



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:25 AM UTC

PDB ID : 7BSI / pdb_00007bsi
EMDB ID : EMD-30162
Title : Epstein-Barr virus, one asymmetric unit structure of the icosahedral tegumented capsid
Authors : Li, Z.; Yu, X.
Deposited on : 2020-03-30
Resolution : 4.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

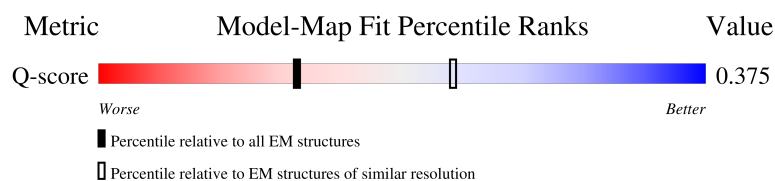
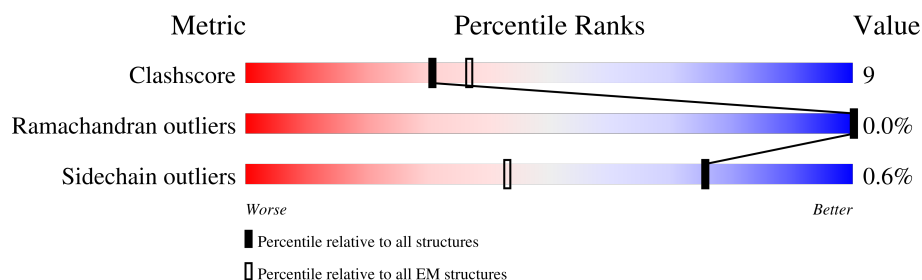
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	6458 (3.60 - 4.60)

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

Mol	Chain	Length	Quality of chain
1	0	176	31% 31% 10% 58%
1	1	176	34% 30% 11% 58%
1	G	176	31% 34% 10% 56%
1	H	176	28% 31% 11% 58%

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Mol	Chain	Length	Quality of chain
1	I	176	
1	J	176	
1	K	176	
1	L	176	
1	P	176	
1	Q	176	
1	R	176	
1	X	176	
1	Y	176	
1	Z	176	
1	m	176	
1	y	176	
2	A	1381	
2	B	1381	
2	C	1381	
2	D	1381	
2	E	1381	
2	F	1381	
2	M	1381	
2	N	1381	
2	O	1381	
2	S	1381	
2	T	1381	
2	U	1381	
2	V	1381	

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Mol	Chain	Length	Quality of chain
2	k	1381	
2	l	1381	
2	x	1381	
3	5	364	
3	a	364	
3	b	364	
3	e	364	
3	h	364	
4	6	301	
4	7	301	
4	8	301	
4	9	301	
4	c	301	
4	d	301	
4	f	301	
4	g	301	
4	i	301	
4	j	301	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 214157 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 Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	71	Total 600	C 381	N 111	O 107	S 1	0	0
1	Y	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	Z	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	P	77	Total 650	C 411	N 122	O 116	S 1	0	0
1	Q	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	R	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	0	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	1	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	X	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	G	77	Total 650	C 411	N 122	O 116	S 1	0	0
1	H	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	I	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	J	77	Total 650	C 411	N 122	O 116	S 1	0	0
1	K	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	L	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	y	74	Total 621	C 394	N 114	O 112	S 1	0	0

- Molecule 2 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	S	1333	Total	C	N	O	S	0	0
			10491	6665	1820	1946	60		
2	T	1323	Total	C	N	O	S	0	0
			10398	6600	1808	1929	61		
2	l	1251	Total	C	N	O	S	0	0
			9883	6283	1717	1824	59		
2	M	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	N	1370	Total	C	N	O	S	0	0
			10761	6828	1871	2001	61		
2	O	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	U	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	V	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	k	1346	Total	C	N	O	S	0	0
			10572	6712	1835	1965	60		
2	A	1370	Total	C	N	O	S	0	0
			10761	6828	1871	2001	61		
2	B	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	C	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	D	1354	Total	C	N	O	S	0	0
			10634	6750	1845	1979	60		
2	E	1370	Total	C	N	O	S	0	0
			10761	6828	1871	2001	61		
2	F	1342	Total	C	N	O	S	0	0
			10546	6694	1831	1961	60		
2	x	1325	Total	C	N	O	S	0	0
			10404	6607	1803	1935	59		

- Molecule 3 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	319	Total	C	N	O	S	0	0
			2505	1608	444	446	7		
3	5	311	Total	C	N	O	S	0	0
			2446	1568	435	436	7		
3	b	317	Total	C	N	O	S	0	0
			2490	1600	439	444	7		
3	h	321	Total	C	N	O	S	0	0
			2519	1616	446	450	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	319	Total	C	N	O	S	0	0
			2505	1609	441	448	7		

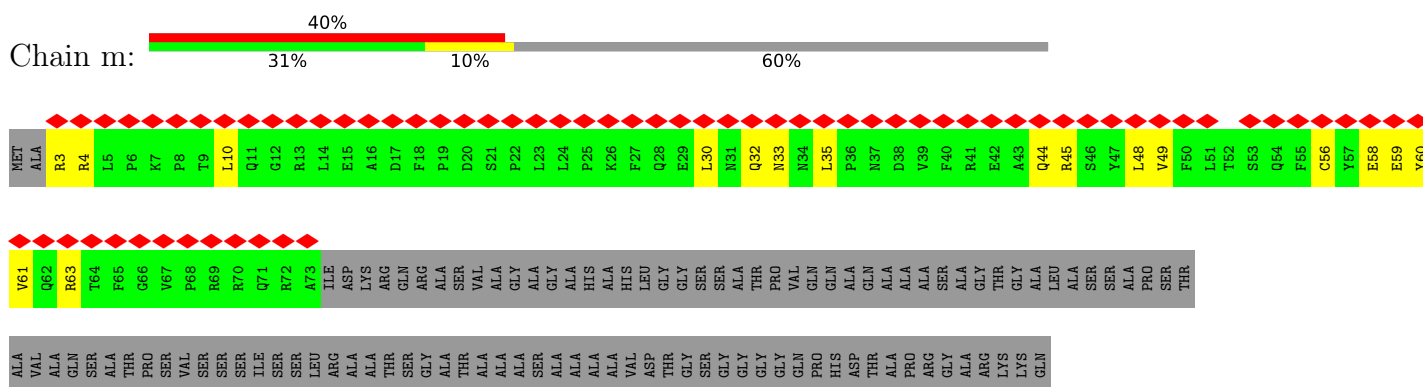
- Molecule 4 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	f	290	Total	C	N	O	S	0	0
			2279	1466	378	419	16		
4	g	292	Total	C	N	O	S	0	0
			2275	1461	373	423	18		
4	6	289	Total	C	N	O	S	0	0
			2272	1461	377	418	16		
4	7	279	Total	C	N	O	S	0	0
			2187	1406	358	405	18		
4	c	290	Total	C	N	O	S	0	0
			2279	1466	378	419	16		
4	d	292	Total	C	N	O	S	0	0
			2275	1461	373	423	18		
4	i	290	Total	C	N	O	S	0	0
			2279	1466	378	419	16		
4	j	292	Total	C	N	O	S	0	0
			2275	1461	373	423	18		
4	8	290	Total	C	N	O	S	0	0
			2279	1466	378	419	16		
4	9	292	Total	C	N	O	S	0	0
			2275	1461	373	423	18		

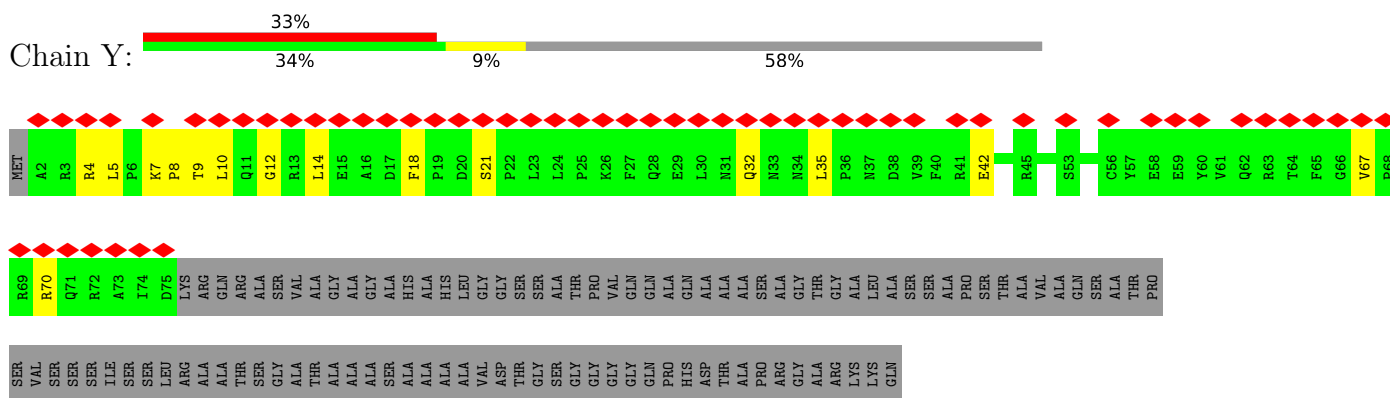
3 Residue-property plots

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.

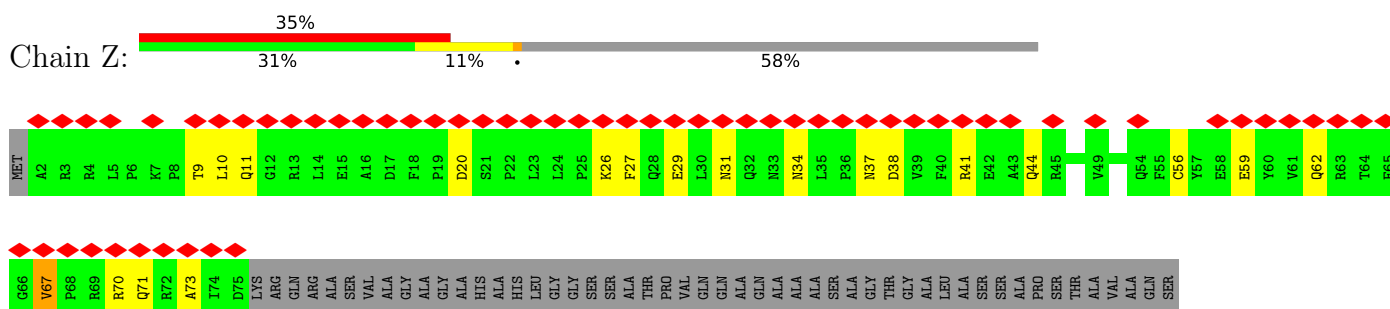
- Molecule 1: Small capsomere-interacting protein



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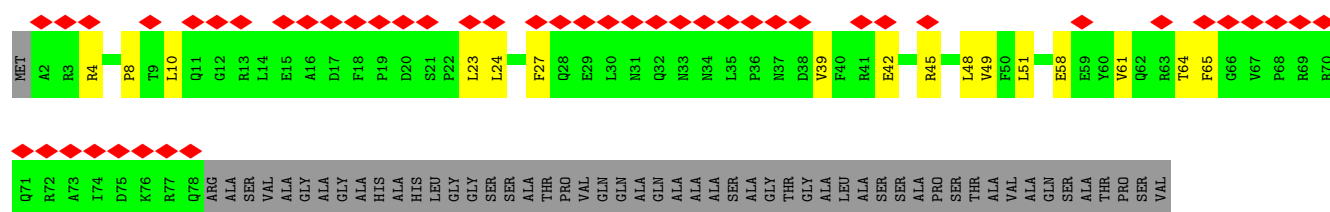
- Molecule 1: Small capsomere-interacting protein



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

• Molecule 1: Small capsomere-interacting protein

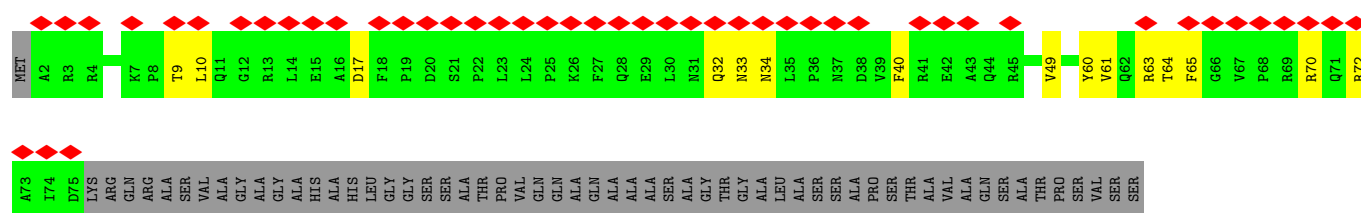
Chain P: 



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• Molecule 1: Small capsomere-interacting protein

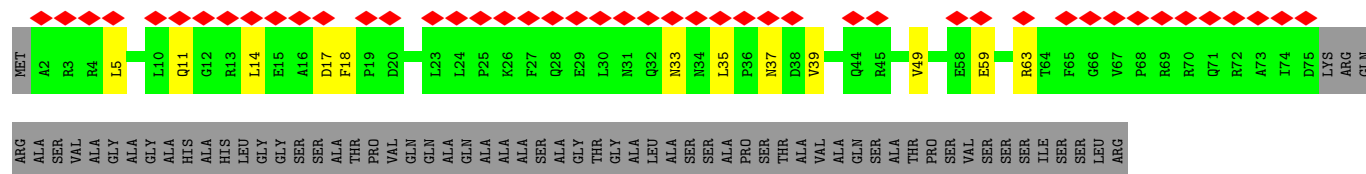
Chain Q: 



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

• Molecule 1: Small capsomere-interacting protein

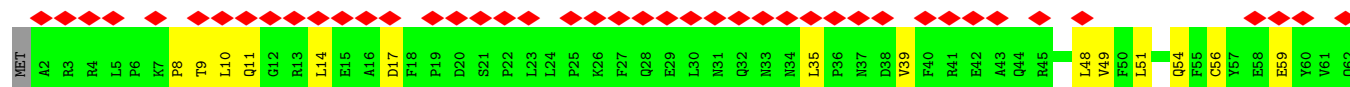
Chain R: 

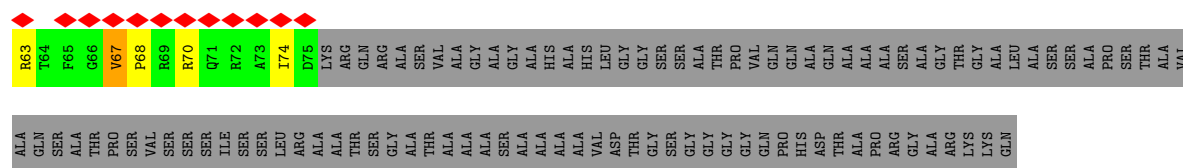


ARG ALA SER VAL GLY ALA GLY ALA HIS HIS LEU GLY GLY SER ASP THR GLY SER VAL GLY GLN GLN GLN PRO HIS ASP THR ALA ALA LYS GLN

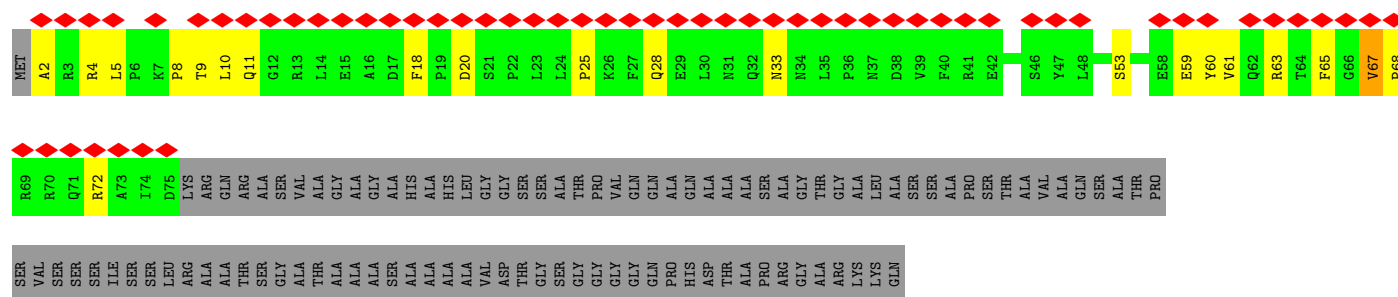
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Chain 0: 

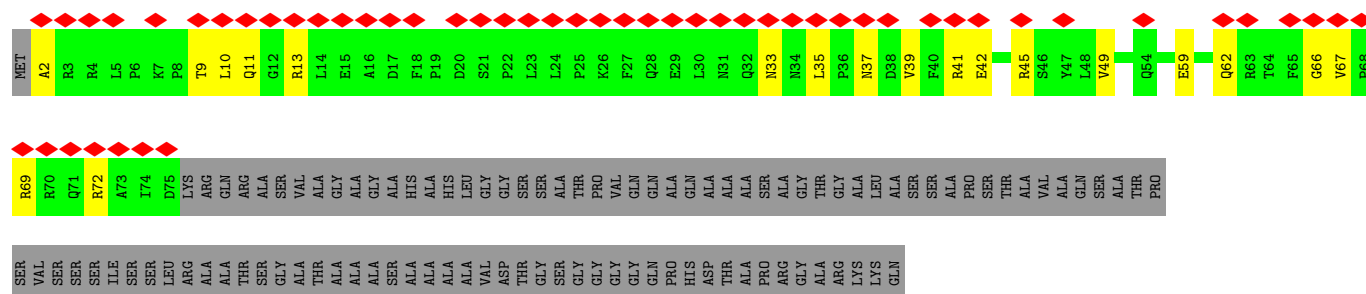
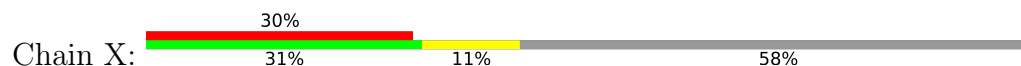




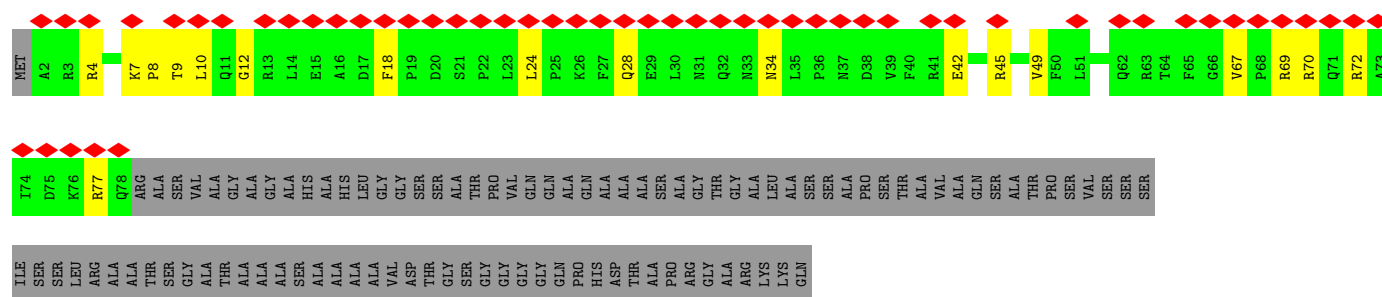
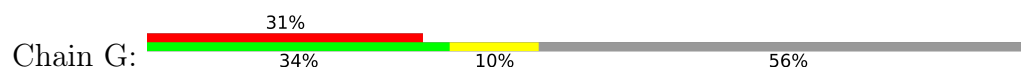
• Molecule 1: Small capsomere-interacting protein



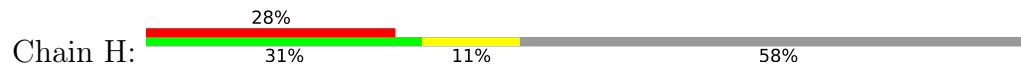
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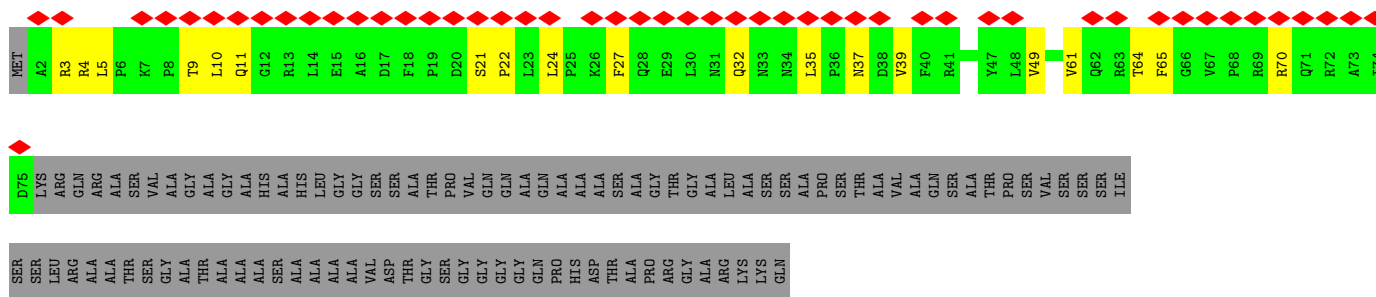


