



wwPDB EM Validation Summary Report ⓘ

Nov 10, 2024 – 05:50 pm GMT

PDB ID : 7Z4B
EMDB ID : EMD-14492
Title : Bacteriophage SU10 virion (C1)
Authors : Siborova, M.; Fuzik, T.; Prochazkova, M.; Novacek, J.; Plevka, P.
Deposited on : 2022-03-03
Resolution : 7.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
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) : 2.39

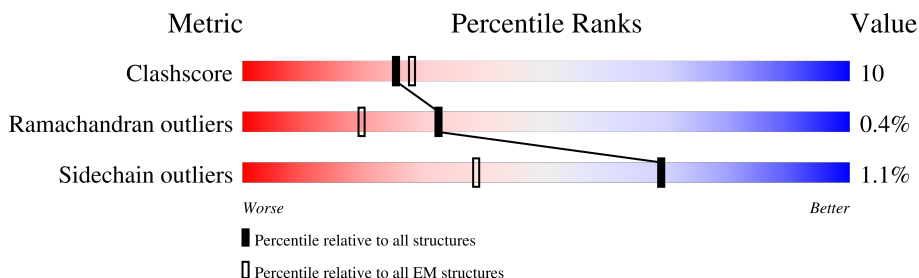
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.40 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
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	AA	352	<div> <div>25%</div> <div>86%</div> <div>12%</div> <div>..</div> </div>
1	AB	352	<div> <div>26%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>
1	AC	352	<div> <div>21%</div> <div>83%</div> <div>14%</div> <div>.</div> </div>
1	AD	352	<div> <div>28%</div> <div>87%</div> <div>11%</div> <div>.</div> </div>
1	AE	352	<div> <div>28%</div> <div>87%</div> <div>12%</div> <div>.</div> </div>
1	AF	352	<div> <div>29%</div> <div>86%</div> <div>12%</div> <div>.</div> </div>
1	AG	352	<div> <div>30%</div> <div>86%</div> <div>13%</div> <div>..</div> </div>
1	AH	352	<div> <div>29%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	AI	352	
1	AJ	352	
1	AK	352	
1	AL	352	
1	AM	352	
1	AN	352	
1	AO	352	
1	AP	352	
1	AQ	352	
1	AR	352	
1	AS	352	
1	AT	352	
1	AU	352	
1	AV	352	
1	AW	352	
1	AX	352	
1	AY	352	
1	AZ	352	
1	BA	352	
1	BB	352	
1	BC	352	
1	BD	352	
1	BE	352	
1	BF	352	
1	BG	352	

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Mol	Chain	Length	Quality of chain
1	BH	352	
1	BI	352	
1	BJ	352	
1	BK	352	
1	BL	352	
1	BM	352	
1	BN	352	
1	BO	352	
1	BP	352	
1	BQ	352	
1	BR	352	
1	BS	352	
1	BT	352	
1	BU	352	
1	BV	352	
1	BW	352	
1	BX	352	
1	BY	352	
1	BZ	352	
1	CA	352	
1	CB	352	
1	CC	352	
1	CD	352	
1	CE	352	
1	CF	352	

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Mol	Chain	Length	Quality of chain
1	CG	352	<div> <div>34%</div> <div>82%</div> <div>16%</div> </div>
1	CH	352	<div> <div>24%</div> <div>88%</div> <div>10%</div> </div>
1	CI	352	<div> <div>24%</div> <div>86%</div> <div>12%</div> </div>
1	CJ	352	<div> <div>24%</div> <div>87%</div> <div>12%</div> </div>
1	CK	352	<div> <div>37%</div> <div>83%</div> <div>16%</div> </div>
1	CL	352	<div> <div>32%</div> <div>79%</div> <div>18%</div> </div>
1	CM	352	<div> <div>19%</div> <div>85%</div> <div>13%</div> </div>
1	CN	352	<div> <div>32%</div> <div>78%</div> <div>19%</div> </div>
1	CO	352	<div> <div>35%</div> <div>81%</div> <div>16%</div> </div>
1	CP	352	<div> <div>34%</div> <div>84%</div> <div>14%</div> </div>
1	CQ	352	<div> <div>19%</div> <div>81%</div> <div>17%</div> </div>
1	CR	352	<div> <div>37%</div> <div>83%</div> <div>15%</div> </div>
1	CS	352	<div> <div>37%</div> <div>73%</div> <div>26%</div> </div>
1	CT	352	<div> <div>24%</div> <div>85%</div> <div>13%</div> </div>
1	CU	352	<div> <div>17%</div> <div>79%</div> <div>19%</div> </div>
1	CV	352	<div> <div>30%</div> <div>84%</div> <div>15%</div> </div>
1	CW	352	<div> <div>41%</div> <div>78%</div> <div>21%</div> </div>
1	CX	352	<div> <div>21%</div> <div>90%</div> <div>9%</div> </div>
1	CY	352	<div> <div>31%</div> <div>83%</div> <div>16%</div> </div>
1	CZ	352	<div> <div>34%</div> <div>77%</div> <div>22%</div> </div>
1	DA	352	<div> <div>36%</div> <div>82%</div> <div>16%</div> </div>
1	DB	352	<div> <div>49%</div> <div>80%</div> <div>19%</div> </div>
1	DC	352	<div> <div>47%</div> <div>83%</div> <div>15%</div> </div>
1	DD	352	<div> <div>42%</div> <div>72%</div> <div>25%</div> </div>
1	DE	352	<div> <div>41%</div> <div>84%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
1	DF	352	<div> <div>39%</div> <div>82%</div> <div>16%</div> </div>
1	DG	352	<div> <div>38%</div> <div>82%</div> <div>16%</div> </div>
1	DH	352	<div> <div>35%</div> <div>80%</div> <div>18%</div> </div>
1	DI	352	<div> <div>41%</div> <div>88%</div> <div>11%</div> </div>
1	DJ	352	<div> <div>32%</div> <div>81%</div> <div>17%</div> </div>
1	DK	352	<div> <div>46%</div> <div>82%</div> <div>16%</div> </div>
1	DL	352	<div> <div>30%</div> <div>86%</div> <div>13%</div> </div>
1	DM	352	<div> <div>36%</div> <div>82%</div> <div>16%</div> </div>
1	DN	352	<div> <div>33%</div> <div>84%</div> <div>15%</div> </div>
1	DO	352	<div> <div>33%</div> <div>84%</div> <div>14%</div> </div>
1	DP	352	<div> <div>34%</div> <div>78%</div> <div>20%</div> </div>
1	DQ	352	<div> <div>49%</div> <div>86%</div> <div>13%</div> </div>
2	DR	267	<div> <div>97%</div> <div>85%</div> <div>13%</div> </div>
2	DS	267	<div> <div>96%</div> <div>87%</div> <div>10%</div> </div>
2	DT	267	<div> <div>96%</div> <div>87%</div> <div>9%</div> </div>
3	DU	250	<div> <div>81%</div> <div>38%</div> <div>45%</div> <div>5%</div> <div>11%</div> </div>
3	DV	250	<div> <div>84%</div> <div>34%</div> <div>47%</div> <div>6%</div> <div>11%</div> </div>
4	DW	1005	<div> <div>88%</div> <div>71%</div> <div>18%</div> <div>9%</div> </div>
5	DX	786	<div> <div>10%</div> <div>5%</div> <div>89%</div> </div>
5	DY	786	<div> <div>10%</div> <div>90%</div> </div>
5	DZ	786	<div> <div>9%</div> <div>5%</div> <div>91%</div> </div>
6	EA	322	<div> <div>95%</div> <div>89%</div> <div>7%</div> </div>
6	EB	322	<div> <div>96%</div> <div>91%</div> <div>7%</div> </div>
6	EC	322	<div> <div>98%</div> <div>89%</div> <div>8%</div> </div>
7	ED	747	<div> <div>77%</div> <div>55%</div> <div>22%</div> <div>19%</div> </div>

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Mol	Chain	Length	Quality of chain
7	EE	747	<div><div></div><div>77%</div><div>56%</div><div>21%</div><div>•</div><div>19%</div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 284597 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major head protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AB	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AC	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AD	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AE	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AF	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AG	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AH	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AI	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AJ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AK	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AL	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AM	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AN	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AO	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	AP	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AQ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AR	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AS	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AT	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AU	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	AV	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AW	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AX	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	AY	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	AZ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BA	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	BB	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BC	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BD	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BE	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BF	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BG	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BH	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BI	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BJ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BK	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	BL	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BM	344	Total	C	N	O	S	0	0
			2663	1671	466	516	10		
1	BN	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BO	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BP	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BQ	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BR	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BS	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BT	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BU	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BV	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	BW	345	Total	C	N	O	S	0	0
			2672	1676	467	519	10		
1	BX	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	BY	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	BZ	345	Total	C	N	O	S	0	0
			2670	1675	467	518	10		
1	CA	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	CB	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CC	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CD	343	Total	C	N	O	S	0	0
			2657	1668	465	514	10		
1	CE	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CF	342	Total	C	N	O	S	0	0
			2644	1656	464	514	10		
1	CG	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CH	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CI	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CJ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CK	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CL	343	Total	C	N	O	S	0	0
			2654	1665	464	515	10		
1	CM	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CN	342	Total	C	N	O	S	0	0
			2644	1656	464	514	10		
1	CO	341	Total	C	N	O	S	0	0
			2637	1651	463	513	10		
1	CP	345	Total	C	N	O	S	0	0
			2668	1674	466	518	10		
1	CQ	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CR	345	Total	C	N	O	S	0	0
			2670	1675	467	518	10		
1	CS	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CT	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	CU	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CV	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CW	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	CX	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	CY	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	CZ	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	DA	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	DB	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	345	Total	C	N	O	S	0	0
			2670	1675	467	518	10		
1	DD	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	DE	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DF	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	DG	343	Total	C	N	O	S	0	0
			2657	1668	465	514	10		
1	DH	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DI	347	Total	C	N	O	S	0	0
			2685	1684	470	521	10		
1	DJ	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DK	343	Total	C	N	O	S	0	0
			2654	1665	464	515	10		
1	DL	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DM	345	Total	C	N	O	S	0	0
			2668	1674	466	518	10		
1	DN	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DO	346	Total	C	N	O	S	0	0
			2677	1680	468	519	10		
1	DP	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		
1	DQ	346	Total	C	N	O	S	0	0
			2676	1678	468	520	10		

- Molecule 2 is a protein called Putative structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DR	263	Total	C	N	O	S	0	0
			1420	809	289	317	5		
2	DS	263	Total	C	N	O	S	0	0
			1424	812	289	317	6		
2	DT	263	Total	C	N	O	S	0	0
			1424	812	289	317	6		

- Molecule 3 is a protein called Adaptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	DU	222	Total	C	N	O	S	0	0
			1813	1171	292	345	5		
3	DV	222	Total	C	N	O	S	0	0
			1813	1171	292	345	5		

- Molecule 4 is a protein called Surface protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DW	910	Total	C	N	O	S	0	0
			7063	4465	1178	1404	16		

- Molecule 5 is a protein called Putative tail fiber.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DX	87	Total	C	N	O	S	0	0
			683	430	112	139	2		
5	DY	80	Total	C	N	O	S	0	0
			628	397	102	127	2		
5	DZ	68	Total	C	N	O	S	0	0
			545	347	87	109	2		

- Molecule 6 is a protein called Putative tail tip fiber protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	EA	322	Total	C	N	O	0	0
			1289	644	322	323		
6	EB	322	Total	C	N	O	0	0
			1289	644	322	323		
6	EC	322	Total	C	N	O	0	0
			1289	644	322	323		

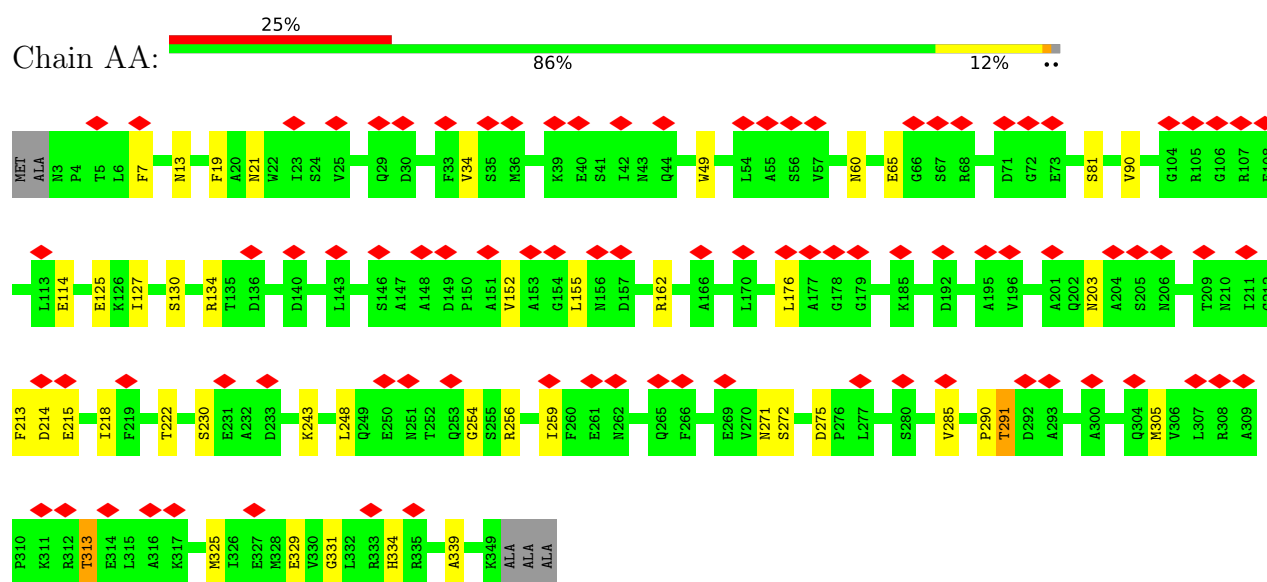
- Molecule 7 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	ED	604	Total	C	N	O	S	0	0
			4838	3038	835	942	23		
7	EE	604	Total	C	N	O	S	0	0
			4838	3038	835	942	23		

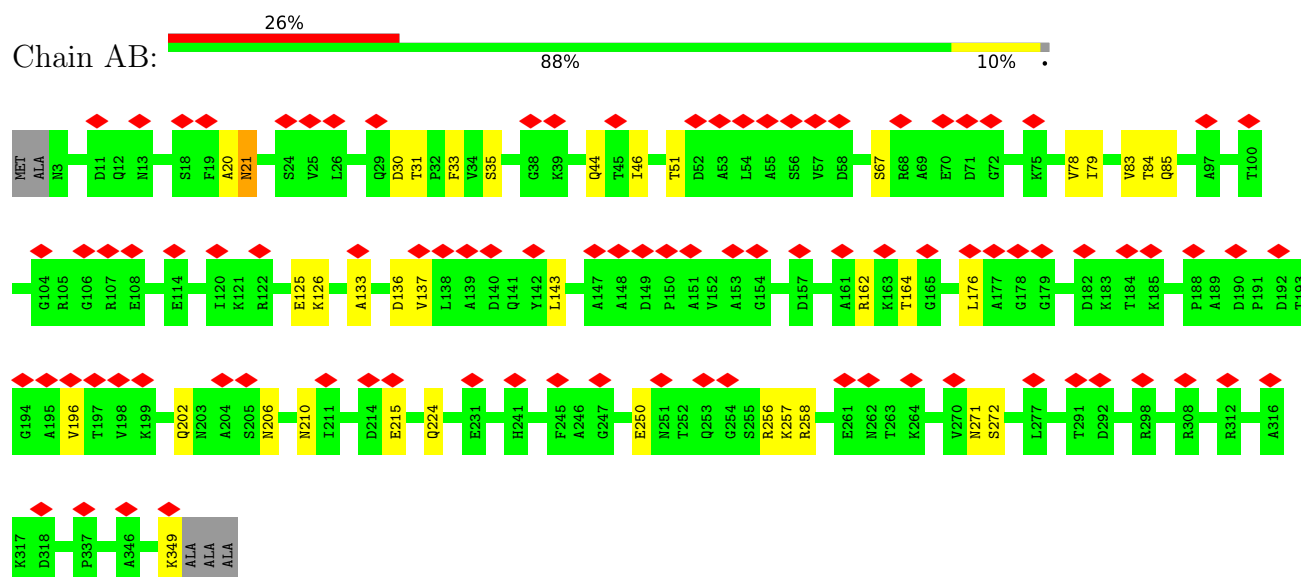
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.


- Molecule 1: Major head protein

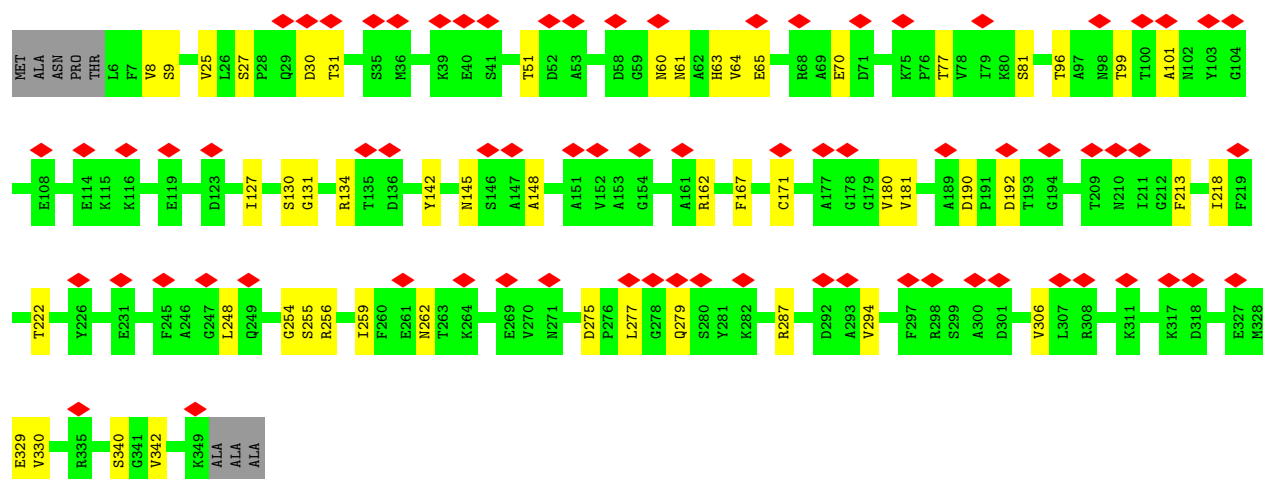


- Molecule 1: Major head protein




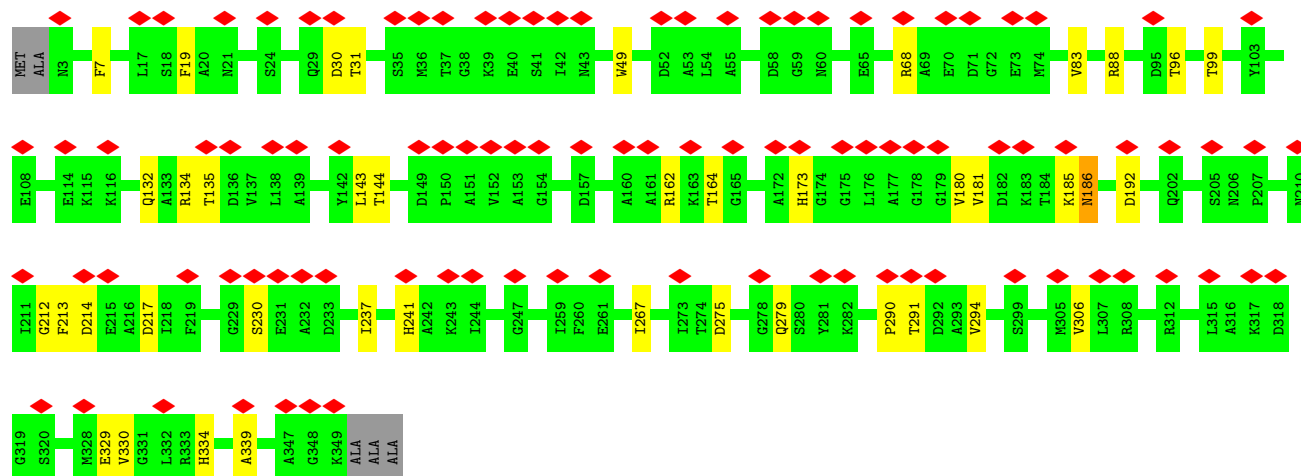
- Molecule 1: Major head protein

Chain AC: 




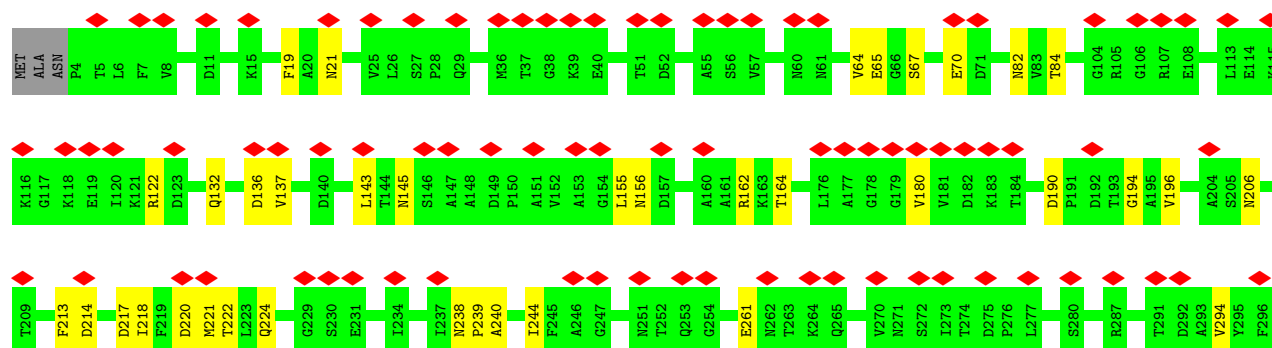
• Molecule 1: Major head protein

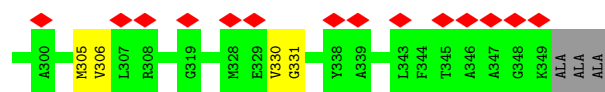
Chain AD: 



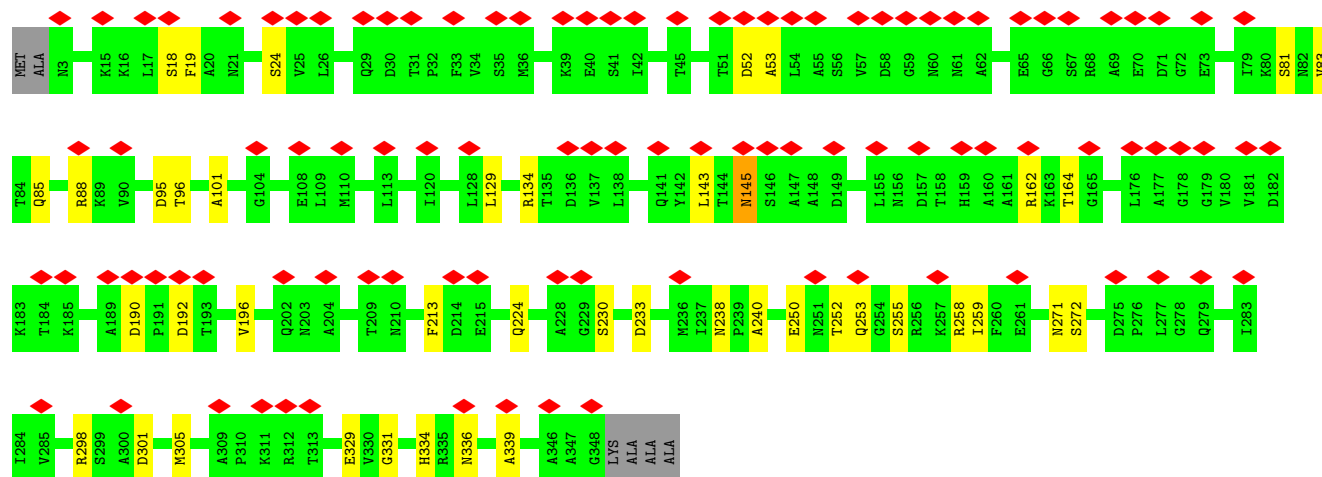
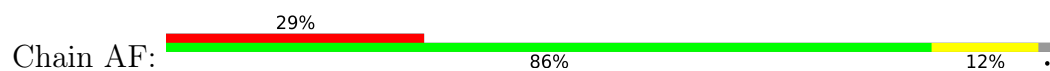
• Molecule 1: Major head protein

Chain AE: 

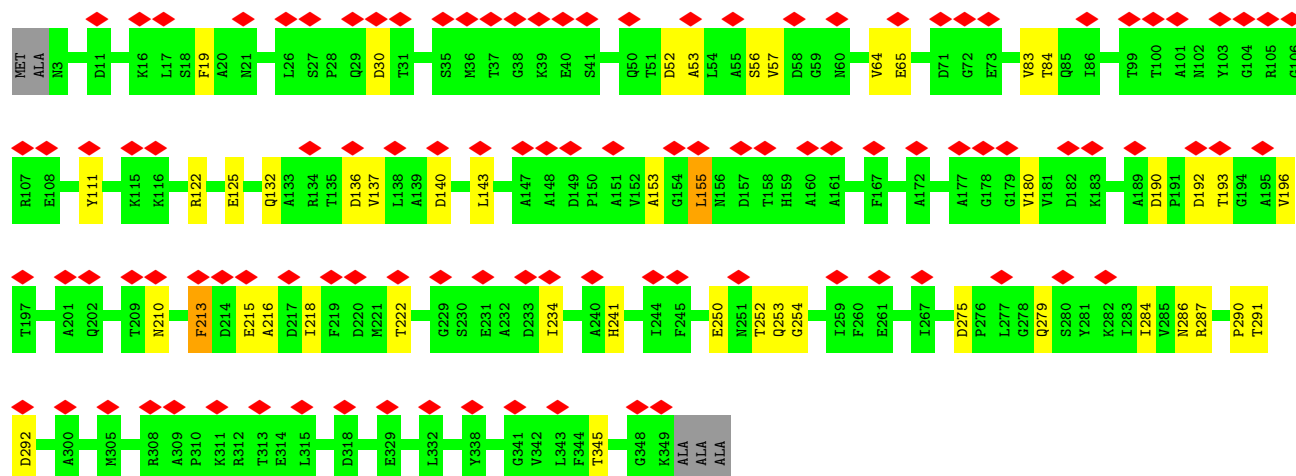
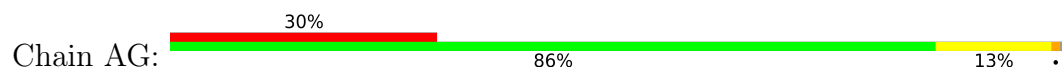




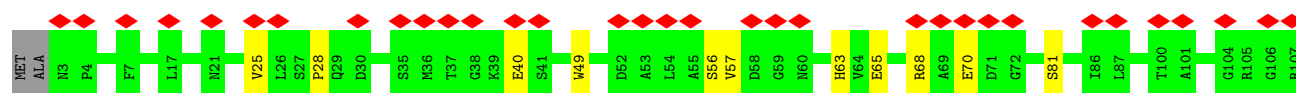
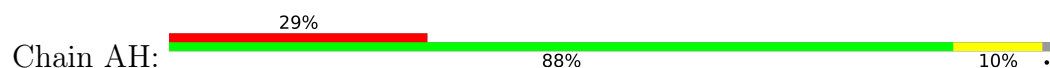
• Molecule 1: Major head protein

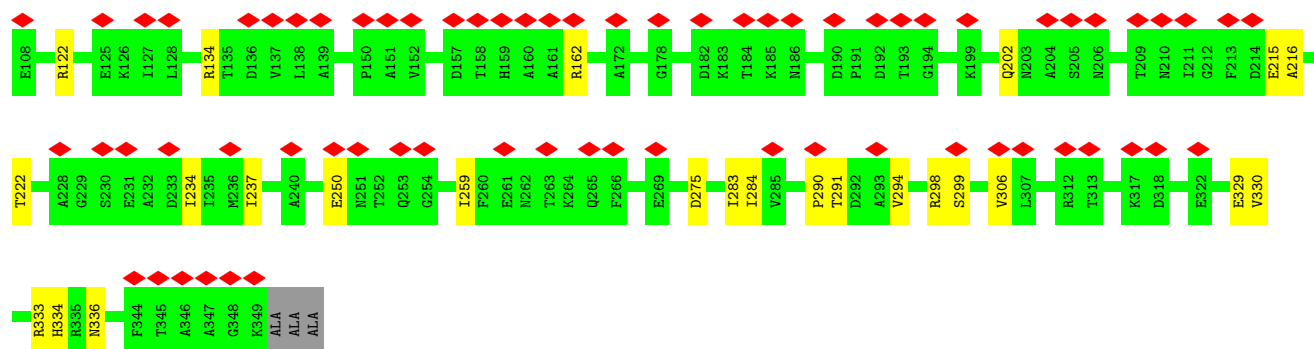


• Molecule 1: Major head protein

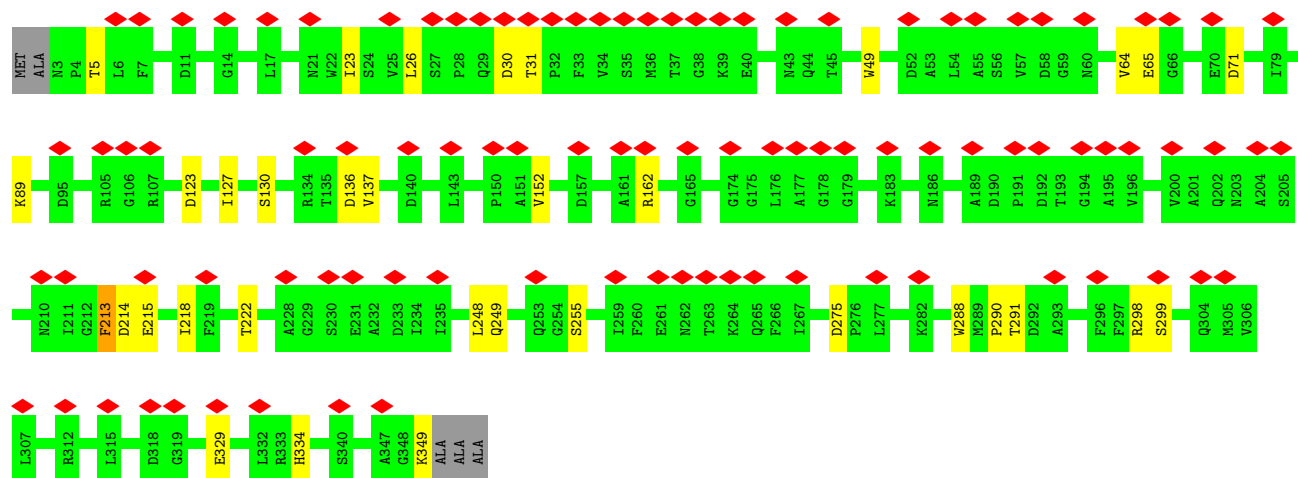


• Molecule 1: Major head protein

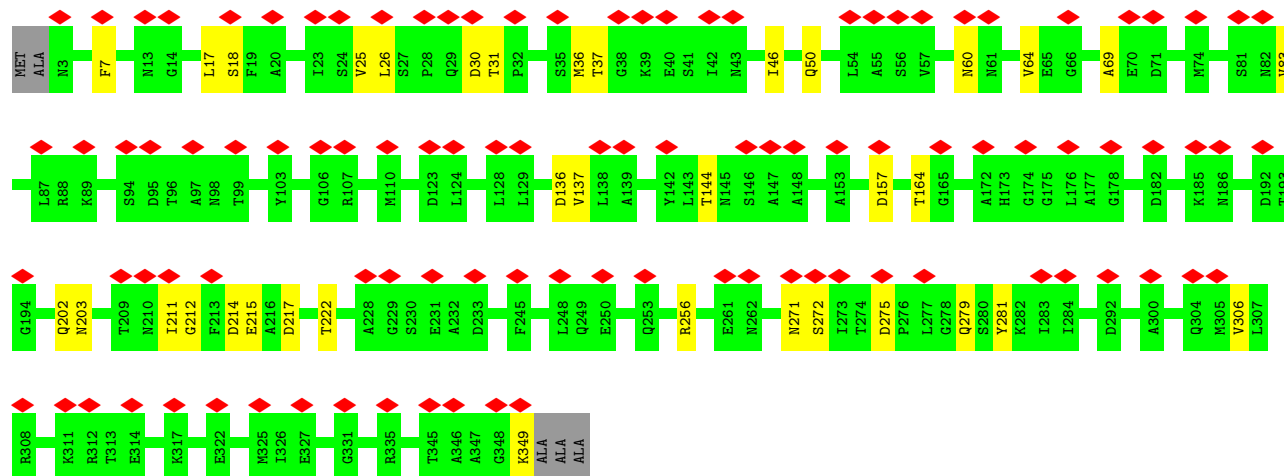
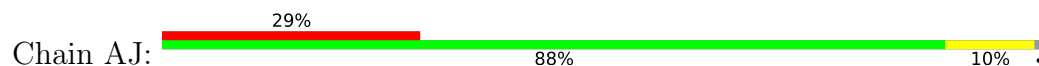




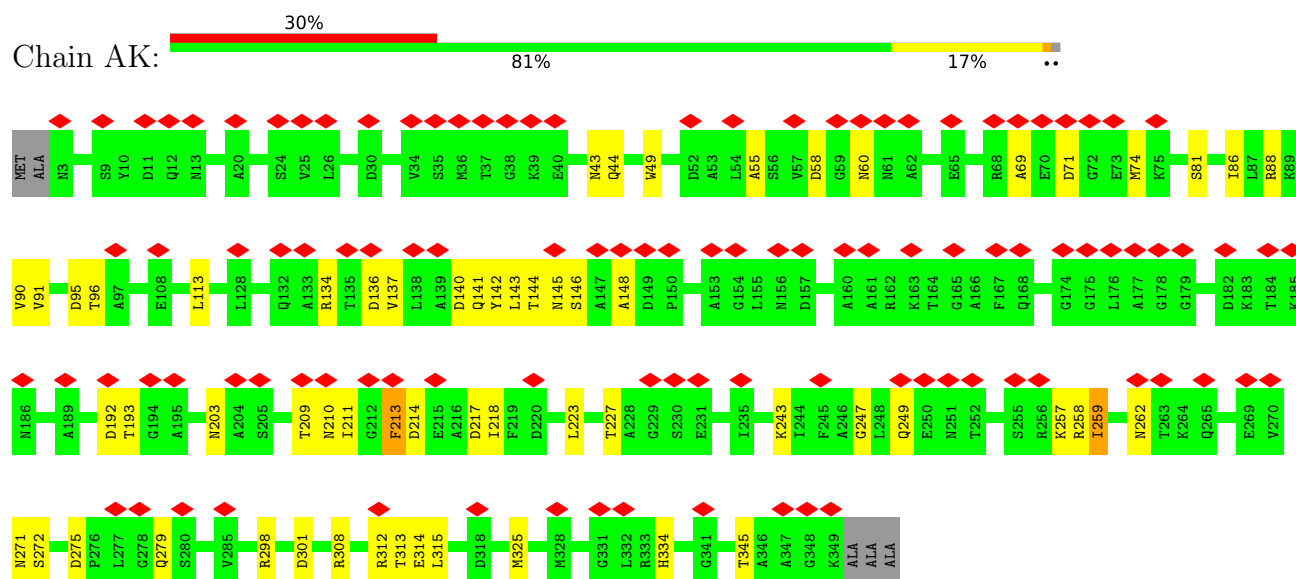
- Molecule 1: Major head protein



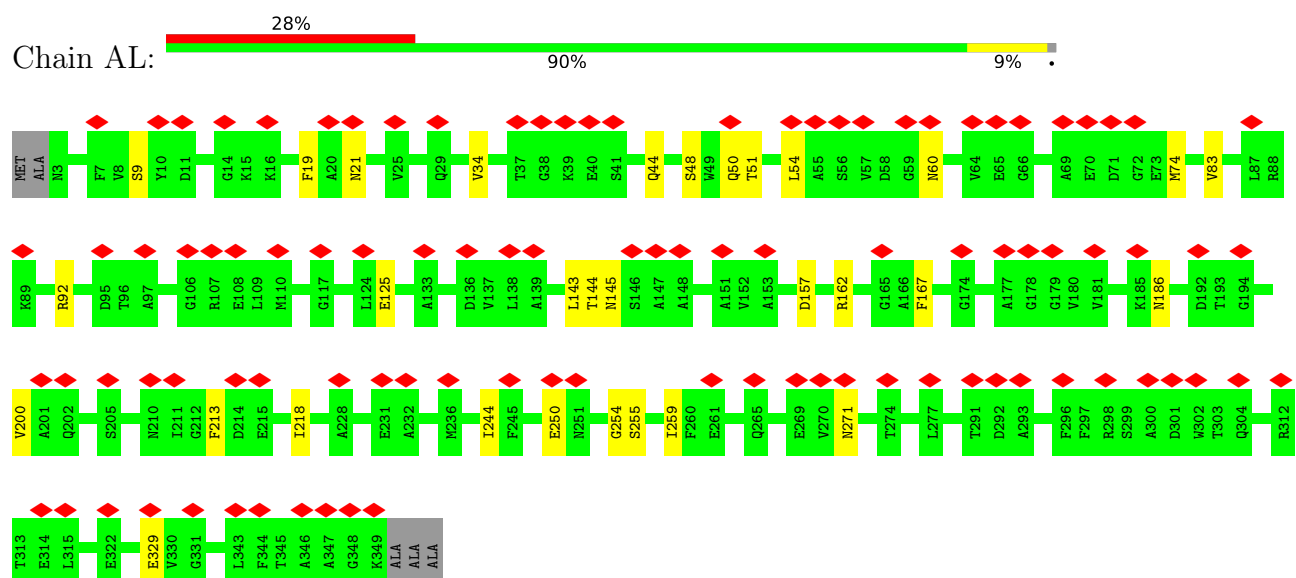
- Molecule 1: Major head protein



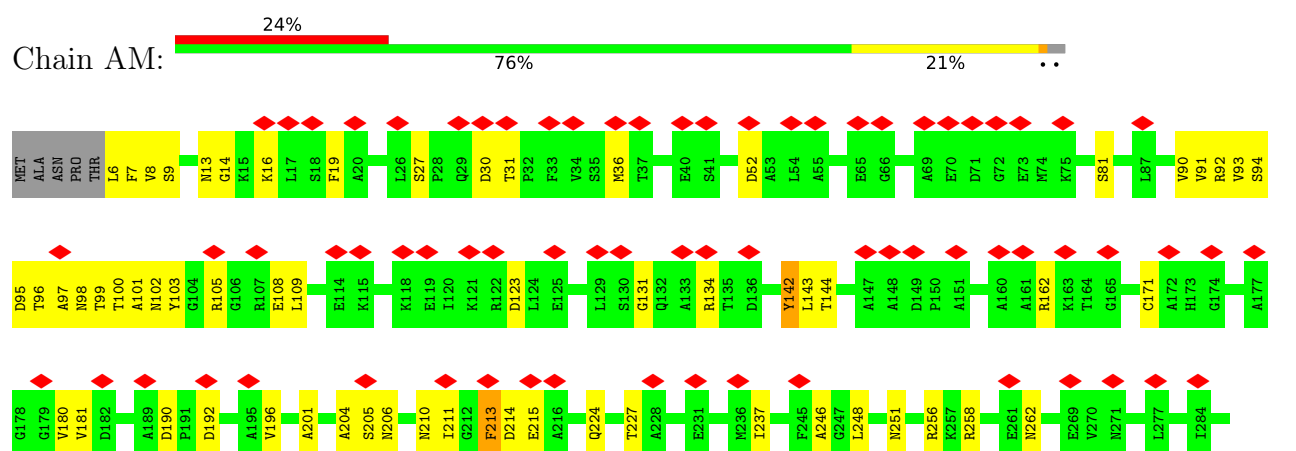
- Molecule 1: Major head protein

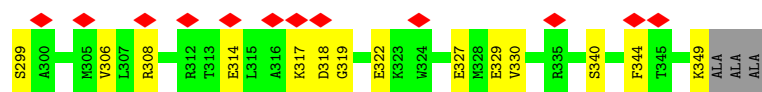


• Molecule 1: Major head protein

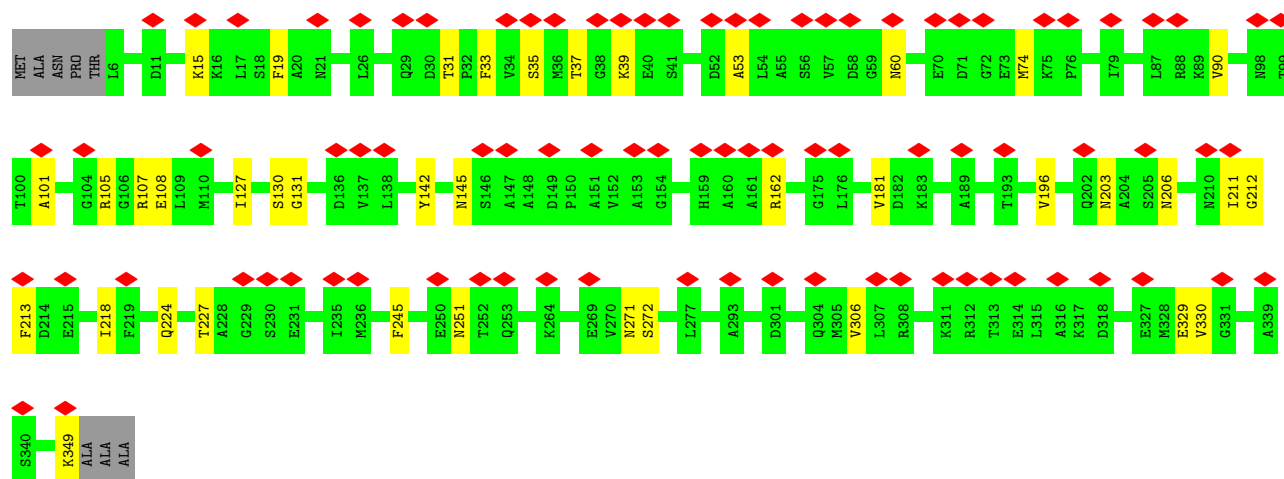
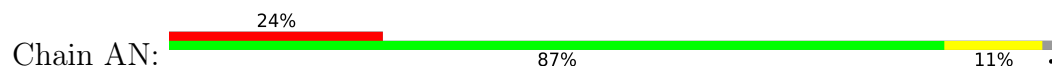


