



## Full wwPDB EM Validation Report ⓘ

Mar 2, 2025 – 10:46 PM EST

PDB ID : 9DOG  
EMDB ID : EMD-47083  
Title : Octahedral small virus-like particles of dengue virus type 2 (octahedral reconstruction)  
Authors : Johnson, A.; Dodes Traian, M.; Walsh, R.M.; Jenni, S.; Harrison, S.C.  
Deposited on : 2024-09-19  
Resolution : 6.50 Å(reported)  
Based on initial model : .

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.41.4

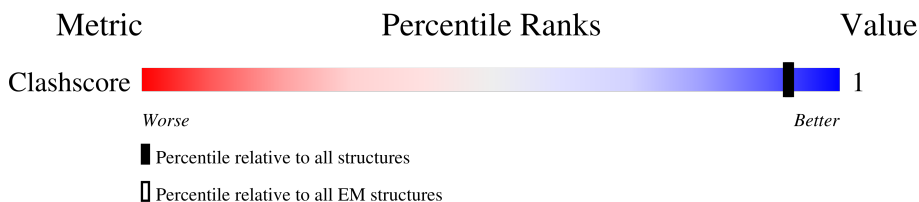
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

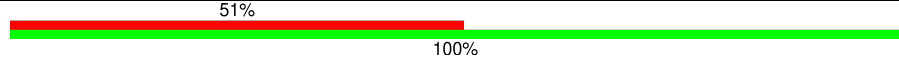
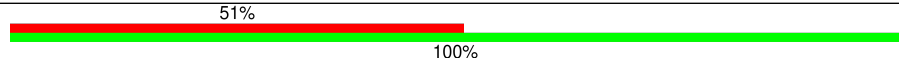
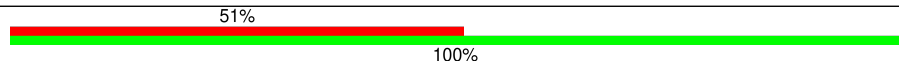
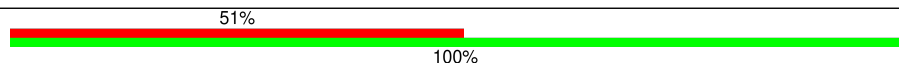
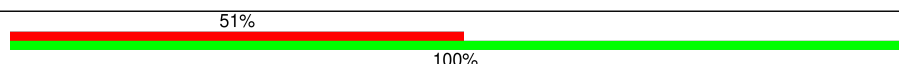
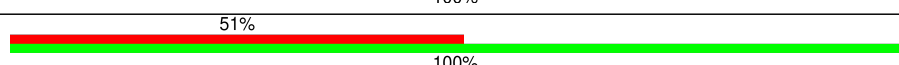
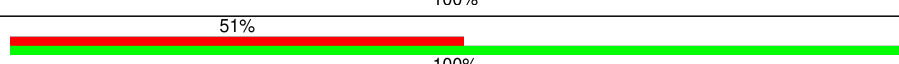
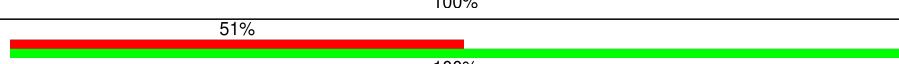
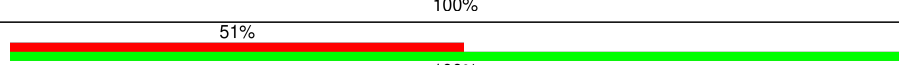
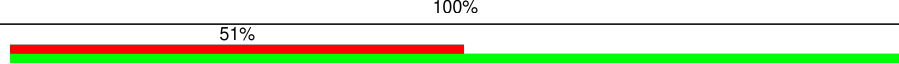
The reported resolution of this entry is 6.50 Å.

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)
Clashscore	210492	15764

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A000	495	 51% 100%
1	A001	495	 51% 100%
1	A002	495	 51% 100%
1	A003	495	 51% 100%
1	A004	495	 51% 100%
1	A005	495	 51% 100%
1	A006	495	 51% 100%
1	A007	495	 51% 100%
1	A008	495	 51% 100%
1	A009	495	 51% 100%

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Mol	Chain	Length	Quality of chain	
1	A010	495	51%	100%
1	A011	495	51%	100%
1	A012	495	51%	100%
1	A013	495	51%	100%
1	A014	495	51%	100%
1	A015	495	51%	100%
1	A016	495	51%	100%
1	A017	495	51%	100%
1	A018	495	51%	100%
1	A019	495	51%	100%
1	A020	495	51%	100%
1	A021	495	51%	100%
1	A022	495	51%	100%
1	A023	495	51%	100%
1	B000	495	60%	100%
1	B001	495	60%	100%
1	B002	495	60%	100%
1	B003	495	60%	100%
1	B004	495	60%	100%
1	B005	495	60%	100%
1	B006	495	60%	100%
1	B007	495	60%	100%
1	B008	495	60%	100%
1	B009	495	60%	100%
1	B010	495	60%	100%

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Mol	Chain	Length	Quality of chain	
1	B011	495	60%	100%
1	B012	495	60%	100%
1	B013	495	60%	100%
1	B014	495	60%	100%
1	B015	495	60%	100%
1	B016	495	60%	100%
1	B017	495	60%	100%
1	B018	495	60%	100%
1	B019	495	60%	100%
1	B020	495	60%	100%
1	B021	495	60%	100%
1	B022	495	60%	100%
1	B023	495	60%	100%
1	C000	495	52%	100%
1	C001	495	52%	100%
1	C002	495	52%	100%
1	C003	495	52%	100%
1	C004	495	52%	100%
1	C005	495	52%	100%
1	C006	495	52%	100%
1	C007	495	52%	100%
1	C008	495	52%	100%
1	C009	495	52%	100%
1	C010	495	52%	100%
1	C011	495	52%	100%

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Mol	Chain	Length	Quality of chain
1	C012	495	52% 100%
1	C013	495	52% 100%
1	C014	495	52% 100%
1	C015	495	52% 100%
1	C016	495	52% 100%
1	C017	495	52% 100%
1	C018	495	52% 100%
1	C019	495	52% 100%
1	C020	495	52% 100%
1	C021	495	52% 100%
1	C022	495	52% 100%
1	C023	495	52% 100%
2	D000	166	80% 100%
2	D001	166	80% 100%
2	D002	166	80% 100%
2	D003	166	80% 100%
2	D004	166	80% 100%
2	D005	166	80% 100%
2	D006	166	80% 100%
2	D007	166	80% 100%
2	D008	166	80% 100%
2	D009	166	80% 100%
2	D010	166	80% 100%
2	D011	166	80% 100%
2	D012	166	80% 100%

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Mol	Chain	Length	Quality of chain
2	D013	166	80%  100%
2	D014	166	80%  100%
2	D015	166	80%  100%
2	D016	166	80%  100%
2	D017	166	80%  100%
2	D018	166	80%  100%
2	D019	166	80%  100%
2	D020	166	80%  100%
2	D021	166	80%  100%
2	D022	166	80%  100%
2	D023	166	80%  100%
2	E000	166	84%  100%
2	E001	166	84%  100%
2	E002	166	84%  100%
2	E003	166	84%  100%
2	E004	166	84%  100%
2	E005	166	84%  100%
2	E006	166	84%  100%
2	E007	166	84%  100%
2	E008	166	84%  100%
2	E009	166	84%  100%
2	E010	166	84%  100%
2	E011	166	84%  100%
2	E012	166	84%  100%
2	E013	166	84%  100%

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Mol	Chain	Length	Quality of chain
2	E014	166	<p>84% 100%</p>
2	E015	166	<p>84% 100%</p>
2	E016	166	<p>84% 100%</p>
2	E017	166	<p>84% 100%</p>
2	E018	166	<p>84% 100%</p>
2	E019	166	<p>84% 100%</p>
2	E020	166	<p>84% 100%</p>
2	E021	166	<p>84% 100%</p>
2	E022	166	<p>84% 100%</p>
2	E023	166	<p>84% 100%</p>
2	F000	166	<p>84% 100%</p>
2	F001	166	<p>84% 100%</p>
2	F002	166	<p>84% 100%</p>
2	F003	166	<p>84% 100%</p>
2	F004	166	<p>84% 100%</p>
2	F005	166	<p>84% 100%</p>
2	F006	166	<p>84% 100%</p>
2	F007	166	<p>84% 100%</p>
2	F008	166	<p>84% 100%</p>
2	F009	166	<p>84% 100%</p>
2	F010	166	<p>84% 100%</p>
2	F011	166	<p>84% 100%</p>
2	F012	166	<p>84% 100%</p>
2	F013	166	<p>84% 100%</p>
2	F014	166	<p>84% 100%</p>

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Mol	Chain	Length	Quality of chain
2	F015	166	<p>84% 100%</p>
2	F016	166	<p>84% 100%</p>
2	F017	166	<p>84% 100%</p>
2	F018	166	<p>84% 100%</p>
2	F019	166	<p>84% 100%</p>
2	F020	166	<p>84% 100%</p>
2	F021	166	<p>84% 100%</p>
2	F022	166	<p>84% 100%</p>
2	F023	166	<p>84% 100%</p>



## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 47592 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 glycoprotein E.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A000	495	Total C 495 495	0	495
1	C004	495	Total C 495 495	0	495
1	A005	495	Total C 495 495	0	495
1	B005	495	Total C 495 495	0	495
1	C005	495	Total C 495 495	0	495
1	A006	495	Total C 495 495	0	495
1	B006	495	Total C 495 495	0	495
1	C006	495	Total C 495 495	0	495
1	A007	495	Total C 495 495	0	495
1	B007	495	Total C 495 495	0	495
1	C007	495	Total C 495 495	0	495
1	A008	495	Total C 495 495	0	495
1	B008	495	Total C 495 495	0	495
1	C008	495	Total C 495 495	0	495
1	B000	495	Total C 495 495	0	495
1	A009	495	Total C 495 495	0	495
1	B009	495	Total C 495 495	0	495

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Mol	Chain	Residues	Atoms	AltConf	Trace
1	C009	495	Total C 495 495	0	495
1	A010	495	Total C 495 495	0	495
1	B010	495	Total C 495 495	0	495
1	C010	495	Total C 495 495	0	495
1	A011	495	Total C 495 495	0	495
1	B011	495	Total C 495 495	0	495
1	C011	495	Total C 495 495	0	495
1	A012	495	Total C 495 495	0	495
1	B012	495	Total C 495 495	0	495
1	C012	495	Total C 495 495	0	495
1	C000	495	Total C 495 495	0	495
1	A013	495	Total C 495 495	0	495
1	B013	495	Total C 495 495	0	495
1	C013	495	Total C 495 495	0	495
1	A014	495	Total C 495 495	0	495
1	B014	495	Total C 495 495	0	495
1	C014	495	Total C 495 495	0	495
1	A015	495	Total C 495 495	0	495
1	B015	495	Total C 495 495	0	495
1	C015	495	Total C 495 495	0	495
1	A016	495	Total C 495 495	0	495

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Mol	Chain	Residues	Atoms	AltConf	Trace
1	B016	495	Total C 495 495	0	495
1	C016	495	Total C 495 495	0	495
1	A017	495	Total C 495 495	0	495
1	B017	495	Total C 495 495	0	495
1	C017	495	Total C 495 495	0	495
1	A018	495	Total C 495 495	0	495
1	B018	495	Total C 495 495	0	495
1	C018	495	Total C 495 495	0	495
1	A019	495	Total C 495 495	0	495
1	B019	495	Total C 495 495	0	495
1	C019	495	Total C 495 495	0	495
1	A020	495	Total C 495 495	0	495
1	B020	495	Total C 495 495	0	495
1	C020	495	Total C 495 495	0	495
1	A021	495	Total C 495 495	0	495
1	B021	495	Total C 495 495	0	495
1	C021	495	Total C 495 495	0	495
1	A022	495	Total C 495 495	0	495
1	B022	495	Total C 495 495	0	495
1	C022	495	Total C 495 495	0	495
1	A023	495	Total C 495 495	0	495

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Mol	Chain	Residues	Atoms	AltConf	Trace
1	B023	495	Total C 495 495	0	495
1	C023	495	Total C 495 495	0	495
1	A001	495	Total C 495 495	0	495
1	B001	495	Total C 495 495	0	495
1	C001	495	Total C 495 495	0	495
1	A002	495	Total C 495 495	0	495
1	B002	495	Total C 495 495	0	495
1	C002	495	Total C 495 495	0	495
1	A003	495	Total C 495 495	0	495
1	B003	495	Total C 495 495	0	495
1	C003	495	Total C 495 495	0	495
1	A004	495	Total C 495 495	0	495
1	B004	495	Total C 495 495	0	495

- Molecule 2 is a protein called Protein prM.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D004	166	Total C 166 166	0	166
2	E004	166	Total C 166 166	0	166
2	F004	166	Total C 166 166	0	166
2	D005	166	Total C 166 166	0	166
2	E005	166	Total C 166 166	0	166
2	F005	166	Total C 166 166	0	166

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Mol	Chain	Residues	Atoms		AltConf	Trace
2	D006	166	Total 166	C 166	0	166
2	E006	166	Total 166	C 166	0	166
2	F006	166	Total 166	C 166	0	166
2	D007	166	Total 166	C 166	0	166
2	E007	166	Total 166	C 166	0	166
2	F007	166	Total 166	C 166	0	166
2	D008	166	Total 166	C 166	0	166
2	E008	166	Total 166	C 166	0	166
2	F008	166	Total 166	C 166	0	166
2	D009	166	Total 166	C 166	0	166
2	E009	166	Total 166	C 166	0	166
2	F009	166	Total 166	C 166	0	166
2	D010	166	Total 166	C 166	0	166
2	E010	166	Total 166	C 166	0	166
2	F010	166	Total 166	C 166	0	166
2	D011	166	Total 166	C 166	0	166
2	E011	166	Total 166	C 166	0	166
2	F011	166	Total 166	C 166	0	166
2	D012	166	Total 166	C 166	0	166
2	E012	166	Total 166	C 166	0	166
2	F012	166	Total 166	C 166	0	166

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Mol	Chain	Residues	Atoms		AltConf	Trace
2	D013	166	Total 166	C 166	0	166
2	E013	166	Total 166	C 166	0	166
2	F013	166	Total 166	C 166	0	166
2	D014	166	Total 166	C 166	0	166
2	E014	166	Total 166	C 166	0	166
2	F014	166	Total 166	C 166	0	166
2	D015	166	Total 166	C 166	0	166
2	E015	166	Total 166	C 166	0	166
2	F015	166	Total 166	C 166	0	166
2	D016	166	Total 166	C 166	0	166
2	E016	166	Total 166	C 166	0	166
2	F016	166	Total 166	C 166	0	166
2	D000	166	Total 166	C 166	0	166
2	D017	166	Total 166	C 166	0	166
2	E017	166	Total 166	C 166	0	166
2	F017	166	Total 166	C 166	0	166
2	D018	166	Total 166	C 166	0	166
2	E018	166	Total 166	C 166	0	166
2	F018	166	Total 166	C 166	0	166
2	D019	166	Total 166	C 166	0	166
2	E019	166	Total 166	C 166	0	166

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Mol	Chain	Residues	Atoms		AltConf	Trace
2	F019	166	Total 166	C 166	0	166
2	D020	166	Total 166	C 166	0	166
2	E020	166	Total 166	C 166	0	166
2	F020	166	Total 166	C 166	0	166
2	D021	166	Total 166	C 166	0	166
2	E000	166	Total 166	C 166	0	166
2	E021	166	Total 166	C 166	0	166
2	F021	166	Total 166	C 166	0	166
2	D022	166	Total 166	C 166	0	166
2	E022	166	Total 166	C 166	0	166
2	F022	166	Total 166	C 166	0	166
2	D023	166	Total 166	C 166	0	166
2	E023	166	Total 166	C 166	0	166
2	F023	166	Total 166	C 166	0	166
2	F000	166	Total 166	C 166	0	166
2	D001	166	Total 166	C 166	0	166
2	E001	166	Total 166	C 166	0	166
2	F001	166	Total 166	C 166	0	166
2	D002	166	Total 166	C 166	0	166
2	E002	166	Total 166	C 166	0	166
2	F002	166	Total 166	C 166	0	166

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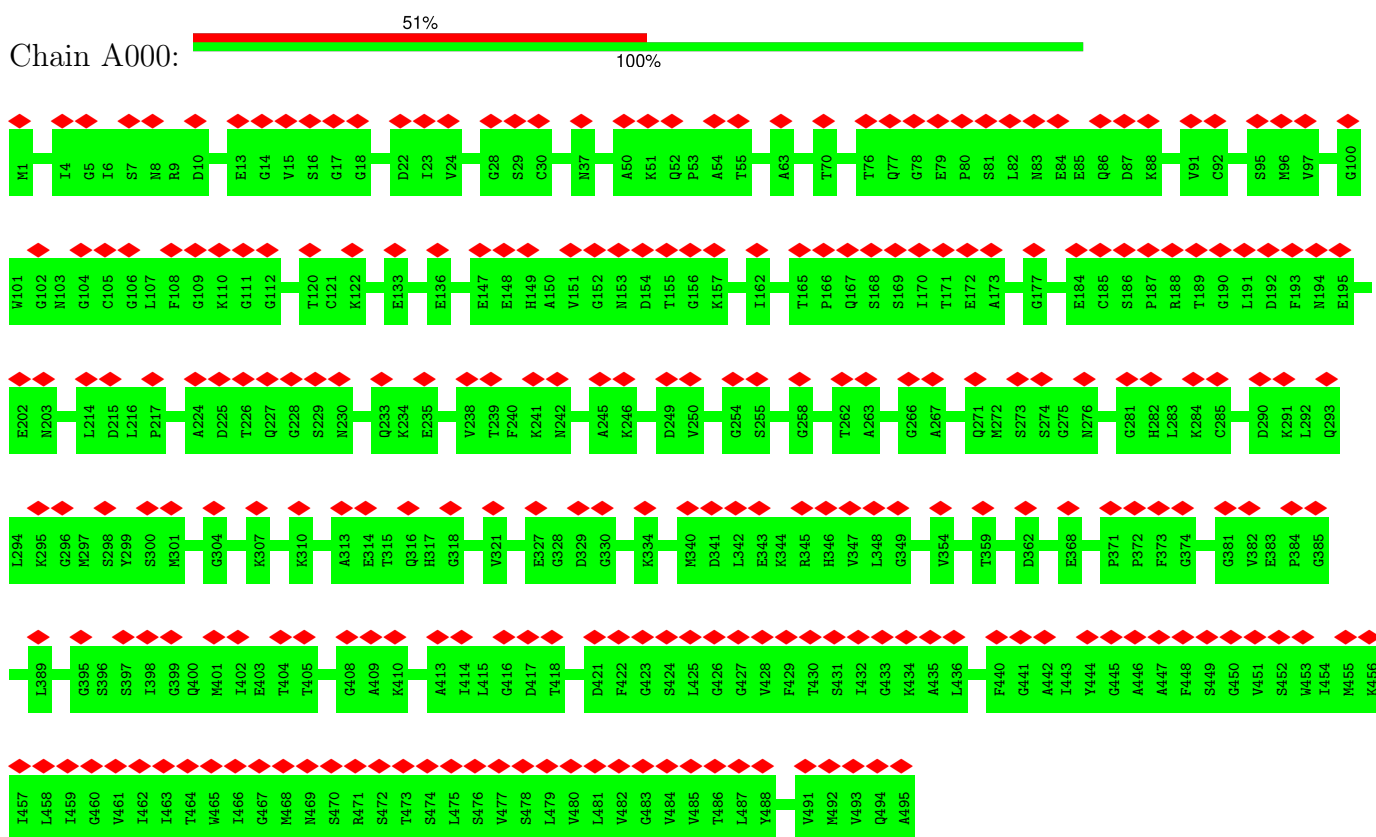
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>	<b>Trace</b>
2	D003	166	Total 166	C 166	0	166
2	E003	166	Total 166	C 166	0	166
2	F003	166	Total 166	C 166	0	166



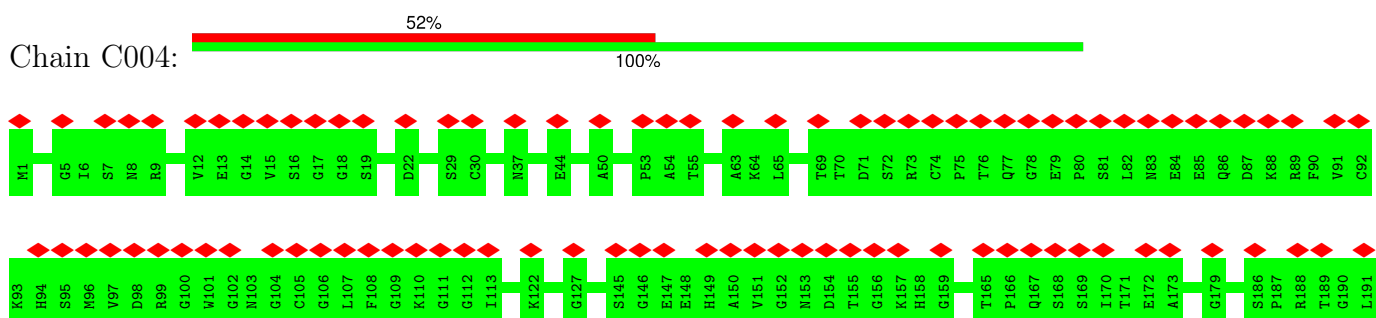
### 3 Residue-property plots [i](#)

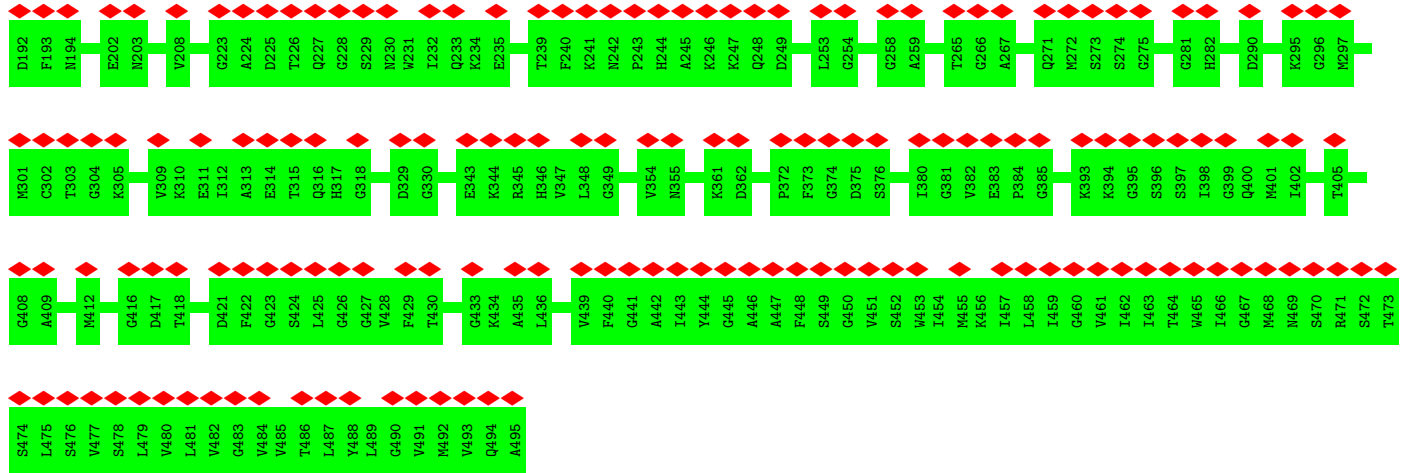
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



- Molecule 1: glycoprotein E

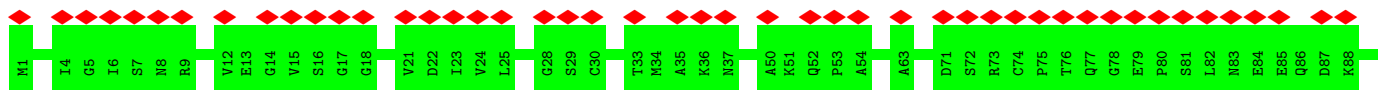


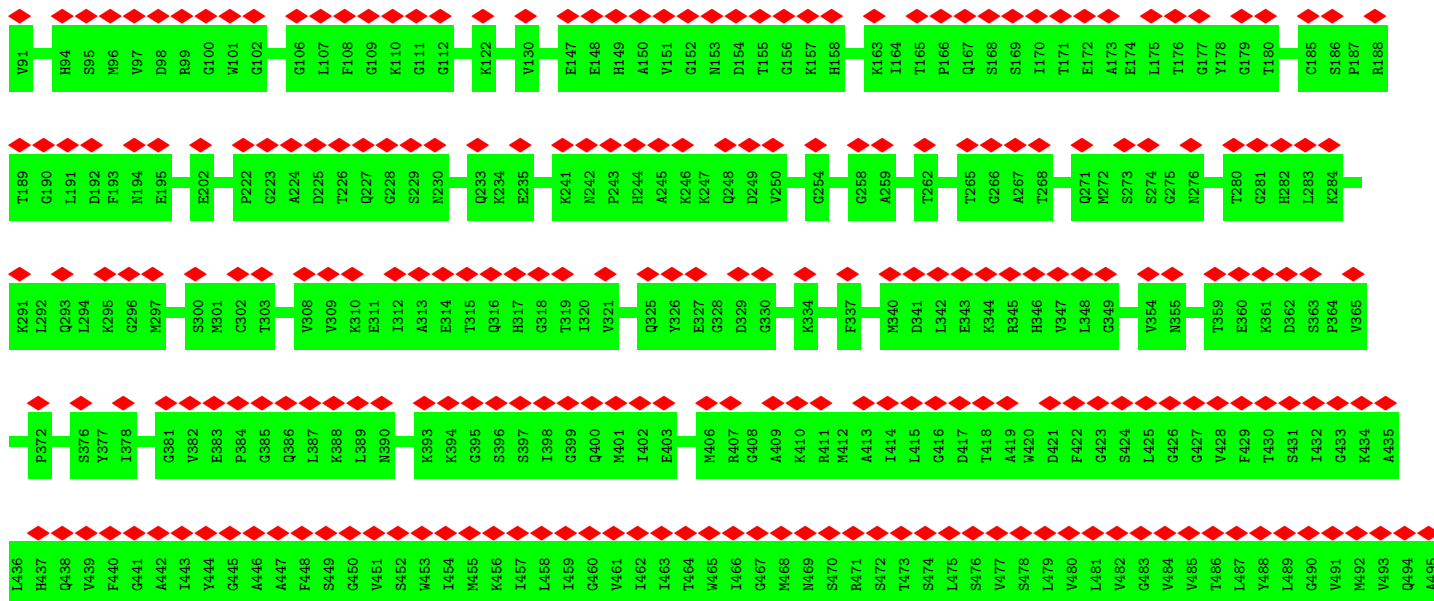


● Molecule 1: glycoprotein E



● Molecule 1: glycoprotein E



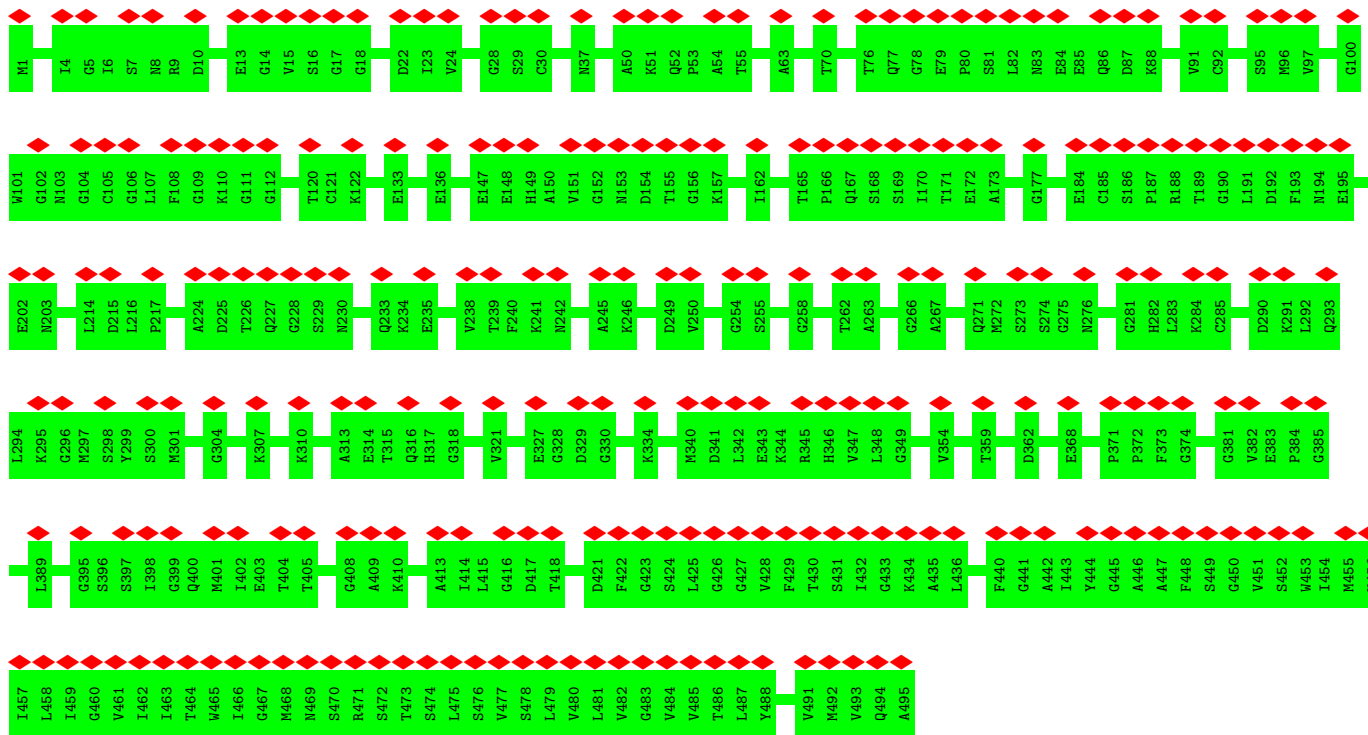


• Molecule 1: glycoprotein E

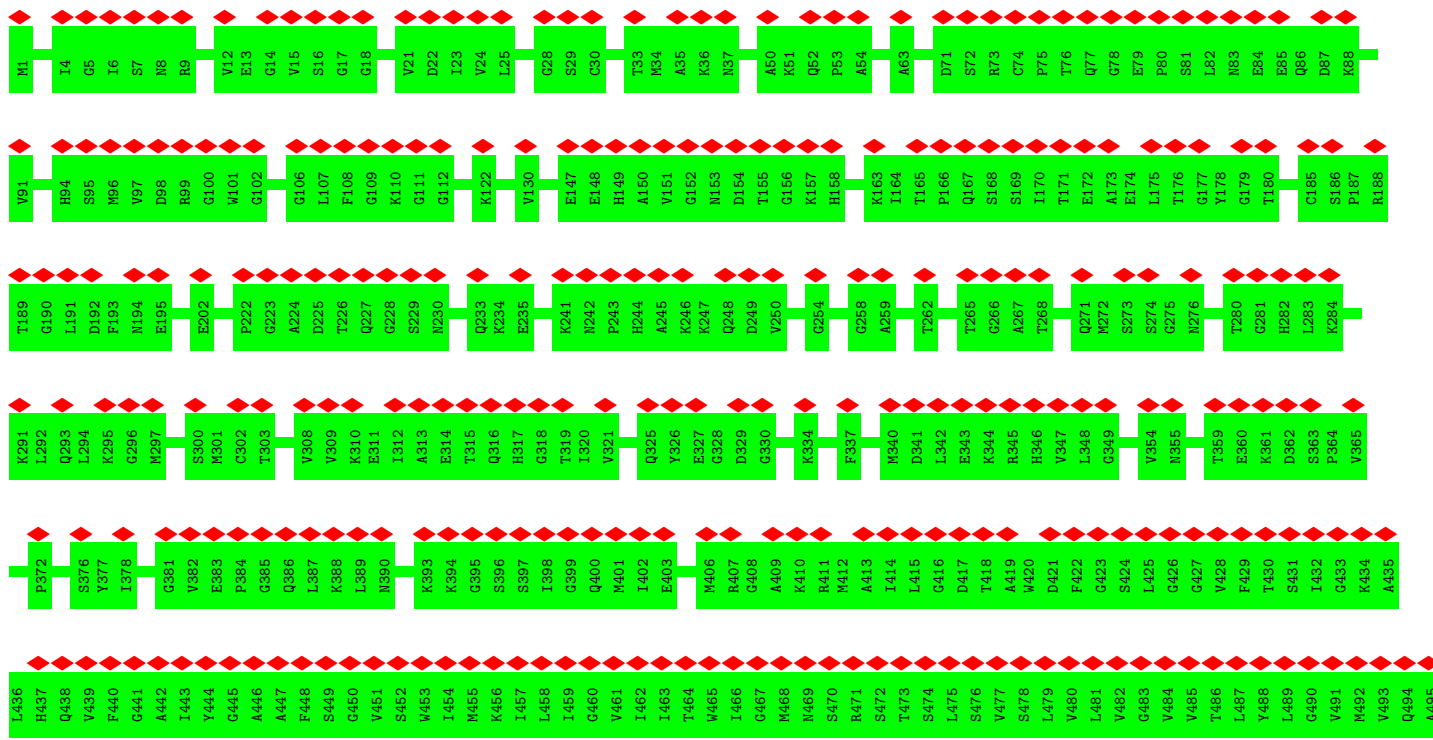


• Molecule 1: glycoprotein E

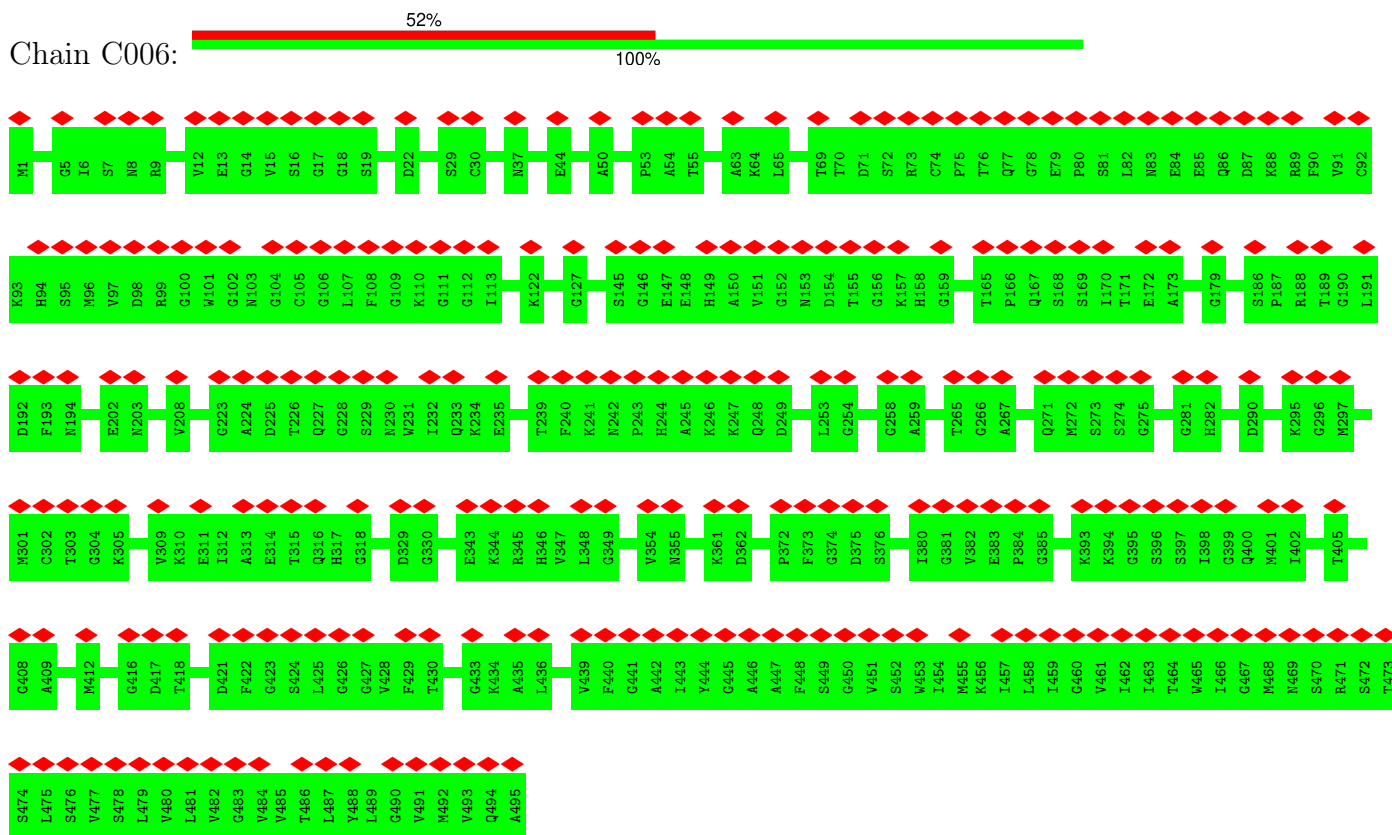




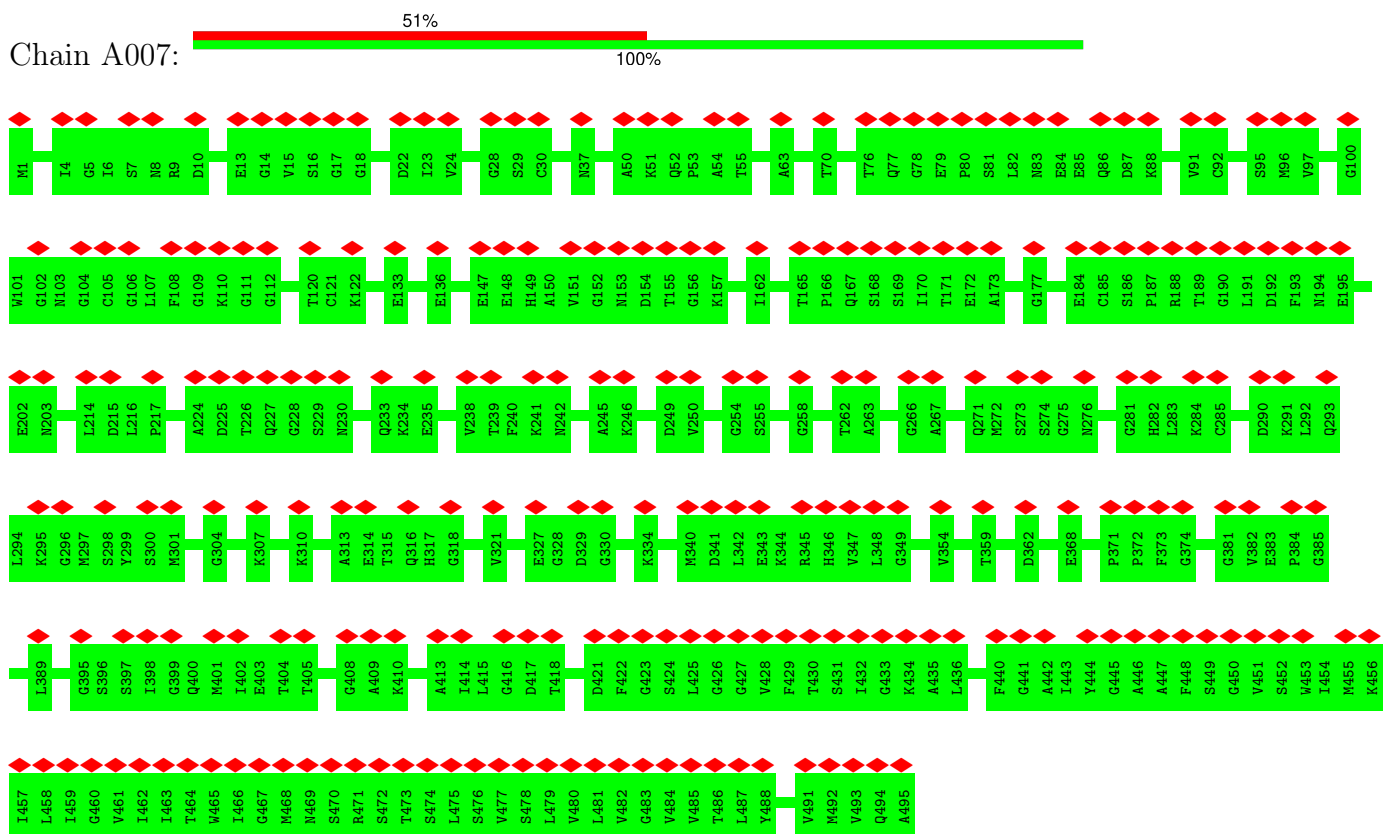
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



