



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:26 AM UTC

PDB ID : 6B43 / pdb_00006b43
EMDB ID : EMD-7047
Title : CryoEM structure and atomic model of the Kaposi's sarcoma-associated herpesvirus capsid
Authors : Dai, X.H.; Gong, D.Y.; Sun, R.; Zhou, Z.H.
Deposited on : 2017-09-25
Resolution : 4.20 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:

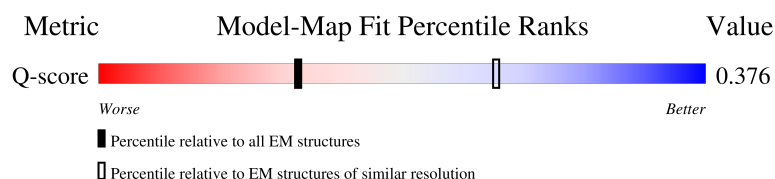
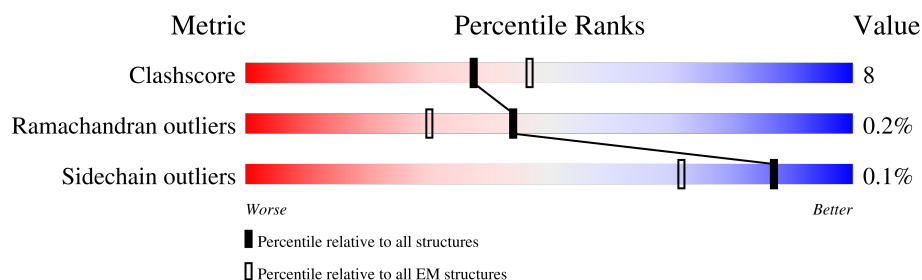
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.20 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	5410 (3.70 - 4.70)

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	4	1376	58% 69% 19% 12%
1	A	1376	9% 80% 19% .
1	B	1376	10% 79% 19% .
1	C	1376	11% 76% 22% ..

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Mol	Chain	Length	Quality of chain
1	D	1376	
1	E	1376	
1	F	1376	
1	M	1376	
1	N	1376	
1	O	1376	
1	S	1376	
1	T	1376	
1	U	1376	
1	V	1376	
1	W	1376	
1	X	1376	
2	0	170	
2	1	170	
2	2	170	
2	3	170	
2	G	170	
2	H	170	
2	I	170	
2	J	170	
2	K	170	
2	L	170	
2	P	170	
2	Q	170	
2	R	170	

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Mol	Chain	Length	Quality of chain
2	Y	170	
2	Z	170	
3	5	331	
3	8	331	
3	b	331	
3	e	331	
3	h	331	
4	6	305	
4	7	305	
4	9	305	
4	a	305	
4	c	305	
4	d	305	
4	f	305	
4	g	305	
4	i	305	
4	j	305	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 214334 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	A	1363	Total	C	N	O	S	0	0
			10682	6786	1854	1969	73		
1	B	1355	Total	C	N	O	S	0	0
			10627	6751	1843	1960	73		
1	C	1354	Total	C	N	O	S	0	0
			10621	6748	1842	1959	72		
1	D	1355	Total	C	N	O	S	0	0
			10627	6751	1843	1960	73		
1	E	1363	Total	C	N	O	S	0	0
			10682	6786	1854	1969	73		
1	F	1356	Total	C	N	O	S	0	0
			10638	6757	1847	1961	73		
1	M	1355	Total	C	N	O	S	0	0
			10627	6751	1843	1960	73		
1	N	1363	Total	C	N	O	S	0	0
			10682	6786	1854	1969	73		
1	O	1355	Total	C	N	O	S	0	0
			10627	6751	1843	1960	73		
1	S	1281	Total	C	N	O	S	0	0
			10060	6397	1737	1855	71		
1	T	1360	Total	C	N	O	S	0	0
			10666	6776	1851	1966	73		
1	U	1355	Total	C	N	O	S	0	0
			10627	6751	1843	1960	73		
1	V	1352	Total	C	N	O	S	0	0
			10604	6739	1839	1954	72		
1	W	1354	Total	C	N	O	S	0	0
			10621	6748	1842	1959	72		
1	X	1345	Total	C	N	O	S	0	0
			10548	6701	1829	1946	72		
1	4	1216	Total	C	N	O	S	0	0
			9586	6102	1665	1748	71		

- Molecule 2 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	H	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	I	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	J	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	K	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	L	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	P	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	Q	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	R	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	Y	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	Z	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	0	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	1	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	2	78	Total 666	C 418	N 130	O 115	S 3	0	0
2	3	78	Total 666	C 418	N 130	O 115	S 3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	319	Total 2463	C 1578	N 421	O 449	S 15	0	0
3	8	321	Total 2477	C 1586	N 424	O 452	S 15	0	0
3	b	321	Total 2477	C 1586	N 424	O 452	S 15	0	0
3	e	319	Total 2460	C 1575	N 422	O 448	S 15	0	0
3	h	321	Total 2477	C 1586	N 424	O 452	S 15	0	0

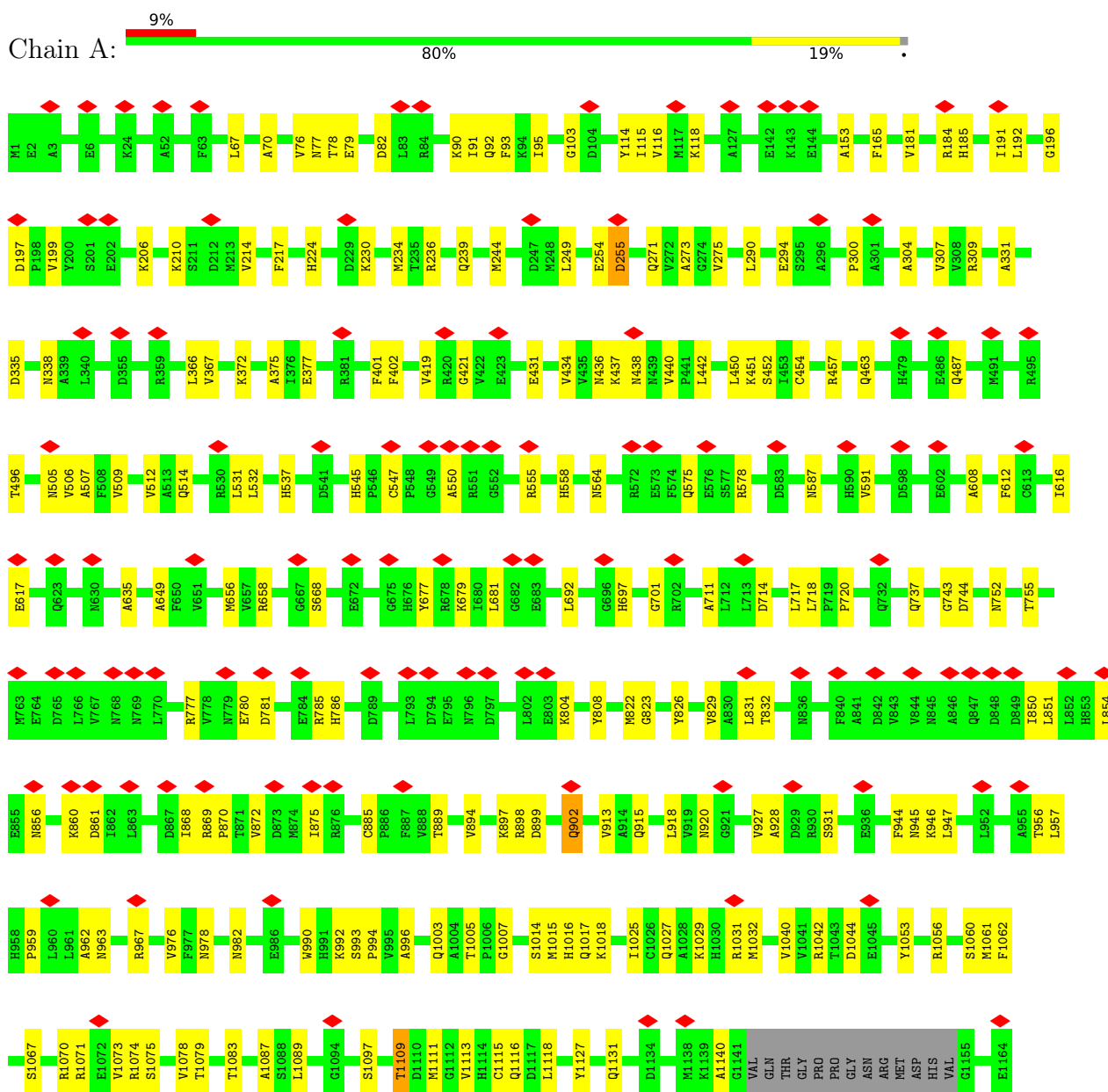
- Molecule 4 is a protein called Triplex capsid protein 2.

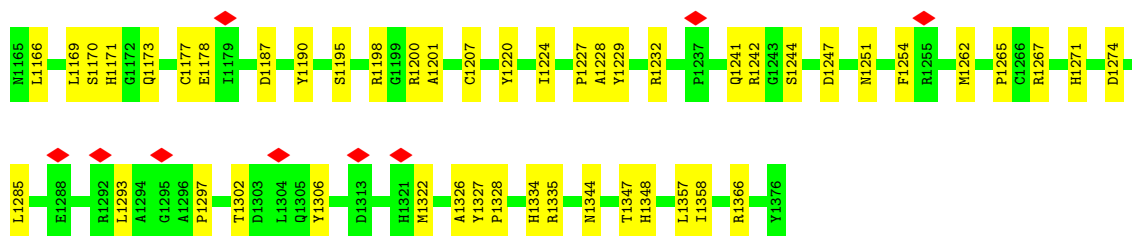
Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	294	Total	C	N	O	S	0	0
			2329	1485	397	433	14		
4	7	300	Total	C	N	O	S	0	0
			2364	1505	401	443	15		
4	9	294	Total	C	N	O	S	0	0
			2329	1485	397	433	14		
4	a	300	Total	C	N	O	S	0	0
			2364	1505	401	443	15		
4	c	294	Total	C	N	O	S	0	0
			2329	1485	397	433	14		
4	d	300	Total	C	N	O	S	0	0
			2364	1505	401	443	15		
4	f	294	Total	C	N	O	S	0	0
			2329	1485	397	433	14		
4	g	300	Total	C	N	O	S	0	0
			2364	1505	401	443	15		
4	i	294	Total	C	N	O	S	0	0
			2329	1485	397	433	14		
4	j	300	Total	C	N	O	S	0	0
			2364	1505	401	443	15		

3 Residue-property plots

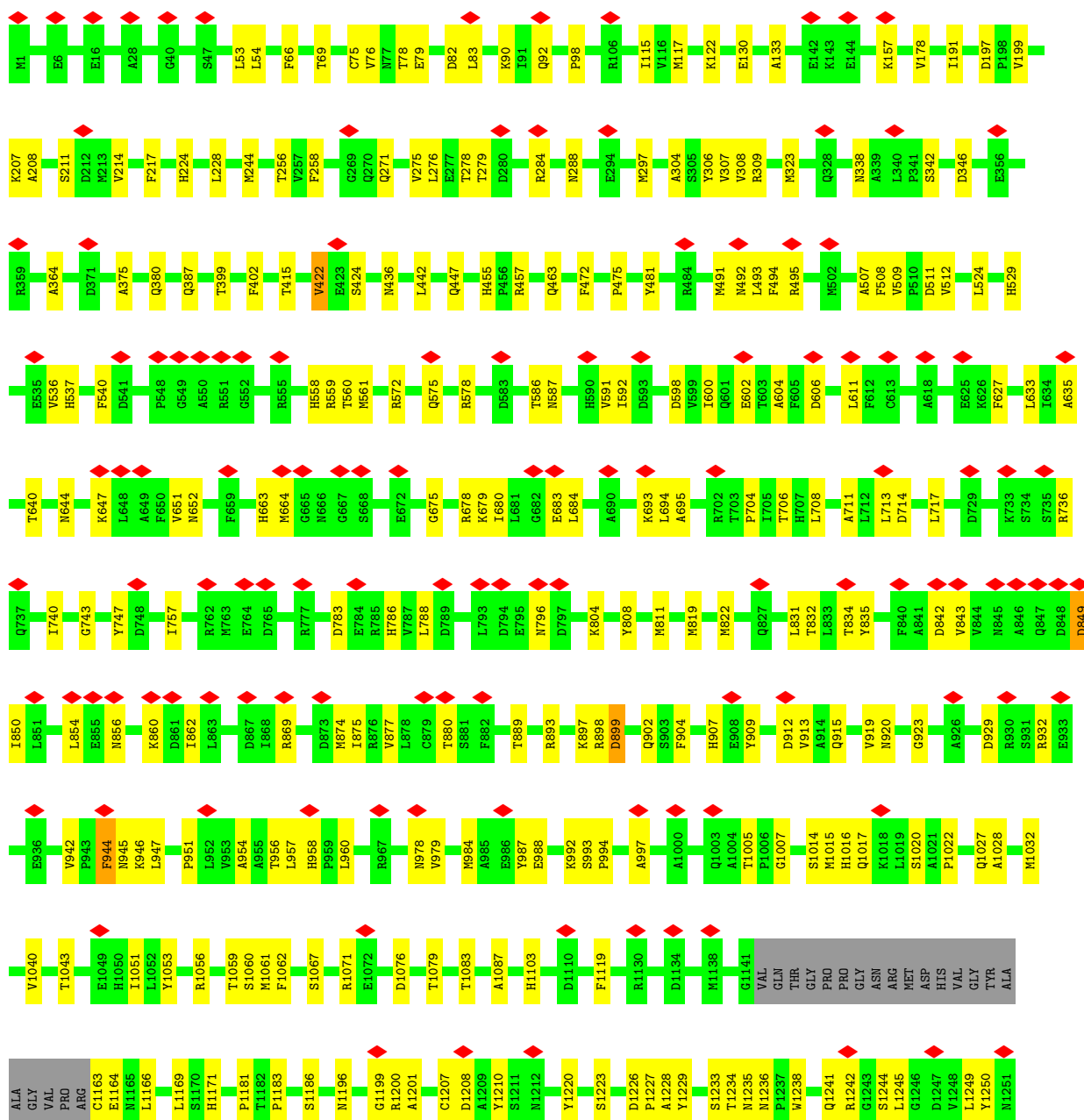
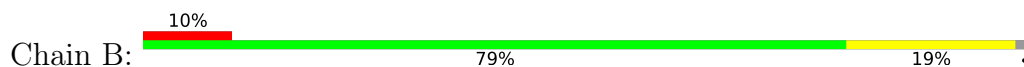
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

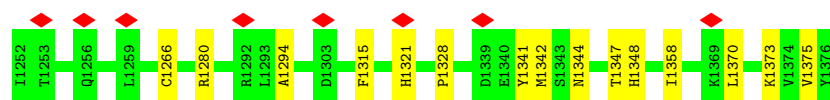
• Molecule 1: Major capsid protein



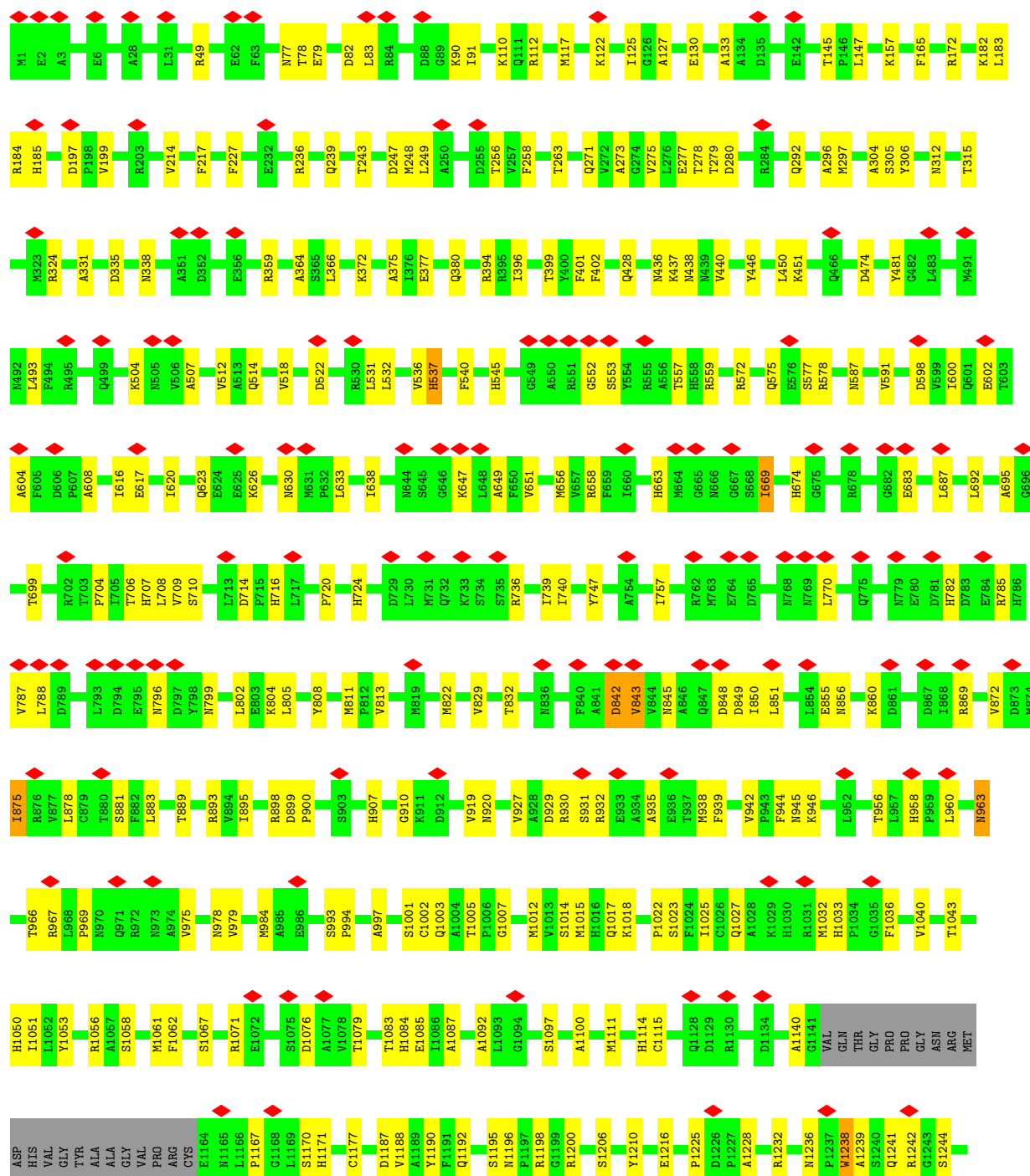
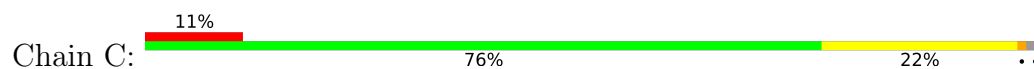


