



wwPDB EM Validation Summary Report ⓘ

Apr 7, 2026 – 11:36 PM UTC

PDB ID : 7FJ1 / pdb_00007fj1
EMDB ID : EMD-31611
Title : Cryo-EM structure of pseudorabies virus C-capsid
Authors : Zheng, Q.; Li, S.; Zha, Z.; Sun, H.
Deposited on : 2021-08-02
Resolution : 4.43 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:

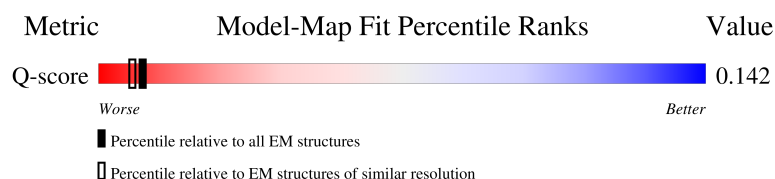
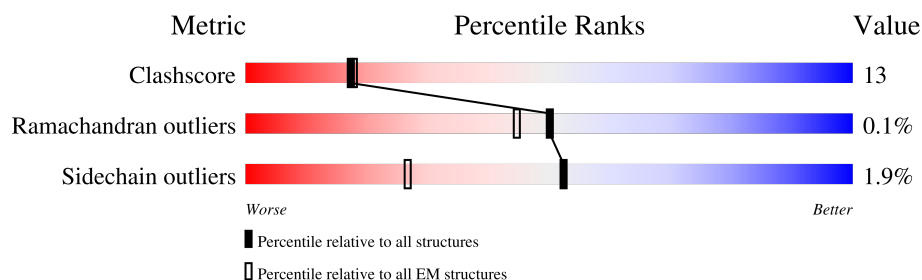
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.48.1

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 4.43 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	3083 (3.93 - 4.93)

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	1330	27% 74% 25%
1	A	1330	22% 71% 27%
1	S	1330	27% 69% 28%
1	U	1330	23% 73% 25%

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Mol	Chain	Length	Quality of chain
1	a	1330	
1	e	1330	
1	f	1330	
1	g	1330	
1	l	1330	
1	m	1330	
1	n	1330	
1	p	1330	
1	q	1330	
1	u	1330	
1	w	1330	
1	y	1330	
2	1	296	
2	2	296	
2	3	296	
2	j	296	
2	k	296	
2	o	296	
2	s	296	
2	v	296	
2	x	296	
2	z	296	
3	B	597	
4	E	103	
4	F	103	

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Mol	Chain	Length	Quality of chain
4	G	103	
4	H	103	
4	I	103	
4	J	103	
4	K	103	
4	L	103	
4	M	103	
4	N	103	
4	O	103	
4	P	103	
4	Q	103	
4	R	103	
4	V	103	
5	T	368	
5	h	368	
5	i	368	
5	r	368	
5	t	368	
6	X	534	
6	c	534	
7	Y	62	
7	Z	62	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 210927 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	A	1308	Total	C	N	O	S	0	0
			10112	6393	1820	1837	62		
1	S	1289	Total	C	N	O	S	0	0
			9975	6307	1797	1812	59		
1	U	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	a	1289	Total	C	N	O	S	0	0
			9974	6311	1797	1805	61		
1	e	1126	Total	C	N	O	S	0	0
			8722	5528	1561	1579	54		
1	f	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	g	1310	Total	C	N	O	S	0	0
			10125	6401	1823	1840	61		
1	l	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	m	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	n	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	p	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	q	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	u	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	w	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		
1	y	1311	Total	C	N	O	S	0	0
			10129	6403	1824	1841	61		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	2	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	3	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	j	267	Total	C	N	O	S	0	0
			2009	1269	365	364	11		
2	k	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	o	296	Total	C	N	O	S	0	0
			2229	1403	414	401	11		
2	s	277	Total	C	N	O	S	0	0
			2088	1318	382	377	11		
2	v	289	Total	C	N	O	S	0	0
			2189	1380	404	394	11		
2	x	296	Total	C	N	O	S	0	0
			2229	1403	414	401	11		
2	z	294	Total	C	N	O	S	0	0
			2210	1391	412	396	11		

- Molecule 3 is a protein called Capsid vertex component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	524	Total	C	N	O	S	0	0
			4023	2540	764	706	13		

- Molecule 4 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	F	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	G	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	H	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	I	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	J	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	K	91	Total	C	N	O	S	0	0
			722	453	139	128	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	M	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	N	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	O	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	P	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	Q	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	R	91	Total	C	N	O	S	0	0
			722	453	139	128	2		
4	V	91	Total	C	N	O	S	0	0
			722	453	139	128	2		

- Molecule 5 is a protein called Triplex capsid protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	T	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
5	h	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
5	i	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
5	r	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		
5	t	327	Total	C	N	O	S	0	0
			2538	1582	494	450	12		

- Molecule 6 is a protein called DNA packaging tegument protein UL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	73	Total	C	N	O	S	0	0
			552	346	109	96	1		
6	c	75	Total	C	N	O	S	0	0
			558	350	111	96	1		

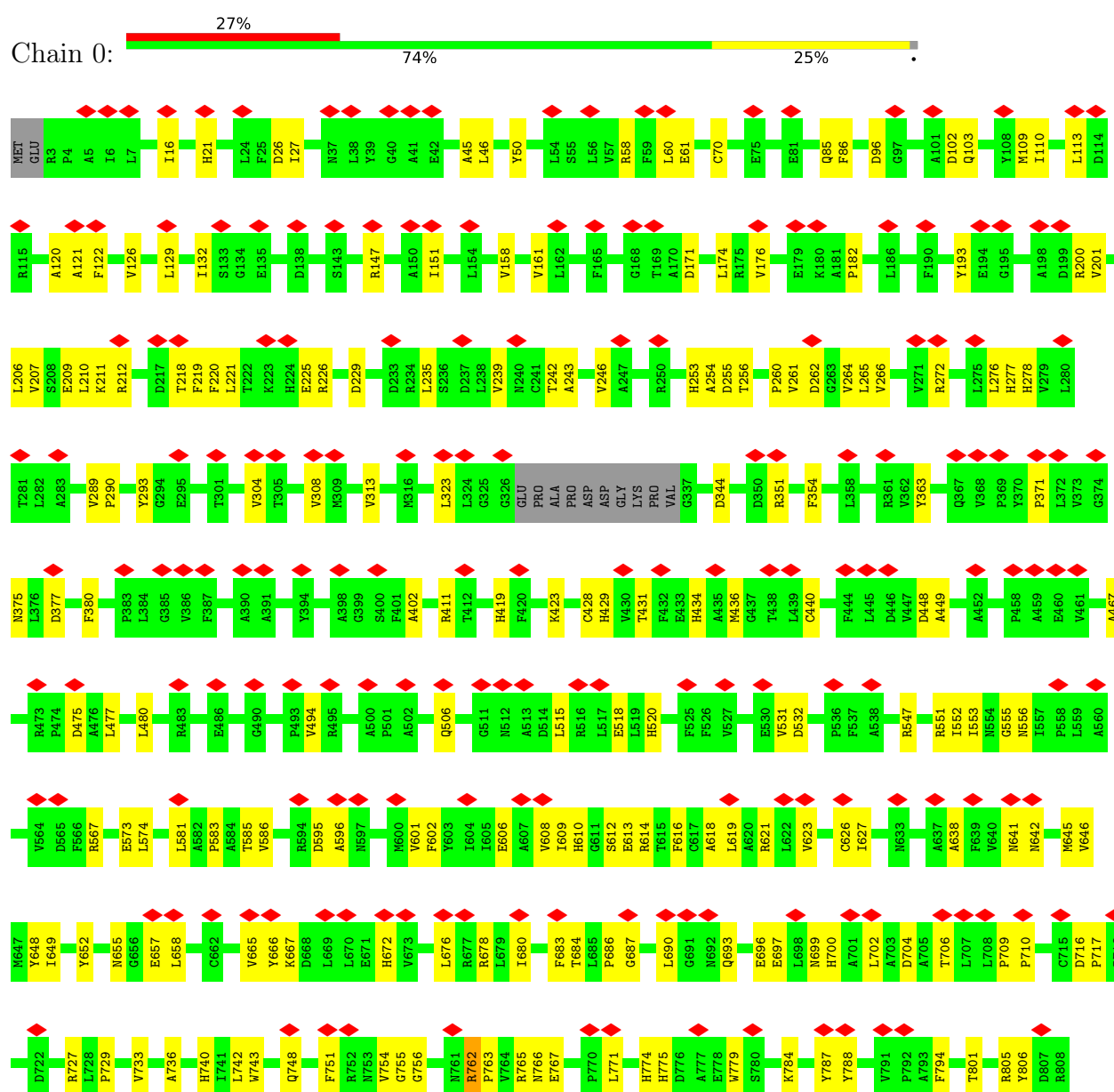
- Molecule 7 is a protein called VP1/2.

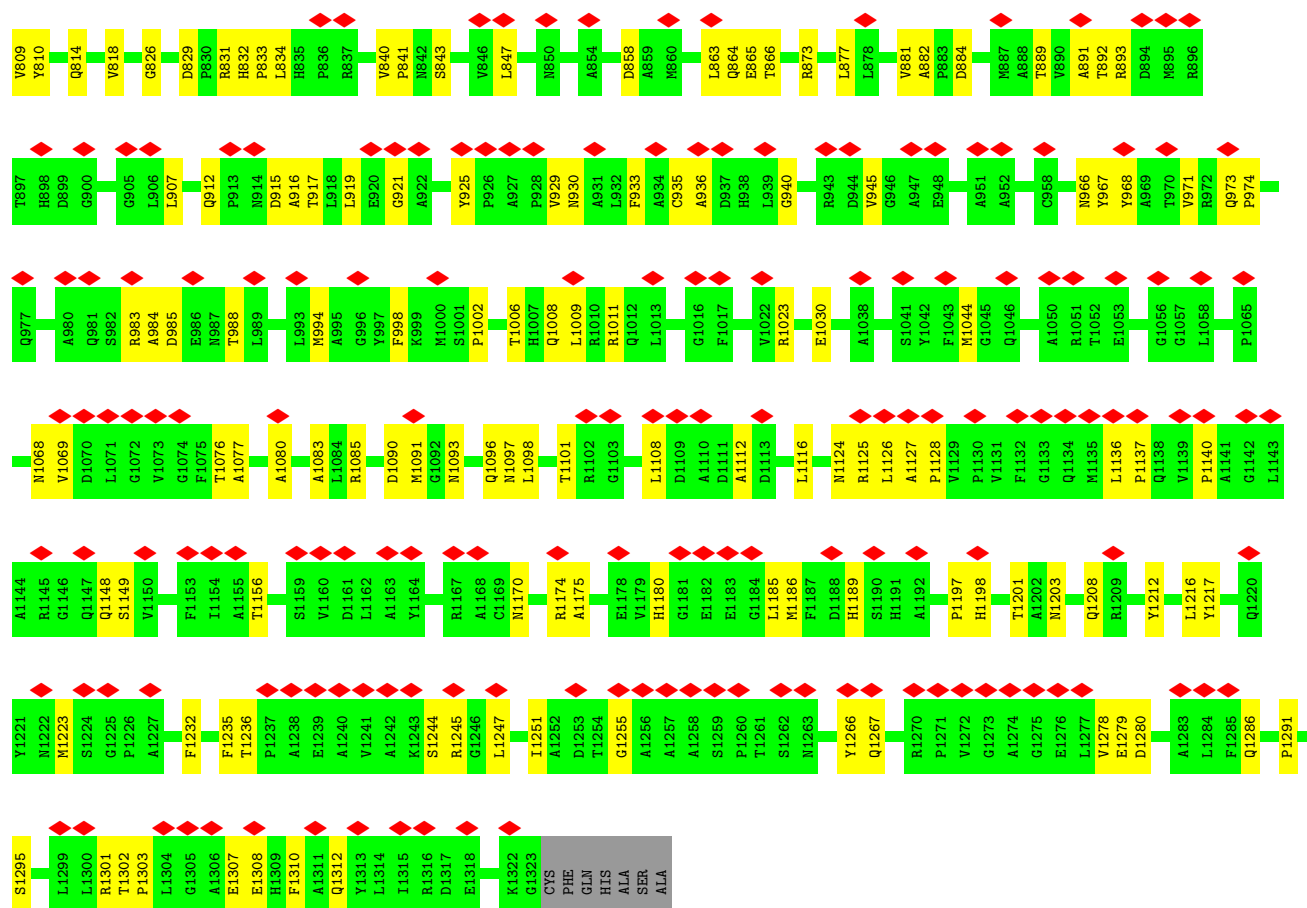
Mol	Chain	Residues	Atoms					AltConf	Trace
7	Y	45	Total	C	N	O	S	0	0
			353	224	72	56	1		
7	Z	35	Total	C	N	O	S	0	0
			288	180	62	45	1		

3 Residue-property plots

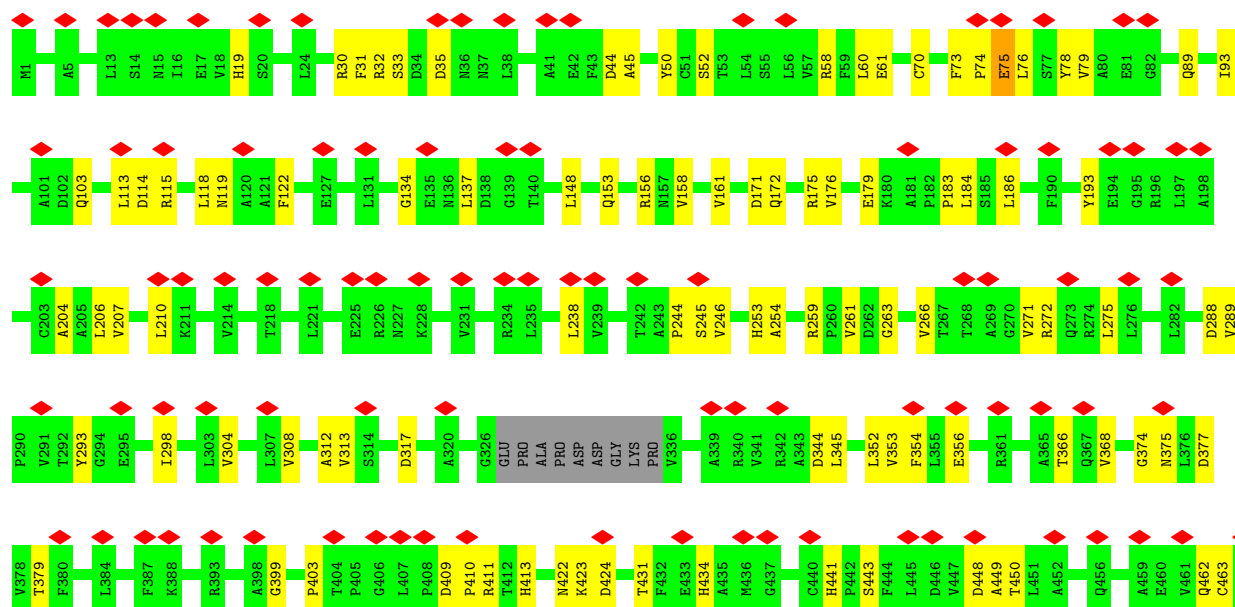
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

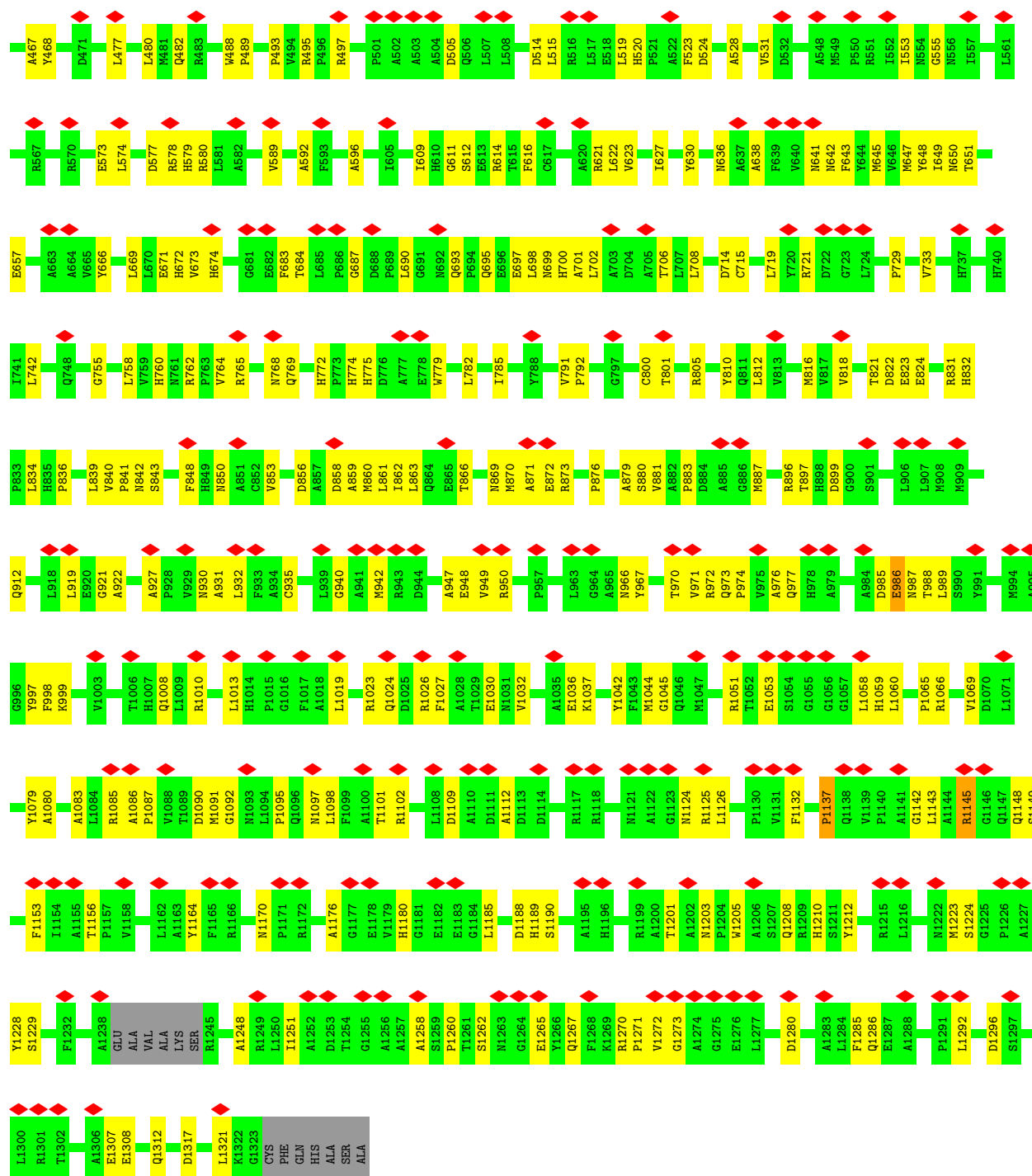
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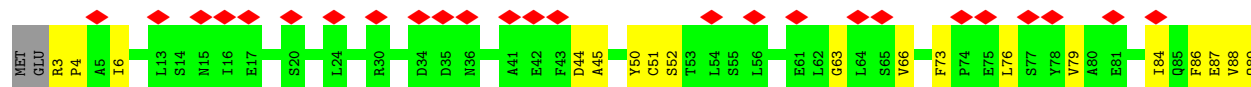


• Molecule 1: Major capsid protein

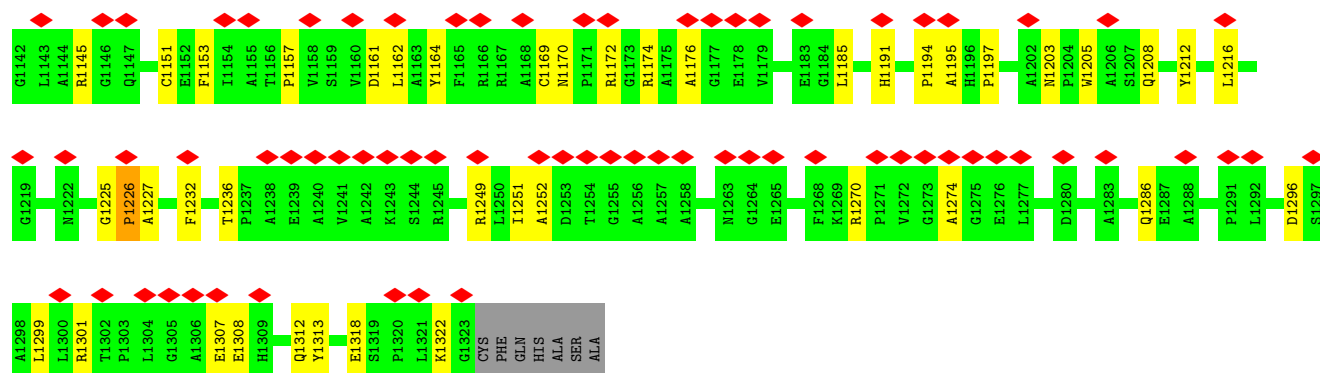




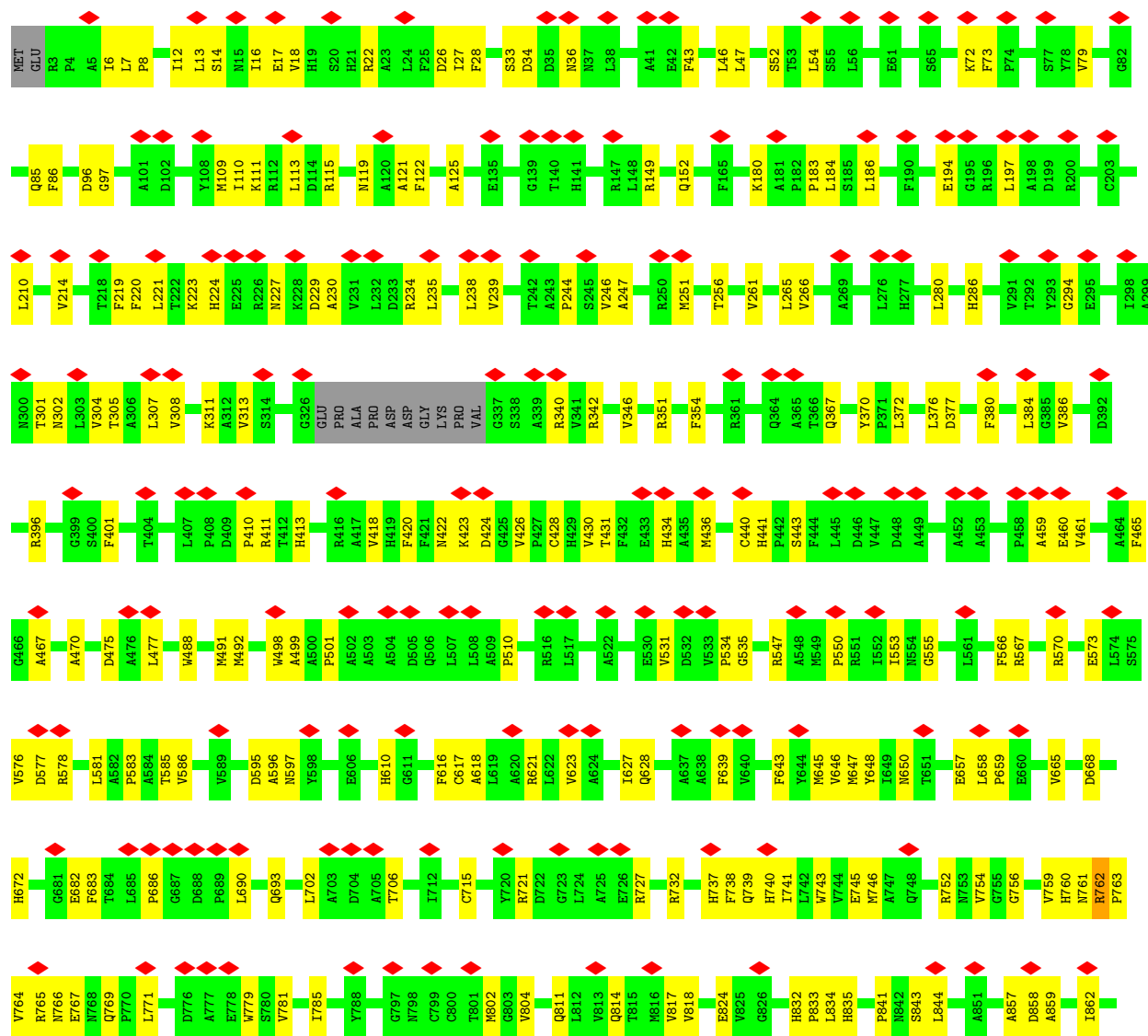
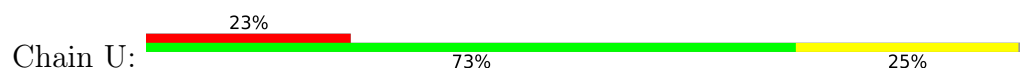
• Molecule 1: Major capsid protein