• Molecule 1: Major head protein

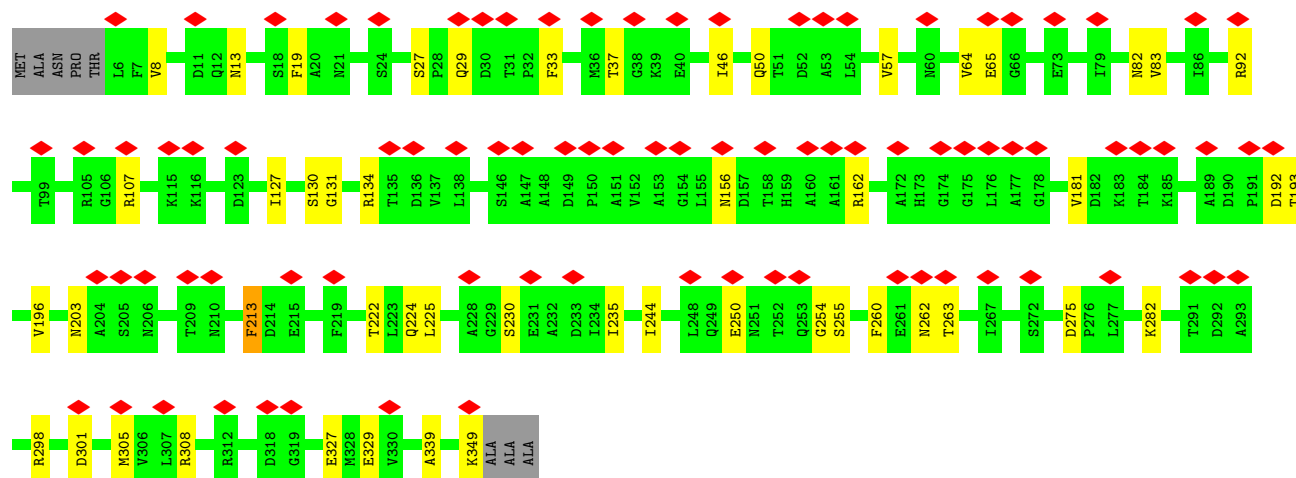
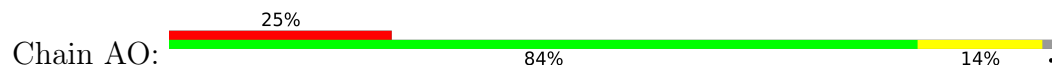




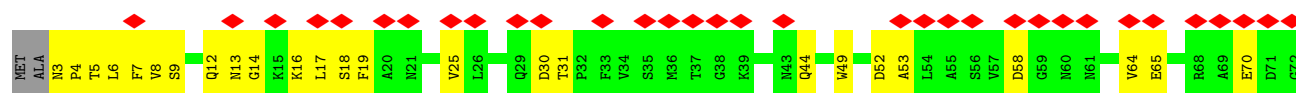
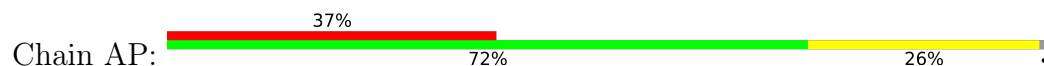
• Molecule 1: Major head protein

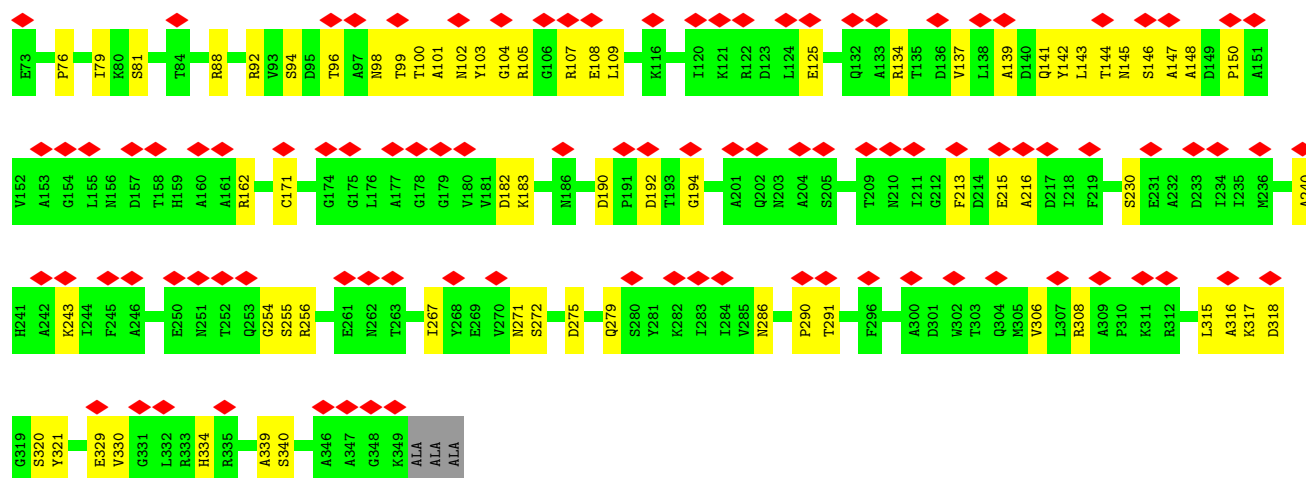


• Molecule 1: Major head protein



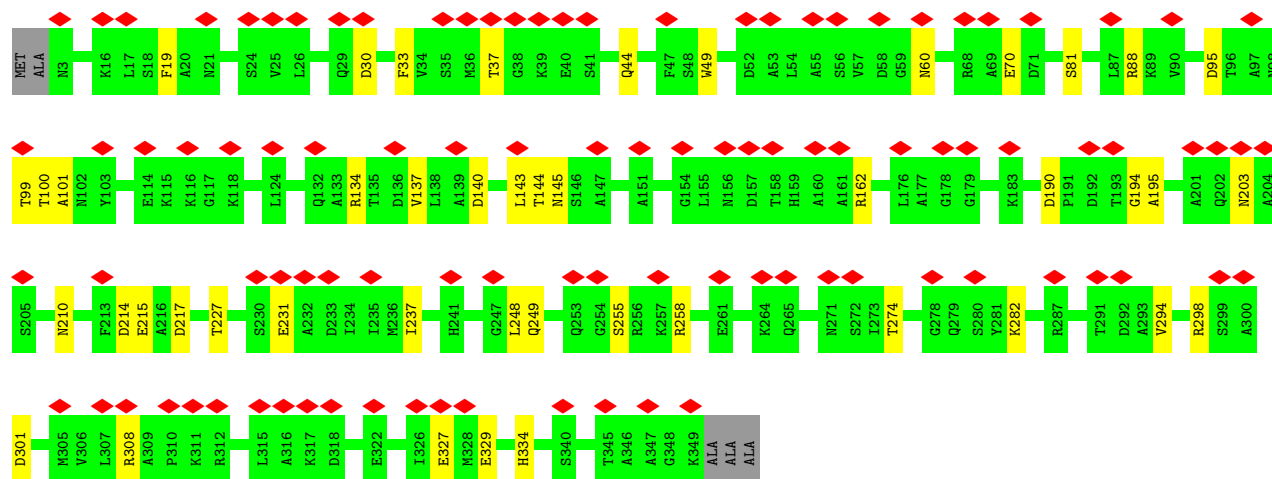
• Molecule 1: Major head protein





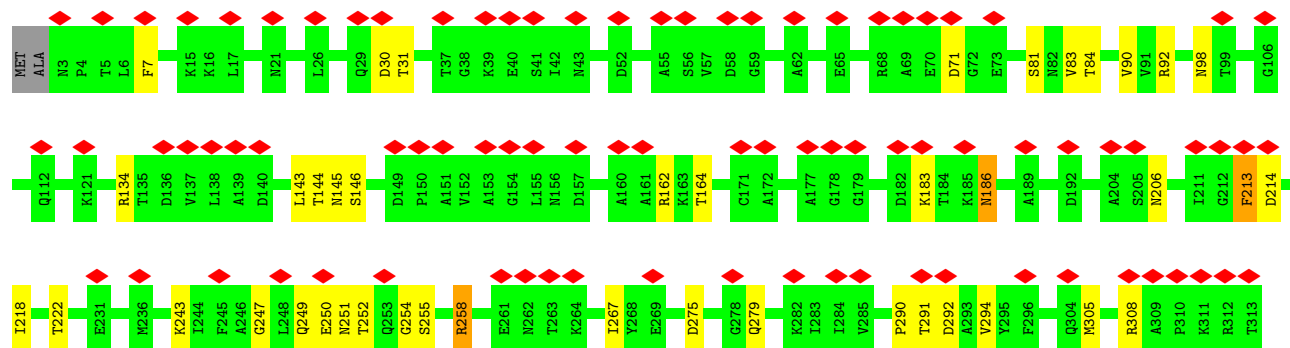
- Molecule 1: Major head protein

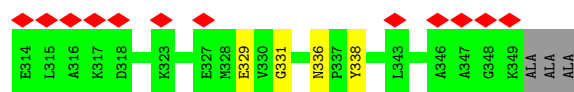
Chain AQ: 28% 86% 13% .



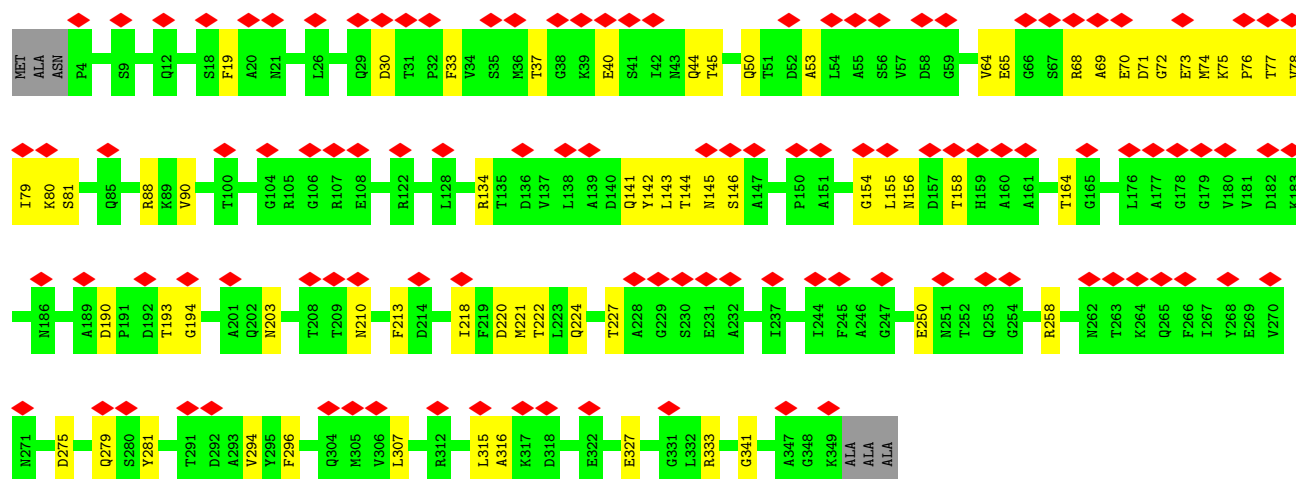
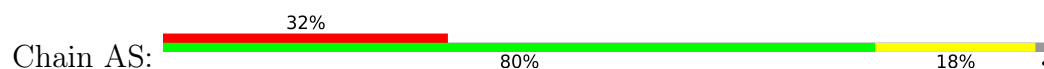
- Molecule 1: Major head protein

Chain AR: 28% 86% 12% ..

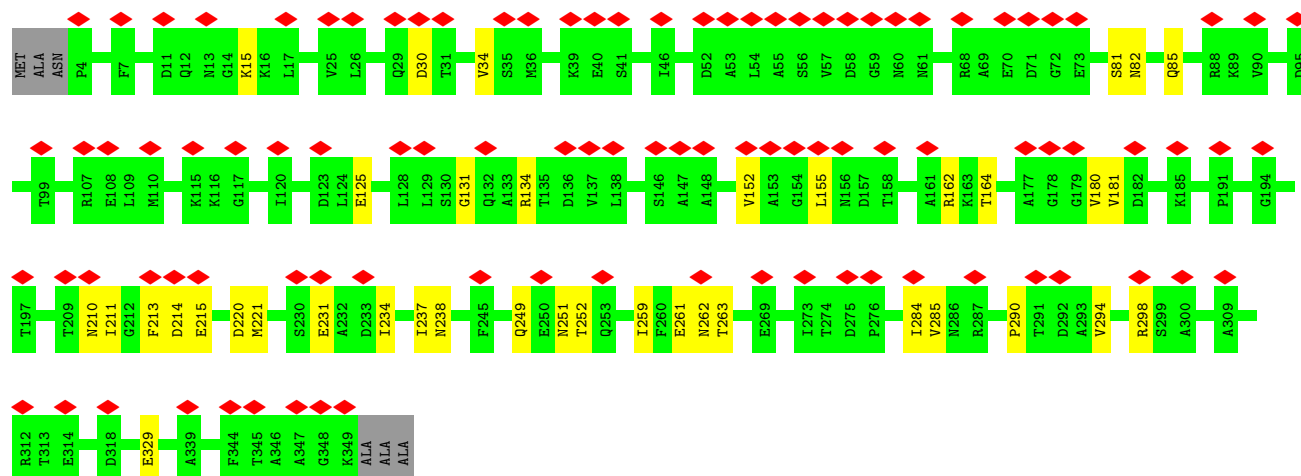
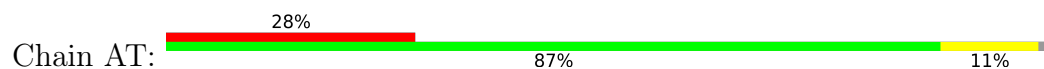




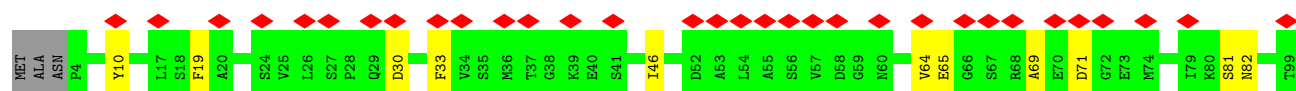
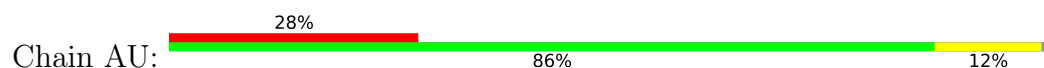
• Molecule 1: Major head protein

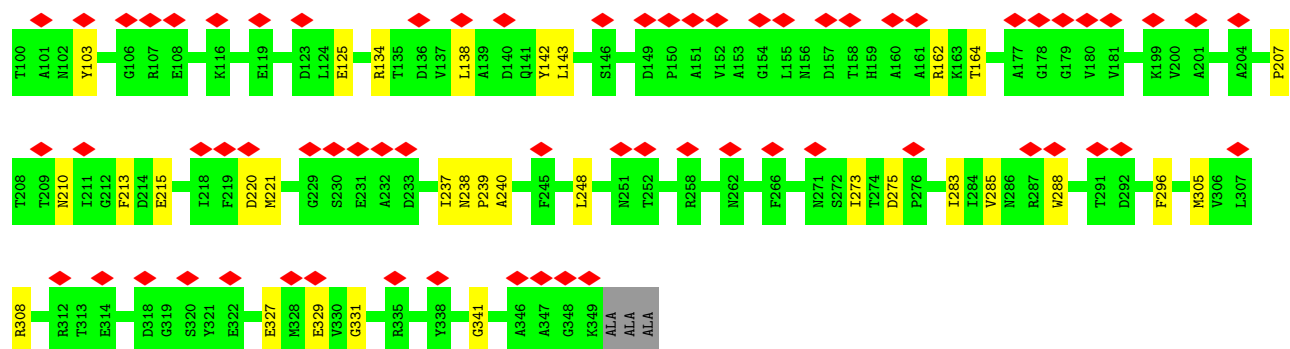


• Molecule 1: Major head protein

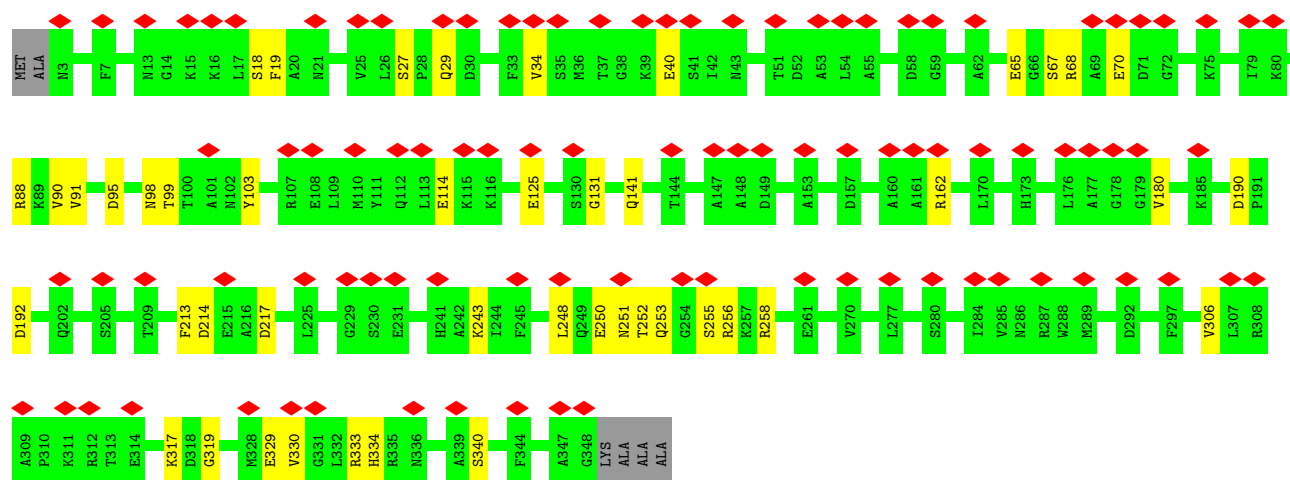
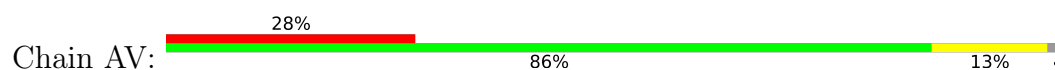


• Molecule 1: Major head protein

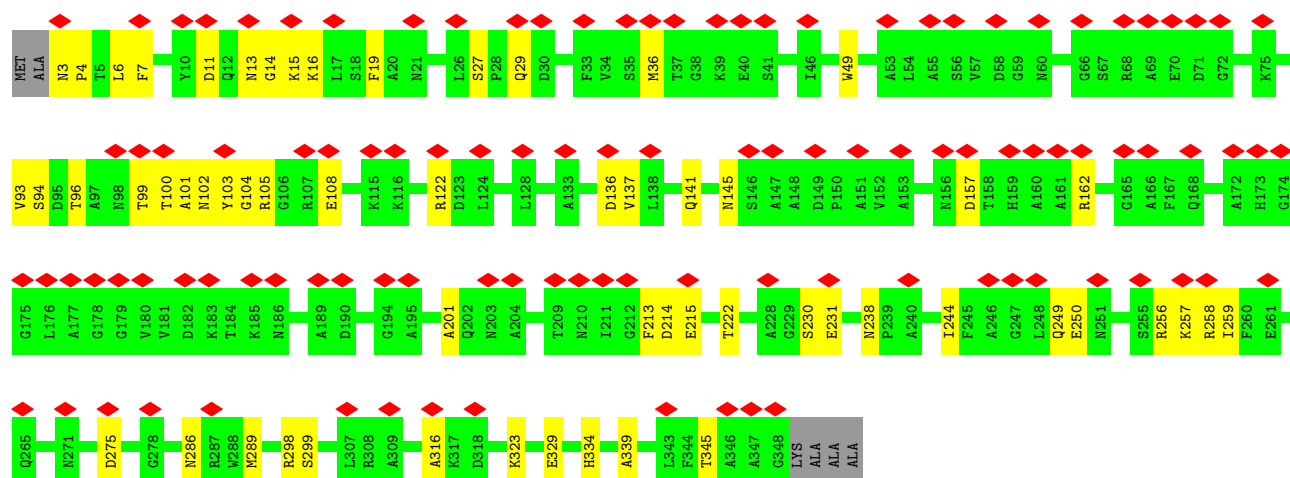
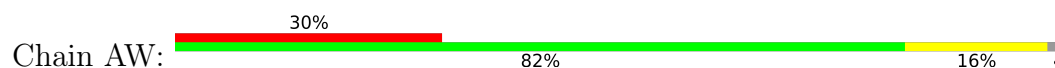




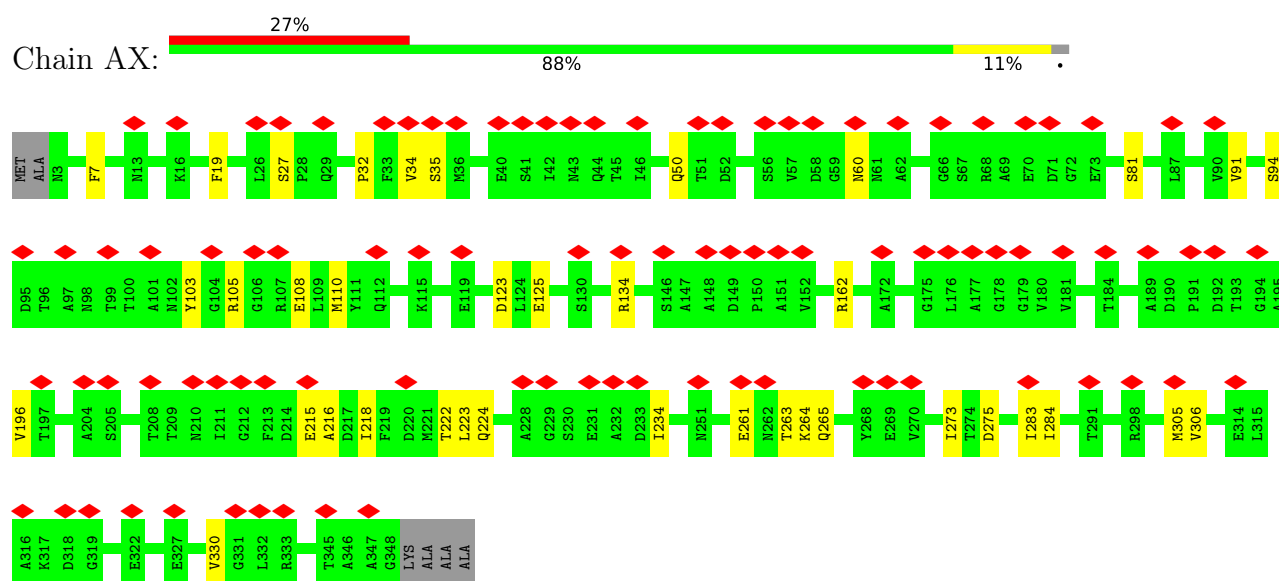
- Molecule 1: Major head protein



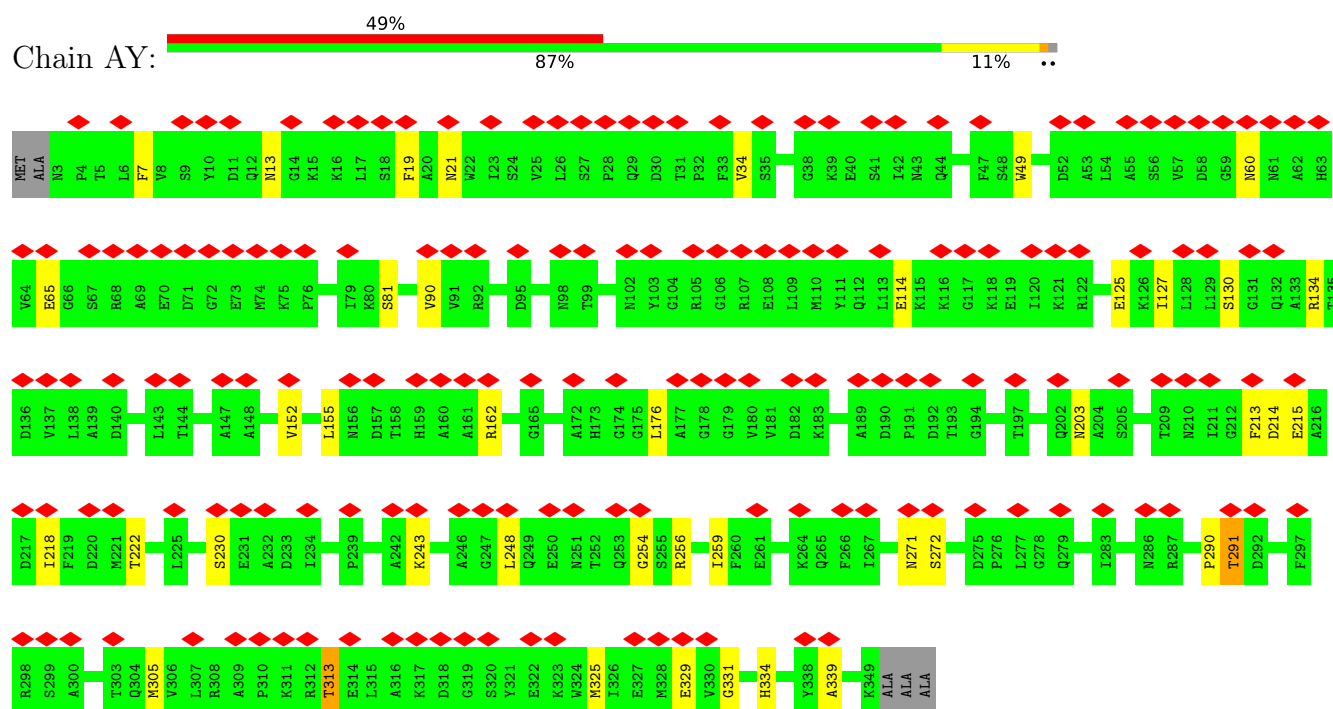
- Molecule 1: Major head protein



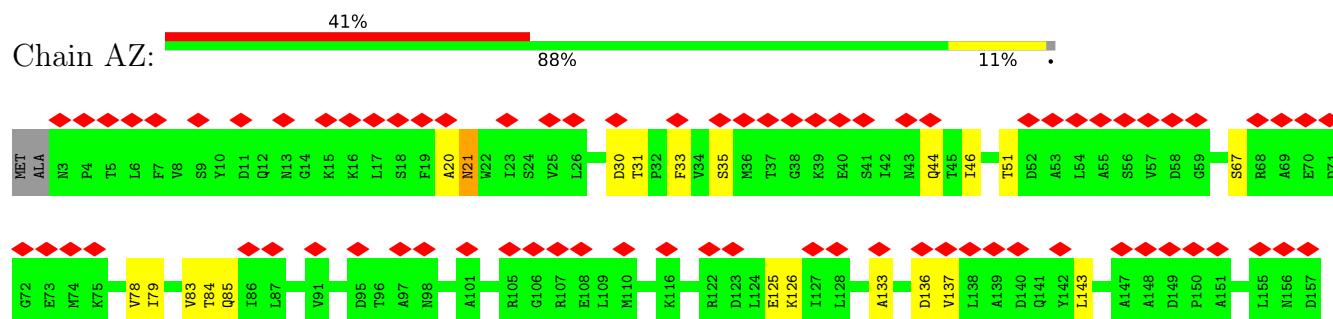
- Molecule 1: Major head protein

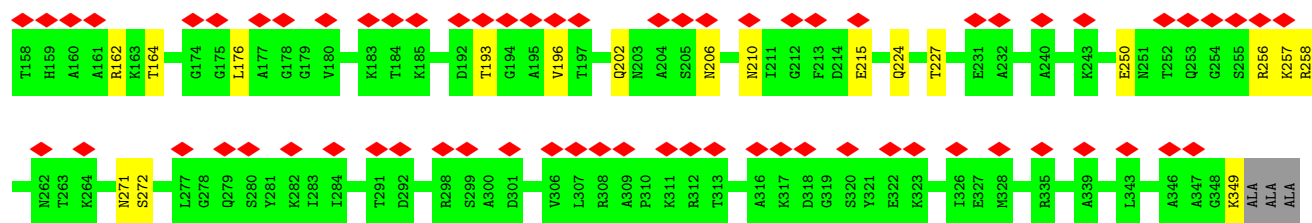


- Molecule 1: Major head protein



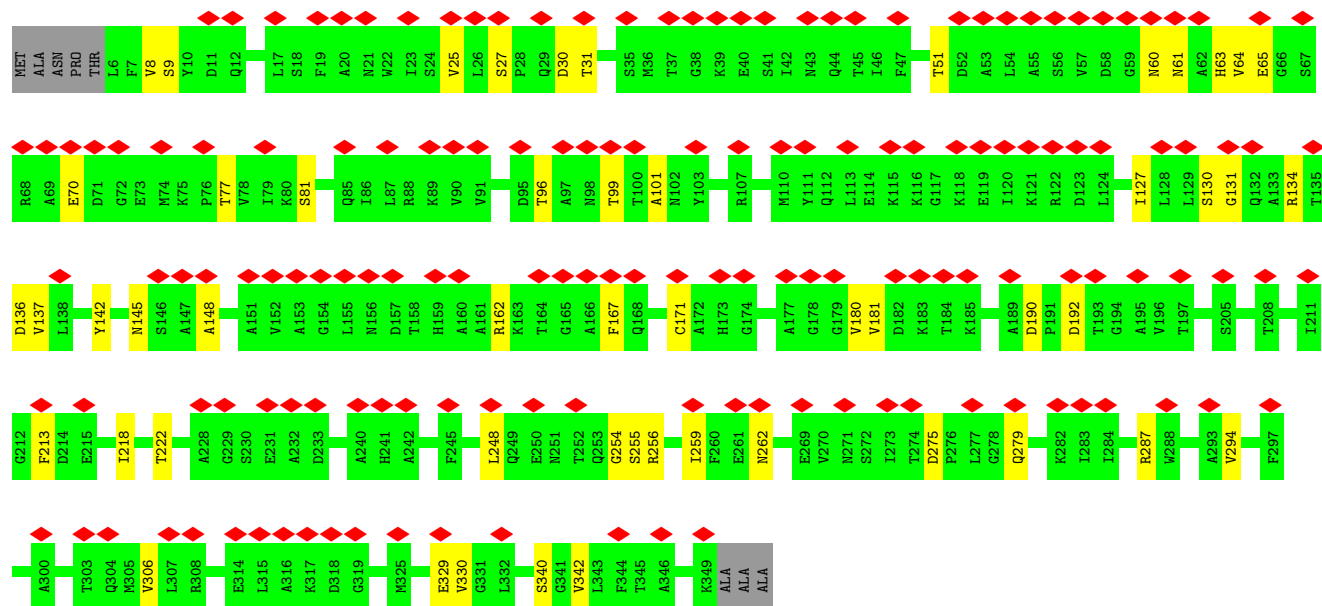
- Molecule 1: Major head protein





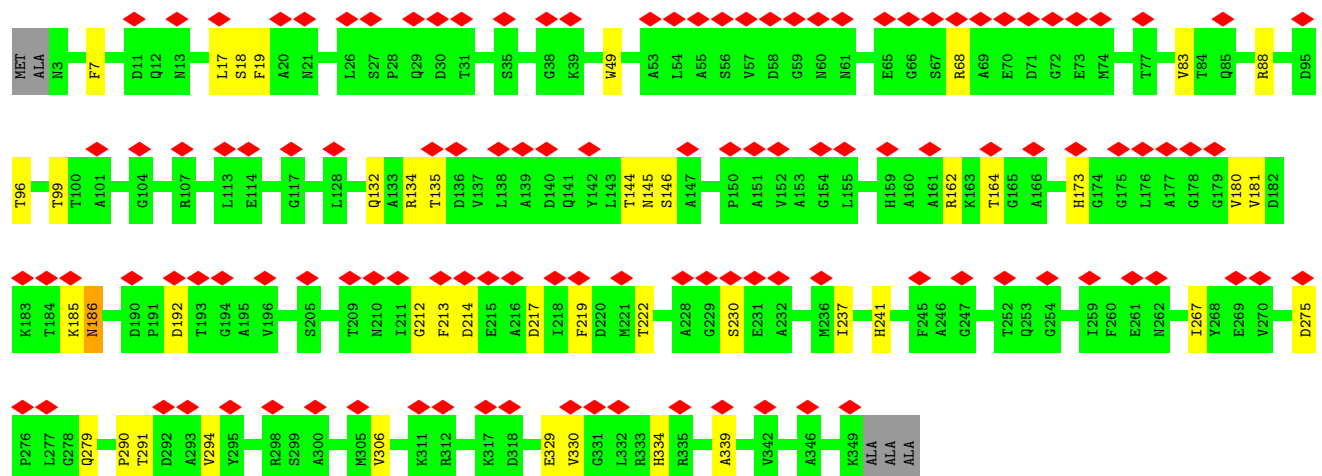
- Molecule 1: Major head protein

Chain BA: 44% 83% 15% .




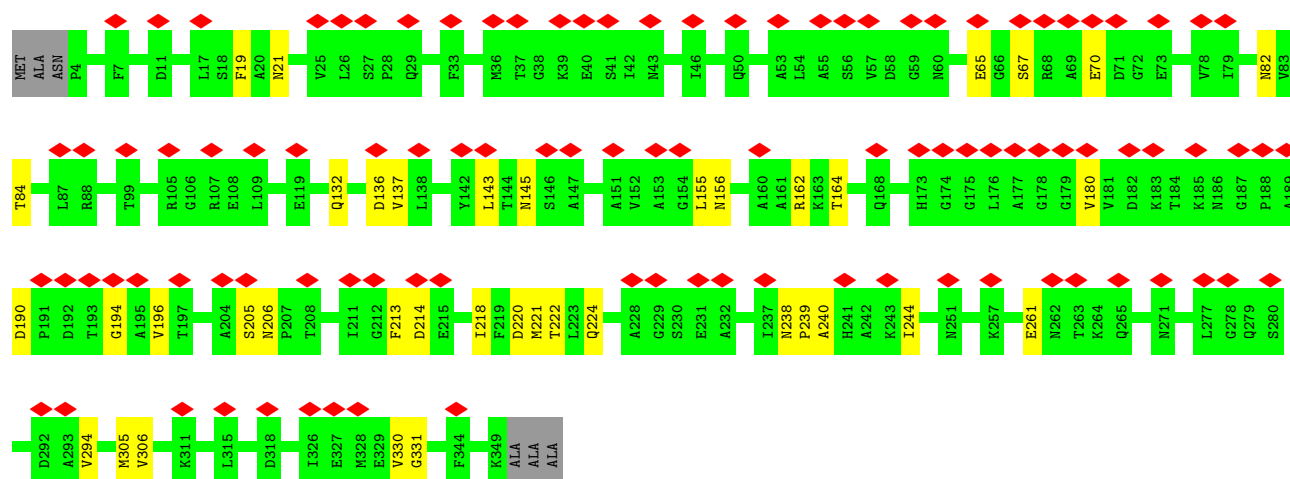
- Molecule 1: Major head protein

Chain BB: 34% 86% 12% .




