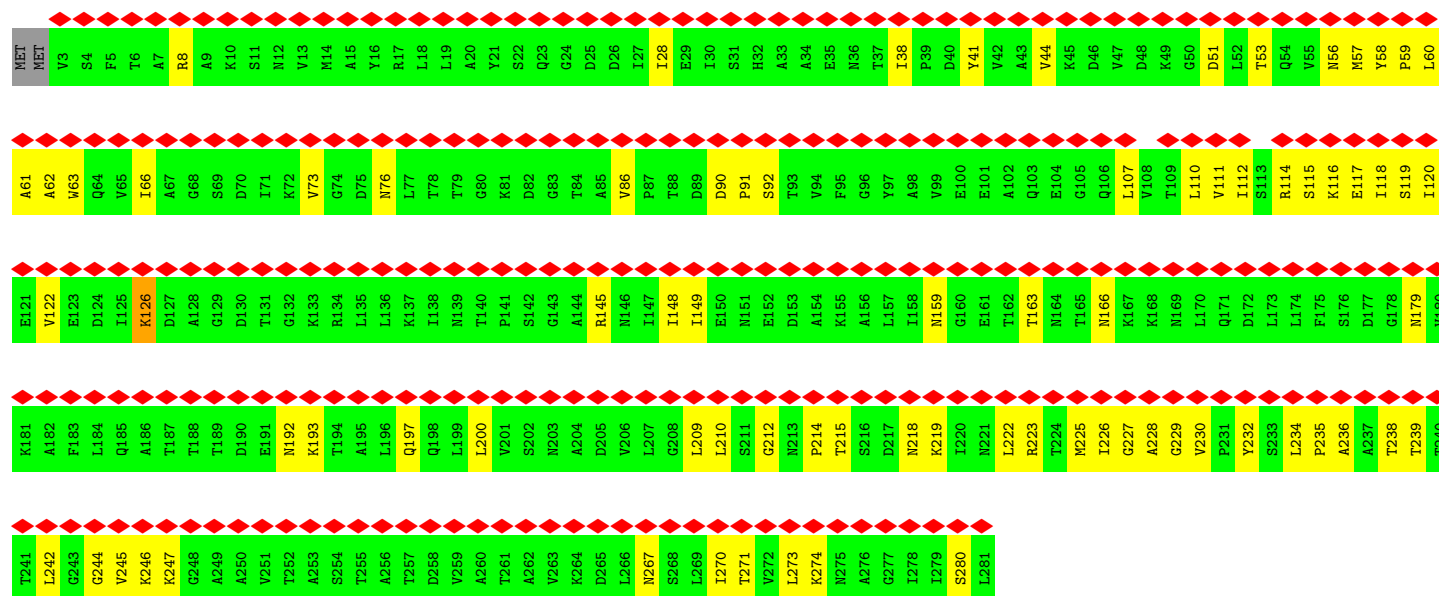


• Molecule 2: Capsid fiber protein

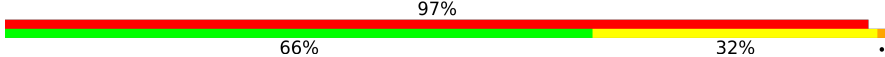


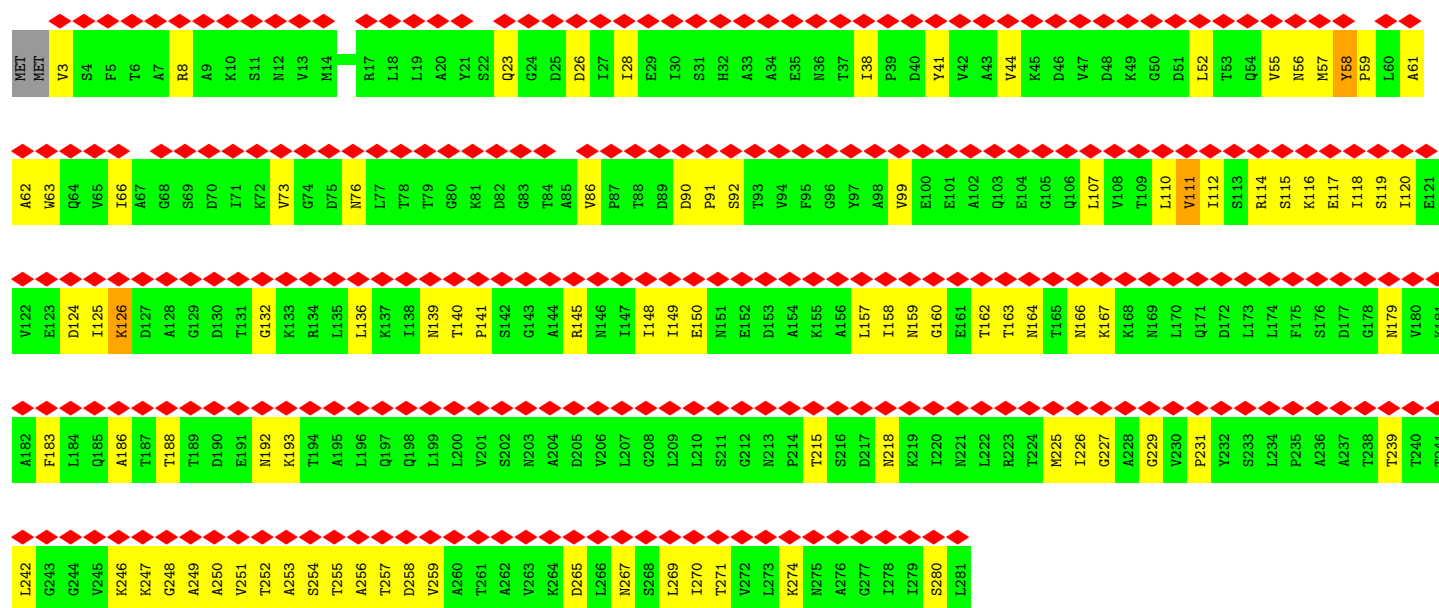
• Molecule 2: Capsid fiber protein

Chain 5f: 



• Molecule 2: Capsid fiber protein

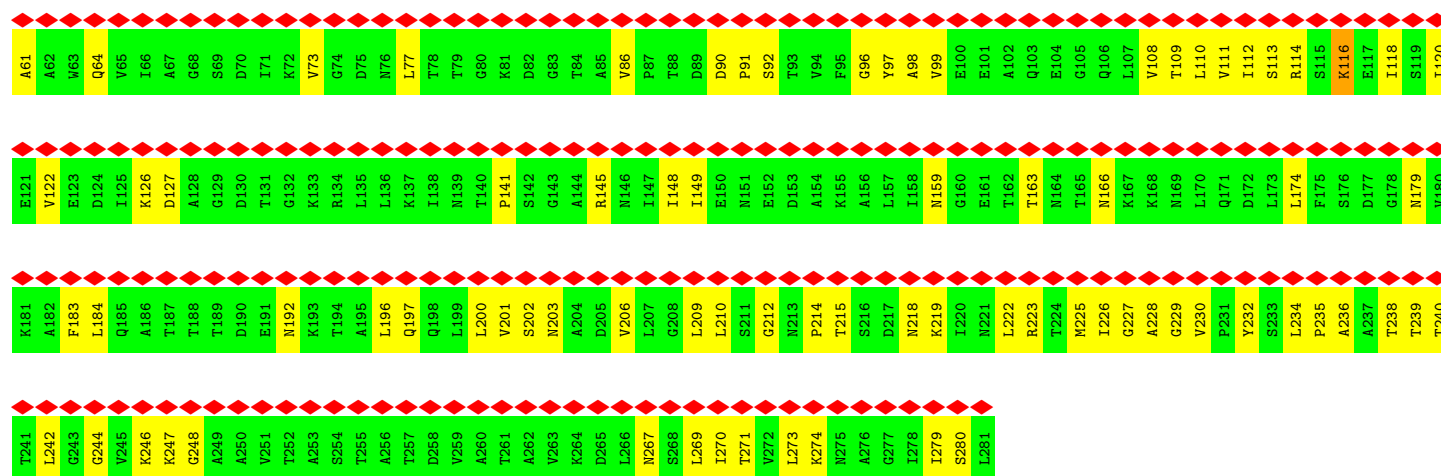
Chain 6e: 



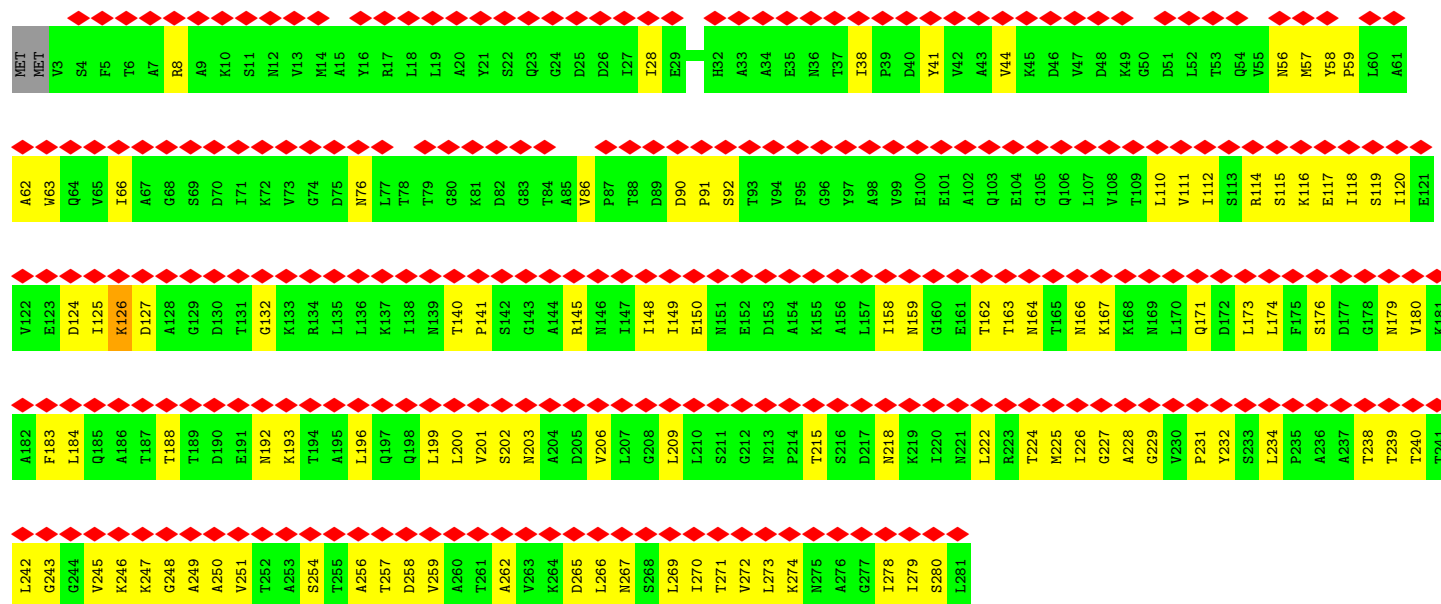
• Molecule 2: Capsid fiber protein

Chain 6f: 

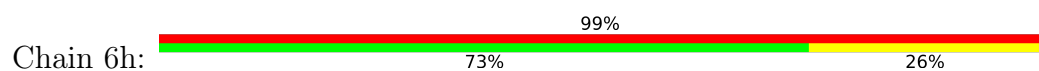




• Molecule 2: Capsid fiber protein

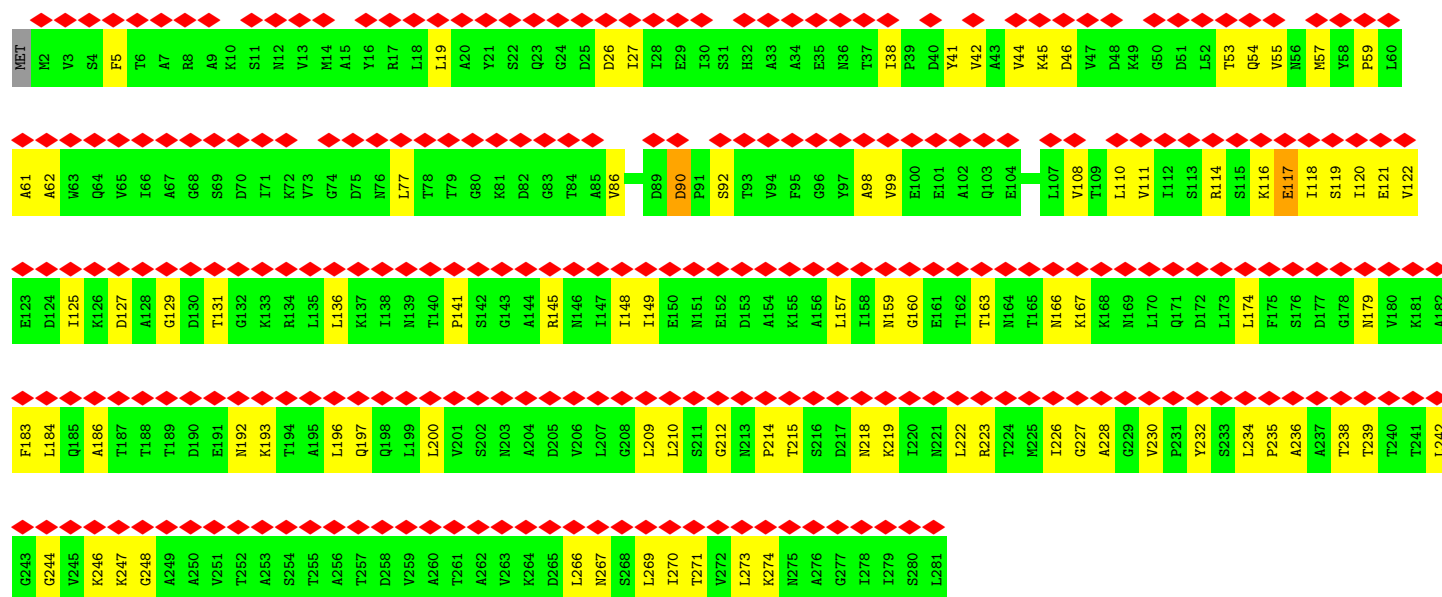


• Molecule 2: Capsid fiber protein

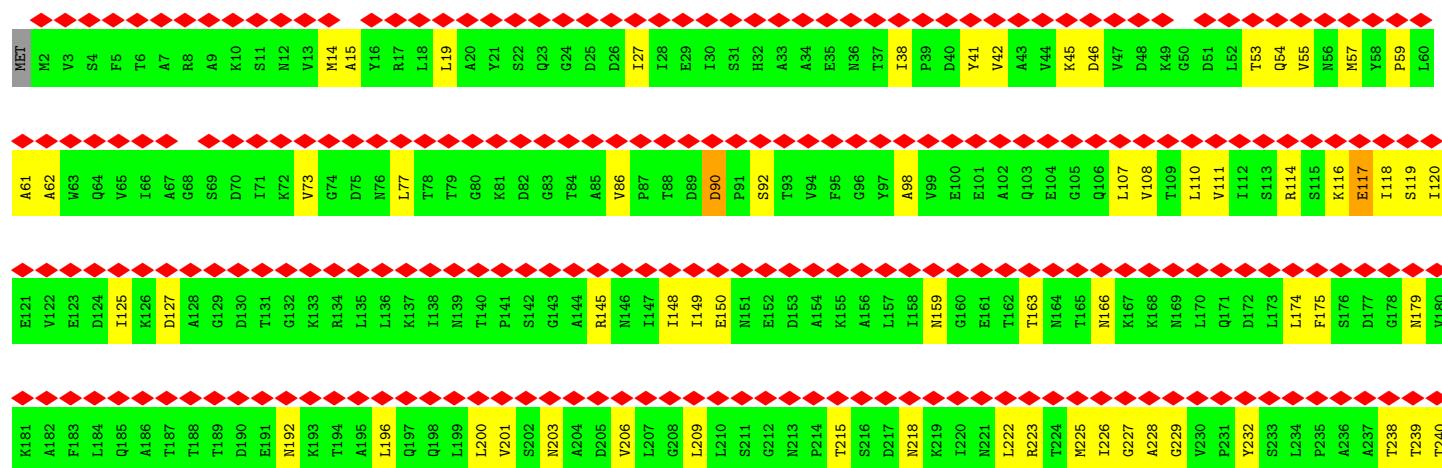
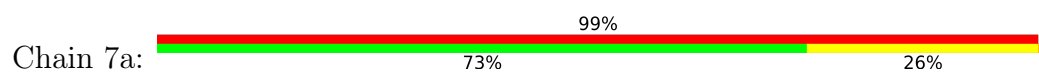


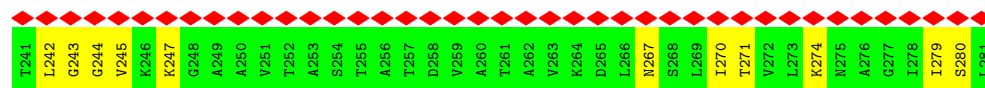


• Molecule 2: Capsid fiber protein

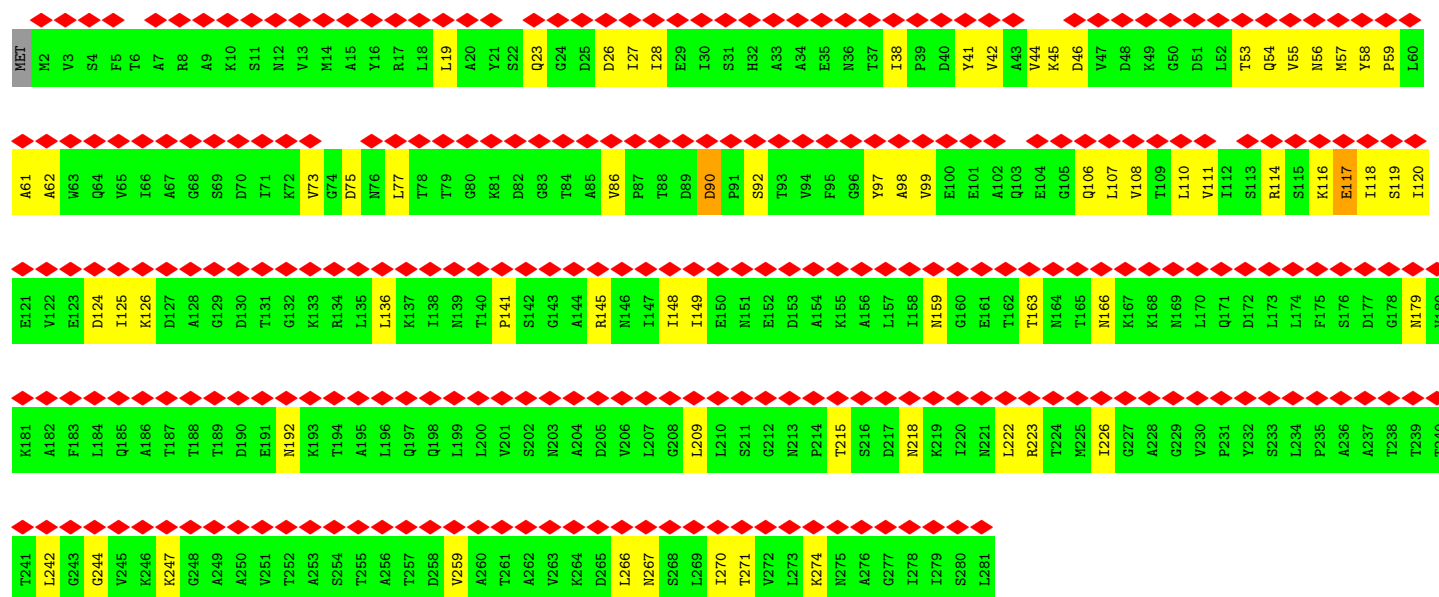
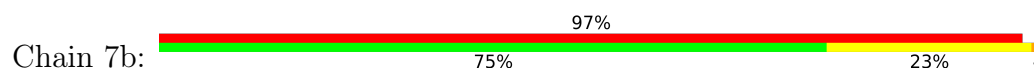


• Molecule 2: Capsid fiber protein

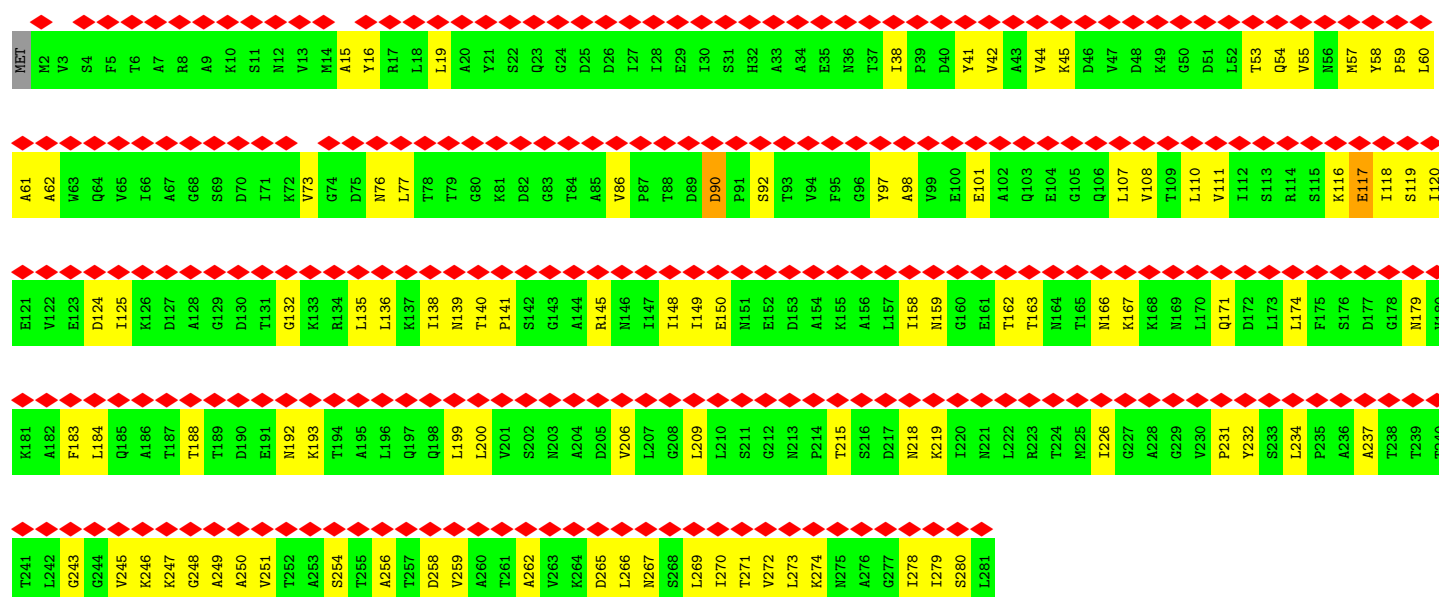




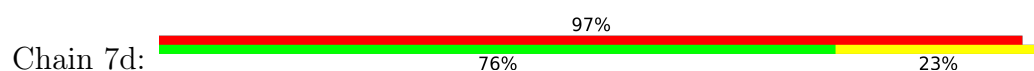
• Molecule 2: Capsid fiber protein

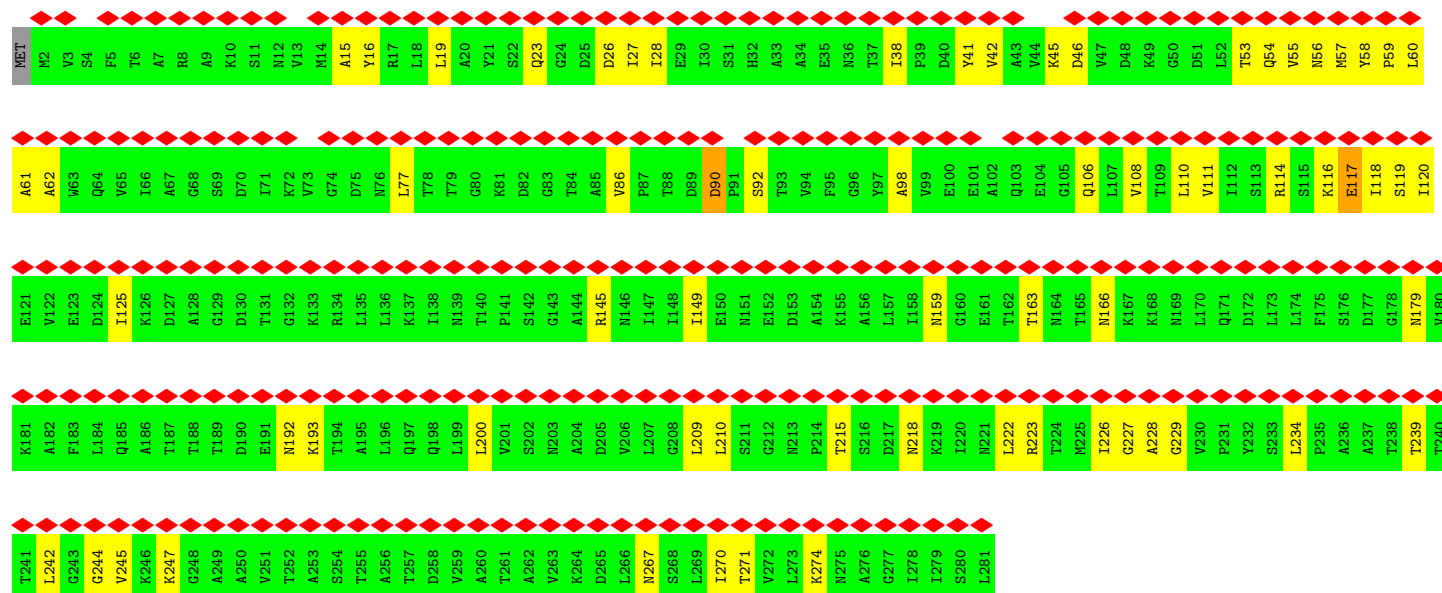


• Molecule 2: Capsid fiber protein

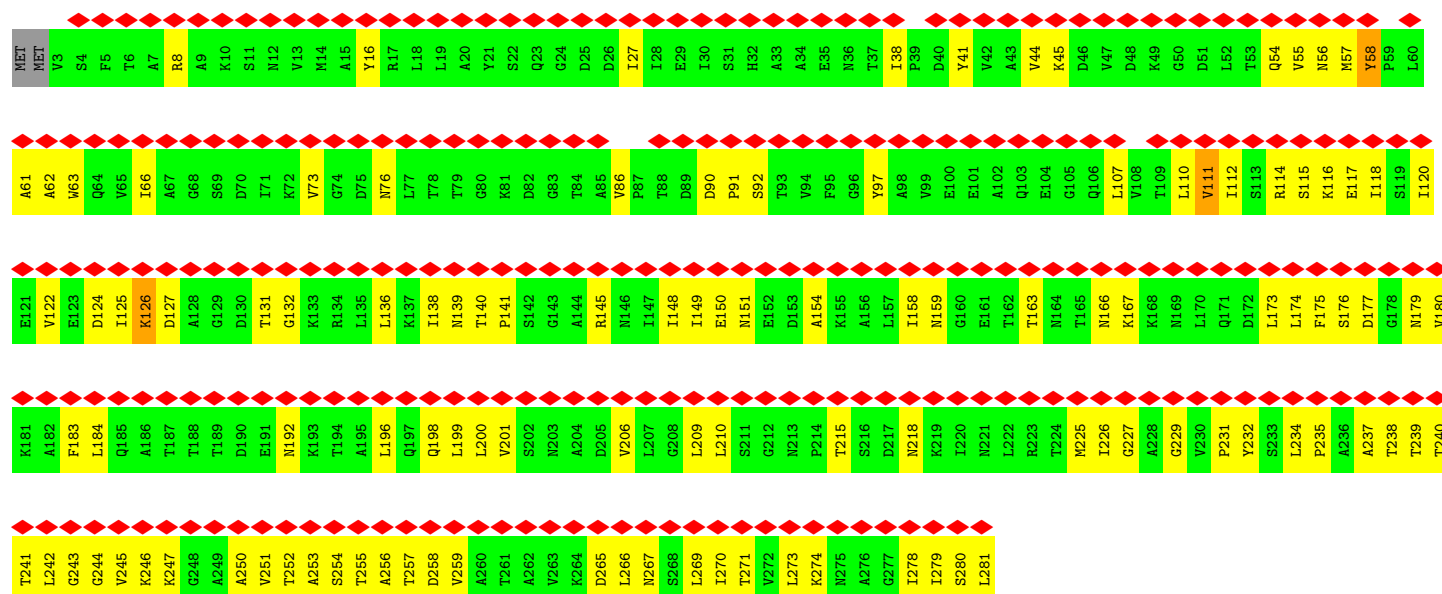


• Molecule 2: Capsid fiber protein

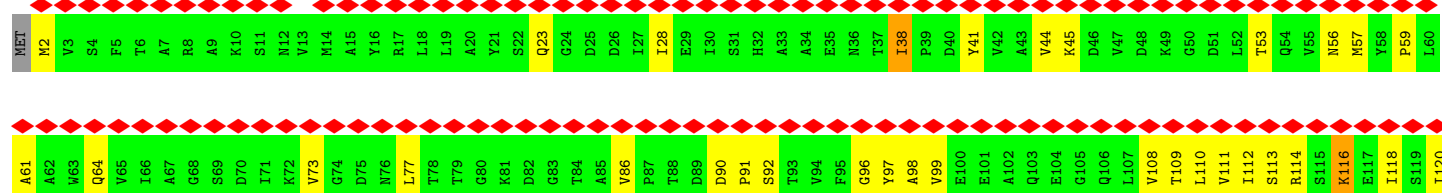
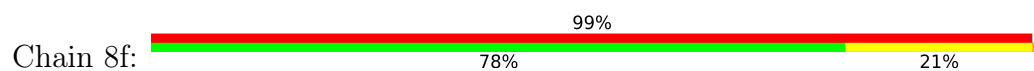


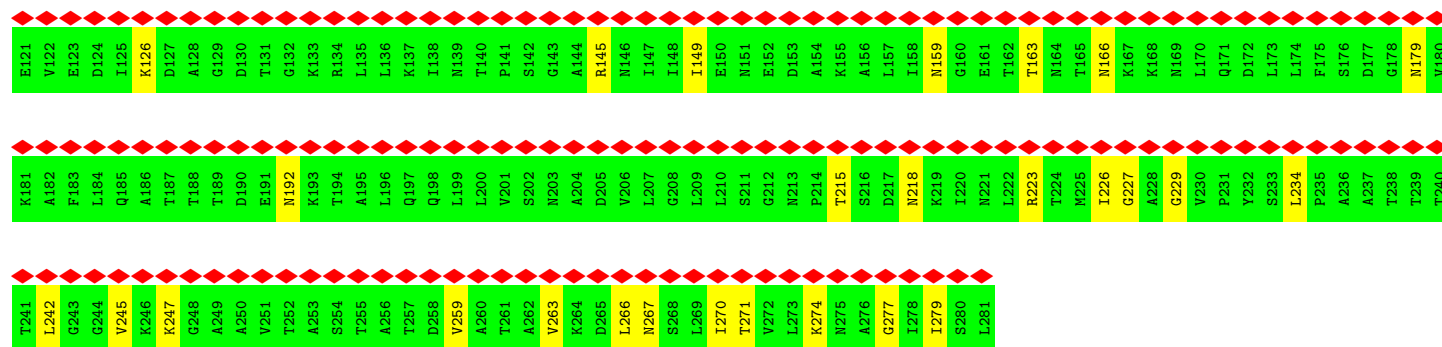


• Molecule 2: Capsid fiber protein

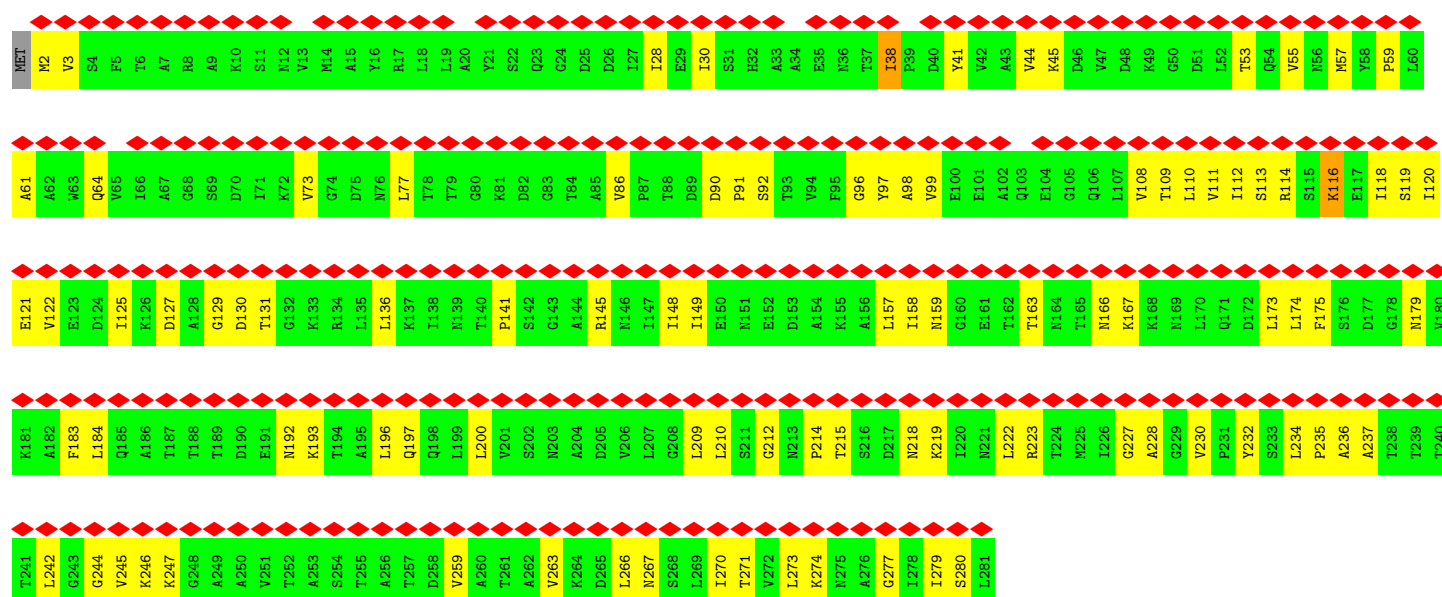


• Molecule 2: Capsid fiber protein

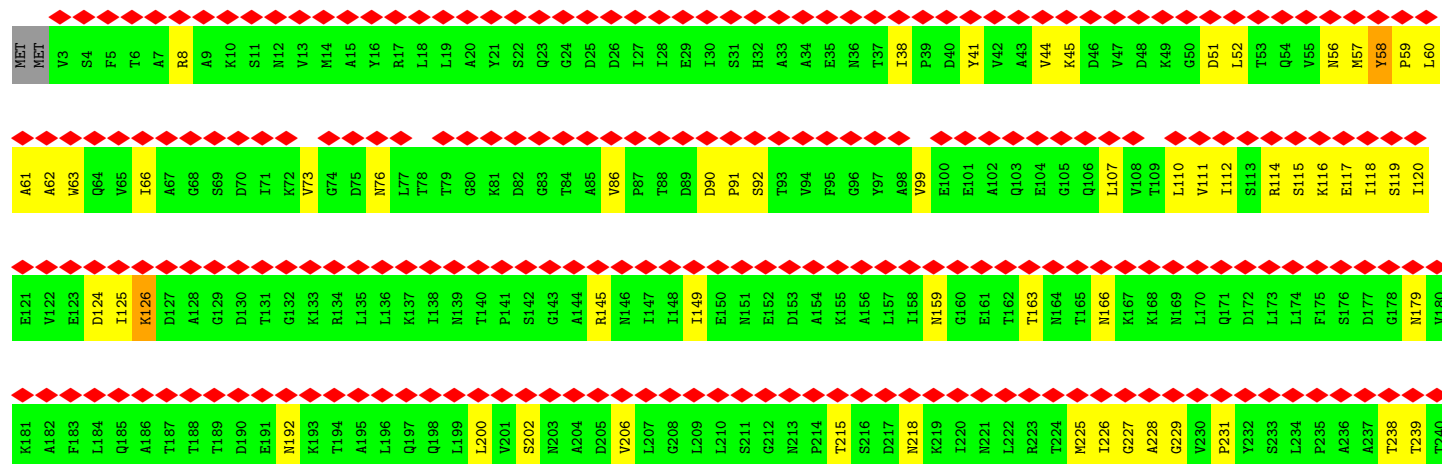
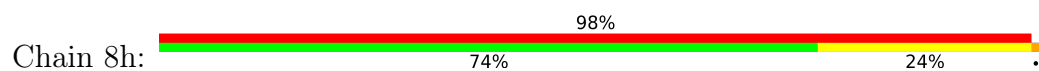




• Molecule 2: Capsid fiber protein

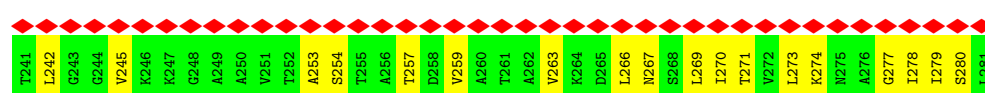
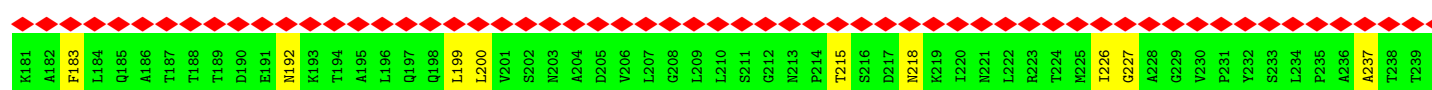


• Molecule 2: Capsid fiber protein

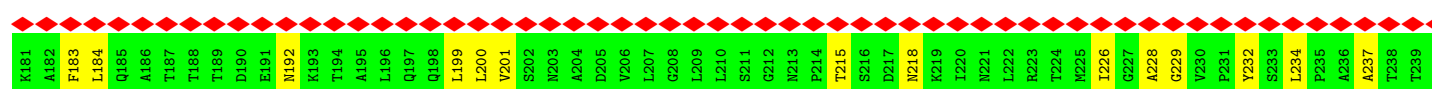
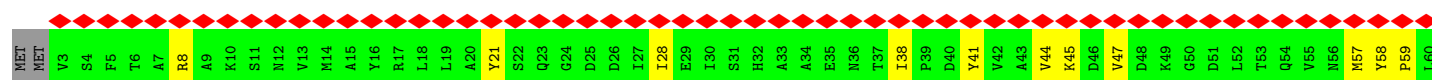




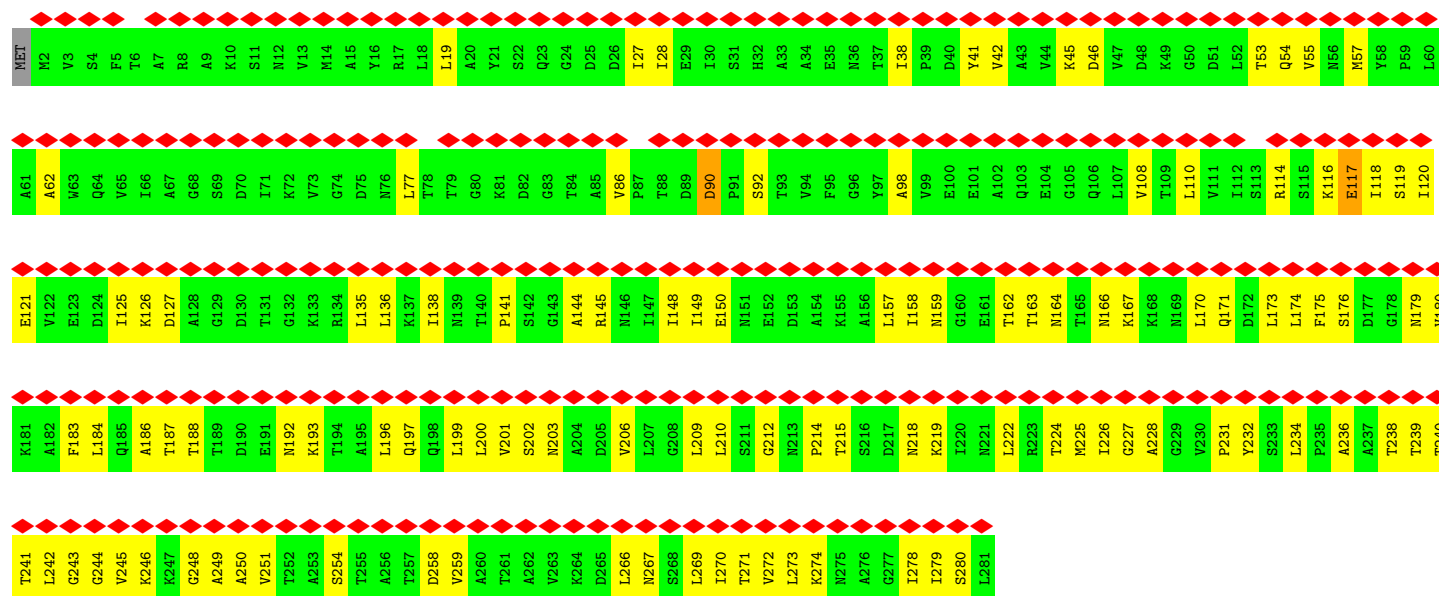
• Molecule 2: Capsid fiber protein



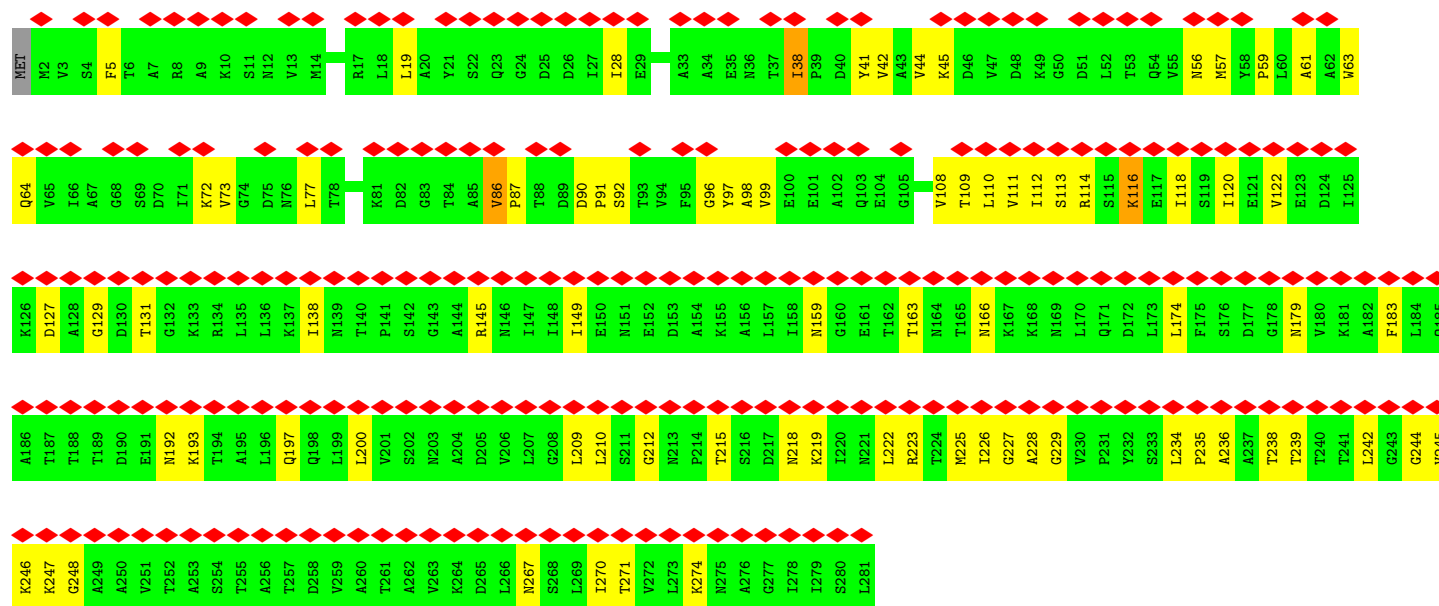
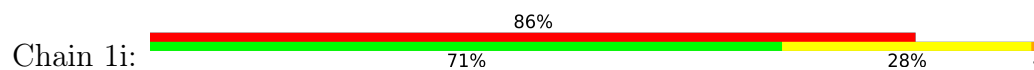
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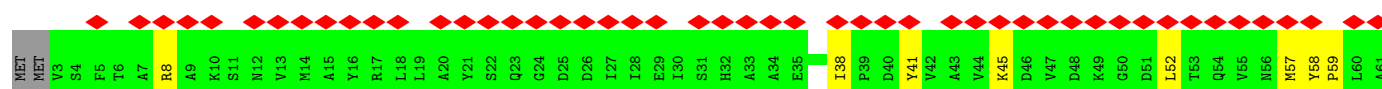
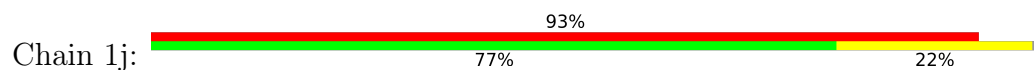
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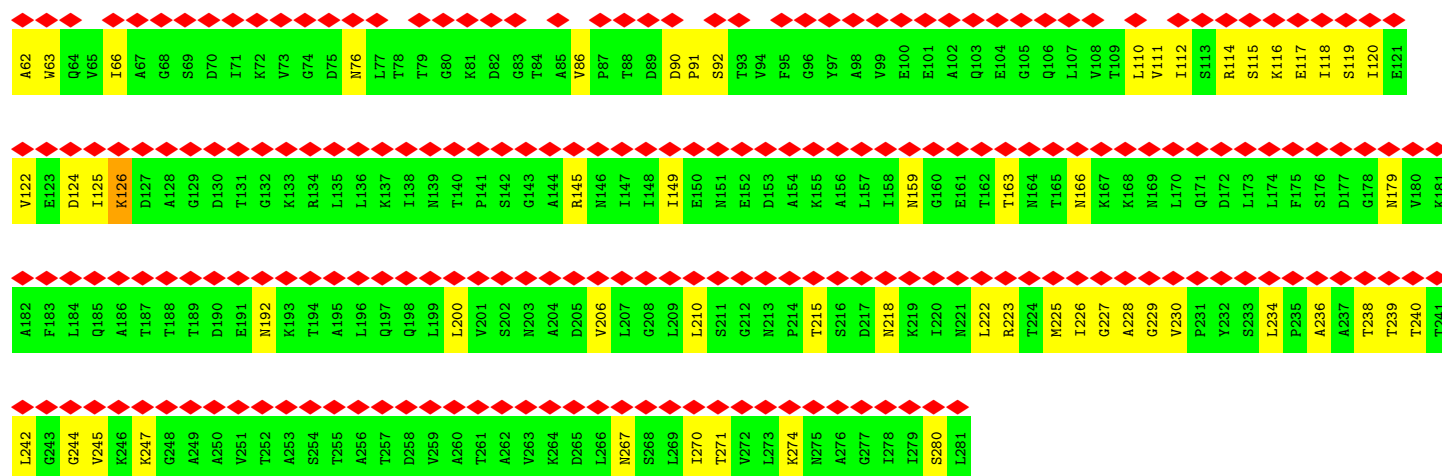


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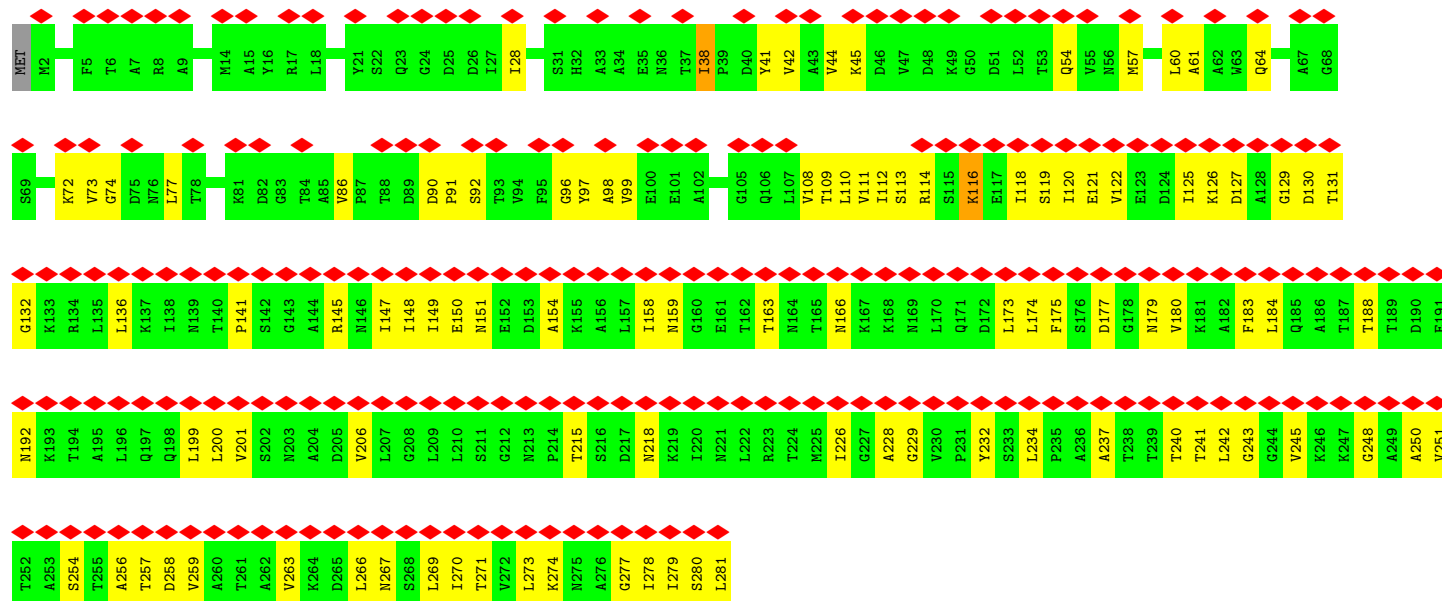
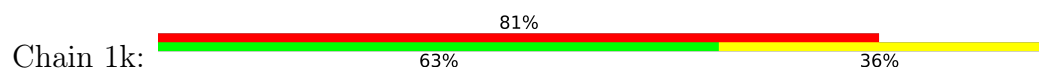


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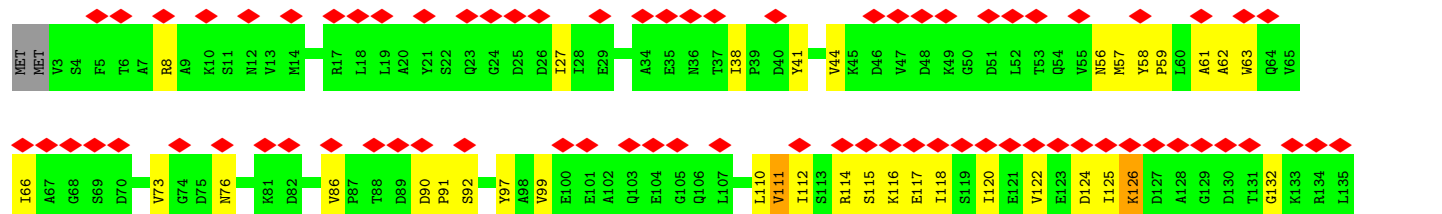
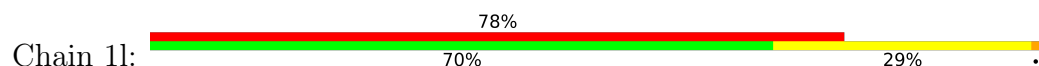


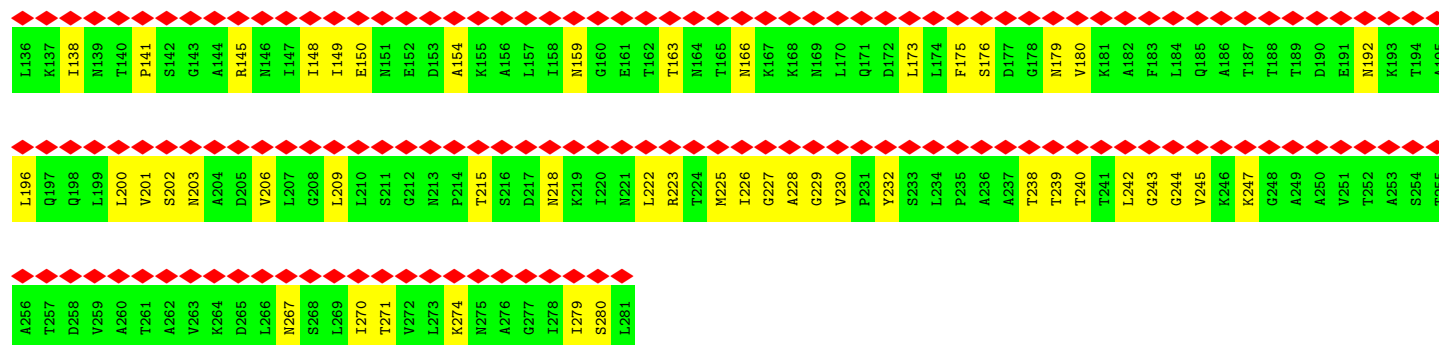


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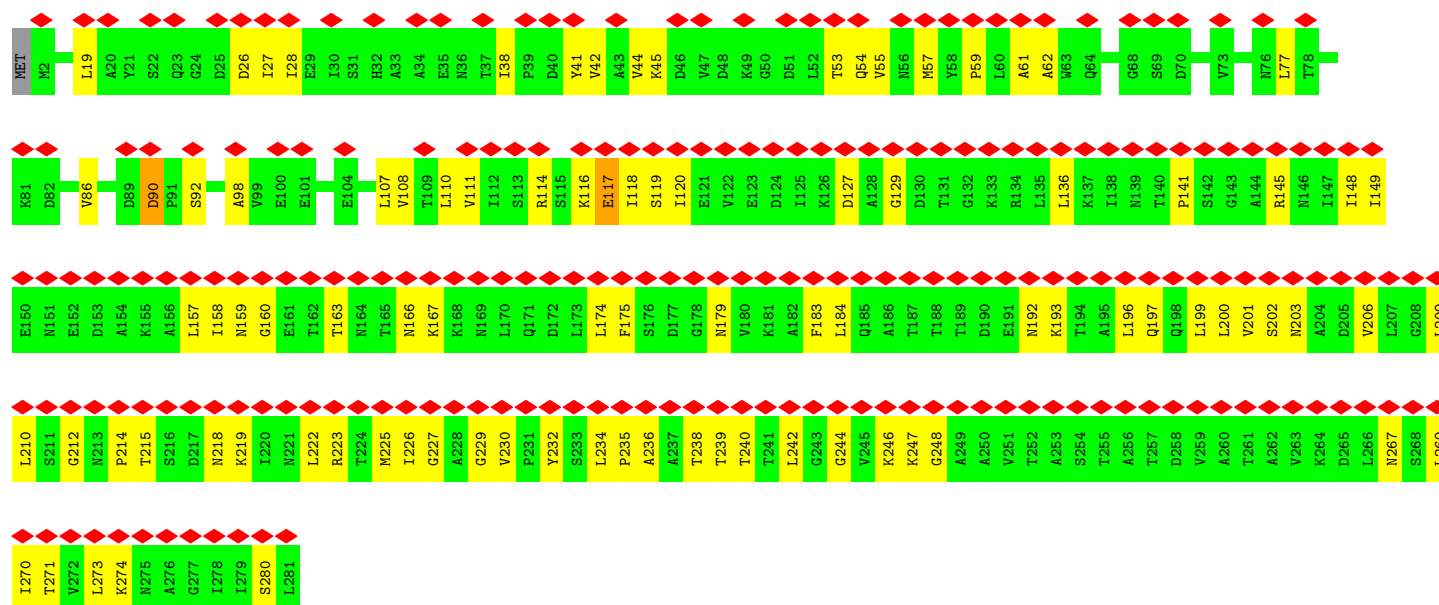
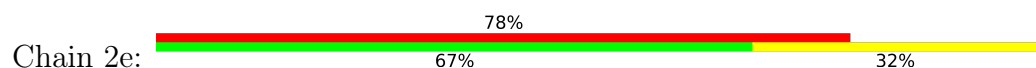