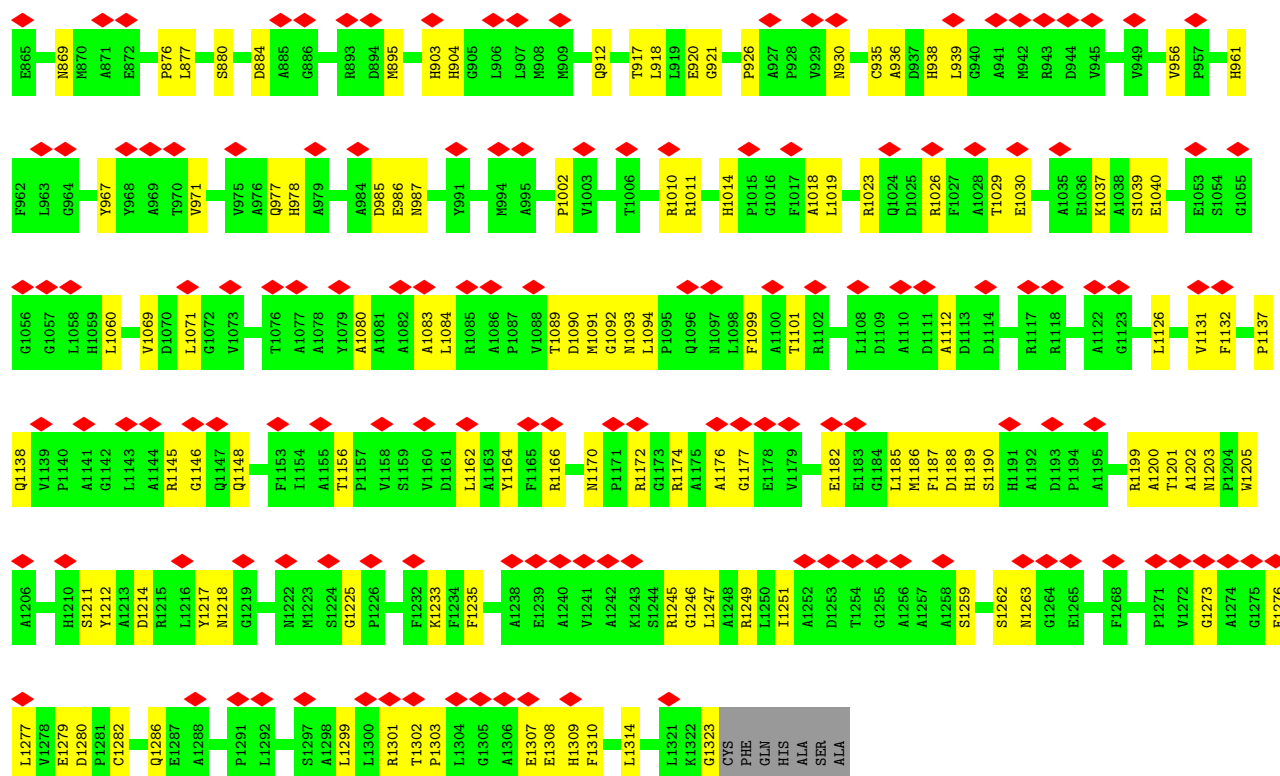




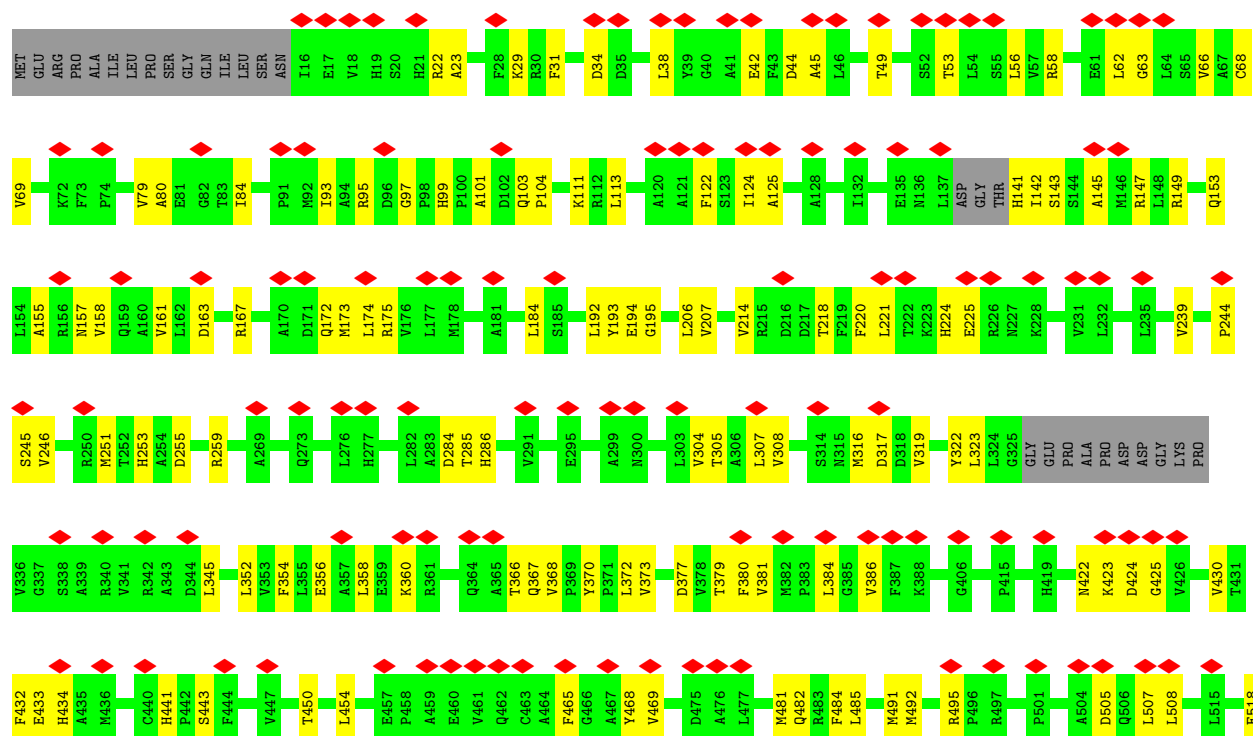


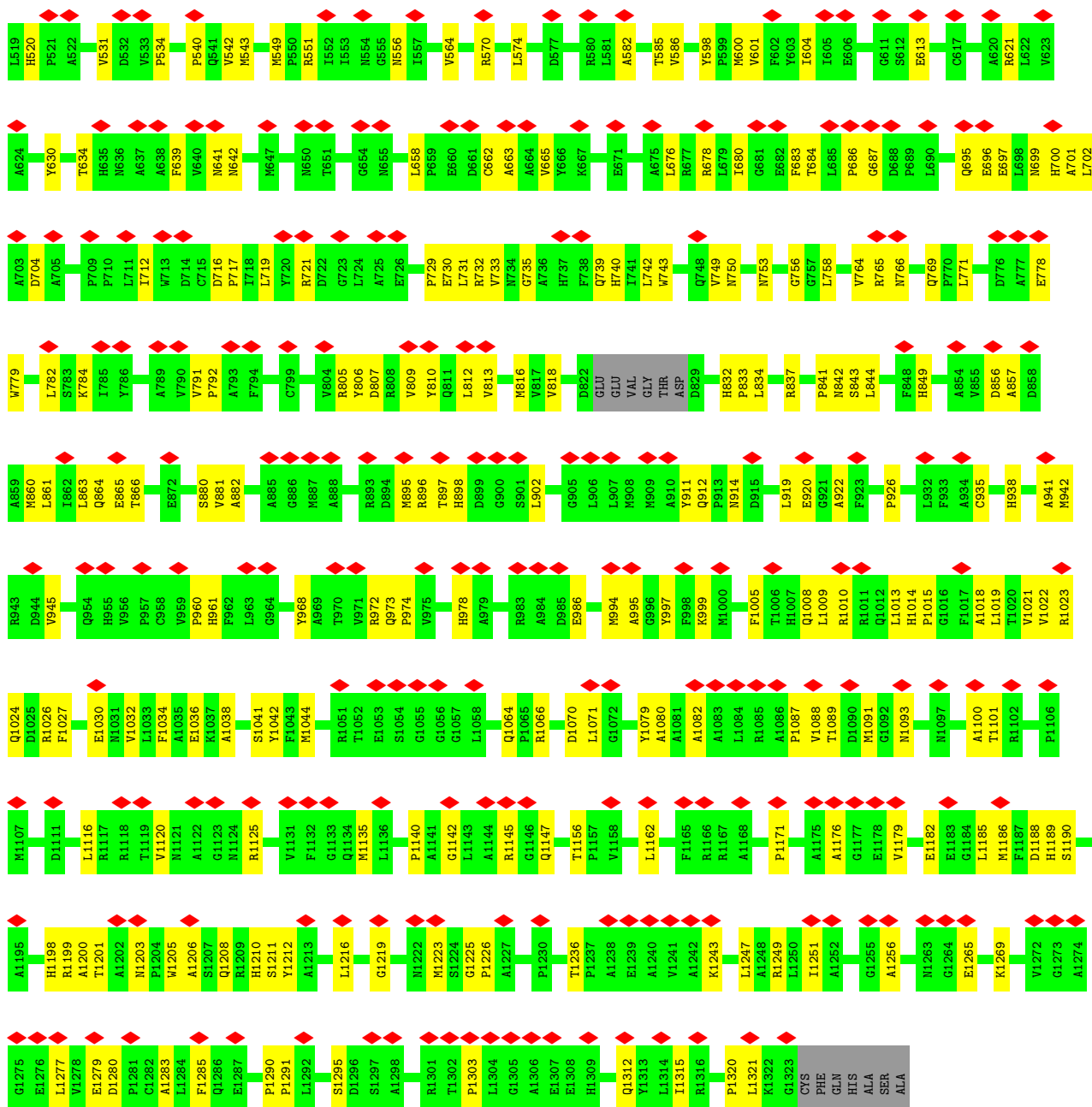
• Molecule 1: Major capsid protein



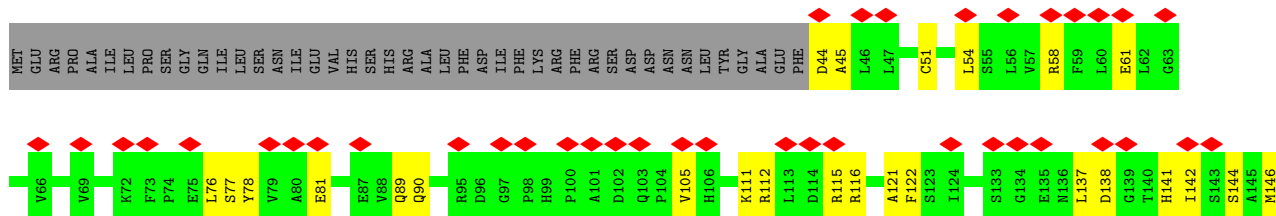


• Molecule 1: Major capsid protein

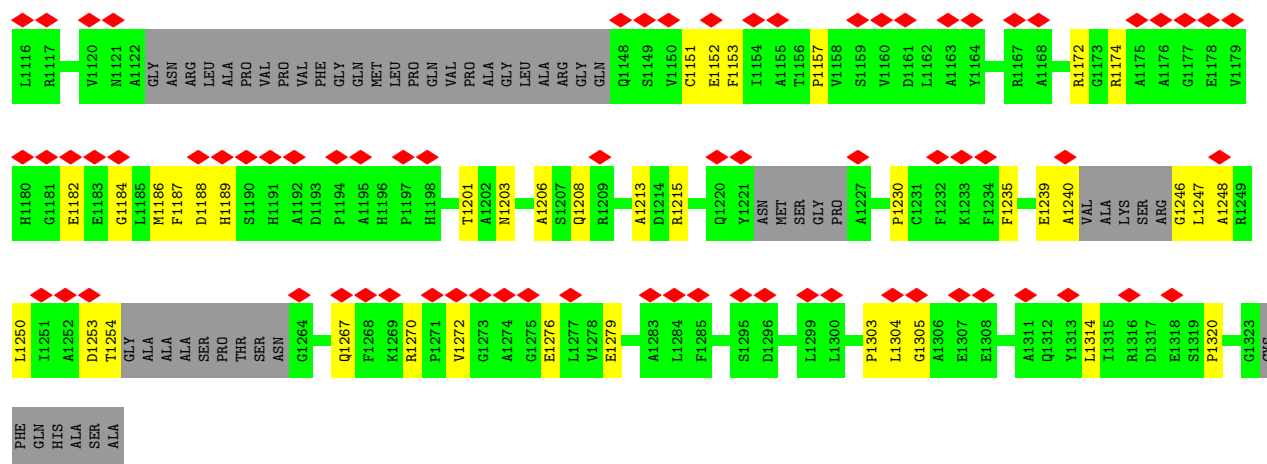




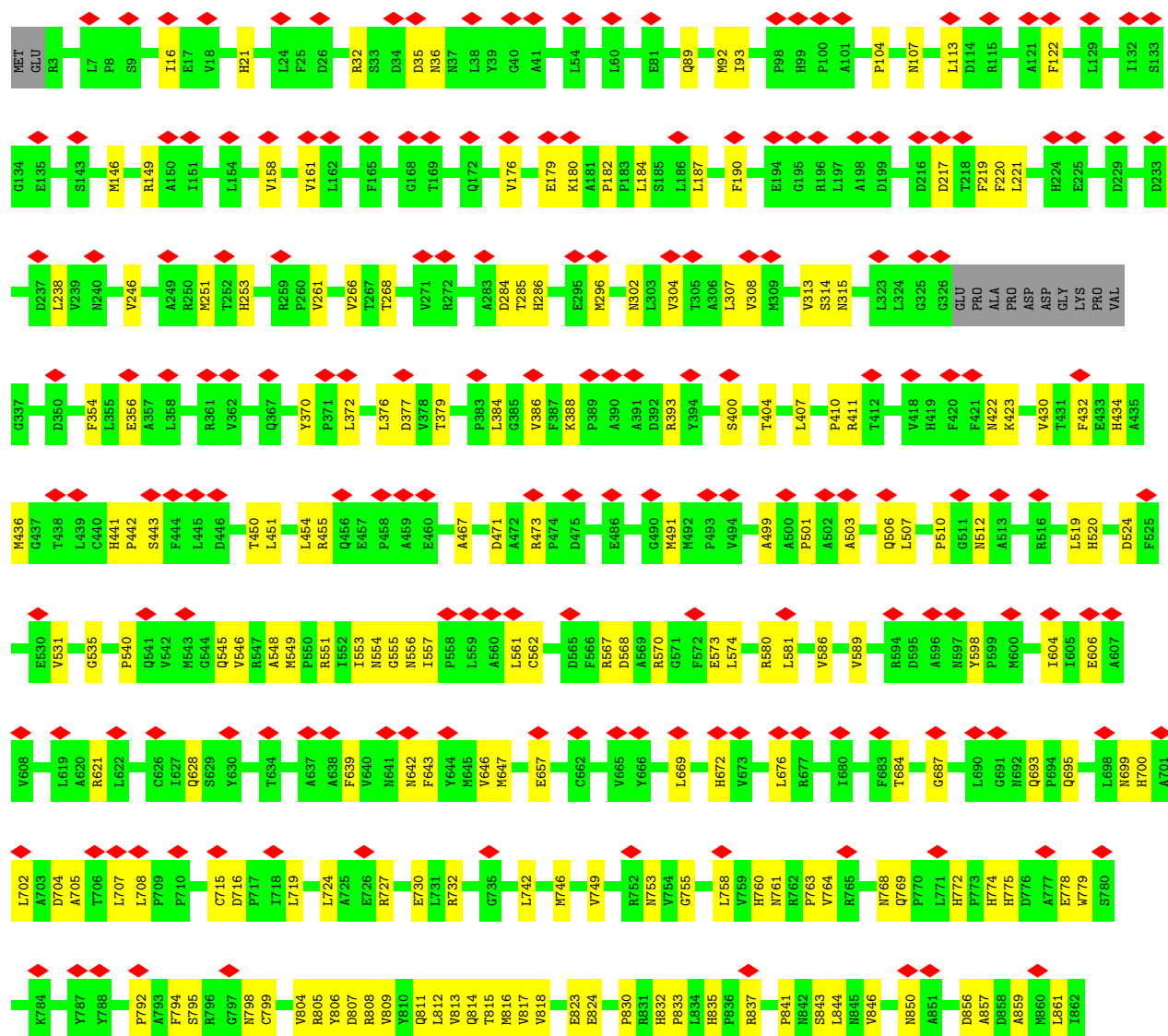
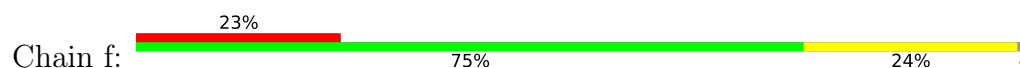
• Molecule 1: Major capsid protein

