



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:51 PM UTC

PDB ID : 7BR8 / pdb_00007br8
EMDB ID : EMD-30159
Title : Epstein-Barr virus, C5 penton vertex, CATC absent.
Authors : Li, Z.; Yu, X.
Deposited on : 2020-03-26
Resolution : 3.80 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:

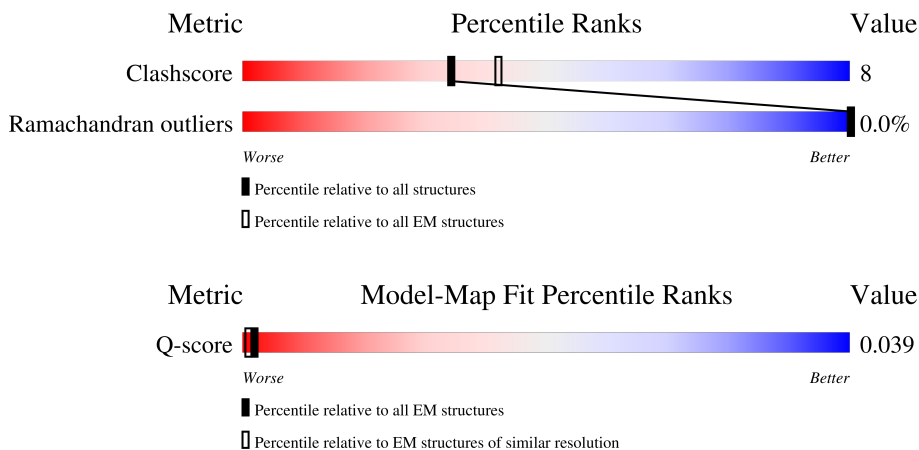
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	2	176	<div style="display: flex; align-items: center;"> <div style="width: 39%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">33% 9% .</div> <div style="width: 58%; height: 10px; background-color: grey; margin-left: 10px;"></div> </div>
1	Y	176	<div style="display: flex; align-items: center;"> <div style="width: 35%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">40% .</div> <div style="width: 58%; height: 10px; background-color: grey; margin-left: 10px;"></div> </div>
1	Z	176	<div style="display: flex; align-items: center;"> <div style="width: 37%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">39% .</div> <div style="width: 58%; height: 10px; background-color: grey; margin-left: 10px;"></div> </div>
1	m	176	<div style="display: flex; align-items: center;"> <div style="width: 38%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">34% 6%</div> <div style="width: 60%; height: 10px; background-color: grey; margin-left: 10px;"></div> </div>
1	y	176	<div style="display: flex; align-items: center;"> <div style="width: 36%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="margin-left: 10px;">32% 10%</div> <div style="width: 58%; height: 10px; background-color: grey; margin-left: 10px;"></div> </div>

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Mol	Chain	Length	Quality of chain
2	S	1381	<p>54% 79% 17%</p>
2	T	1381	<p>49% 76% 19%</p>
2	W	1381	<p>43% 79% 18%</p>
2	l	1381	<p>57% 74% 16% 9%</p>
2	x	1381	<p>49% 76% 19%</p>
3	5	364	<p>54% 72% 13% 15%</p>
3	e	364	<p>35% 74% 13% 12%</p>
4	6	301	<p>73% 76% 19%</p>
4	7	301	<p>77% 74% 19% 7%</p>
4	f	301	<p>41% 75% 21%</p>
4	g	301	<p>41% 77% 17% 7%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 68602 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	m	71	Total 600	C 381	N 111	O 107	S 1	0	0
1	Y	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	Z	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	2	74	Total 621	C 394	N 114	O 112	S 1	0	0
1	y	74	Total 621	C 394	N 114	O 112	S 1	0	0

- Molecule 2 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	S	1333	Total 10491	C 6665	N 1820	O 1946	S 60	0	0
2	T	1323	Total 10398	C 6600	N 1808	O 1929	S 61	0	0
2	W	1331	Total 10463	C 6650	N 1810	O 1944	S 59	0	0
2	x	1325	Total 10404	C 6607	N 1803	O 1935	S 59	0	0
2	l	1251	Total 9883	C 6283	N 1717	O 1824	S 59	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	e	319	Total 2505	C 1608	N 444	O 446	S 7	0	0
3	5	311	Total 2446	C 1568	N 435	O 436	S 7	0	0

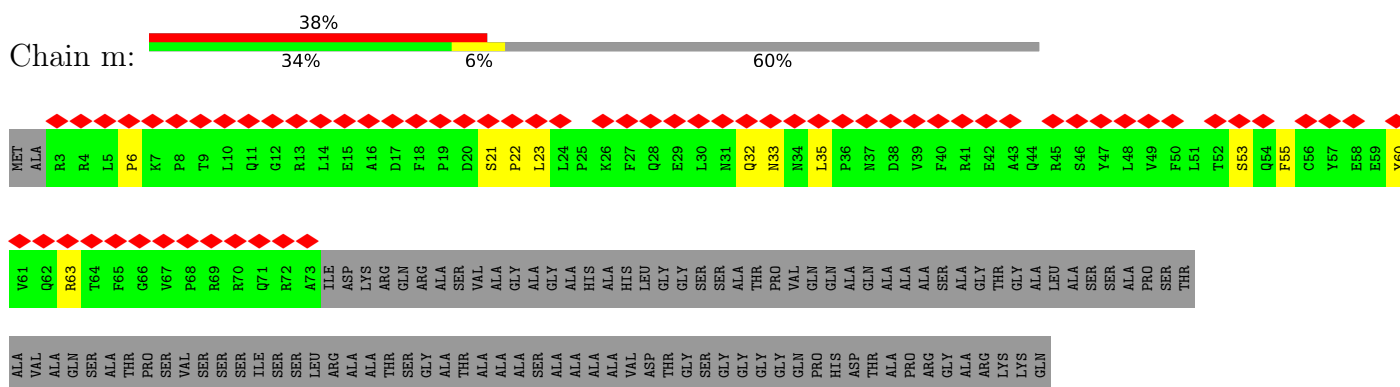
- Molecule 4 is a protein called Triplex capsid protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	f	290	Total 2279	C 1466	N 378	O 419	S 16	0	0
4	g	281	Total 2190	C 1413	N 358	O 401	S 18	0	0
4	6	289	Total 2272	C 1461	N 377	O 418	S 16	0	0
4	7	279	Total 2187	C 1406	N 358	O 405	S 18	0	0

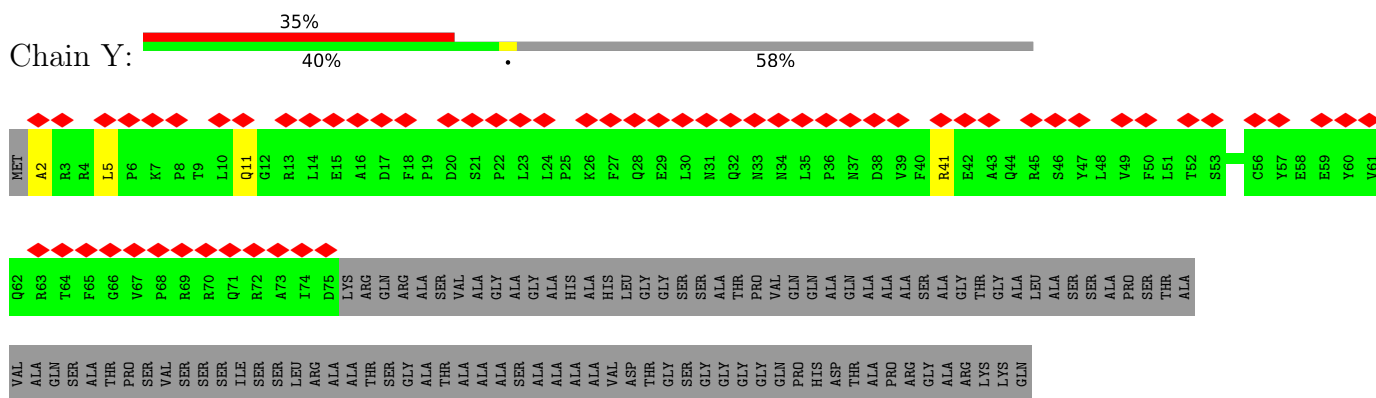
3 Residue-property plots

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.

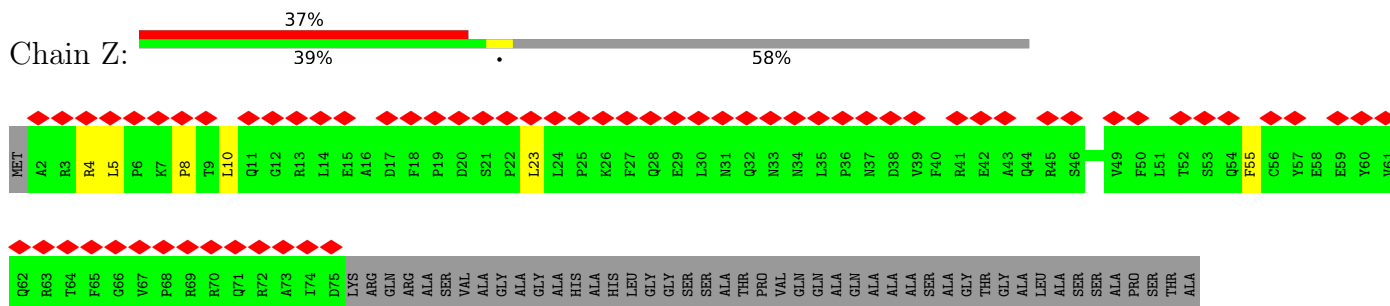
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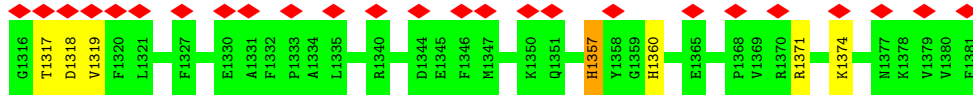
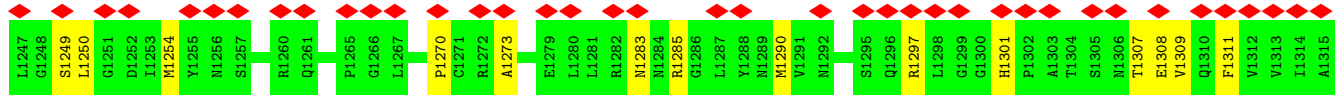
- Molecule 1: Small capsomere-interacting protein