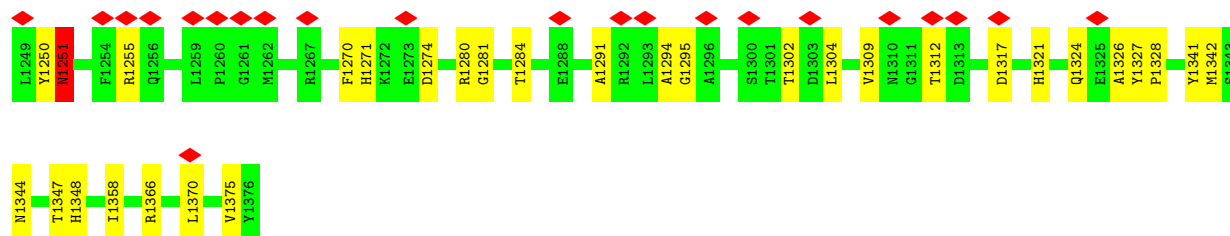
• Molecule 1: Major capsid protein



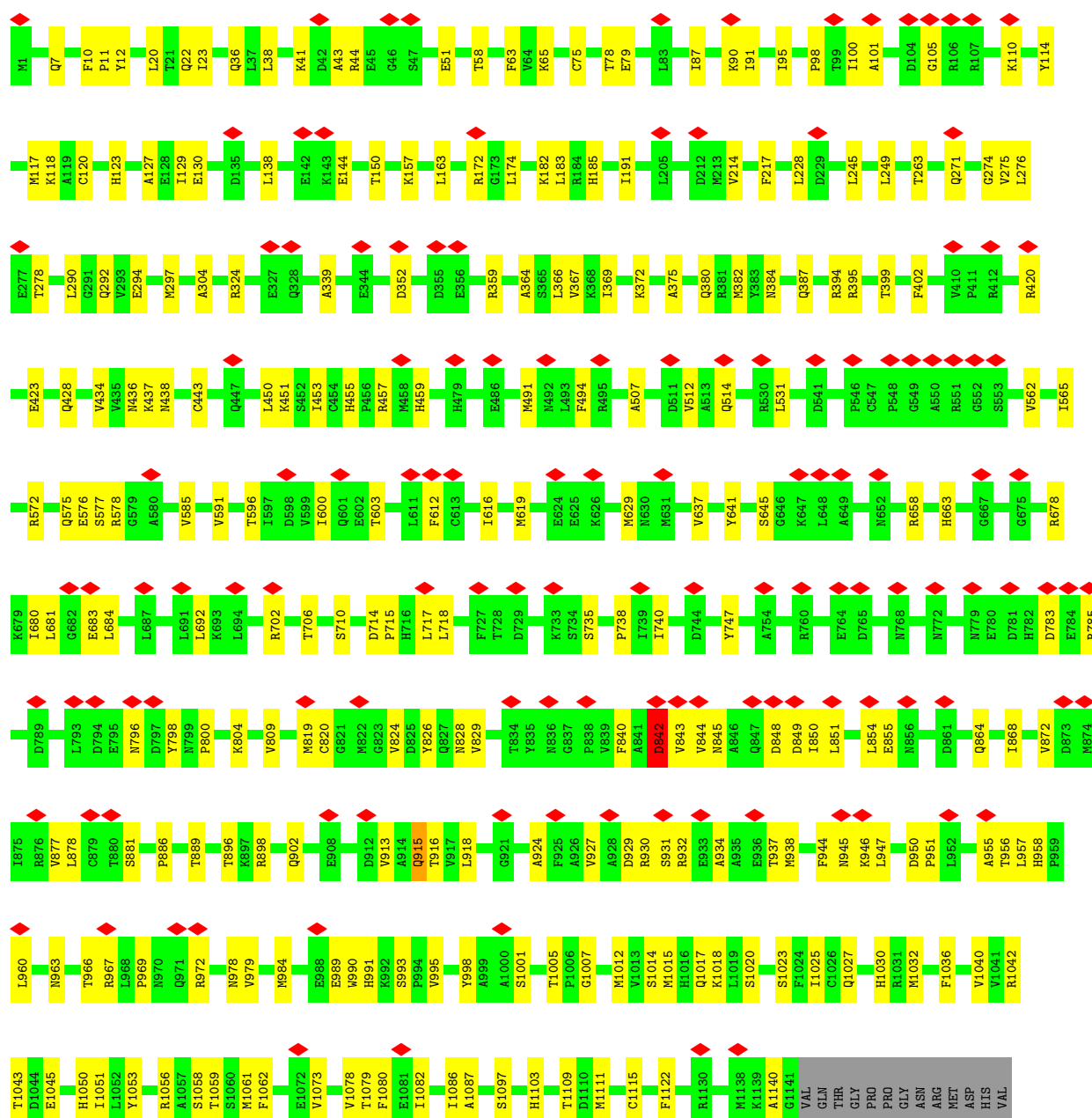
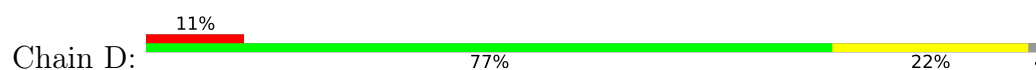


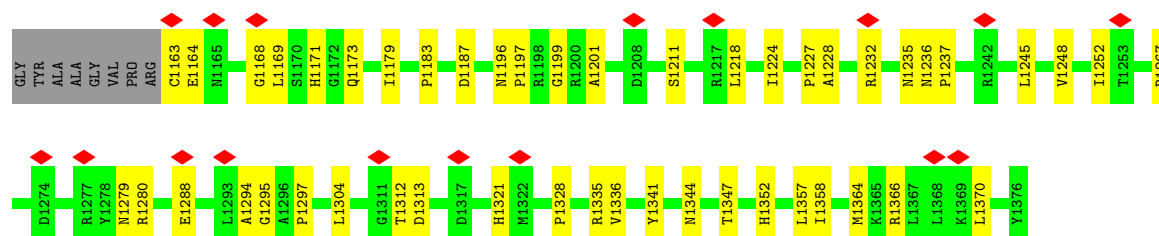
• Molecule 1: Major capsid protein



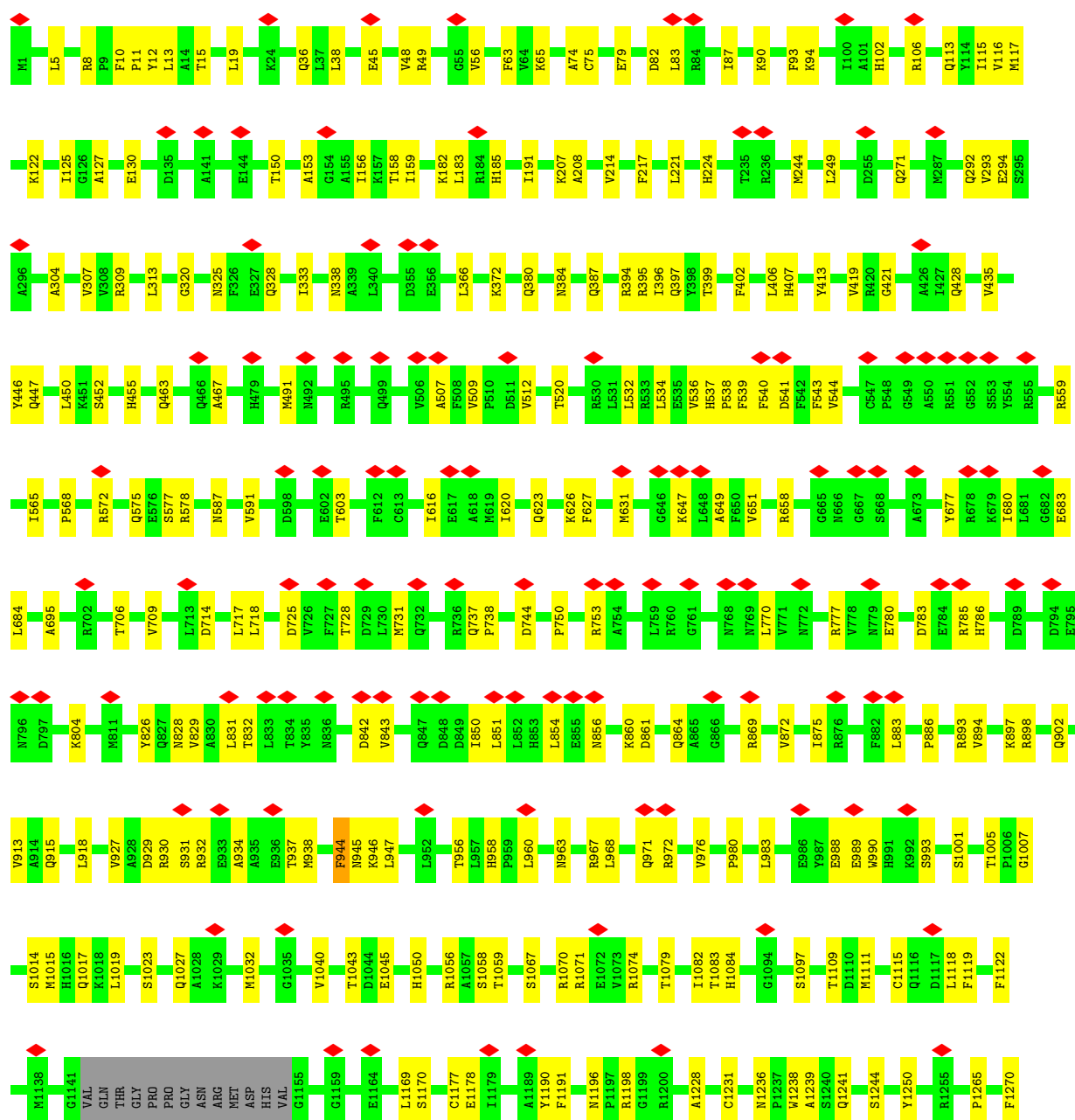
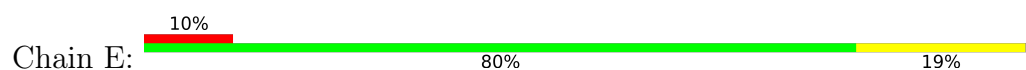


• Molecule 1: Major capsid protein



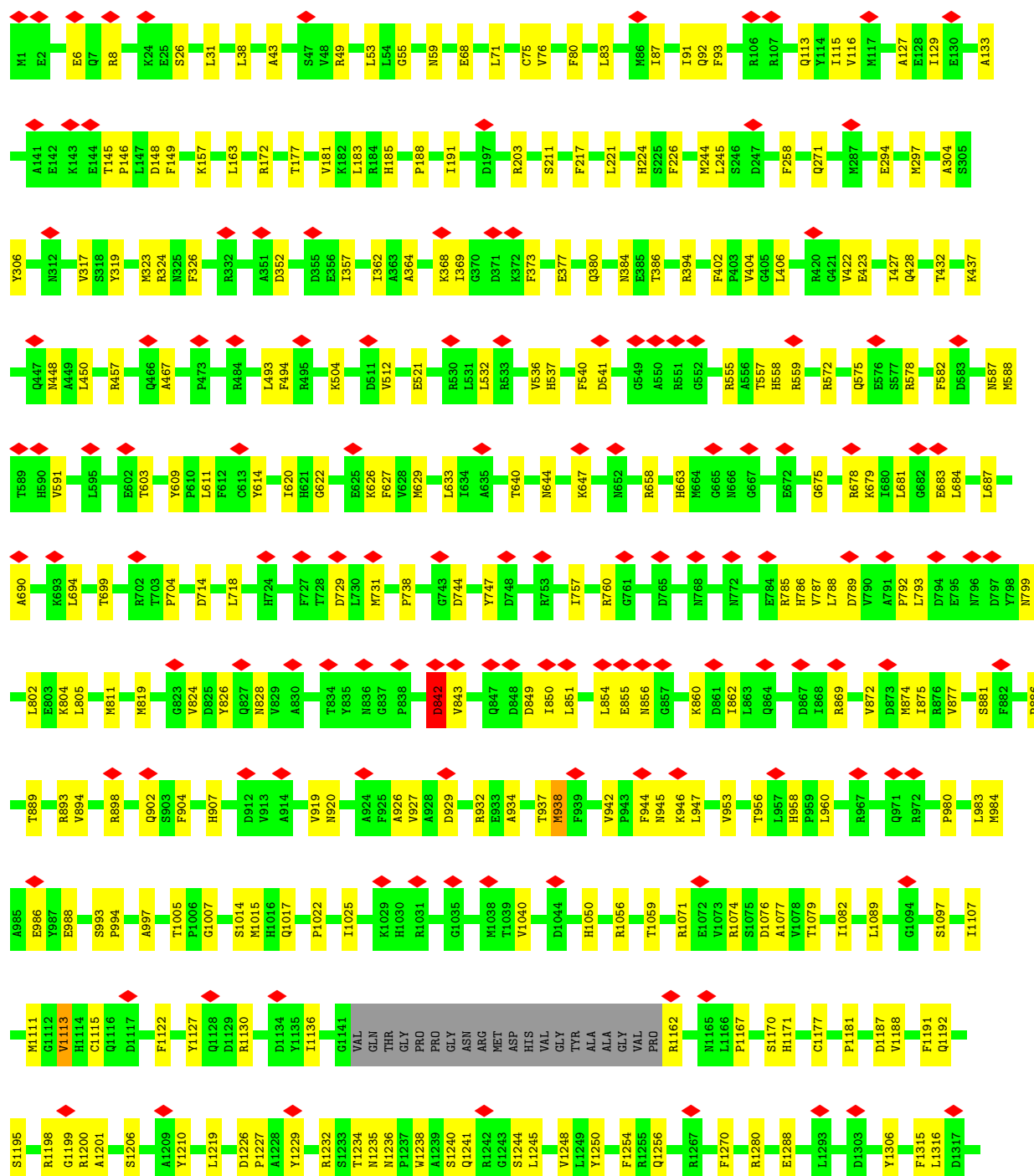
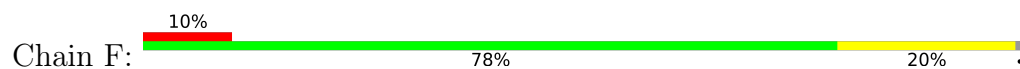


• Molecule 1: Major capsid protein



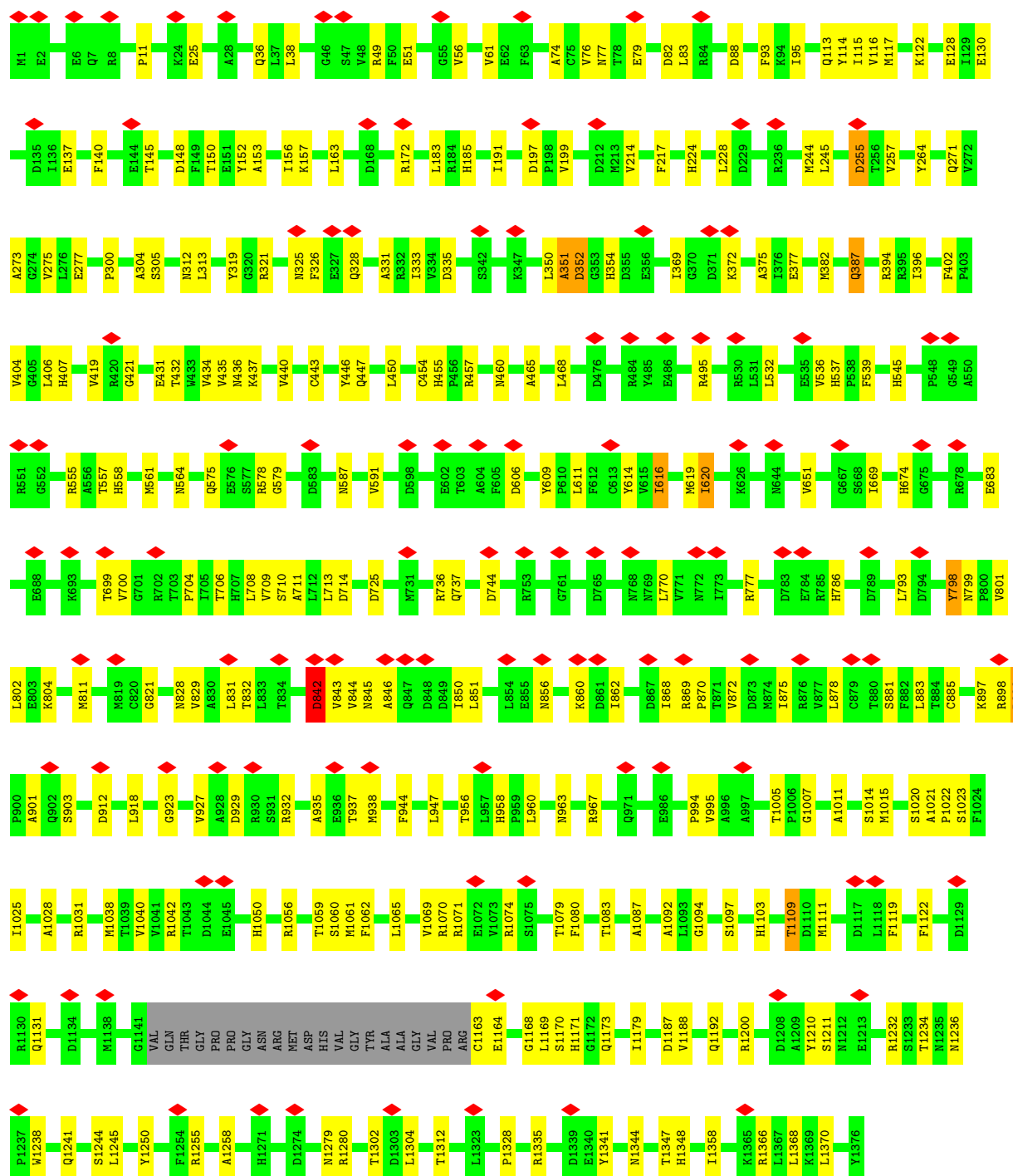
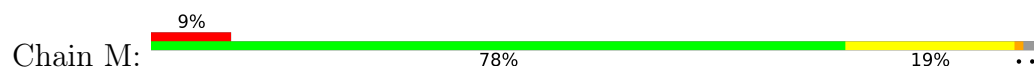