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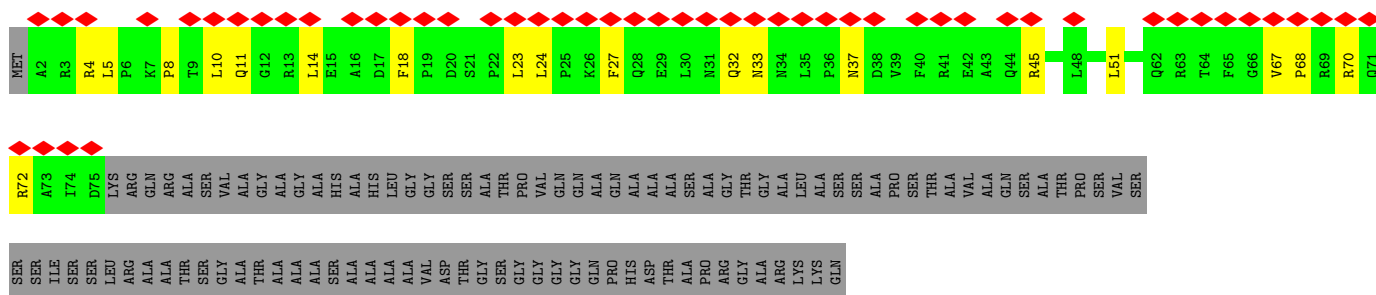


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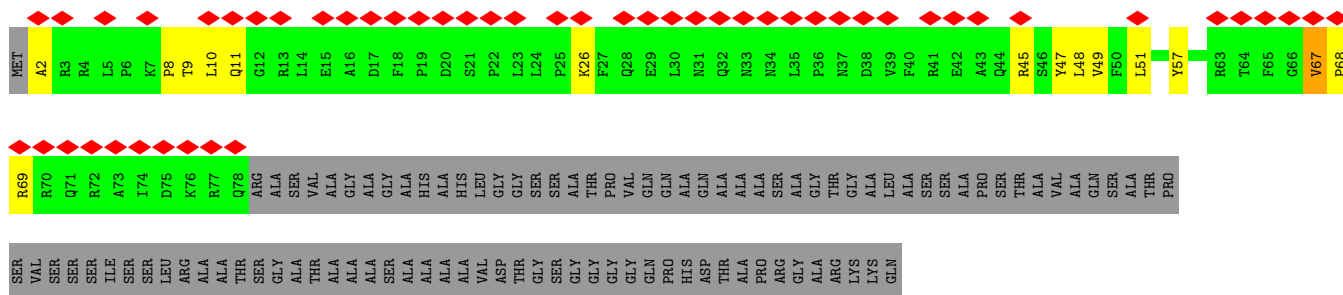
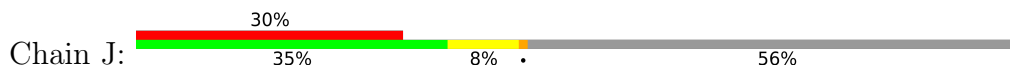




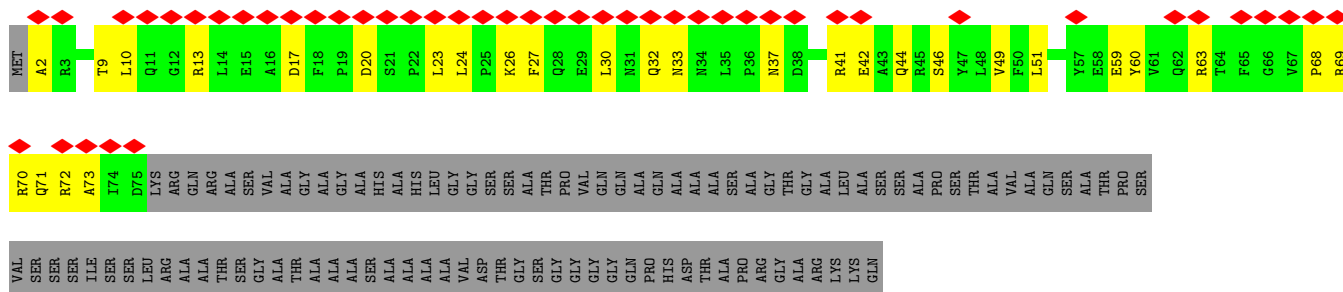
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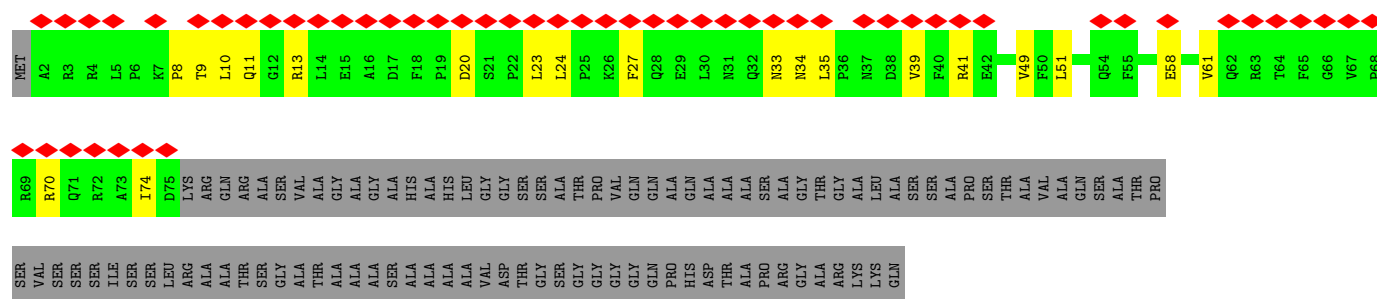
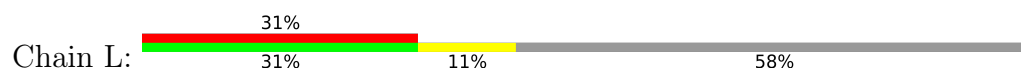
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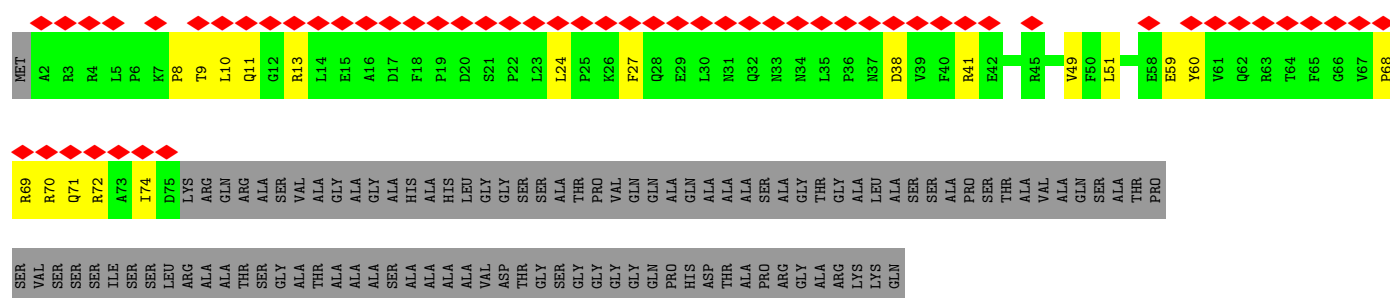
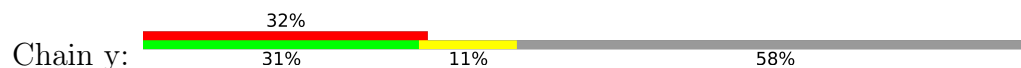
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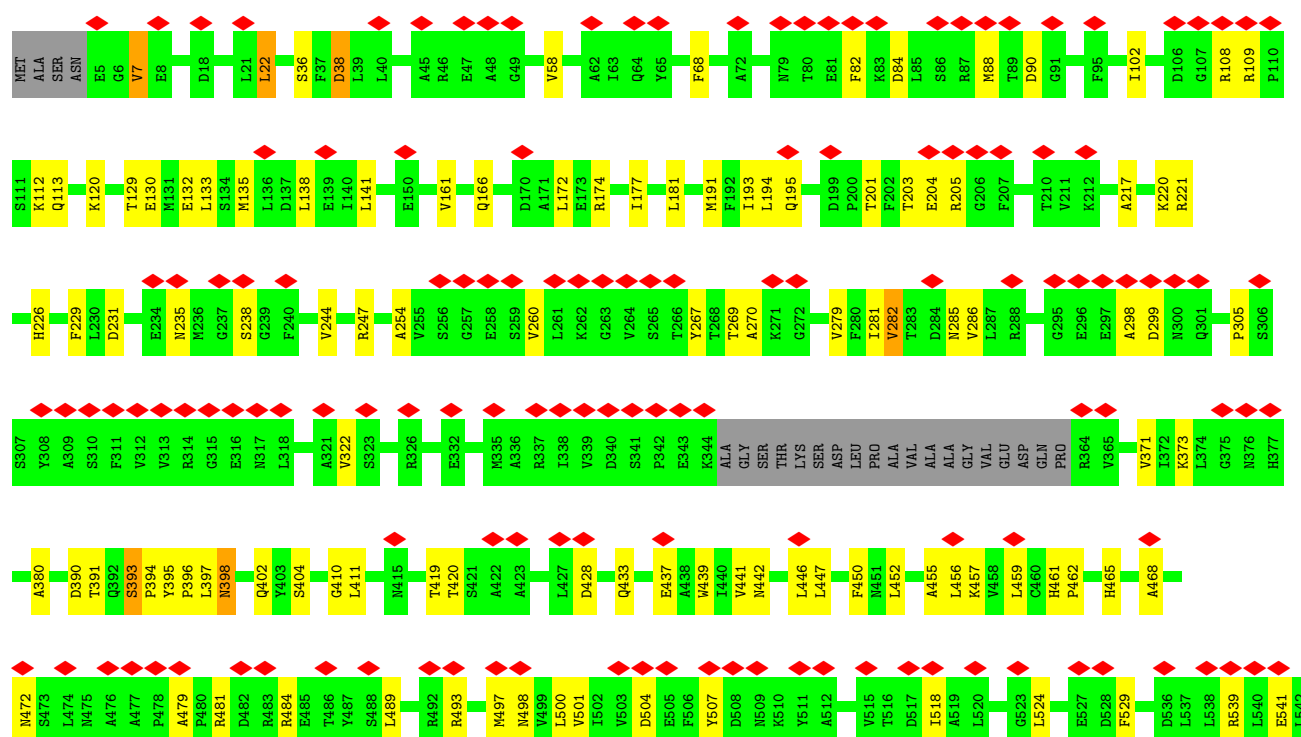
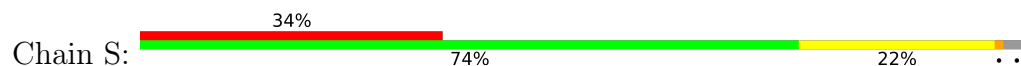
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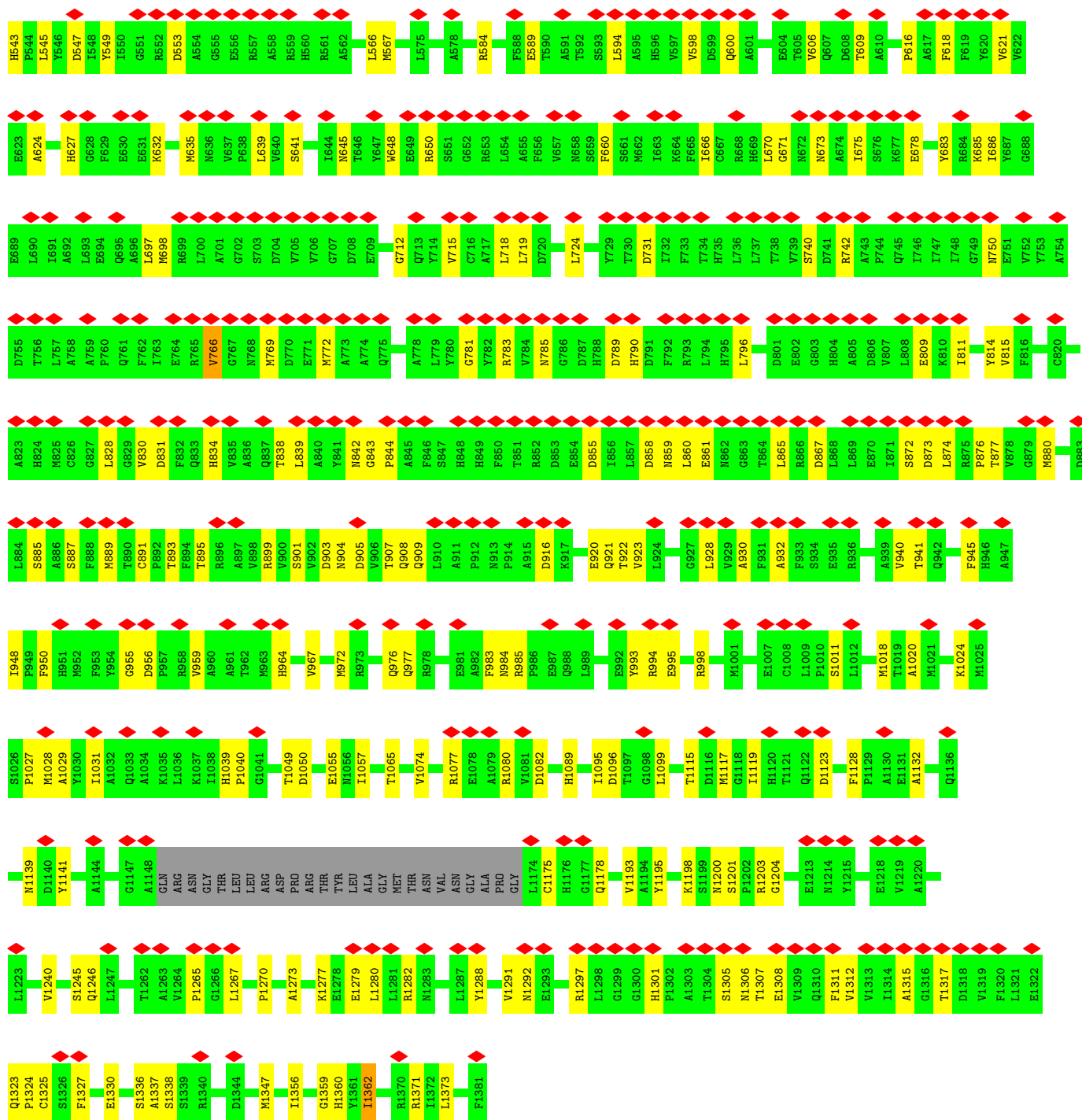


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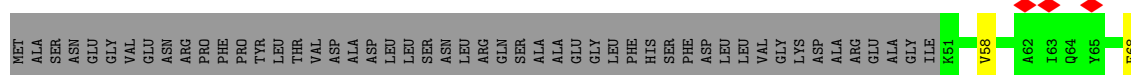