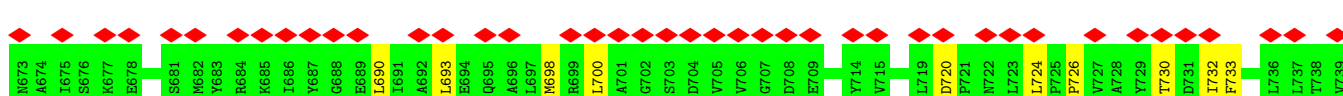
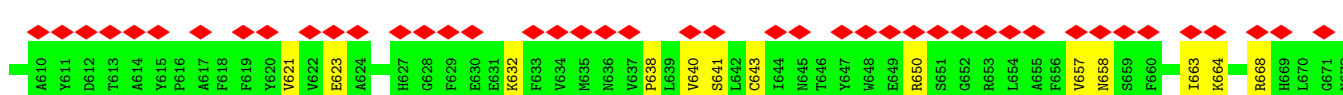
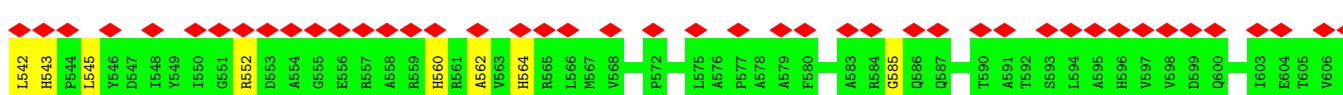
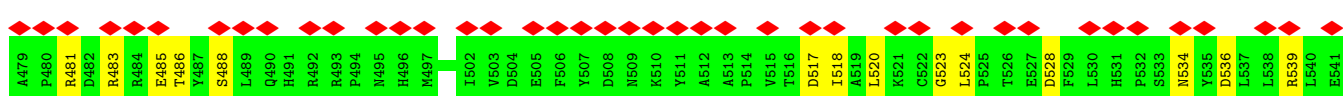
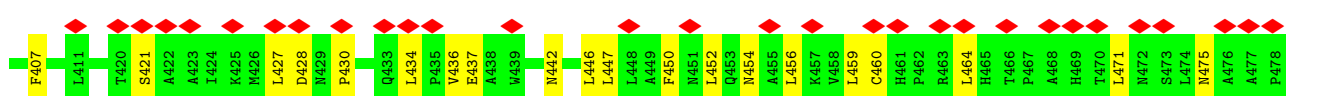
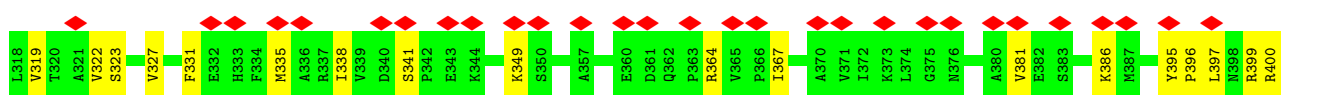
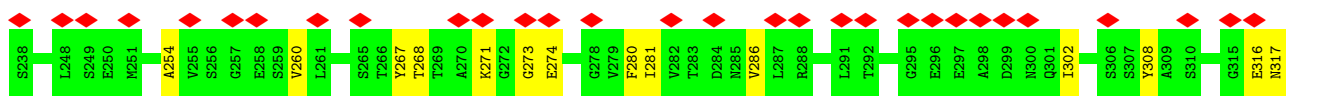
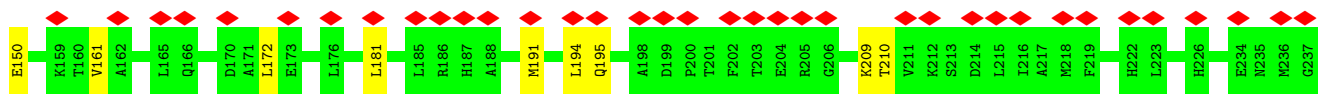
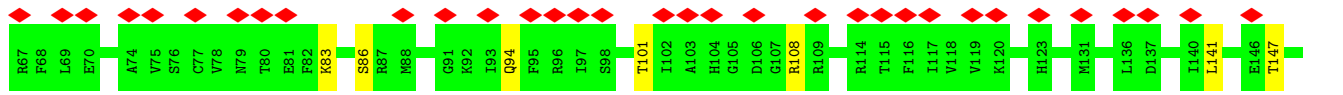
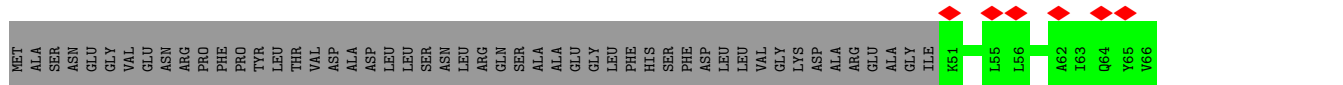
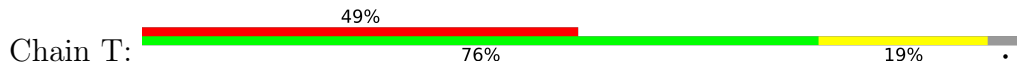
- Molecule 1: Small capsomere-interacting protein