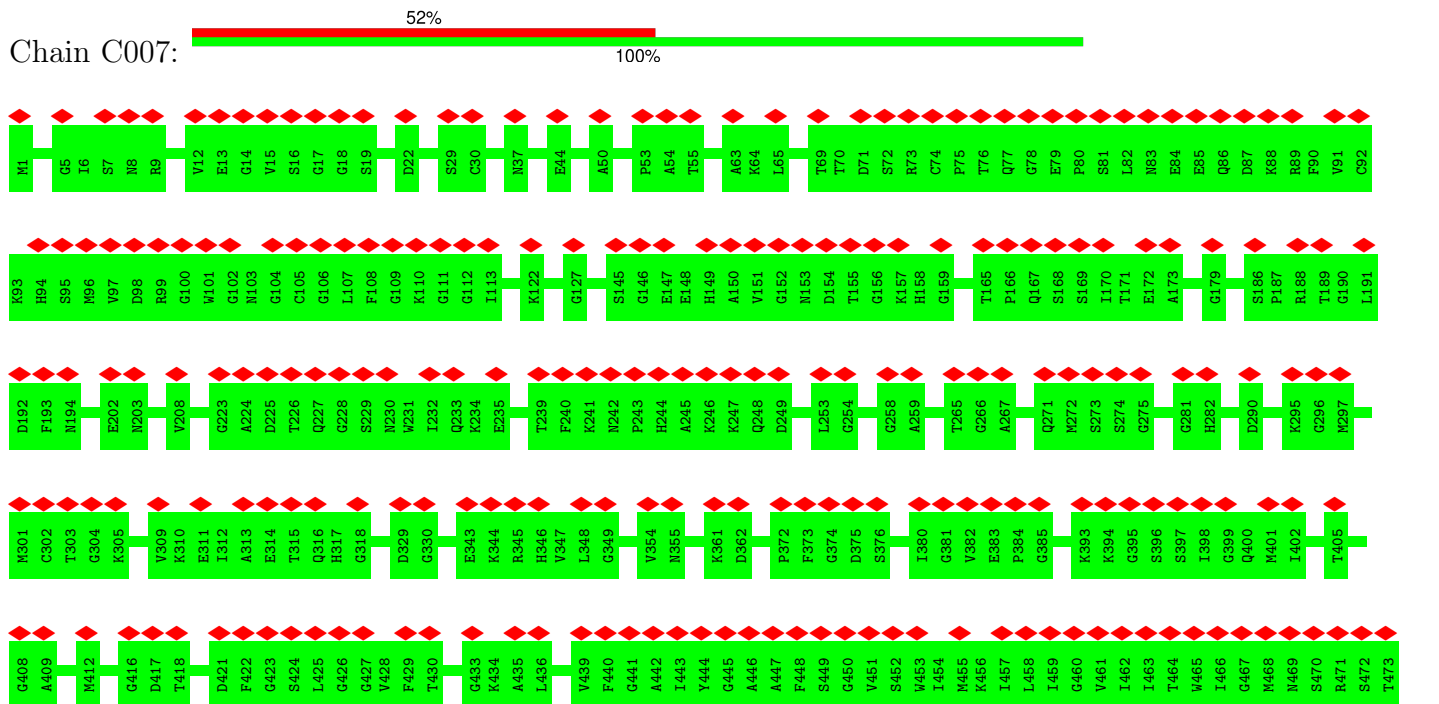
• Molecule 1: glycoprotein E

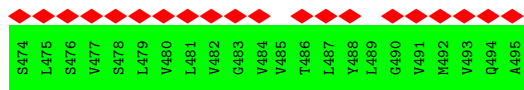


• Molecule 1: glycoprotein E

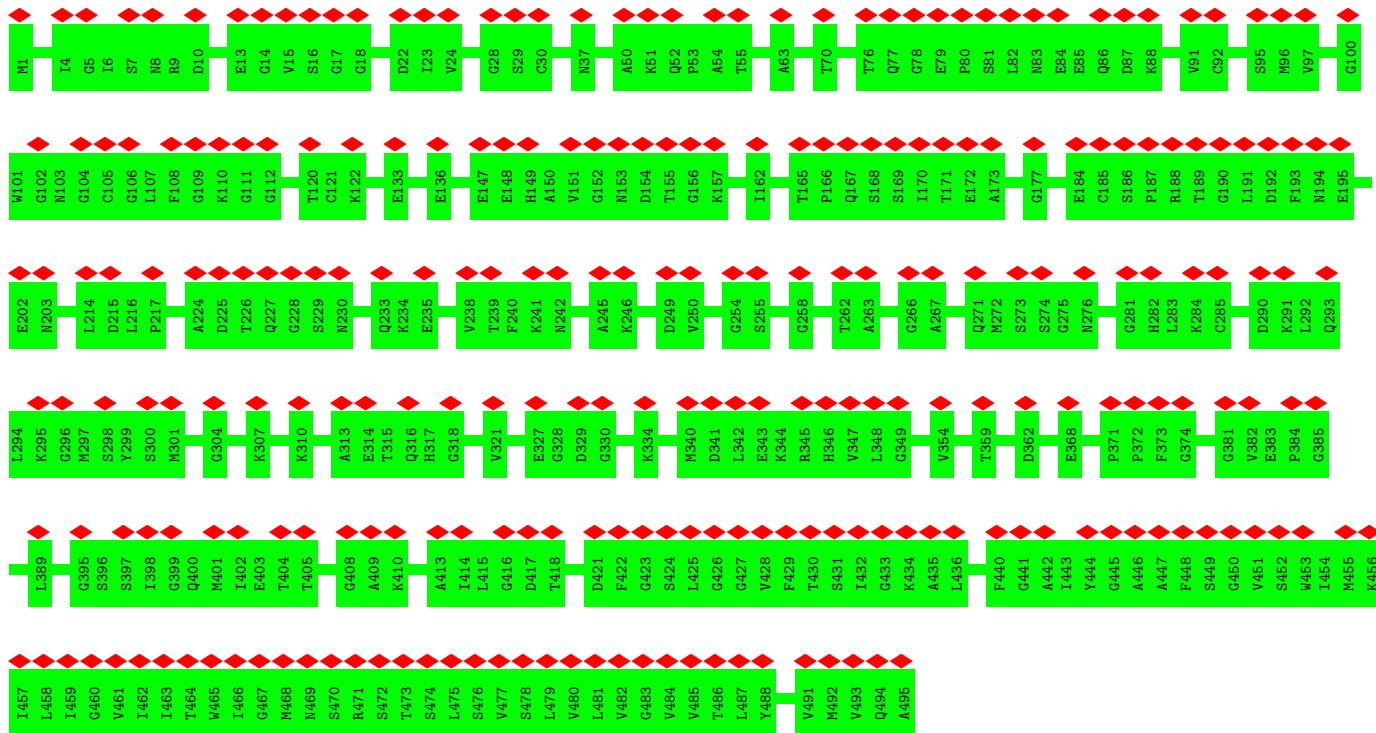


• Molecule 1: glycoprotein E

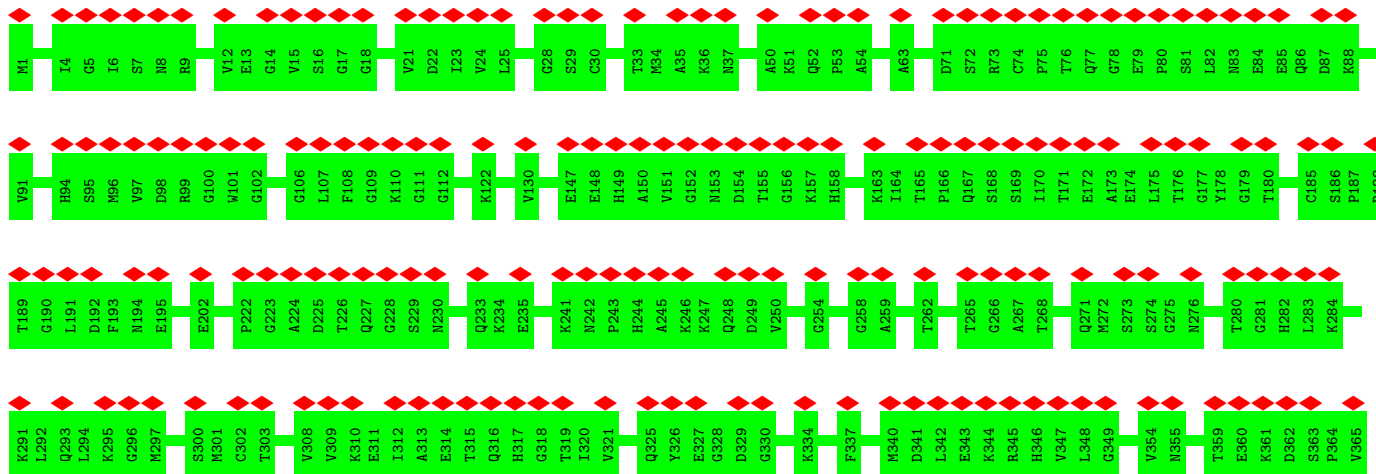


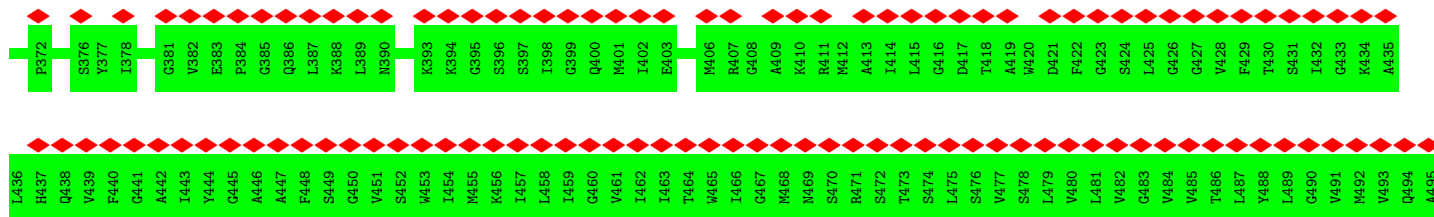


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

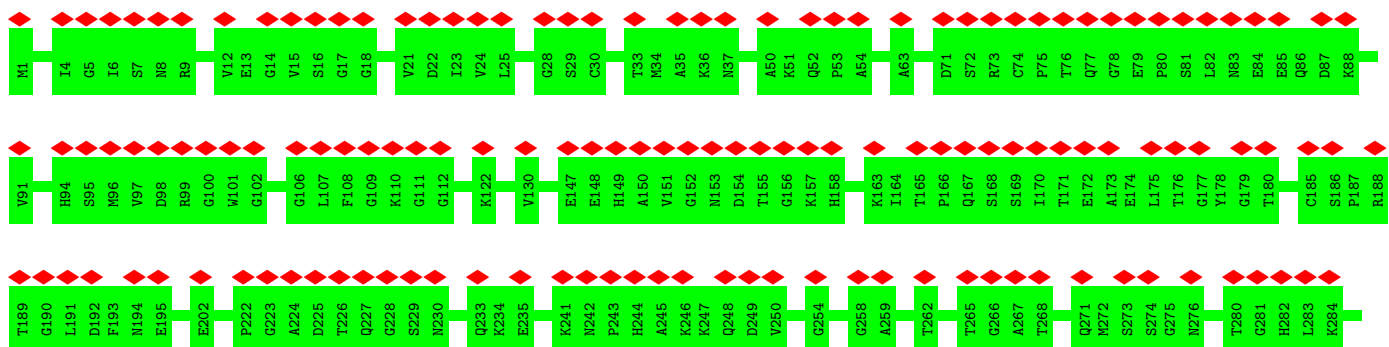




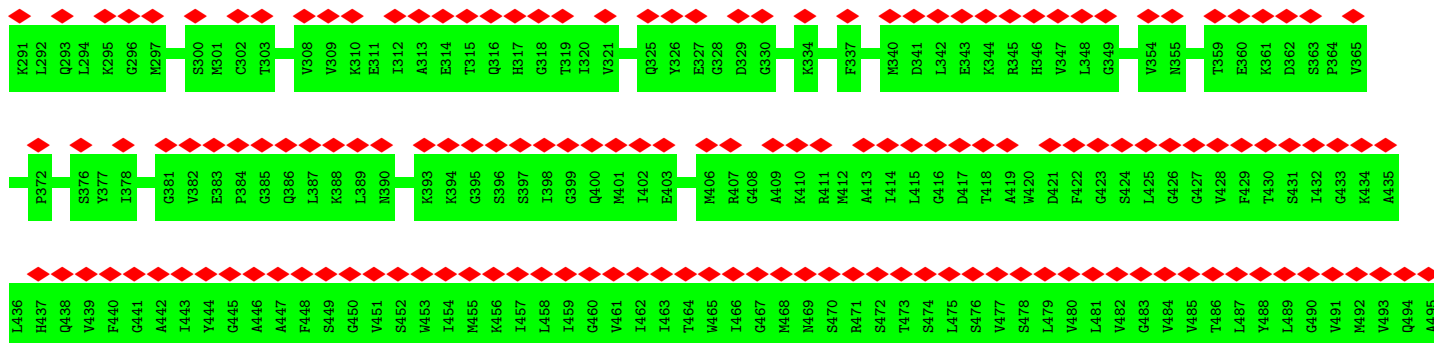
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



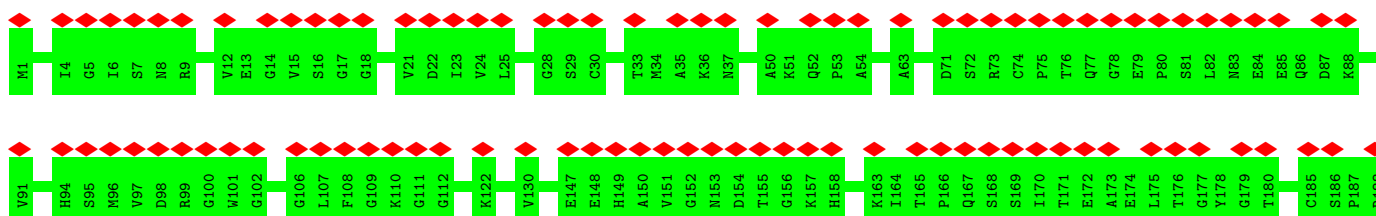


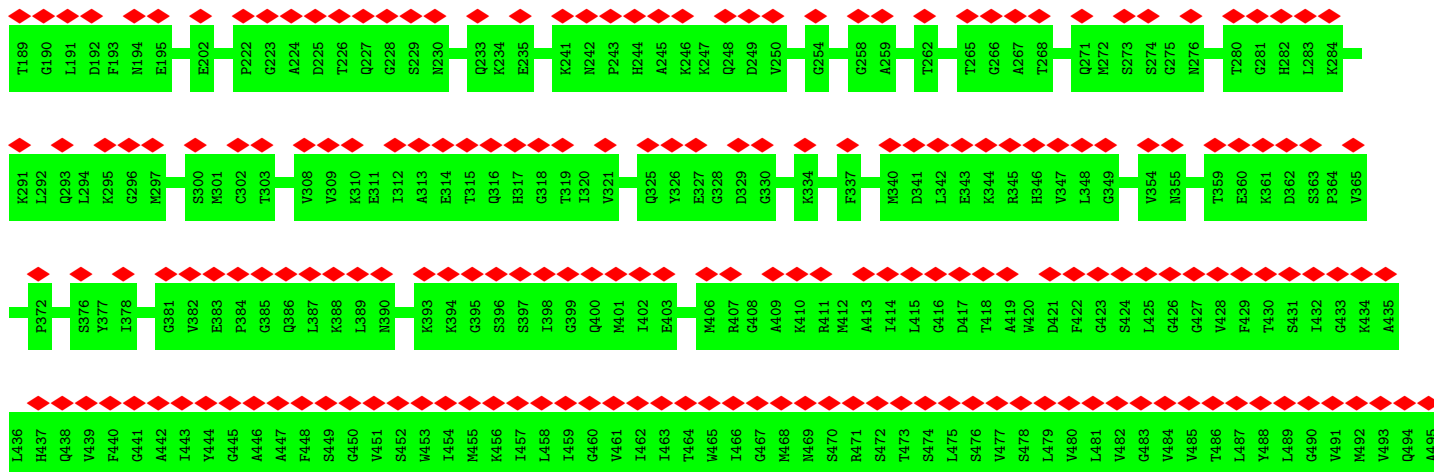


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

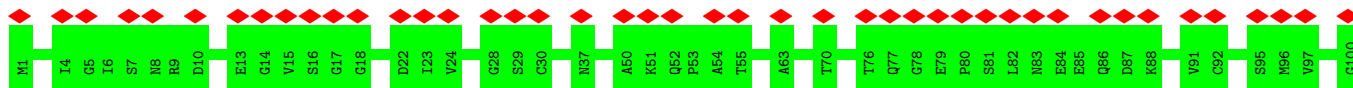


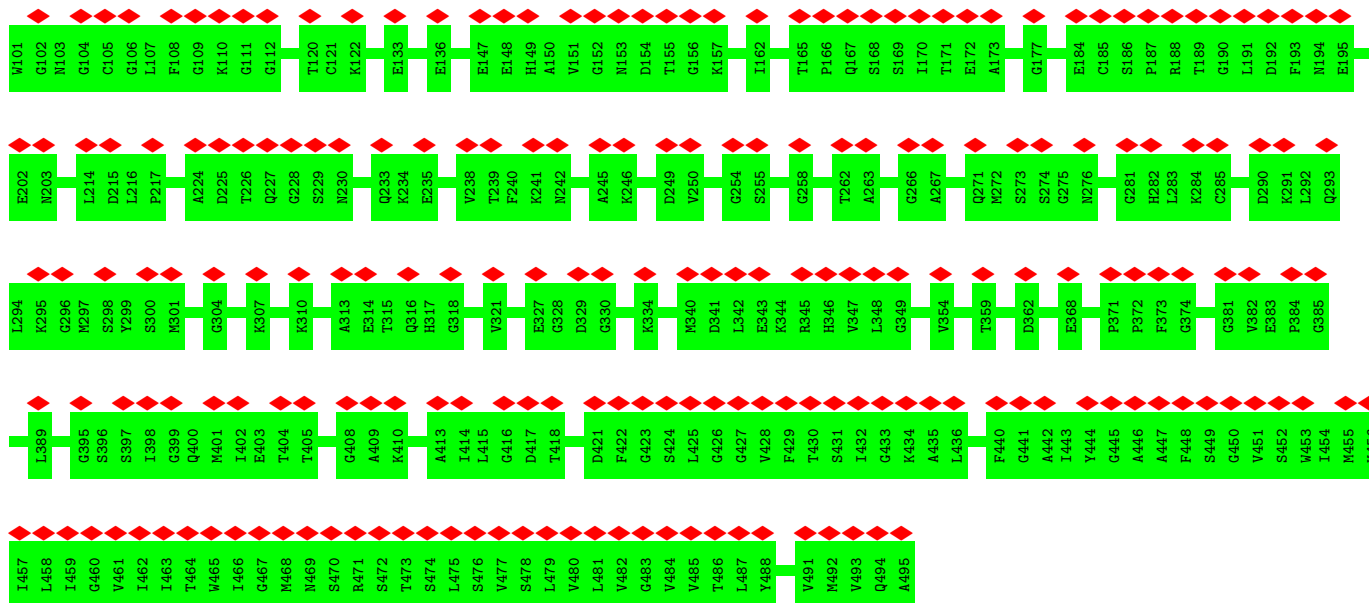


• Molecule 1: glycoprotein E

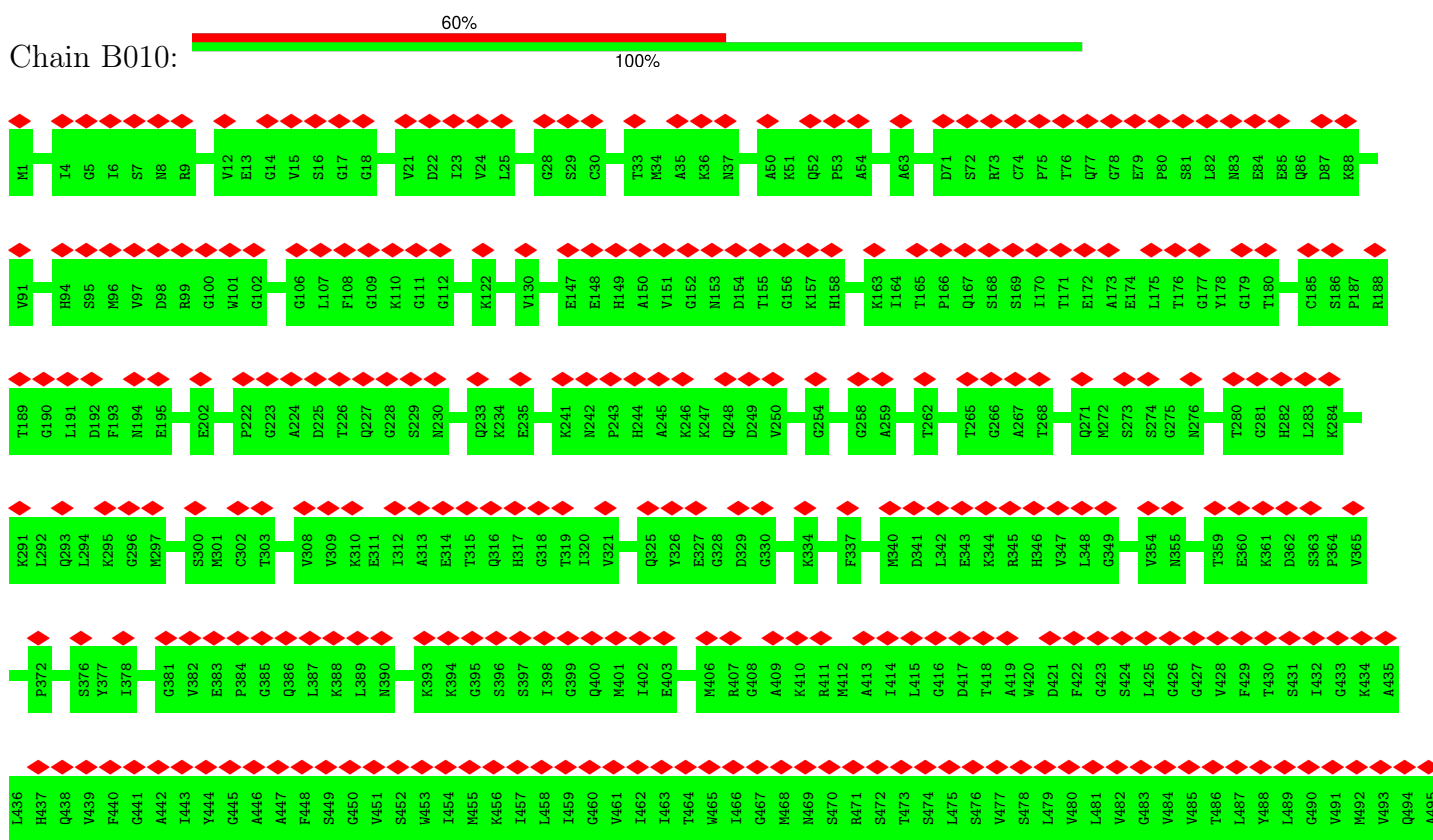


• Molecule 1: glycoprotein E



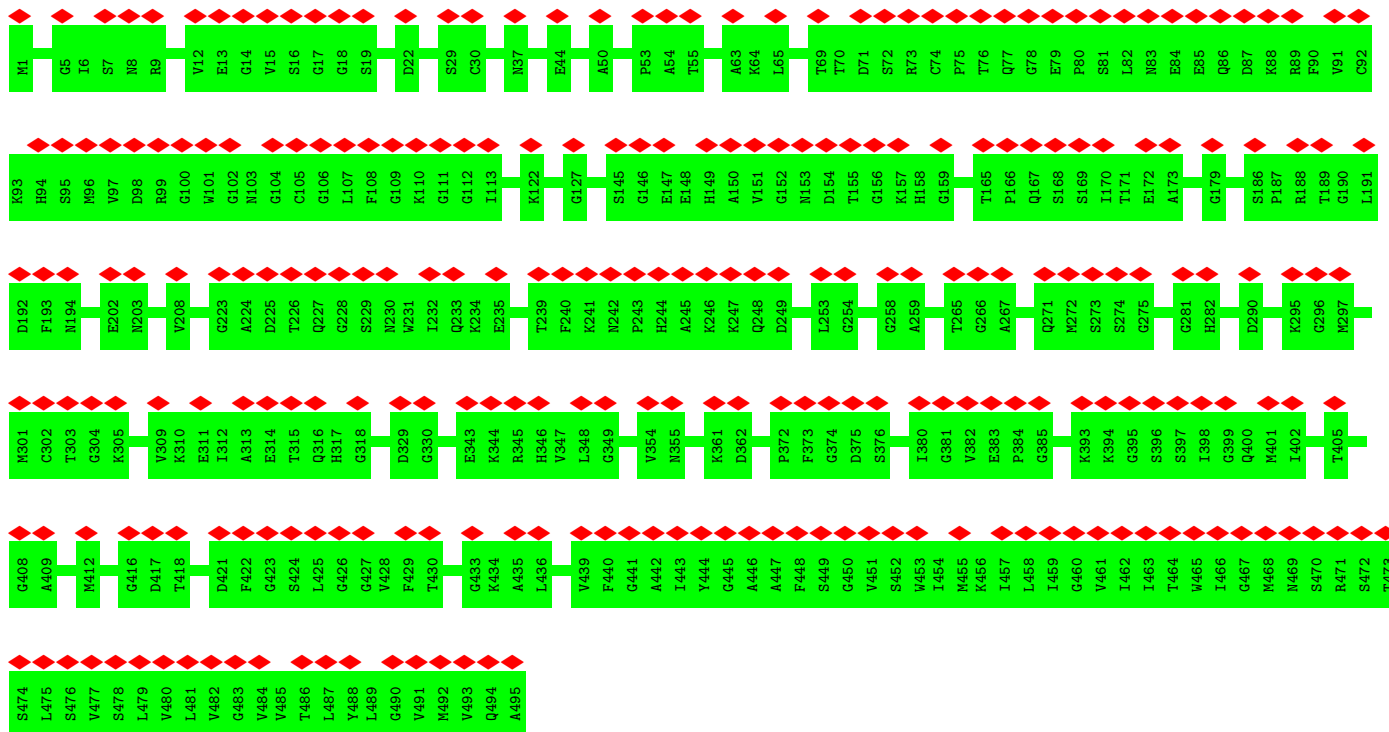


• Molecule 1: glycoprotein E

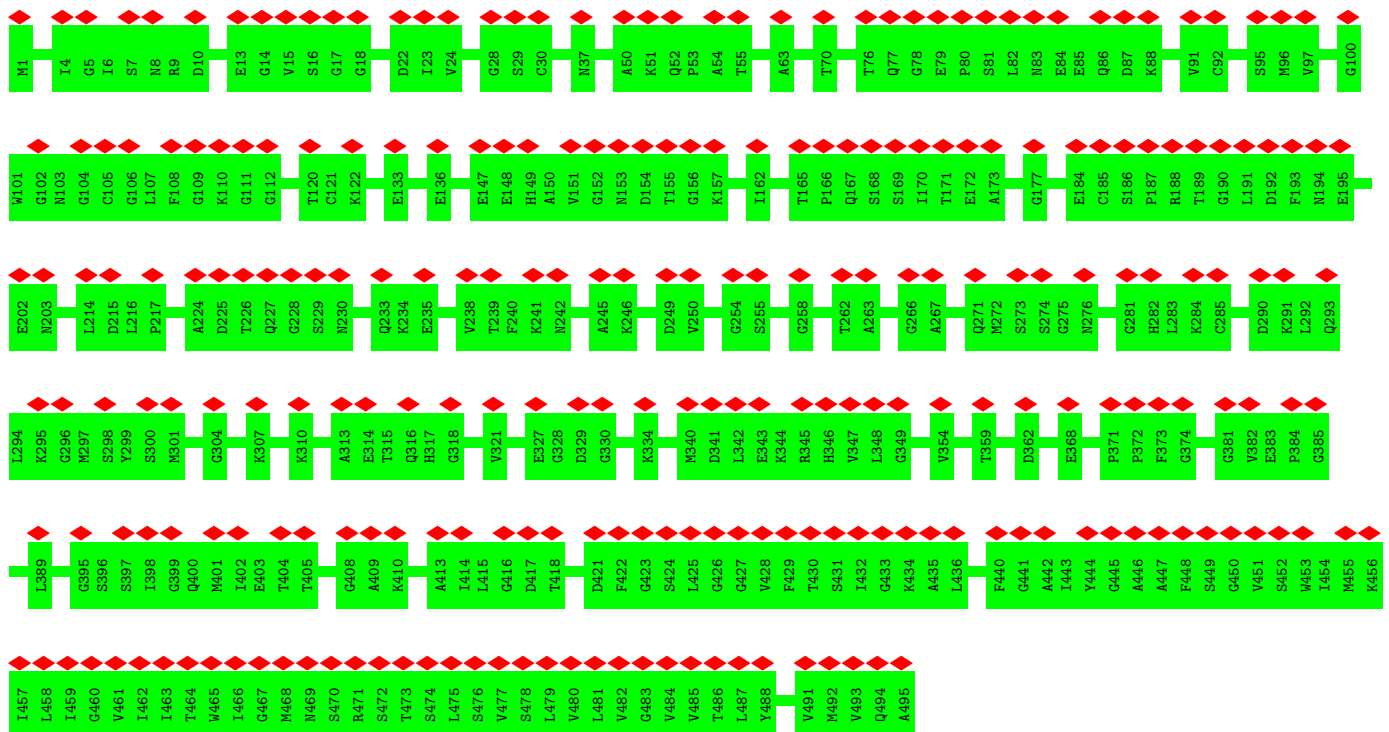


• Molecule 1: glycoprotein E

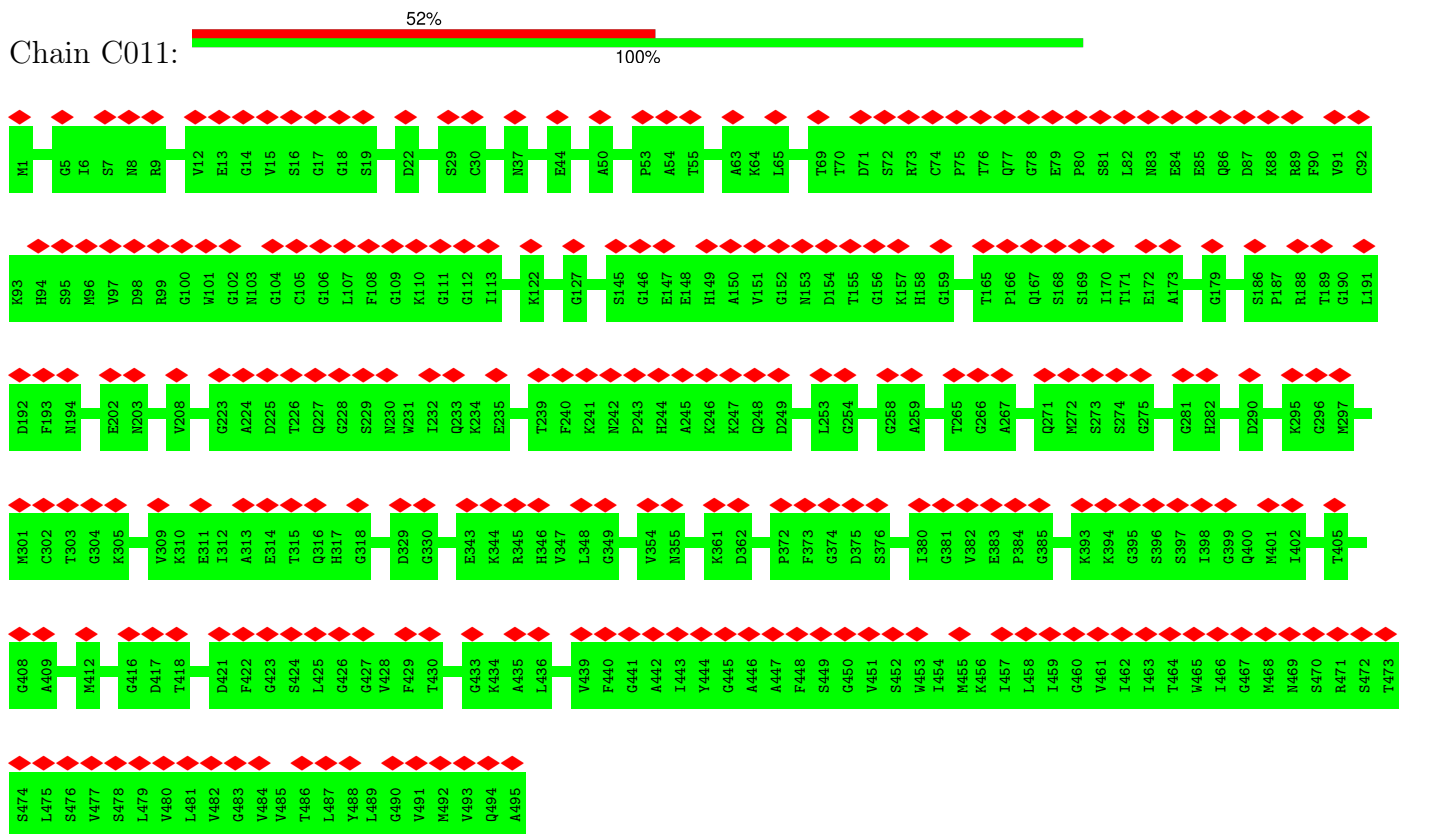
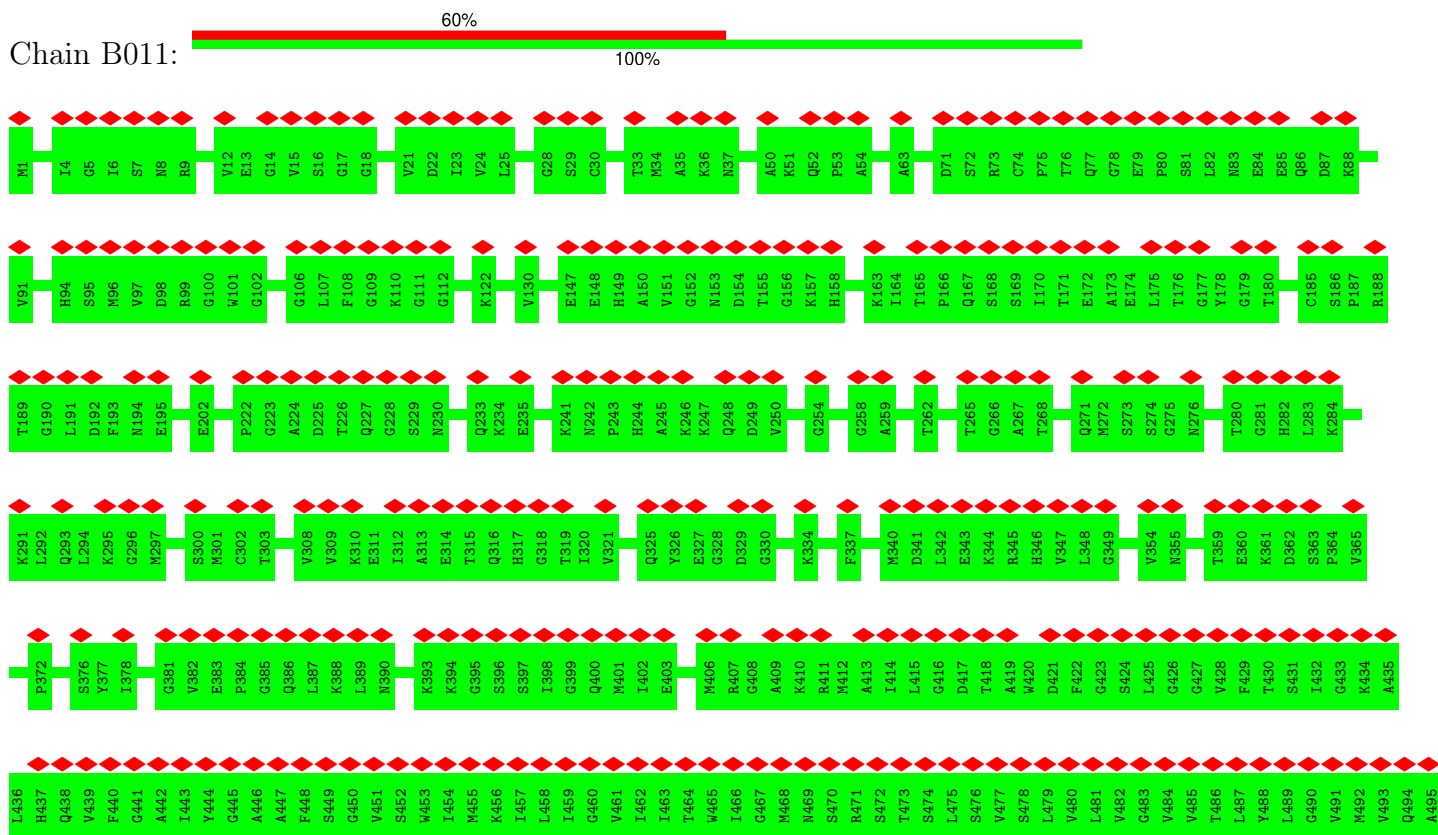




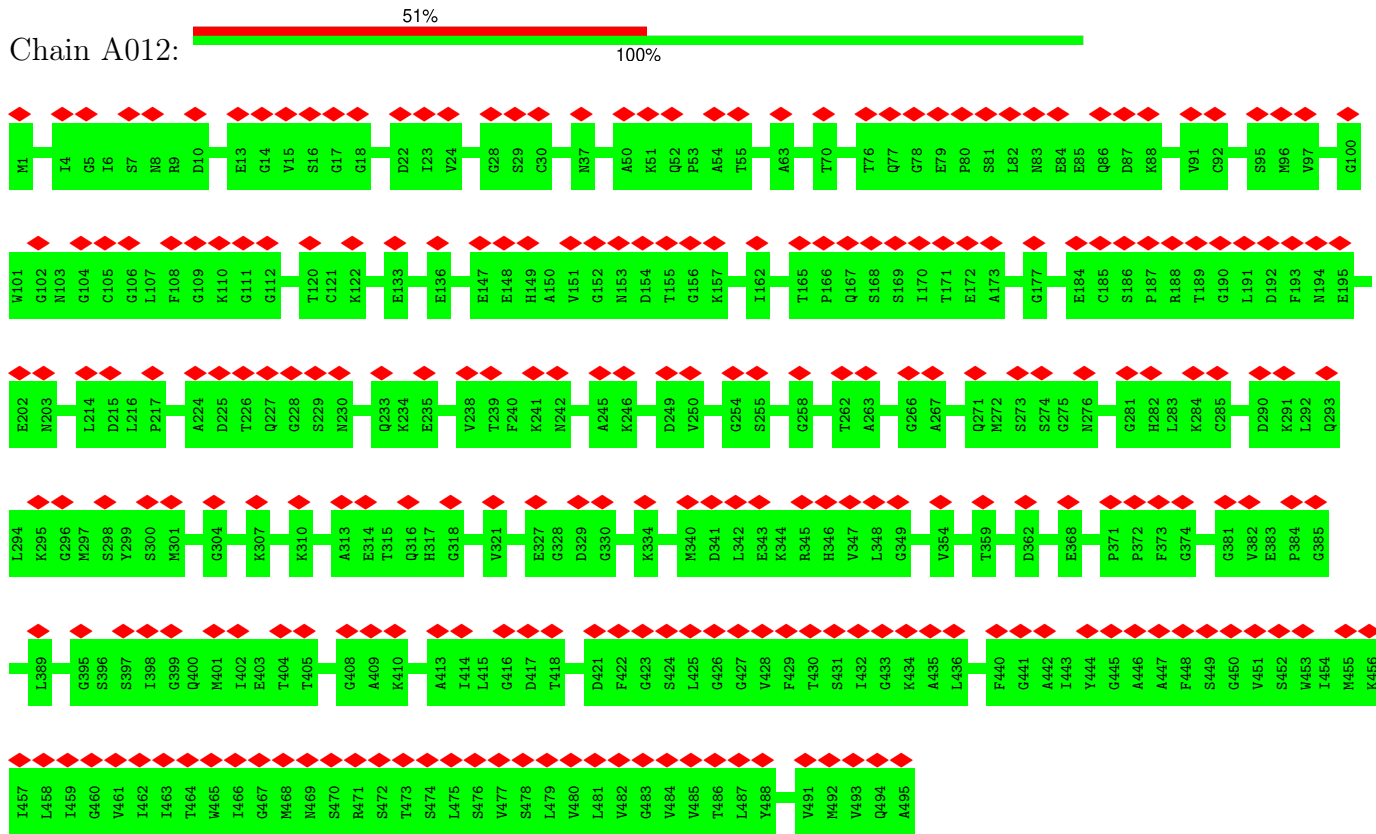
• Molecule 1: glycoprotein E



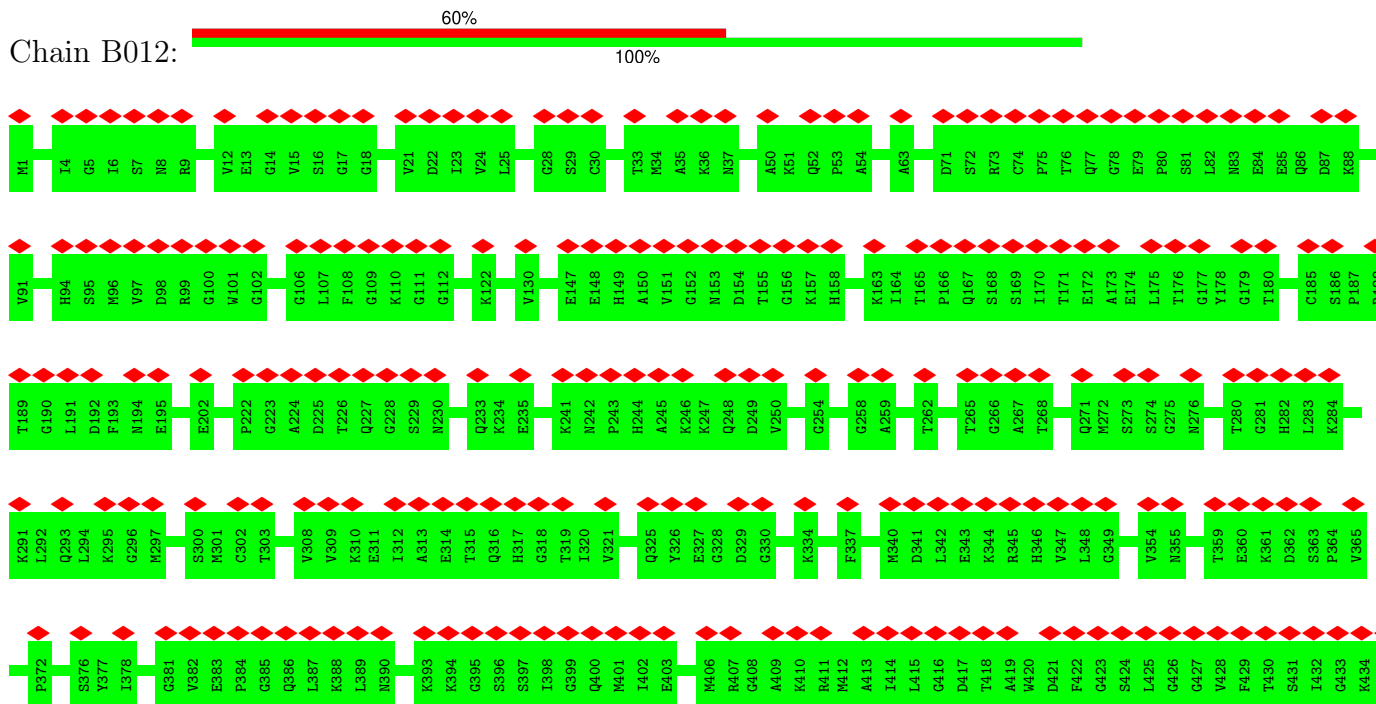
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