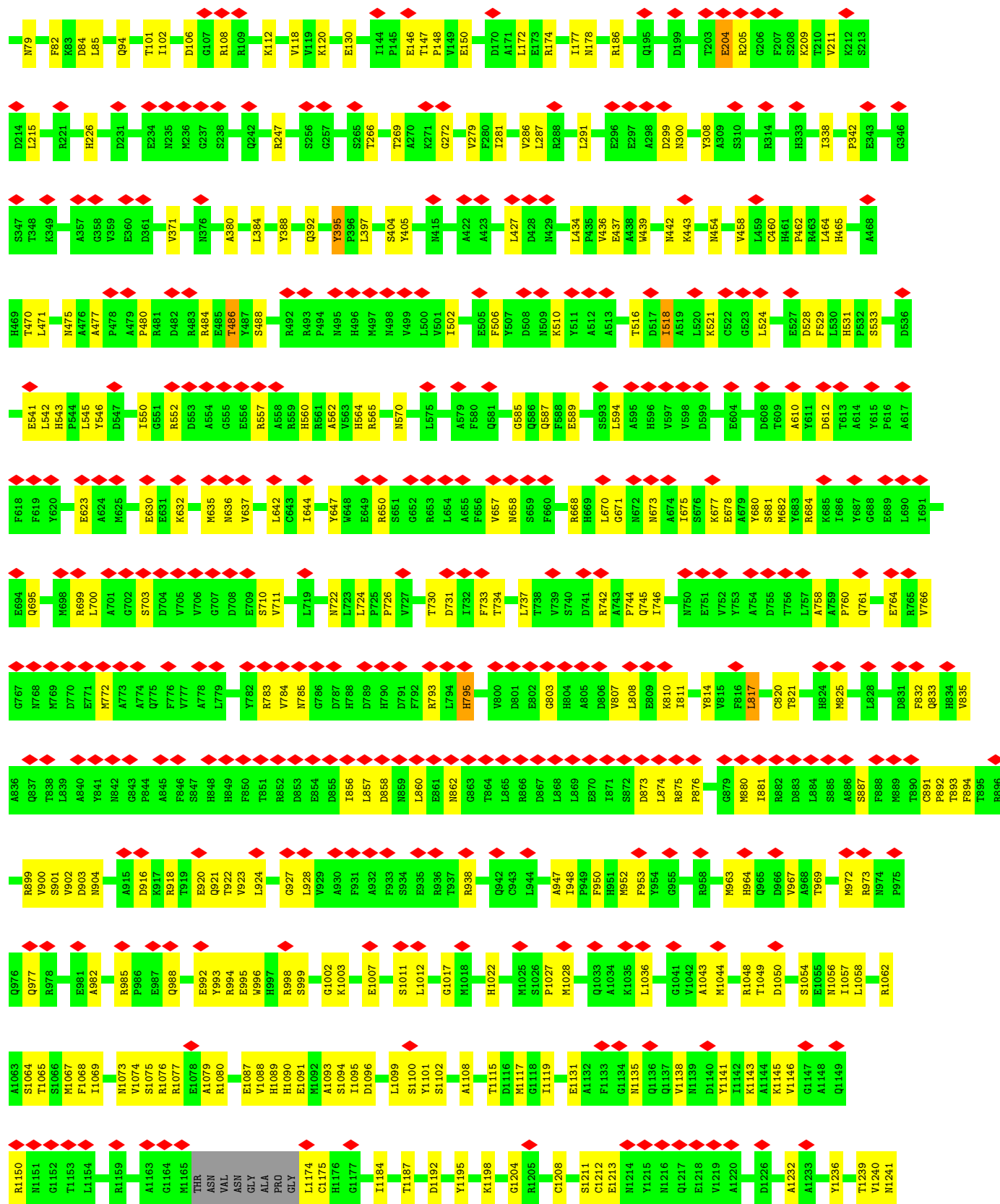
• Molecule 2: Major capsid protein

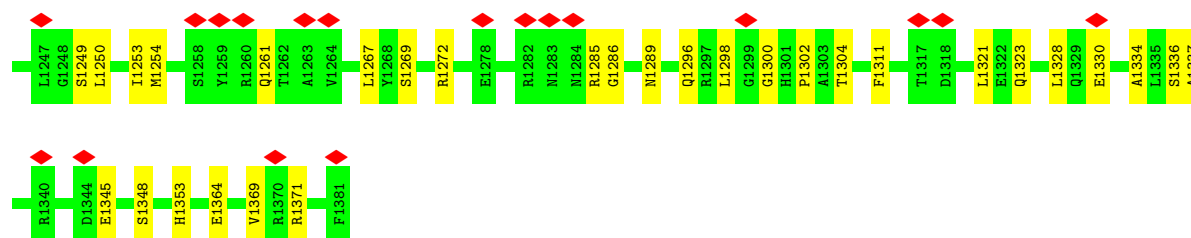




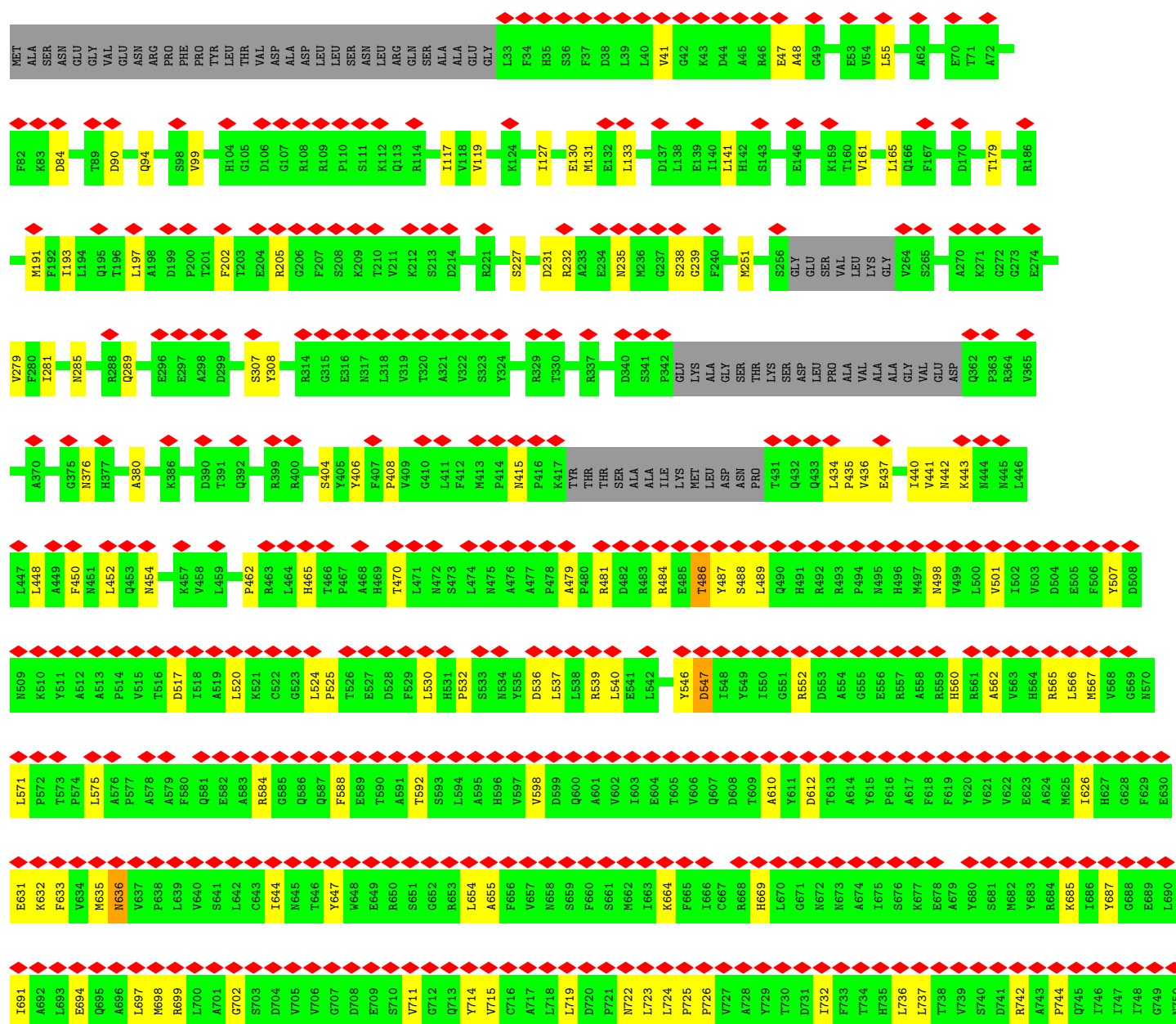
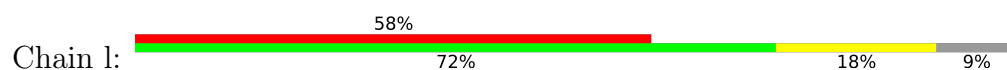
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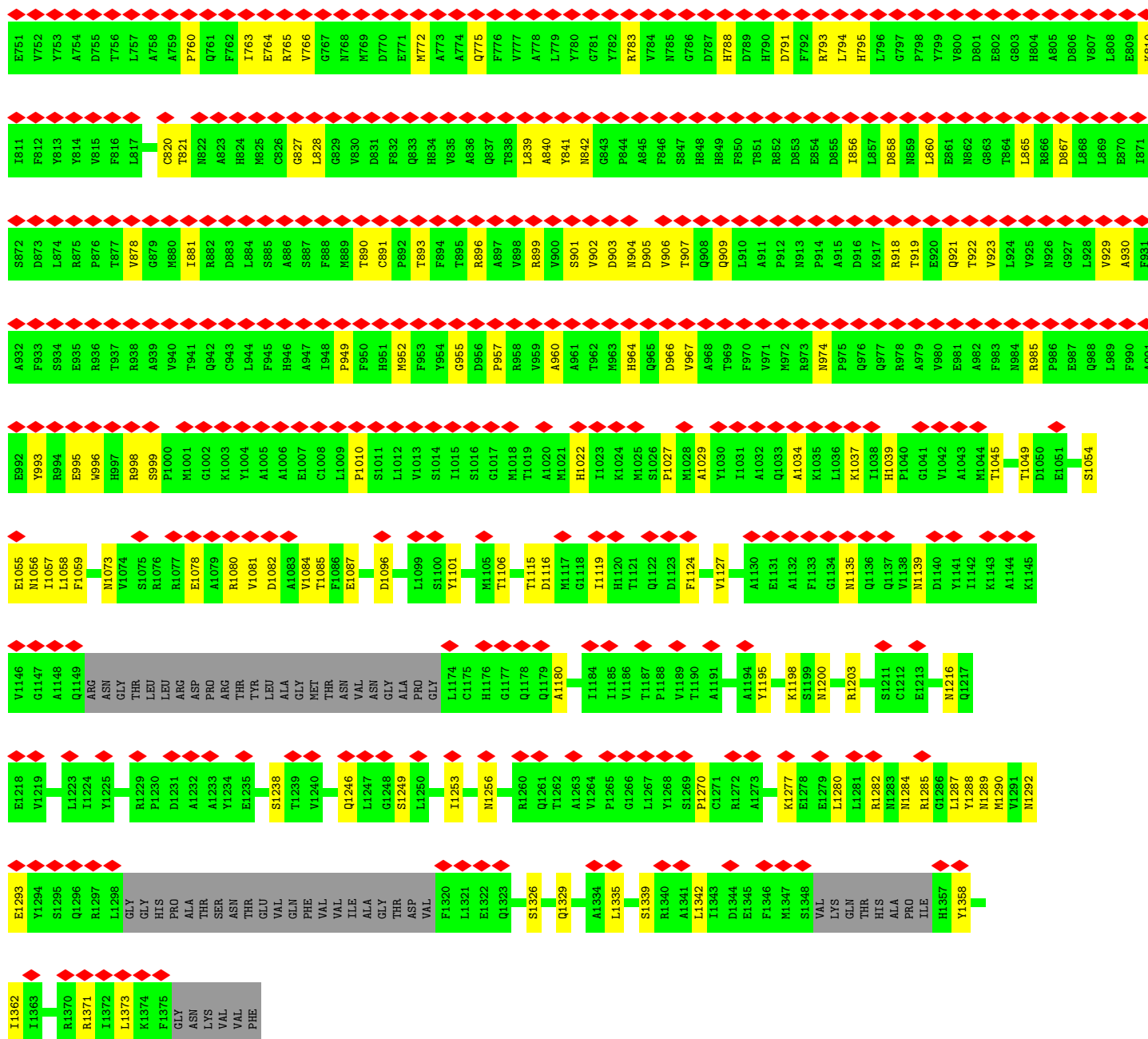




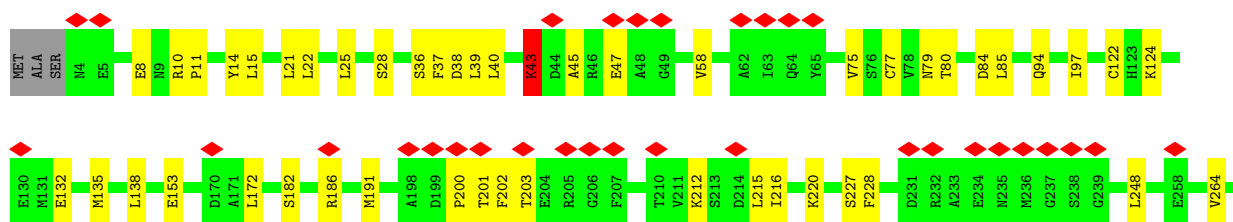
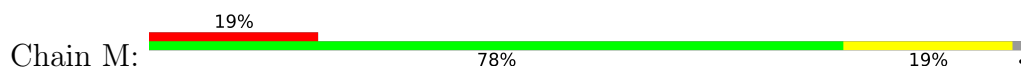


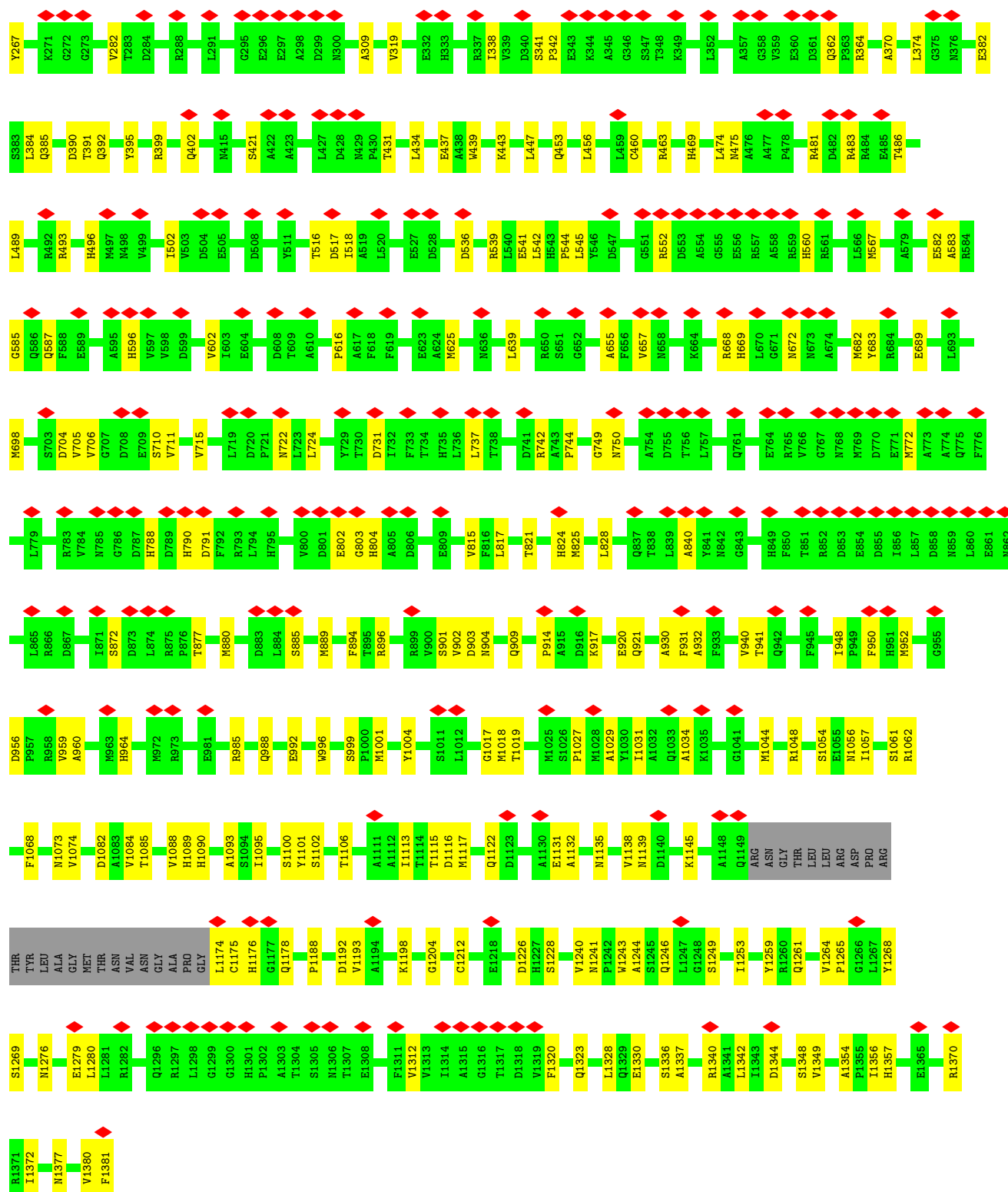
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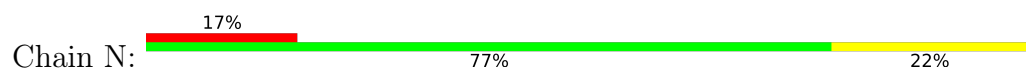


• Molecule 2: Major capsid protein

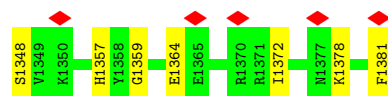




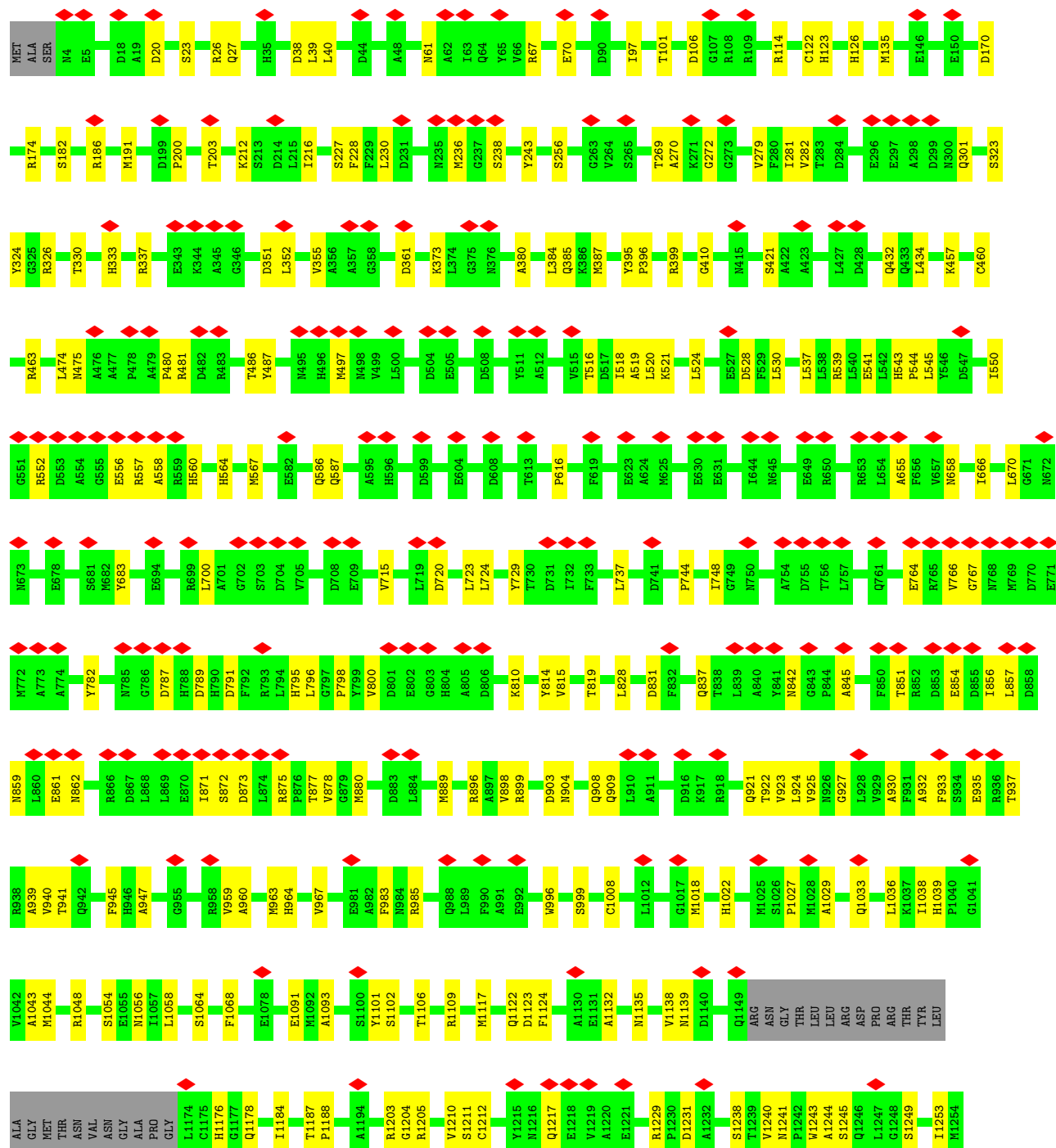
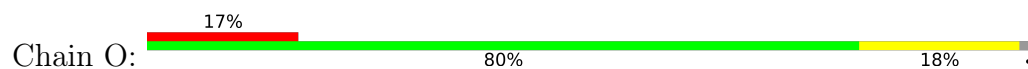
• Molecule 2: Major capsid protein





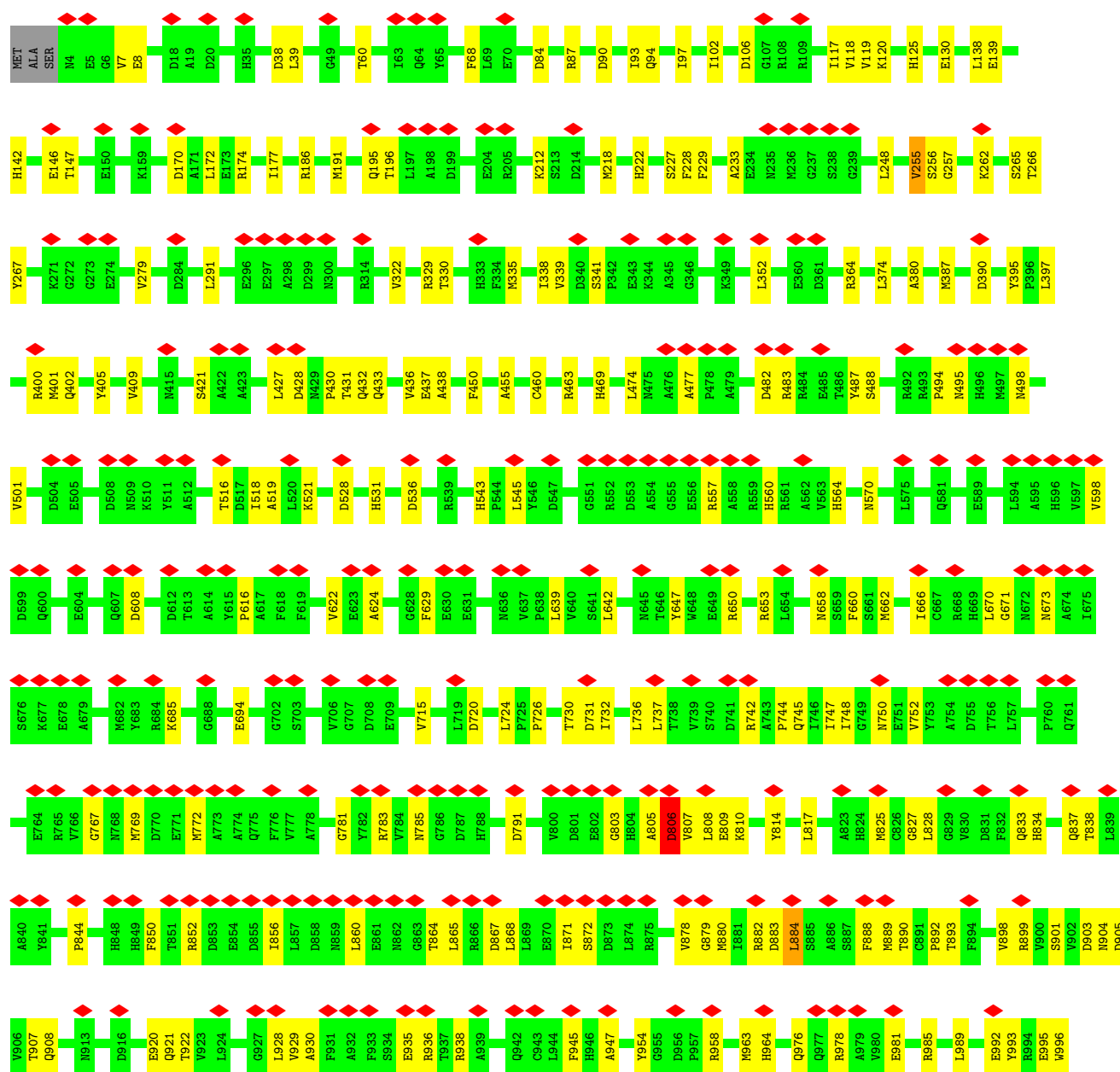
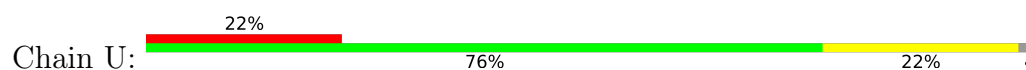