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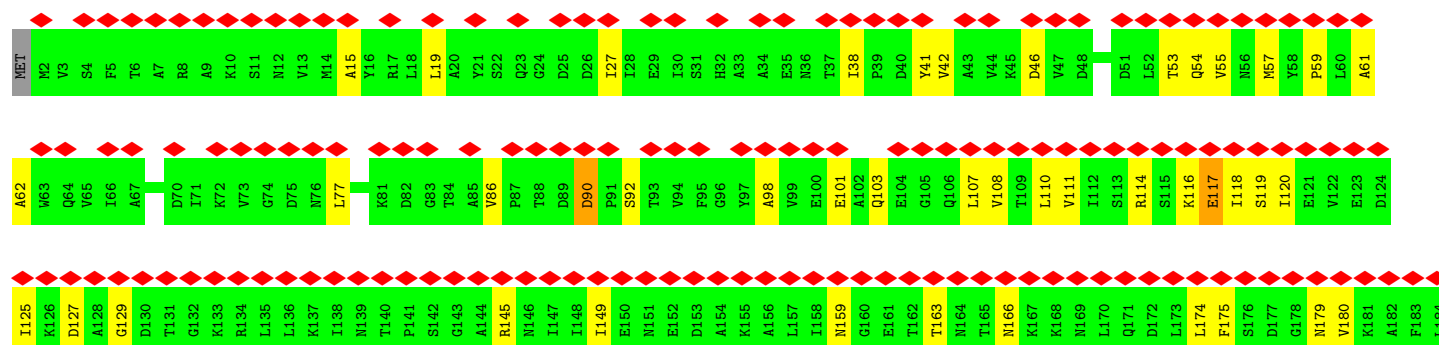
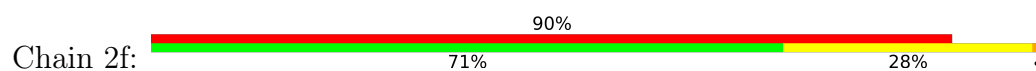


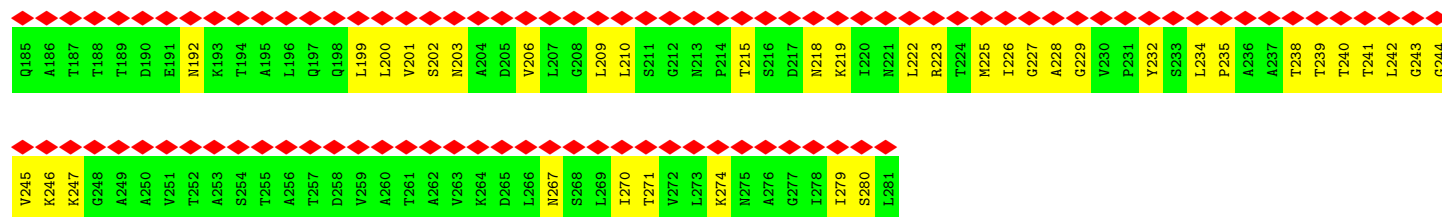


- Molecule 2: Capsid fiber protein

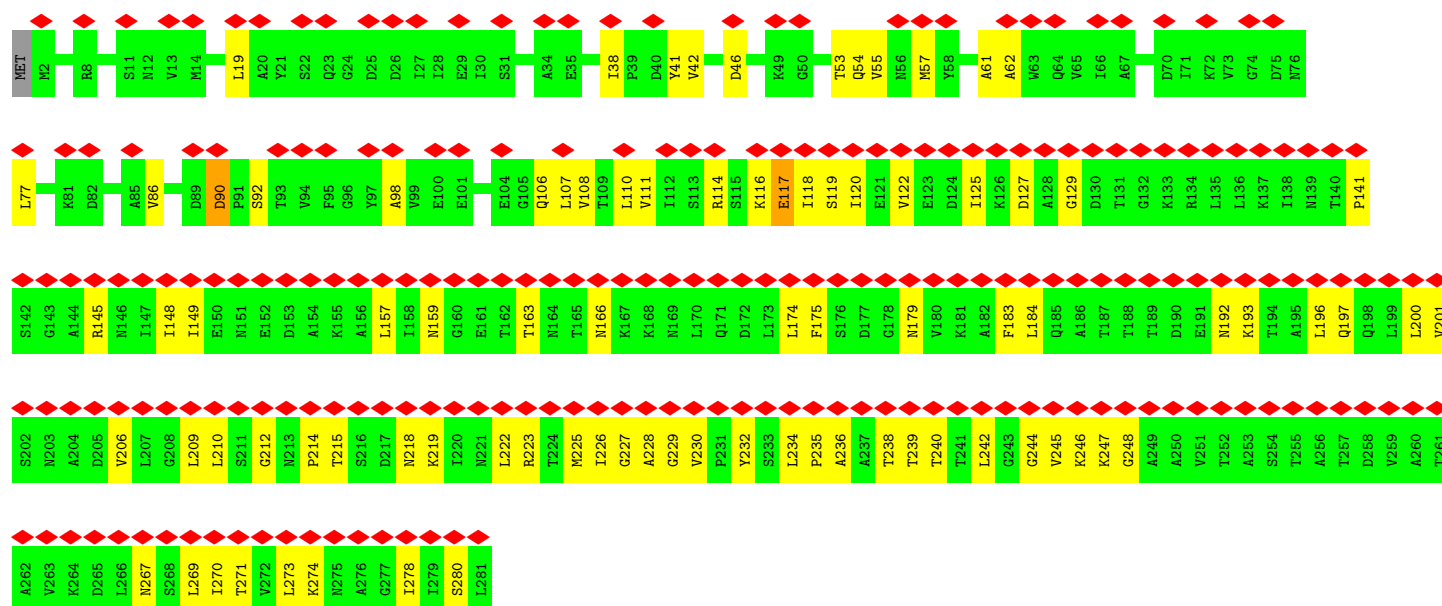
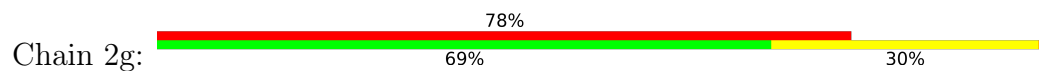


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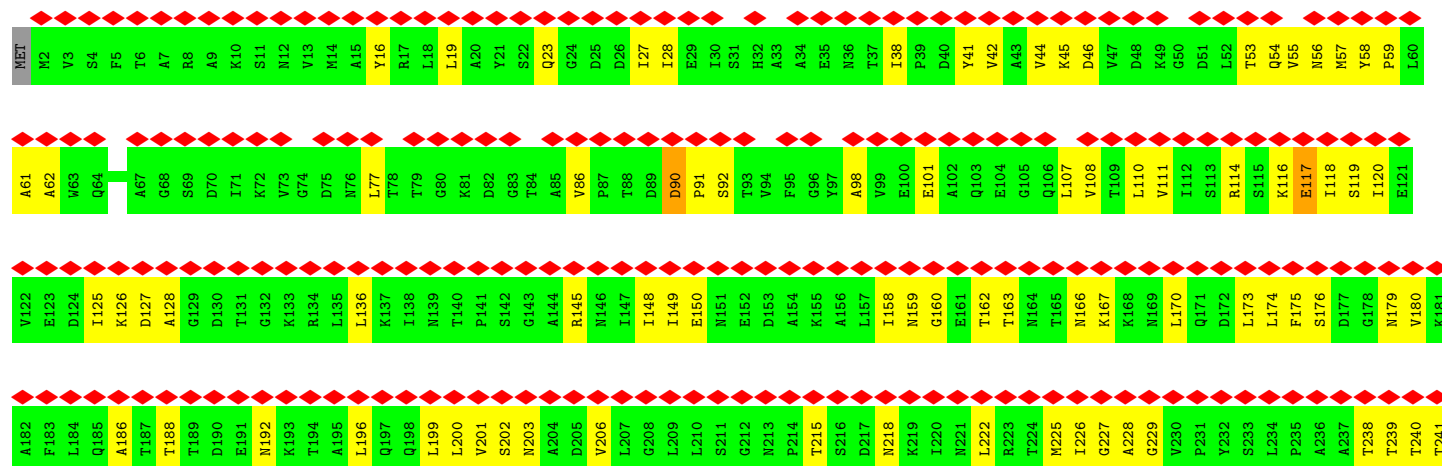


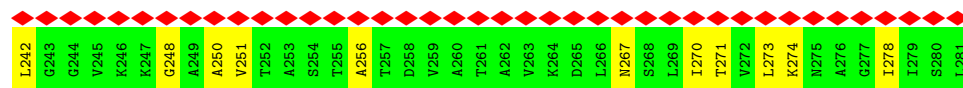


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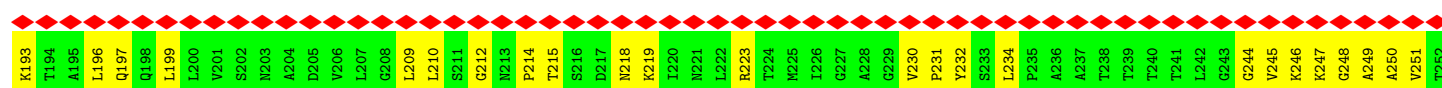
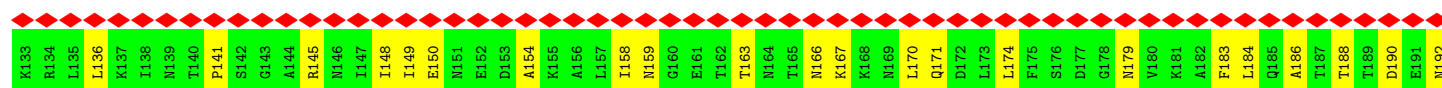
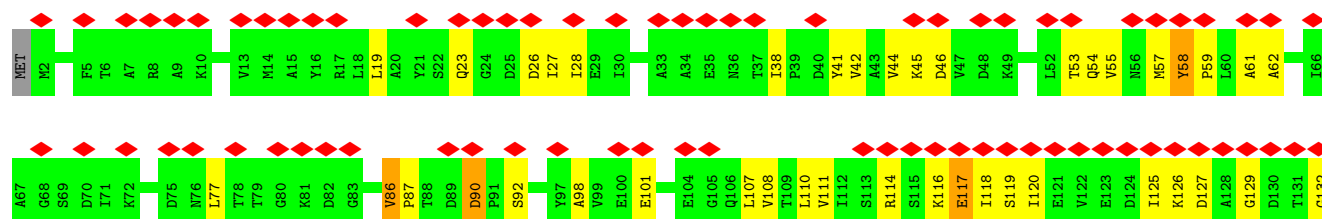
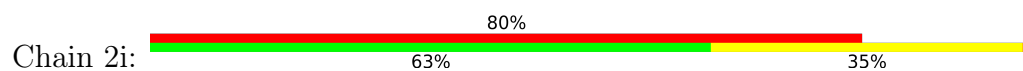


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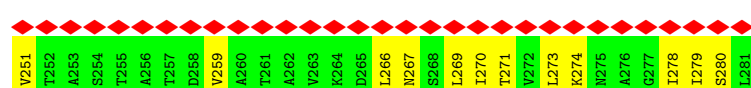
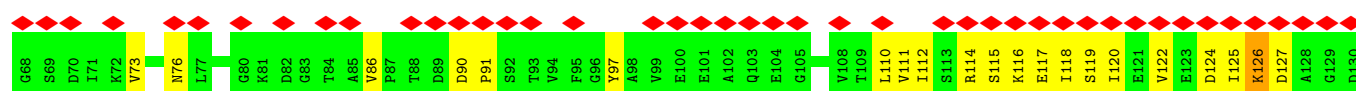
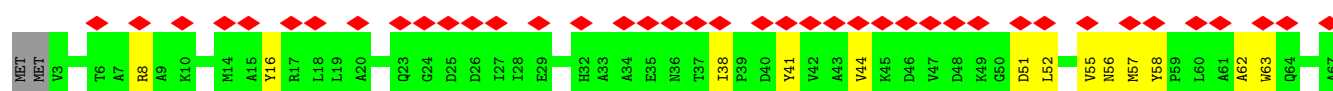
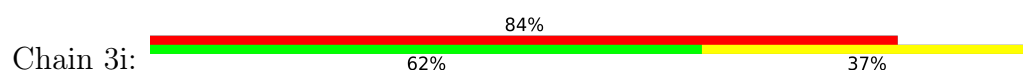




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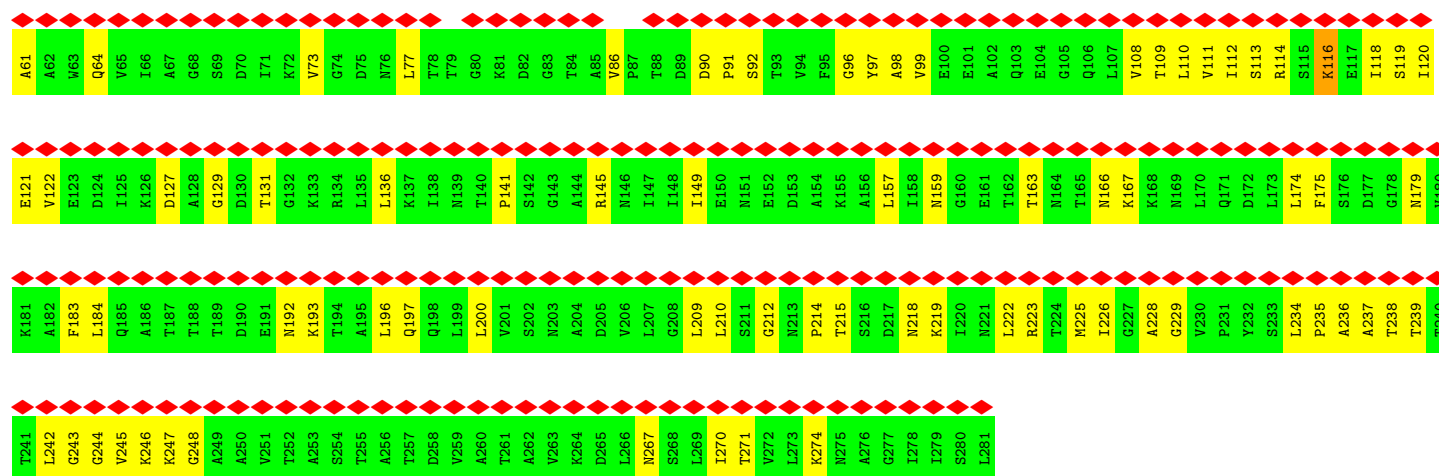


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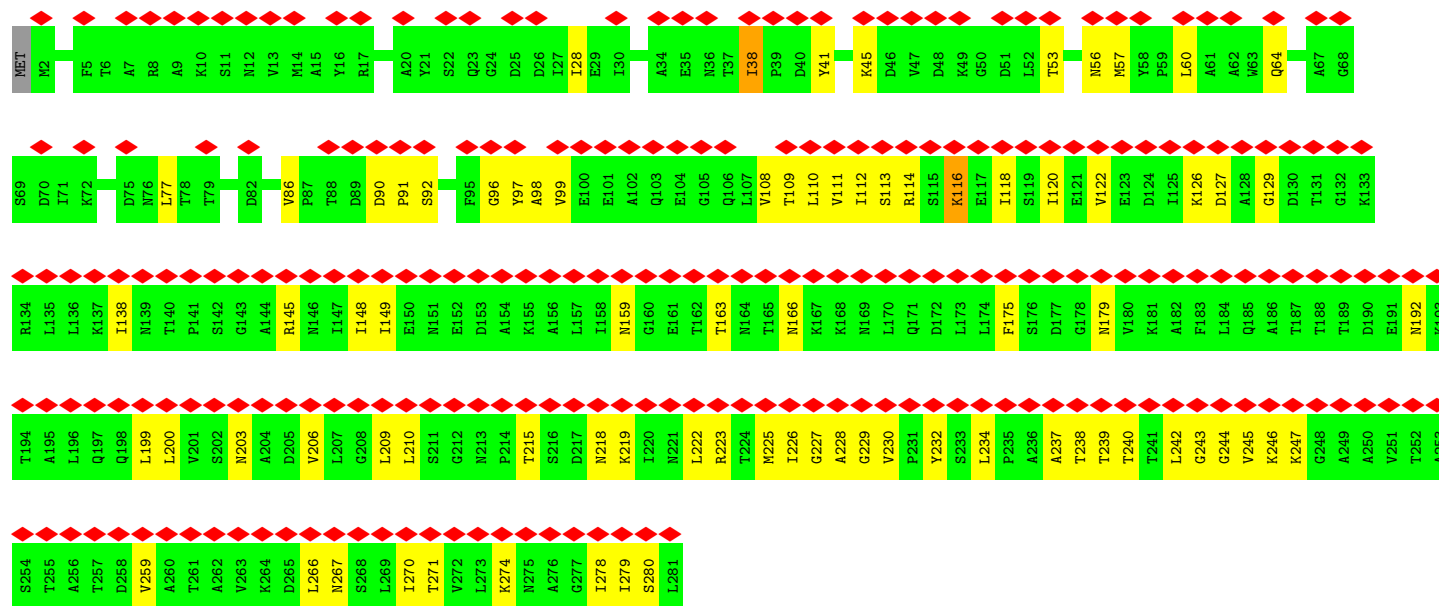
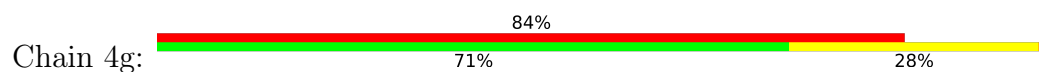


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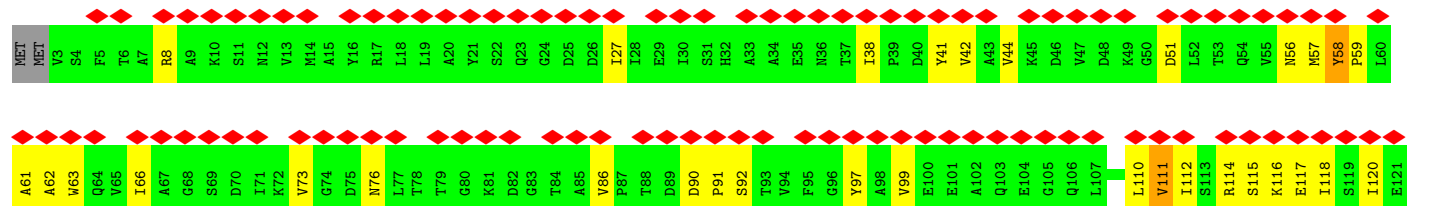
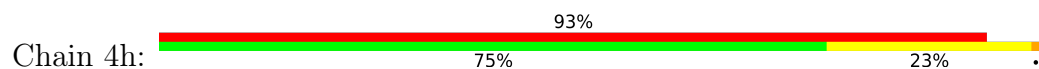




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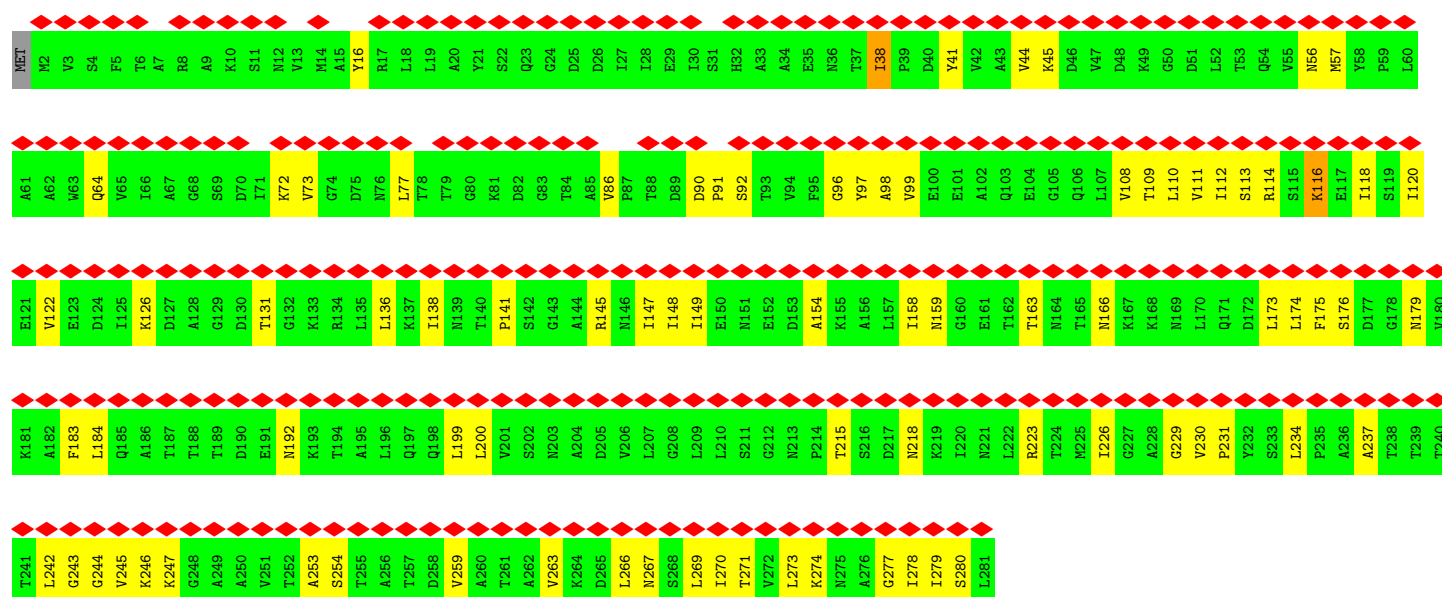


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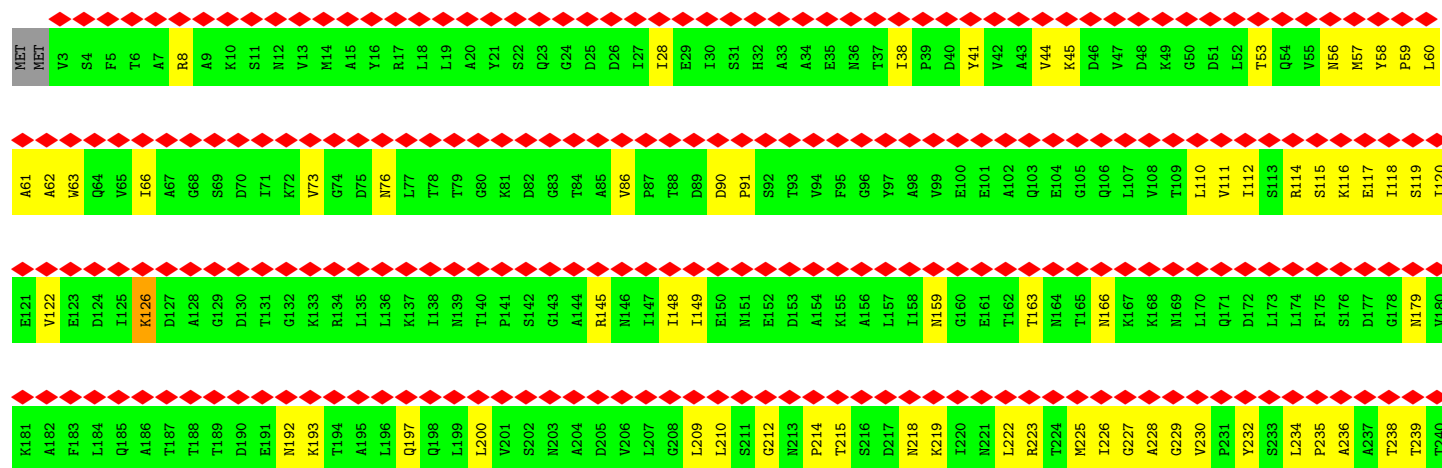
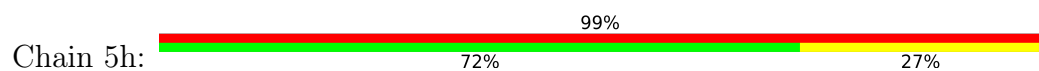


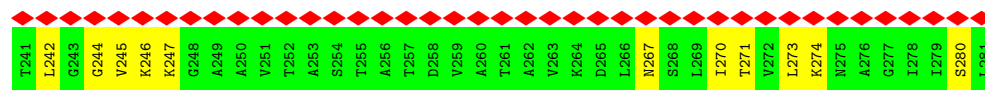


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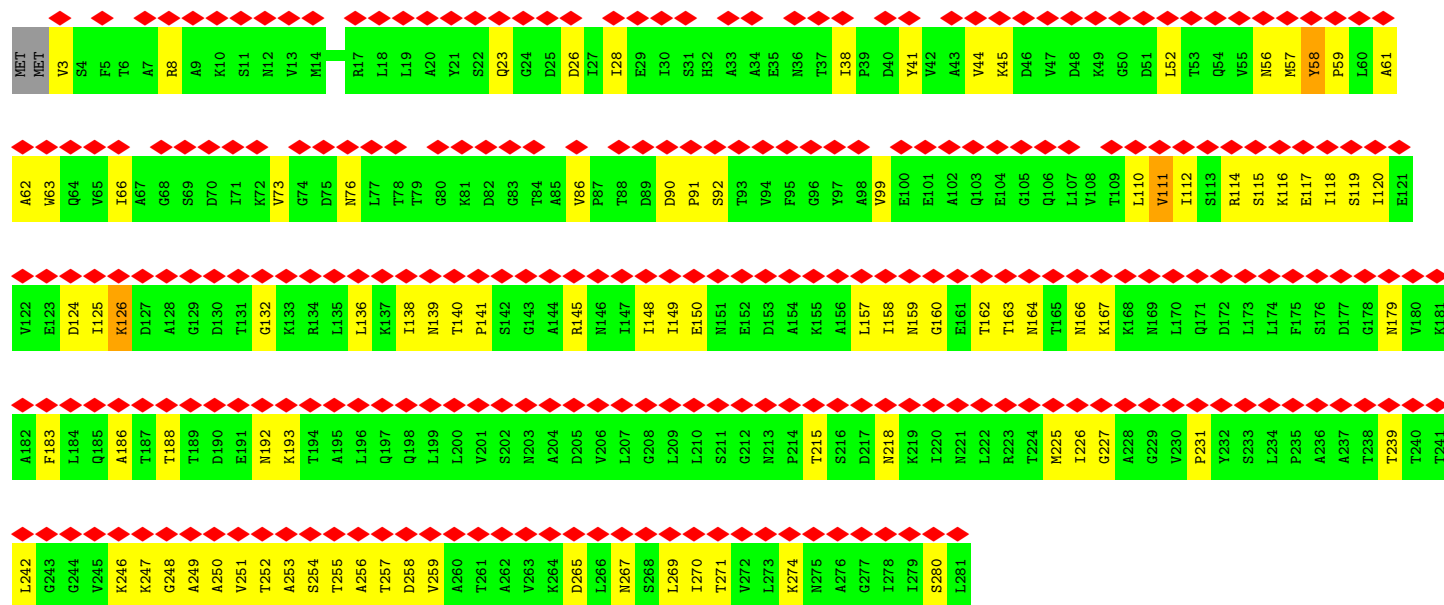
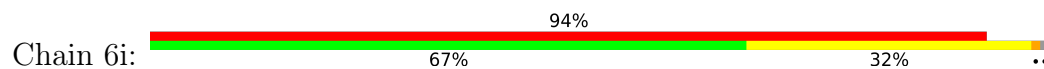


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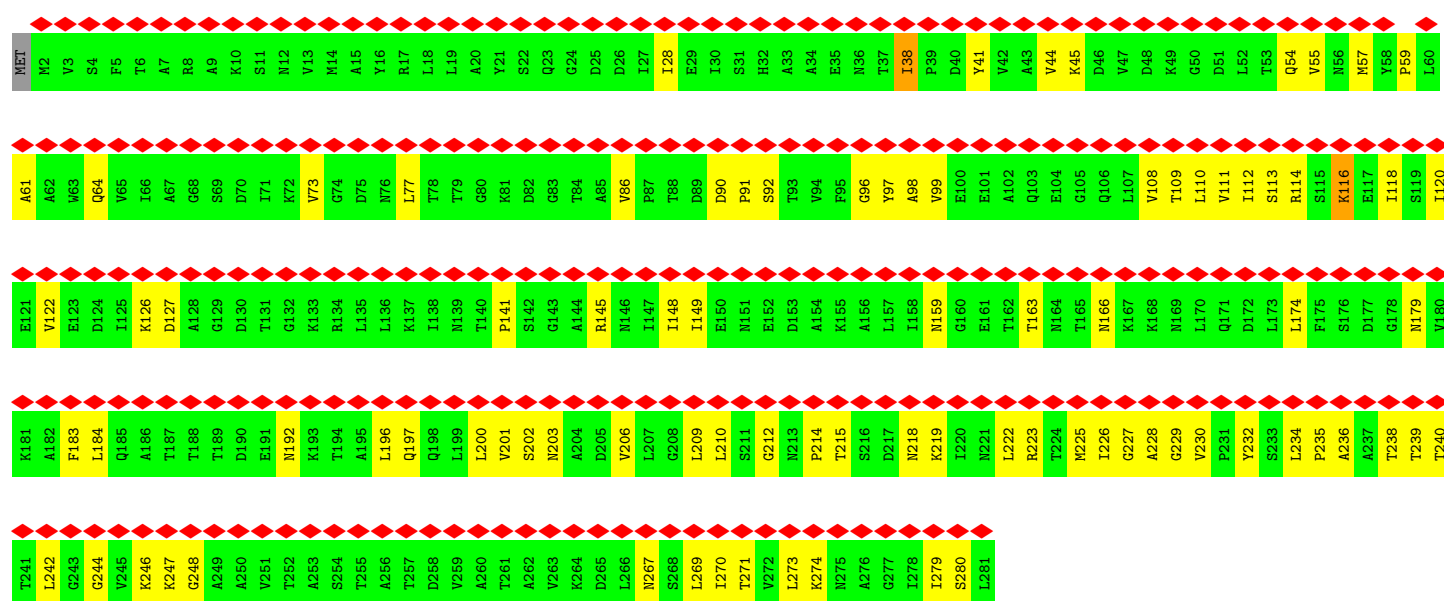




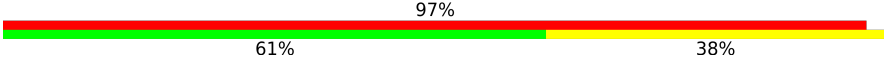
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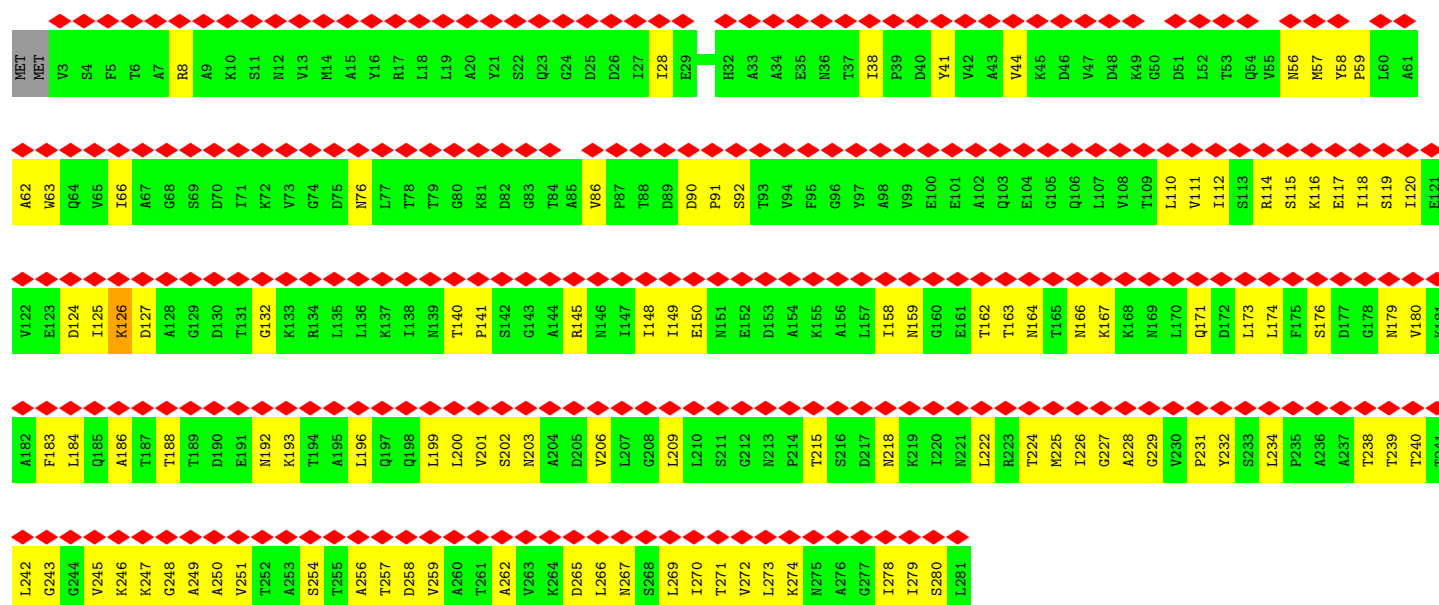


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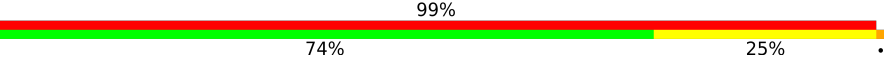


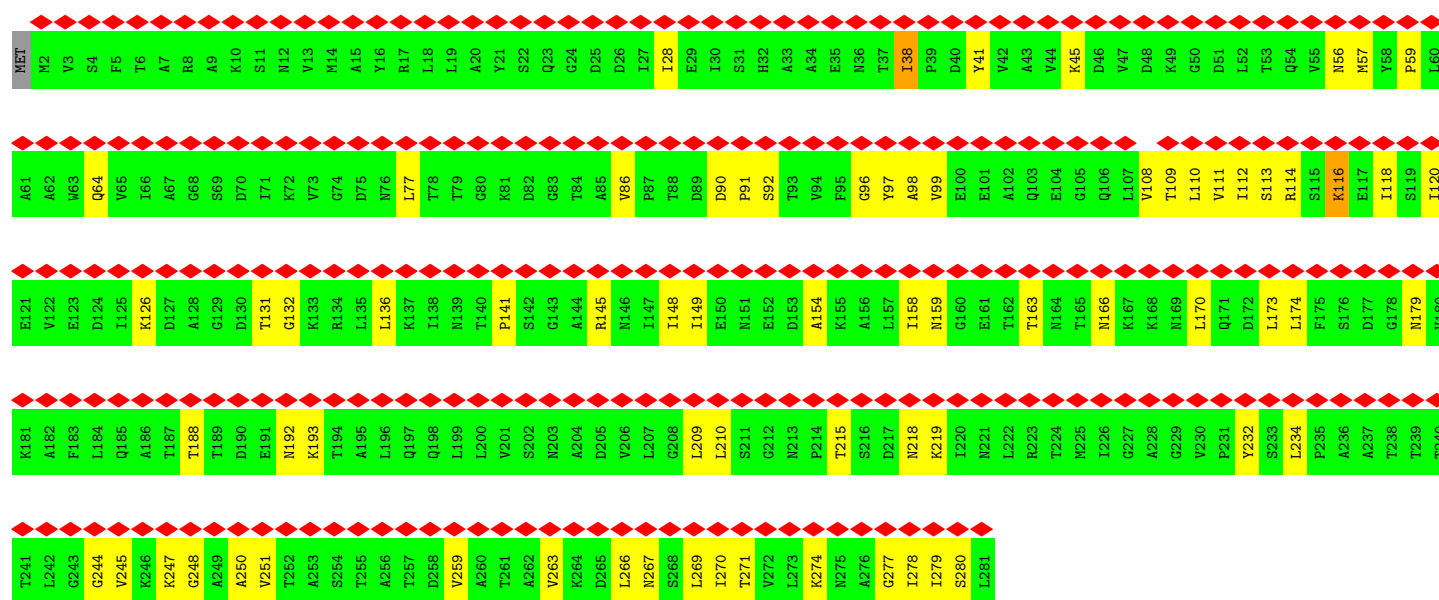
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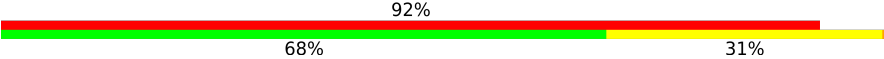


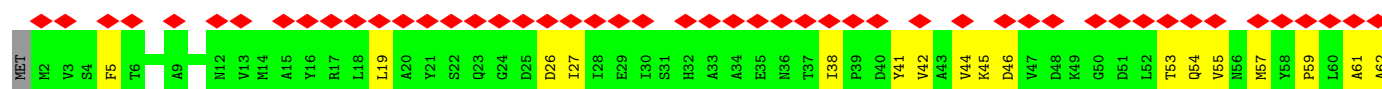
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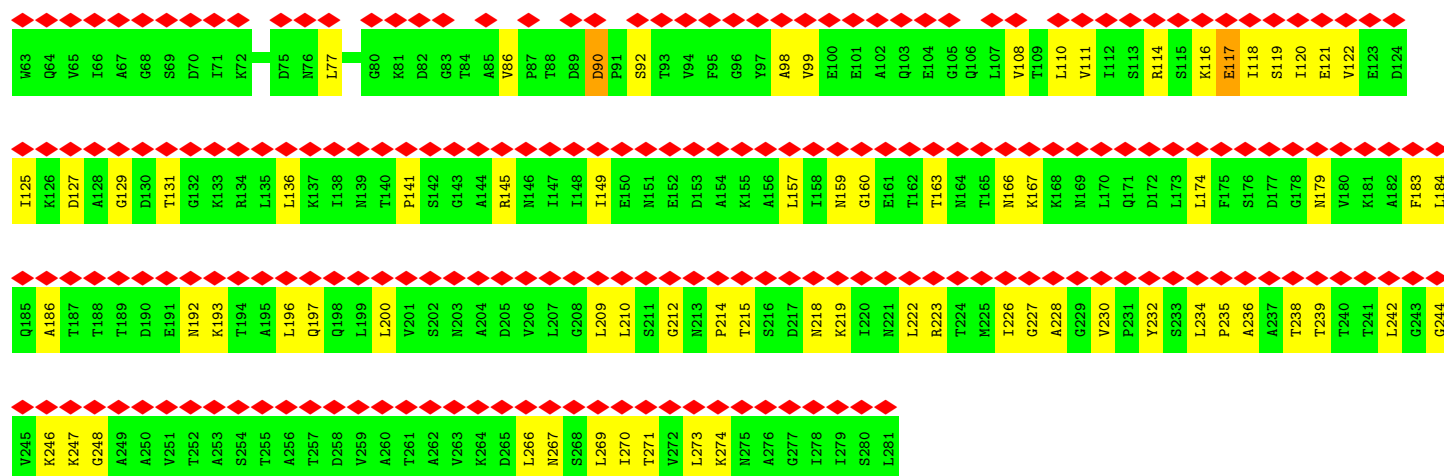
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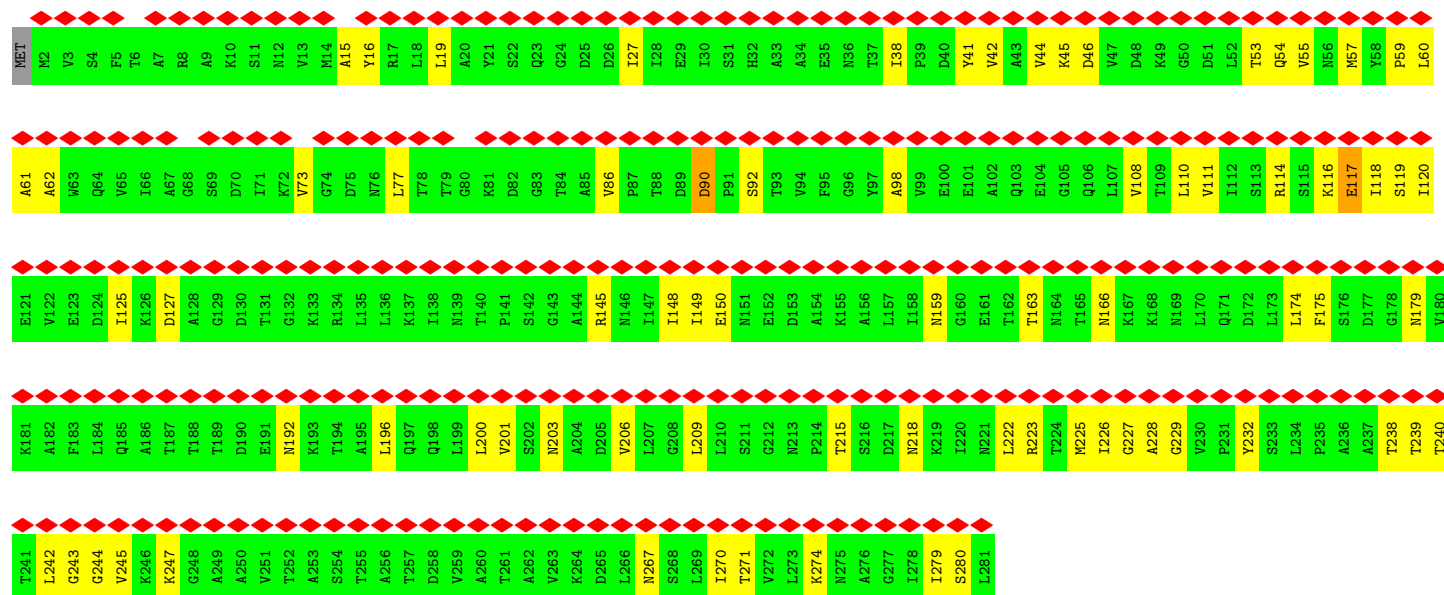
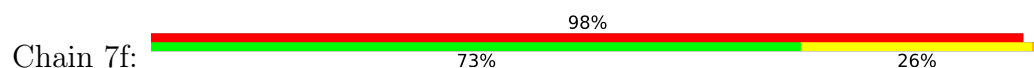
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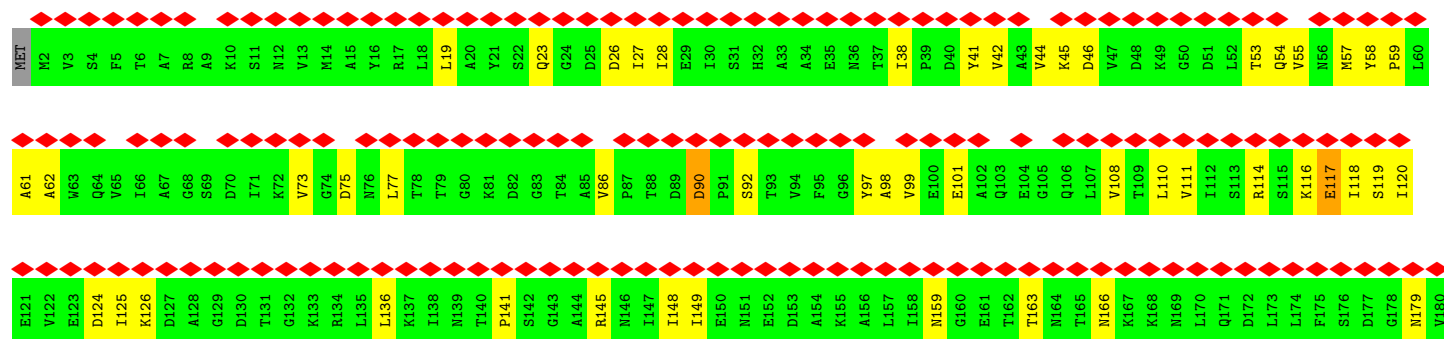
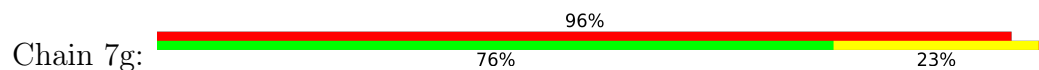


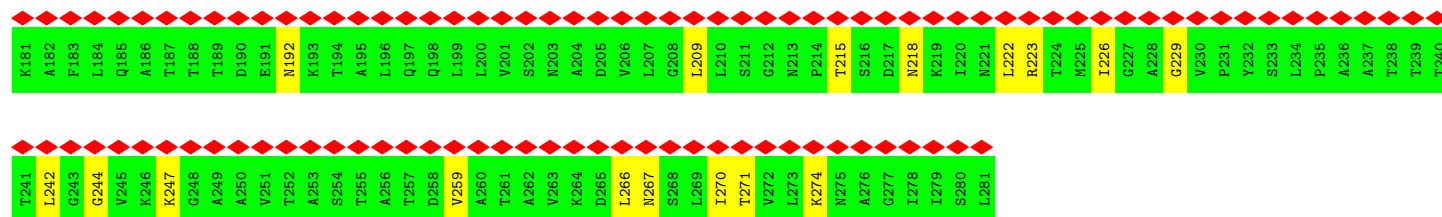


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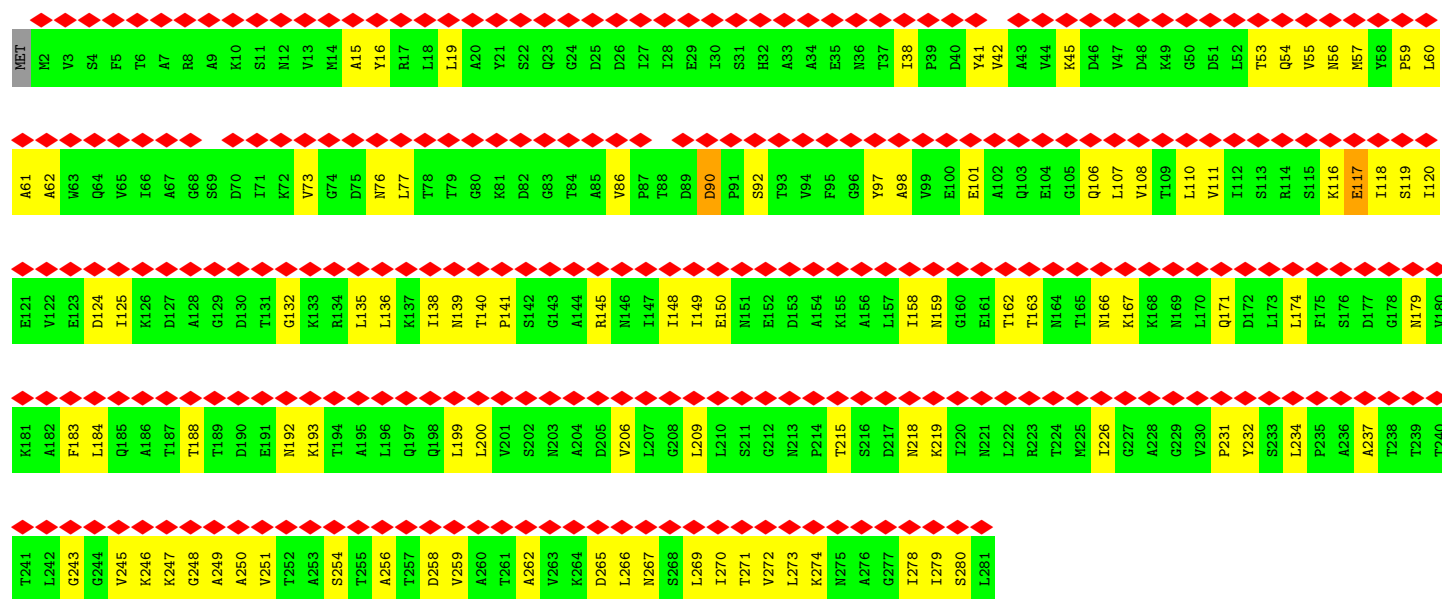


• Molecule 2: Capsid fiber protein

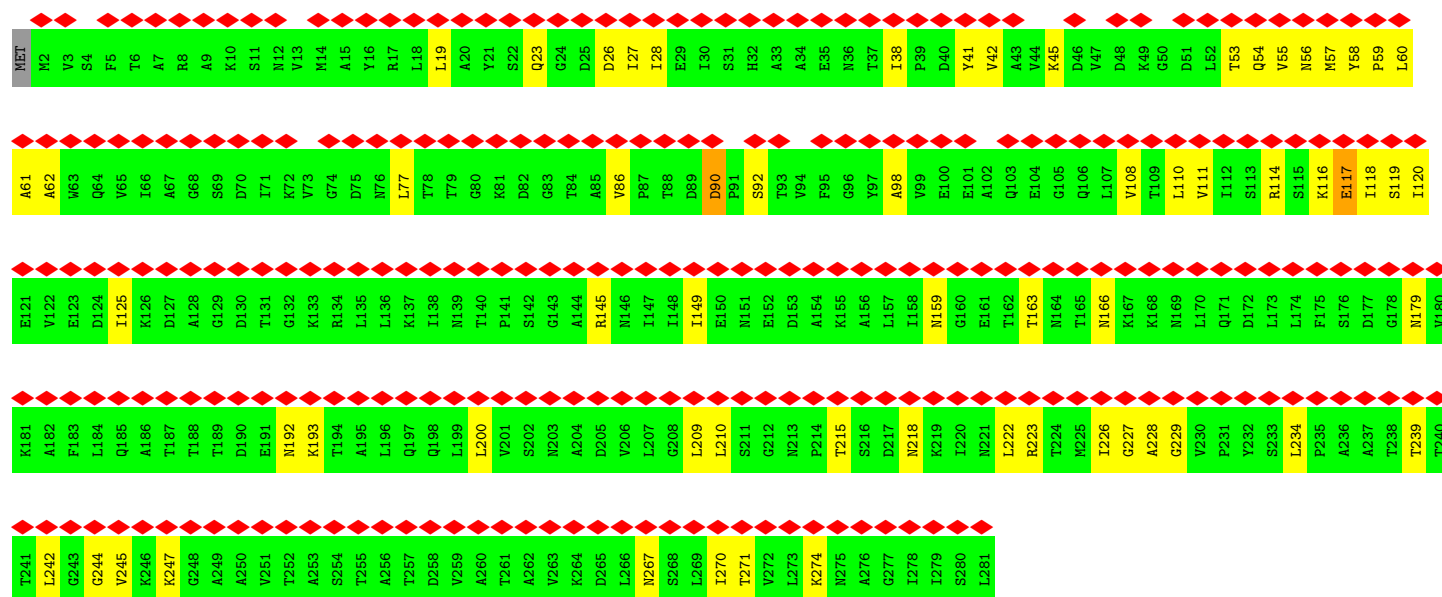
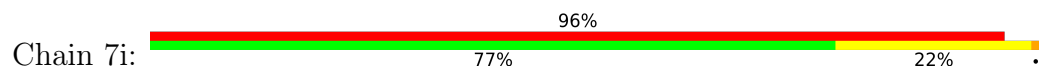




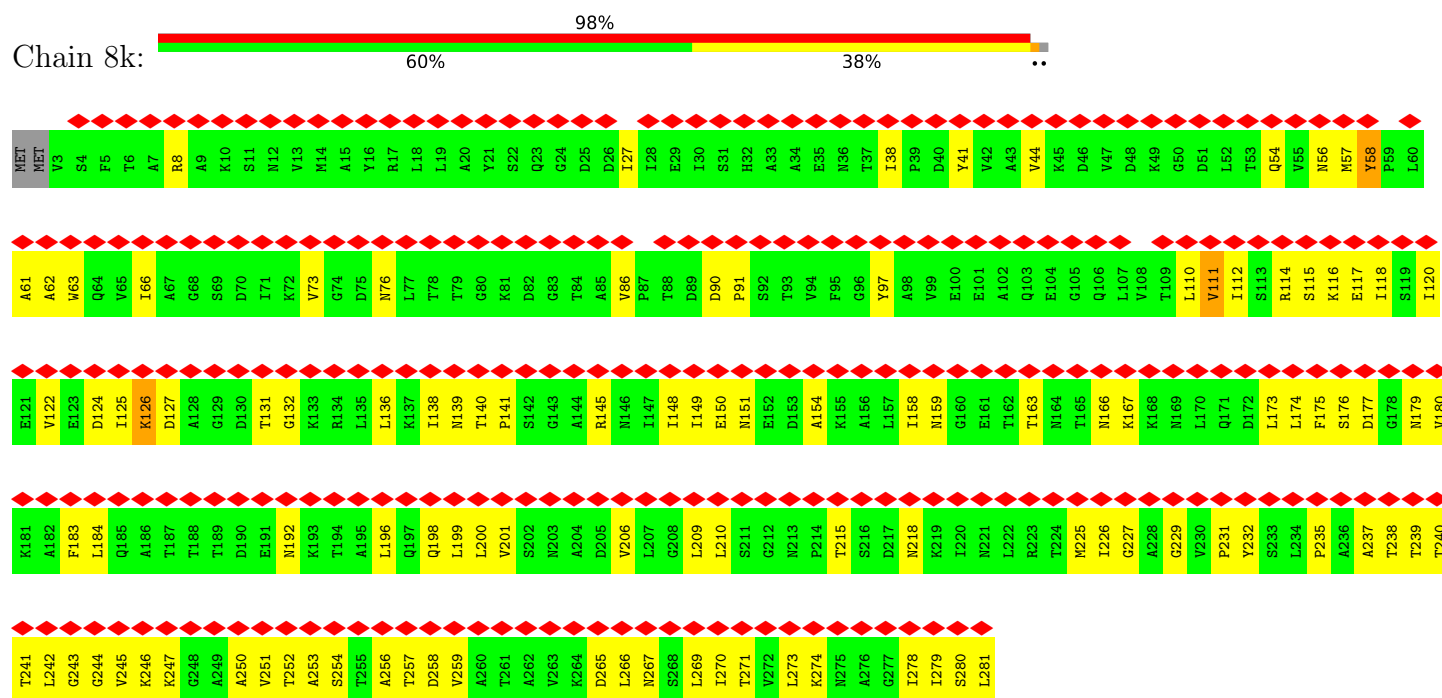
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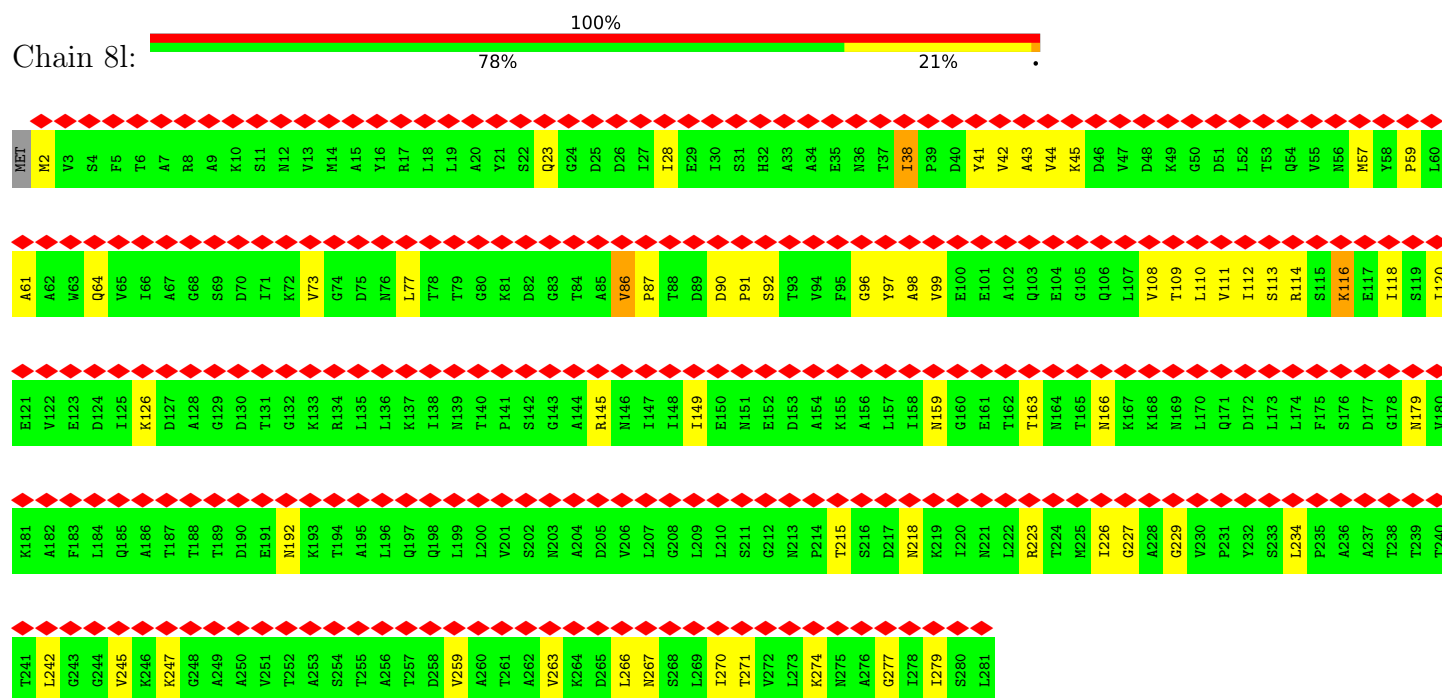
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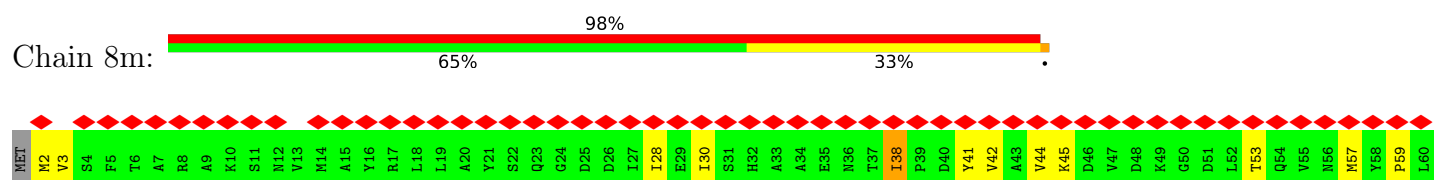
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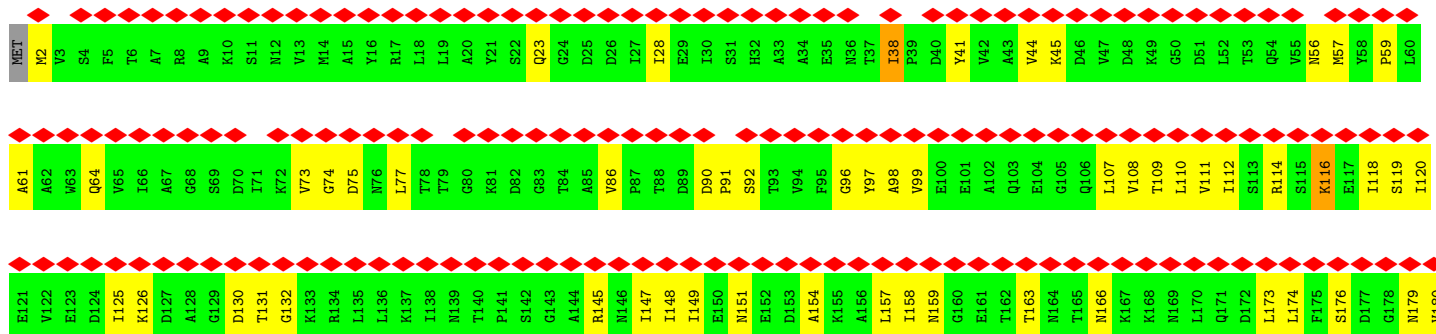