• Molecule 1: Major capsid protein

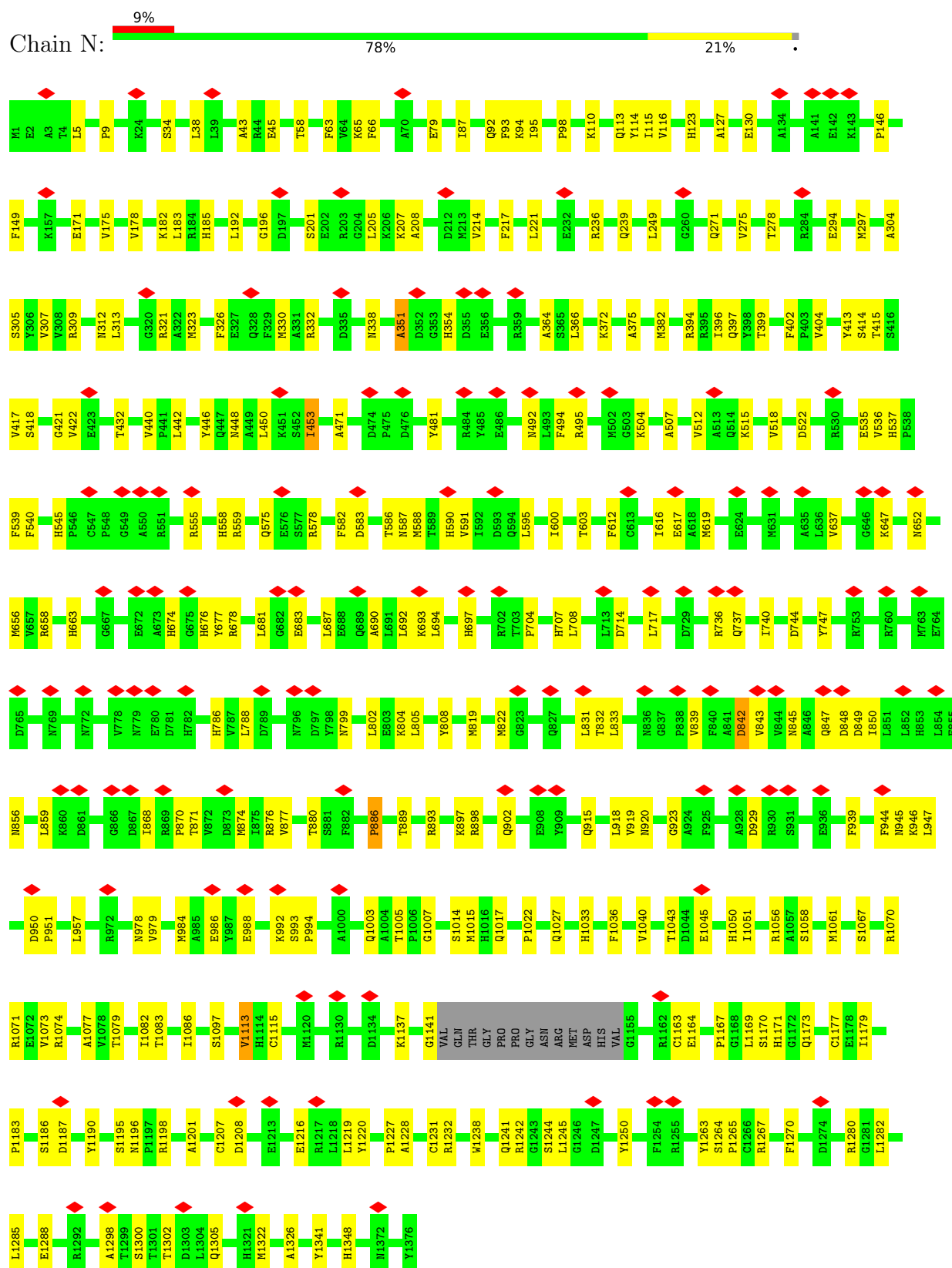




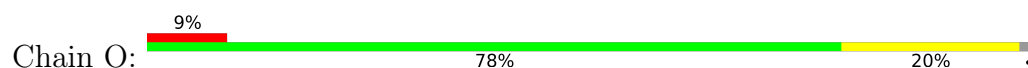
• Molecule 1: Major capsid protein



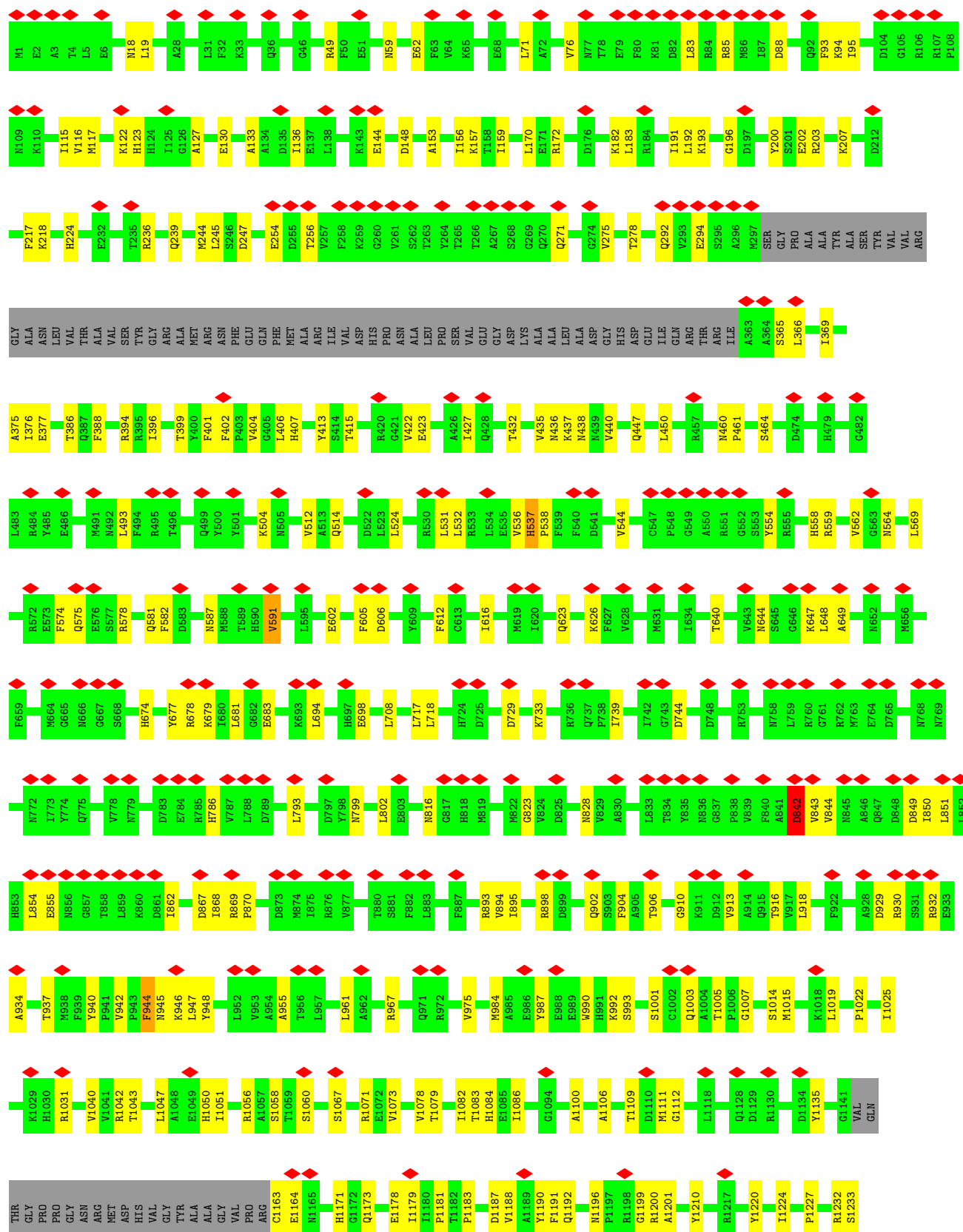
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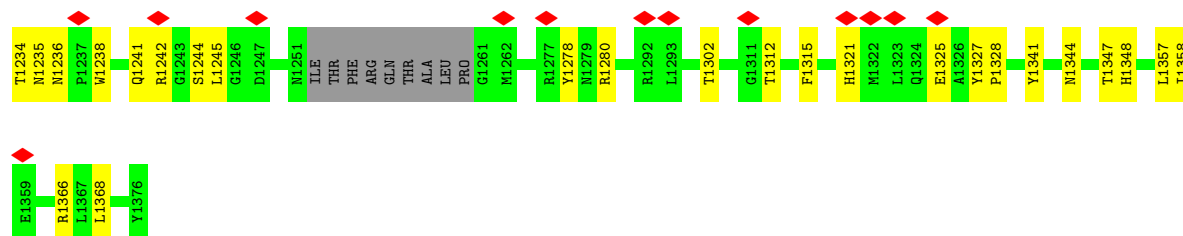


• Molecule 1: Major capsid protein

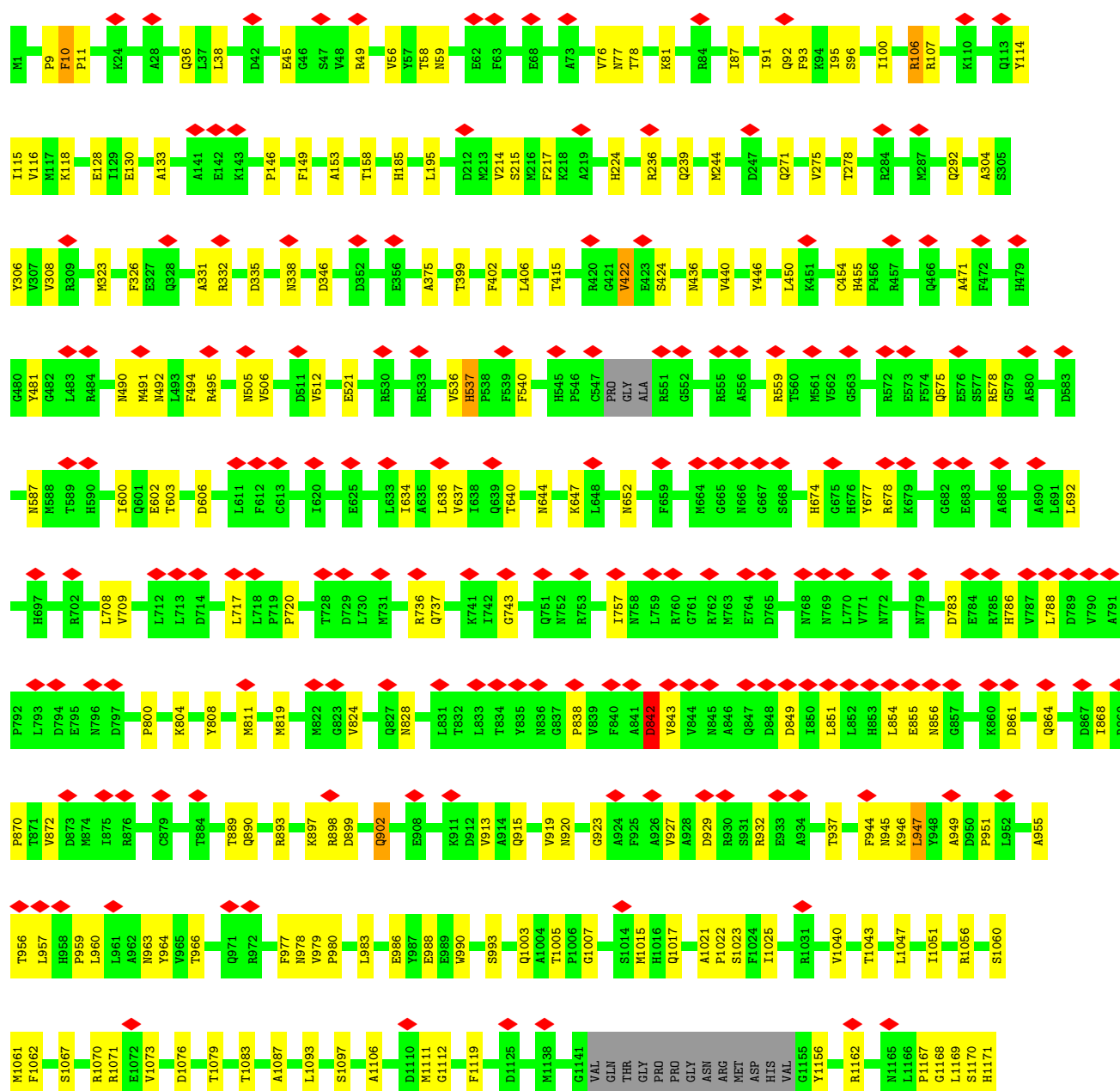
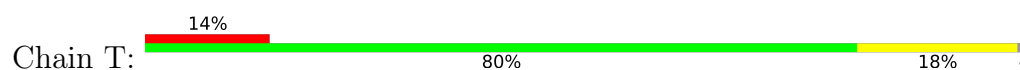


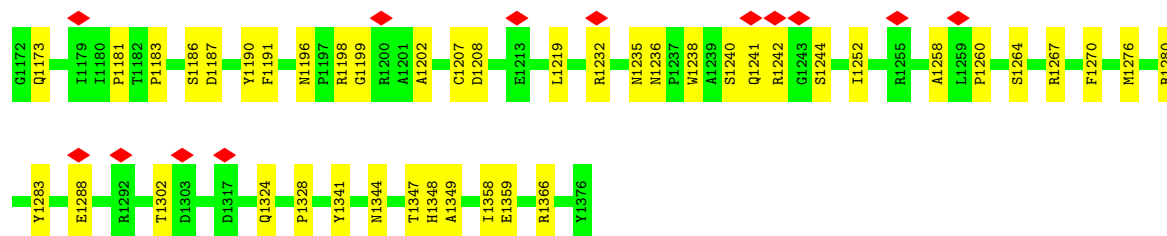




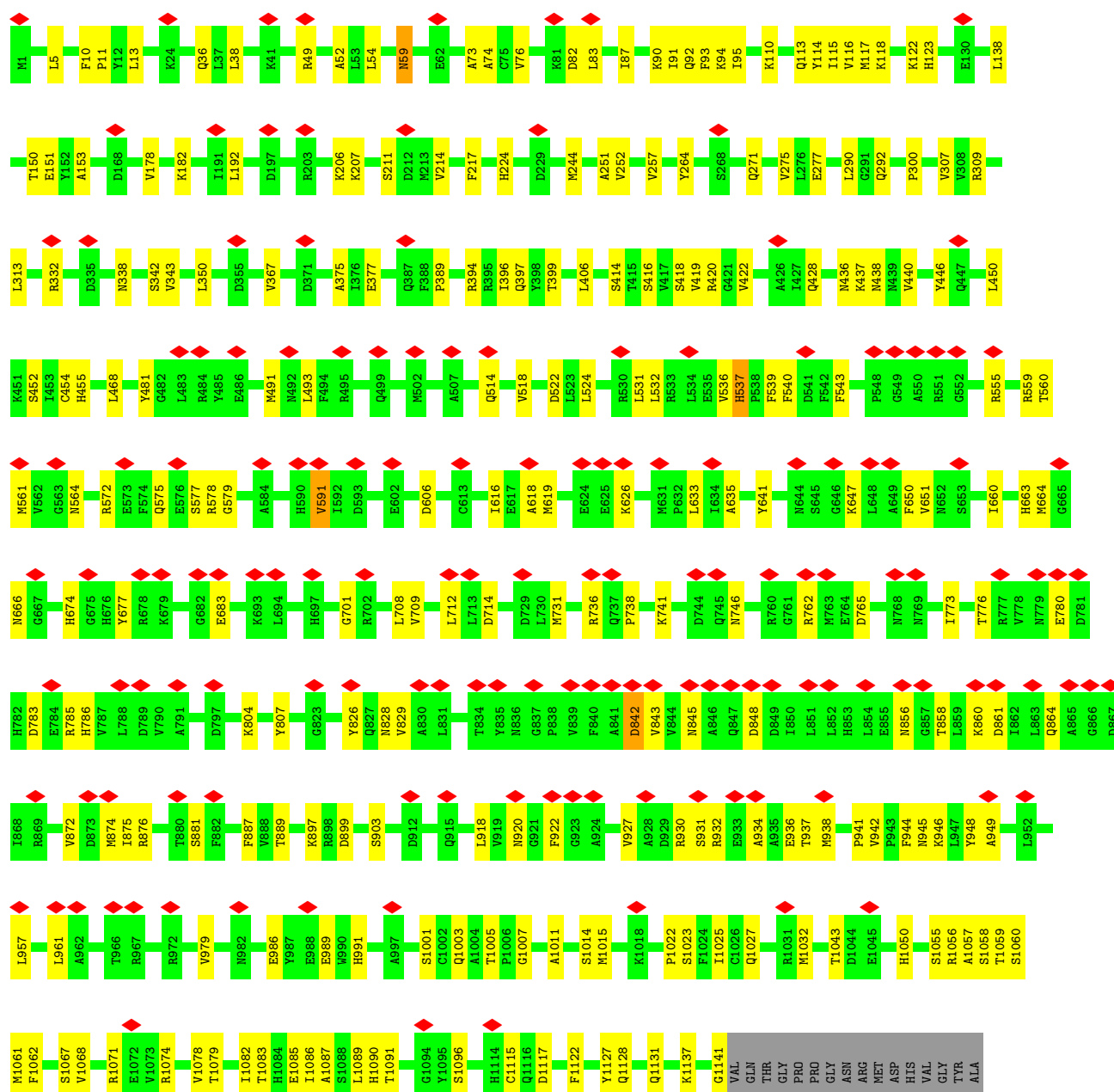
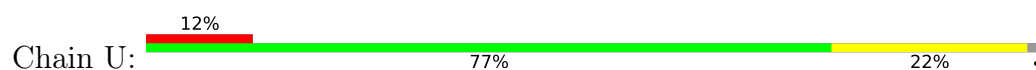


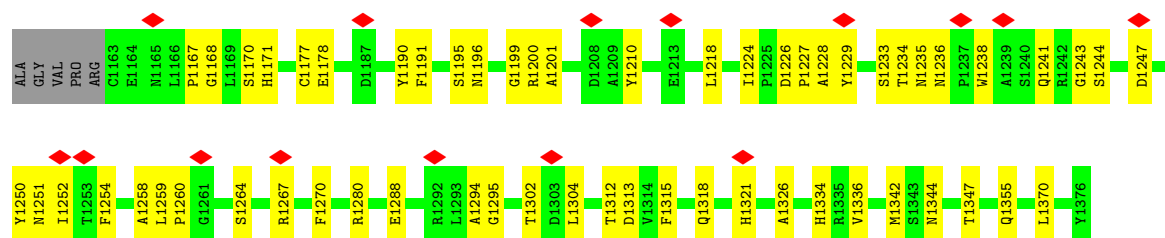
• Molecule 1: Major capsid protein



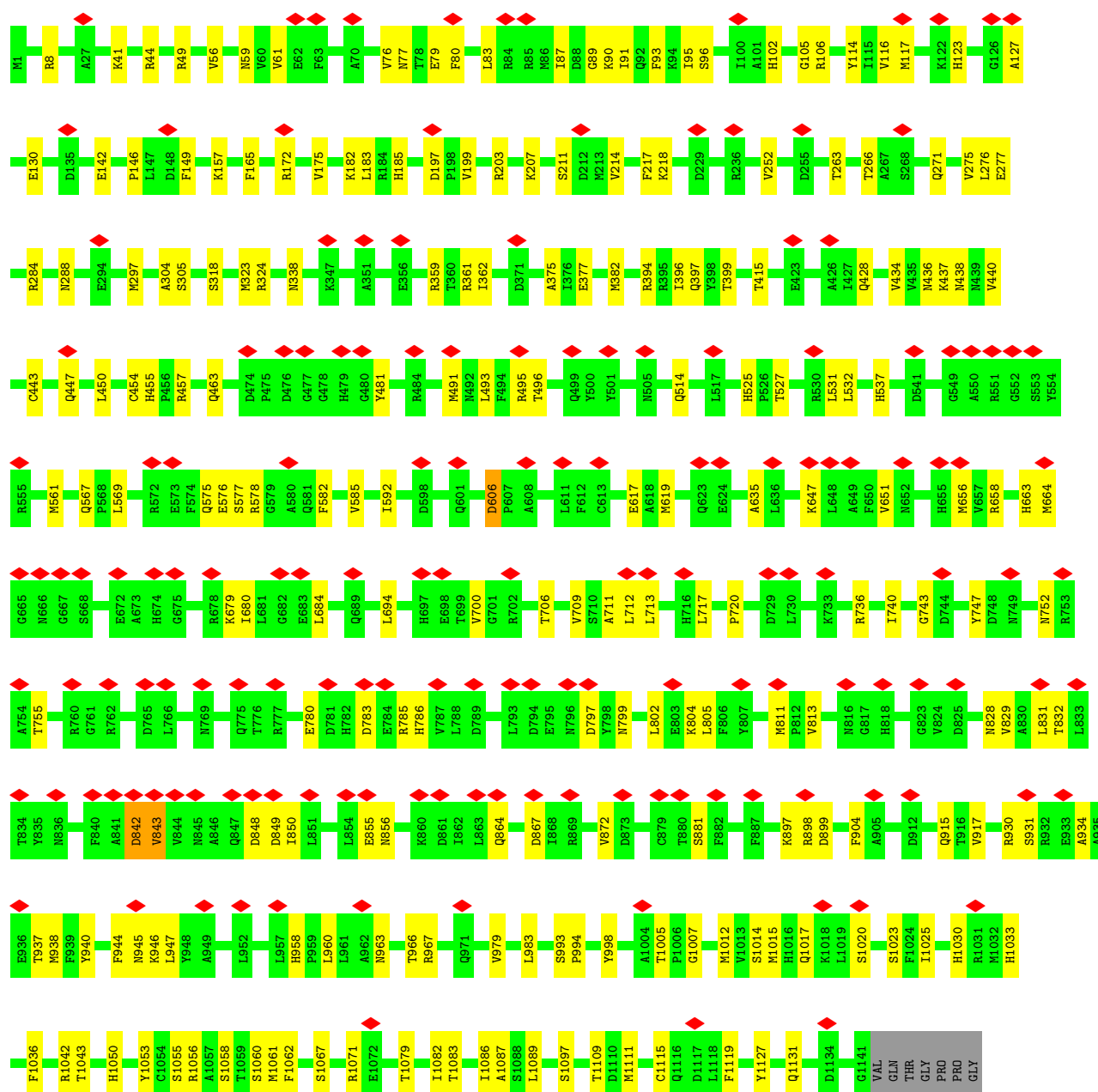
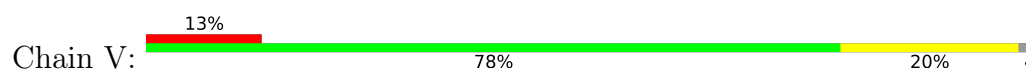