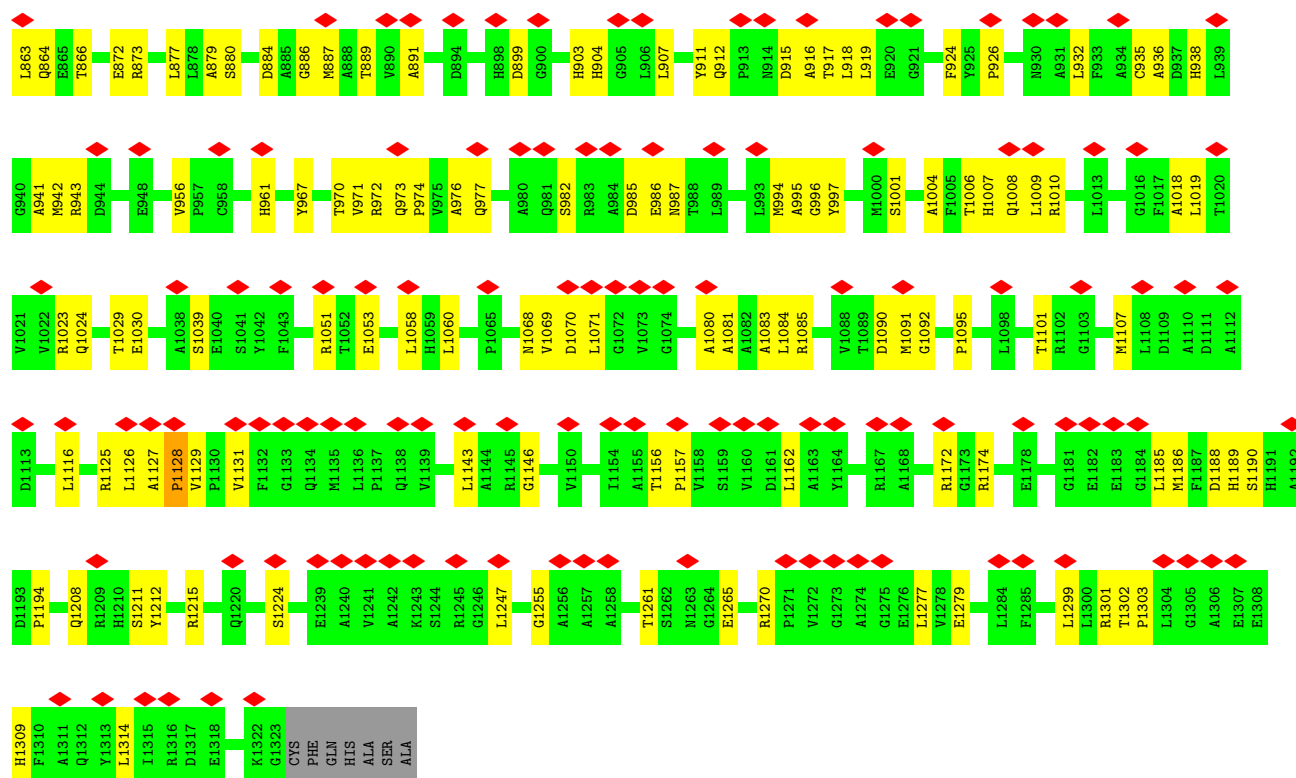




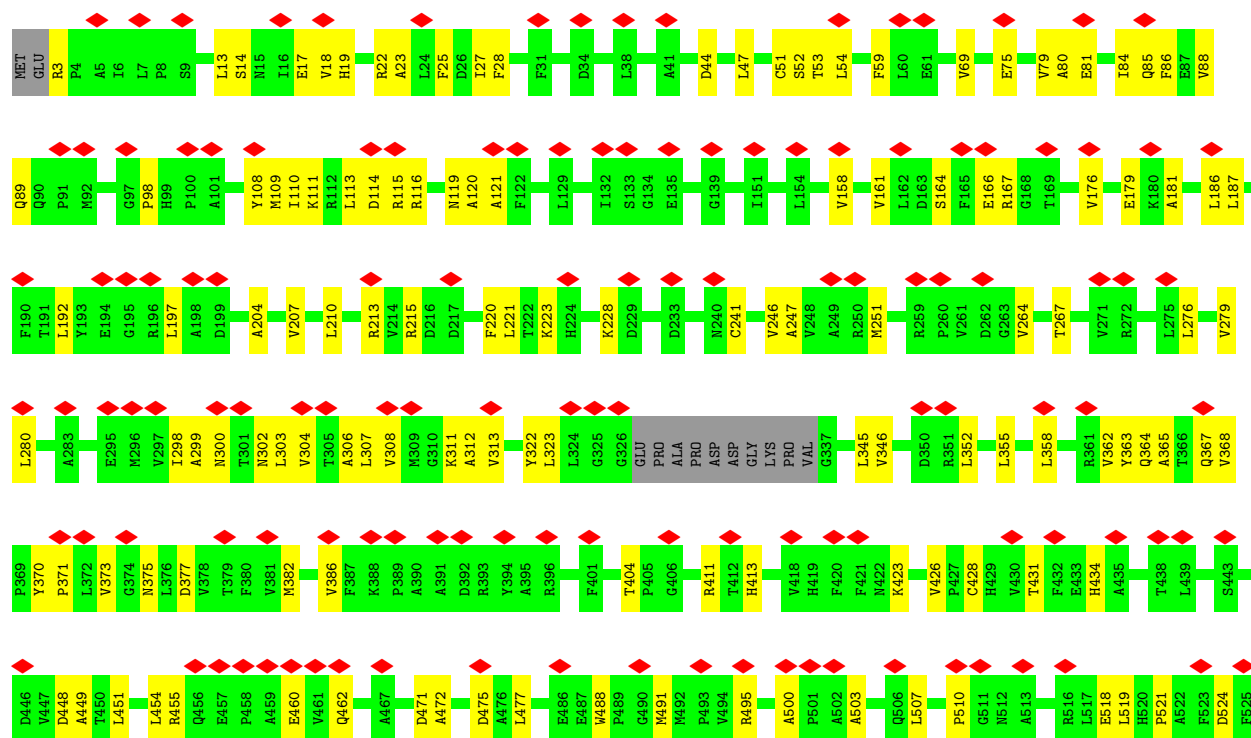


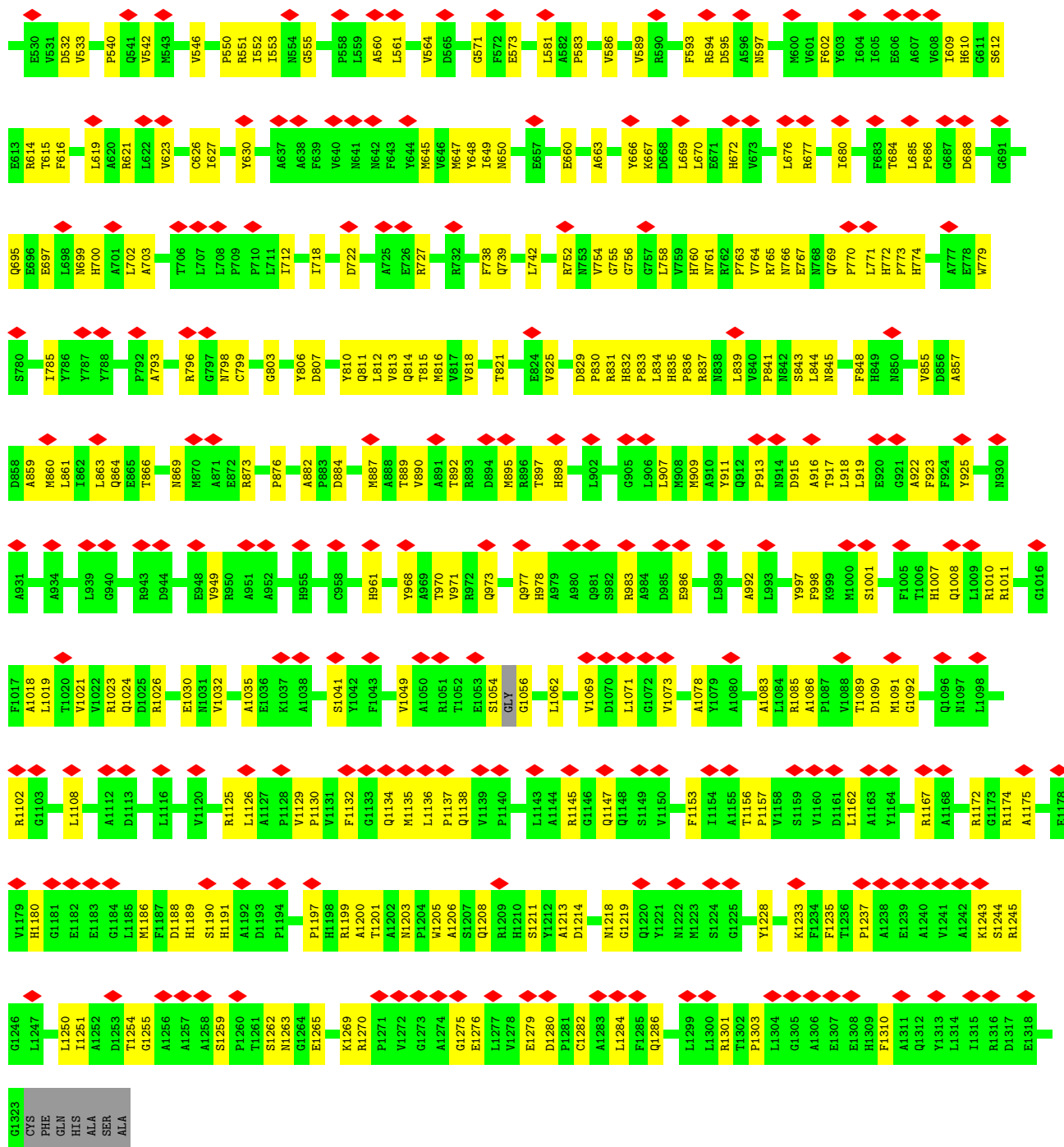
• Molecule 1: Major capsid protein



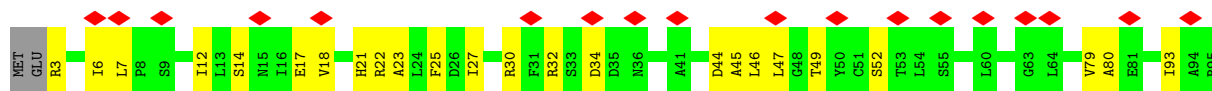


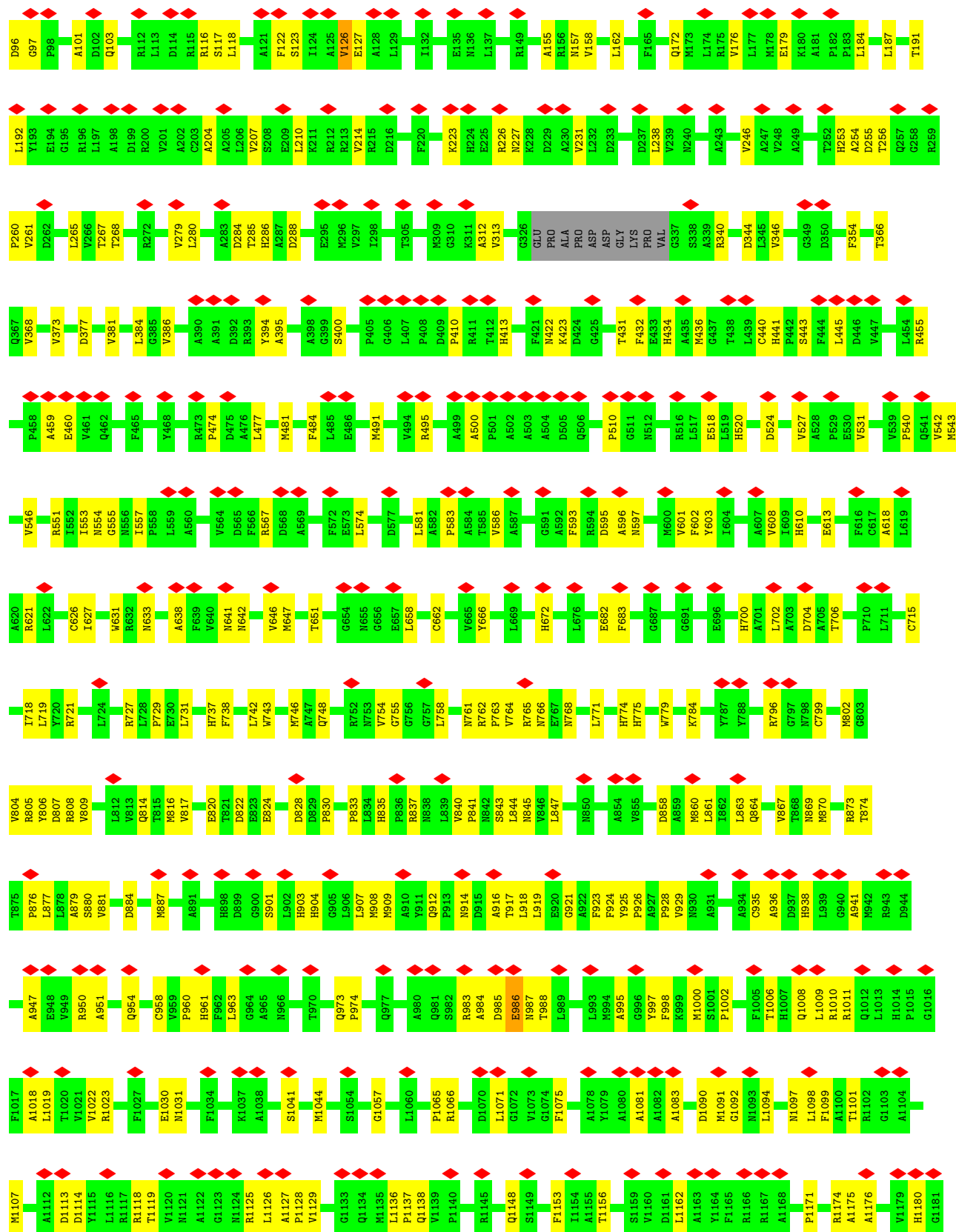
• Molecule 1: Major capsid protein

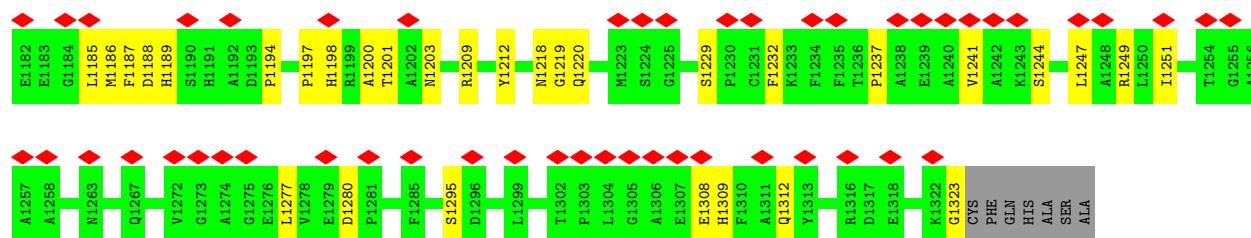




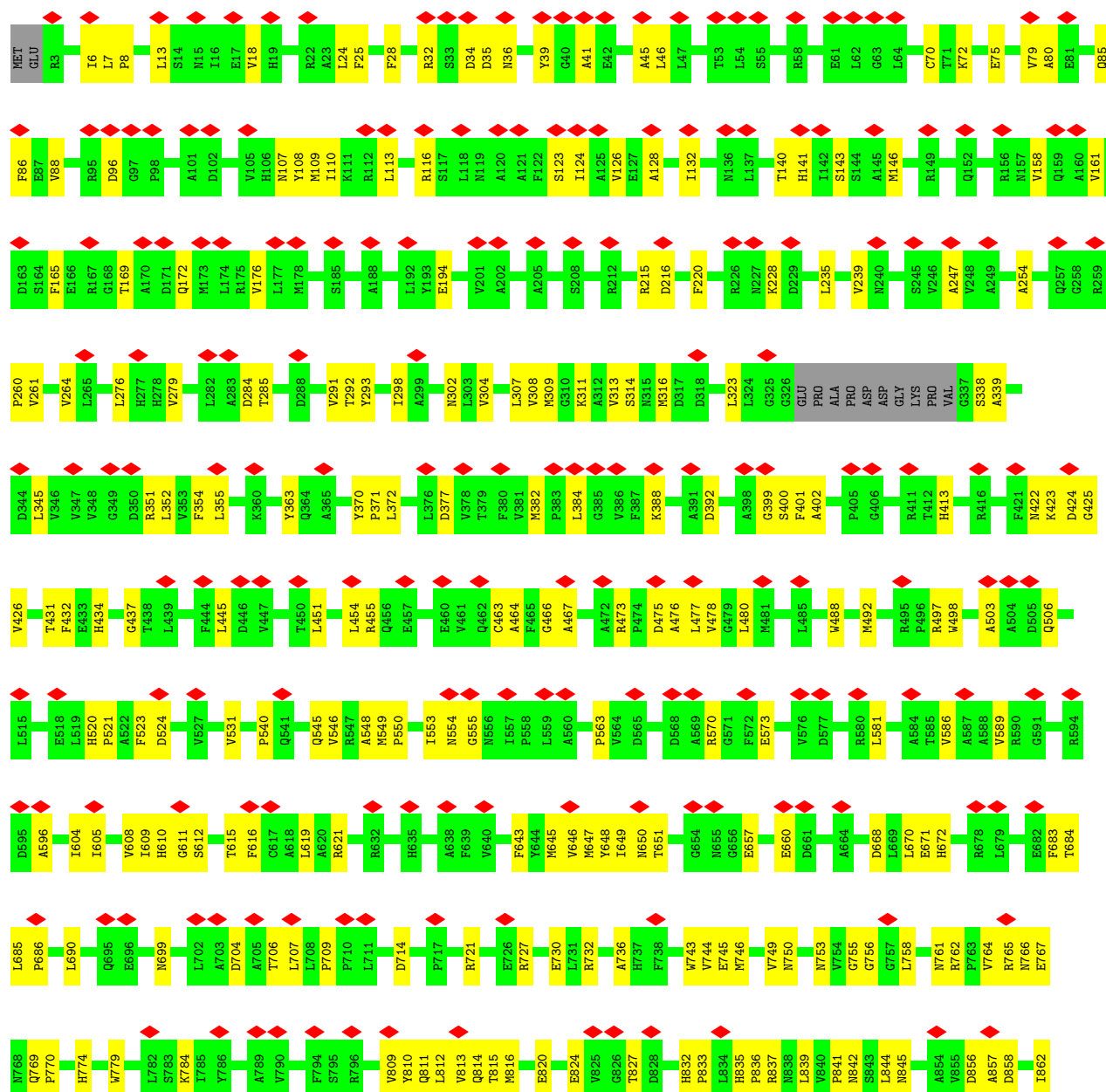
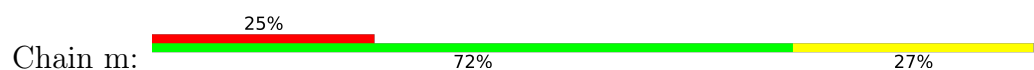
• Molecule 1: Major capsid protein

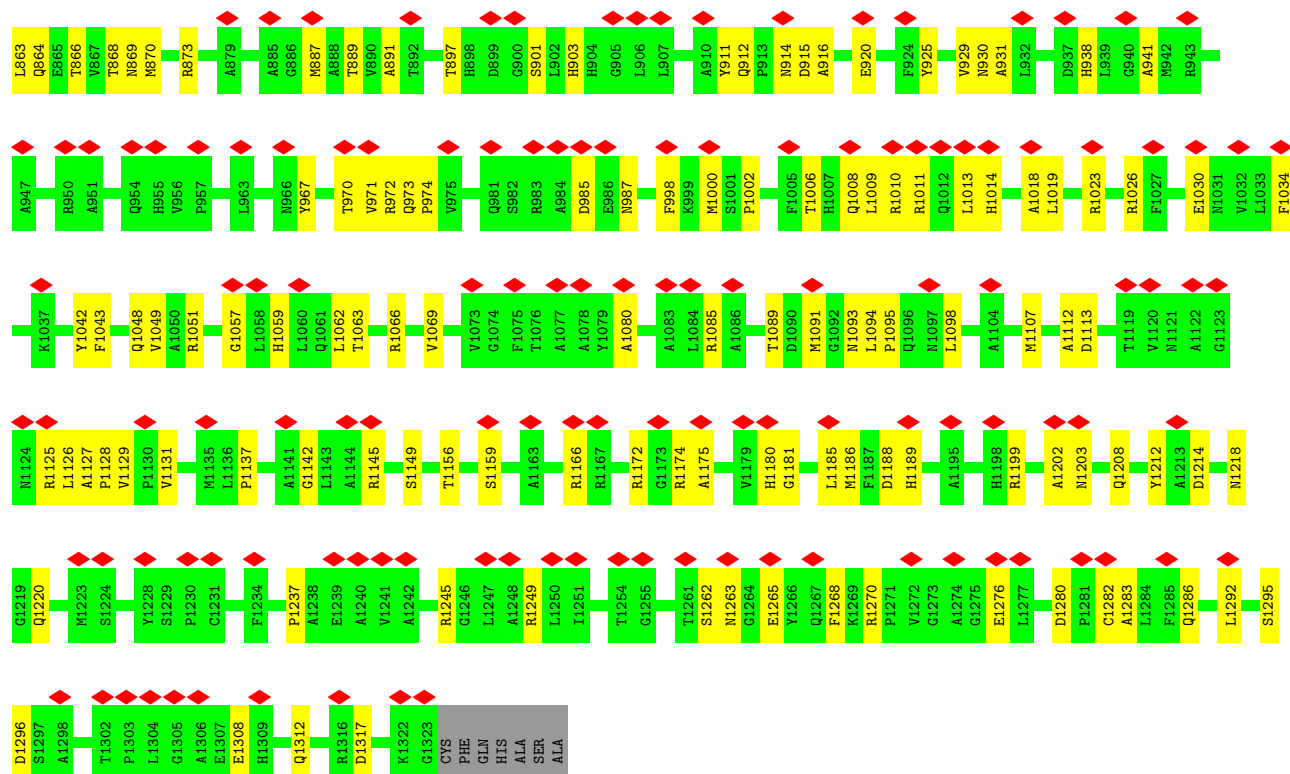




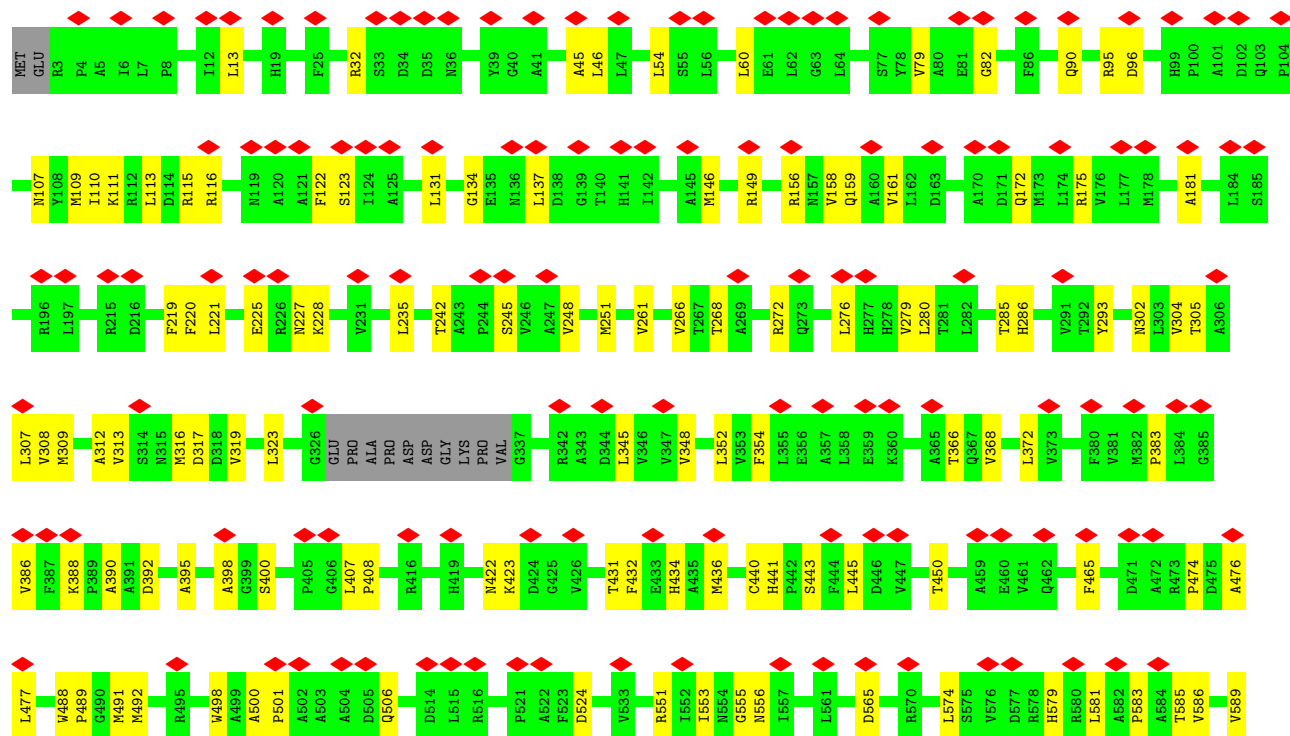
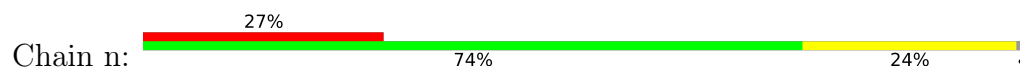


• Molecule 1: Major capsid protein

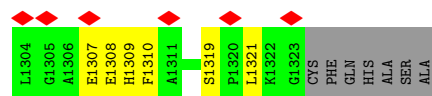




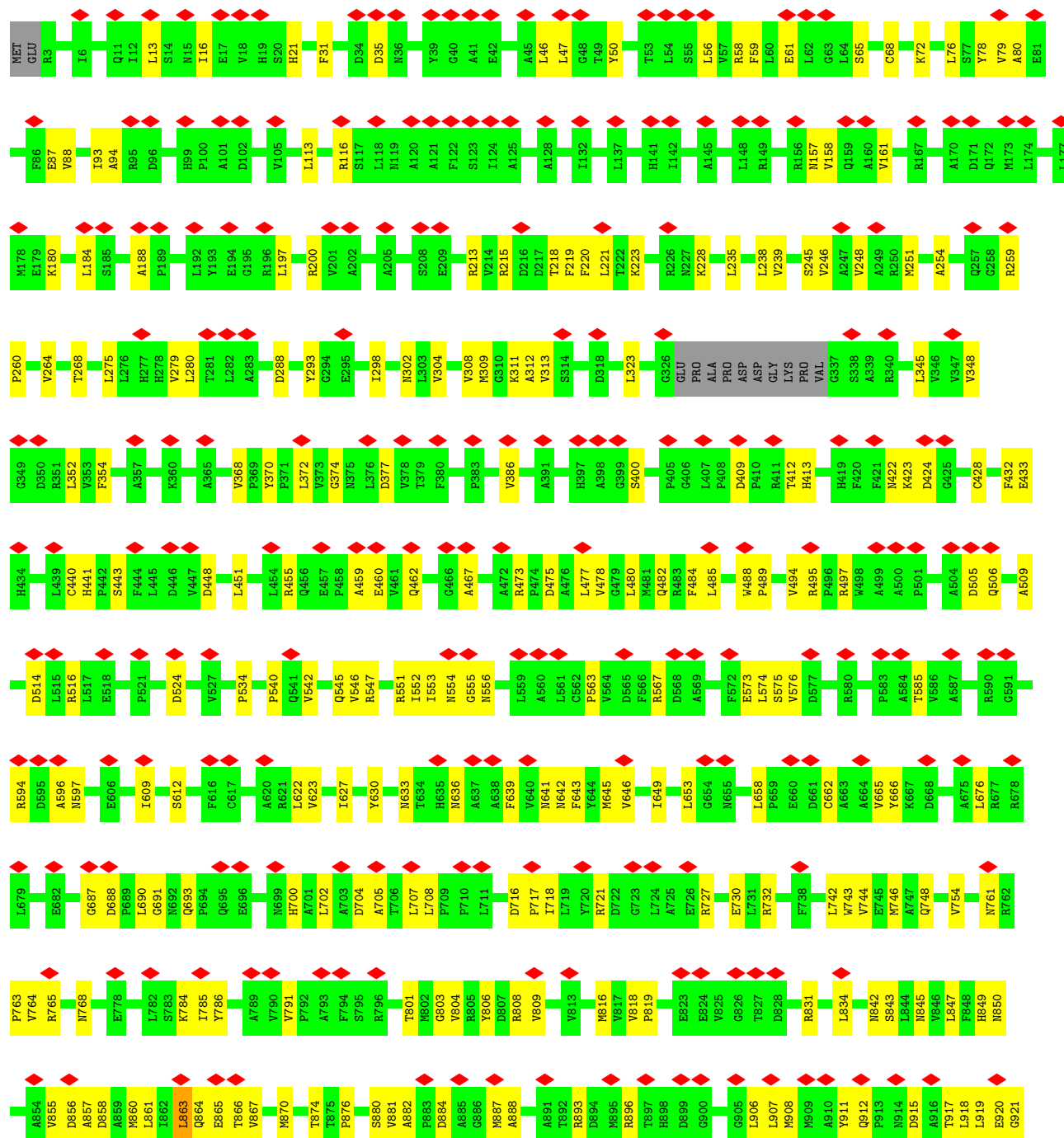
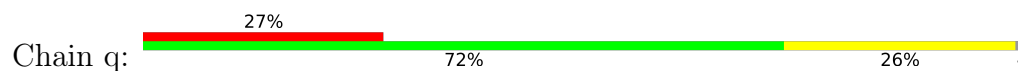
• Molecule 1: Major capsid protein

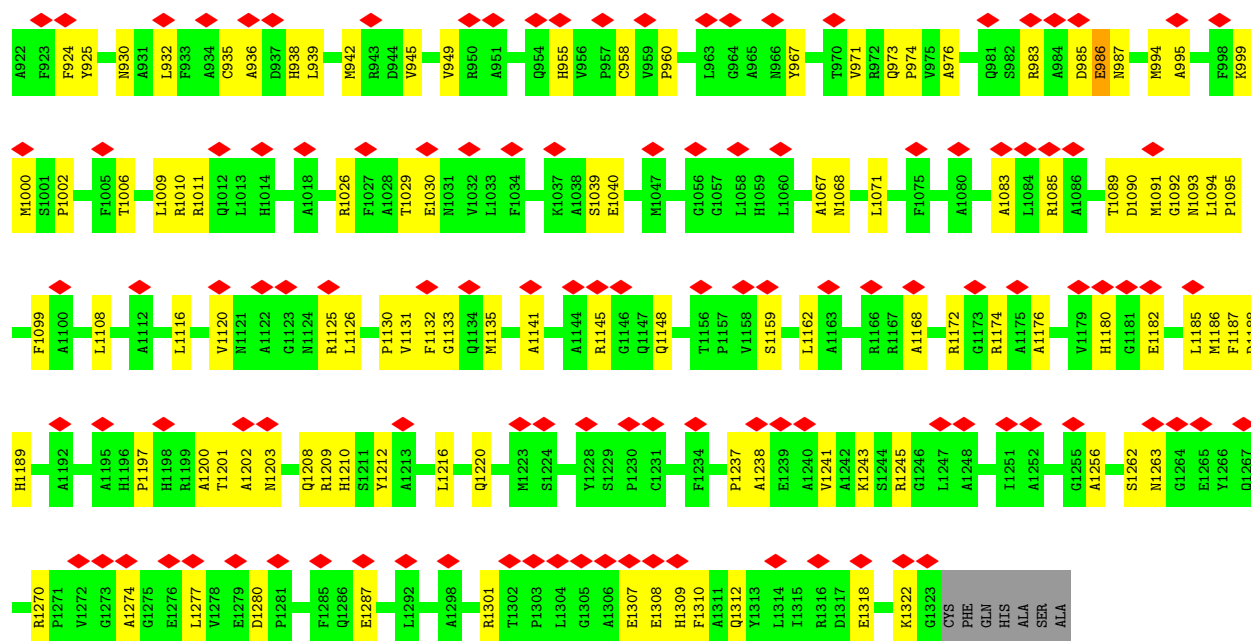


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		R274	L275	L276		V279	L280	D284	T285		Y293		I298	A299	N300	N301	L302	L303	V304		L307	V308	M309		A312	V313	M316	D317		A320	L324	G325	G326	GLU	PRQ	ALA	ASP	ASP	GLY	LYS	PRQ	VAL	G337	S338	A339	R340	V341	D350	F354	L355	E356	A357	L358	E359					
K360		D471		Q367	V368	P371		N375	L376	D377		V386	F387		D392	A395	R396		S400	F401		L407	P408	D409	P410	R411	T412	H413		F420		V430		T438	L439	C440	H441	P442	S443	F444	L445	D446	V447	D448	A449	A452	Q456	E457	P458	A459	E460	V461	A464	Y468					
A470		D471		D475		A476	L477	V478	G479	L480	M481		F484	L485	E486	E487	M488	P489	G490	M491	M492	P493	V494	R495	P496	R497	W498		A502	R594	D595	A596		M600		Y603	I604	I605	E606	A607	V608	I609	H610		E613	R614	T615	F616	L619	A620	R621	L622	V623	C626	I627	Q628	S629	Y630	A637
N554	G555	N556	I557	A560	L561		D565	F566	R567	F568	D568	A569	R570	L574	S575	V576	D577	R578		A582		T585	V586	F593	R594	D595	A596		M600		Y603	I604	I605	E606	A607	V608	I609	H610		E613	R614	T615	F616	L619	A620	R621	L622	V623	C626	I627	Q628	S629	Y630	A637					
A638	F639	V640	N641		Y644	M645	V646	M647	Y648	I649		Y652	L653	G654	G656	E657	L658	P659		C662		V665	Y666	L669	V673	R677	I680	F683	T684	L685	P686	G687	D688	P689	L690	G691	Q695	L698	N699	H700	A701	D704	A705	T706	L707	L708	D714	C715	D716										
P717		D722		A725	E726	R727		R732		L742	W743	W746	A747	Q748		R752	N753	V754	G755		H760	N761	R762	P763	V764	R765	N768	Q769	P770	L771		H774	H775	D776	A777	E778	W779	S780		Y787	Y788	P792	A793	F794		G797	N798	C799	Y806	V809	L812	W813	Q814						
T815	H816	T821	E824	D828	D829	P830	P833	L834	H835	R837	W840	P841	N842	S843	L844	N845	W846	L847	F848	H849	N850	A851	D856	A857		X860	L863	Q864	V867	A871	E872	R873	T874	P883	D884	A885	G886	H887	V890	R893	D894	G905	L906	L907	P908														
H909	A910	Y911	N914	E920	G921	P926	A927	P928	Y929	N930	A931	F933	A934	C935	A936	P937	H938	L939	G940	A941	N942	R943	D944	Y945		E948	V949	R950	A951	A952	A953	Q954	H955	Y956	P960	L963	N966	Y967	T970	Q973	Q981	S982	R983	A984	D985	E986	N987	A995											
F998	K999	M1000	S1001	P1002	V1003	T1006	H1007	Q1008	L1009	R1010	L1013	H1014	P1015	G1016	F1017	A1018	R1023	Q1024	D1025	R1026	E1030	N1031	V1032	A1035	A1038	Y1042	F1043	Q1046	M1047	Q1048	V1049	A1050	R1051	T1052	E1053	G1056	G1057	L1058	P1065	R1066	A1067	N1068	V1069	D1070	A1071	L1071	G1072	V1073	G1074										
F1075	T1076	Y1079	A1080	A1081	A1082	L1084	R1085	V1088	T1089	D1090	M1091	G1092	L1094	A1100	T1101	R1102	G1103	A1104	L1108	D1109	A1110	N1111	A1112	D1113	L1116	R1117	R1118	T1119	A1122	R1125	V1129	P1130	V1131	F1132	G1133	Q1134	M1135	L1136	V1139	P1140	A1141	G1142	L1143	A1144	R1145	Q1148	S1149												
V1150	G1151	E1152	F1153	T1154	A1155	T1156	P1157	V1158	S1159	D1161	L1162	F1165	R1166	R1167	A1168	R1172	G1173	R1174	A1175	A1176	G1177	E1178	G1181	E1182	E1183	G1184	L1185	L1186	F1187	L1188	H1189	D1193	P1194	A1195	H1196	P1197	H1198	R1199	A1200	T1201	A1202	N1203	P1204	W1205	Q1208	S1211	Y1212	A1213	D1214	N1218	G1219								
Q1220	Y1221	N1222	M1223	K1233	T1236	P1237	A1238	E1239	A1240	V1241	A1242	K1243	S1244	R1245	G1246	L1247	A1248	R1249	L1250	L1251	A1252	D1253	A1256	A1257	A1258	F1268	K1269	L1270	P1271	V1272	G1273	A1274	G1275	E1276	L1277	V1278	E1279	D1280	A1283	L1284	F1285	Q1286	L1292	L1299	L1300	T1302	P1303												