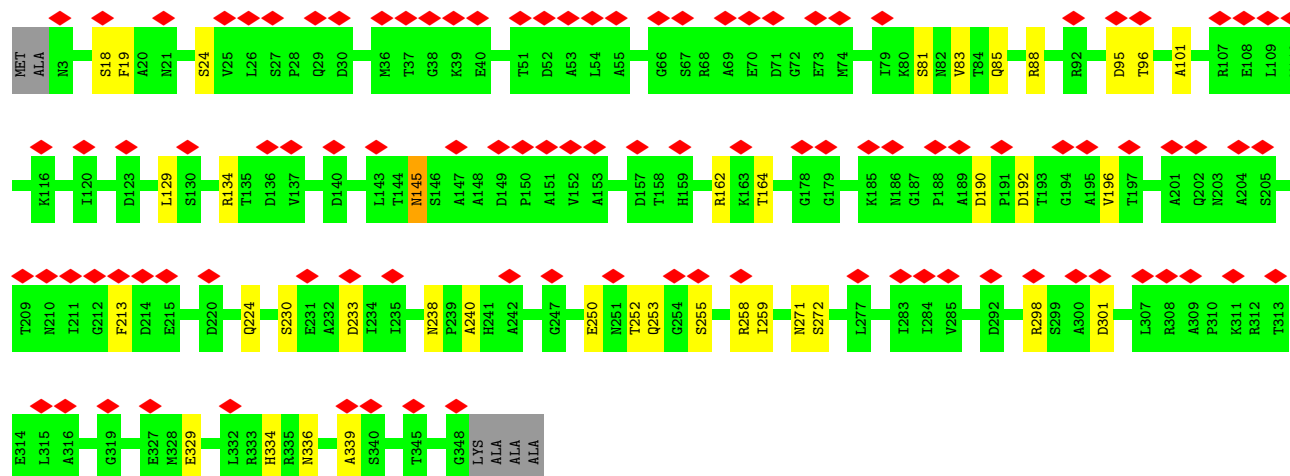
- Molecule 1: Major head protein

Chain BC: 




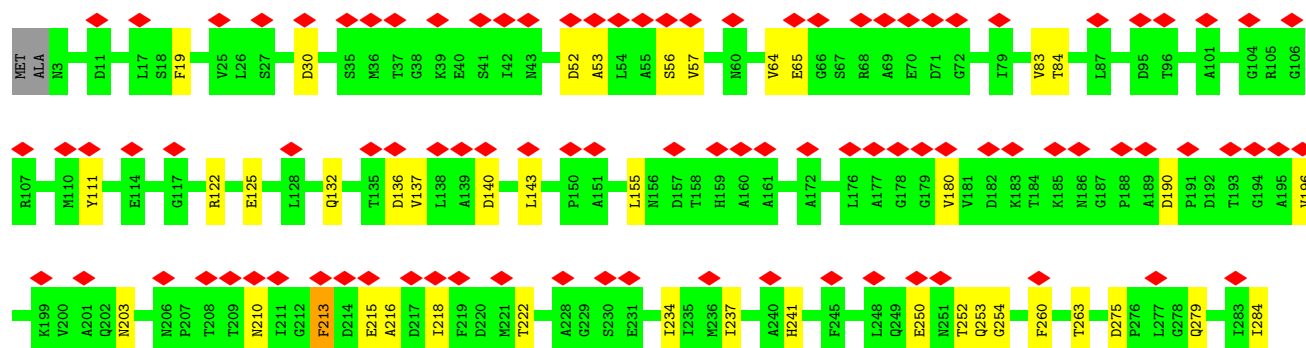
• Molecule 1: Major head protein

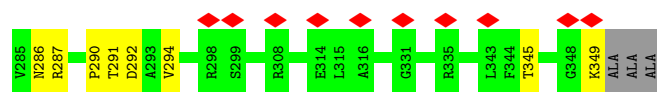
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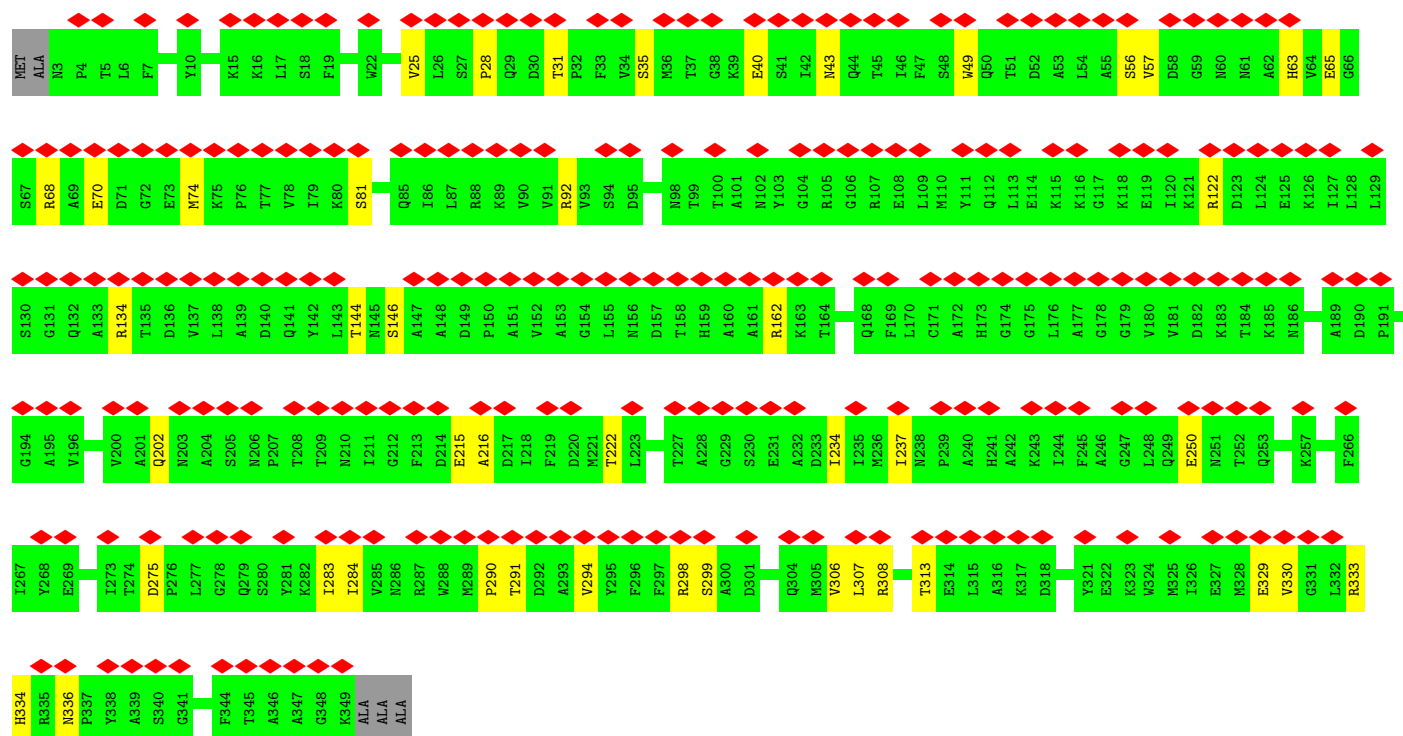
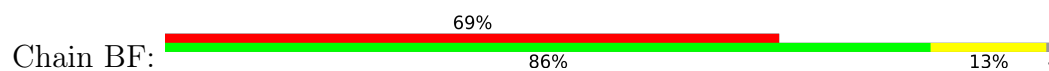
• Molecule 1: Major head protein

Chain BE: 

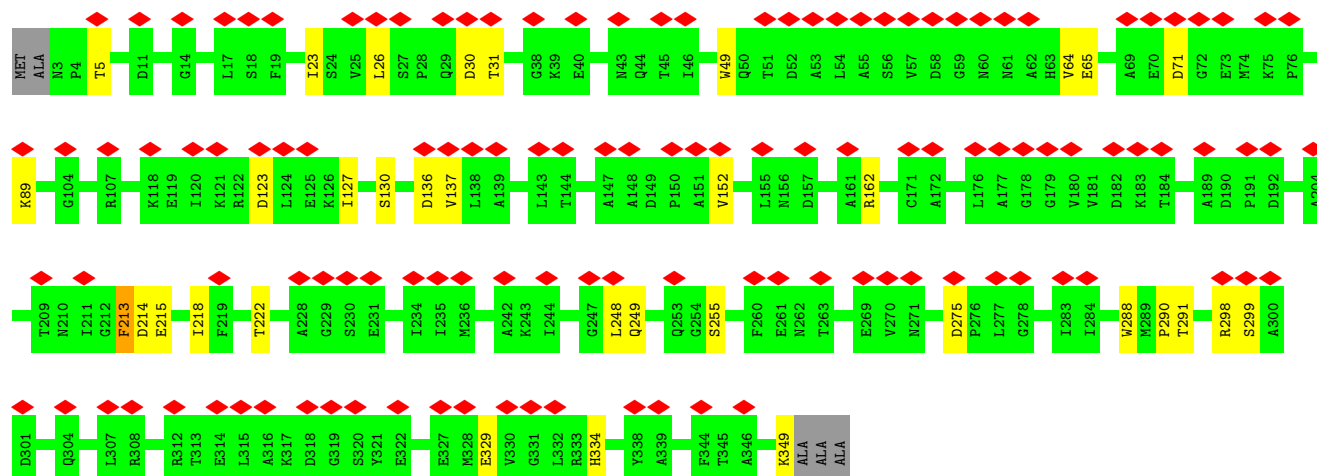
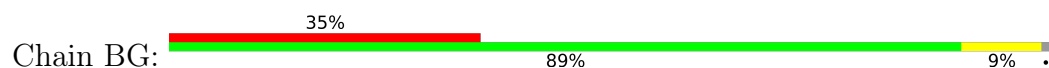




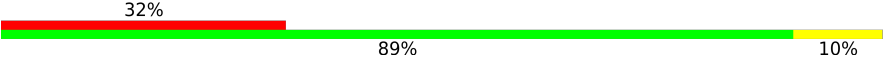
- Molecule 1: Major head protein

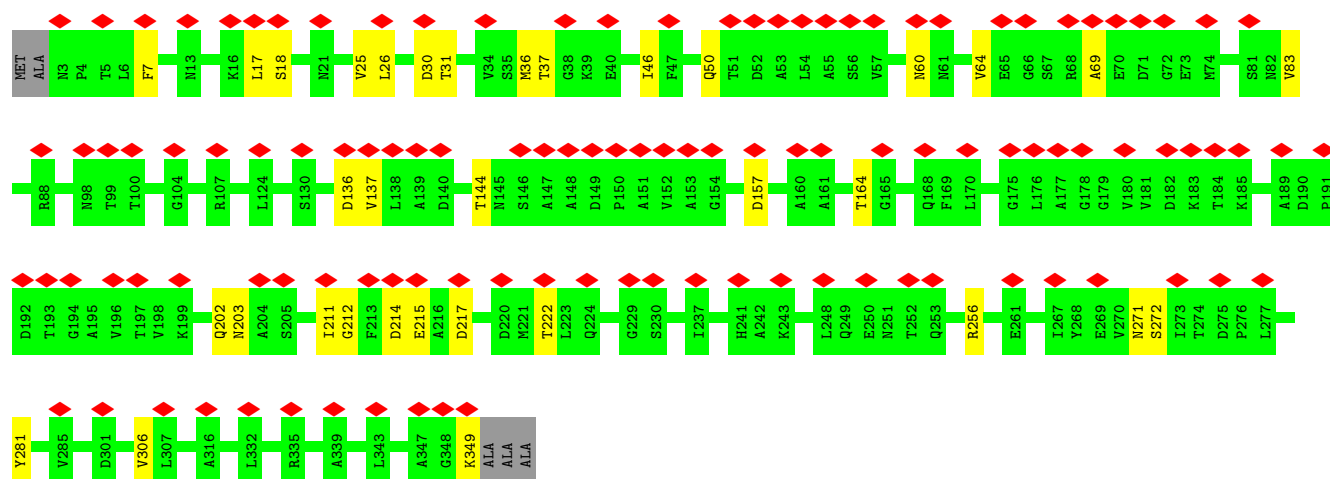


- Molecule 1: Major head protein




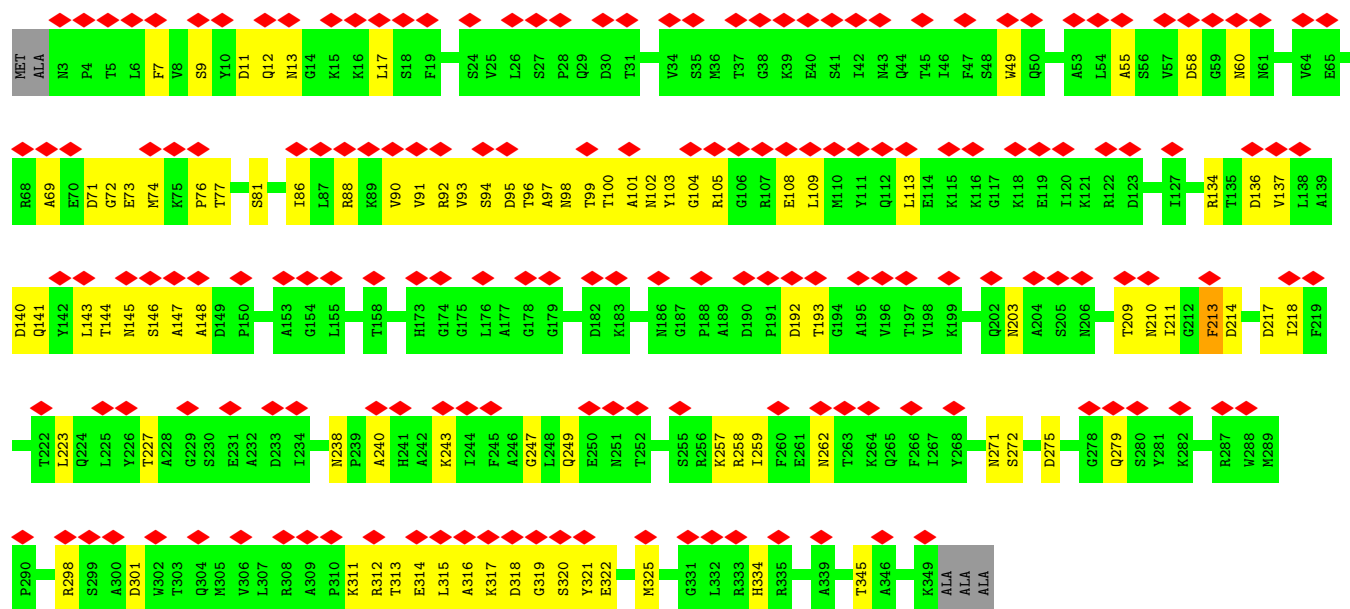
- Molecule 1: Major head protein

Chain BH: 




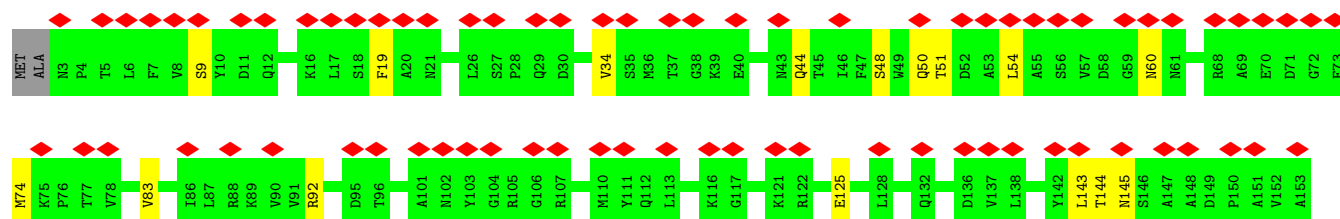
• Molecule 1: Major head protein

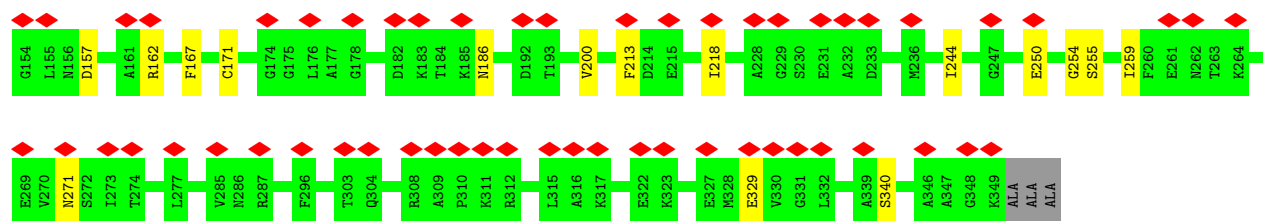
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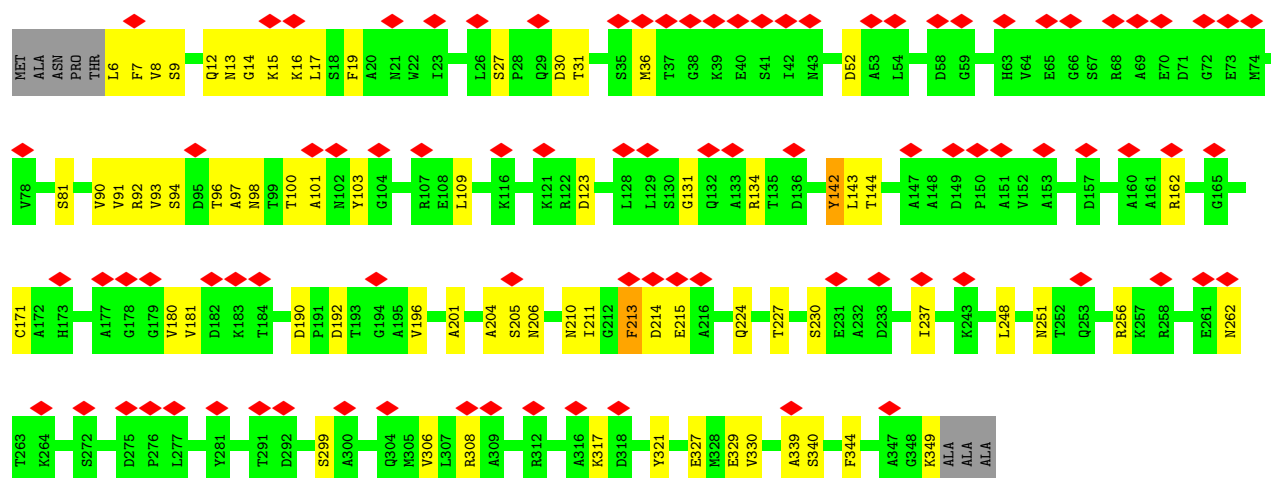
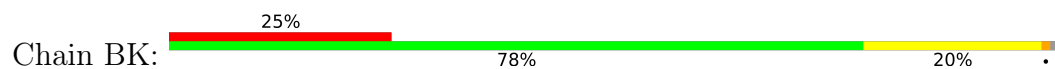
• Molecule 1: Major head protein

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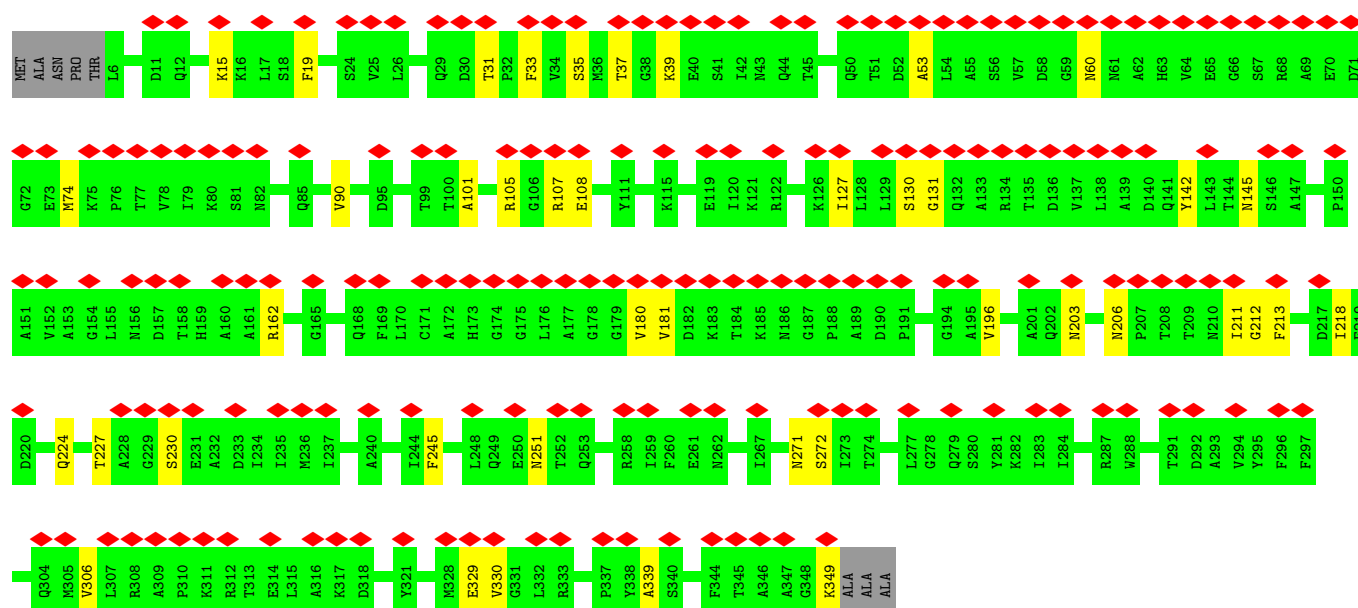
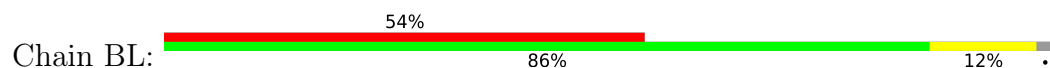




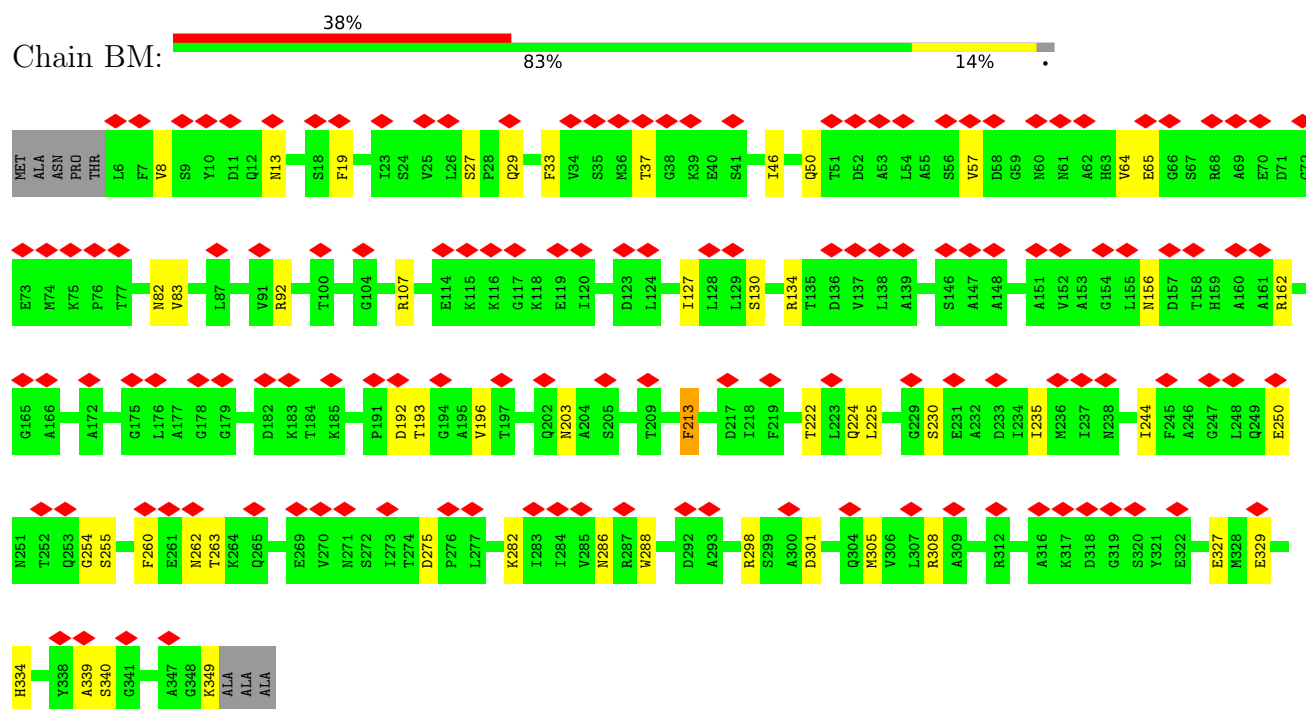
- Molecule 1: Major head protein



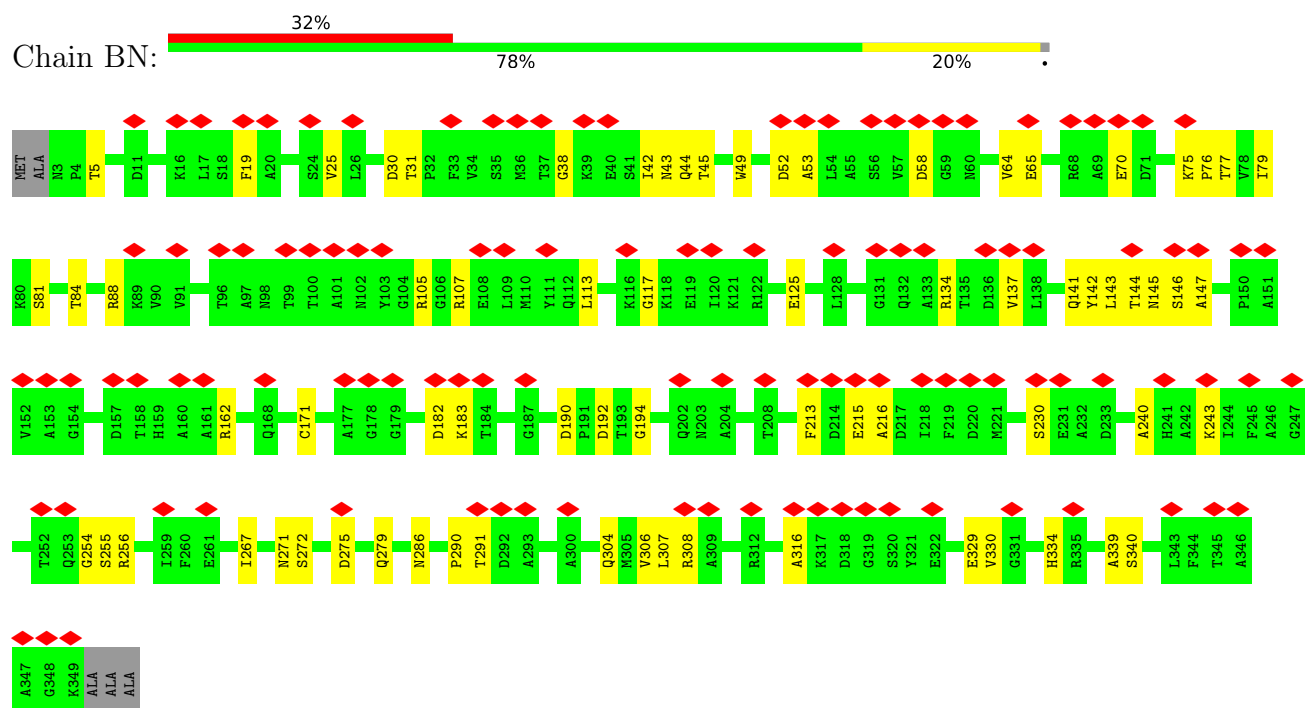
- Molecule 1: Major head protein



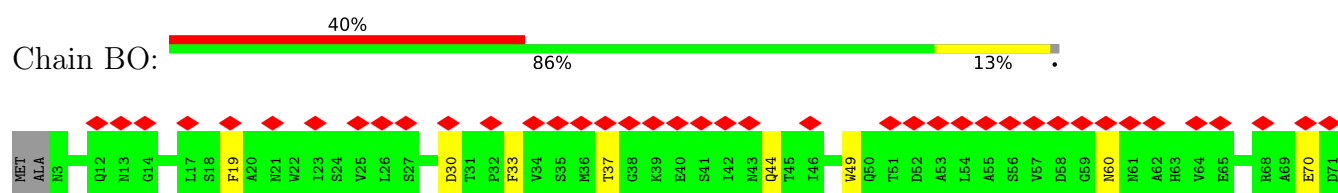
- Molecule 1: Major head protein

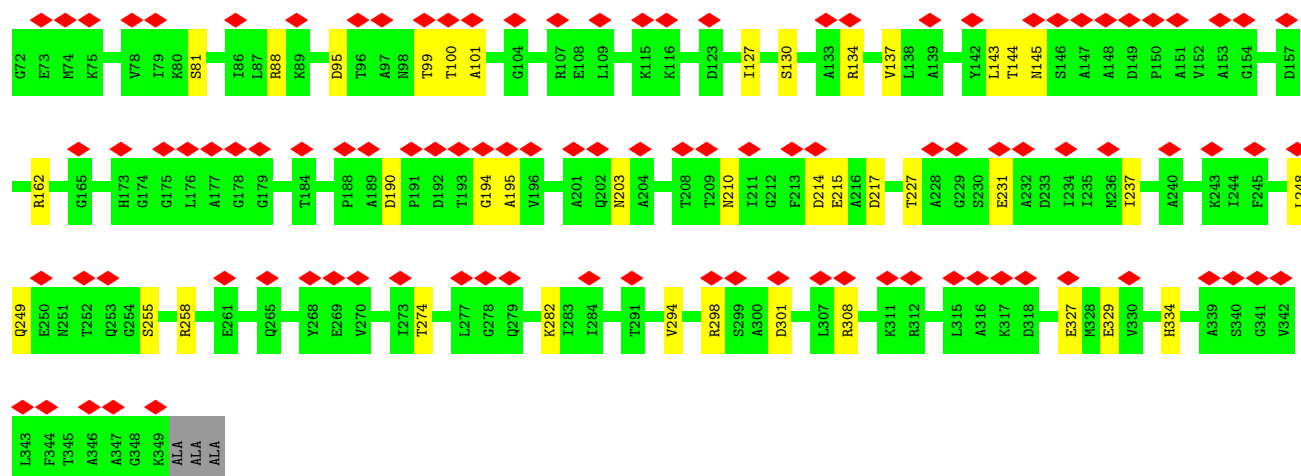


• Molecule 1: Major head protein

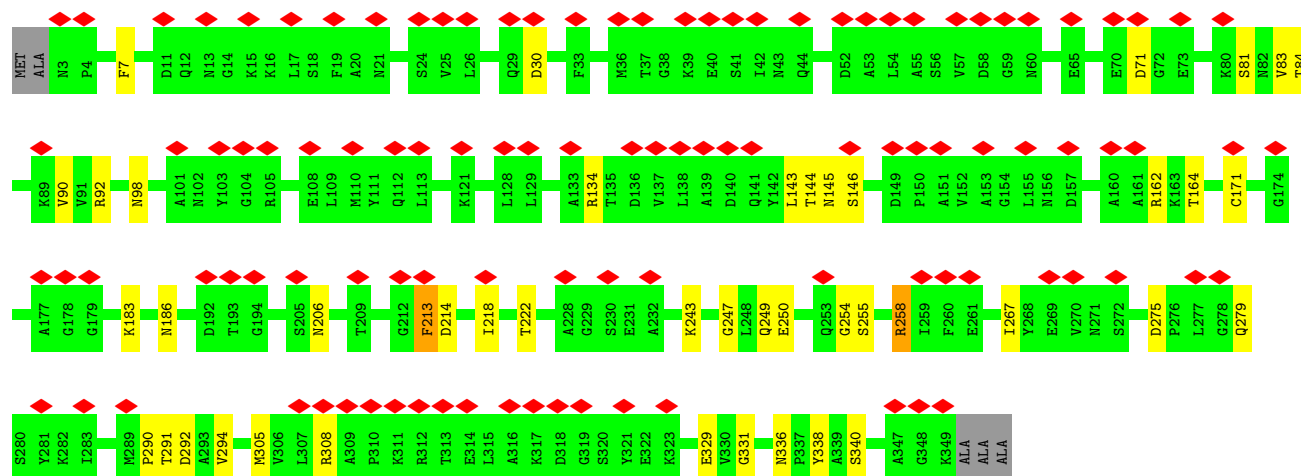
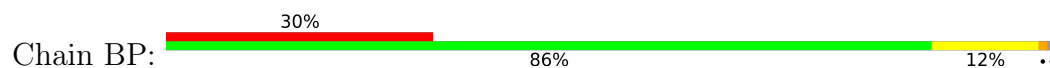


• Molecule 1: Major head protein

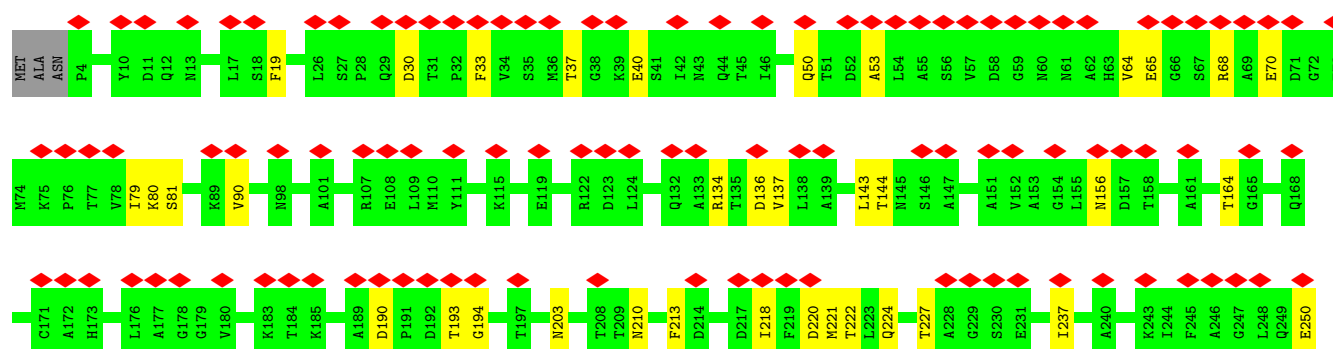
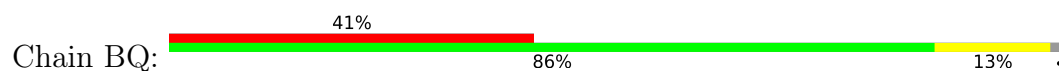


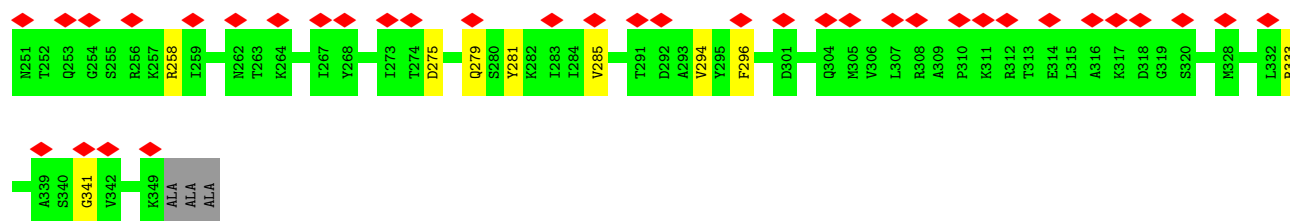


- Molecule 1: Major head protein

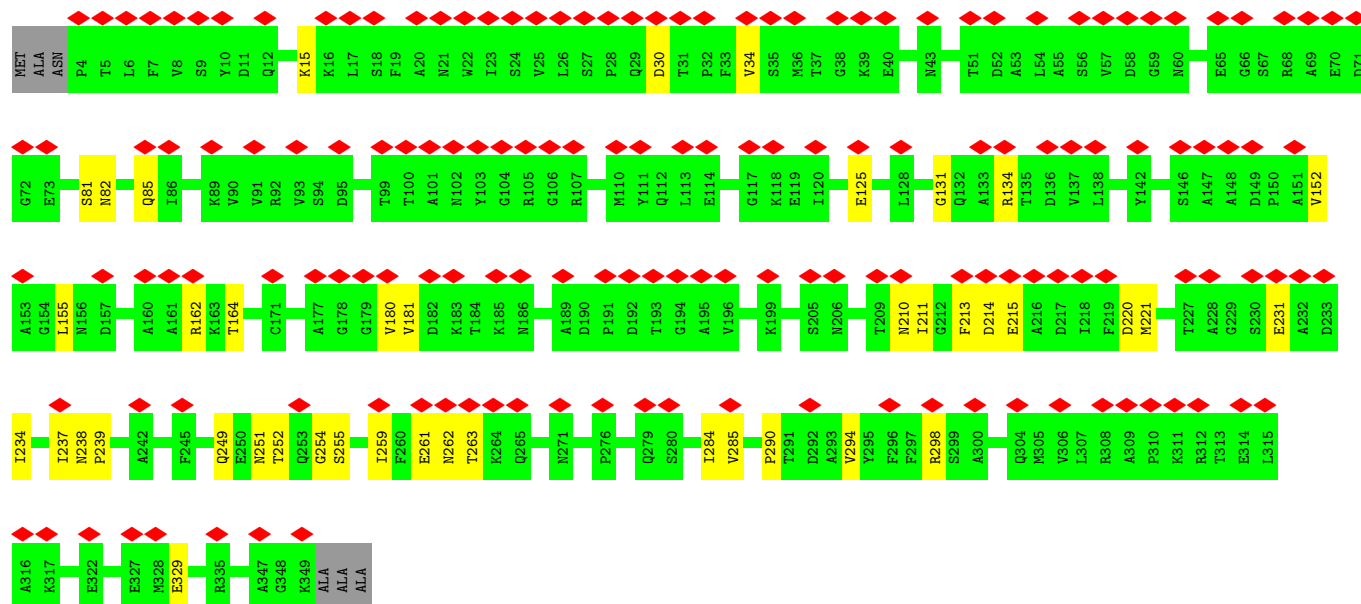
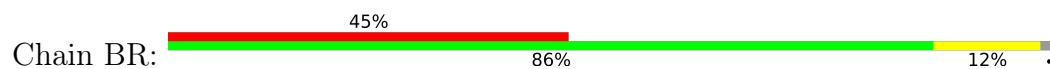


- Molecule 1: Major head protein

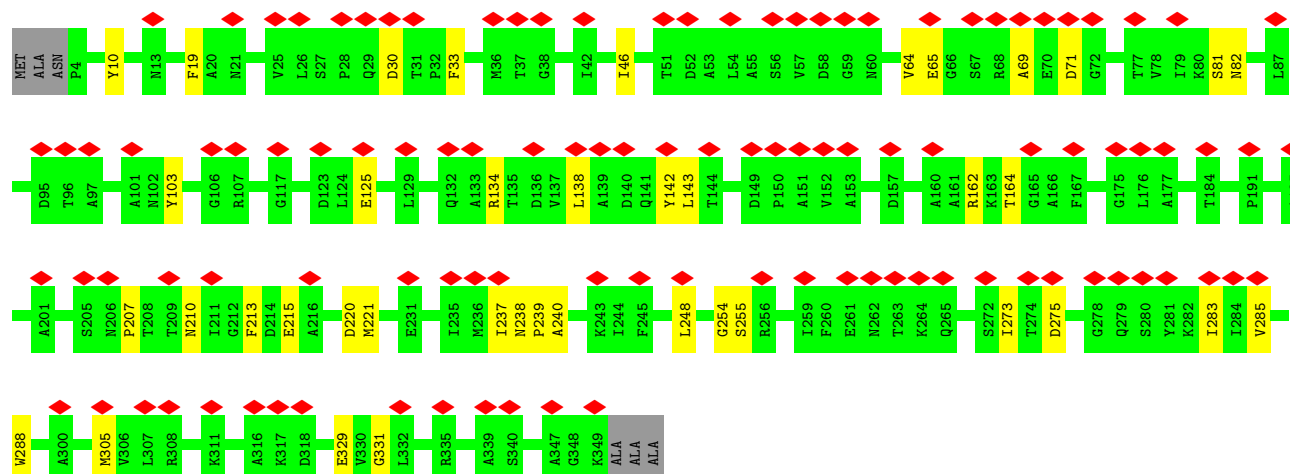
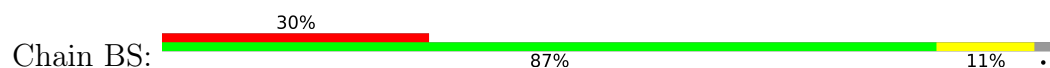





- Molecule 1: Major head protein

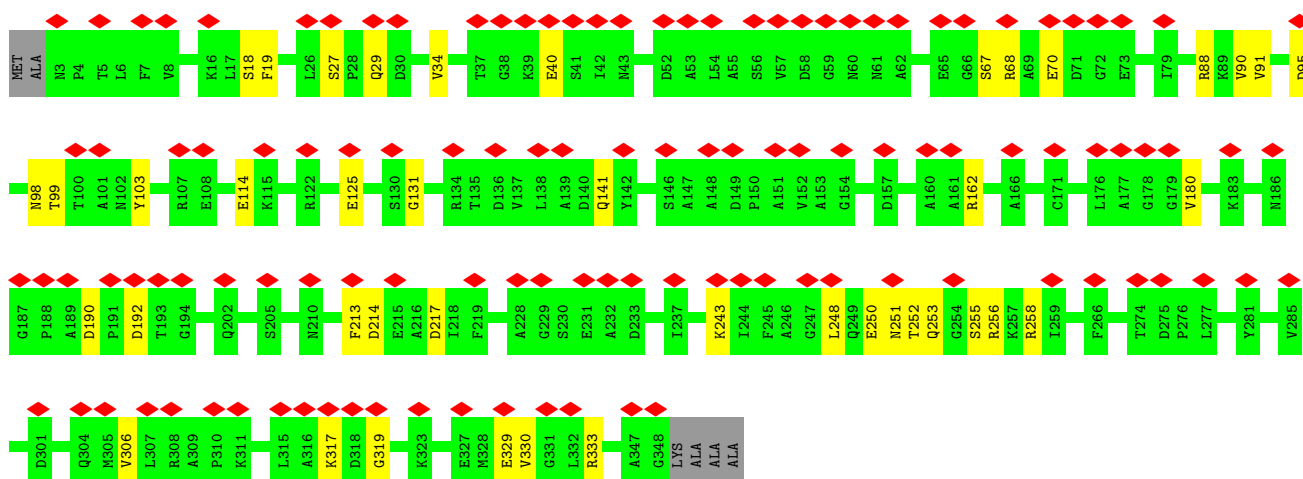


- Molecule 1: Major head protein




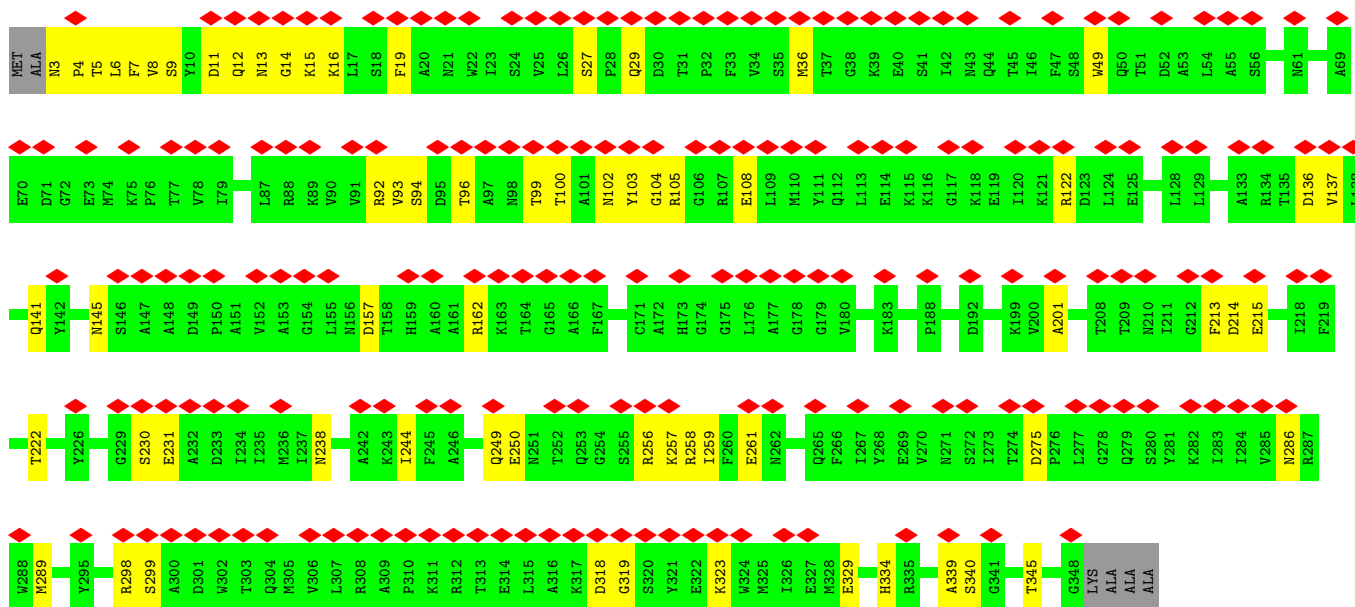
- Molecule 1: Major head protein

Chain BT: 