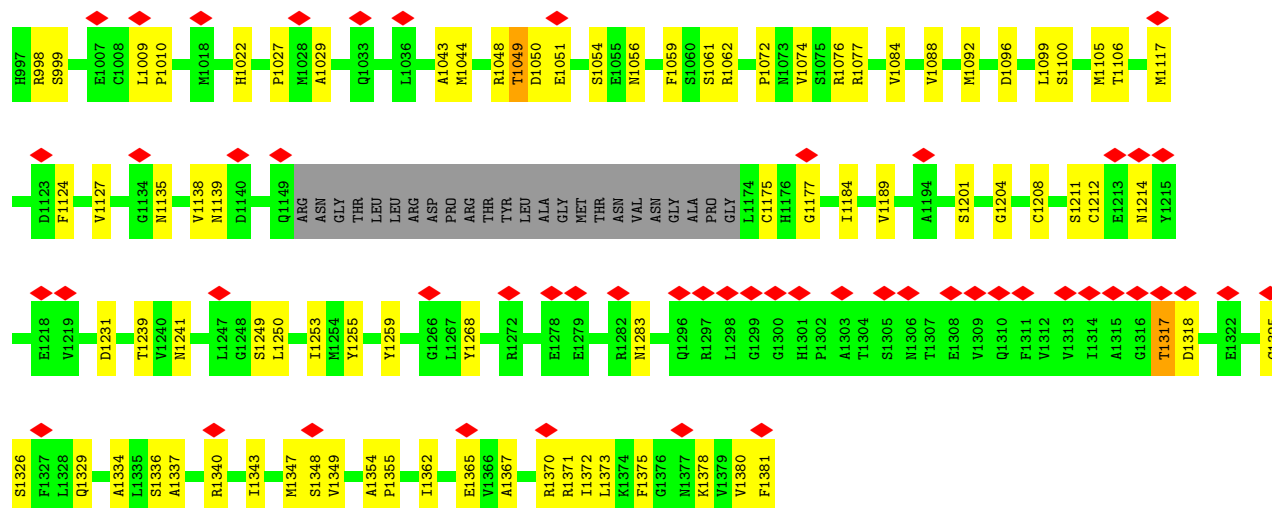
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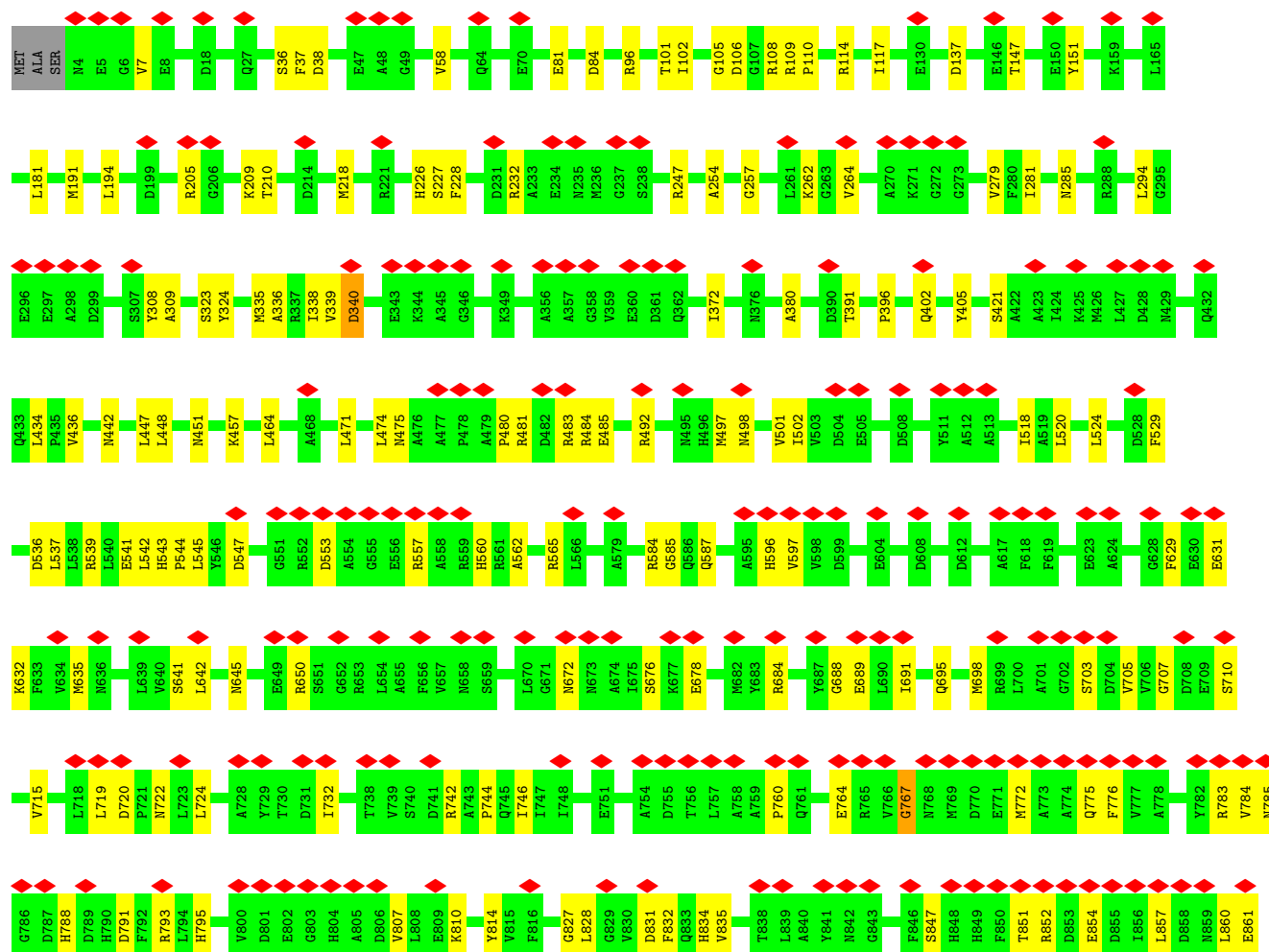
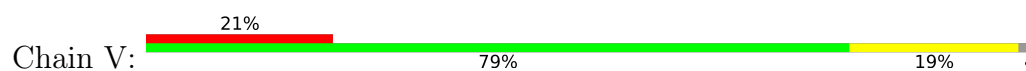


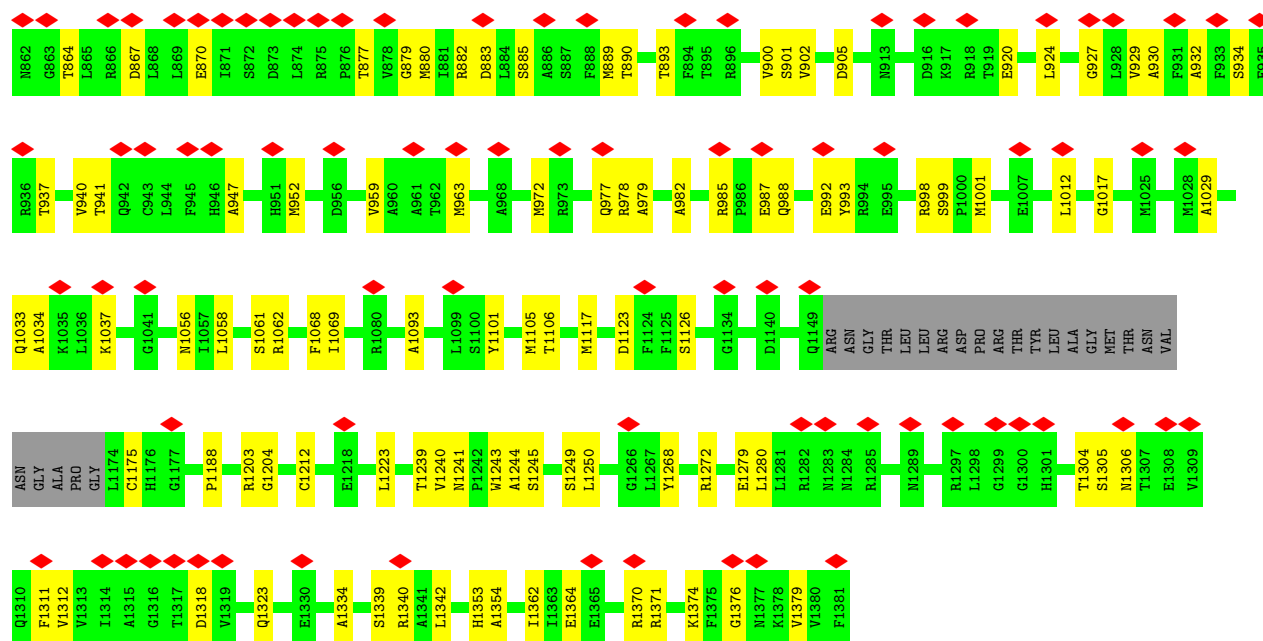
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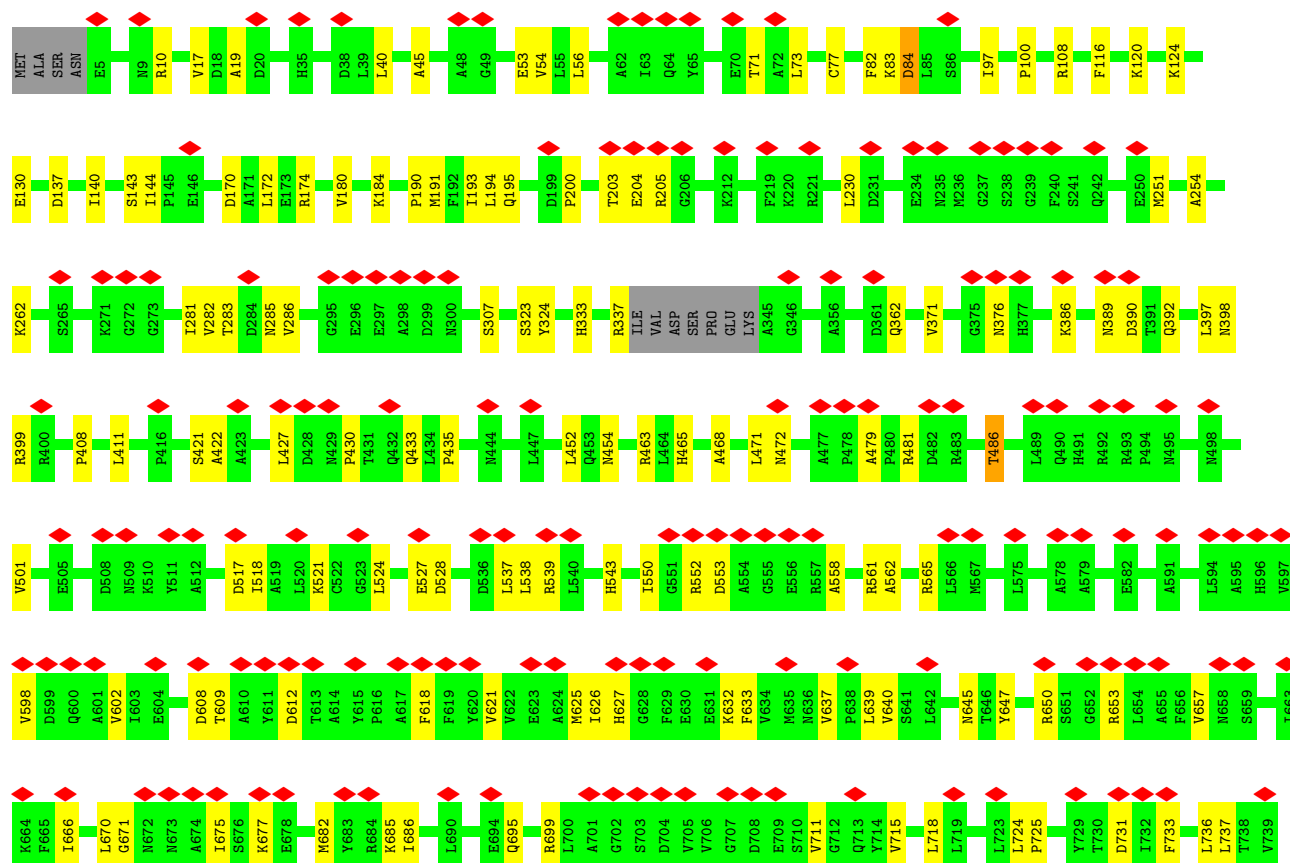
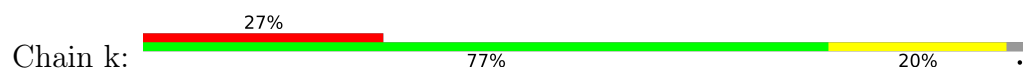


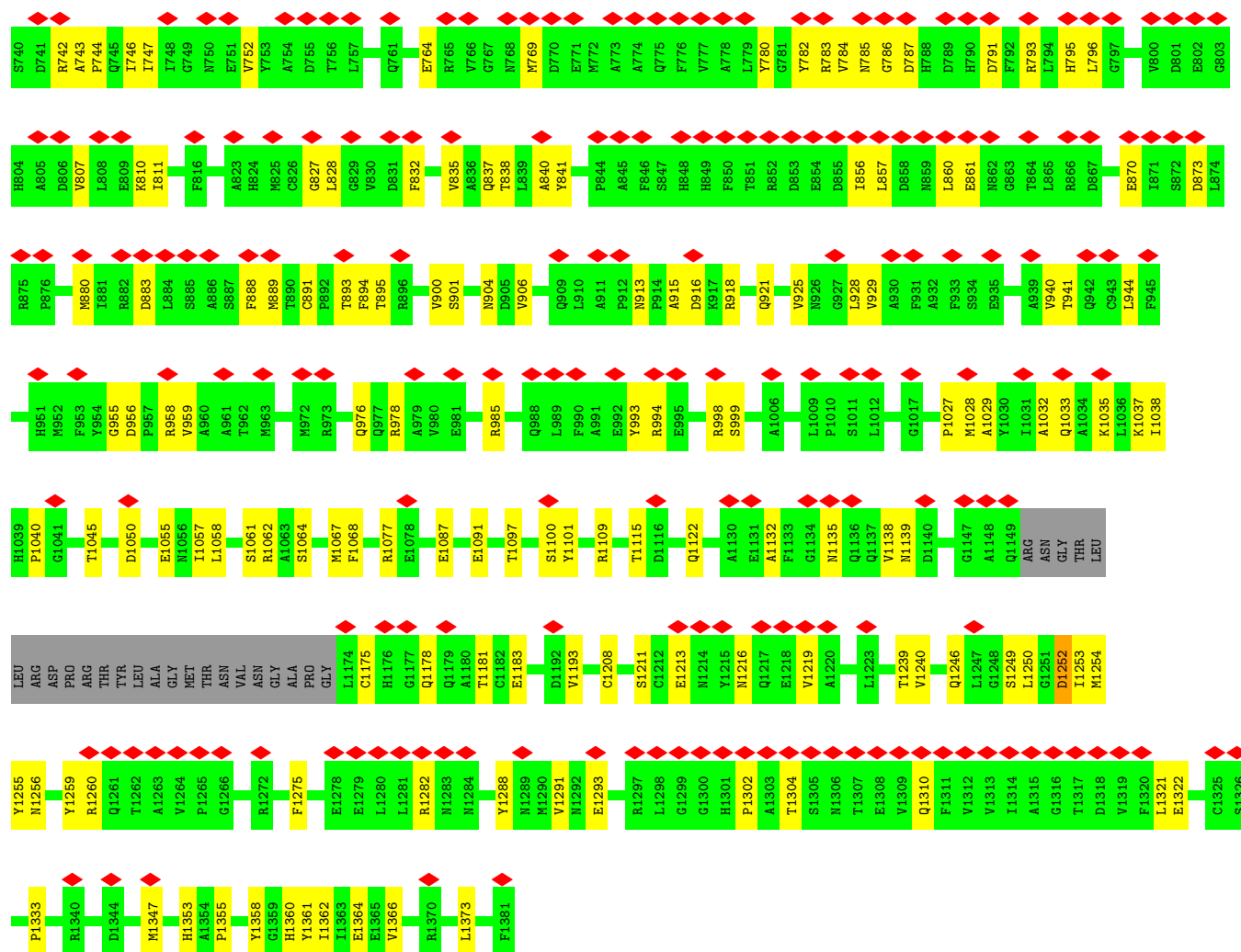
• Molecule 2: Major capsid protein



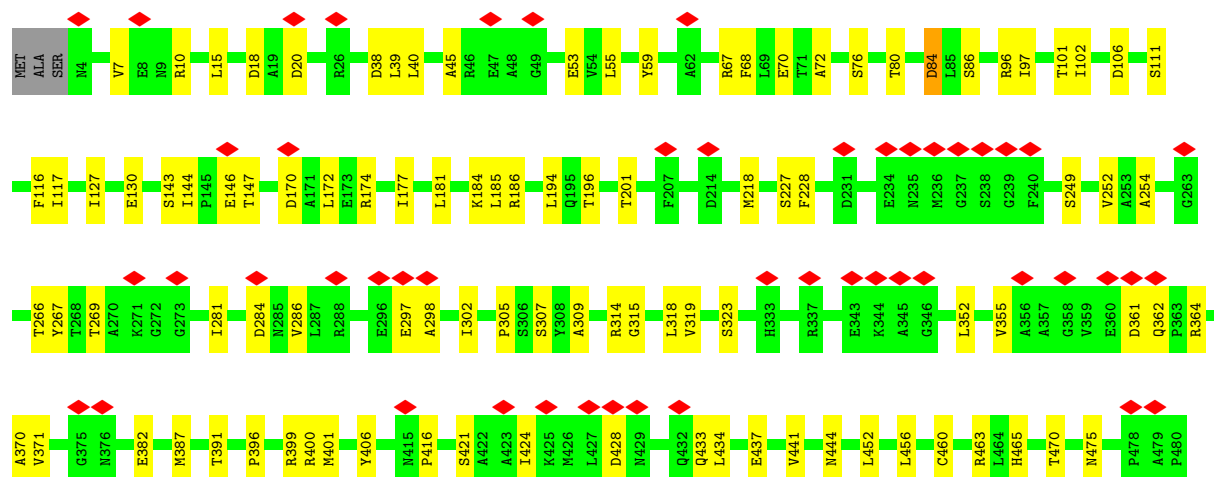
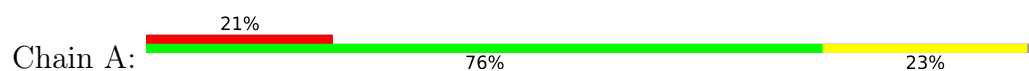


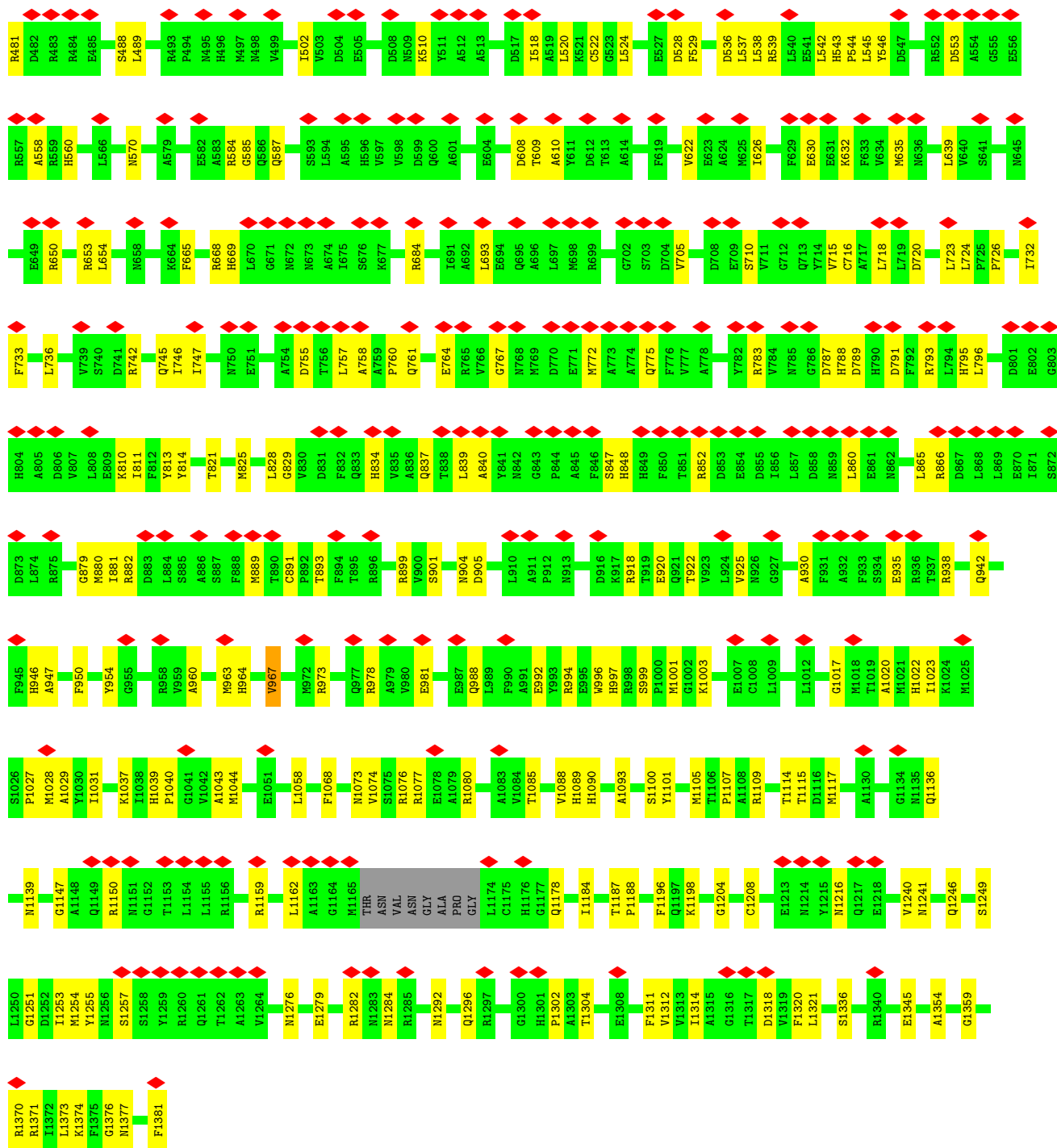
• Molecule 2: Major capsid protein



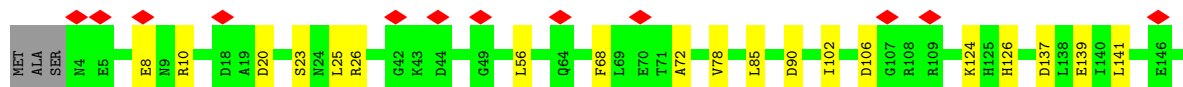
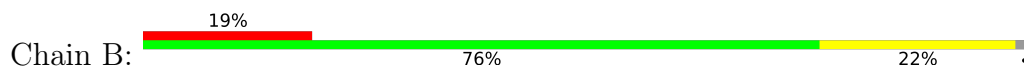