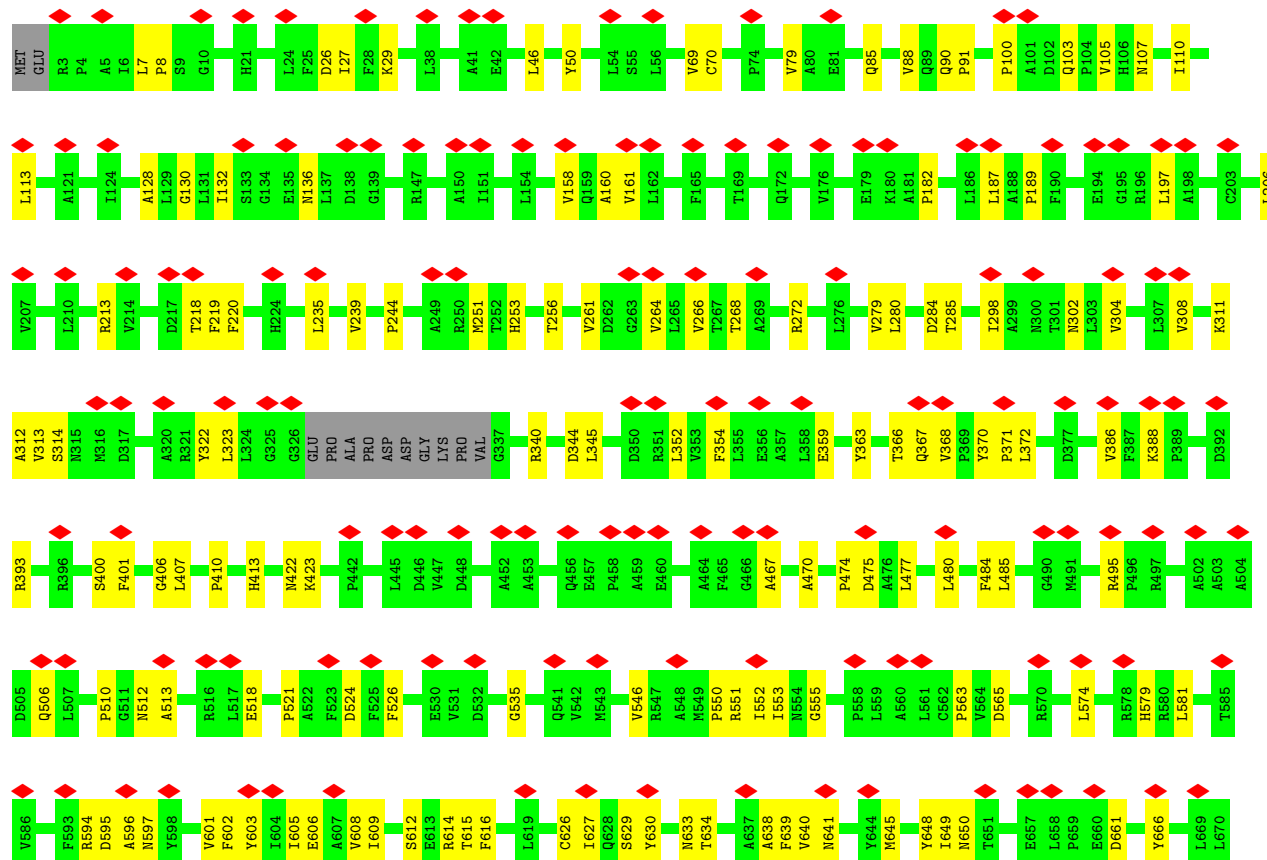
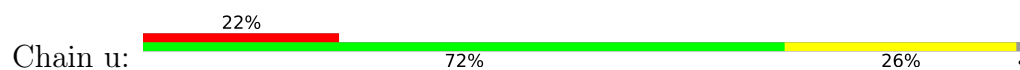