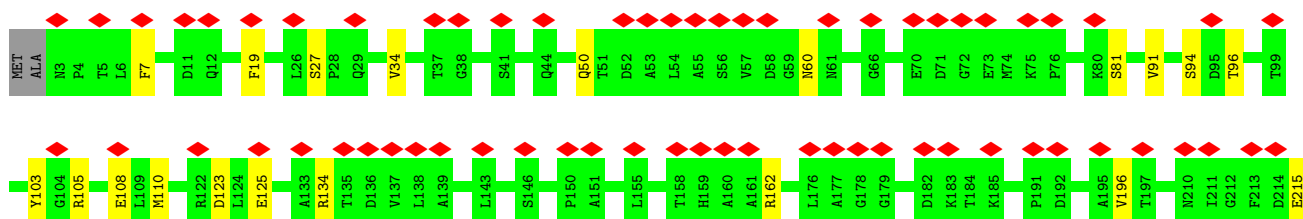
• Molecule 1: Major head protein

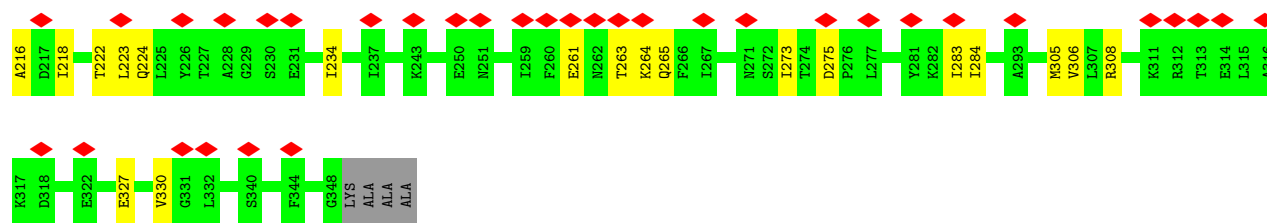
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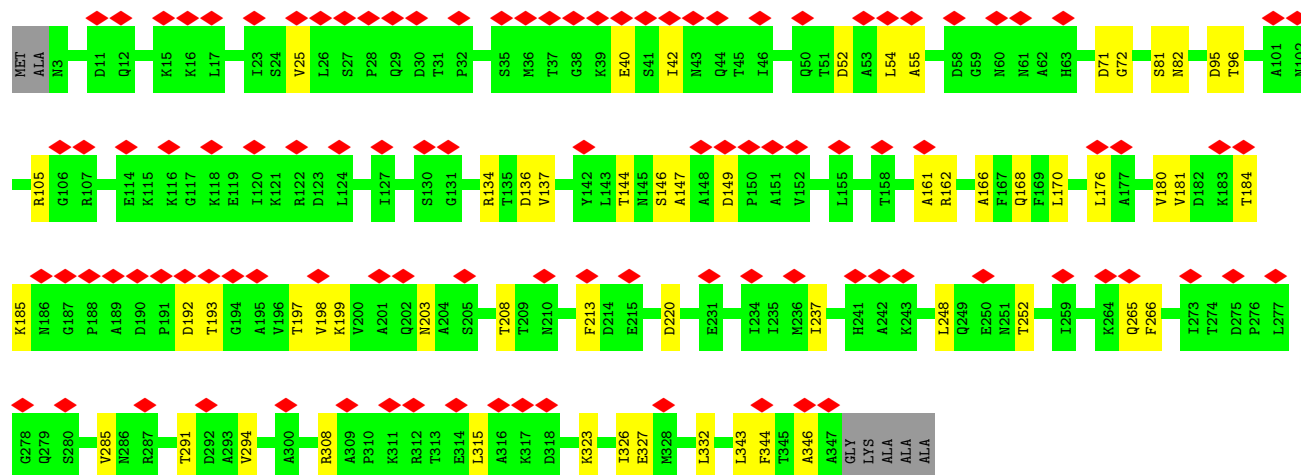
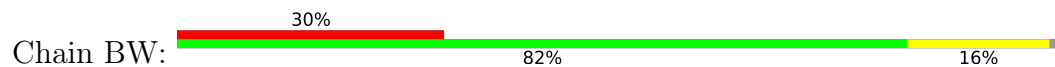
• Molecule 1: Major head protein

Chain BV: 

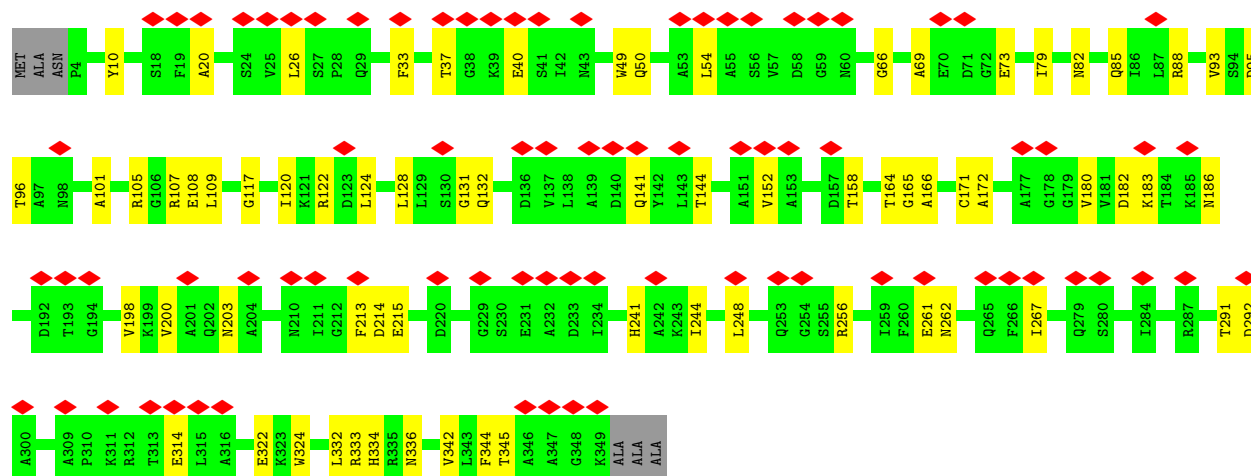
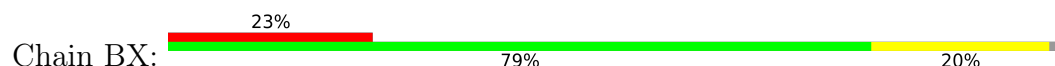




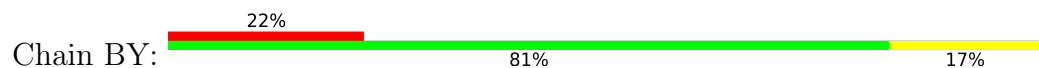
- Molecule 1: Major head protein

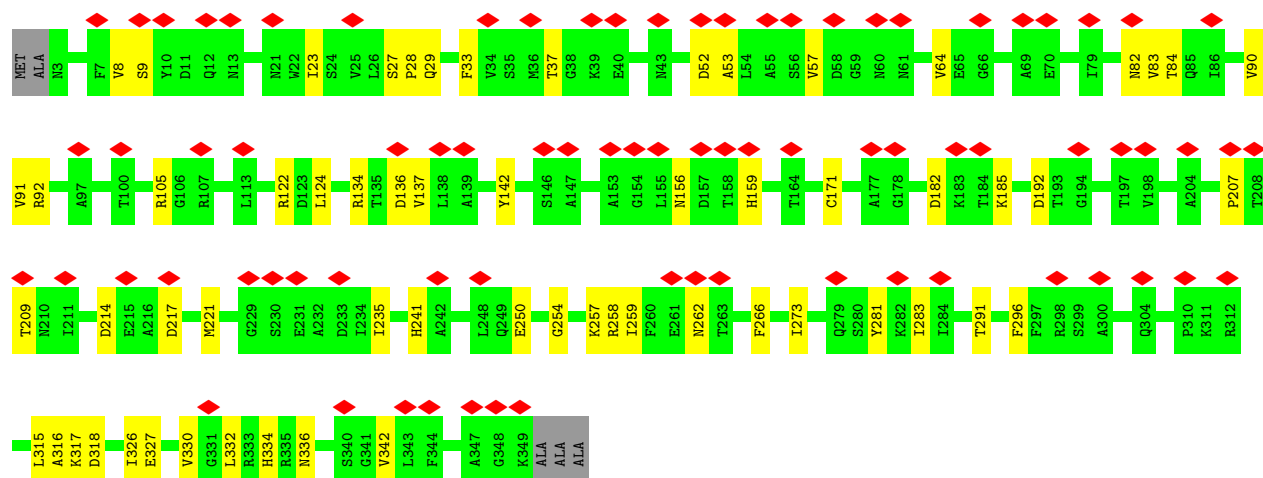


- Molecule 1: Major head protein

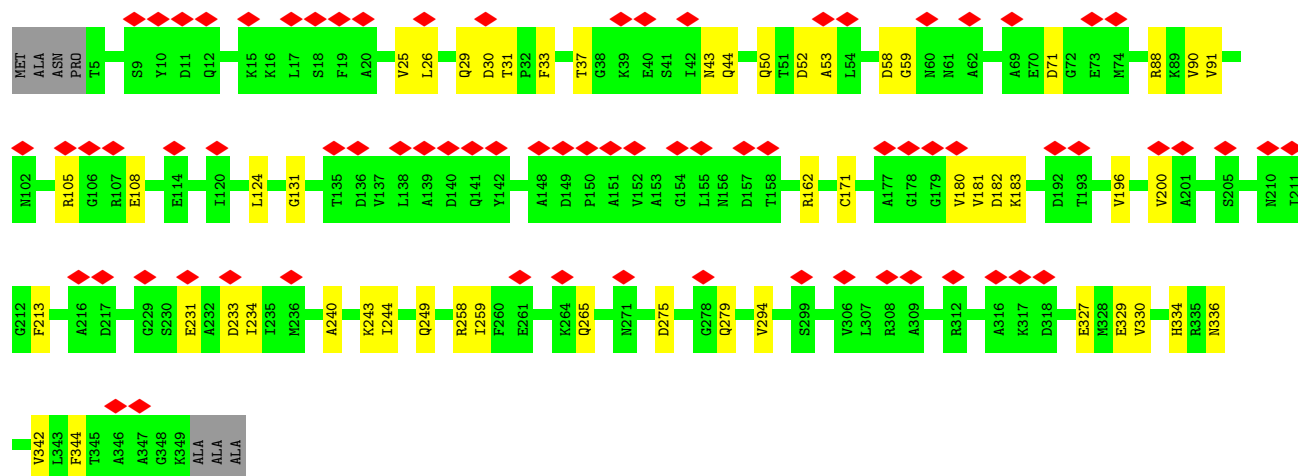
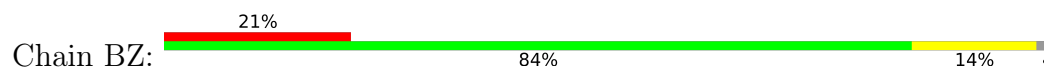


- Molecule 1: Major head protein

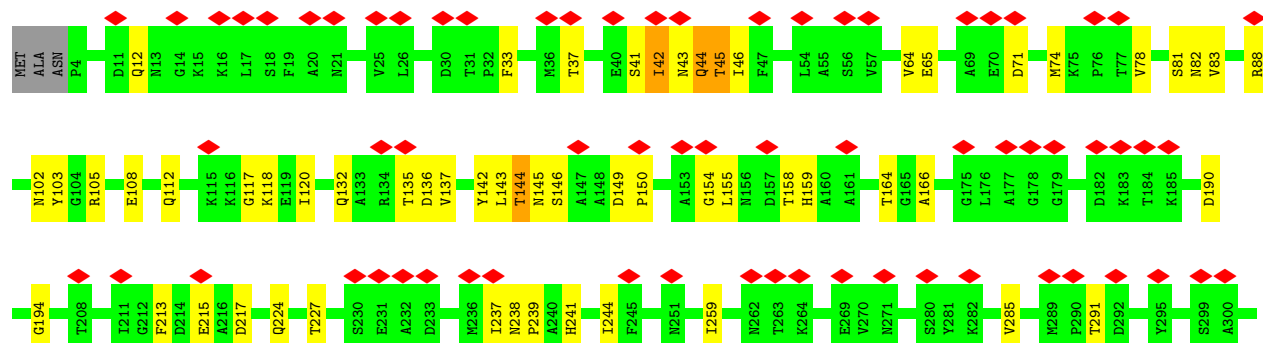
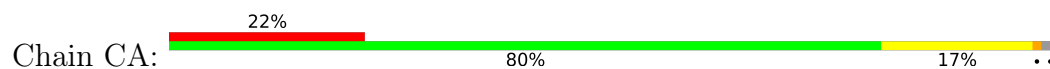


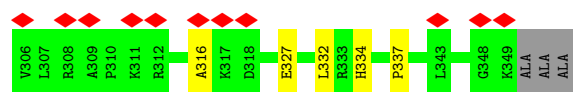


• Molecule 1: Major head protein

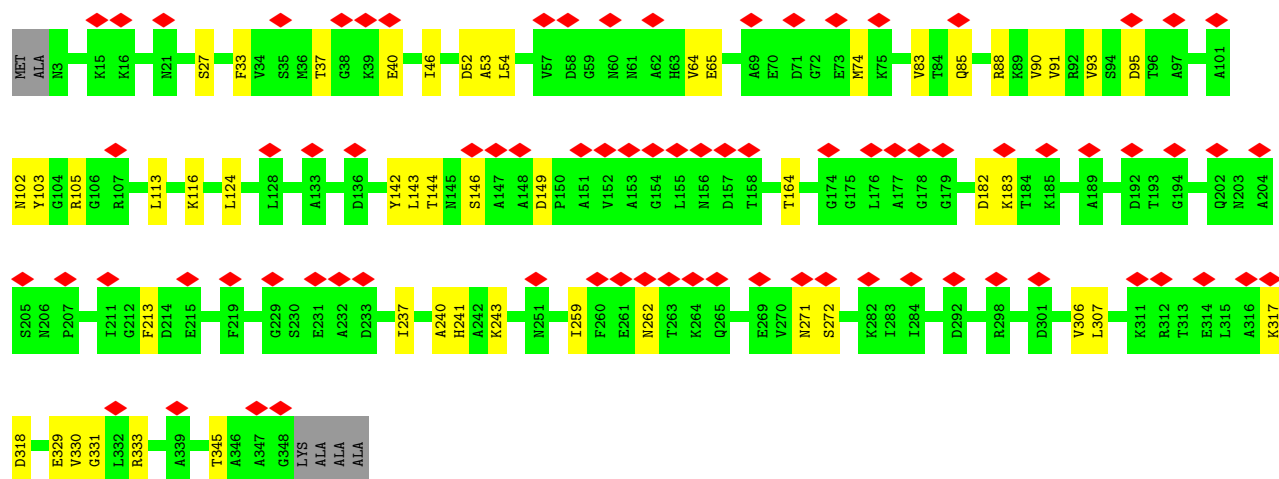
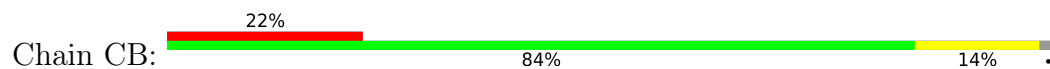


• Molecule 1: Major head protein

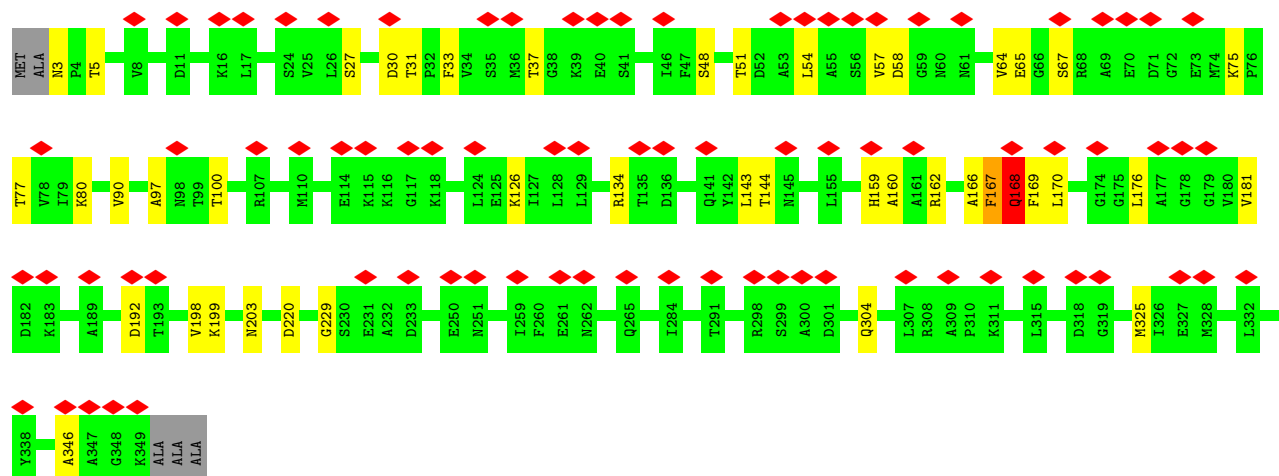
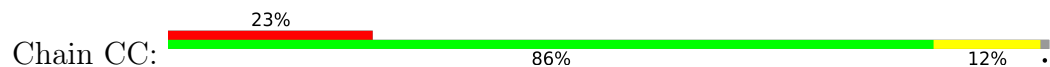




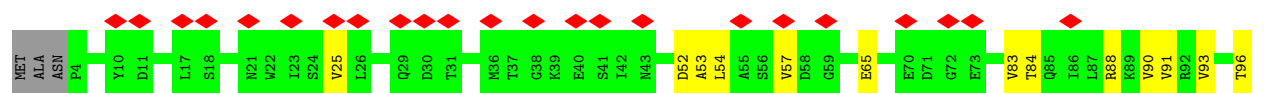
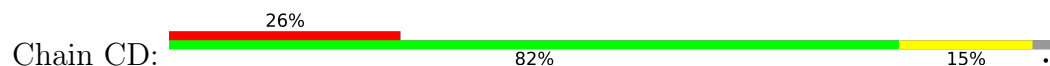
- Molecule 1: Major head protein

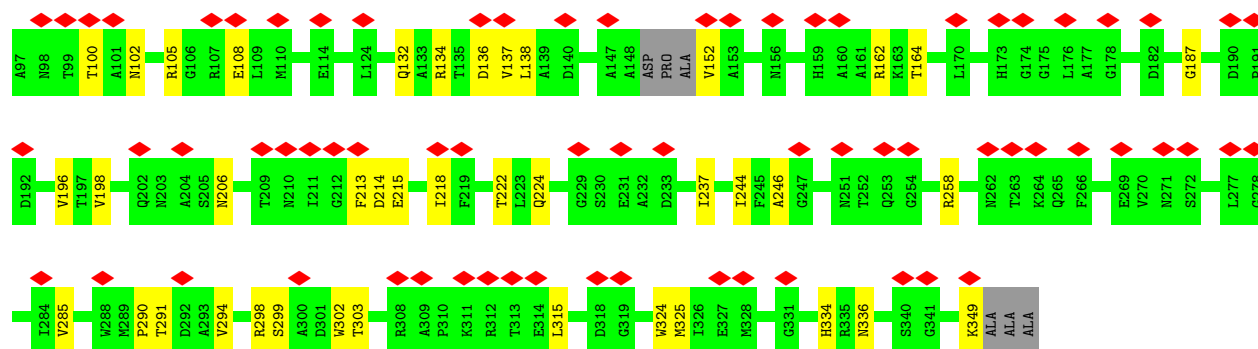


- Molecule 1: Major head protein

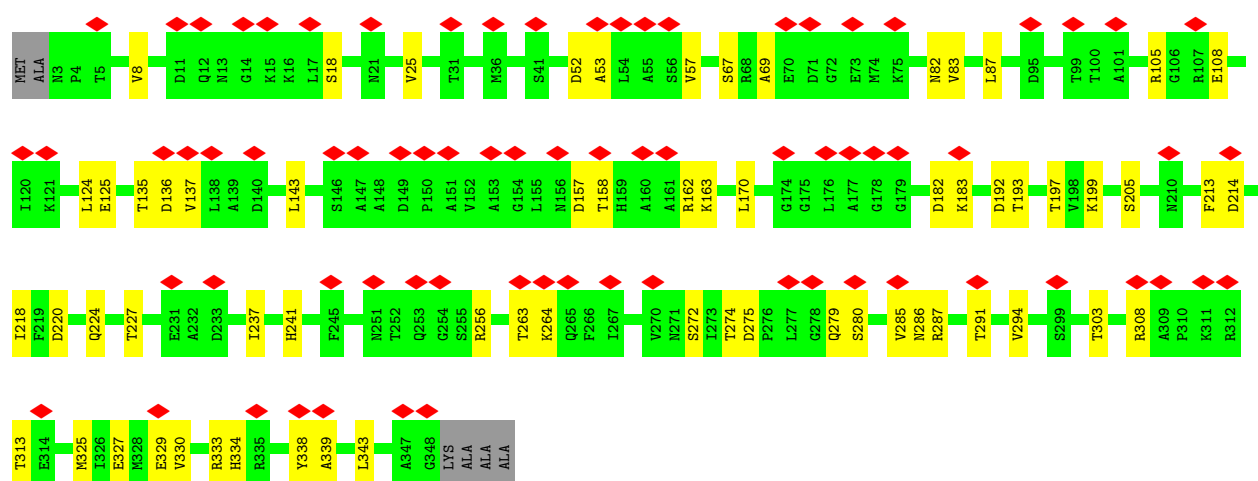
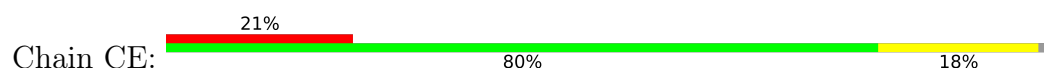


- Molecule 1: Major head protein

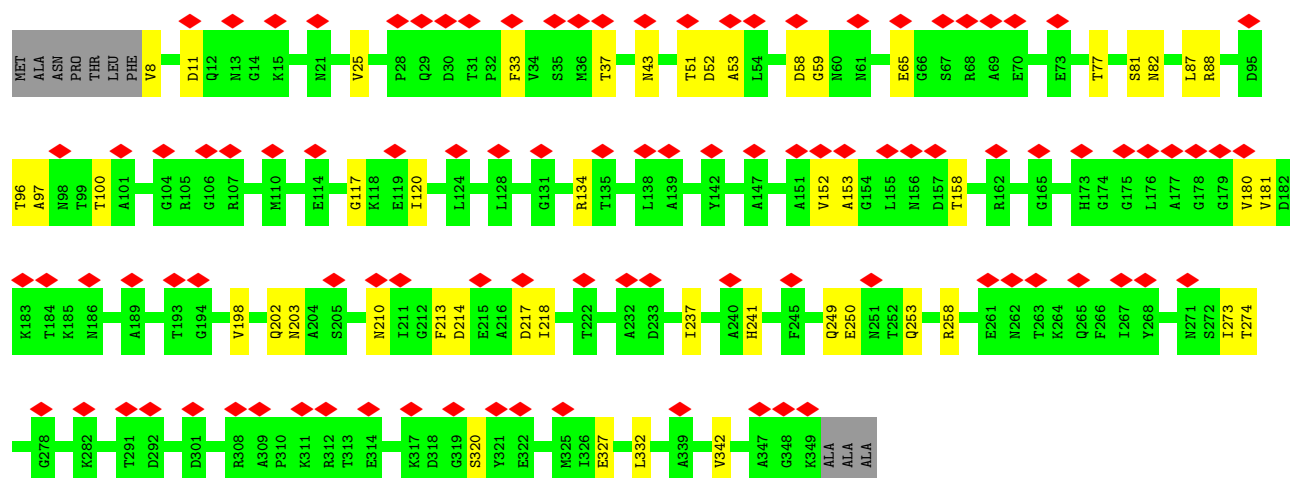
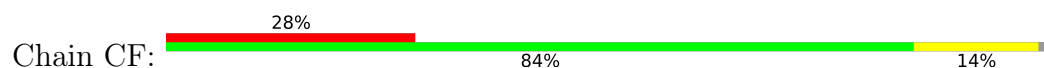




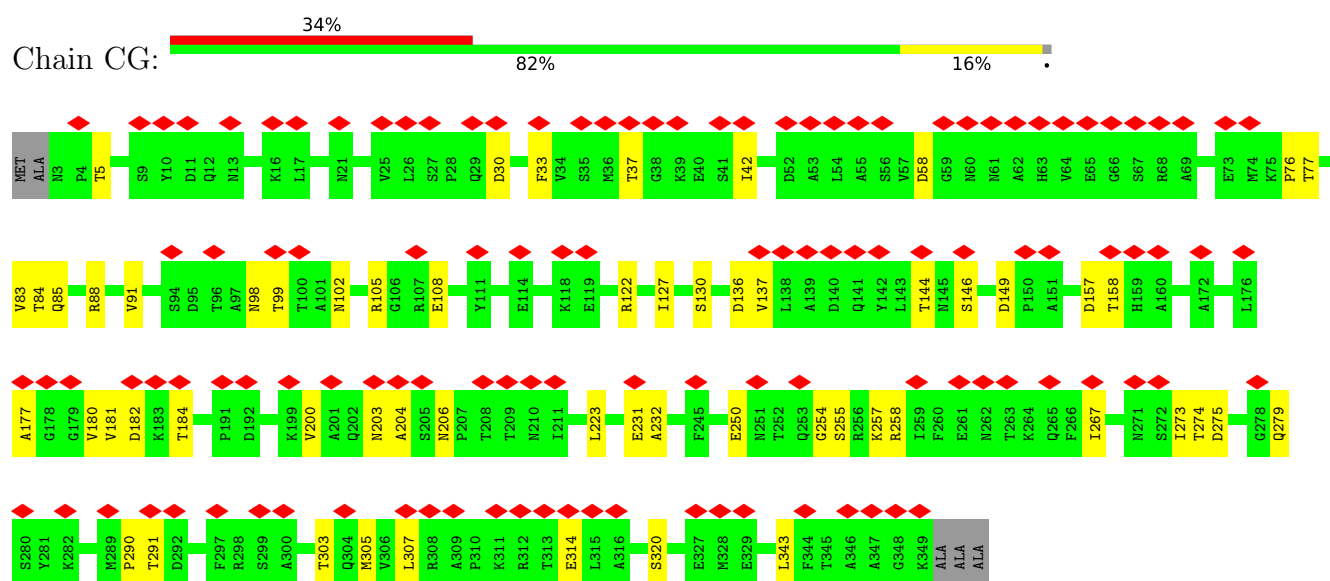
• Molecule 1: Major head protein



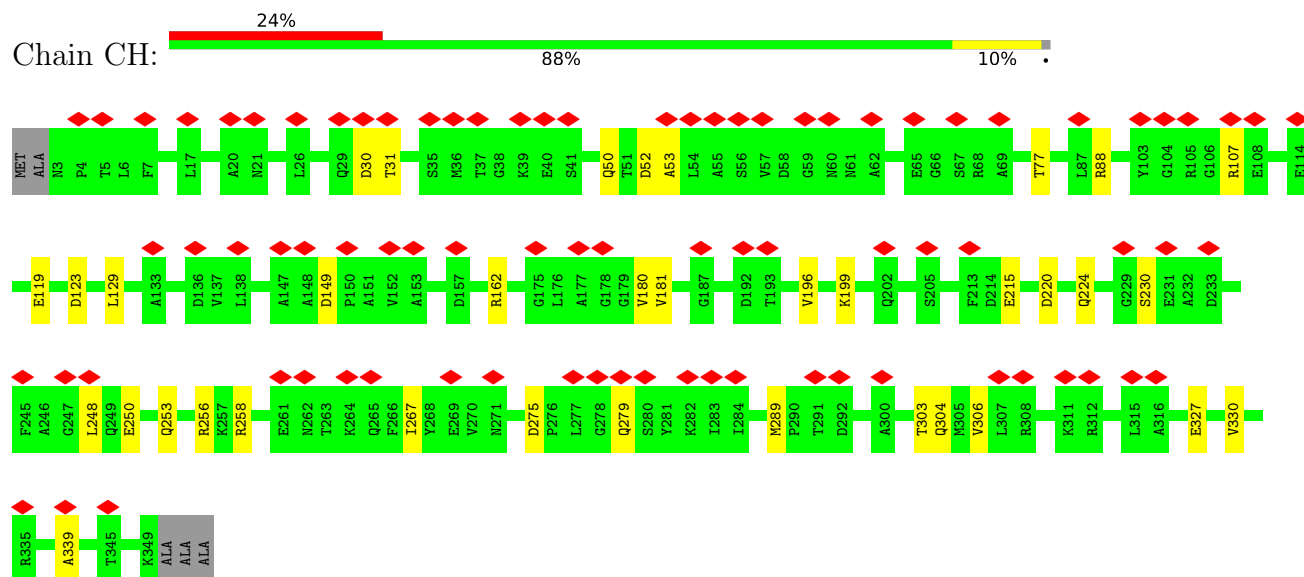
• Molecule 1: Major head protein



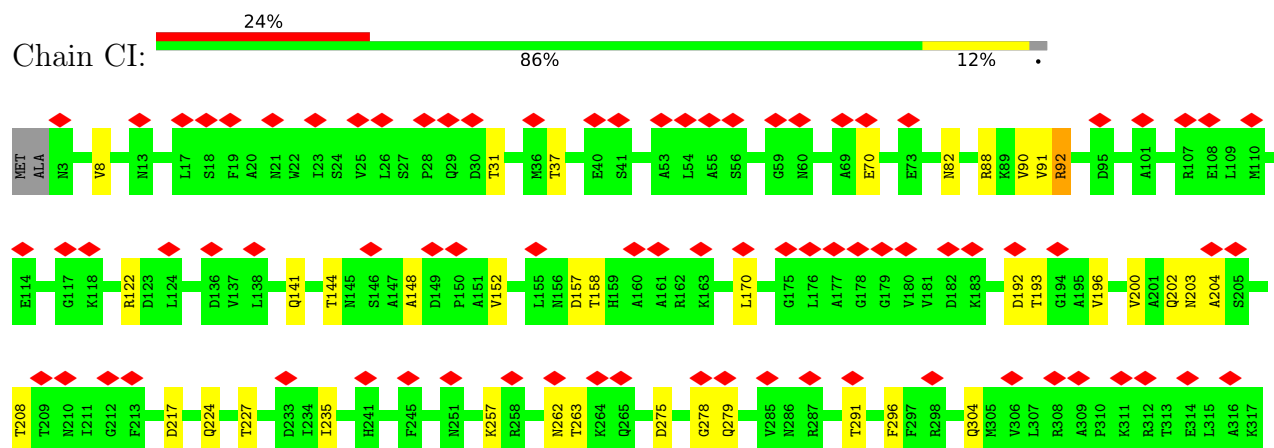
• Molecule 1: Major head protein

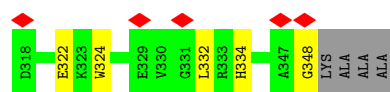


• Molecule 1: Major head protein

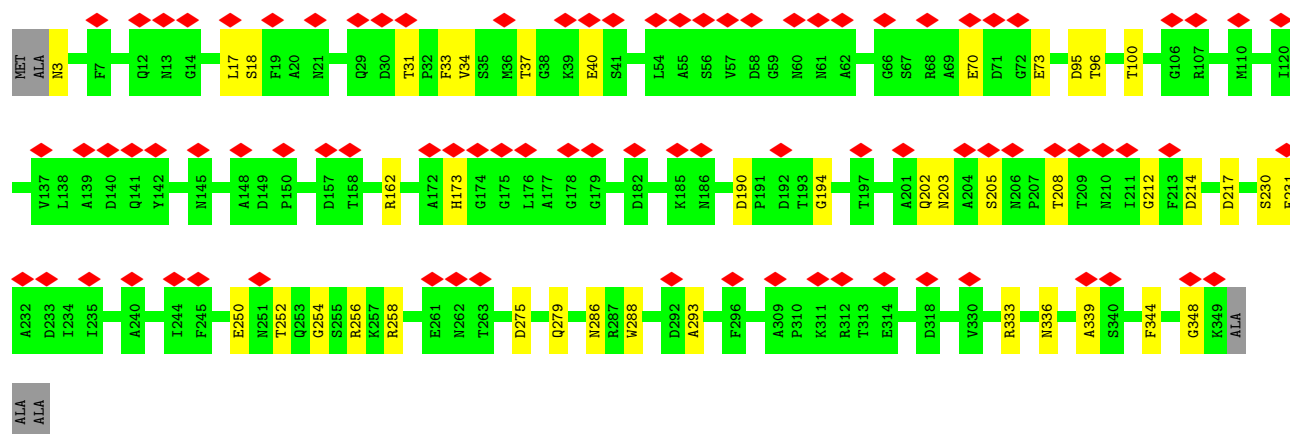
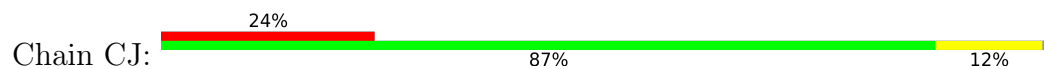


• Molecule 1: Major head protein

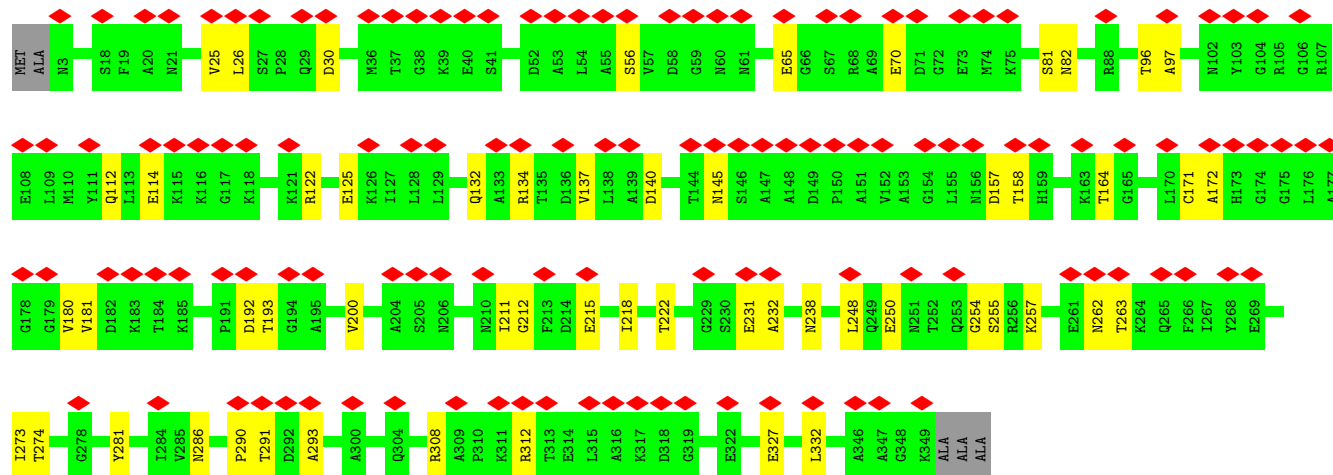
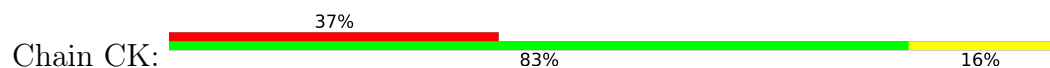




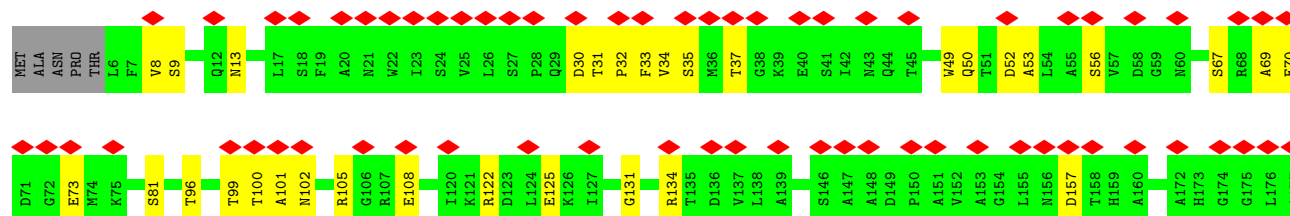
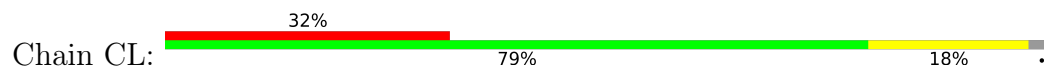
• Molecule 1: Major head protein

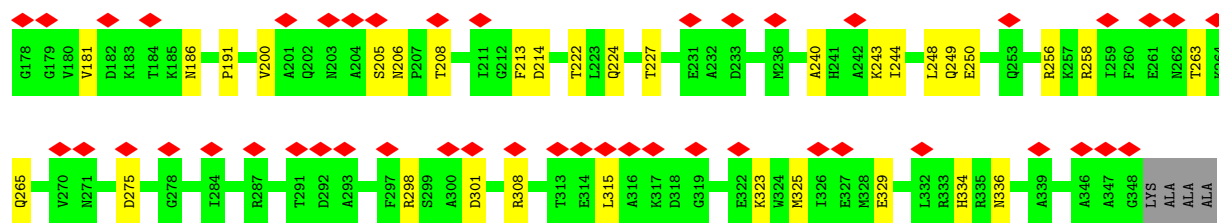


• Molecule 1: Major head protein

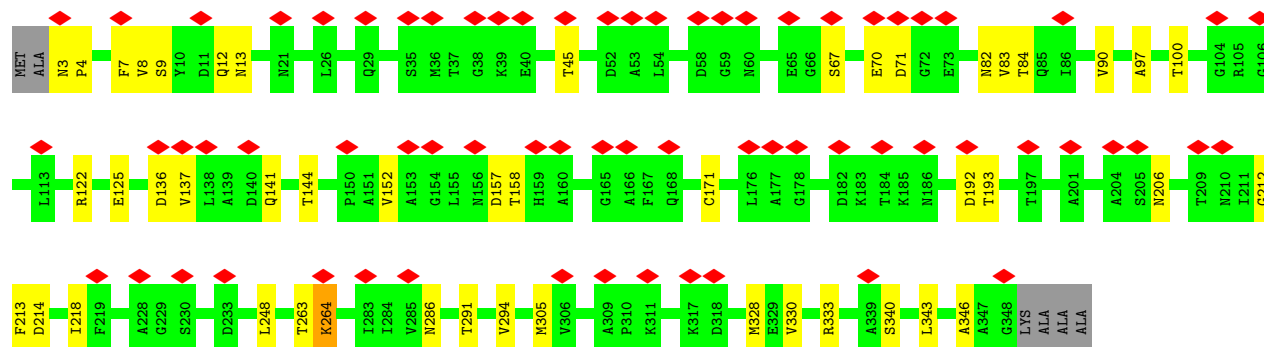
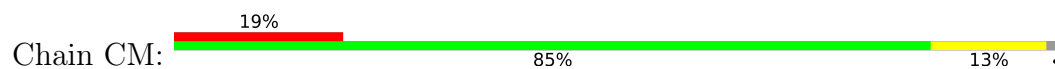