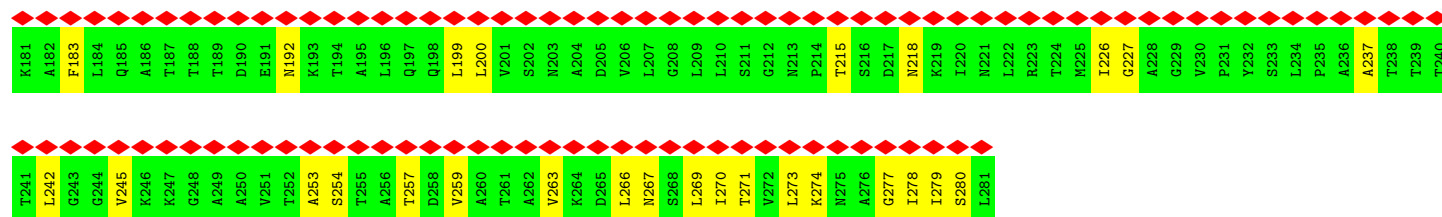
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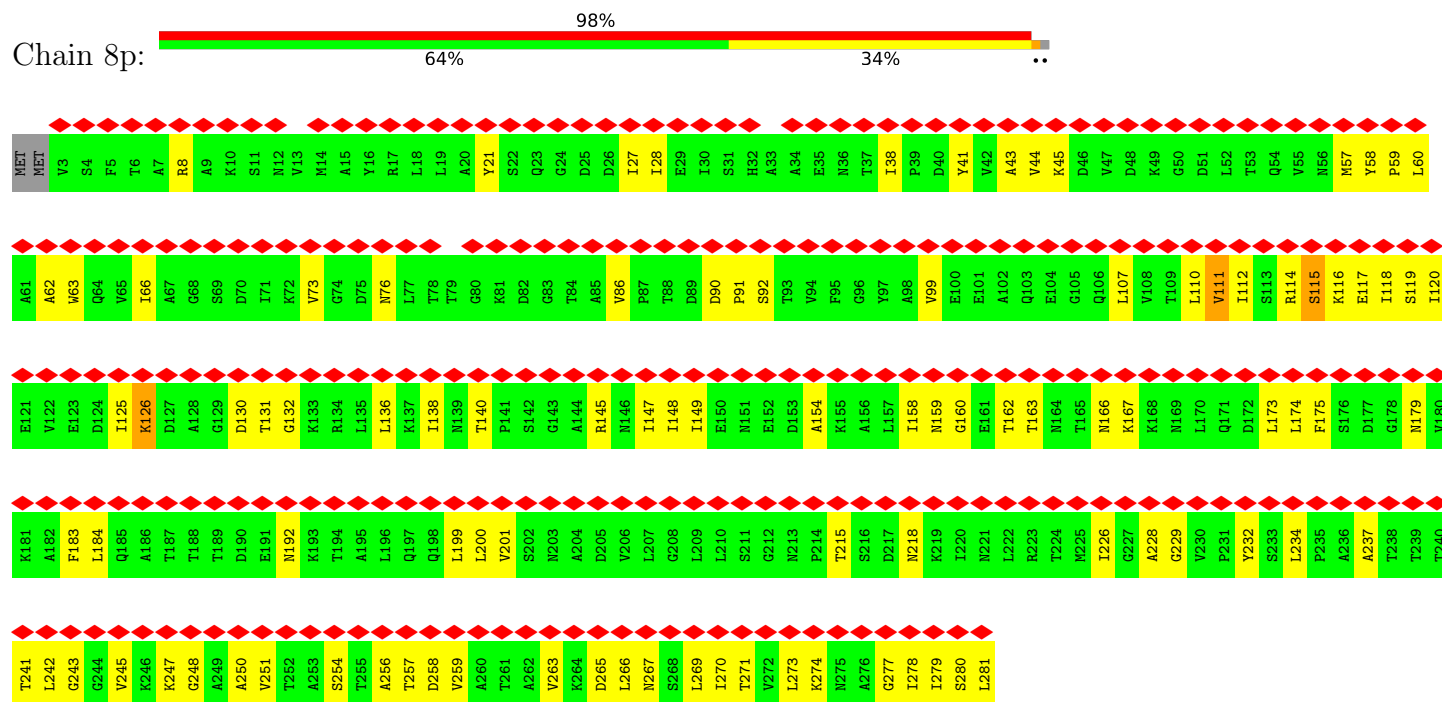
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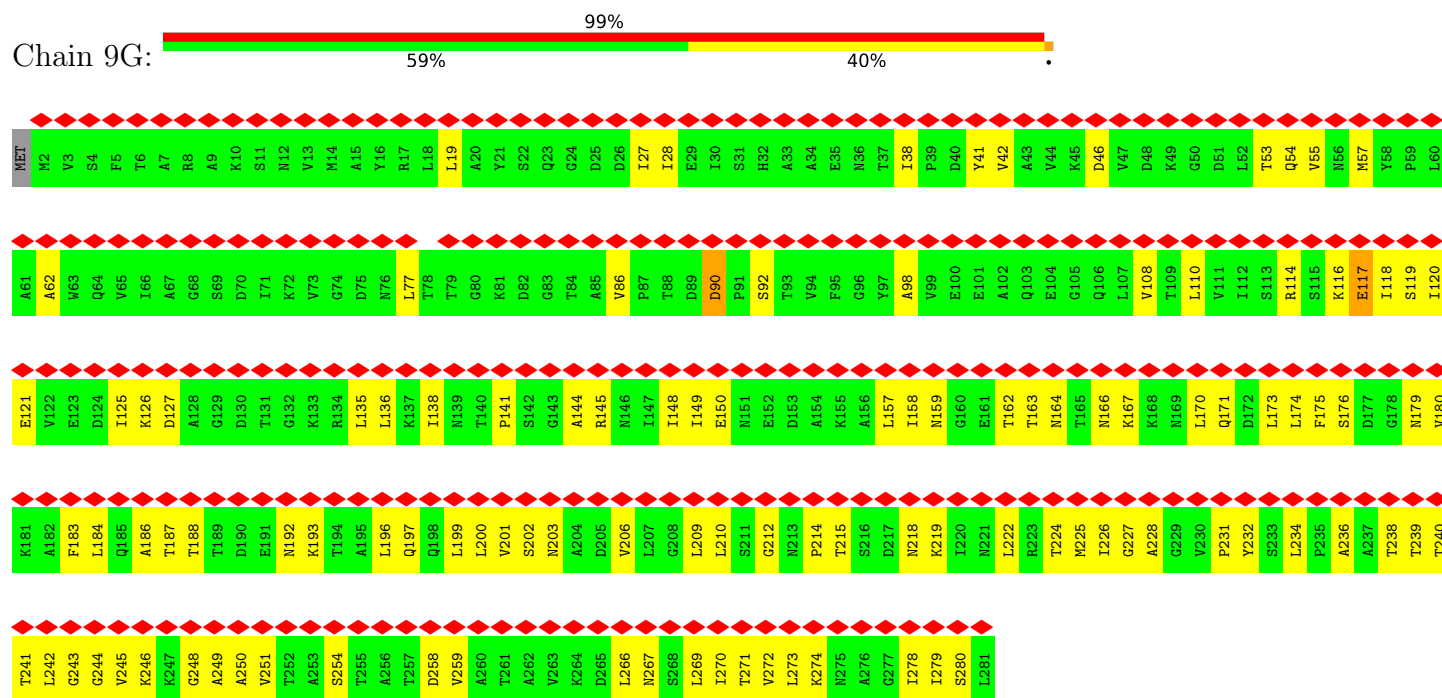




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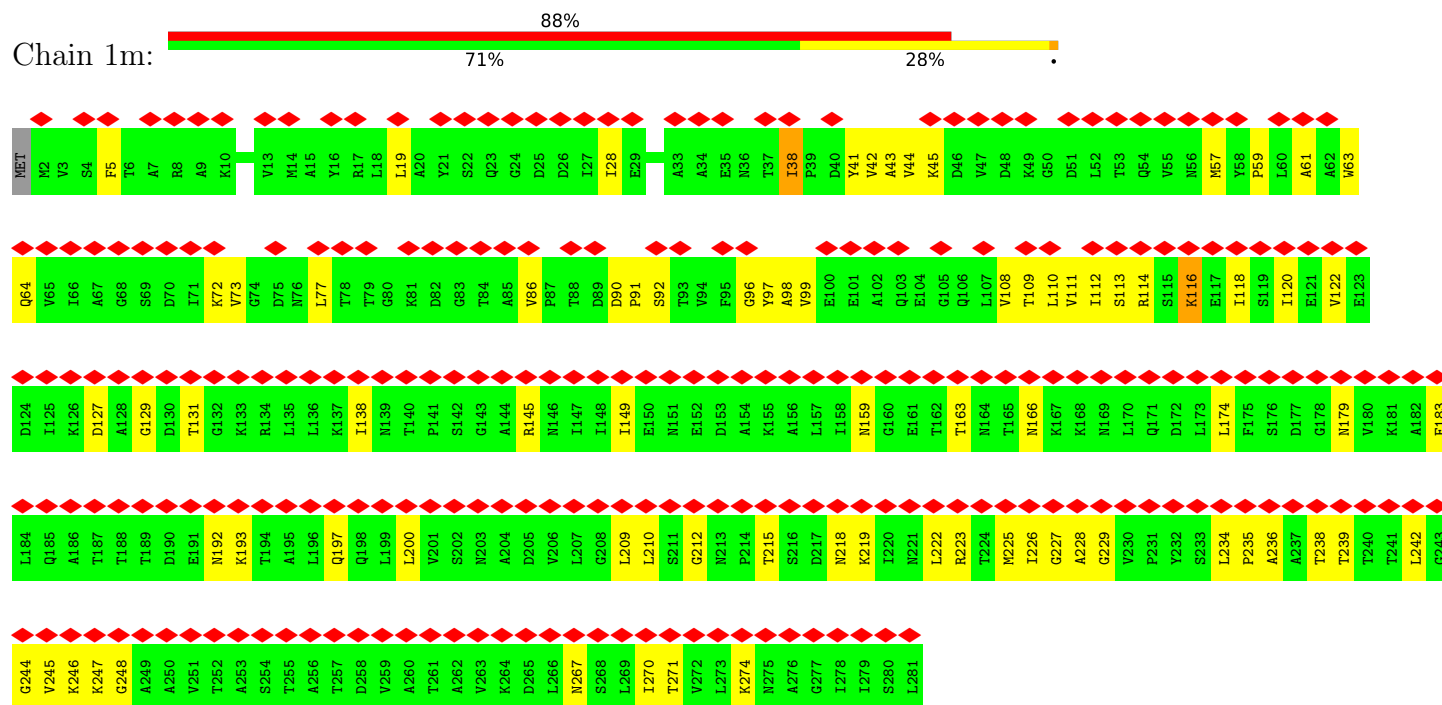


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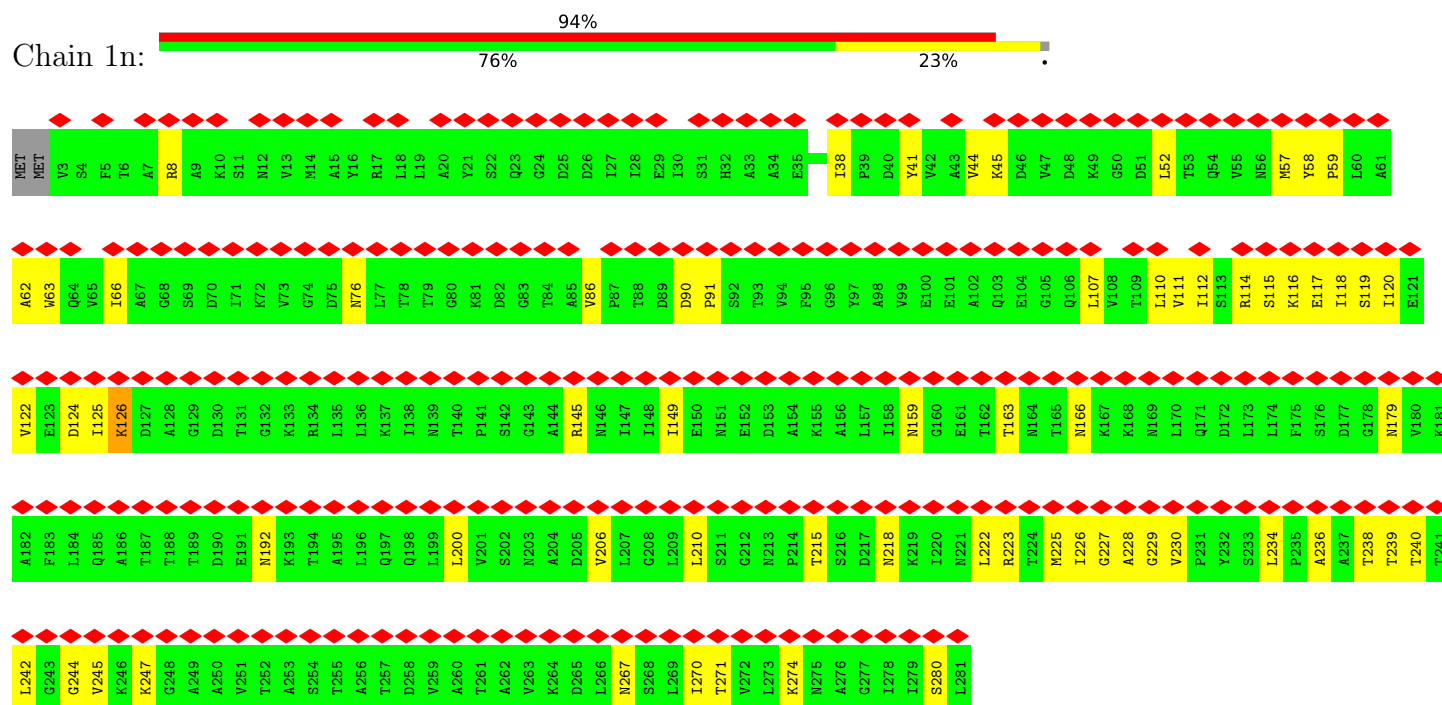
● Molecule 2: Capsid fiber protein

Chain 1m:



● Molecule 2: Capsid fiber protein

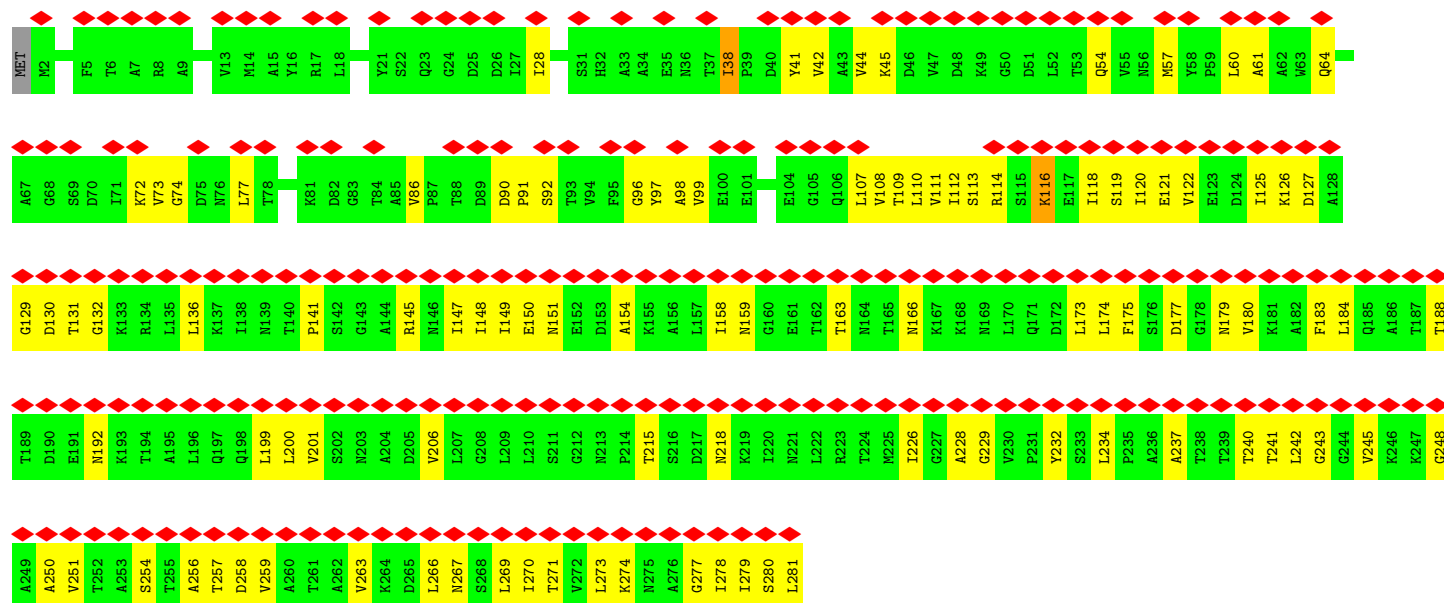
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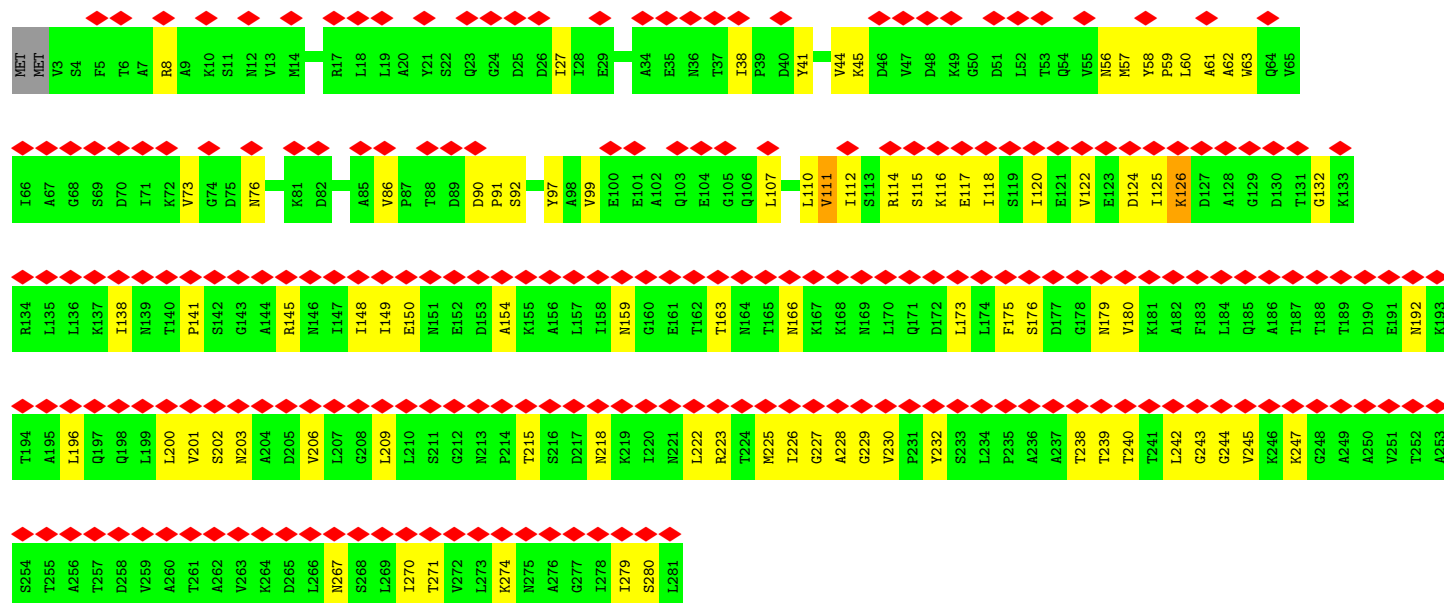
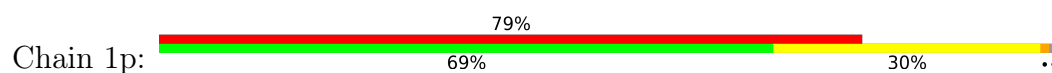
● Molecule 2: Capsid fiber protein

Chain 1o:

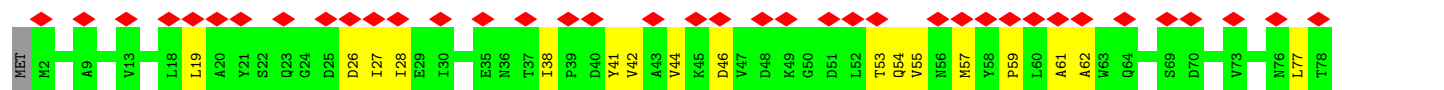
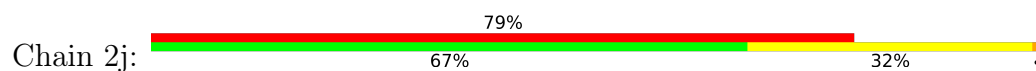




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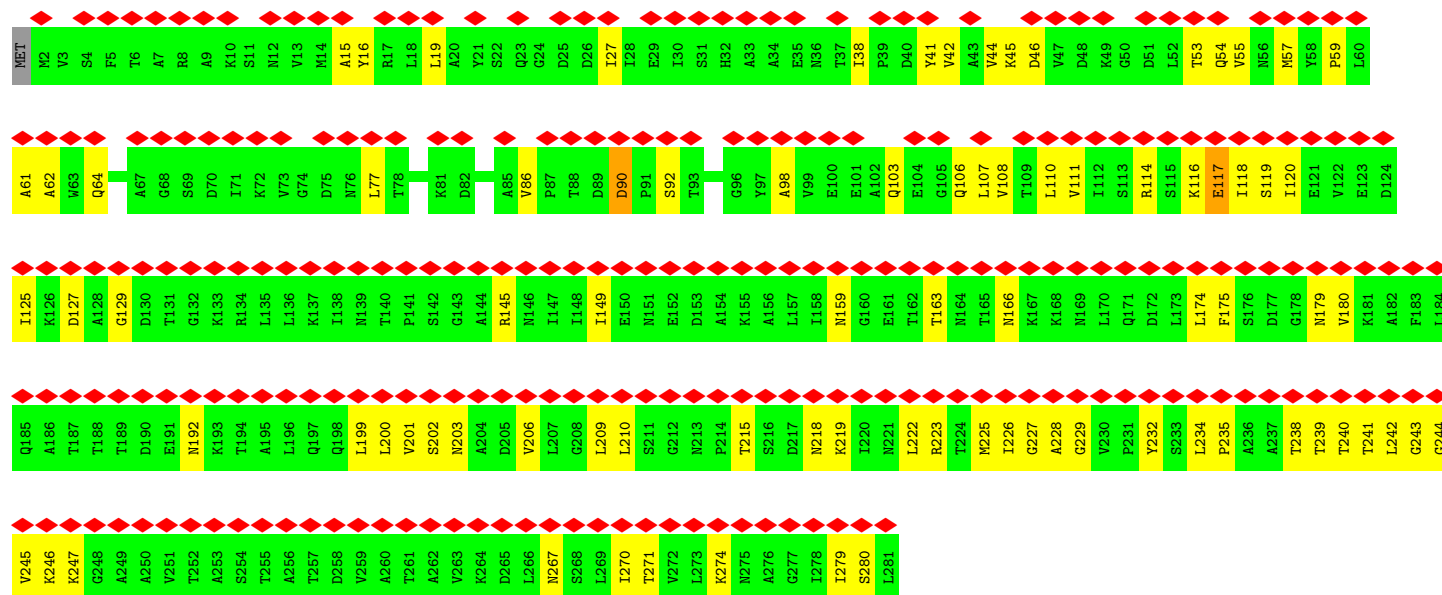
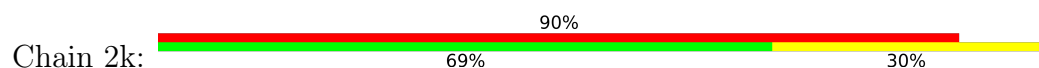


• Molecule 2: Capsid fiber protein

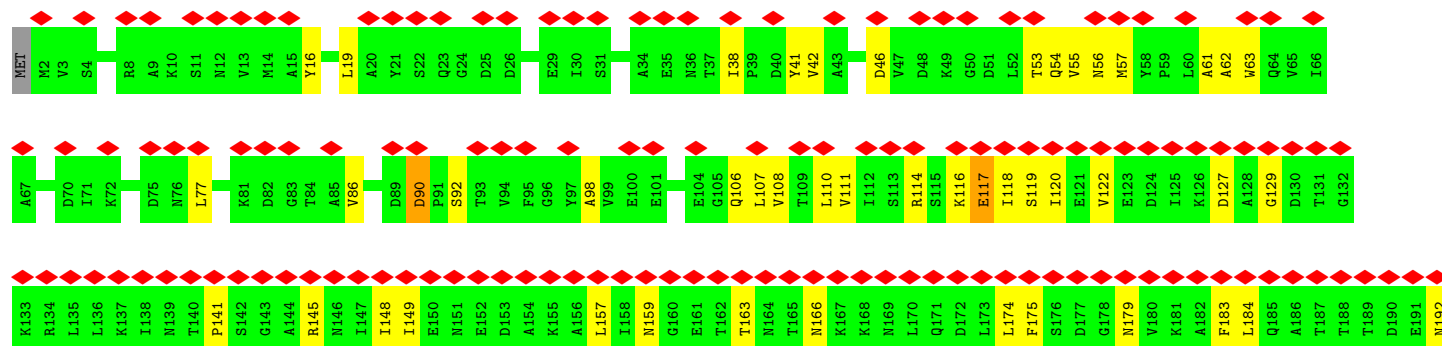
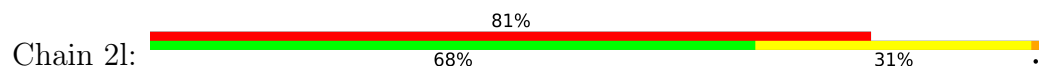


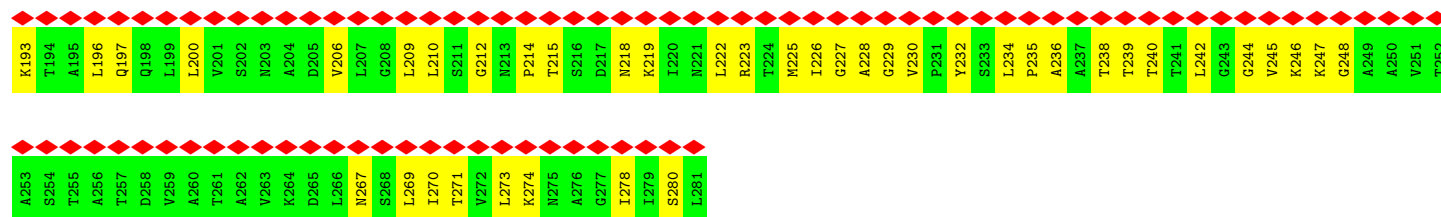


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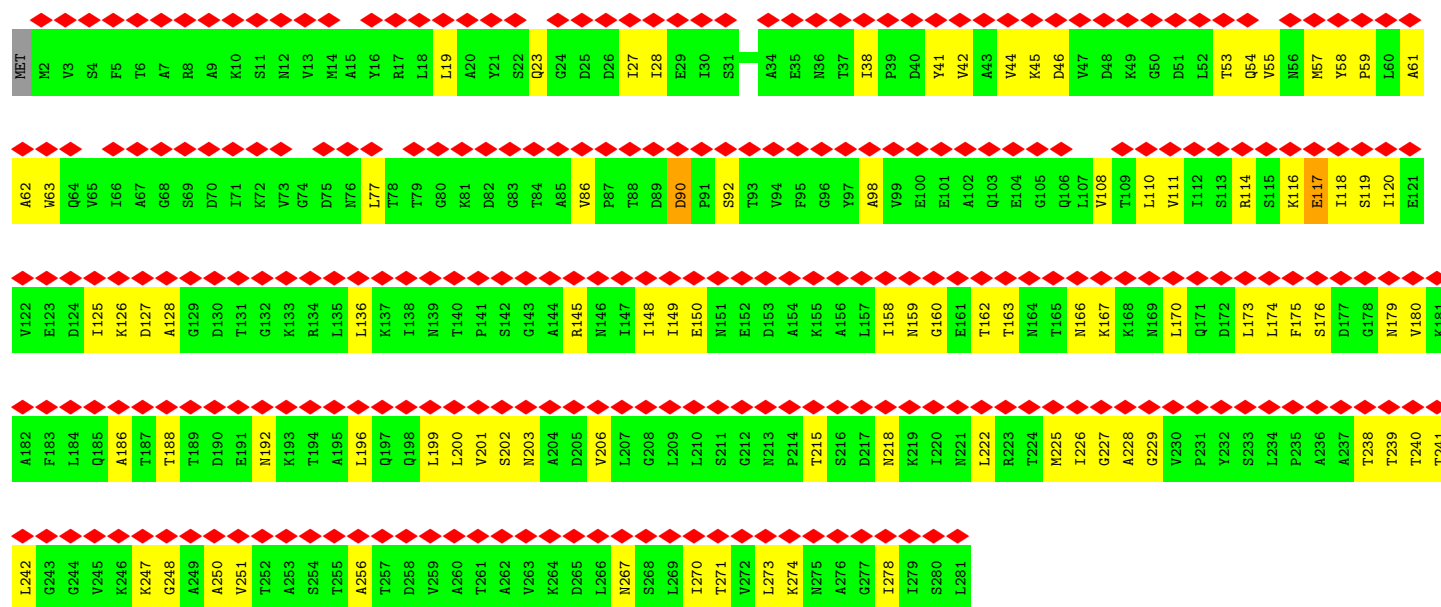


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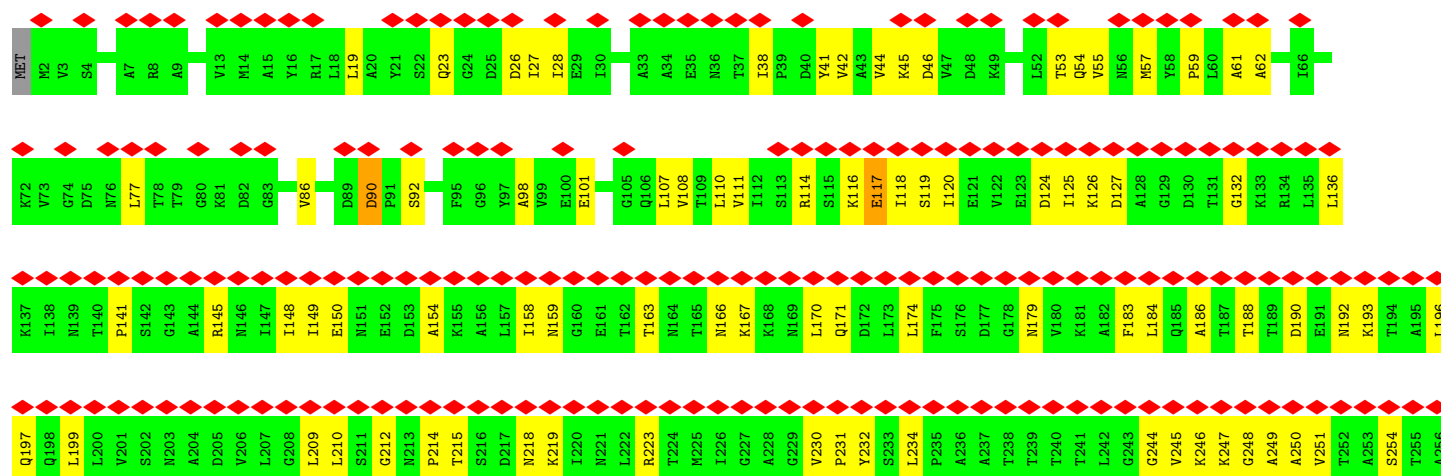
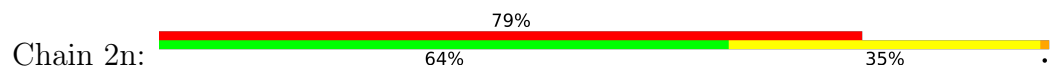




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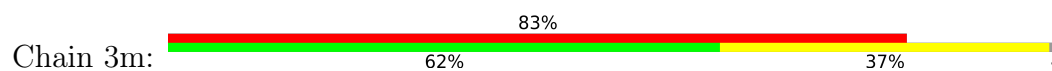


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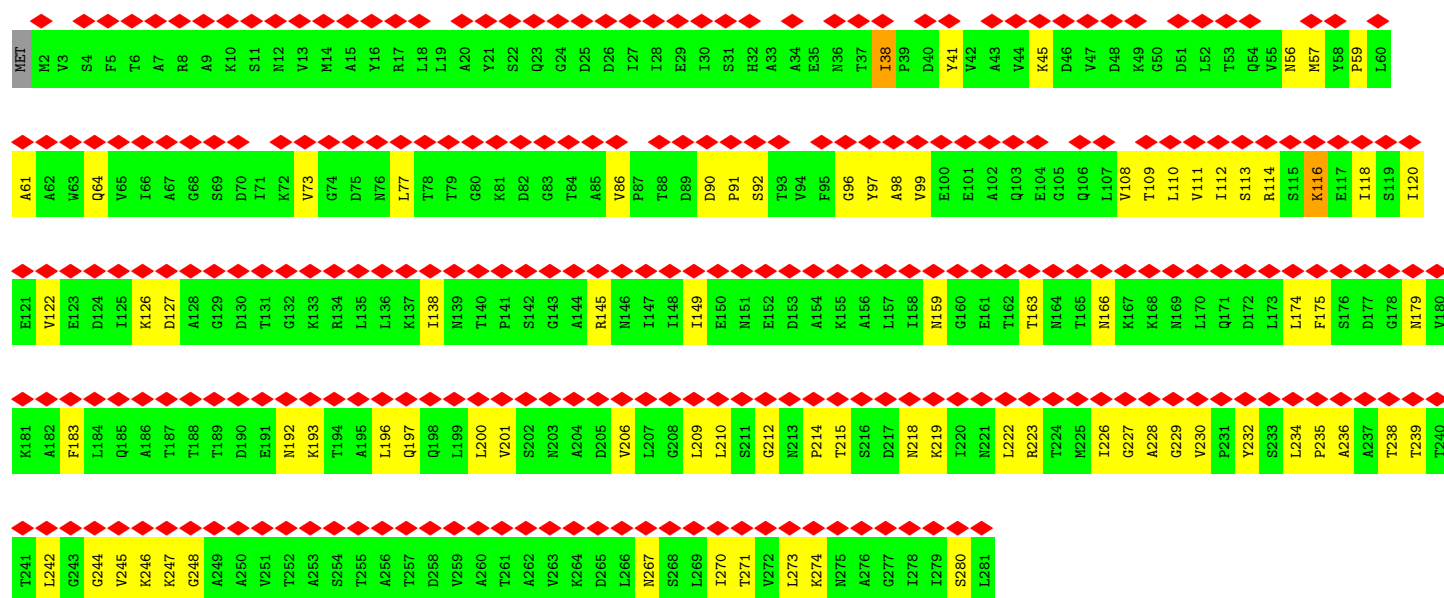
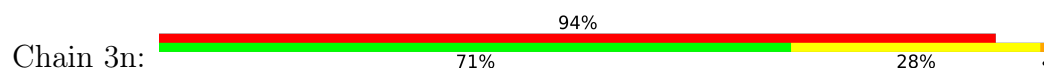




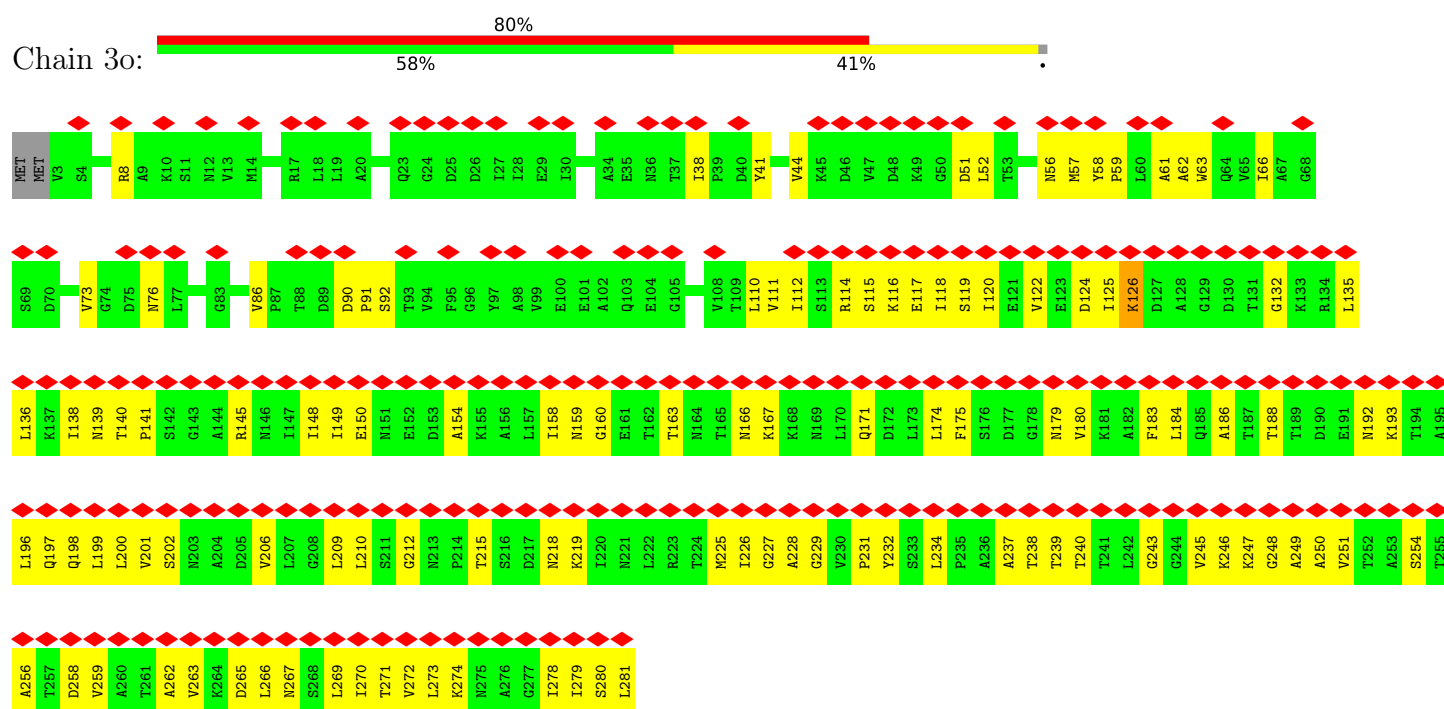
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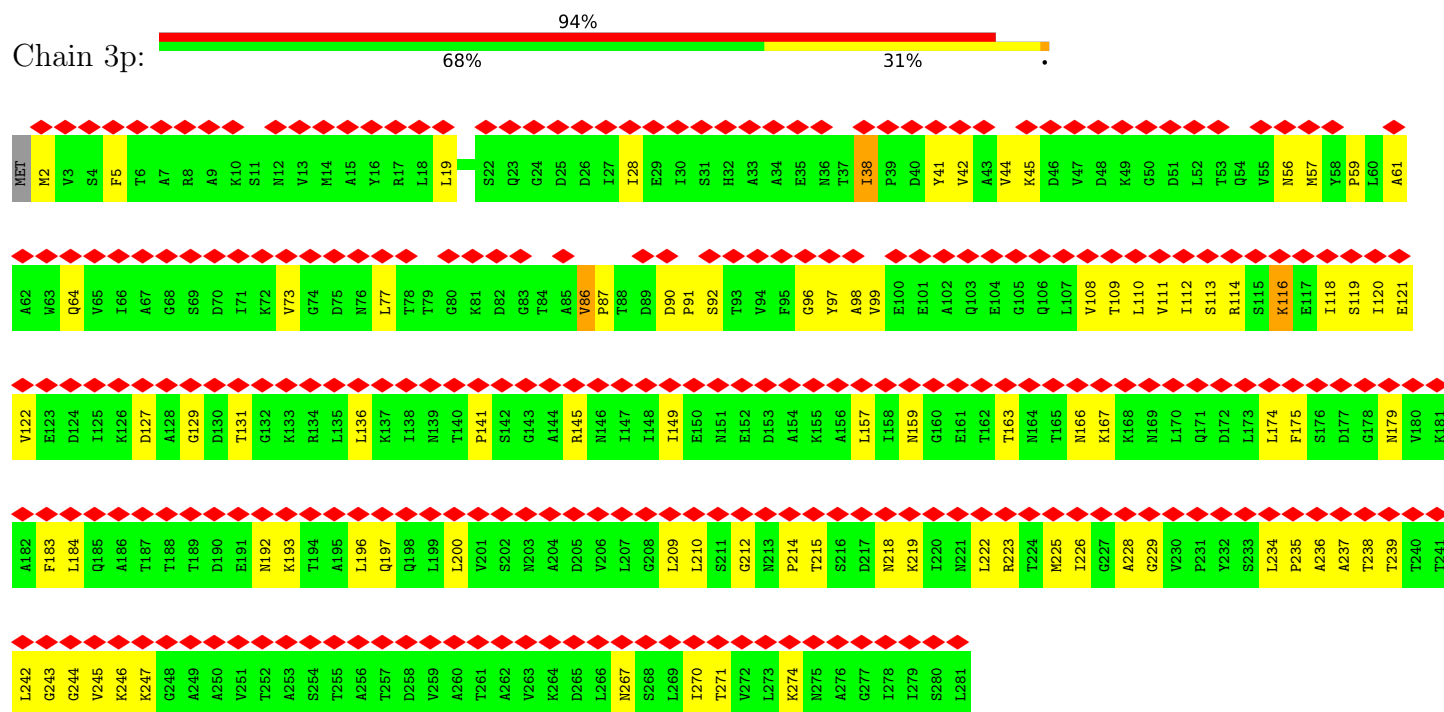
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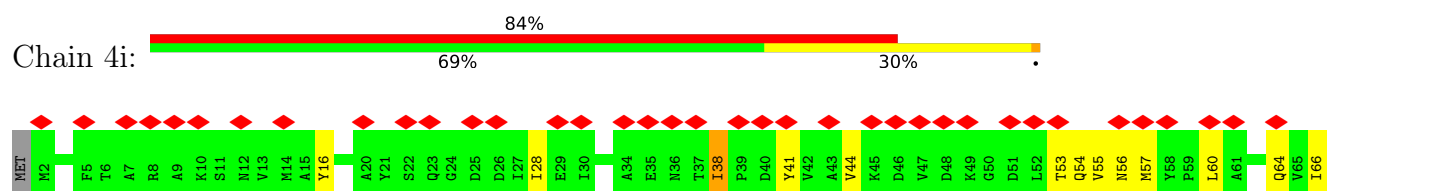
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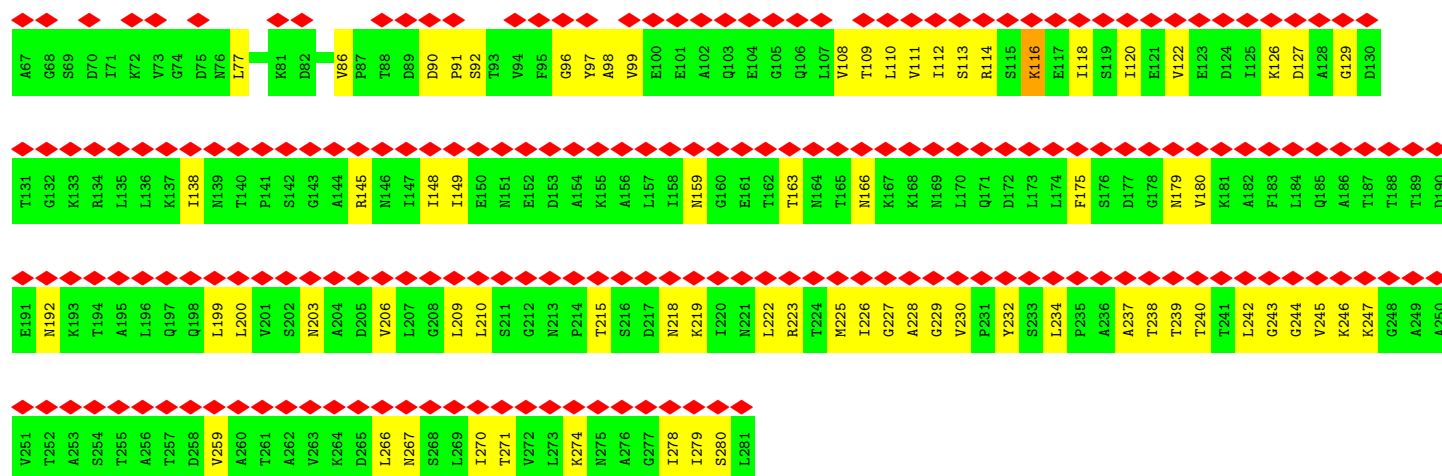


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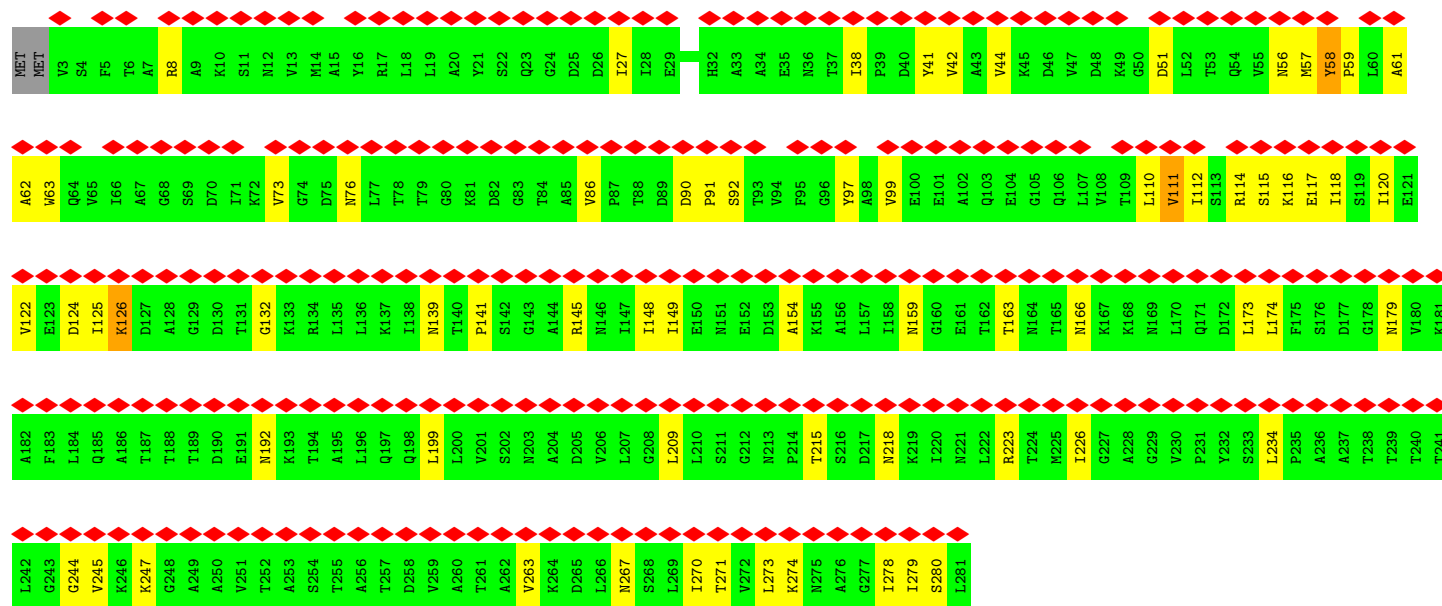
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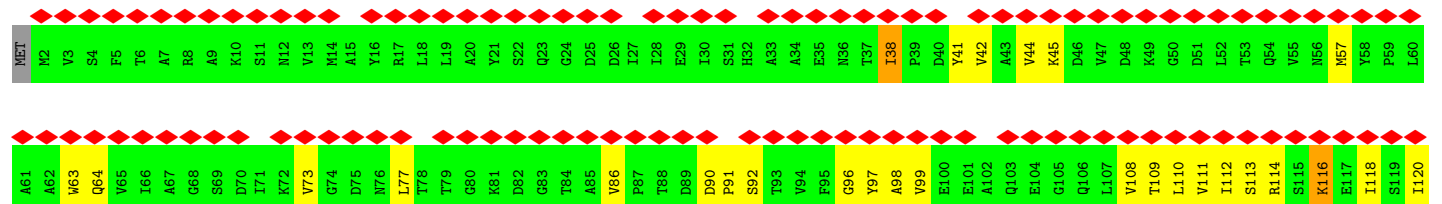
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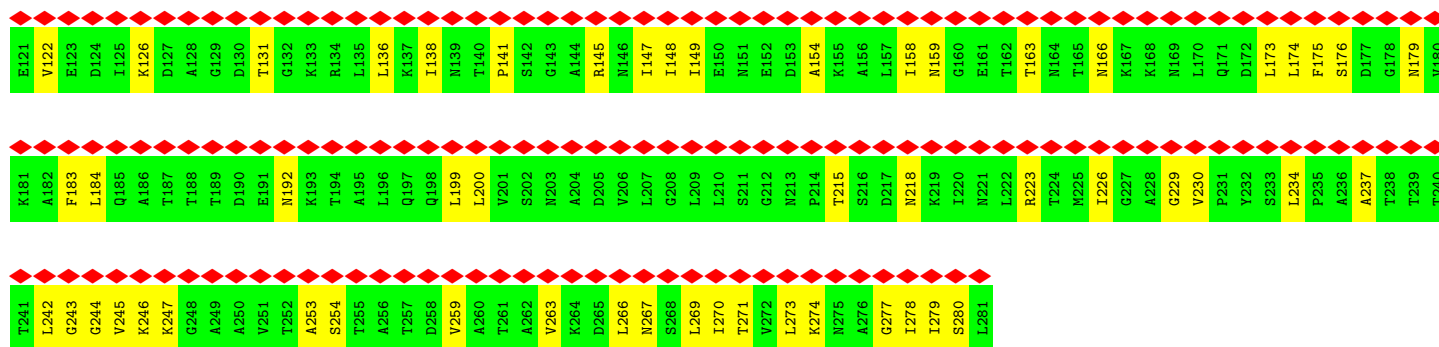
Chain 4j: 95% 75% 23% ..



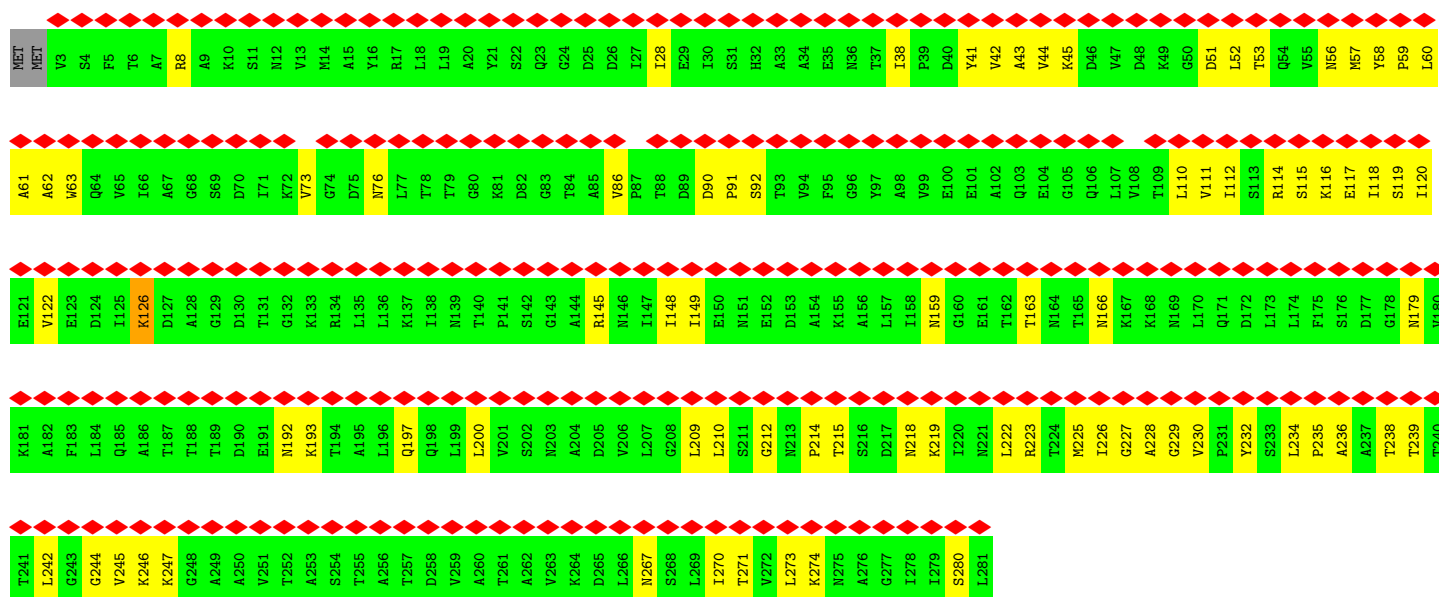
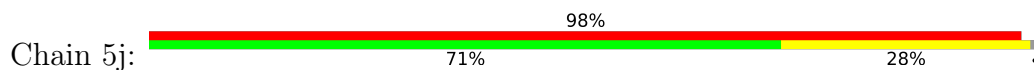
• Molecule 2: Capsid fiber protein

Chain 5i: 97% 70% 28% .