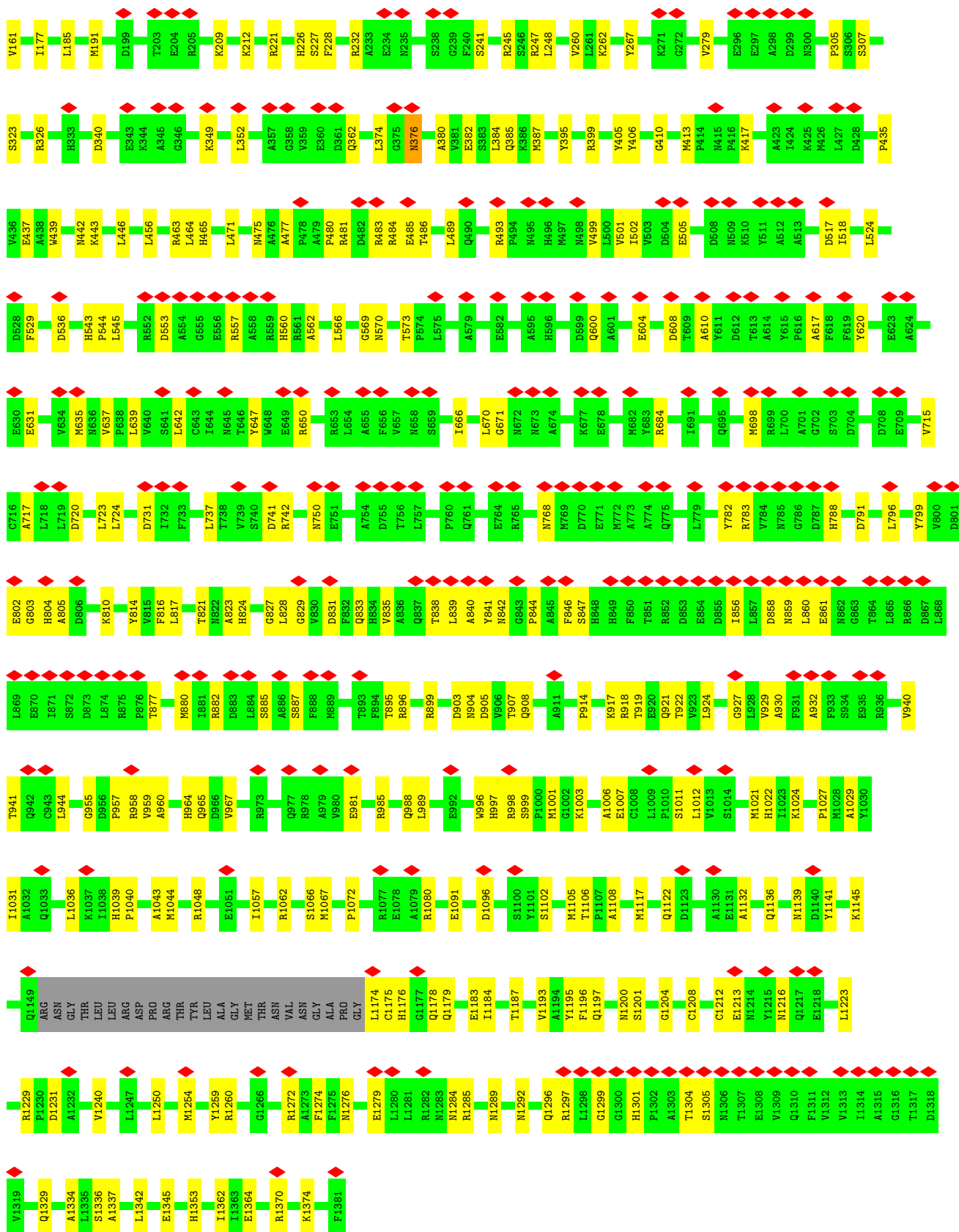
• Molecule 2: Major capsid protein





• Molecule 2: Major capsid protein



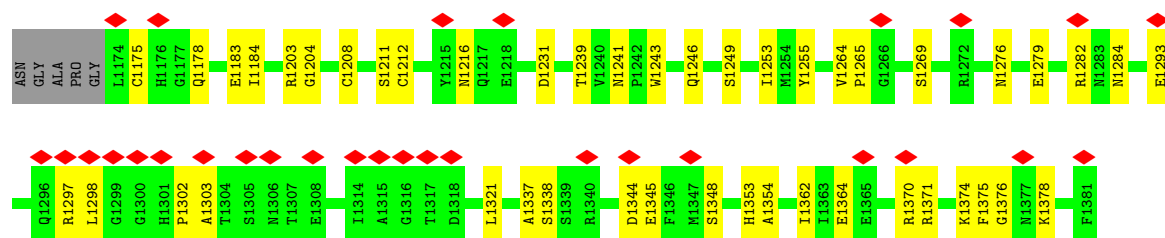


- Molecule 2: Major capsid protein

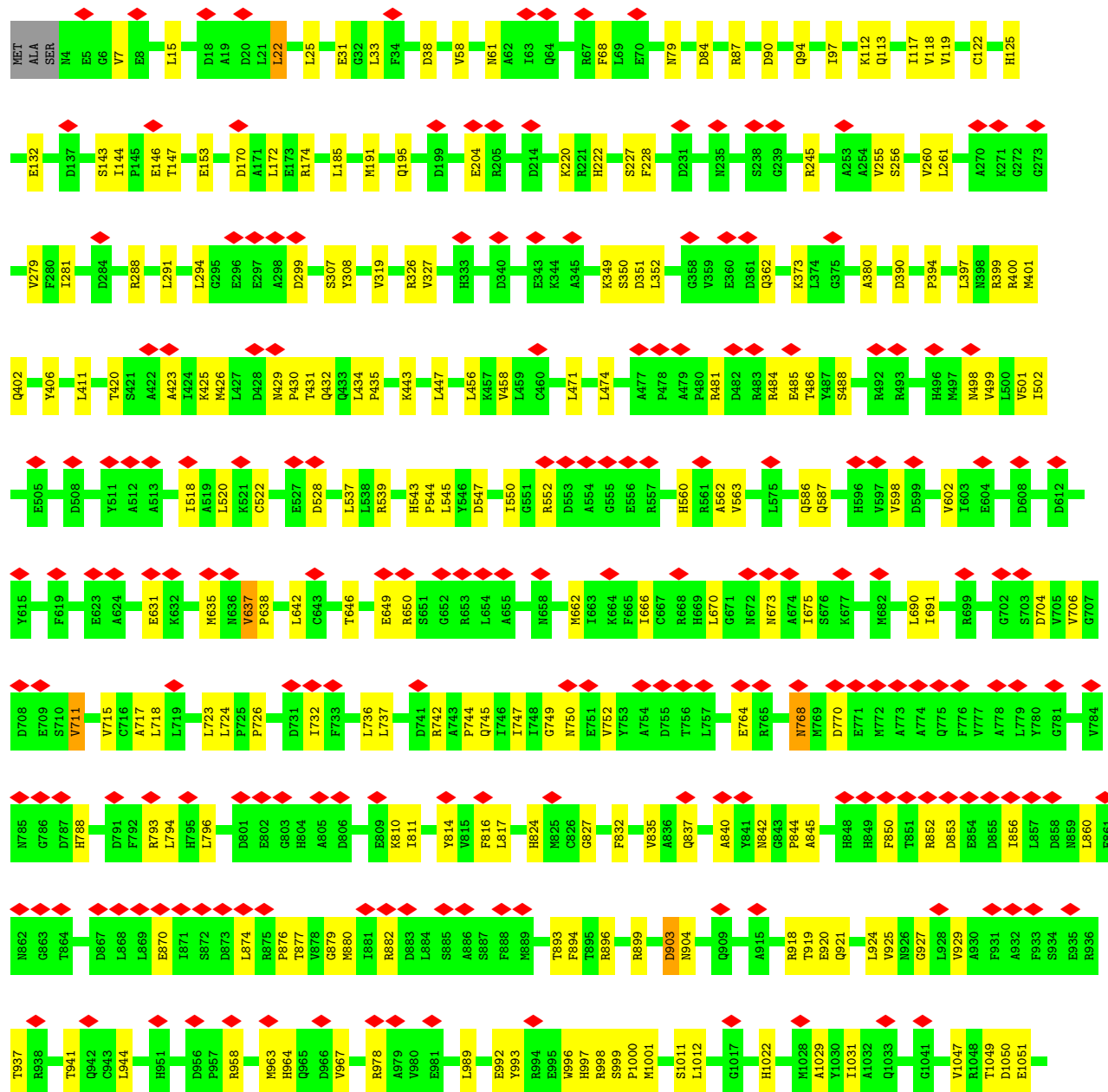
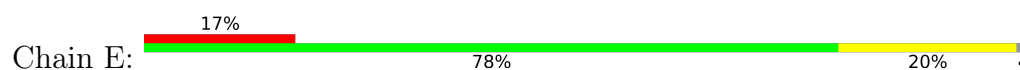


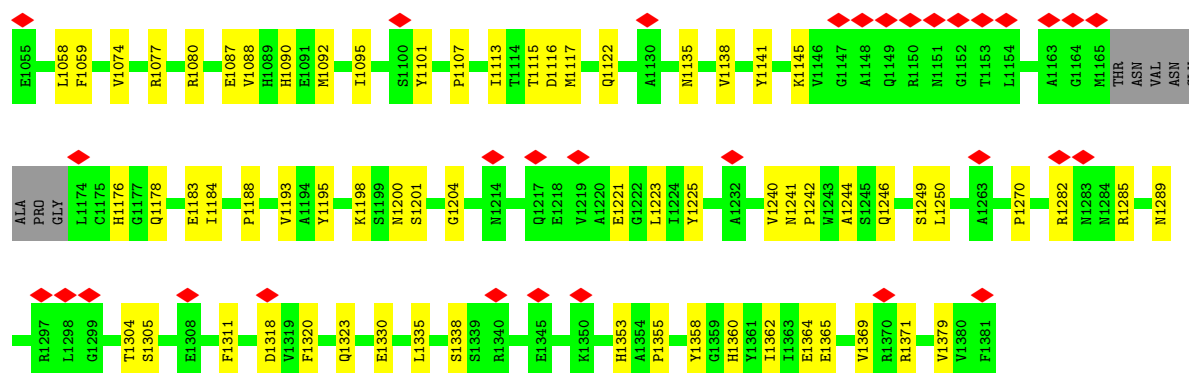
Chain D:



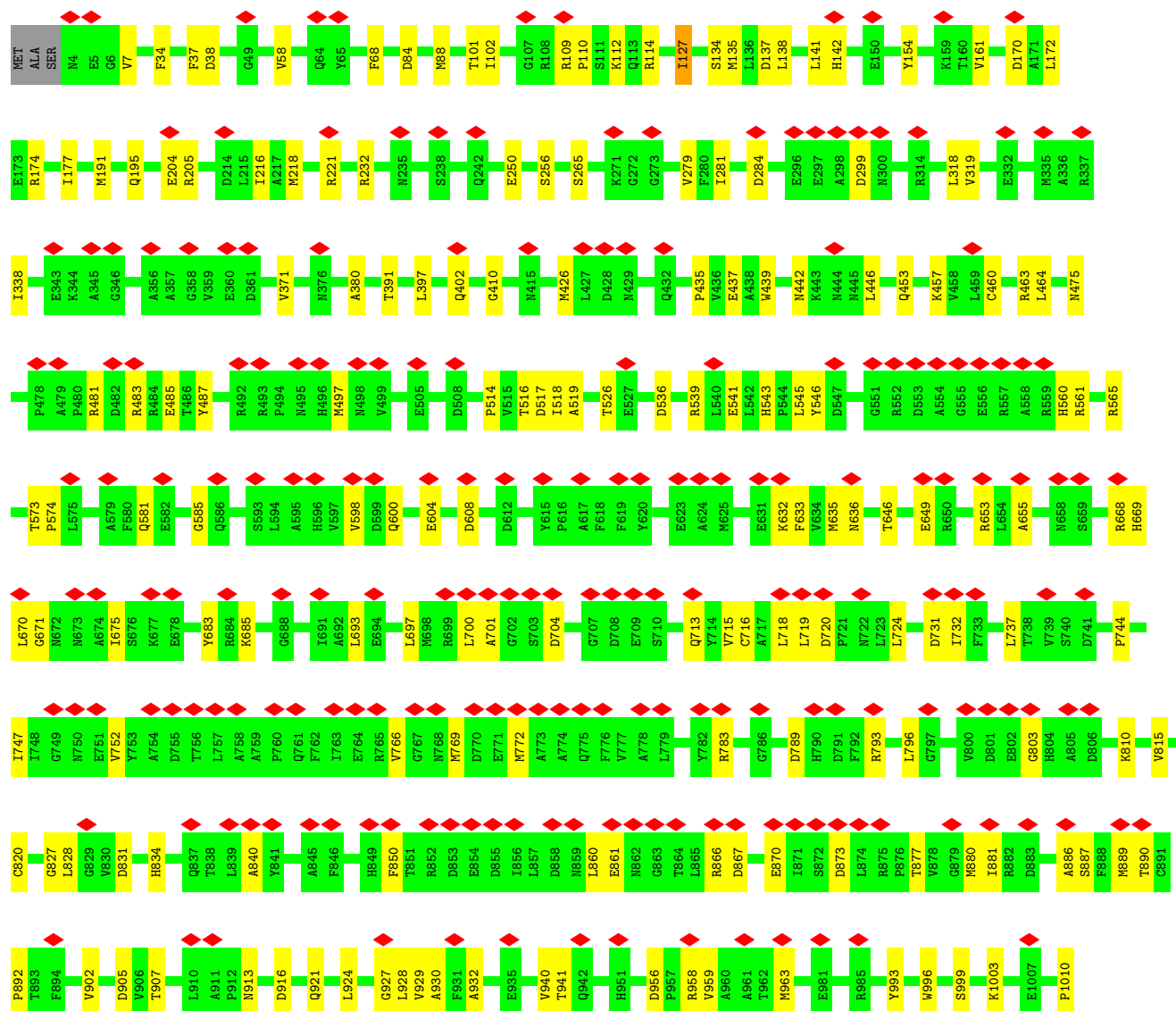
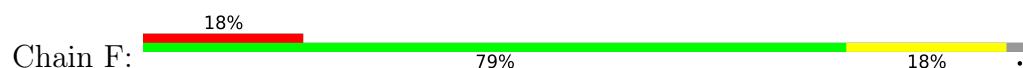


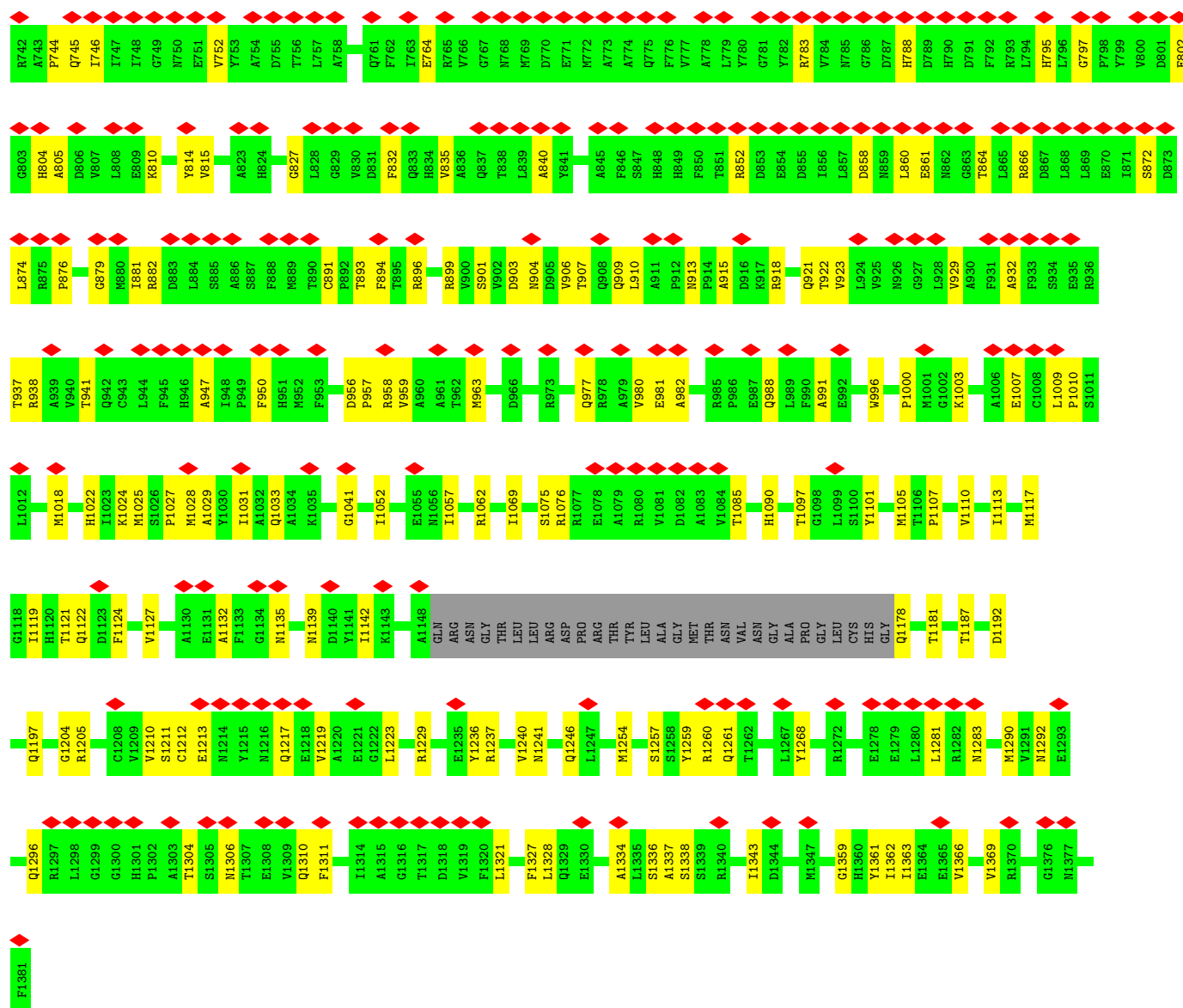
• Molecule 2: Major capsid protein



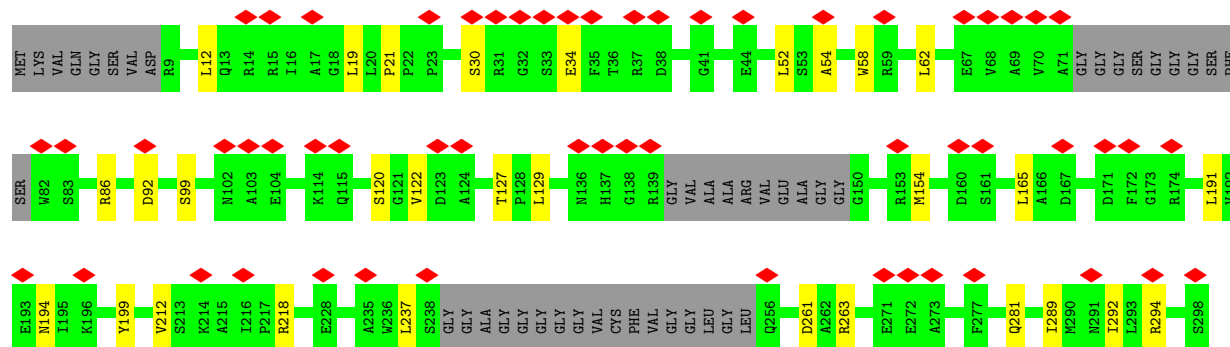
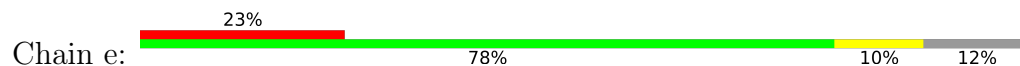