• Molecule 1: Major head protein

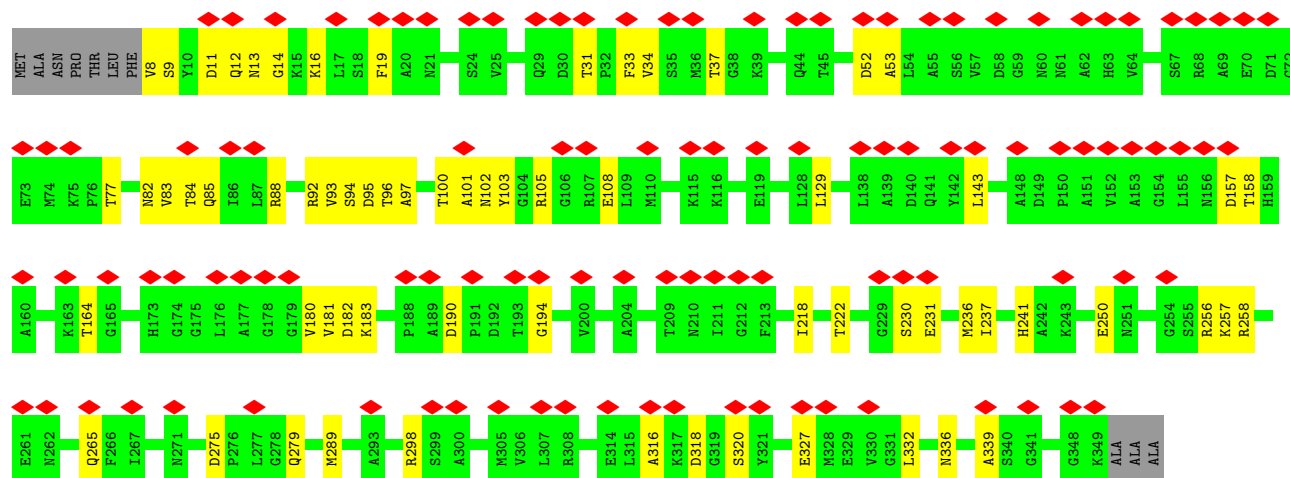
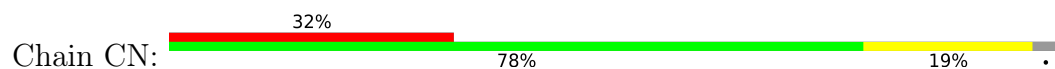




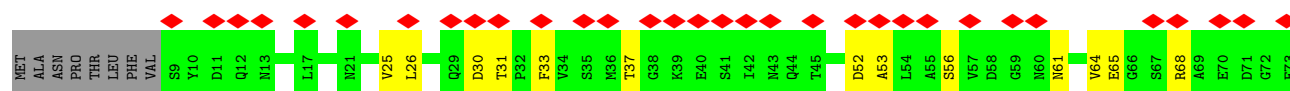
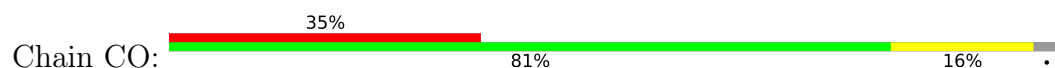
• Molecule 1: Major head protein

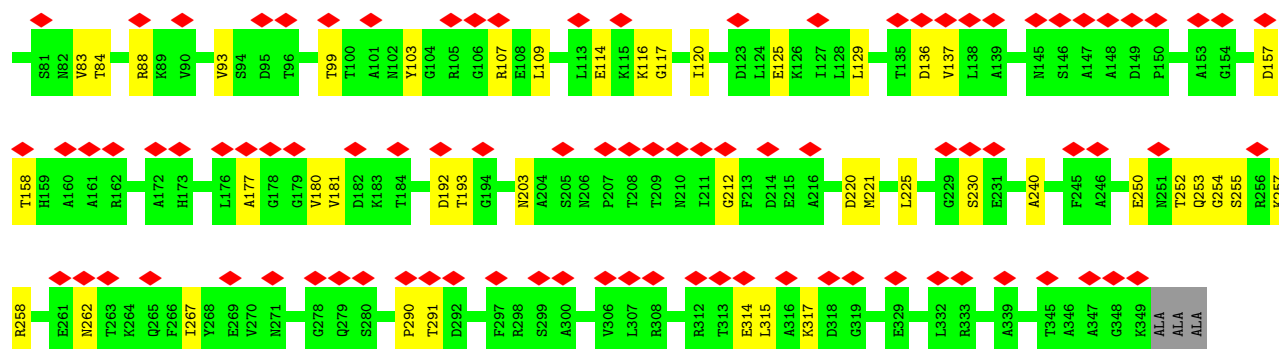


• Molecule 1: Major head protein

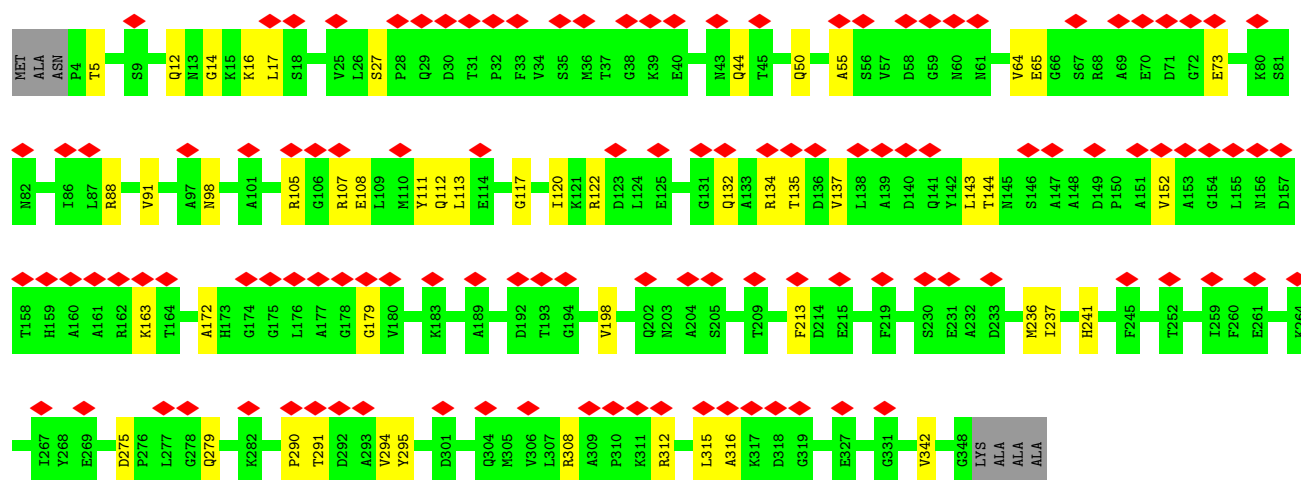
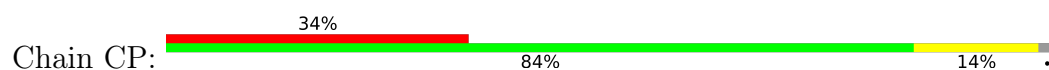


• Molecule 1: Major head protein

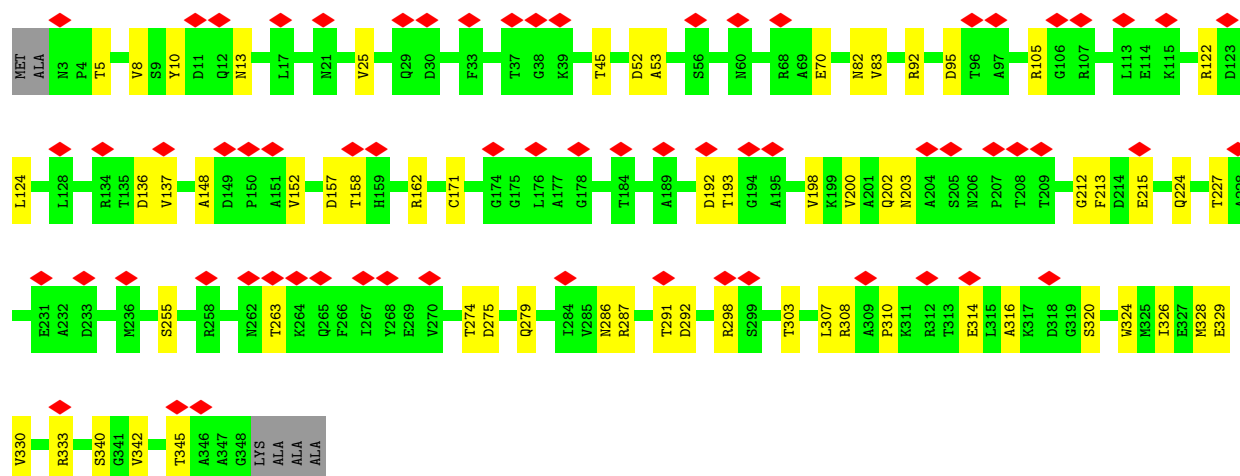
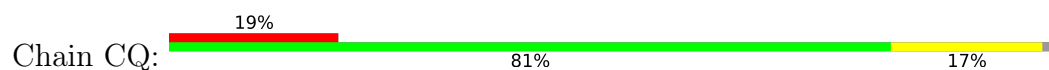





- Molecule 1: Major head protein

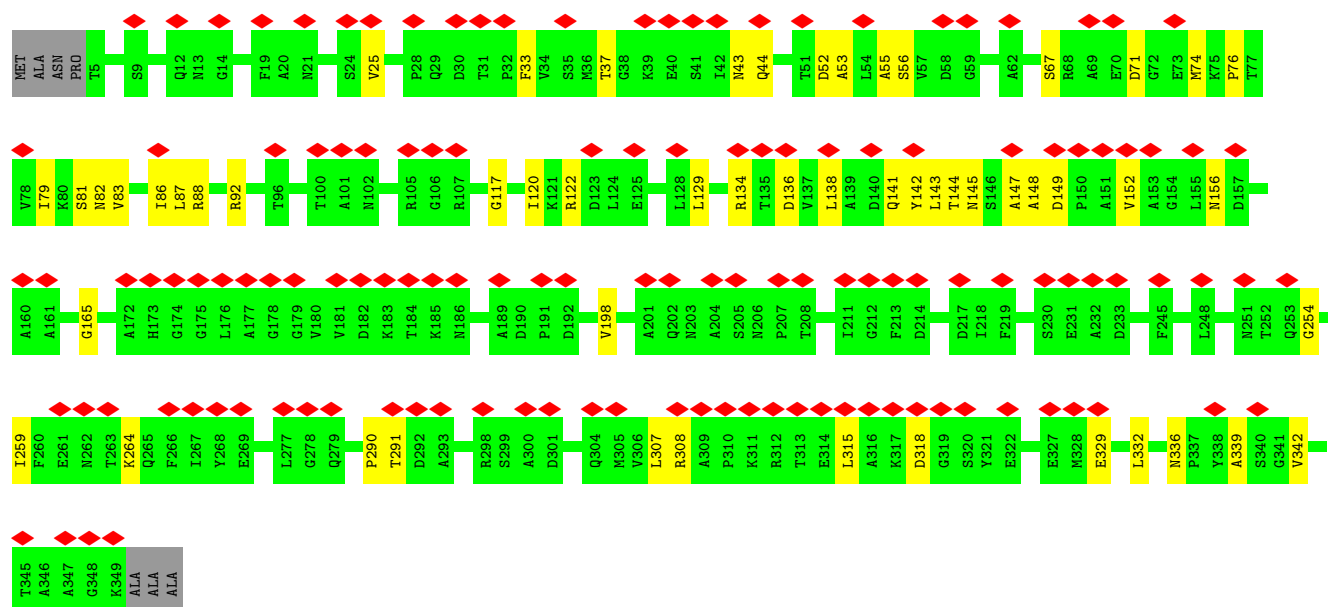


- Molecule 1: Major head protein




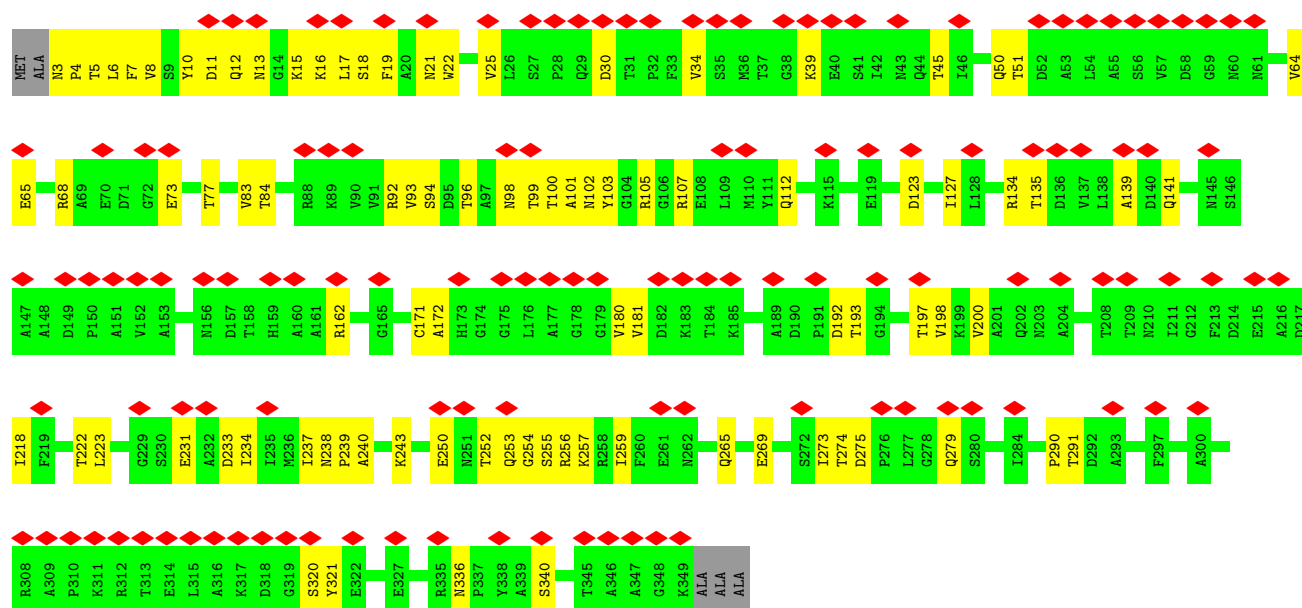
- Molecule 1: Major head protein

Chain CR: 




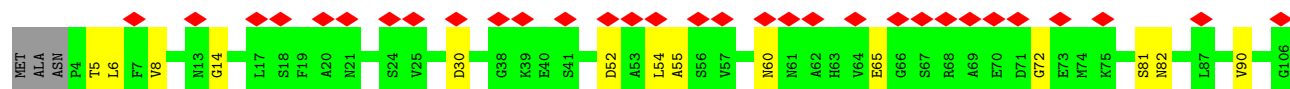
• Molecule 1: Major head protein

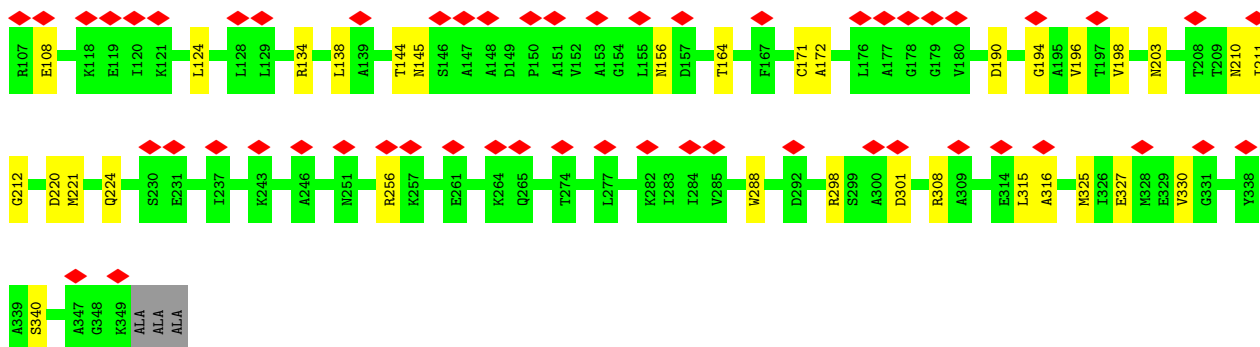
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• Molecule 1: Major head protein

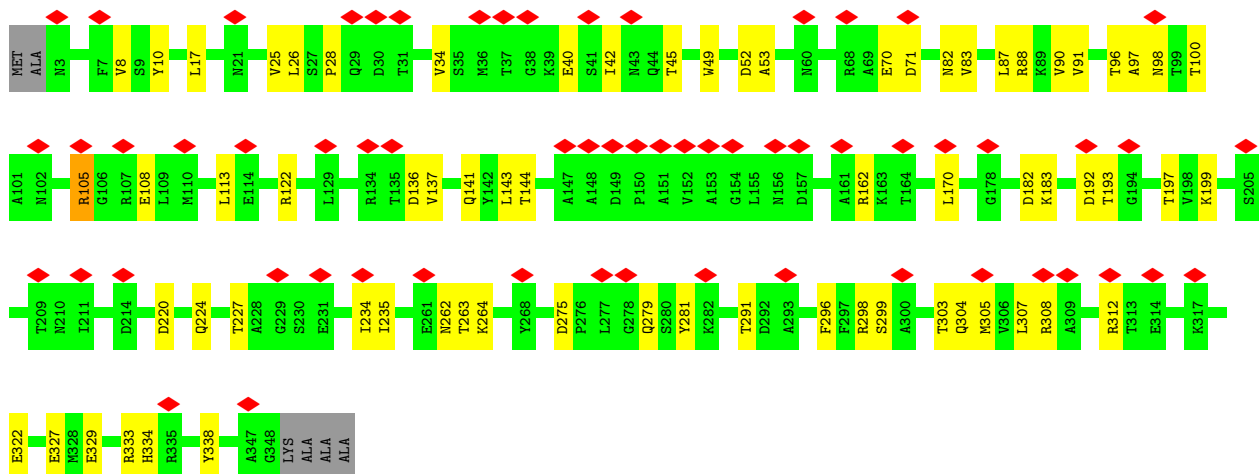
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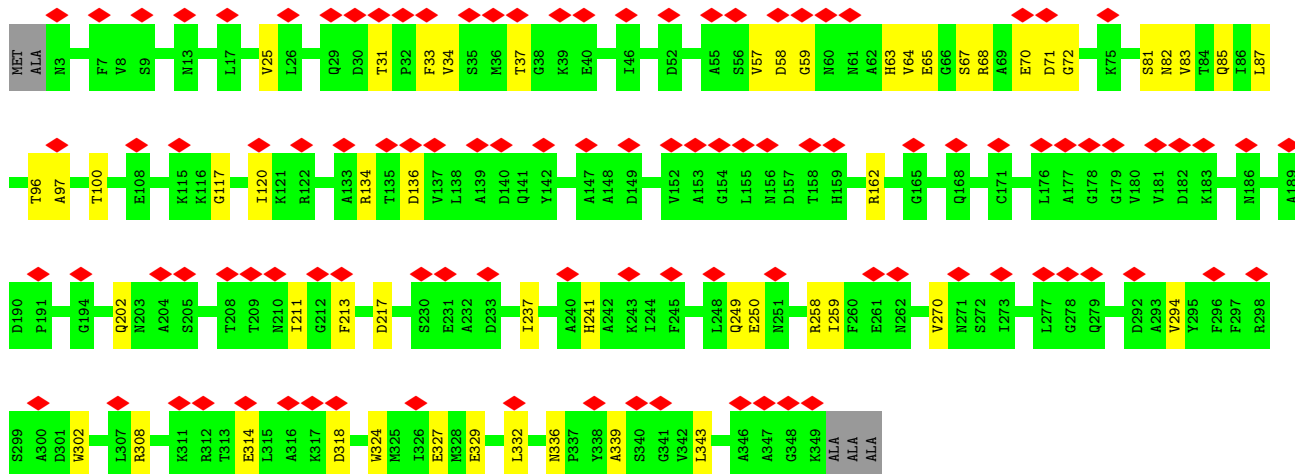
- Molecule 1: Major head protein

Chain CU: 17% 79% 19% .

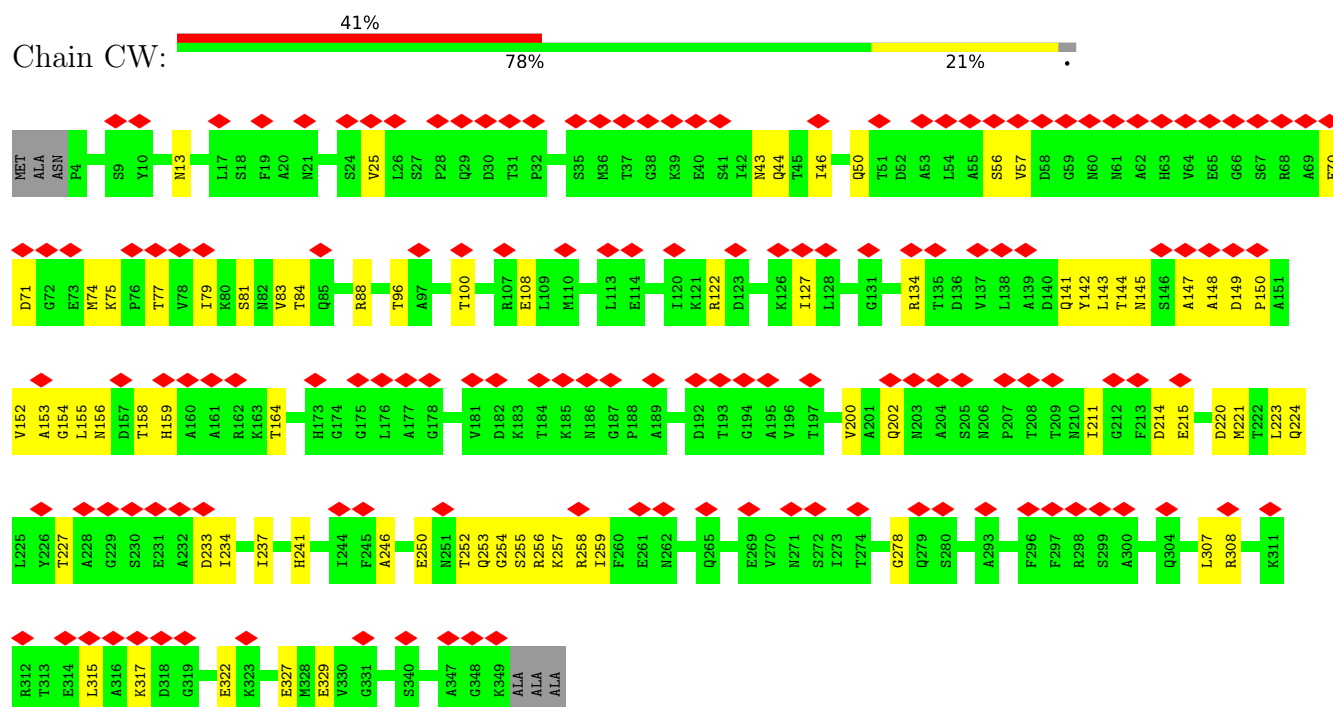


- Molecule 1: Major head protein

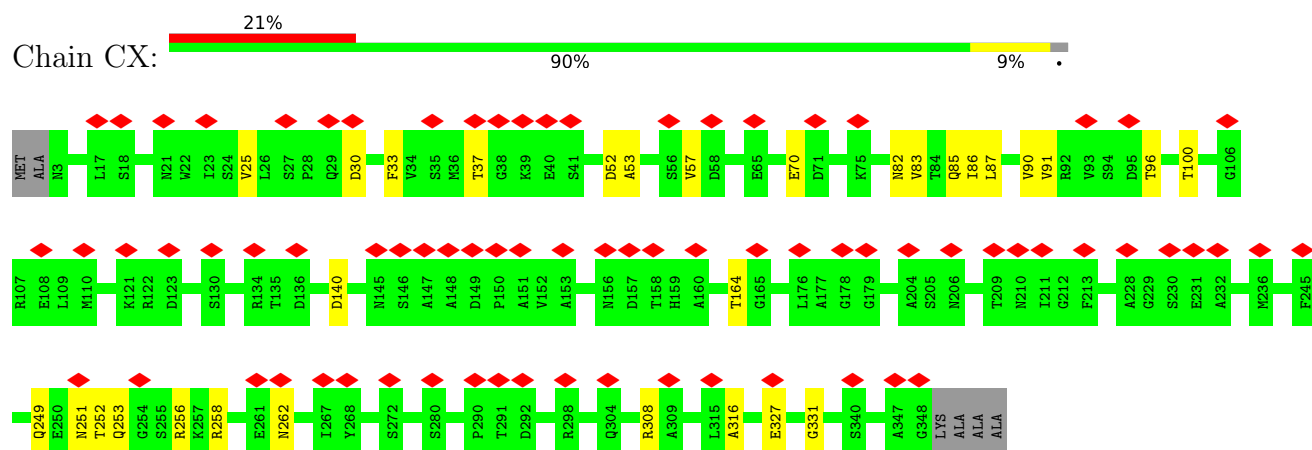
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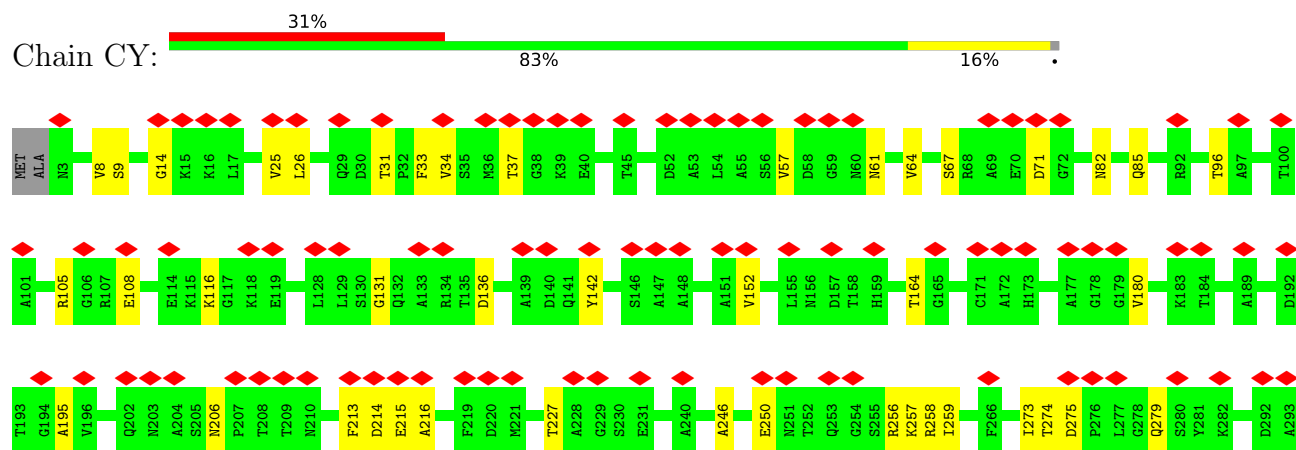
- Molecule 1: Major head protein



• Molecule 1: Major head protein

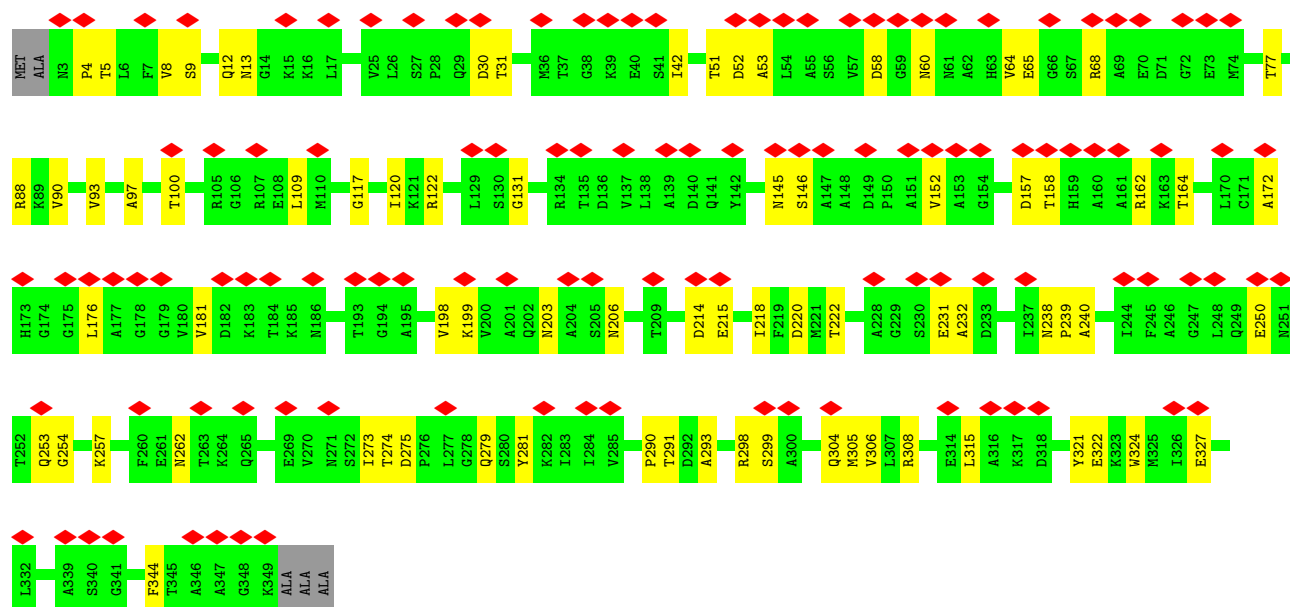
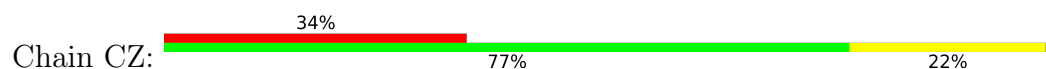


• Molecule 1: Major head protein

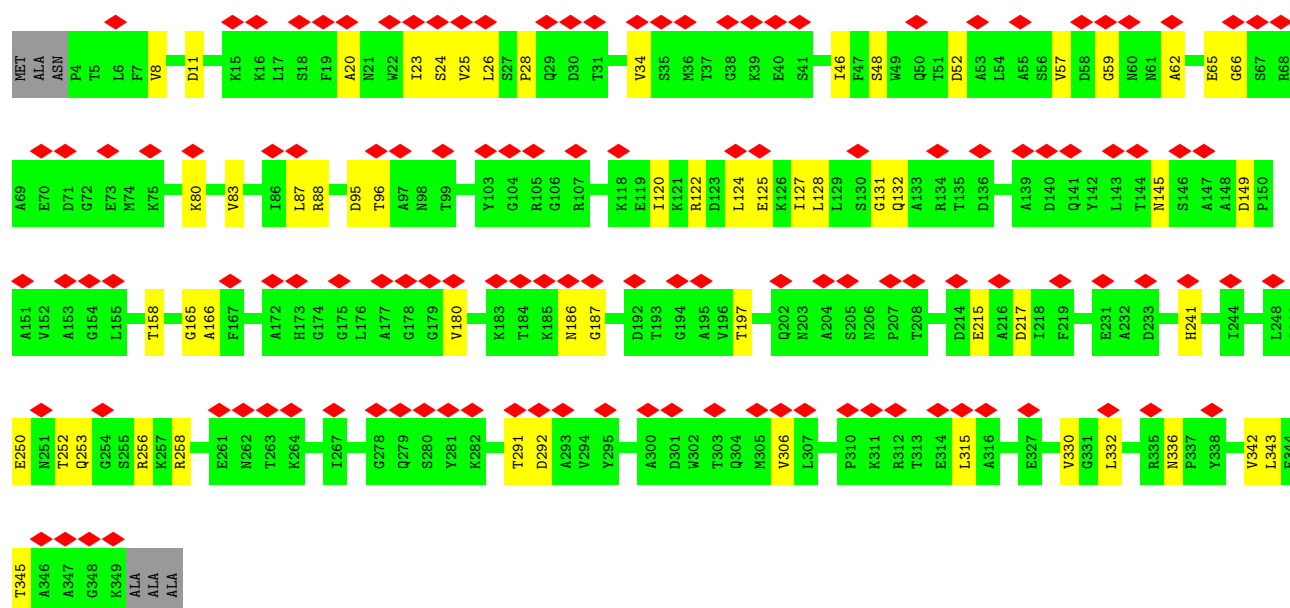
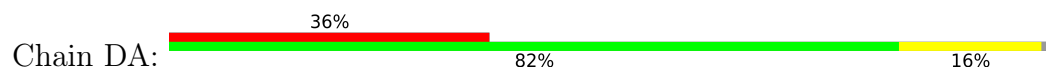




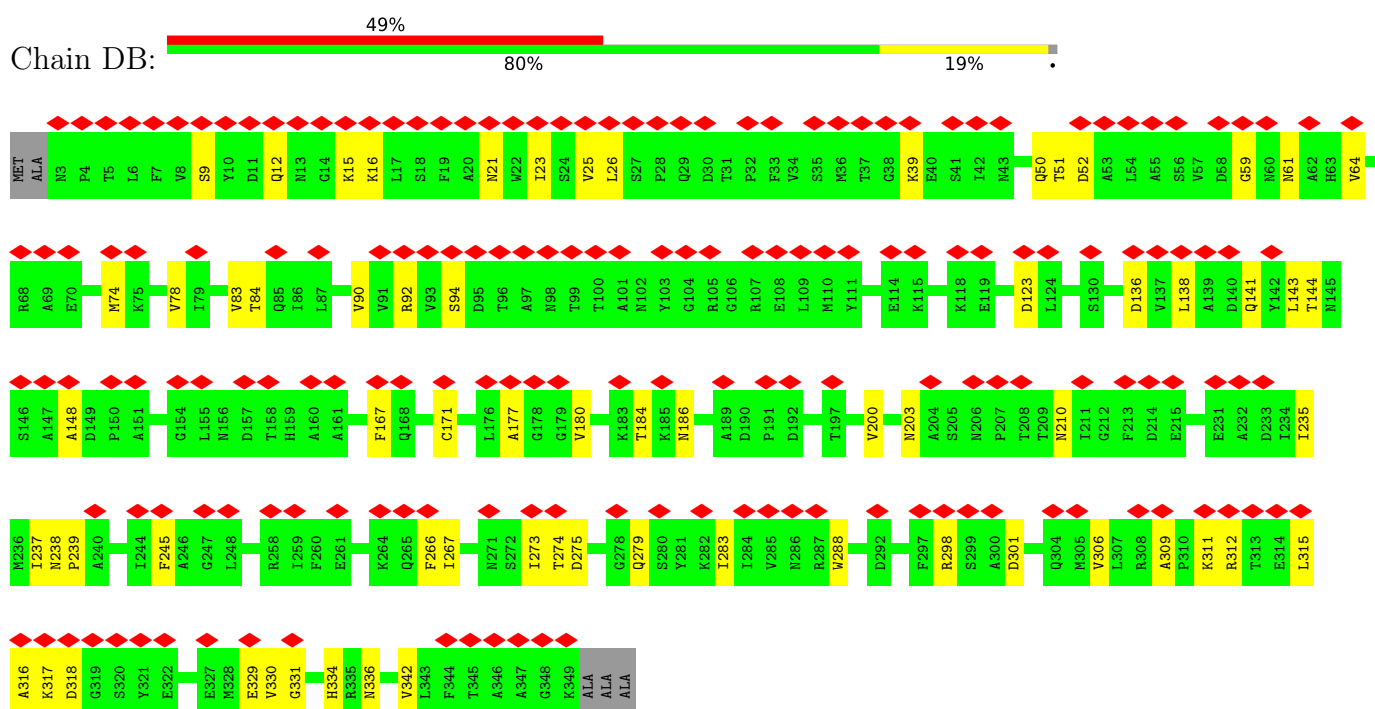
- Molecule 1: Major head protein

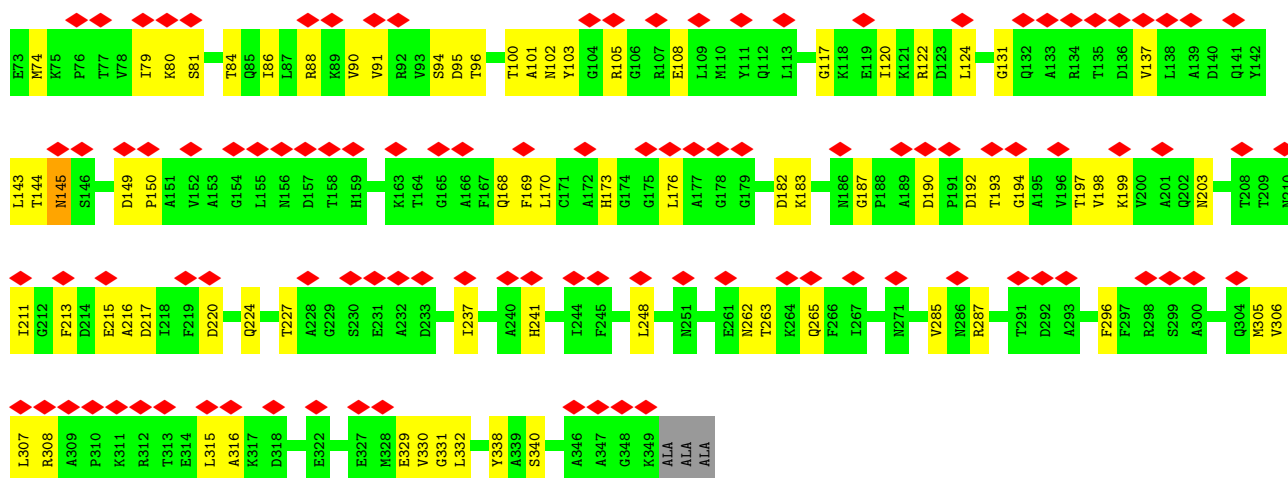


- Molecule 1: Major head protein

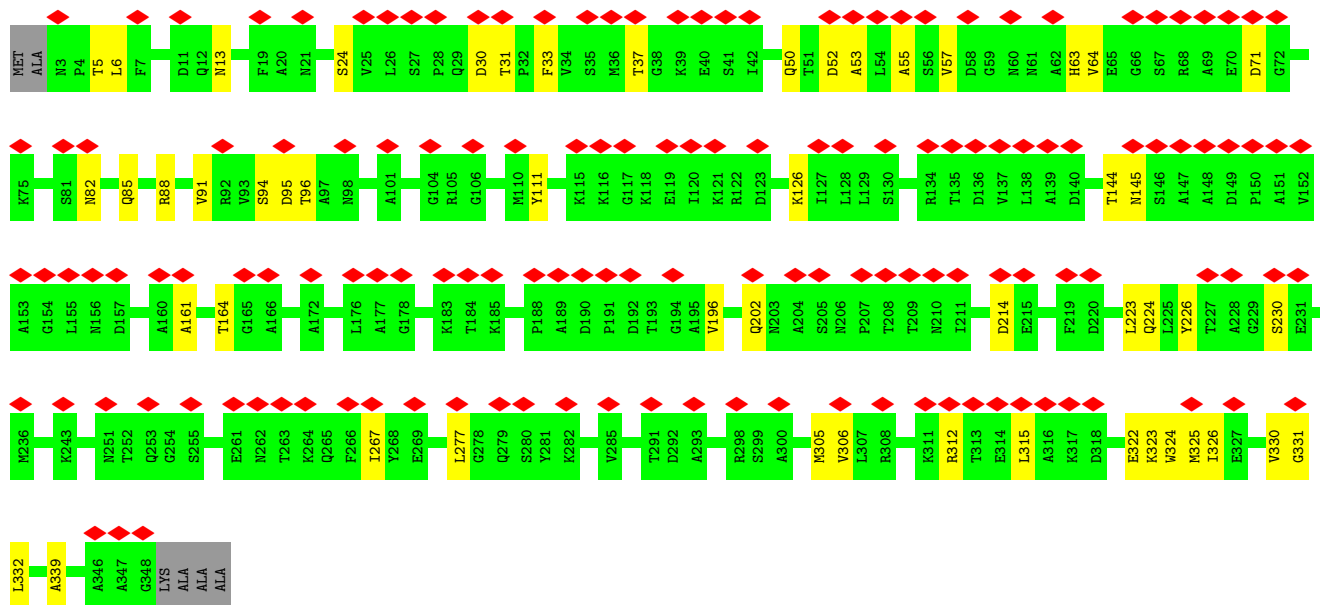
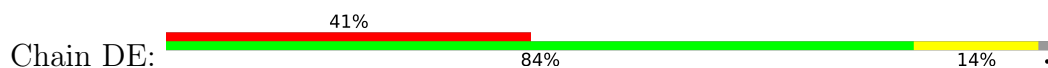


- Molecule 1: Major head protein

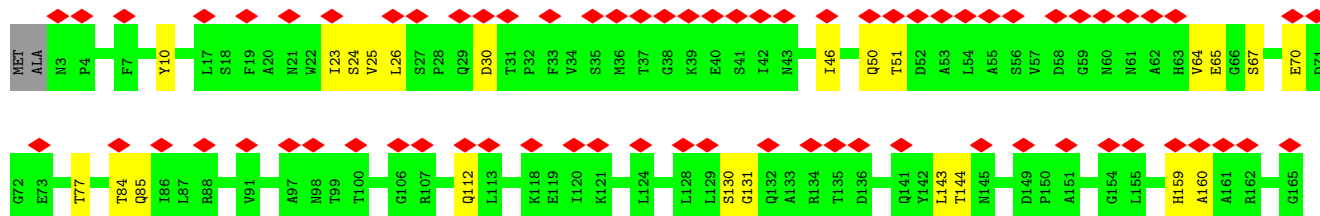
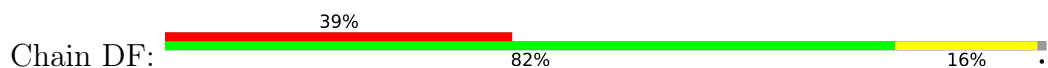