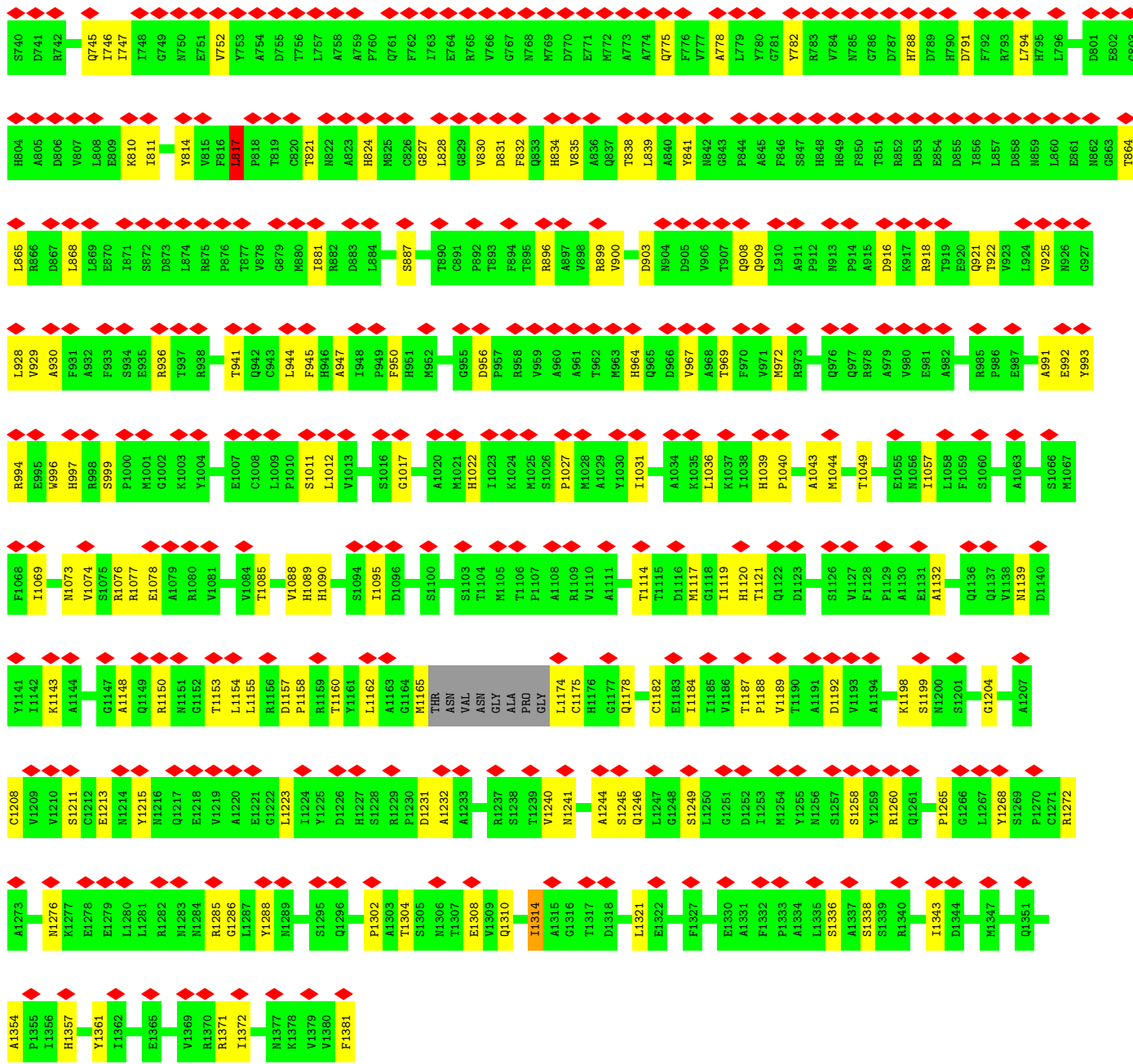


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T470	L471	M472	S473	L474	M475	A476	A477	P478	A479	P480	R481	D482	R483	R484	E485	T486	Y487	S488	A489	Q490	H491	R492	R493	P494	M495	H496	M497	M498	V499	L500	V501	I502	V503	D504	E505	F506	Y507	D508	N509	K510	A512	A513	P514	V515	V516	D517	I518	K521	C522	G523	L524	P525	T526	E527	F528	L530				
H531	N534	Y535	L538	R539	L540	E541	L542	H543	Y546	D547	Y549	I550	T551	R552	D553	A554	G555	E556	A558	R559	H560	A562	V563	H564	R565	L566	M567	V568	G569	N570	L571	F572	T573	P574	L575	A579	F580	Q581	E582	R584	G585	T586	N587	Q588	F589	T590	P591	T592	S593	L594	A595									
H596	V597	V598	D599	Q600	I603	E604	V606	Q607	D608	T609	A610	Y611	I612	T613	A614	G551	R552	D553	A554	F618	F619	Y620	P621	V622	E623	A624	M625	I626	G627	F629	E630	G631	K632	F633	V634	M635	N636	V637	P638	L639	V640	S641	L642	C643	I644	N645	T646	Y647	W648	E649	R650	S651	G652	R653	L654	A655	F656			
V657	N658	S659	F660	I663	K664	F665	I666	C667	R668	H669	L670	G671	N672	N673	A674	I675	S676	K677	E678	A679	Y680	M682	Y683	R684	K685	I686	E689	A692	L693	Q695	A696	L697	M698	R699	L700	A701	G702	S703	D704	V705	V706	G707	D708	E709	S710	V711	G712	Q713	Y714	V715	C716	A717	L718	L719						
D720	P721	N722	L723	L724	P725	P726	V727	A728	Y729	T730	D731	I732	F733	I734	H735	L736	L737	T738	V739	S740	D741	R742	A743	P744	Q745	I746	L747	L748	G749	N750	E751	V752	L753	A754	D755	T756	L757	A758	A759	P760	Q761	F762	I763	E764	G765	V766	G767	N768	M769	D770	E771	N772	A773	A774	Q775	L776	V777	A778	L779	
Y780	G781	Y782	R783	W784	N785	G786	D787	H788	D789	H790	D791	F792	R793	L794	H795	L796	G797	P798	Y799	W800	D801	E802	G803	H804	A805	D806	W807	L808	E809	K810	L811	W815	F816	L817	P818	T819	C820	T821	N822	A823	H824	K825	C826	G827	L828	G829	W830	D831	F832	Q833	H834	W835	A836	D837	T838	L839	A840	Y841		
H843	G844	F844	A845	F846	S847	H848	H849	F850	T851	R852	D853	E854	D855	L856	L857	D858	R859	L860	E861	H862	G863	T864	L865	R866	D867	L868	L869	E870	L871	S872	D873	L874	R875	P876	M880	L881	D882	D883	L884	S885	A886	S887	F888	H889	T890	C891	F892	T893	R896	A897	H898	R899	Y900	S901	Y902	D903	H904			
D905	Y906	T907	L910	A911	P912	H913	D916	R917	R918	T919	E920	Q921	T922	Y923	L924	Y925	R926	G927	L928	Y929	A930	F931	A932	F933	S934	E935	Y936	T937	R938	A939	Y940	T941	Q942	F945	H946	I947	I948	P949	F950	H951	N952	F953	Y954	G955	D956	F957	R958	Y959	A960	A961	T962	H963	H964	Q965	P966	Y967				
A968	V971	M972	R973	N974	P975	Q976	Q977	R978	A979	V980	E981	A982	F983	N984	R985	P986	L988	F989	Q988	E992	Y993	R994	E995	W996	H997	R998	S999	P1000	M1001	G1002	K1003	Y1004	E1007	C1008	L1009	P1010	S1011	L1012	V1013	S1016	G1017	A1020	M1021	H1022	I1023	K1024	M1025	S1026	P1027	M1028	A1029	A960	A897	H898	R899	Y900	S901	Y902	D903	H904
A1034	K1035	L1036	K1037	I1038	H1039	P1040	M1044	T1045	V1046	R1047	T1048	T1049	D1050	E1055	M1056	I1057	L1058	F1059	S1060	S1061	R1062	A1063	S1066	M1067	F1068	T1071	F1072	M1073	G1002	E1078	A1079	R1080	V1081	D1082	A1083	V1084	H1089	H1090	L1095	D1096	T1097	S1100	Y1101	S1102	S1103	T1104	M1105	P1107	A1108	R1109	V1110									
A1111	D1116	M1117	G1118	I1119	H1120	Q1121	D1123	S1126	V1127	A1130	E1131	M1136	Q1136	S1137	V1138	M1139	D1140	Y1141	I1142	K1143	K1145	V1146	G1147	A1148	G11	ARG	ASN	GLY	THR	LEU	LEU	LEU	ASP	PRO	ARG	THR	THR	THR	ALA	ALA	GLY	GLY	PRO	PRO	GLY	ASN	VAL	ASN	GLY	ALA	PRO	GLY	L1174	C1175	H1176	G1177				
Q1178	Q1179	A1180	T1181	C1182	E1183	I1184	I1185	V1186	T1187	P1188	V1189	D1192	V1193	A1194	Y1195	K1198	S1199	M1200	S1201	P1202	R1203	G1204	R1205	A1206	V1210	S1211	C1212	E1213	M1214	Y1215	M1216	Q1217	E1218	V1219	A1220	L1223	I1224	Y1225	D1226	H1227	S1228	R1229	A1232	A1233	R1237	S1238	T1239	V1240	M1241	A1244	S1245	Q1246								

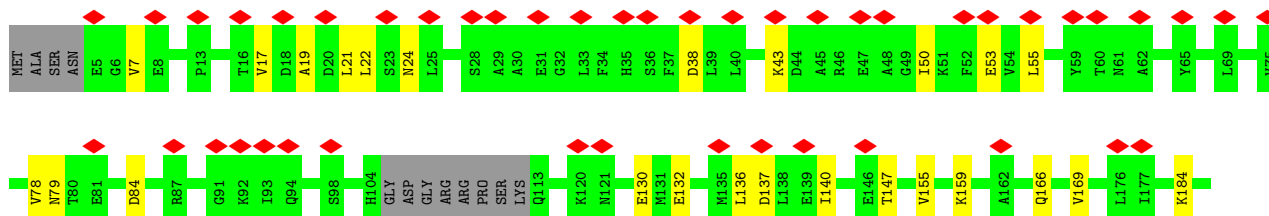
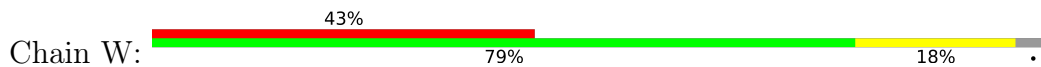