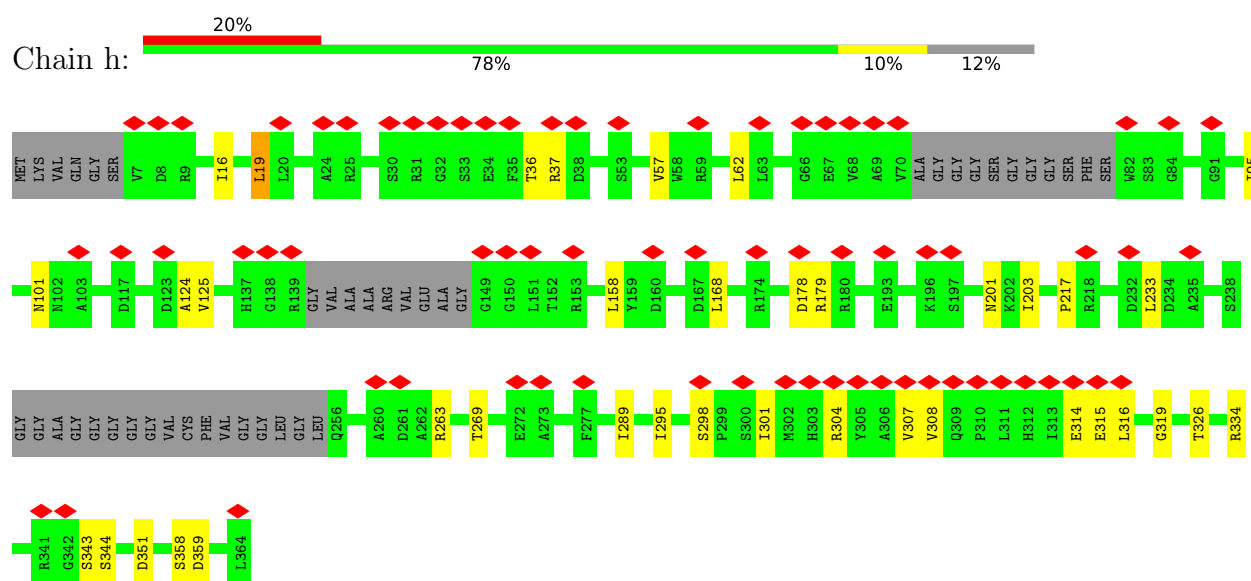
• Molecule 2: Major capsid protein



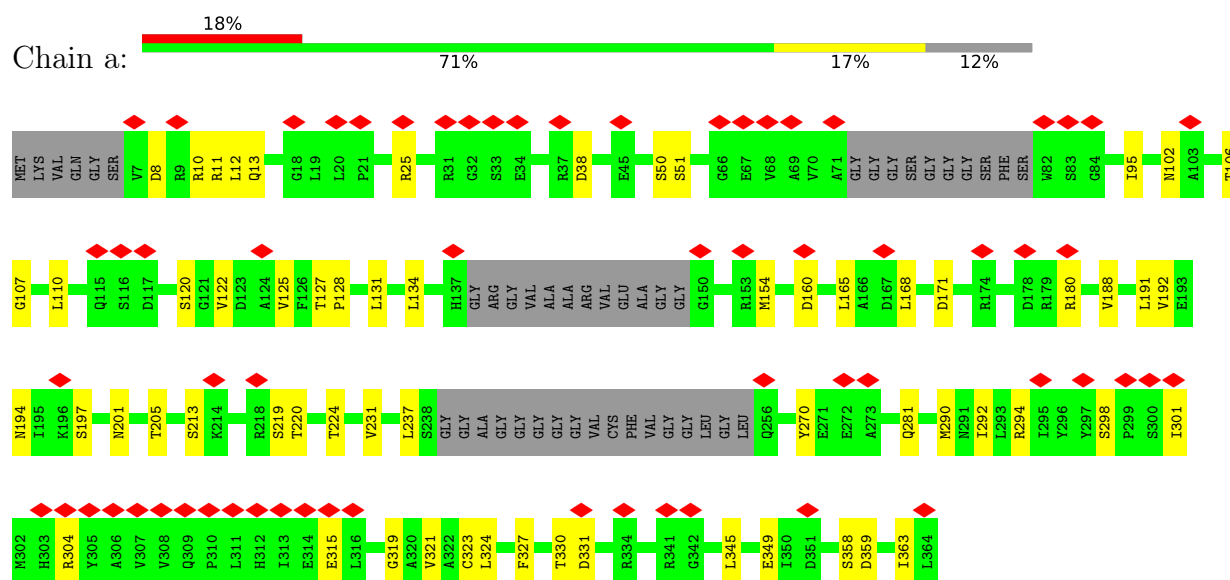


• Molecule 3: Triplex capsid protein 1

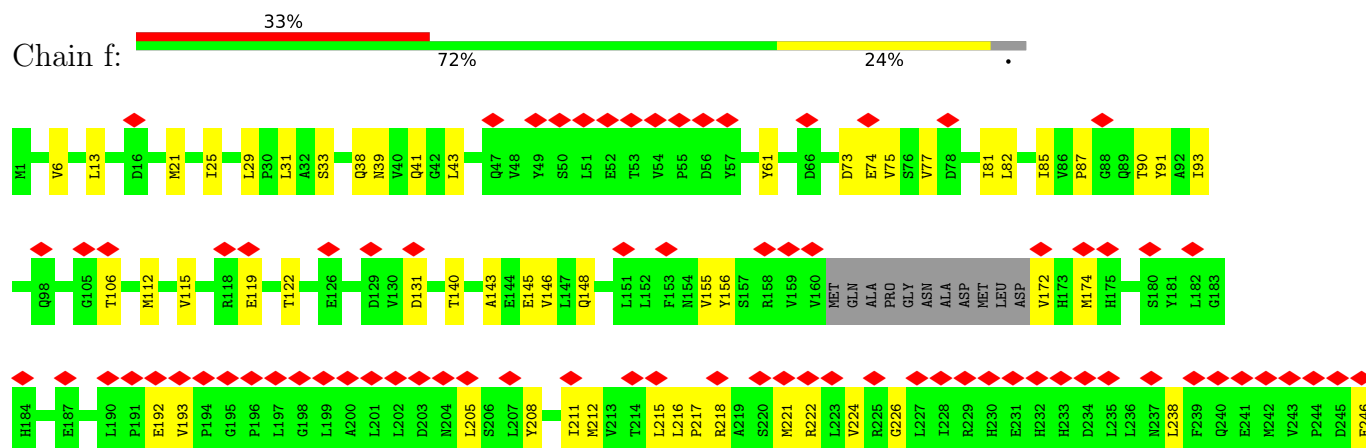


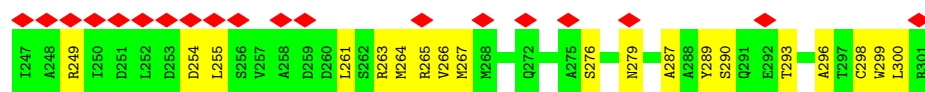


• Molecule 3: Triplex capsid protein 1

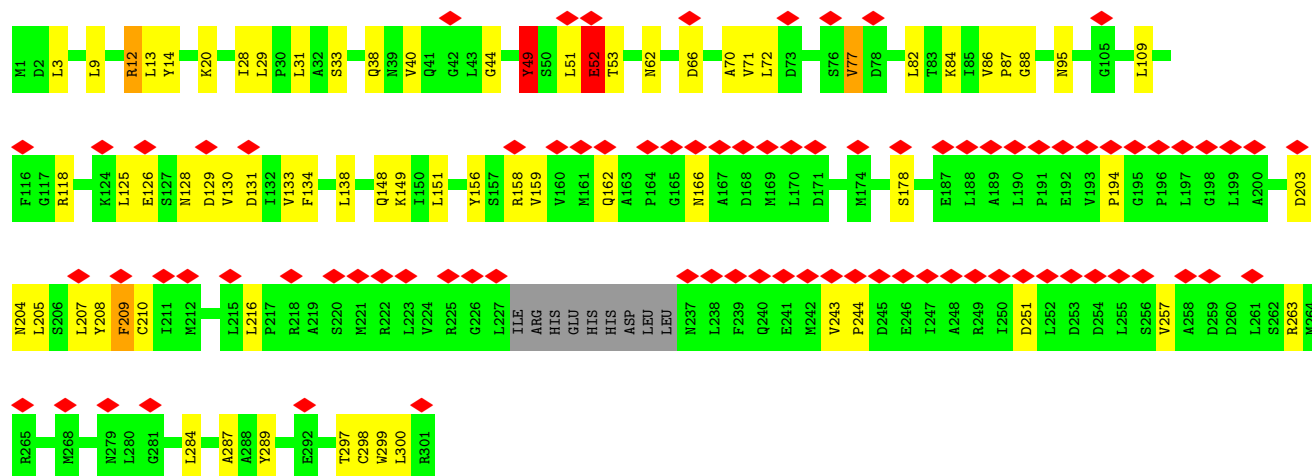
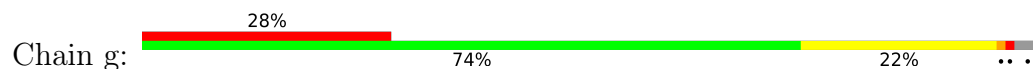


• Molecule 4: Triplex capsid protein 2

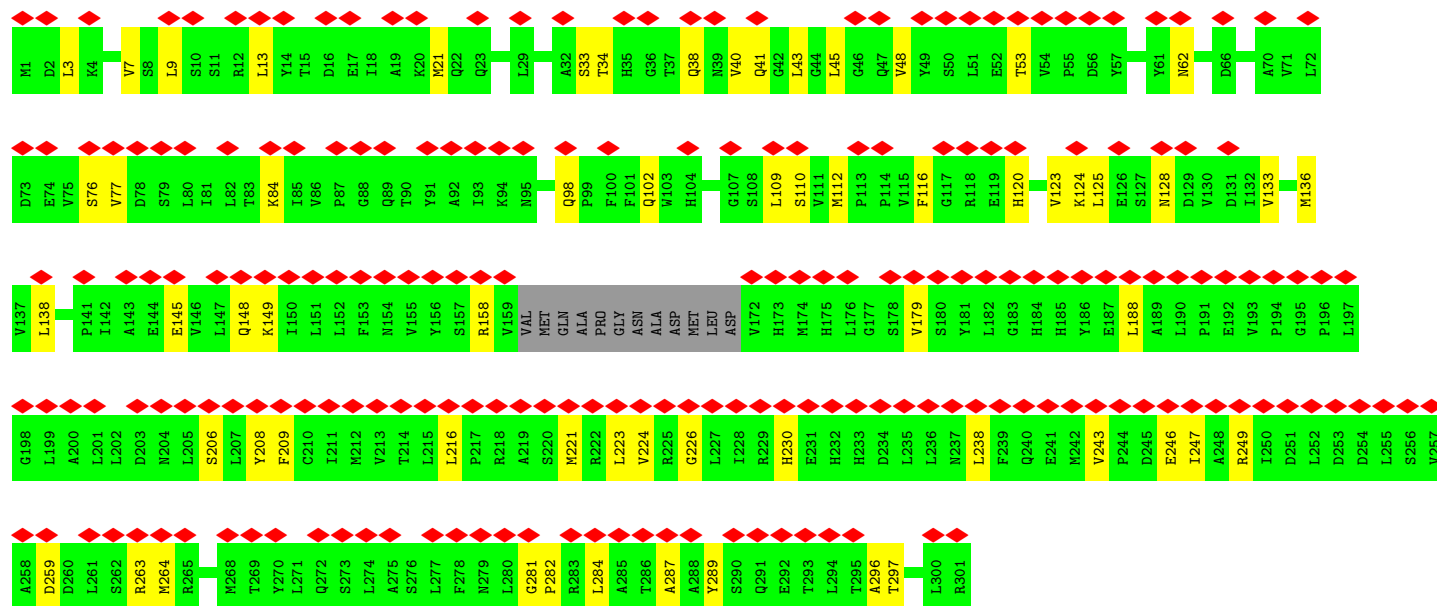
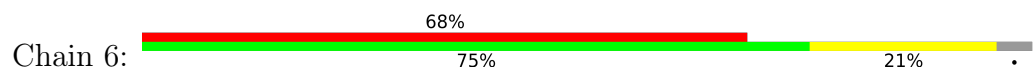




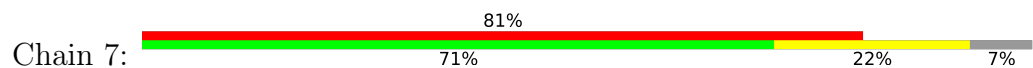
• Molecule 4: Triplex capsid protein 2

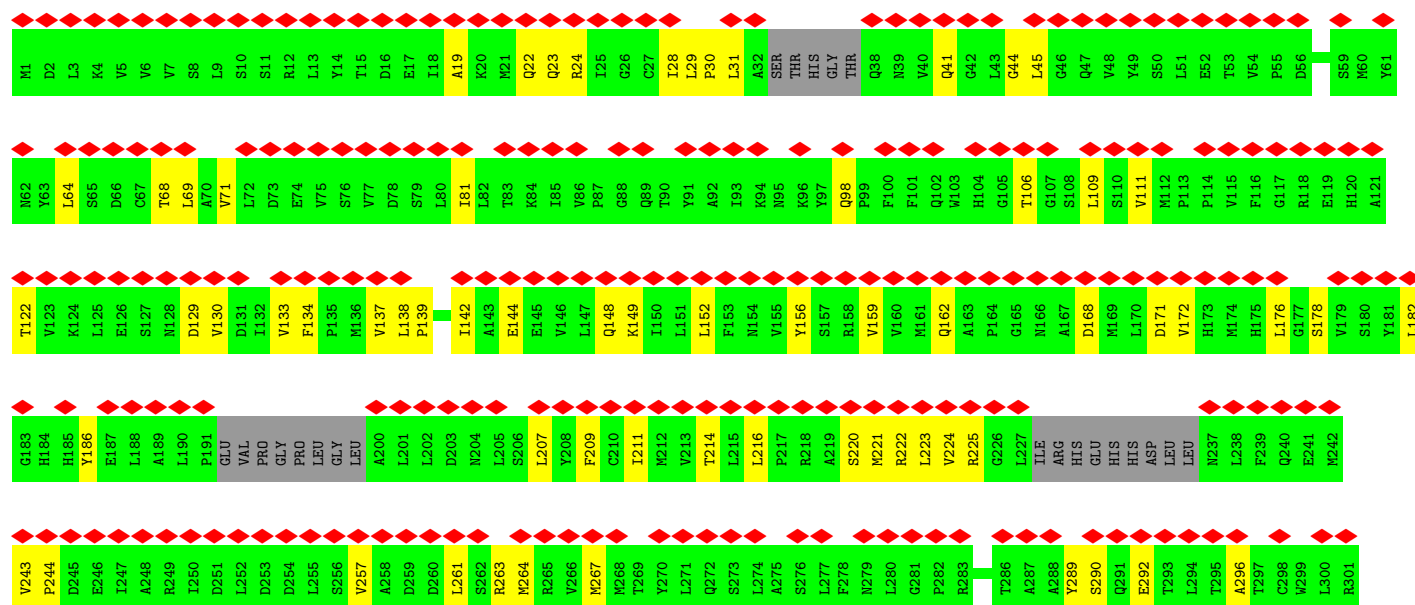


• Molecule 4: Triplex capsid protein 2

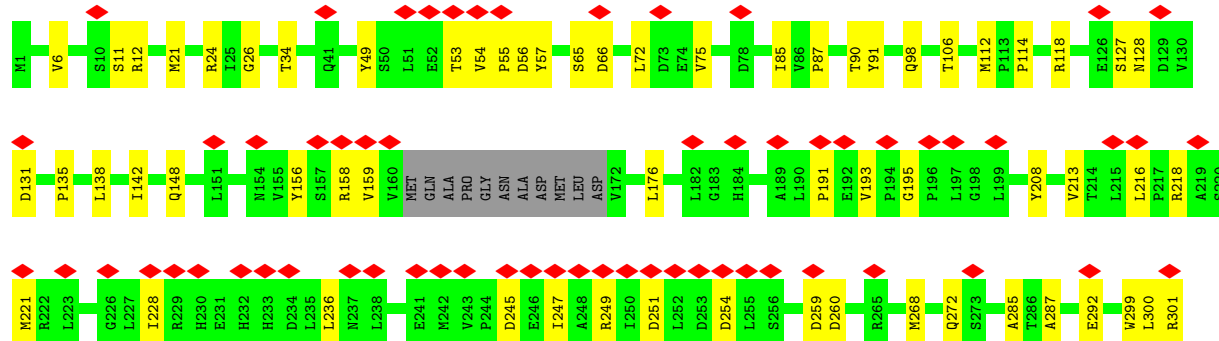
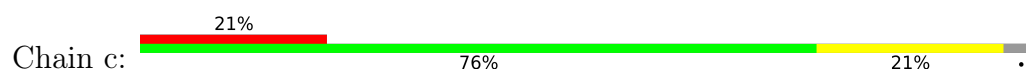


• Molecule 4: Triplex capsid protein 2

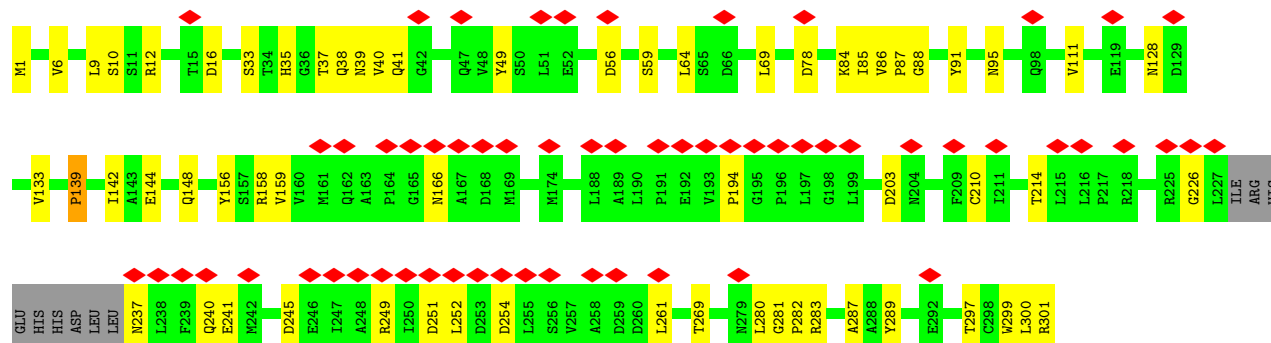
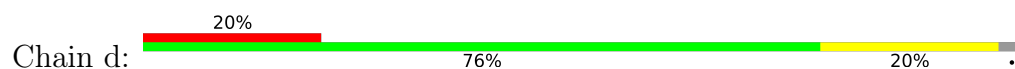




• Molecule 4: Triplex capsid protein 2

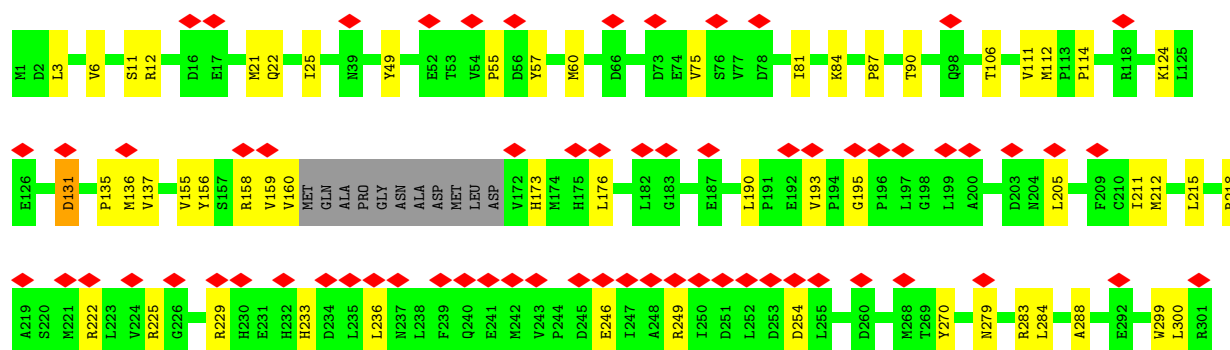


• Molecule 4: Triplex capsid protein 2



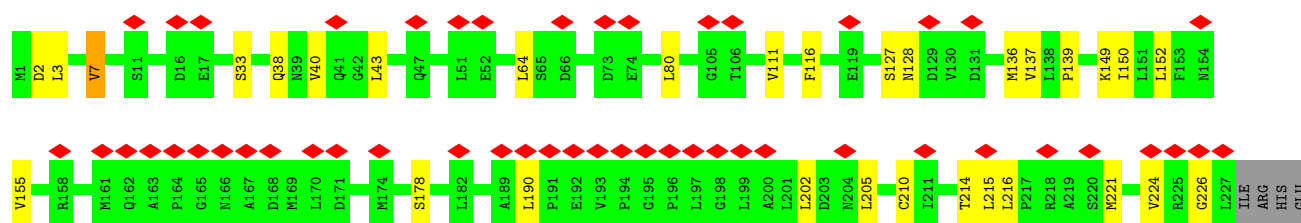
• Molecule 4: Triplex capsid protein 2

Chain i: 



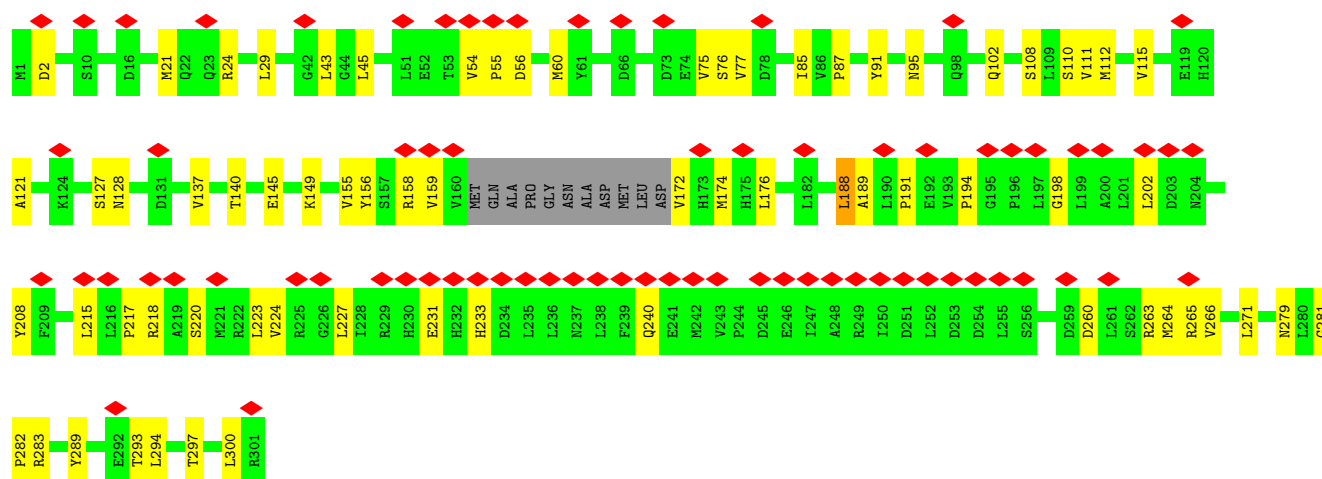
• Molecule 4: Triplex capsid protein 2

Chain j: 