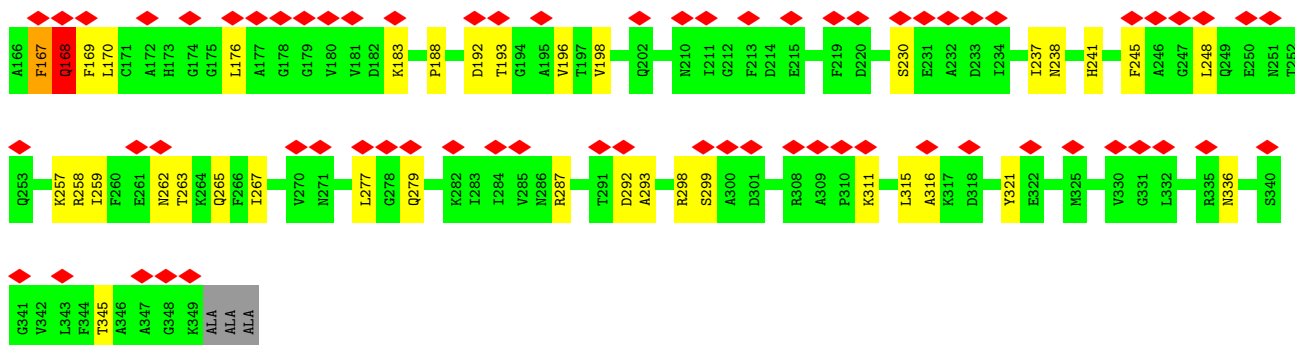


• Molecule 1: Major head protein

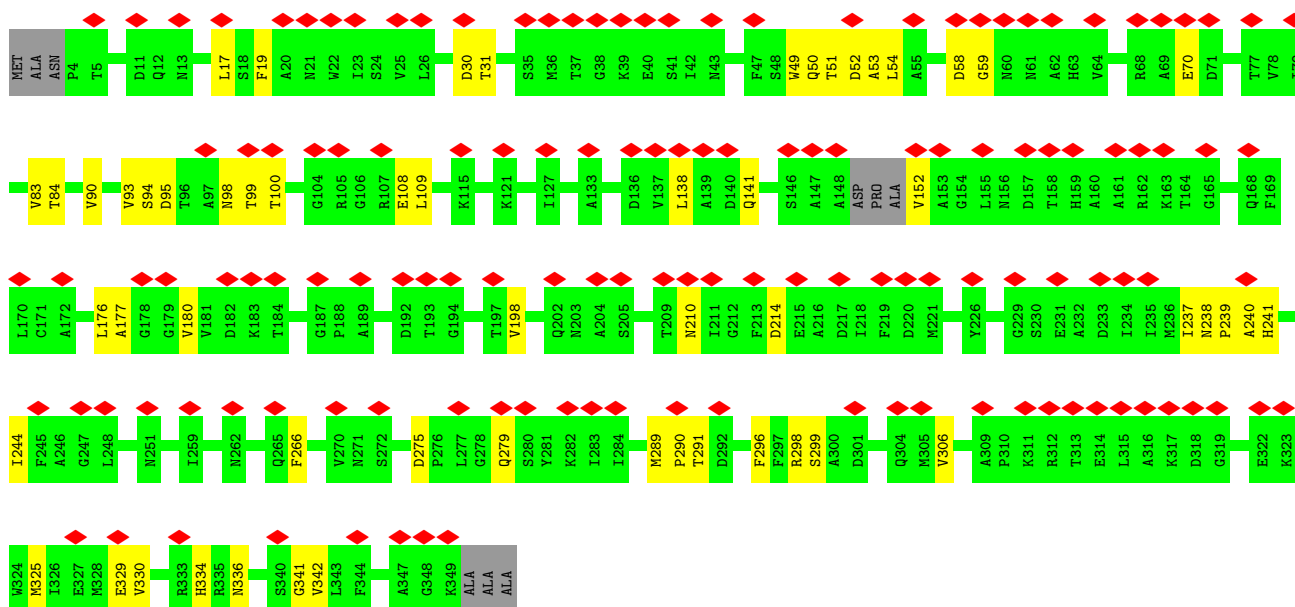
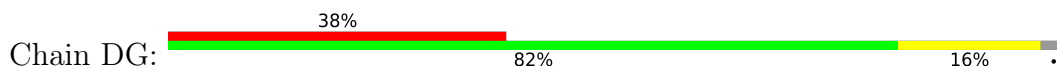


• Molecule 1: Major head protein

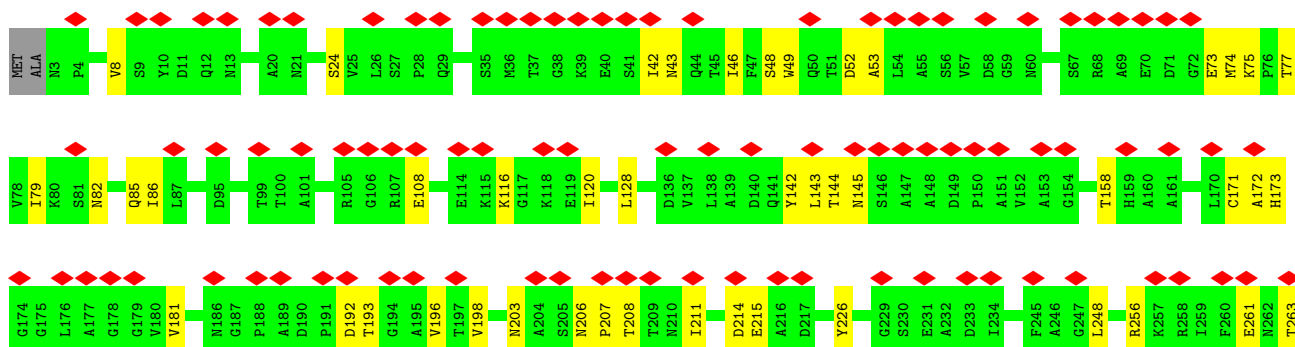
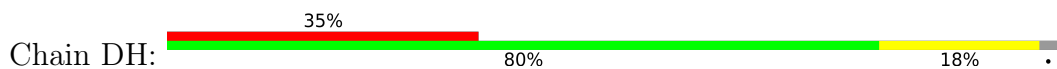


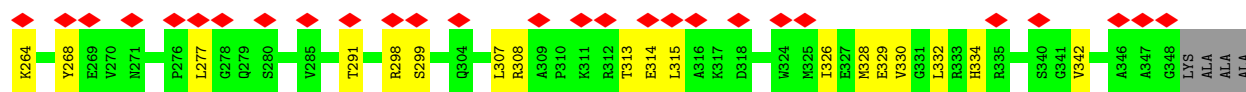


- Molecule 1: Major head protein

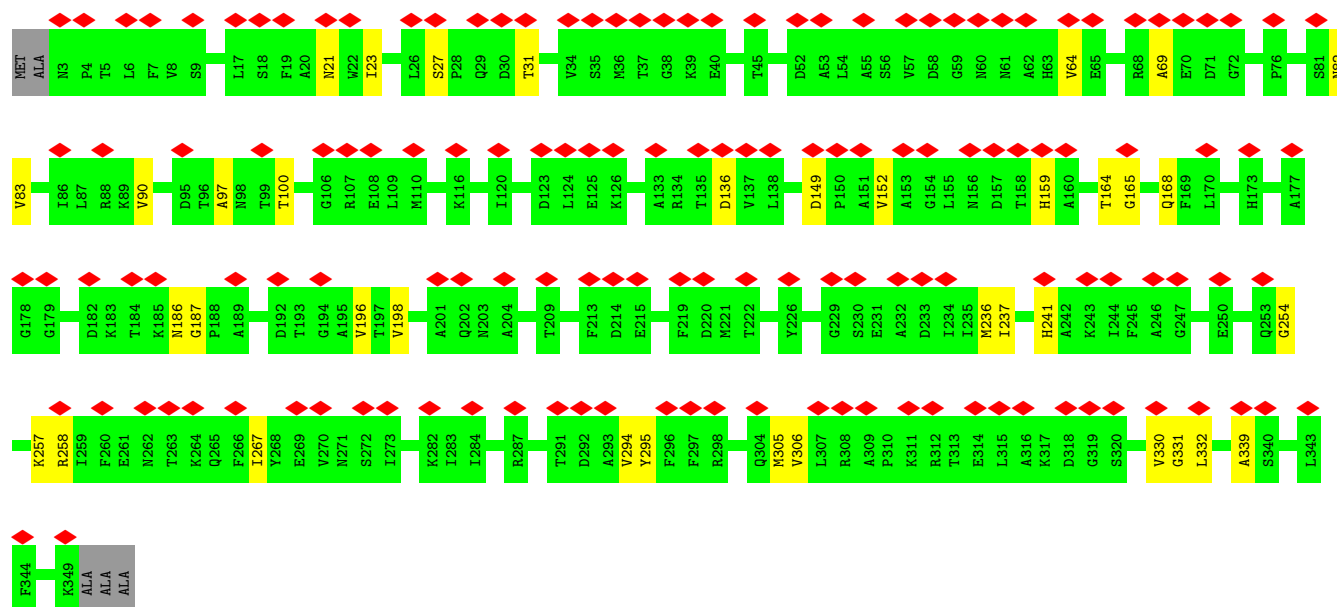
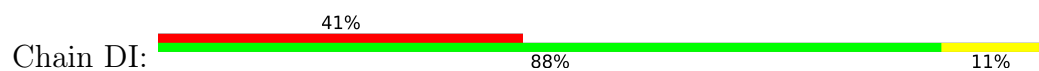


- Molecule 1: Major head protein

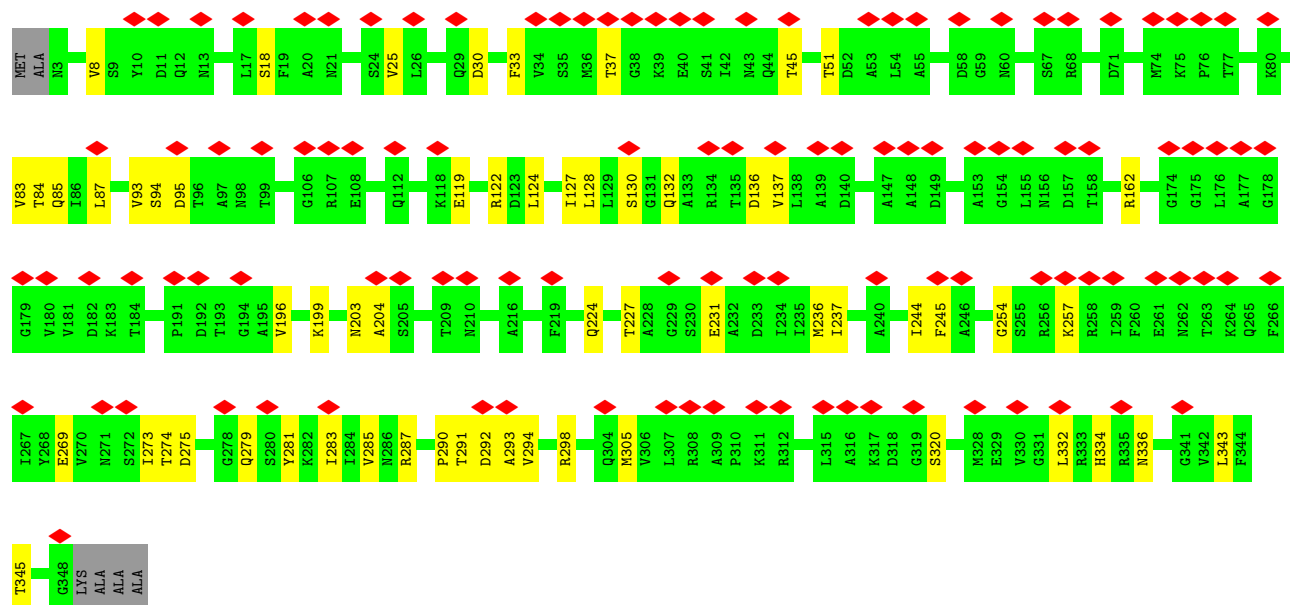
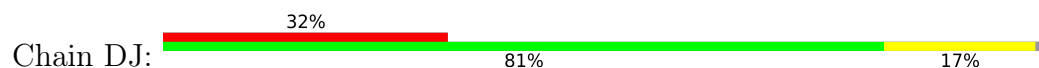




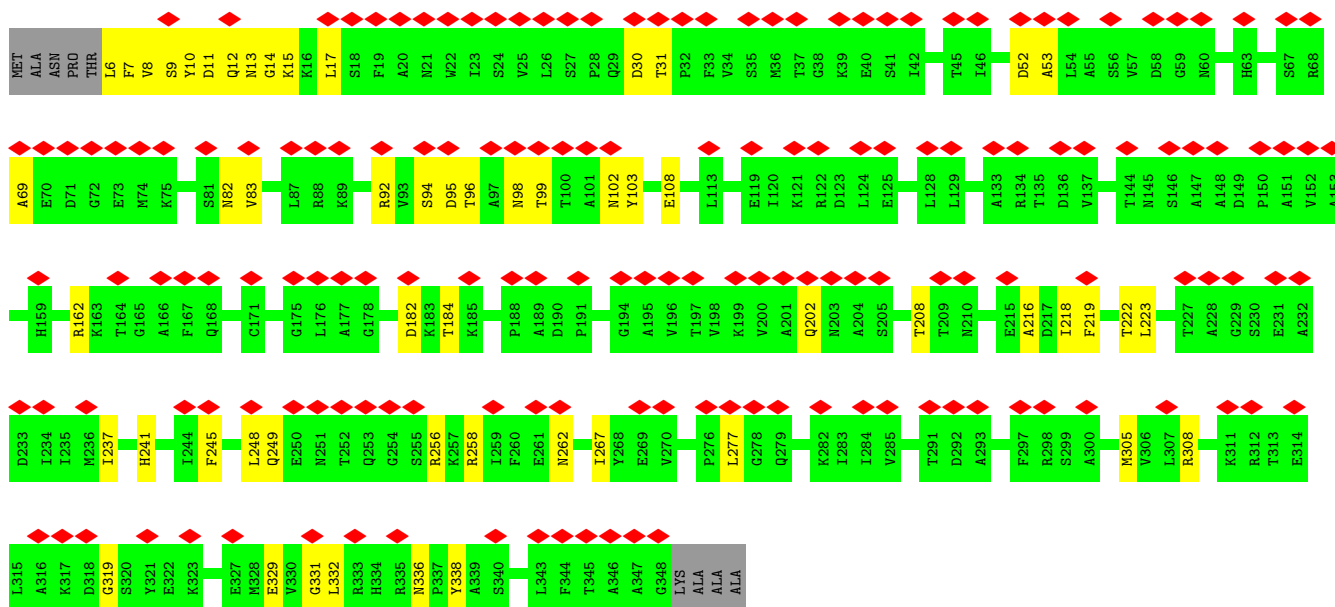
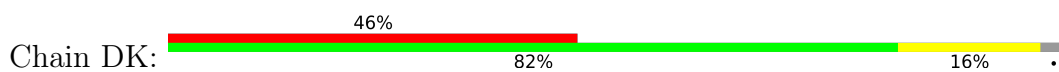
- Molecule 1: Major head protein



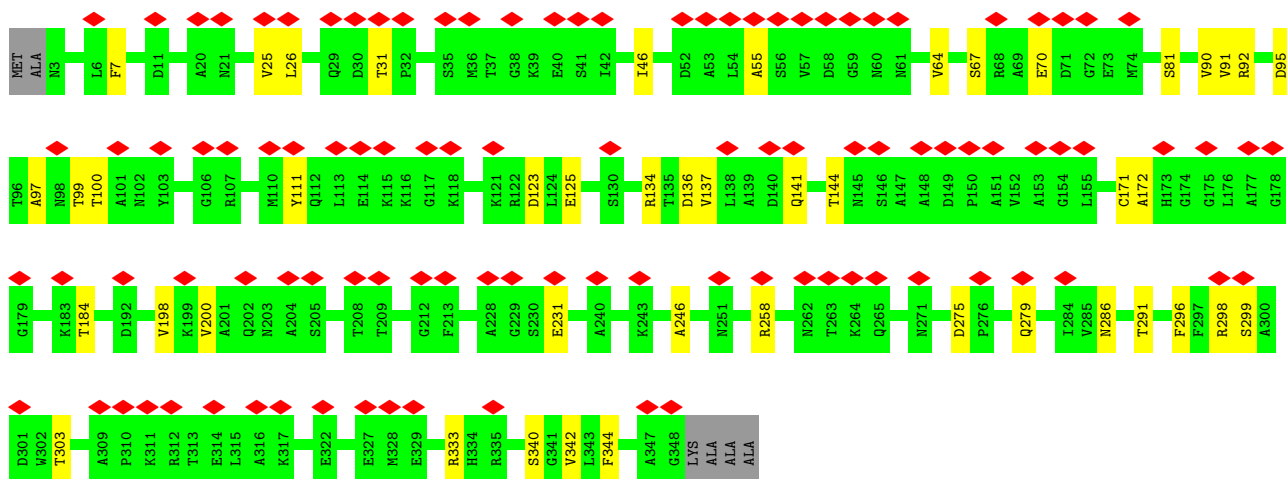
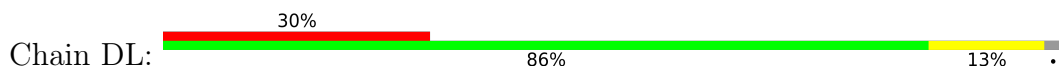
- Molecule 1: Major head protein



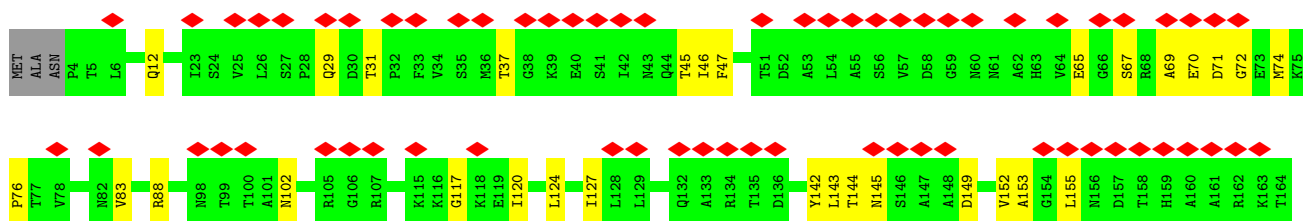
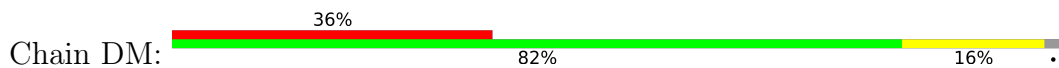
- Molecule 1: Major head protein

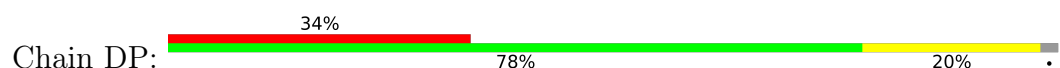


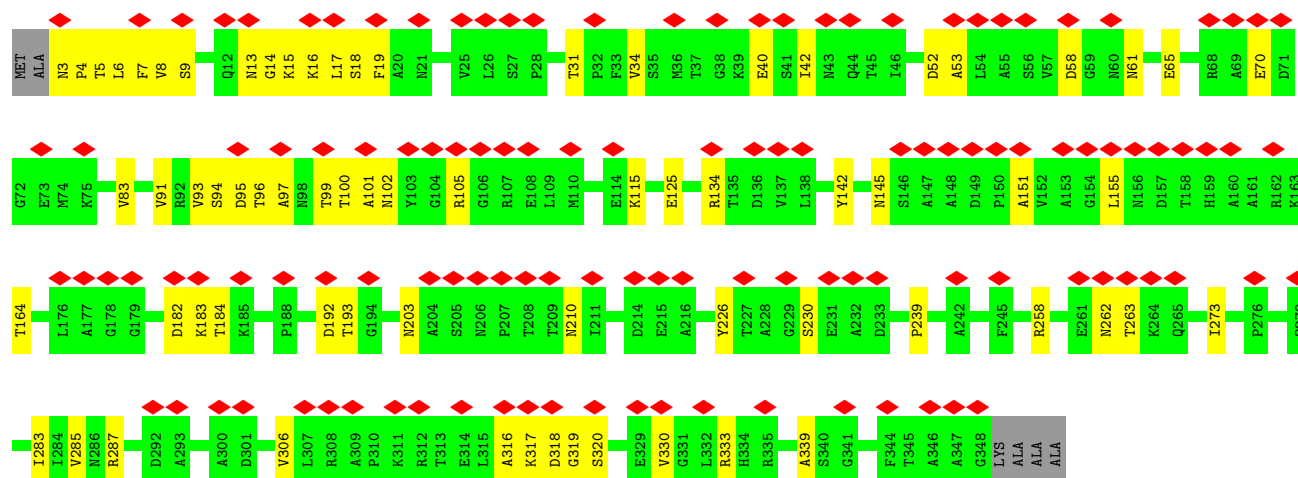
• Molecule 1: Major head protein



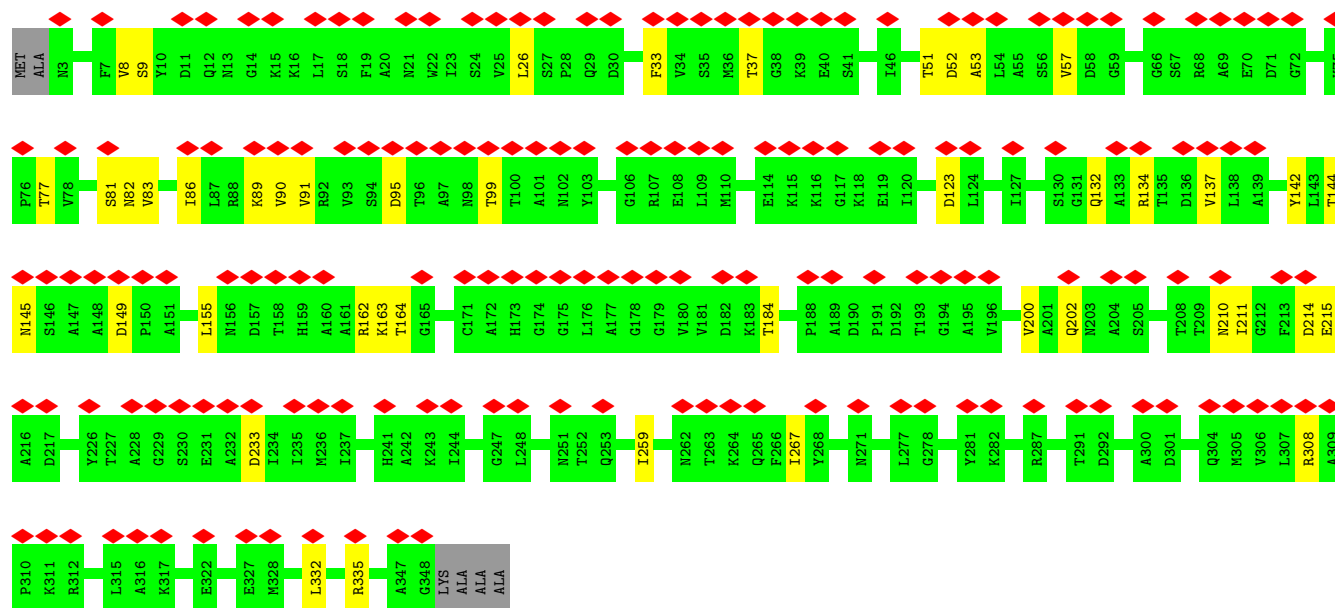
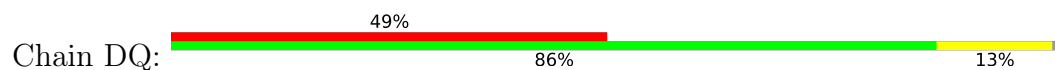
• Molecule 1: Major head protein



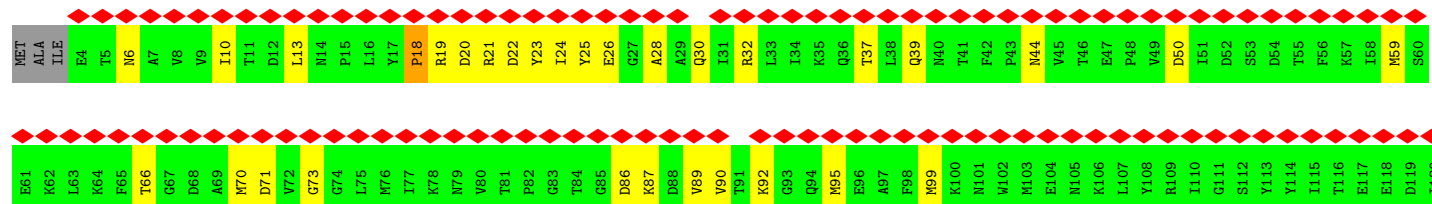
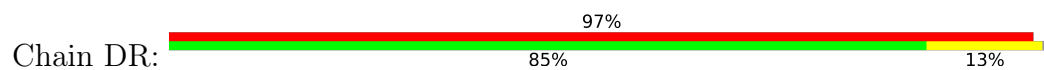


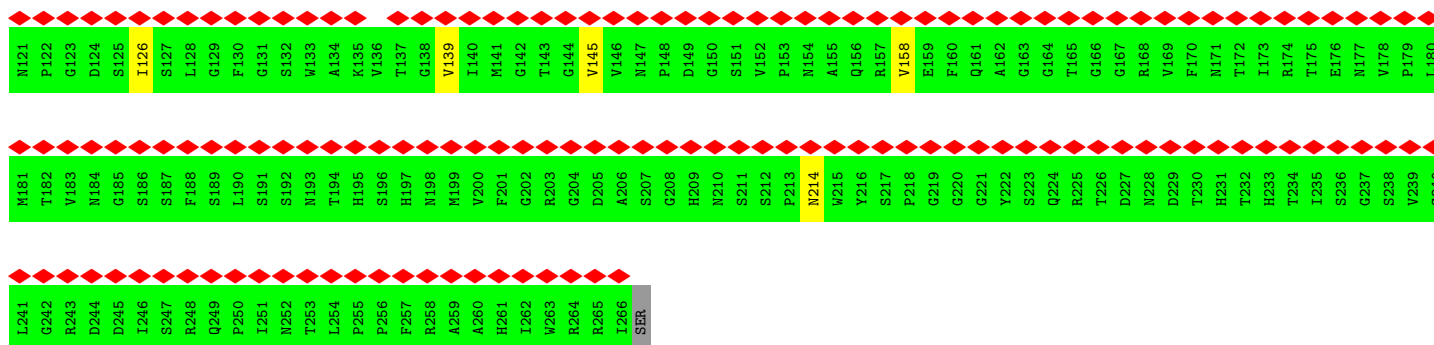


• Molecule 1: Major head protein

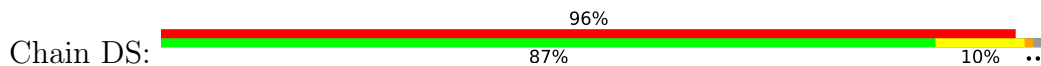


• Molecule 2: Putative structural protein

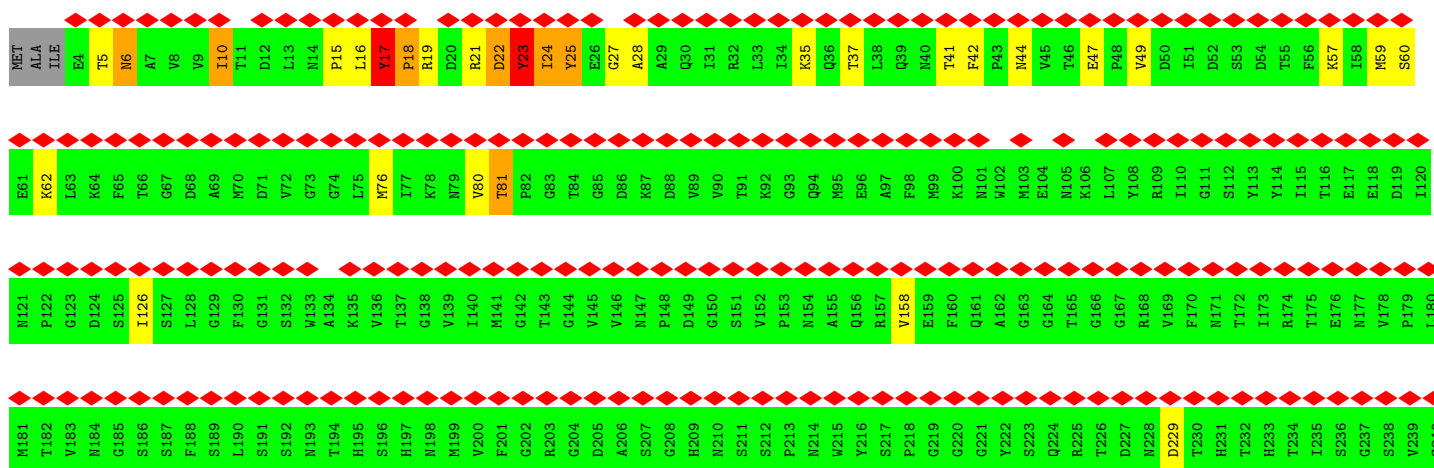
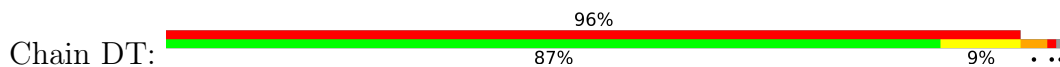


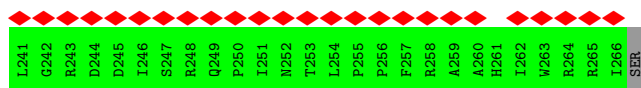


• Molecule 2: Putative structural protein

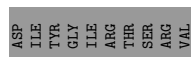
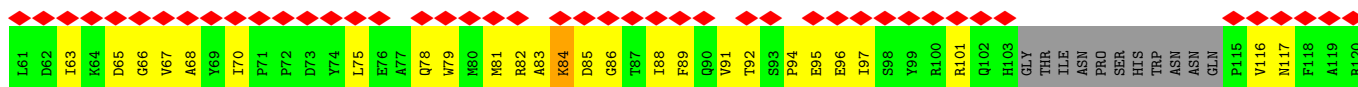
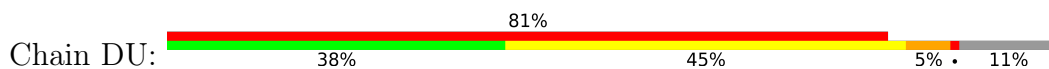


• Molecule 2: Putative structural protein

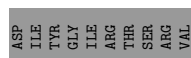
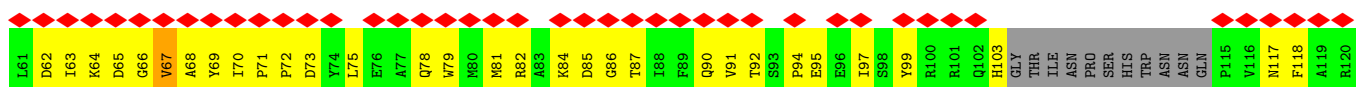
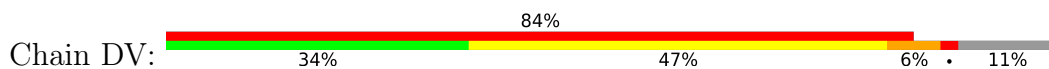




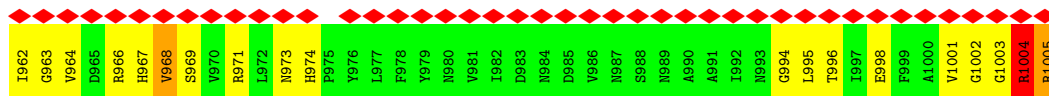
• Molecule 3: Adaptor



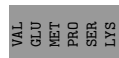
• Molecule 3: Adaptor



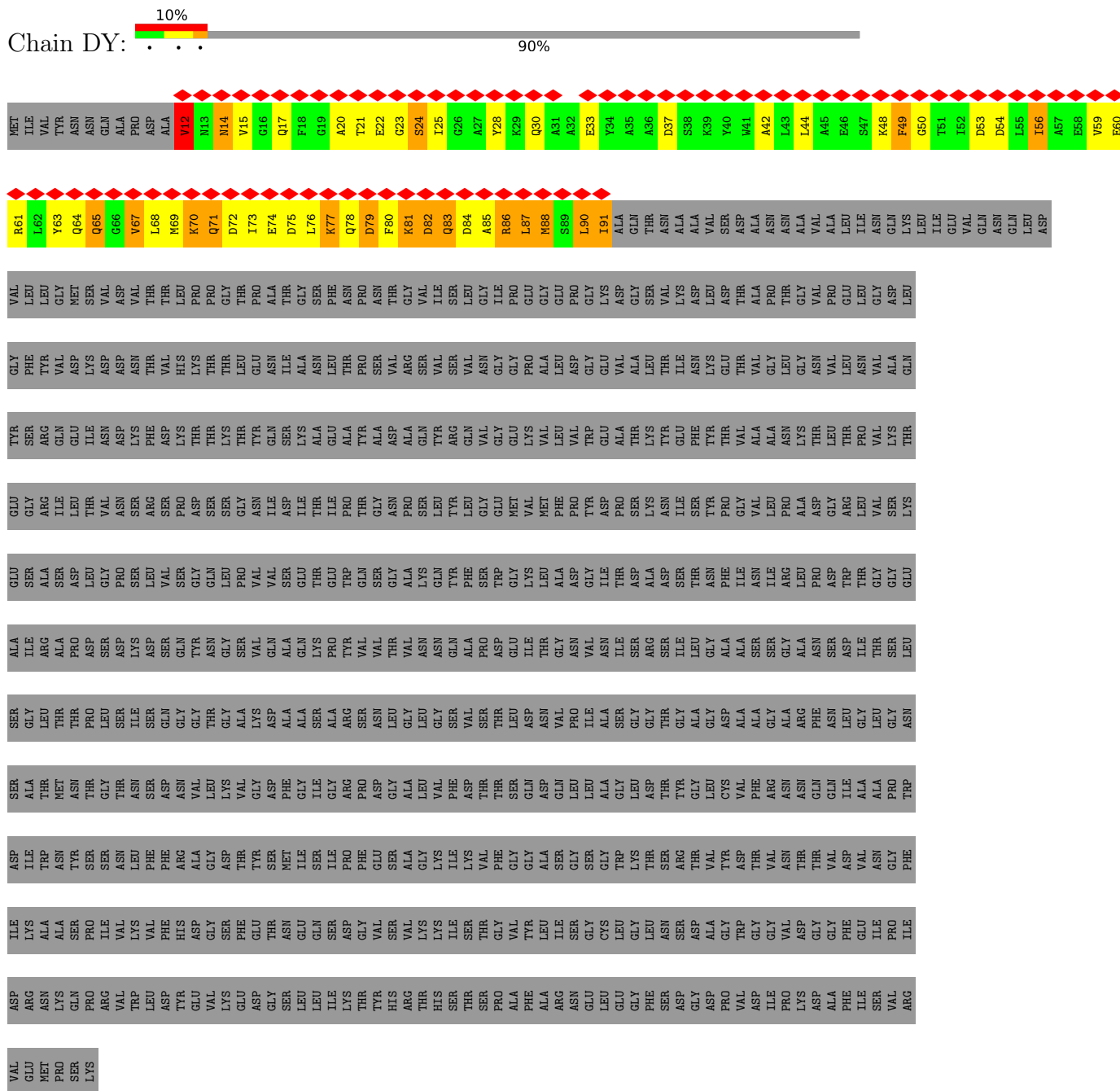




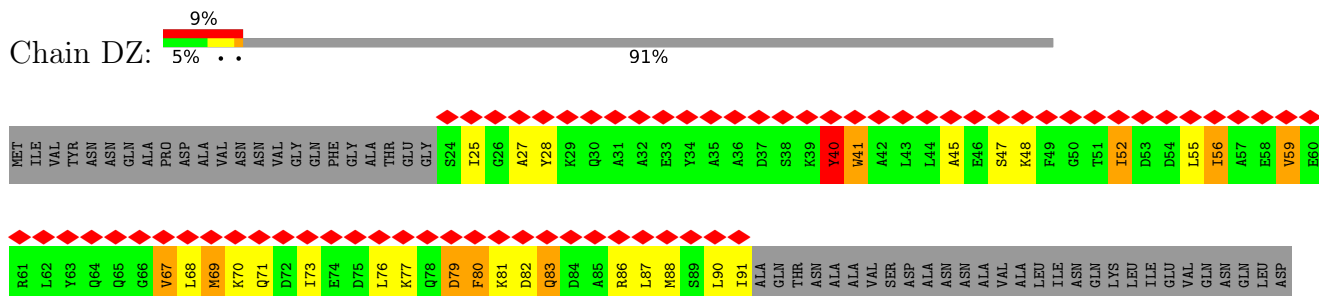
Chain DX:  10% 5% 89%



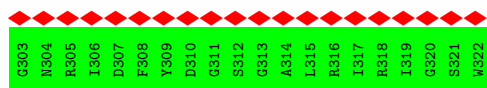
- Molecule 5: Putative tail fiber



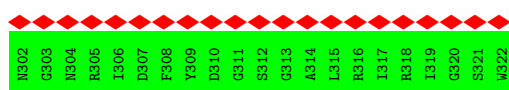
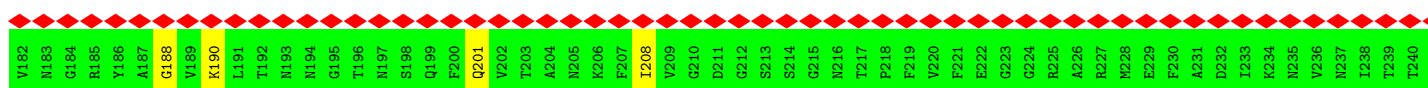
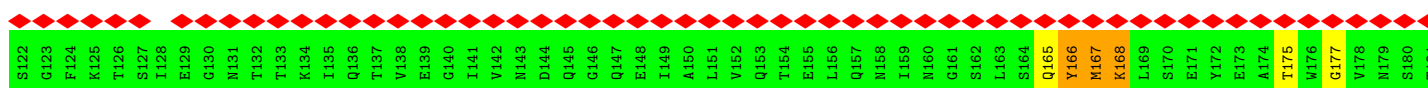
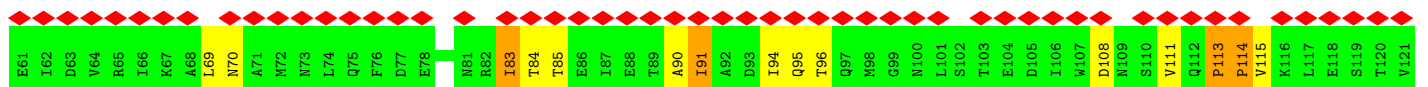
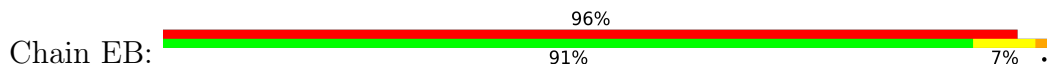
- Molecule 5: Putative tail fiber



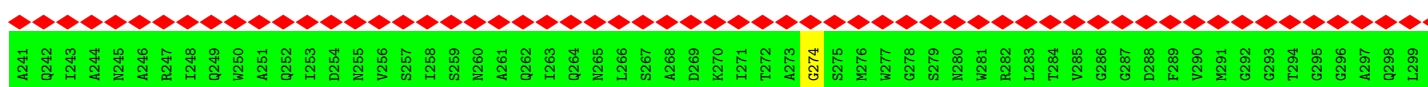
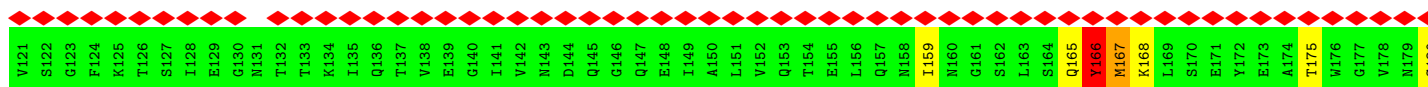
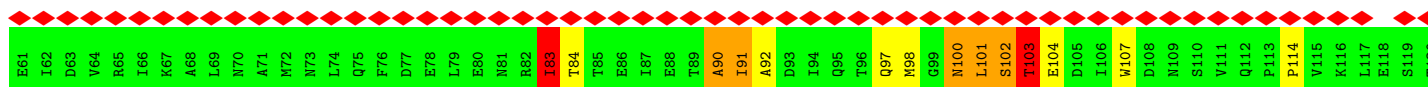
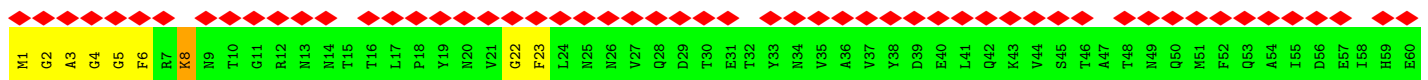
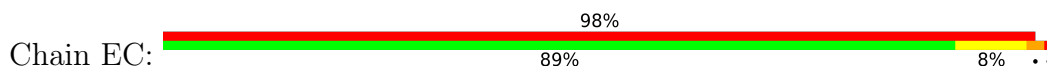