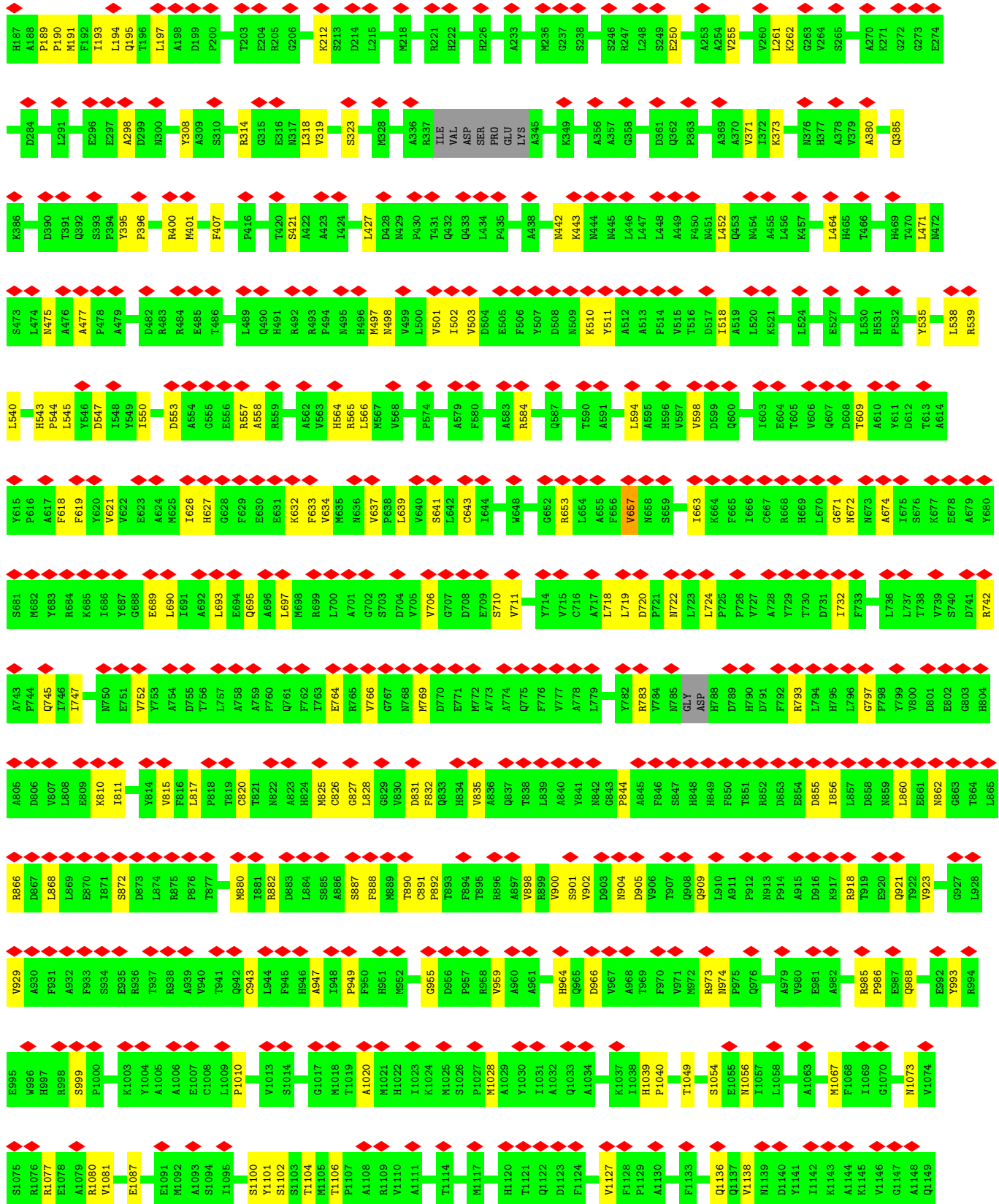
• Molecule 2: Major capsid protein

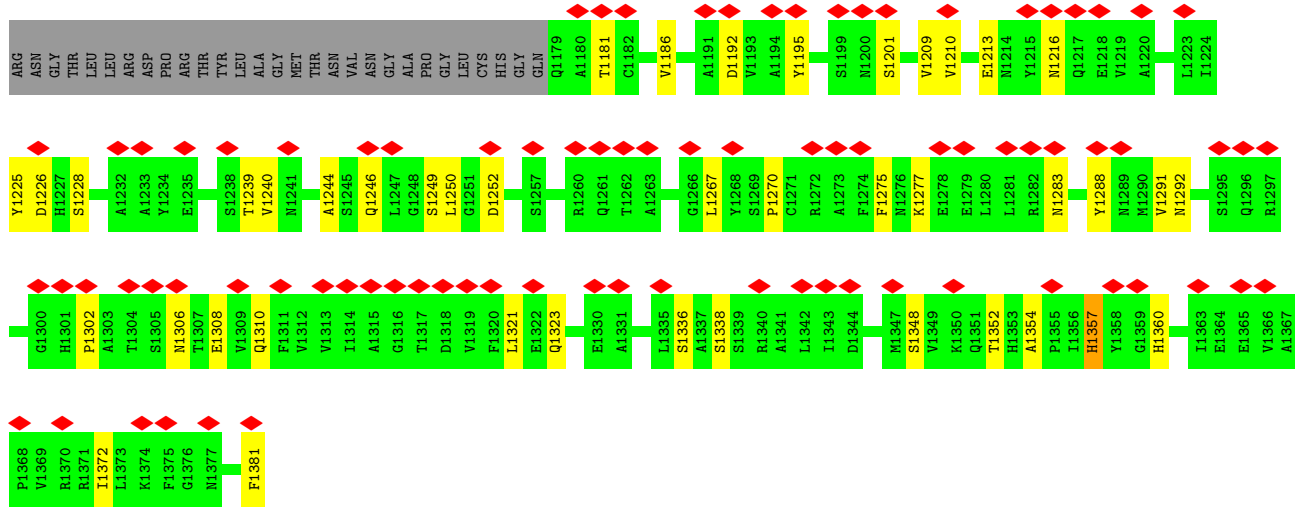




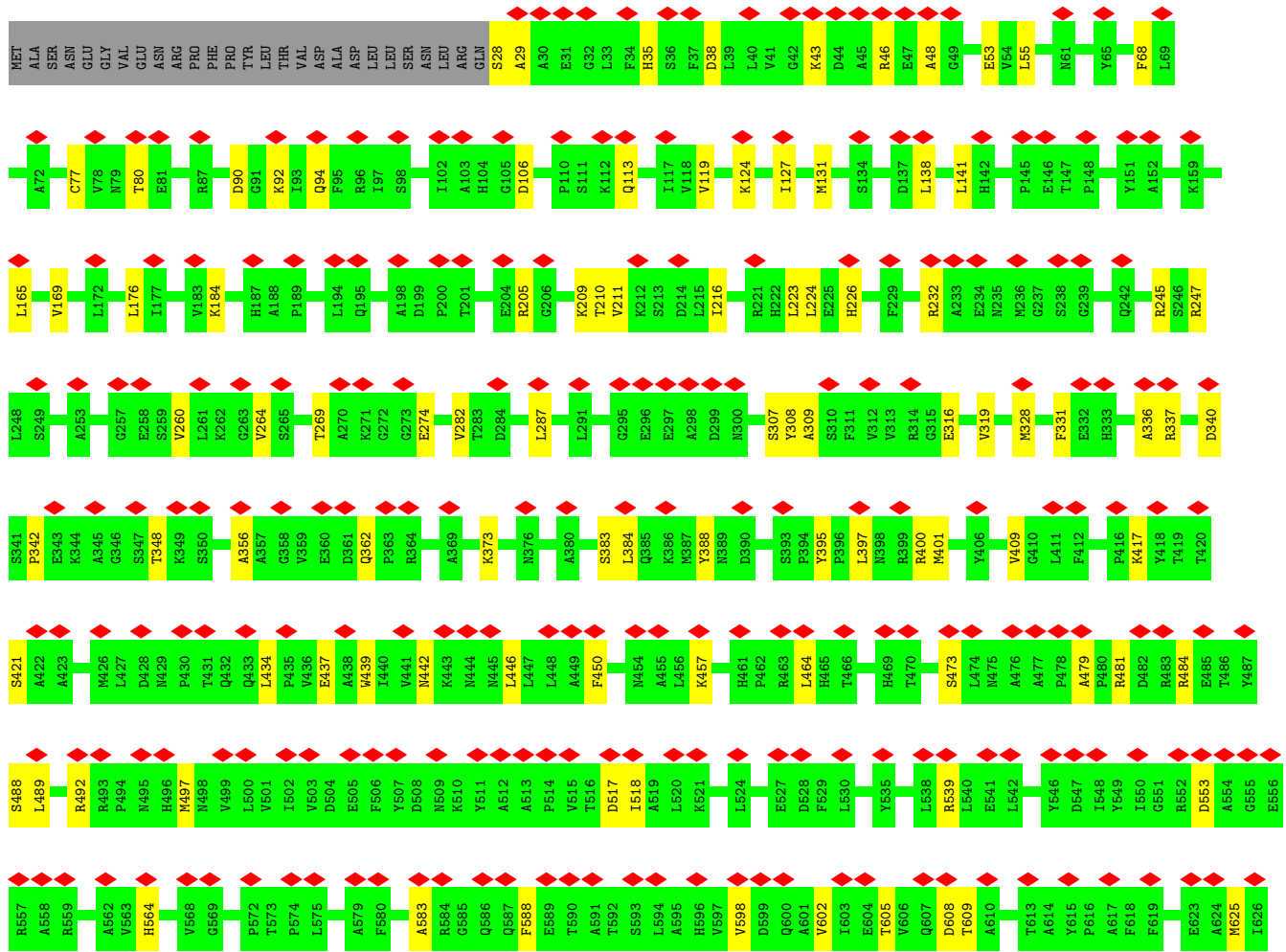
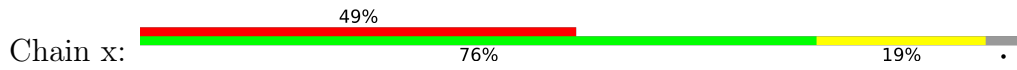
• Molecule 2: Major capsid protein