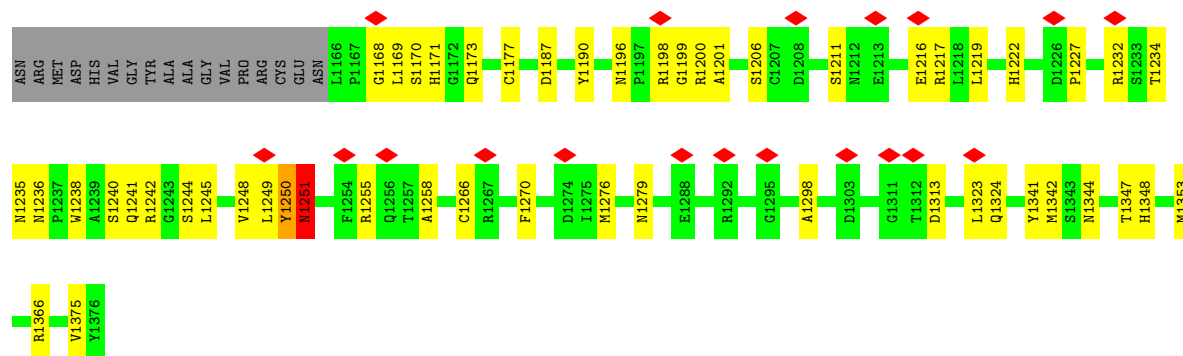
• Molecule 1: Major capsid protein



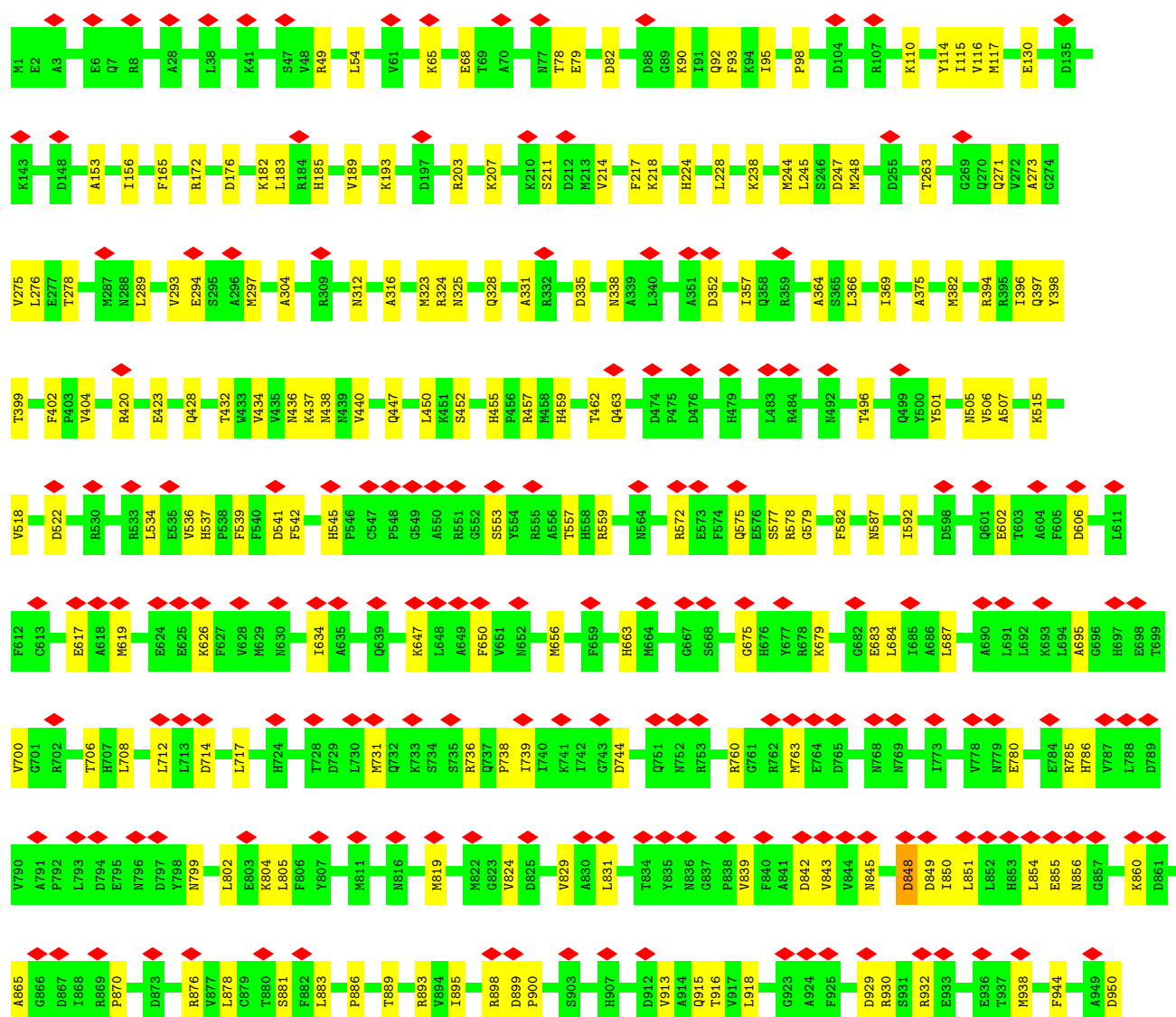
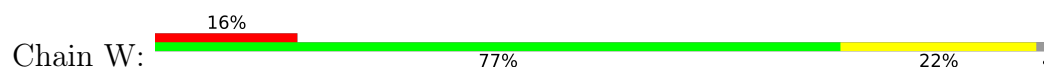


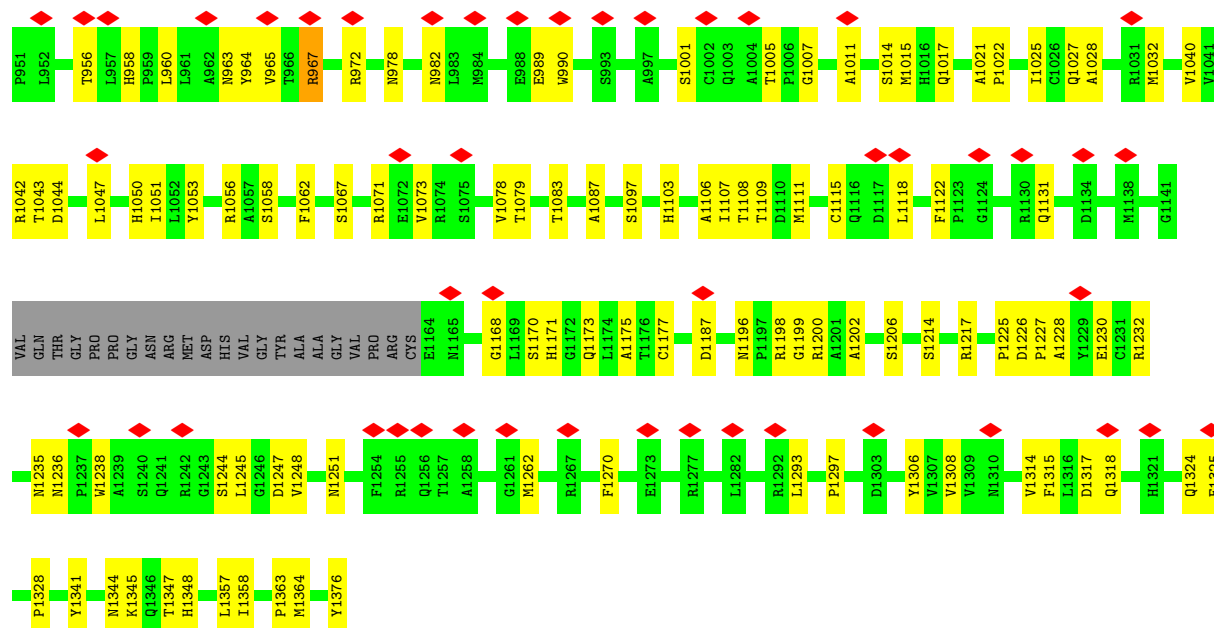
• Molecule 1: Major capsid protein



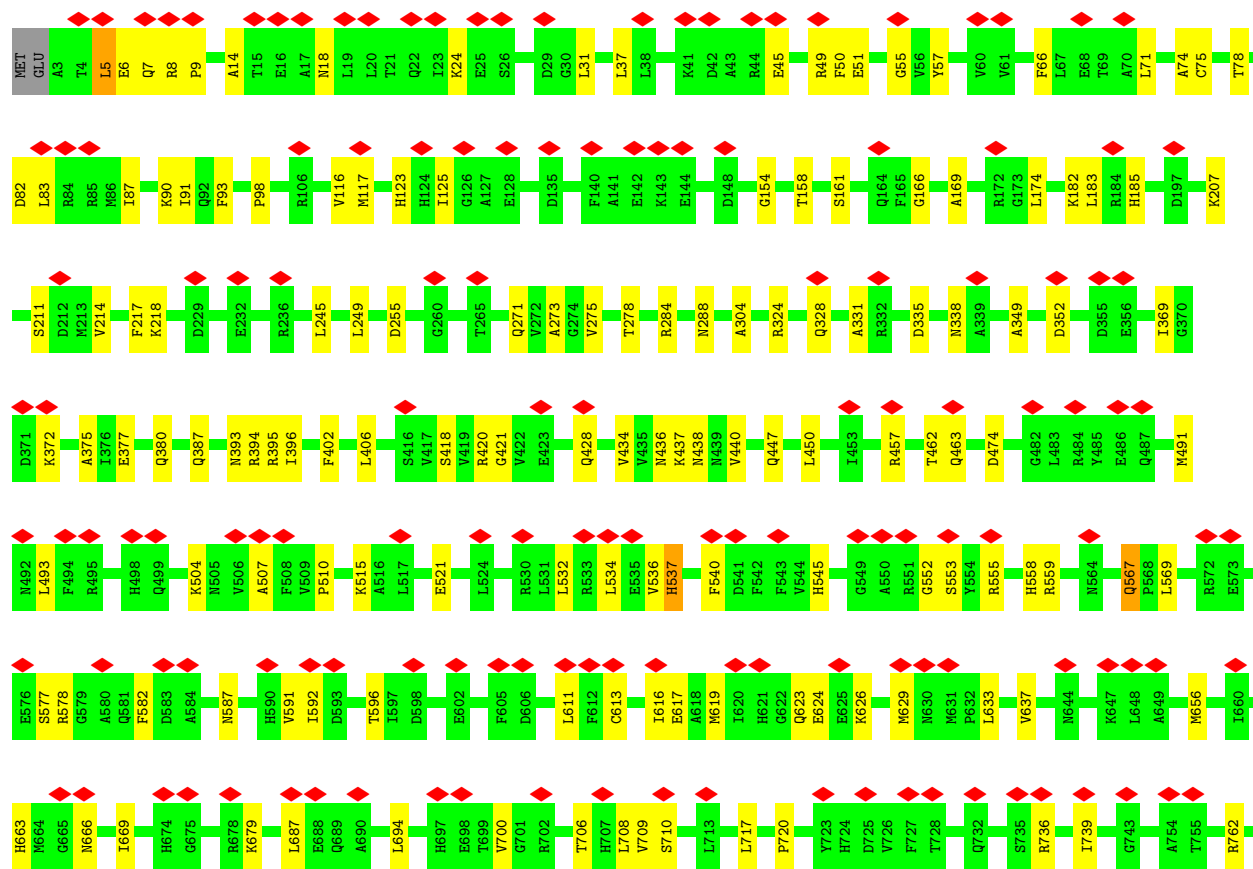
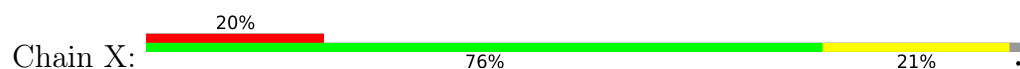


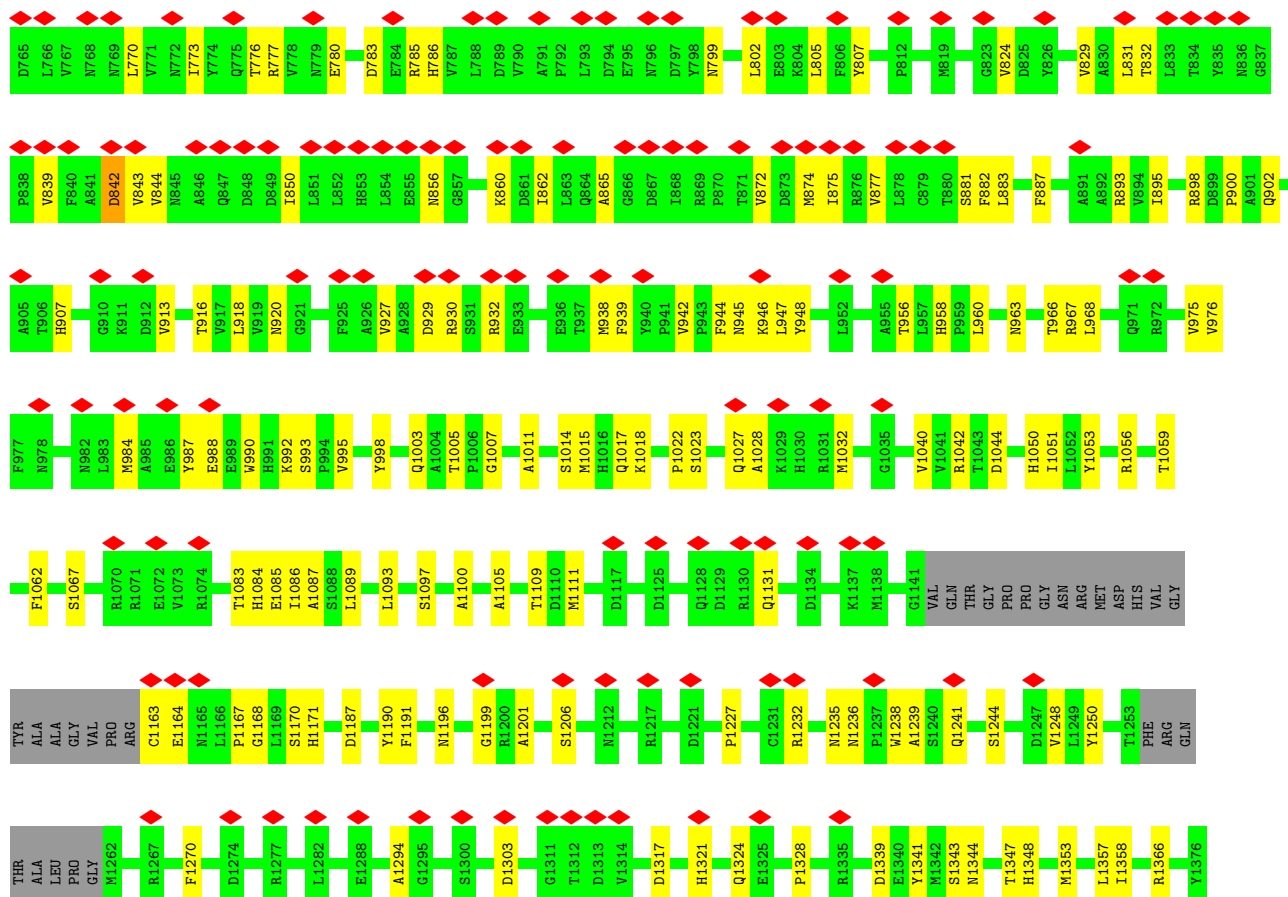
• Molecule 1: Major capsid protein



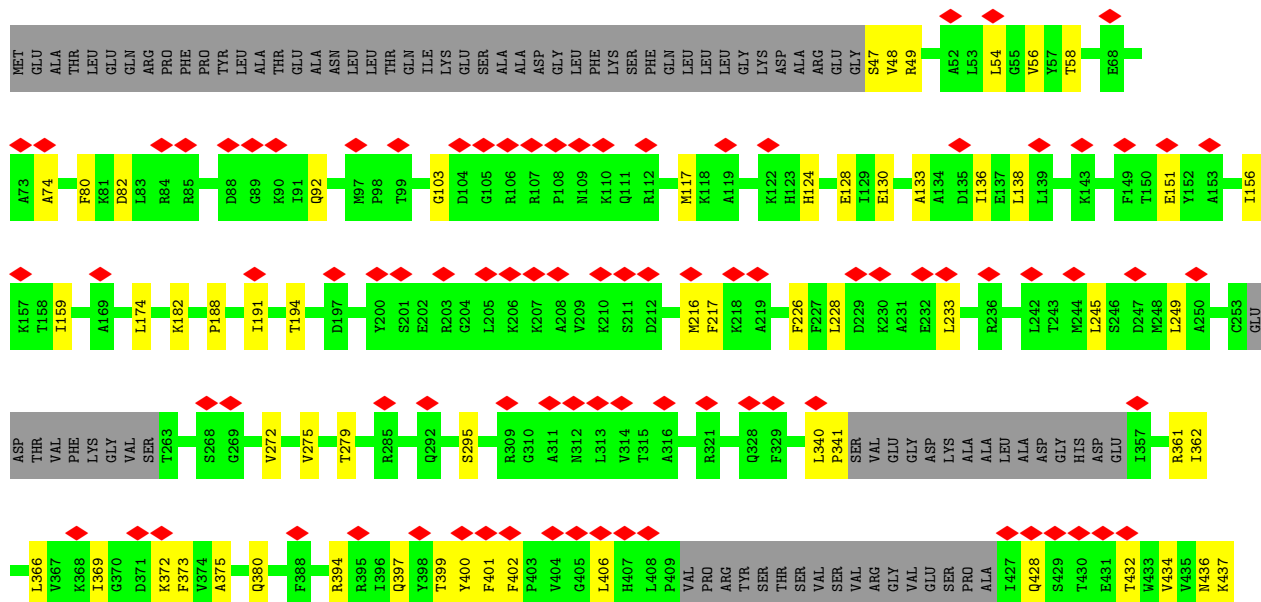


• Molecule 1: Major capsid protein

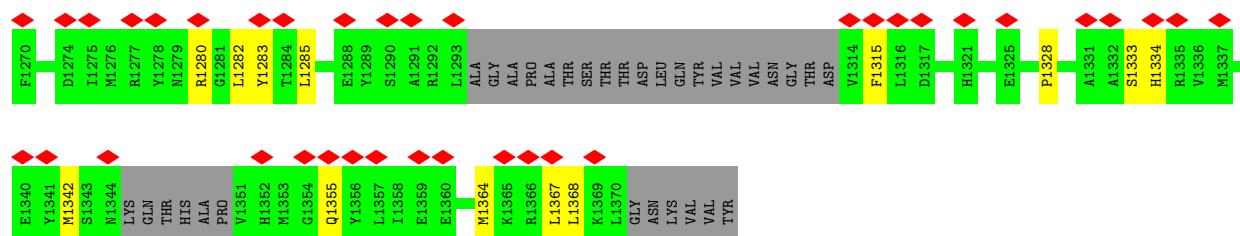




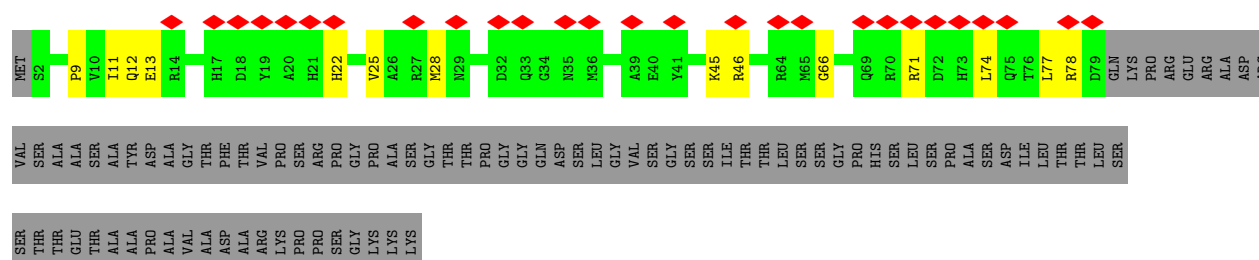
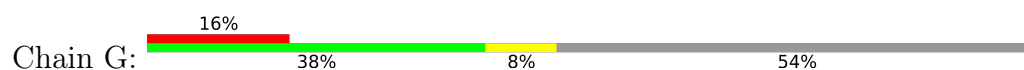
• Molecule 1: Major capsid protein