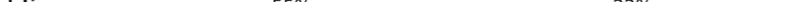


• Molecule 6: Putative tail tip fiber protein



• Molecule 6: Putative tail tip fiber protein

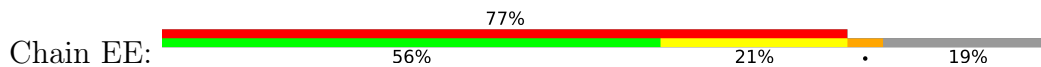


Chain ED: 



THR
LYS
LYS
GLU
GLN
GLN
ALA
SER
SER
LYS
LYS
ASP
SER
SER
ARG
ILE
PRO
GLY
LYS
ARG
LEU
GLY
SER
LYS
LYS

● Molecule 7: Portal protein



E661	ASP	ASN	ASN	ALA	ALA	THR	LEU	LEU	GLN	ALA	LYS	HIS	LYS	LEU	ALA	LEU	MET	GLN	GLN	VAL	ARG	GLN	TTR	GLU	SER	VAL	LEU	LYS	GLU	LEU	GLN	MET	VAL	VAL	GLN	LEU	LEU	SER	HIS	GLN	VAL	ASP	GLU	LYS	ILE	VAL	VAL	GLN	GLN	ALA	ARG	VAL	VAL	GLN	ASP	LYS	THR	LEU	GLU	LEU	GLN	LYS
K601	A602	Q603	V604	E605	N606	V607	Q608	A609	S610	S611	Q612	K613	M614	I615	A616	D617	A618	F619	D620	Q621	R622	E623	R624	T625	T626	F627	E628	Q629	Q630	K631	A632	A633	D634	E635	L636	S637	L638	R639	Q640	E641	E642	L643	Q644	F645	K646	Q647	E648	N649	A650	A651	D652	A653	M654	T655	L656	E657	N658	R659	K660			
Q541	L542	I543	A544	A545	D546	A547	Q548	L549	A550	P551	Q552	F553	G554	L555	E556	Q557	D558	R559	Y560	M561	T562	A563	Q564	I565	F566	E567	L568	M569	Q570	I571	K572	D573	T574	H575	K576	Y577	L578	L579	P580	L581	E582	Q583	Y584	Q585	P586	P587	E588	P589	A650	P591	M592	E593	I594	L595	Q596	L597	E598	M599	T600			
M481	R482	G483	I484	Y485	M486	L487	I488	R489	E490	M491	G492	E493	V494	P495	I496	E497	V498	Q499	T500	P501	R502	G503	M504	I505	Q506	V507	N508	P509	K510	Q511	L512	P513	A514	R515	H516	N517	L518	Q519	V520	V521	V522	A523	I524	S525	P526	N527	E528	K529	A530	E531	R532	A533	Q534	K535	L536	I537	S538	L539	K540			
G421	M422	S423	E424	E425	L426	K427	E428	T429	R430	T431	G432	V433	T434	K435	L436	G437	M438	G439	I440	N441	P442	D443	V444	F445	K446	N447	D448	N449	A450	Y451	A452	T453	V454	G455	L456	M457	M458	N459	A460	A461	Q462	M463	R464	L465	R466	M467	V468	C469	N470	N471	I472	A473	Q474	H475	N476	M477	V478	E479	L480			
R361	G362	Y363	I364	D365	N366	V367	N368	N369	A370	N371	Y372	G373	R374	Y375	K376	A377	L378	V379	G380	A381	Y382	D383	R384	R385	S386	L387	L388	D389	N390	K391	P392	G393	G394	V395	V396	E397	M398	E399	R400	Q401	D402	A403	I404	D405	L406	F407	P408	Y409	H410	N411	L412	P413	Q414	G415	I416	D417	G418	L419	L420			
K301	N302	K303	E304	S305	K306	L307	Y308	Q309	V310	I311	Q312	A313	G314	E315	H316	I317	L318	H319	T320	E321	E322	D323	T324	H325	I326	P327	F328	V329	T330	D331	C332	P333	P335	I336	P337	G338	S339	F340	Y341	G342	Q343	S344	V345	Y346	D347	I348	T349	K350	D351	I352	Q353	D354	L355	R356	T357	A358	L359	V360				
K241	D242	E243	I244	E245	A246	PHE	ASN	ASP	TRP	THR	ASP	THR	MET	ASP	T256	T257	Q258	S259	V260	A262	W263	S264	R265	T266	D267	W268	R269	Q270	D271	I272	D273	A274	D275	T276	G277	T278	D279	E280	E281	D282	I283	A284	S285	M286	V287	W288	V289	Y290	E291	H292	Y293	I294	R295	T296	G297	V298	L299	D300				
GLU	ASP	GLY	THR	VAL	ASP	VAL	LYS	V189	T190	TRP	Y191	E192	Q193	T194	V195	K196	R197	V198	K199	V200	E201	Y202	V203	P204	S205	E206	Q207	R208	F209	V210	D211	E212	H213	A214	T215	S216	F217	A218	D219	A220	Q221	Y222	F223	C224	H225	R226	V227	R228	R229	S230	K231	E232	D233	L234	V235	A236	W237	G238	F239	P240		
S121	S122	A123	A124	Q125	E126	C127	L128	Y129	T130	R131	Q132	S133	F134	I135	K136	Y137	W138	W139	D140	E141	T142	T143	S144	THR	GLN	GLU	ALA	GLY	VAL	PRO	PRO	GLU	ALA	LEU	ALA	ALA	TYR	VAL	GLN	GLY	LEU	GLU	GLY	ASN	LEU	GLU	VAL	PHE	THR	GLU	GLU	ASN	R112	D113	N114	P115	G116	Y117	N118	I119	I120	
D61	R62	T63	V64	W65	E66	S67	V68	N69	G70	T71	L72	Q73	W74	I75	T76	W77	V78	W79	C80	S81	C82	D83	E84	A85	V86	T87	F88	V89	D90	D91	N92	Q93	Q94	D95	S96	D97	Y98	A99	D100	W101	A102	T103	K104	LEU	L105	V106	N107	Q108	A50	P51	T109	L110	T53	A54	G55	S56	S57	S58	W59	V60		

GLU
ALA
ASN
VAL
THR
LYS
LYS
GLU
GLN
ALA
SER
LEU
LYS
ASP
SER
ARG
ILE
PRO
GLY
LYS
ARG
LEU
GLY
SER
LYS
LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9418	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.075	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	1788.48, 1788.48, 1788.48	wwPDB
Map dimensions	1296, 1296, 1296	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.25	0/2736	0.43	0/3706
1	AB	0.24	0/2736	0.41	0/3706
1	AC	0.25	0/2713	0.42	0/3673
1	AD	0.25	0/2736	0.43	0/3706
1	AE	0.25	0/2728	0.43	0/3694
1	AF	0.24	0/2727	0.41	0/3695
1	AG	0.25	0/2736	0.44	0/3706
1	AH	0.24	0/2736	0.43	0/3706
1	AI	0.25	0/2736	0.44	0/3706
1	AJ	0.24	0/2736	0.42	0/3706
1	AK	0.24	0/2736	0.42	0/3706
1	AL	0.25	0/2736	0.43	0/3706
1	AM	0.25	0/2713	0.43	0/3673
1	AN	0.25	0/2713	0.42	0/3673
1	AO	0.25	0/2713	0.42	0/3673
1	AP	0.24	0/2736	0.43	0/3706
1	AQ	0.25	0/2736	0.42	0/3706
1	AR	0.25	0/2736	0.42	0/3706
1	AS	0.24	0/2728	0.43	0/3694
1	AT	0.24	0/2728	0.44	0/3694
1	AU	0.25	0/2728	0.44	0/3694
1	AV	0.25	0/2727	0.42	0/3695
1	AW	0.24	0/2727	0.42	0/3695
1	AX	0.24	0/2727	0.42	0/3695
1	AY	0.25	0/2736	0.43	0/3706
1	AZ	0.24	0/2736	0.42	0/3706
1	BA	0.25	0/2713	0.42	0/3673
1	BB	0.25	0/2736	0.43	0/3706
1	BC	0.25	0/2728	0.43	0/3694
1	BD	0.24	0/2727	0.41	0/3695
1	BE	0.25	0/2736	0.44	0/3706
1	BF	0.24	0/2736	0.43	0/3706
1	BG	0.25	0/2736	0.44	0/3706
1	BH	0.24	0/2736	0.42	0/3706

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.24	0/2736	0.42	0/3706
1	BJ	0.25	0/2736	0.43	0/3706
1	BK	0.25	0/2713	0.43	0/3673
1	BL	0.25	0/2713	0.42	0/3673
1	BM	0.25	0/2713	0.42	0/3673
1	BN	0.25	0/2736	0.43	0/3706
1	BO	0.25	0/2736	0.42	0/3706
1	BP	0.25	0/2736	0.42	0/3706
1	BQ	0.24	0/2728	0.43	0/3694
1	BR	0.24	0/2728	0.44	0/3694
1	BS	0.25	0/2728	0.44	0/3694
1	BT	0.25	0/2727	0.42	0/3695
1	BU	0.24	0/2727	0.42	0/3695
1	BV	0.24	0/2727	0.42	0/3695
1	BW	0.25	0/2723	0.44	0/3690
1	BX	0.24	0/2728	0.44	0/3694
1	BY	0.25	0/2736	0.43	0/3706
1	BZ	0.25	0/2720	0.43	0/3683
1	CA	0.24	0/2728	0.45	0/3694
1	CB	0.25	0/2727	0.44	0/3695
1	CC	0.24	0/2736	0.46	0/3706
1	CD	0.25	0/2706	0.45	0/3661
1	CE	0.25	0/2727	0.44	0/3695
1	CF	0.25	0/2693	0.43	0/3646
1	CG	0.25	0/2736	0.45	0/3706
1	CH	0.24	0/2736	0.42	0/3706
1	CI	0.25	0/2727	0.45	0/3695
1	CJ	0.25	0/2736	0.44	0/3706
1	CK	0.24	0/2736	0.44	0/3706
1	CL	0.25	0/2704	0.43	0/3662
1	CM	0.25	0/2727	0.45	0/3695
1	CN	0.25	0/2693	0.44	0/3646
1	CO	0.25	0/2686	0.45	0/3636
1	CP	0.25	0/2719	0.43	0/3683
1	CQ	0.25	0/2727	0.44	0/3695
1	CR	0.25	0/2720	0.44	0/3683
1	CS	0.25	0/2736	0.43	0/3706
1	CT	0.25	0/2728	0.42	0/3694
1	CU	0.25	0/2727	0.45	0/3695
1	CV	0.25	0/2736	0.43	0/3706
1	CW	0.25	0/2728	0.45	0/3694
1	CX	0.25	0/2727	0.43	0/3695
1	CY	0.25	0/2736	0.44	0/3706

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.25	0/2736	0.46	0/3706
1	DA	0.25	0/2728	0.44	0/3694
1	DB	0.25	0/2736	0.44	0/3706
1	DC	0.25	0/2720	0.44	0/3683
1	DD	0.25	0/2728	0.44	0/3694
1	DE	0.25	0/2727	0.44	0/3695
1	DF	0.25	0/2736	0.45	0/3706
1	DG	0.25	0/2706	0.45	0/3661
1	DH	0.25	0/2727	0.44	0/3695
1	DI	0.25	0/2736	0.43	0/3706
1	DJ	0.25	0/2727	0.45	0/3695
1	DK	0.25	0/2704	0.43	0/3662
1	DL	0.25	0/2727	0.44	0/3695
1	DM	0.24	0/2719	0.43	0/3683
1	DN	0.25	0/2727	0.44	0/3695
1	DO	0.25	0/2728	0.43	0/3694
1	DP	0.25	0/2727	0.44	0/3695
1	DQ	0.25	0/2727	0.42	0/3695
2	DR	0.26	0/1431	0.51	0/1867
2	DS	0.36	2/1435 (0.1%)	0.92	7/1872 (0.4%)
2	DT	0.28	0/1435	0.66	3/1872 (0.2%)
3	DU	0.89	0/1866	0.78	4/2545 (0.2%)
3	DV	1.10	11/1866 (0.6%)	1.48	27/2545 (1.1%)
4	DW	1.49	138/7215 (1.9%)	1.30	54/9852 (0.5%)
5	DX	0.67	1/693 (0.1%)	0.95	4/935 (0.4%)
5	DY	0.64	0/635	0.80	1/852 (0.1%)
5	DZ	0.97	1/552 (0.2%)	1.02	3/741 (0.4%)
6	EA	1.16	18/1288 (1.4%)	1.35	21/1607 (1.3%)
6	EB	0.69	0/1288	0.94	1/1607 (0.1%)
6	EC	0.95	6/1288 (0.5%)	1.12	11/1607 (0.7%)
7	ED	1.28	45/4930 (0.9%)	1.27	35/6682 (0.5%)
7	EE	1.28	46/4930 (0.9%)	1.26	37/6682 (0.6%)
All	All	0.44	268/289915 (0.1%)	0.56	208/392151 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AF	0	1
1	BD	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	CA	0	1
1	CC	0	2
1	DF	0	2
2	DT	0	1
3	DU	0	1
3	DV	1	6
4	DW	0	2
5	DX	0	2
5	DZ	0	1
6	EA	0	5
6	EB	0	7
6	EC	0	11
7	ED	0	1
All	All	1	44

The worst 5 of 268 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	DZ	41	TRP	C-O	15.14	1.52	1.23
6	EA	102	SER	C-O	14.54	1.50	1.23
6	EC	101	LEU	C-O	13.22	1.48	1.23
3	DV	28	ASP	C-O	-11.08	1.02	1.23
6	EA	101	LEU	C-O	10.11	1.42	1.23

The worst 5 of 208 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	DV	24	ALA	CB-CA-C	-27.15	69.38	110.10
3	DV	27	ASP	CB-CA-C	-26.89	56.61	110.40
3	DV	26	ARG	CB-CA-C	-26.87	56.66	110.40
2	DS	23	TYR	CB-CG-CD1	-22.54	107.48	121.00
3	DV	28	ASP	CB-CA-C	-19.23	71.94	110.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	DV	25	ASP	CA

5 of 44 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AF	213	PHE	Peptide

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Mol	Chain	Res	Type	Group
1	BD	213	PHE	Peptide
1	CA	144	THR	Peptide
1	CC	167	PHE	Peptide
1	CC	168	GLN	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	2685	0	2651	29	0
1	AB	2685	0	2651	24	0
1	AC	2663	0	2631	33	0
1	AD	2685	0	2651	26	0
1	AE	2677	0	2646	26	0
1	AF	2676	0	2638	26	0
1	AG	2685	0	2651	27	0
1	AH	2685	0	2651	29	0
1	AI	2685	0	2651	23	0
1	AJ	2685	0	2651	23	0
1	AK	2685	0	2645	88	0
1	AL	2685	0	2651	23	0
1	AM	2663	0	2625	169	0
1	AN	2663	0	2631	26	0
1	AO	2663	0	2631	32	0
1	AP	2685	0	2626	376	0
1	AQ	2685	0	2651	26	0
1	AR	2685	0	2651	30	0
1	AS	2677	0	2641	155	0
1	AT	2677	0	2646	25	0
1	AU	2677	0	2646	26	0
1	AV	2676	0	2638	33	0
1	AW	2676	0	2619	212	0
1	AX	2676	0	2638	23	0
1	AY	2685	0	2651	27	0
1	AZ	2685	0	2651	26	0
1	BA	2663	0	2631	34	0
1	BB	2685	0	2651	27	0
1	BC	2677	0	2646	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BD	2676	0	2638	23	0
1	BE	2685	0	2651	28	0
1	BF	2685	0	2651	52	0
1	BG	2685	0	2651	24	0
1	BH	2685	0	2651	22	0
1	BI	2685	0	2629	426	0
1	BJ	2685	0	2651	22	0
1	BK	2663	0	2622	168	0
1	BL	2663	0	2631	29	0
1	BM	2663	0	2631	31	0
1	BN	2685	0	2642	145	0
1	BO	2685	0	2651	26	0
1	BP	2685	0	2651	28	0
1	BQ	2677	0	2646	31	0
1	BR	2677	0	2646	27	0
1	BS	2677	0	2646	25	0
1	BT	2676	0	2638	29	0
1	BU	2676	0	2622	275	0
1	BV	2676	0	2638	24	0
1	BW	2672	0	2635	40	0
1	BX	2677	0	2646	53	0
1	BY	2685	0	2651	41	0
1	BZ	2670	0	2638	34	0
1	CA	2677	0	2646	45	0
1	CB	2676	0	2638	40	0
1	CC	2685	0	2651	33	0
1	CD	2657	0	2629	39	0
1	CE	2676	0	2638	45	0
1	CF	2644	0	2611	34	0
1	CG	2685	0	2651	38	0
1	CH	2685	0	2651	22	0
1	CI	2676	0	2638	28	0
1	CJ	2685	0	2651	26	0
1	CK	2685	0	2651	41	0
1	CL	2654	0	2618	41	0
1	CM	2676	0	2638	31	0
1	CN	2644	0	2608	118	0
1	CO	2637	0	2602	39	0
1	CP	2668	0	2633	37	0
1	CQ	2676	0	2638	43	0
1	CR	2670	0	2631	139	0
1	CS	2685	0	2642	275	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CT	2677	0	2646	34	0
1	CU	2676	0	2638	48	0
1	CV	2685	0	2647	48	0
1	CW	2677	0	2629	165	0
1	CX	2676	0	2638	22	0
1	CY	2685	0	2651	37	0
1	CZ	2685	0	2647	95	0
1	DA	2677	0	2646	36	0
1	DB	2685	0	2649	117	0
1	DC	2670	0	2636	72	0
1	DD	2677	0	2646	68	0
1	DE	2676	0	2638	42	0
1	DF	2685	0	2651	44	0
1	DG	2657	0	2629	37	0
1	DH	2676	0	2634	172	0
1	DI	2685	0	2651	28	0
1	DJ	2676	0	2638	38	0
1	DK	2654	0	2606	204	0
1	DL	2676	0	2638	30	0
1	DM	2668	0	2633	104	0
1	DN	2676	0	2638	38	0
1	DO	2677	0	2642	53	0
1	DP	2676	0	2623	296	0
1	DQ	2676	0	2638	30	0
2	DR	1420	0	954	74	0
2	DS	1424	0	965	40	0
2	DT	1424	0	965	36	0
3	DU	1813	0	1736	191	0
3	DV	1813	0	1738	300	0
4	DW	7063	0	6881	199	0
5	DX	683	0	653	167	0
5	DY	628	0	610	132	0
5	DZ	545	0	536	116	0
6	EA	1289	0	384	10	0
6	EB	1289	0	384	10	0
6	EC	1289	0	384	18	0
7	ED	4838	0	4692	509	0
7	EE	4838	0	4692	462	0
All	All	284597	0	276368	5691	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 10.

The worst 5 of 5691 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BI:96:THR:HB	1:DM:152:VAL:CG2	1.26	1.63
1:AW:16:LYS:HG3	1:BK:103:TYR:CD2	1.21	1.62
1:AP:320:SER:CB	1:CZ:65:GLU:CG	1.74	1.62
1:BI:92:ARG:CZ	1:DK:6:LEU:HD23	1.20	1.62
1:AP:79:ILE:HD13	1:CR:147:ALA:CB	1.15	1.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	345/352 (98%)	327 (95%)	18 (5%)	0	100	100
1	AB	345/352 (98%)	318 (92%)	27 (8%)	0	100	100
1	AC	342/352 (97%)	320 (94%)	22 (6%)	0	100	100
1	AD	345/352 (98%)	321 (93%)	24 (7%)	0	100	100
1	AE	344/352 (98%)	308 (90%)	36 (10%)	0	100	100
1	AF	344/352 (98%)	317 (92%)	27 (8%)	0	100	100
1	AG	345/352 (98%)	314 (91%)	31 (9%)	0	100	100
1	AH	345/352 (98%)	319 (92%)	26 (8%)	0	100	100
1	AI	345/352 (98%)	322 (93%)	23 (7%)	0	100	100
1	AJ	345/352 (98%)	313 (91%)	32 (9%)	0	100	100
1	AK	345/352 (98%)	318 (92%)	27 (8%)	0	100	100
1	AL	345/352 (98%)	313 (91%)	32 (9%)	0	100	100
1	AM	342/352 (97%)	319 (93%)	22 (6%)	1 (0%)	37	73
1	AN	342/352 (97%)	311 (91%)	31 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AO	342/352 (97%)	315 (92%)	27 (8%)	0	100	100
1	AP	345/352 (98%)	318 (92%)	27 (8%)	0	100	100
1	AQ	345/352 (98%)	321 (93%)	24 (7%)	0	100	100
1	AR	345/352 (98%)	324 (94%)	21 (6%)	0	100	100
1	AS	344/352 (98%)	316 (92%)	28 (8%)	0	100	100
1	AT	344/352 (98%)	309 (90%)	35 (10%)	0	100	100
1	AU	344/352 (98%)	300 (87%)	44 (13%)	0	100	100
1	AV	344/352 (98%)	320 (93%)	24 (7%)	0	100	100
1	AW	344/352 (98%)	319 (93%)	25 (7%)	0	100	100
1	AX	344/352 (98%)	321 (93%)	23 (7%)	0	100	100
1	AY	345/352 (98%)	327 (95%)	18 (5%)	0	100	100
1	AZ	345/352 (98%)	319 (92%)	26 (8%)	0	100	100
1	BA	342/352 (97%)	319 (93%)	23 (7%)	0	100	100
1	BB	345/352 (98%)	320 (93%)	25 (7%)	0	100	100
1	BC	344/352 (98%)	308 (90%)	36 (10%)	0	100	100
1	BD	344/352 (98%)	319 (93%)	25 (7%)	0	100	100
1	BE	345/352 (98%)	314 (91%)	31 (9%)	0	100	100
1	BF	345/352 (98%)	319 (92%)	26 (8%)	0	100	100
1	BG	345/352 (98%)	323 (94%)	22 (6%)	0	100	100
1	BH	345/352 (98%)	314 (91%)	31 (9%)	0	100	100
1	BI	345/352 (98%)	316 (92%)	29 (8%)	0	100	100
1	BJ	345/352 (98%)	315 (91%)	30 (9%)	0	100	100
1	BK	342/352 (97%)	319 (93%)	22 (6%)	1 (0%)	37	73
1	BL	342/352 (97%)	311 (91%)	31 (9%)	0	100	100
1	BM	342/352 (97%)	316 (92%)	26 (8%)	0	100	100
1	BN	345/352 (98%)	318 (92%)	27 (8%)	0	100	100
1	BO	345/352 (98%)	321 (93%)	24 (7%)	0	100	100
1	BP	345/352 (98%)	323 (94%)	22 (6%)	0	100	100
1	BQ	344/352 (98%)	317 (92%)	27 (8%)	0	100	100
1	BR	344/352 (98%)	308 (90%)	36 (10%)	0	100	100
1	BS	344/352 (98%)	300 (87%)	44 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BT	344/352 (98%)	320 (93%)	24 (7%)	0	100	100
1	BU	344/352 (98%)	320 (93%)	24 (7%)	0	100	100
1	BV	344/352 (98%)	321 (93%)	23 (7%)	0	100	100
1	BW	343/352 (97%)	286 (83%)	57 (17%)	0	100	100
1	BX	344/352 (98%)	284 (83%)	59 (17%)	1 (0%)	37	73
1	BY	345/352 (98%)	309 (90%)	36 (10%)	0	100	100
1	BZ	343/352 (97%)	308 (90%)	35 (10%)	0	100	100
1	CA	344/352 (98%)	275 (80%)	65 (19%)	4 (1%)	11	44
1	CB	344/352 (98%)	298 (87%)	46 (13%)	0	100	100
1	CC	345/352 (98%)	288 (84%)	56 (16%)	1 (0%)	37	73
1	CD	339/352 (96%)	305 (90%)	34 (10%)	0	100	100
1	CE	344/352 (98%)	322 (94%)	22 (6%)	0	100	100
1	CF	340/352 (97%)	307 (90%)	33 (10%)	0	100	100
1	CG	345/352 (98%)	276 (80%)	68 (20%)	1 (0%)	37	73
1	CH	345/352 (98%)	314 (91%)	31 (9%)	0	100	100
1	CI	344/352 (98%)	318 (92%)	26 (8%)	0	100	100
1	CJ	345/352 (98%)	315 (91%)	30 (9%)	0	100	100
1	CK	345/352 (98%)	264 (76%)	81 (24%)	0	100	100
1	CL	341/352 (97%)	294 (86%)	47 (14%)	0	100	100
1	CM	344/352 (98%)	324 (94%)	20 (6%)	0	100	100
1	CN	340/352 (97%)	310 (91%)	30 (9%)	0	100	100
1	CO	339/352 (96%)	286 (84%)	53 (16%)	0	100	100
1	CP	343/352 (97%)	306 (89%)	37 (11%)	0	100	100
1	CQ	344/352 (98%)	313 (91%)	31 (9%)	0	100	100
1	CR	343/352 (97%)	307 (90%)	36 (10%)	0	100	100
1	CS	345/352 (98%)	298 (86%)	47 (14%)	0	100	100
1	CT	344/352 (98%)	312 (91%)	32 (9%)	0	100	100
1	CU	344/352 (98%)	319 (93%)	25 (7%)	0	100	100
1	CV	345/352 (98%)	323 (94%)	22 (6%)	0	100	100
1	CW	344/352 (98%)	284 (83%)	60 (17%)	0	100	100
1	CX	344/352 (98%)	328 (95%)	16 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CY	345/352 (98%)	311 (90%)	34 (10%)	0	100	100
1	CZ	345/352 (98%)	285 (83%)	60 (17%)	0	100	100
1	DA	344/352 (98%)	288 (84%)	54 (16%)	2 (1%)	22	60
1	DB	345/352 (98%)	317 (92%)	28 (8%)	0	100	100
1	DC	343/352 (97%)	305 (89%)	38 (11%)	0	100	100
1	DD	344/352 (98%)	290 (84%)	51 (15%)	3 (1%)	14	52
1	DE	344/352 (98%)	302 (88%)	42 (12%)	0	100	100
1	DF	345/352 (98%)	286 (83%)	58 (17%)	1 (0%)	37	73
1	DG	339/352 (96%)	303 (89%)	36 (11%)	0	100	100
1	DH	344/352 (98%)	315 (92%)	29 (8%)	0	100	100
1	DI	345/352 (98%)	313 (91%)	32 (9%)	0	100	100
1	DJ	344/352 (98%)	322 (94%)	22 (6%)	0	100	100
1	DK	341/352 (97%)	303 (89%)	38 (11%)	0	100	100
1	DL	344/352 (98%)	324 (94%)	20 (6%)	0	100	100
1	DM	343/352 (97%)	312 (91%)	31 (9%)	0	100	100
1	DN	344/352 (98%)	326 (95%)	18 (5%)	0	100	100
1	DO	344/352 (98%)	317 (92%)	27 (8%)	0	100	100
1	DP	344/352 (98%)	327 (95%)	17 (5%)	0	100	100
1	DQ	344/352 (98%)	318 (92%)	26 (8%)	0	100	100
2	DR	261/267 (98%)	212 (81%)	43 (16%)	6 (2%)	5	28
2	DS	261/267 (98%)	219 (84%)	37 (14%)	5 (2%)	6	32
2	DT	261/267 (98%)	222 (85%)	30 (12%)	9 (3%)	3	21
3	DU	218/250 (87%)	163 (75%)	47 (22%)	8 (4%)	2	20
3	DV	218/250 (87%)	170 (78%)	43 (20%)	5 (2%)	5	28
4	DW	904/1005 (90%)	758 (84%)	131 (14%)	15 (2%)	7	37
5	DX	85/786 (11%)	63 (74%)	15 (18%)	7 (8%)	1	9
5	DY	76/786 (10%)	61 (80%)	13 (17%)	2 (3%)	4	26
5	DZ	66/786 (8%)	58 (88%)	7 (11%)	1 (2%)	8	40
6	EA	320/322 (99%)	272 (85%)	33 (10%)	15 (5%)	2	16
6	EB	320/322 (99%)	269 (84%)	37 (12%)	14 (4%)	2	17
6	EC	320/322 (99%)	271 (85%)	32 (10%)	17 (5%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	ED	598/747 (80%)	533 (89%)	56 (9%)	9 (2%)	8	40
7	EE	598/747 (80%)	533 (89%)	57 (10%)	8 (1%)	10	43
All	All	37172/40564 (92%)	33351 (90%)	3685 (10%)	136 (0%)	32	68

5 of 136 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	DR	6	ASN
2	DR	18	PRO
2	DR	126	ILE
2	DR	139	VAL
2	DR	158	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	286/287 (100%)	279 (98%)	7 (2%)	44	62
1	AB	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	AC	283/287 (99%)	282 (100%)	1 (0%)	89	91
1	AD	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	AE	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	AF	285/287 (99%)	281 (99%)	4 (1%)	62	75
1	AG	286/287 (100%)	282 (99%)	4 (1%)	62	75
1	AH	286/287 (100%)	285 (100%)	1 (0%)	91	92
1	AI	286/287 (100%)	283 (99%)	3 (1%)	73	82
1	AJ	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	AK	286/287 (100%)	282 (99%)	4 (1%)	62	75
1	AL	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	AM	283/287 (99%)	280 (99%)	3 (1%)	70	80
1	AN	283/287 (99%)	281 (99%)	2 (1%)	81	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AO	283/287 (99%)	278 (98%)	5 (2%)	54	71
1	AP	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	AQ	286/287 (100%)	280 (98%)	6 (2%)	48	66
1	AR	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	AS	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	AT	285/287 (99%)	285 (100%)	0	100	100
1	AU	285/287 (99%)	280 (98%)	5 (2%)	54	71
1	AV	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	AW	285/287 (99%)	284 (100%)	1 (0%)	89	91
1	AX	285/287 (99%)	281 (99%)	4 (1%)	62	75
1	AY	286/287 (100%)	279 (98%)	7 (2%)	44	62
1	AZ	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	BA	283/287 (99%)	282 (100%)	1 (0%)	89	91
1	BB	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	BC	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	BD	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	BE	286/287 (100%)	282 (99%)	4 (1%)	62	75
1	BF	286/287 (100%)	285 (100%)	1 (0%)	91	92
1	BG	286/287 (100%)	283 (99%)	3 (1%)	73	82
1	BH	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	BI	286/287 (100%)	282 (99%)	4 (1%)	62	75
1	BJ	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	BK	283/287 (99%)	280 (99%)	3 (1%)	70	80
1	BL	283/287 (99%)	281 (99%)	2 (1%)	81	87
1	BM	283/287 (99%)	278 (98%)	5 (2%)	54	71
1	BN	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	BO	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	BP	286/287 (100%)	281 (98%)	5 (2%)	56	72
1	BQ	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	BR	285/287 (99%)	285 (100%)	0	100	100
1	BS	285/287 (99%)	280 (98%)	5 (2%)	54	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BT	285/287 (99%)	282 (99%)	3 (1%)	70	80
1	BU	285/287 (99%)	284 (100%)	1 (0%)	89	91
1	BV	285/287 (99%)	281 (99%)	4 (1%)	62	75
1	BW	285/287 (99%)	284 (100%)	1 (0%)	89	91
1	BX	285/287 (99%)	284 (100%)	1 (0%)	89	91
1	BY	286/287 (100%)	286 (100%)	0	100	100
1	BZ	284/287 (99%)	284 (100%)	0	100	100
1	CA	285/287 (99%)	285 (100%)	0	100	100
1	CB	285/287 (99%)	285 (100%)	0	100	100
1	CC	286/287 (100%)	286 (100%)	0	100	100
1	CD	283/287 (99%)	283 (100%)	0	100	100
1	CE	285/287 (99%)	285 (100%)	0	100	100
1	CF	281/287 (98%)	281 (100%)	0	100	100
1	CG	286/287 (100%)	286 (100%)	0	100	100
1	CH	286/287 (100%)	284 (99%)	2 (1%)	81	87
1	CI	285/287 (99%)	283 (99%)	2 (1%)	81	87
1	CJ	286/287 (100%)	286 (100%)	0	100	100
1	CK	286/287 (100%)	286 (100%)	0	100	100
1	CL	282/287 (98%)	282 (100%)	0	100	100
1	CM	285/287 (99%)	283 (99%)	2 (1%)	81	87
1	CN	281/287 (98%)	281 (100%)	0	100	100
1	CO	280/287 (98%)	279 (100%)	1 (0%)	89	91
1	CP	284/287 (99%)	284 (100%)	0	100	100
1	CQ	285/287 (99%)	283 (99%)	2 (1%)	81	87
1	CR	284/287 (99%)	283 (100%)	1 (0%)	89	91
1	CS	286/287 (100%)	285 (100%)	1 (0%)	91	92
1	CT	285/287 (99%)	284 (100%)	1 (0%)	89	91
1	CU	285/287 (99%)	283 (99%)	2 (1%)	81	87
1	CV	286/287 (100%)	286 (100%)	0	100	100
1	CW	285/287 (99%)	285 (100%)	0	100	100
1	CX	285/287 (99%)	285 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CY	286/287 (100%)	286 (100%)	0	100	100
1	CZ	286/287 (100%)	286 (100%)	0	100	100
1	DA	285/287 (99%)	285 (100%)	0	100	100
1	DB	286/287 (100%)	286 (100%)	0	100	100
1	DC	284/287 (99%)	284 (100%)	0	100	100
1	DD	285/287 (99%)	285 (100%)	0	100	100
1	DE	285/287 (99%)	284 (100%)	1 (0%)	89	91
1	DF	286/287 (100%)	285 (100%)	1 (0%)	91	92
1	DG	283/287 (99%)	283 (100%)	0	100	100
1	DH	285/287 (99%)	285 (100%)	0	100	100
1	DI	286/287 (100%)	286 (100%)	0	100	100
1	DJ	285/287 (99%)	285 (100%)	0	100	100
1	DK	282/287 (98%)	282 (100%)	0	100	100
1	DL	285/287 (99%)	285 (100%)	0	100	100
1	DM	284/287 (99%)	284 (100%)	0	100	100
1	DN	285/287 (99%)	285 (100%)	0	100	100
1	DO	285/287 (99%)	285 (100%)	0	100	100
1	DP	285/287 (99%)	285 (100%)	0	100	100
1	DQ	285/287 (99%)	285 (100%)	0	100	100
2	DR	85/227 (37%)	84 (99%)	1 (1%)	67	78
2	DS	86/227 (38%)	84 (98%)	2 (2%)	45	64
2	DT	86/227 (38%)	83 (96%)	3 (4%)	31	51
3	DU	197/223 (88%)	179 (91%)	18 (9%)	7	24
3	DV	197/223 (88%)	183 (93%)	14 (7%)	12	32
4	DW	792/870 (91%)	782 (99%)	10 (1%)	65	77
5	DX	69/640 (11%)	51 (74%)	18 (26%)	0	3
5	DY	64/640 (10%)	41 (64%)	23 (36%)	0	1
5	DZ	56/640 (9%)	45 (80%)	11 (20%)	1	7
7	ED	523/647 (81%)	493 (94%)	30 (6%)	17	38
7	EE	523/647 (81%)	493 (94%)	30 (6%)	17	38
All	All	29746/32476 (92%)	29410 (99%)	336 (1%)	69	80

5 of 336 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	DX	62	LEU
7	ED	363	TYR
5	DX	81	LYS
5	DY	86	ARG
7	ED	617	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 212 such sidechains are listed below:

Mol	Chain	Res	Type
1	DD	202	GLN
1	DJ	336	ASN
7	EE	77	ASN
1	DE	60	ASN
1	DH	29	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
5	DY	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DY	81:LYS	C	82:ASP	N	3.02

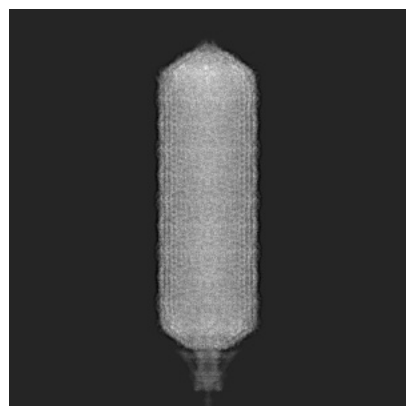
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14492. These allow visual inspection of the internal detail of the map and identification of artifacts.