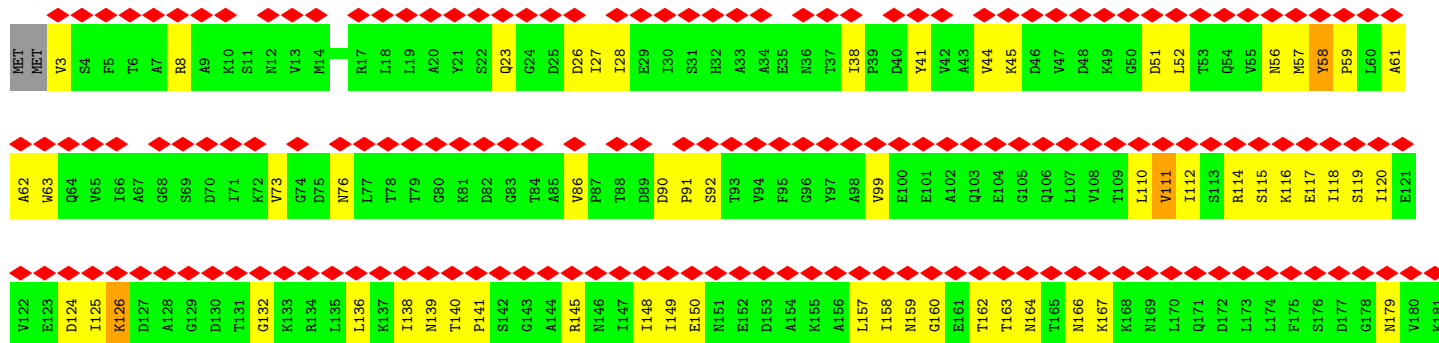


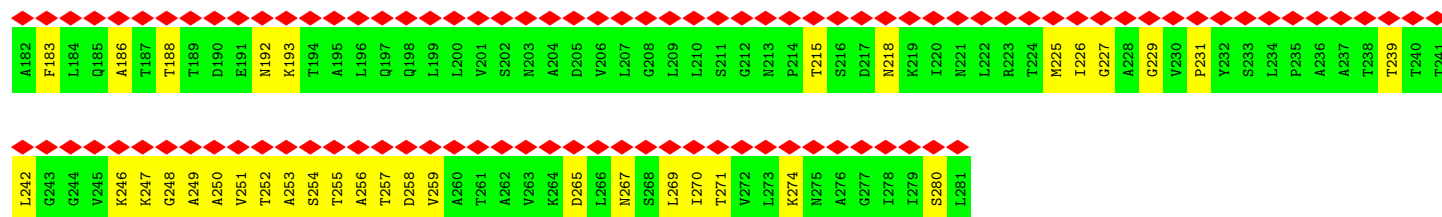


• Molecule 2: Capsid fiber protein

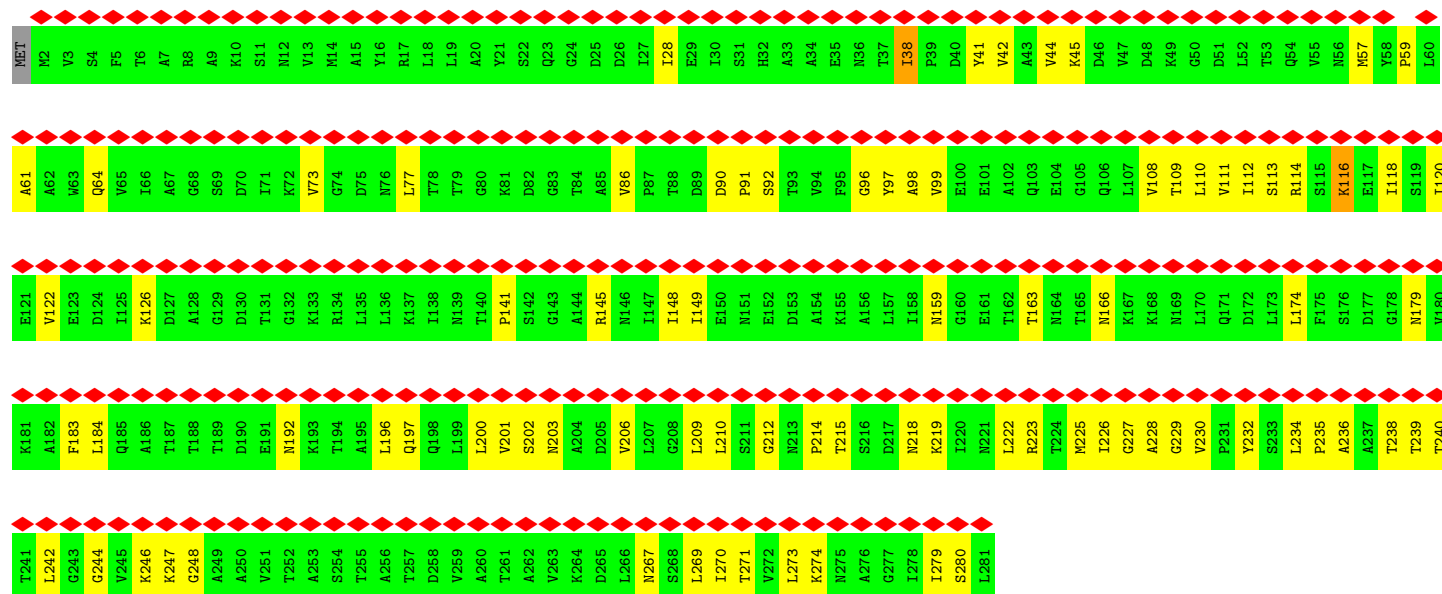


• Molecule 2: Capsid fiber protein

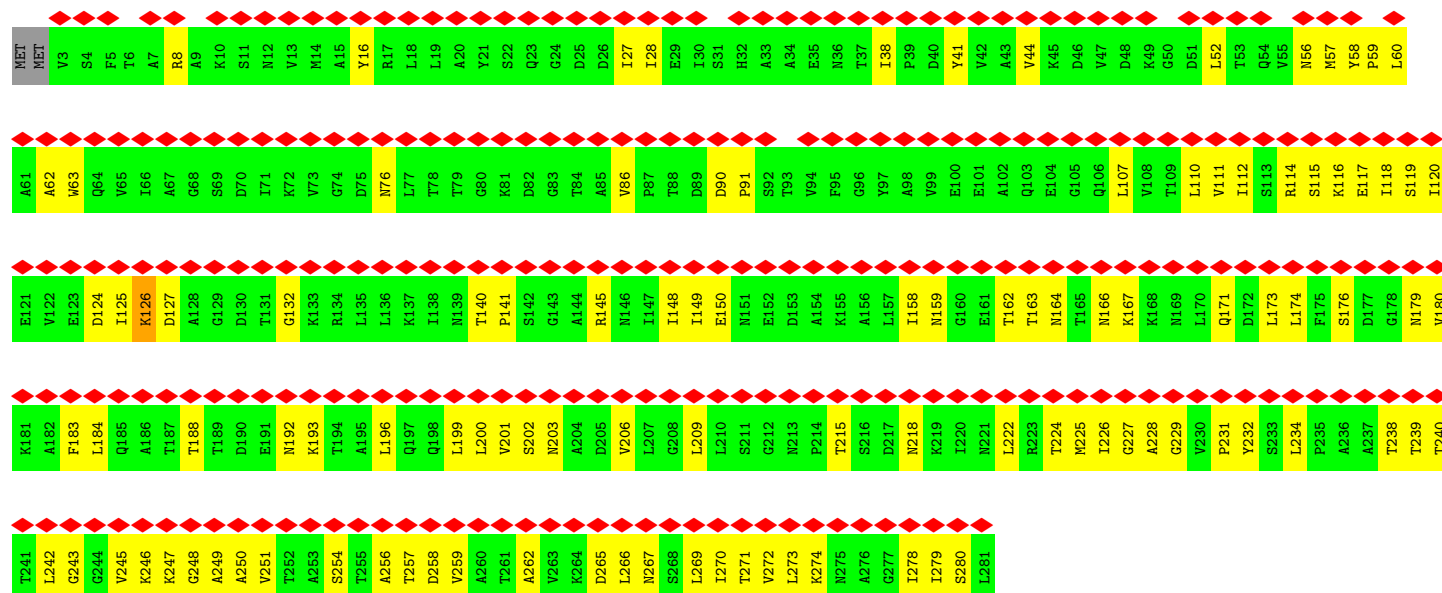




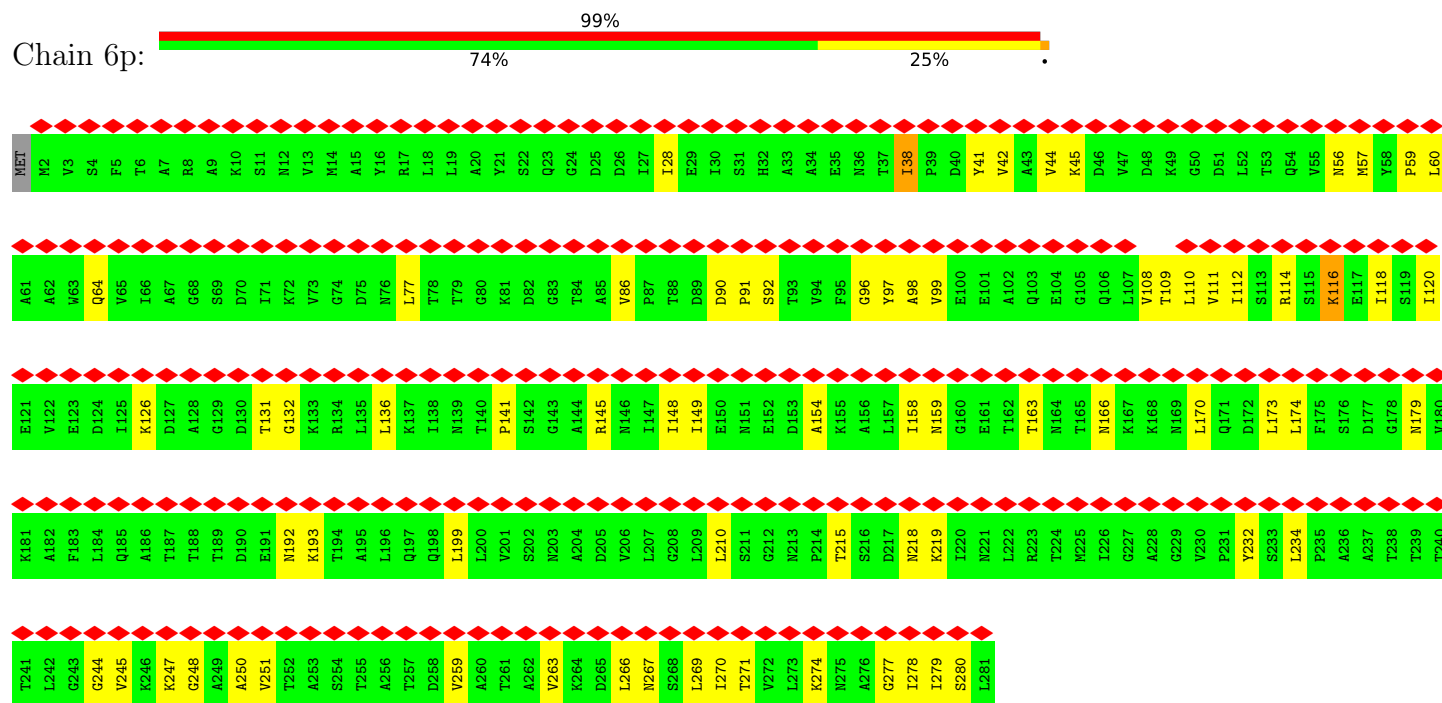
• Molecule 2: Capsid fiber protein

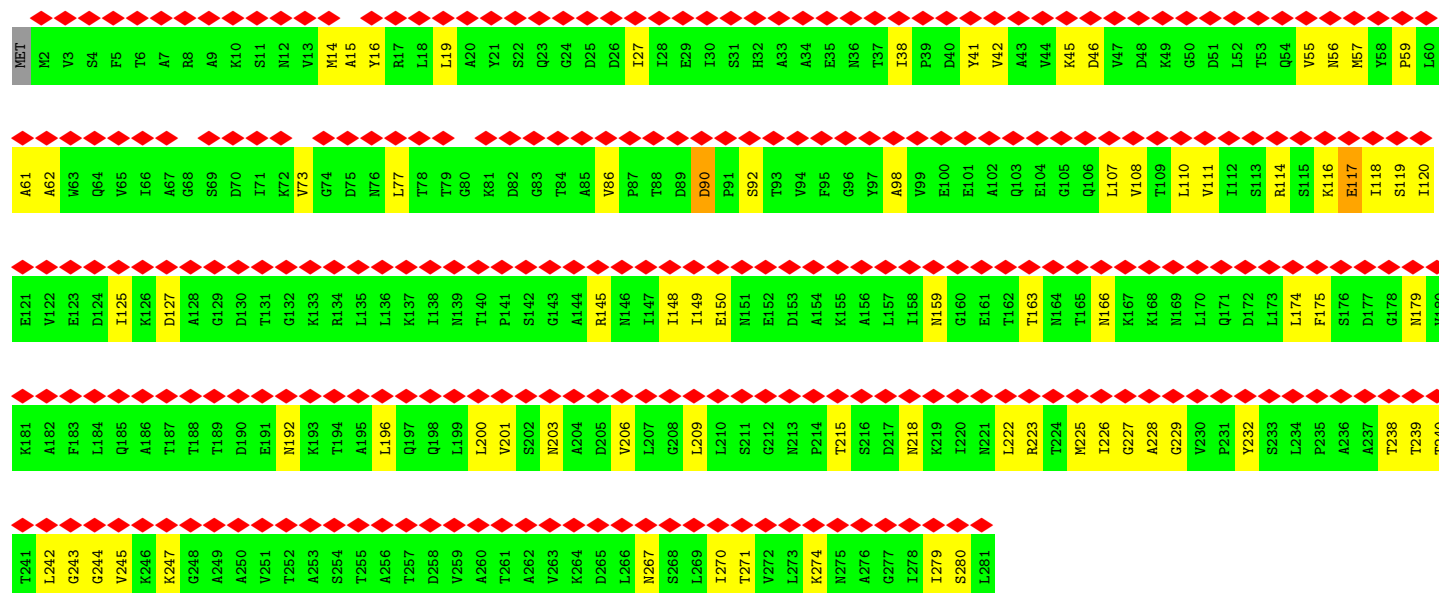


• Molecule 2: Capsid fiber protein

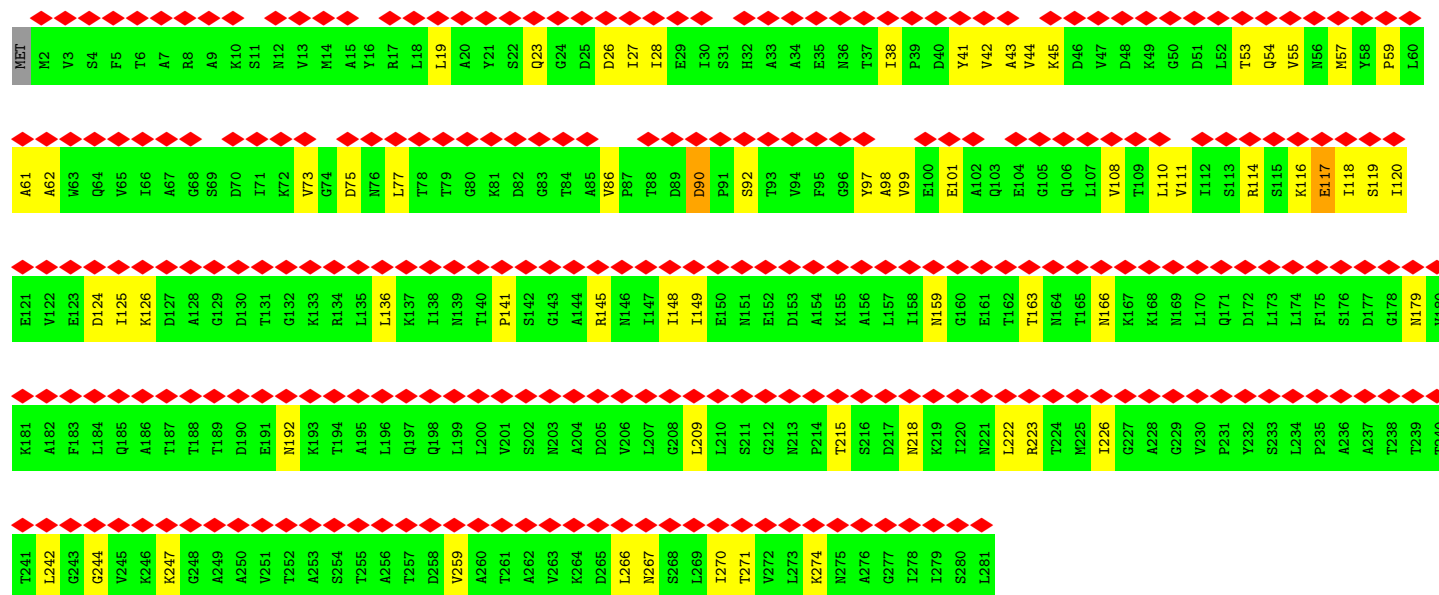
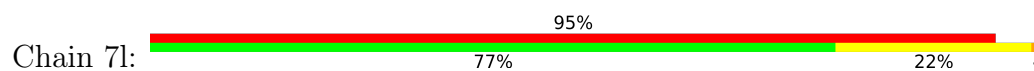


• Molecule 2: Capsid fiber protein

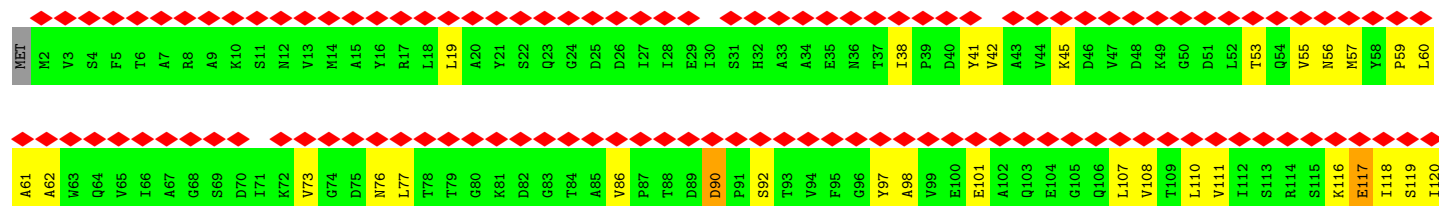




• Molecule 2: Capsid fiber protein

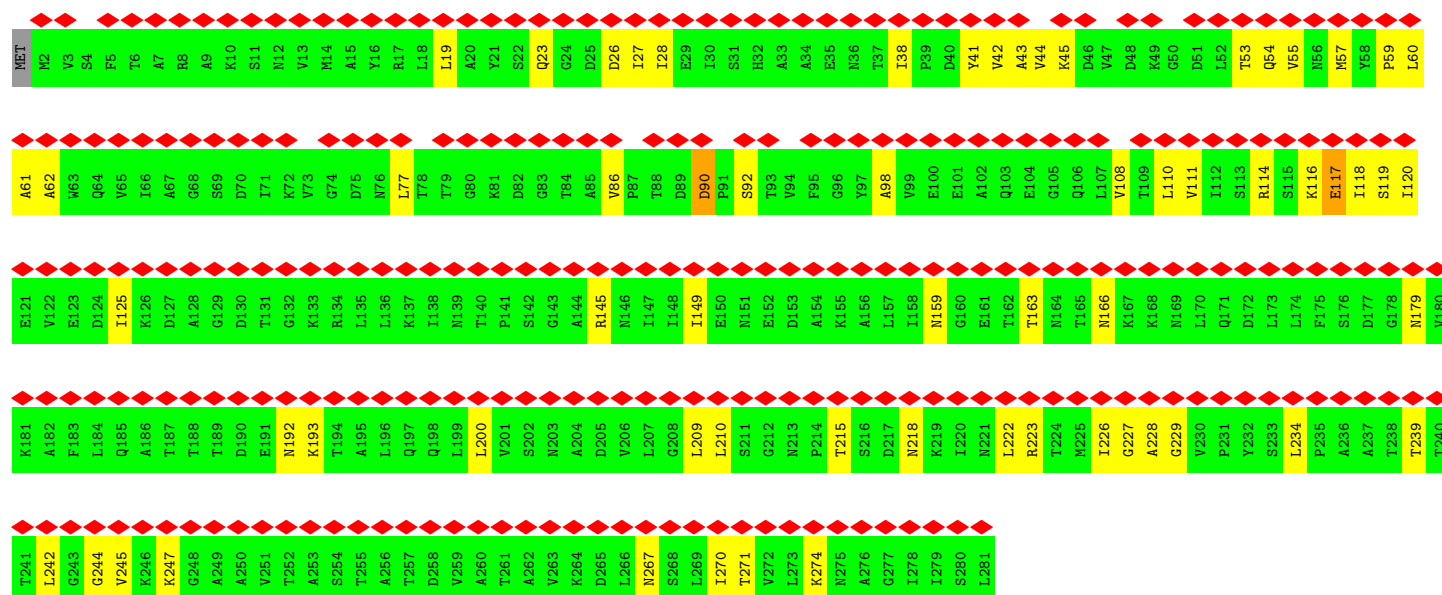
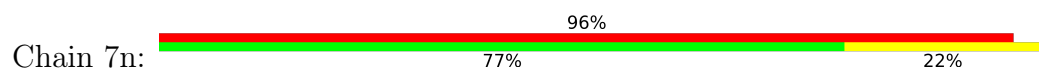


• Molecule 2: Capsid fiber protein

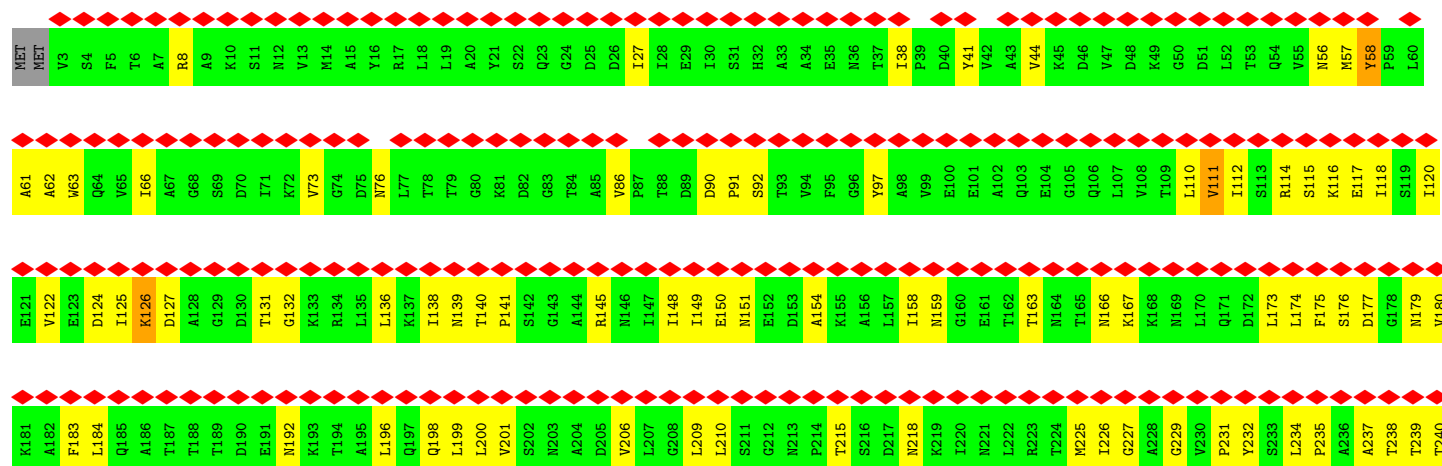




• Molecule 2: Capsid fiber protein



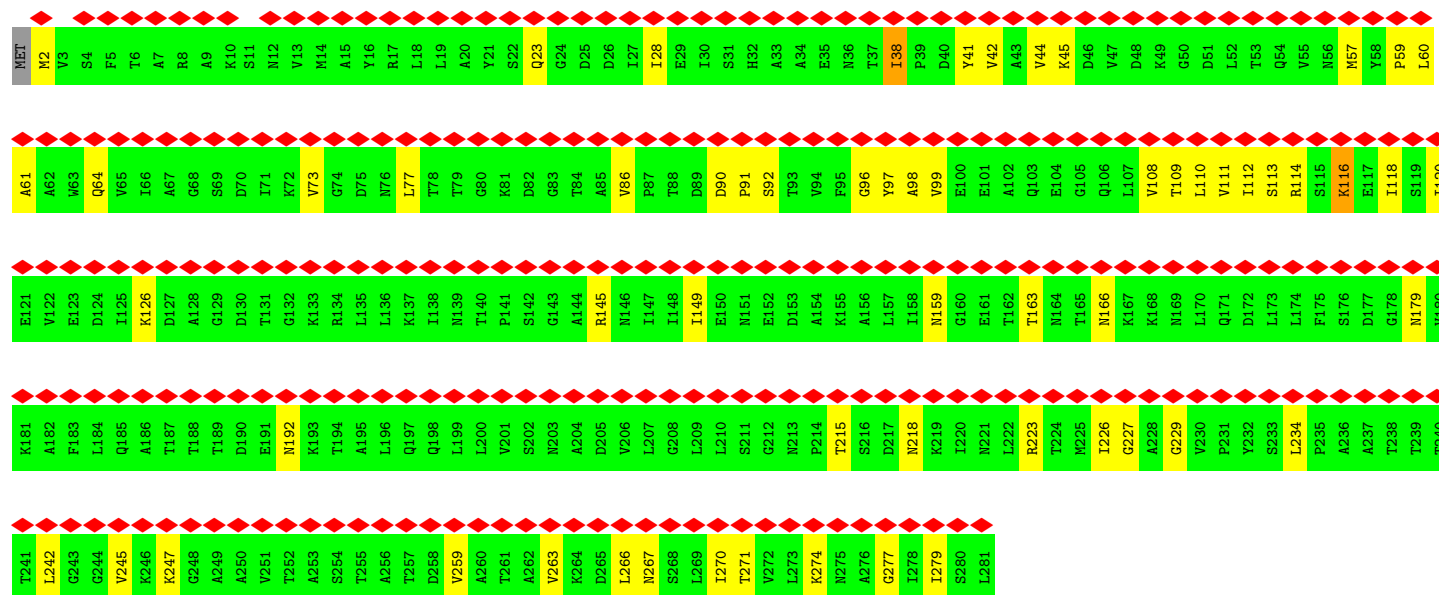
• Molecule 2: Capsid fiber protein





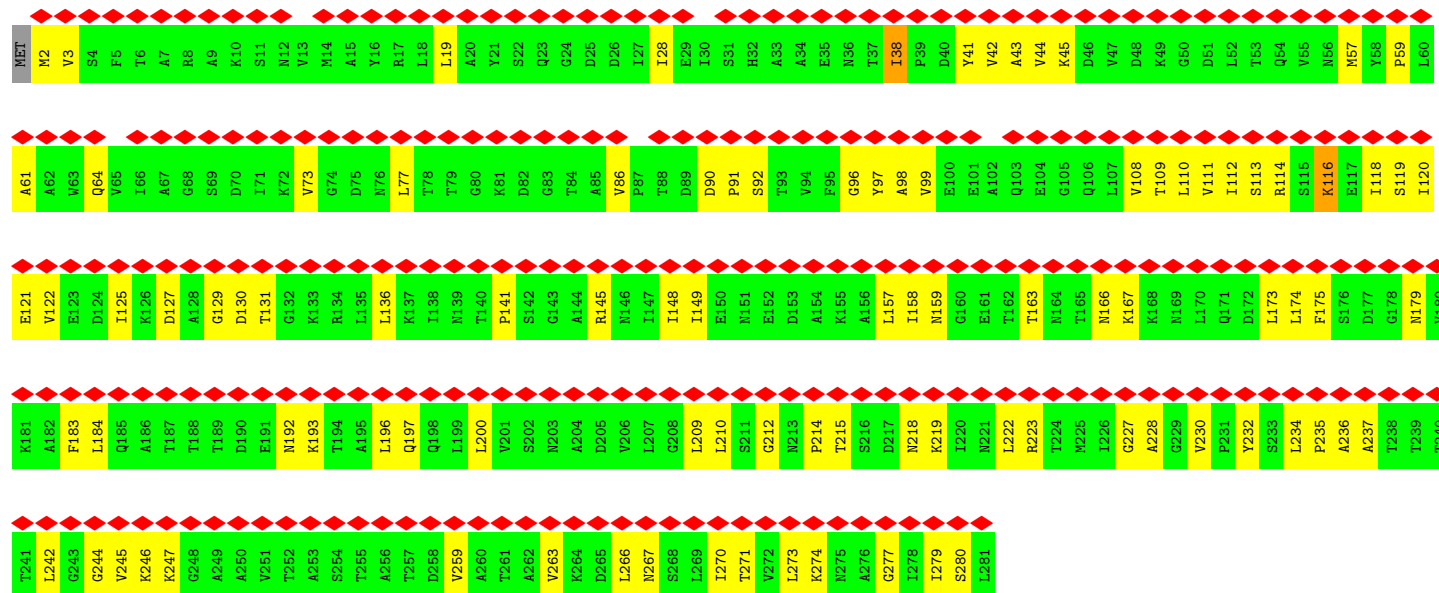
• Molecule 2: Capsid fiber protein

Chain 8r:



• Molecule 2: Capsid fiber protein

Chain 8s:

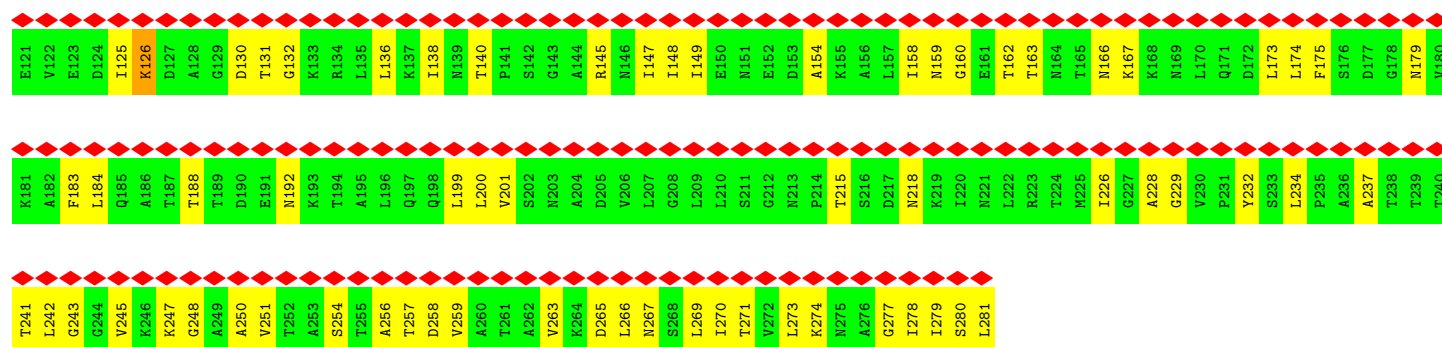


• Molecule 2: Capsid fiber protein

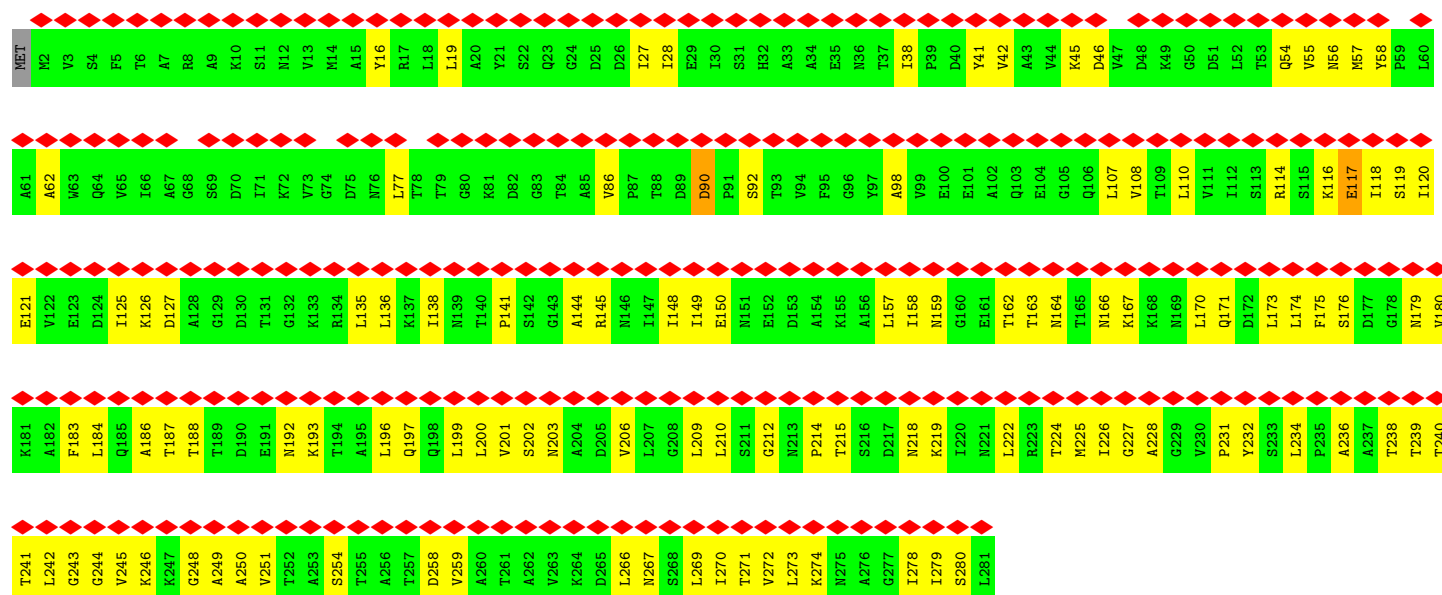
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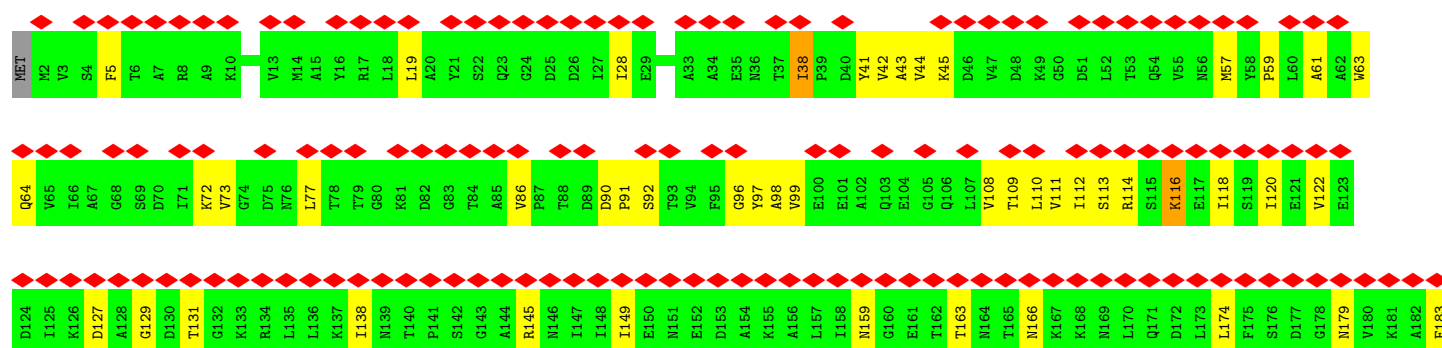
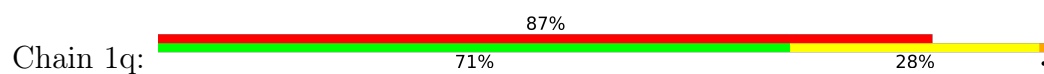


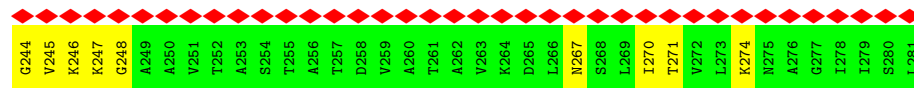
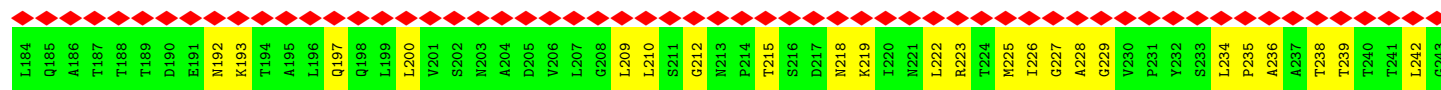


• Molecule 2: Capsid fiber protein

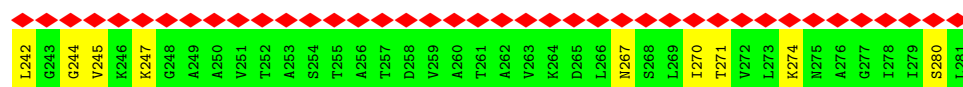
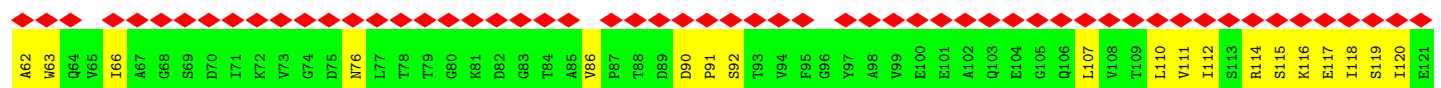
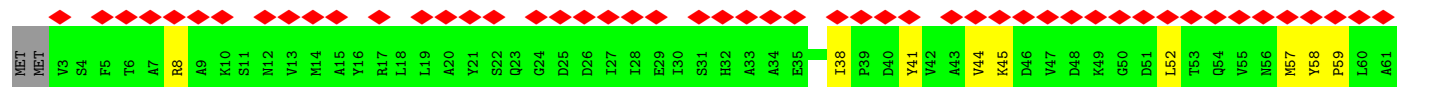
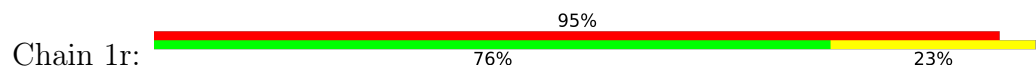


• Molecule 2: Capsid fiber protein

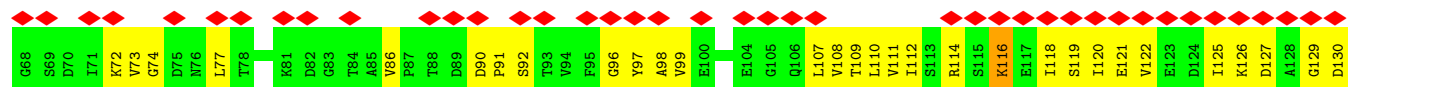
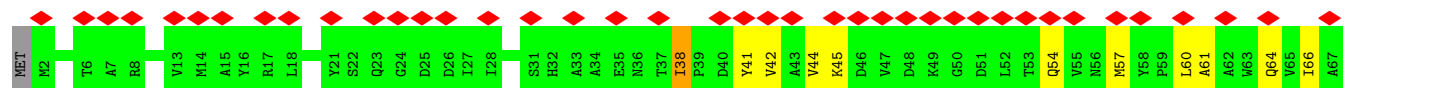
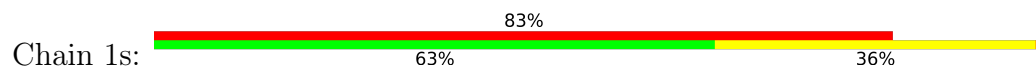


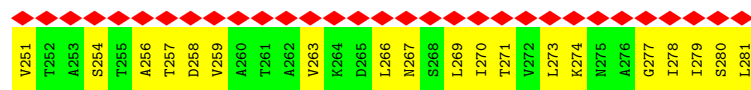


• Molecule 2: Capsid fiber protein

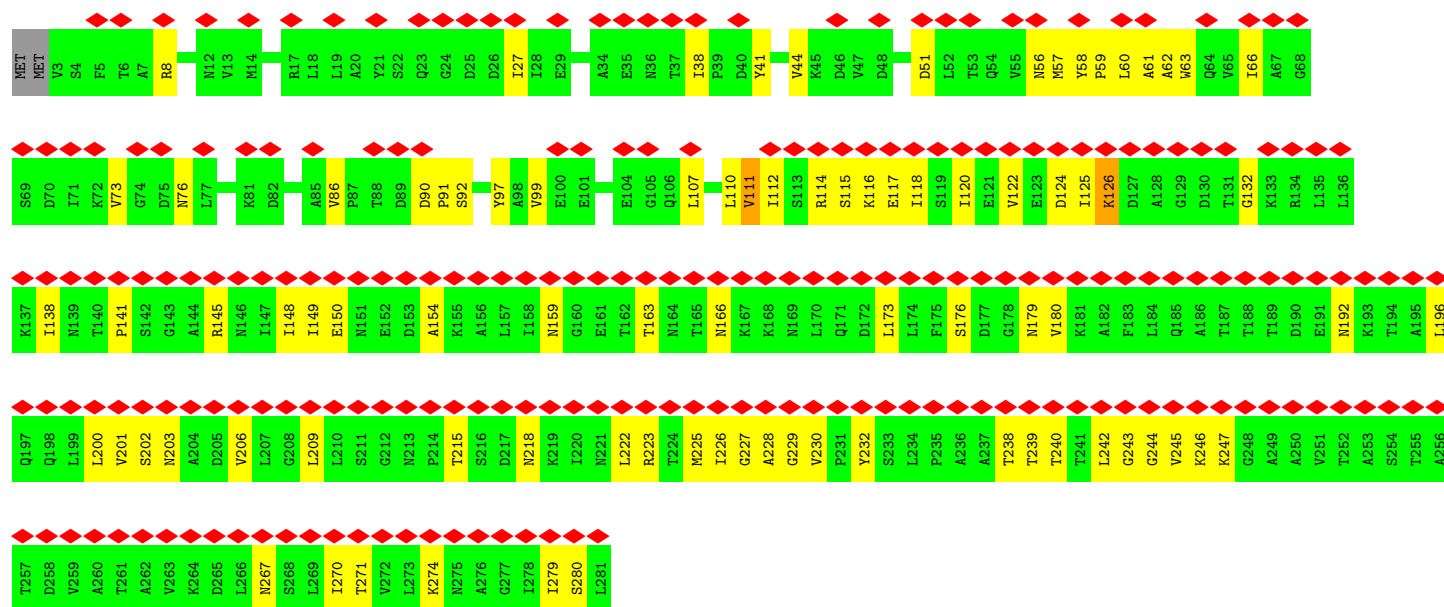
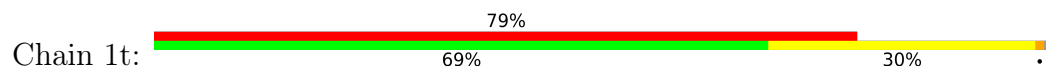


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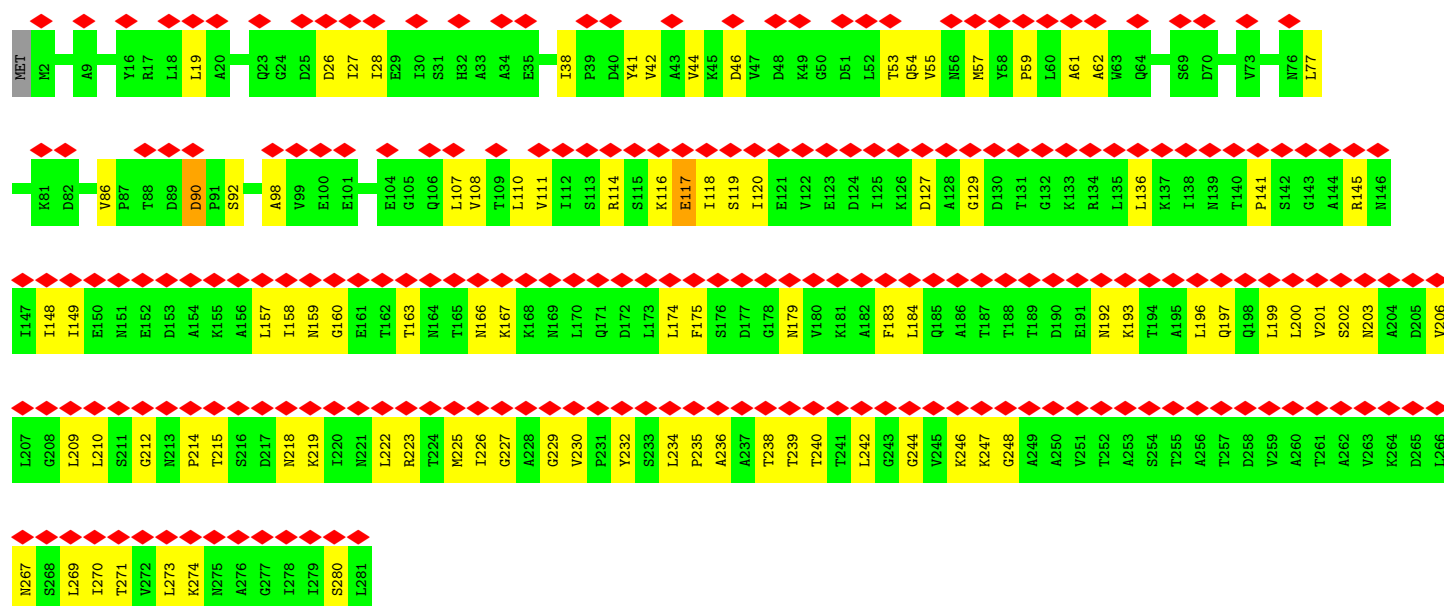
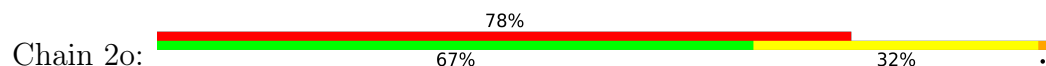




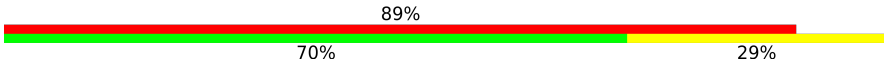
• Molecule 2: Capsid fiber protein

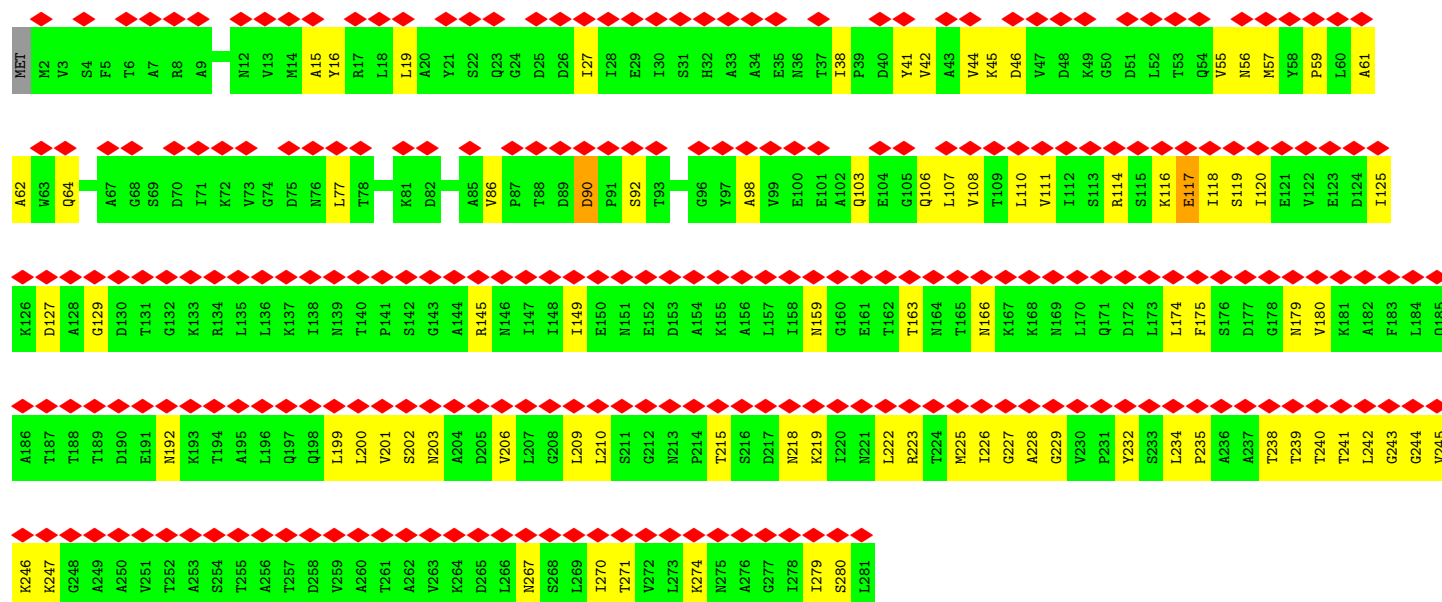


• Molecule 2: Capsid fiber protein



• Molecule 2: Capsid fiber protein

Chain 2p: 

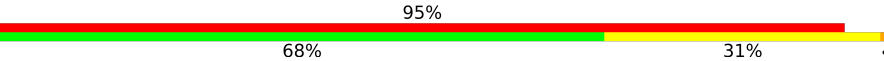


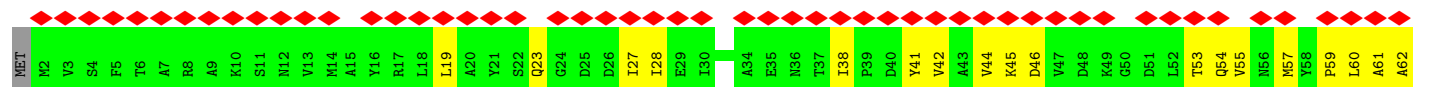
• Molecule 2: Capsid fiber protein

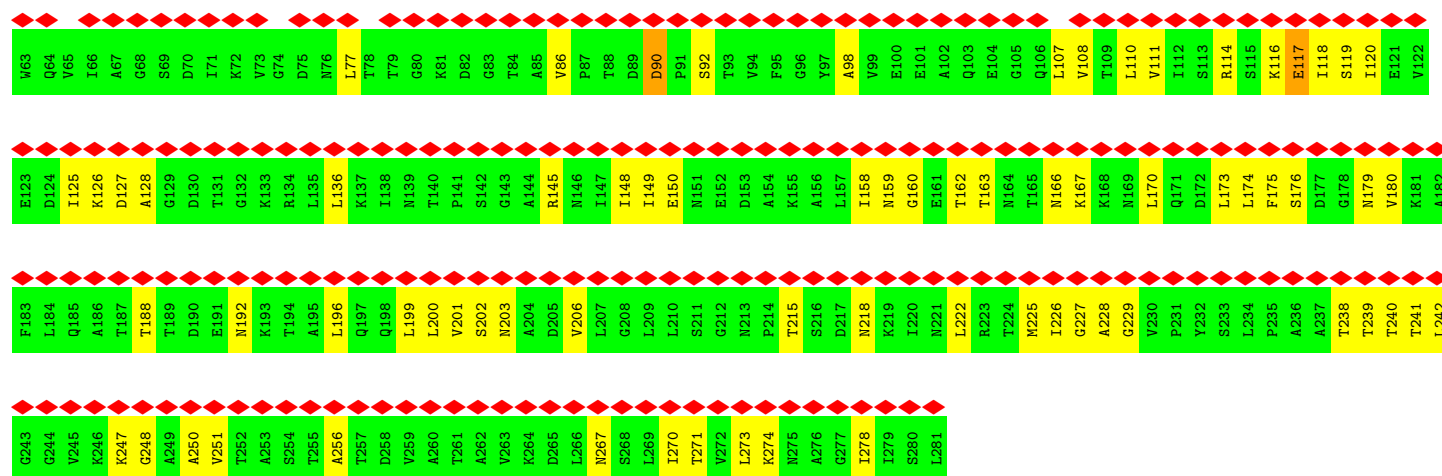
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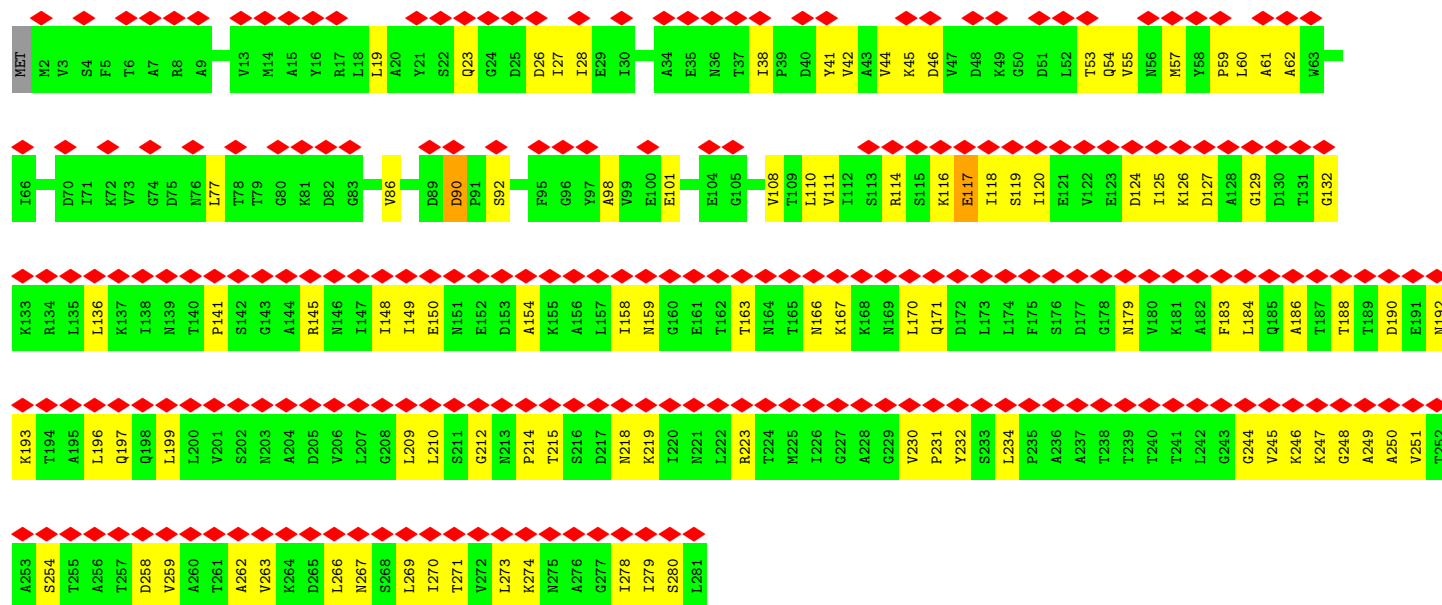
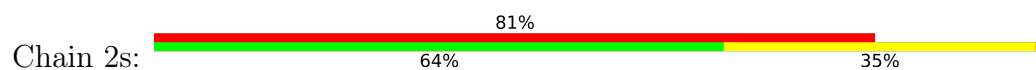
• Molecule 2: Capsid fiber protein

Chain 2r: 

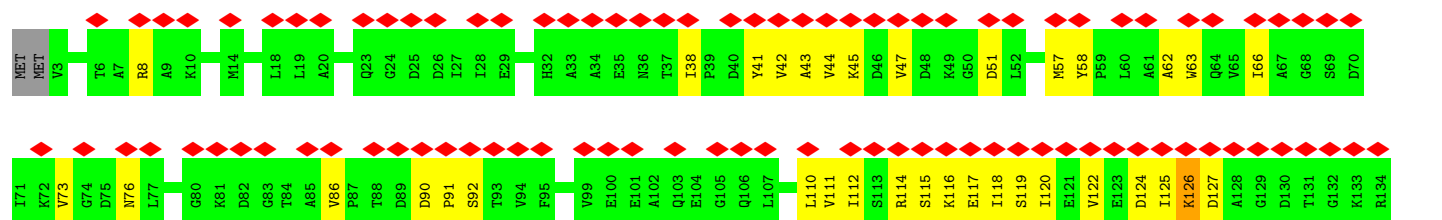
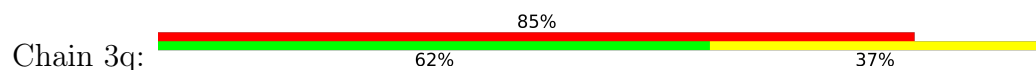