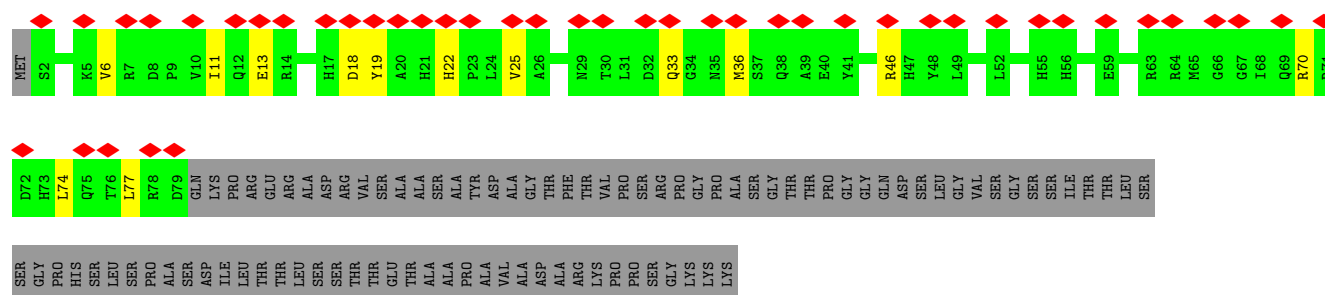
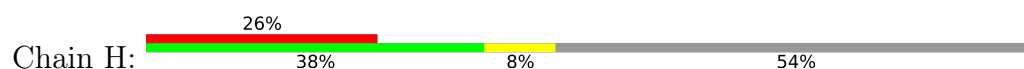
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PRO	D1208	M438	K504	E624	L684	D744	K804	Q864	A924	M884	D1044	PRO
GLY	A1209	M439	N505	E625	I685	Q745	L805	A865	F925	A885	E1045	GLY
ASN	S1211	L442	V506	K626	A686	N746	F806	Q866	A926	E886	S1058	ASN
MET	N1212	Y446	A507	F627	L687	Y747	Y807	Q867	Y927	Y987	V1063	MET
ASP	E1213	Q447	F508	V628	E688	D748	Y808	I868	A928	E888	G1064	ASP
HIS	S1214	Q448	V509	M629	Q889	N749	V809	R869	D929	E889	L1065	HIS
VAL	A1215	A449	P510	N630	A690	P750	L810	P870	R930	W990	L1071	VAL
THR	E1216	A450	D511	M631	L691	Q751	M811	T871	S931	H991	R1072	THR
ALA	L1217	L451	V512	P632	L692	N752	P812	V872	R932	K992	E1073	ALA
GLY	L1218	S452	A513	L633	K693	R753	V613	D873	E933	S993	V1074	GLY
VAL	D1221	I453	Q514	I634	L694	A754	C614	M874	A934	P994	R1075	VAL
PRO	I1222	C454	K615	A635	A695	T755	S815	L875	A935	V995	S1076	PRO
ARG	S1223	H455	A516	L636	G696	F756	N816	R876	E936	A996	D1076	ARG
CYS	I1224	P456	L517	V637	H697	I757	G817	V877	T937	A997	A1077	CYS
GLU	P1225	R457	V518	I638	E698	N758	H818	L878	N938	Y998	V1078	GLU
ASN	P1226	M458	T519	Q639	T699	L759	M819	C879	F939	A999	T1079	ASN
LEU	D1228	H459	T520	T640	V700	R760	C820	T880	Y940	A1000	H1084	LEU
PRO	Y1229	M460	E521	Y641	G701	G761	G821	S881	P941	S1001	E1085	PRO
GLY	C1230	P461	D522	W642	R702	R762	M822	F882	Y942	C1002	I1086	GLY
GLN	R1231	Q463	L523	V643	T703	M763	G823	L883	F943	A1004	A1087	GLN
LEU	S1233	Q466	L524	N644	P704	E764	V824	T884	N945	L1005	H1103	LEU
ALA	N1235	A467	H525	S645	I705	D765	D825	C885	N946	P1006	M1111	ALA
THR	P1236	A468	P526	G646	T706	L766	Y826	P886	K946	G1007	G1112	THR
LEU	P1237	L468	T527	T647	H707	V767	Q827	F887	L947	A1008	V1113	LEU
GLY	W1238	M469	S528	L648	L708	N768	N828	V888	Y948	I1009	H1114	GLY
GLN	A1239	Q470	H529	A649	V709	N769	V829	T889	A949	S1010	Q1116	GLN
LEU	S1240	P473	B530	F650	S710	L770	A830	Q890	D950	A1011	Q1117	LEU
ALA	Q1241	D474	L532	N652	L712	V771	L831	A891	P951	M1012	D1118	ALA
THR	R1242	M475	L533	S653	L713	I772	T832	A892	L952	A1013	L1119	THR
LEU	S1244	P476	L534	Y654	D714	I773	L833	R893	V953	S1014	T1120	LEU
GLY	G1246	D477	E535	H655	T715	V774	T834	V894	A954	M1015	M1121	GLY
GLN	L1245	Q477	V536	M656	H716	T775	Y835	I895	A955	H1016	F1122	GLN
THR	P1247	G478	H537	L717	L718	R777	G837	R897	L957	Q1017	T1123	THR
ALA	V1248	H479	P538	V657	L719	N778	P838	R898	H958	K1018	G1124	ALA
PRO	L1249	G480	F539	F659	T719	N779	V839	D899	P959	L1019	D1125	PRO
ARG	Y1250	Y481	D540	I660	F720	E780	F840	P900	L960	A1020	A1126	ARG
GLN	M1251	G482	F542	C661	A721	D781	A841	A901	L961	P1021	Y1127	GLN
THR	I1252	L483	D541	E602	T723	H782	D842	Q902	A962	S1022	Q1128	THR
ALA	S1253	R484	F543	T603	H724	D783	V843	S903	N963	I1023	D1129	ALA
LEU	V1254	Y485	V544	A604	D725	E784	V844	F904	Y964	F1024	R1130	LEU
PRO	G1261	E486	H545	F605	V726	R785	N845	A905	V965	I1025	Q1131	PRO
GLY	M1262	Q487	P546	D606	T727	H786	A846	T906	T966	Q1027	L1132	GLY
GLN	Y1263	T488	C547	G607	T728	V787	Q847	H907	R967	A1028	H1133	GLN
THR	S1264	P489	P548	A608	D729	L788	D848	E908	L968	K1029	D1134	THR
ALA	R1267	M490	G549	V609	I669	D789	D849	Y909	P969	H1030	Y1135	ALA
PRO	Q1268	M491	A550	P610	P670	V790	L850	G910	N970	R1031	I1136	PRO
GLY	F1269	M492	R551	R611	Q732	A791	L851	X911	Q971	M1032	L1137	GLY
GLN		L493	G552	E672	K733	P792	L852	D912	R972	H1033	M1138	GLN
THR		F494	S553	C613	A673	L793	H853	V913	N973	P1034	G1141	THR
ALA		R495	Y554	Y614	H674	D794	L854	A914	A974	G1035	VAL	ALA
LEU		T496	R555	V615	G675	E795	E855	Q915	V975	F1036	GLN	LEU
PRO		F497	A556	I616	H676	N796	N856	T916	V976	A1037	THR	PRO
ARG		H498	T557	E617	Q737	D797	G857	V917	F977	M1038	GLN	ARG
GLY		Q499	H558	A618	R678	Y798	T858	L918	N978	T1039	THR	GLY
GLN		Y501	R559	M619	K679	N799	L859	V919	V979	V1040	ALA	GLN
THR		M502	T560	I620	I680	P800	K860	N920	P980	V1041	LEU	THR
ALA			M561	G621	L681	V801	D861	G921	S981	R1042	THR	ALA
LEU			V562	G822	I742	L302	T862	F922	N982			LEU



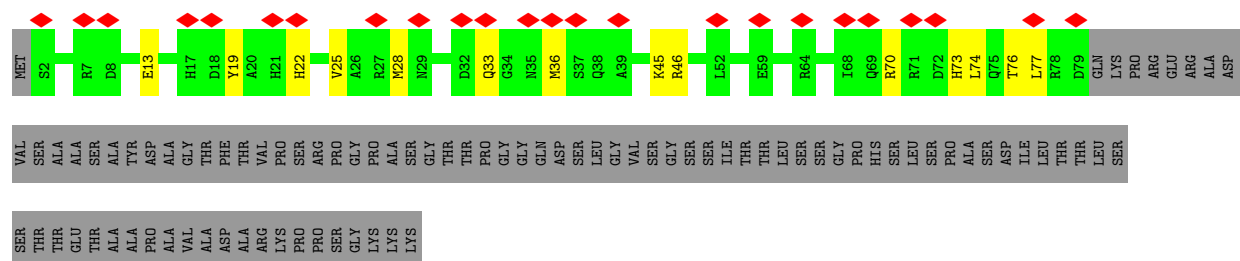
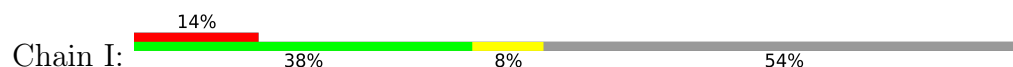
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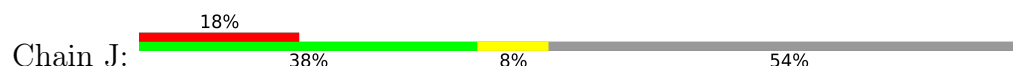
• Molecule 2: Small capsomere-interacting protein

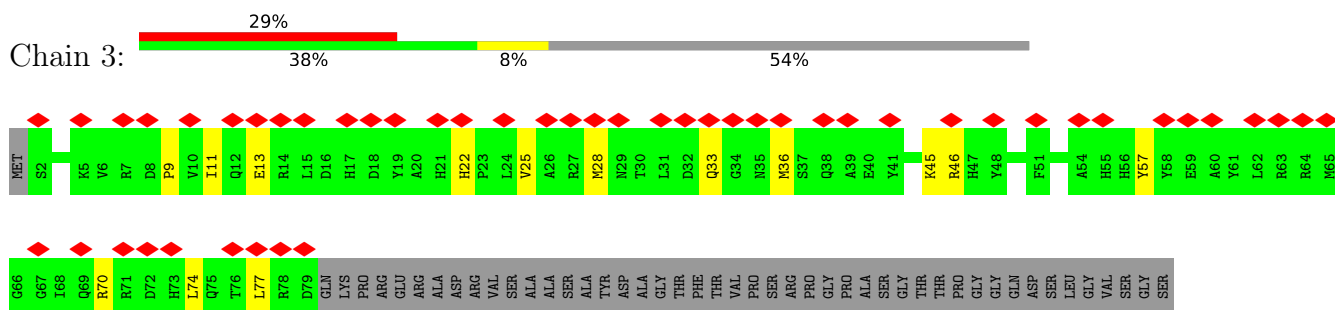


• Molecule 2: Small capsomere-interacting protein



• Molecule 2: Small capsomere-interacting protein

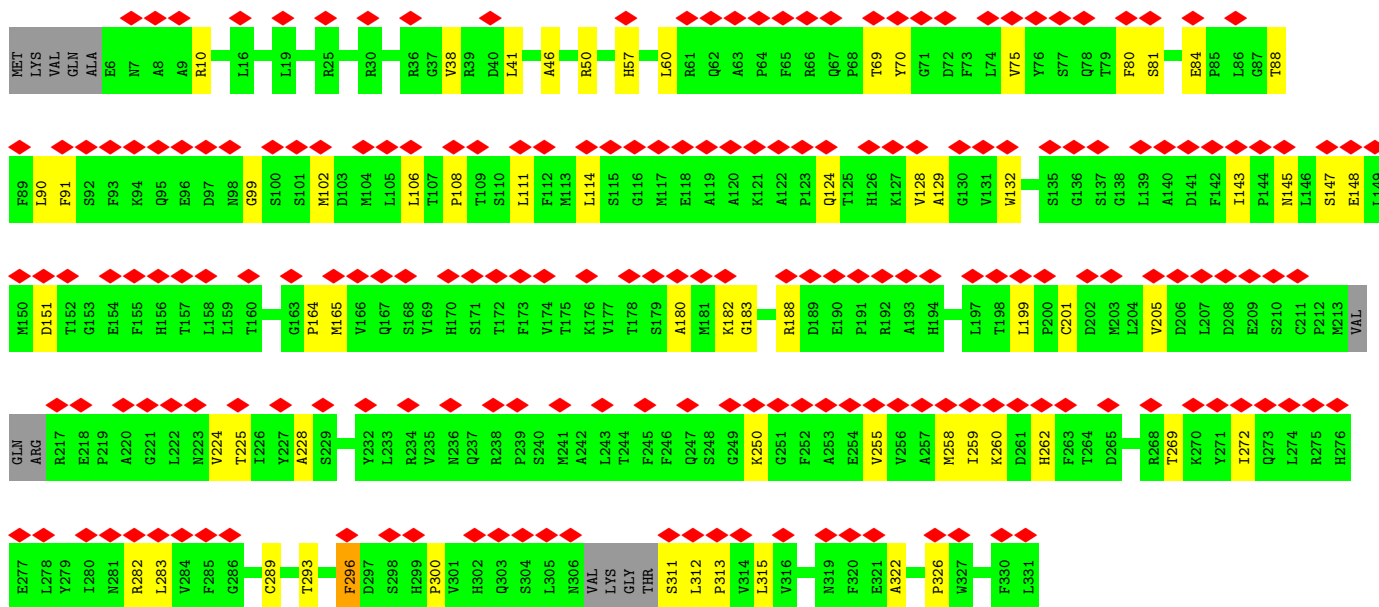




SER ILE THR THR LEU SER SER GLY HIS SER LEU SER PRO PRO ALA ALA SER ASP ILE LEU THR THR SER SER SER THR THR THR GLU THR ALA ALA ALA PRO ALA VAL ALA ASP ARG LYS LYS PRO PRO SER GLY LYS LYS

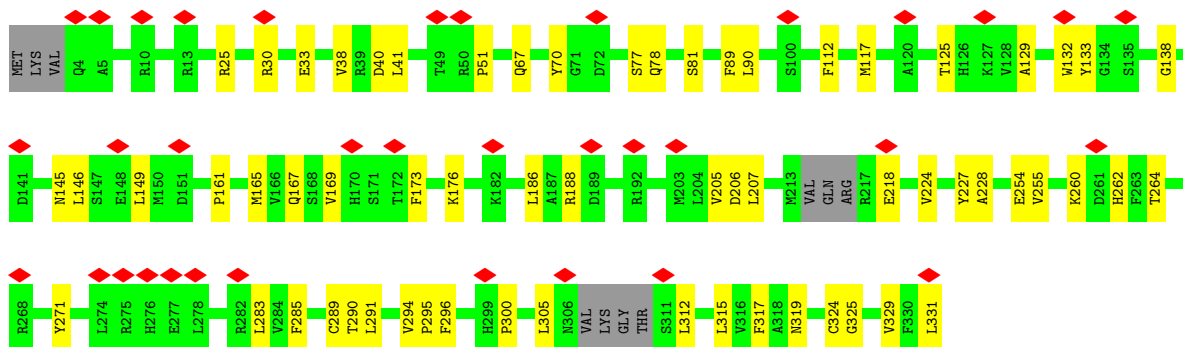
• Molecule 3: Triplex capsid protein 1

Chain 5: 



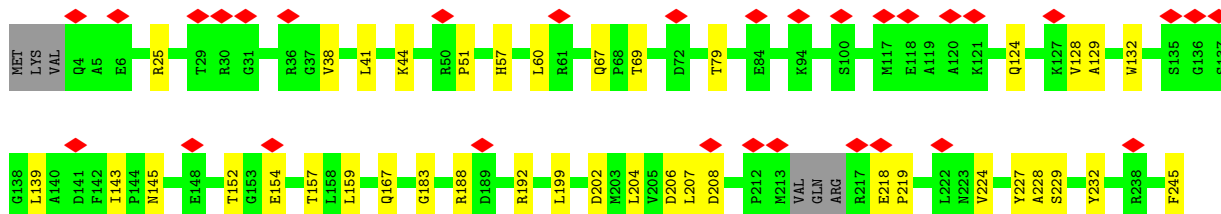
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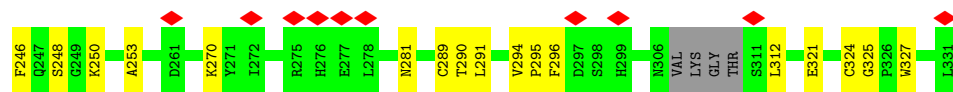
Chain 8: 



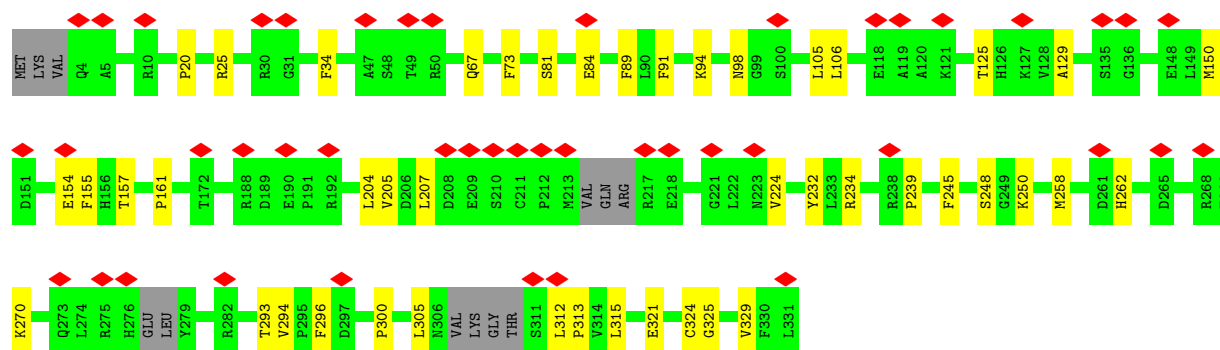
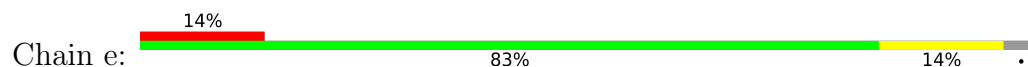
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Chain b: 

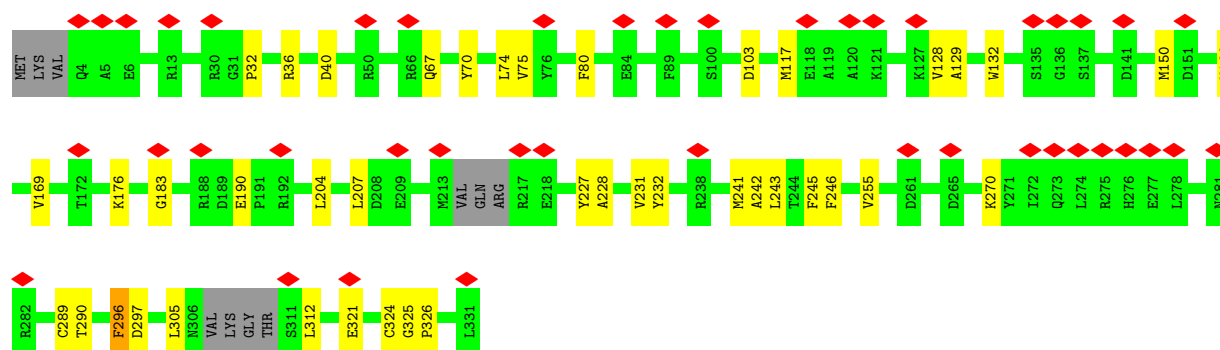
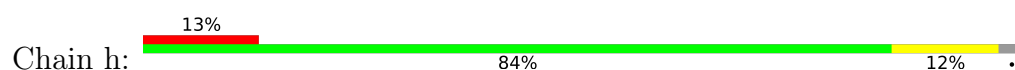




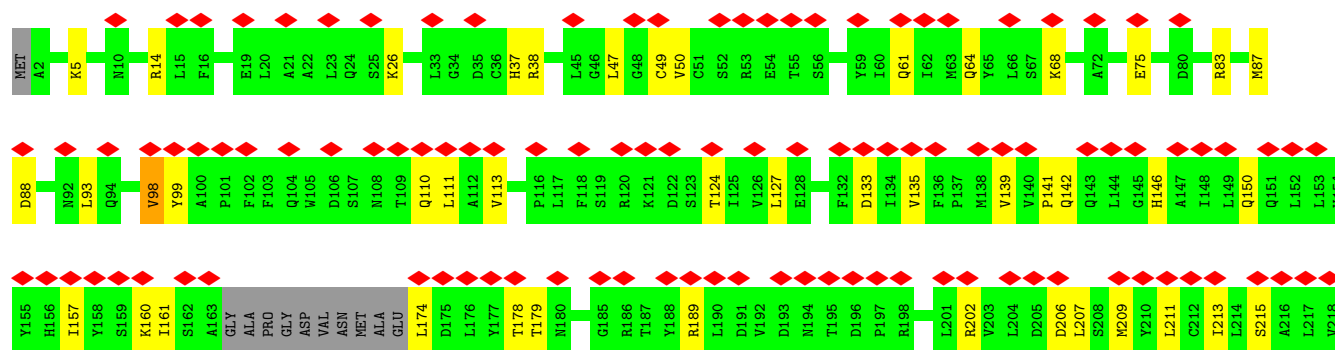
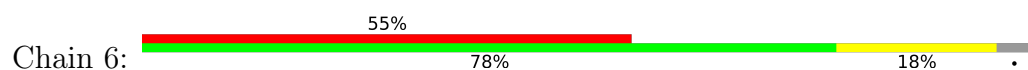
• Molecule 3: Triplex capsid protein 1