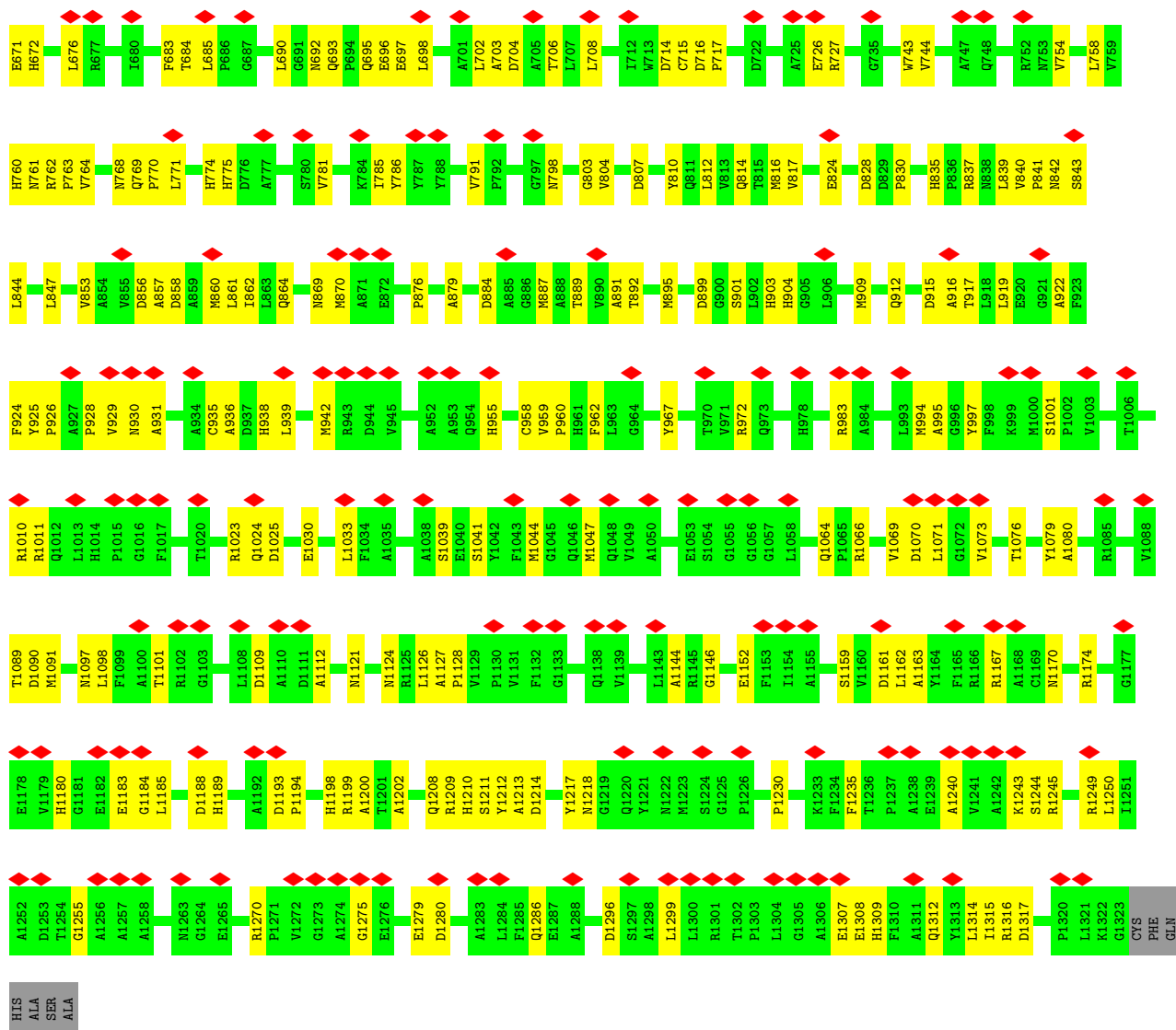
• Molecule 1: Major capsid protein



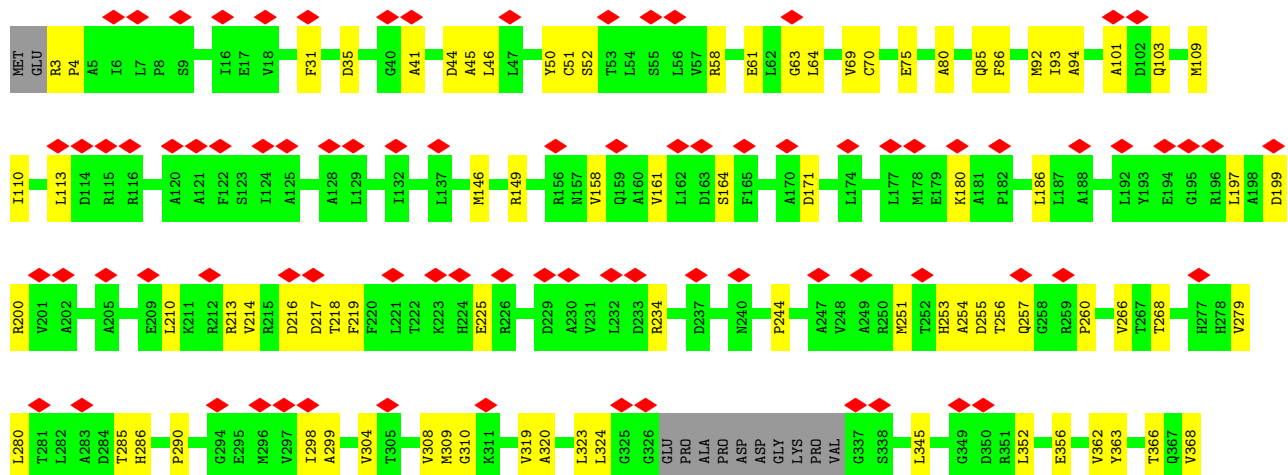


• Molecule 1: Major capsid protein

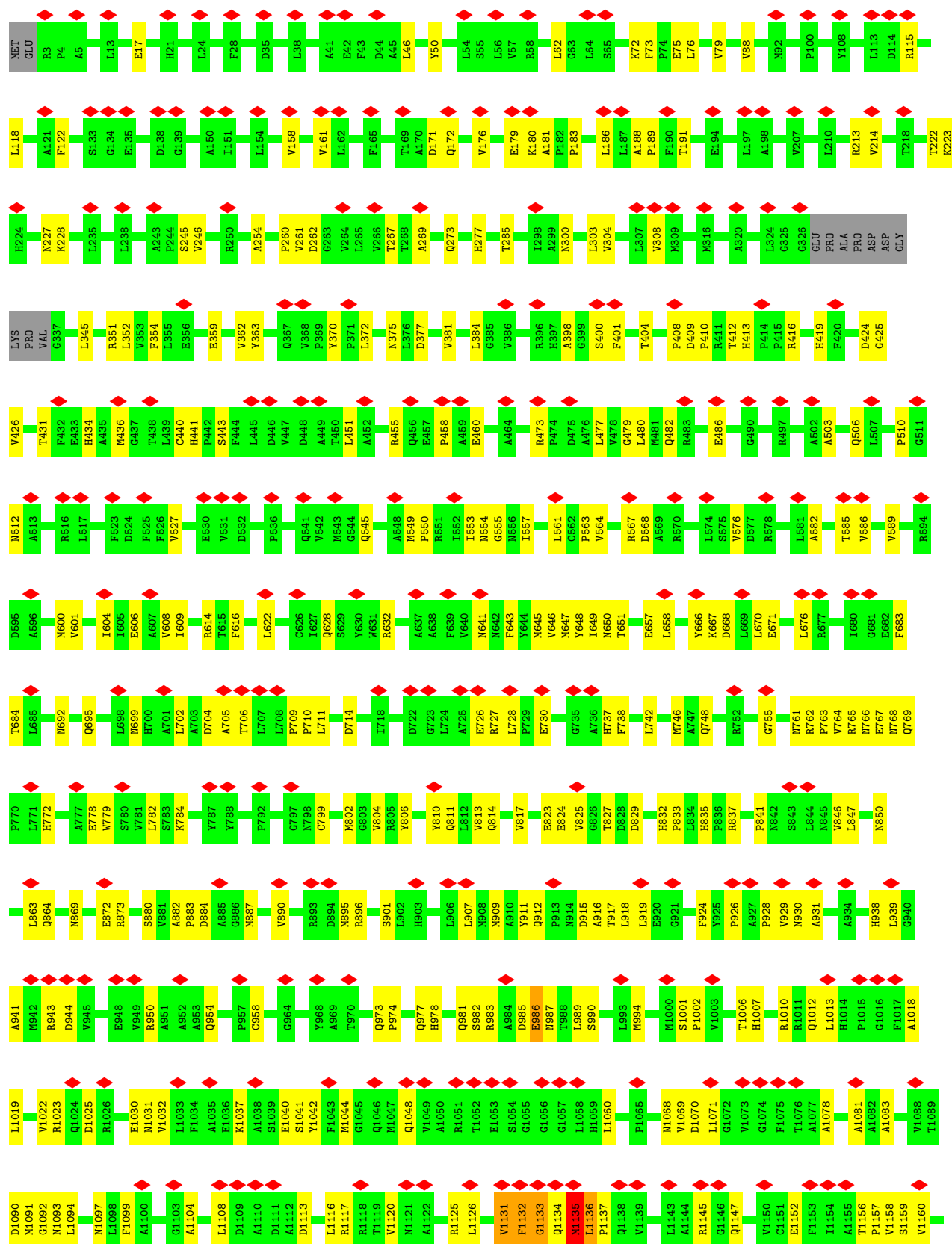


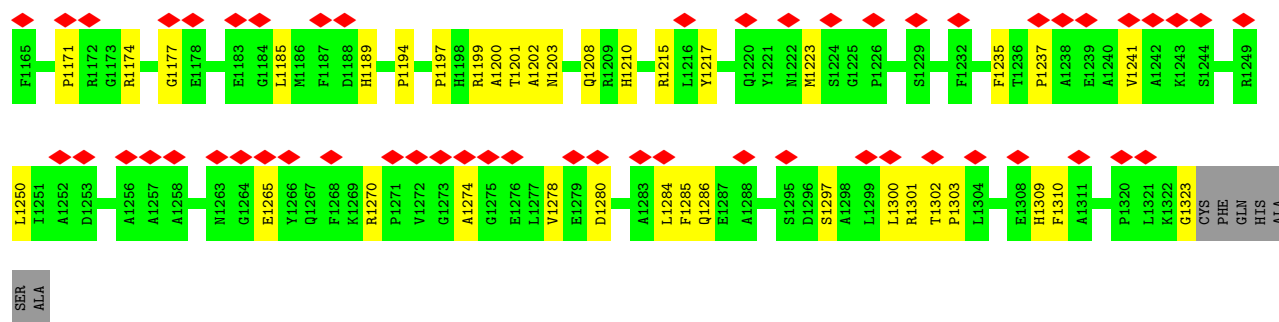


• Molecule 1: Major capsid protein

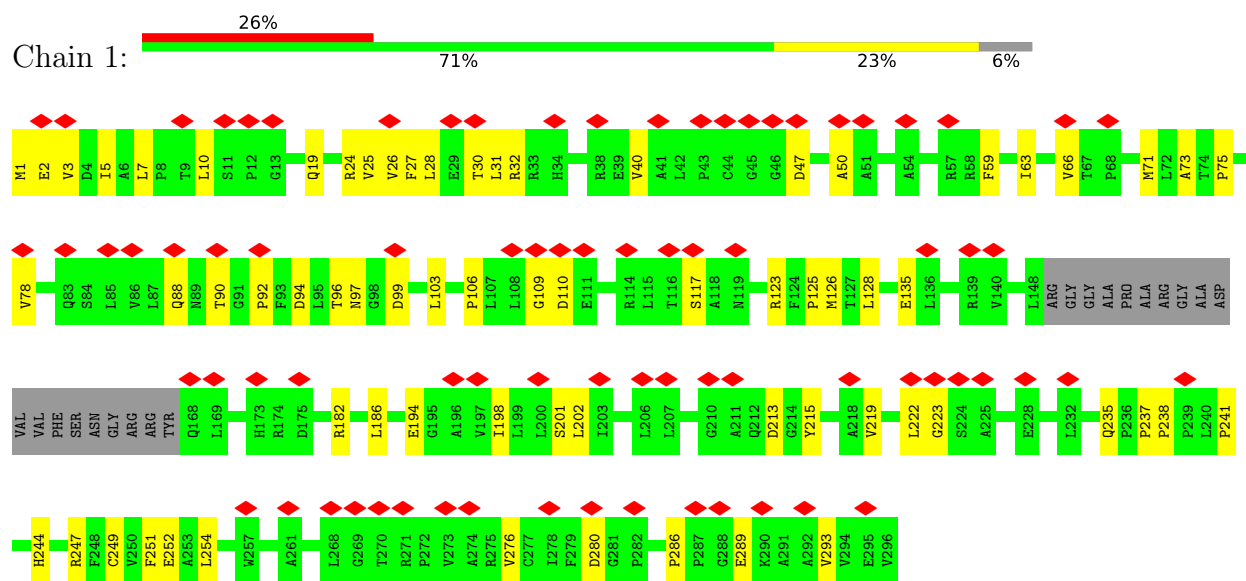




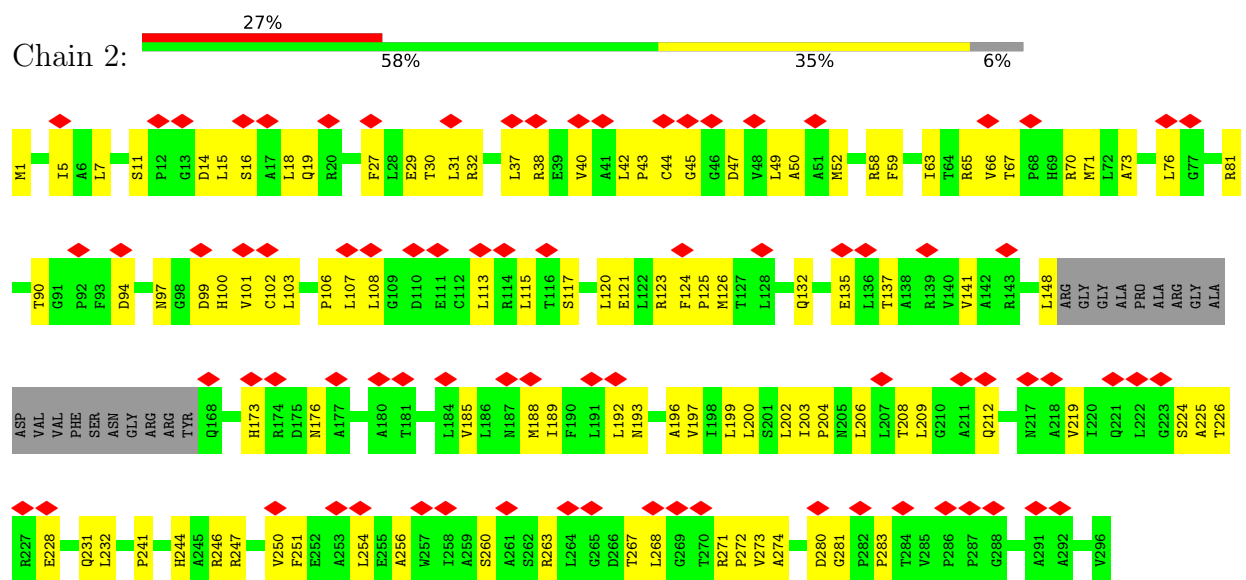




• Molecule 2: Triplex capsid protein 2

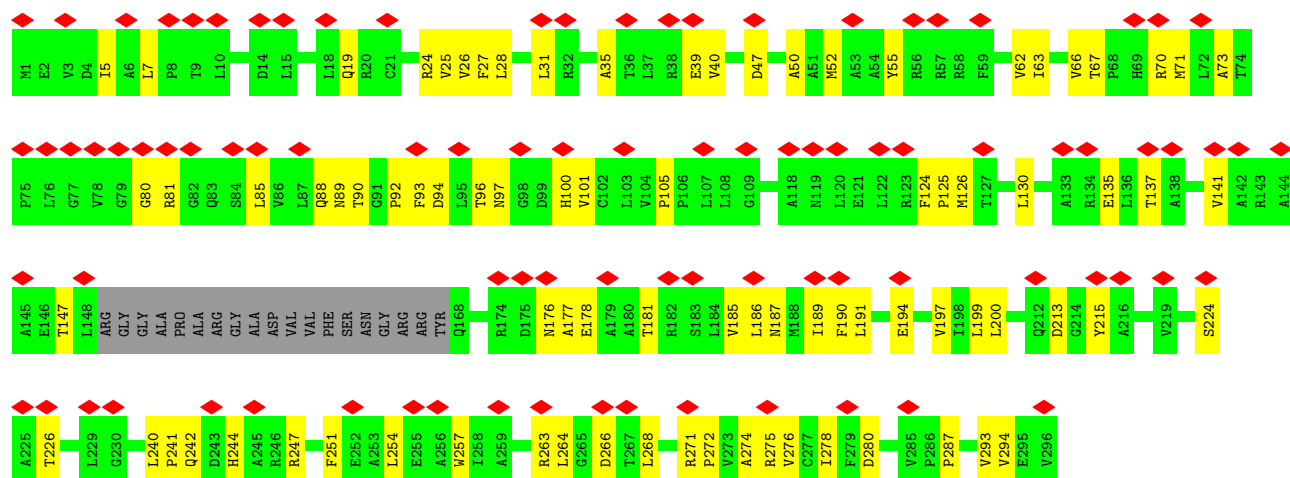


• Molecule 2: Triplex capsid protein 2

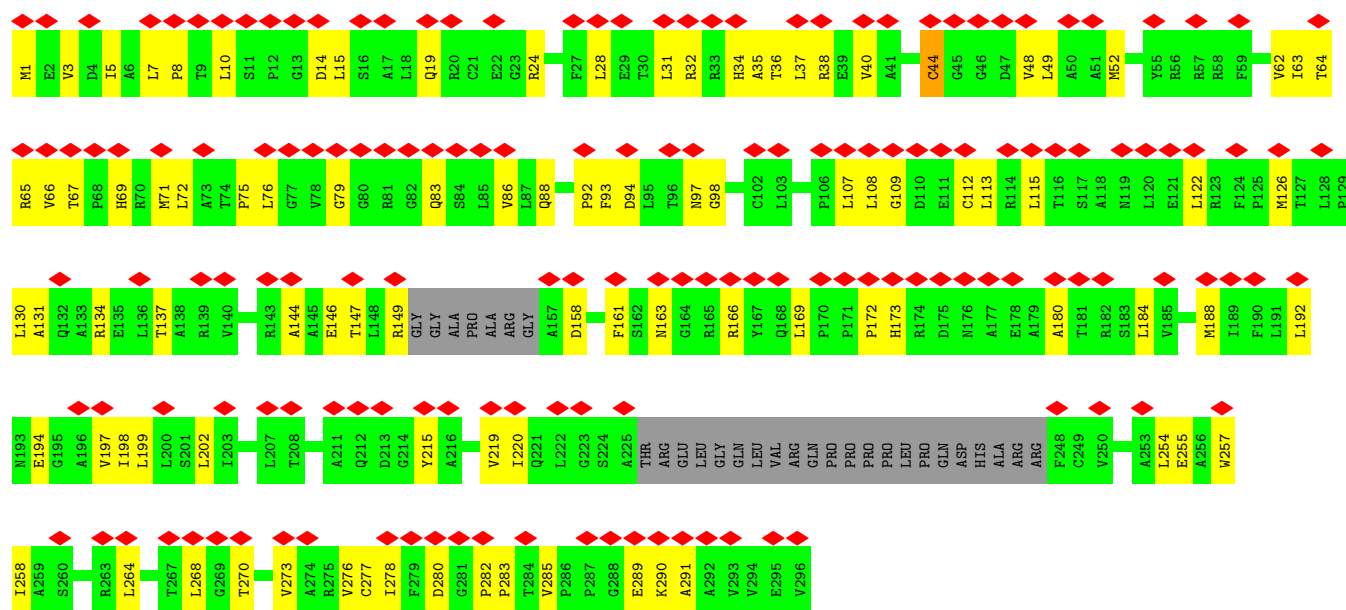


• Molecule 2: Triplex capsid protein 2

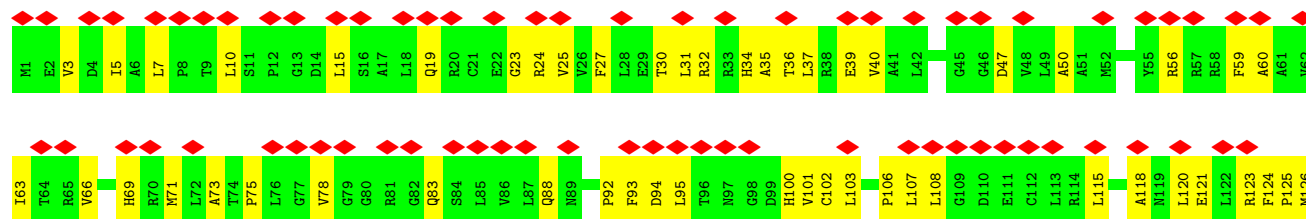


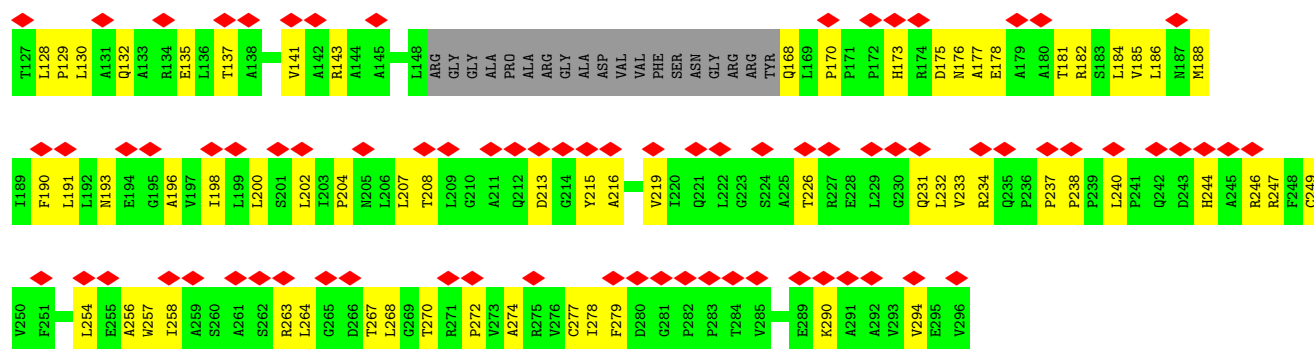


• Molecule 2: Triplex capsid protein 2

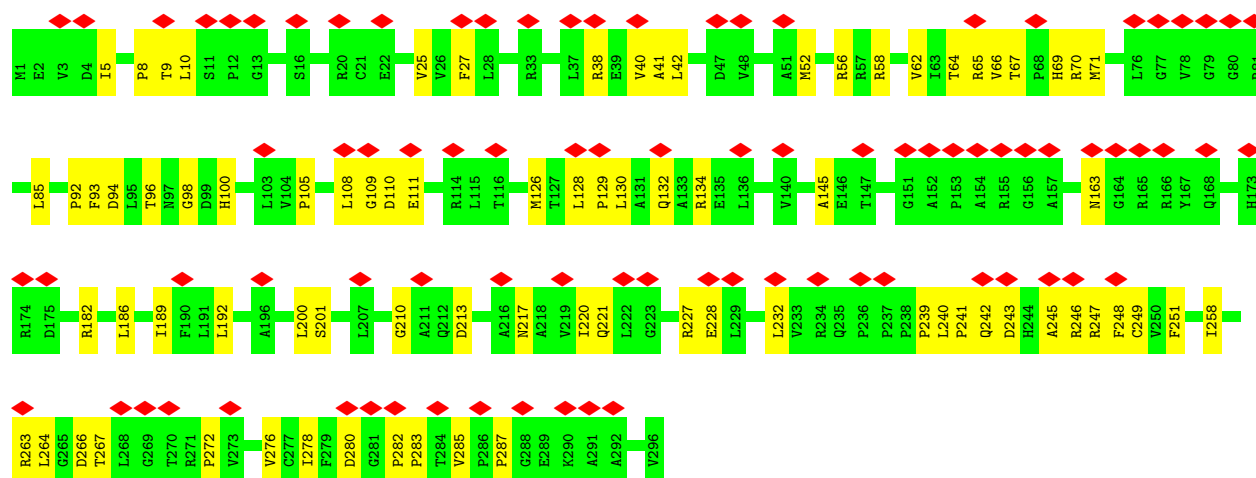


• Molecule 2: Triplex capsid protein 2

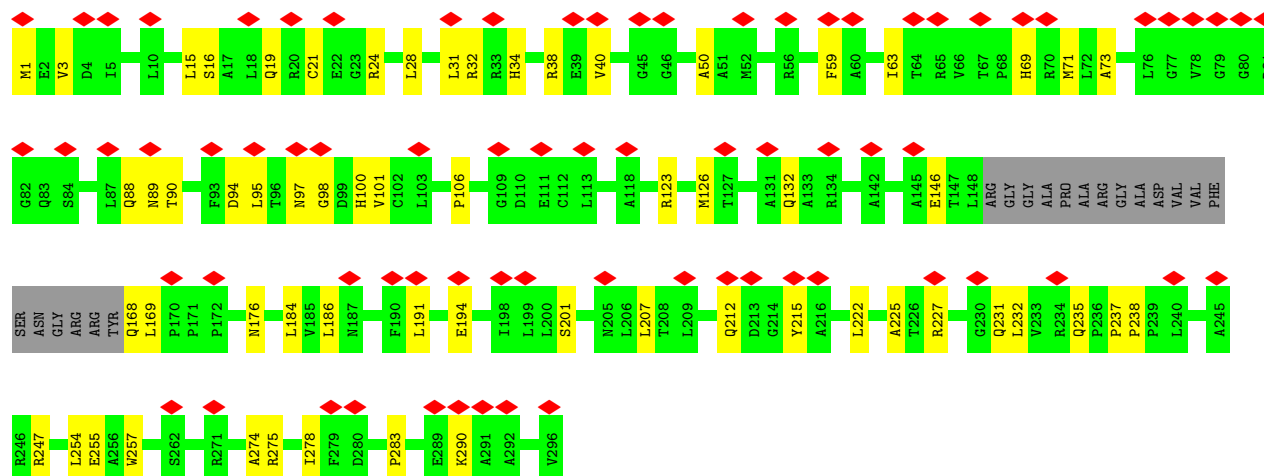




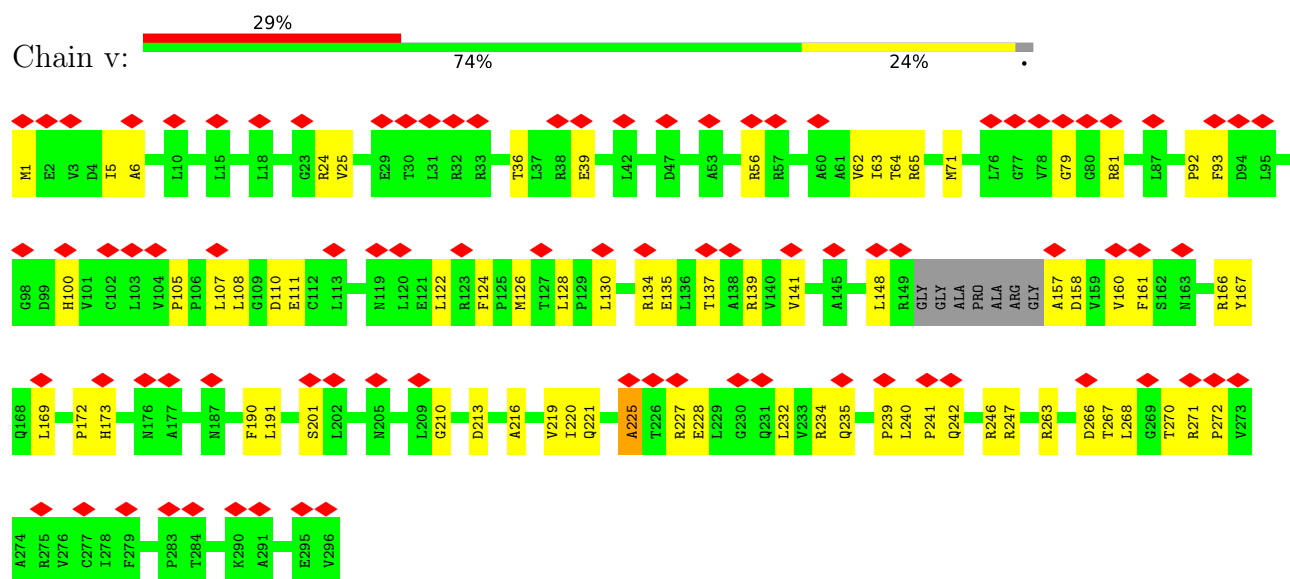
• Molecule 2: Triplex capsid protein 2



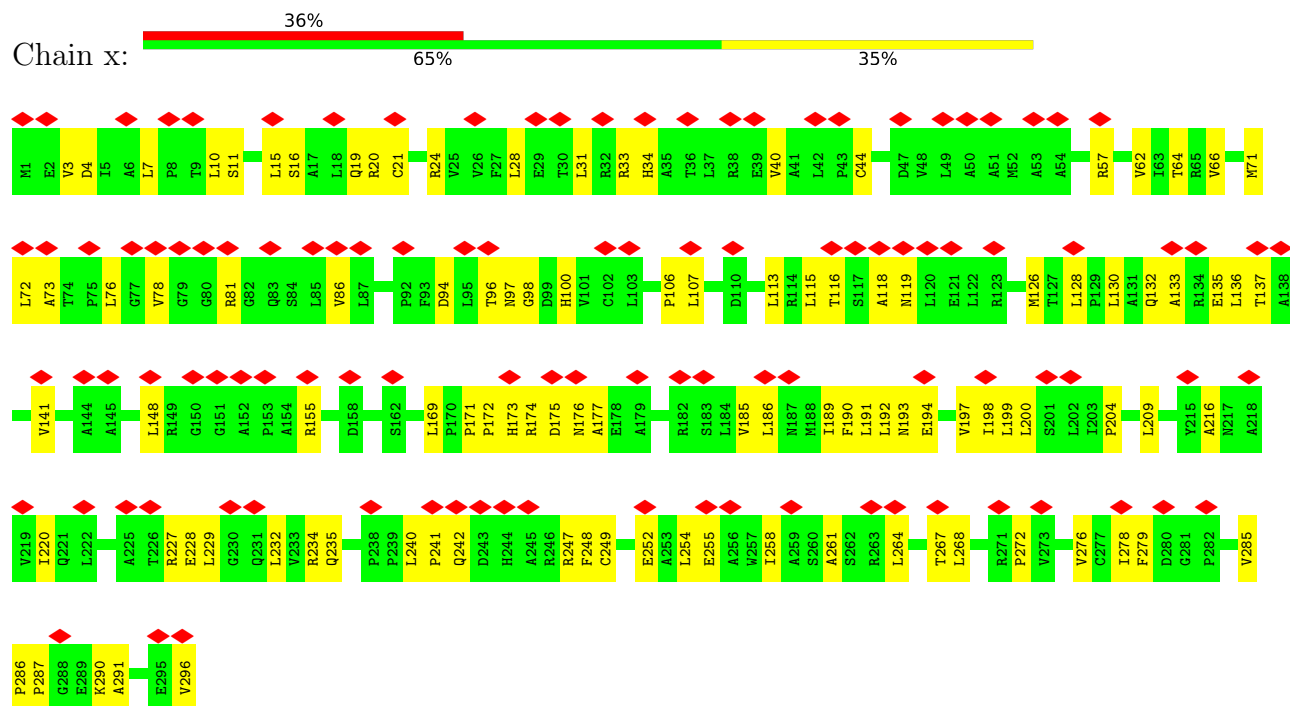
• Molecule 2: Triplex capsid protein 2



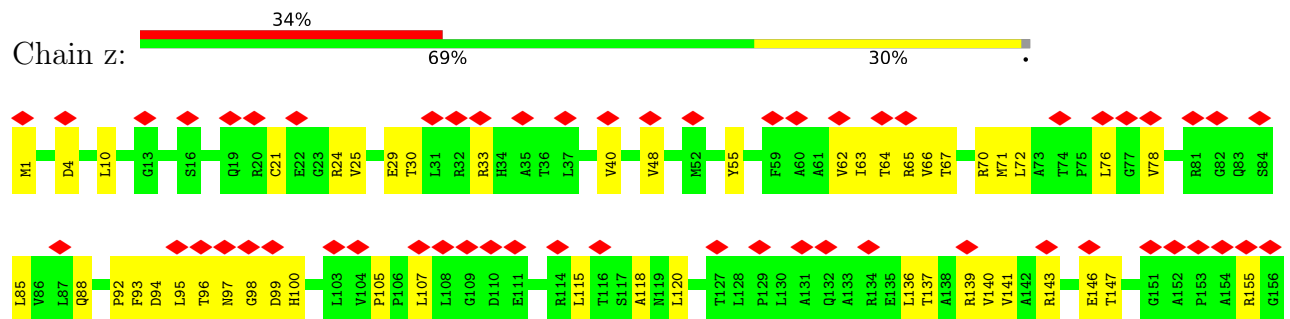
• Molecule 2: Triplex capsid protein 2

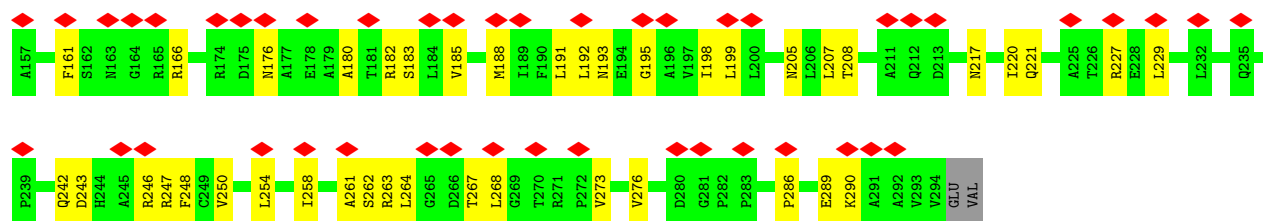


• Molecule 2: Triplex capsid protein 2

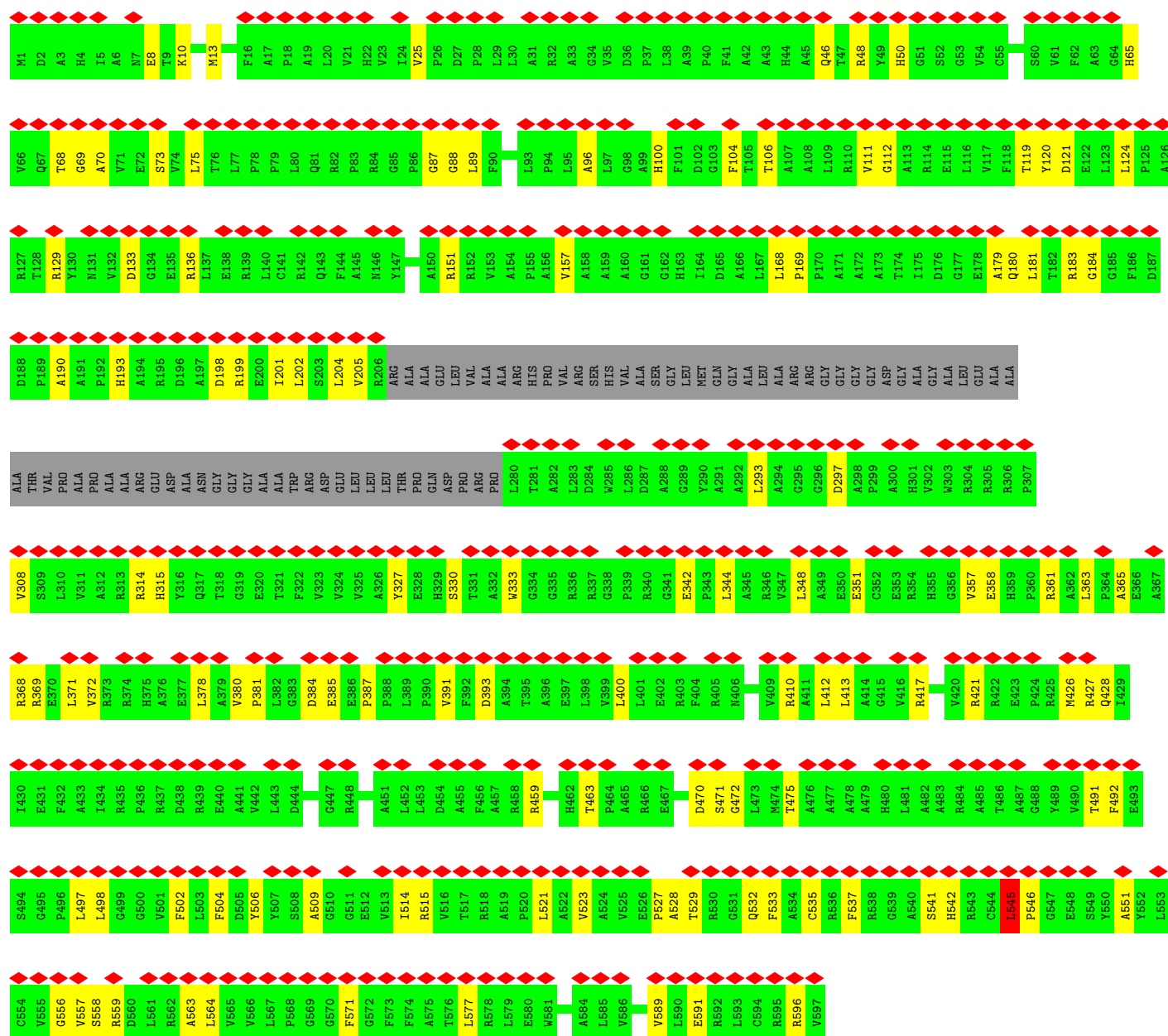


• Molecule 2: Triplex capsid protein 2

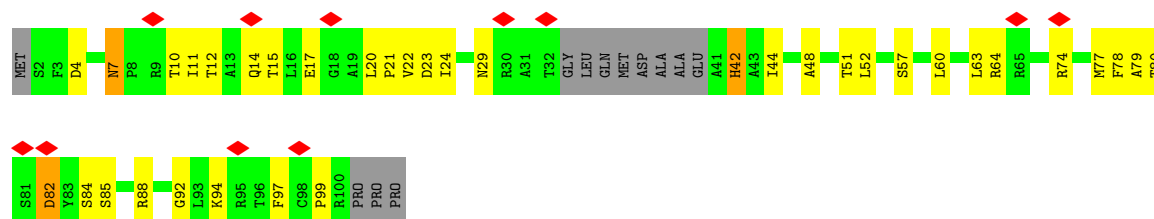




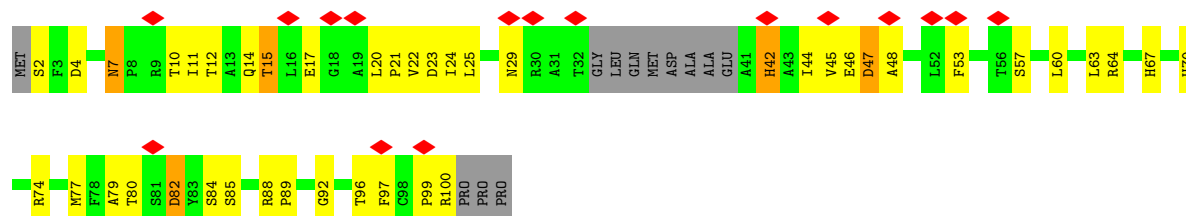
• Molecule 3: Capsid vertex component 1



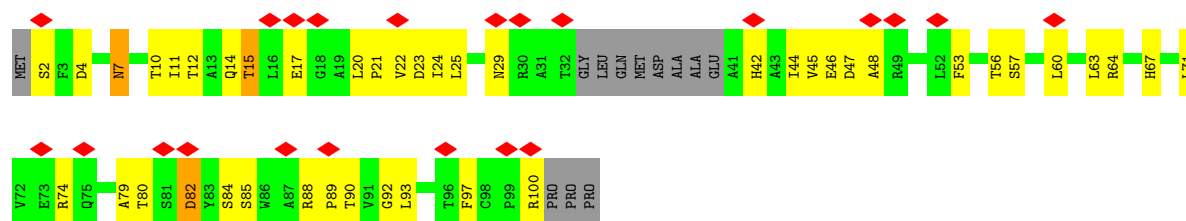
• Molecule 4: Small capsomere-interacting protein



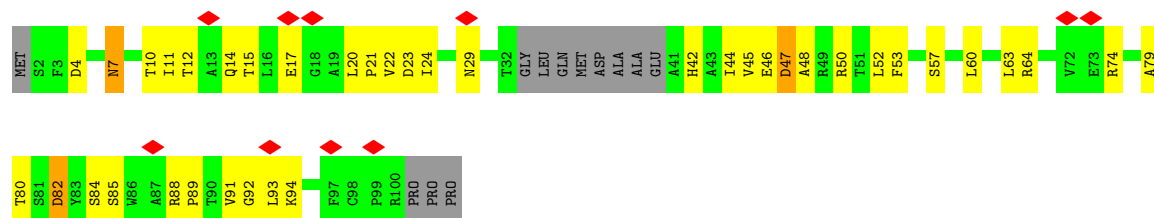
- Molecule 4: Small capsomere-interacting protein



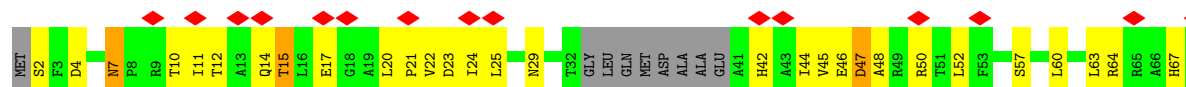
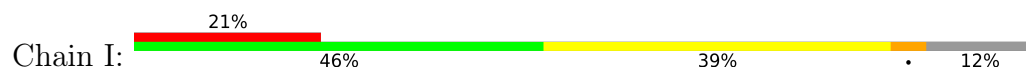
- Molecule 4: Small capsomere-interacting protein

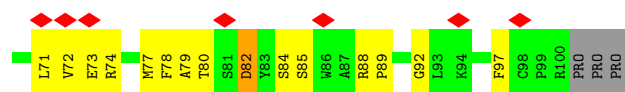


- Molecule 4: Small capsomere-interacting protein

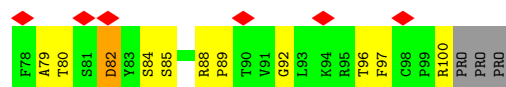


- Molecule 4: Small capsomere-interacting protein

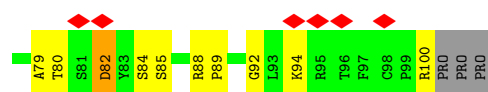
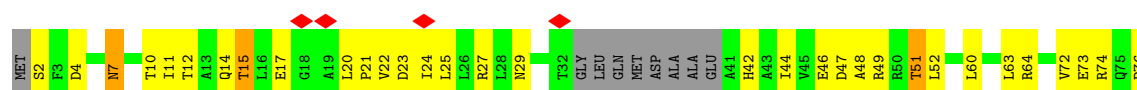




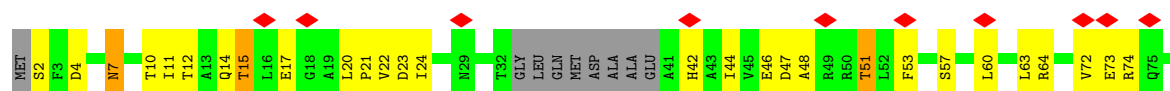
- Molecule 4: Small capsomere-interacting protein



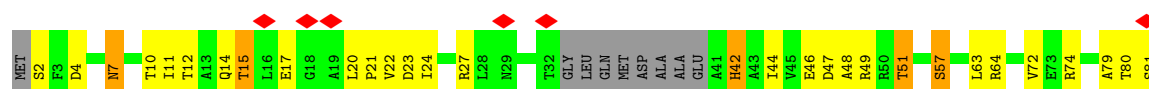
- Molecule 4: Small capsomere-interacting protein