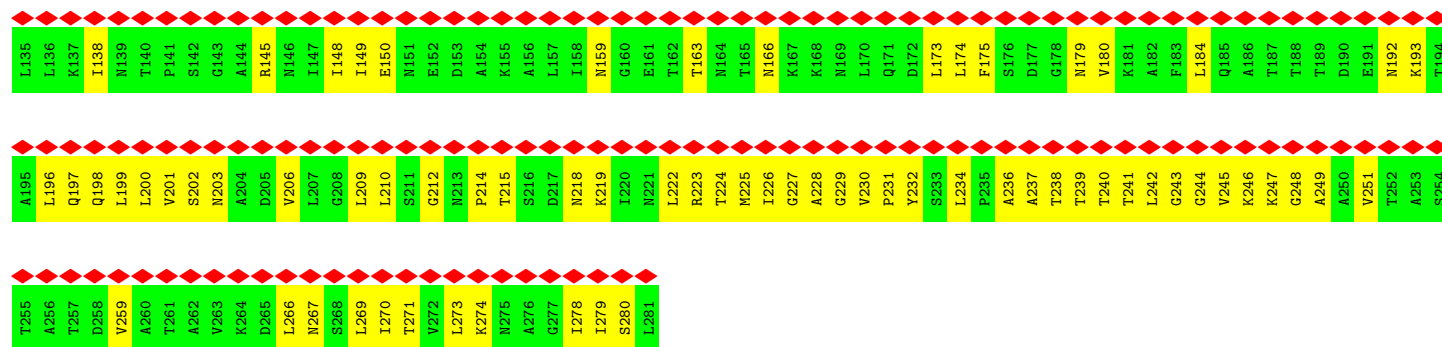


• Molecule 2: Capsid fiber protein

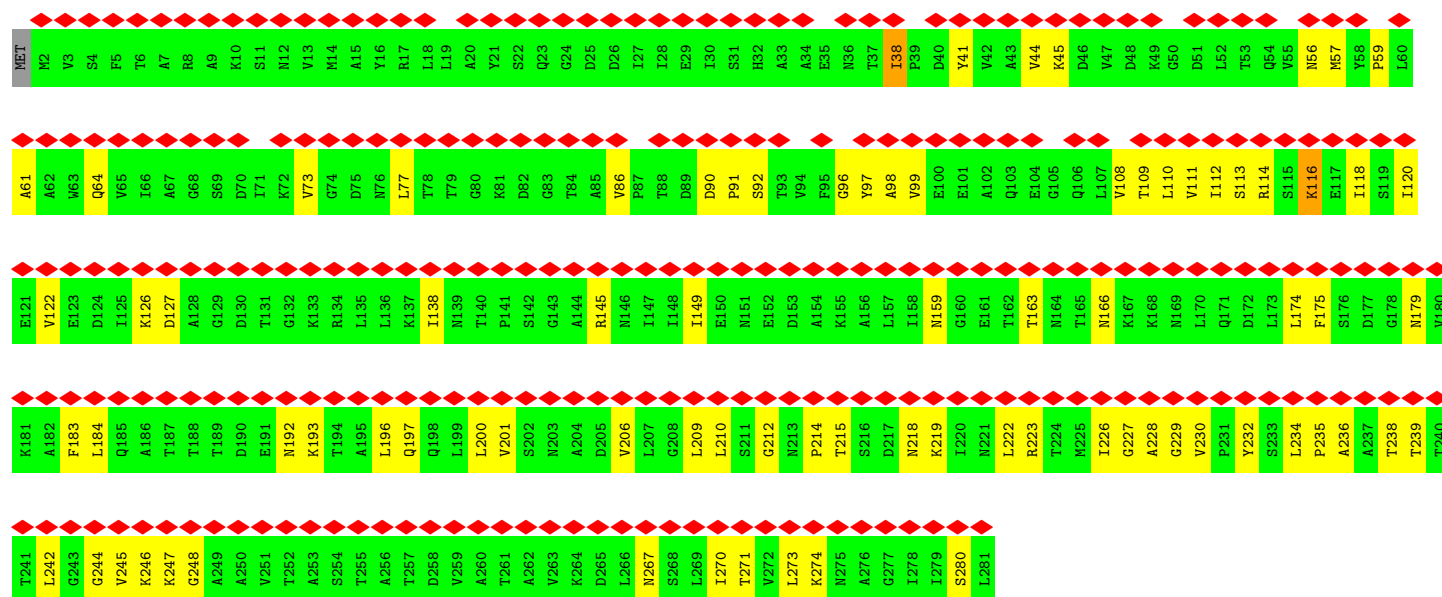
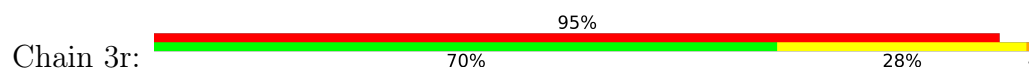


• Molecule 2: Capsid fiber protein

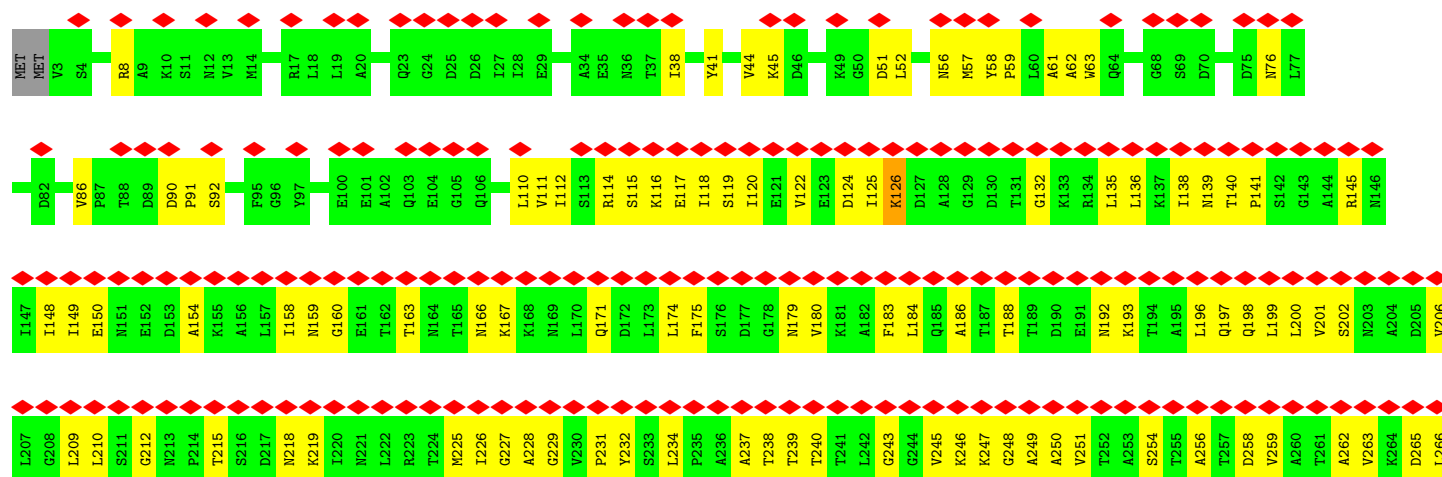
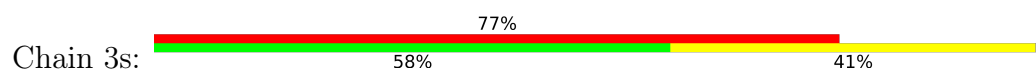




• Molecule 2: Capsid fiber protein

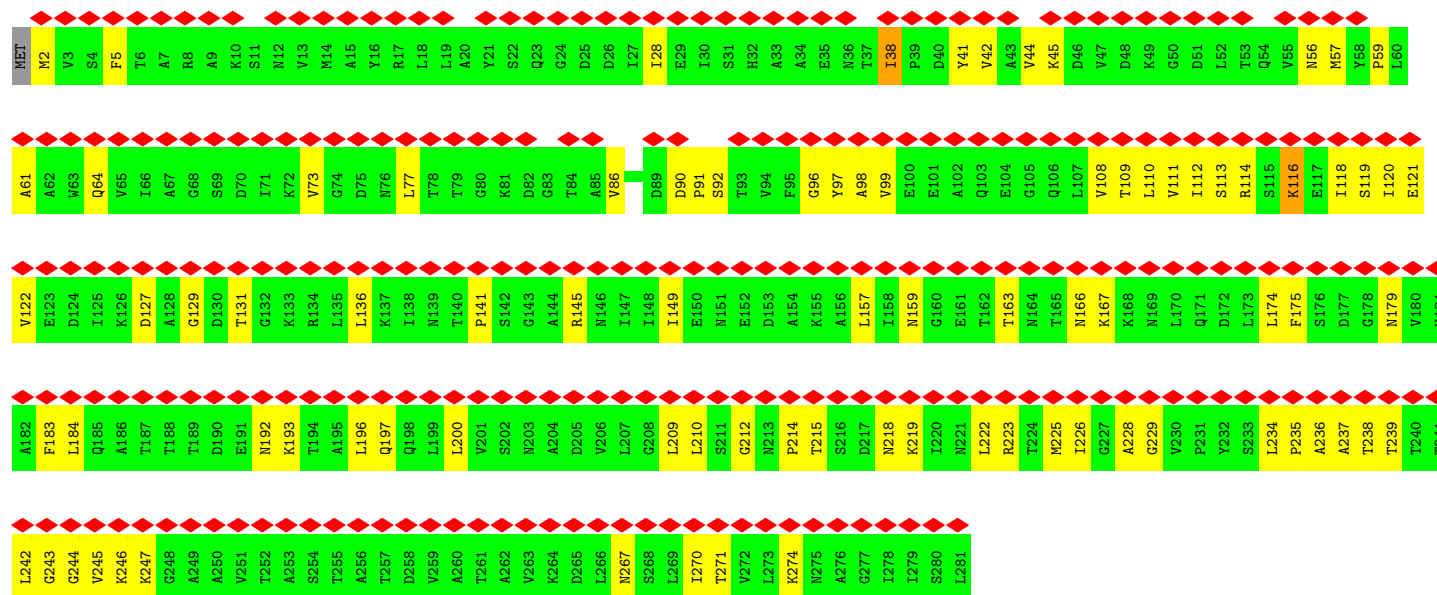


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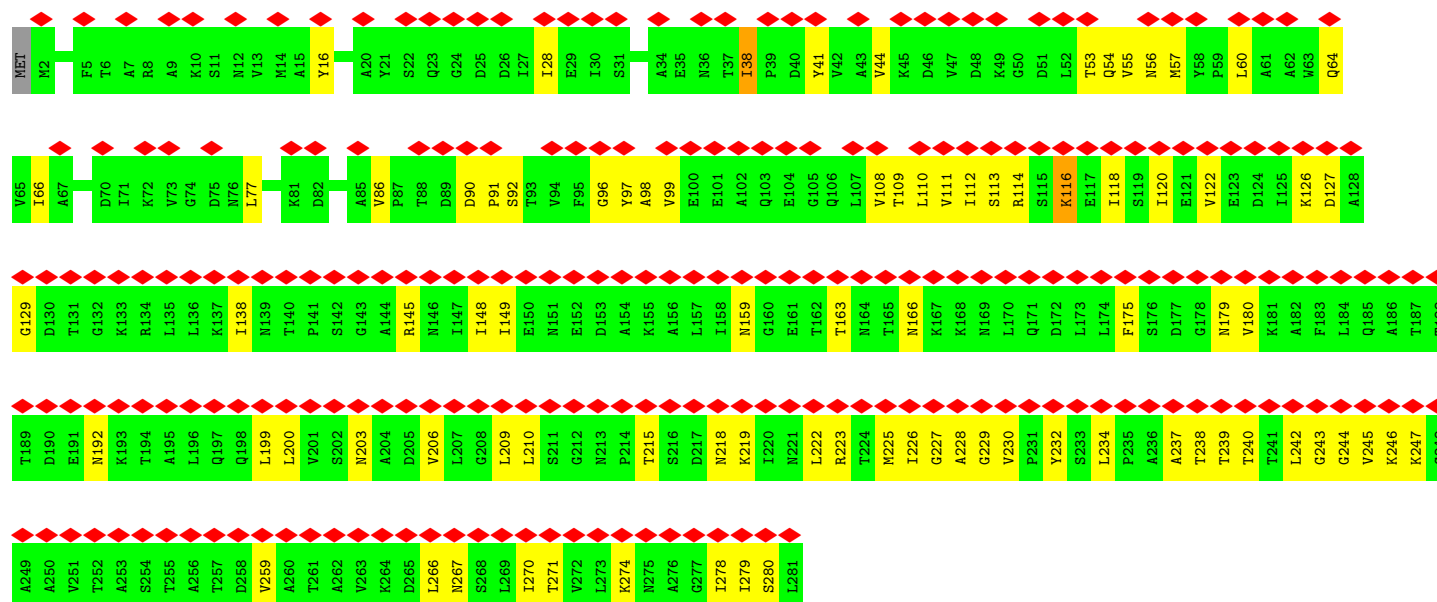
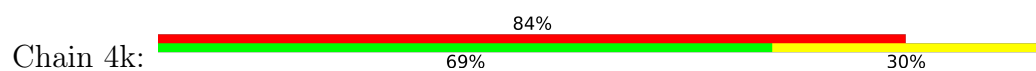




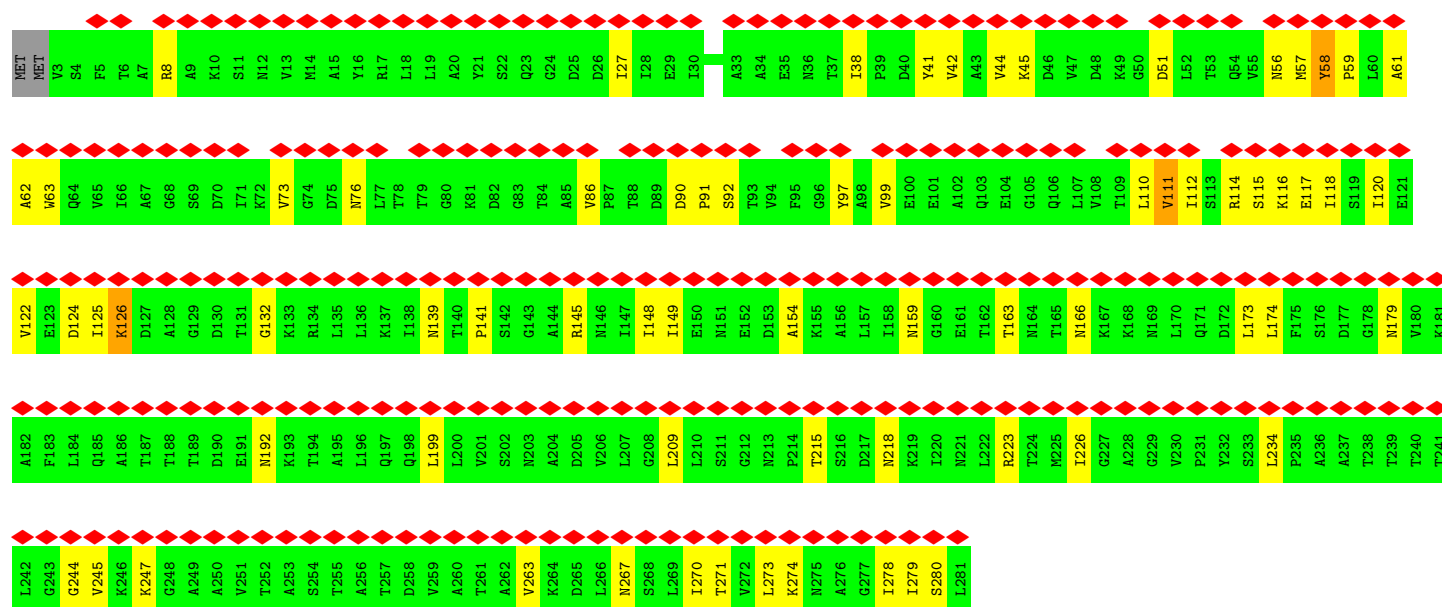
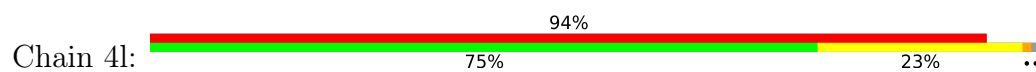
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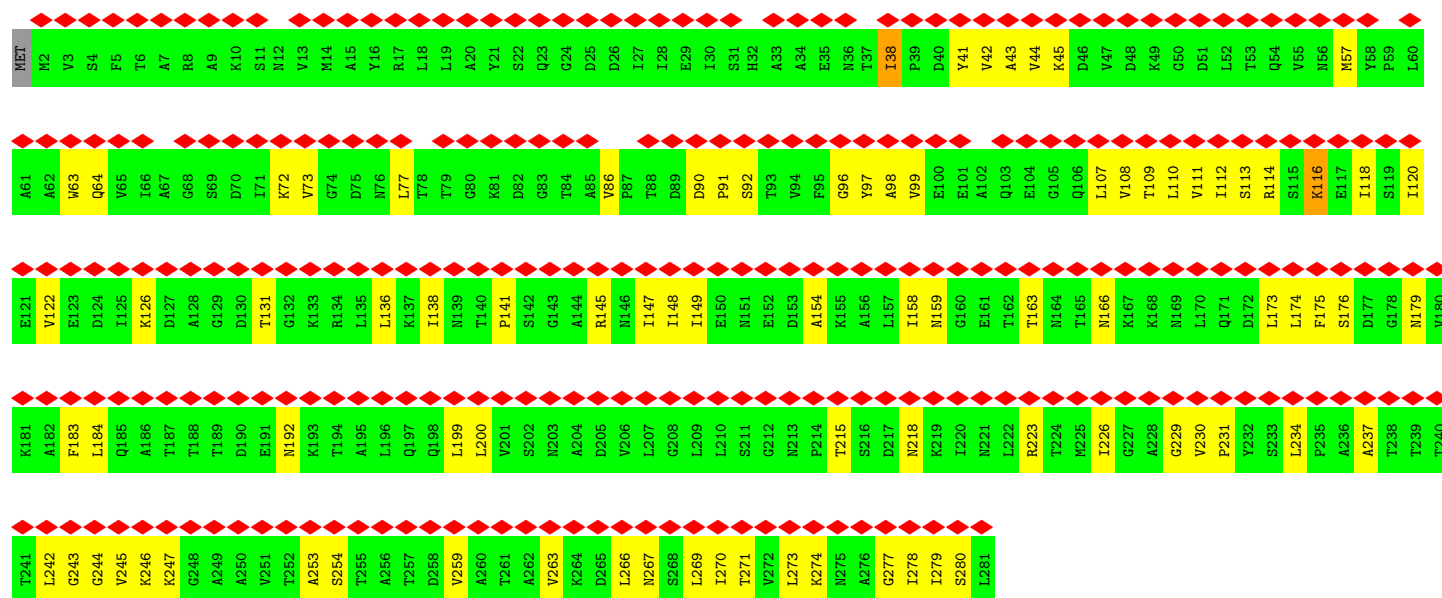
• Molecule 2: Capsid fiber protein



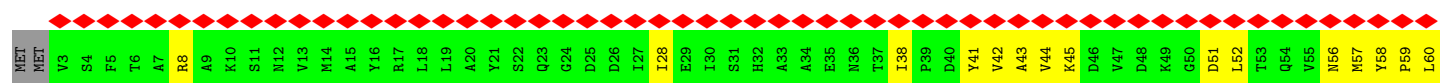
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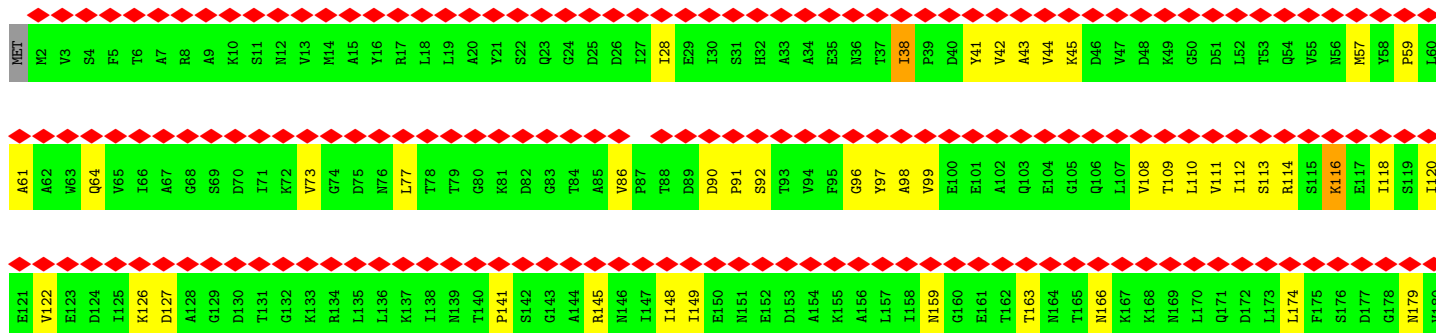


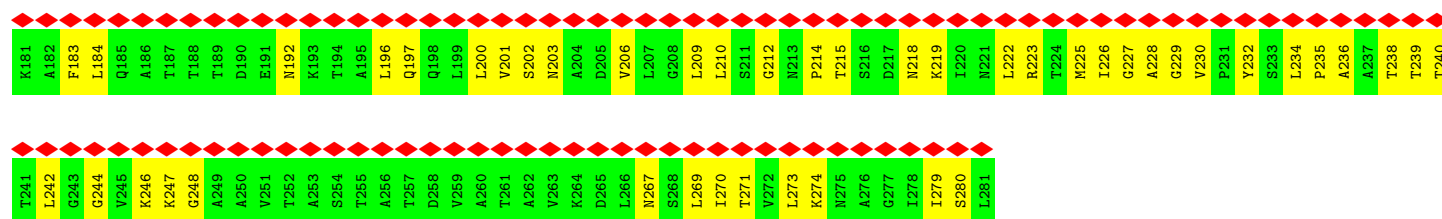
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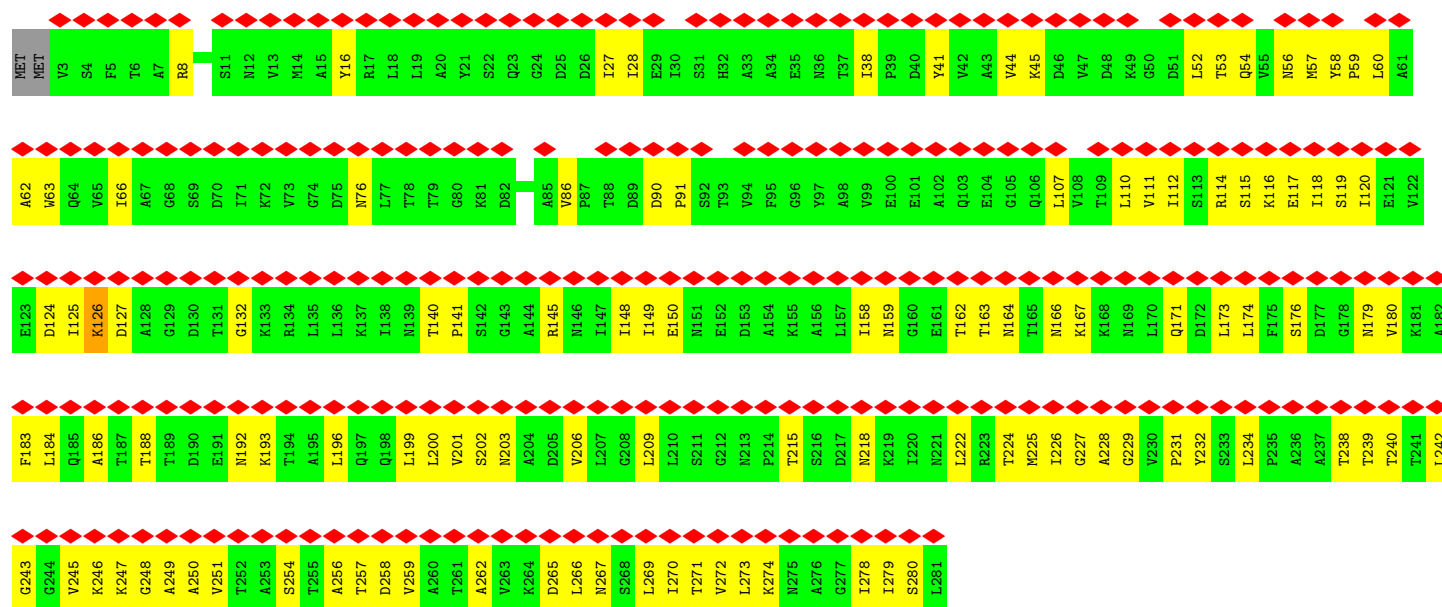
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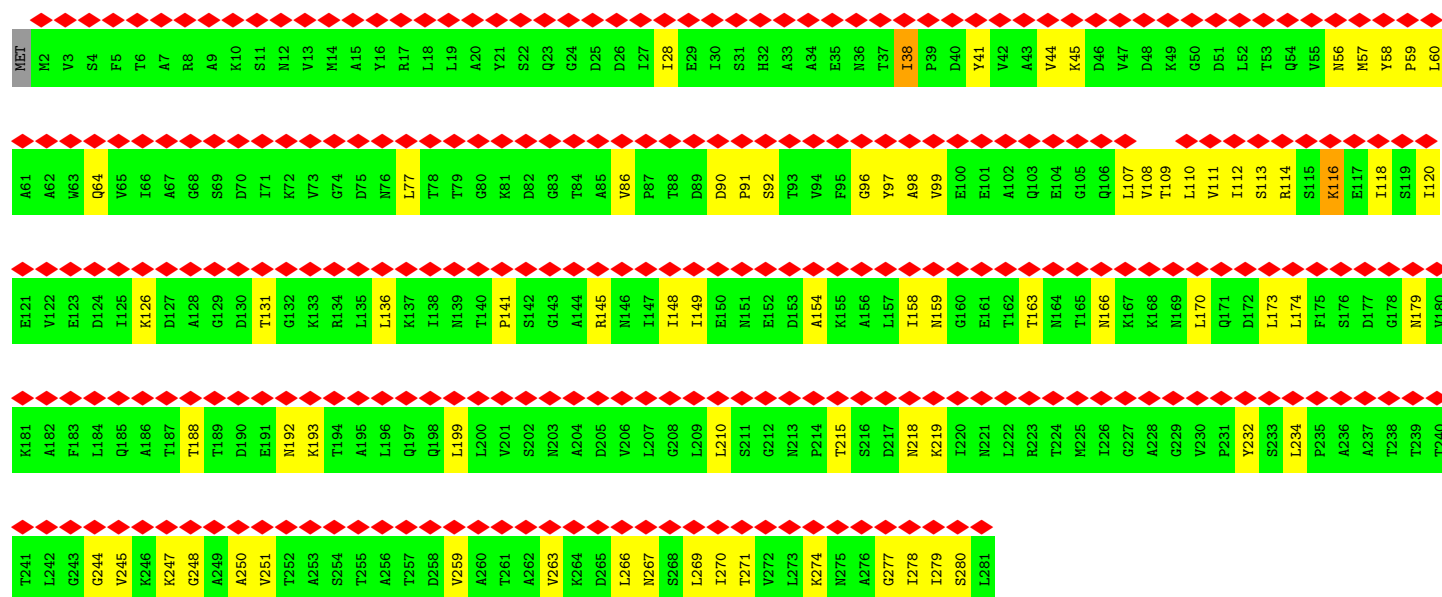
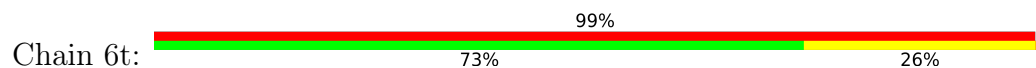




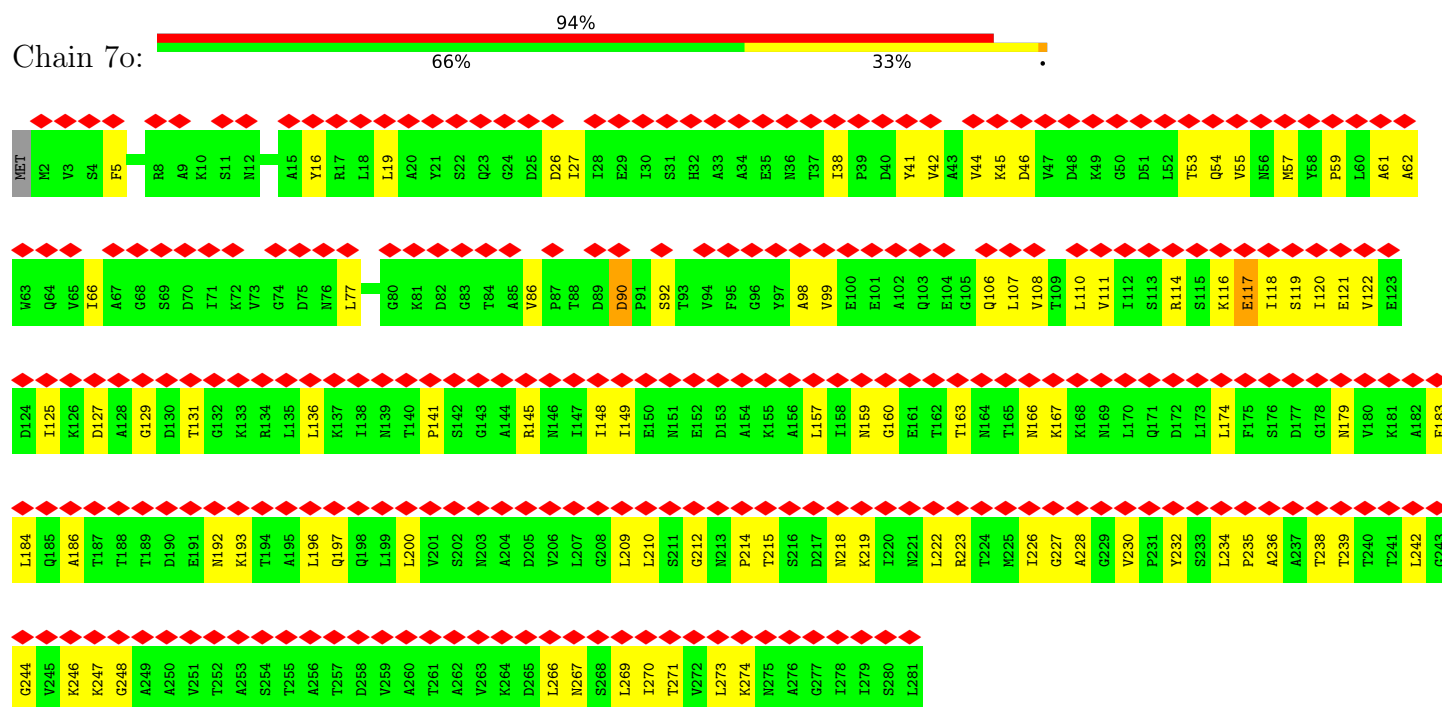
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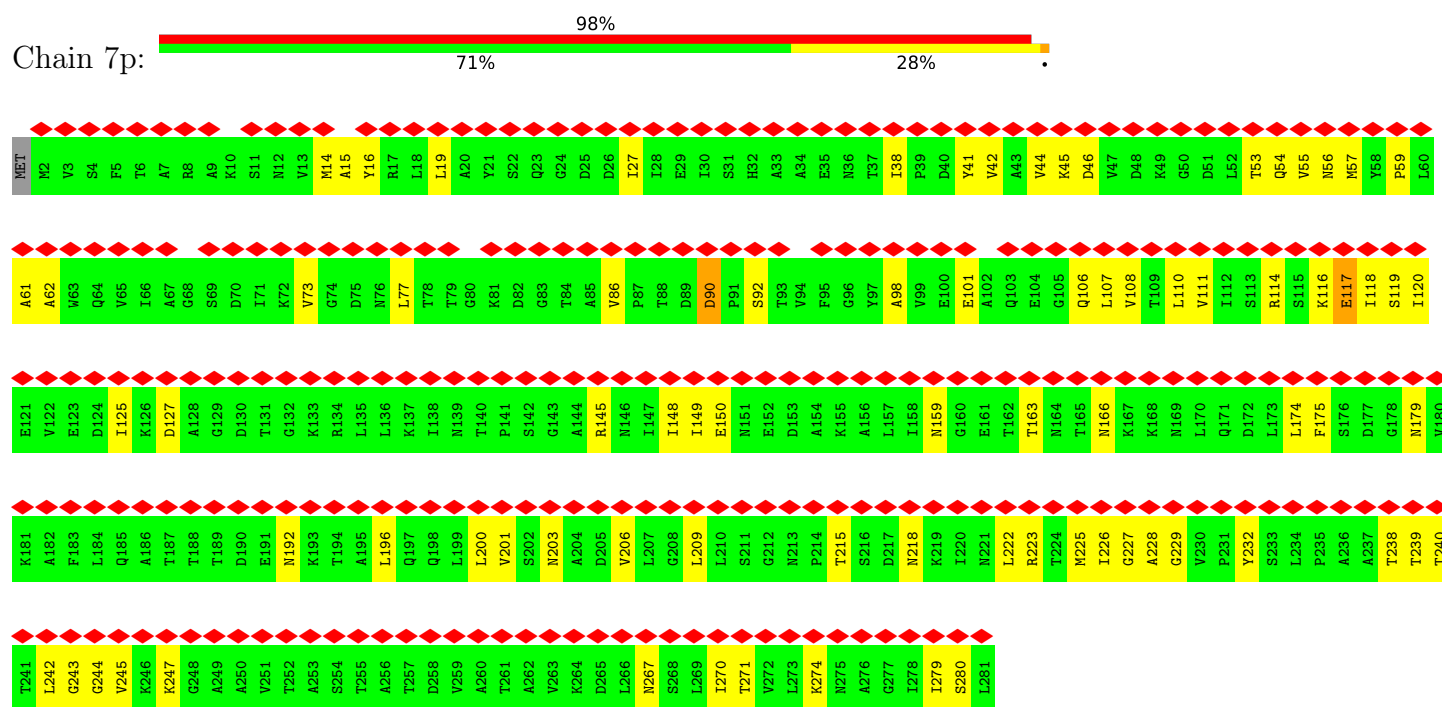
• Molecule 2: Capsid fiber protein



- Molecule 2: Capsid fiber protein

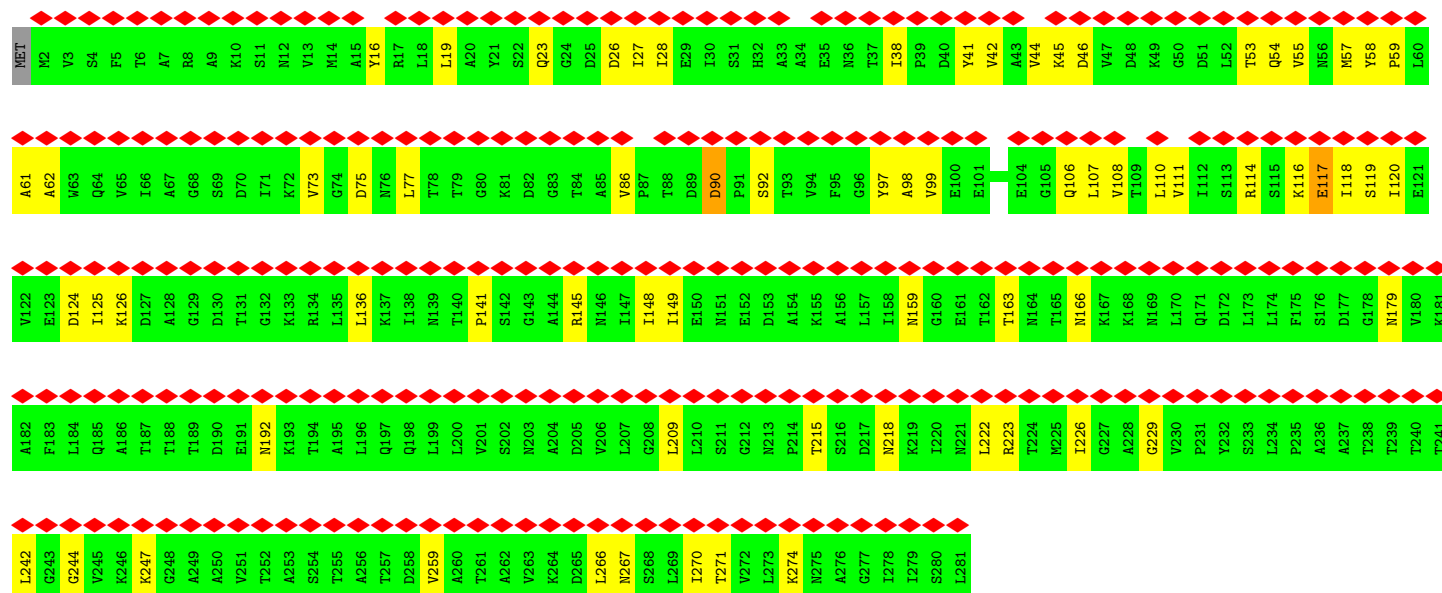


- Molecule 2: Capsid fiber protein

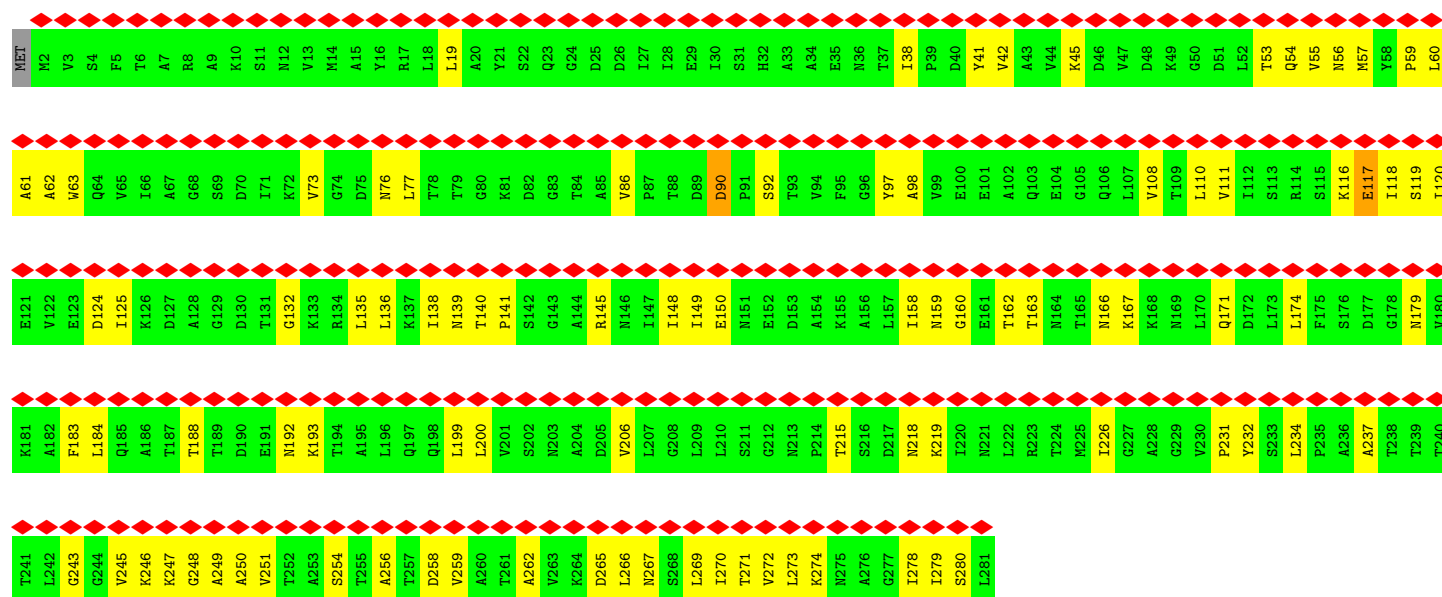


- Molecule 2: Capsid fiber protein

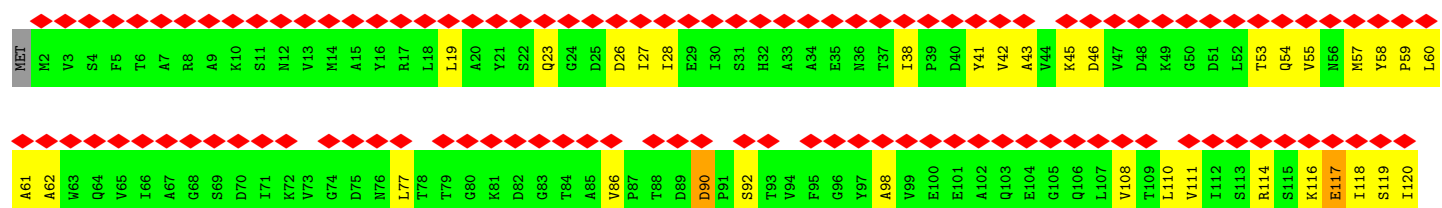
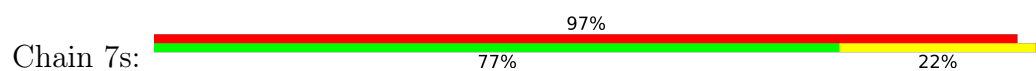




• Molecule 2: Capsid fiber protein

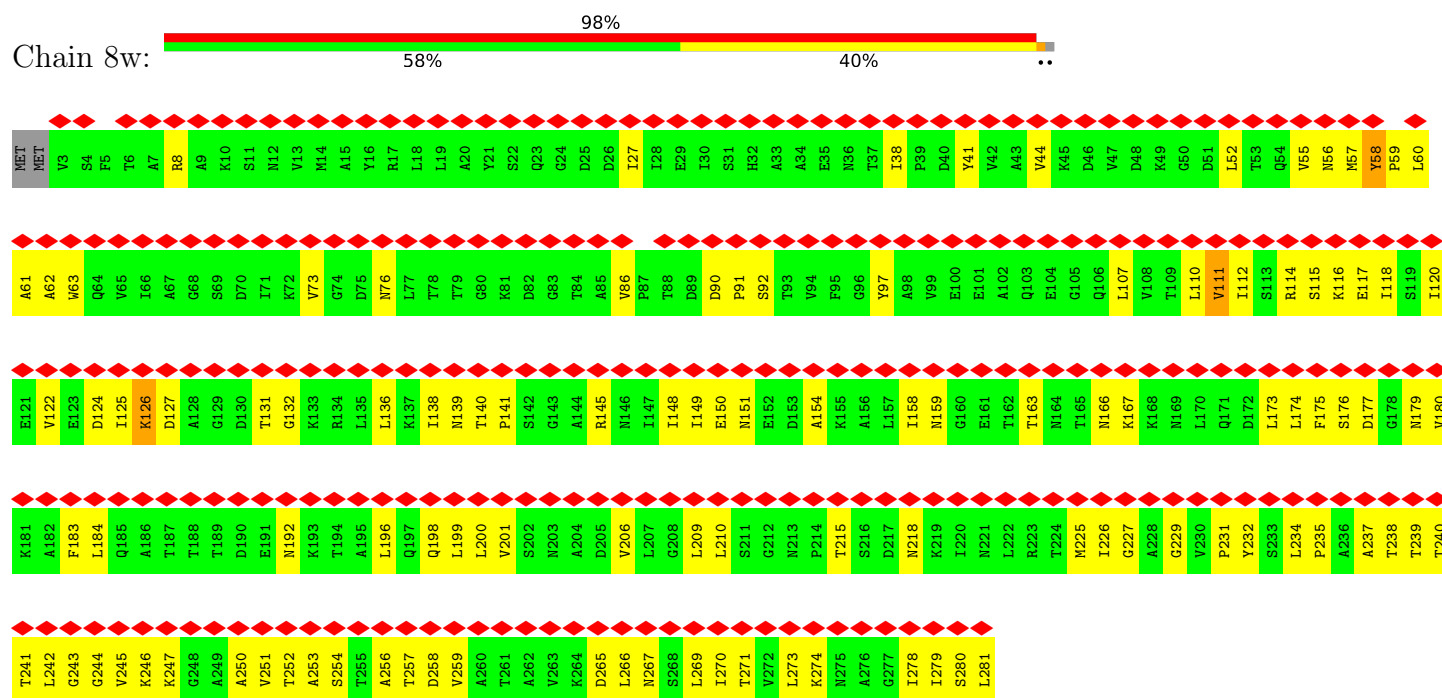


• Molecule 2: Capsid fiber protein

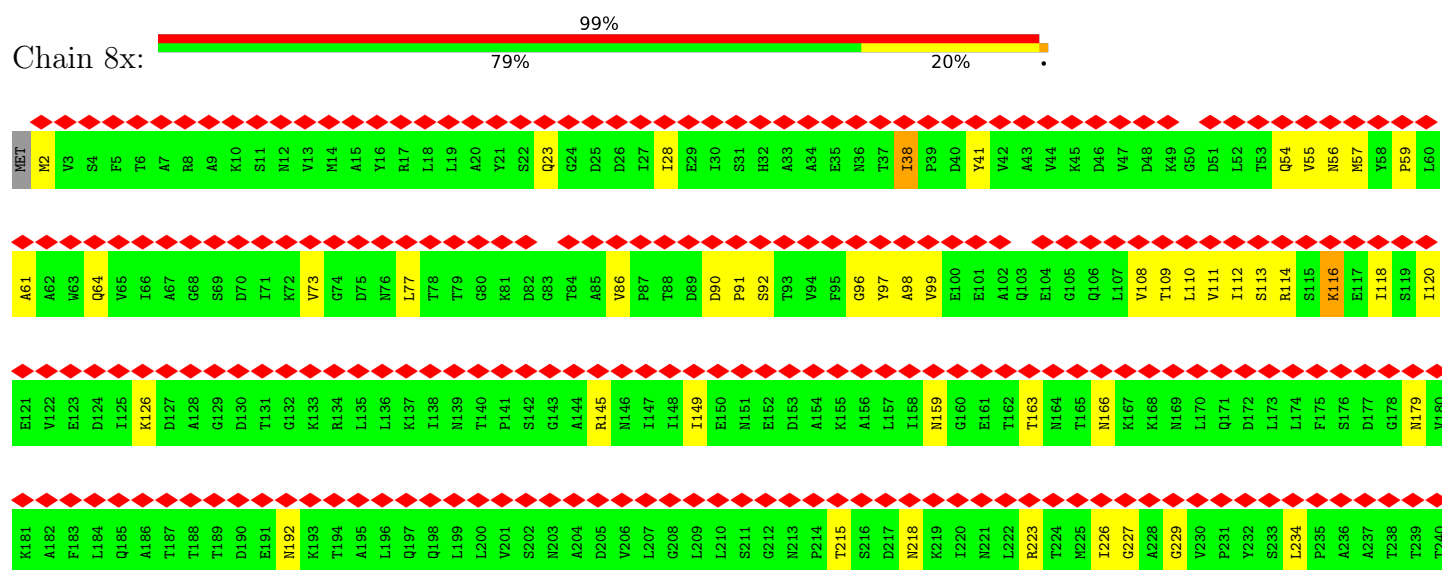




• Molecule 2: Capsid fiber protein

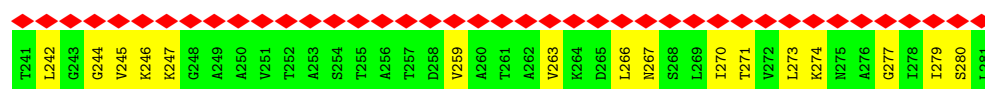
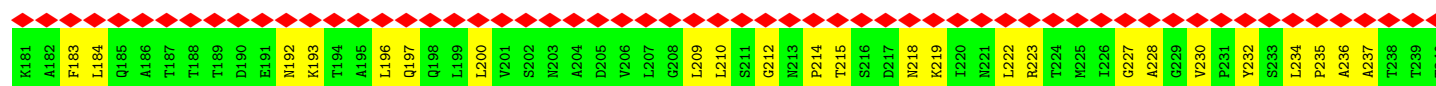
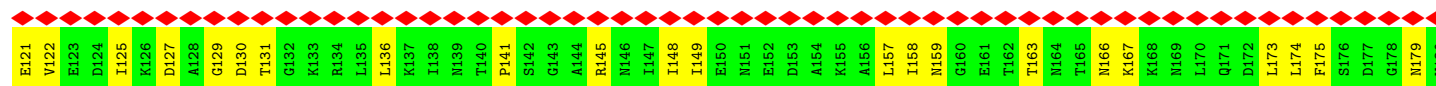
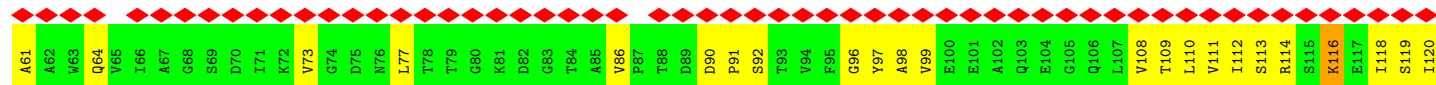
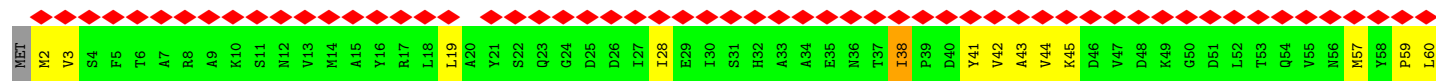


• Molecule 2: Capsid fiber protein

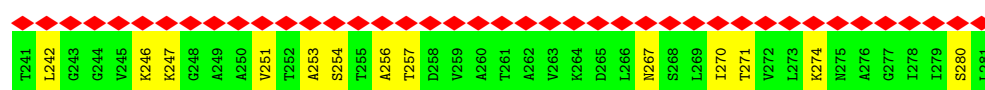
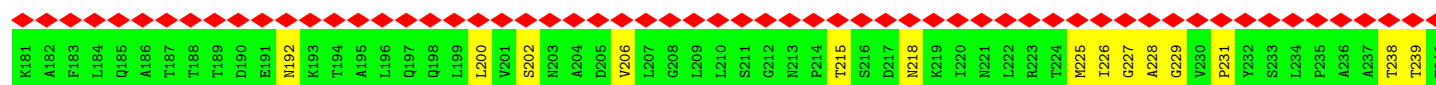
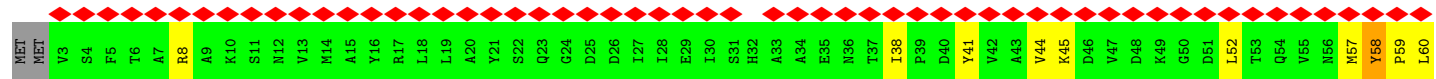
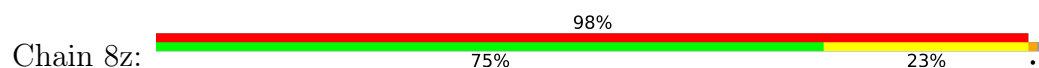




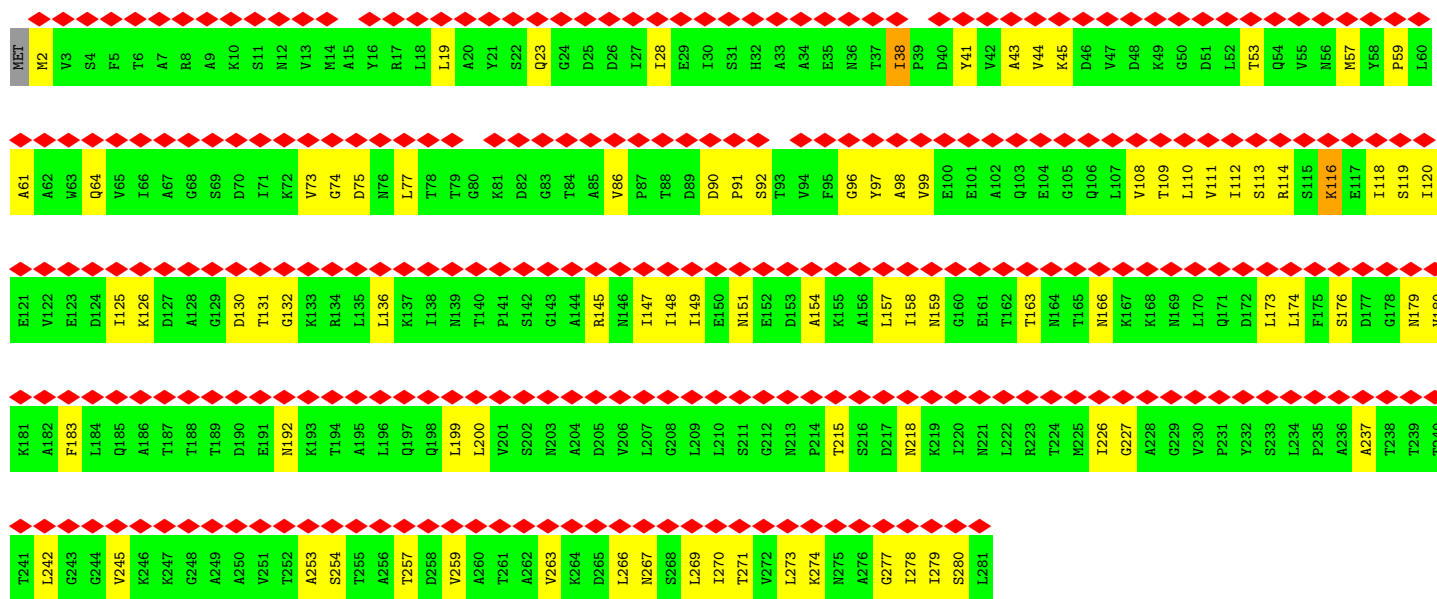
• Molecule 2: Capsid fiber protein



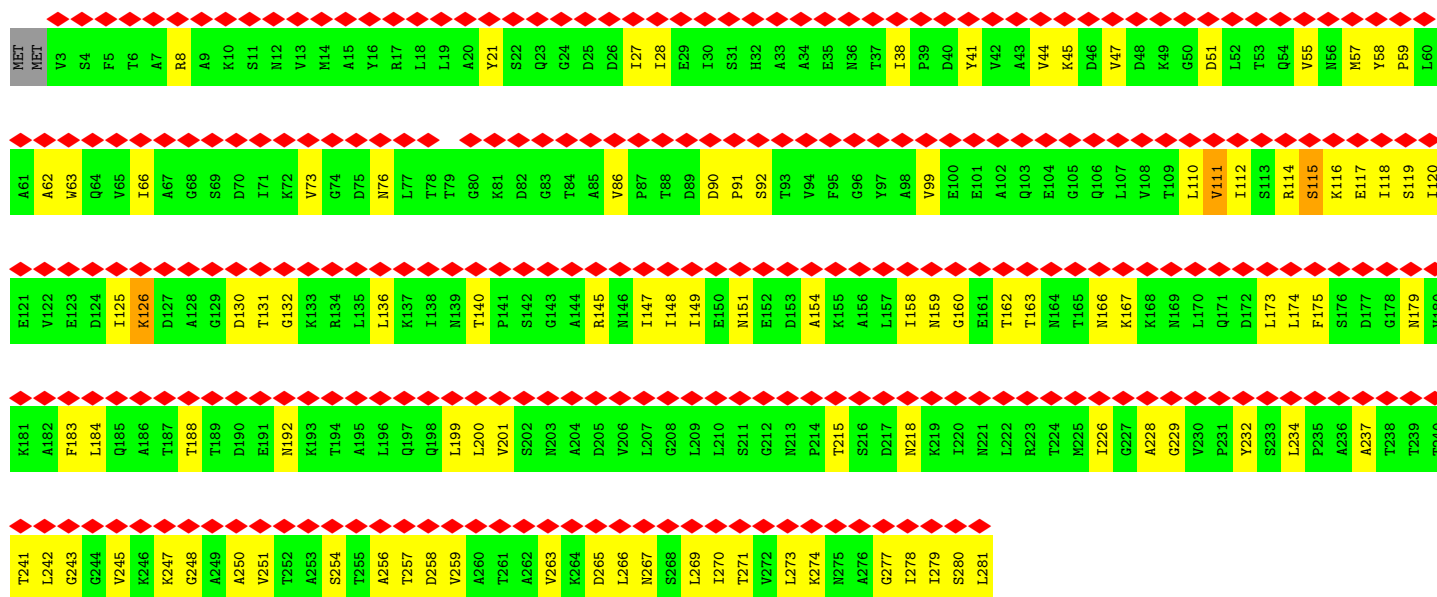
• Molecule 2: Capsid fiber protein



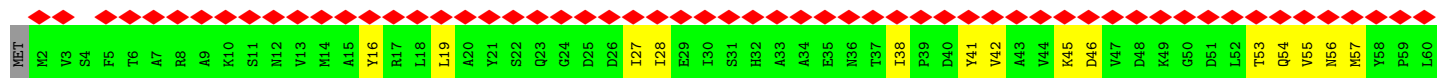
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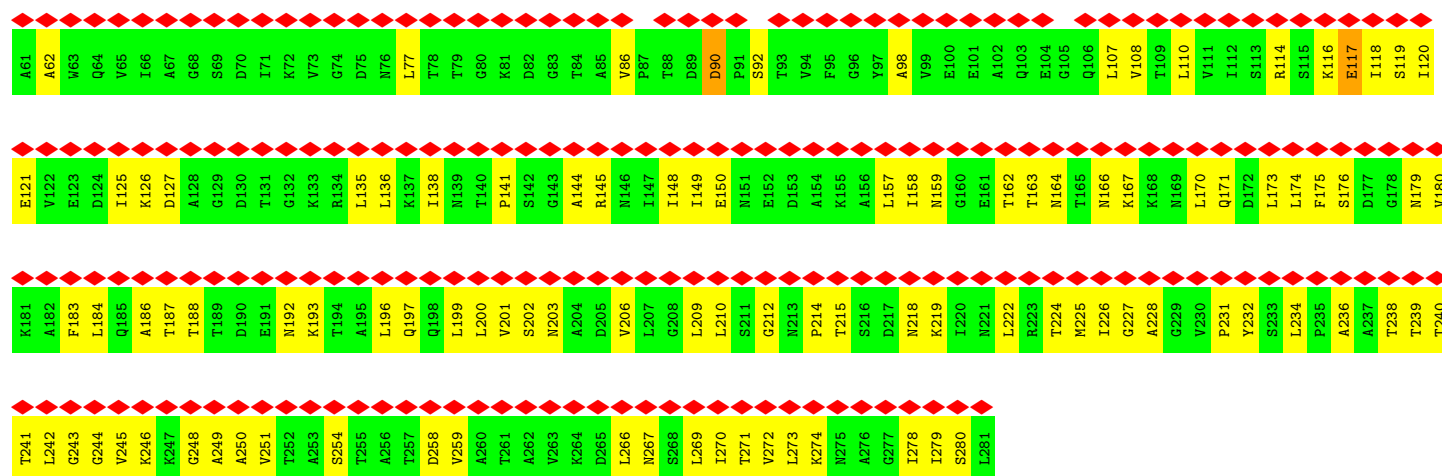