• Molecule 3: Triplex capsid protein 1

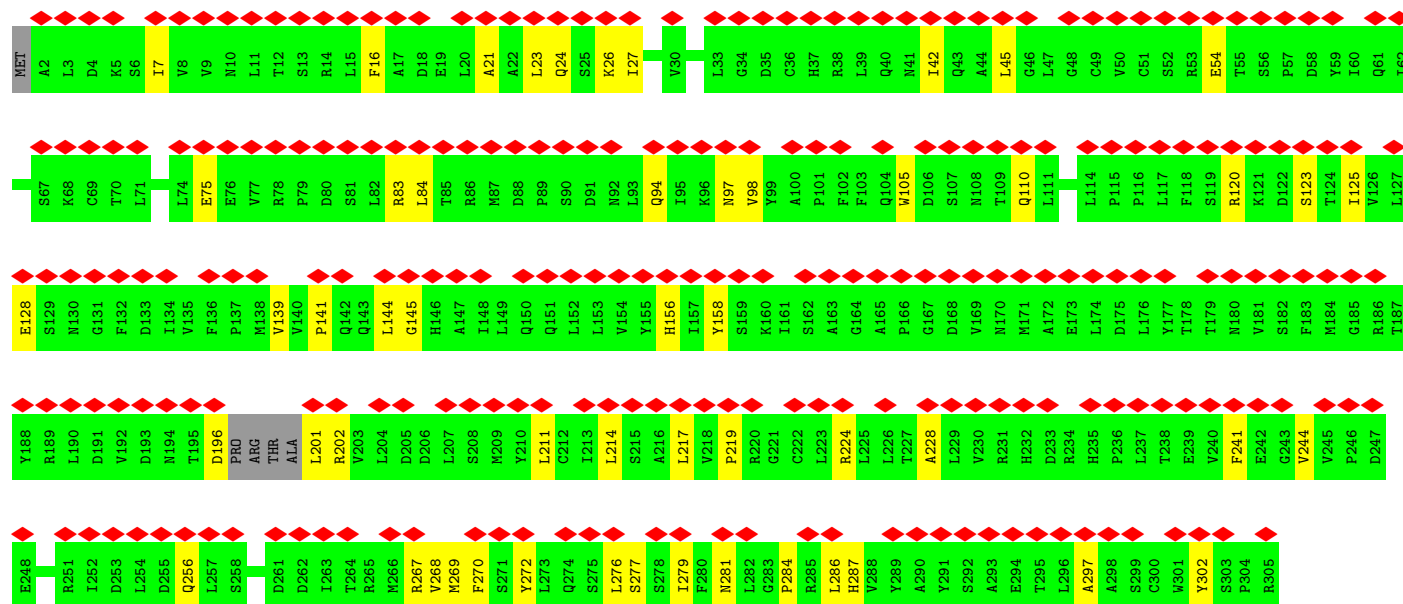
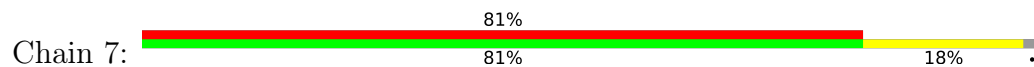


• Molecule 4: Triplex capsid protein 2

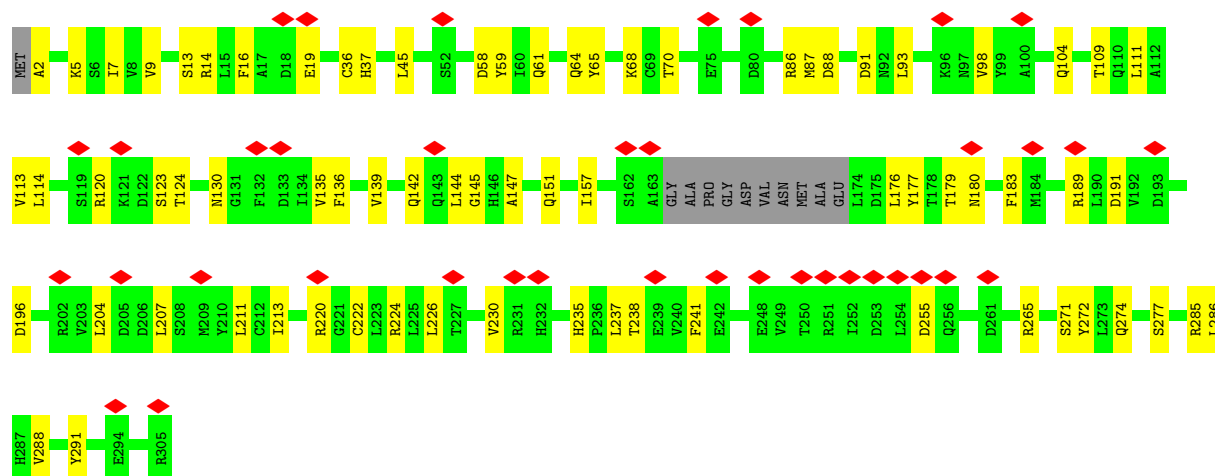




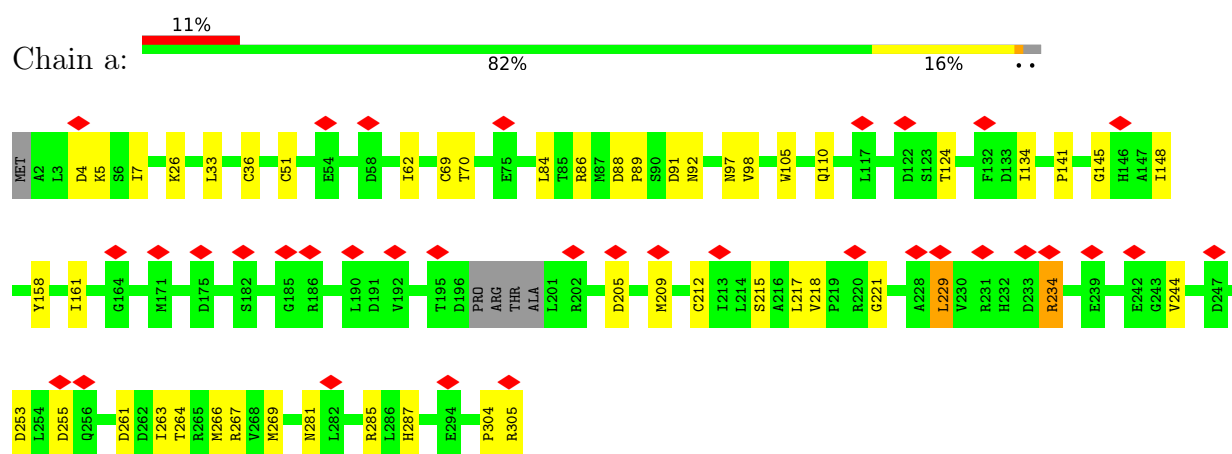
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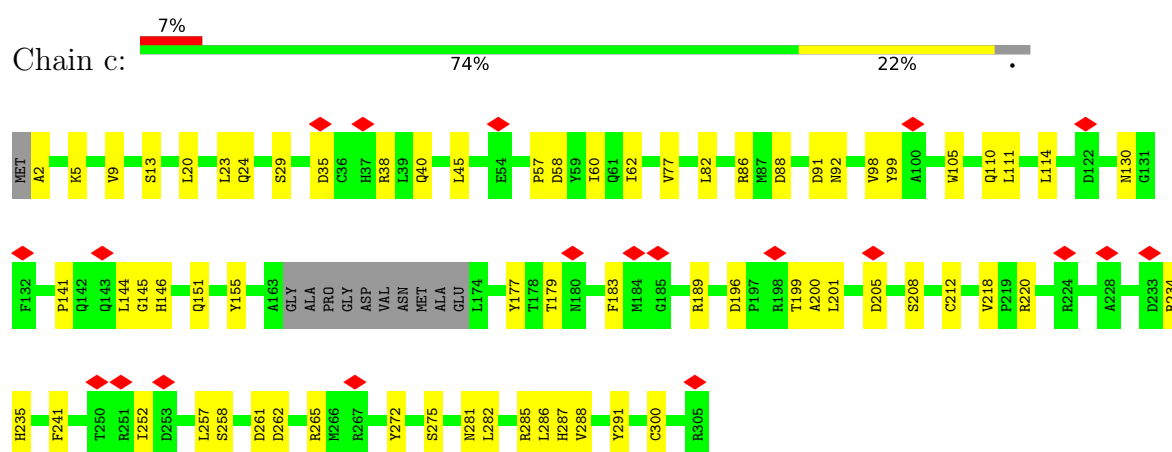
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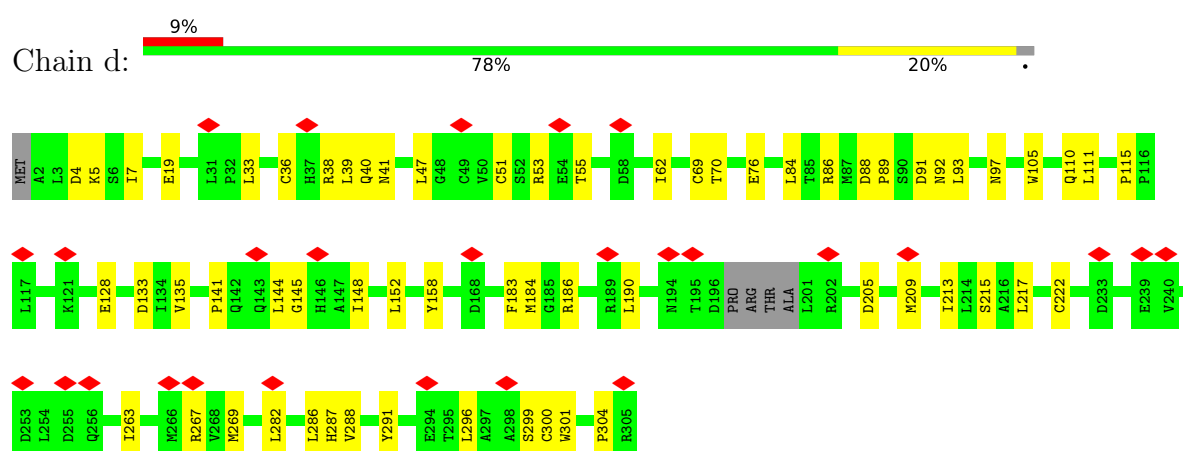
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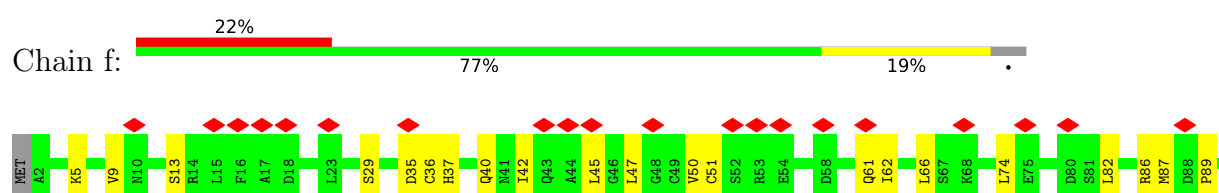
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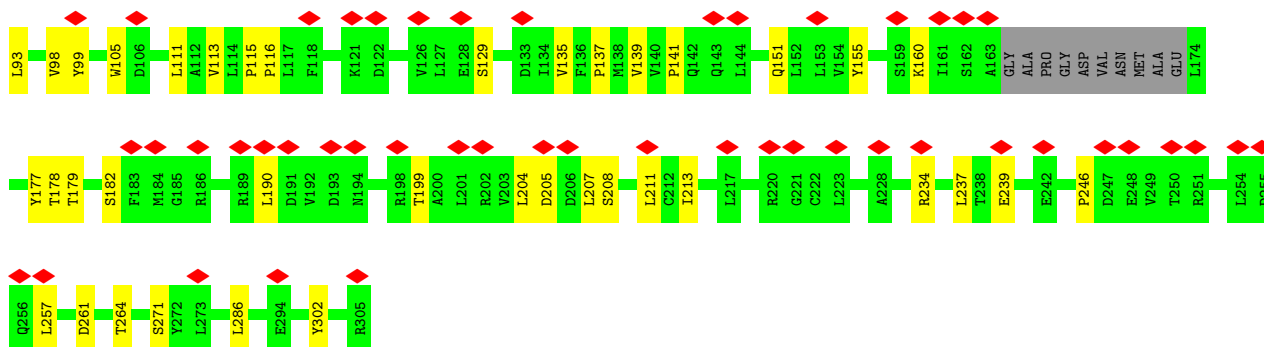


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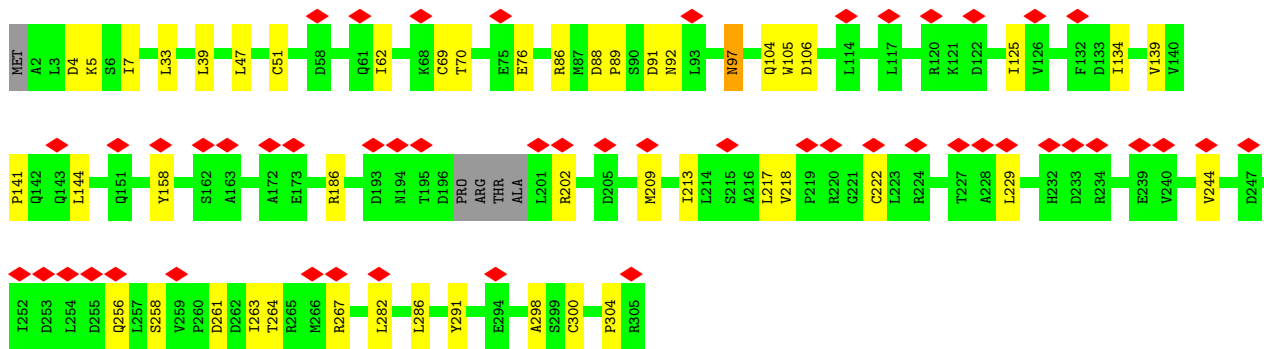
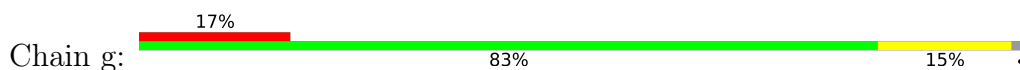


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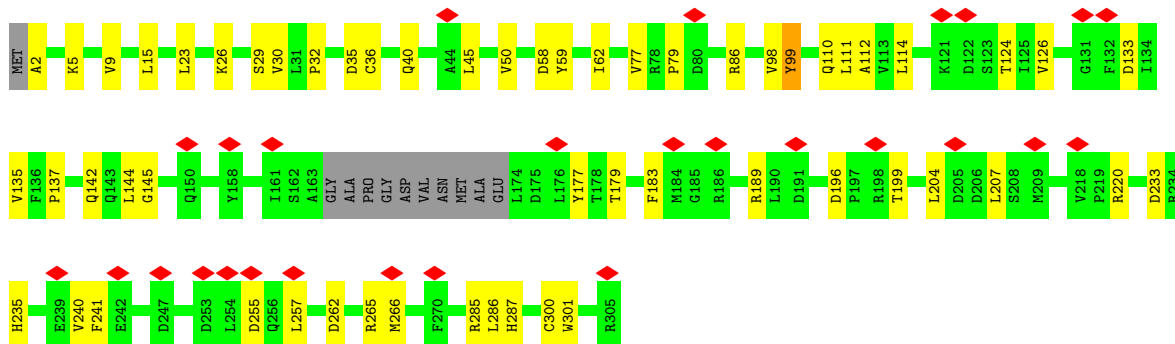
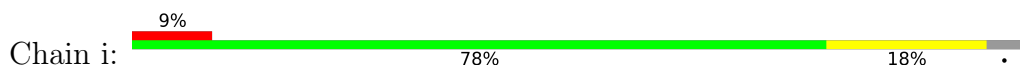




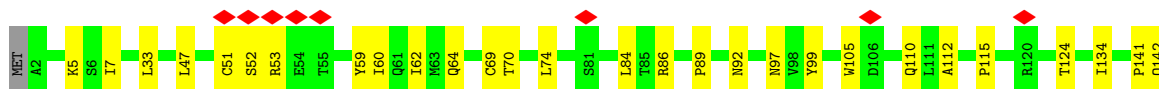
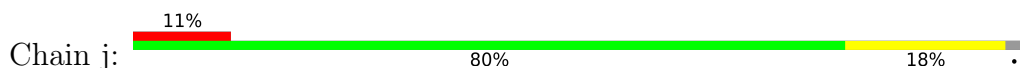
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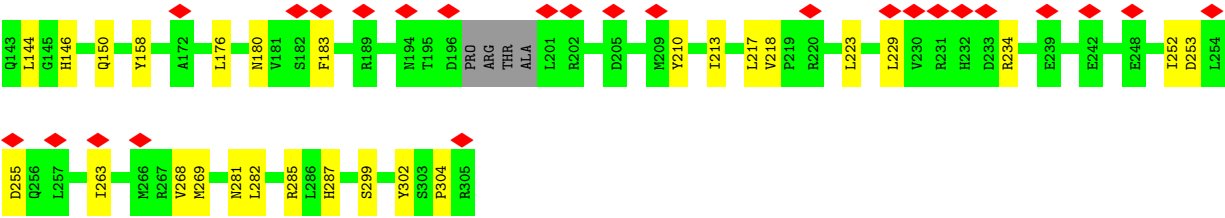


• Molecule 4: Triplex capsid protein 2



• Molecule 4: Triplex capsid protein 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	25315	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	24271	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	15.720	Depositor
Minimum map value	-11.596	Depositor
Average map value	0.008	Depositor
Map value standard deviation	1.070	Depositor
Recommended contour level	2.5	Depositor
Map size (Å)	1318.3999, 1318.3999, 1318.3999	wwPDB
Map dimensions	1280, 1280, 1280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.03, 1.03, 1.03	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	4	0.26	0/9812	0.61	4/13326 (0.0%)
1	A	0.36	0/10936	0.63	1/14866 (0.0%)
1	B	0.37	0/10879	0.67	10/14788 (0.1%)
1	C	0.35	0/10873	0.63	6/14780 (0.0%)
1	D	0.36	0/10879	0.66	2/14788 (0.0%)
1	E	0.37	0/10936	0.64	2/14866 (0.0%)
1	F	0.37	0/10890	0.65	7/14802 (0.0%)
1	M	0.38	0/10879	0.66	6/14788 (0.0%)
1	N	0.37	0/10936	0.66	10/14866 (0.1%)
1	O	0.37	0/10879	0.65	2/14788 (0.0%)
1	S	0.33	0/10298	0.64	3/13995 (0.0%)
1	T	0.35	0/10918	0.65	4/14839 (0.0%)
1	U	0.36	0/10879	0.65	4/14788 (0.0%)
1	V	0.36	0/10856	0.65	3/14757 (0.0%)
1	W	0.37	1/10873 (0.0%)	0.63	0/14780
1	X	0.33	0/10797	0.62	4/14676 (0.0%)
2	0	0.38	0/682	0.47	0/919
2	1	0.38	0/682	0.47	0/919
2	2	0.37	0/682	0.47	0/919
2	3	0.38	0/682	0.48	0/919
2	G	0.38	0/682	0.47	0/919
2	H	0.38	0/682	0.48	0/919
2	I	0.37	0/682	0.47	0/919
2	J	0.37	0/682	0.47	0/919
2	K	0.38	0/682	0.47	0/919
2	L	0.37	0/682	0.47	0/919
2	P	0.37	0/682	0.47	0/919
2	Q	0.37	0/682	0.47	0/919
2	R	0.37	0/682	0.47	0/919
2	Y	0.38	0/682	0.48	0/919
2	Z	0.37	0/682	0.48	0/919
3	5	0.26	0/2525	0.58	2/3433 (0.1%)
3	8	0.35	0/2539	0.58	2/3452 (0.1%)
3	b	0.35	0/2539	0.58	2/3452 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	e	0.33	0/2521	0.56	2/3426 (0.1%)
3	h	0.34	0/2539	0.57	2/3452 (0.1%)
4	6	0.28	0/2375	0.60	0/3234
4	7	0.26	0/2410	0.58	1/3281 (0.0%)
4	9	0.36	0/2375	0.63	0/3234
4	a	0.41	2/2410 (0.1%)	0.61	0/3281
4	c	0.38	0/2375	0.62	0/3234
4	d	0.38	0/2410	0.62	0/3281
4	f	0.32	0/2375	0.59	0/3234
4	g	0.36	0/2410	0.60	0/3281
4	i	0.37	0/2375	0.60	0/3234
4	j	0.38	0/2410	0.63	0/3281
All	All	0.36	3/219338 (0.0%)	0.63	79/298068 (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	4	0	9
1	A	0	4
1	B	0	7
1	C	0	8
1	D	0	10
1	E	0	5
1	F	0	4
1	M	0	6
1	N	0	7
1	O	0	6
1	S	0	6
1	T	0	11
1	U	0	4
1	V	0	6
1	W	0	2
1	X	0	1
3	h	0	1
4	6	0	1
4	7	0	1
4	9	0	2
4	a	0	1
4	c	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	d	0	1
4	f	0	2
4	g	0	2
4	i	0	1
4	j	0	2
All	All	0	111

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	a	234	ARG	CZ-NH2	-6.90	1.24	1.33
1	W	967	ARG	CD-NE	-6.15	1.37	1.46
4	a	234	ARG	CD-NE	5.45	1.53	1.46

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1181	PRO	CA-C-N	9.55	148.86	120.69
1	B	1181	PRO	C-N-CA	9.55	148.86	120.69
1	F	1113	VAL	N-CA-C	-8.53	105.01	113.20
1	T	308	VAL	N-CA-C	-7.42	105.31	111.91
1	N	417	VAL	N-CA-C	-7.03	105.20	113.42

There are no chirality outliers.