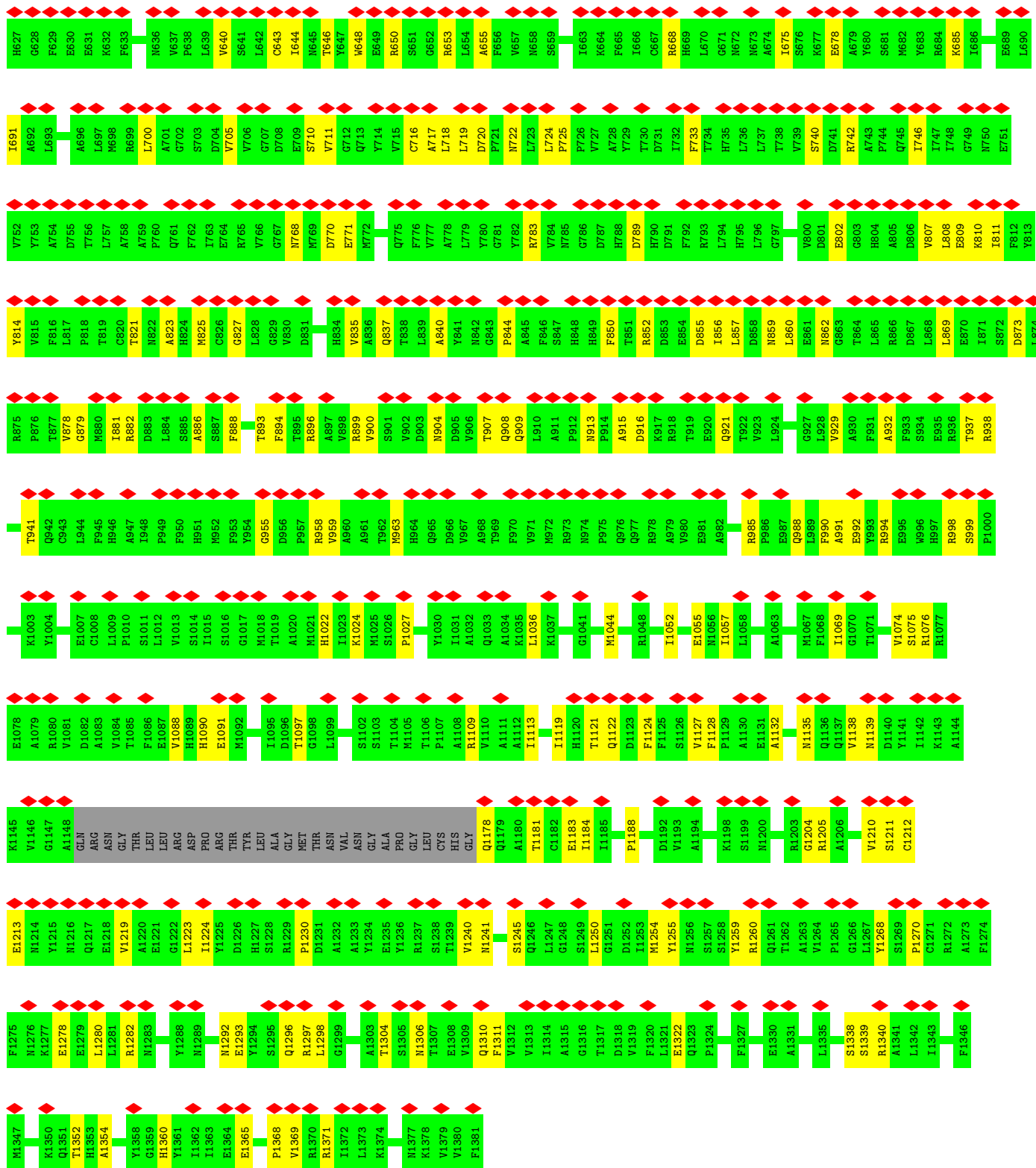




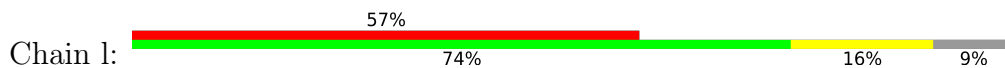


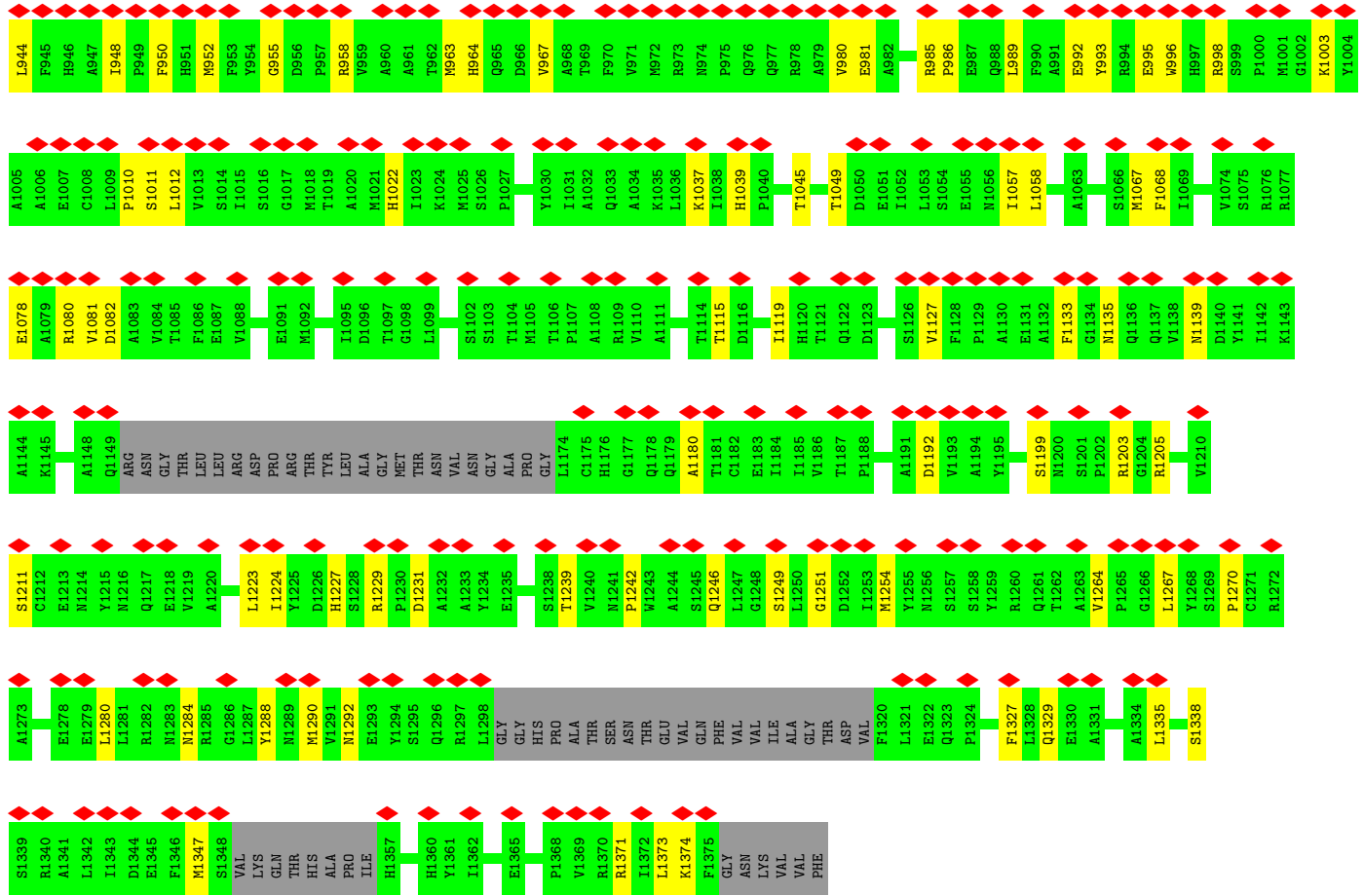
• Molecule 2: Major capsid protein



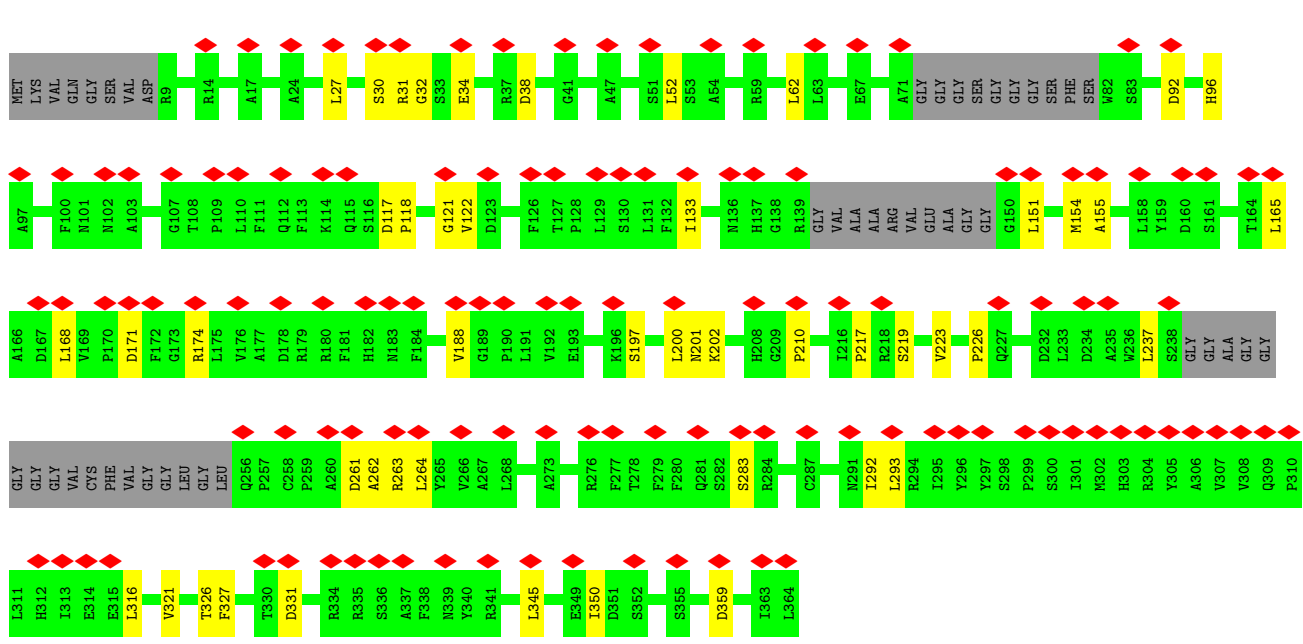
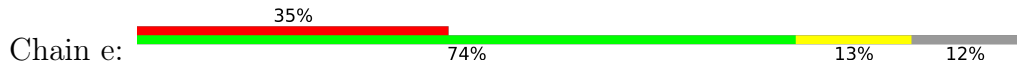


• Molecule 2: Major capsid protein

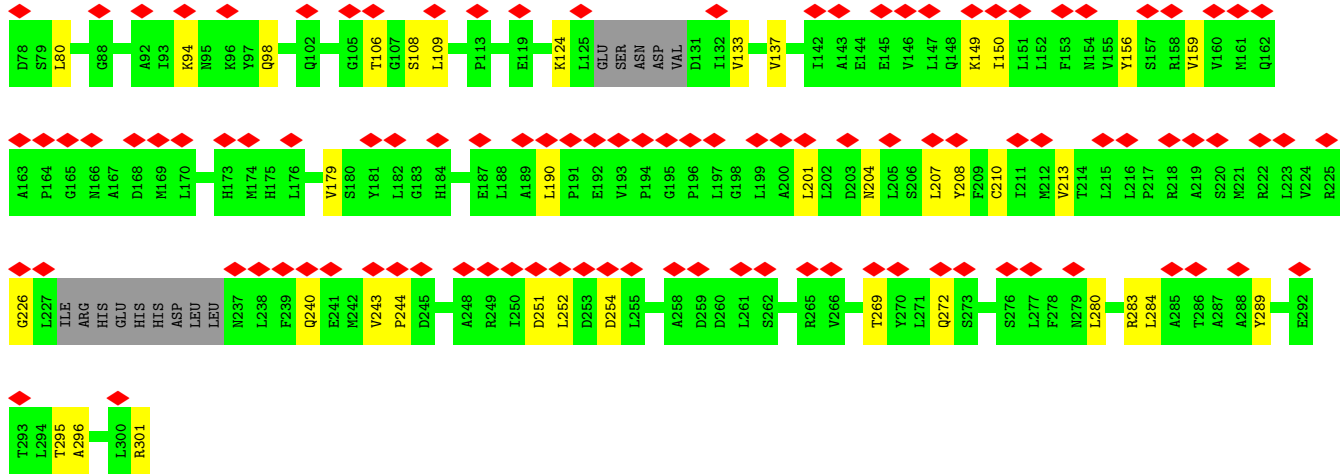




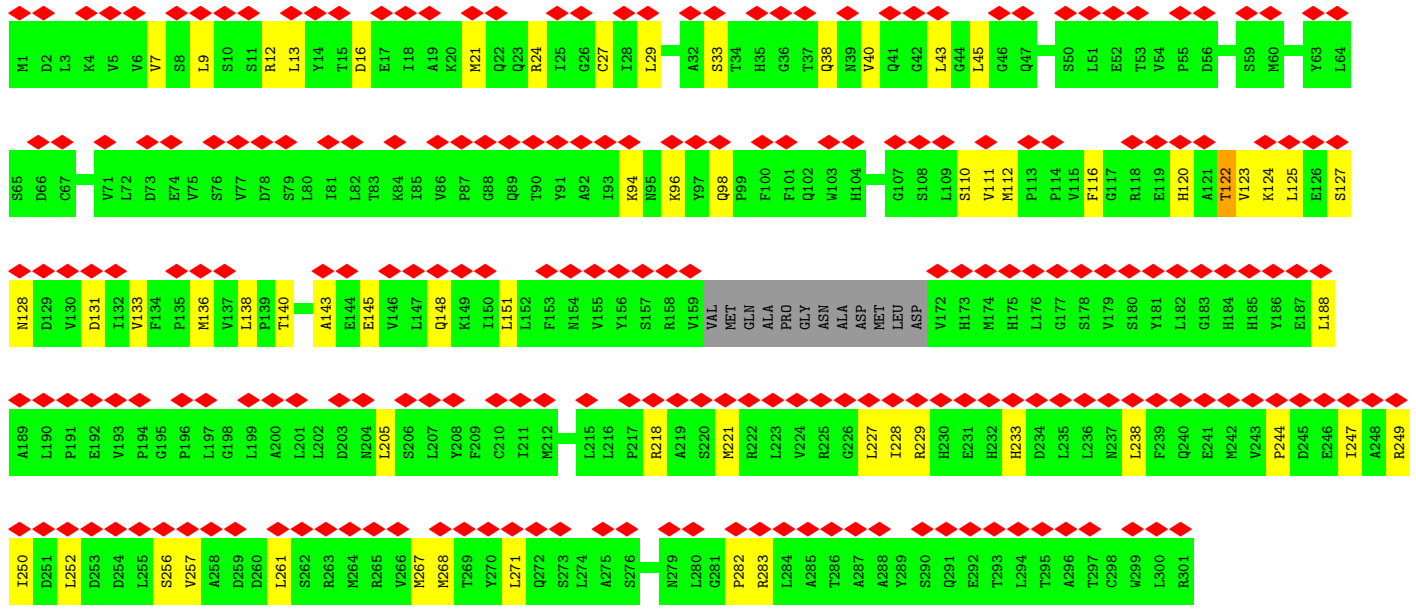
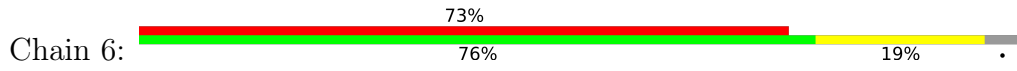
• Molecule 3: Triplex capsid protein 1