• Molecule 2: Capsid fiber protein

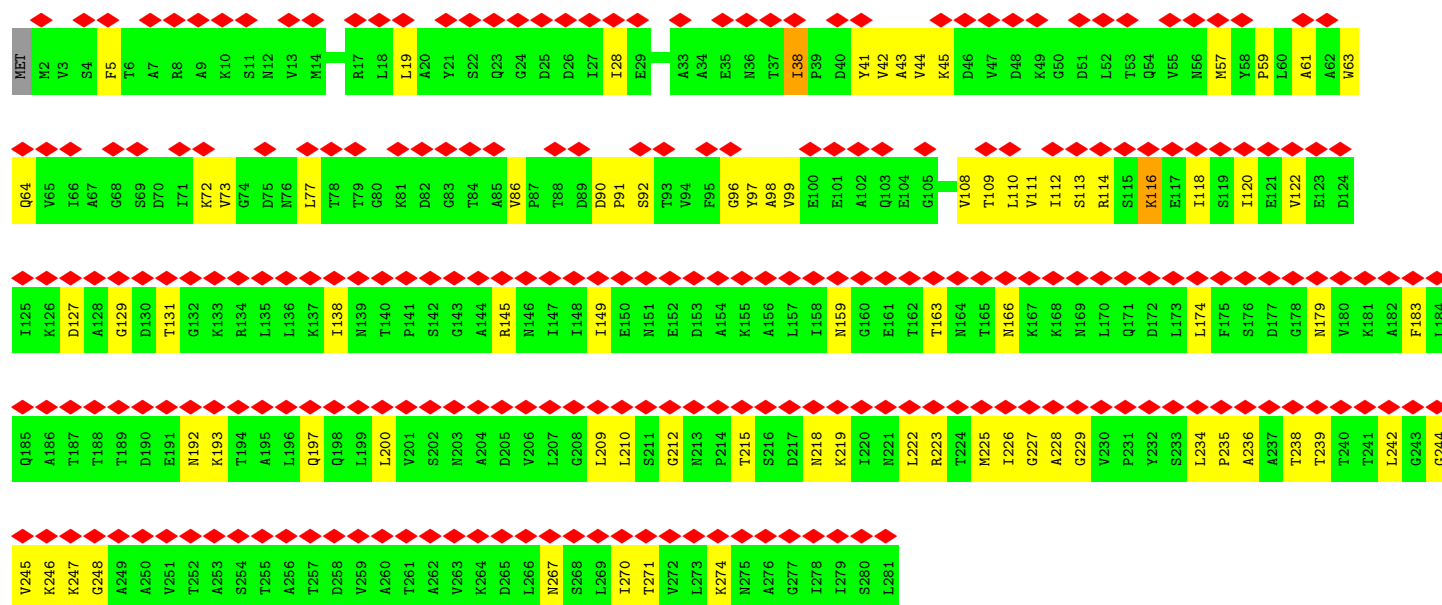
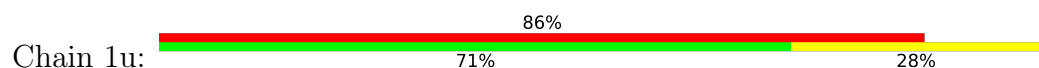


• Molecule 2: Capsid fiber protein

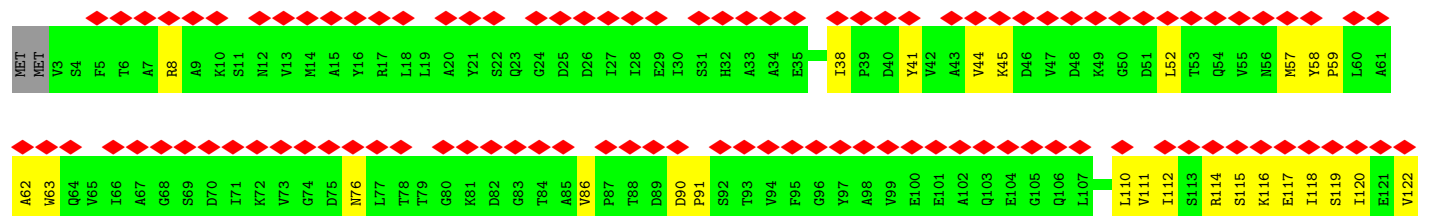
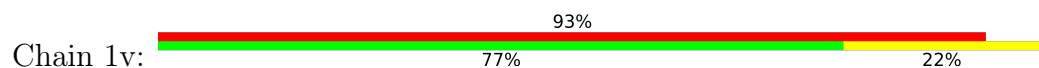


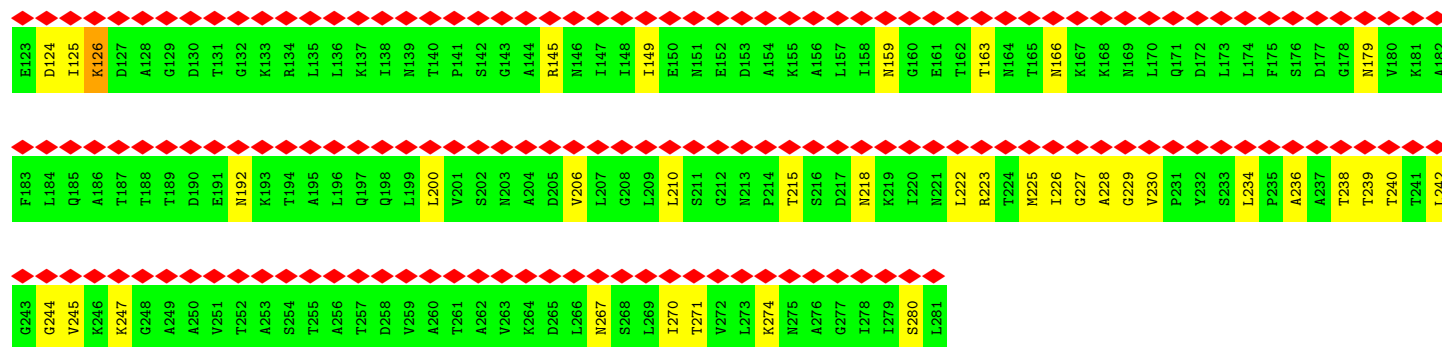


• Molecule 2: Capsid fiber protein

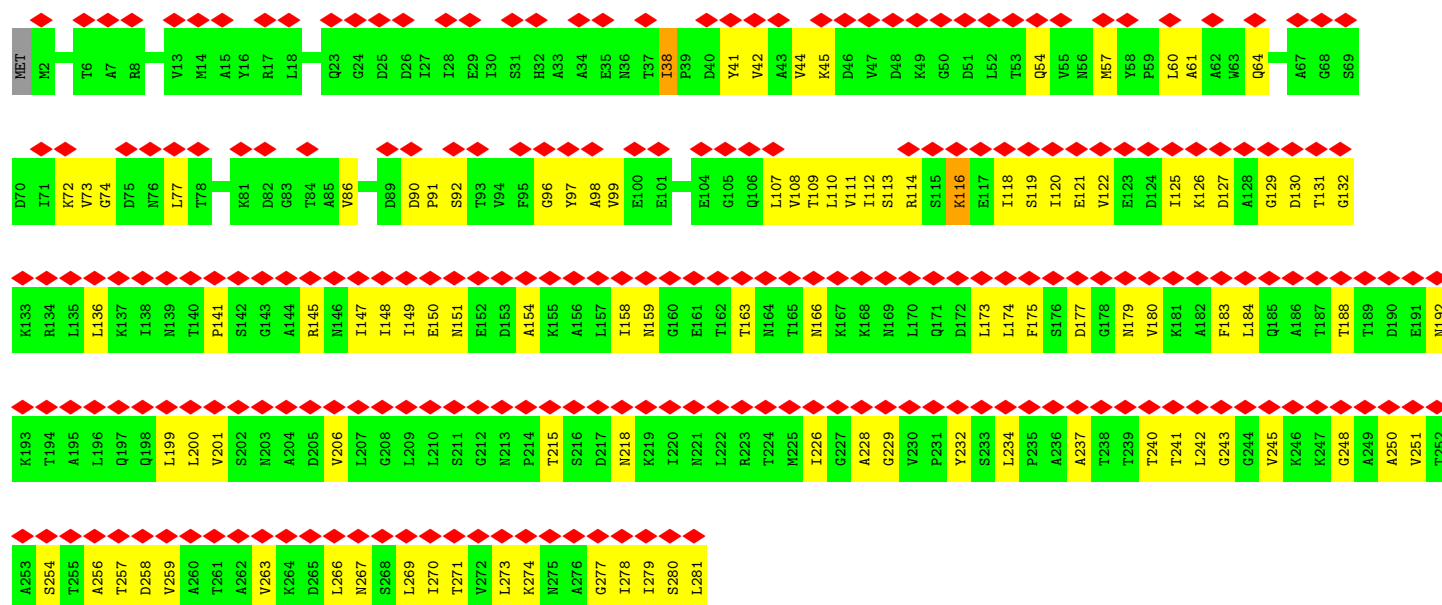
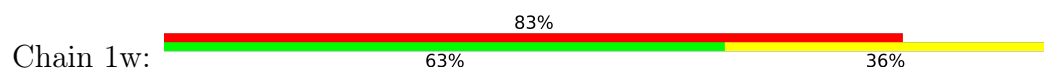


• Molecule 2: Capsid fiber protein

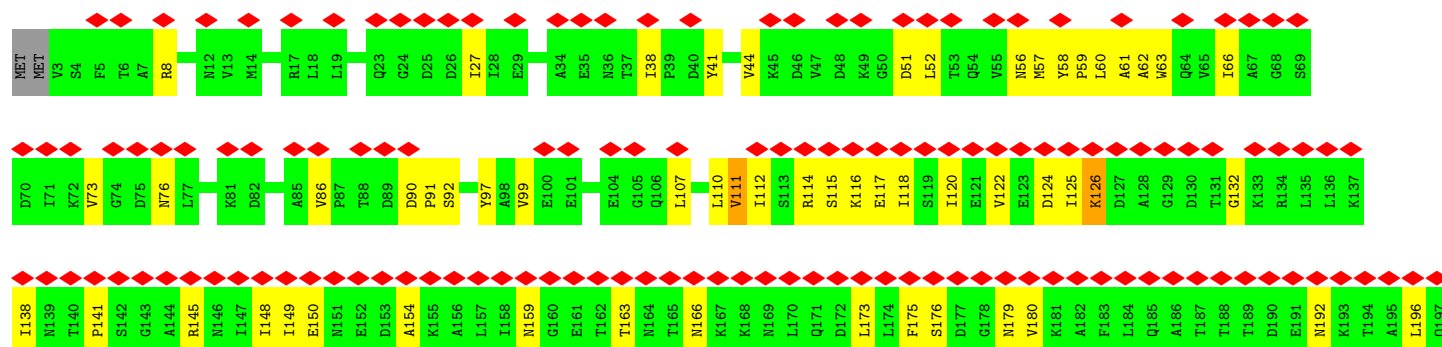
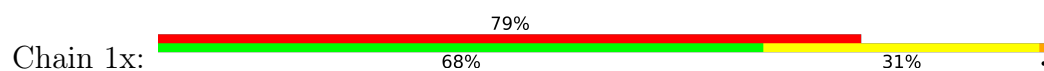




• Molecule 2: Capsid fiber protein

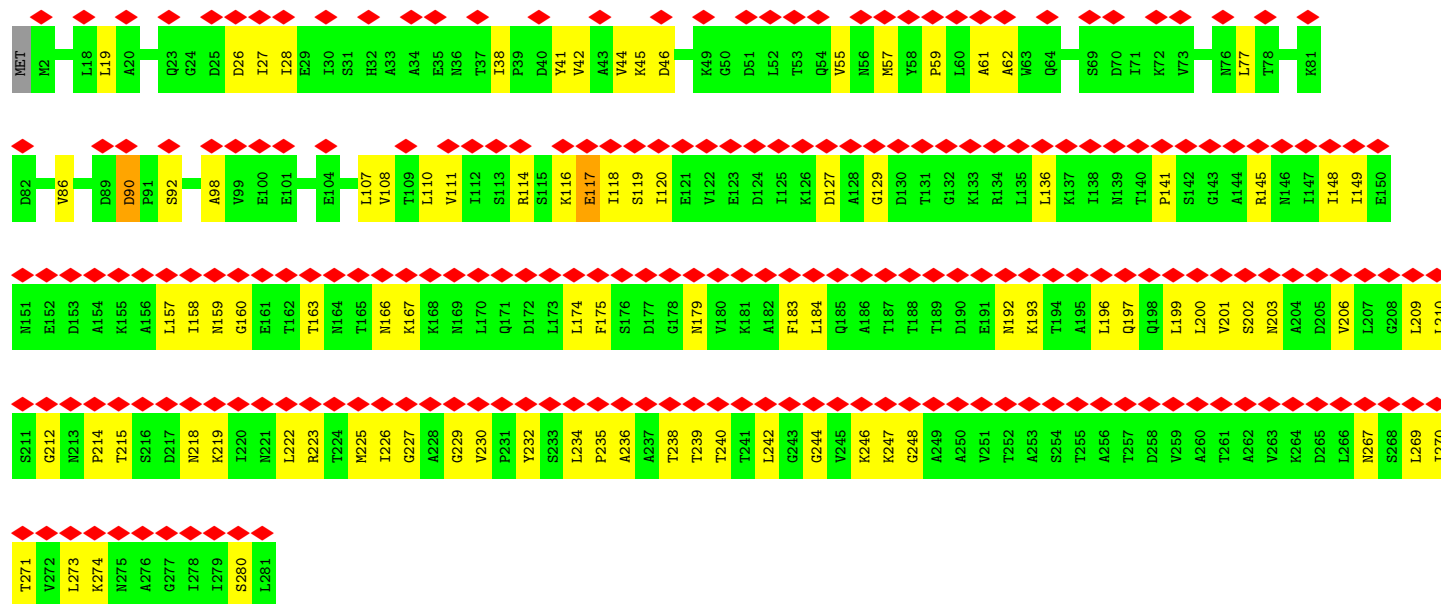
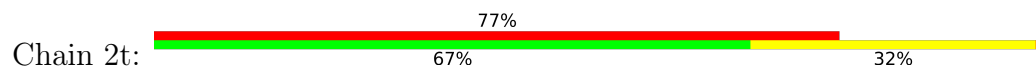


• Molecule 2: Capsid fiber protein

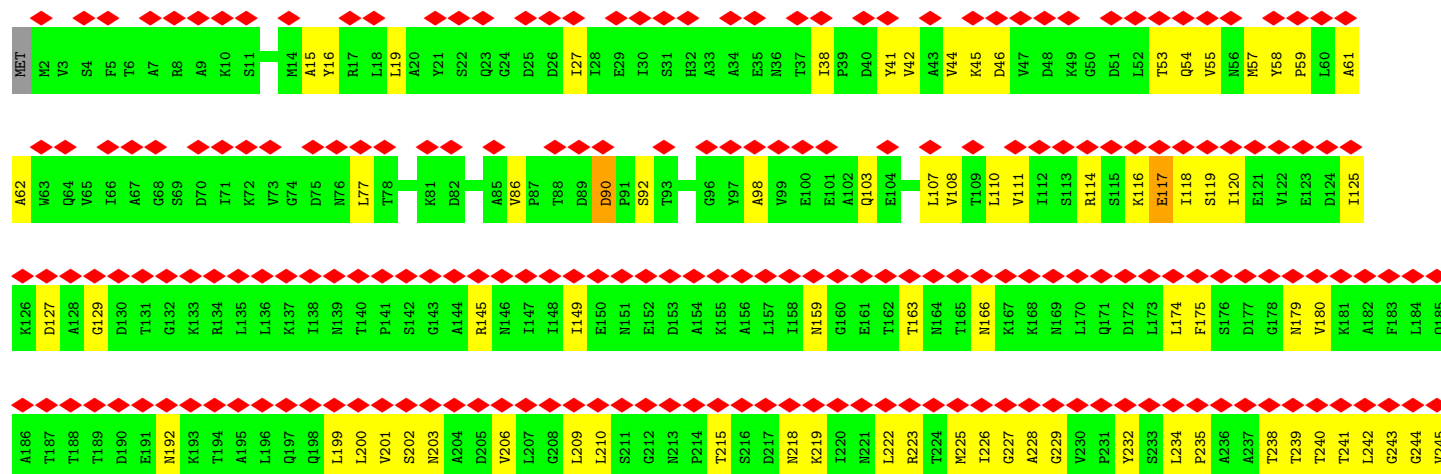
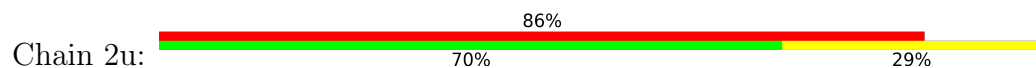


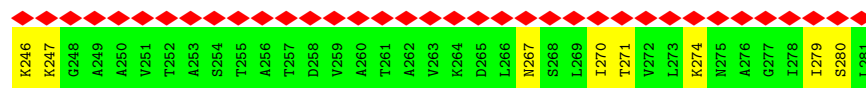


• Molecule 2: Capsid fiber protein

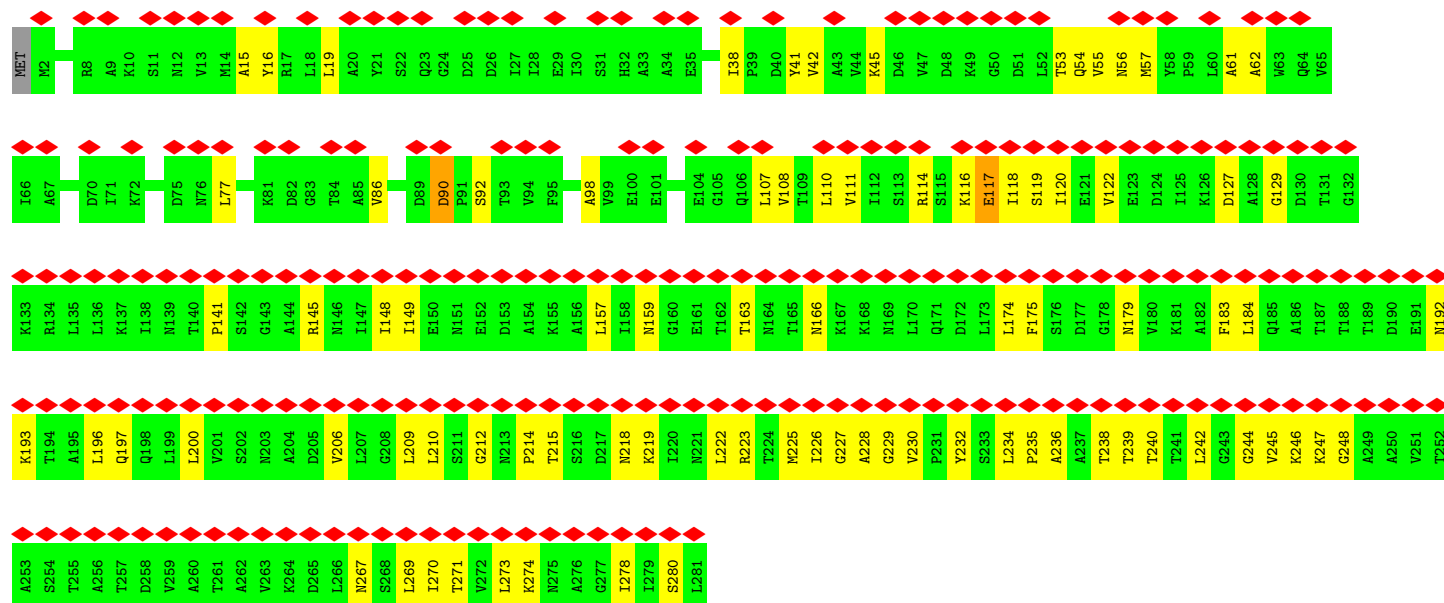
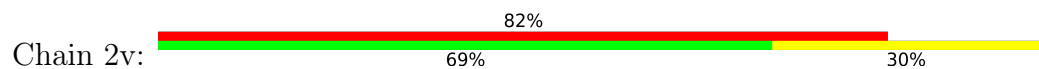


• Molecule 2: Capsid fiber protein

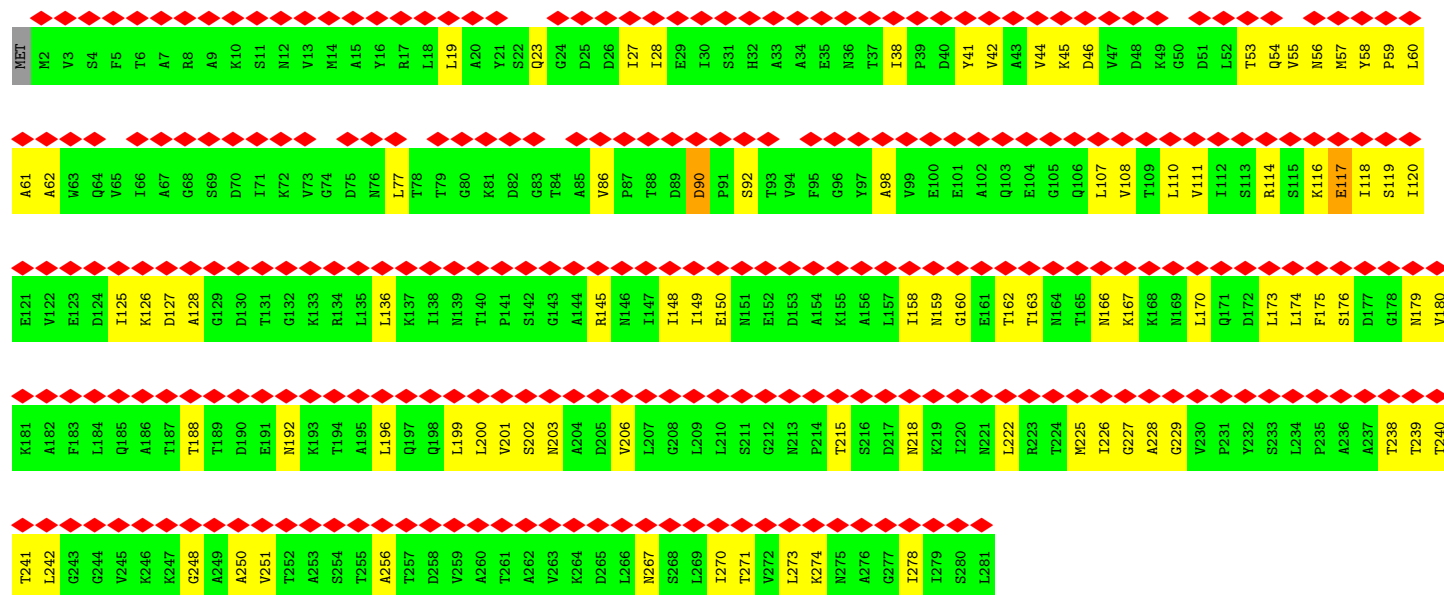




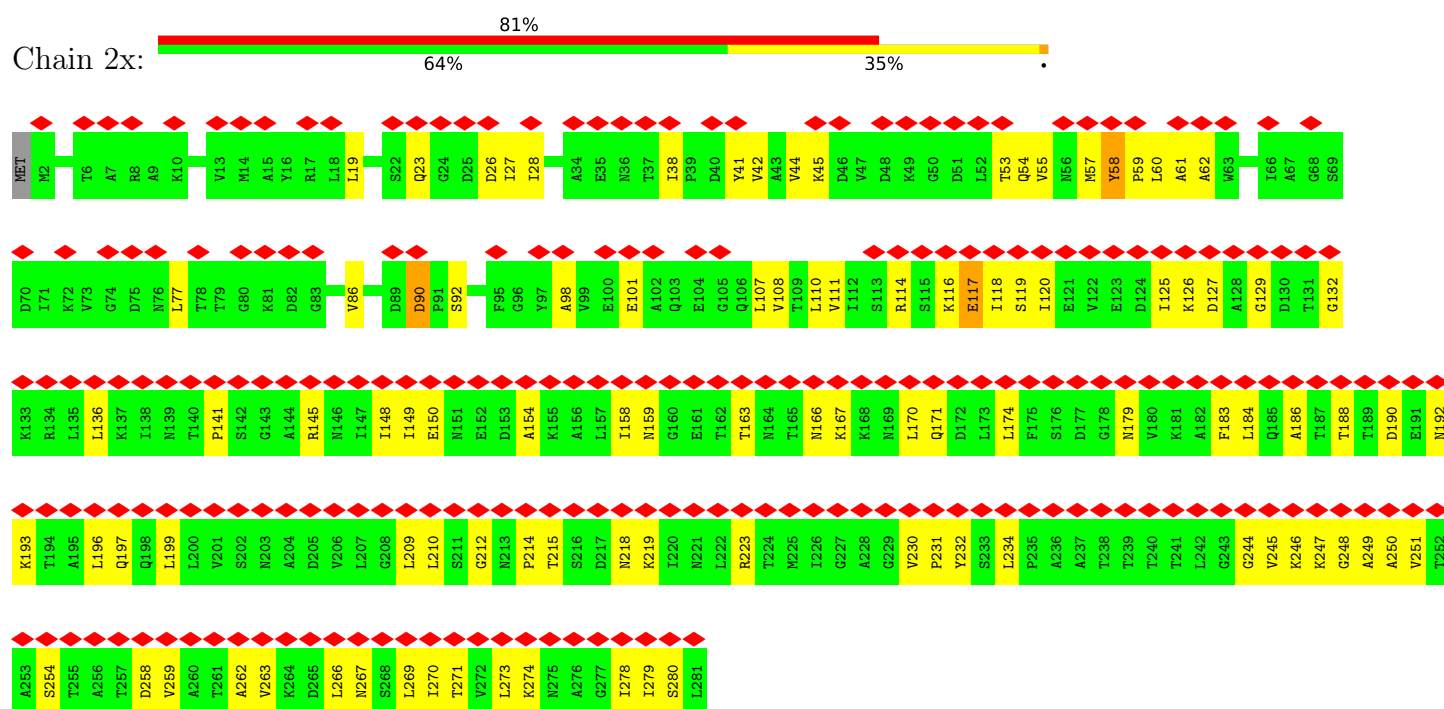
• Molecule 2: Capsid fiber protein



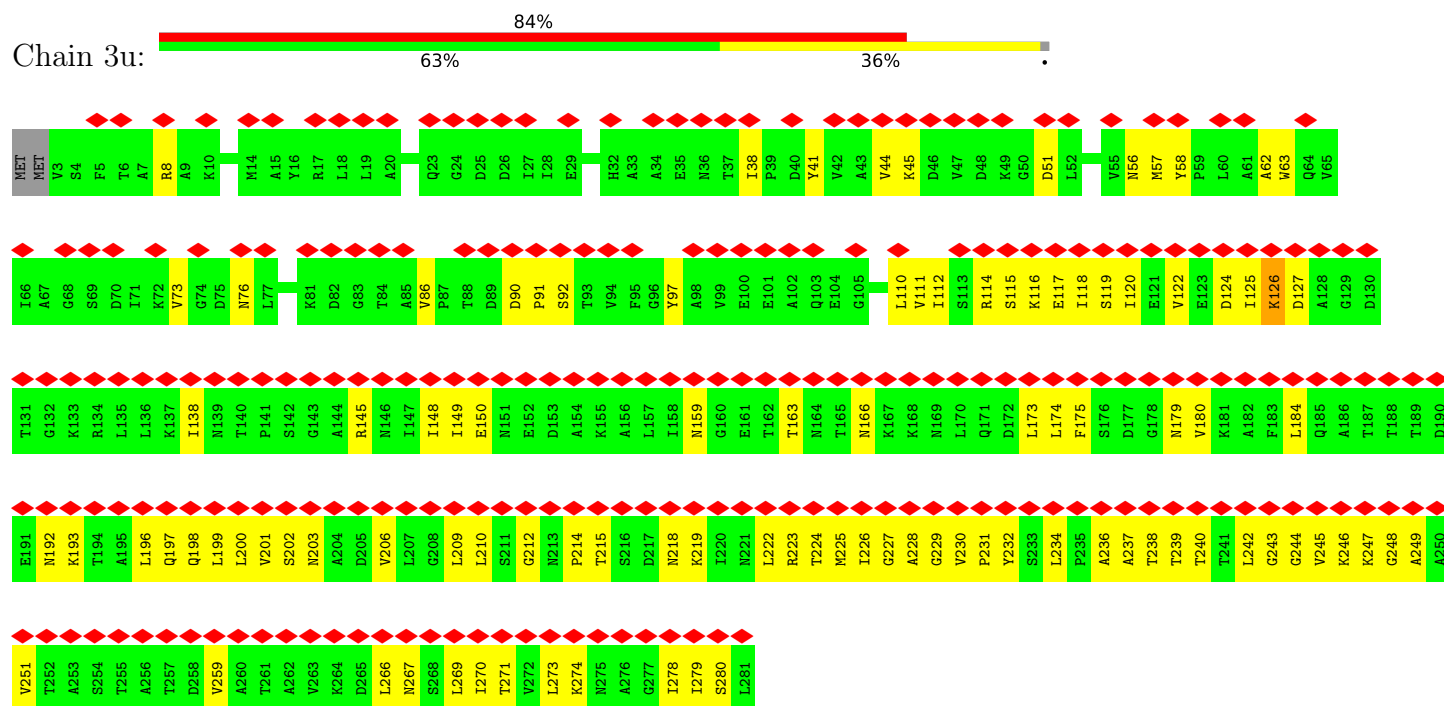
• Molecule 2: Capsid fiber protein



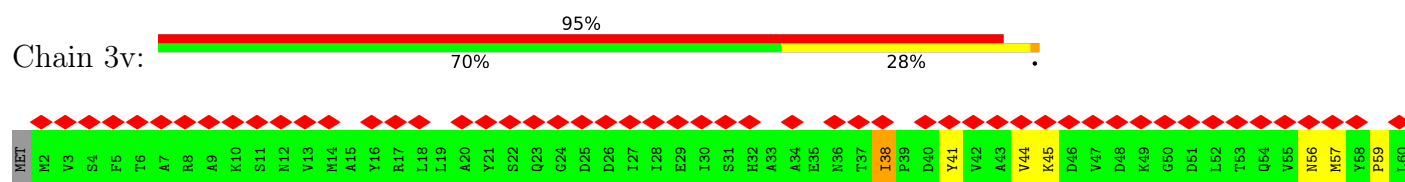
• Molecule 2: Capsid fiber protein

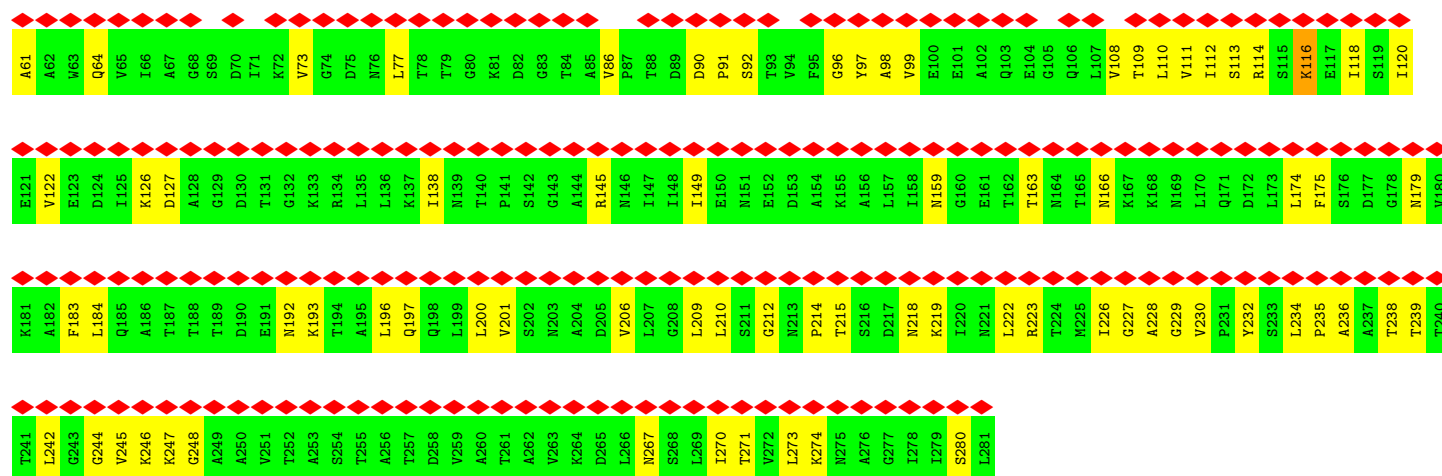


• Molecule 2: Capsid fiber protein

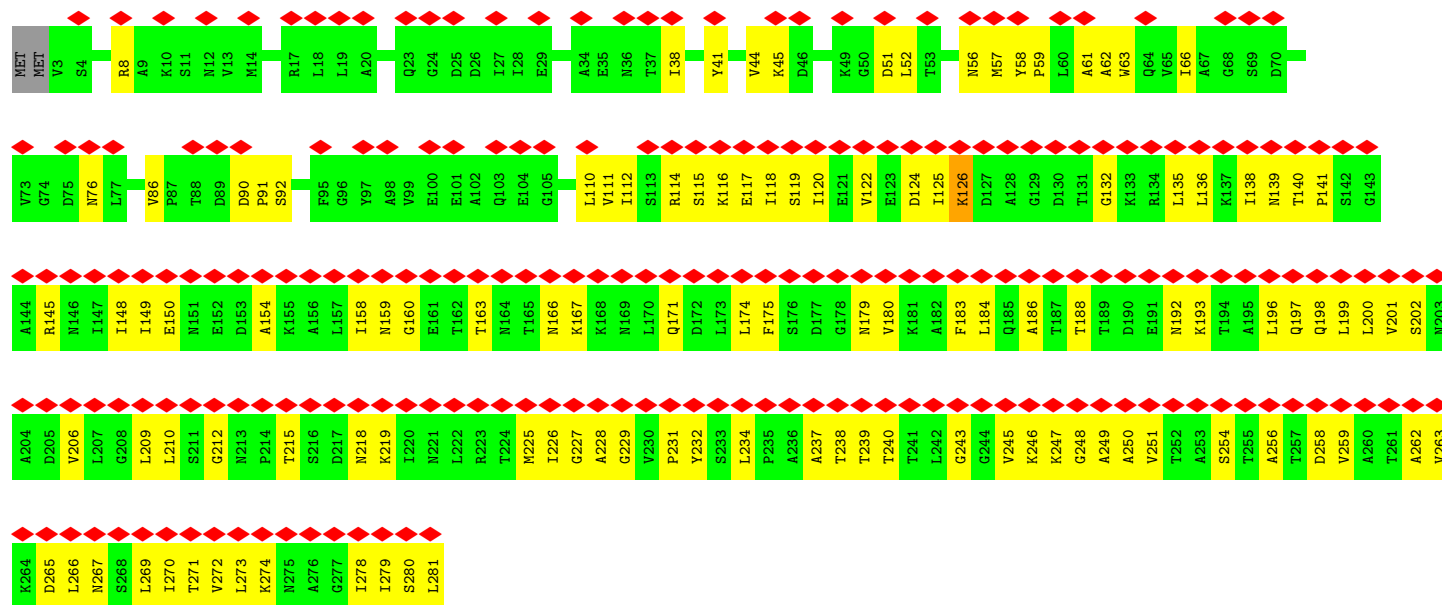
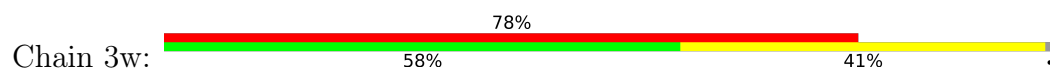


• Molecule 2: Capsid fiber protein

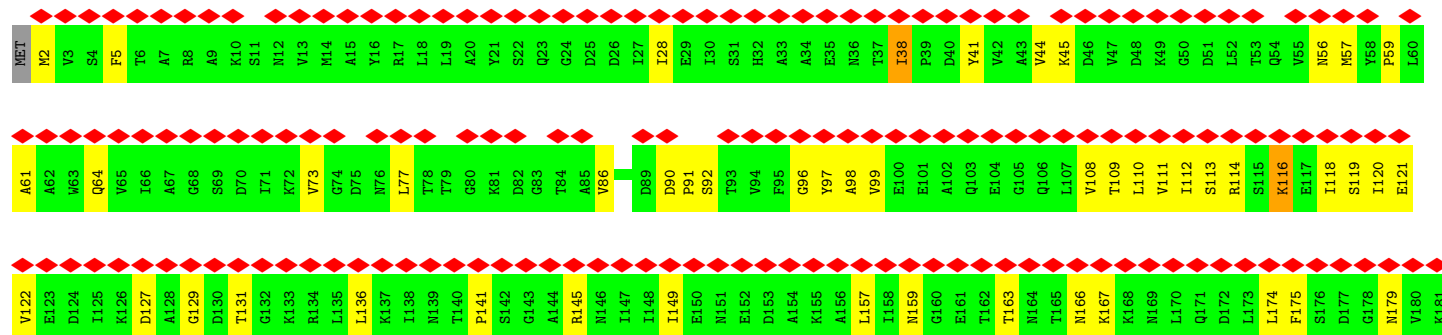




• Molecule 2: Capsid fiber protein

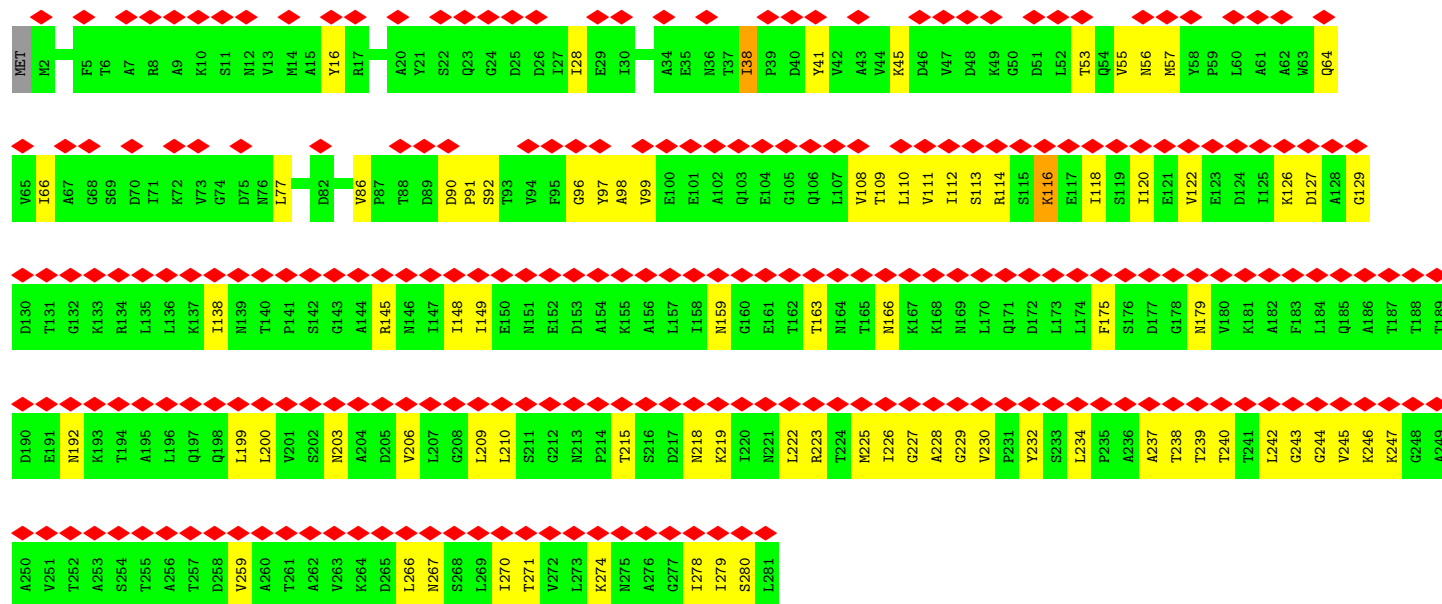
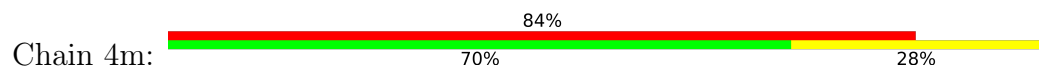


• Molecule 2: Capsid fiber protein

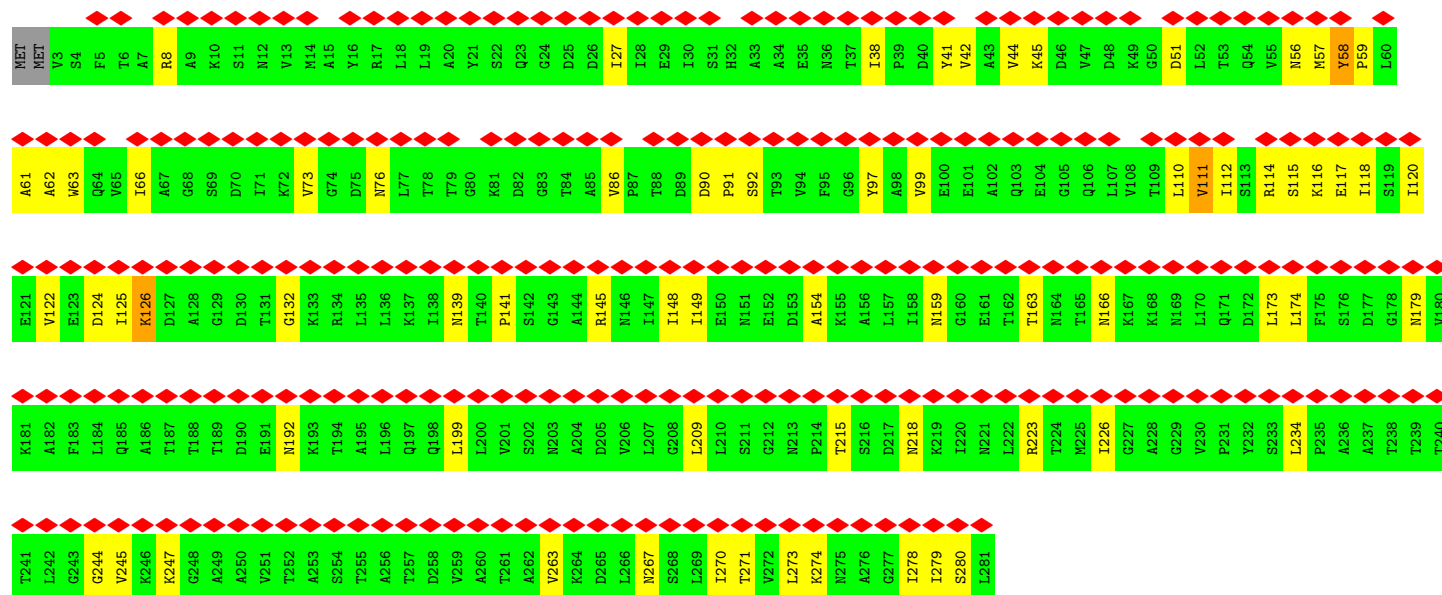
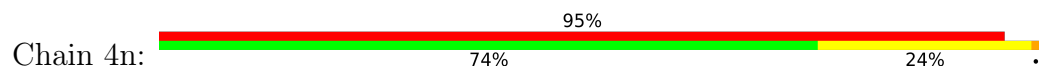




• Molecule 2: Capsid fiber protein

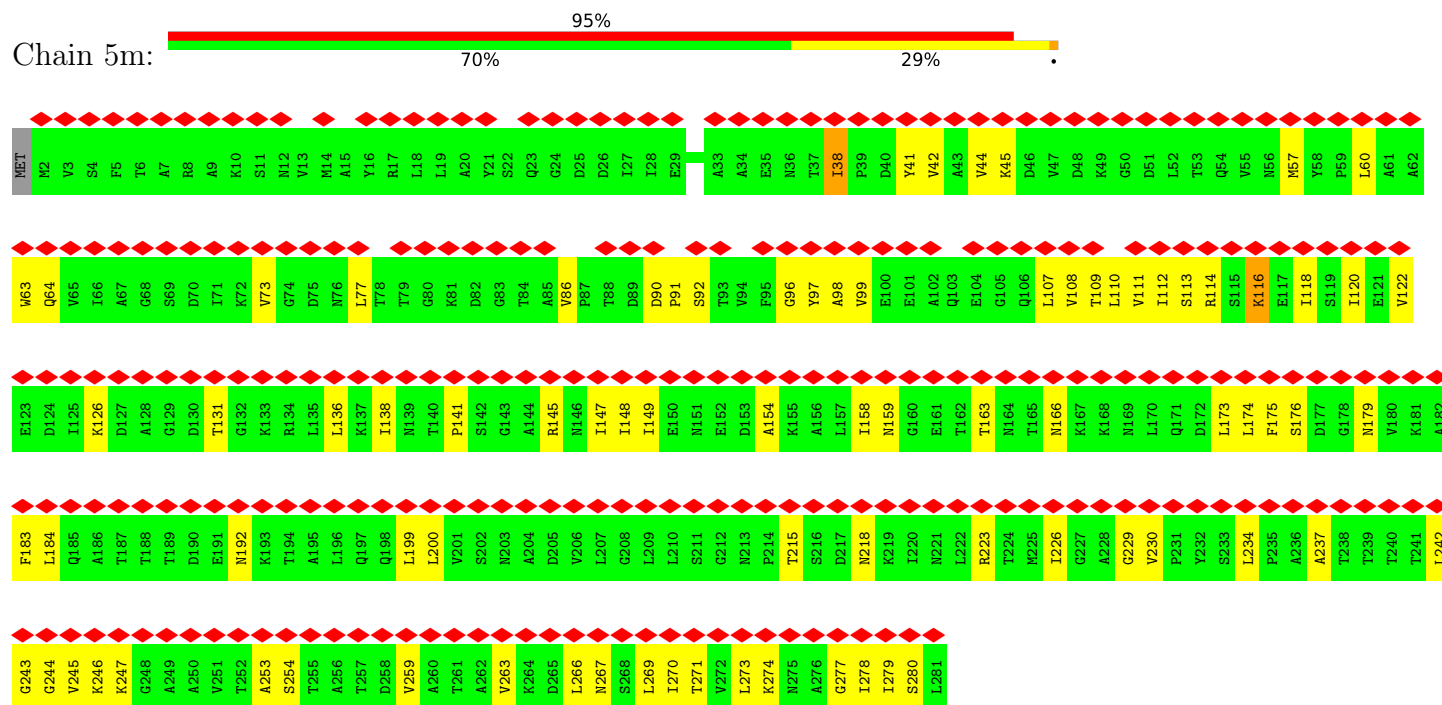


• Molecule 2: Capsid fiber protein



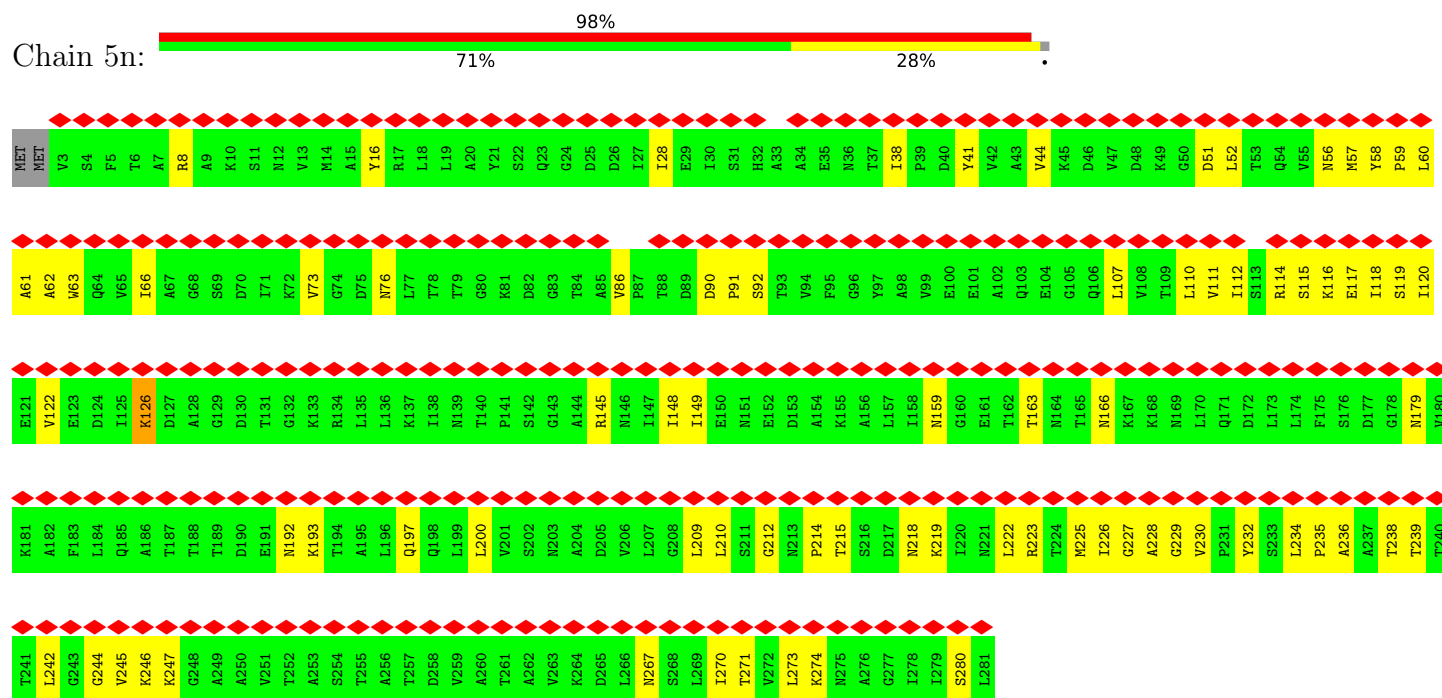
● Molecule 2: Capsid fiber protein

Chain 5m:



● Molecule 2: Capsid fiber protein

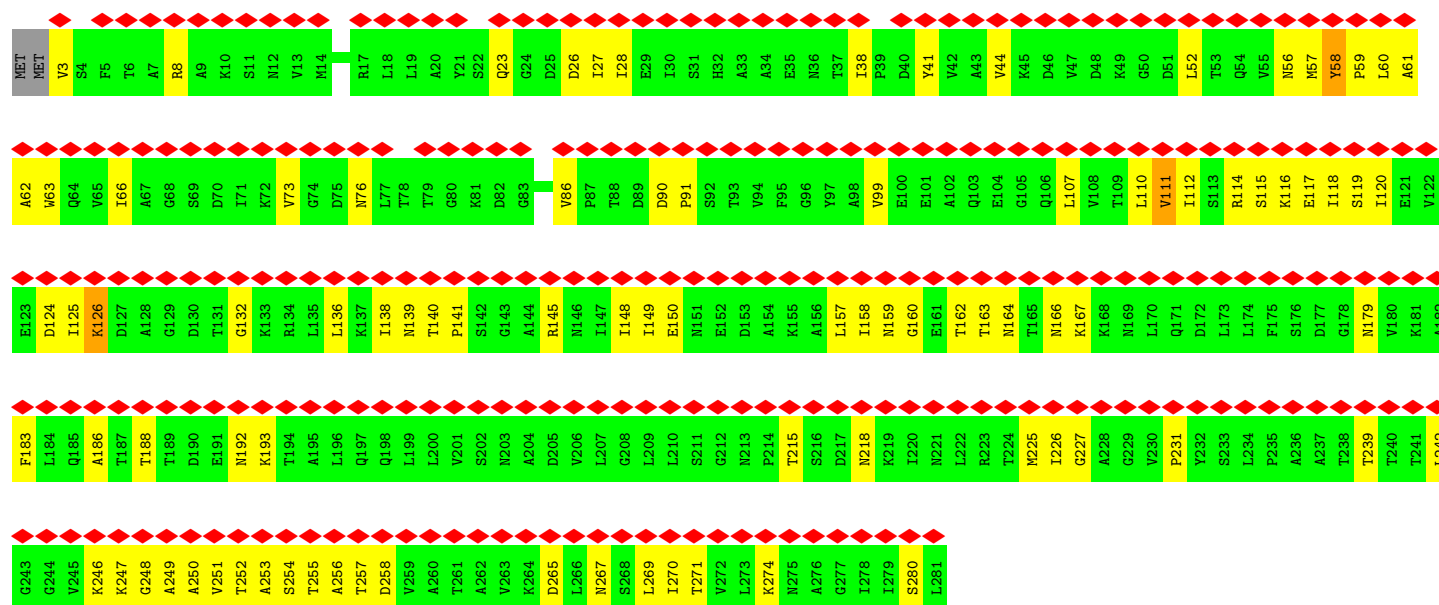
Chain 5n:



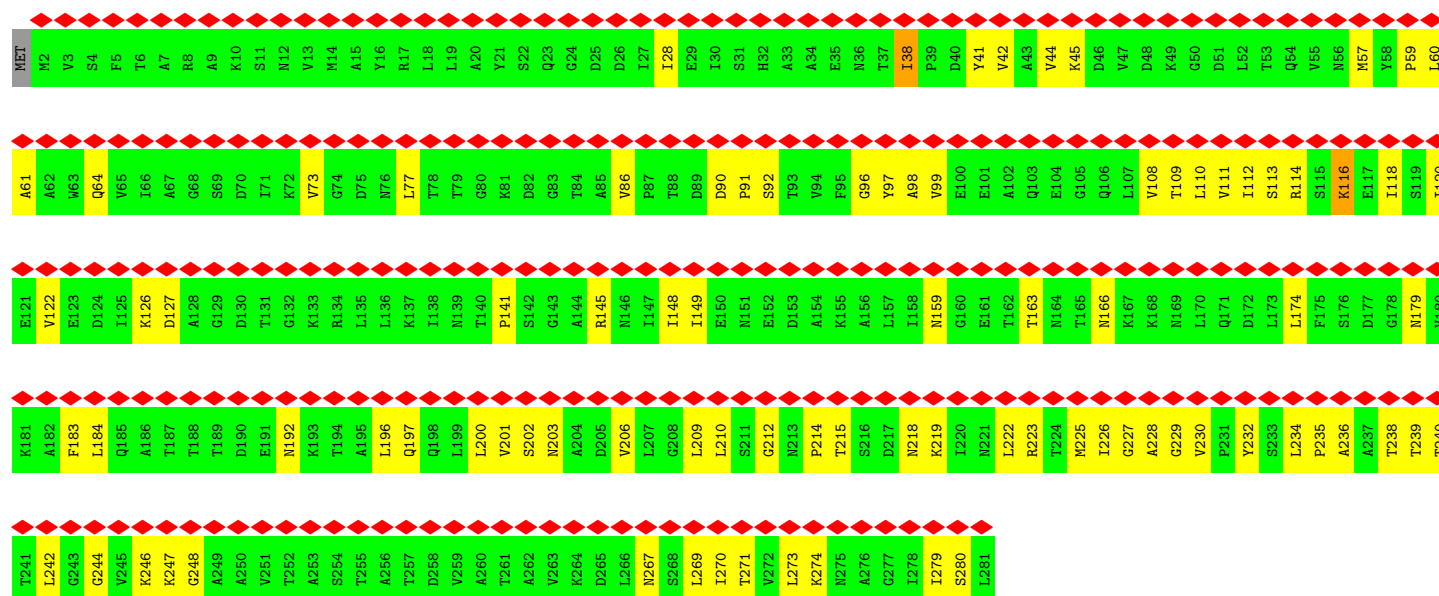
● Molecule 2: Capsid fiber protein

Chain 6u:

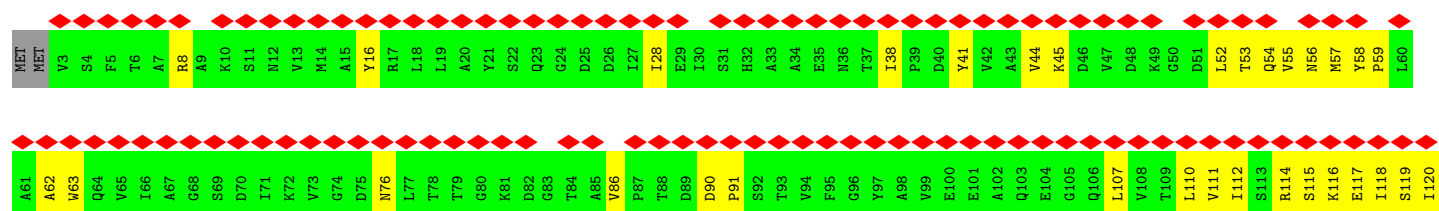




• Molecule 2: Capsid fiber protein

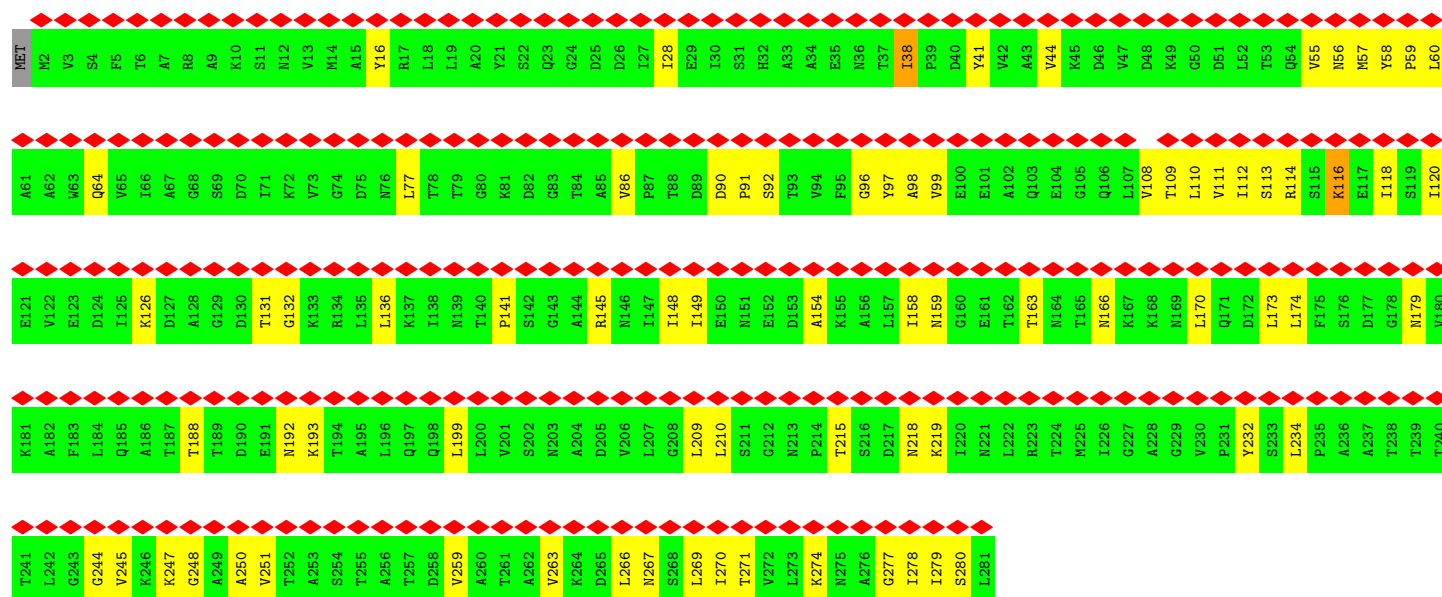
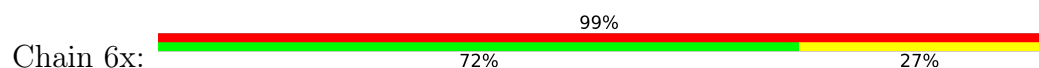


• Molecule 2: Capsid fiber protein

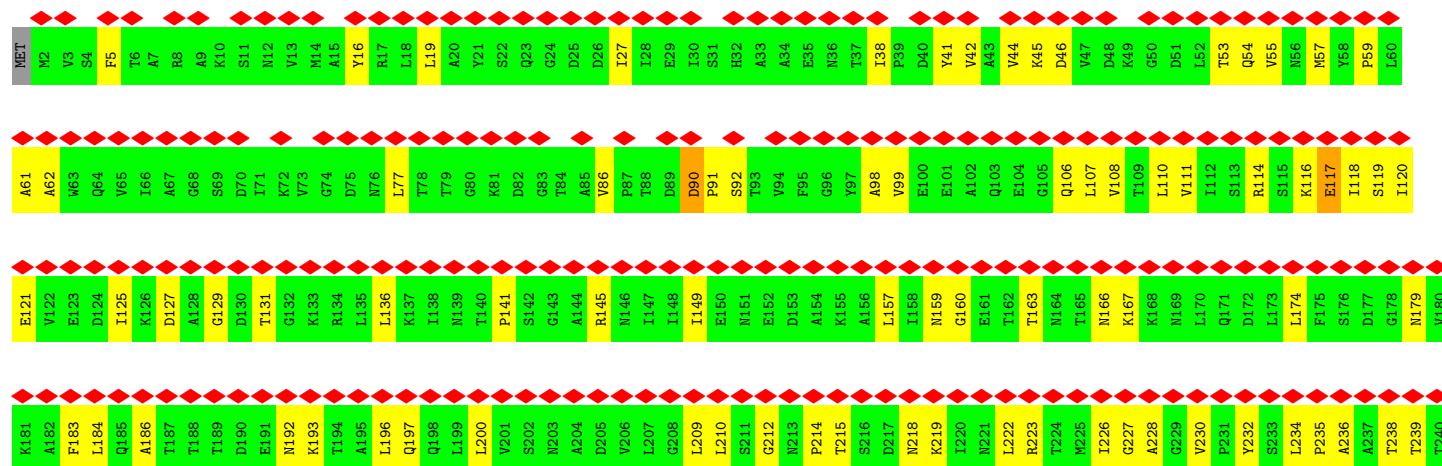


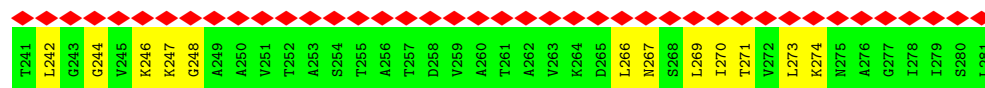


• Molecule 2: Capsid fiber protein

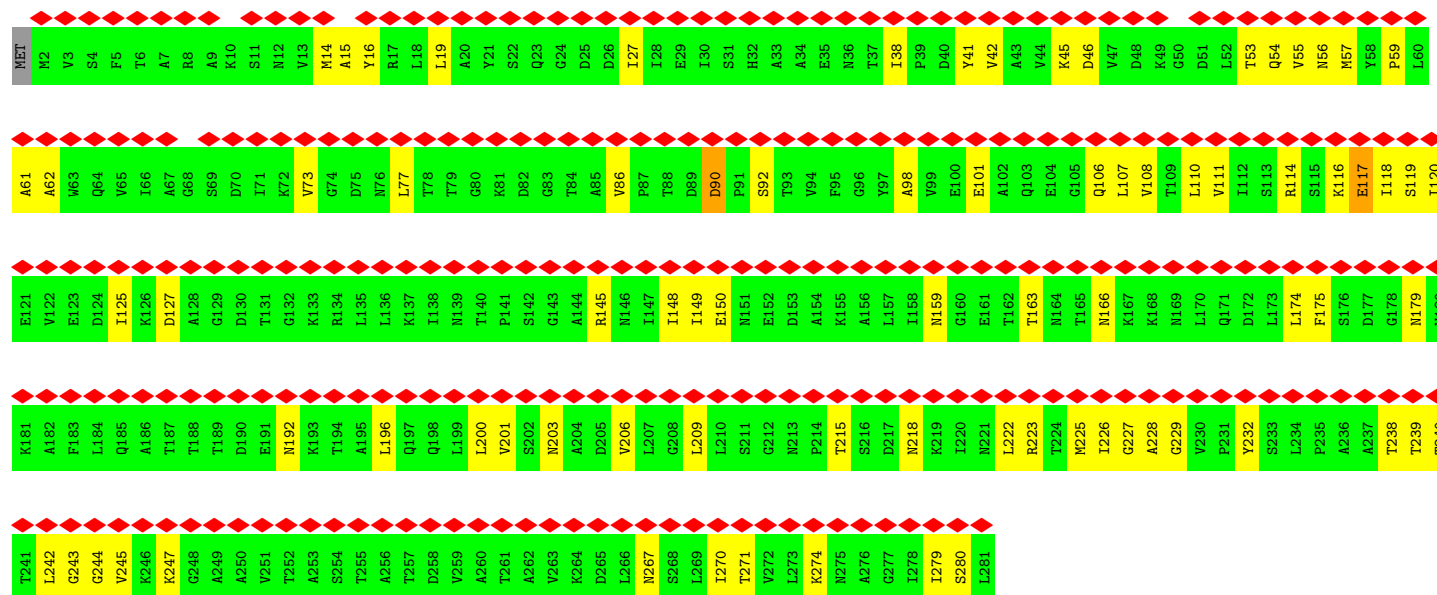
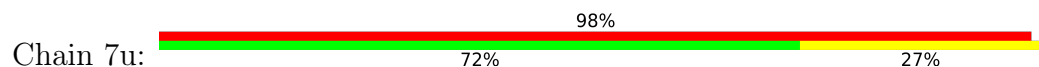


• Molecule 2: Capsid fiber protein

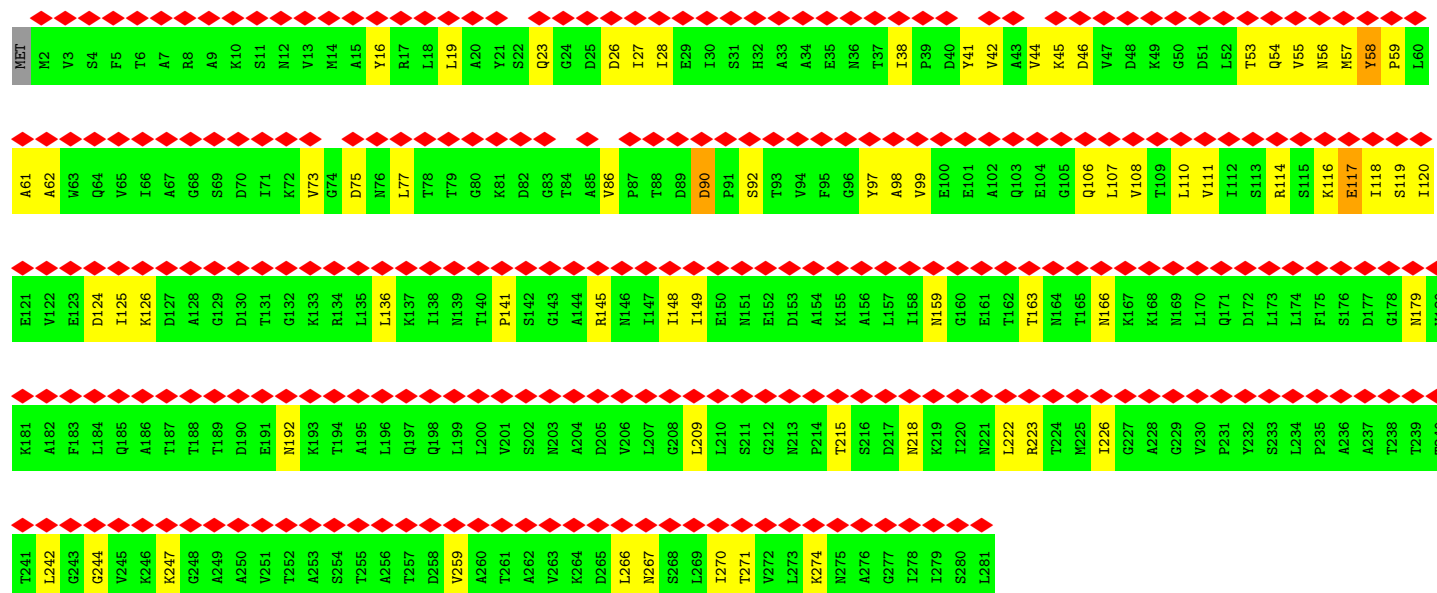
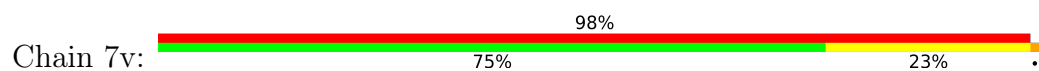




- Molecule 2: Capsid fiber protein

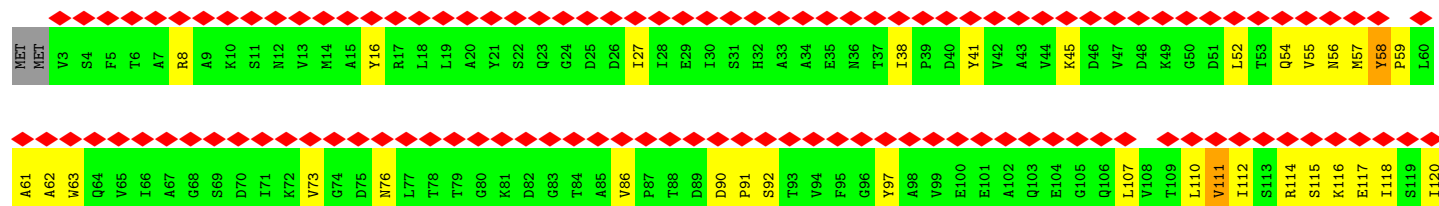


- Molecule 2: Capsid fiber protein



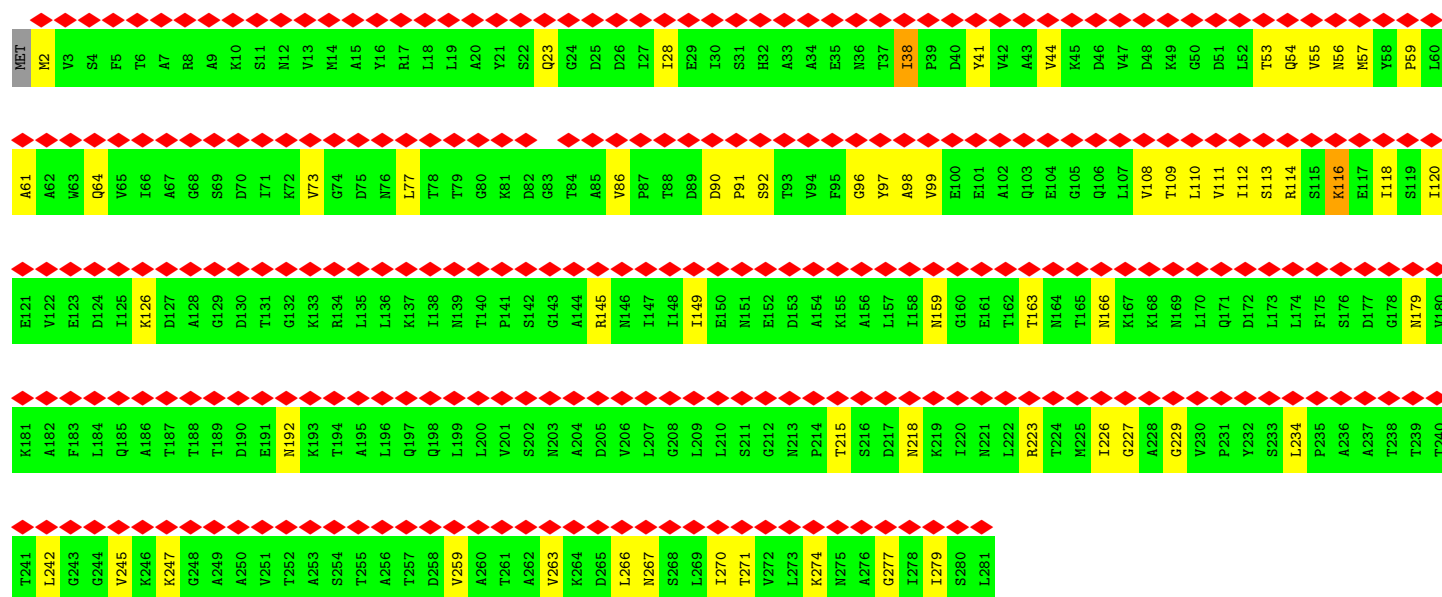
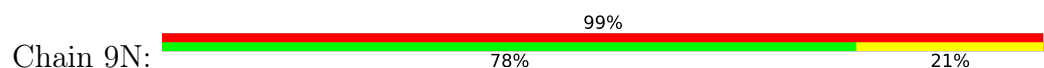
- Molecule 2: Capsid fiber protein



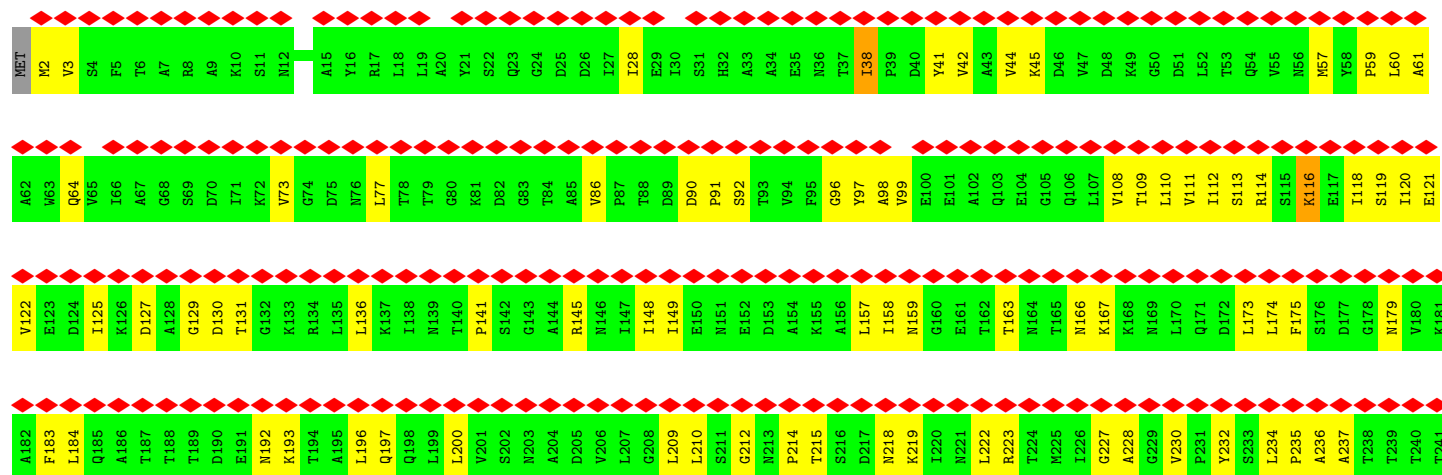




• Molecule 2: Capsid fiber protein

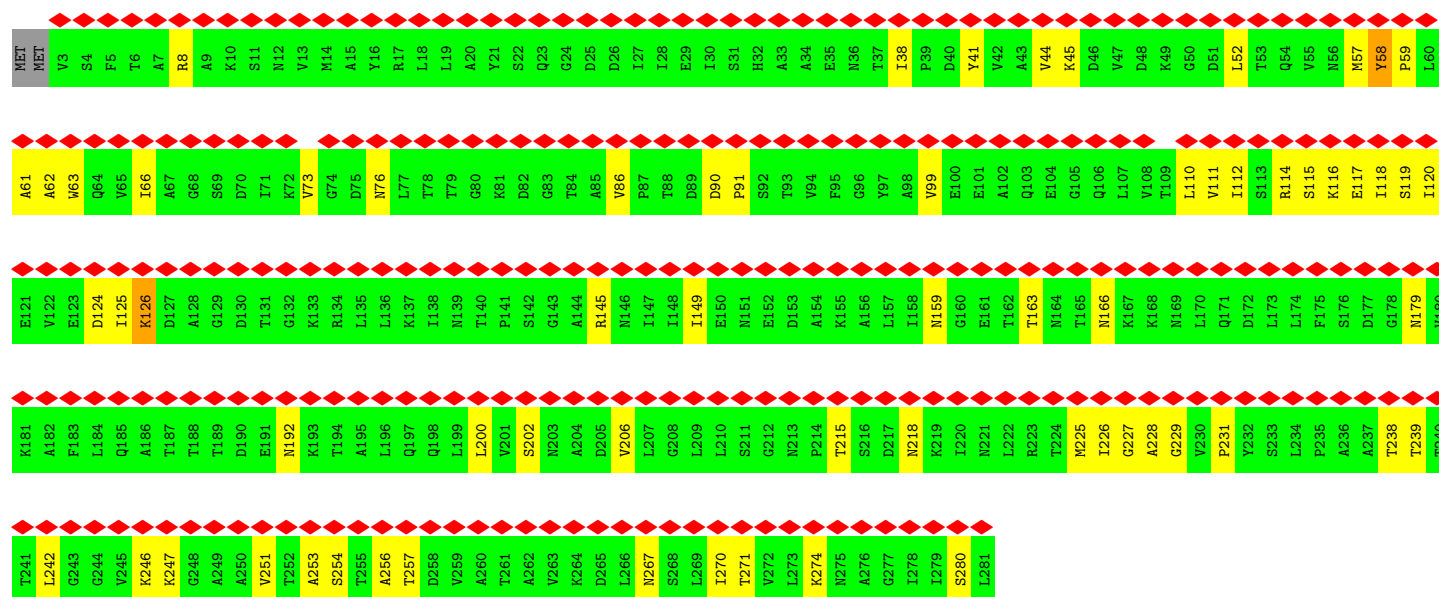
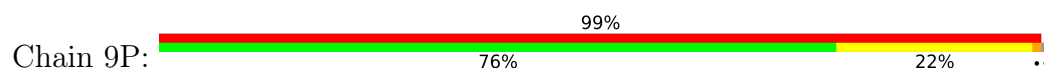


• Molecule 2: Capsid fiber protein

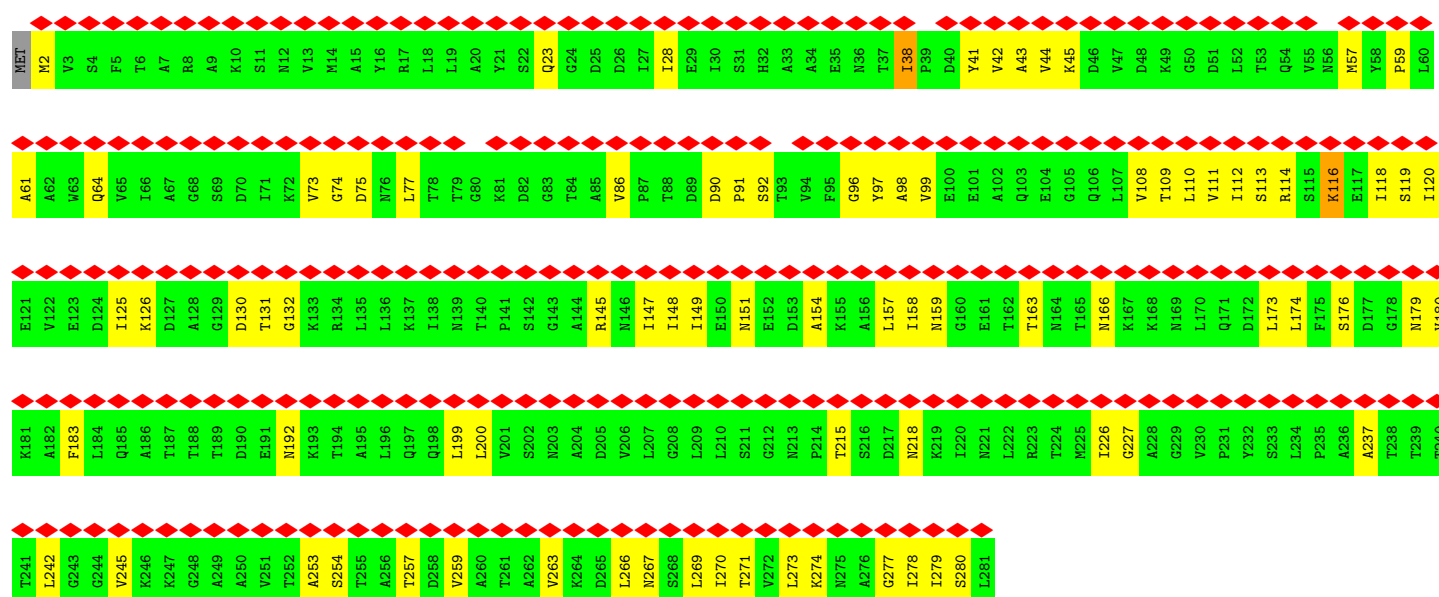
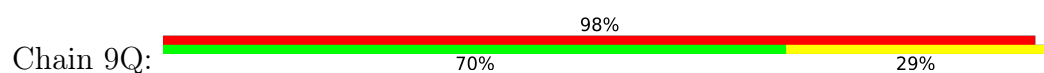




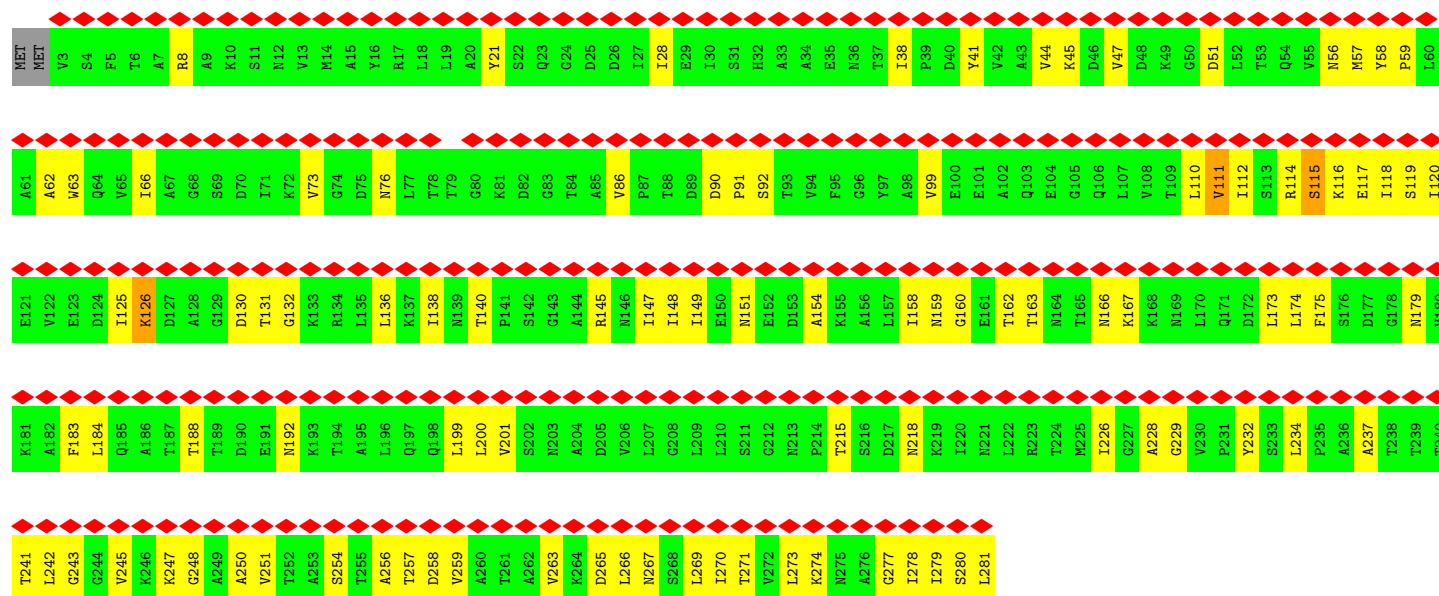
• Molecule 2: Capsid fiber protein



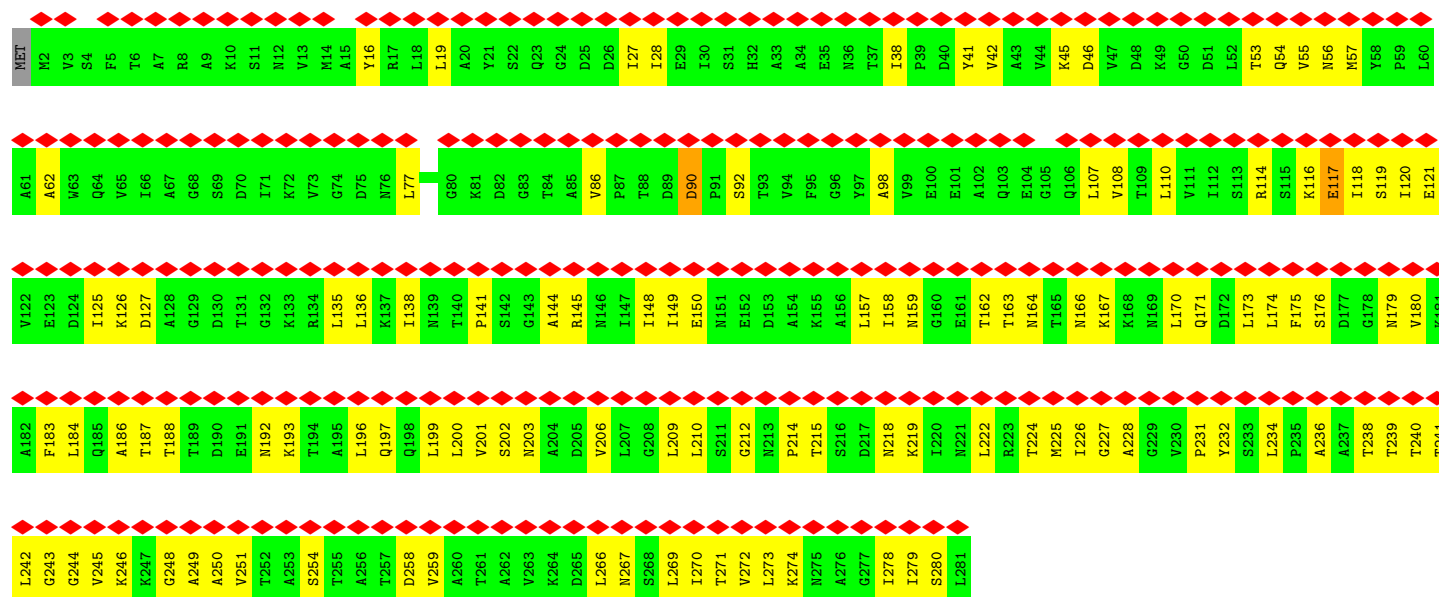
• Molecule 2: Capsid fiber protein



• Molecule 2: Capsid fiber protein



• Molecule 2: Capsid fiber protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18230	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	22.243	Depositor
Minimum map value	-0.425	Depositor
Average map value	0.118	Depositor
Map value standard deviation	0.805	Depositor
Recommended contour level	4.5	Depositor
Map size ($\text{\AA}$)	754.688, 754.688, 754.688	wwPDB
Map dimensions	704, 704, 704	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.072, 1.072, 1.072	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	1A	0.86	0/3460	1.03	7/4698 (0.1%)
1	1B	1.04	0/3551	1.16	23/4822 (0.5%)
1	1C	1.05	0/3551	1.12	22/4822 (0.5%)
1	1D	1.05	0/3551	1.16	17/4822 (0.4%)
1	1E	1.04	0/3489	1.13	16/4737 (0.3%)
1	1F	1.02	0/3513	1.17	23/4771 (0.5%)
1	1G	0.86	0/3460	1.03	7/4698 (0.1%)
1	1H	1.04	0/3551	1.16	23/4822 (0.5%)
1	1I	1.05	0/3551	1.12	22/4822 (0.5%)
1	1J	1.05	0/3551	1.16	17/4822 (0.4%)
1	1K	1.04	0/3489	1.13	16/4737 (0.3%)
1	1L	1.02	0/3513	1.17	23/4771 (0.5%)
1	1M	0.86	0/3460	1.03	7/4698 (0.1%)
1	1N	1.04	0/3551	1.16	23/4822 (0.5%)
1	1O	1.05	0/3551	1.12	22/4822 (0.5%)
1	1P	1.05	0/3551	1.16	17/4822 (0.4%)
1	1Q	1.04	0/3489	1.13	16/4737 (0.3%)
1	1R	1.03	0/3513	1.17	23/4771 (0.5%)
1	1S	0.86	1/3460 (0.0%)	1.02	7/4698 (0.1%)
1	1T	1.04	0/3551	1.16	23/4822 (0.5%)
1	1U	1.05	0/3551	1.12	23/4822 (0.5%)
1	1V	1.05	0/3551	1.16	17/4822 (0.4%)
1	1W	1.04	0/3489	1.13	16/4737 (0.3%)
1	1X	1.03	0/3513	1.17	23/4771 (0.5%)
1	1Y	0.86	1/3460 (0.0%)	1.03	7/4698 (0.1%)
1	1Z	1.04	0/3551	1.16	23/4822 (0.5%)
1	1a	1.05	0/3551	1.12	23/4822 (0.5%)
1	1b	1.05	0/3551	1.16	17/4822 (0.4%)
1	1c	1.04	0/3489	1.13	16/4737 (0.3%)
1	1d	1.03	0/3513	1.17	23/4771 (0.5%)
1	2A	1.04	0/3493	1.11	22/4743 (0.5%)
1	2B	1.08	0/3551	1.18	23/4822 (0.5%)
1	2C	1.04	0/3551	1.14	23/4822 (0.5%)
1	2D	1.06	0/3551	1.14	23/4822 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2E	1.06	0/3551	1.16	25/4822 (0.5%)
1	2F	1.04	0/3493	1.12	22/4743 (0.5%)
1	2G	1.08	0/3551	1.18	23/4822 (0.5%)
1	2H	1.04	0/3551	1.14	23/4822 (0.5%)
1	2I	1.06	0/3551	1.14	23/4822 (0.5%)
1	2J	1.06	0/3551	1.16	26/4822 (0.5%)
1	2K	1.04	0/3493	1.11	22/4743 (0.5%)
1	2L	1.08	0/3551	1.18	23/4822 (0.5%)
1	2M	1.04	0/3551	1.14	23/4822 (0.5%)
1	2N	1.06	0/3551	1.14	23/4822 (0.5%)
1	2O	1.06	0/3551	1.16	25/4822 (0.5%)
1	2P	1.04	0/3493	1.12	22/4743 (0.5%)
1	2Q	1.08	0/3551	1.18	23/4822 (0.5%)
1	2R	1.04	0/3551	1.14	23/4822 (0.5%)
1	2S	1.06	0/3551	1.14	23/4822 (0.5%)
1	2T	1.06	0/3551	1.16	25/4822 (0.5%)
1	2U	1.04	0/3493	1.12	22/4743 (0.5%)
1	2V	1.08	0/3551	1.18	23/4822 (0.5%)
1	2W	1.04	0/3551	1.14	23/4822 (0.5%)
1	2X	1.06	0/3551	1.14	23/4822 (0.5%)
1	2Y	1.06	0/3551	1.16	25/4822 (0.5%)
1	3A	1.07	0/3489	1.14	17/4737 (0.4%)
1	3B	1.08	0/3489	1.16	22/4737 (0.5%)
1	3C	1.09	0/3551	1.14	17/4822 (0.4%)
1	3D	1.10	0/3551	1.14	22/4822 (0.5%)
1	3E	1.08	0/3551	1.14	22/4822 (0.5%)
1	3F	1.08	0/3551	1.15	23/4822 (0.5%)
1	3G	1.07	0/3489	1.14	17/4737 (0.4%)
1	3H	1.08	0/3489	1.16	22/4737 (0.5%)
1	3I	1.09	0/3551	1.14	17/4822 (0.4%)
1	3J	1.10	0/3551	1.14	22/4822 (0.5%)
1	3K	1.08	0/3551	1.14	22/4822 (0.5%)
1	3L	1.08	0/3551	1.15	23/4822 (0.5%)
1	3M	1.07	0/3489	1.14	19/4737 (0.4%)
1	3N	1.08	0/3489	1.16	22/4737 (0.5%)
1	3O	1.09	0/3551	1.14	17/4822 (0.4%)
1	3P	1.10	0/3551	1.14	22/4822 (0.5%)
1	3Q	1.08	0/3551	1.14	22/4822 (0.5%)
1	3R	1.08	0/3551	1.15	23/4822 (0.5%)
1	3S	1.07	0/3489	1.14	17/4737 (0.4%)
1	3T	1.08	0/3489	1.16	22/4737 (0.5%)
1	3U	1.09	0/3551	1.14	17/4822 (0.4%)
1	3V	1.10	0/3551	1.14	22/4822 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	3W	1.08	0/3551	1.14	22/4822 (0.5%)
1	3X	1.08	0/3551	1.15	23/4822 (0.5%)
1	3Y	1.07	0/3489	1.14	17/4737 (0.4%)
1	3Z	1.08	0/3489	1.16	22/4737 (0.5%)
1	3a	1.09	0/3551	1.14	17/4822 (0.4%)
1	3b	1.10	0/3551	1.15	22/4822 (0.5%)
1	3c	1.08	0/3551	1.14	22/4822 (0.5%)
1	3d	1.08	0/3551	1.15	23/4822 (0.5%)
1	4A	1.10	0/3489	1.14	18/4737 (0.4%)
1	4B	1.09	0/3489	1.16	21/4737 (0.4%)
1	4C	1.10	0/3489	1.16	19/4737 (0.4%)
1	4D	1.09	0/3489	1.14	24/4737 (0.5%)
1	4E	1.10	0/3551	1.15	24/4822 (0.5%)
1	4F	1.08	1/3551 (0.0%)	1.16	19/4822 (0.4%)
1	4G	1.10	0/3489	1.14	18/4737 (0.4%)
1	4H	1.09	0/3489	1.16	21/4737 (0.4%)
1	4I	1.10	0/3489	1.16	19/4737 (0.4%)
1	4J	1.09	0/3489	1.14	24/4737 (0.5%)
1	4K	1.10	0/3551	1.15	24/4822 (0.5%)
1	4L	1.08	1/3551 (0.0%)	1.16	19/4822 (0.4%)
1	4M	1.10	0/3489	1.14	18/4737 (0.4%)
1	4N	1.09	0/3489	1.16	21/4737 (0.4%)
1	4O	1.10	0/3489	1.16	19/4737 (0.4%)
1	4P	1.09	0/3489	1.14	23/4737 (0.5%)
1	4Q	1.10	0/3551	1.15	24/4822 (0.5%)
1	4R	1.08	1/3551 (0.0%)	1.16	19/4822 (0.4%)
1	4S	1.10	0/3489	1.14	18/4737 (0.4%)
1	4T	1.09	0/3489	1.16	21/4737 (0.4%)
1	4U	1.10	0/3489	1.16	19/4737 (0.4%)
1	4V	1.09	0/3489	1.14	23/4737 (0.5%)
1	4W	1.10	0/3551	1.15	24/4822 (0.5%)
1	4X	1.08	1/3551 (0.0%)	1.16	19/4822 (0.4%)
1	4Y	1.10	0/3489	1.14	18/4737 (0.4%)
1	4Z	1.09	0/3489	1.16	21/4737 (0.4%)
1	4a	1.10	0/3489	1.16	19/4737 (0.4%)
1	4b	1.09	0/3489	1.14	24/4737 (0.5%)
1	4c	1.10	0/3551	1.15	24/4822 (0.5%)
1	4d	1.08	0/3551	1.16	19/4822 (0.4%)
1	5A	1.10	0/3489	1.15	15/4737 (0.3%)
1	5B	1.06	0/3489	1.19	21/4737 (0.4%)
1	5C	1.08	0/3489	1.15	24/4737 (0.5%)
1	5D	1.09	0/3489	1.12	20/4737 (0.4%)
1	5E	1.09	1/3551 (0.0%)	1.15	19/4822 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	5F	1.06	0/3551	1.17	23/4822 (0.5%)
1	5G	1.10	0/3489	1.15	15/4737 (0.3%)
1	5H	1.06	0/3489	1.19	21/4737 (0.4%)
1	5I	1.08	0/3489	1.15	24/4737 (0.5%)
1	5J	1.09	0/3489	1.12	20/4737 (0.4%)
1	5K	1.09	1/3551 (0.0%)	1.15	19/4822 (0.4%)
1	5L	1.06	0/3551	1.17	23/4822 (0.5%)
1	5M	1.10	0/3489	1.15	15/4737 (0.3%)
1	5N	1.06	0/3489	1.19	23/4737 (0.5%)
1	5O	1.08	0/3489	1.15	24/4737 (0.5%)
1	5P	1.09	0/3489	1.12	20/4737 (0.4%)
1	5Q	1.09	1/3551 (0.0%)	1.15	19/4822 (0.4%)
1	5R	1.06	0/3551	1.17	23/4822 (0.5%)
1	5S	1.10	0/3489	1.15	15/4737 (0.3%)
1	5T	1.06	0/3489	1.19	21/4737 (0.4%)
1	5U	1.08	0/3489	1.15	24/4737 (0.5%)
1	5V	1.09	0/3489	1.12	20/4737 (0.4%)
1	5W	1.09	1/3551 (0.0%)	1.15	19/4822 (0.4%)
1	5X	1.06	0/3551	1.17	23/4822 (0.5%)
1	5Y	1.10	0/3489	1.15	15/4737 (0.3%)
1	5Z	1.06	0/3489	1.19	21/4737 (0.4%)
1	5a	1.08	0/3489	1.15	24/4737 (0.5%)
1	5b	1.09	0/3489	1.12	20/4737 (0.4%)
1	5c	1.09	1/3551 (0.0%)	1.15	19/4822 (0.4%)
1	5d	1.06	0/3551	1.17	23/4822 (0.5%)
1	6A	1.03	0/3551	1.17	21/4822 (0.4%)
1	6B	1.03	0/3551	1.13	23/4822 (0.5%)
1	6C	1.03	0/3489	1.12	20/4737 (0.4%)
1	6D	1.05	0/3489	1.17	23/4737 (0.5%)
1	6E	1.05	0/3551	1.17	26/4822 (0.5%)
1	6F	1.04	0/3551	1.15	24/4822 (0.5%)
1	6G	1.03	0/3551	1.17	21/4822 (0.4%)
1	6H	1.03	0/3551	1.13	23/4822 (0.5%)
1	6I	1.03	0/3489	1.12	20/4737 (0.4%)
1	6J	1.06	0/3489	1.16	24/4737 (0.5%)
1	6K	1.05	0/3551	1.17	27/4822 (0.6%)
1	6L	1.04	0/3551	1.15	24/4822 (0.5%)
1	6M	1.03	0/3551	1.17	21/4822 (0.4%)
1	6N	1.03	0/3551	1.13	23/4822 (0.5%)
1	6O	1.03	0/3489	1.12	20/4737 (0.4%)
1	6P	1.06	0/3489	1.17	23/4737 (0.5%)
1	6Q	1.05	0/3551	1.17	27/4822 (0.6%)
1	6R	1.04	0/3551	1.15	24/4822 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	6S	1.03	0/3551	1.17	21/4822 (0.4%)
1	6T	1.03	0/3551	1.13	23/4822 (0.5%)
1	6U	1.03	0/3489	1.12	20/4737 (0.4%)
1	6V	1.06	0/3489	1.17	24/4737 (0.5%)
1	6W	1.05	0/3551	1.17	26/4822 (0.5%)
1	6X	1.04	0/3551	1.15	24/4822 (0.5%)
1	6Y	1.03	0/3551	1.17	21/4822 (0.4%)
1	6Z	1.03	0/3551	1.13	23/4822 (0.5%)
1	6a	1.03	0/3489	1.12	20/4737 (0.4%)
1	6b	1.06	0/3489	1.17	23/4737 (0.5%)
1	6c	1.05	0/3551	1.17	27/4822 (0.6%)
1	6d	1.04	0/3551	1.15	23/4822 (0.5%)
1	7A	0.99	0/3551	1.16	25/4822 (0.5%)
1	7B	0.96	0/3551	1.13	21/4822 (0.4%)
1	7C	0.99	1/3551 (0.0%)	1.17	23/4822 (0.5%)
1	7D	0.99	0/3551	1.13	21/4822 (0.4%)
1	7E	0.98	0/3551	1.16	26/4822 (0.5%)
1	7F	0.99	0/3551	1.16	25/4822 (0.5%)
1	7G	0.97	0/3551	1.13	21/4822 (0.4%)
1	7H	0.99	1/3551 (0.0%)	1.17	23/4822 (0.5%)
1	7I	0.99	0/3551	1.13	21/4822 (0.4%)
1	7J	0.98	0/3551	1.16	26/4822 (0.5%)
1	7K	0.99	0/3551	1.16	27/4822 (0.6%)
1	7L	0.97	0/3551	1.13	21/4822 (0.4%)
1	7M	0.99	1/3551 (0.0%)	1.17	23/4822 (0.5%)
1	7N	0.99	0/3551	1.13	21/4822 (0.4%)
1	7O	0.98	0/3551	1.16	26/4822 (0.5%)
1	7P	0.99	0/3551	1.16	26/4822 (0.5%)
1	7Q	0.97	0/3551	1.13	21/4822 (0.4%)
1	7R	0.99	1/3551 (0.0%)	1.17	23/4822 (0.5%)
1	7S	0.99	1/3551 (0.0%)	1.13	21/4822 (0.4%)
1	7T	0.98	0/3551	1.16	26/4822 (0.5%)
1	7U	0.99	0/3551	1.16	25/4822 (0.5%)
1	7V	0.96	0/3551	1.13	21/4822 (0.4%)
1	7W	0.99	1/3551 (0.0%)	1.17	23/4822 (0.5%)
1	7X	0.99	0/3551	1.13	21/4822 (0.4%)
1	7Y	0.98	0/3551	1.16	26/4822 (0.5%)
1	8A	0.99	0/3551	1.17	34/4822 (0.7%)
1	8B	0.97	0/3551	1.14	19/4822 (0.4%)
1	8C	0.98	0/3551	1.15	24/4822 (0.5%)
1	8D	0.98	0/3551	1.13	25/4822 (0.5%)
1	8E	0.99	0/3551	1.14	23/4822 (0.5%)
1	8F	0.99	0/3551	1.13	26/4822 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	8G	0.99	0/3551	1.17	34/4822 (0.7%)
1	8H	0.97	0/3551	1.14	19/4822 (0.4%)
1	8I	0.98	0/3551	1.14	23/4822 (0.5%)
1	8J	0.98	0/3551	1.13	26/4822 (0.5%)
1	8K	0.99	0/3551	1.14	23/4822 (0.5%)
1	8L	0.99	0/3551	1.13	26/4822 (0.5%)
1	8M	0.99	0/3551	1.17	34/4822 (0.7%)
1	8N	0.97	0/3551	1.14	19/4822 (0.4%)
1	8O	0.98	0/3551	1.15	24/4822 (0.5%)
1	8P	0.98	0/3551	1.13	26/4822 (0.5%)
1	8Q	0.99	0/3551	1.14	23/4822 (0.5%)
1	8R	0.99	0/3551	1.13	26/4822 (0.5%)
1	8S	0.99	0/3551	1.17	34/4822 (0.7%)
1	8T	0.97	0/3551	1.14	19/4822 (0.4%)
1	8U	0.98	0/3551	1.15	24/4822 (0.5%)
1	8V	0.98	0/3551	1.13	26/4822 (0.5%)
1	8W	0.99	0/3551	1.14	23/4822 (0.5%)
1	8X	0.99	0/3551	1.13	26/4822 (0.5%)
1	8Y	0.99	0/3551	1.17	34/4822 (0.7%)
1	8Z	0.97	0/3551	1.14	19/4822 (0.4%)
1	8a	0.98	0/3551	1.15	24/4822 (0.5%)
1	8b	0.98	0/3551	1.13	25/4822 (0.5%)
1	8c	0.99	0/3551	1.14	23/4822 (0.5%)
1	8d	0.99	0/3551	1.13	26/4822 (0.5%)
1	9A	0.97	1/3551 (0.0%)	1.14	17/4822 (0.4%)
1	9B	0.97	1/3551 (0.0%)	1.14	17/4822 (0.4%)
1	9C	0.97	1/3551 (0.0%)	1.14	17/4822 (0.4%)
1	9D	0.97	1/3551 (0.0%)	1.14	17/4822 (0.4%)
1	9E	0.97	1/3551 (0.0%)	1.14	17/4822 (0.4%)
2	1e	0.80	0/2150	0.94	7/2925 (0.2%)
2	1f	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1g	0.80	0/2150	0.94	7/2925 (0.2%)
2	1h	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1i	0.80	0/2150	0.94	7/2925 (0.2%)
2	1j	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1k	0.80	0/2150	0.94	7/2925 (0.2%)
2	1l	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1m	0.80	0/2150	0.94	7/2925 (0.2%)
2	1n	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1o	0.80	0/2150	0.94	7/2925 (0.2%)
2	1p	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1q	0.80	0/2150	0.94	7/2925 (0.2%)
2	1r	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	1s	0.80	0/2150	0.94	7/2925 (0.2%)
2	1t	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1u	0.80	0/2150	0.94	7/2925 (0.2%)
2	1v	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	1w	0.80	0/2150	0.94	7/2925 (0.2%)
2	1x	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	2Z	0.81	0/2150	0.96	7/2925 (0.2%)
2	2a	0.81	0/2150	0.96	7/2925 (0.2%)
2	2b	0.81	0/2150	0.96	7/2925 (0.2%)
2	2c	0.81	0/2150	0.96	7/2925 (0.2%)
2	2d	0.81	0/2150	0.96	7/2925 (0.2%)
2	2e	0.81	0/2150	0.96	7/2925 (0.2%)
2	2f	0.81	0/2150	0.96	7/2925 (0.2%)
2	2g	0.81	0/2150	0.96	7/2925 (0.2%)
2	2h	0.81	0/2150	0.96	9/2925 (0.3%)
2	2i	0.81	0/2150	0.96	9/2925 (0.3%)
2	2j	0.81	0/2150	0.96	7/2925 (0.2%)
2	2k	0.81	0/2150	0.96	7/2925 (0.2%)
2	2l	0.81	0/2150	0.96	7/2925 (0.2%)
2	2m	0.81	0/2150	0.96	9/2925 (0.3%)
2	2n	0.81	0/2150	0.96	7/2925 (0.2%)
2	2o	0.81	0/2150	0.96	7/2925 (0.2%)
2	2p	0.81	0/2150	0.96	7/2925 (0.2%)
2	2q	0.81	0/2150	0.96	9/2925 (0.3%)
2	2r	0.81	0/2150	0.96	7/2925 (0.2%)
2	2s	0.81	0/2150	0.96	7/2925 (0.2%)
2	2t	0.81	0/2150	0.96	7/2925 (0.2%)
2	2u	0.81	0/2150	0.96	7/2925 (0.2%)
2	2v	0.81	0/2150	0.96	7/2925 (0.2%)
2	2w	0.81	0/2150	0.96	9/2925 (0.3%)
2	2x	0.81	0/2150	0.96	9/2925 (0.3%)
2	3e	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3f	0.80	0/2150	0.94	7/2925 (0.2%)
2	3g	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3h	0.80	0/2150	0.94	7/2925 (0.2%)
2	3i	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3j	0.80	0/2150	0.94	7/2925 (0.2%)
2	3k	0.84	1/2142 (0.0%)	0.99	12/2915 (0.4%)
2	3l	0.80	0/2150	0.94	7/2925 (0.2%)
2	3m	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3n	0.80	0/2150	0.94	7/2925 (0.2%)
2	3o	0.84	1/2142 (0.0%)	0.99	12/2915 (0.4%)
2	3p	0.80	0/2150	0.94	7/2925 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	3q	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3r	0.80	0/2150	0.94	7/2925 (0.2%)
2	3s	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3t	0.80	0/2150	0.94	7/2925 (0.2%)
2	3u	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	3v	0.80	0/2150	0.94	7/2925 (0.2%)
2	3w	0.84	1/2142 (0.0%)	0.99	12/2915 (0.4%)
2	3x	0.80	0/2150	0.94	7/2925 (0.2%)
2	4e	0.80	0/2150	0.94	7/2925 (0.2%)
2	4f	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	4g	0.80	0/2150	0.94	7/2925 (0.2%)
2	4h	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	4i	0.80	0/2150	0.94	7/2925 (0.2%)
2	4j	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	4k	0.80	0/2150	0.94	7/2925 (0.2%)
2	4l	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	4m	0.80	0/2150	0.94	7/2925 (0.2%)
2	4n	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	5e	0.80	0/2150	0.94	7/2925 (0.2%)
2	5f	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	5g	0.80	0/2150	0.94	7/2925 (0.2%)
2	5h	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	5i	0.80	0/2150	0.94	7/2925 (0.2%)
2	5j	0.84	1/2142 (0.0%)	0.99	12/2915 (0.4%)
2	5k	0.80	0/2150	0.94	7/2925 (0.2%)
2	5l	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	5m	0.80	0/2150	0.94	7/2925 (0.2%)
2	5n	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6e	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6f	0.80	0/2150	0.94	7/2925 (0.2%)
2	6g	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6h	0.80	0/2150	0.94	7/2925 (0.2%)
2	6i	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6j	0.80	0/2150	0.94	7/2925 (0.2%)
2	6k	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6l	0.80	0/2150	0.94	7/2925 (0.2%)
2	6m	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6n	0.80	0/2150	0.94	7/2925 (0.2%)
2	6o	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6p	0.80	0/2150	0.94	7/2925 (0.2%)
2	6q	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6r	0.80	0/2150	0.94	7/2925 (0.2%)
2	6s	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	6t	0.80	0/2150	0.94	7/2925 (0.2%)
2	6u	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6v	0.80	0/2150	0.94	7/2925 (0.2%)
2	6w	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	6x	0.80	0/2150	0.94	7/2925 (0.2%)
2	7Z	0.81	0/2150	0.96	7/2925 (0.2%)
2	7a	0.81	0/2150	0.96	7/2925 (0.2%)
2	7b	0.81	0/2150	0.96	7/2925 (0.2%)
2	7c	0.81	0/2150	0.96	7/2925 (0.2%)
2	7d	0.81	0/2150	0.96	7/2925 (0.2%)
2	7e	0.81	0/2150	0.96	7/2925 (0.2%)
2	7f	0.81	0/2150	0.96	7/2925 (0.2%)
2	7g	0.81	0/2150	0.96	9/2925 (0.3%)
2	7h	0.81	0/2150	0.96	7/2925 (0.2%)
2	7i	0.81	0/2150	0.96	7/2925 (0.2%)
2	7j	0.81	0/2150	0.96	7/2925 (0.2%)
2	7k	0.81	0/2150	0.96	7/2925 (0.2%)
2	7l	0.81	0/2150	0.96	7/2925 (0.2%)
2	7m	0.81	0/2150	0.96	7/2925 (0.2%)
2	7n	0.81	0/2150	0.96	7/2925 (0.2%)
2	7o	0.81	0/2150	0.96	7/2925 (0.2%)
2	7p	0.81	0/2150	0.96	7/2925 (0.2%)
2	7q	0.81	0/2150	0.96	7/2925 (0.2%)
2	7r	0.81	0/2150	0.96	7/2925 (0.2%)
2	7s	0.81	0/2150	0.96	9/2925 (0.3%)
2	7t	0.81	0/2150	0.96	7/2925 (0.2%)
2	7u	0.81	0/2150	0.96	7/2925 (0.2%)
2	7v	0.81	0/2150	0.96	9/2925 (0.3%)
2	7w	0.81	0/2150	0.96	7/2925 (0.2%)
2	7x	0.81	0/2150	0.96	7/2925 (0.2%)
2	8e	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8f	0.80	0/2150	0.94	7/2925 (0.2%)
2	8g	0.80	0/2150	0.94	7/2925 (0.2%)
2	8h	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8i	0.80	0/2150	0.94	7/2925 (0.2%)
2	8j	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8k	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8l	0.80	0/2150	0.94	7/2925 (0.2%)
2	8m	0.80	0/2150	0.94	7/2925 (0.2%)
2	8n	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8o	0.80	0/2150	0.94	7/2925 (0.2%)
2	8p	0.83	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8q	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	8r	0.80	0/2150	0.94	7/2925 (0.2%)
2	8s	0.80	0/2150	0.94	7/2925 (0.2%)
2	8t	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8u	0.80	0/2150	0.94	7/2925 (0.2%)
2	8v	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8w	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	8x	0.80	0/2150	0.94	7/2925 (0.2%)
2	8y	0.80	0/2150	0.94	7/2925 (0.2%)
2	8z	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	9F	0.81	0/2150	0.96	7/2925 (0.2%)
2	9G	0.81	0/2150	0.96	7/2925 (0.2%)
2	9H	0.81	0/2150	0.96	7/2925 (0.2%)
2	9I	0.81	0/2150	0.96	7/2925 (0.2%)
2	9J	0.81	0/2150	0.96	7/2925 (0.2%)
2	9K	0.80	0/2150	0.94	7/2925 (0.2%)
2	9L	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	9M	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	9N	0.80	0/2150	0.94	7/2925 (0.2%)
2	9O	0.80	0/2150	0.94	7/2925 (0.2%)
2	9P	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
2	9Q	0.80	0/2150	0.94	7/2925 (0.2%)
2	9R	0.84	1/2142 (0.0%)	1.00	12/2915 (0.4%)
All	All	0.98	77/1183830 (0.0%)	1.10	6537/1608450 (0.4%)