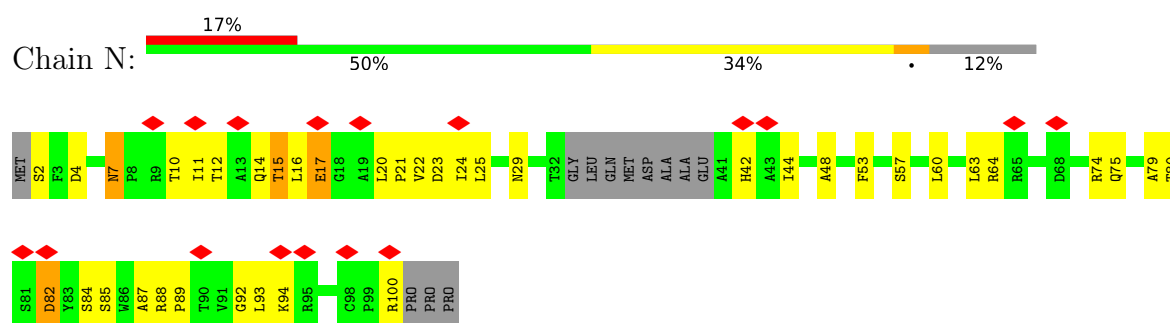
- Molecule 4: Small capsomere-interacting protein



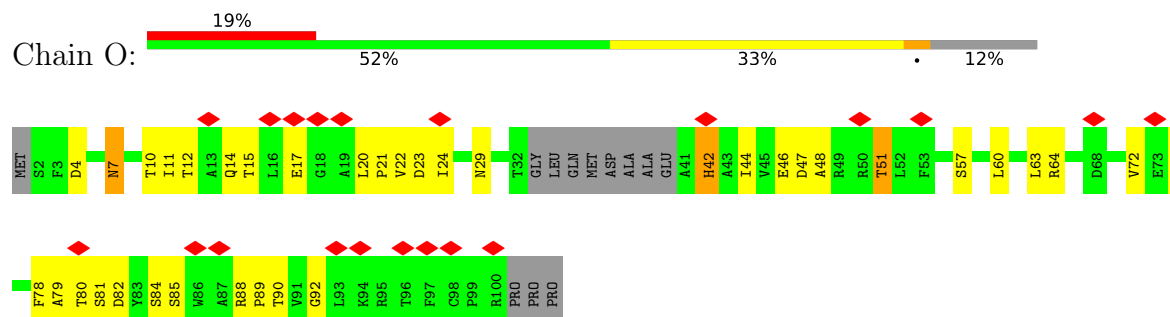
- Molecule 4: Small capsomere-interacting protein



- Molecule 4: Small capsomere-interacting protein



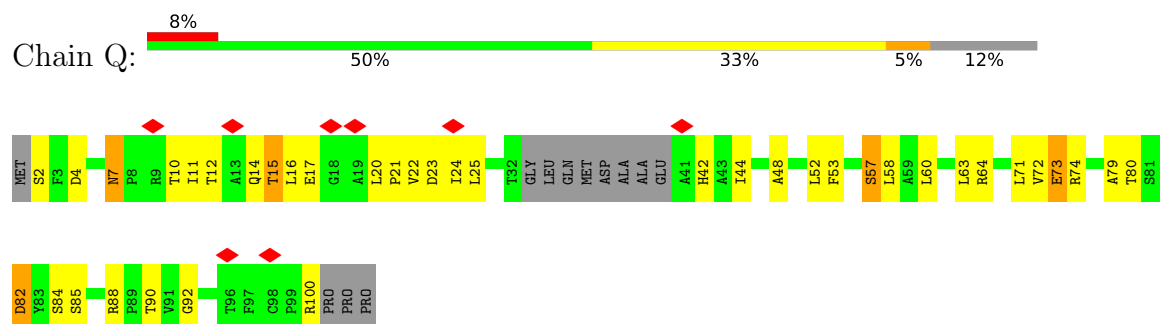
• Molecule 4: Small capsomere-interacting protein



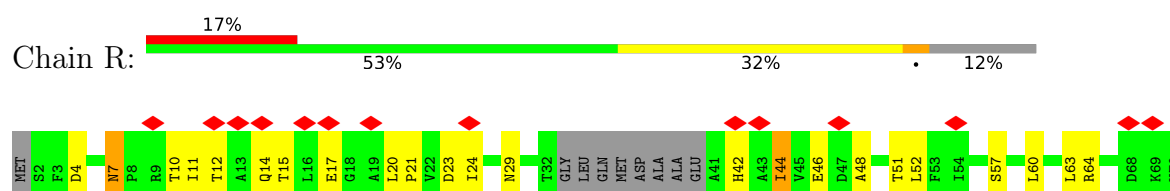
• Molecule 4: Small capsomere-interacting protein

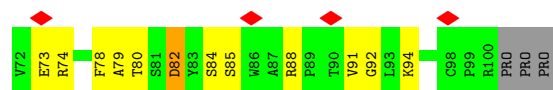


• Molecule 4: Small capsomere-interacting protein

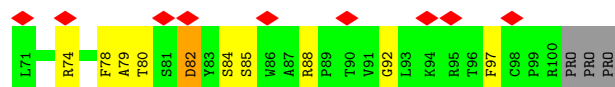
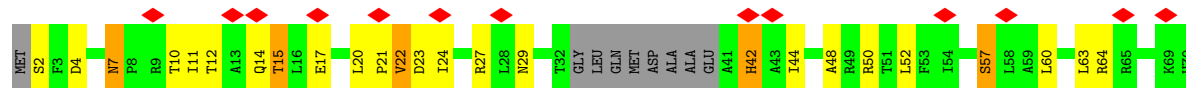


• Molecule 4: Small capsomere-interacting protein

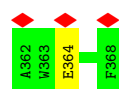
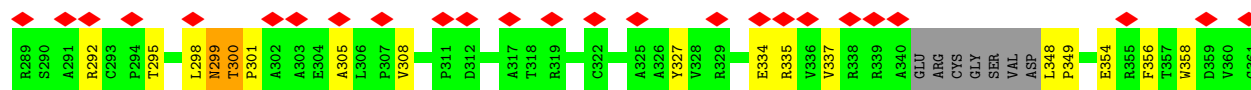
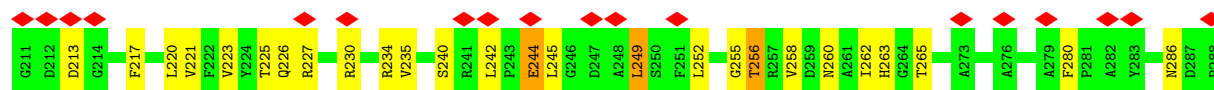
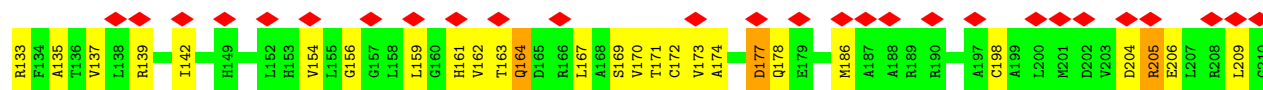
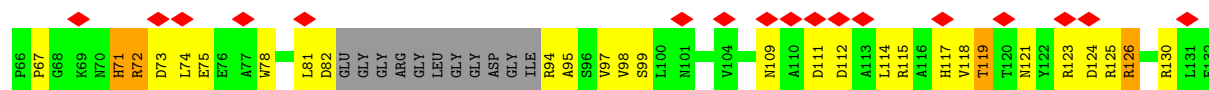
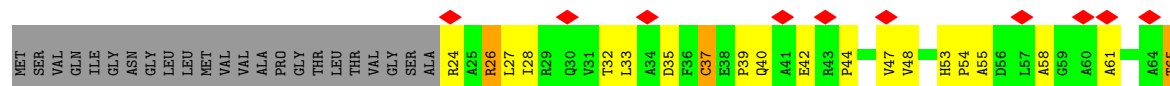




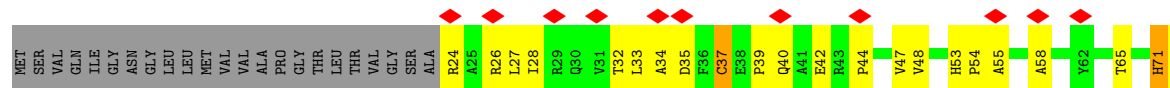
- Molecule 4: Small capsomere-interacting protein

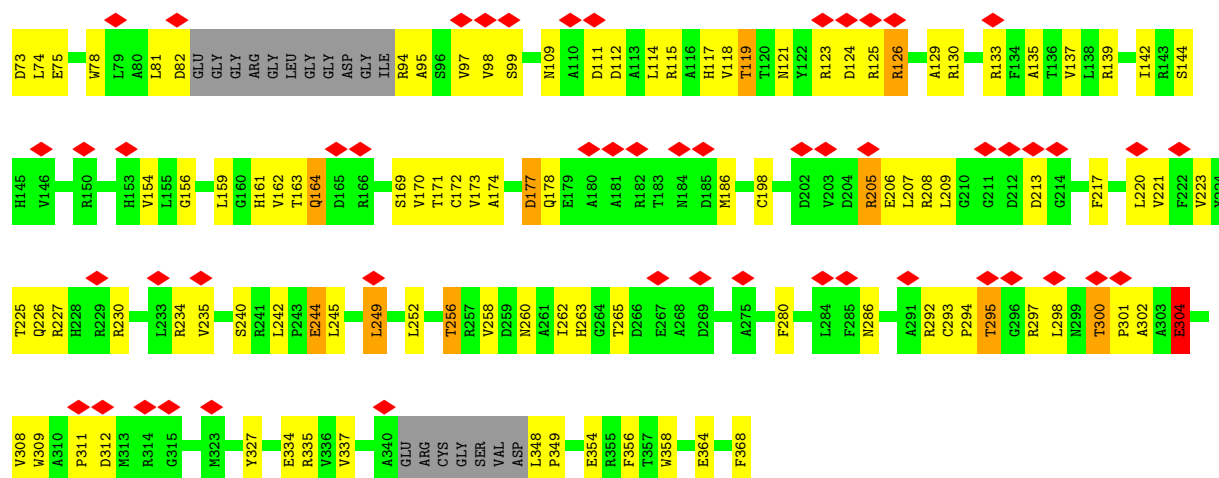


- Molecule 5: Triplex capsid protein 1

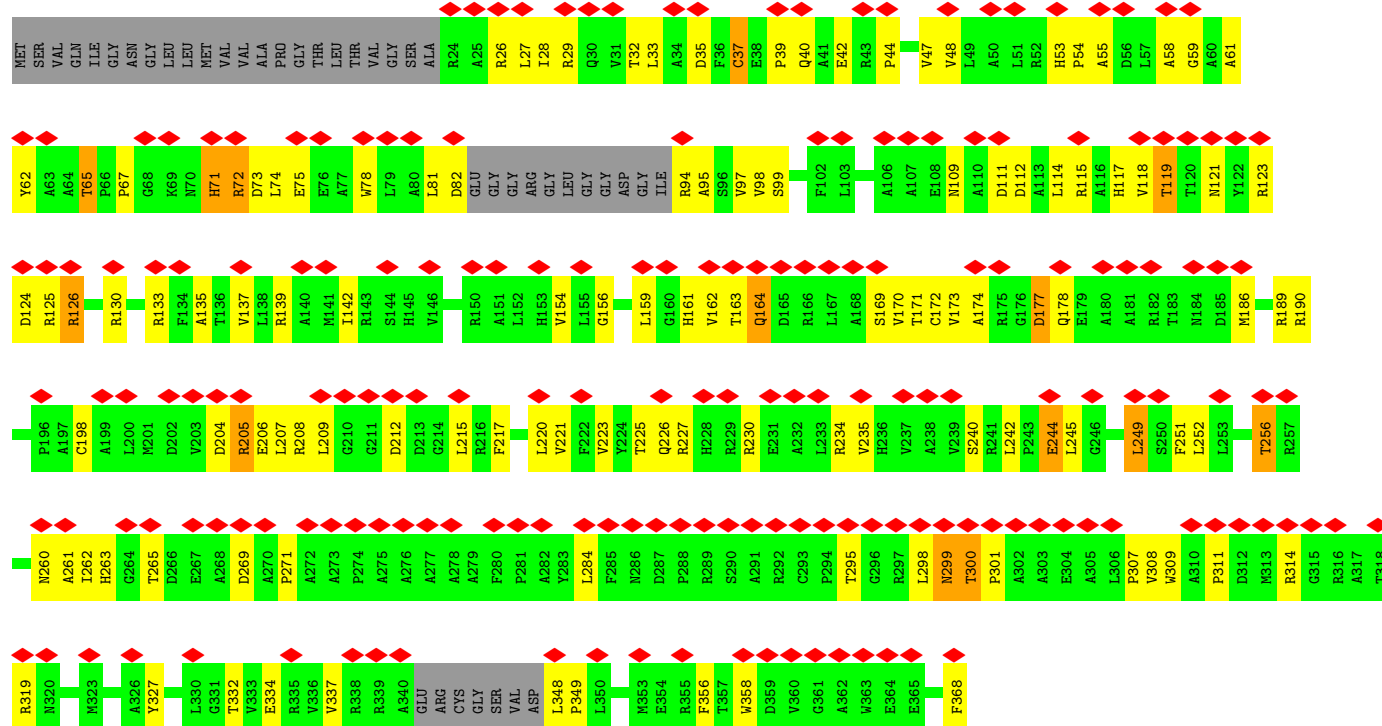


- Molecule 5: Triplex capsid protein 1



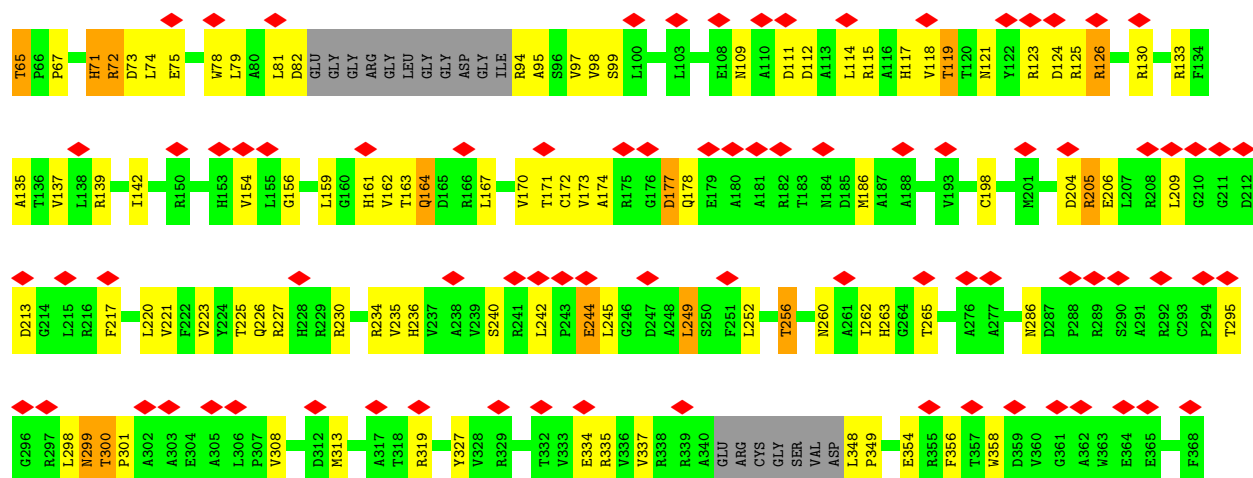


• Molecule 5: Triplex capsid protein 1

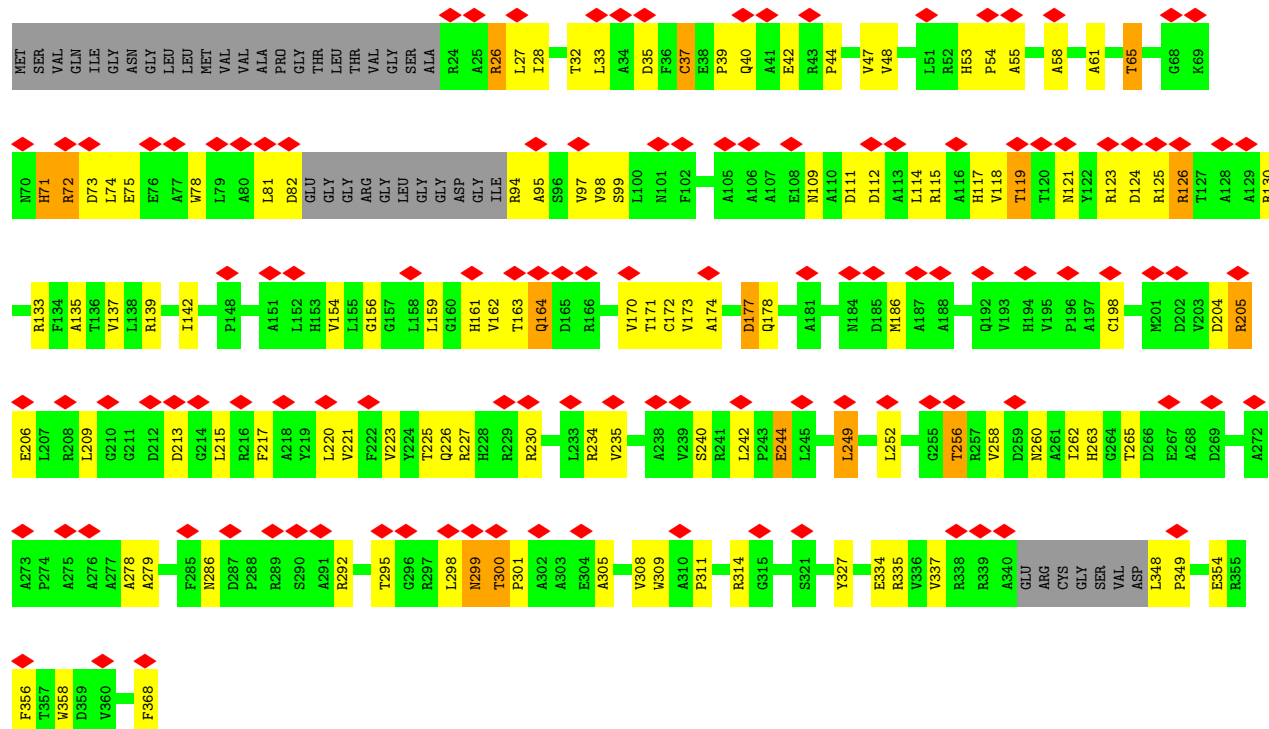


• Molecule 5: Triplex capsid protein 1

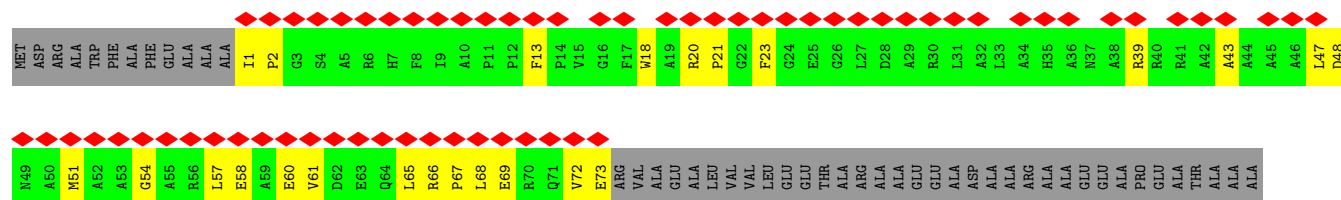




• Molecule 5: Triplex capsid protein 1

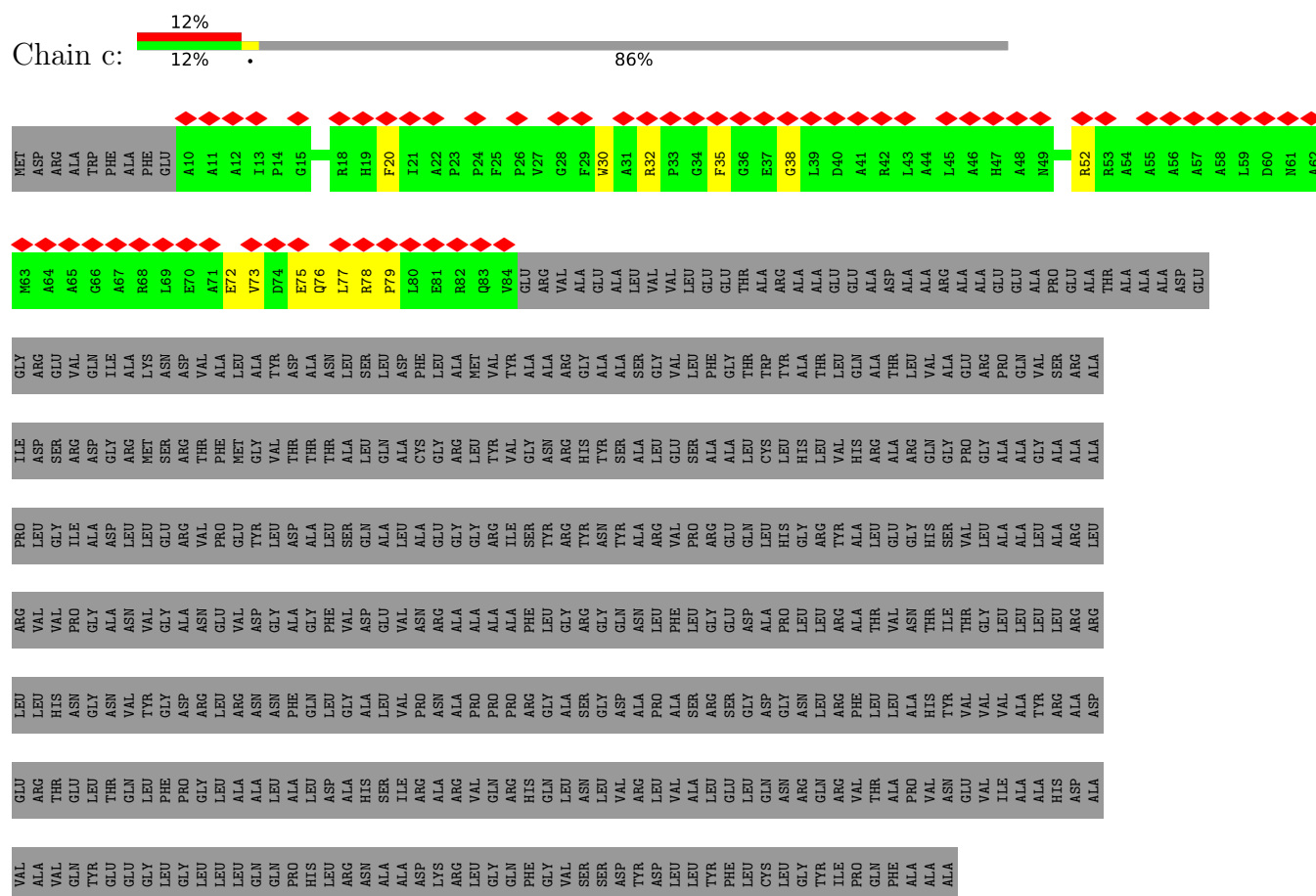


• Molecule 6: DNA packaging tegument protein UL25



ASP	ALA	ARG	ARG	ALA	ARG	ASP
ASP	ASP	ARG	LEU	ALA	LEU	GLY
VAL	GLU	LEU	ARG	PRO	ILE	GLY
ALA	ALA	HIS	VAL	LEU	ASP	ARG
VAL	THR	HIS	VAL	GLY	SER	GLU
GLN	GLU	ASN	PRO	ILE	ARG	VAL
TYR	LEU	GLY	GLY	ALA	ASP	GLN
GLU	THR	ASN	ALA	ASP	ILE	ALA
GLU	GLN	VAL	ASN	LEU	MET	ALA
GLY	PHE	TYR	GLY	LEU	MET	LYS
LEU	LEU	GLY	GLY	GLU	SER	ASN
GLY	PRO	ASP	ALA	ARG	ASP	ASP
LEU	GLY	ASP	ASN	VAL	THR	VAL
LEU	LEU	LEU	GLU	PRO	ALA	VAL
LEU	ALA	ARG	VAL	GLU	MET	LEU
GLN	ALA	ASN	ASP	TYR	GLY	GLY
GLN	LEU	ASN	GLY	LEU	VAL	TYR
PRO	ALA	PHE	ALA	ASP	THR	ASP
HIS	LEU	GLN	GLY	ALA	THR	ALA
LEU	ASP	LEU	PHE	LEU	THR	ASN
ARG	ALA	GLY	VAL	SER	ALA	LEU
ASN	HIS	ALA	ASP	GLN	LEU	SER
ALA	ALA	SER	LEU	ALA	GLN	LEU
ALA	ILE	VAL	VAL	LEU	ALA	ASP
ASP	ARG	PRO	ASN	ALA	CYS	PHE
LYS	ARG	ALA	ASN	ARG	GLY	LEU
ARG	ALA	ALA	ALA	GLY	ARG	ALA
LEU	VAL	PRO	ALA	GLY	LEU	MET
GLY	GLN	ARG	PRO	ALA	TYR	VAL
GLN	ARG	PRO	ALA	ILE	VAL	TYR
PHE	HIS	ARG	PHE	SER	GLY	ALA
GLY	GLN	GLY	GLY	TYR	ASN	ALA
VAL	LEU	ALA	GLY	TYR	HIS	ARG
SER	ASN	SER	ARG	TYR	ASN	ALA
SER	LEU	GLY	GLY	ASN	TYR	SER
ASP	VAL	ASP	GLN	TYR	SER	ALA
TYR	ARG	ALA	ASN	ALA	ALA	SER
ASP	LEU	PRO	LEU	ARG	LEU	GLY
LEU	VAL	ALA	PHE	VAL	GLU	VAL
LEU	ALA	SER	LEU	PRO	SER	LEU
TYR	LEU	ARG	GLY	ARG	ALA	PHE
PHE	GLU	SER	GLU	GLU	ALA	GLY
LEU	LEU	GLY	ASP	GLN	LEU	THR
CYS	GLN	ASP	ALA	LEU	CYS	TRP
LEU	ASN	GLY	PRO	HIS	LEU	TYR
GLY	ARG	ASN	LEU	GLY	HIS	THR
ILE	GLN	ARG	LEU	TYR	VAL	LEU
PRO	VAL	PHE	ALA	ALA	HIS	GLN
GLN	THR	LEU	LEU	LEU	ARG	ALA
PHE	ALA	LEU	VAL	GLY	ALA	THR
ALA	PRO	ALA	ASN	GLY	ARG	LEU
ALA	VAL	HIS	THR	SER	GLN	VAL
ALA	ASN	TYR	ILE	SER	GLY	ALA
	GLU	VAL	THR	VAL	PRO	GLU
	VAL	VAL	VAL	GLY	GLY	ARG
	ILE	VAL	VAL	LEU	ALA	PRO
	ALA	ALA	VAL	LEU	ALA	GLN
	ALA	THR	THR	LEU	GLY	VAL
		ASP	LEU	ALA	ALA	SER