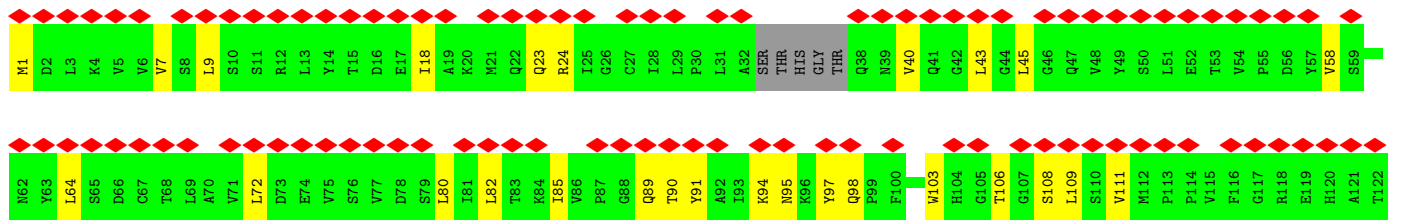
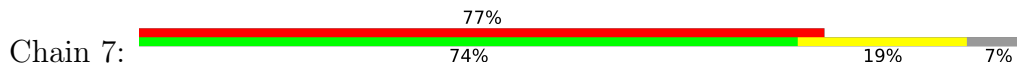
• Molecule 3: Triplex capsid protein 1

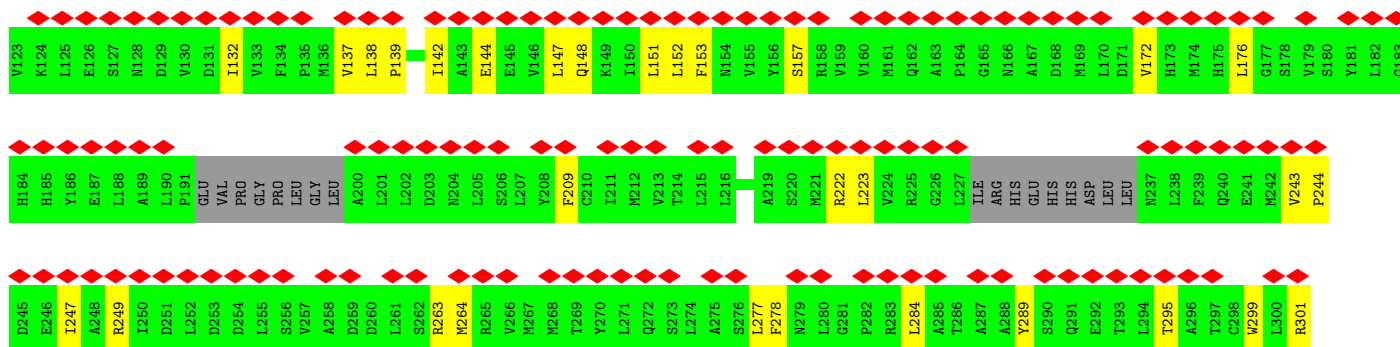


• Molecule 4: Triplex capsid protein 2



• Molecule 4: Triplex capsid protein 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	137356	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	392.99997, 392.99997, 392.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.24	0/636	0.61	1/861 (0.1%)
1	Y	0.20	0/636	0.53	0/861
1	Z	0.21	0/636	0.53	0/861
1	m	0.30	0/615	0.58	0/832
1	y	0.27	0/636	0.54	0/861
2	S	0.32	0/10737	0.55	2/14589 (0.0%)
2	T	0.32	0/10642	0.57	4/14463 (0.0%)
2	W	0.28	0/10706	0.53	1/14549 (0.0%)
2	l	0.25	0/10114	0.57	2/13734 (0.0%)
2	x	0.30	0/10648	0.54	1/14471 (0.0%)
3	5	0.23	0/2511	0.62	2/3418 (0.1%)
3	e	0.30	0/2572	0.61	0/3503
4	6	0.24	0/2320	0.59	0/3159
4	7	0.23	0/2228	0.58	0/3029
4	f	0.24	0/2327	0.59	0/3169
4	g	0.26	0/2233	0.57	0/3037
All	All	0.29	0/70197	0.56	13/95397 (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
2	S	0	1
2	T	0	2
2	W	0	1
3	5	0	1
4	6	0	1
4	7	0	1
All	All	0	7

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	523	GLY	CA-C-N	8.24	133.20	120.68
2	T	523	GLY	C-N-CA	8.24	133.20	120.68
2	T	1314	ILE	N-CA-C	-6.44	107.59	113.71
3	5	159	TYR	CA-C-N	6.41	129.15	120.38
3	5	159	TYR	C-N-CA	6.41	129.15	120.38

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	5	307	VAL	Peptide
2	S	1357	HIS	Peptide
2	T	1357	HIS	Peptide
2	T	817	LEU	Peptide
2	W	1357	HIS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	621	0	611	15	0
1	Y	621	0	611	4	0
1	Z	621	0	611	6	0
1	m	600	0	591	10	0
1	y	621	0	611	13	0
2	S	10491	0	10318	194	0
2	T	10398	0	10232	227	0
2	W	10463	0	10288	184	0
2	l	9883	0	9710	150	0
2	x	10404	0	10234	183	0
3	5	2446	0	2422	31	0
3	e	2505	0	2479	42	0
4	6	2272	0	2307	41	0
4	7	2187	0	2222	35	0
4	f	2279	0	2316	42	0
4	g	2190	0	2228	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	68602	0	67791	1104	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 1104 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:1160:THR:HG21	2:T:1314:ILE:CD1	1.05	1.50
2:T:1160:THR:CG2	2:T:1314:ILE:CD1	1.93	1.47
2:T:1160:THR:CG2	2:T:1314:ILE:HD11	1.47	1.41
2:S:788:HIS:NE2	2:S:893:THR:CG2	1.84	1.38
2:W:518:ILE:HD11	2:W:547:ASP:OD2	1.27	1.31

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	2	72/176 (41%)	64 (89%)	8 (11%)	0	100	100
1	Y	72/176 (41%)	65 (90%)	7 (10%)	0	100	100
1	Z	72/176 (41%)	67 (93%)	5 (7%)	0	100	100
1	m	69/176 (39%)	64 (93%)	5 (7%)	0	100	100
1	y	72/176 (41%)	65 (90%)	7 (10%)	0	100	100
2	S	1327/1381 (96%)	1246 (94%)	80 (6%)	1 (0%)	48	79
2	T	1319/1381 (96%)	1222 (93%)	97 (7%)	0	100	100
2	W	1321/1381 (96%)	1243 (94%)	78 (6%)	0	100	100
2	l	1237/1381 (90%)	1164 (94%)	73 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	x	1321/1381 (96%)	1243 (94%)	78 (6%)	0	100	100
3	5	303/364 (83%)	285 (94%)	17 (6%)	1 (0%)	36	67
3	e	311/364 (85%)	300 (96%)	11 (4%)	0	100	100
4	6	285/301 (95%)	269 (94%)	16 (6%)	0	100	100
4	7	271/301 (90%)	255 (94%)	16 (6%)	0	100	100
4	f	286/301 (95%)	276 (96%)	10 (4%)	0	100	100
4	g	271/301 (90%)	261 (96%)	10 (4%)	0	100	100
All	All	8609/9717 (89%)	8089 (94%)	518 (6%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	S	1176	HIS
3	5	308	VAL

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

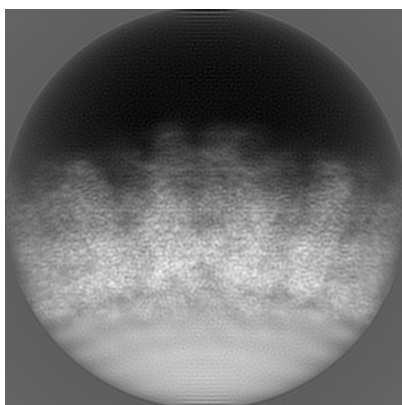
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30159. These allow visual inspection of the internal detail of the map and identification of artifacts.