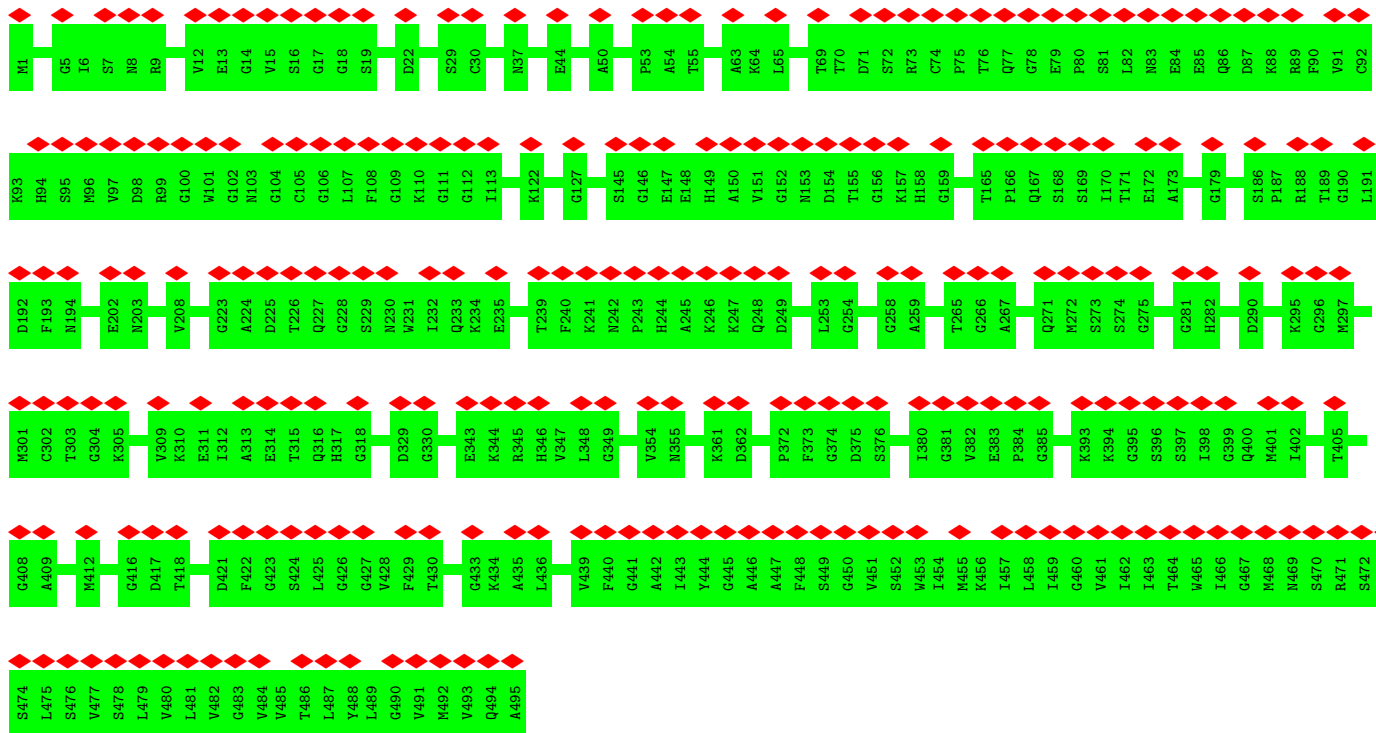


• Molecule 1: glycoprotein E

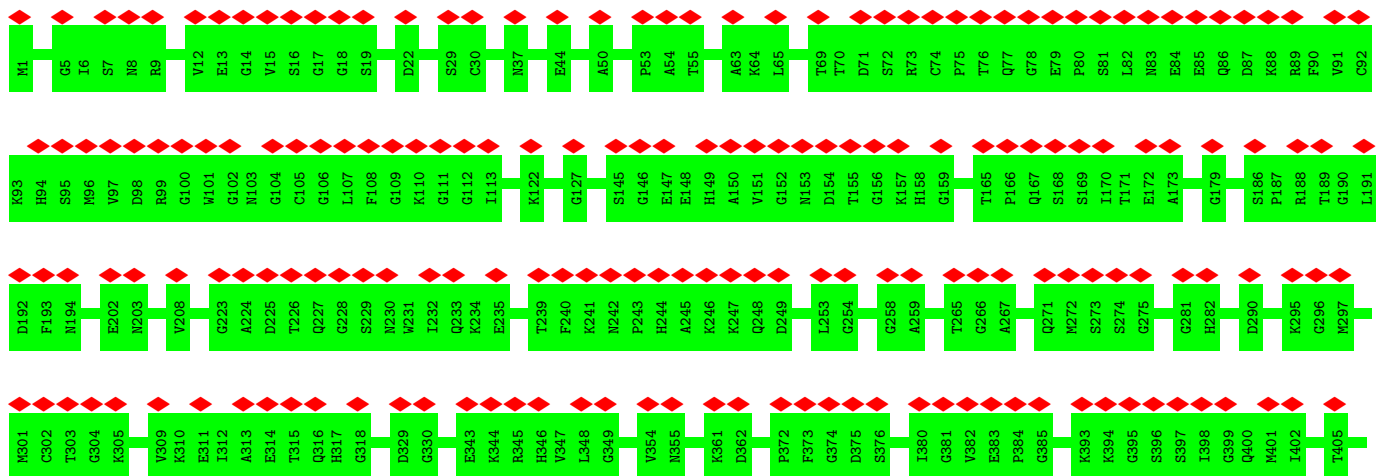




• Molecule 1: glycoprotein E

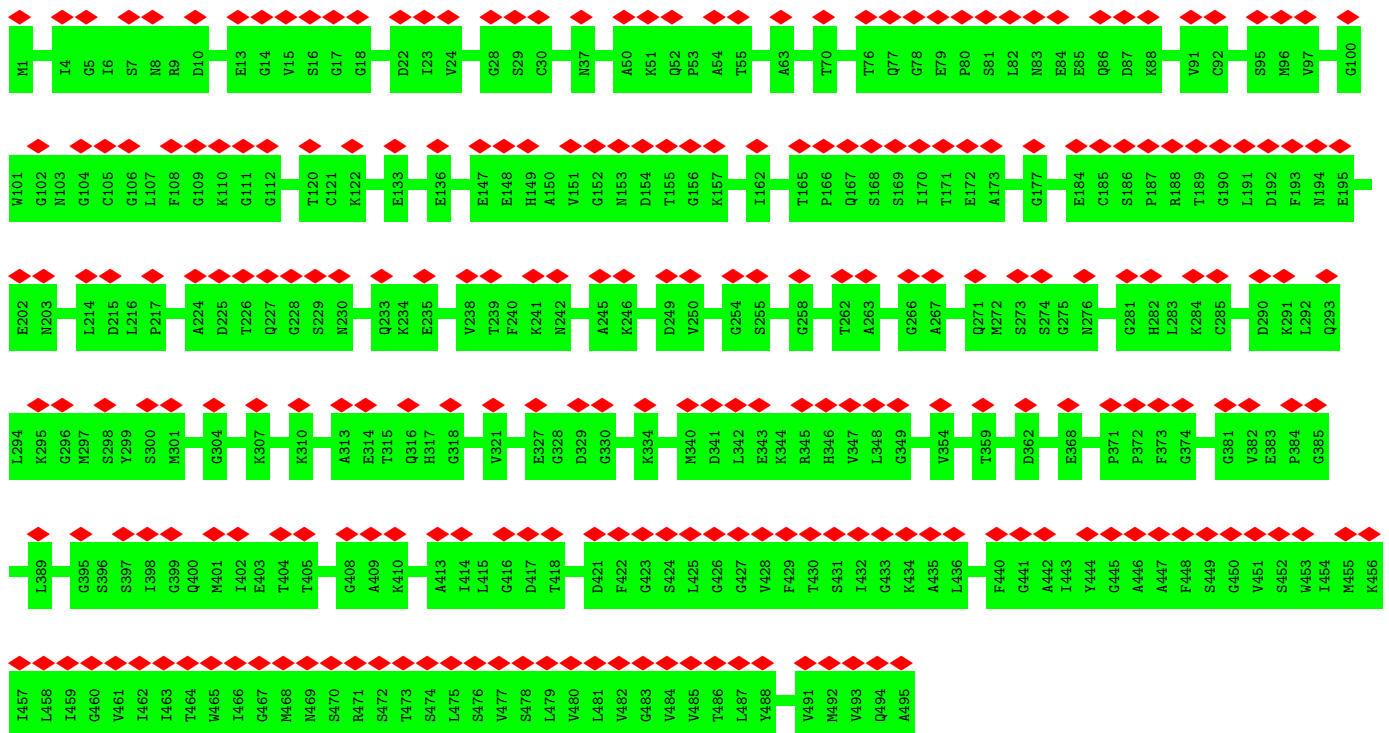


• Molecule 1: glycoprotein E

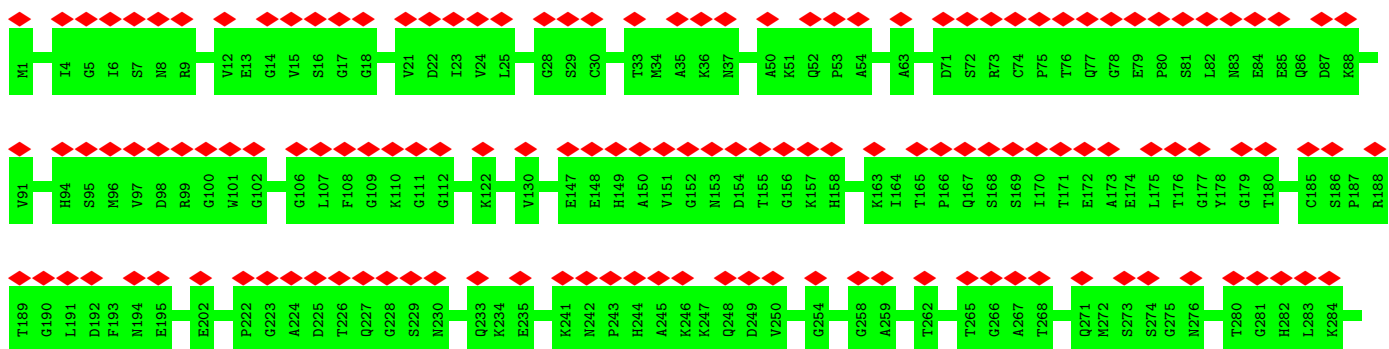




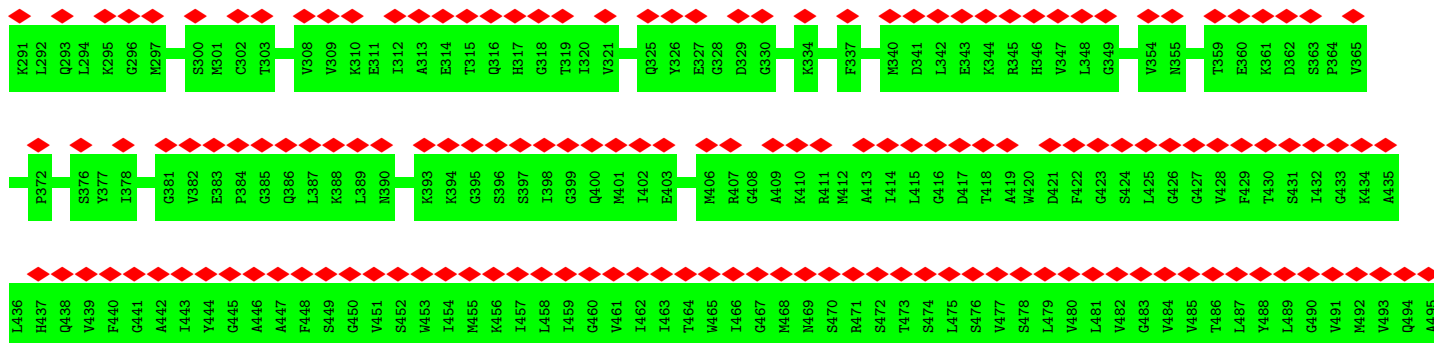
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



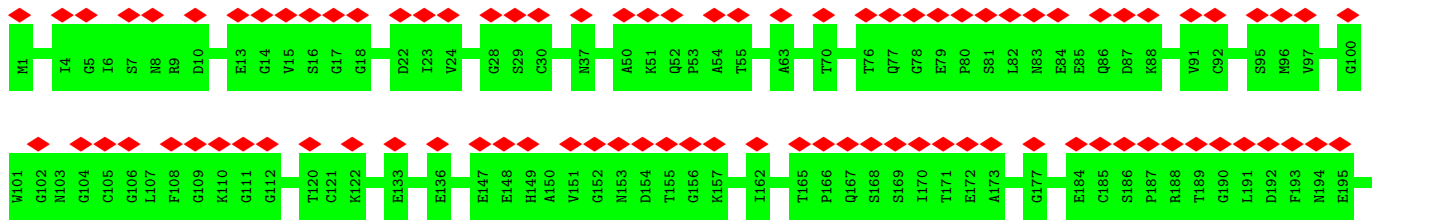


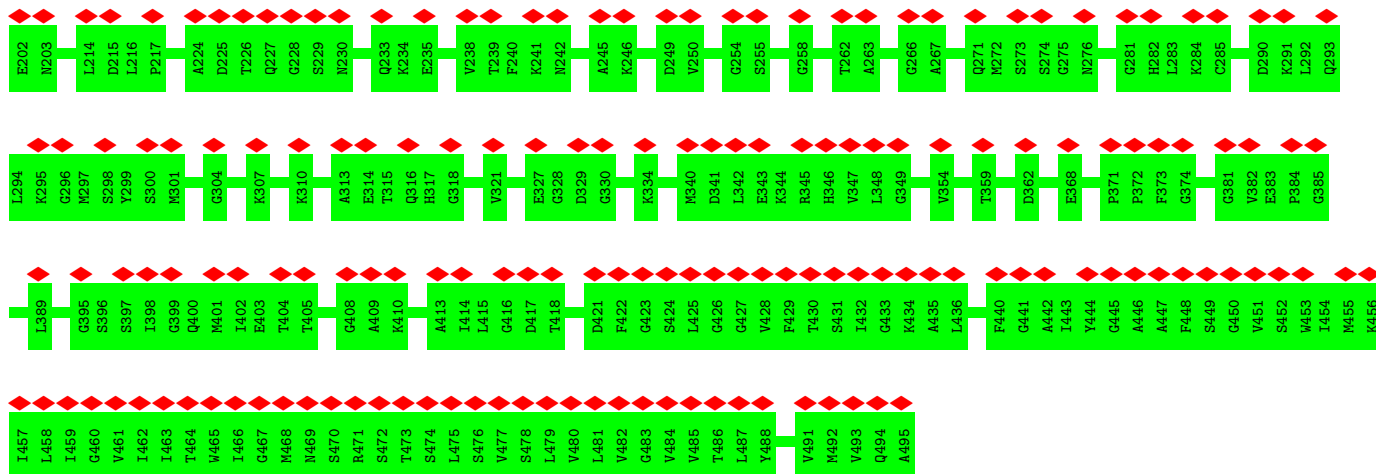


• Molecule 1: glycoprotein E

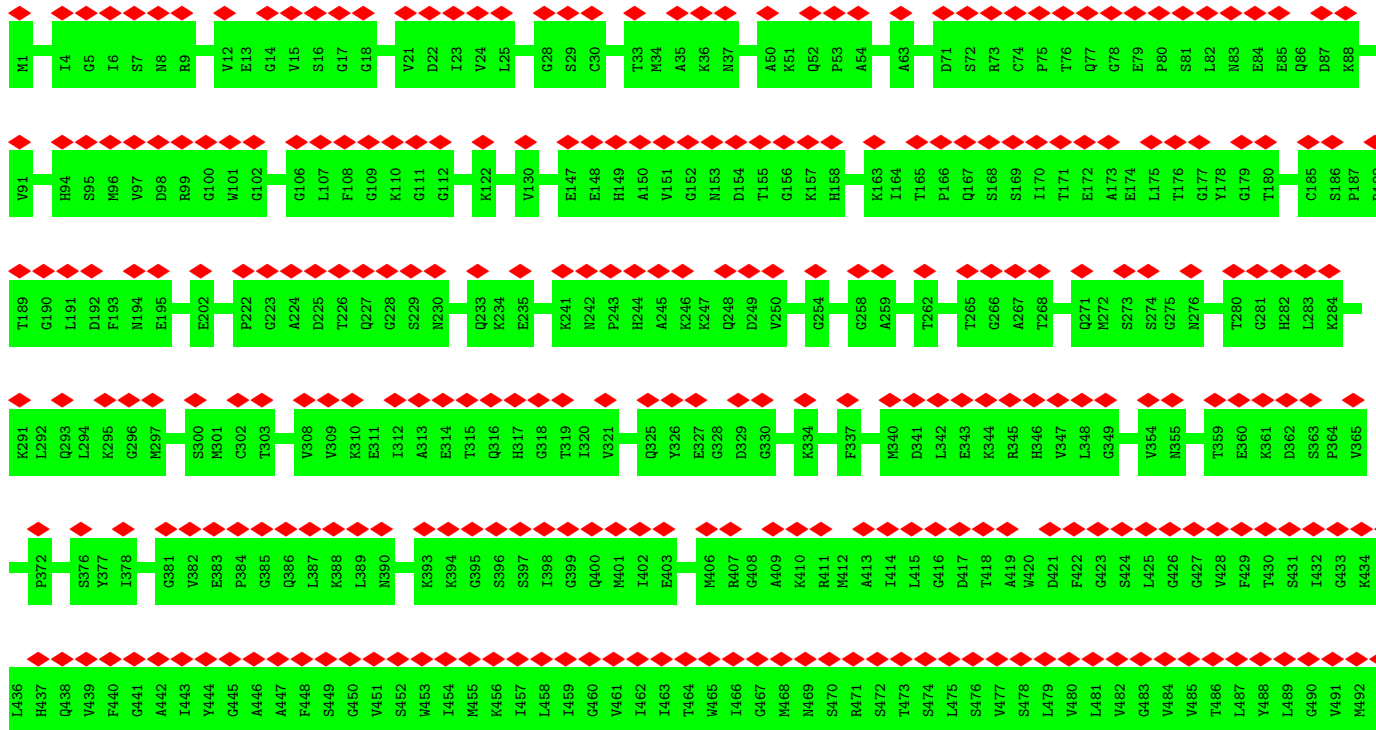


• Molecule 1: glycoprotein E

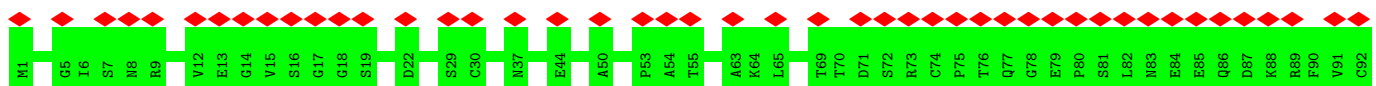


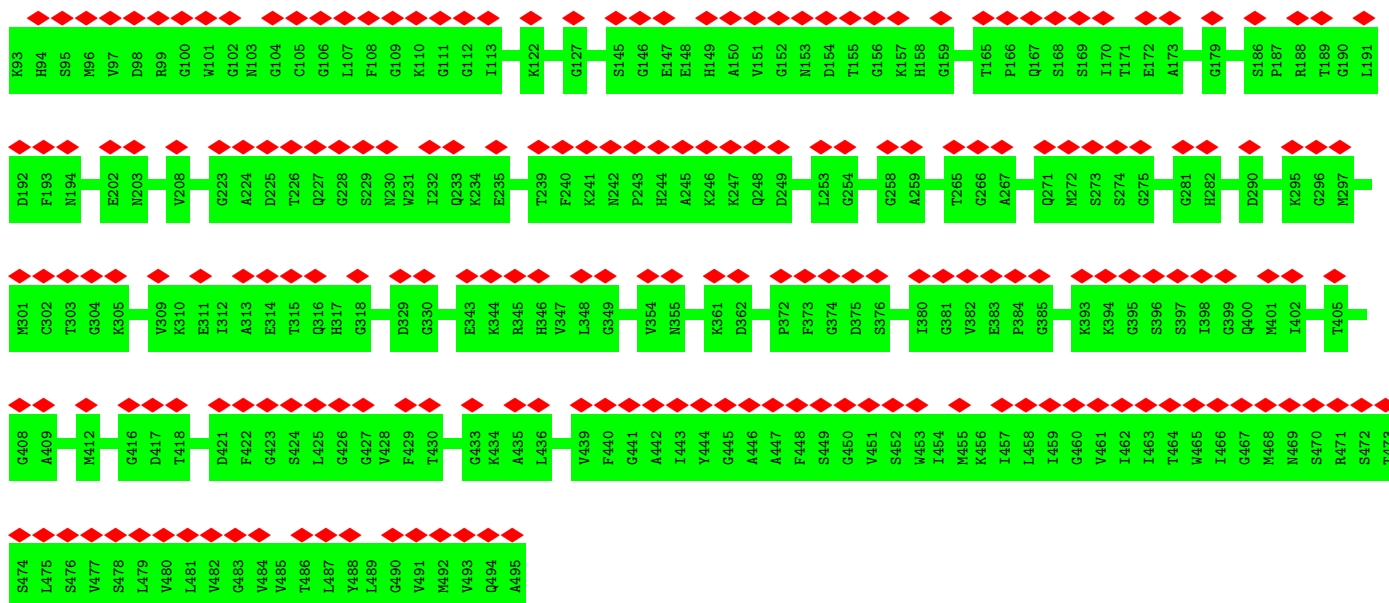


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



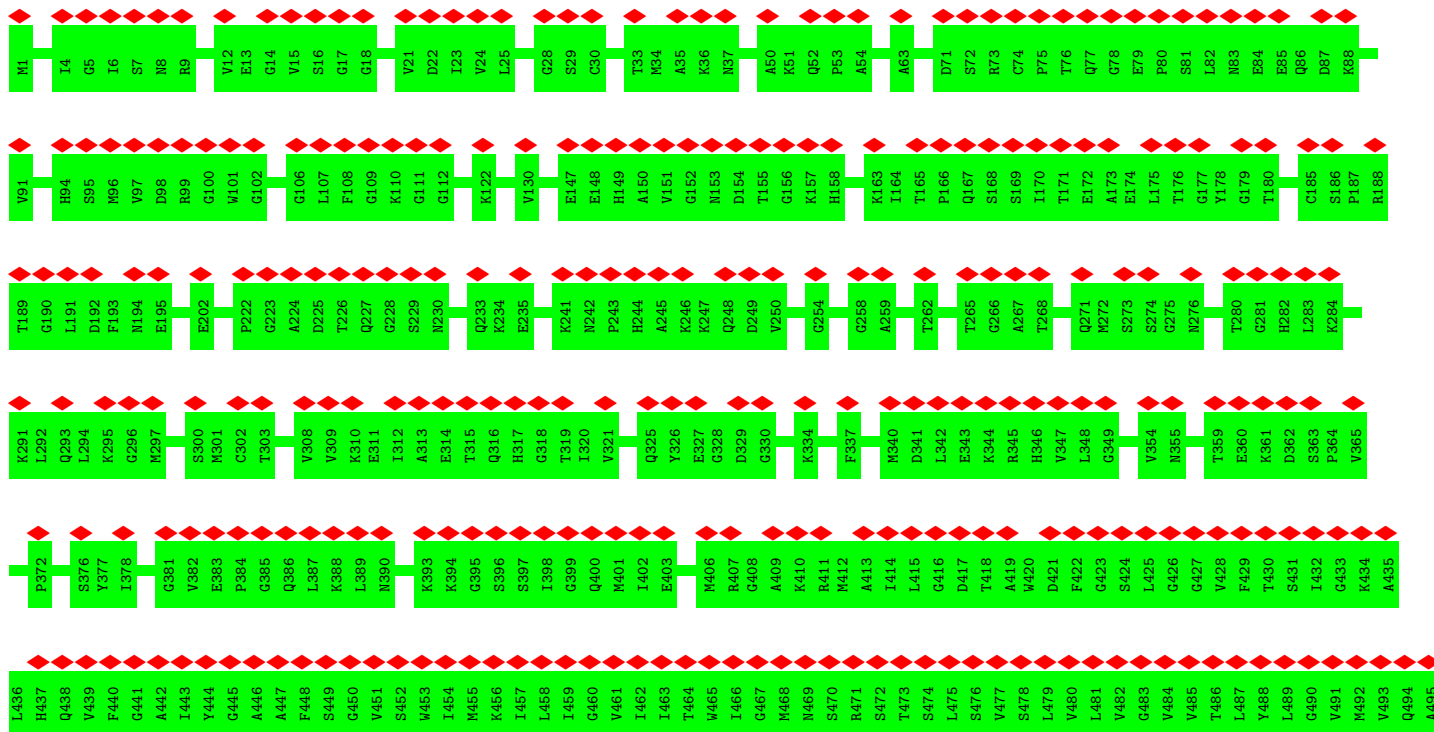


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

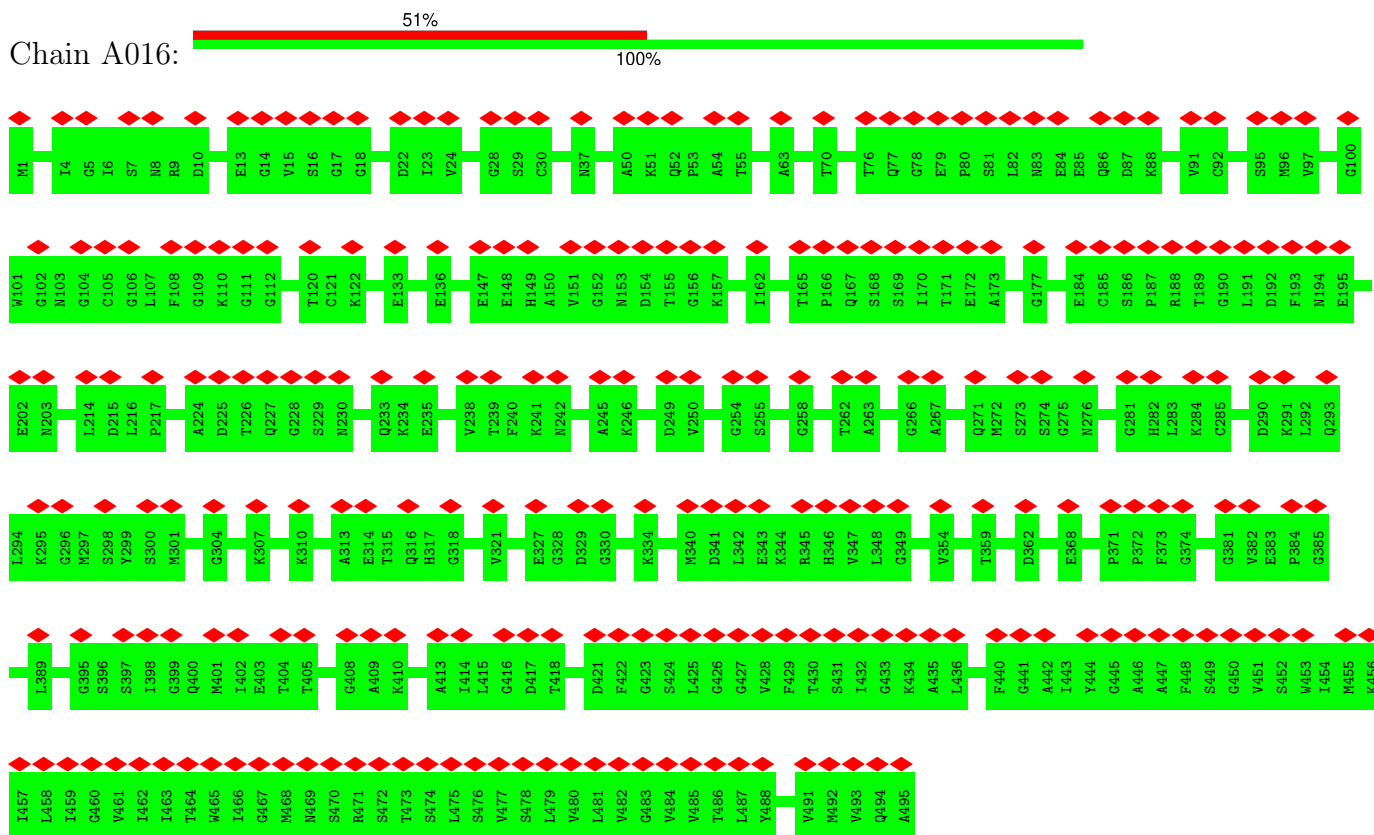




• Molecule 1: glycoprotein E



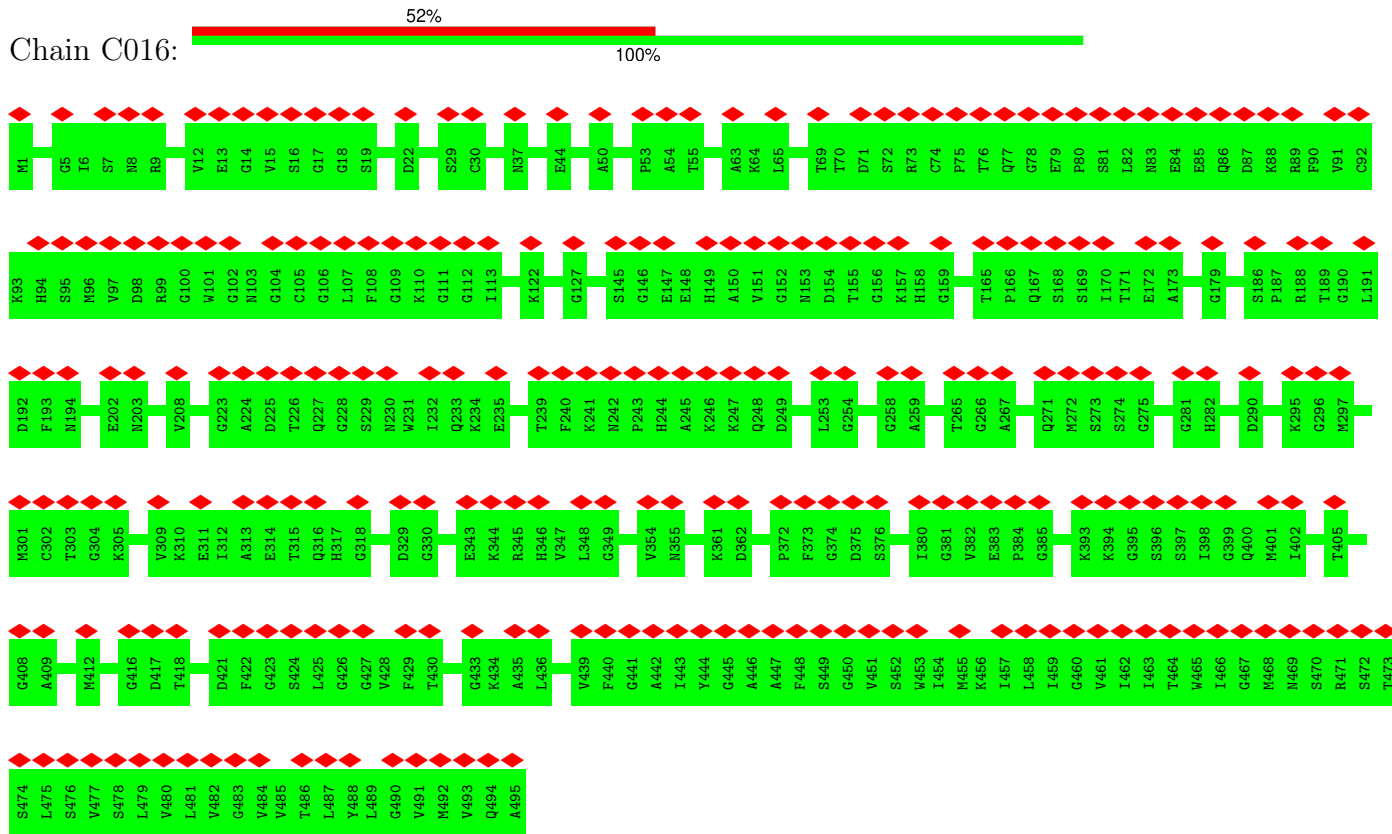
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

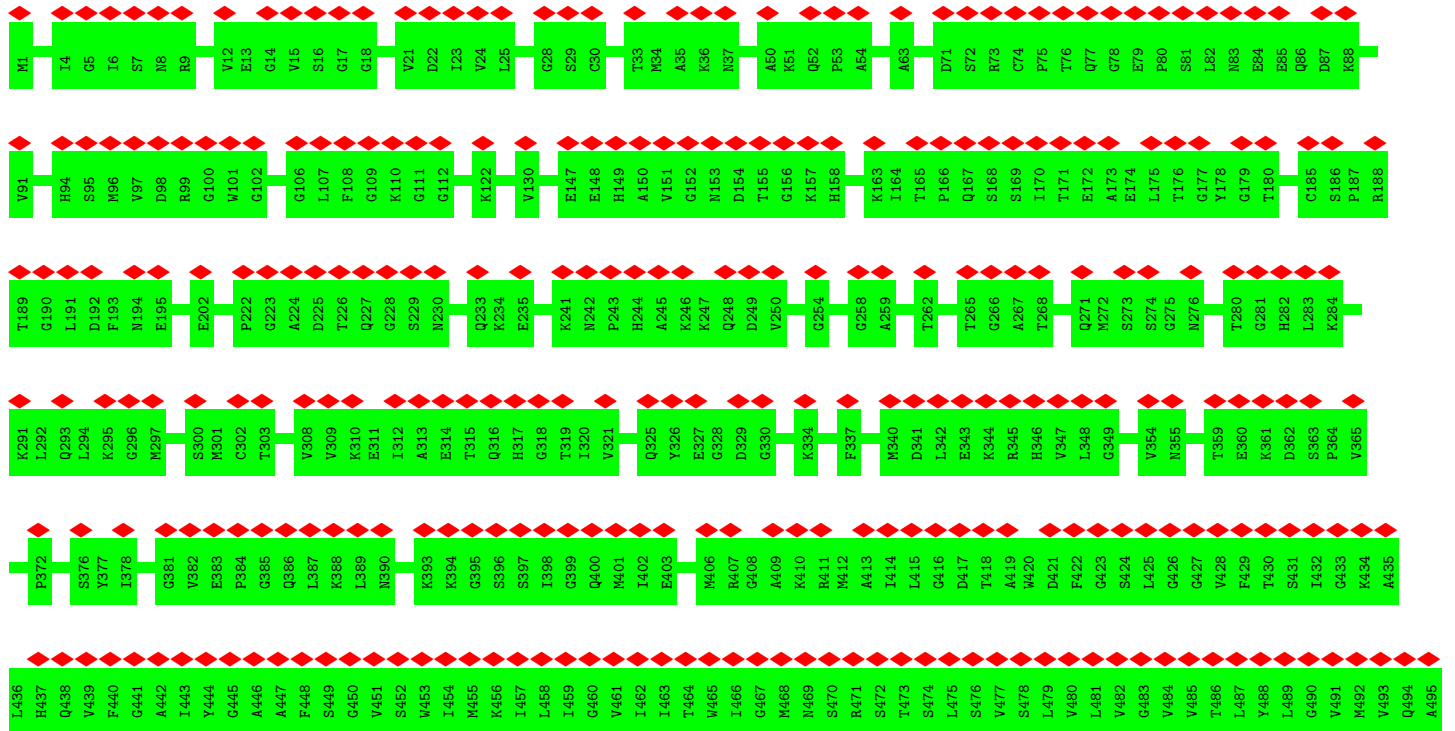


• Molecule 1: glycoprotein E

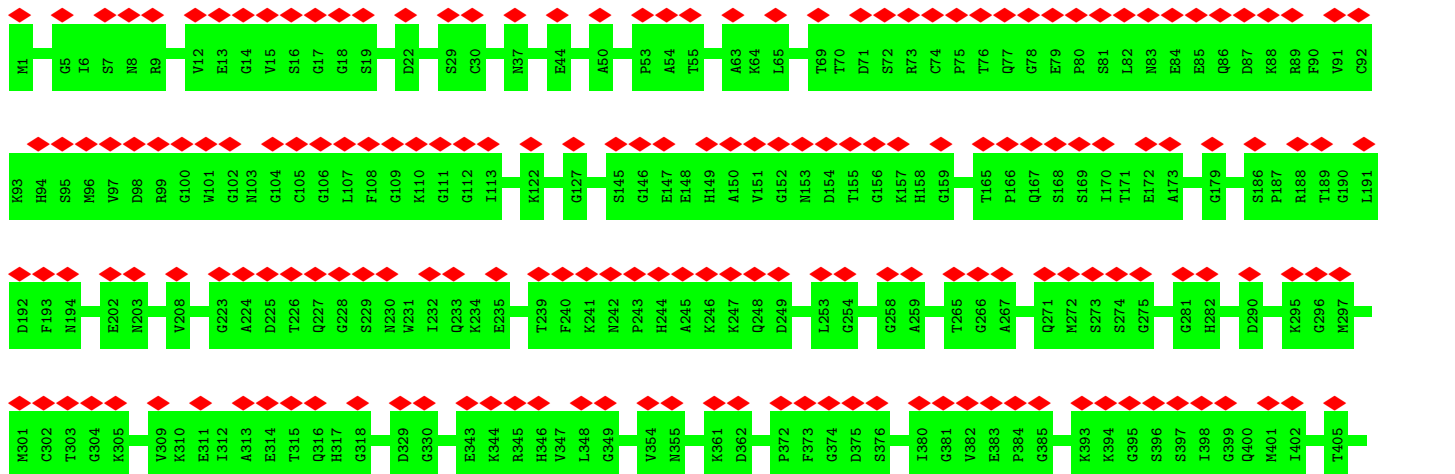


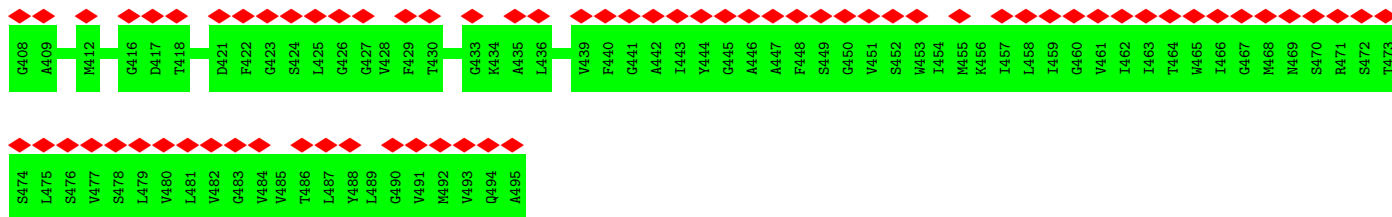


● Molecule 1: glycoprotein E



● Molecule 1: glycoprotein E

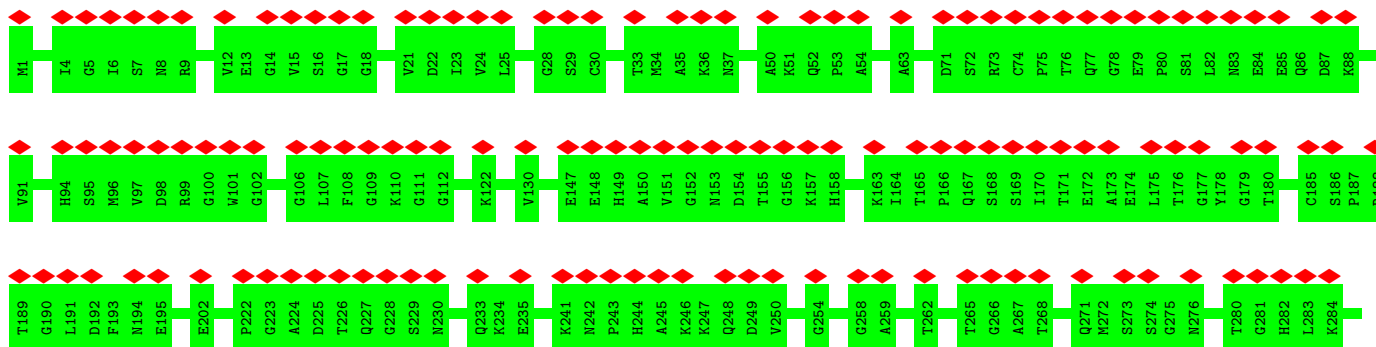




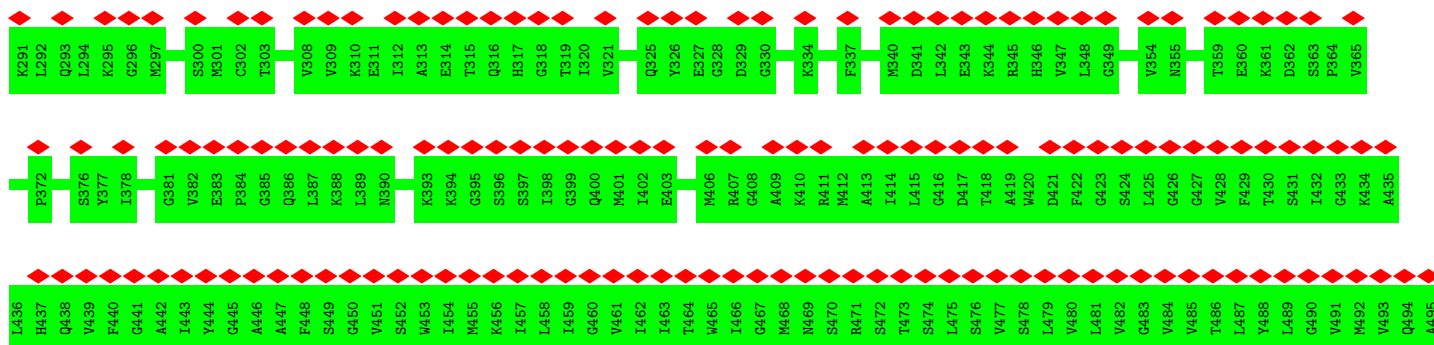
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E



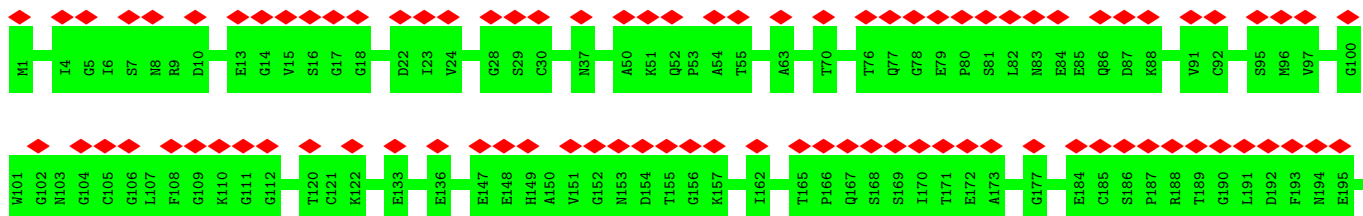


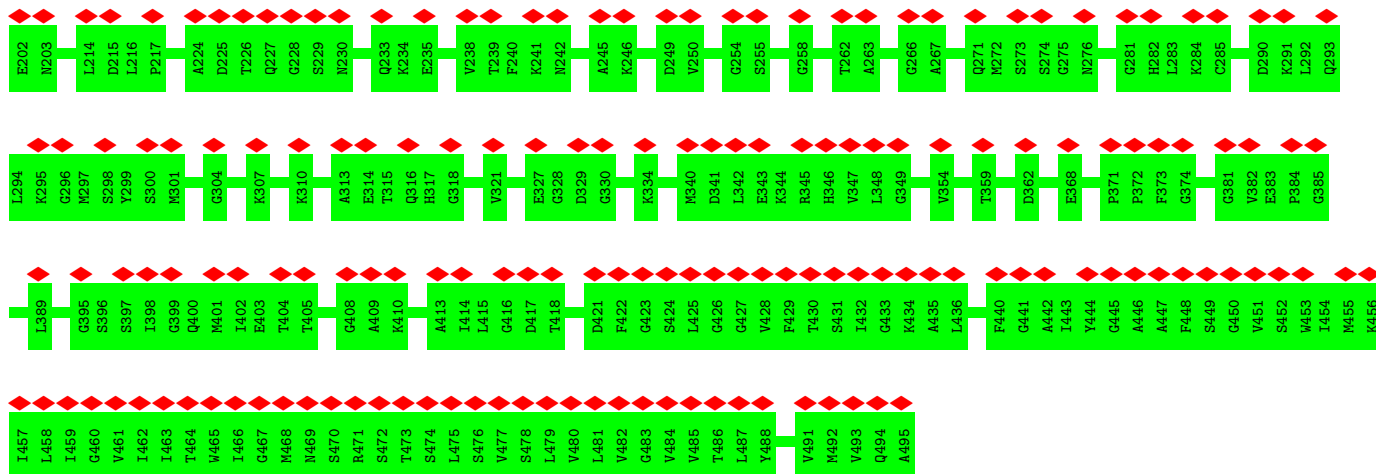


- Molecule 1: glycoprotein E



- Molecule 1: glycoprotein E

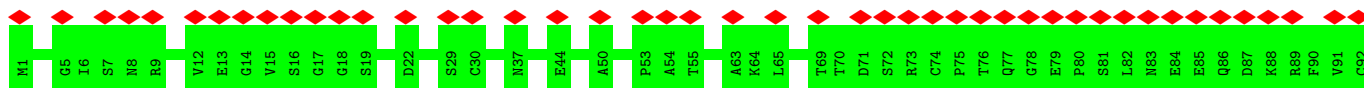


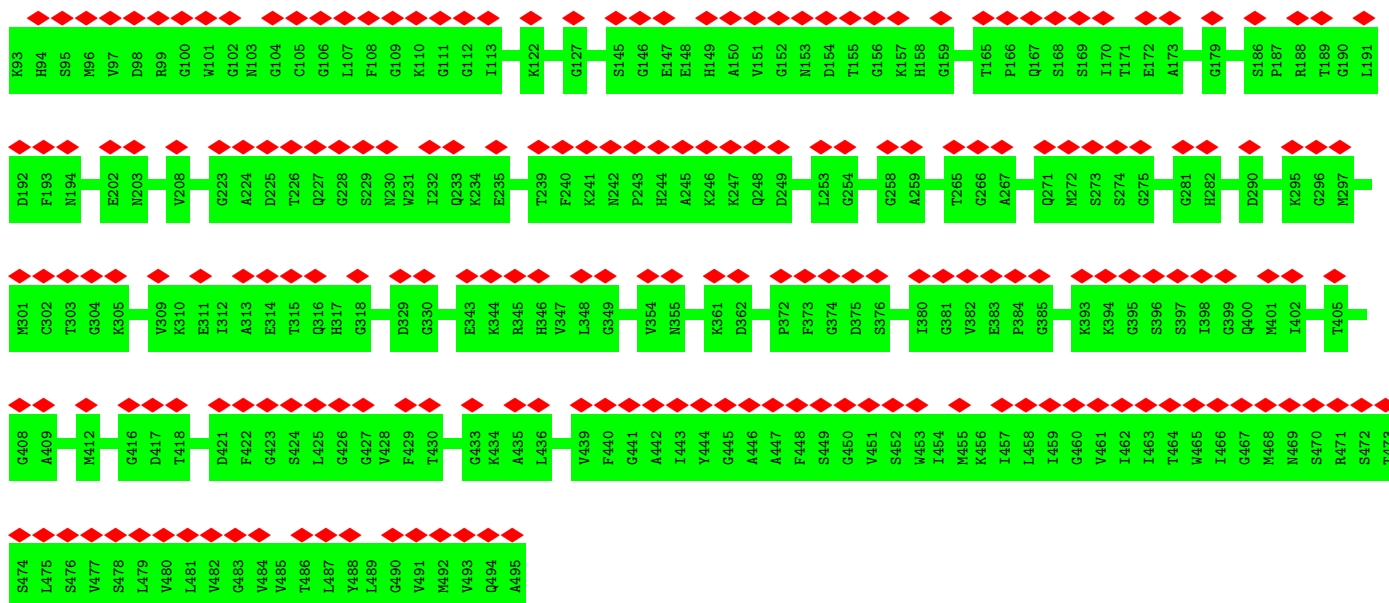


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E





• Molecule 1: glycoprotein E



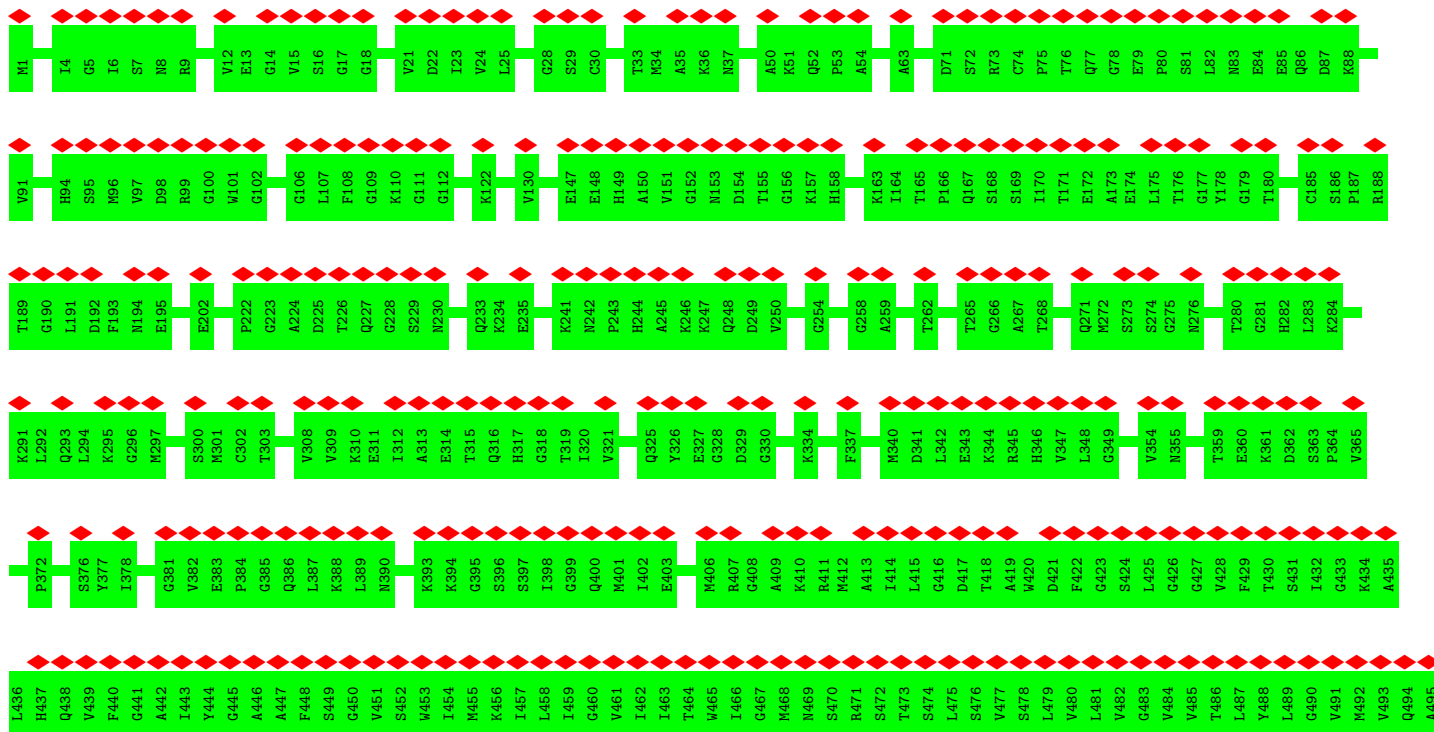
Chain A020:



• Molecule 1: glycoprotein E



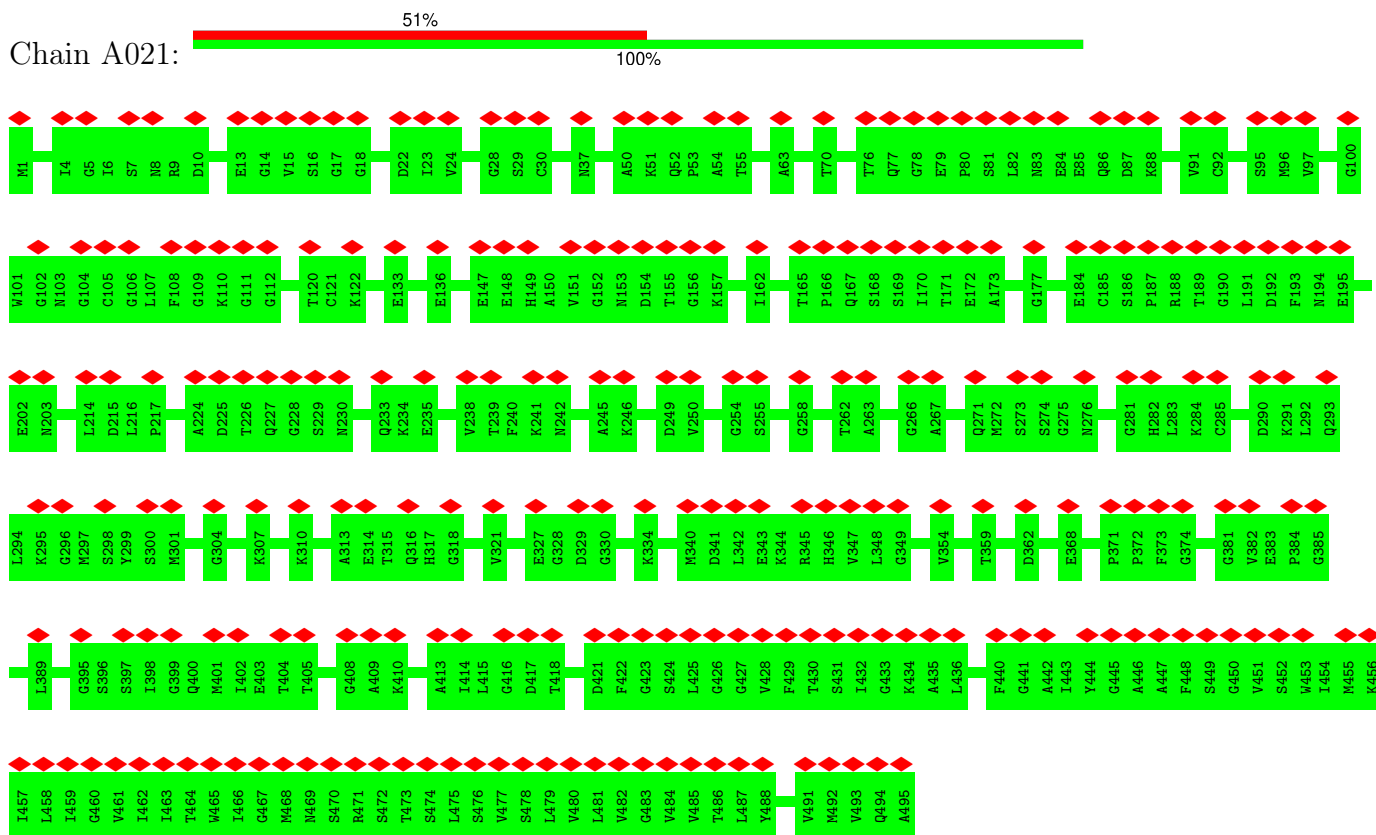
Chain B020:



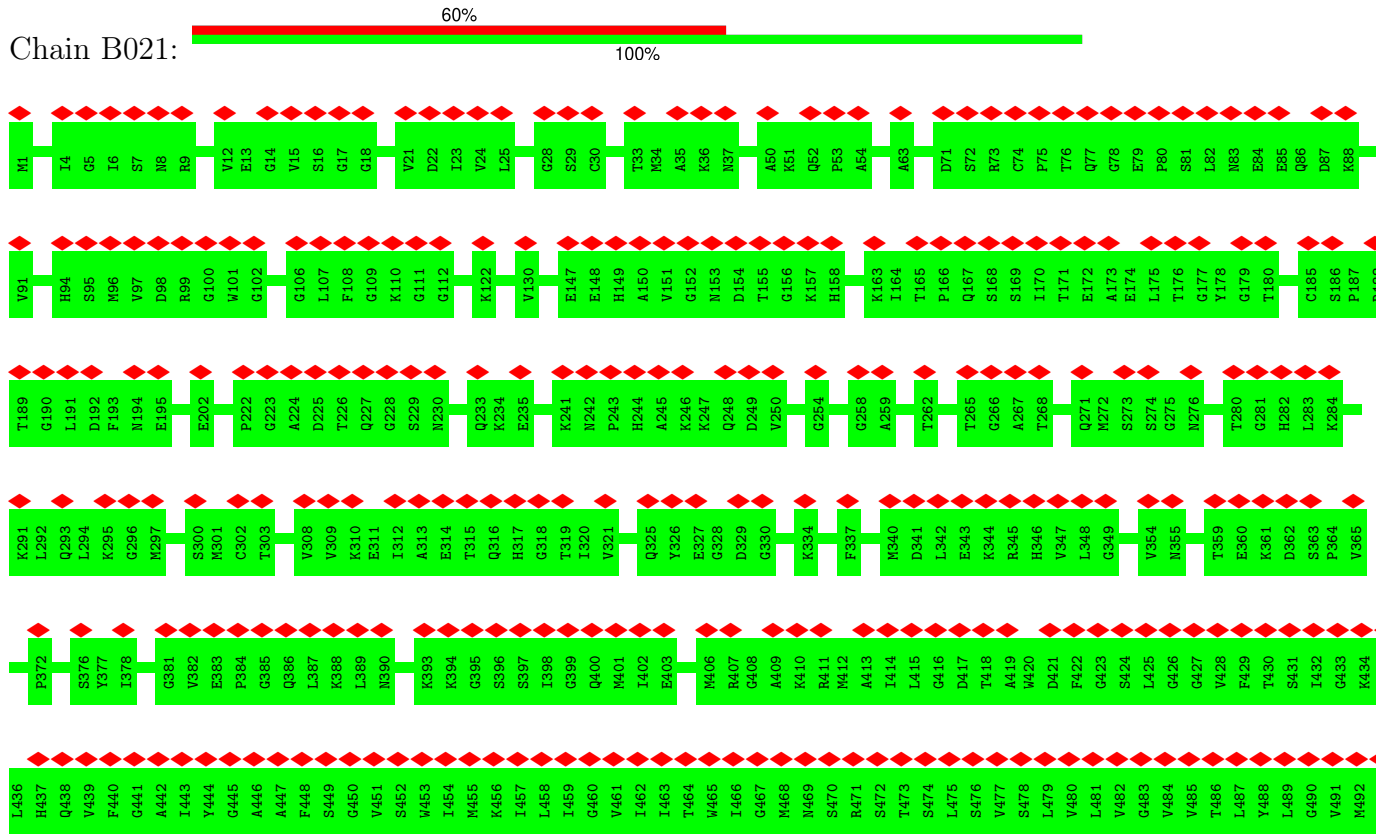
• Molecule 1: glycoprotein E



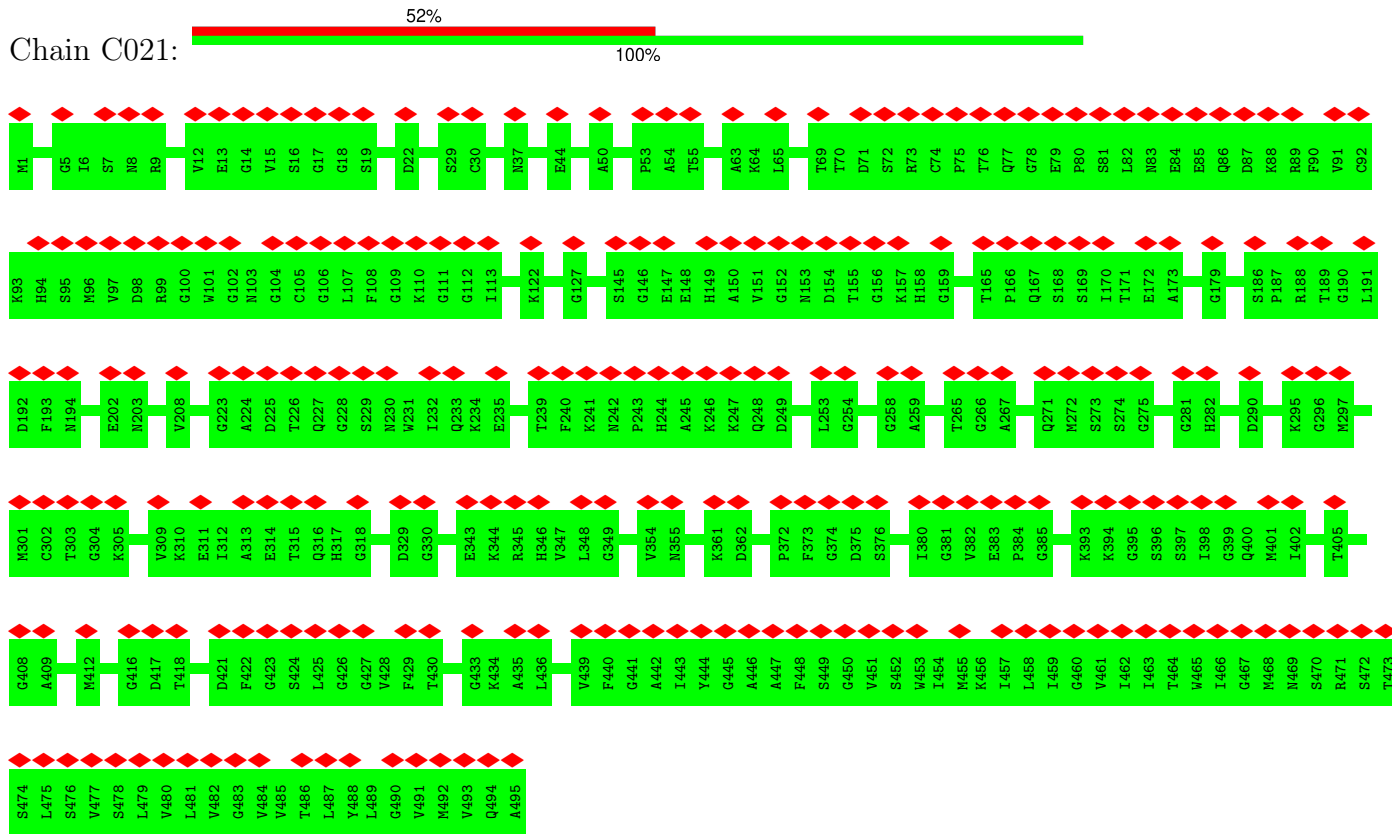
• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

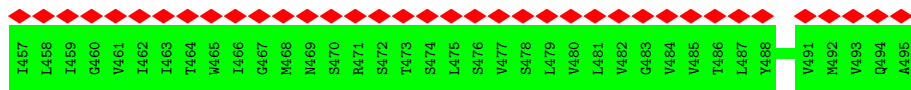


• Molecule 1: glycoprotein E

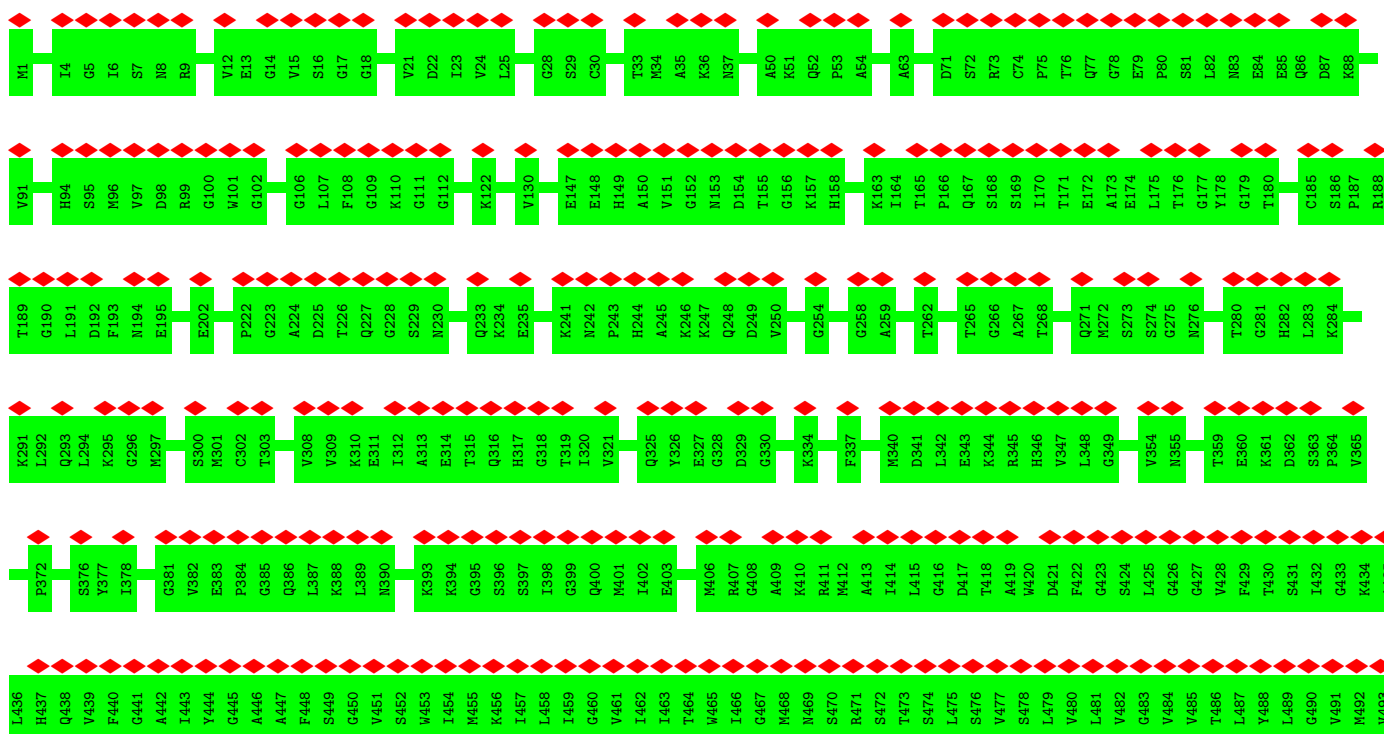


• Molecule 1: glycoprotein E

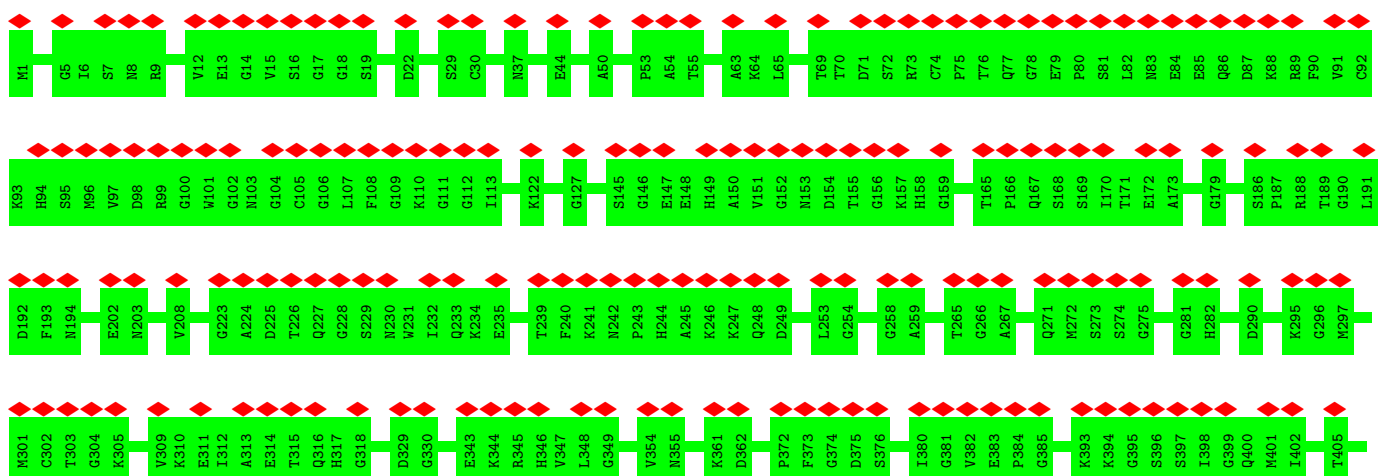


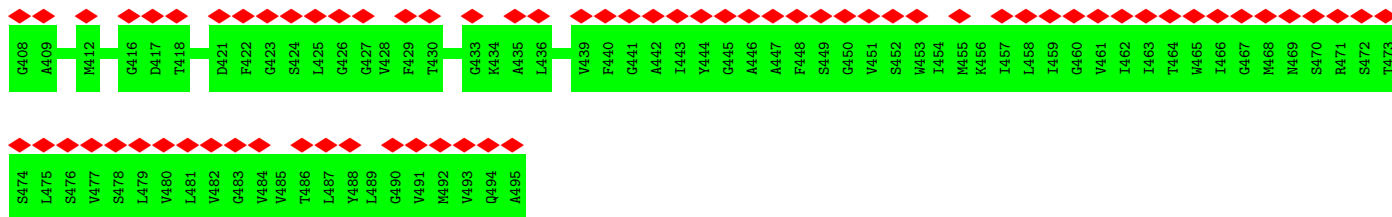


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E

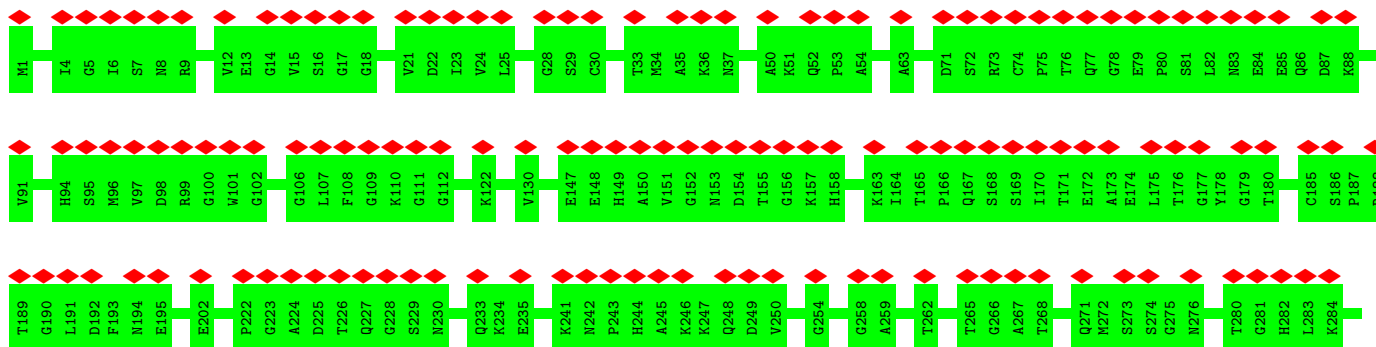




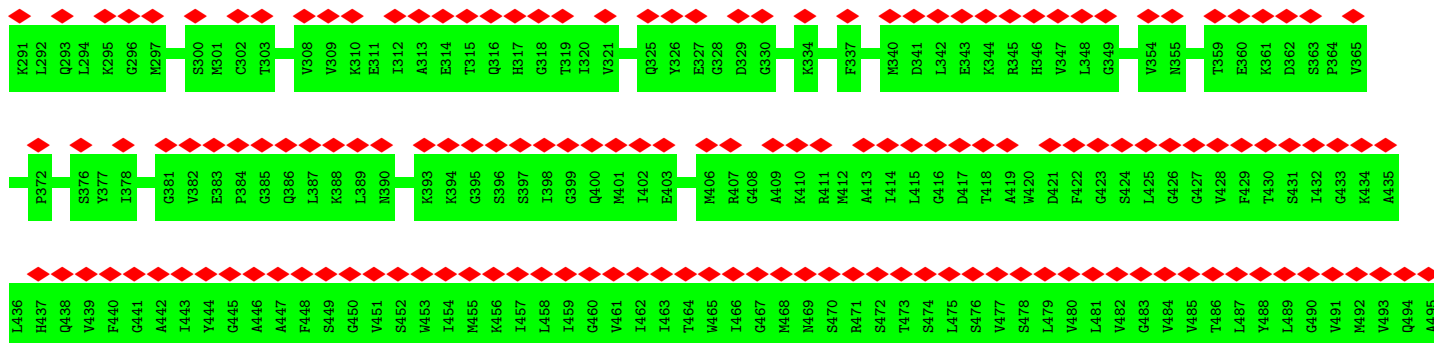
• Molecule 1: glycoprotein E



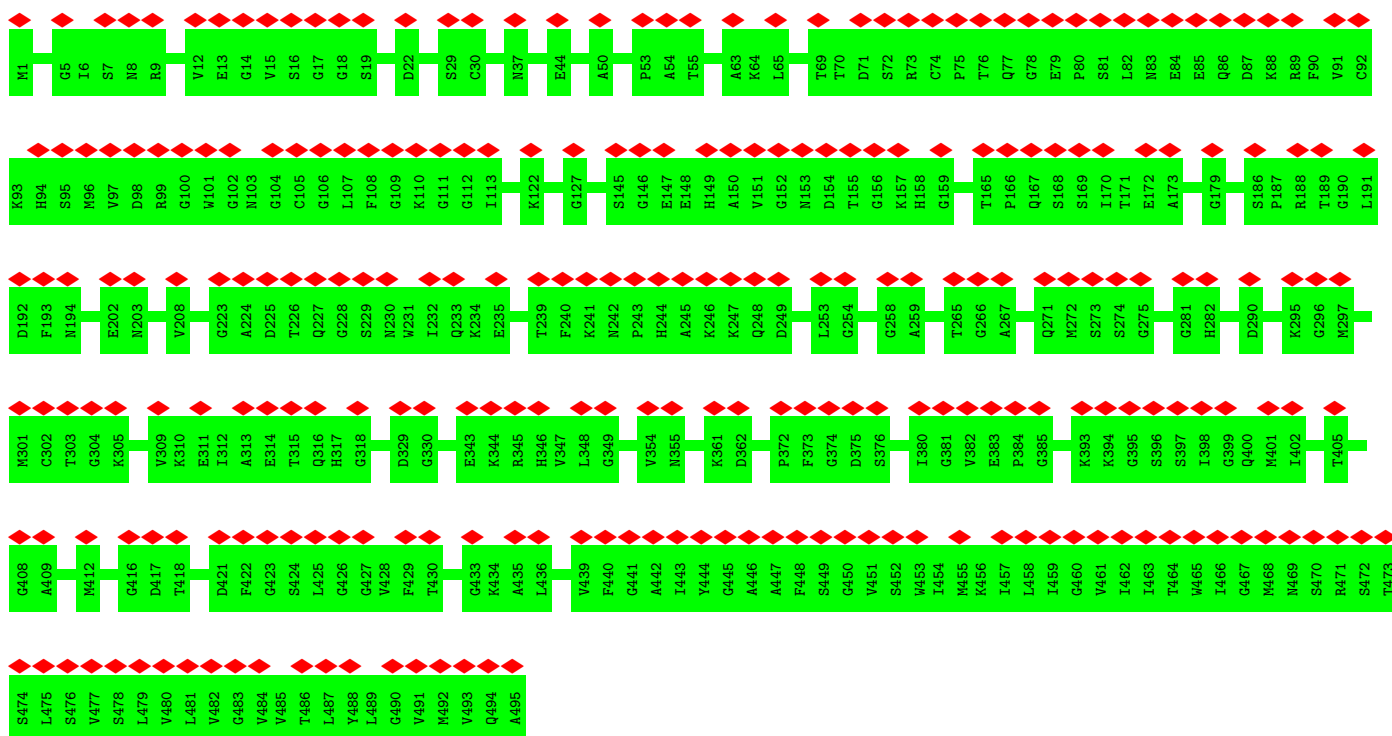
• Molecule 1: glycoprotein E



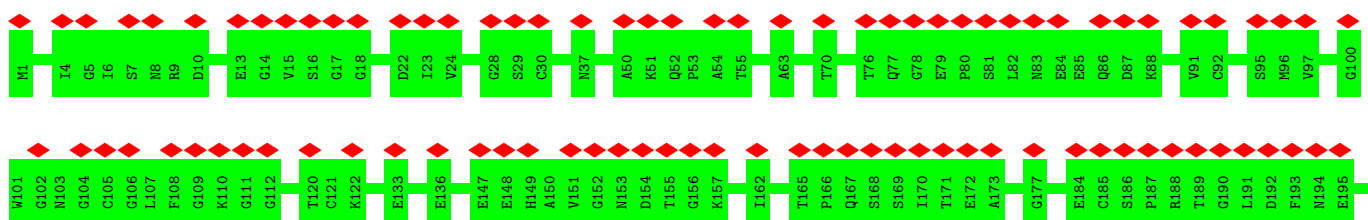


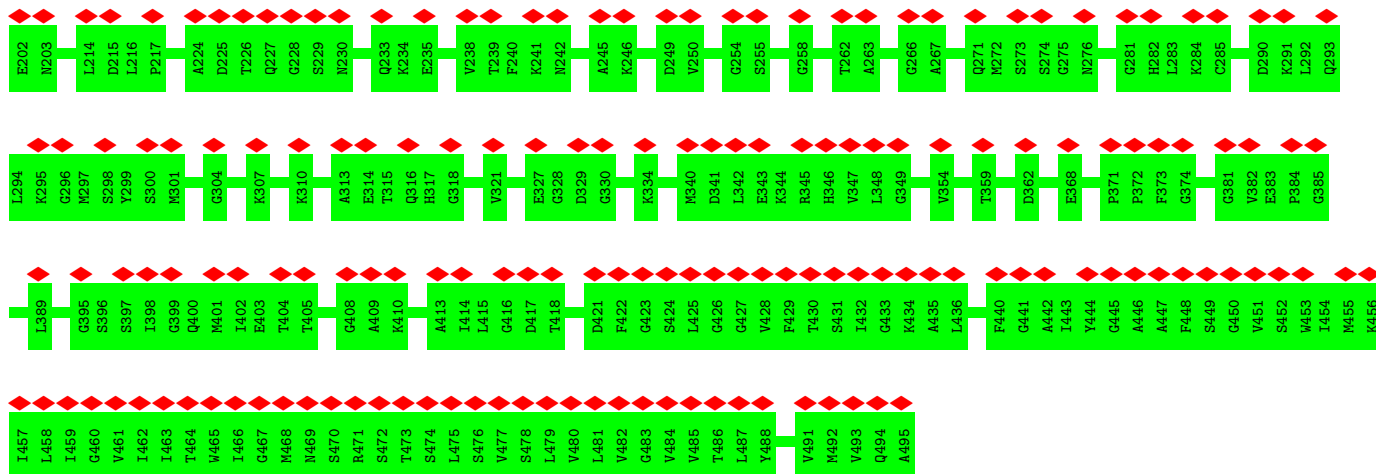


• Molecule 1: glycoprotein E

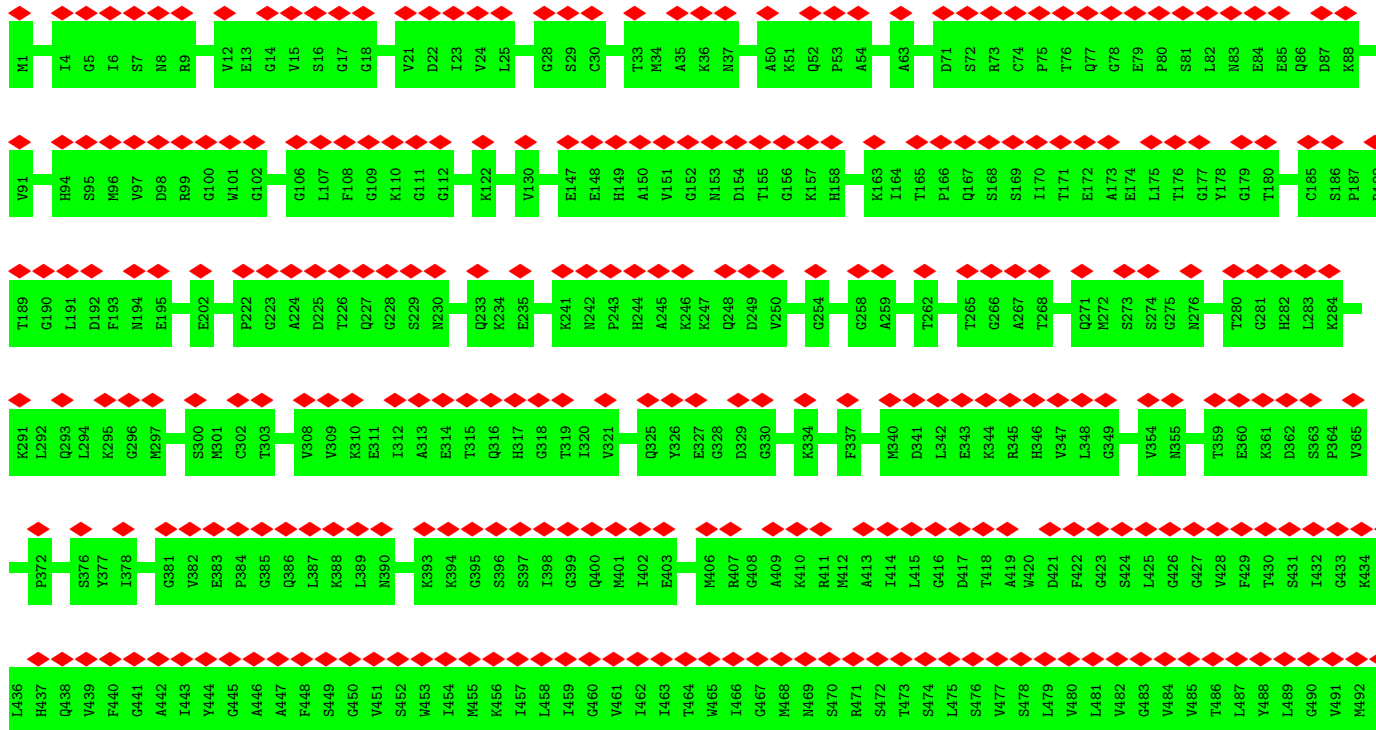


• Molecule 1: glycoprotein E

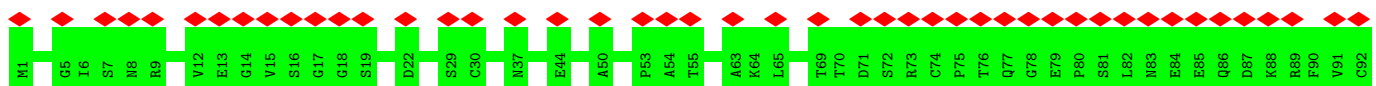


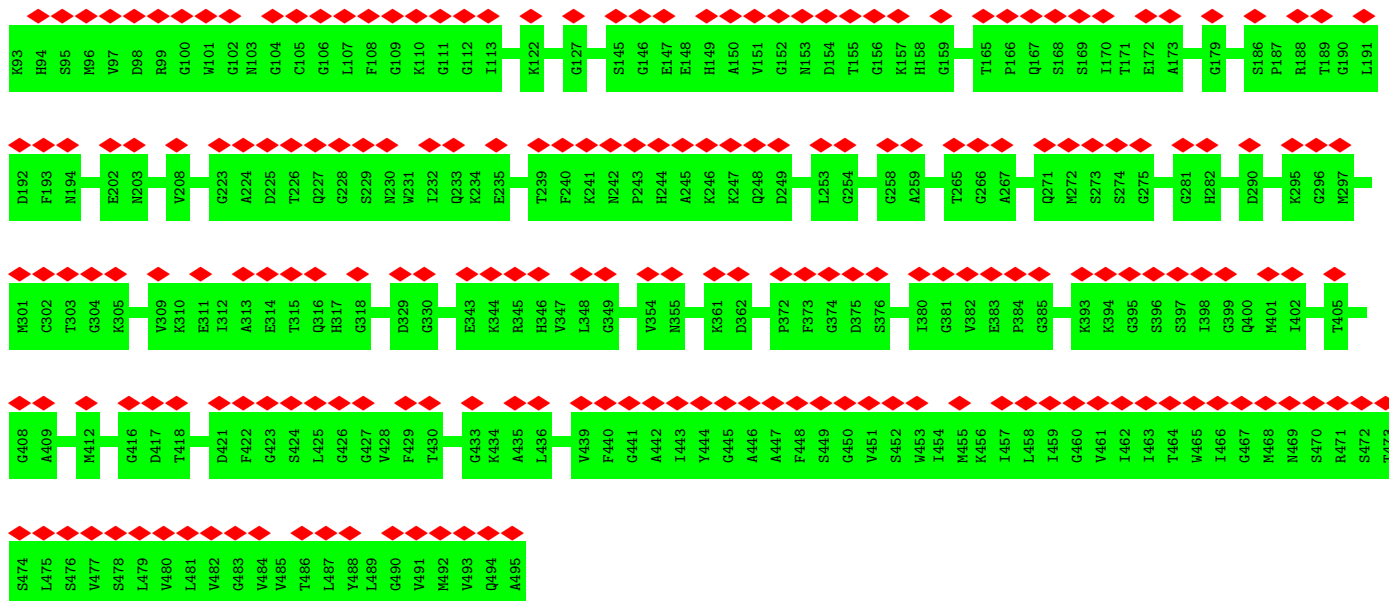


• Molecule 1: glycoprotein E



• Molecule 1: glycoprotein E





• Molecule 1: glycoprotein E



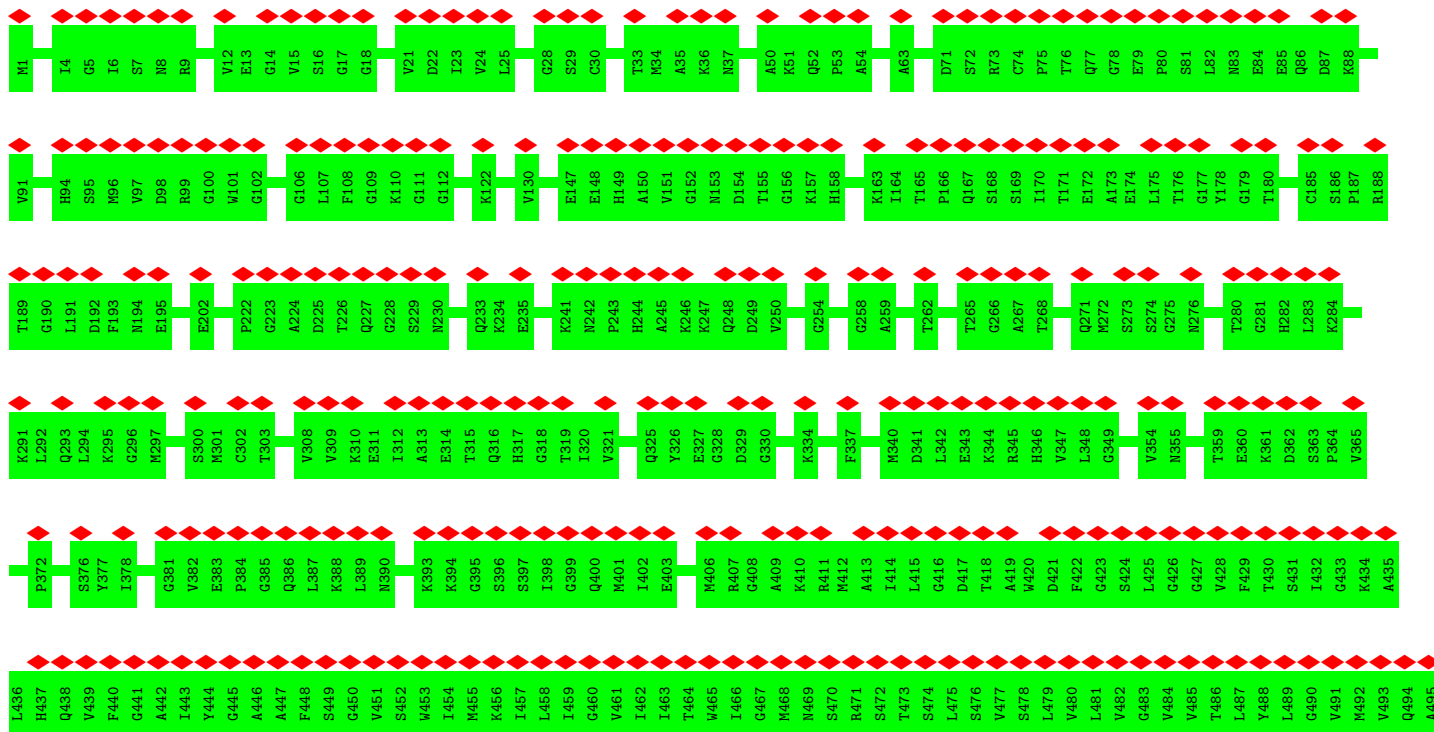
Chain A002:



• Molecule 1: glycoprotein E



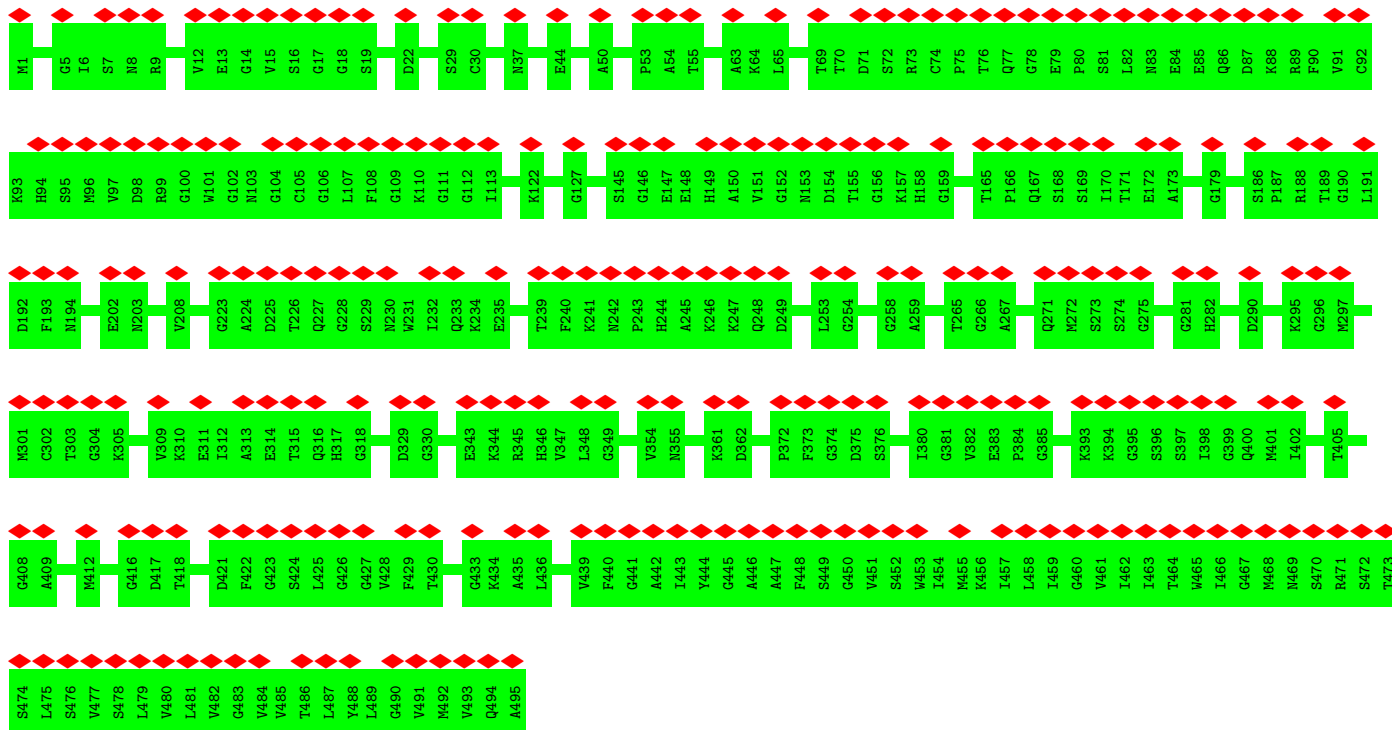
Chain B002:



• Molecule 1: glycoprotein E



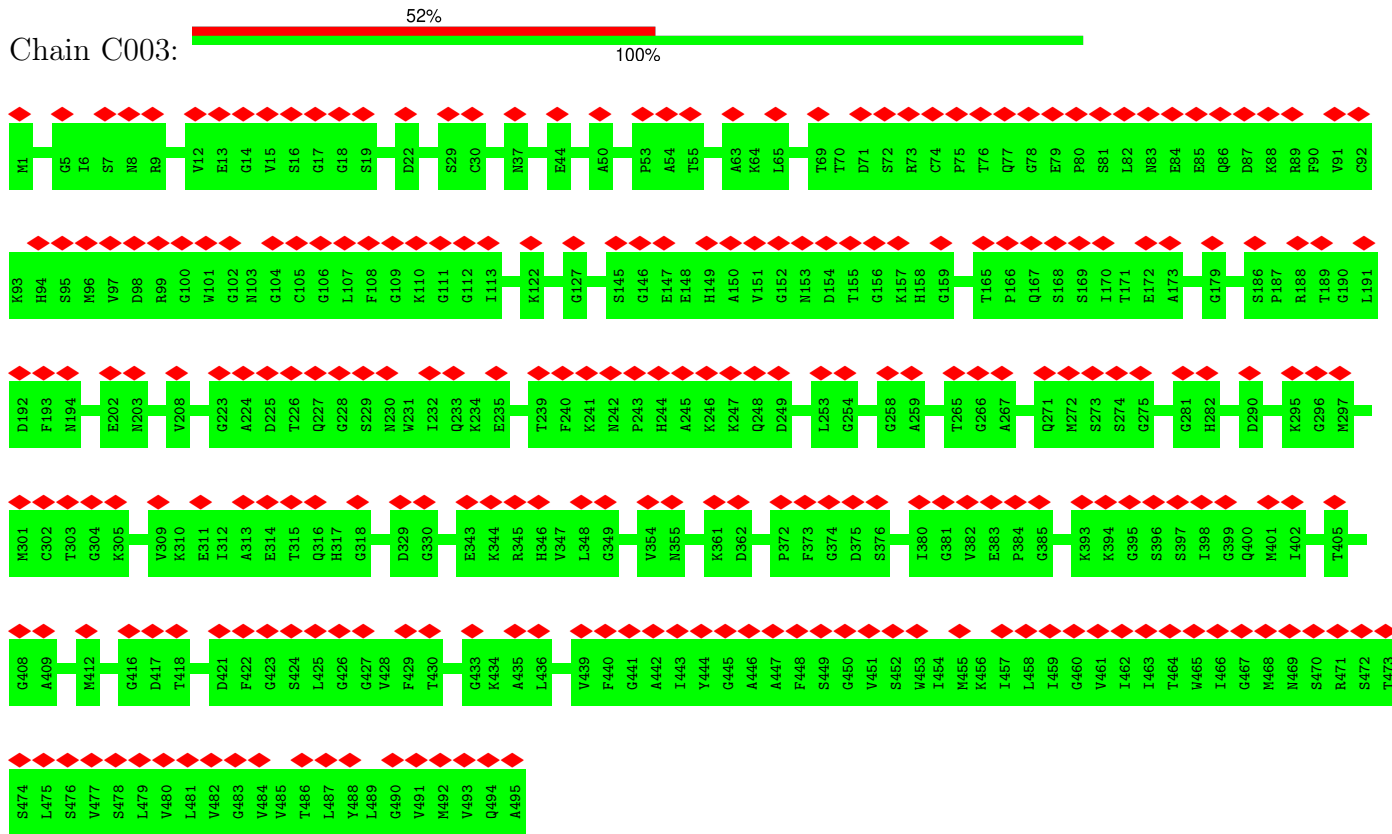
Chain C002:



• Molecule 1: glycoprotein E

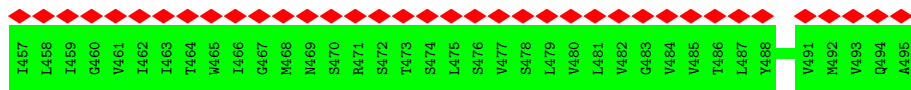


• Molecule 1: glycoprotein E

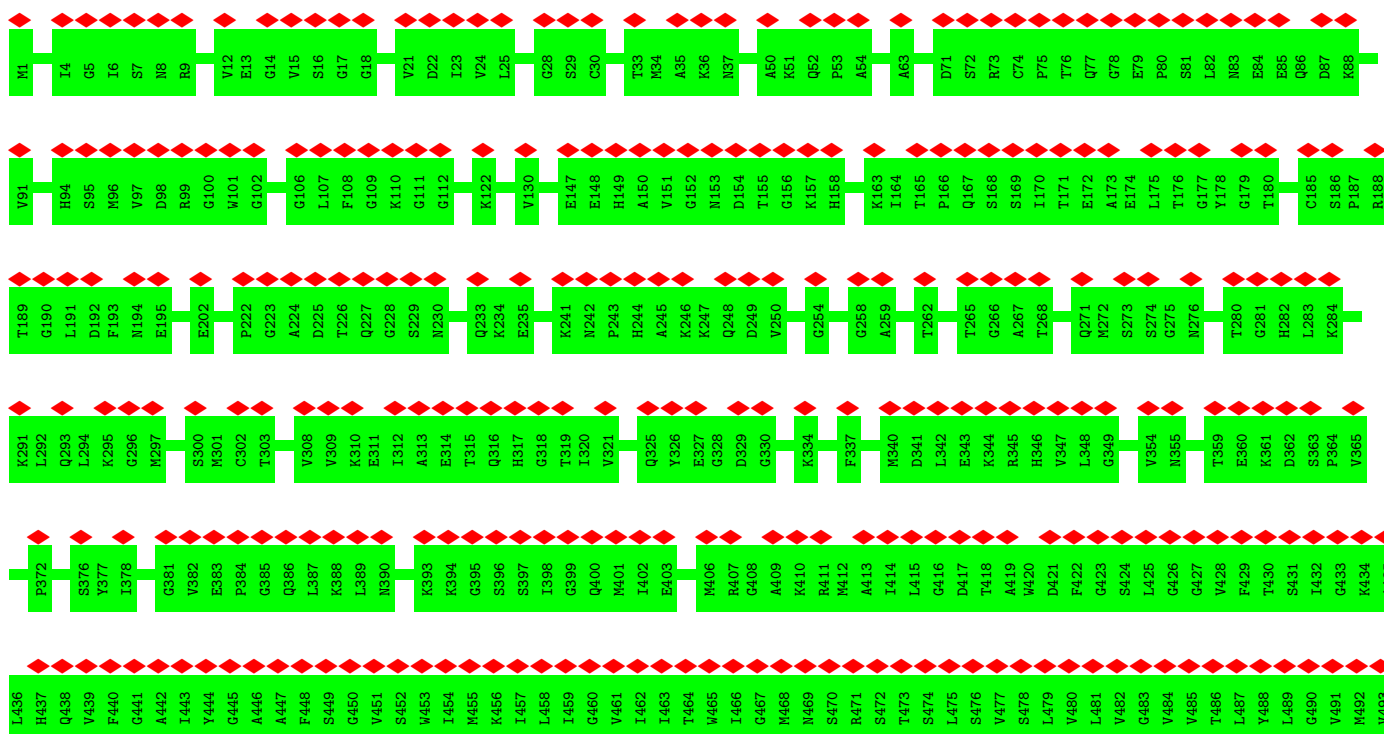


• Molecule 1: glycoprotein E

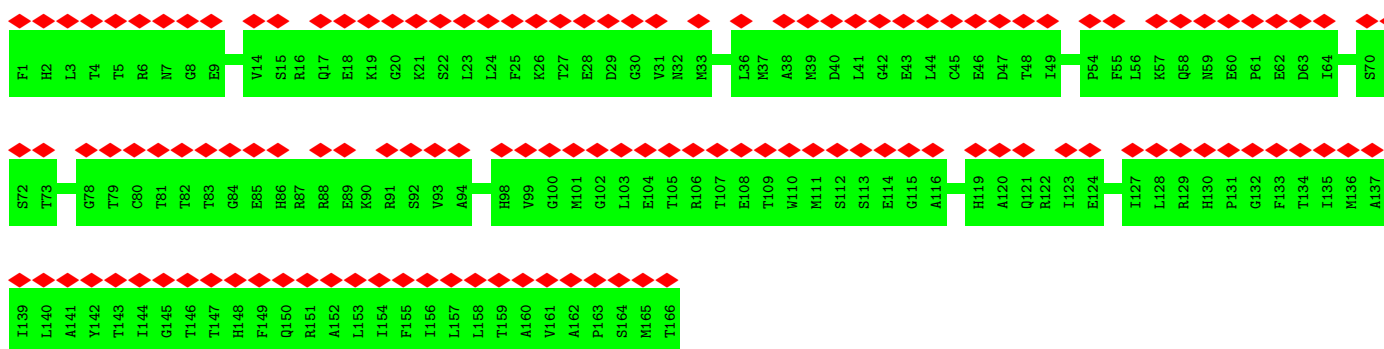
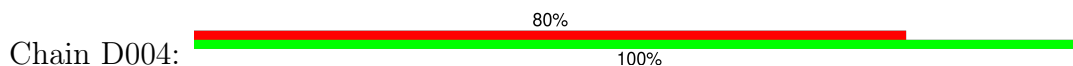




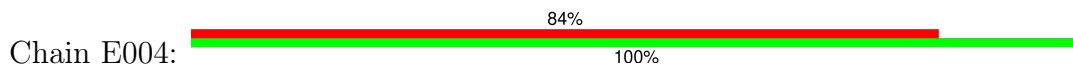
• Molecule 1: glycoprotein E

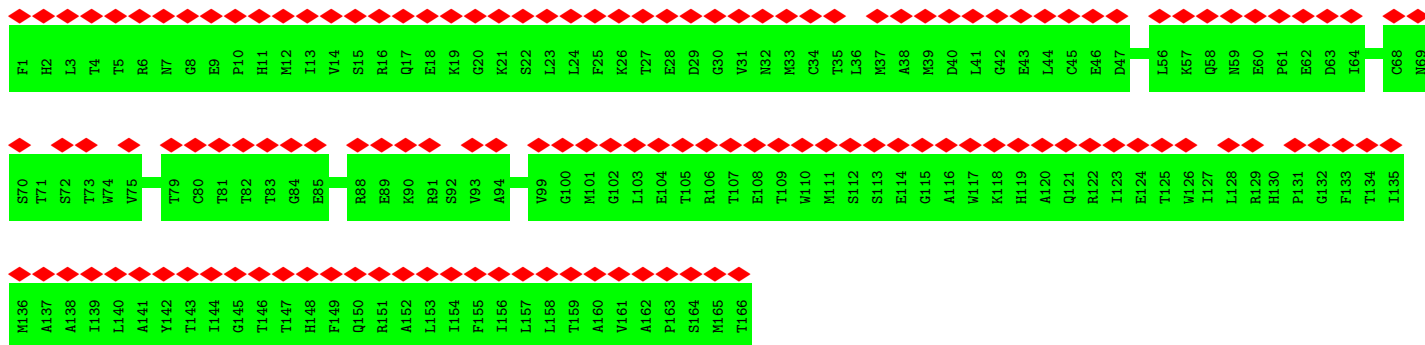


• Molecule 2: Protein prM

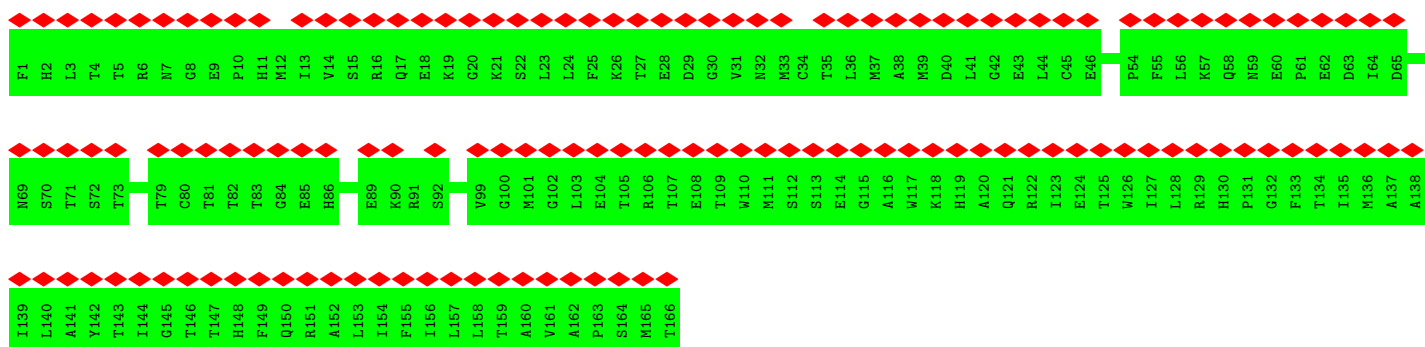
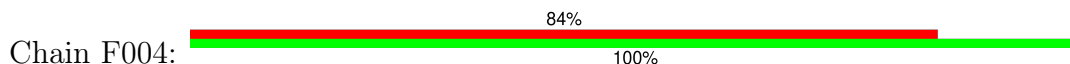


• Molecule 2: Protein prM

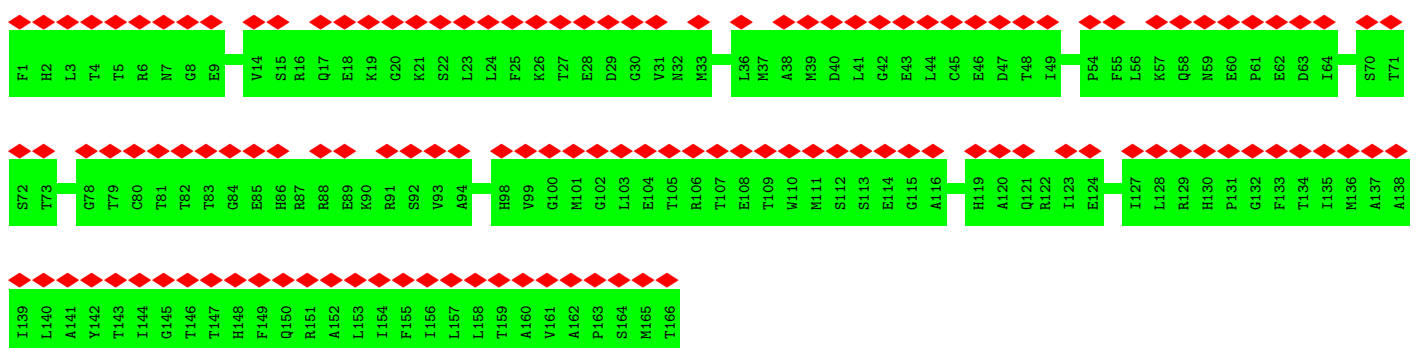
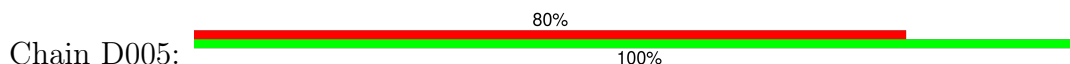




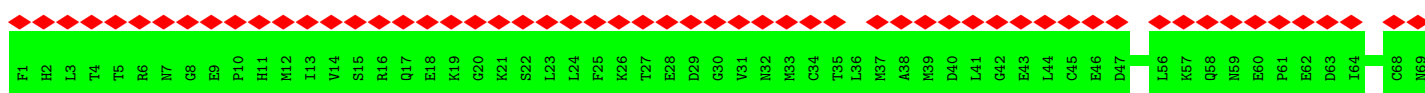
• Molecule 2: Protein prM



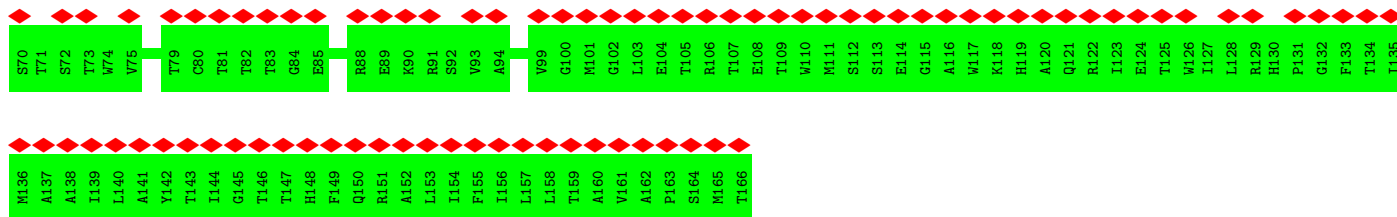
• Molecule 2: Protein prM



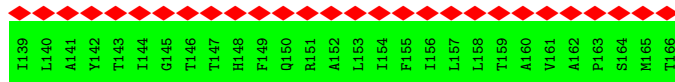
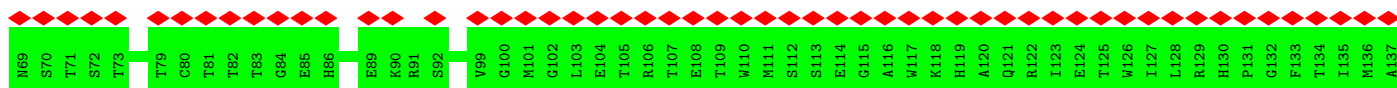
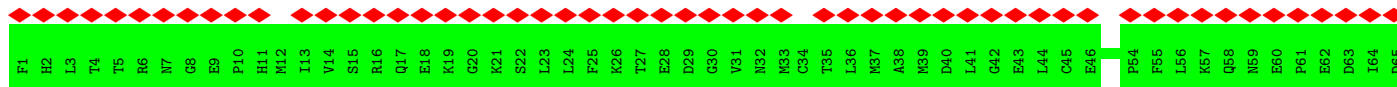
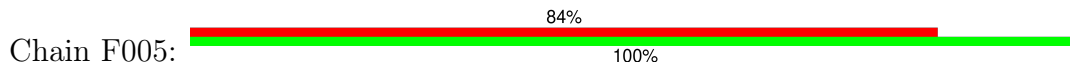
• Molecule 2: Protein prM



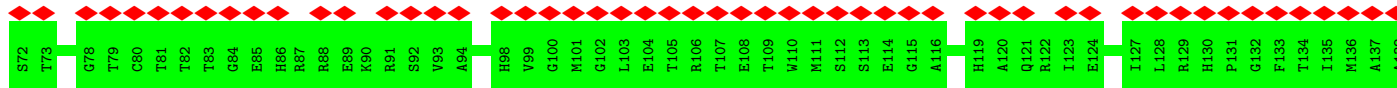
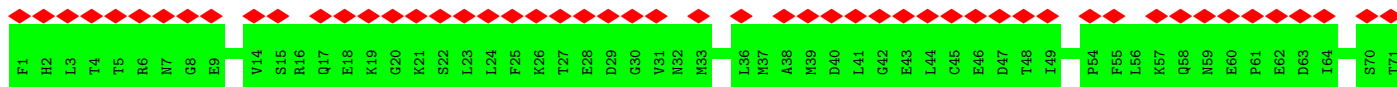
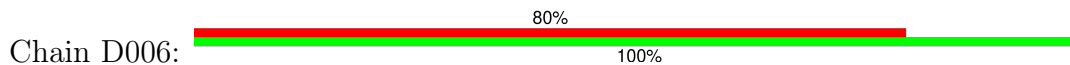




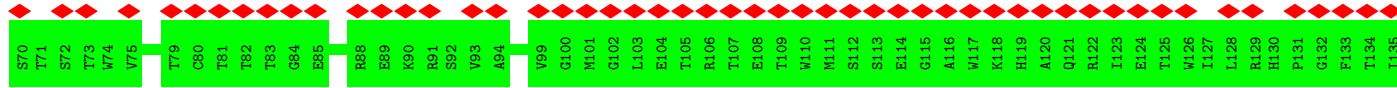
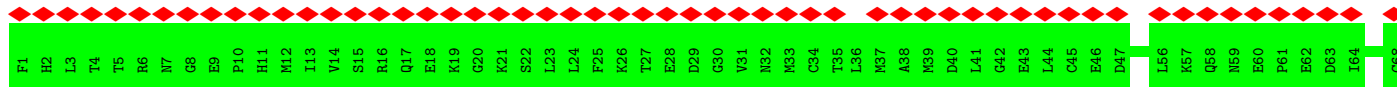
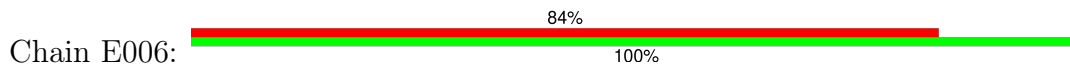
• Molecule 2: Protein prM

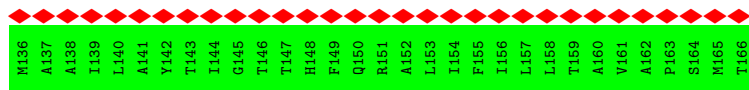


• Molecule 2: Protein prM

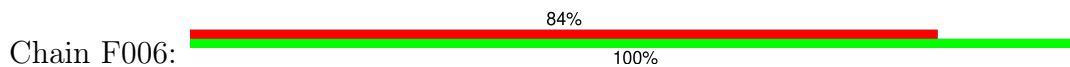


• Molecule 2: Protein prM

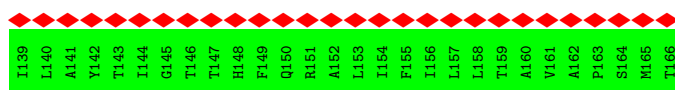
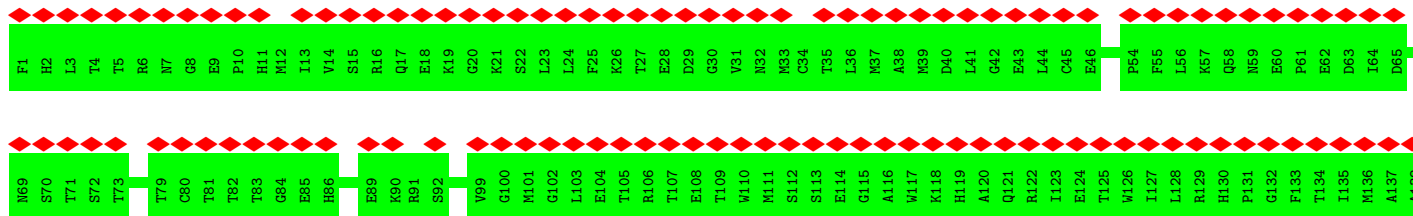




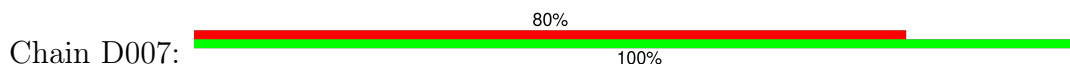
• Molecule 2: Protein prM



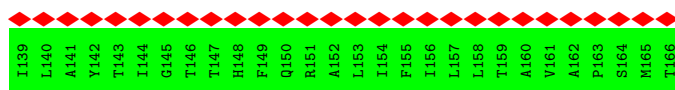
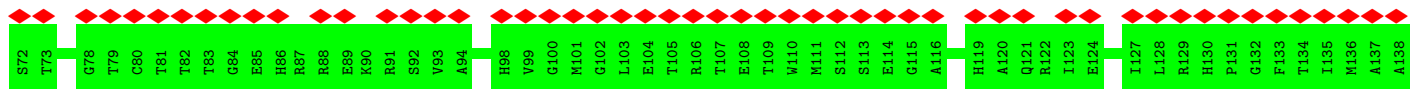
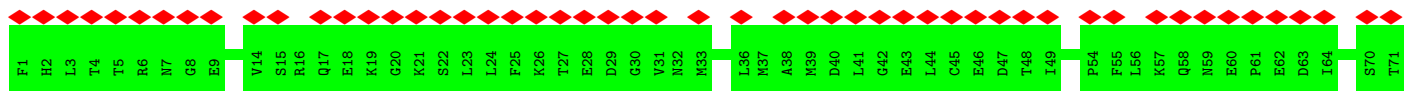
Chain F006:



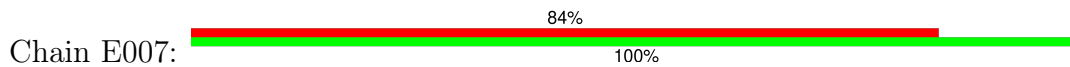
• Molecule 2: Protein prM



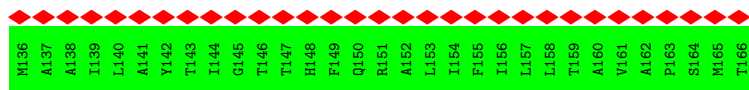
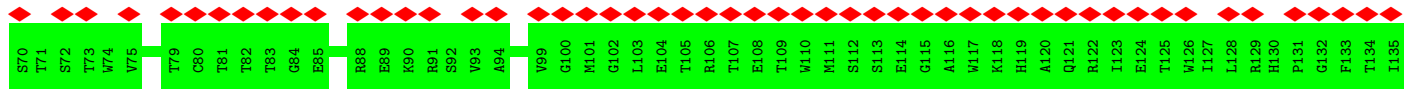
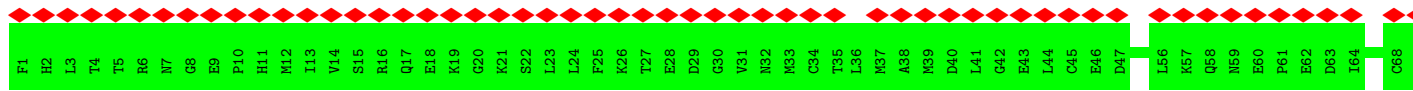
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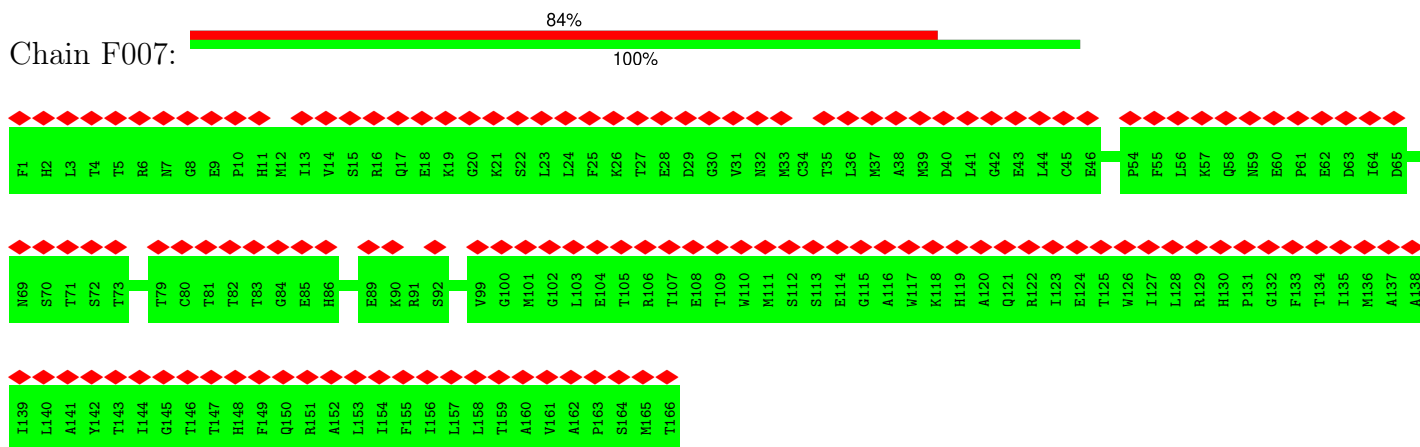
• Molecule 2: Protein prM



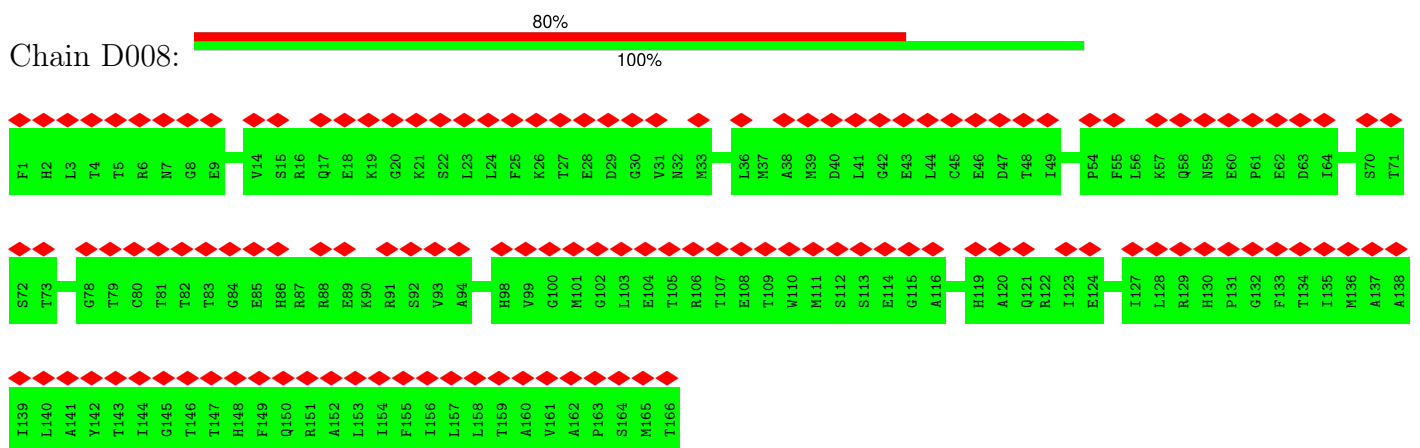
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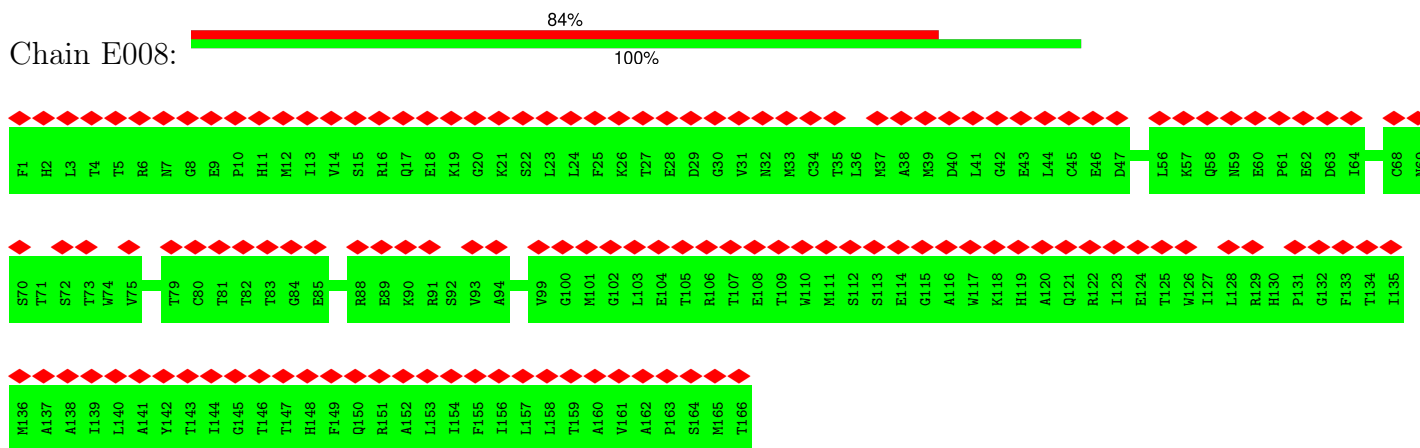
• Molecule 2: Protein prM



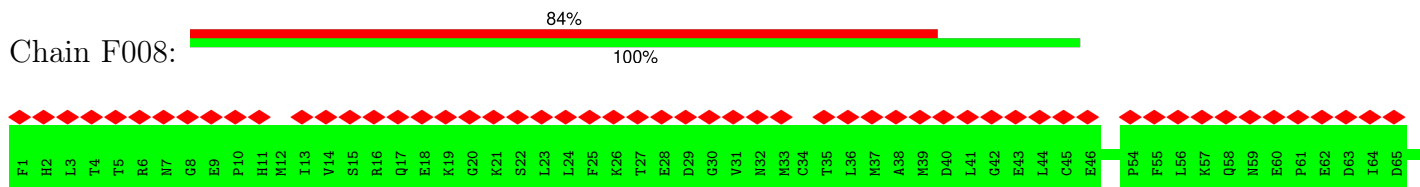
• Molecule 2: Protein prM

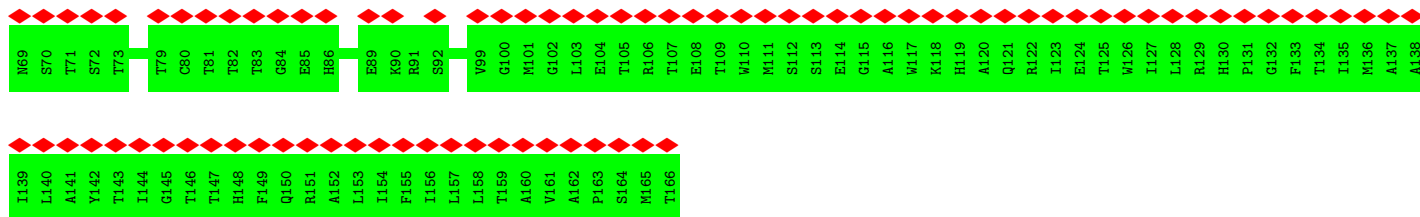


• Molecule 2: Protein prM

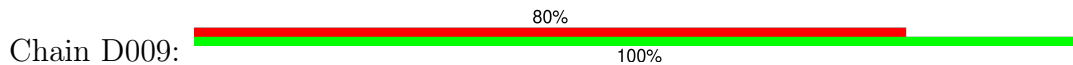


• Molecule 2: Protein prM

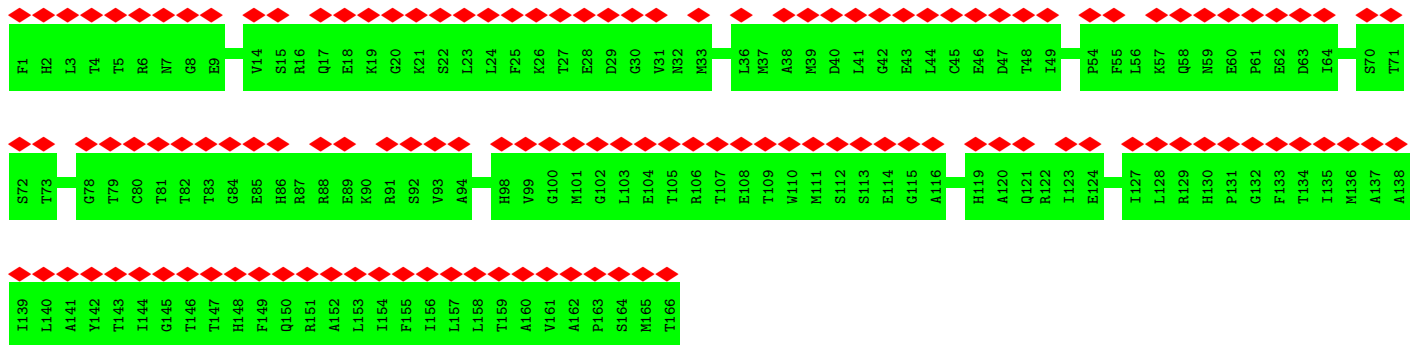




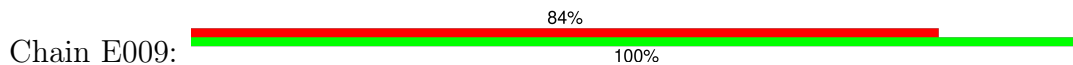
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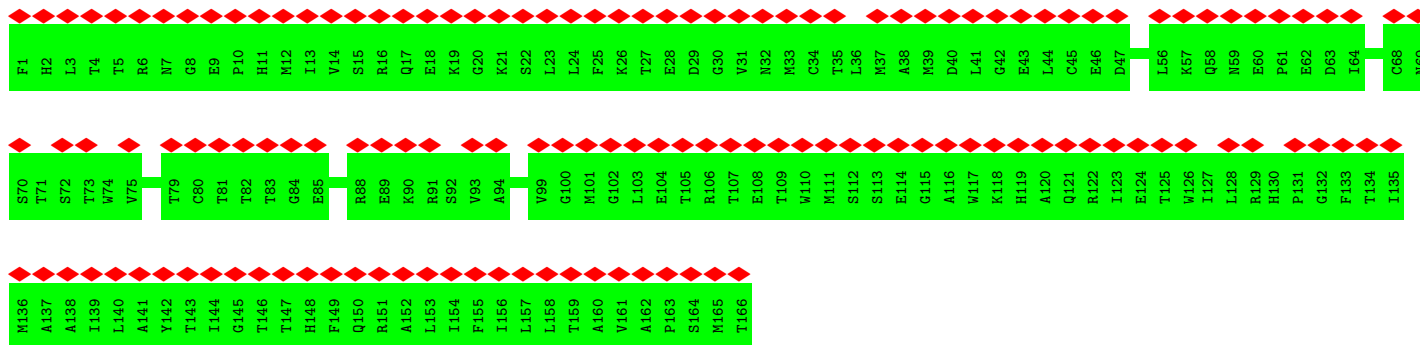
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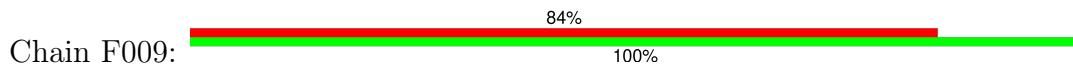
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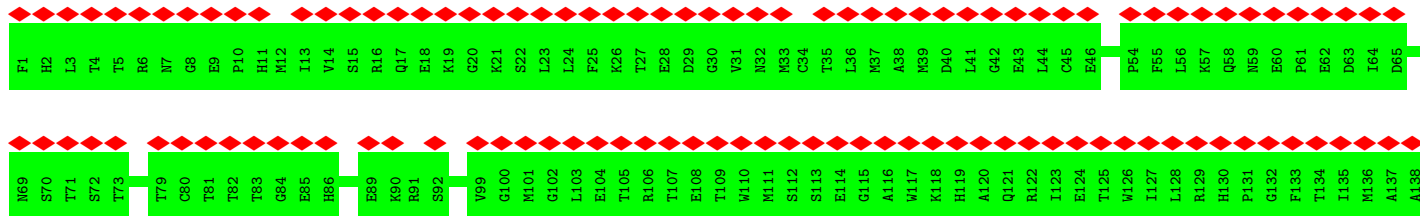
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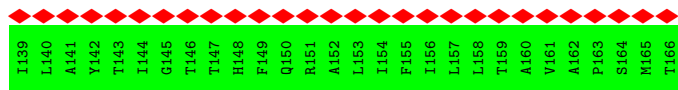


• Molecule 2: Protein prM

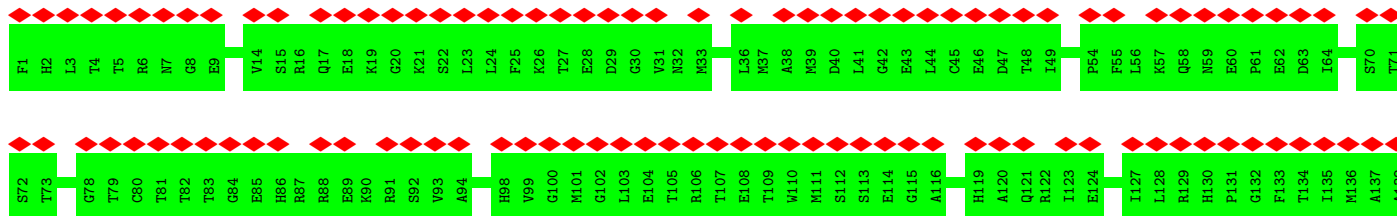
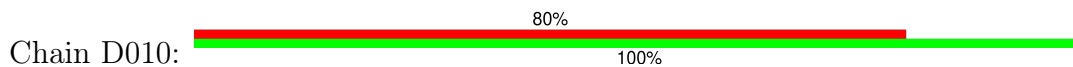


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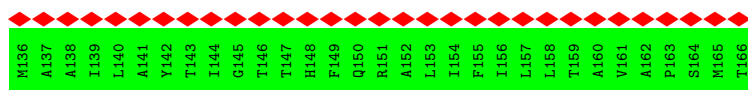
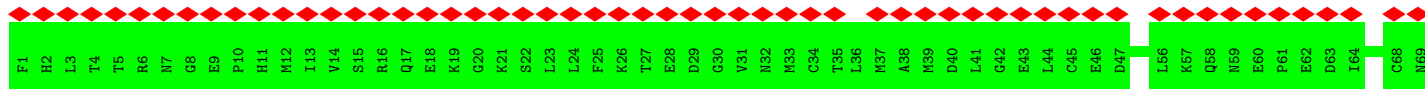
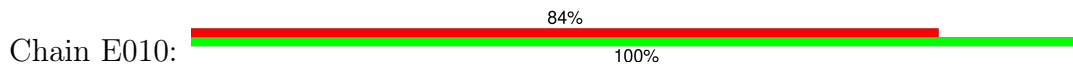




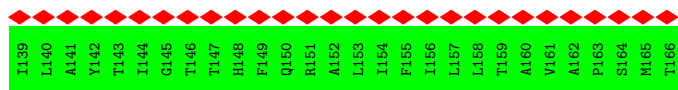
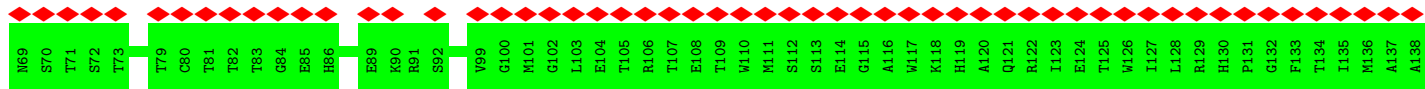
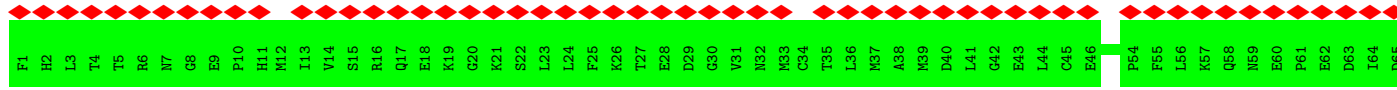
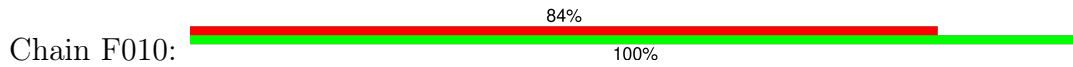
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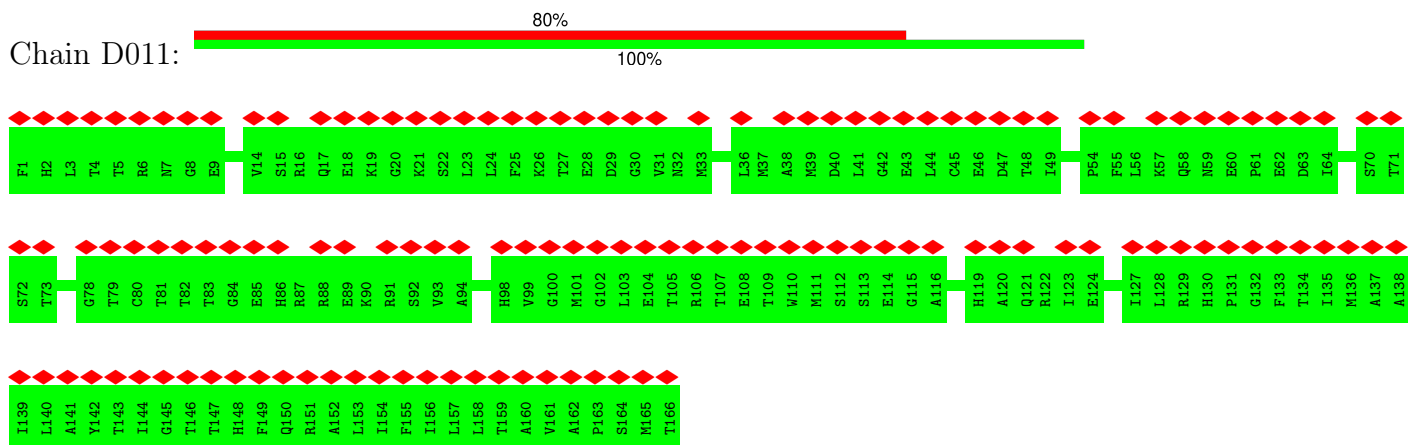
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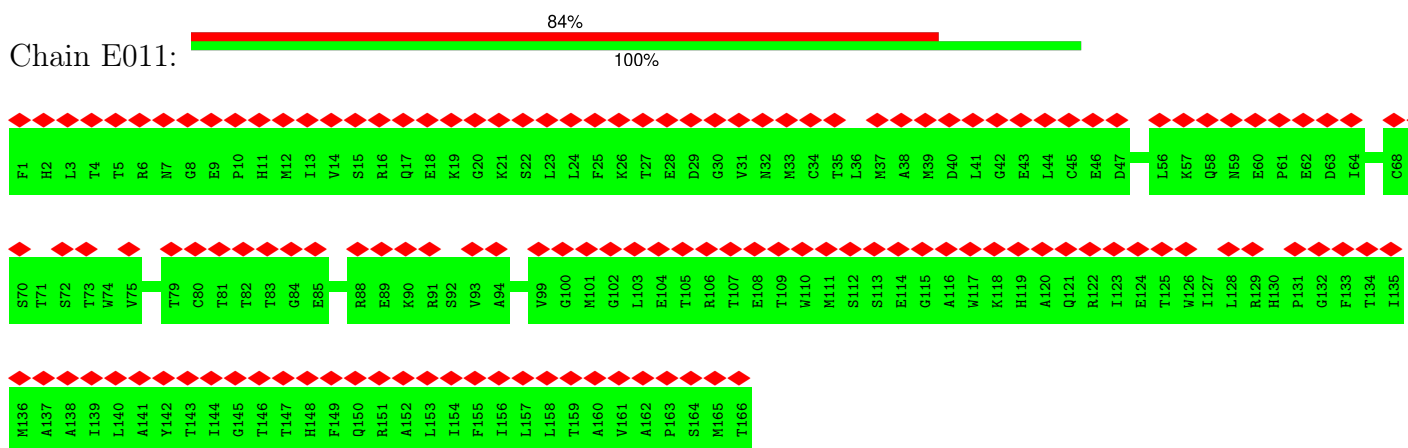
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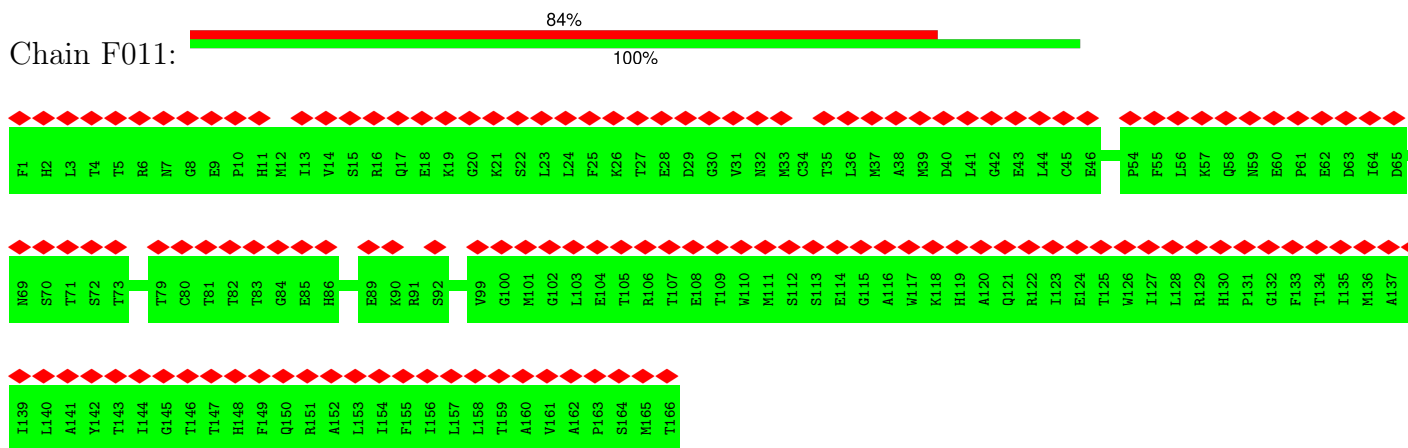
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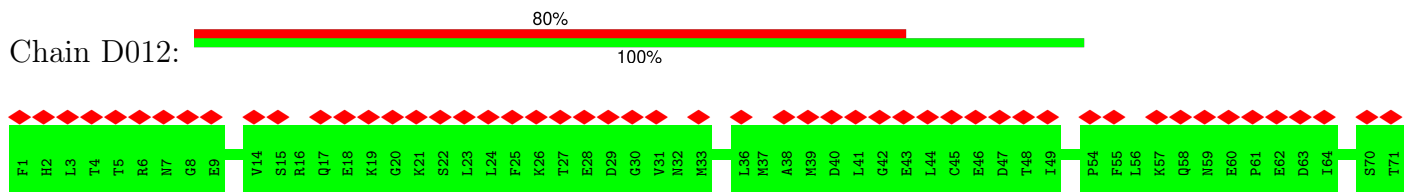
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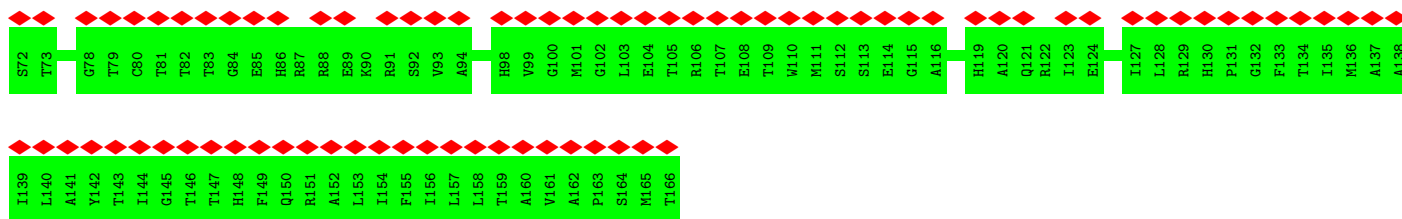