- Molecule 6: DNA packaging tegument protein UL25



- Molecule 7: VP1/2

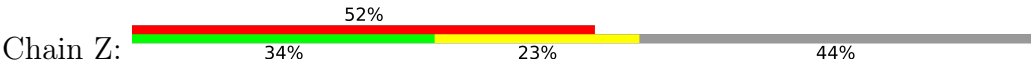


ARG	VAL	VAL	GLU	SER	ASP	THR	LEU	ILE	ASN	ARG	ARG	TYR	MET	ARG	ALA	T3093	G3094	L3095	G3096	A3097	L3098	A3099	L3100	L3101	T3102	A3103	A3104	C3105	R3106	L3107	T3108	A3109	R3110	R3111	L3112	R3113	E3114	T3115	R3116	T3117	T3118	L3119	K3120	G3121	S3122	A3123	R3124	R3125	F3126	N3127	V3128	D3129	L3130	F3131	Q3132	V3133	R3134	L3135	T3136
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GLY

● Molecule 7: VP1/2



ARG	VAL	VAL	GLU	SER	ASP	THR	LEU	ILE	ASN	ARG	ARG	TYR	MET	ARG	ALA	THR	GLY	LEU	GLY	ALA	LEU	ALA	LEU	LEU	ILE	A3103	A3104	C3105	R3106	L3107	T3108	A3109	R3110	R3111	L3112	R3113	E3114	T3115	R3116	T3117	T3118	L3119	K3120	G3121	S3122	A3123	R3124	R3125	F3126	N3127	V3128	D3129	L3130	F3131	Q3132	V3133	R3134	L3135	T3136
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

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GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14252	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	9.391	Depositor
Minimum map value	-6.027	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.915	Depositor
Recommended contour level	2	Depositor
Map size (Å)	1429.76, 1429.76, 1429.76	wwPDB
Map dimensions	1280, 1280, 1280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.117, 1.117, 1.117	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	0.16	0/10384	0.44	2/14158 (0.0%)
1	A	0.17	1/10366 (0.0%)	0.45	3/14132 (0.0%)
1	S	0.16	0/10229	0.43	0/13950
1	U	0.16	0/10384	0.40	0/14158
1	a	0.16	0/10225	0.43	0/13938
1	e	0.18	0/8938	0.39	0/12175
1	f	0.15	0/10384	0.39	0/14158
1	g	0.16	0/10379	0.41	0/14150
1	l	0.16	0/10384	0.42	0/14158
1	m	0.16	0/10384	0.42	0/14158
1	n	0.20	1/10384 (0.0%)	0.43	2/14158 (0.0%)
1	p	0.16	0/10384	0.43	0/14158
1	q	0.17	0/10384	0.44	2/14158 (0.0%)
1	u	0.15	0/10384	0.39	0/14158
1	w	0.15	0/10384	0.40	2/14158 (0.0%)
1	y	0.16	0/10384	0.43	0/14158
2	1	0.23	0/2127	0.42	0/2903
2	2	0.31	1/2127 (0.0%)	0.50	4/2903 (0.1%)
2	3	0.21	0/2127	0.44	0/2903
2	j	0.22	0/2043	0.50	1/2783 (0.0%)
2	k	0.19	0/2127	0.42	0/2903
2	o	0.25	0/2272	0.44	0/3099
2	s	0.25	0/2127	0.42	0/2903
2	v	0.23	0/2230	0.43	0/3041
2	x	0.23	0/2272	0.45	0/3099
2	z	0.20	0/2253	0.44	1/3074 (0.0%)
3	B	0.27	0/4120	0.47	0/5609
4	E	0.24	0/736	0.66	1/999 (0.1%)
4	F	0.25	0/736	0.68	3/999 (0.3%)
4	G	0.25	0/736	0.69	3/999 (0.3%)
4	H	0.27	0/736	0.79	5/999 (0.5%)
4	I	0.27	0/736	0.80	6/999 (0.6%)
4	J	0.24	0/736	0.61	0/999
4	K	0.24	0/736	0.65	0/999

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	L	0.25	0/736	0.66	3/999 (0.3%)
4	M	0.23	0/736	0.52	0/999
4	N	0.30	0/736	0.77	2/999 (0.2%)
4	O	0.23	0/736	0.54	0/999
4	P	0.25	0/736	0.81	4/999 (0.4%)
4	Q	0.26	0/736	0.79	3/999 (0.3%)
4	R	0.28	0/736	0.82	4/999 (0.4%)
4	V	0.25	0/736	0.71	2/999 (0.2%)
5	T	0.27	0/2591	0.61	3/3521 (0.1%)
5	h	0.28	0/2591	0.68	6/3521 (0.2%)
5	i	0.27	0/2591	0.61	2/3521 (0.1%)
5	r	0.27	0/2591	0.60	2/3521 (0.1%)
5	t	0.27	0/2591	0.61	3/3521 (0.1%)
6	X	0.22	0/565	0.44	0/766
6	c	0.22	0/571	0.39	0/775
7	Y	0.22	0/354	0.47	0/474
7	Z	0.21	0/289	0.54	0/385
All	All	0.19	3/215960 (0.0%)	0.46	69/294293 (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	0	0	1
1	U	0	1
1	e	0	1
1	n	0	2
1	w	0	1
2	v	0	1
3	B	0	1
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	n	1130	PRO	N-CD	-11.67	1.31	1.47
2	2	272	PRO	N-CD	10.57	1.62	1.47
1	A	75	GLU	CA-C	6.30	1.59	1.53

The worst 5 of 69 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	46	GLU	N-CA-C	8.86	120.55	111.07
4	N	16	LEU	N-CA-C	8.70	123.68	112.89
1	q	865	GLU	N-CA-C	-8.63	101.85	112.38
1	A	76	LEU	N-CA-C	-8.51	101.75	112.90
1	0	984	ALA	N-CA-C	8.36	121.20	107.23

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	762	ARG	Peptide
3	B	545	LEU	Peptide
1	U	762	ARG	Peptide
1	e	298	ILE	Peptide
1	n	476	ALA	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	0	10129	0	9939	264	0
1	A	10112	0	9922	279	0
1	S	9975	0	9780	296	0
1	U	10129	0	9939	279	0
1	a	9974	0	9791	275	0
1	e	8722	0	8537	181	0
1	f	10129	0	9939	233	0
1	g	10125	0	9935	315	0
1	l	10129	0	9939	316	0
1	m	10129	0	9939	321	0
1	n	10129	0	9939	271	0
1	p	10129	0	9939	296	0
1	q	10129	0	9939	298	0
1	u	10129	0	9939	302	0
1	w	10129	0	9937	309	0
1	y	10129	0	9939	277	0
2	1	2088	0	2157	47	0
2	2	2088	0	2157	88	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	3	2088	0	2157	72	0
2	j	2009	0	2067	73	0
2	k	2088	0	2157	101	0
2	o	2229	0	2293	64	0
2	s	2088	0	2157	61	0
2	v	2189	0	2253	61	0
2	x	2229	0	2293	84	0
2	z	2210	0	2271	80	0
3	B	4023	0	4020	107	0
4	E	722	0	734	43	0
4	F	722	0	734	75	0
4	G	722	0	734	63	0
4	H	722	0	734	31	0
4	I	722	0	734	55	0
4	J	722	0	734	49	0
4	K	722	0	734	51	0
4	L	722	0	734	48	0
4	M	722	0	734	51	0
4	N	722	0	734	63	0
4	O	722	0	734	49	0
4	P	722	0	734	73	0
4	Q	722	0	734	43	0
4	R	722	0	734	32	0
4	V	722	0	734	37	0
5	T	2538	0	2514	91	0
5	h	2538	0	2514	95	0
5	i	2538	0	2512	100	0
5	r	2538	0	2514	97	0
5	t	2538	0	2514	72	0
6	X	552	0	545	37	0
6	c	558	0	551	17	0
7	Y	353	0	396	16	0
7	Z	288	0	318	13	0
All	All	210927	0	208662	5603	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 13.

The worst 5 of 5603 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)
4:M:80:THR:HG22	1:q:919:LEU:CD2	1.28	1.61
5:T:255:GLY:CA	6:X:2:PRO:HB3	1.25	1.59
4:M:80:THR:CG2	1:q:919:LEU:CD2	1.81	1.56
1:A:841:PRO:CG	4:R:29:ASN:HD21	1.28	1.44
1:A:841:PRO:HG2	4:R:29:ASN:ND2	1.29	1.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	1307/1330 (98%)	1200 (92%)	107 (8%)	0	100	100
1	A	1302/1330 (98%)	1193 (92%)	106 (8%)	3 (0%)	44	78
1	S	1285/1330 (97%)	1174 (91%)	108 (8%)	3 (0%)	44	78
1	U	1307/1330 (98%)	1184 (91%)	122 (9%)	1 (0%)	48	83
1	a	1281/1330 (96%)	1143 (89%)	138 (11%)	0	100	100
1	e	1102/1330 (83%)	993 (90%)	109 (10%)	0	100	100
1	f	1307/1330 (98%)	1182 (90%)	123 (9%)	2 (0%)	44	78
1	g	1304/1330 (98%)	1174 (90%)	130 (10%)	0	100	100
1	l	1307/1330 (98%)	1200 (92%)	106 (8%)	1 (0%)	48	83
1	m	1307/1330 (98%)	1197 (92%)	110 (8%)	0	100	100
1	n	1307/1330 (98%)	1201 (92%)	103 (8%)	3 (0%)	44	78
1	p	1307/1330 (98%)	1199 (92%)	107 (8%)	1 (0%)	48	83
1	q	1307/1330 (98%)	1214 (93%)	92 (7%)	1 (0%)	48	83
1	u	1307/1330 (98%)	1186 (91%)	120 (9%)	1 (0%)	48	83
1	w	1307/1330 (98%)	1189 (91%)	118 (9%)	0	100	100
1	y	1307/1330 (98%)	1190 (91%)	112 (9%)	5 (0%)	30	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	1	273/296 (92%)	252 (92%)	21 (8%)	0	100	100
2	2	273/296 (92%)	251 (92%)	22 (8%)	0	100	100
2	3	273/296 (92%)	250 (92%)	23 (8%)	0	100	100
2	j	261/296 (88%)	236 (90%)	25 (10%)	0	100	100
2	k	273/296 (92%)	252 (92%)	21 (8%)	0	100	100
2	o	294/296 (99%)	264 (90%)	30 (10%)	0	100	100
2	s	273/296 (92%)	248 (91%)	25 (9%)	0	100	100
2	v	285/296 (96%)	256 (90%)	29 (10%)	0	100	100
2	x	294/296 (99%)	257 (87%)	37 (13%)	0	100	100
2	z	292/296 (99%)	260 (89%)	32 (11%)	0	100	100
3	B	520/597 (87%)	459 (88%)	60 (12%)	1 (0%)	44	78
4	E	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	F	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	G	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	H	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	I	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	J	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	K	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	L	87/103 (84%)	80 (92%)	7 (8%)	0	100	100
4	M	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	N	87/103 (84%)	80 (92%)	7 (8%)	0	100	100
4	O	87/103 (84%)	80 (92%)	7 (8%)	0	100	100
4	P	87/103 (84%)	80 (92%)	7 (8%)	0	100	100
4	Q	87/103 (84%)	80 (92%)	7 (8%)	0	100	100
4	R	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
4	V	87/103 (84%)	81 (93%)	6 (7%)	0	100	100
5	T	321/368 (87%)	292 (91%)	29 (9%)	0	100	100
5	h	321/368 (87%)	294 (92%)	26 (8%)	1 (0%)	37	72
5	i	321/368 (87%)	292 (91%)	29 (9%)	0	100	100
5	r	321/368 (87%)	292 (91%)	29 (9%)	0	100	100
5	t	321/368 (87%)	292 (91%)	29 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	X	71/534 (13%)	67 (94%)	4 (6%)	0	100	100
6	c	73/534 (14%)	67 (92%)	6 (8%)	0	100	100
7	Y	43/62 (69%)	42 (98%)	1 (2%)	0	100	100
7	Z	33/62 (53%)	32 (97%)	1 (3%)	0	100	100
All	All	27092/29414 (92%)	24684 (91%)	2385 (9%)	23 (0%)	50	83

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	h	302	ALA
1	U	986	GLU
1	n	1127	ALA
1	p	986	GLU
1	y	986	GLU

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	1057/1072 (99%)	1057 (100%)	0	100	100
1	A	1056/1072 (98%)	1055 (100%)	1 (0%)	92	95
1	S	1042/1072 (97%)	1041 (100%)	1 (0%)	92	95
1	U	1057/1072 (99%)	1056 (100%)	1 (0%)	92	95
1	a	1040/1072 (97%)	1040 (100%)	0	100	100
1	e	909/1072 (85%)	909 (100%)	0	100	100
1	f	1057/1072 (99%)	1057 (100%)	0	100	100
1	g	1057/1072 (99%)	1057 (100%)	0	100	100
1	l	1057/1072 (99%)	1056 (100%)	1 (0%)	92	95
1	m	1057/1072 (99%)	1057 (100%)	0	100	100
1	n	1057/1072 (99%)	1057 (100%)	0	100	100
1	p	1057/1072 (99%)	1057 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	q	1057/1072 (99%)	1057 (100%)	0	100	100
1	u	1057/1072 (99%)	1057 (100%)	0	100	100
1	w	1057/1072 (99%)	1057 (100%)	0	100	100
1	y	1057/1072 (99%)	1054 (100%)	3 (0%)	91	91
2	1	223/235 (95%)	223 (100%)	0	100	100
2	2	223/235 (95%)	223 (100%)	0	100	100
2	3	223/235 (95%)	223 (100%)	0	100	100
2	j	213/235 (91%)	212 (100%)	1 (0%)	86	89
2	k	223/235 (95%)	223 (100%)	0	100	100
2	o	235/235 (100%)	235 (100%)	0	100	100
2	s	223/235 (95%)	223 (100%)	0	100	100
2	v	233/235 (99%)	233 (100%)	0	100	100
2	x	235/235 (100%)	234 (100%)	1 (0%)	89	90
2	z	232/235 (99%)	232 (100%)	0	100	100
3	B	396/440 (90%)	395 (100%)	1 (0%)	91	91
4	E	78/87 (90%)	68 (87%)	10 (13%)	3	15
4	F	78/87 (90%)	68 (87%)	10 (13%)	3	15
4	G	78/87 (90%)	68 (87%)	10 (13%)	3	15
4	H	78/87 (90%)	68 (87%)	10 (13%)	3	15
4	I	78/87 (90%)	68 (87%)	10 (13%)	3	15
4	J	78/87 (90%)	66 (85%)	12 (15%)	2	12
4	K	78/87 (90%)	67 (86%)	11 (14%)	3	14
4	L	78/87 (90%)	66 (85%)	12 (15%)	2	12
4	M	78/87 (90%)	65 (83%)	13 (17%)	2	10
4	N	78/87 (90%)	71 (91%)	7 (9%)	8	25
4	O	78/87 (90%)	65 (83%)	13 (17%)	2	10
4	P	78/87 (90%)	70 (90%)	8 (10%)	6	21
4	Q	78/87 (90%)	70 (90%)	8 (10%)	6	21
4	R	78/87 (90%)	69 (88%)	9 (12%)	4	18
4	V	78/87 (90%)	68 (87%)	10 (13%)	3	15
5	T	251/279 (90%)	199 (79%)	52 (21%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	h	251/279 (90%)	201 (80%)	50 (20%)	1	7
5	i	251/279 (90%)	201 (80%)	50 (20%)	1	7
5	r	251/279 (90%)	199 (79%)	52 (21%)	1	6
5	t	251/279 (90%)	199 (79%)	52 (21%)	1	6
6	X	49/387 (13%)	49 (100%)	0	100	100
6	c	48/387 (12%)	48 (100%)	0	100	100
7	Y	36/51 (71%)	36 (100%)	0	100	100
7	Z	30/51 (59%)	30 (100%)	0	100	100
All	All	21978/23518 (94%)	21559 (98%)	419 (2%)	52	69

5 of 419 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	h	162	VAL
5	i	170	VAL
5	t	213	ASP
5	h	186	MET
5	i	35	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 550 such sidechains are listed below:

Mol	Chain	Res	Type
1	u	835	HIS
2	v	221	GLN
1	u	814	GLN
1	y	240	ASN
1	a	1210	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [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.

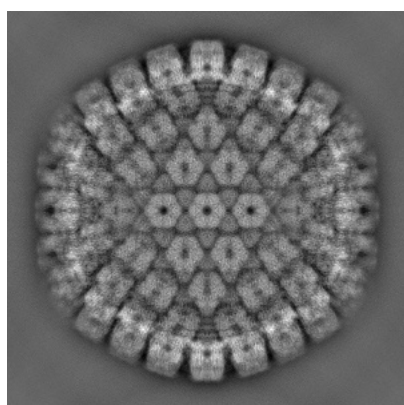
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31611. These allow visual inspection of the internal detail of the map and identification of artifacts.

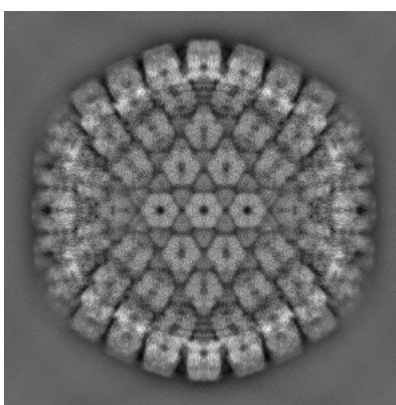
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

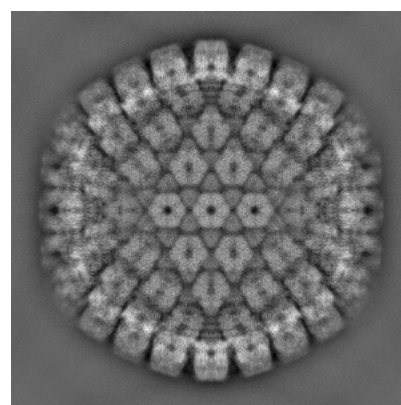
6.1.1 Primary map



X



Y

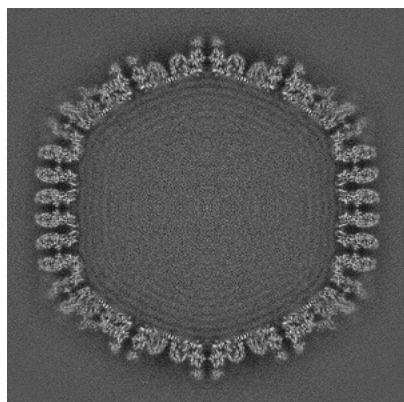


Z

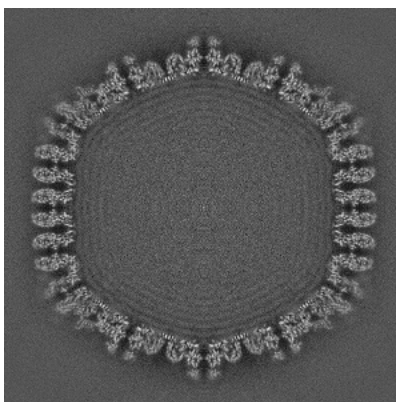
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

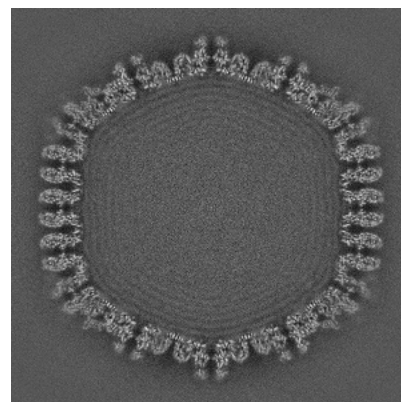
6.2.1 Primary map



X Index: 640



Y Index: 640

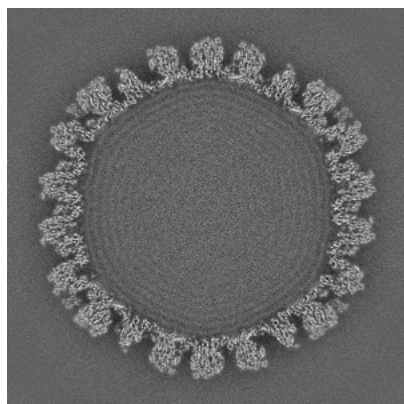


Z Index: 640

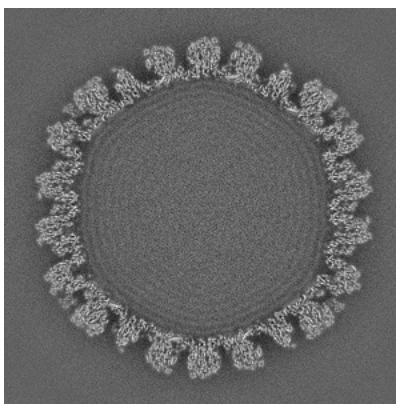
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

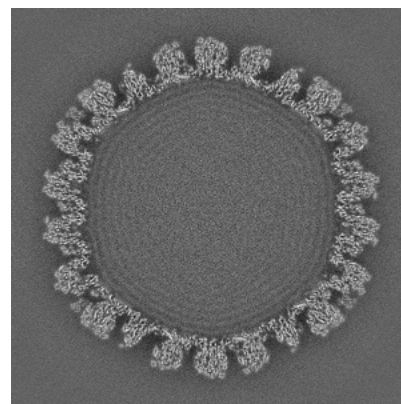
6.3.1 Primary map



X Index: 750



Y Index: 750

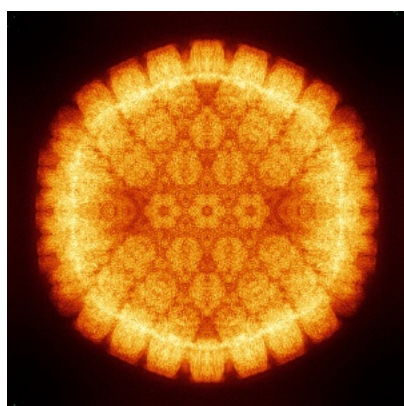


Z Index: 529

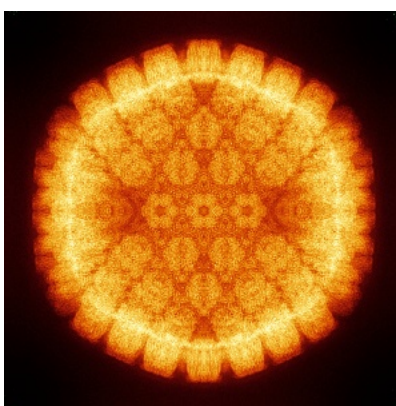
The images above show the largest variance slices of the map in three orthogonal directions.