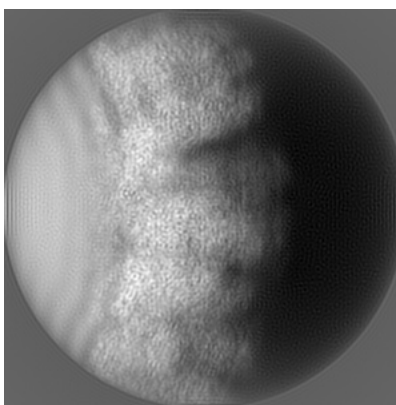
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

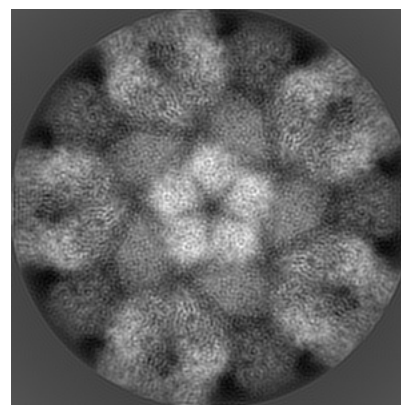
6.1.1 Primary map



X



Y

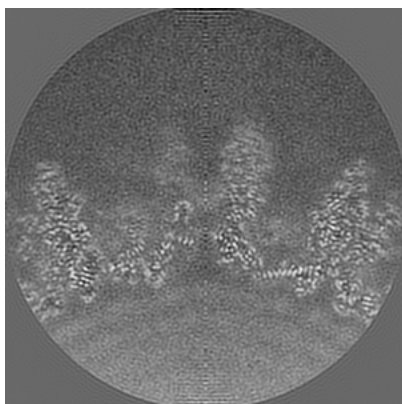


Z

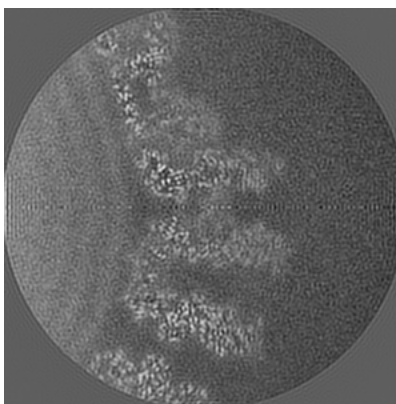
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

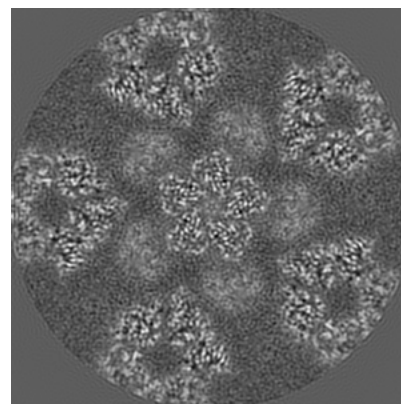
6.2.1 Primary map



X Index: 150



Y Index: 150

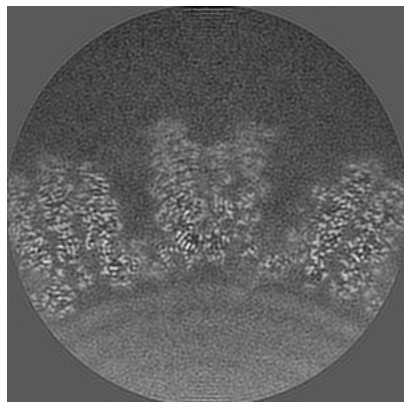


Z Index: 150

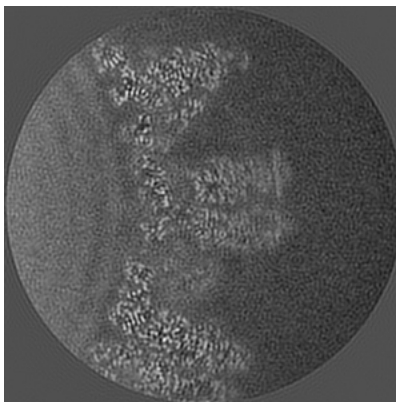
The images above show central slices of the map in three orthogonal directions.

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

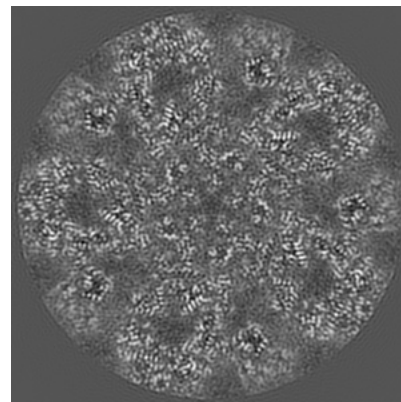
6.3.1 Primary map



X Index: 137



Y Index: 122

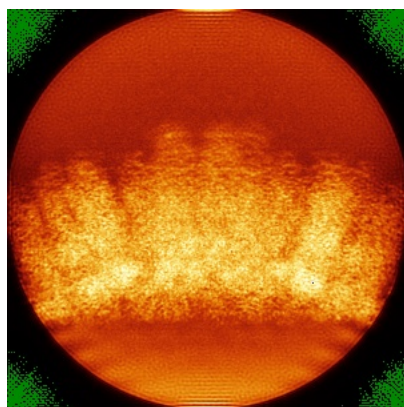


Z Index: 108

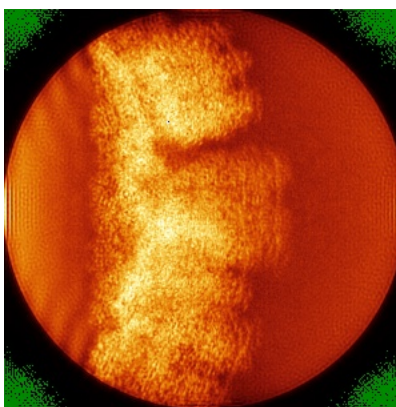
The images above show the largest variance slices of the map in three orthogonal directions.

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

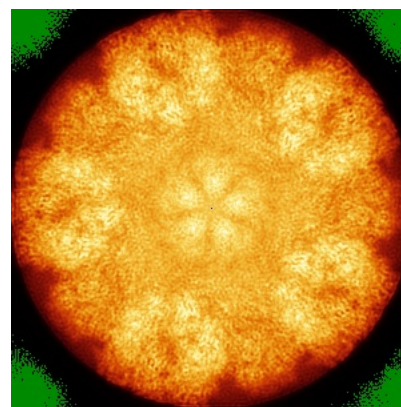
6.4.1 Primary map



X



Y

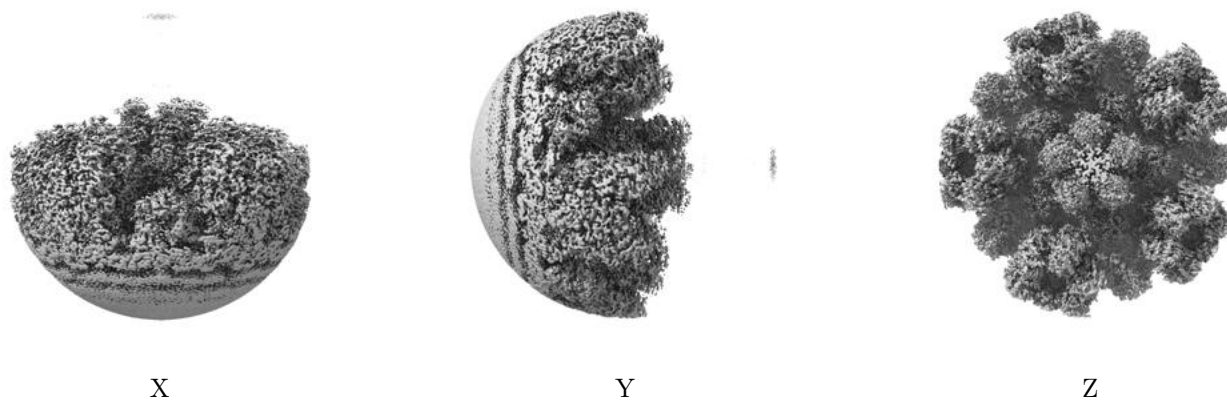


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

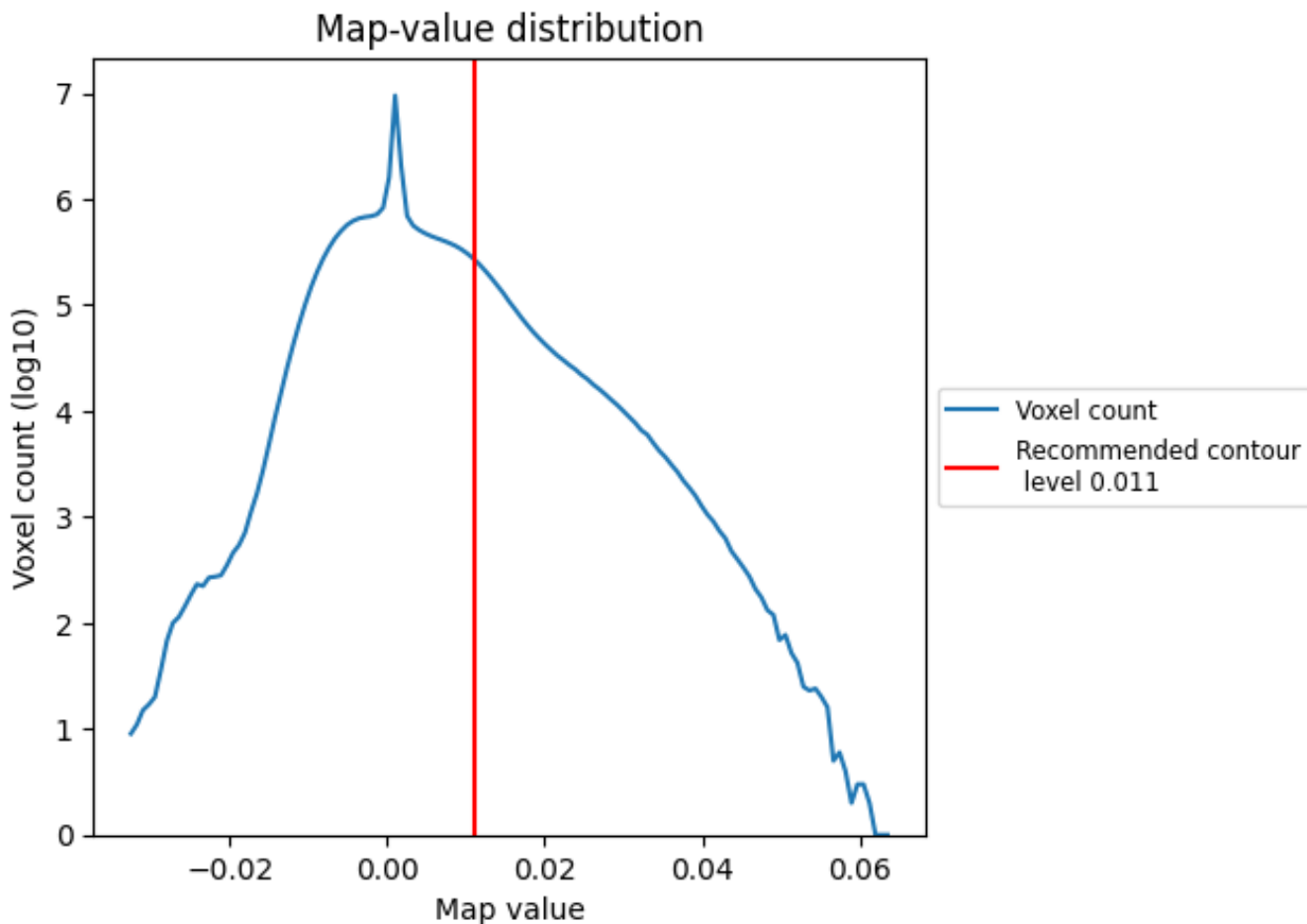
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