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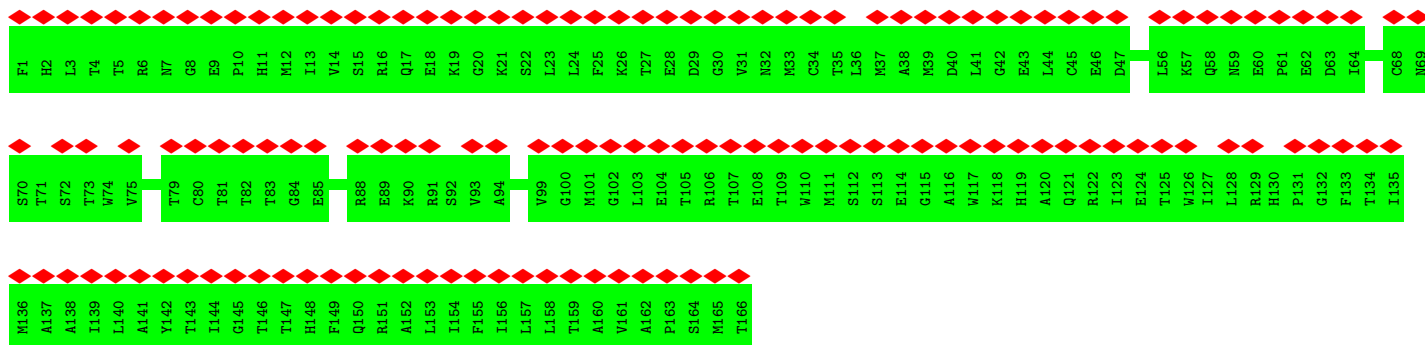
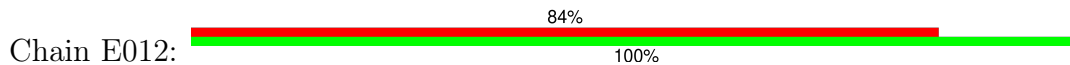


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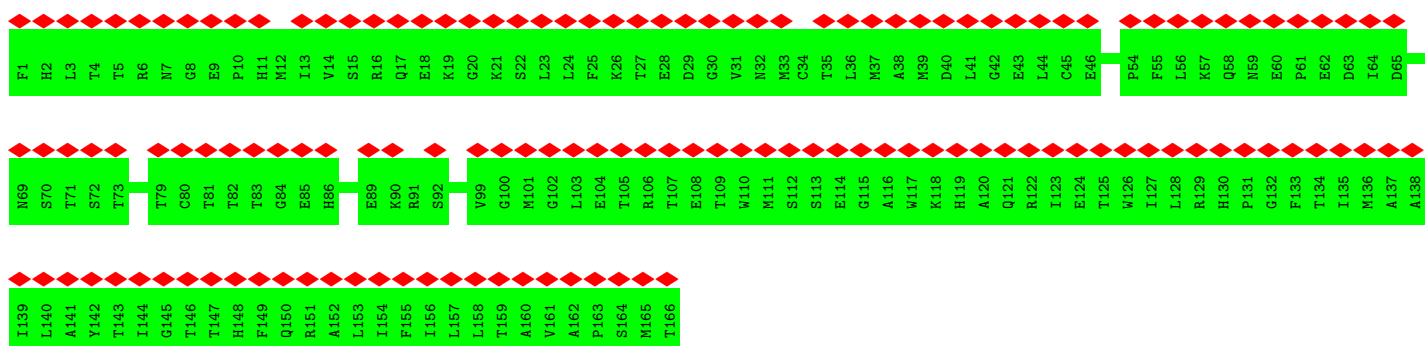
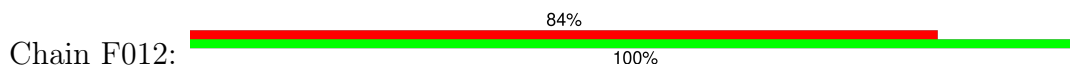




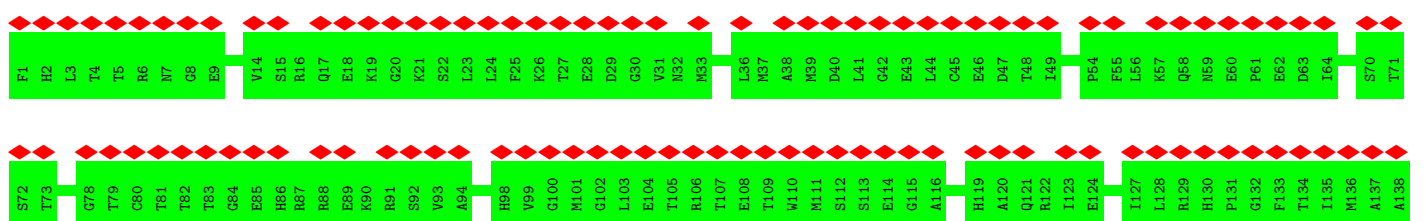
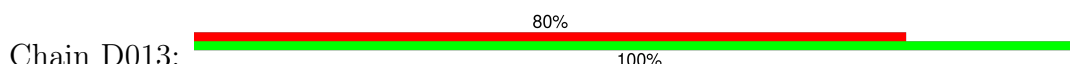
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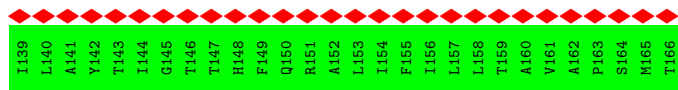


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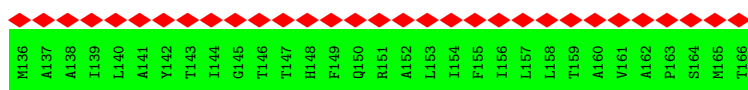
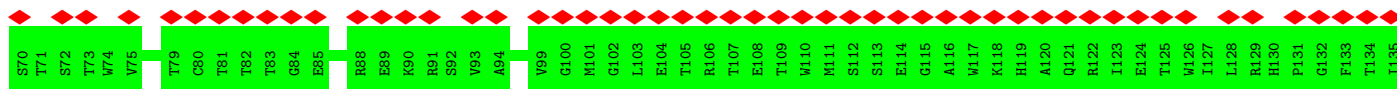
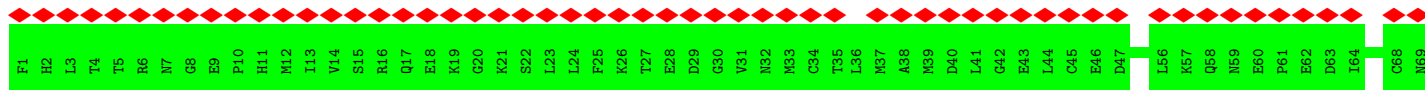
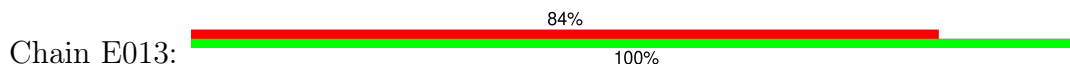


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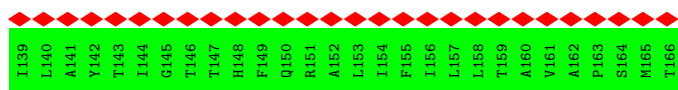
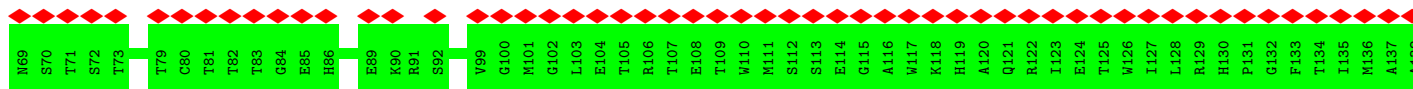
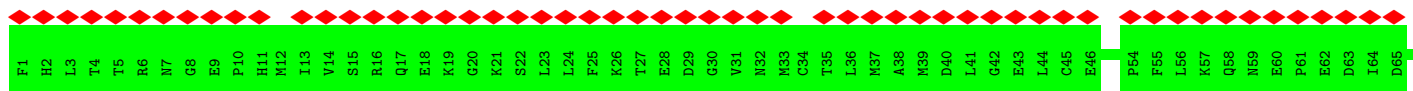
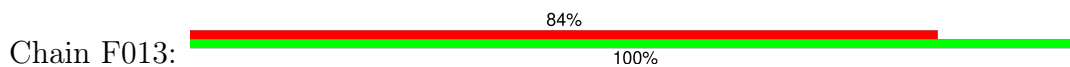




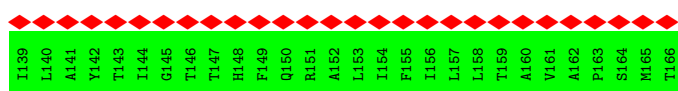
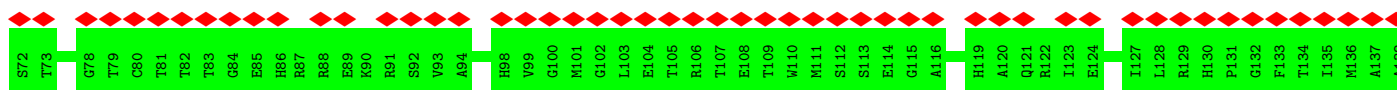
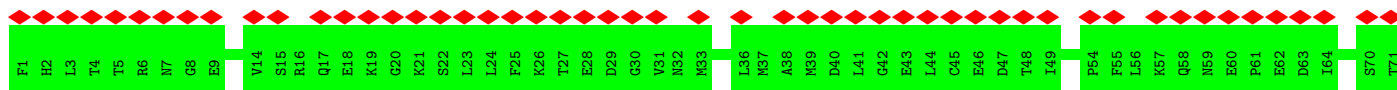
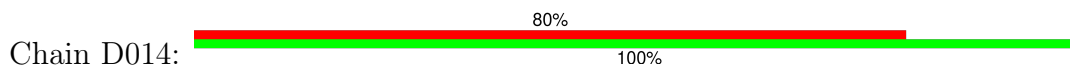
• Molecule 2: Protein prM



• Molecule 2: Protein prM

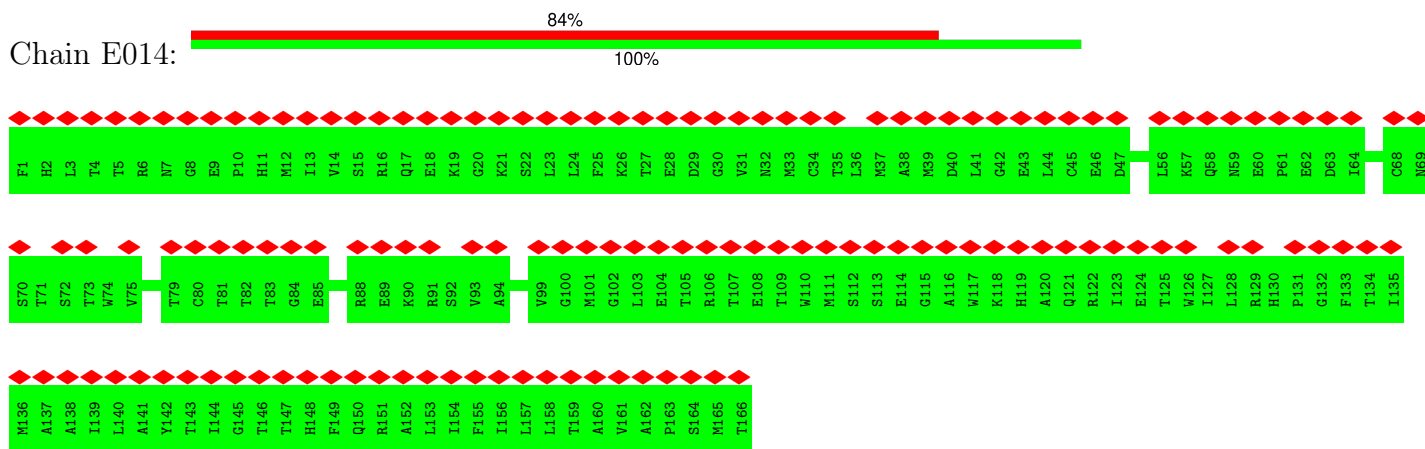


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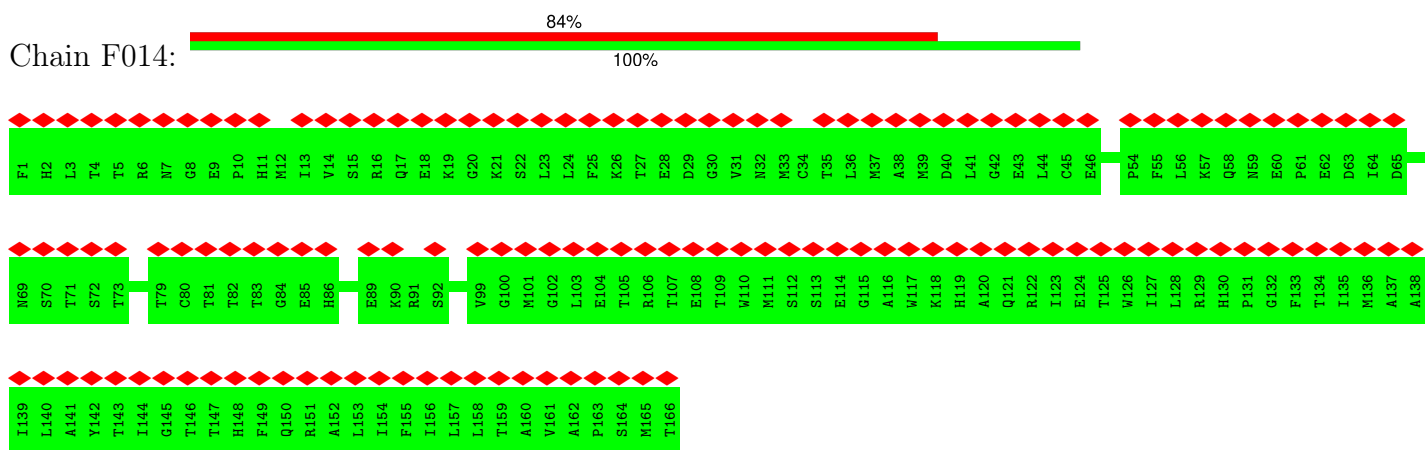


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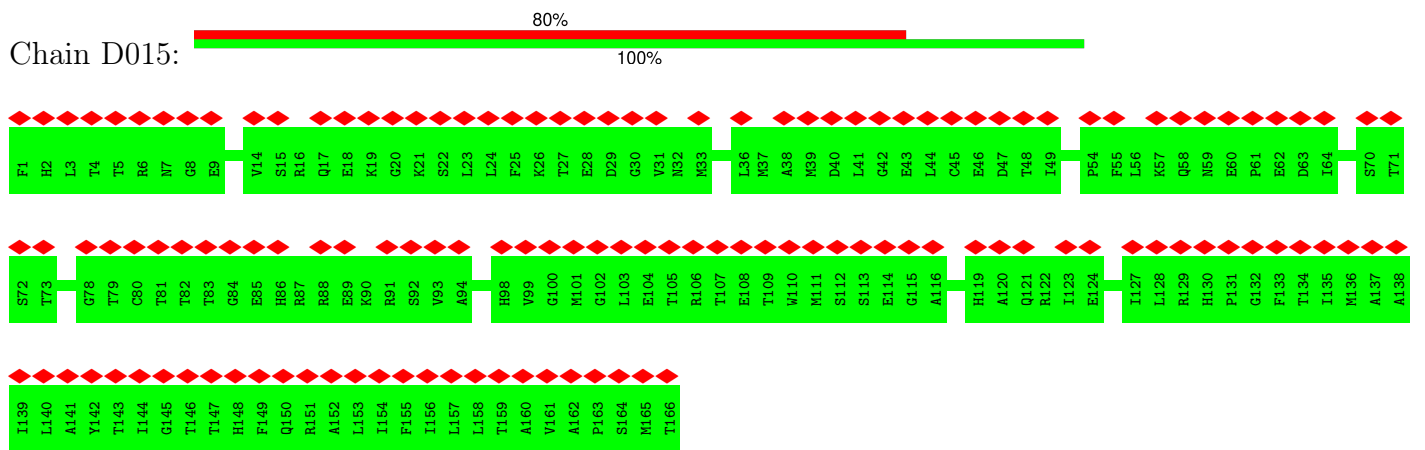




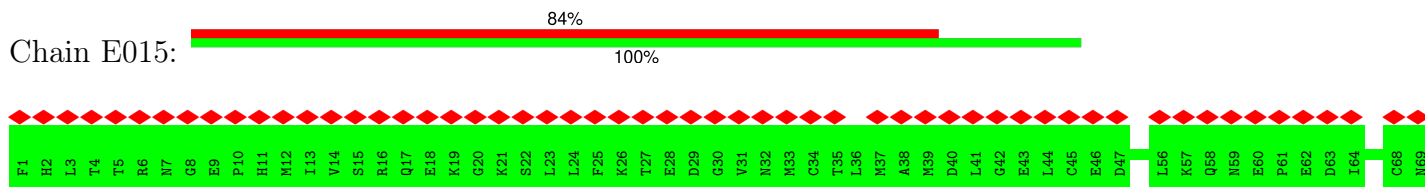
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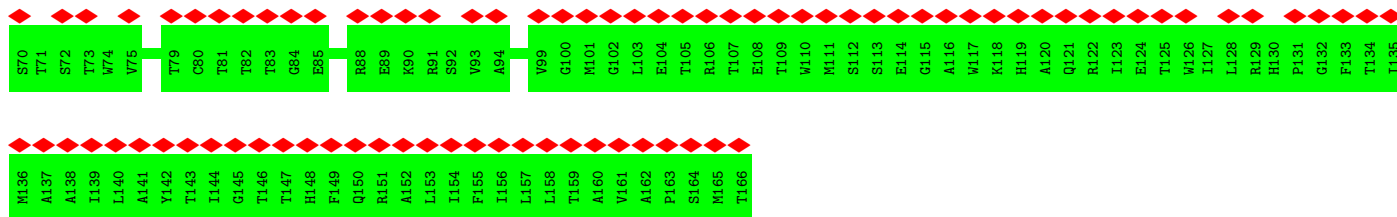


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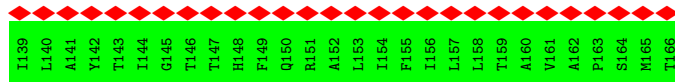
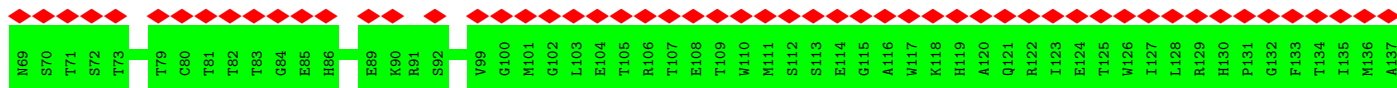
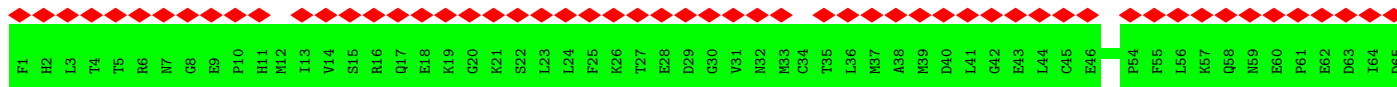
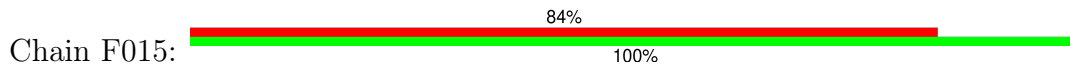


• Molecule 2: Protein prM

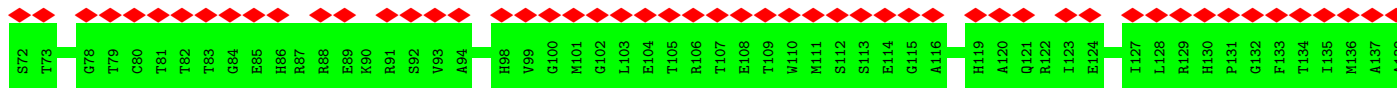
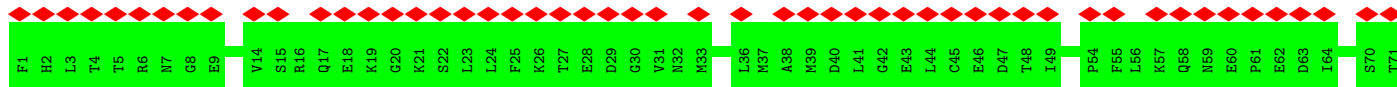
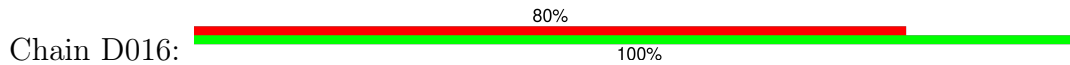




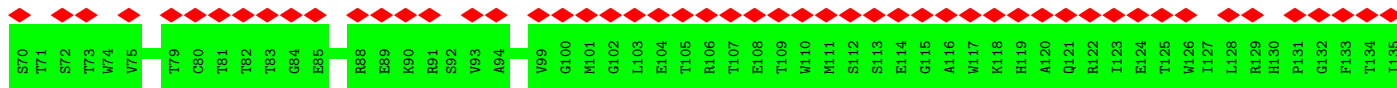
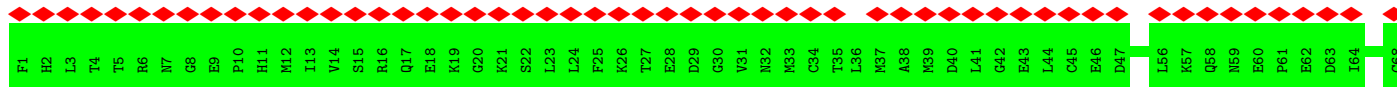
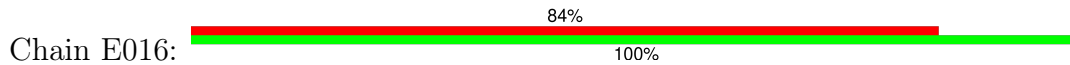
• Molecule 2: Protein prM

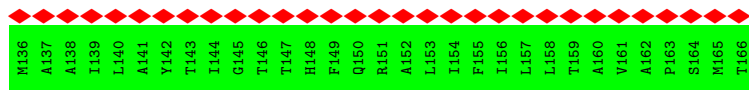


• Molecule 2: Protein prM

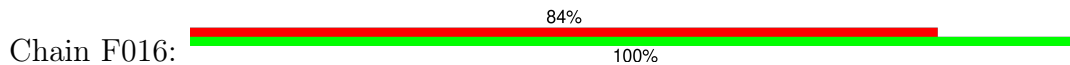


• Molecule 2: Protein prM

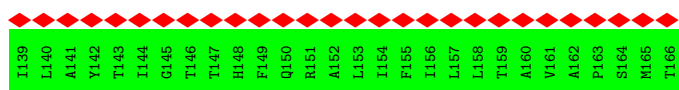
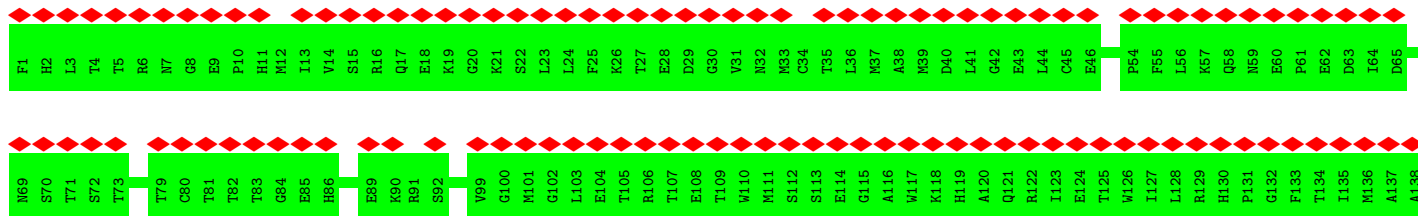




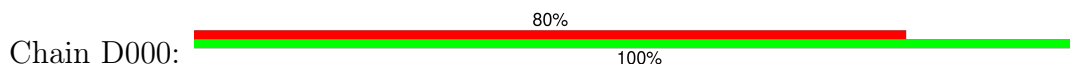
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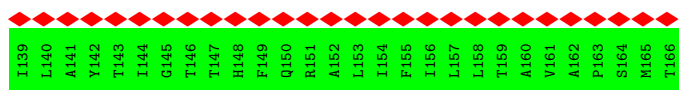
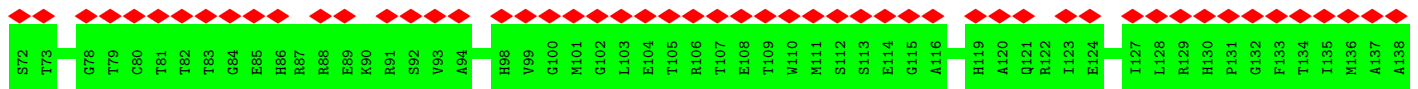
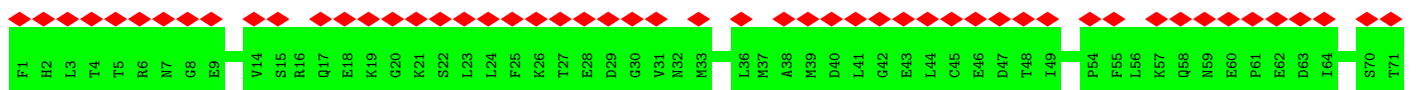
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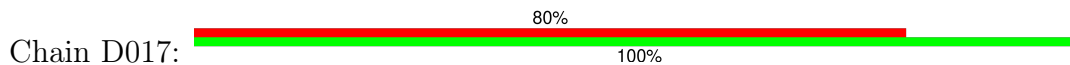
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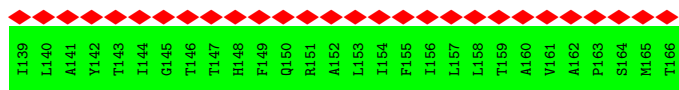
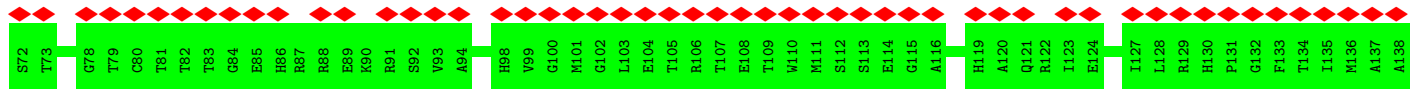
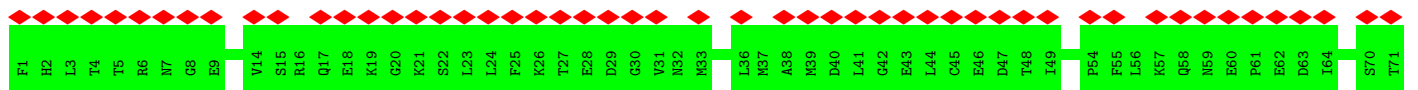
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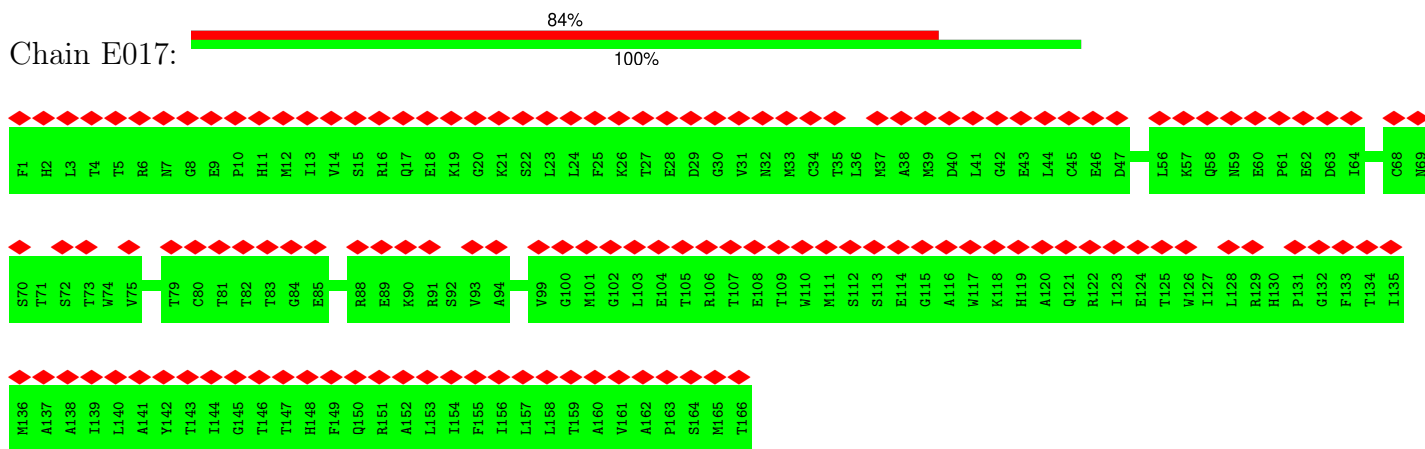
• Molecule 2: Protein prM



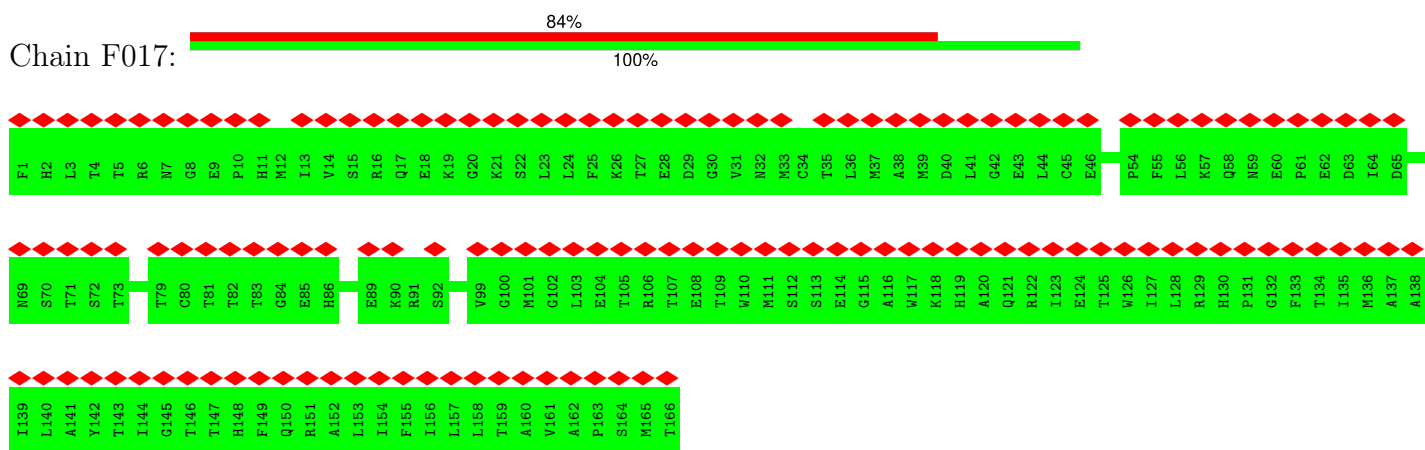
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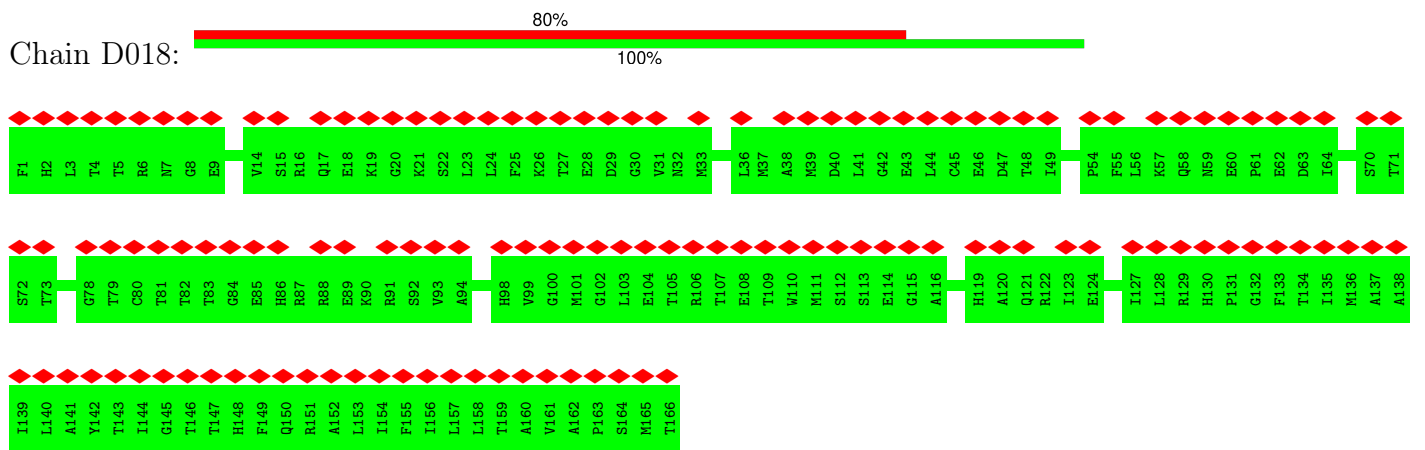
• Molecule 2: Protein prM



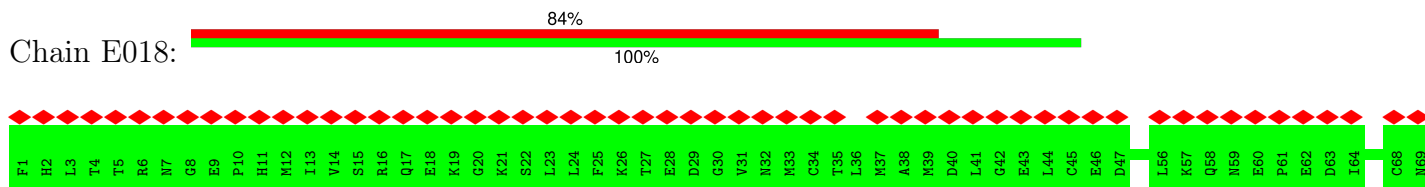
• Molecule 2: Protein prM

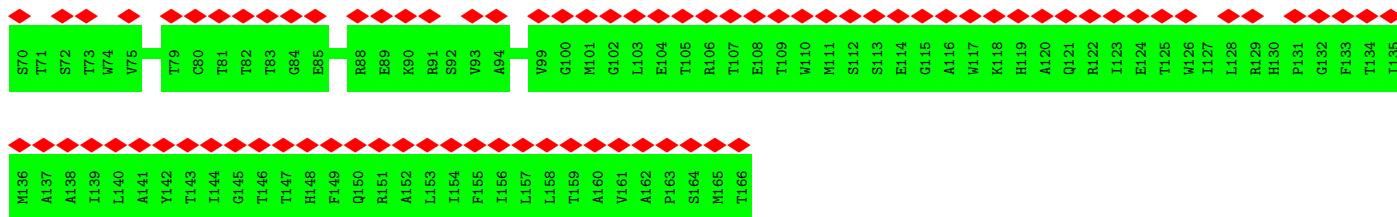


• Molecule 2: Protein prM

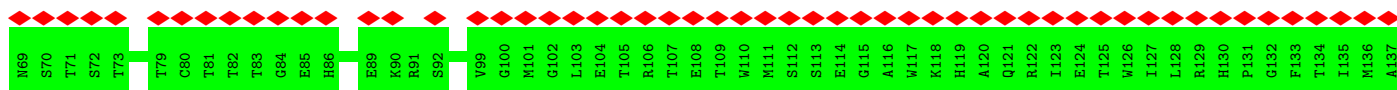
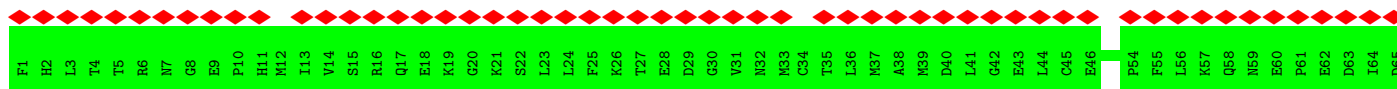
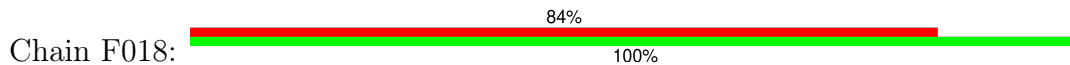


• Molecule 2: Protein prM

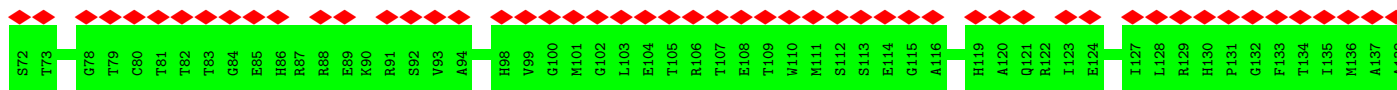
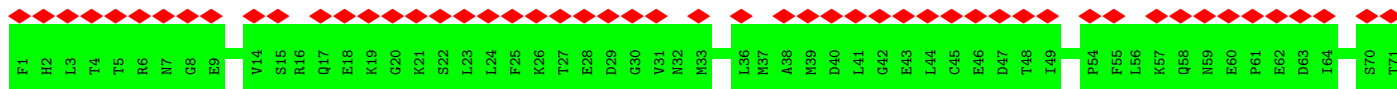
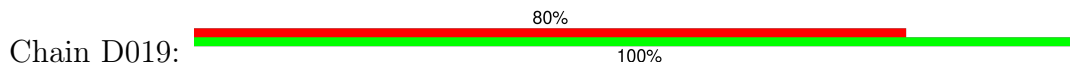




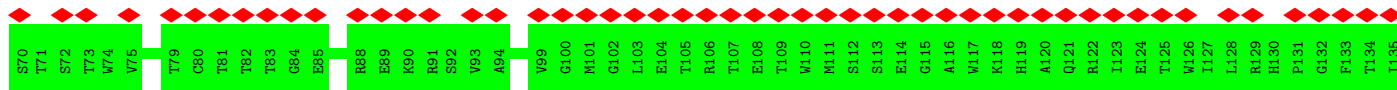
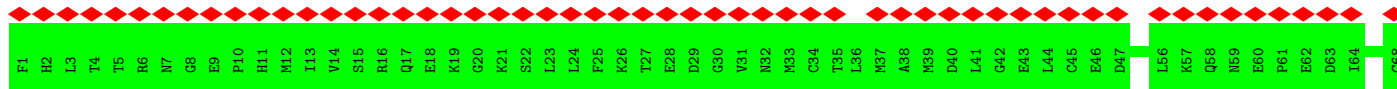
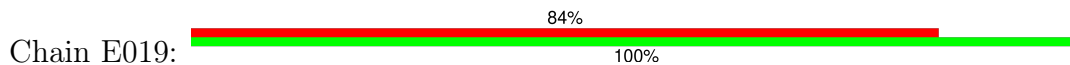
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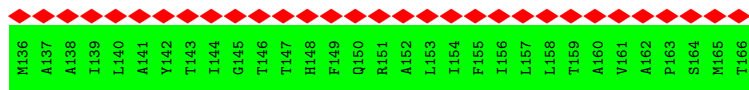


• Molecule 2: Protein prM

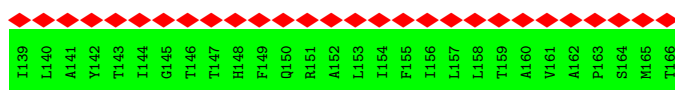
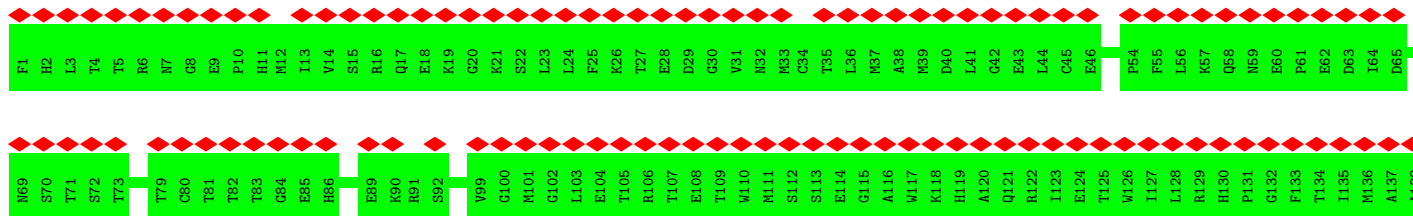
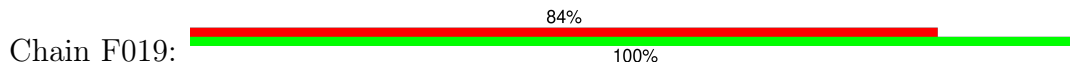


• Molecule 2: Protein prM

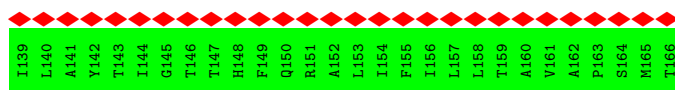
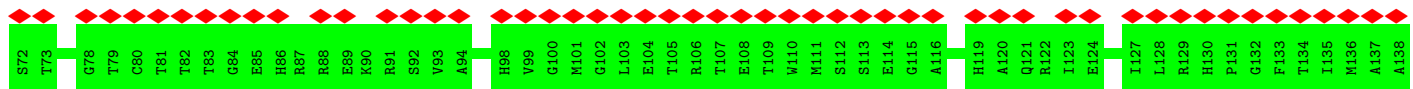
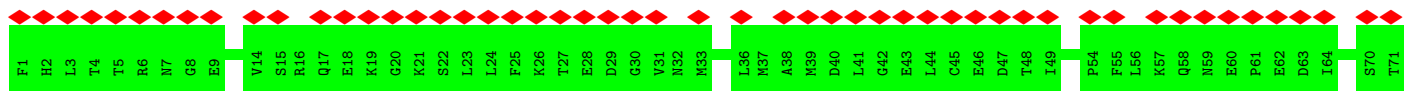
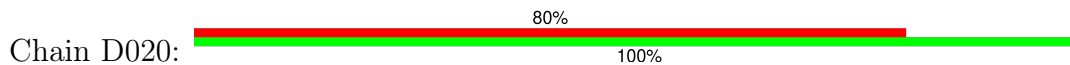




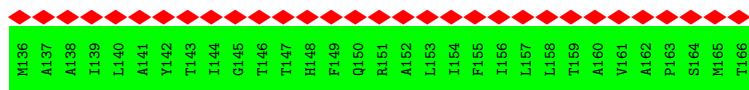
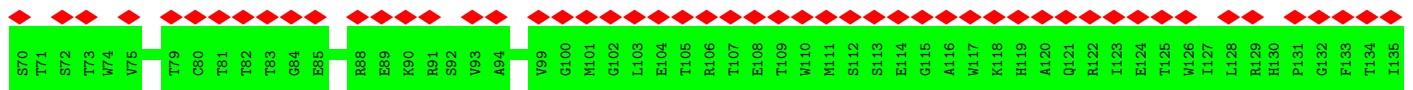
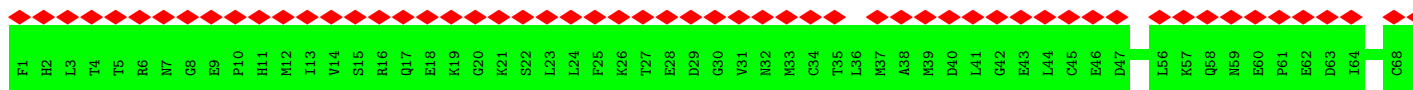
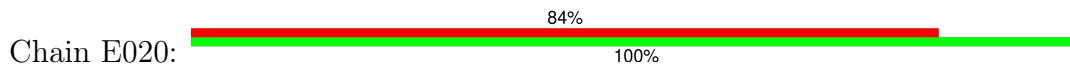
• Molecule 2: Protein prM