5 of 111 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1109	THR	Peptide
1	A	255	ASP	Peptide
1	A	537	HIS	Peptide
1	A	899	ASP	Peptide
1	B	422	VAL	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	4	9586	0	9478	160	0
1	A	10682	0	10559	167	0
1	B	10627	0	10504	164	0
1	C	10621	0	10498	195	0
1	D	10627	0	10503	194	0
1	E	10682	0	10558	187	0
1	F	10638	0	10517	180	0
1	M	10627	0	10503	185	0
1	N	10682	0	10558	182	0
1	O	10627	0	10505	178	0
1	S	10060	0	9942	176	0
1	T	10666	0	10542	159	0
1	U	10627	0	10504	211	0
1	V	10604	0	10486	177	0
1	W	10621	0	10499	198	0
1	X	10548	0	10422	186	0
2	0	666	0	647	9	0
2	1	666	0	647	11	0
2	2	666	0	647	5	0
2	3	666	0	647	10	0
2	G	666	0	647	10	0
2	H	666	0	647	9	0
2	I	666	0	647	8	0
2	J	666	0	647	8	0
2	K	666	0	647	8	0
2	L	666	0	647	8	0
2	P	666	0	647	8	0
2	Q	666	0	647	11	0
2	R	666	0	647	8	0
2	Y	666	0	647	8	0
2	Z	666	0	647	8	0
3	5	2463	0	2453	38	0
3	8	2477	0	2466	39	0
3	b	2477	0	2465	35	0
3	e	2460	0	2448	29	0
3	h	2477	0	2466	26	0
4	6	2329	0	2354	42	0
4	7	2364	0	2379	36	0
4	9	2329	0	2354	46	0
4	a	2364	0	2379	36	0
4	c	2329	0	2354	47	0
4	d	2364	0	2379	50	0
4	f	2329	0	2354	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	g	2364	0	2379	34	0
4	i	2329	0	2354	35	0
4	j	2364	0	2379	40	0
All	All	214334	0	212246	3214	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 8.

The worst 5 of 3214 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:736:ARG:HH22	1:C:899:ASP:HA	1.49	0.77
1:F:172:ARG:HH12	1:F:386:THR:HG21	1.49	0.77
1:X:558:HIS:HB3	1:X:898:ARG:HH12	1.50	0.76
1:4:457:ARG:HH12	1:4:463:GLN:HB3	1.50	0.75
1:W:865:ALA:HA	1:W:930:ARG:HH12	1.51	0.75

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	4	1200/1376 (87%)	1061 (88%)	136 (11%)	3 (0%)	36	71
1	A	1359/1376 (99%)	1204 (89%)	155 (11%)	0	100	100
1	B	1351/1376 (98%)	1192 (88%)	158 (12%)	1 (0%)	48	82
1	C	1350/1376 (98%)	1200 (89%)	148 (11%)	2 (0%)	48	82
1	D	1351/1376 (98%)	1186 (88%)	163 (12%)	2 (0%)	48	82
1	E	1359/1376 (99%)	1203 (88%)	155 (11%)	1 (0%)	48	82
1	F	1352/1376 (98%)	1197 (88%)	149 (11%)	6 (0%)	30	66

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	1351/1376 (98%)	1185 (88%)	163 (12%)	3 (0%)	43	77
1	N	1359/1376 (99%)	1189 (88%)	168 (12%)	2 (0%)	48	82
1	O	1351/1376 (98%)	1191 (88%)	155 (12%)	5 (0%)	30	66
1	S	1273/1376 (92%)	1126 (88%)	145 (11%)	2 (0%)	43	77
1	T	1354/1376 (98%)	1195 (88%)	154 (11%)	5 (0%)	30	66
1	U	1351/1376 (98%)	1199 (89%)	150 (11%)	2 (0%)	48	82
1	V	1348/1376 (98%)	1200 (89%)	146 (11%)	2 (0%)	48	82
1	W	1350/1376 (98%)	1211 (90%)	136 (10%)	3 (0%)	43	77
1	X	1339/1376 (97%)	1198 (90%)	140 (10%)	1 (0%)	48	82
2	0	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	1	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	2	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	3	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	G	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	H	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	I	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	J	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	K	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	L	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	P	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	Q	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	R	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	Y	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
2	Z	76/170 (45%)	73 (96%)	3 (4%)	0	100	100
3	5	313/331 (95%)	279 (89%)	34 (11%)	0	100	100
3	8	315/331 (95%)	293 (93%)	22 (7%)	0	100	100
3	b	315/331 (95%)	288 (91%)	27 (9%)	0	100	100
3	e	311/331 (94%)	288 (93%)	23 (7%)	0	100	100
3	h	315/331 (95%)	288 (91%)	26 (8%)	1 (0%)	36	71
4	6	290/305 (95%)	263 (91%)	27 (9%)	0	100	100
4	7	296/305 (97%)	261 (88%)	35 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	9	290/305 (95%)	264 (91%)	26 (9%)	0	100	100
4	a	296/305 (97%)	270 (91%)	26 (9%)	0	100	100
4	c	290/305 (95%)	265 (91%)	25 (9%)	0	100	100
4	d	296/305 (97%)	277 (94%)	19 (6%)	0	100	100
4	f	290/305 (95%)	263 (91%)	27 (9%)	0	100	100
4	g	296/305 (97%)	269 (91%)	27 (9%)	0	100	100
4	i	290/305 (95%)	264 (91%)	26 (9%)	0	100	100
4	j	296/305 (97%)	272 (92%)	24 (8%)	0	100	100
All	All	27037/29271 (92%)	24136 (89%)	2860 (11%)	41 (0%)	44	77

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	1251	ASN
1	O	144	GLU
1	T	10	PHE
1	V	1251	ASN
1	B	843	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4	1039/1166 (89%)	1038 (100%)	1 (0%)	88	88
1	A	1155/1166 (99%)	1155 (100%)	0	100	100
1	B	1151/1166 (99%)	1150 (100%)	1 (0%)	88	88
1	C	1150/1166 (99%)	1149 (100%)	1 (0%)	88	88
1	D	1151/1166 (99%)	1151 (100%)	0	100	100
1	E	1155/1166 (99%)	1153 (100%)	2 (0%)	87	85
1	F	1152/1166 (99%)	1151 (100%)	1 (0%)	88	88
1	M	1151/1166 (99%)	1149 (100%)	2 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	N	1155/1166 (99%)	1154 (100%)	1 (0%)	88	88
1	O	1151/1166 (99%)	1149 (100%)	2 (0%)	87	85
1	S	1094/1166 (94%)	1092 (100%)	2 (0%)	87	85
1	T	1154/1166 (99%)	1153 (100%)	1 (0%)	88	88
1	U	1151/1166 (99%)	1149 (100%)	2 (0%)	87	85
1	V	1148/1166 (98%)	1147 (100%)	1 (0%)	88	88
1	W	1150/1166 (99%)	1150 (100%)	0	100	100
1	X	1143/1166 (98%)	1141 (100%)	2 (0%)	87	85
2	0	70/141 (50%)	70 (100%)	0	100	100
2	1	70/141 (50%)	70 (100%)	0	100	100
2	2	70/141 (50%)	70 (100%)	0	100	100
2	3	70/141 (50%)	70 (100%)	0	100	100
2	G	70/141 (50%)	70 (100%)	0	100	100
2	H	70/141 (50%)	70 (100%)	0	100	100
2	I	70/141 (50%)	70 (100%)	0	100	100
2	J	70/141 (50%)	70 (100%)	0	100	100
2	K	70/141 (50%)	70 (100%)	0	100	100
2	L	70/141 (50%)	70 (100%)	0	100	100
2	P	70/141 (50%)	70 (100%)	0	100	100
2	Q	70/141 (50%)	70 (100%)	0	100	100
2	R	70/141 (50%)	70 (100%)	0	100	100
2	Y	70/141 (50%)	70 (100%)	0	100	100
2	Z	70/141 (50%)	70 (100%)	0	100	100
3	5	271/281 (96%)	271 (100%)	0	100	100
3	8	272/281 (97%)	272 (100%)	0	100	100
3	b	272/281 (97%)	272 (100%)	0	100	100
3	e	270/281 (96%)	270 (100%)	0	100	100
3	h	272/281 (97%)	272 (100%)	0	100	100
4	6	267/274 (97%)	267 (100%)	0	100	100
4	7	270/274 (98%)	270 (100%)	0	100	100
4	9	267/274 (97%)	267 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	a	270/274 (98%)	270 (100%)	0	100	100
4	c	267/274 (97%)	267 (100%)	0	100	100
4	d	270/274 (98%)	270 (100%)	0	100	100
4	f	267/274 (97%)	267 (100%)	0	100	100
4	g	270/274 (98%)	270 (100%)	0	100	100
4	i	267/274 (97%)	267 (100%)	0	100	100
4	j	270/274 (98%)	270 (100%)	0	100	100
All	All	23342/24916 (94%)	23323 (100%)	19 (0%)	87	88

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	U	961	LEU
1	X	669	ILE
1	4	947	LEU
1	X	616	ILE
1	O	616	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 509 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	1173	GLN
3	8	194	HIS
1	U	113	GLN
4	7	94	GLN
3	e	7	ASN

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	N	1
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	9:PRO	C	10:PHE	N	1.20
1	F	454:CYS	C	455:HIS	N	1.17

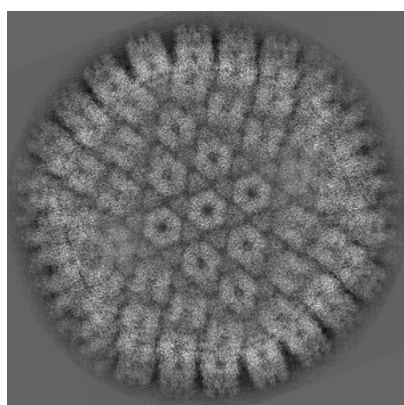
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7047. These allow visual inspection of the internal detail of the map and identification of artifacts.

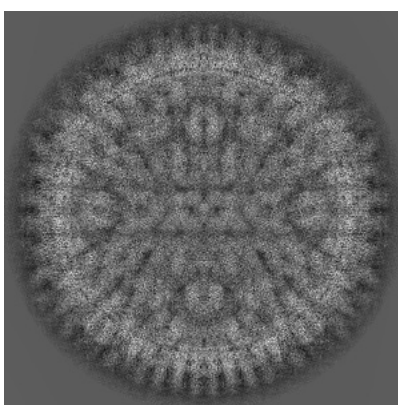
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

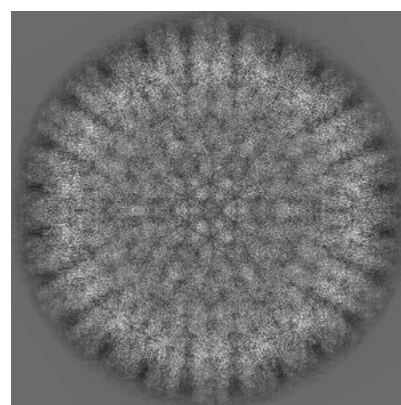
6.1.1 Primary map



X



Y

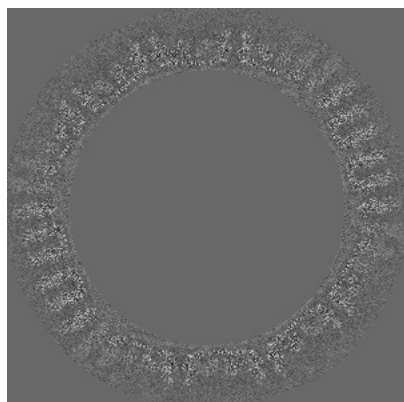


Z

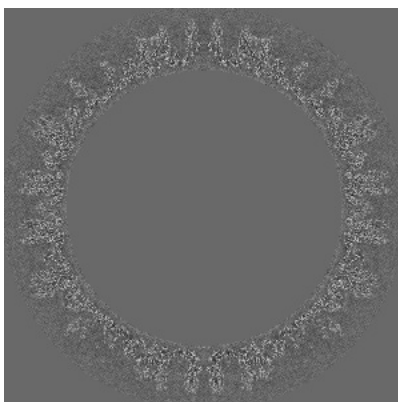
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

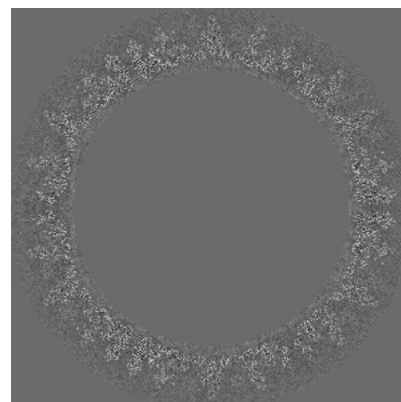
6.2.1 Primary map



X Index: 640



Y Index: 640

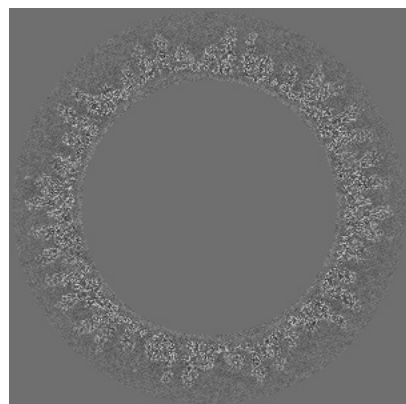


Z Index: 640

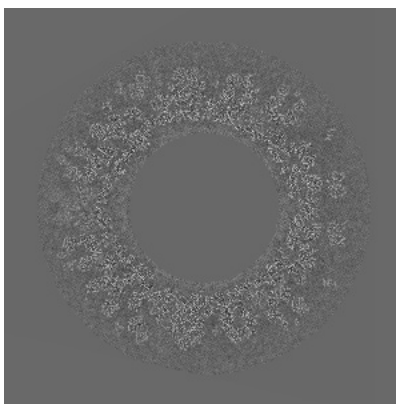
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

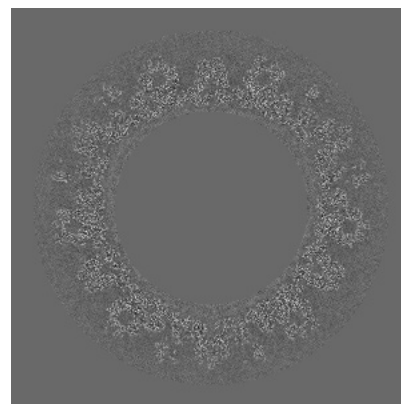
6.3.1 Primary map



X Index: 475



Y Index: 270

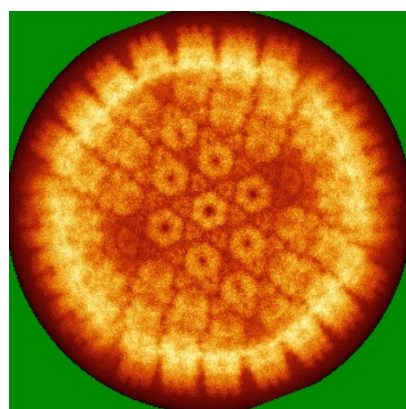


Z Index: 326

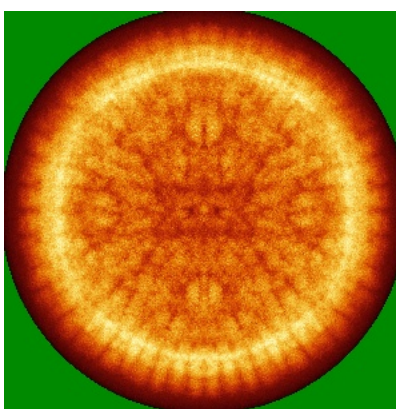
The images above show the largest variance slices of the map in three orthogonal directions.