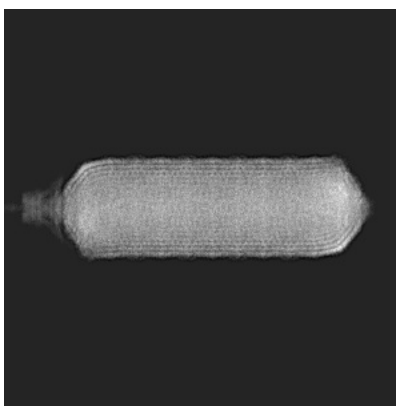
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

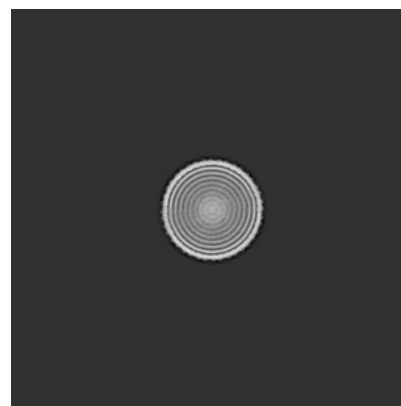
6.1.1 Primary map



X

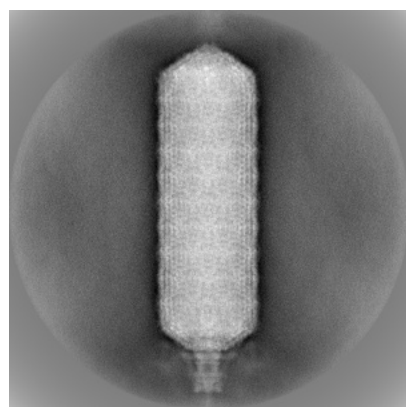


Y

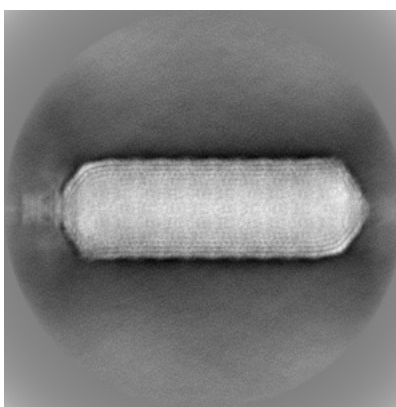


Z

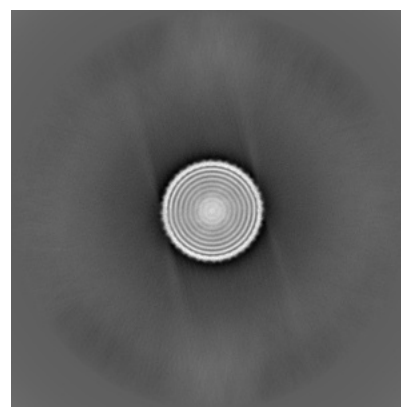
6.1.2 Raw map



X



Y

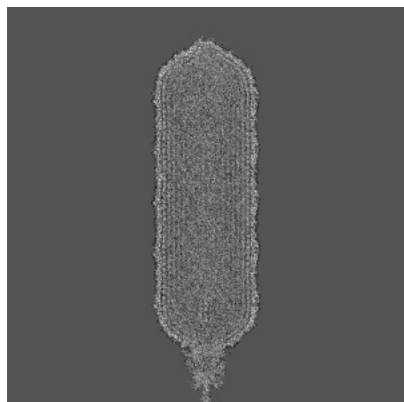


Z

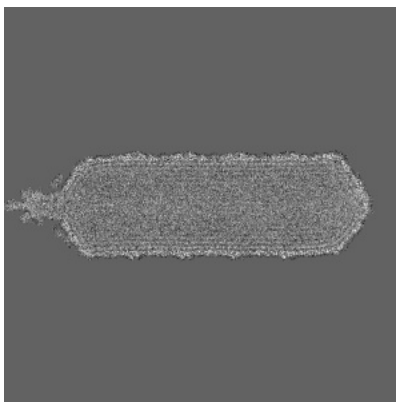
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

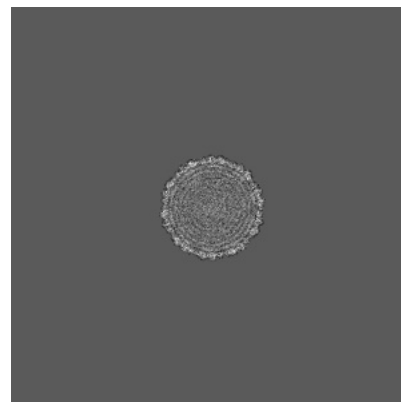
6.2.1 Primary map



X Index: 648

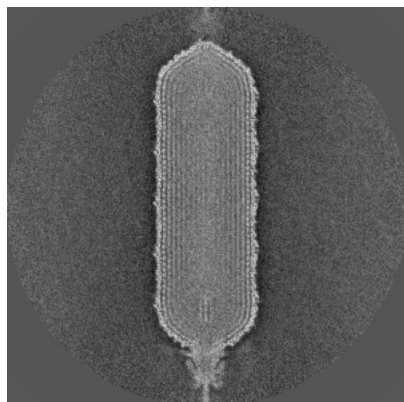


Y Index: 648

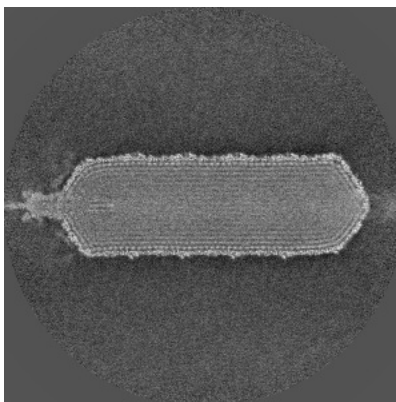


Z Index: 648

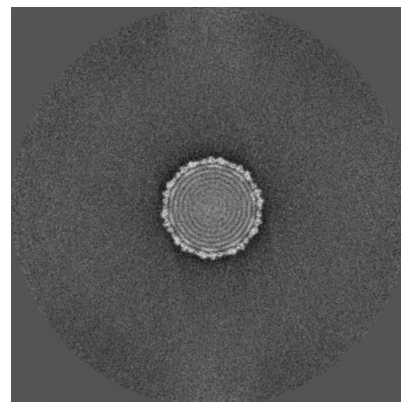
6.2.2 Raw map



X Index: 648



Y Index: 648

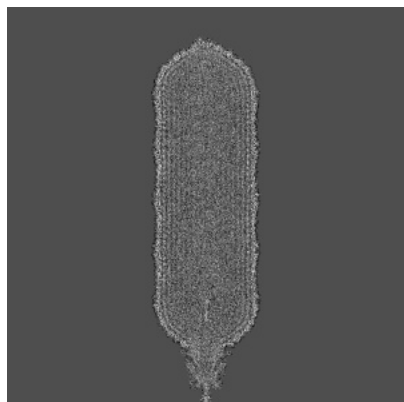


Z Index: 648

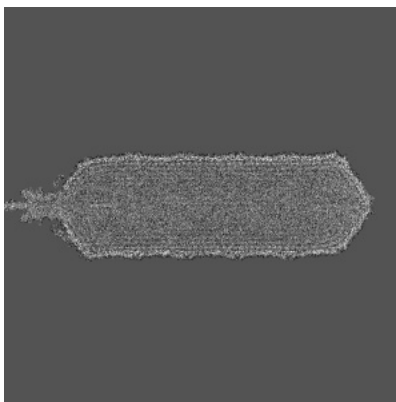
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

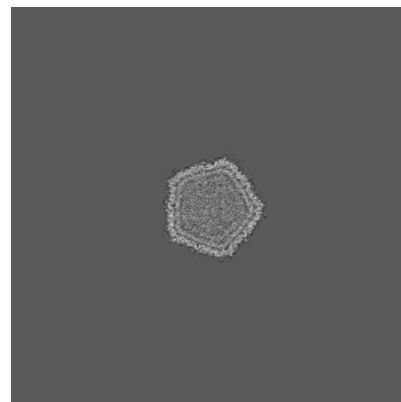
6.3.1 Primary map



X Index: 651

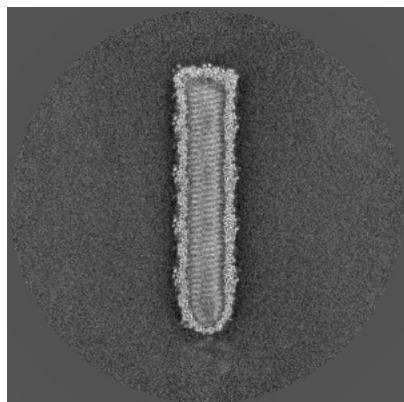


Y Index: 644

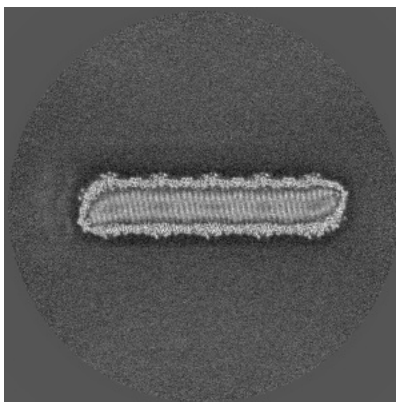


Z Index: 1085

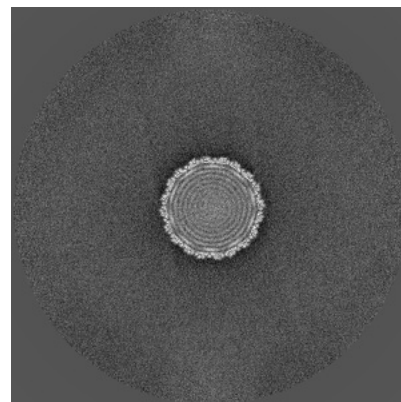
6.3.2 Raw map



X Index: 519



Y Index: 511

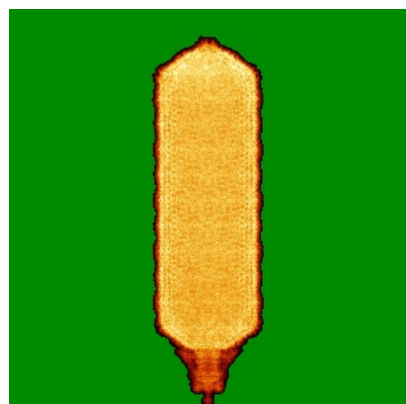


Z Index: 757

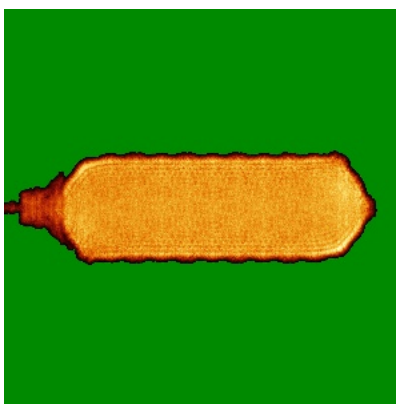
The images above show the largest variance slices of the map in three orthogonal directions.

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

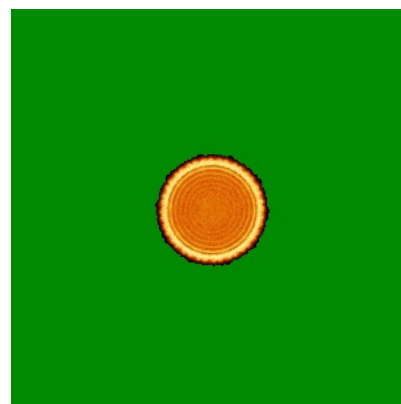
6.4.1 Primary map



X

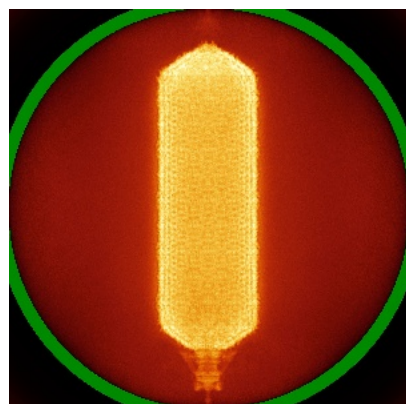


Y

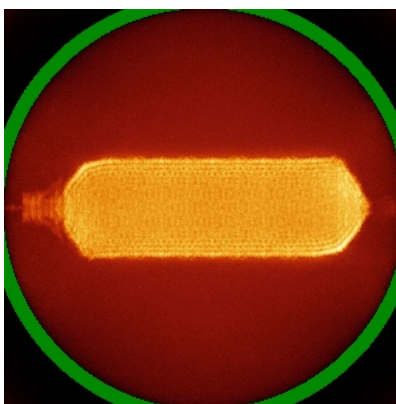


Z

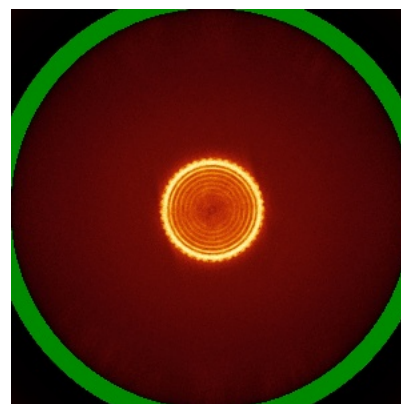
6.4.2 Raw map



X



Y

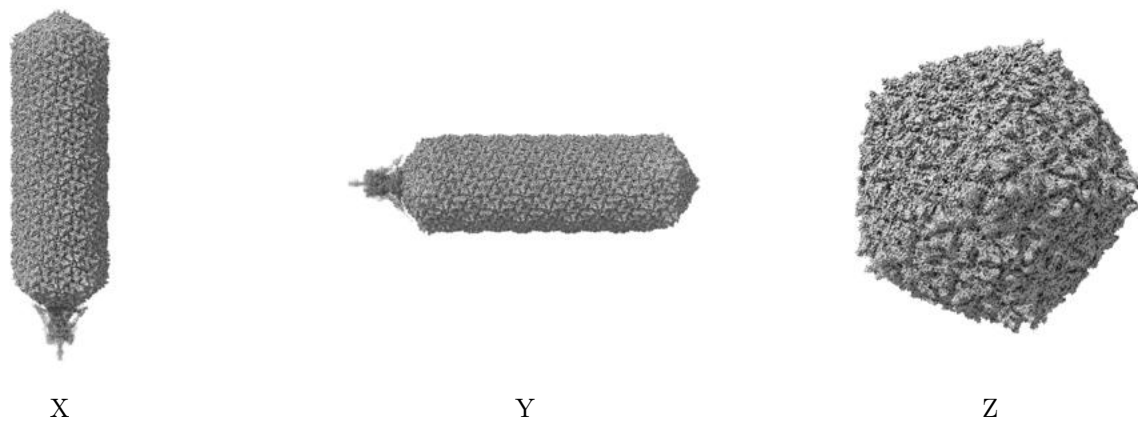


Z

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.

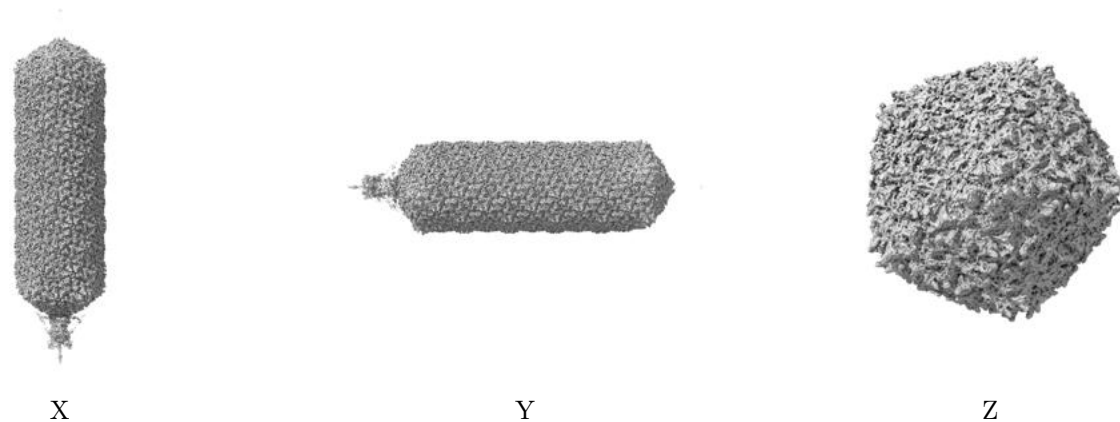
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

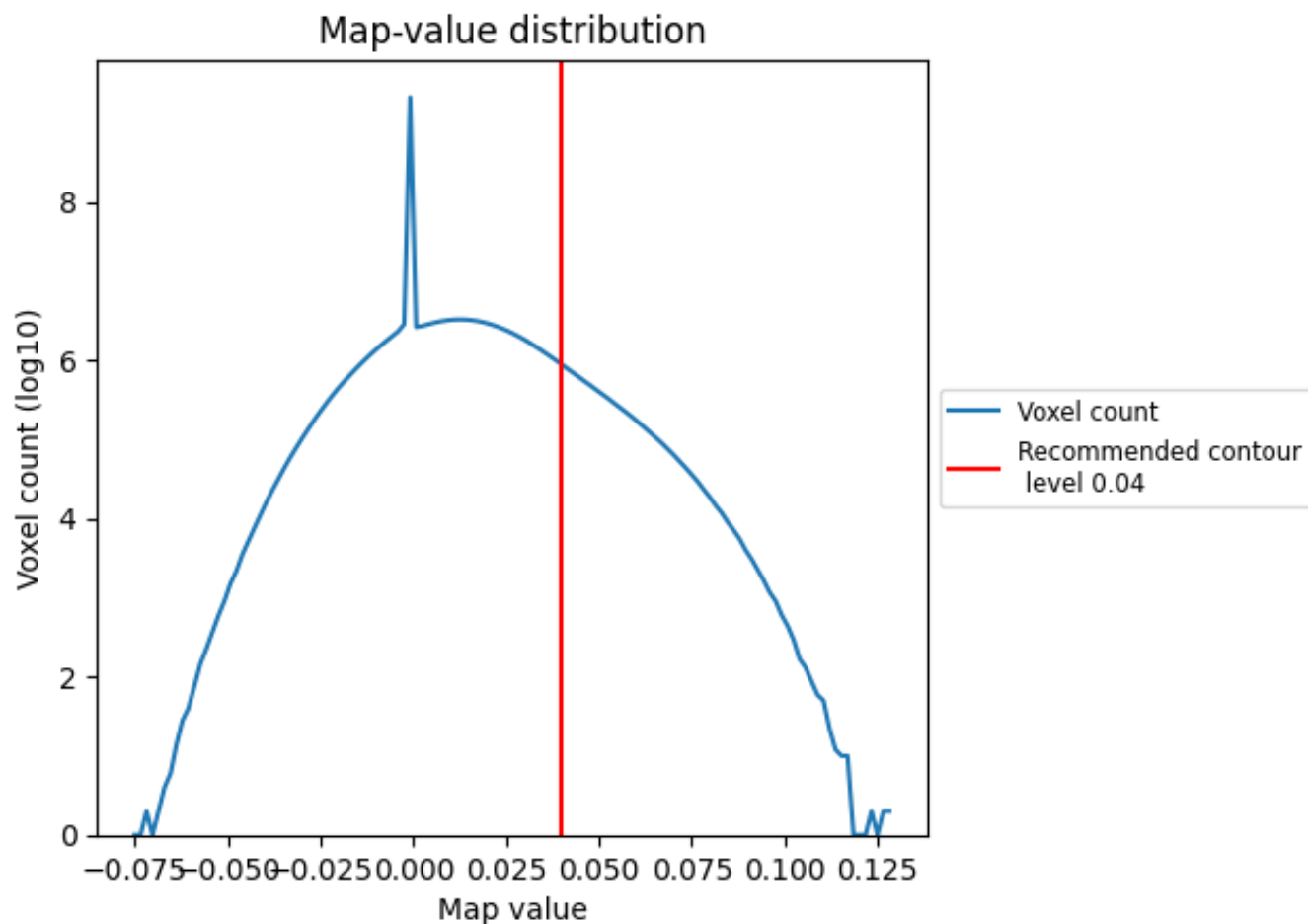
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

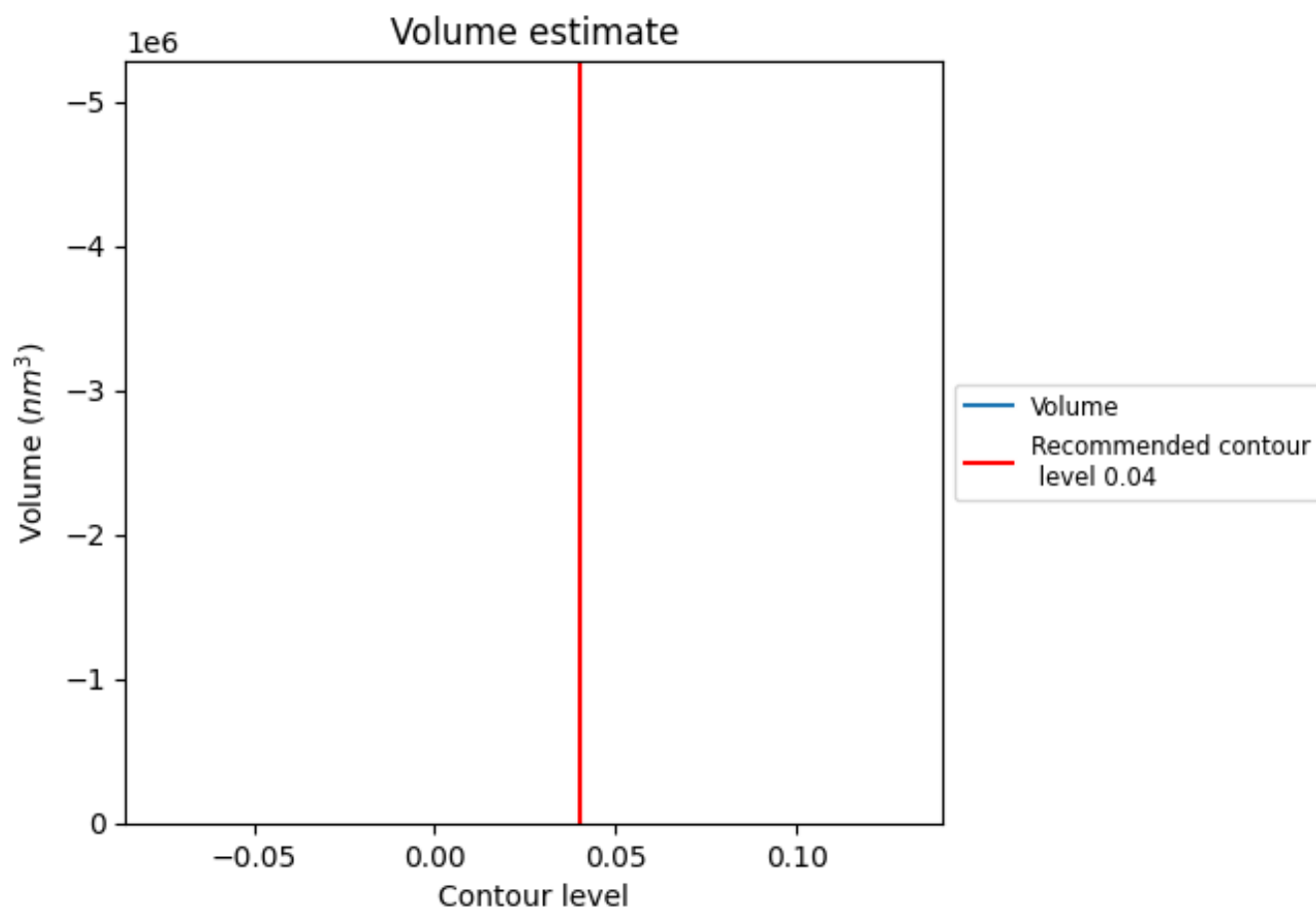
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

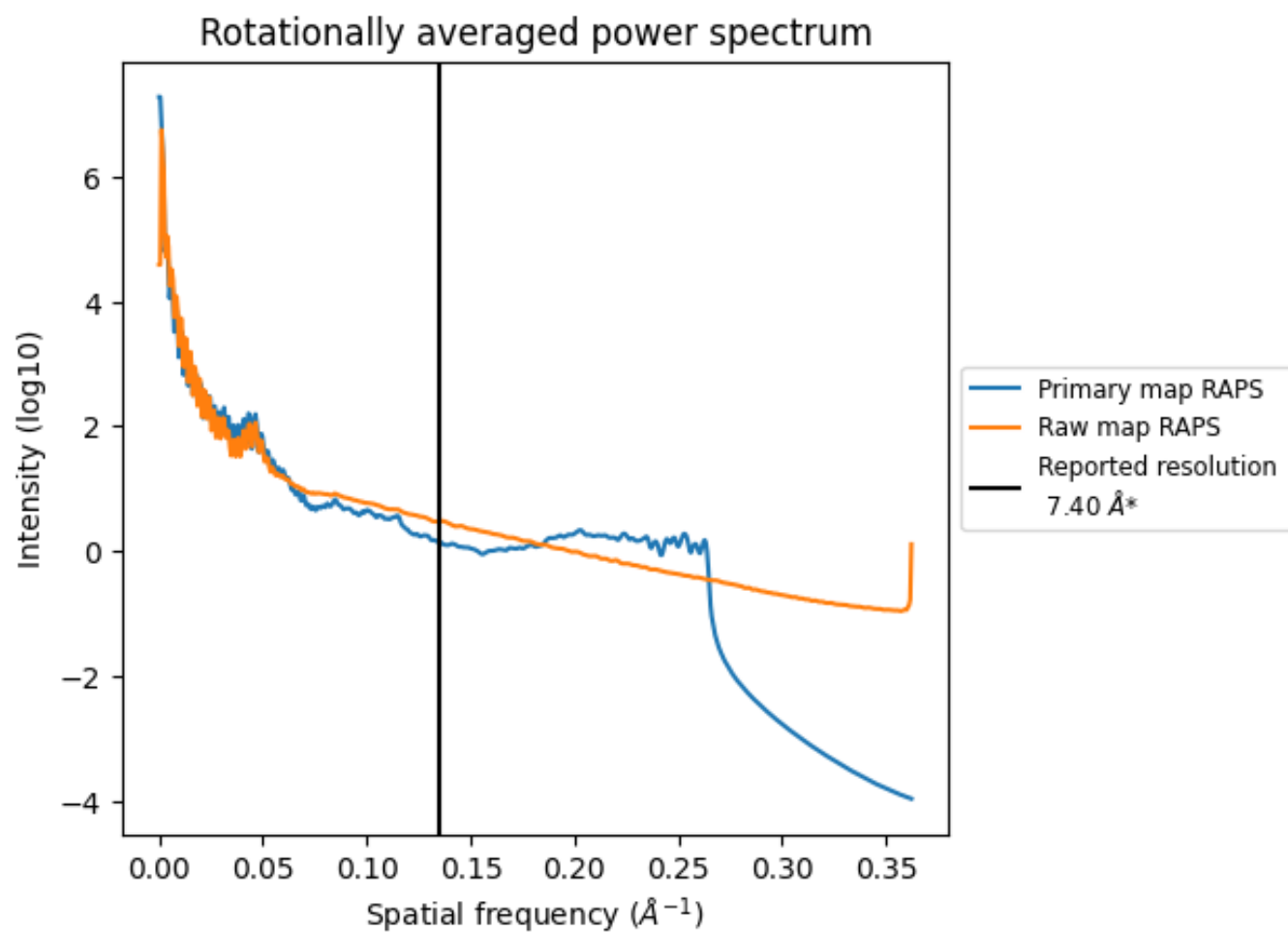
7.2 Volume estimate [i](#)



The volume at the recommended contour level is -11269269 nm³; this corresponds to an approximate mass of -10179824 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

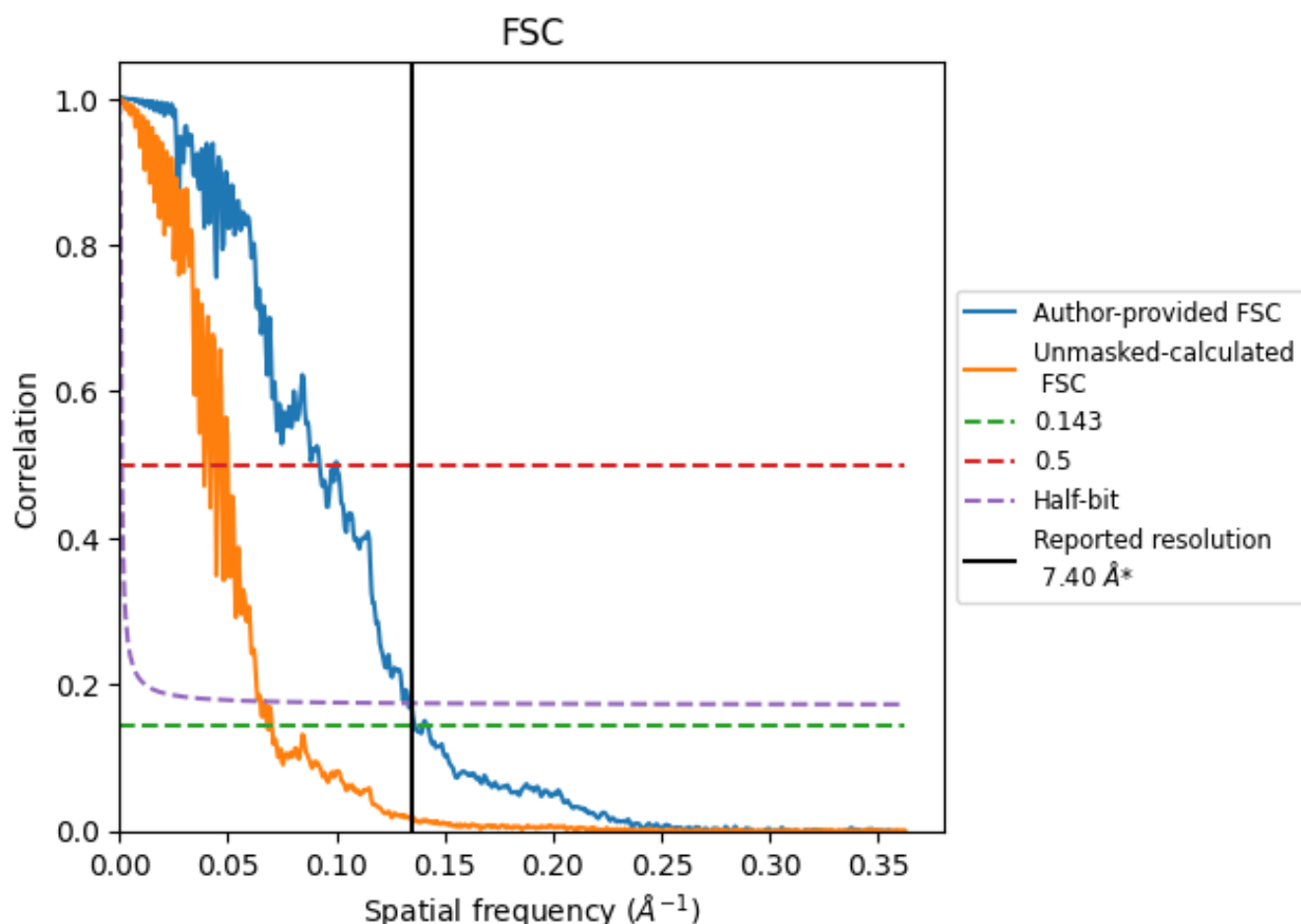


*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.33	10.83	7.50
Unmasked-calculated*	14.66	25.64	15.38

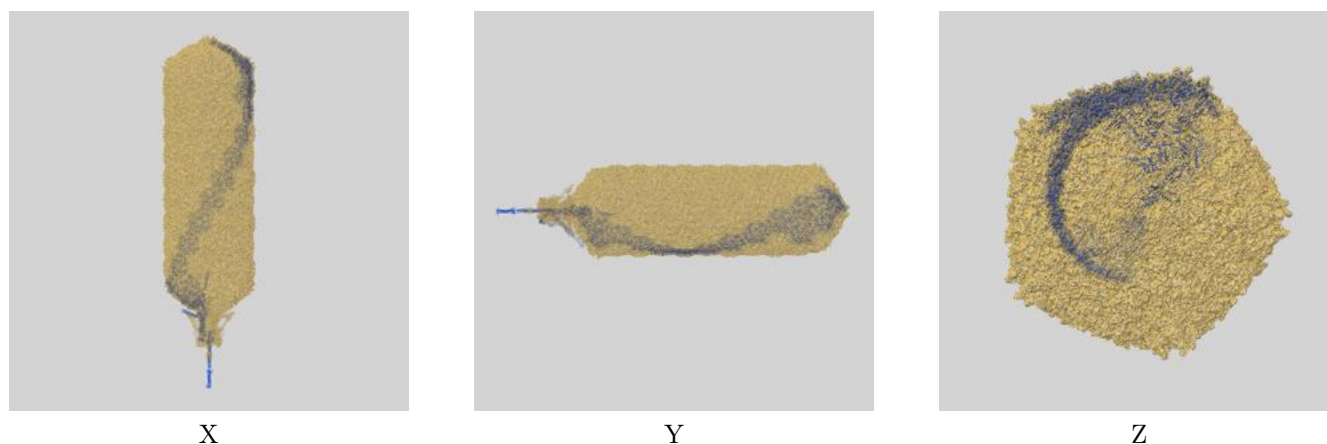
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 14.66 differs from the reported value 7.4 by more than 10 %

9 Map-model fit [i](#)

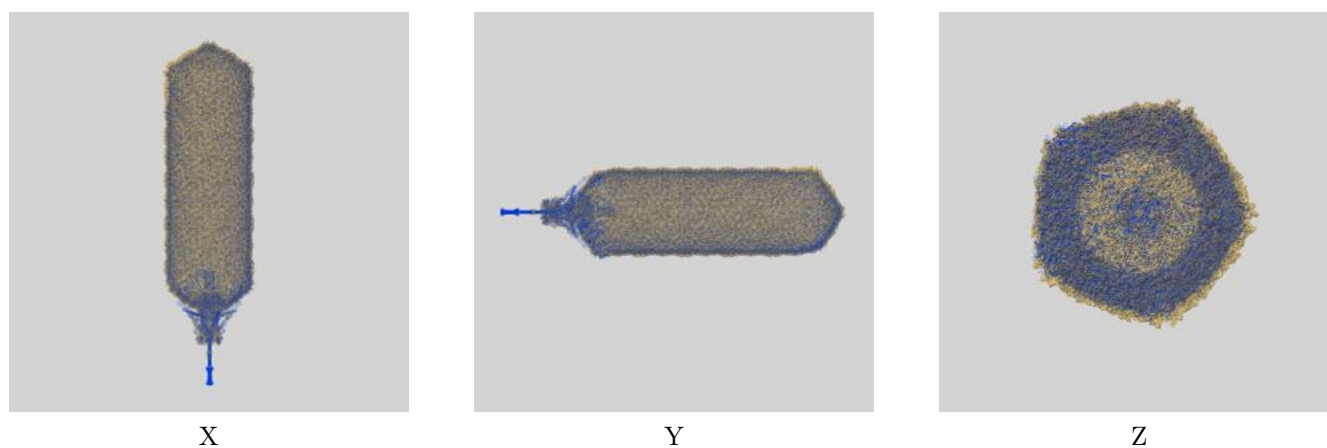
This section contains information regarding the fit between EMDB map EMD-14492 and PDB model 7Z4B. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



9.1.2 Map-model assembly overlay [i](#)



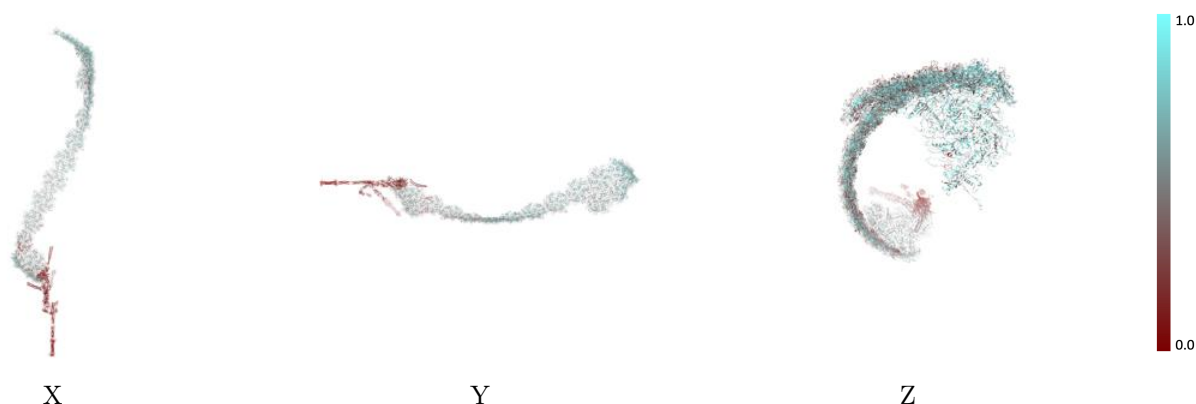
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



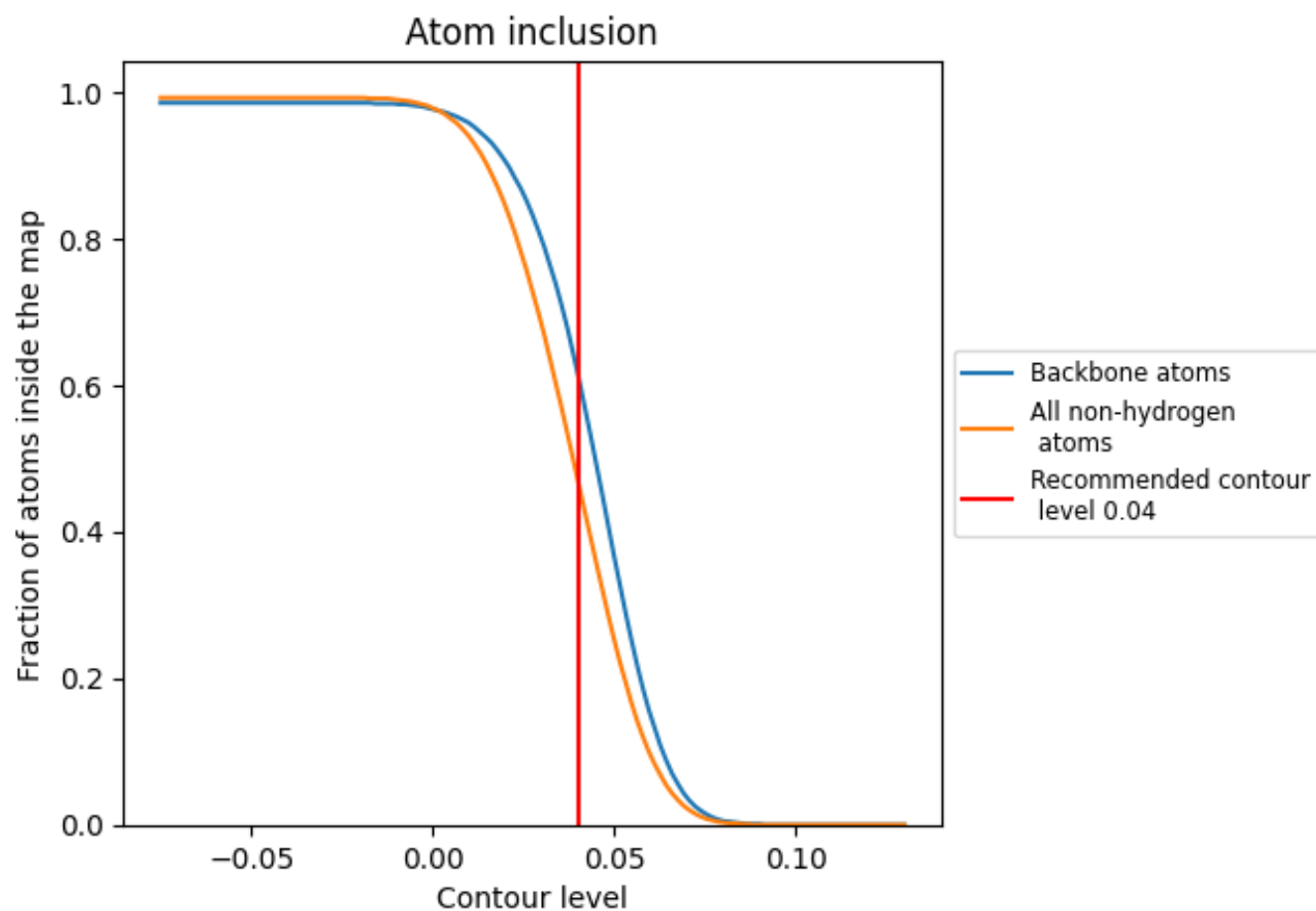
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 47% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4680	 0.1940
AA	 0.5570	 0.2700
AB	 0.5490	 0.2600
AC	 0.5700	 0.2630
AD	 0.5310	 0.2520
AE	 0.5260	 0.2670
AF	 0.5340	 0.2620
AG	 0.5420	 0.2370
AH	 0.5500	 0.2540
AI	 0.5500	 0.2470
AJ	 0.5470	 0.2380
AK	 0.5350	 0.2540
AL	 0.5320	 0.2460
AM	 0.5670	 0.2400
AN	 0.5410	 0.2570
AO	 0.5530	 0.2440
AP	 0.5030	 0.2270
AQ	 0.5330	 0.2620
AR	 0.5430	 0.2470
AS	 0.5190	 0.2230
AT	 0.5390	 0.2620
AU	 0.5230	 0.2280
AV	 0.5450	 0.2460
AW	 0.5180	 0.2690
AX	 0.5360	 0.2510
AY	 0.4120	 0.2240
AZ	 0.4590	 0.2310
BA	 0.4440	 0.2390
BB	 0.4900	 0.2560
BC	 0.5190	 0.2480
BD	 0.5220	 0.2500
BE	 0.5380	 0.2600
BF	 0.2710	 0.0450
BG	 0.5040	 0.2510
BH	 0.4960	 0.2480





































































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Chain	Atom inclusion	Q-score
BI	 0.4060	 0.0790
BJ	 0.4810	 0.2490
BK	 0.5570	 0.2580
BL	 0.3870	 0.1680
BM	 0.4870	 0.2550
BN	 0.5100	 0.2570
BO	 0.4720	 0.2200
BP	 0.4950	 0.2580
BQ	 0.4640	 0.2360
BR	 0.4430	 0.1820
BS	 0.5260	 0.2500
BT	 0.5000	 0.2690
BU	 0.3650	 0.0680
BV	 0.5260	 0.2660
BW	 0.5470	 0.1400
BX	 0.5990	 0.1870
BY	 0.5940	 0.1890
BZ	 0.6100	 0.1870
CA	 0.6000	 0.1820
CB	 0.6030	 0.2020
CC	 0.6020	 0.1780
CD	 0.5460	 0.1730
CE	 0.5790	 0.1950
CF	 0.5410	 0.2090
CG	 0.5170	 0.1720
CH	 0.5770	 0.2020
CI	 0.5850	 0.2030
CJ	 0.5680	 0.2190
CK	 0.4780	 0.1710
CL	 0.5040	 0.1870
CM	 0.6060	 0.2050
CN	 0.5140	 0.2080
CO	 0.5040	 0.1970
CP	 0.5170	 0.1650
CQ	 0.6090	 0.2020
CR	 0.4860	 0.1950
CS	 0.4840	 0.1760
CT	 0.5910	 0.1860
CU	 0.6060	 0.1940
CV	 0.5270	 0.2090
CW	 0.4620	 0.1900
CX	 0.5980	 0.2030

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Chain	Atom inclusion	Q-score
CY	 0.5470	 0.1940
CZ	 0.5040	 0.1900
DA	 0.4870	 0.1930
DB	 0.4230	 0.1710
DC	 0.4080	 0.1790
DD	 0.4620	 0.1710
DE	 0.4770	 0.1880
DF	 0.4890	 0.1940
DG	 0.4750	 0.1930
DH	 0.5140	 0.1840
DI	 0.4780	 0.1910
DJ	 0.5320	 0.1800
DK	 0.4330	 0.1770
DL	 0.5450	 0.1930
DM	 0.4910	 0.1860
DN	 0.5140	 0.1900
DO	 0.5030	 0.2040
DP	 0.5140	 0.1780
DQ	 0.4330	 0.1780
DR	 0.0330	 0.0210
DS	 0.0370	 0.0130
DT	 0.0570	 0.0350
DU	 0.1420	 0.0390
DV	 0.0950	 0.0290
DW	 0.0670	 0.0320
DX	 0.1080	 0.0360
DY	 0.0370	 0.0310
DZ	 0.0450	 0.0160
EA	 0.0540	 0.0050
EB	 0.0360	 0.0050
EC	 0.0220	 -0.0070
ED	 0.0830	 0.0630
EE	 0.0900	 0.0770