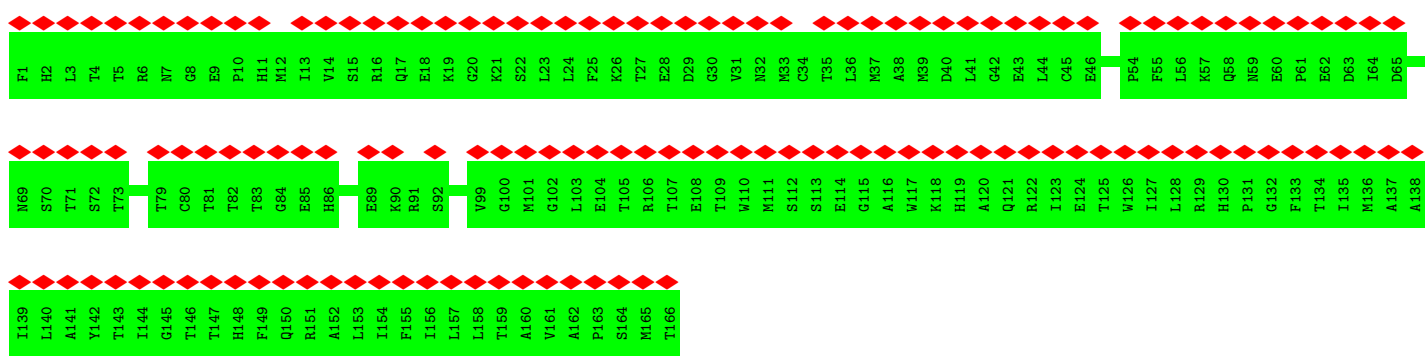
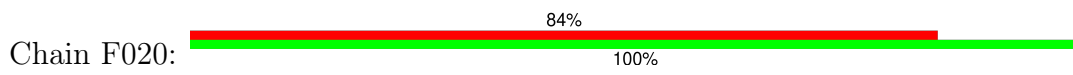
• Molecule 2: Protein prM



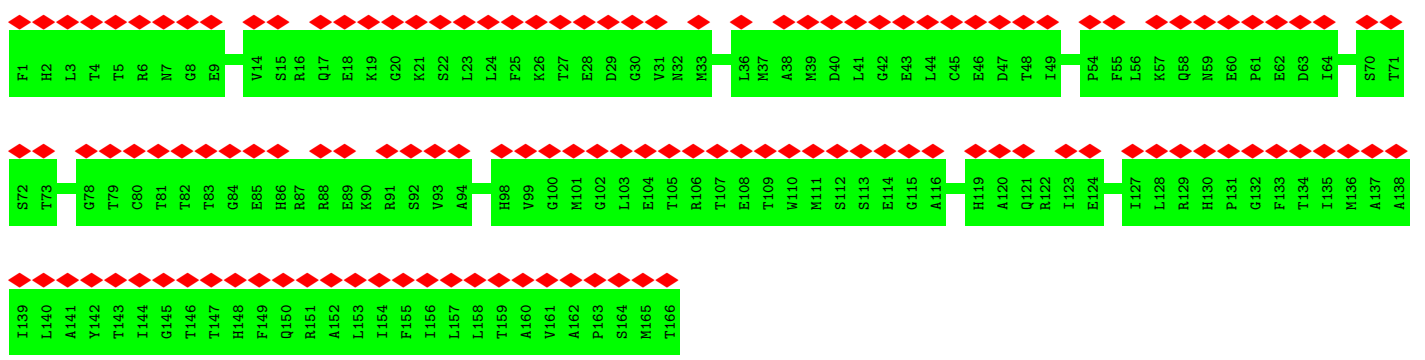
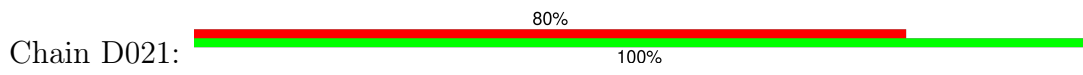
• Molecule 2: Protein prM



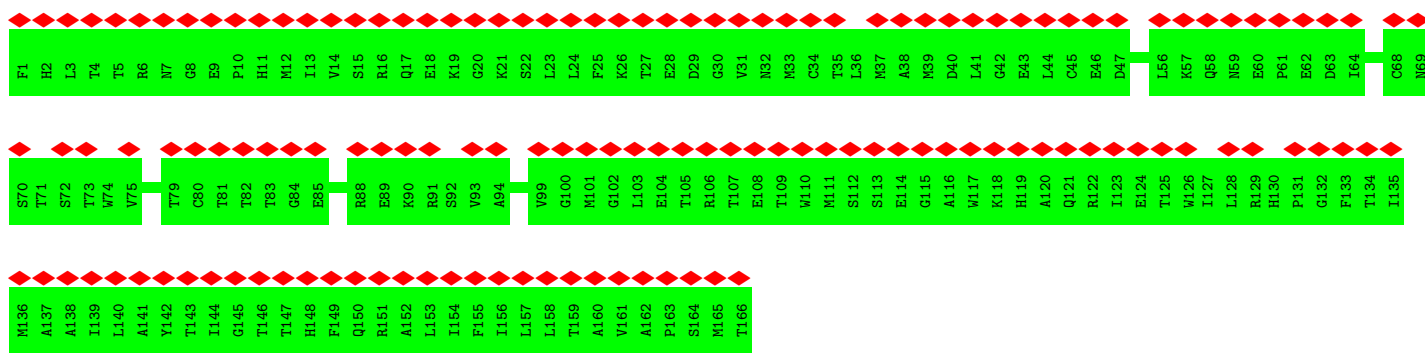
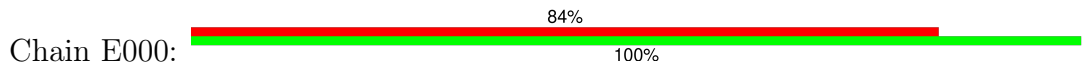
• Molecule 2: Protein prM



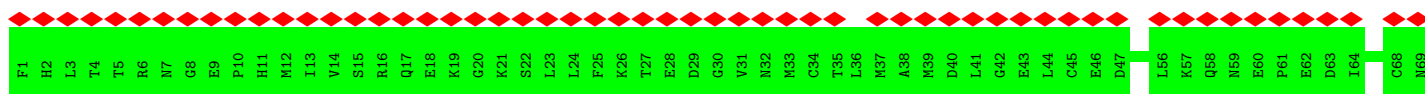
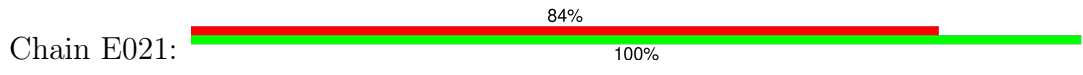
• Molecule 2: Protein prM

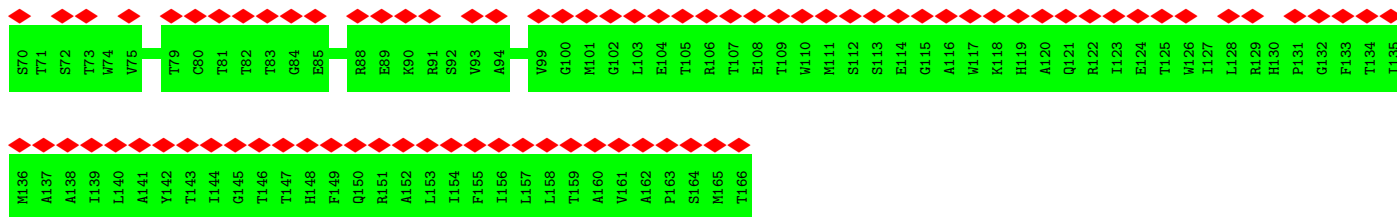


• Molecule 2: Protein prM

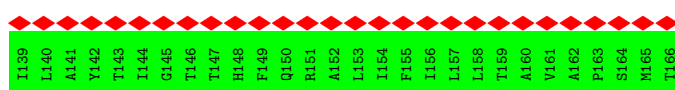
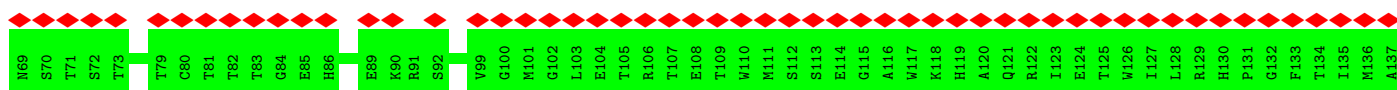
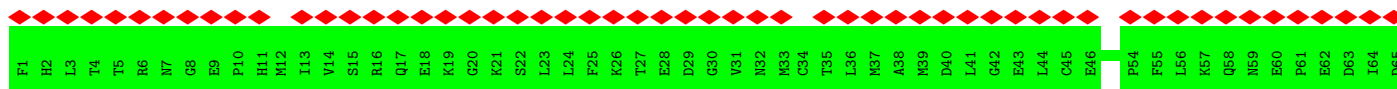
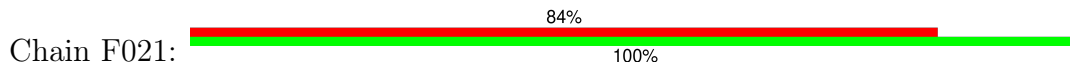


• Molecule 2: Protein prM

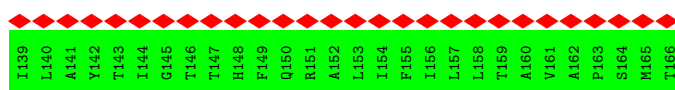
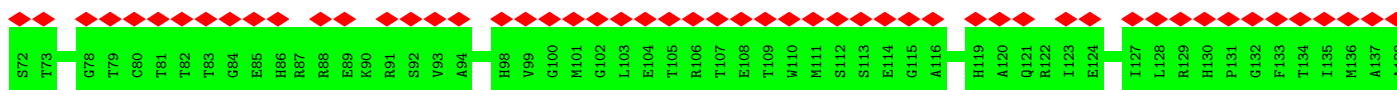
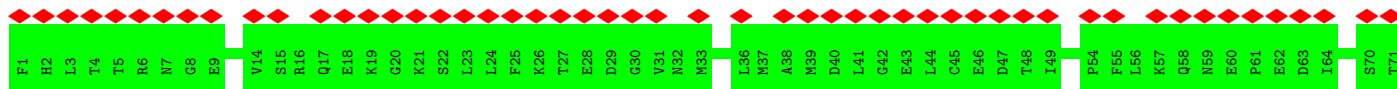
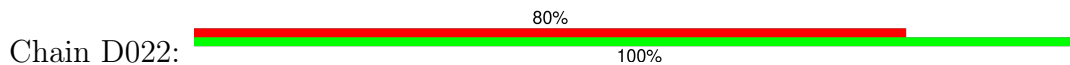




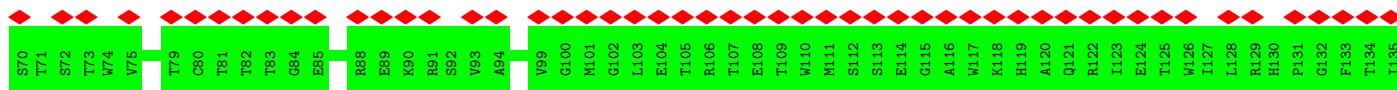
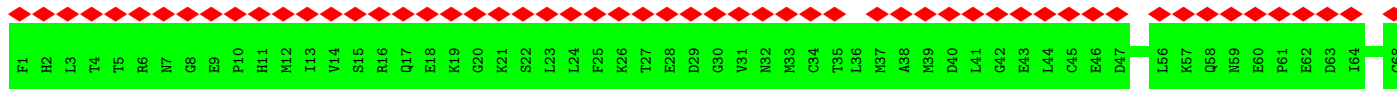
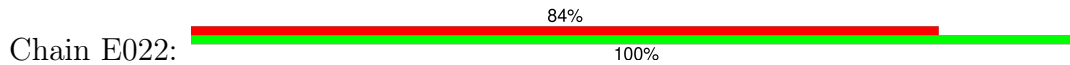
• Molecule 2: Protein prM



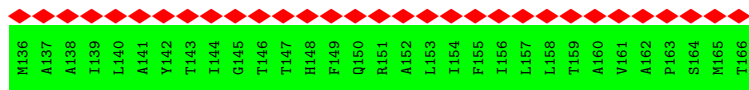
• Molecule 2: Protein prM



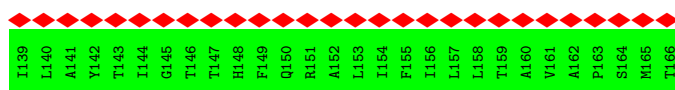
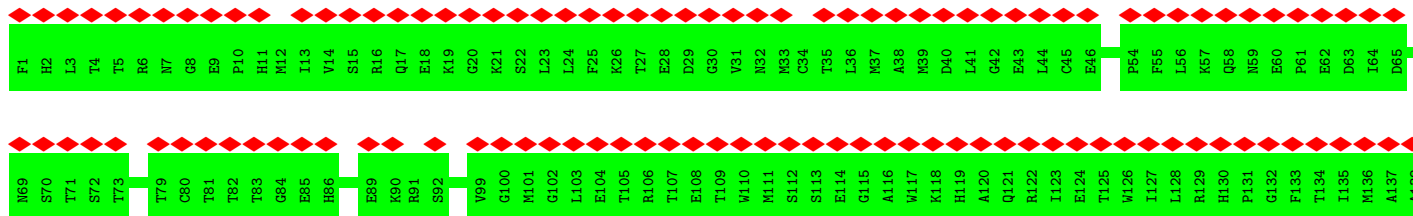
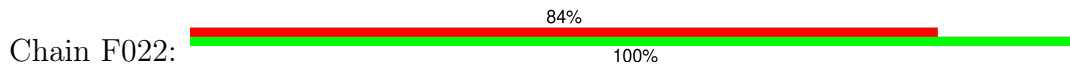
• Molecule 2: Protein prM



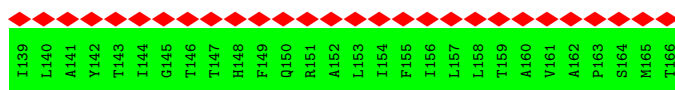
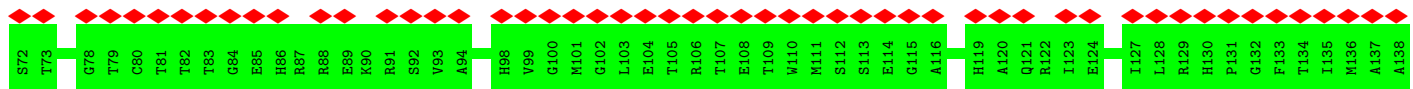
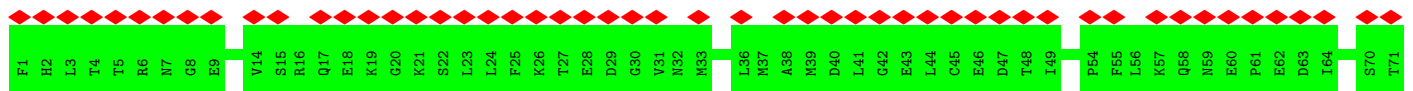
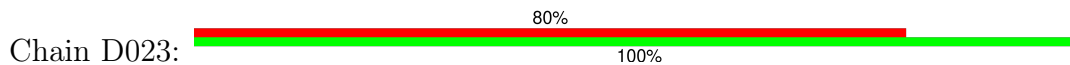




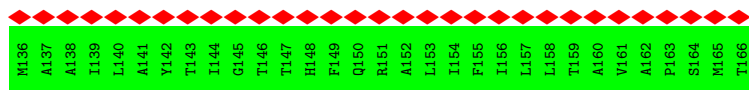
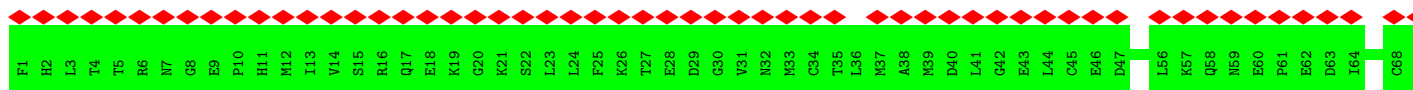
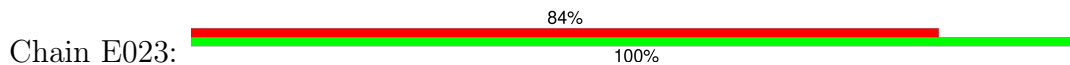
• Molecule 2: Protein prM



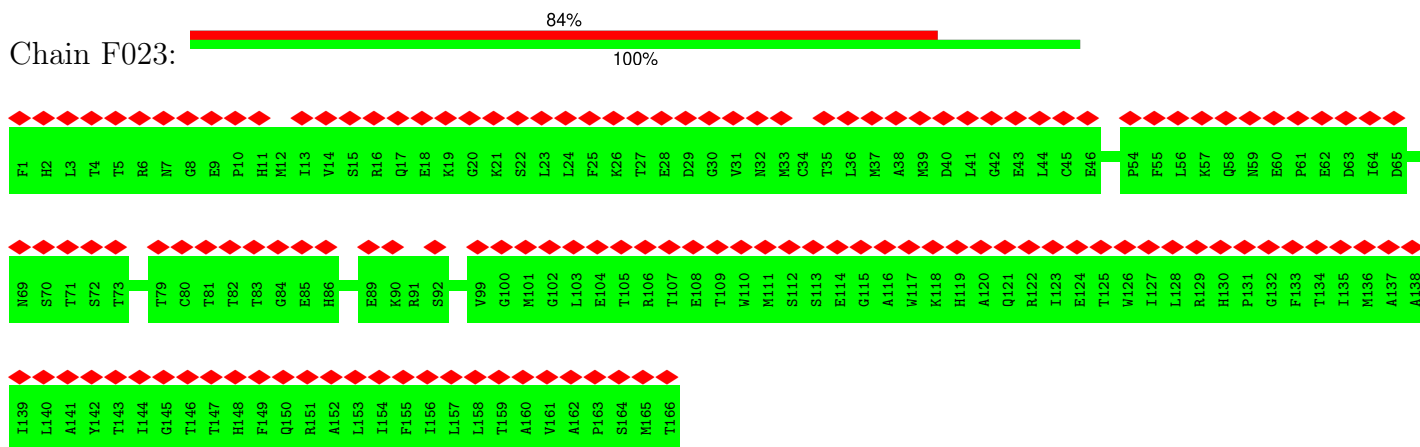
• Molecule 2: Protein prM



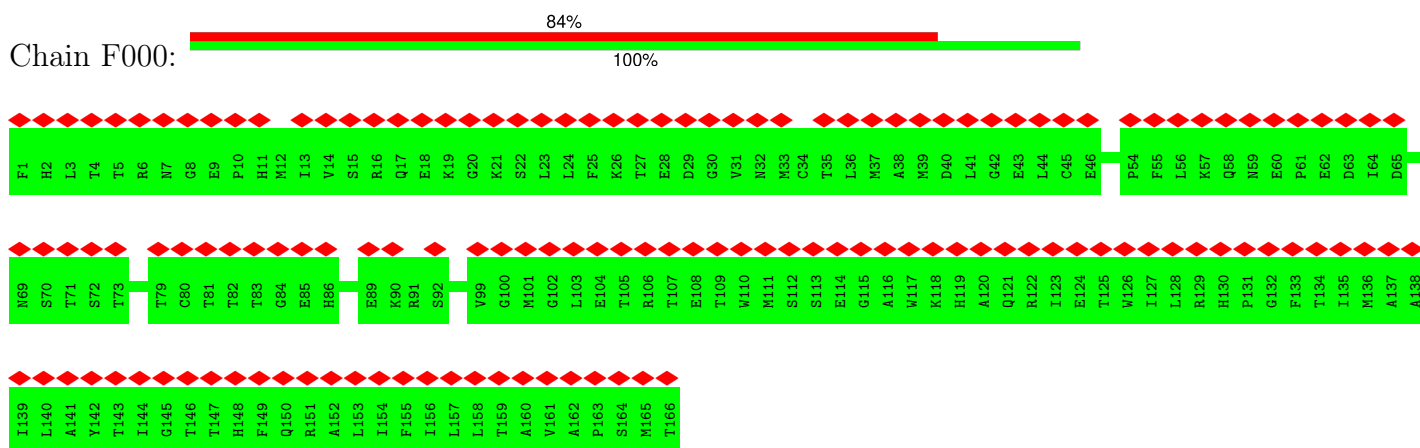
• Molecule 2: Protein prM



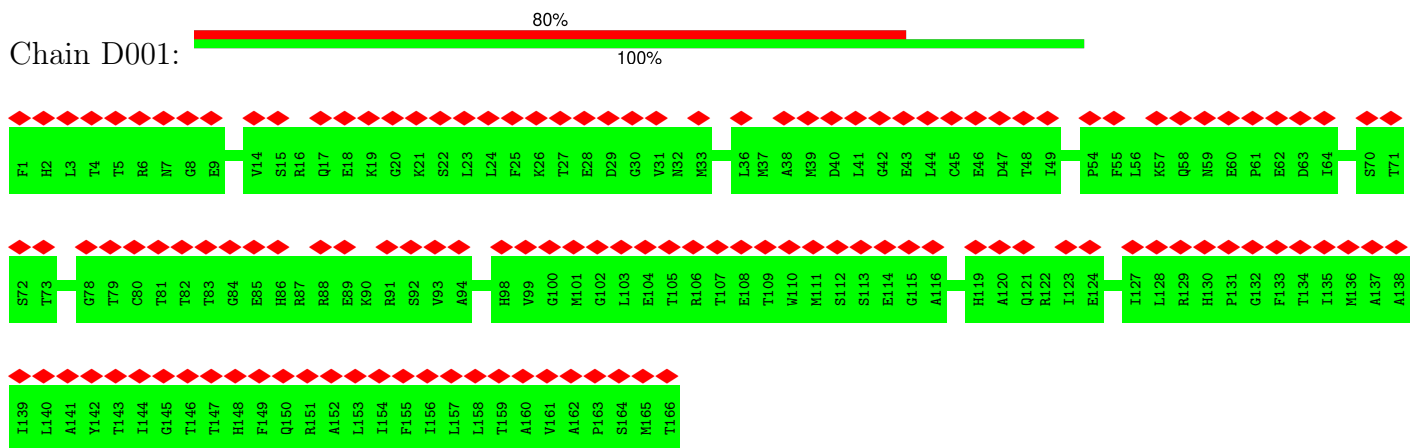
• Molecule 2: Protein prM



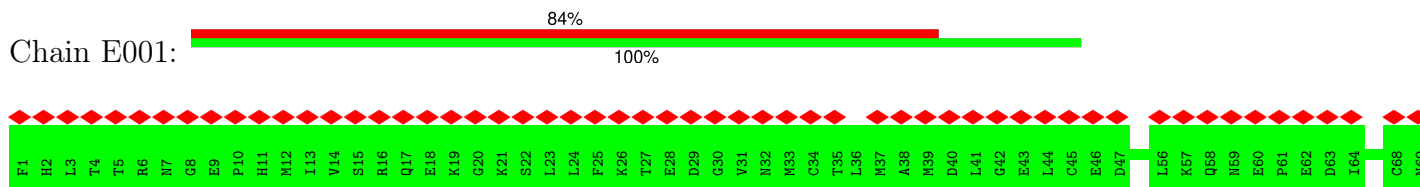
• Molecule 2: Protein prM

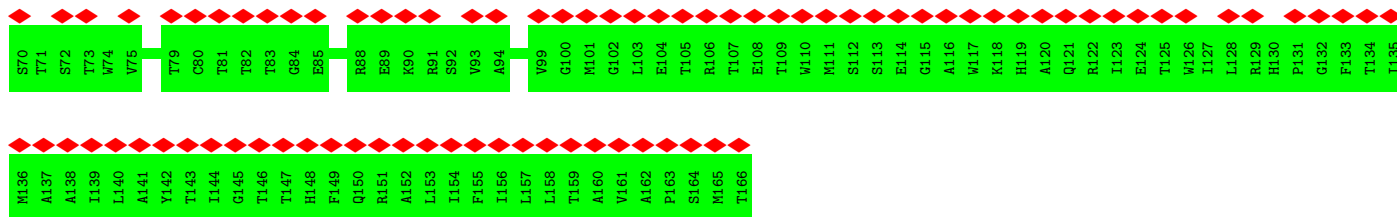


• Molecule 2: Protein prM

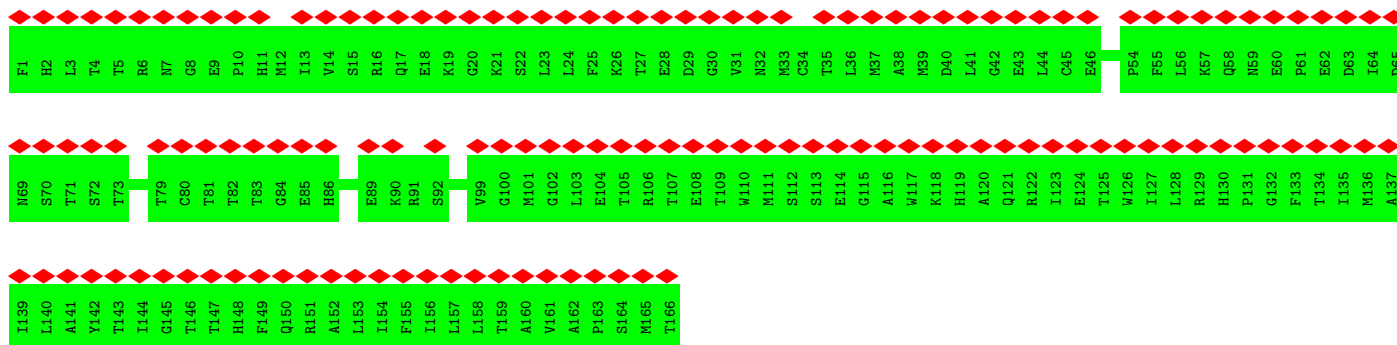
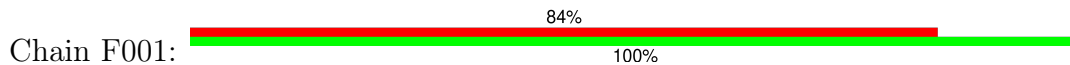


• Molecule 2: Protein prM

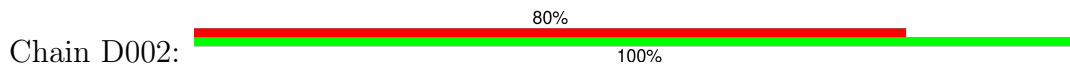




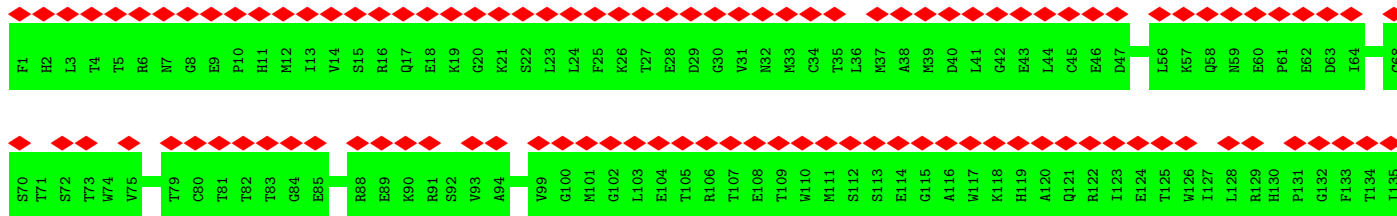
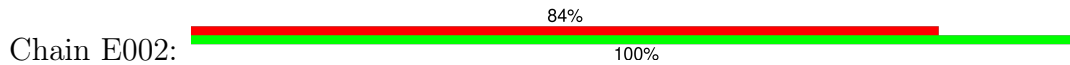
• Molecule 2: Protein prM

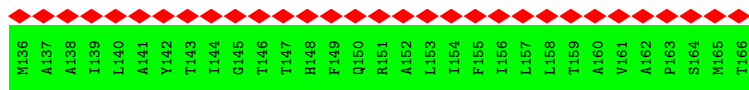


• Molecule 2: Protein prM

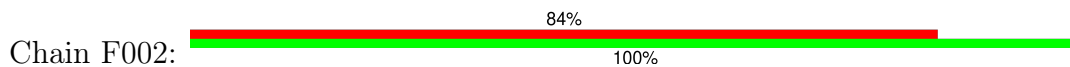


• Molecule 2: Protein prM

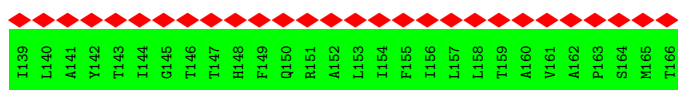
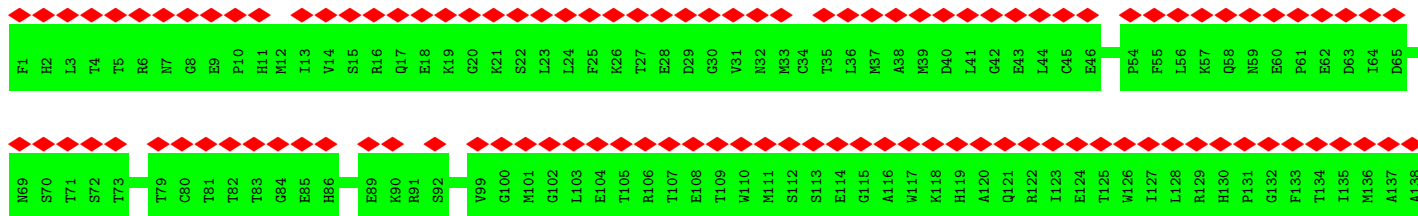




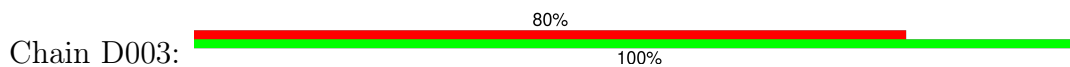
• Molecule 2: Protein prM



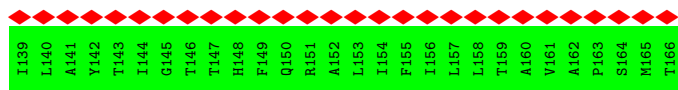
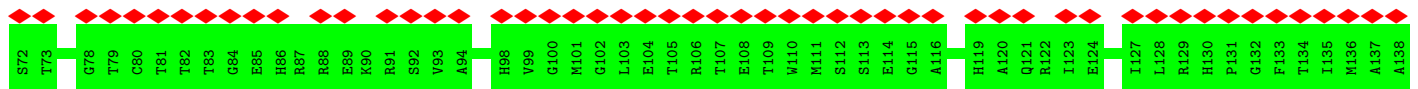
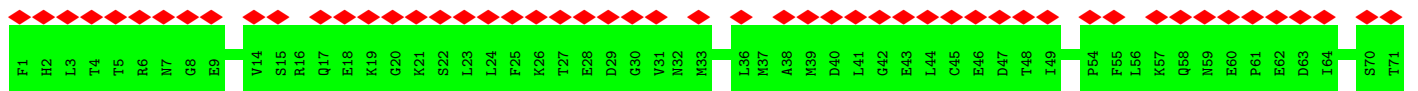
Chain F002:



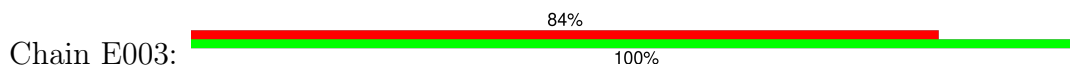
• Molecule 2: Protein prM



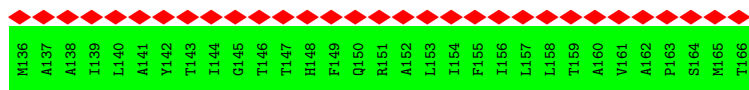
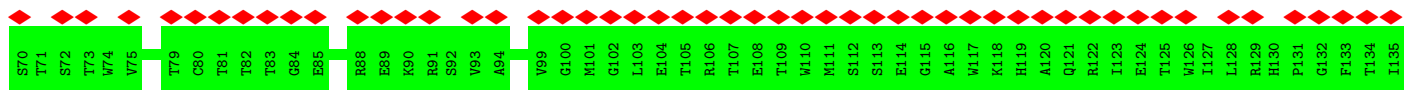
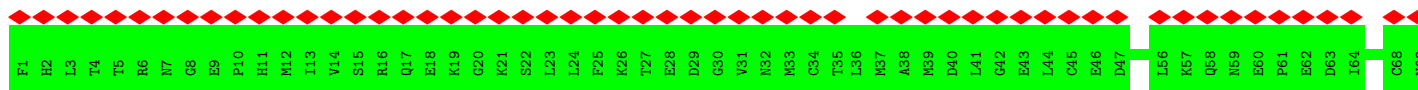
Chain D003:



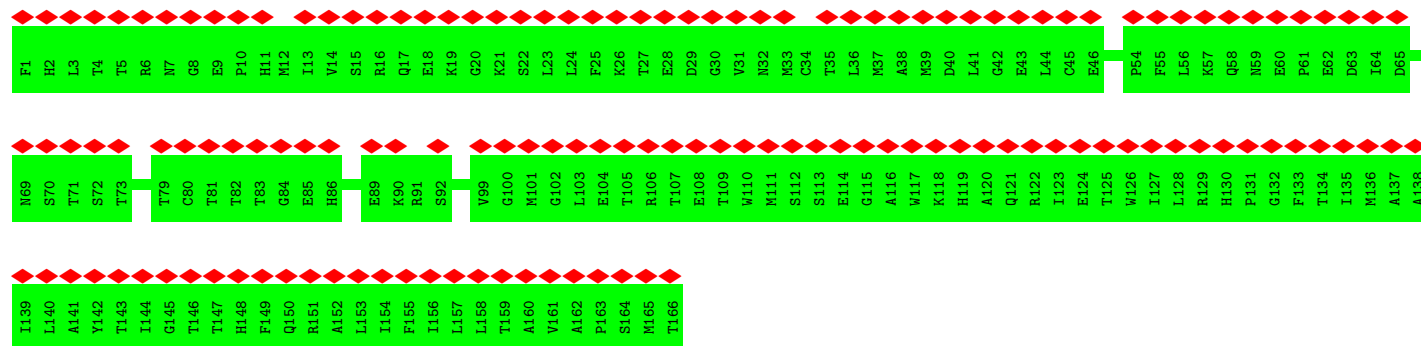
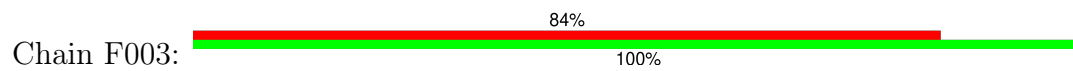
• Molecule 2: Protein prM



Chain E003:



• Molecule 2: Protein prM



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	42.3	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.022	Depositor
Minimum map value	-0.006	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size ( $\text{\AA}$ )	629.76, 629.76, 629.76	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.23, 1.23, 1.23	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	A000	495	0	0	0	0
1	A001	495	0	0	0	0
1	A002	495	0	0	0	0
1	A003	495	0	0	0	0
1	A004	495	0	0	0	0
1	A005	495	0	0	0	0
1	A006	495	0	0	0	0
1	A007	495	0	0	0	0
1	A008	495	0	0	0	0
1	A009	495	0	0	0	0
1	A010	495	0	0	0	0
1	A011	495	0	0	0	0
1	A012	495	0	0	0	0
1	A013	495	0	0	0	0
1	A014	495	0	0	0	0
1	A015	495	0	0	0	0
1	A016	495	0	0	0	0
1	A017	495	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A018	495	0	0	0	0
1	A019	495	0	0	0	0
1	A020	495	0	0	0	0
1	A021	495	0	0	0	0
1	A022	495	0	0	0	0
1	A023	495	0	0	0	0
1	B000	495	0	0	0	0
1	B001	495	0	0	0	0
1	B002	495	0	0	0	0
1	B003	495	0	0	0	0
1	B004	495	0	0	0	0
1	B005	495	0	0	0	0
1	B006	495	0	0	0	0
1	B007	495	0	0	0	0
1	B008	495	0	0	0	0
1	B009	495	0	0	0	0
1	B010	495	0	0	0	0
1	B011	495	0	0	0	0
1	B012	495	0	0	0	0
1	B013	495	0	0	0	0
1	B014	495	0	0	0	0
1	B015	495	0	0	0	0
1	B016	495	0	0	0	0
1	B017	495	0	0	0	0
1	B018	495	0	0	0	0
1	B019	495	0	0	0	0
1	B020	495	0	0	0	0
1	B021	495	0	0	0	0
1	B022	495	0	0	0	0
1	B023	495	0	0	0	0
1	C000	495	0	0	0	0
1	C001	495	0	0	0	0
1	C002	495	0	0	0	0
1	C003	495	0	0	0	0
1	C004	495	0	0	0	0
1	C005	495	0	0	0	0
1	C006	495	0	0	0	0
1	C007	495	0	0	0	0
1	C008	495	0	0	0	0
1	C009	495	0	0	0	0
1	C010	495	0	0	0	0
1	C011	495	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C012	495	0	0	0	0
1	C013	495	0	0	0	0
1	C014	495	0	0	0	0
1	C015	495	0	0	0	0
1	C016	495	0	0	0	0
1	C017	495	0	0	0	0
1	C018	495	0	0	0	0
1	C019	495	0	0	0	0
1	C020	495	0	0	0	0
1	C021	495	0	0	0	0
1	C022	495	0	0	0	0
1	C023	495	0	0	0	0
2	D000	166	0	0	0	0
2	D001	166	0	0	0	0
2	D002	166	0	0	0	0
2	D003	166	0	0	0	0
2	D004	166	0	0	0	0
2	D005	166	0	0	0	0
2	D006	166	0	0	0	0
2	D007	166	0	0	0	0
2	D008	166	0	0	0	0
2	D009	166	0	0	0	0
2	D010	166	0	0	0	0
2	D011	166	0	0	0	0
2	D012	166	0	0	0	0
2	D013	166	0	0	0	0
2	D014	166	0	0	0	0
2	D015	166	0	0	0	0
2	D016	166	0	0	0	0
2	D017	166	0	0	0	0
2	D018	166	0	0	0	0
2	D019	166	0	0	0	0
2	D020	166	0	0	0	0
2	D021	166	0	0	0	0
2	D022	166	0	0	0	0
2	D023	166	0	0	0	0
2	E000	166	0	0	0	0
2	E001	166	0	0	0	0
2	E002	166	0	0	0	0
2	E003	166	0	0	0	0
2	E004	166	0	0	0	0
2	E005	166	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E006	166	0	0	0	0
2	E007	166	0	0	0	0
2	E008	166	0	0	0	0
2	E009	166	0	0	0	0
2	E010	166	0	0	0	0
2	E011	166	0	0	0	0
2	E012	166	0	0	0	0
2	E013	166	0	0	0	0
2	E014	166	0	0	0	0
2	E015	166	0	0	0	0
2	E016	166	0	0	0	0
2	E017	166	0	0	0	0
2	E018	166	0	0	0	0
2	E019	166	0	0	0	0
2	E020	166	0	0	0	0
2	E021	166	0	0	0	0
2	E022	166	0	0	0	0
2	E023	166	0	0	0	0
2	F000	166	0	0	0	0
2	F001	166	0	0	0	0
2	F002	166	0	0	0	0
2	F003	166	0	0	0	0
2	F004	166	0	0	0	0
2	F005	166	0	0	0	0
2	F006	166	0	0	0	0
2	F007	166	0	0	0	0
2	F008	166	0	0	0	0
2	F009	166	0	0	0	0
2	F010	166	0	0	0	0
2	F011	166	0	0	0	0
2	F012	166	0	0	0	0
2	F013	166	0	0	0	0
2	F014	166	0	0	0	0
2	F015	166	0	0	0	0
2	F016	166	0	0	0	0
2	F017	166	0	0	0	0
2	F018	166	0	0	0	0
2	F019	166	0	0	0	0
2	F020	166	0	0	0	0
2	F021	166	0	0	0	0
2	F022	166	0	0	0	0
2	F023	166	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	47592	0	0	0	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 1.

There are no clashes within the asymmetric unit.

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.

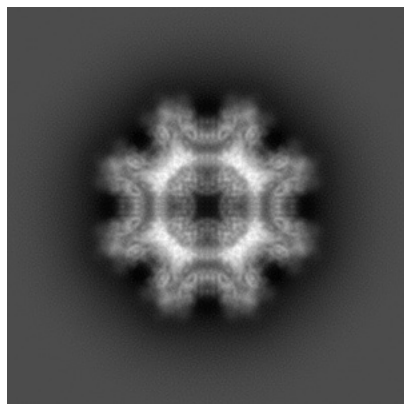
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47083. These allow visual inspection of the internal detail of the map and identification of artifacts.

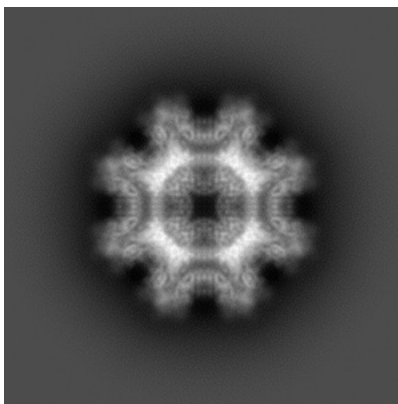
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

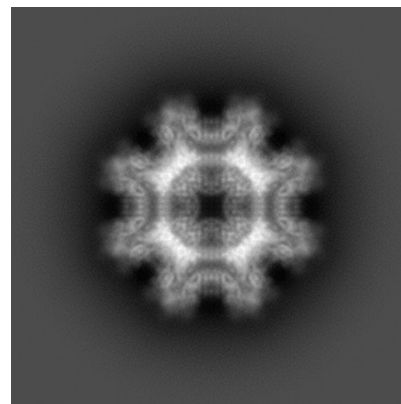
#### 6.1.1 Primary map



X

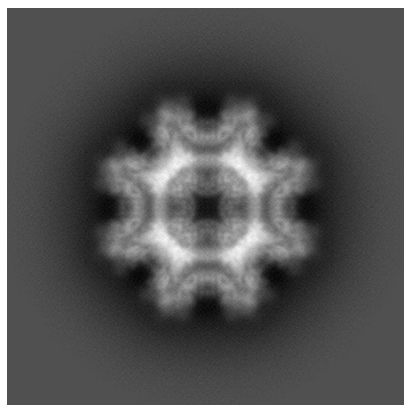


Y

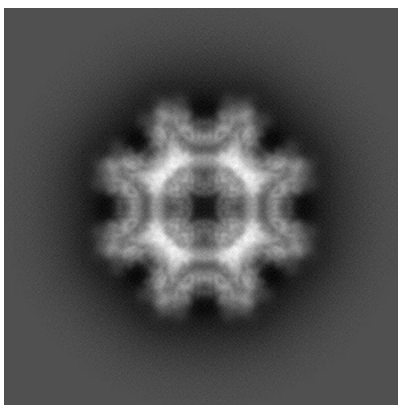


Z

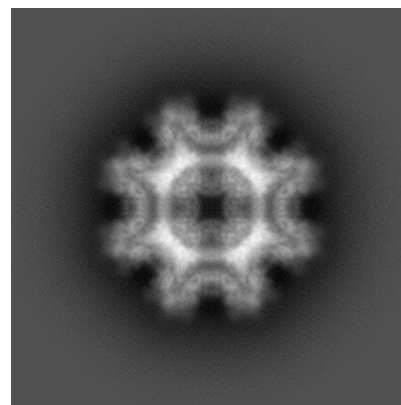
#### 6.1.2 Raw map



X



Y

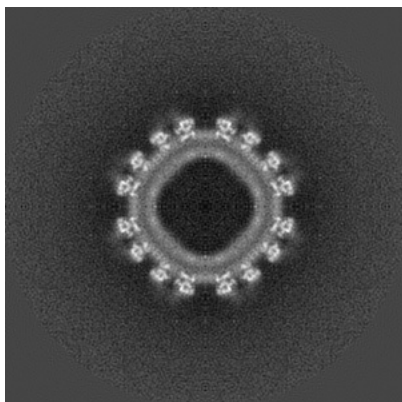


Z

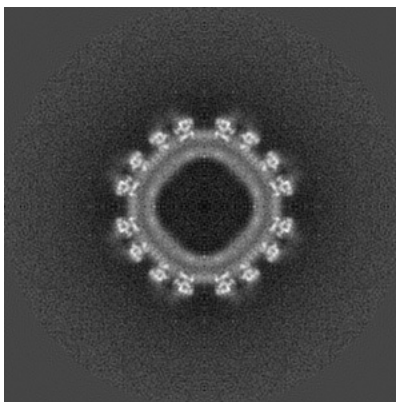
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

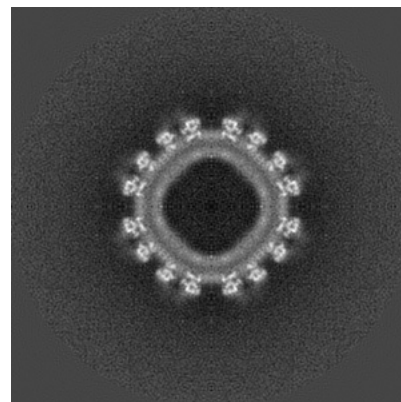
### 6.2.1 Primary map



X Index: 256

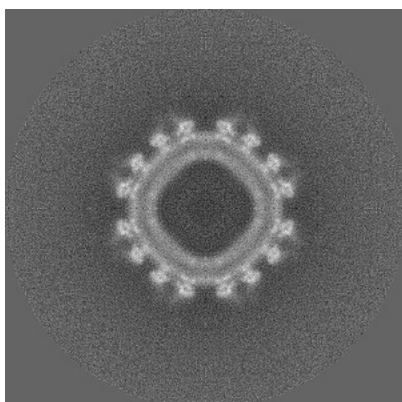


Y Index: 256

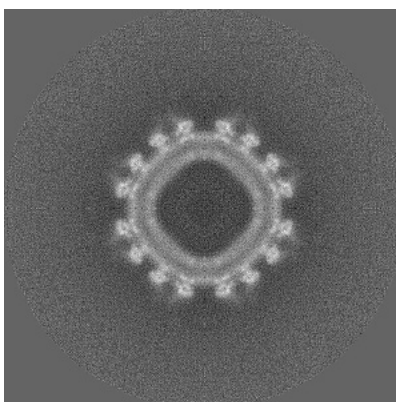


Z Index: 256

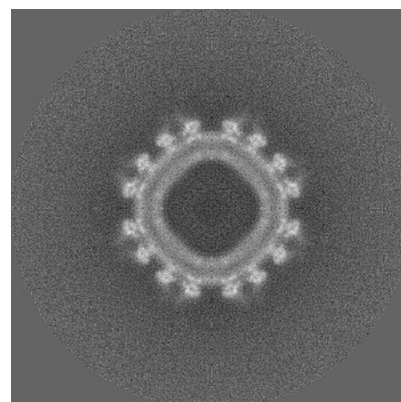
### 6.2.2 Raw map



X Index: 256



Y Index: 256

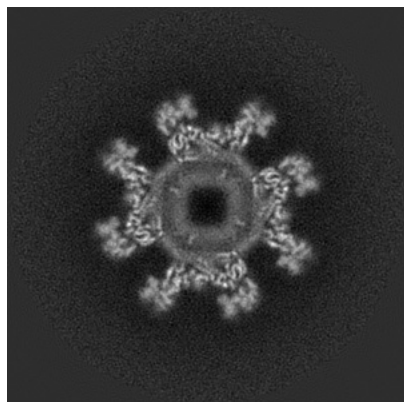


Z Index: 256

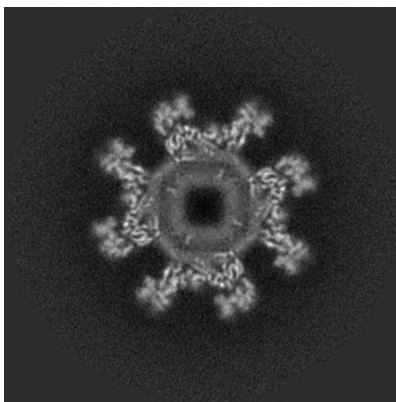
The images above show central slices of the map in three orthogonal directions.