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

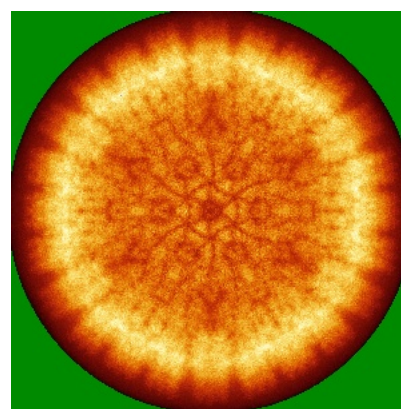
6.4.1 Primary map



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](#)

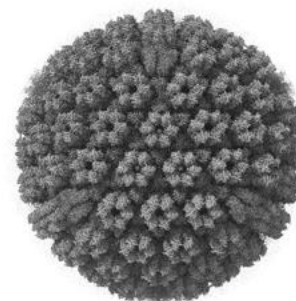
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

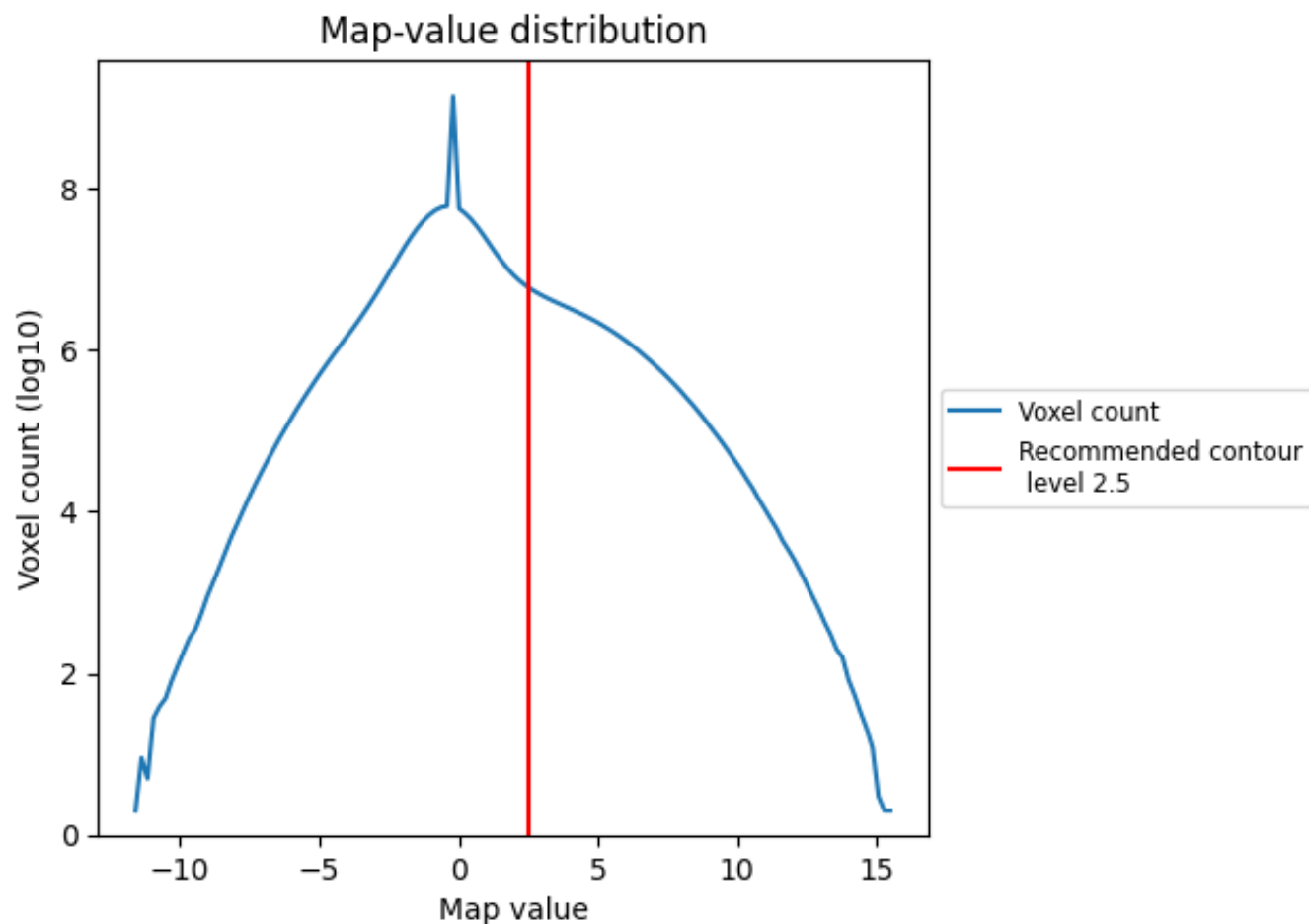
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

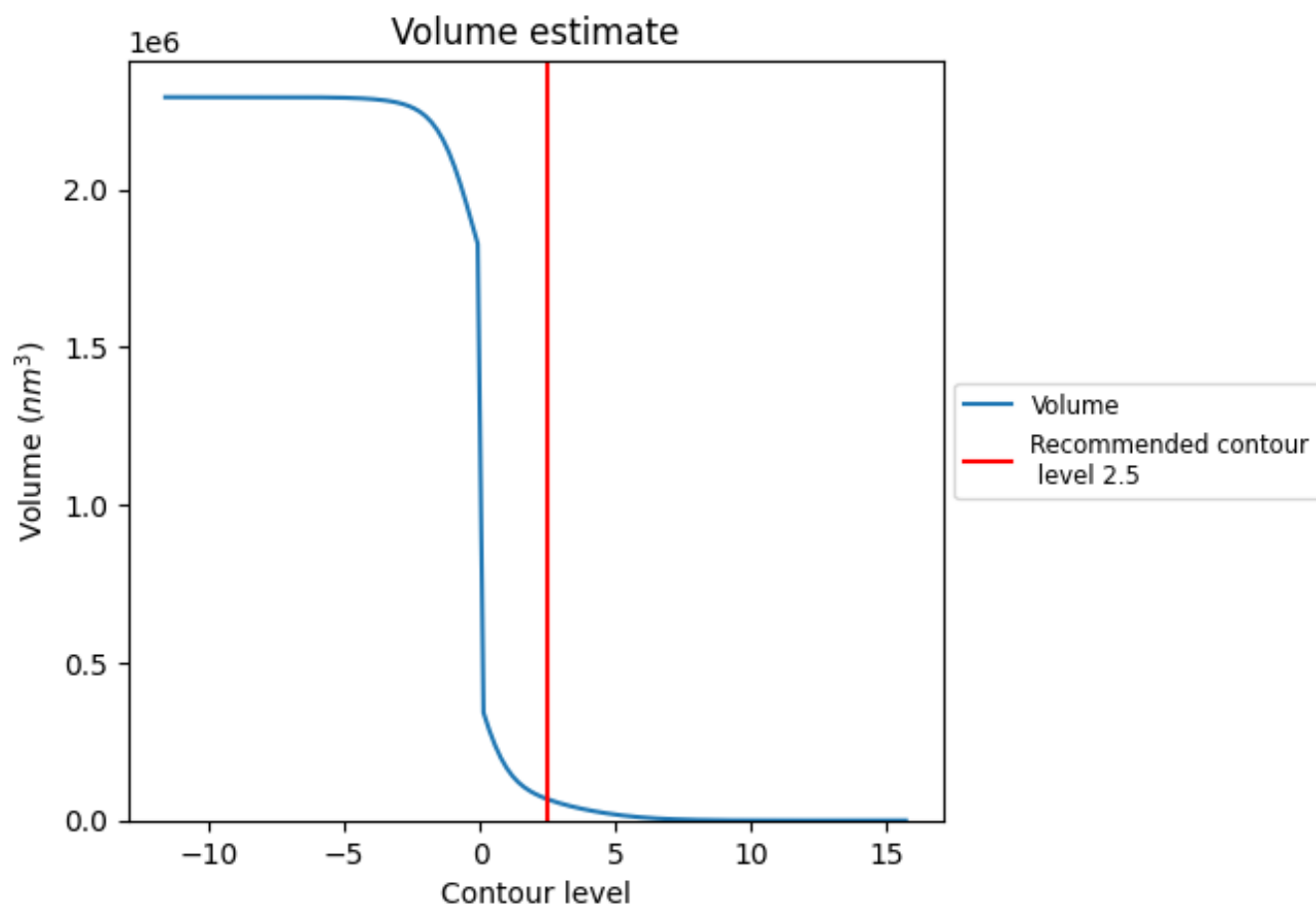
This section contains the results of statistical analysis of the map.

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.

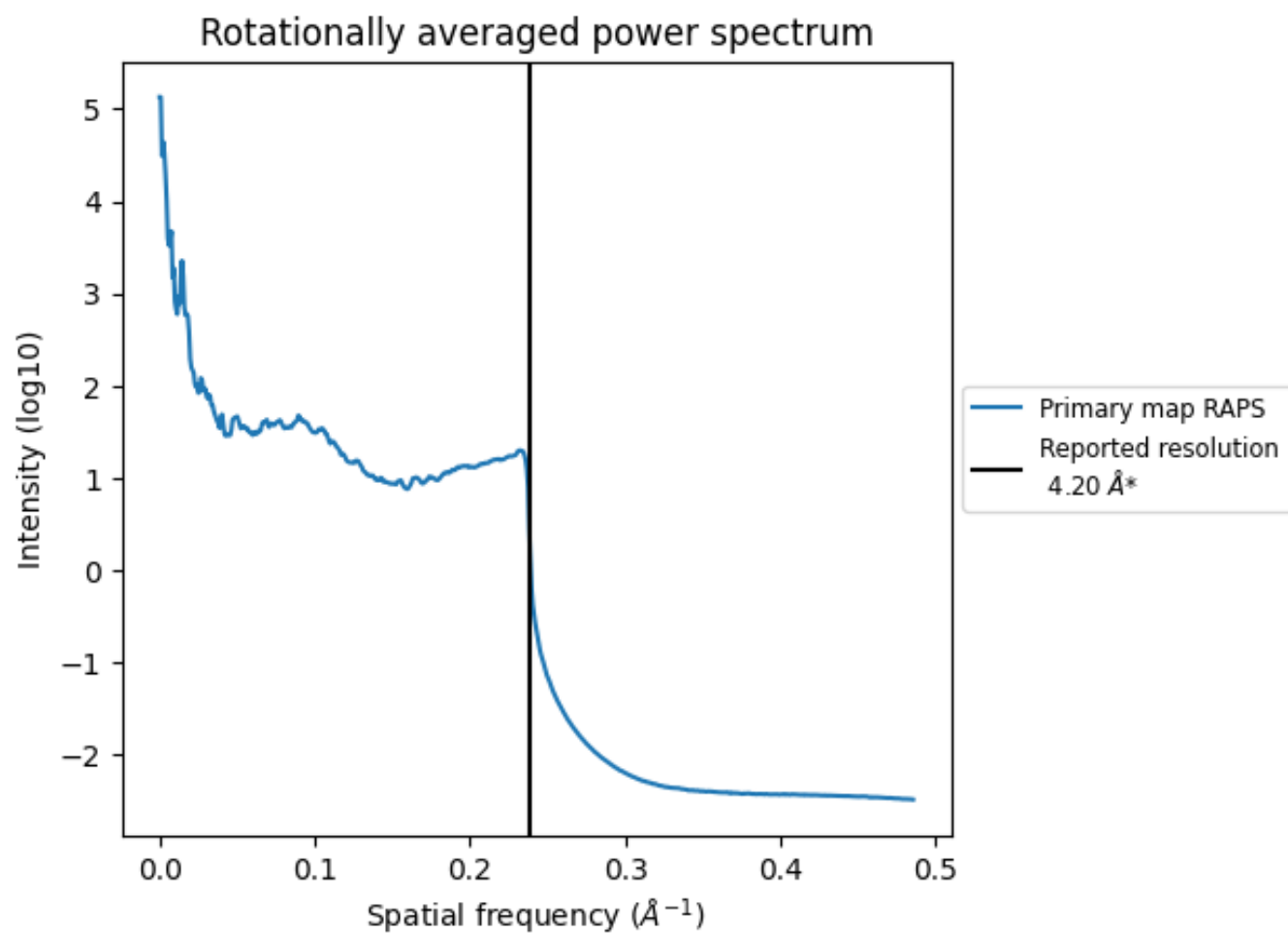
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 67318 nm³; this corresponds to an approximate mass of 60810 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 0.238 Å⁻¹

8 Fourier-Shell correlation

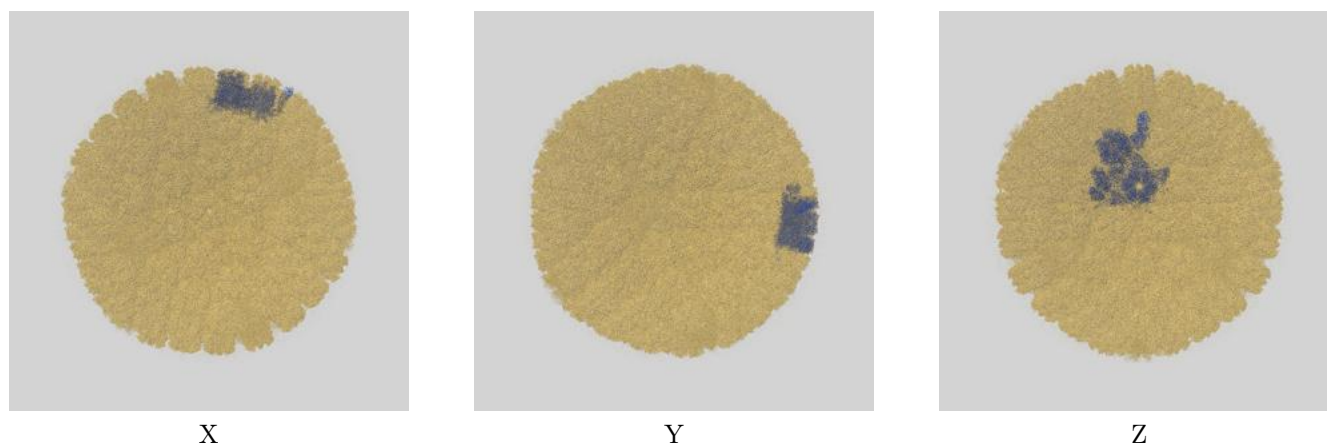
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7047 and PDB model 6B43. Per-residue inclusion information can be found in section [3](#) on page [8](#).

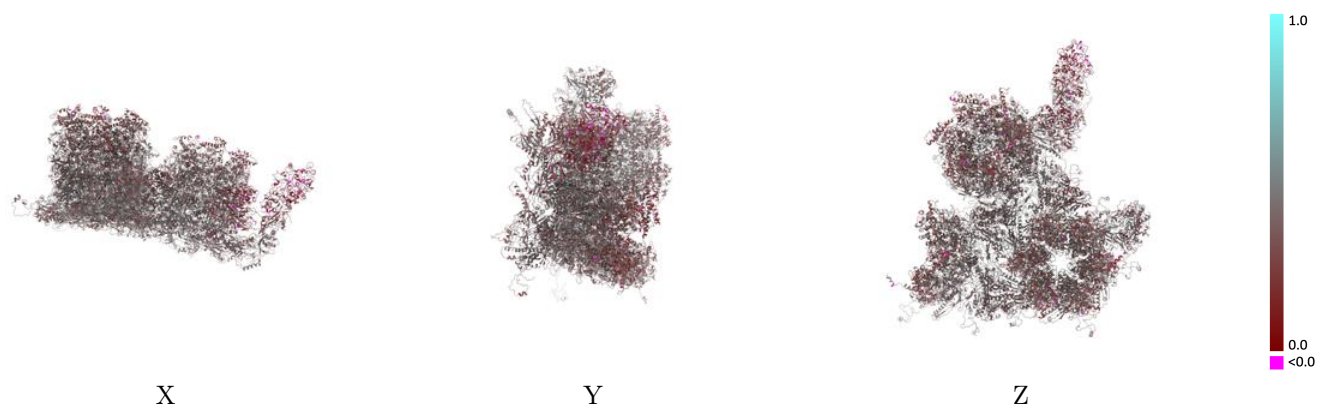
9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



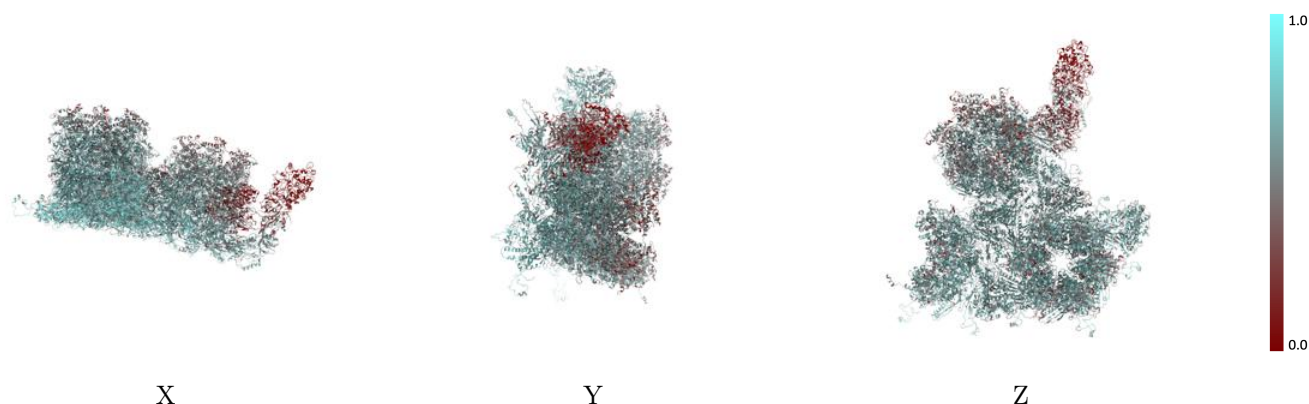
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



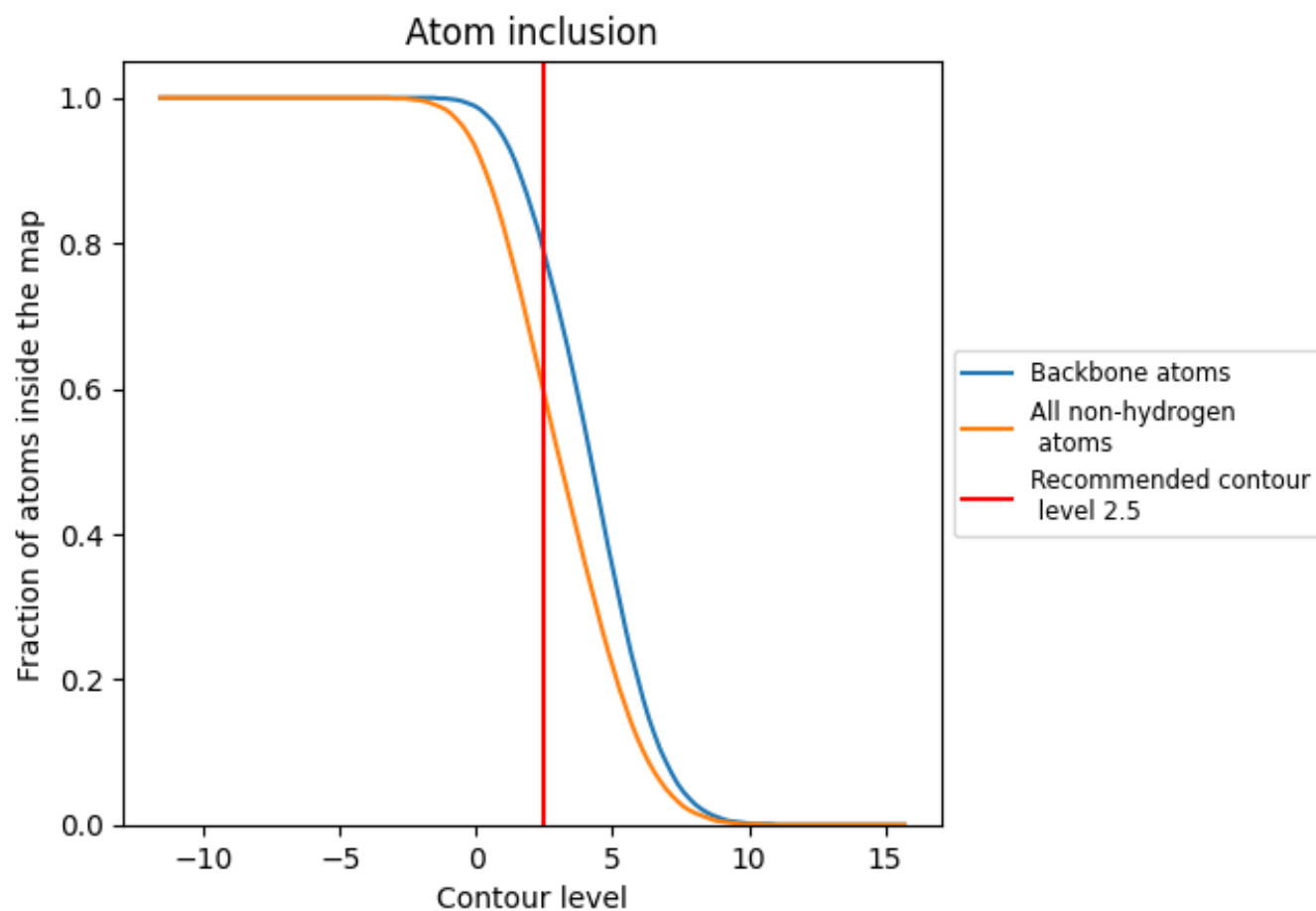
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 59% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5910	 0.3760
0	 0.4380	 0.2910
1	 0.4520	 0.3070
2	 0.3660	 0.2610
3	 0.3600	 0.2470
4	 0.2800	 0.2860
5	 0.3310	 0.3130
6	 0.3450	 0.2850
7	 0.1930	 0.2500
8	 0.6510	 0.3990
9	 0.6270	 0.3870
A	 0.6420	 0.3980
B	 0.6390	 0.3880
C	 0.6270	 0.3870
D	 0.6330	 0.3840
E	 0.6450	 0.3990
F	 0.6420	 0.3960
G	 0.4830	 0.3050
H	 0.4020	 0.2270
I	 0.5030	 0.3280
J	 0.4730	 0.2980
K	 0.4830	 0.2990
L	 0.4840	 0.3170
M	 0.6510	 0.3990
N	 0.6490	 0.3980
O	 0.6500	 0.3960
P	 0.5000	 0.3220
Q	 0.4840	 0.2840
R	 0.4950	 0.2980
S	 0.5690	 0.3780
T	 0.6080	 0.3870
U	 0.6240	 0.3890
V	 0.6210	 0.3830
W	 0.5950	 0.3780
X	 0.5730	 0.3720



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Chain	Atom inclusion	Q-score
Y	 0.3890	 0.2760
Z	 0.3520	 0.2410
a	 0.6350	 0.3950
b	 0.6460	 0.4070
c	 0.6560	 0.3980
d	 0.6500	 0.3980
e	 0.6140	 0.3910
f	 0.5620	 0.3680
g	 0.5930	 0.3790
h	 0.6380	 0.3950
i	 0.6420	 0.3950
j	 0.6410	 0.3940