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

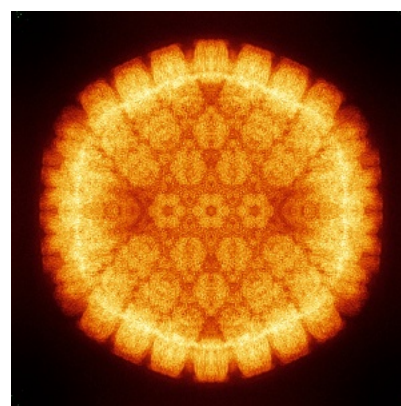
6.4.1 Primary map



X



Y

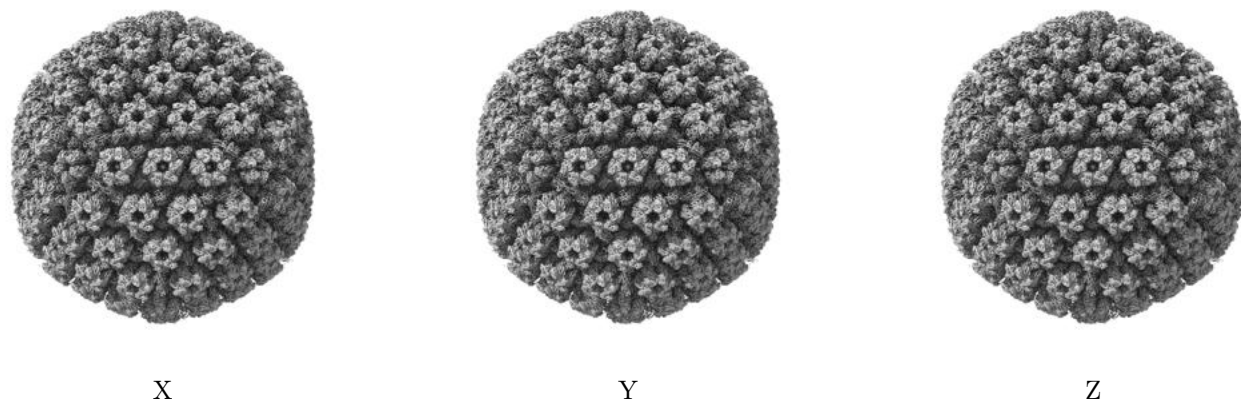


Z

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 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

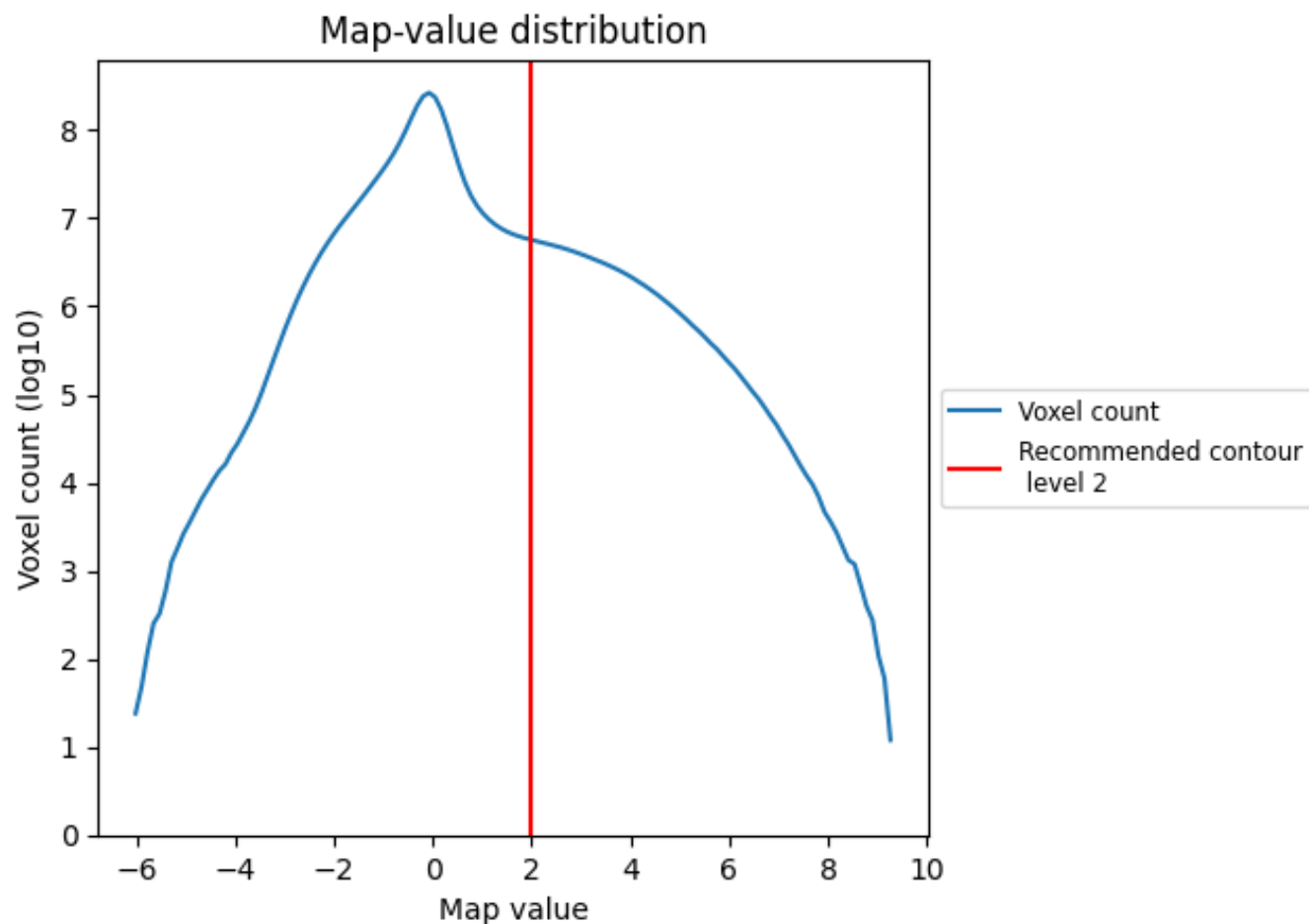
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

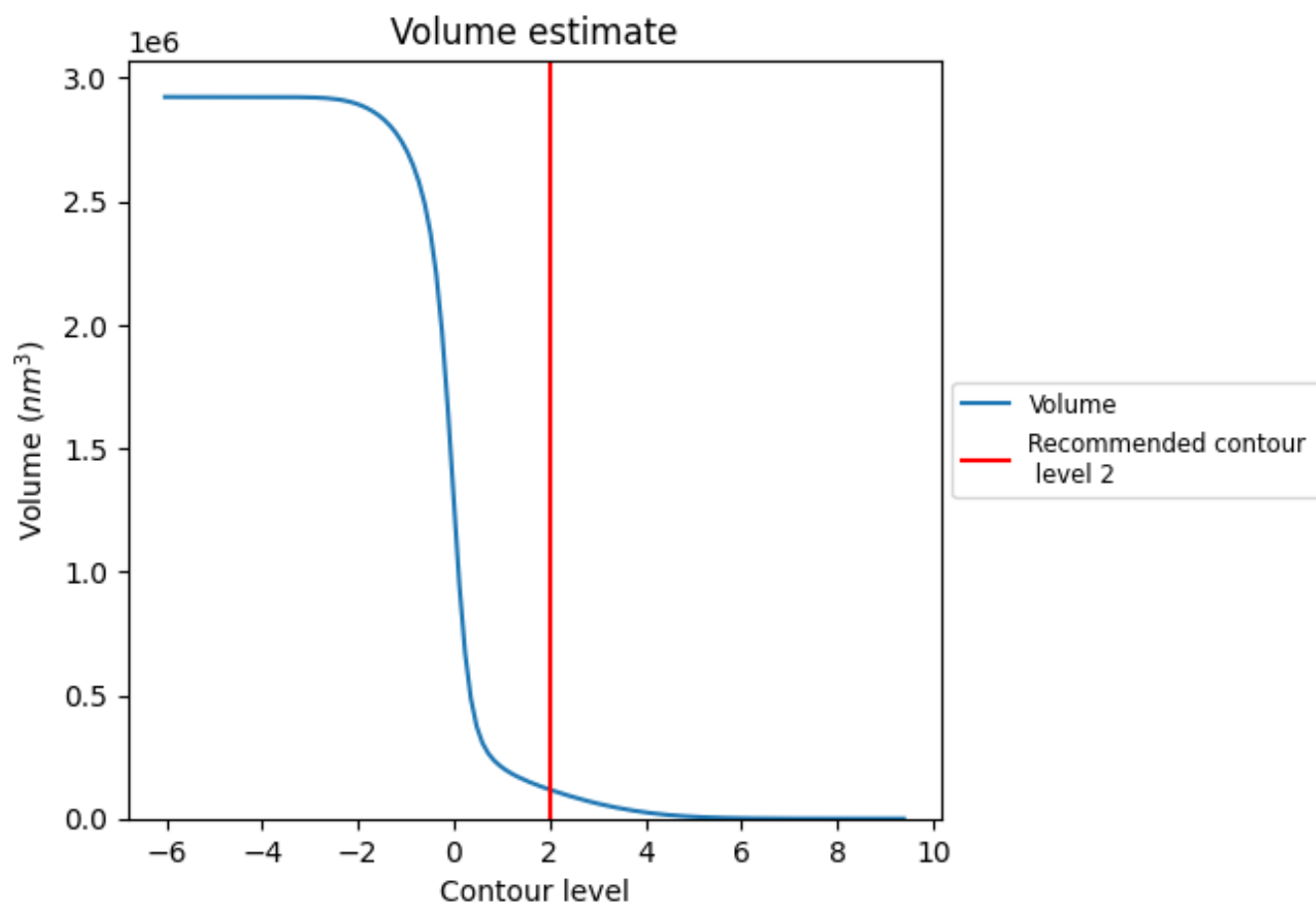
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

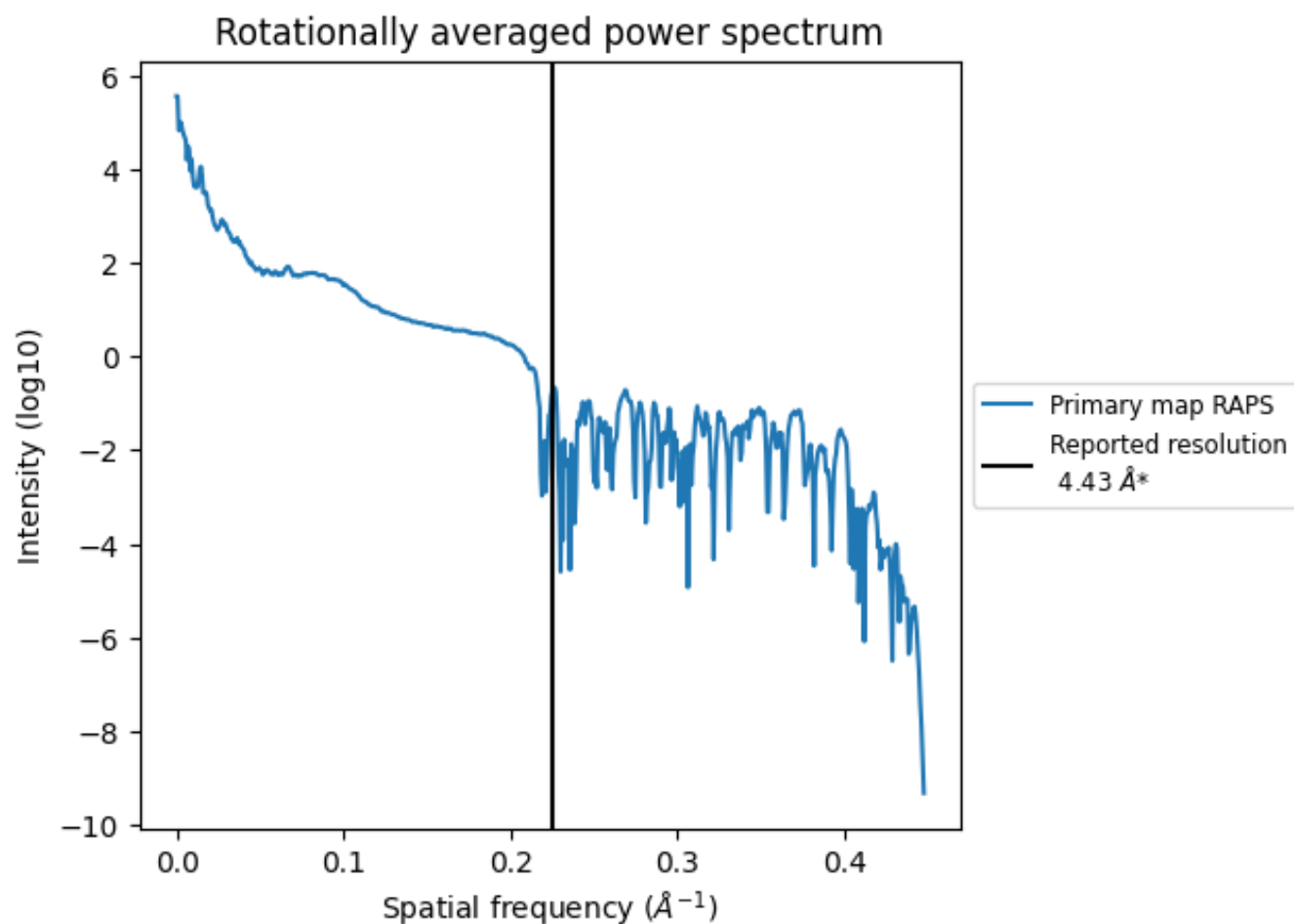
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117685 nm³; this corresponds to an approximate mass of 106308 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 0.226 Å⁻¹

8 Fourier-Shell correlation

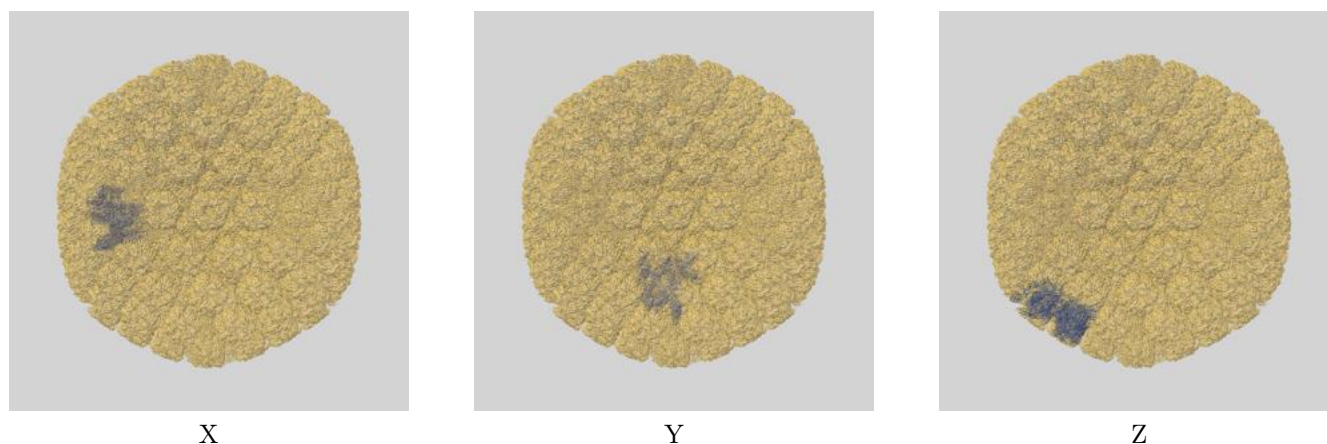
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

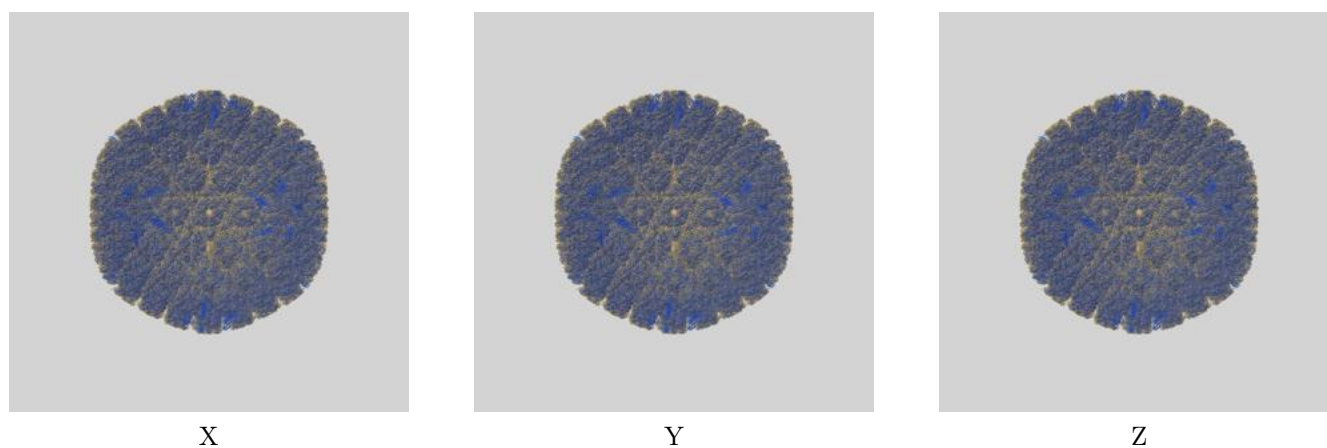
This section contains information regarding the fit between EMDB map EMD-31611 and PDB model 7FJ1. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

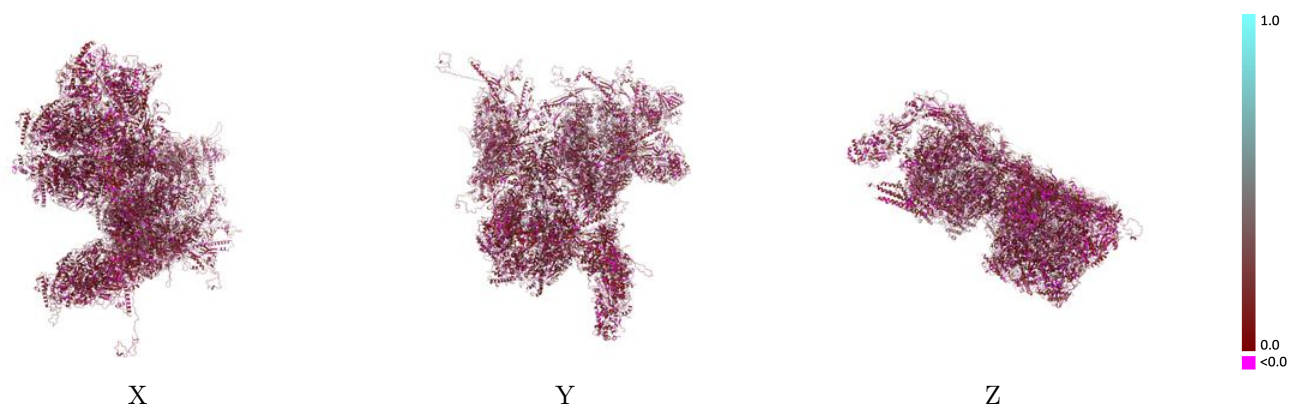


9.1.2 Map-model assembly overlay [i](#)



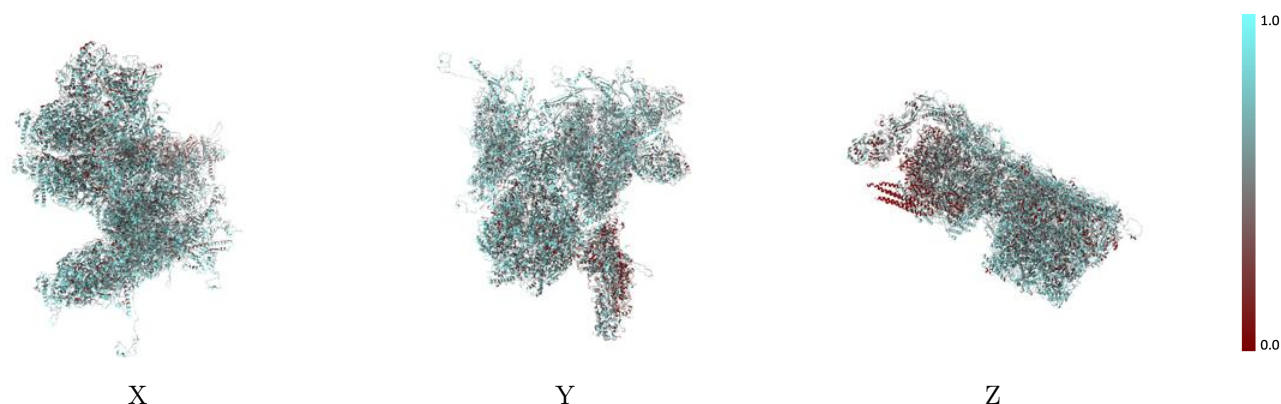
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



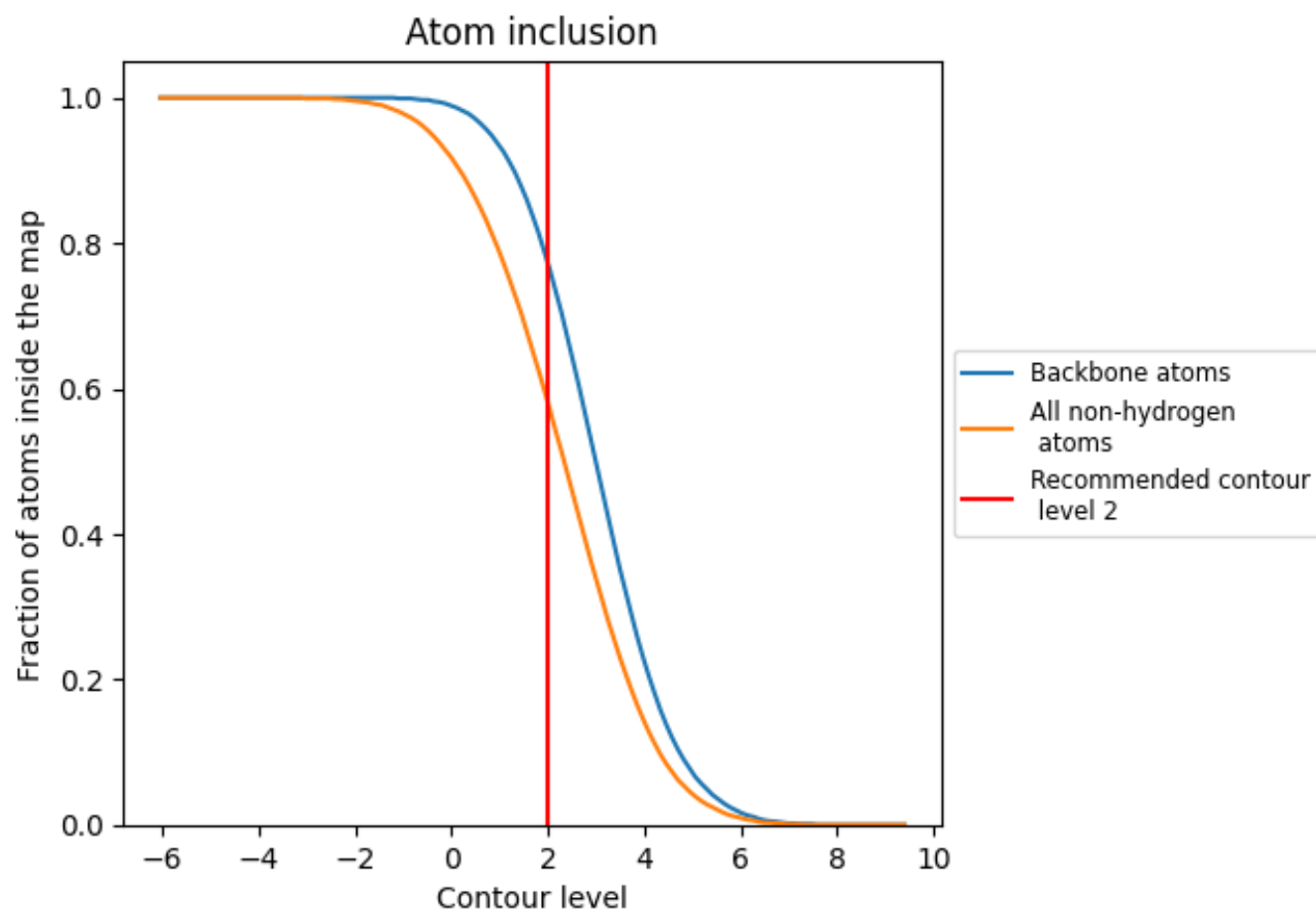
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 58% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5810	 0.1420
0	 0.6010	 0.1380
1	 0.5760	 0.1580
2	 0.5600	 0.1460
3	 0.5650	 0.1330
A	 0.6230	 0.1420
B	 0.1850	 0.1400
E	 0.6680	 0.1500
F	 0.6750	 0.1480
G	 0.6800	 0.1350
H	 0.6800	 0.1420
I	 0.6060	 0.1580
J	 0.6690	 0.1530
K	 0.6950	 0.1700
L	 0.6630	 0.1610
M	 0.7030	 0.1710
N	 0.6760	 0.1590
O	 0.6150	 0.1490
P	 0.6760	 0.1820
Q	 0.7220	 0.1670
R	 0.6620	 0.1600
S	 0.5820	 0.1450
T	 0.5940	 0.1400
U	 0.6080	 0.1450
V	 0.6400	 0.1450
X	 0.1330	 0.1370
Y	 0.1220	 0.1220
Z	 0.0550	 0.0980
a	 0.5870	 0.1370
c	 0.2060	 0.1530
e	 0.4760	 0.1350
f	 0.6240	 0.1460
g	 0.6070	 0.1440
h	 0.6340	 0.1690
i	 0.3910	 0.1260



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Chain	Atom inclusion	Q-score
j	 0.3620	 0.1500
k	 0.3820	 0.1550
l	 0.6030	 0.1430
m	 0.6150	 0.1380
n	 0.6030	 0.1360
o	 0.5490	 0.1580
p	 0.6080	 0.1440
q	 0.6000	 0.1400
r	 0.5780	 0.1310
s	 0.5790	 0.1550
t	 0.5590	 0.1180
u	 0.6260	 0.1480
v	 0.5680	 0.1420
w	 0.5980	 0.1420
x	 0.5280	 0.1360
y	 0.6200	 0.1400
z	 0.5370	 0.1330