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

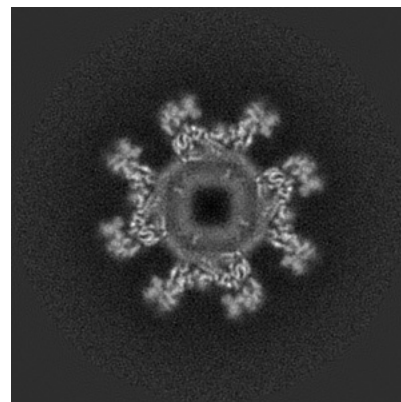
### 6.3.1 Primary map



X Index: 201

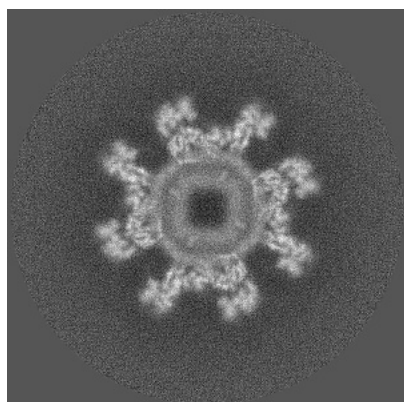


Y Index: 201

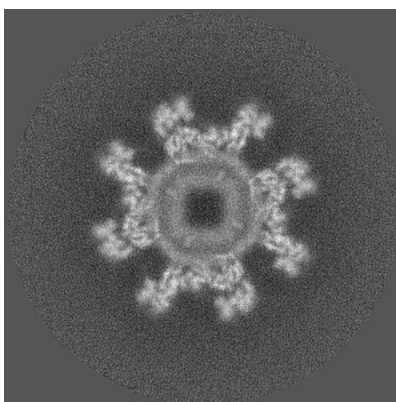


Z Index: 201

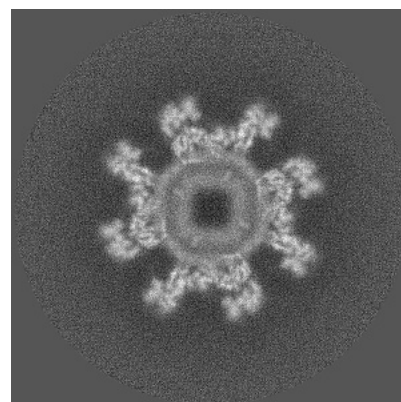
### 6.3.2 Raw map



X Index: 201



Y Index: 201

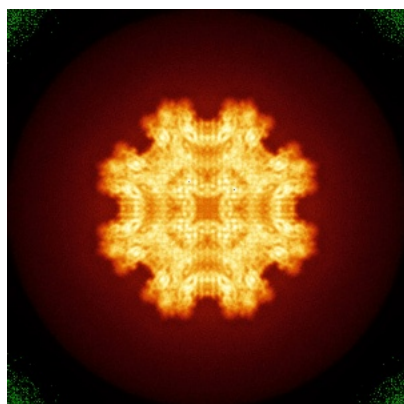


Z Index: 201

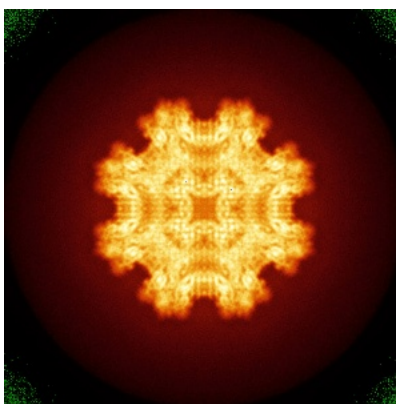
The images above show the largest variance slices of the map in three orthogonal directions.

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

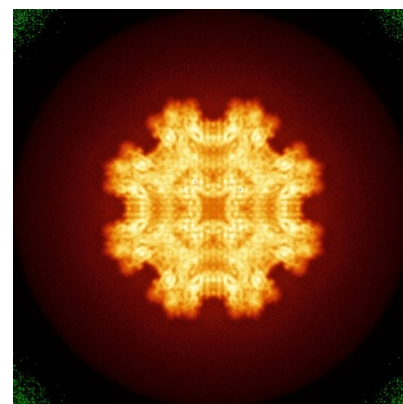
### 6.4.1 Primary map



X

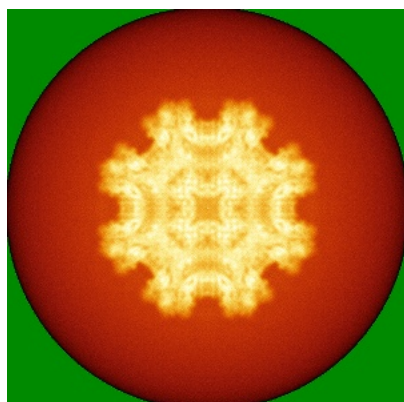


Y

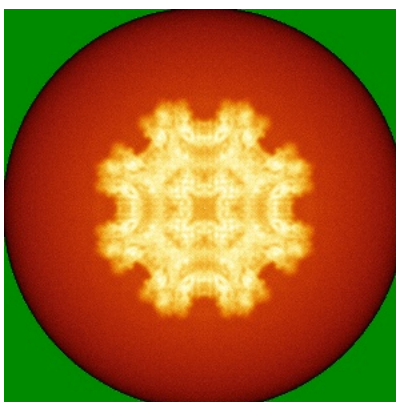


Z

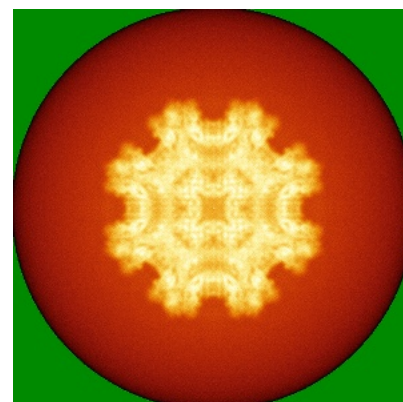
### 6.4.2 Raw map



X



Y



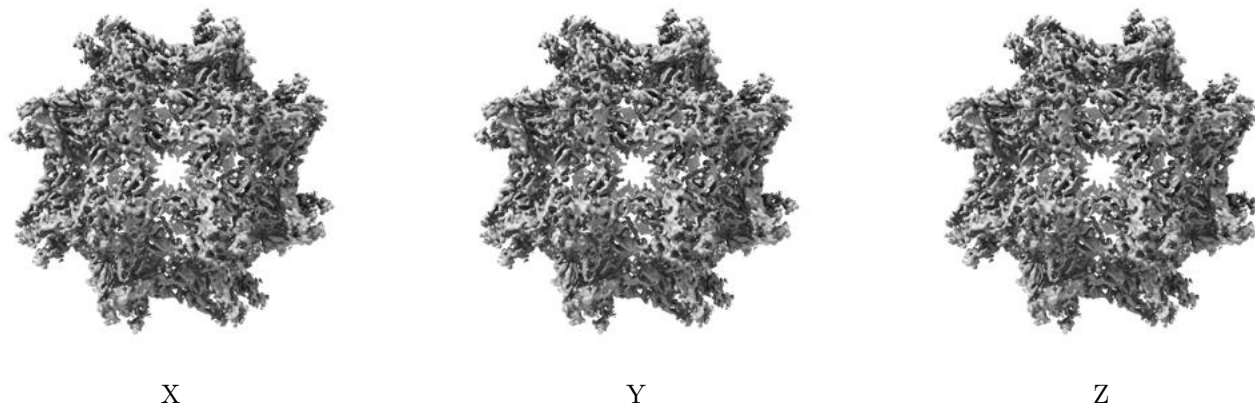
Z

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



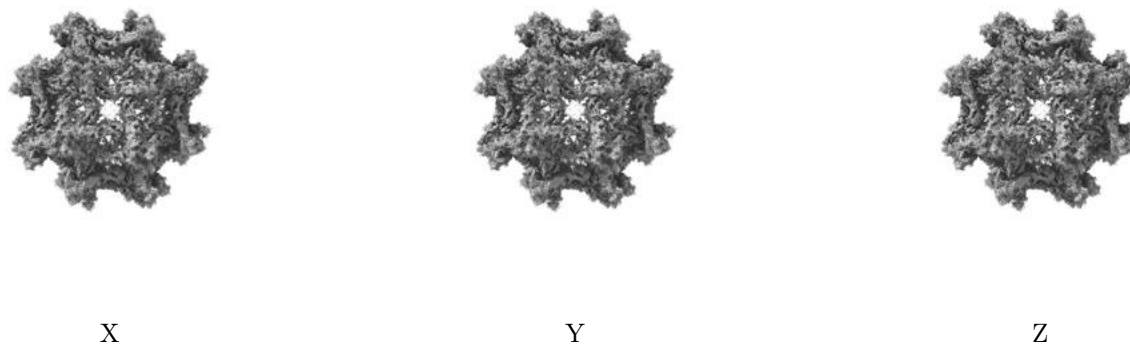
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

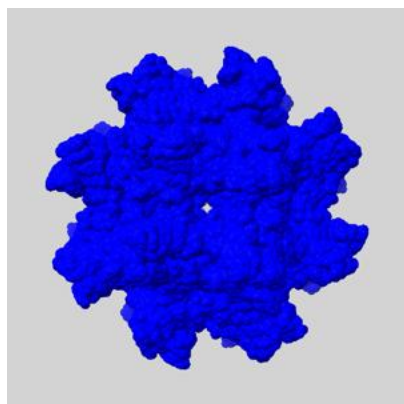
## 6.6 Mask visualisation [i](#)

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

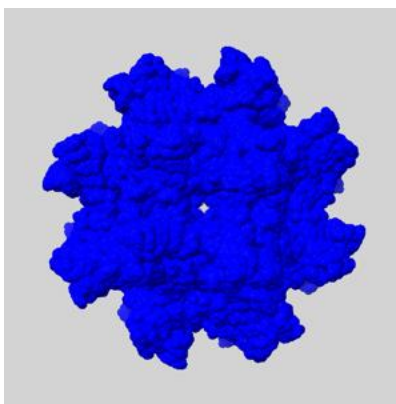
A mask typically either:

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

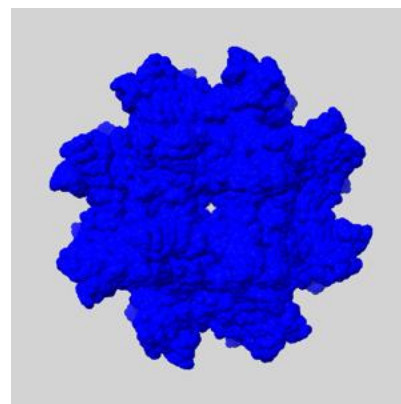
### 6.6.1 emd\_47083\_msk\_1.map [i](#)



X



Y

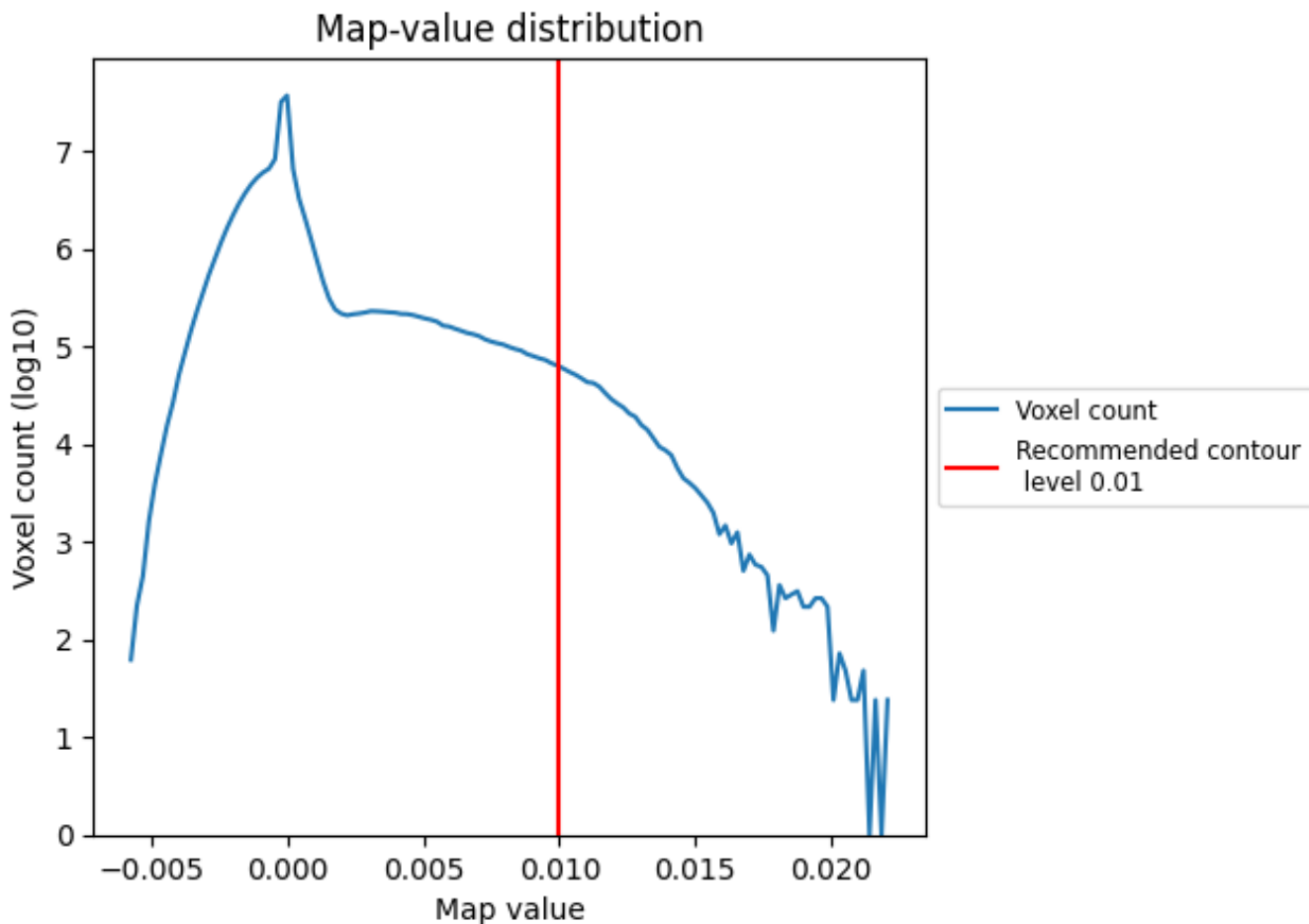


Z

## 7 Map analysis [i](#)

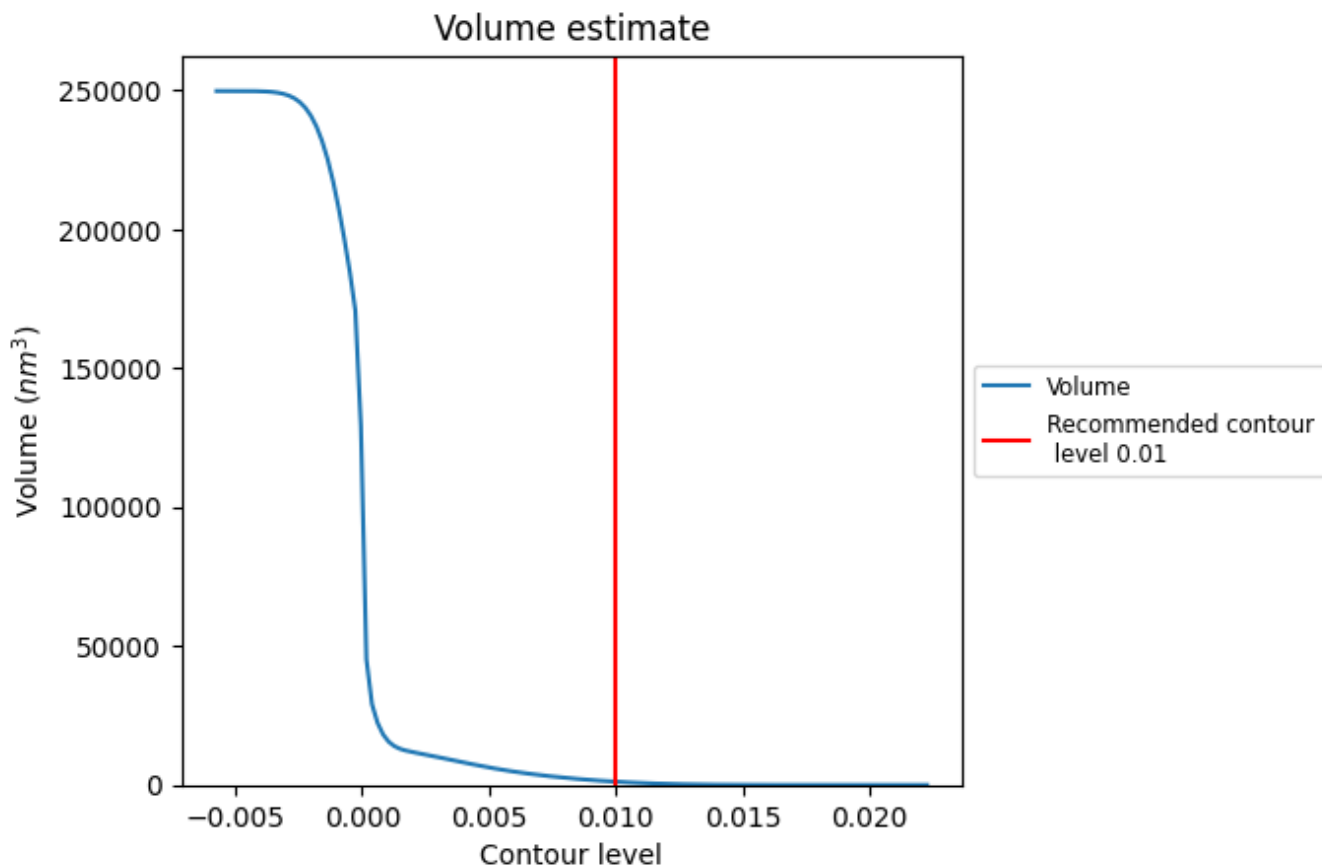
This section contains the results of statistical analysis of the map.

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



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

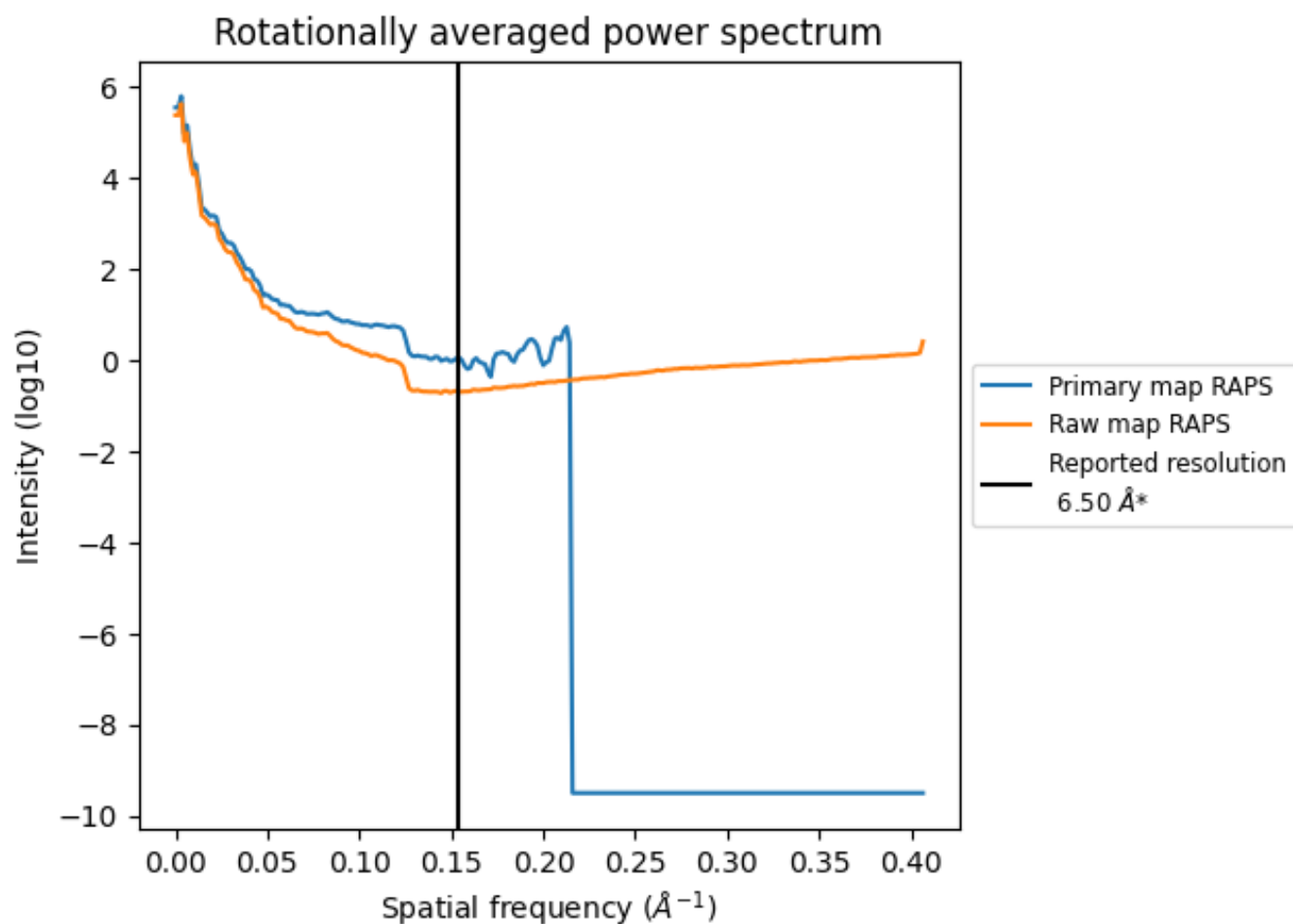
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1176 nm<sup>3</sup>; this corresponds to an approximate mass of 1062 kDa.

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

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

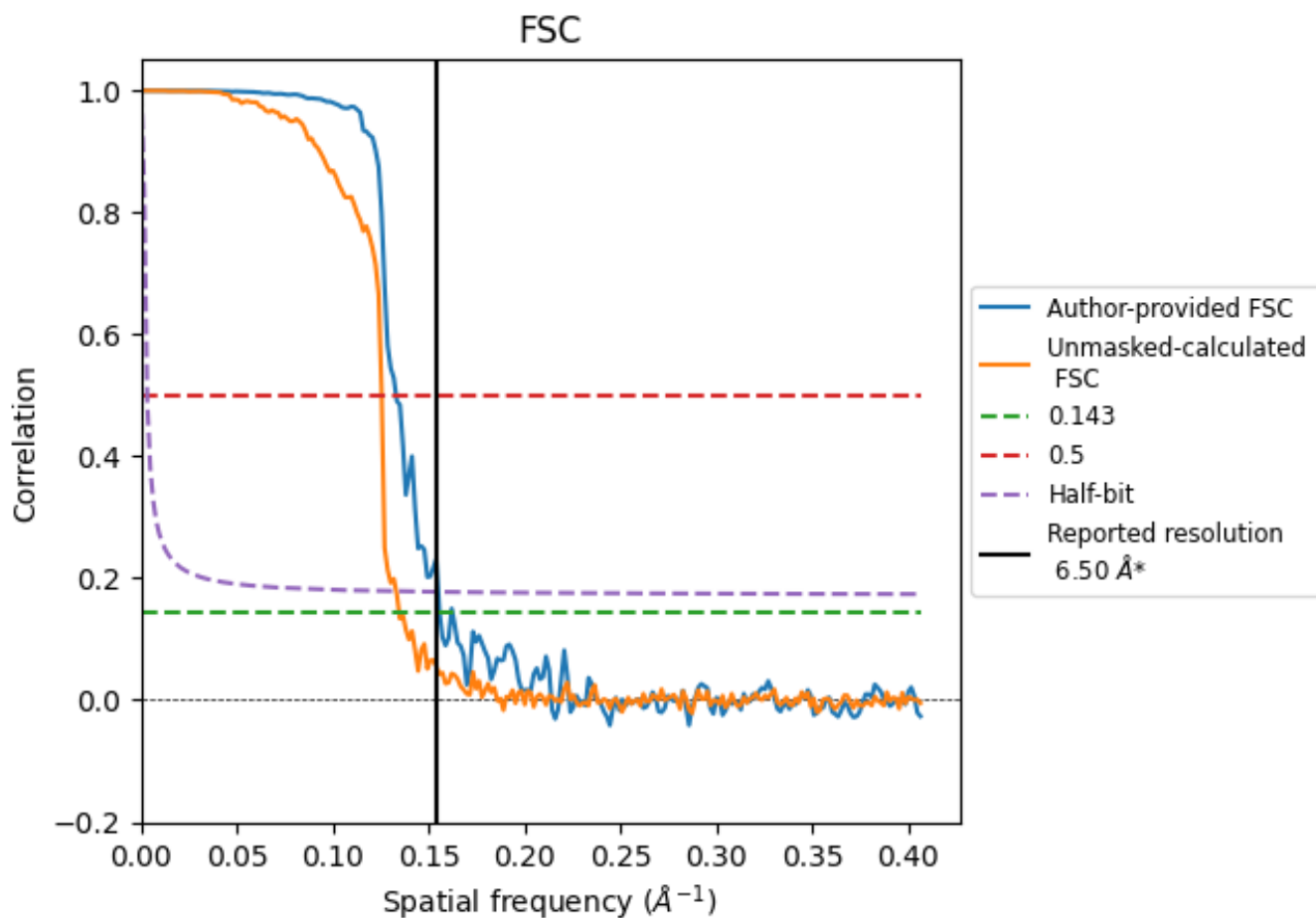


\*Reported resolution corresponds to spatial frequency of 0.154 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.154 \text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

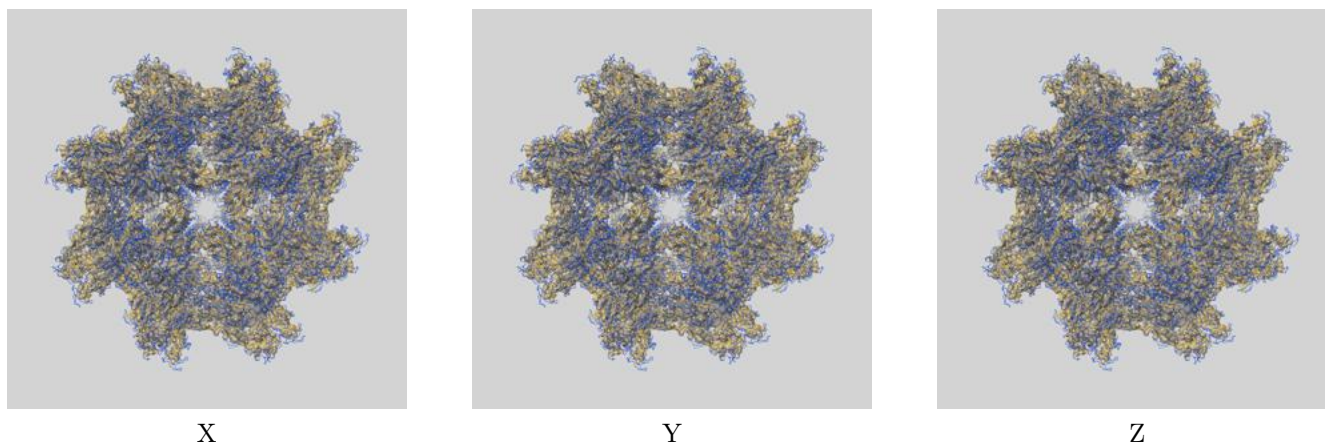
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.50	-	-
Author-provided FSC curve	6.42	7.52	6.45
Unmasked-calculated*	7.43	7.97	7.51

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.43 differs from the reported value 6.5 by more than 10 %

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

This section contains information regarding the fit between EMDB map EMD-47083 and PDB model 9DOG. Per-residue inclusion information can be found in section [3](#) on page [17](#).

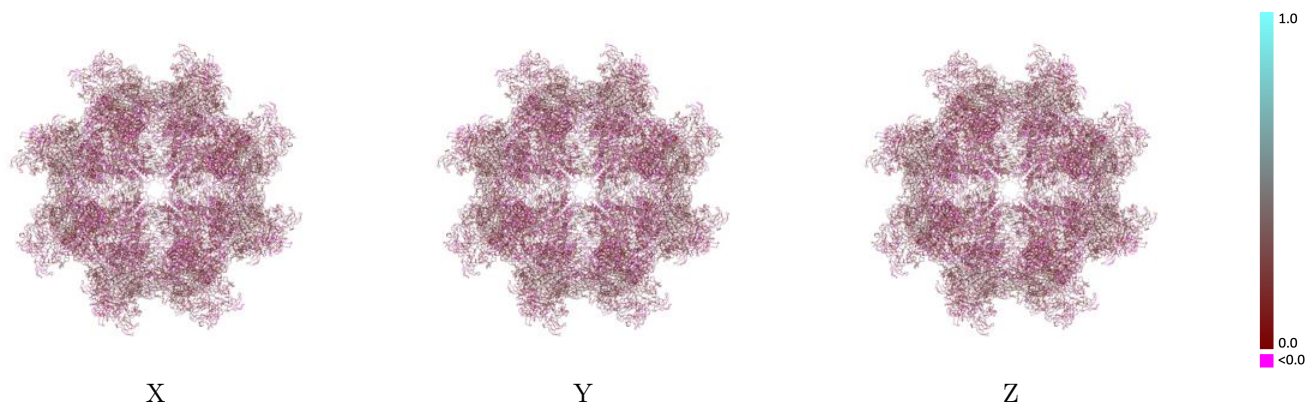
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

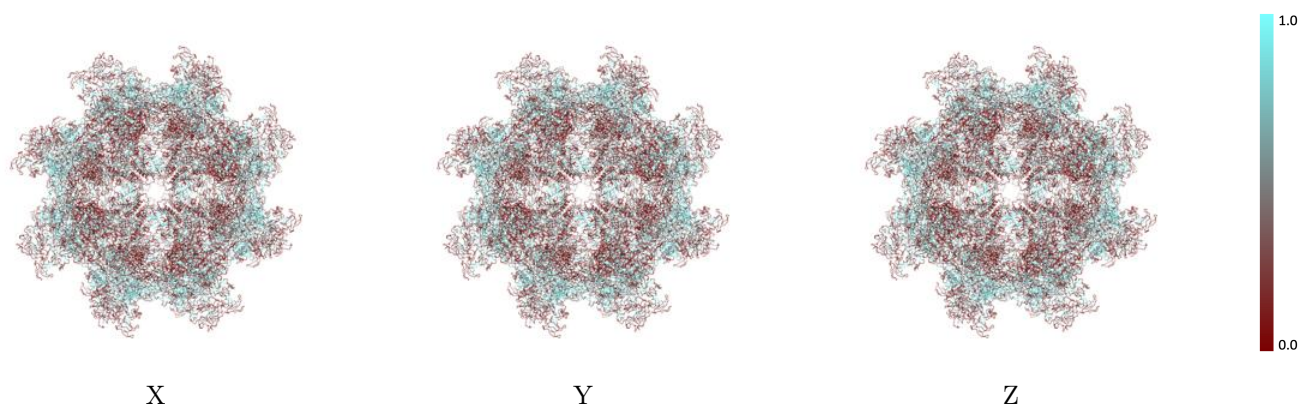


## 9.2 Q-score mapped to coordinate model [i](#)



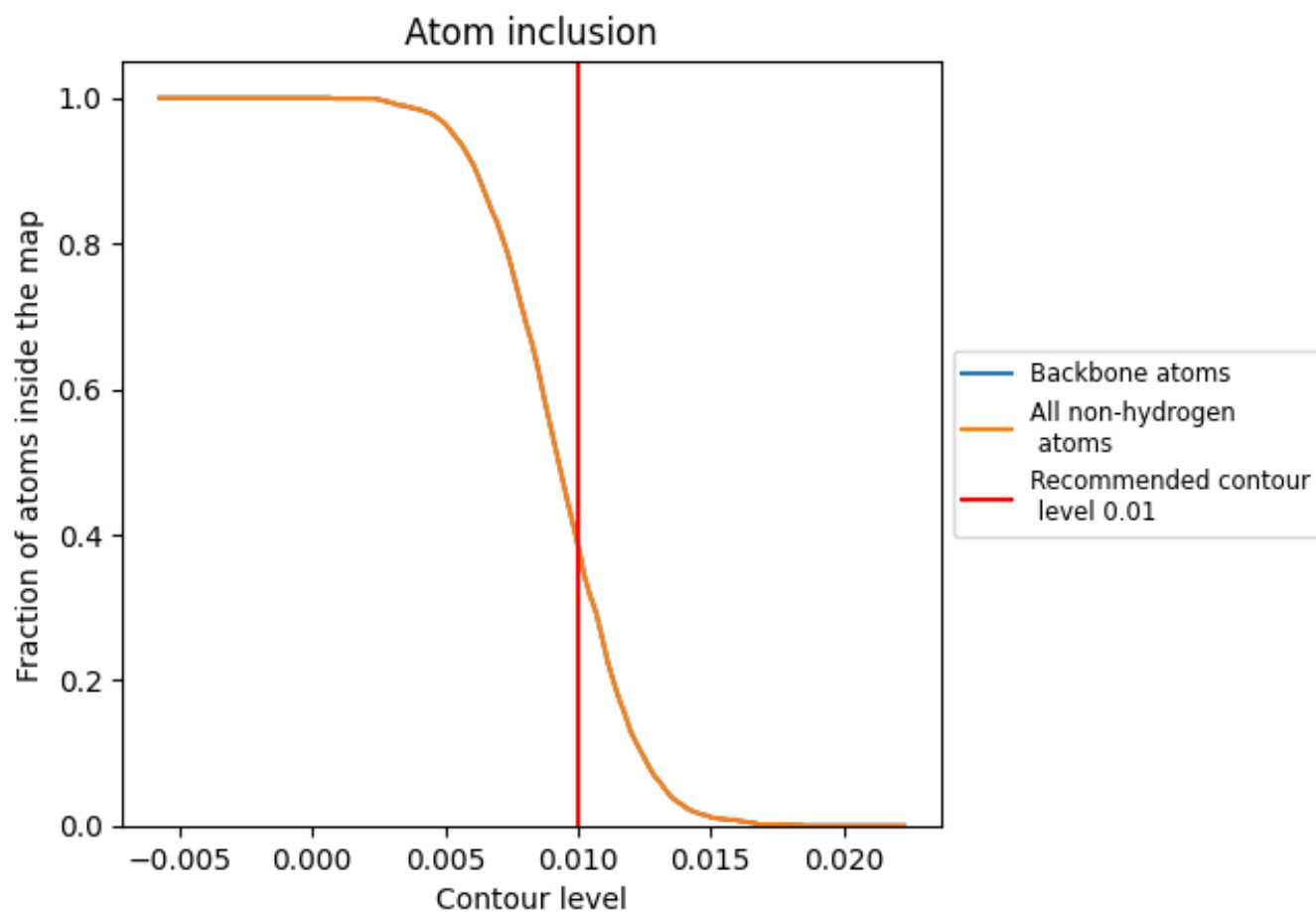
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 39% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3870	 0.1860
A000	 0.4890	 0.2080
A001	 0.4890	 0.2160
A002	 0.4890	 0.2130
A003	 0.4890	 0.2120
A004	 0.4890	 0.2180
A005	 0.4890	 0.2120
A006	 0.4890	 0.2130
A007	 0.4890	 0.2190
A008	 0.4890	 0.2130
A009	 0.4890	 0.2160
A010	 0.4890	 0.2180
A011	 0.4890	 0.2150
A012	 0.4890	 0.2120
A013	 0.4890	 0.2160
A014	 0.4890	 0.2110
A015	 0.4890	 0.2190
A016	 0.4890	 0.2160
A017	 0.4890	 0.2140
A018	 0.4890	 0.2130
A019	 0.4890	 0.2160
A020	 0.4890	 0.2130
A021	 0.4890	 0.2140
A022	 0.4890	 0.2090
A023	 0.4890	 0.2100
B000	 0.4040	 0.1840
B001	 0.4040	 0.1830
B002	 0.4040	 0.1820
B003	 0.4040	 0.1800
B004	 0.4040	 0.1780
B005	 0.4040	 0.1820
B006	 0.4040	 0.1790
B007	 0.4040	 0.1880
B008	 0.4040	 0.1800
B009	 0.4040	 0.1830



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Chain	Atom inclusion	Q-score
B010	■ 0.4040	■ 0.1880
B011	■ 0.4040	■ 0.1780
B012	■ 0.4040	■ 0.1780
B013	■ 0.4040	■ 0.1870
B014	■ 0.4040	■ 0.1810
B015	■ 0.4040	■ 0.1860
B016	■ 0.4040	■ 0.1810
B017	■ 0.4040	■ 0.1840
B018	■ 0.4040	■ 0.1790
B019	■ 0.4040	■ 0.1750
B020	■ 0.4040	■ 0.1830
B021	■ 0.4040	■ 0.1800
B022	■ 0.4040	■ 0.1810
B023	■ 0.4040	■ 0.1860
C000	■ 0.4850	■ 0.2110
C001	■ 0.4850	■ 0.2130
C002	■ 0.4850	■ 0.2200
C003	■ 0.4850	■ 0.2200
C004	■ 0.4850	■ 0.2150
C005	■ 0.4850	■ 0.2090
C006	■ 0.4850	■ 0.2200
C007	■ 0.4850	■ 0.2090
C008	■ 0.4850	■ 0.2160
C009	■ 0.4850	■ 0.2100
C010	■ 0.4850	■ 0.2090
C011	■ 0.4850	■ 0.2160
C012	■ 0.4850	■ 0.2170
C013	■ 0.4850	■ 0.2070
C014	■ 0.4850	■ 0.2160
C015	■ 0.4850	■ 0.2120
C016	■ 0.4850	■ 0.2120
C017	■ 0.4850	■ 0.2100
C018	■ 0.4850	■ 0.2120
C019	■ 0.4850	■ 0.2150
C020	■ 0.4850	■ 0.2150
C021	■ 0.4850	■ 0.2210
C022	■ 0.4850	■ 0.2220
C023	■ 0.4850	■ 0.2130
D000	■ 0.1990	■ 0.1220
D001	■ 0.1990	■ 0.1280
D002	■ 0.1990	■ 0.1250
D003	■ 0.1990	■ 0.1190

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Chain	Atom inclusion	Q-score
D004	■ 0.1990	■ 0.1250
D005	■ 0.1990	■ 0.1250
D006	■ 0.1990	■ 0.1220
D007	■ 0.1990	■ 0.1320
D008	■ 0.1990	■ 0.1350
D009	■ 0.1990	■ 0.1340
D010	■ 0.1990	■ 0.1330
D011	■ 0.1990	■ 0.1390
D012	■ 0.1990	■ 0.1290
D013	■ 0.1990	■ 0.1310
D014	■ 0.1990	■ 0.1300
D015	■ 0.1990	■ 0.1260
D016	■ 0.1990	■ 0.1320
D017	■ 0.1990	■ 0.1280
D018	■ 0.1990	■ 0.1260
D019	■ 0.1990	■ 0.1240
D020	■ 0.1990	■ 0.1210
D021	■ 0.1990	■ 0.1280
D022	■ 0.1990	■ 0.1190
D023	■ 0.1990	■ 0.1220
E000	■ 0.1570	■ 0.1390
E001	■ 0.1570	■ 0.1420
E002	■ 0.1570	■ 0.1450
E003	■ 0.1570	■ 0.1370
E004	■ 0.1570	■ 0.1400
E005	■ 0.1570	■ 0.1420
E006	■ 0.1570	■ 0.1410
E007	■ 0.1570	■ 0.1510
E008	■ 0.1570	■ 0.1350
E009	■ 0.1570	■ 0.1480
E010	■ 0.1570	■ 0.1430
E011	■ 0.1570	■ 0.1400
E012	■ 0.1570	■ 0.1320
E013	■ 0.1570	■ 0.1470
E014	■ 0.1570	■ 0.1360
E015	■ 0.1570	■ 0.1370
E016	■ 0.1570	■ 0.1420
E017	■ 0.1570	■ 0.1380
E018	■ 0.1570	■ 0.1400
E019	■ 0.1570	■ 0.1340
E020	■ 0.1570	■ 0.1370
E021	■ 0.1570	■ 0.1420

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Chain	Atom inclusion	Q-score
E022	■ 0.1570	■ 0.1350
E023	■ 0.1570	■ 0.1400
F000	■ 0.1570	■ 0.1400
F001	■ 0.1570	■ 0.1400
F002	■ 0.1570	■ 0.1430
F003	■ 0.1570	■ 0.1390
F004	■ 0.1570	■ 0.1320
F005	■ 0.1570	■ 0.1320
F006	■ 0.1570	■ 0.1360
F007	■ 0.1570	■ 0.1460
F008	■ 0.1570	■ 0.1360
F009	■ 0.1570	■ 0.1460
F010	■ 0.1570	■ 0.1370
F011	■ 0.1570	■ 0.1380
F012	■ 0.1570	■ 0.1300
F013	■ 0.1570	■ 0.1430
F014	■ 0.1570	■ 0.1380
F015	■ 0.1570	■ 0.1340
F016	■ 0.1570	■ 0.1430
F017	■ 0.1570	■ 0.1380
F018	■ 0.1570	■ 0.1330
F019	■ 0.1570	■ 0.1320
F020	■ 0.1570	■ 0.1410
F021	■ 0.1570	■ 0.1370
F022	■ 0.1570	■ 0.1350
F023	■ 0.1570	■ 0.1400