The worst 5 of 77 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	6i	111	VAL	C-N	-10.36	1.21	1.33
2	1j	111	VAL	C-N	-10.35	1.21	1.33
2	6u	111	VAL	C-N	-10.33	1.21	1.33
2	1f	111	VAL	C-N	-10.33	1.21	1.33
2	6m	111	VAL	C-N	-10.33	1.21	1.33

The worst 5 of 6537 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2T	355	SER	N-CA-C	10.60	127.17	112.75
1	2E	355	SER	N-CA-C	10.58	127.13	112.75
1	2J	355	SER	N-CA-C	10.57	127.13	112.75
1	2Y	355	SER	N-CA-C	10.57	127.13	112.75
1	1Z	275	PHE	CA-CB-CG	-10.43	103.37	113.80

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	1A	3397	0	3342	46	0
1	1B	3487	0	3434	32	0
1	1C	3487	0	3434	60	0
1	1D	3487	0	3434	54	0
1	1E	3426	0	3381	60	0
1	1F	3449	0	3400	46	0
1	1G	3397	0	3342	49	0
1	1H	3487	0	3434	35	0
1	1I	3487	0	3434	63	0
1	1J	3487	0	3434	45	0
1	1K	3426	0	3381	60	0
1	1L	3449	0	3400	45	0
1	1M	3397	0	3342	54	0
1	1N	3487	0	3434	38	0
1	1O	3487	0	3434	63	0
1	1P	3487	0	3434	52	0
1	1Q	3426	0	3381	57	0
1	1R	3449	0	3400	46	0
1	1S	3397	0	3342	59	0
1	1T	3487	0	3434	39	0
1	1U	3487	0	3434	74	0
1	1V	3487	0	3434	63	0
1	1W	3426	0	3381	62	0
1	1X	3449	0	3400	49	0
1	1Y	3397	0	3342	47	0
1	1Z	3487	0	3434	38	0
1	1a	3487	0	3434	71	0
1	1b	3487	0	3434	62	0
1	1c	3426	0	3381	60	0
1	1d	3449	0	3400	47	0
1	2A	3430	0	3378	35	0
1	2B	3487	0	3433	56	0
1	2C	3487	0	3432	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2D	3487	0	3433	23	0
1	2E	3487	0	3433	49	0
1	2F	3430	0	3378	35	0
1	2G	3487	0	3433	53	0
1	2H	3487	0	3433	39	0
1	2I	3487	0	3433	27	0
1	2J	3487	0	3434	44	0
1	2K	3430	0	3378	35	0
1	2L	3487	0	3433	59	0
1	2M	3487	0	3431	52	0
1	2N	3487	0	3434	25	0
1	2O	3487	0	3433	48	0
1	2P	3430	0	3378	40	0
1	2Q	3487	0	3433	68	0
1	2R	3487	0	3431	63	0
1	2S	3487	0	3434	28	0
1	2T	3487	0	3433	49	0
1	2U	3430	0	3378	34	0
1	2V	3487	0	3432	53	0
1	2W	3487	0	3431	48	0
1	2X	3487	0	3433	26	0
1	2Y	3487	0	3433	51	0
1	3A	3426	0	3381	31	0
1	3B	3426	0	3381	29	0
1	3C	3487	0	3434	103	0
1	3D	3487	0	3434	31	0
1	3E	3487	0	3434	32	0
1	3F	3487	0	3434	35	0
1	3G	3426	0	3381	33	0
1	3H	3426	0	3381	31	0
1	3I	3487	0	3434	111	0
1	3J	3487	0	3434	35	0
1	3K	3487	0	3434	30	0
1	3L	3487	0	3434	41	0
1	3M	3426	0	3381	35	0
1	3N	3426	0	3381	33	0
1	3O	3487	0	3434	109	0
1	3P	3487	0	3434	36	0
1	3Q	3487	0	3434	32	0
1	3R	3487	0	3434	43	0
1	3S	3426	0	3381	34	0
1	3T	3426	0	3381	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3U	3487	0	3434	97	0
1	3V	3487	0	3434	38	0
1	3W	3487	0	3434	36	0
1	3X	3487	0	3434	44	0
1	3Y	3426	0	3381	34	0
1	3Z	3426	0	3381	32	0
1	3a	3487	0	3434	91	0
1	3b	3487	0	3434	38	0
1	3c	3487	0	3434	35	0
1	3d	3487	0	3434	35	0
1	4A	3426	0	3381	34	0
1	4B	3426	0	3381	46	0
1	4C	3426	0	3381	28	0
1	4D	3426	0	3381	24	0
1	4E	3487	0	3434	59	0
1	4F	3487	0	3434	66	0
1	4G	3426	0	3381	36	0
1	4H	3426	0	3381	49	0
1	4I	3426	0	3381	25	0
1	4J	3426	0	3381	24	0
1	4K	3487	0	3434	56	0
1	4L	3487	0	3434	65	0
1	4M	3426	0	3381	36	0
1	4N	3426	0	3381	50	0
1	4O	3426	0	3381	28	0
1	4P	3426	0	3381	23	0
1	4Q	3487	0	3434	56	0
1	4R	3487	0	3434	60	0
1	4S	3426	0	3381	35	0
1	4T	3426	0	3381	51	0
1	4U	3426	0	3381	28	0
1	4V	3426	0	3381	26	0
1	4W	3487	0	3434	62	0
1	4X	3487	0	3434	59	0
1	4Y	3426	0	3381	37	0
1	4Z	3426	0	3381	49	0
1	4a	3426	0	3381	27	0
1	4b	3426	0	3381	23	0
1	4c	3487	0	3434	59	0
1	4d	3487	0	3434	71	0
1	5A	3426	0	3381	30	0
1	5B	3426	0	3381	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5C	3426	0	3381	29	0
1	5D	3426	0	3381	29	0
1	5E	3487	0	3434	65	0
1	5F	3487	0	3434	86	0
1	5G	3426	0	3381	31	0
1	5H	3426	0	3381	42	0
1	5I	3426	0	3381	30	0
1	5J	3426	0	3381	27	0
1	5K	3487	0	3434	60	0
1	5L	3487	0	3434	94	0
1	5M	3426	0	3381	30	0
1	5N	3426	0	3381	42	0
1	5O	3426	0	3381	30	0
1	5P	3426	0	3381	29	0
1	5Q	3487	0	3434	71	0
1	5R	3487	0	3434	93	0
1	5S	3426	0	3381	29	0
1	5T	3426	0	3381	44	0
1	5U	3426	0	3381	29	0
1	5V	3426	0	3381	28	0
1	5W	3487	0	3434	77	0
1	5X	3487	0	3434	83	0
1	5Y	3426	0	3381	27	0
1	5Z	3426	0	3381	42	0
1	5a	3426	0	3381	29	0
1	5b	3426	0	3381	27	0
1	5c	3487	0	3434	64	0
1	5d	3487	0	3434	90	0
1	6A	3487	0	3434	56	0
1	6B	3487	0	3434	39	0
1	6C	3426	0	3381	24	0
1	6D	3426	0	3381	32	0
1	6E	3487	0	3434	47	0
1	6F	3487	0	3432	42	0
1	6G	3487	0	3434	47	0
1	6H	3487	0	3434	36	0
1	6I	3426	0	3381	24	0
1	6J	3426	0	3381	33	0
1	6K	3487	0	3434	45	0
1	6L	3487	0	3433	51	0
1	6M	3487	0	3434	44	0
1	6N	3487	0	3434	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	6O	3426	0	3381	24	0
1	6P	3426	0	3381	34	0
1	6Q	3487	0	3434	52	0
1	6R	3487	0	3434	62	0
1	6S	3487	0	3434	44	0
1	6T	3487	0	3434	56	0
1	6U	3426	0	3381	25	0
1	6V	3426	0	3381	34	0
1	6W	3487	0	3434	62	0
1	6X	3487	0	3434	65	0
1	6Y	3487	0	3434	54	0
1	6Z	3487	0	3434	63	0
1	6a	3426	0	3381	24	0
1	6b	3426	0	3381	31	0
1	6c	3487	0	3434	57	0
1	6d	3487	0	3432	44	0
1	7A	3487	0	3433	49	0
1	7B	3487	0	3432	44	0
1	7C	3487	0	3433	80	0
1	7D	3487	0	3434	54	0
1	7E	3487	0	3434	47	0
1	7F	3487	0	3433	37	0
1	7G	3487	0	3433	50	0
1	7H	3487	0	3434	62	0
1	7I	3487	0	3434	38	0
1	7J	3487	0	3433	43	0
1	7K	3487	0	3433	58	0
1	7L	3487	0	3434	56	0
1	7M	3487	0	3434	59	0
1	7N	3487	0	3434	45	0
1	7O	3487	0	3434	50	0
1	7P	3487	0	3434	66	0
1	7Q	3487	0	3433	37	0
1	7R	3487	0	3433	71	0
1	7S	3487	0	3434	67	0
1	7T	3487	0	3433	57	0
1	7U	3487	0	3434	56	0
1	7V	3487	0	3431	44	0
1	7W	3487	0	3433	76	0
1	7X	3487	0	3434	70	0
1	7Y	3487	0	3434	45	0
1	8A	3487	0	3434	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	8B	3487	0	3434	47	0
1	8C	3487	0	3434	41	0
1	8D	3487	0	3434	48	0
1	8E	3487	0	3434	43	0
1	8F	3487	0	3434	53	0
1	8G	3487	0	3434	62	0
1	8H	3487	0	3434	50	0
1	8I	3487	0	3434	41	0
1	8J	3487	0	3434	40	0
1	8K	3487	0	3434	34	0
1	8L	3487	0	3434	80	0
1	8M	3487	0	3434	50	0
1	8N	3487	0	3434	32	0
1	8O	3487	0	3434	40	0
1	8P	3487	0	3434	39	0
1	8Q	3487	0	3434	34	0
1	8R	3487	0	3434	79	0
1	8S	3487	0	3434	54	0
1	8T	3487	0	3434	30	0
1	8U	3487	0	3434	33	0
1	8V	3487	0	3434	59	0
1	8W	3487	0	3434	50	0
1	8X	3487	0	3434	75	0
1	8Y	3487	0	3434	72	0
1	8Z	3487	0	3434	46	0
1	8a	3487	0	3434	36	0
1	8b	3487	0	3433	56	0
1	8c	3487	0	3434	39	0
1	8d	3487	0	3434	55	0
1	9A	3487	0	3433	32	0
1	9B	3487	0	3433	28	0
1	9C	3487	0	3433	58	0
1	9D	3487	0	3433	89	0
1	9E	3487	0	3433	52	0
2	1e	2106	0	2162	280	0
2	1f	2098	0	2154	217	0
2	1g	2106	0	2160	495	0
2	1h	2098	0	2153	346	0
2	1i	2106	0	2162	282	0
2	1j	2098	0	2154	218	0
2	1k	2106	0	2160	499	0
2	1l	2098	0	2153	339	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	1m	2106	0	2160	288	0
2	1n	2098	0	2154	220	0
2	1o	2106	0	2160	494	0
2	1p	2098	0	2153	341	0
2	1q	2106	0	2161	291	0
2	1r	2098	0	2154	224	0
2	1s	2106	0	2160	506	0
2	1t	2098	0	2153	351	0
2	1u	2106	0	2161	280	0
2	1v	2098	0	2154	219	0
2	1w	2106	0	2160	508	0
2	1x	2098	0	2153	356	0
2	2Z	2106	0	2161	411	0
2	2a	2106	0	2162	337	0
2	2b	2106	0	2162	348	0
2	2c	2106	0	2159	307	0
2	2d	2106	0	2162	345	0
2	2e	2106	0	2161	406	0
2	2f	2106	0	2161	337	0
2	2g	2106	0	2162	356	0
2	2h	2106	0	2159	309	0
2	2i	2106	0	2162	347	0
2	2j	2106	0	2159	405	0
2	2k	2106	0	2162	352	0
2	2l	2106	0	2162	359	0
2	2m	2106	0	2159	307	0
2	2n	2106	0	2162	348	0
2	2o	2106	0	2159	410	0
2	2p	2106	0	2162	362	0
2	2q	2106	0	2162	367	0
2	2r	2106	0	2159	308	0
2	2s	2106	0	2162	346	0
2	2t	2106	0	2159	405	0
2	2u	2106	0	2162	348	0
2	2v	2106	0	2162	347	0
2	2w	2106	0	2159	304	0
2	2x	2106	0	2162	346	0
2	3e	2098	0	2153	406	0
2	3f	2106	0	2162	401	0
2	3g	2098	0	2152	650	0
2	3h	2106	0	2160	377	0
2	3i	2098	0	2153	415	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	3j	2106	0	2162	396	0
2	3k	2098	0	2152	659	0
2	3l	2106	0	2160	387	0
2	3m	2098	0	2153	419	0
2	3n	2106	0	2162	403	0
2	3o	2098	0	2152	652	0
2	3p	2106	0	2160	385	0
2	3q	2098	0	2153	421	0
2	3r	2106	0	2162	407	0
2	3s	2098	0	2152	657	0
2	3t	2106	0	2160	369	0
2	3u	2098	0	2153	406	0
2	3v	2106	0	2162	399	0
2	3w	2098	0	2152	659	0
2	3x	2106	0	2160	366	0
2	4e	2106	0	2163	243	0
2	4f	2098	0	2154	181	0
2	4g	2106	0	2163	242	0
2	4h	2098	0	2154	182	0
2	4i	2106	0	2163	241	0
2	4j	2098	0	2154	179	0
2	4k	2106	0	2163	250	0
2	4l	2098	0	2154	177	0
2	4m	2106	0	2163	245	0
2	4n	2098	0	2154	187	0
2	5e	2106	0	2163	324	0
2	5f	2098	0	2154	254	0
2	5g	2106	0	2163	322	0
2	5h	2098	0	2154	264	0
2	5i	2106	0	2162	330	0
2	5j	2098	0	2154	275	0
2	5k	2106	0	2161	342	0
2	5l	2098	0	2154	273	0
2	5m	2106	0	2162	327	0
2	5n	2098	0	2154	264	0
2	6e	2098	0	2151	332	0
2	6f	2106	0	2162	340	0
2	6g	2098	0	2152	499	0
2	6h	2106	0	2163	200	0
2	6i	2098	0	2151	338	0
2	6j	2106	0	2162	341	0
2	6k	2098	0	2152	494	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	6l	2106	0	2163	190	0
2	6m	2098	0	2153	354	0
2	6n	2106	0	2161	348	0
2	6o	2098	0	2152	506	0
2	6p	2106	0	2163	190	0
2	6q	2098	0	2153	370	0
2	6r	2106	0	2162	353	0
2	6s	2098	0	2152	531	0
2	6t	2106	0	2163	186	0
2	6u	2098	0	2151	333	0
2	6v	2106	0	2162	342	0
2	6w	2098	0	2152	527	0
2	6x	2106	0	2163	201	0
2	7Z	2106	0	2162	382	0
2	7a	2106	0	2163	246	0
2	7b	2106	0	2162	150	0
2	7c	2106	0	2162	373	0
2	7d	2106	0	2162	193	0
2	7e	2106	0	2162	374	0
2	7f	2106	0	2161	234	0
2	7g	2106	0	2162	157	0
2	7h	2106	0	2162	366	0
2	7i	2106	0	2162	178	0
2	7j	2106	0	2162	376	0
2	7k	2106	0	2162	240	0
2	7l	2106	0	2162	154	0
2	7m	2106	0	2162	360	0
2	7n	2106	0	2162	190	0
2	7o	2106	0	2162	395	0
2	7p	2106	0	2162	255	0
2	7q	2106	0	2162	139	0
2	7r	2106	0	2162	368	0
2	7s	2106	0	2163	193	0
2	7t	2106	0	2162	387	0
2	7u	2106	0	2163	256	0
2	7v	2106	0	2162	149	0
2	7w	2106	0	2162	373	0
2	7x	2106	0	2162	193	0
2	8e	2098	0	2147	671	0
2	8f	2106	0	2163	162	0
2	8g	2106	0	2162	452	0
2	8h	2098	0	2154	206	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	8i	2106	0	2160	364	0
2	8j	2098	0	2152	374	0
2	8k	2098	0	2148	653	0
2	8l	2106	0	2163	164	0
2	8m	2106	0	2162	475	0
2	8n	2098	0	2154	190	0
2	8o	2106	0	2161	351	0
2	8p	2098	0	2152	377	0
2	8q	2098	0	2149	643	0
2	8r	2106	0	2163	148	0
2	8s	2106	0	2159	482	0
2	8t	2098	0	2154	182	0
2	8u	2106	0	2160	357	0
2	8v	2098	0	2152	381	0
2	8w	2098	0	2149	657	0
2	8x	2106	0	2163	143	0
2	8y	2106	0	2159	473	0
2	8z	2098	0	2154	201	0
2	9F	2106	0	2160	750	0
2	9G	2106	0	2160	748	0
2	9H	2106	0	2160	774	0
2	9I	2106	0	2160	816	0
2	9J	2106	0	2160	774	0
2	9K	2106	0	2160	376	0
2	9L	2098	0	2152	377	0
2	9M	2098	0	2148	675	0
2	9N	2106	0	2163	158	0
2	9O	2106	0	2162	451	0
2	9P	2098	0	2154	203	0
2	9Q	2106	0	2160	369	0
2	9R	2098	0	2152	378	0
All	All	1161605	0	1158735	41996	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 18.

The worst 5 of 41996 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)
1:4d:448:ALA:HB2	2:4n:41:TYR:CD1	1.22	1.69
2:9K:120:ILE:CD1	2:7v:120:ILE:HD13	1.22	1.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2i:120:ILE:HD13	2:1o:120:ILE:CD1	1.20	1.67
1:7D:446:ALA:HB1	2:7Z:41:TYR:CE2	1.17	1.66
1:7C:446:ALA:HB1	2:7a:41:TYR:CE2	1.17	1.65

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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 ⓘ

There are no chain breaks in this entry.

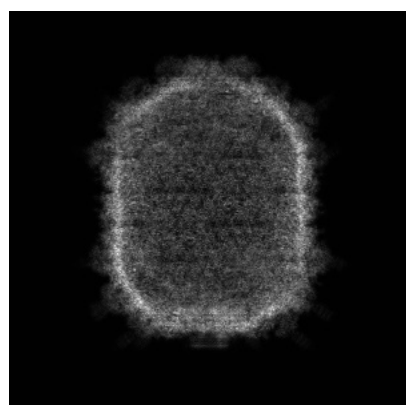
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4655. These allow visual inspection of the internal detail of the map and identification of artifacts.

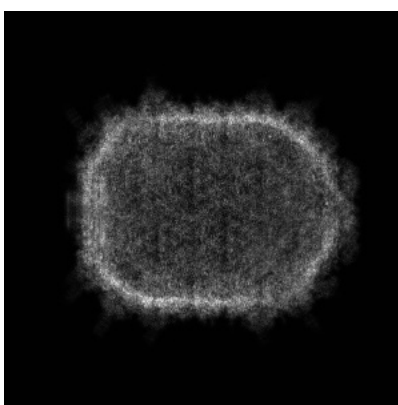
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

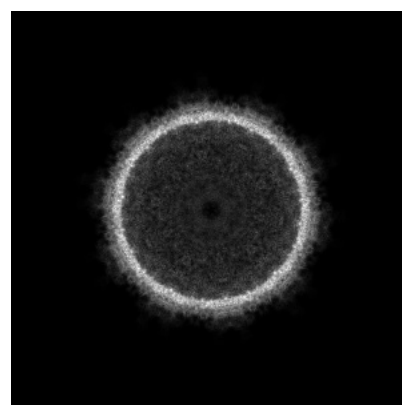
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

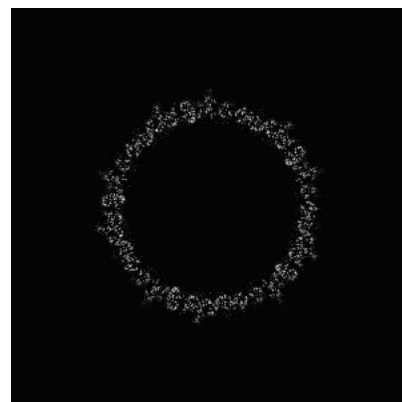
6.2.1 Primary map



X Index: 352



Y Index: 352

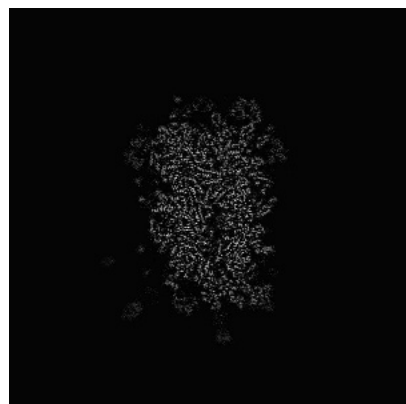


Z Index: 352

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: 511



Y Index: 192

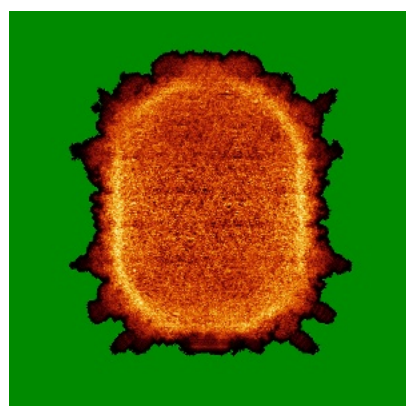


Z Index: 280

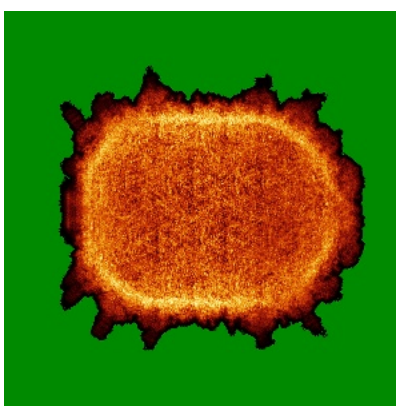
The images above show the largest variance slices of the map in three orthogonal directions.

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

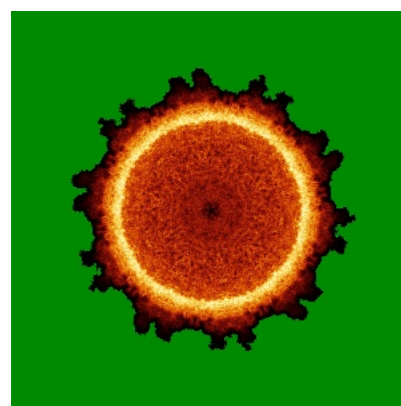
6.4.1 Primary map



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

This section was not generated.

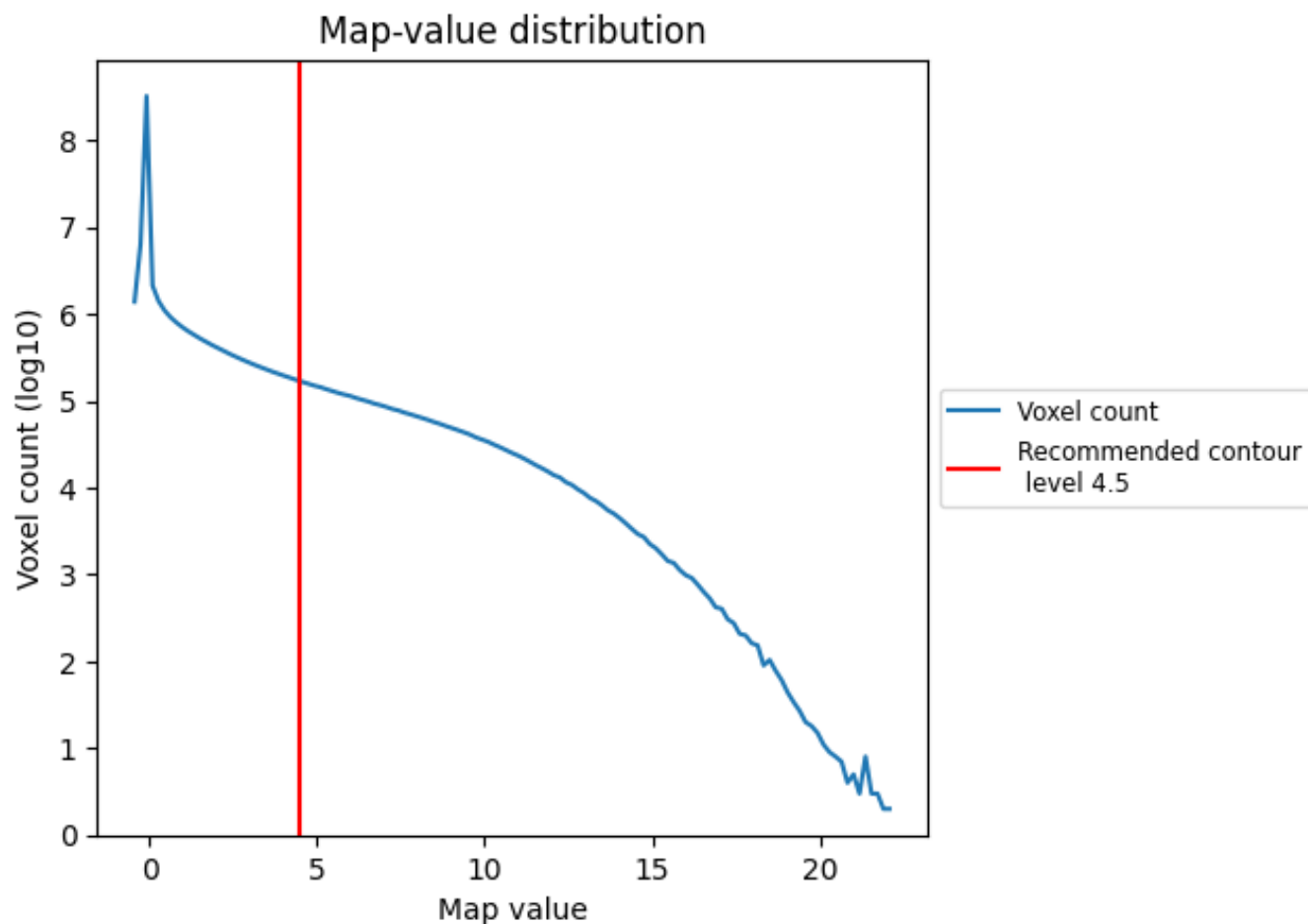
6.6 Mask visualisation

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

7 Map analysis [i](#)

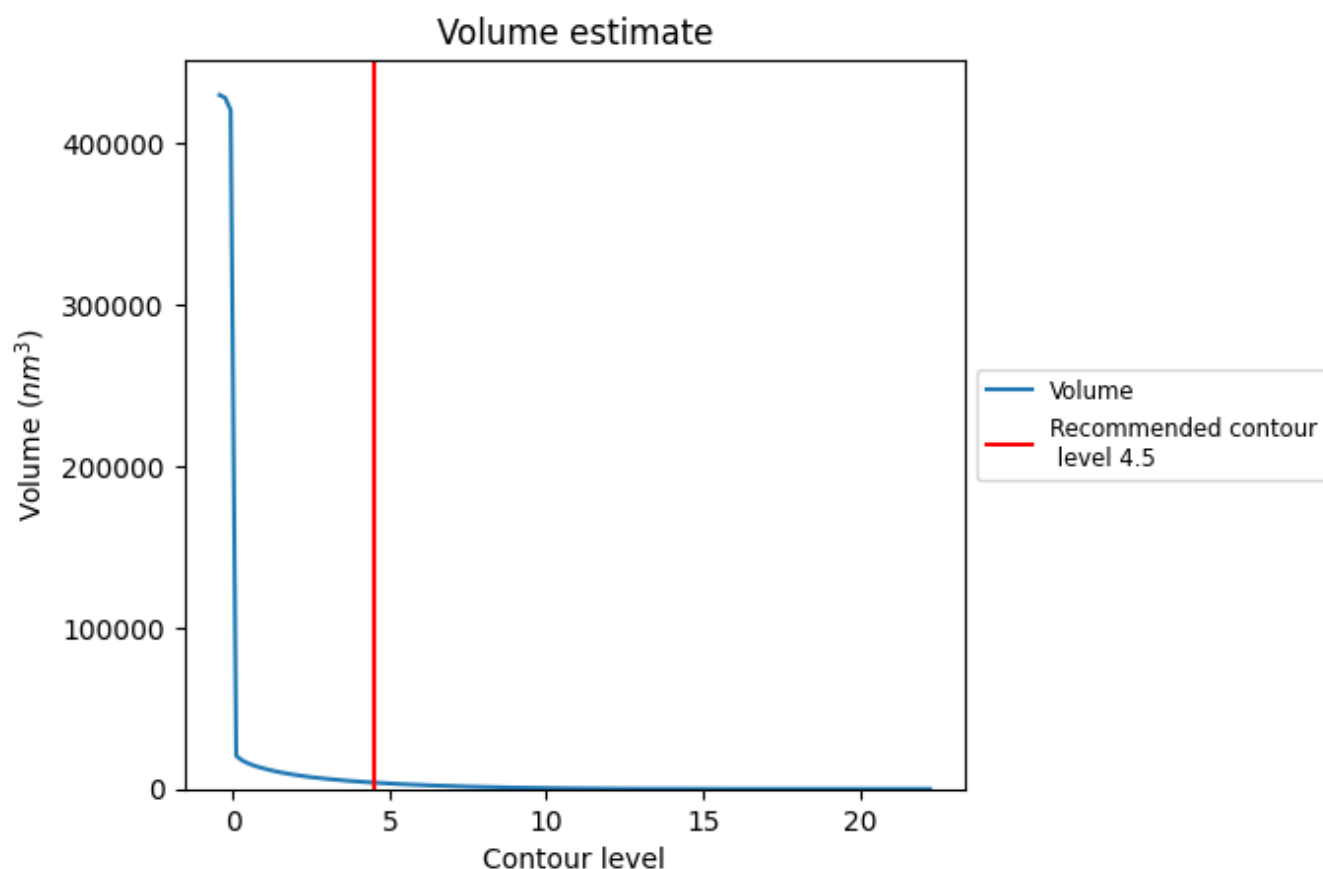
This section contains the results of statistical analysis of the map.

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.

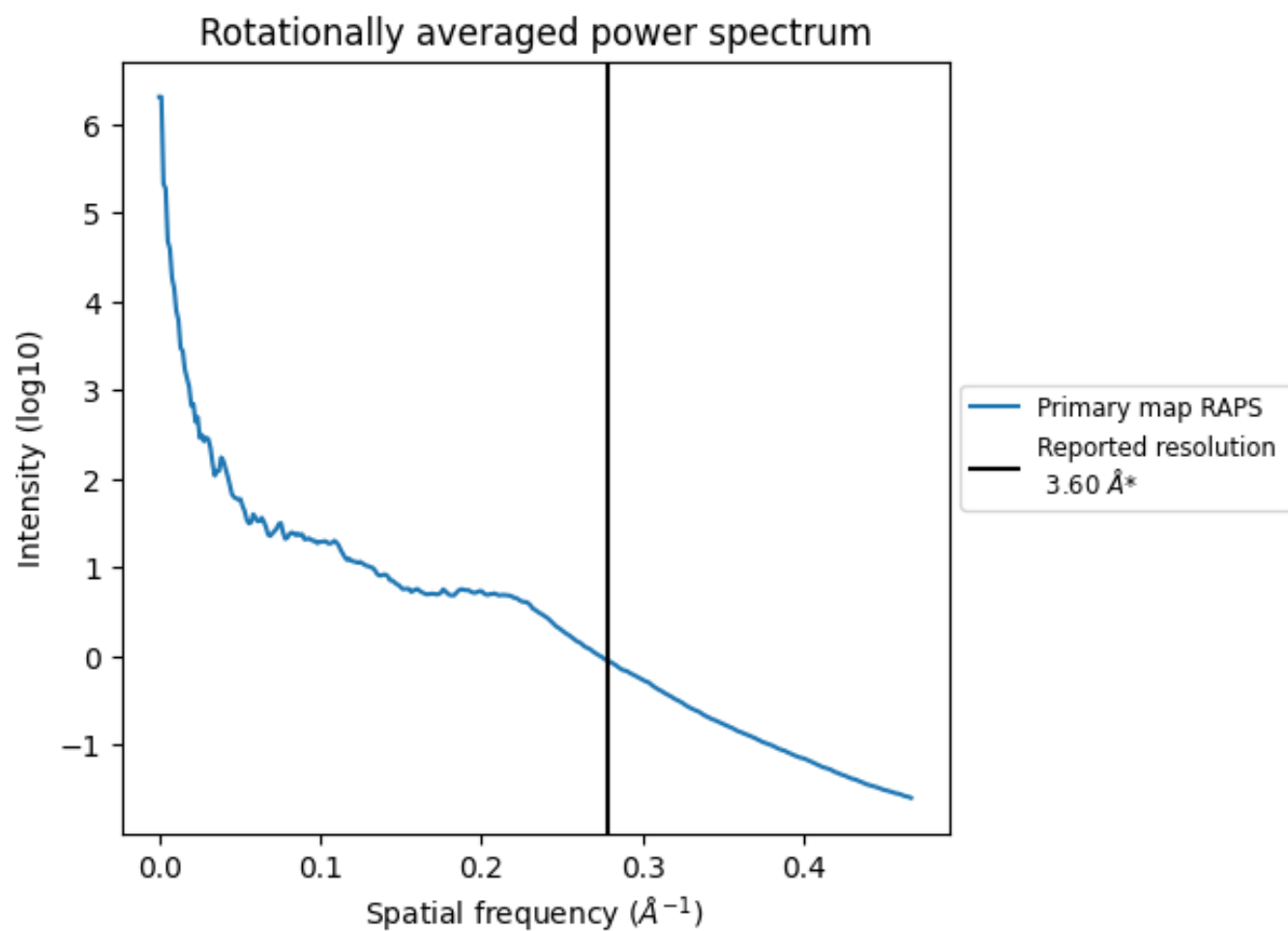
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3930 nm^3 ; this corresponds to an approximate mass of 3550 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 0.278 Å⁻¹

8 Fourier-Shell correlation

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

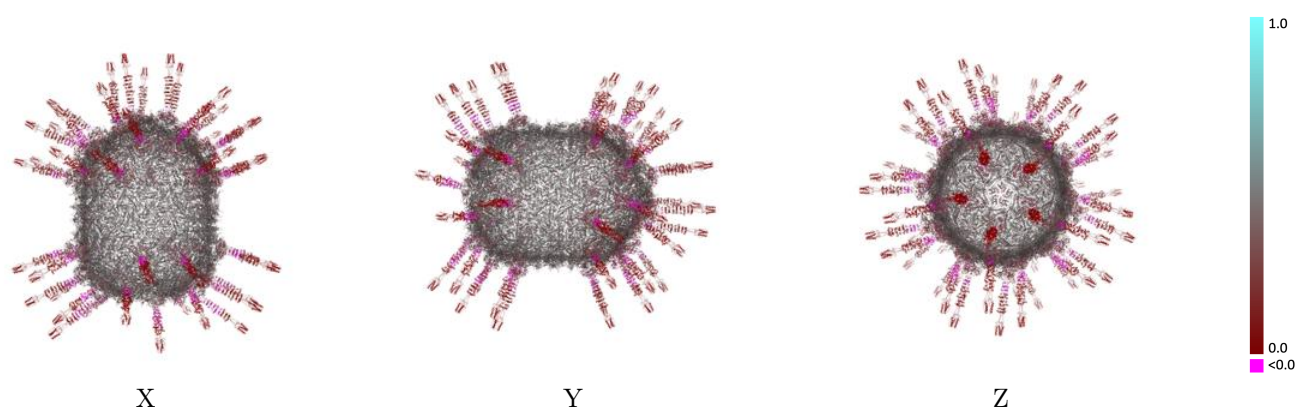
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4655 and PDB model 6QVK. Per-residue inclusion information can be found in section 3 on page 47.

9.1 Map-model overlay [i](#)

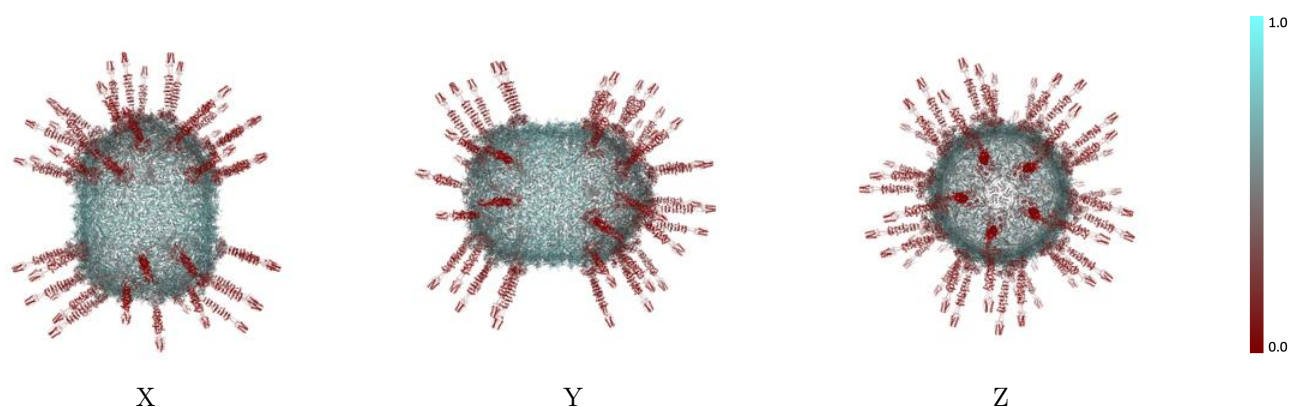
This section was not generated.

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



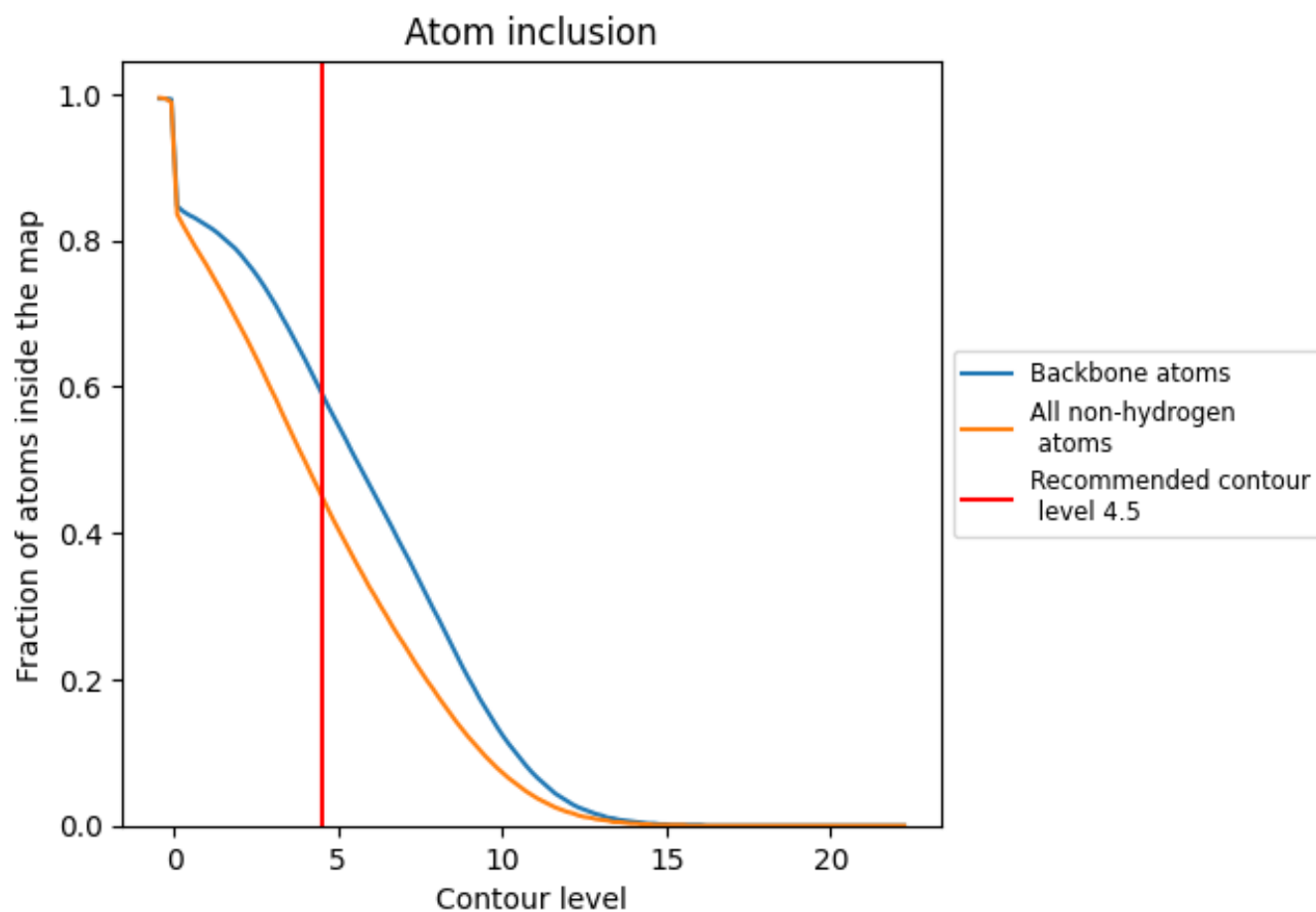
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 45% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4510	 0.3280
1A	 0.5290	 0.4160
1B	 0.6150	 0.4310
1C	 0.6070	 0.4240
1D	 0.6260	 0.4330
1E	 0.6050	 0.4310
1F	 0.5260	 0.4070
1G	 0.5250	 0.4130
1H	 0.6180	 0.4320
1I	 0.6070	 0.4240
1J	 0.6270	 0.4330
1K	 0.6040	 0.4320
1L	 0.5280	 0.4080
1M	 0.5300	 0.4130
1N	 0.6160	 0.4330
1O	 0.6080	 0.4240
1P	 0.6260	 0.4320
1Q	 0.6020	 0.4320
1R	 0.5240	 0.4090
1S	 0.5290	 0.4130
1T	 0.6170	 0.4310
1U	 0.6080	 0.4230
1V	 0.6230	 0.4320
1W	 0.6040	 0.4320
1X	 0.5240	 0.4100
1Y	 0.5300	 0.4130
1Z	 0.6180	 0.4310
1a	 0.6100	 0.4230
1b	 0.6260	 0.4330
1c	 0.6010	 0.4320
1d	 0.5250	 0.4070
1e	 0.1460	 0.1390
1f	 0.0930	 0.1260
1g	 0.1580	 0.1300
1h	 0.1680	 0.1580



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Chain	Atom inclusion	Q-score
1i	 0.1430	 0.1360
1j	 0.0940	 0.1270
1k	 0.1530	 0.1290
1l	 0.1690	 0.1560
1m	 0.1360	 0.1260
1n	 0.0900	 0.1230
1o	 0.1530	 0.1310
1p	 0.1690	 0.1570
1q	 0.1350	 0.1260
1r	 0.0880	 0.1200
1s	 0.1540	 0.1260
1t	 0.1690	 0.1540
1u	 0.1400	 0.1330
1v	 0.0950	 0.1260
1w	 0.1520	 0.1300
1x	 0.1680	 0.1560
2A	 0.6060	 0.4300
2B	 0.6180	 0.4310
2C	 0.5950	 0.4240
2D	 0.5970	 0.4290
2E	 0.5910	 0.4250
2F	 0.6020	 0.4300
2G	 0.6160	 0.4290
2H	 0.5980	 0.4230
2I	 0.5970	 0.4280
2J	 0.5860	 0.4240
2K	 0.6060	 0.4310
2L	 0.6170	 0.4310
2M	 0.5960	 0.4240
2N	 0.6000	 0.4280
2O	 0.5900	 0.4240
2P	 0.6080	 0.4290
2Q	 0.6190	 0.4310
2R	 0.5960	 0.4230
2S	 0.6000	 0.4280
2T	 0.5910	 0.4230
2U	 0.6080	 0.4300
2V	 0.6160	 0.4290
2W	 0.5980	 0.4230
2X	 0.5970	 0.4290
2Y	 0.5910	 0.4230
2Z	 0.1670	 0.1460

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Chain	Atom inclusion	Q-score
2a	 0.1110	 0.1400
2b	 0.1620	 0.1410
2c	 0.0740	 0.1100
2d	 0.1650	 0.1460
2e	 0.1720	 0.1480
2f	 0.1130	 0.1420
2g	 0.1660	 0.1450
2h	 0.0800	 0.1160
2i	 0.1670	 0.1520
2j	 0.1680	 0.1380
2k	 0.1110	 0.1350
2l	 0.1570	 0.1370
2m	 0.0800	 0.1130
2n	 0.1660	 0.1480
2o	 0.1690	 0.1340
2p	 0.1110	 0.1320
2q	 0.1550	 0.1300
2r	 0.0780	 0.1090
2s	 0.1640	 0.1460
2t	 0.1700	 0.1400
2u	 0.1130	 0.1360
2v	 0.1560	 0.1390
2w	 0.0750	 0.1100
2x	 0.1650	 0.1450
3A	 0.6590	 0.4270
3B	 0.6640	 0.4230
3C	 0.6710	 0.4240
3D	 0.6450	 0.4320
3E	 0.6410	 0.4350
3F	 0.6450	 0.4310
3G	 0.6590	 0.4270
3H	 0.6630	 0.4220
3I	 0.6700	 0.4260
3J	 0.6440	 0.4320
3K	 0.6450	 0.4350
3L	 0.6430	 0.4300
3M	 0.6570	 0.4260
3N	 0.6650	 0.4220
3O	 0.6730	 0.4260
3P	 0.6440	 0.4330
3Q	 0.6430	 0.4370
3R	 0.6430	 0.4300

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Chain	Atom inclusion	Q-score
3S	 0.6590	 0.4240
3T	 0.6630	 0.4230
3U	 0.6680	 0.4270
3V	 0.6450	 0.4300
3W	 0.6430	 0.4350
3X	 0.6460	 0.4300
3Y	 0.6610	 0.4260
3Z	 0.6600	 0.4220
3a	 0.6670	 0.4240
3b	 0.6450	 0.4310
3c	 0.6430	 0.4360
3d	 0.6430	 0.4300
3e	 0.1400	 0.1230
3f	 0.0890	 0.1100
3g	 0.1640	 0.1300
3h	 0.0700	 0.1020
3i	 0.1460	 0.1250
3j	 0.0860	 0.1080
3k	 0.1590	 0.1300
3l	 0.0740	 0.1000
3m	 0.1420	 0.1190
3n	 0.0880	 0.1090
3o	 0.1710	 0.1410
3p	 0.0790	 0.1080
3q	 0.1380	 0.1150
3r	 0.0810	 0.1030
3s	 0.1780	 0.1420
3t	 0.0770	 0.1070
3u	 0.1410	 0.1180
3v	 0.0840	 0.1050
3w	 0.1750	 0.1390
3x	 0.0760	 0.1060
4A	 0.6630	 0.4350
4B	 0.6720	 0.4210
4C	 0.6790	 0.4260
4D	 0.6840	 0.4380
4E	 0.6600	 0.4230
4F	 0.6600	 0.4370
4G	 0.6620	 0.4360
4H	 0.6720	 0.4200
4I	 0.6810	 0.4250
4J	 0.6800	 0.4370

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Chain	Atom inclusion	Q-score
4K	 0.6570	 0.4230
4L	 0.6570	 0.4370
4M	 0.6650	 0.4360
4N	 0.6770	 0.4200
4O	 0.6840	 0.4270
4P	 0.6810	 0.4370
4Q	 0.6590	 0.4240
4R	 0.6560	 0.4360
4S	 0.6650	 0.4350
4T	 0.6750	 0.4200
4U	 0.6820	 0.4270
4V	 0.6790	 0.4370
4W	 0.6590	 0.4210
4X	 0.6570	 0.4340
4Y	 0.6640	 0.4350
4Z	 0.6700	 0.4200
4a	 0.6790	 0.4250
4b	 0.6830	 0.4380
4c	 0.6610	 0.4220
4d	 0.6570	 0.4360
4e	 0.1430	 0.1200
4f	 0.0790	 0.1110
4g	 0.1430	 0.1230
4h	 0.0860	 0.1220
4i	 0.1450	 0.1150
4j	 0.0810	 0.1190
4k	 0.1420	 0.1060
4l	 0.0810	 0.1110
4m	 0.1430	 0.1120
4n	 0.0790	 0.1100
5A	 0.6350	 0.4180
5B	 0.6710	 0.4220
5C	 0.6830	 0.4340
5D	 0.6760	 0.4330
5E	 0.6370	 0.4160
5F	 0.6210	 0.4110
5G	 0.6350	 0.4200
5H	 0.6710	 0.4220
5I	 0.6820	 0.4340
5J	 0.6760	 0.4320
5K	 0.6380	 0.4170
5L	 0.6180	 0.4100

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Chain	Atom inclusion	Q-score
5M	 0.6360	 0.4180
5N	 0.6660	 0.4210
5O	 0.6830	 0.4340
5P	 0.6750	 0.4340
5Q	 0.6390	 0.4160
5R	 0.6200	 0.4100
5S	 0.6330	 0.4180
5T	 0.6700	 0.4220
5U	 0.6790	 0.4310
5V	 0.6800	 0.4300
5W	 0.6390	 0.4160
5X	 0.6190	 0.4100
5Y	 0.6360	 0.4170
5Z	 0.6680	 0.4210
5a	 0.6830	 0.4330
5b	 0.6770	 0.4310
5c	 0.6420	 0.4150
5d	 0.6190	 0.4100
5e	 0.0760	 0.1000
5f	 0.0300	 0.0910
5g	 0.0750	 0.1060
5h	 0.0360	 0.0970
5i	 0.0750	 0.0990
5j	 0.0410	 0.1100
5k	 0.0650	 0.0890
5l	 0.0350	 0.1030
5m	 0.0690	 0.0950
5n	 0.0350	 0.0960
6A	 0.5760	 0.4080
6B	 0.5980	 0.4150
6C	 0.6180	 0.4130
6D	 0.6470	 0.4140
6E	 0.6380	 0.4190
6F	 0.6200	 0.4190
6G	 0.5800	 0.4090
6H	 0.5970	 0.4150
6I	 0.6230	 0.4130
6J	 0.6480	 0.4150
6K	 0.6370	 0.4180
6L	 0.6240	 0.4190
6M	 0.5800	 0.4090
6N	 0.6000	 0.4140

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Chain	Atom inclusion	Q-score
6O	 0.6230	 0.4130
6P	 0.6490	 0.4130
6Q	 0.6360	 0.4180
6R	 0.6240	 0.4200
6S	 0.5820	 0.4090
6T	 0.5990	 0.4130
6U	 0.6220	 0.4140
6V	 0.6500	 0.4130
6W	 0.6380	 0.4180
6X	 0.6210	 0.4180
6Y	 0.5800	 0.4080
6Z	 0.6000	 0.4130
6a	 0.6200	 0.4130
6b	 0.6490	 0.4120
6c	 0.6420	 0.4180
6d	 0.6260	 0.4180
6e	 0.0700	 0.0780
6f	 0.0340	 0.0900
6g	 0.0700	 0.0930
6h	 0.0280	 0.0840
6i	 0.0870	 0.0910
6j	 0.0360	 0.1010
6k	 0.0740	 0.1030
6l	 0.0280	 0.0900
6m	 0.0780	 0.0830
6n	 0.0330	 0.0920
6o	 0.0780	 0.1070
6p	 0.0300	 0.0910
6q	 0.0670	 0.0670
6r	 0.0340	 0.0880
6s	 0.0720	 0.0970
6t	 0.0330	 0.0900
6u	 0.0700	 0.0690
6v	 0.0340	 0.0880
6w	 0.0700	 0.0920
6x	 0.0250	 0.0870
7A	 0.5050	 0.3990
7B	 0.5040	 0.4010
7C	 0.5140	 0.4040
7D	 0.5280	 0.4040
7E	 0.5120	 0.3930
7F	 0.5010	 0.4010

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Chain	Atom inclusion	Q-score
7G	 0.5080	 0.4010
7H	 0.5100	 0.4050
7I	 0.5300	 0.4040
7J	 0.5110	 0.3940
7K	 0.5060	 0.4010
7L	 0.5050	 0.4030
7M	 0.5110	 0.4030
7N	 0.5290	 0.4030
7O	 0.5130	 0.3930
7P	 0.5020	 0.3990
7Q	 0.5030	 0.4030
7R	 0.5120	 0.4020
7S	 0.5310	 0.4000
7T	 0.5100	 0.3920
7U	 0.5030	 0.3990
7V	 0.5070	 0.4020
7W	 0.5150	 0.4030
7X	 0.5260	 0.4020
7Y	 0.5170	 0.3930
7Z	 0.0900	 0.1180
7a	 0.0380	 0.0960
7b	 0.0690	 0.0990
7c	 0.0350	 0.0780
7d	 0.0600	 0.0990
7e	 0.0980	 0.1230
7f	 0.0410	 0.0970
7g	 0.0710	 0.1010
7h	 0.0380	 0.0890
7i	 0.0640	 0.1050
7j	 0.0960	 0.1190
7k	 0.0390	 0.1030
7l	 0.0760	 0.1130
7m	 0.0480	 0.1060
7n	 0.0670	 0.1120
7o	 0.0840	 0.1070
7p	 0.0410	 0.1000
7q	 0.0700	 0.1100
7r	 0.0390	 0.0950
7s	 0.0610	 0.1080
7t	 0.0870	 0.1130
7u	 0.0360	 0.0970
7v	 0.0710	 0.1030

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Chain	Atom inclusion	Q-score
7w	 0.0350	 0.0850
7x	 0.0590	 0.1020
8A	 0.5420	 0.4110
8B	 0.5340	 0.4050
8C	 0.5530	 0.4110
8D	 0.5550	 0.4120
8E	 0.5620	 0.4090
8F	 0.5380	 0.4150
8G	 0.5430	 0.4110
8H	 0.5330	 0.4060
8I	 0.5550	 0.4120
8J	 0.5530	 0.4120
8K	 0.5600	 0.4100
8L	 0.5380	 0.4150
8M	 0.5430	 0.4100
8N	 0.5280	 0.4040
8O	 0.5550	 0.4110
8P	 0.5550	 0.4100
8Q	 0.5610	 0.4080
8R	 0.5340	 0.4150
8S	 0.5420	 0.4090
8T	 0.5300	 0.4040
8U	 0.5500	 0.4110
8V	 0.5560	 0.4090
8W	 0.5600	 0.4060
8X	 0.5380	 0.4140
8Y	 0.5410	 0.4090
8Z	 0.5310	 0.4040
8a	 0.5480	 0.4110
8b	 0.5540	 0.4100
8c	 0.5640	 0.4080
8d	 0.5360	 0.4130
8e	 0.0520	 0.1020
8f	 0.0370	 0.0830
8g	 0.0550	 0.1200
8h	 0.0410	 0.0740
8i	 0.0560	 0.0840
8j	 0.0290	 0.0720
8k	 0.0550	 0.0990
8l	 0.0430	 0.0890
8m	 0.0510	 0.1100
8n	 0.0570	 0.0960

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Chain	Atom inclusion	Q-score
8o	 0.0680	 0.1000
8p	 0.0380	 0.0870
8q	 0.0580	 0.0890
8r	 0.0440	 0.1030
8s	 0.0490	 0.0980
8t	 0.0500	 0.0930
8u	 0.0650	 0.0960
8v	 0.0420	 0.1080
8w	 0.0480	 0.0870
8x	 0.0490	 0.1070
8y	 0.0500	 0.0970
8z	 0.0420	 0.0770
9A	 0.4630	 0.4000
9B	 0.4650	 0.3990
9C	 0.4680	 0.4020
9D	 0.4670	 0.4010
9E	 0.4670	 0.3980
9F	 0.0590	 0.1160
9G	 0.0600	 0.1210
9H	 0.0570	 0.1070
9I	 0.0570	 0.0970
9J	 0.0580	 0.1040
9K	 0.0540	 0.0840
9L	 0.0390	 0.1040
9M	 0.0540	 0.0910
9N	 0.0400	 0.0930
9O	 0.0570	 0.1120
9P	 0.0330	 0.0630
9Q	 0.0490	 0.0740
9R	 0.0330	 0.0880