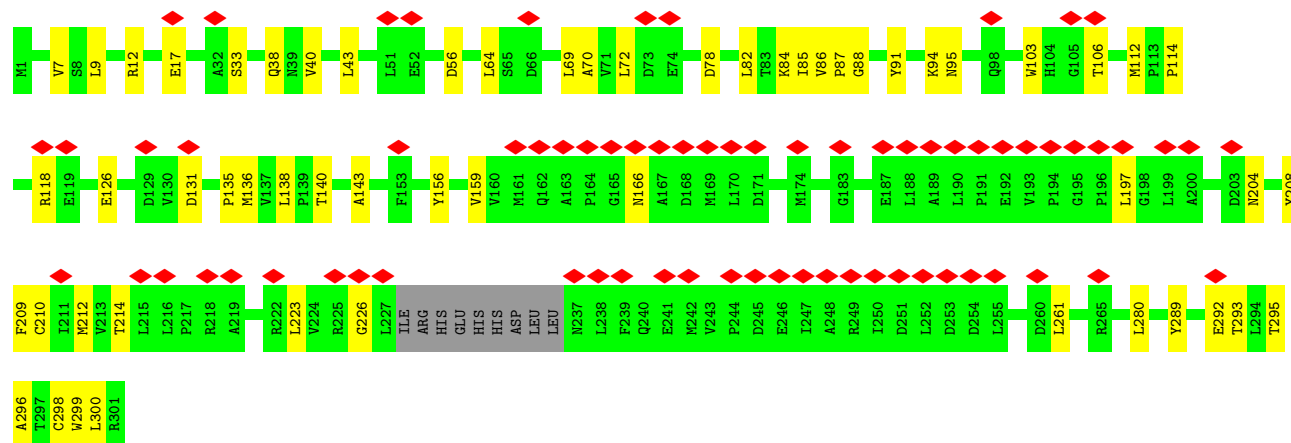
• Molecule 4: Triplex capsid protein 2

Chain 8: 



• Molecule 4: Triplex capsid protein 2

Chain 9: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	32721	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 ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.036	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	1341.44, 1341.44, 1341.44	wwPDB
Map dimensions	1024, 1024, 1024	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.26	0/636	0.64	0/861
1	1	0.23	0/636	0.60	0/861
1	G	0.38	1/665 (0.2%)	0.54	0/898
1	H	0.26	0/636	0.57	0/861
1	I	0.26	0/636	0.60	0/861
1	J	0.29	0/665	0.64	0/898
1	K	0.28	0/636	0.54	0/861
1	L	0.27	0/636	0.60	0/861
1	P	0.29	0/665	0.59	0/898
1	Q	0.37	1/636 (0.2%)	0.62	2/861 (0.2%)
1	R	0.25	0/636	0.54	0/861
1	X	0.25	0/636	0.61	0/861
1	Y	0.30	0/636	0.54	0/861
1	Z	0.26	0/636	0.62	2/861 (0.2%)
1	m	0.23	0/615	0.61	0/832
1	y	0.24	0/636	0.59	0/861
2	A	0.32	0/11012	0.60	2/14965 (0.0%)
2	B	0.32	0/10883	0.57	0/14791
2	C	0.31	0/10883	0.58	2/14791 (0.0%)
2	D	0.31	0/10883	0.58	1/14791 (0.0%)
2	E	0.33	0/11012	0.59	0/14965
2	F	0.33	1/10793 (0.0%)	0.58	0/14666
2	M	0.32	0/10883	0.59	1/14791 (0.0%)
2	N	0.34	0/11012	0.60	1/14965 (0.0%)
2	O	0.31	0/10883	0.56	1/14791 (0.0%)
2	S	0.30	0/10737	0.56	4/14589 (0.0%)
2	T	0.34	0/10642	0.61	1/14463 (0.0%)
2	U	0.32	0/10883	0.59	1/14791 (0.0%)
2	V	0.32	0/10883	0.59	2/14791 (0.0%)
2	k	0.32	0/10819	0.59	1/14702 (0.0%)
2	l	0.24	0/10114	0.54	2/13734 (0.0%)
2	x	0.28	0/10648	0.56	0/14471
3	5	0.25	0/2511	0.53	0/3418
3	a	0.30	0/2572	0.57	0/3505

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	b	0.32	0/2557	0.57	0/3484
3	e	0.29	0/2572	0.58	0/3503
3	h	0.30	0/2586	0.59	0/3522
4	6	0.25	0/2320	0.59	1/3159 (0.0%)
4	7	0.24	0/2228	0.57	1/3029 (0.0%)
4	8	0.30	0/2327	0.57	0/3169
4	9	0.32	0/2321	0.59	0/3161
4	c	0.31	0/2327	0.59	0/3169
4	d	0.31	0/2321	0.63	2/3161 (0.1%)
4	f	0.27	0/2327	0.56	0/3169
4	g	0.44	1/2321 (0.0%)	1.00	4/3161 (0.1%)
4	i	0.29	0/2327	0.58	0/3169
4	j	0.30	0/2321	0.60	2/3161 (0.1%)
All	All	0.31	4/219150 (0.0%)	0.59	33/297855 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Z	0	1
2	F	0	1
2	M	0	1
2	N	0	1
2	O	0	1
2	T	0	1
3	b	0	2
4	g	0	1
All	All	0	9

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	g	52	GLU	C-N	-7.74	1.22	1.33
1	G	67	VAL	C-N	7.65	1.40	1.33
1	Q	34	ASN	C-N	-6.04	1.24	1.33
2	F	84	ASP	CA-CB	-5.16	1.45	1.53

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	g	52	GLU	CA-C-N	23.50	153.84	120.95
4	g	52	GLU	C-N-CA	23.50	153.84	120.95
4	g	52	GLU	O-C-N	-22.41	92.78	122.59
2	N	395	TYR	CB-CA-C	-7.34	98.46	109.26
4	g	49	TYR	O-C-N	-7.22	112.83	122.22

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	M	43	LYS	Peptide
2	N	395	TYR	Sidechain
2	T	817	LEU	Peptide
1	Z	67	VAL	Peptide
4	g	49	TYR	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	621	0	611	16	0
1	1	621	0	611	18	0
1	G	650	0	645	15	0
1	H	621	0	611	16	0
1	I	621	0	611	16	0
1	J	650	0	645	12	0
1	K	621	0	611	23	0
1	L	621	0	611	14	0
1	P	650	0	645	10	0
1	Q	621	0	611	11	0
1	R	621	0	611	11	0
1	X	621	0	611	14	0
1	Y	621	0	611	13	0
1	Z	621	0	611	14	0
1	m	600	0	591	11	0
1	y	621	0	611	15	0
2	A	10761	0	10585	201	0
2	B	10634	0	10452	218	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	10634	0	10453	208	0
2	D	10634	0	10453	233	0
2	E	10761	0	10584	195	0
2	F	10546	0	10365	164	0
2	M	10634	0	10453	198	0
2	N	10761	0	10584	205	0
2	O	10634	0	10453	172	0
2	S	10491	0	10317	227	0
2	T	10398	0	10235	242	0
2	U	10634	0	10452	248	0
2	V	10634	0	10452	186	0
2	k	10572	0	10390	201	0
2	l	9883	0	9710	169	0
2	x	10404	0	10233	216	0
3	5	2446	0	2422	45	0
3	a	2505	0	2477	42	0
3	b	2490	0	2464	38	0
3	e	2505	0	2480	26	0
3	h	2519	0	2491	25	0
4	6	2272	0	2307	42	0
4	7	2187	0	2222	44	0
4	8	2279	0	2316	47	0
4	9	2275	0	2310	41	0
4	c	2279	0	2316	43	0
4	d	2275	0	2310	45	0
4	f	2279	0	2316	46	0
4	g	2275	0	2307	86	0
4	i	2279	0	2316	37	0
4	j	2275	0	2310	30	0
All	All	214157	0	211393	3778	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 9.

The worst 5 of 3778 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)
2:D:395:TYR:HE1	2:D:397:LEU:CG	1.25	1.45
2:D:395:TYR:HE1	2:D:397:LEU:CB	1.30	1.40
2:D:395:TYR:CE1	2:D:397:LEU:CG	2.04	1.39
2:D:395:TYR:CE1	2:D:397:LEU:HG	1.59	1.35

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:395:TYR:CE1	2:D:397:LEU:HB2	1.63	1.32

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	0	72/176 (41%)	69 (96%)	3 (4%)	0	100	100
1	1	72/176 (41%)	67 (93%)	5 (7%)	0	100	100
1	G	75/176 (43%)	72 (96%)	3 (4%)	0	100	100
1	H	72/176 (41%)	66 (92%)	6 (8%)	0	100	100
1	I	72/176 (41%)	66 (92%)	6 (8%)	0	100	100
1	J	75/176 (43%)	69 (92%)	6 (8%)	0	100	100
1	K	72/176 (41%)	67 (93%)	5 (7%)	0	100	100
1	L	72/176 (41%)	69 (96%)	3 (4%)	0	100	100
1	P	75/176 (43%)	70 (93%)	5 (7%)	0	100	100
1	Q	72/176 (41%)	65 (90%)	7 (10%)	0	100	100
1	R	72/176 (41%)	68 (94%)	4 (6%)	0	100	100
1	X	72/176 (41%)	64 (89%)	8 (11%)	0	100	100
1	Y	72/176 (41%)	67 (93%)	5 (7%)	0	100	100
1	Z	72/176 (41%)	68 (94%)	4 (6%)	0	100	100
1	m	69/176 (39%)	64 (93%)	5 (7%)	0	100	100
1	y	72/176 (41%)	67 (93%)	5 (7%)	0	100	100
2	A	1366/1381 (99%)	1274 (93%)	92 (7%)	0	100	100
2	B	1350/1381 (98%)	1252 (93%)	98 (7%)	0	100	100
2	C	1350/1381 (98%)	1258 (93%)	92 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	1350/1381 (98%)	1266 (94%)	84 (6%)	0	100	100
2	E	1366/1381 (99%)	1264 (92%)	101 (7%)	1 (0%)	48	81
2	F	1336/1381 (97%)	1252 (94%)	84 (6%)	0	100	100
2	M	1350/1381 (98%)	1267 (94%)	83 (6%)	0	100	100
2	N	1366/1381 (99%)	1275 (93%)	91 (7%)	0	100	100
2	O	1350/1381 (98%)	1253 (93%)	97 (7%)	0	100	100
2	S	1327/1381 (96%)	1250 (94%)	77 (6%)	0	100	100
2	T	1319/1381 (96%)	1227 (93%)	92 (7%)	0	100	100
2	U	1350/1381 (98%)	1261 (93%)	89 (7%)	0	100	100
2	V	1350/1381 (98%)	1264 (94%)	86 (6%)	0	100	100
2	k	1340/1381 (97%)	1258 (94%)	82 (6%)	0	100	100
2	l	1237/1381 (90%)	1169 (94%)	68 (6%)	0	100	100
2	x	1321/1381 (96%)	1238 (94%)	83 (6%)	0	100	100
3	5	303/364 (83%)	288 (95%)	15 (5%)	0	100	100
3	a	311/364 (85%)	294 (94%)	17 (6%)	0	100	100
3	b	309/364 (85%)	289 (94%)	20 (6%)	0	100	100
3	e	311/364 (85%)	291 (94%)	20 (6%)	0	100	100
3	h	313/364 (86%)	295 (94%)	18 (6%)	0	100	100
4	6	285/301 (95%)	274 (96%)	11 (4%)	0	100	100
4	7	271/301 (90%)	254 (94%)	17 (6%)	0	100	100
4	8	286/301 (95%)	271 (95%)	15 (5%)	0	100	100
4	9	288/301 (96%)	265 (92%)	23 (8%)	0	100	100
4	c	286/301 (95%)	270 (94%)	16 (6%)	0	100	100
4	d	288/301 (96%)	266 (92%)	22 (8%)	0	100	100
4	f	286/301 (95%)	273 (96%)	13 (4%)	0	100	100
4	g	288/301 (96%)	266 (92%)	20 (7%)	2 (1%)	18	55
4	i	286/301 (95%)	269 (94%)	17 (6%)	0	100	100
4	j	288/301 (96%)	270 (94%)	18 (6%)	0	100	100
All	All	26985/29742 (91%)	25241 (94%)	1741 (6%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	g	129	ASP
4	g	52	GLU
2	E	768	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	68/128 (53%)	67 (98%)	1 (2%)	57	70
1	1	68/128 (53%)	67 (98%)	1 (2%)	57	70
1	G	71/128 (56%)	71 (100%)	0	100	100
1	H	68/128 (53%)	67 (98%)	1 (2%)	57	70
1	I	68/128 (53%)	68 (100%)	0	100	100
1	J	71/128 (56%)	70 (99%)	1 (1%)	59	71
1	K	68/128 (53%)	68 (100%)	0	100	100
1	L	68/128 (53%)	68 (100%)	0	100	100
1	P	71/128 (56%)	71 (100%)	0	100	100
1	Q	68/128 (53%)	68 (100%)	0	100	100
1	R	68/128 (53%)	68 (100%)	0	100	100
1	X	68/128 (53%)	67 (98%)	1 (2%)	57	70
1	Y	68/128 (53%)	68 (100%)	0	100	100
1	Z	68/128 (53%)	67 (98%)	1 (2%)	57	70
1	m	66/128 (52%)	66 (100%)	0	100	100
1	y	68/128 (53%)	68 (100%)	0	100	100
2	A	1164/1171 (99%)	1159 (100%)	5 (0%)	84	83
2	B	1151/1171 (98%)	1148 (100%)	3 (0%)	86	85
2	C	1151/1171 (98%)	1146 (100%)	5 (0%)	84	83
2	D	1151/1171 (98%)	1144 (99%)	7 (1%)	78	80
2	E	1164/1171 (99%)	1155 (99%)	9 (1%)	73	77
2	F	1141/1171 (97%)	1135 (100%)	6 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	M	1151/1171 (98%)	1144 (99%)	7 (1%)	78	80
2	N	1164/1171 (99%)	1159 (100%)	5 (0%)	84	83
2	O	1151/1171 (98%)	1144 (99%)	7 (1%)	78	80
2	S	1136/1171 (97%)	1126 (99%)	10 (1%)	70	76
2	T	1126/1171 (96%)	1119 (99%)	7 (1%)	78	80
2	U	1151/1171 (98%)	1142 (99%)	9 (1%)	73	77
2	V	1151/1171 (98%)	1148 (100%)	3 (0%)	86	85
2	k	1143/1171 (98%)	1137 (100%)	6 (0%)	81	82
2	l	1070/1171 (91%)	1065 (100%)	5 (0%)	81	82
2	x	1125/1171 (96%)	1116 (99%)	9 (1%)	73	77
3	5	263/289 (91%)	261 (99%)	2 (1%)	73	77
3	a	269/289 (93%)	267 (99%)	2 (1%)	76	79
3	b	267/289 (92%)	266 (100%)	1 (0%)	84	83
3	e	268/289 (93%)	268 (100%)	0	100	100
3	h	270/289 (93%)	269 (100%)	1 (0%)	84	83
4	6	258/267 (97%)	258 (100%)	0	100	100
4	7	248/267 (93%)	248 (100%)	0	100	100
4	8	259/267 (97%)	256 (99%)	3 (1%)	63	73
4	9	258/267 (97%)	258 (100%)	0	100	100
4	c	259/267 (97%)	258 (100%)	1 (0%)	84	83
4	d	258/267 (97%)	257 (100%)	1 (0%)	84	83
4	f	259/267 (97%)	257 (99%)	2 (1%)	73	77
4	g	258/267 (97%)	251 (97%)	7 (3%)	39	60
4	i	259/267 (97%)	258 (100%)	1 (0%)	84	83
4	j	258/267 (97%)	257 (100%)	1 (0%)	84	83
All	All	23296/24899 (94%)	23165 (99%)	131 (1%)	76	80

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	x	327	VAL
2	x	1110	VAL
4	8	293	THR

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Mol	Chain	Res	Type
2	O	766	VAL
2	O	550	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 502 such sidechains are listed below:

Mol	Chain	Res	Type
1	X	54	GLN
2	F	984	ASN
2	A	600	GLN
2	F	645	ASN
2	x	1310	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

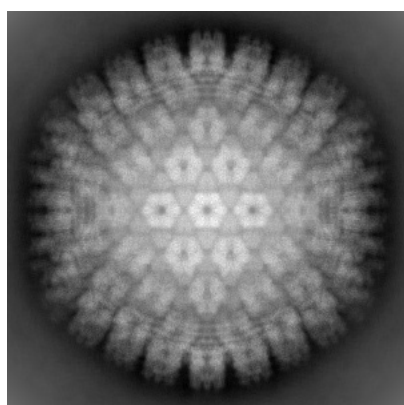
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30162. These allow visual inspection of the internal detail of the map and identification of artifacts.

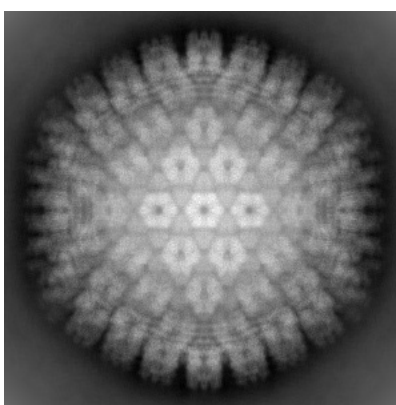
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

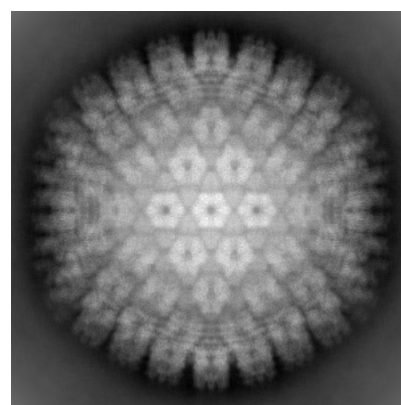
6.1.1 Primary map



X



Y

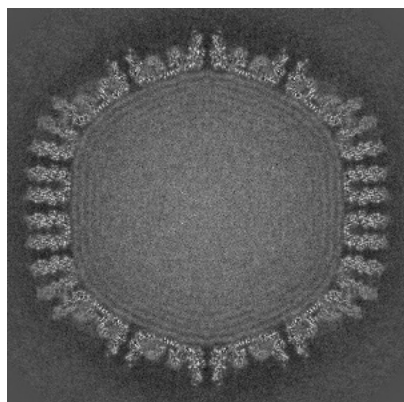


Z

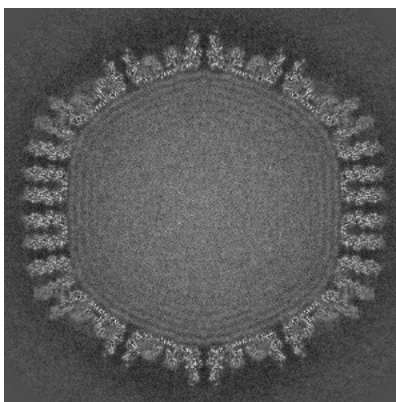
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

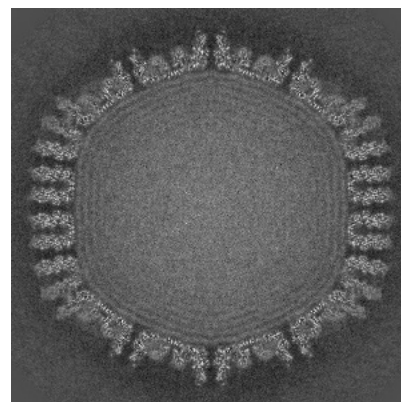
6.2.1 Primary map



X Index: 512



Y Index: 512

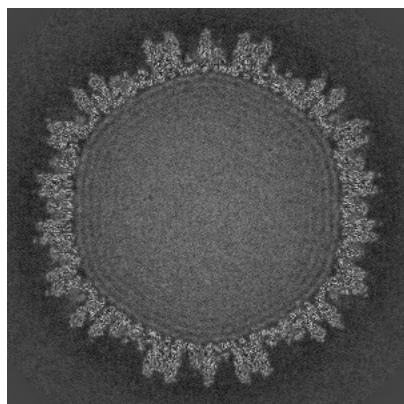


Z Index: 512

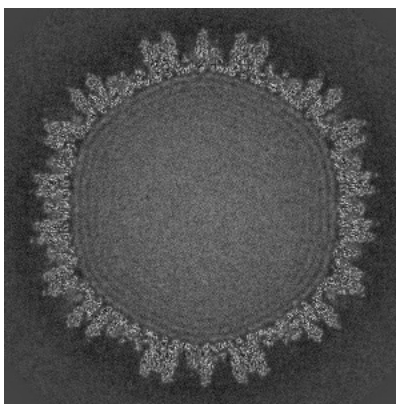
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

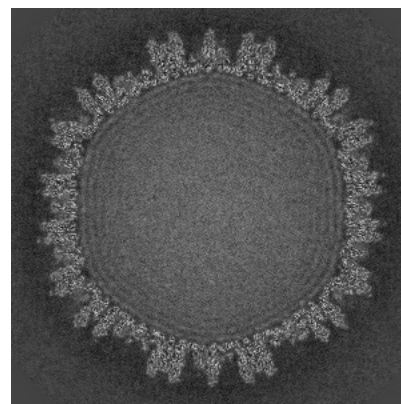
6.3.1 Primary map



X Index: 432



Y Index: 432

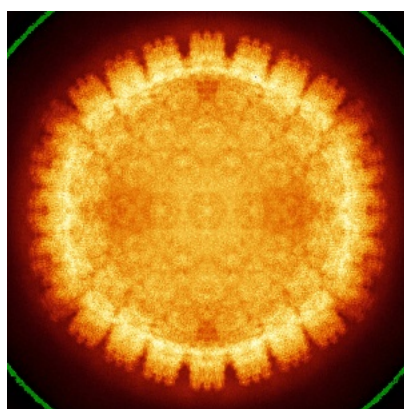


Z Index: 432

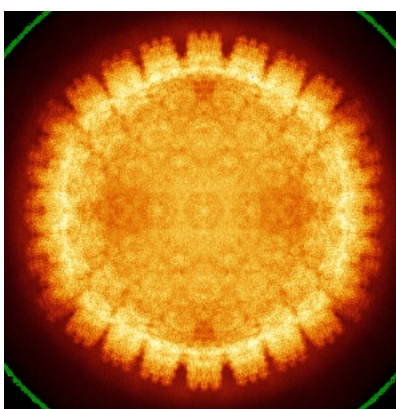
The images above show the largest variance slices of the map in three orthogonal directions.

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

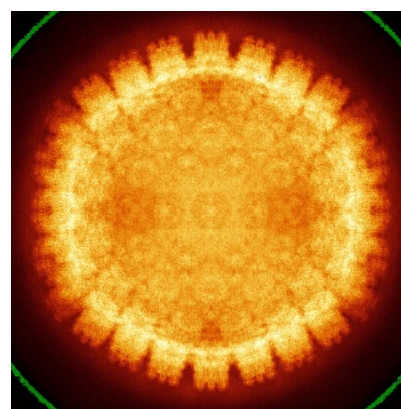
6.4.1 Primary map



X



Y

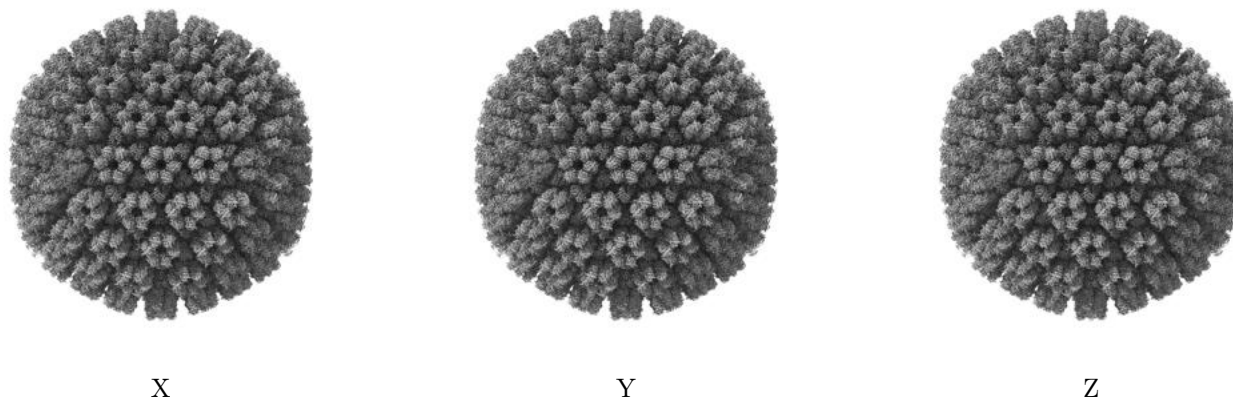


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

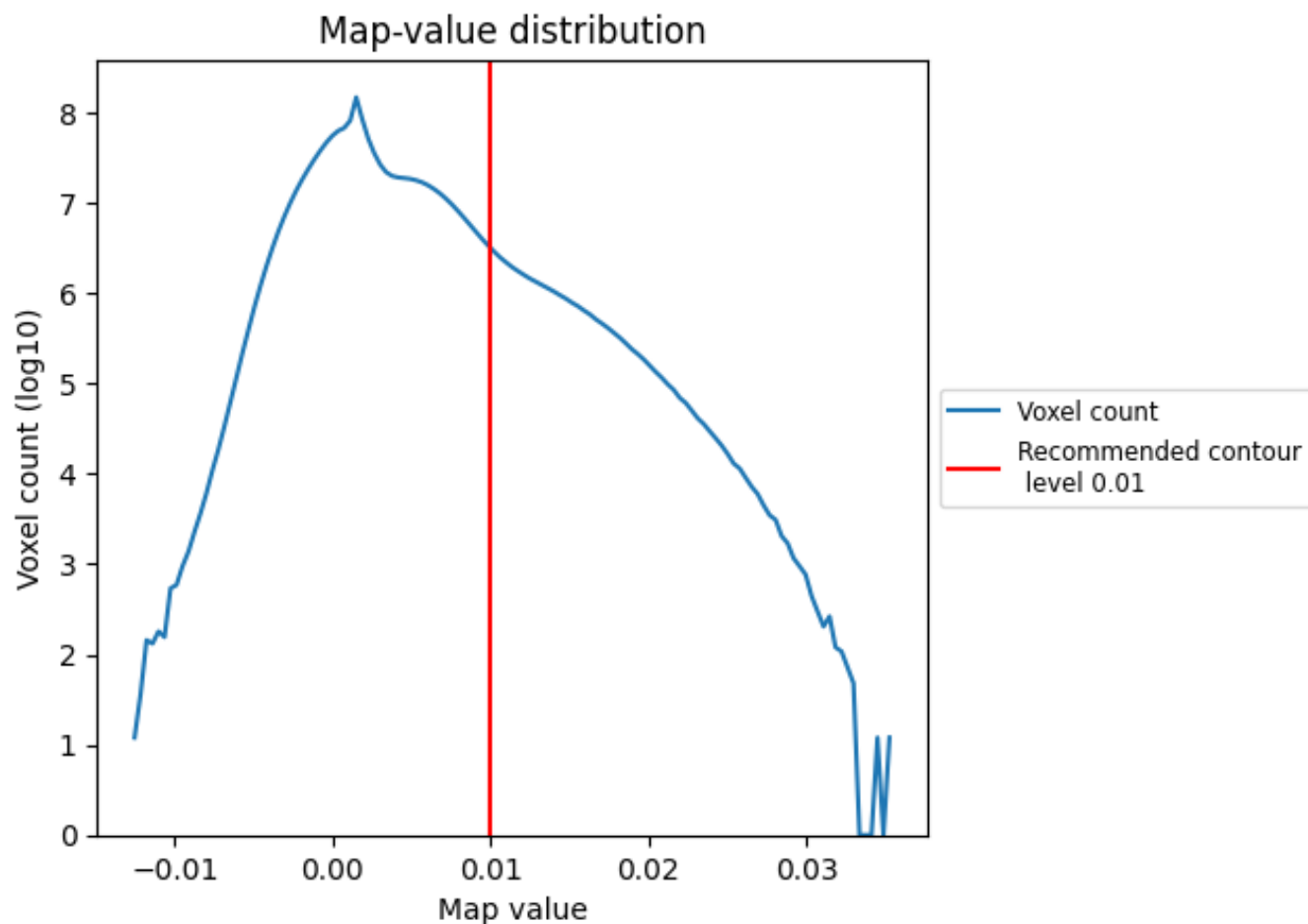
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

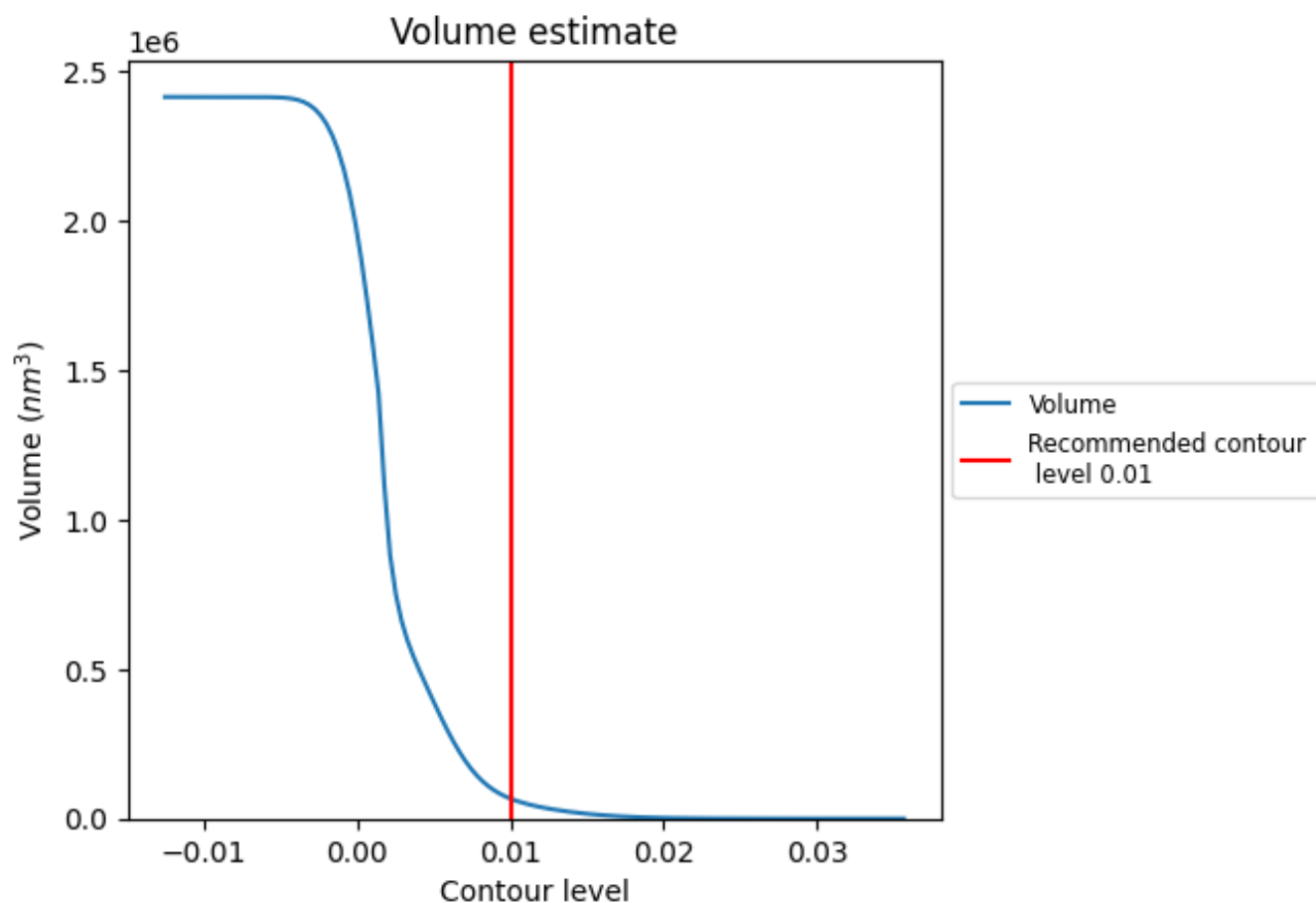
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

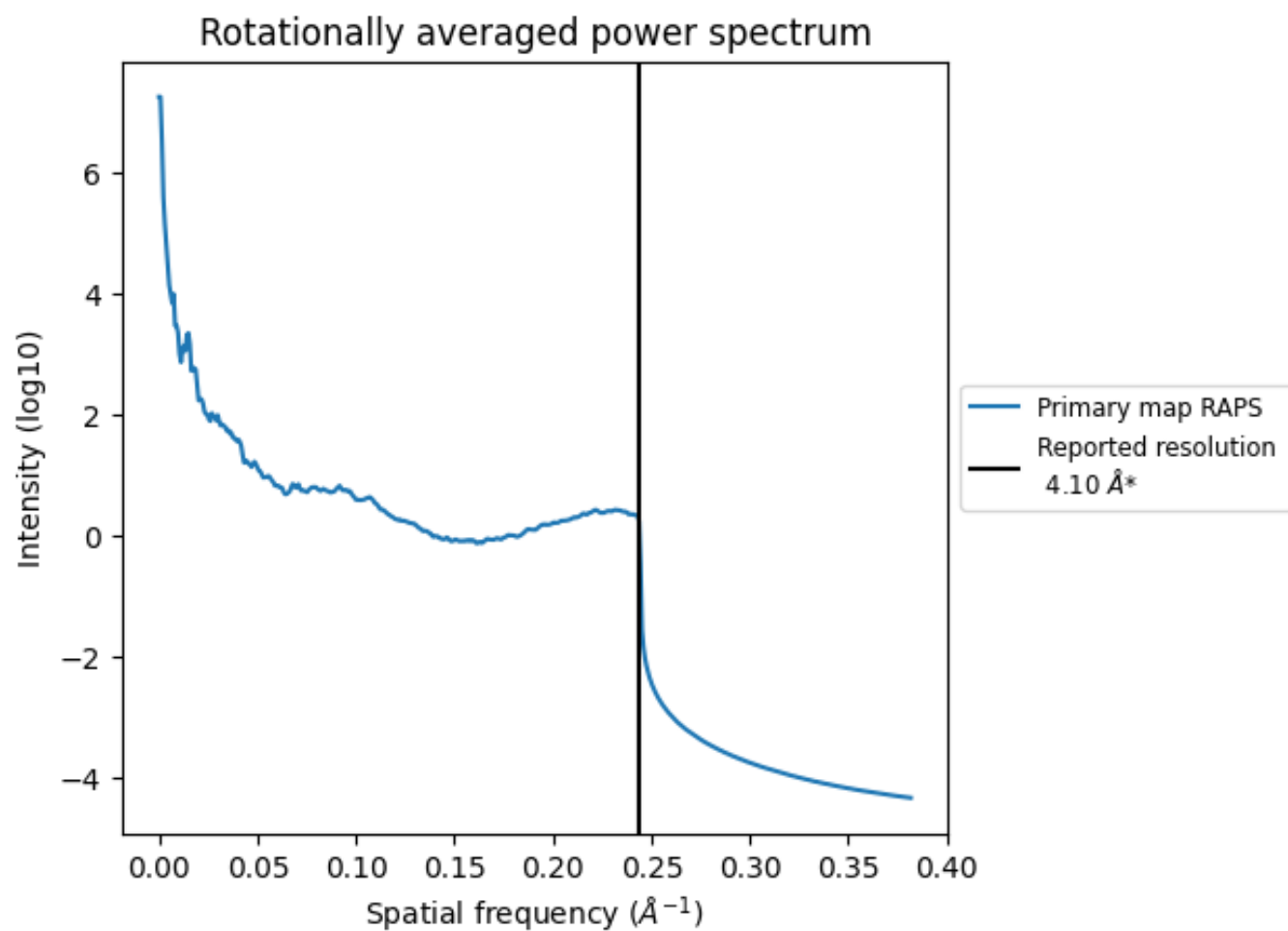
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 67041 nm³; this corresponds to an approximate mass of 60560 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 0.244 Å⁻¹

8 Fourier-Shell correlation

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

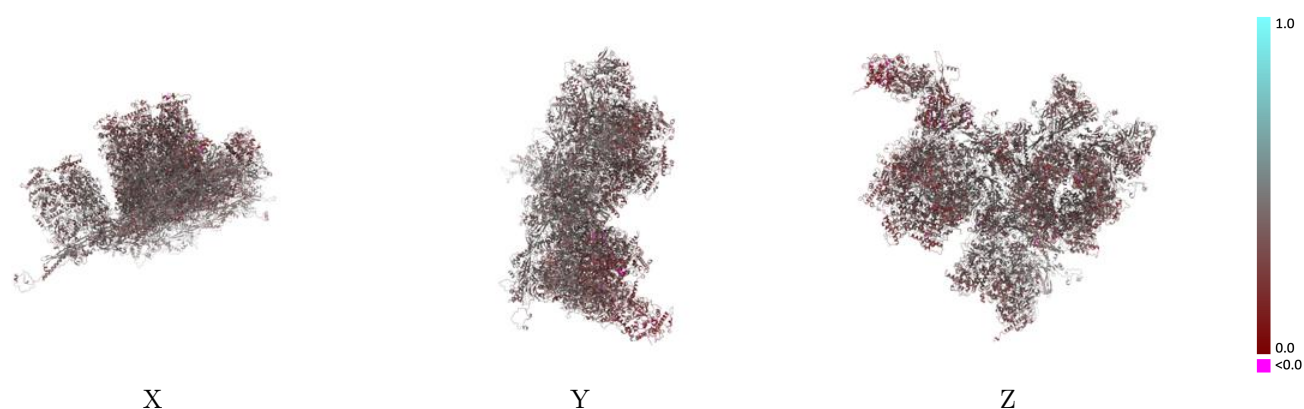
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30162 and PDB model 7BSI. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

This section was not generated.

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

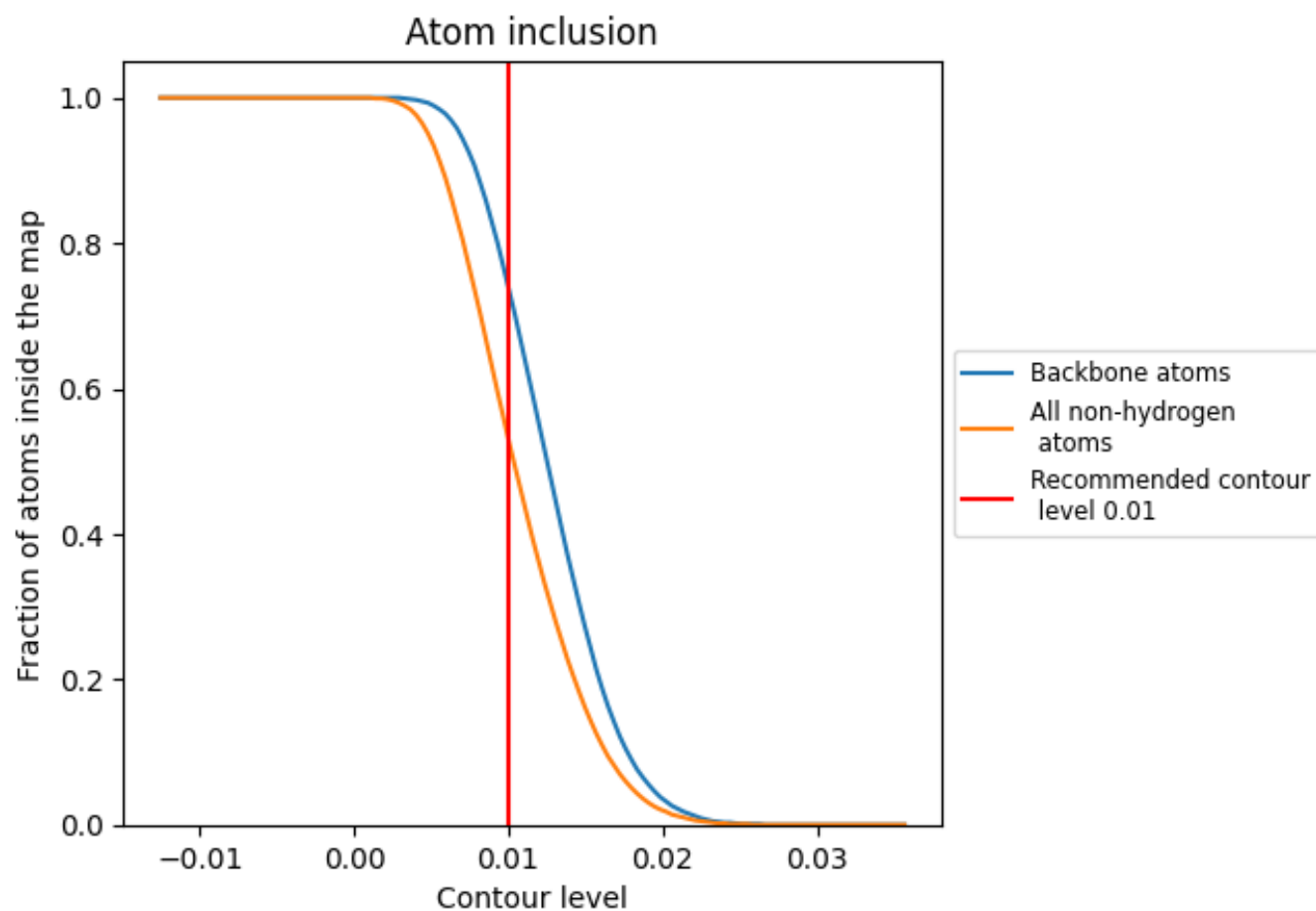


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 53% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

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

Chain	Atom inclusion	Q-score
All	 0.5310	 0.3750
0	 0.2380	 0.2930
1	 0.2380	 0.2830
5	 0.2760	 0.3010
6	 0.2530	 0.2980
7	 0.1620	 0.2670
8	 0.5520	 0.3700
9	 0.5570	 0.3770
A	 0.5820	 0.3880
B	 0.5920	 0.3860
C	 0.5870	 0.3830
D	 0.5980	 0.3890
E	 0.6020	 0.3920
F	 0.5900	 0.3910
G	 0.2570	 0.2980
H	 0.2970	 0.3000
I	 0.3000	 0.3330
J	 0.3030	 0.3220
K	 0.2980	 0.3240
L	 0.2620	 0.3130
M	 0.5920	 0.3940
N	 0.6070	 0.3970
O	 0.5960	 0.3960
P	 0.3140	 0.3210
Q	 0.3200	 0.3200
R	 0.3480	 0.3330
S	 0.4880	 0.3650
T	 0.5390	 0.3790
U	 0.5660	 0.3890
V	 0.5710	 0.3880
X	 0.2580	 0.2830
Y	 0.2130	 0.2620
Z	 0.1900	 0.2680
a	 0.5980	 0.3910
b	 0.6060	 0.3910



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Chain	Atom inclusion	Q-score
c	 0.5690	 0.3880
d	 0.5810	 0.3900
e	 0.5570	 0.3930
f	 0.4880	 0.3590
g	 0.5260	 0.3770
h	 0.5770	 0.3880
i	 0.5560	 0.3750
j	 0.5550	 0.3750
k	 0.5310	 0.3760
l	 0.2970	 0.3250
m	 0.0350	 0.2160
x	 0.5100	 0.3720
y	 0.1950	 0.2610