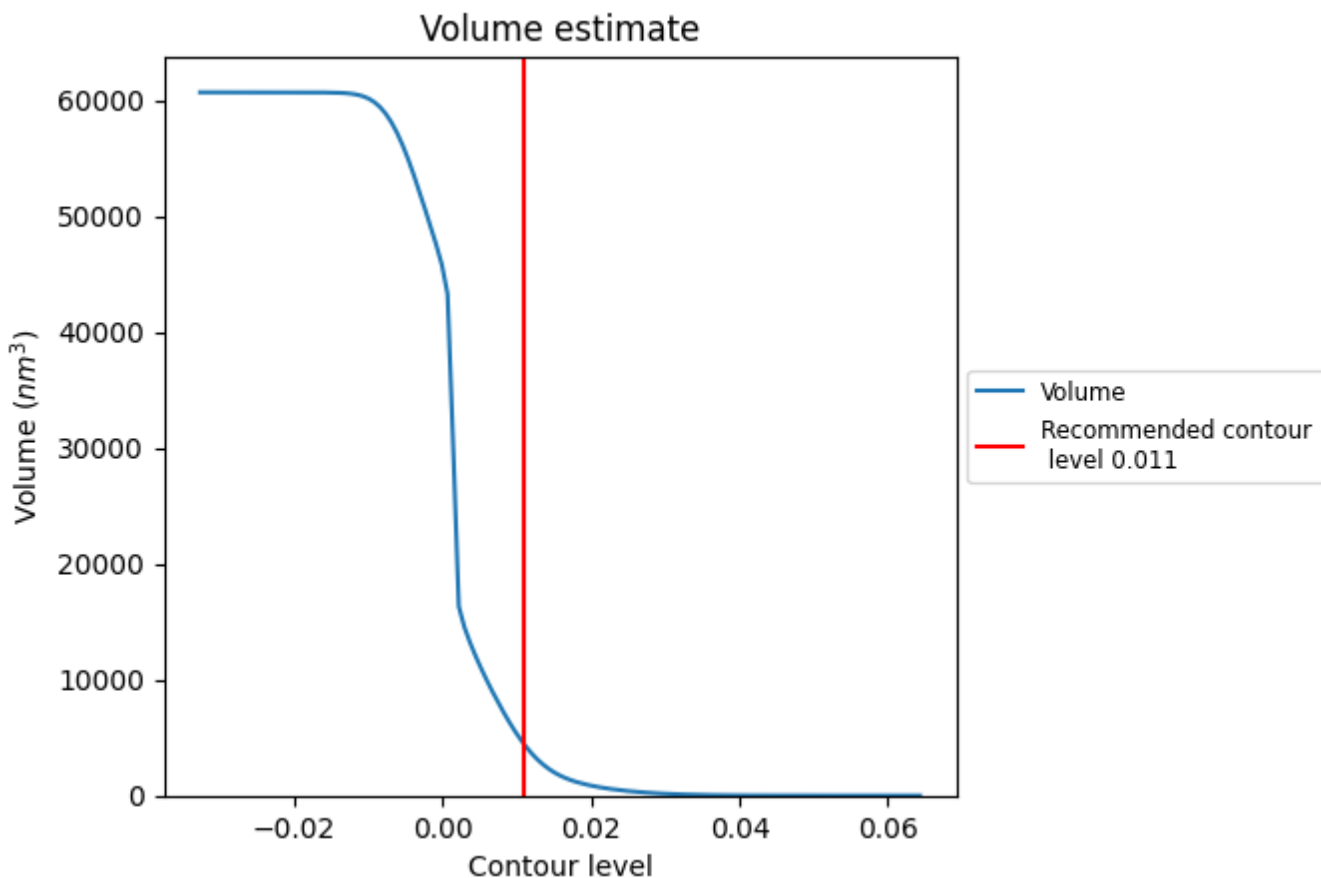
This section contains the results of statistical analysis of the map.

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.

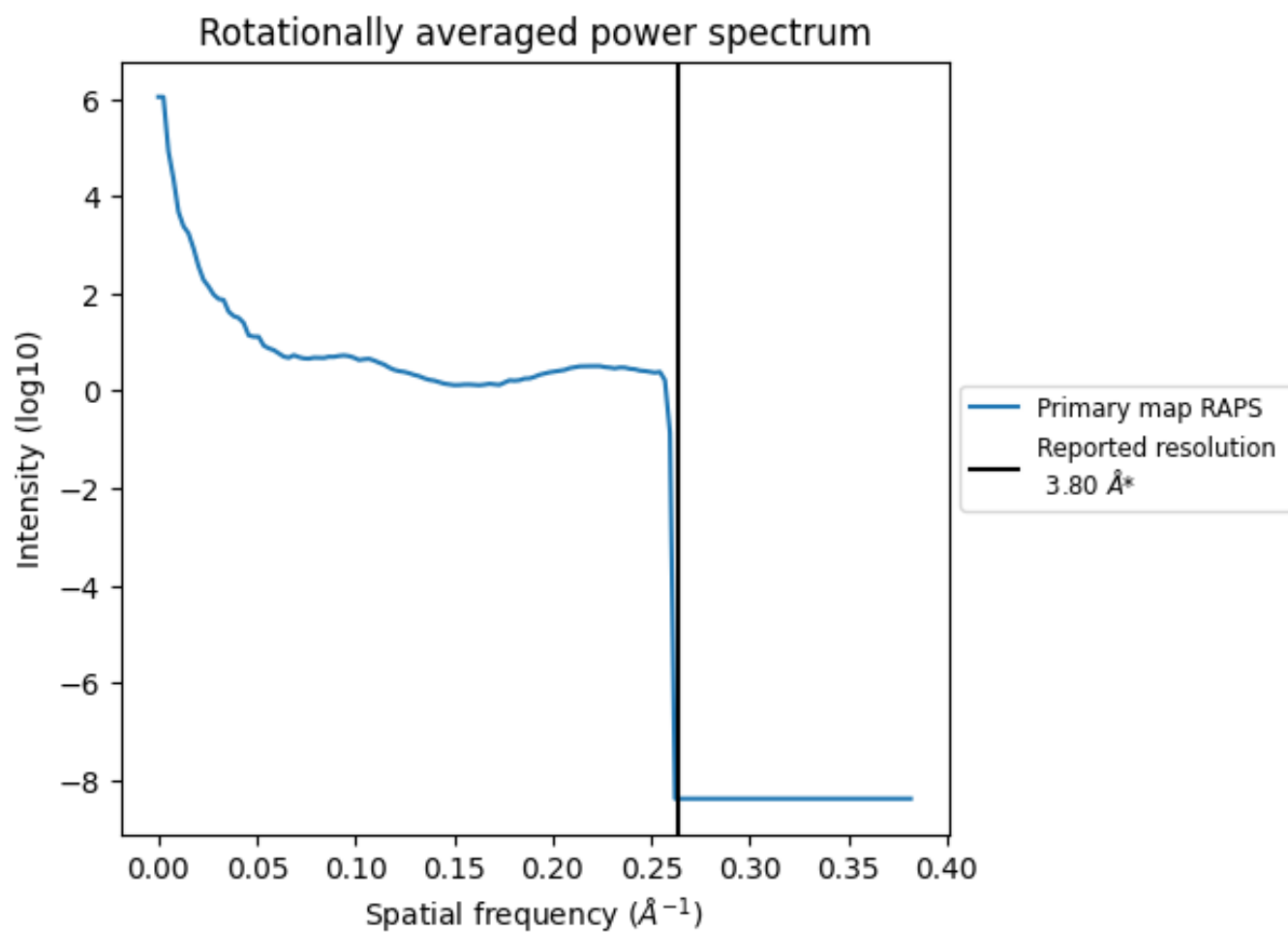
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4476 nm³; this corresponds to an approximate mass of 4043 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation

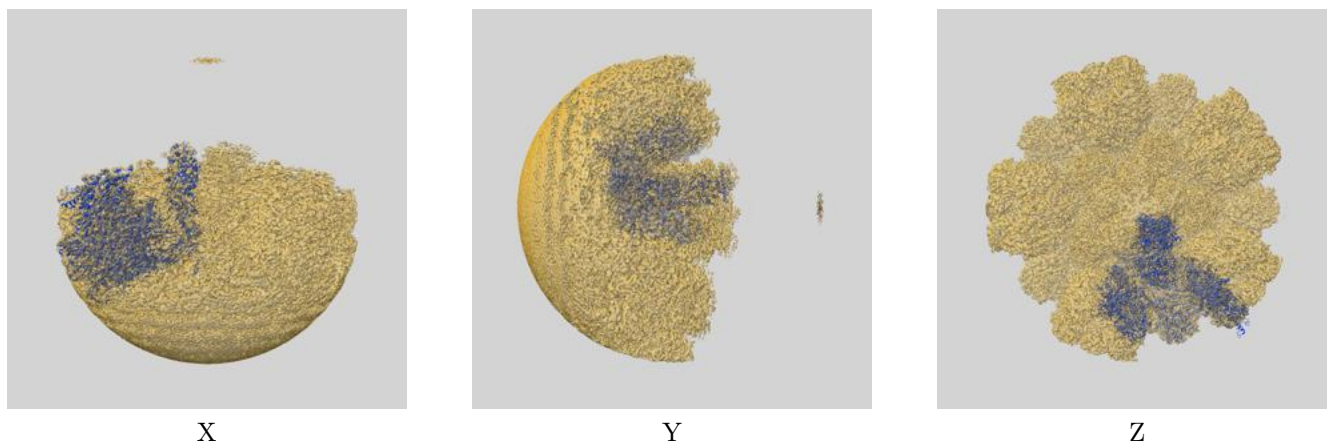
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30159 and PDB model 7BR8. Per-residue inclusion information can be found in section 3 on page 6.

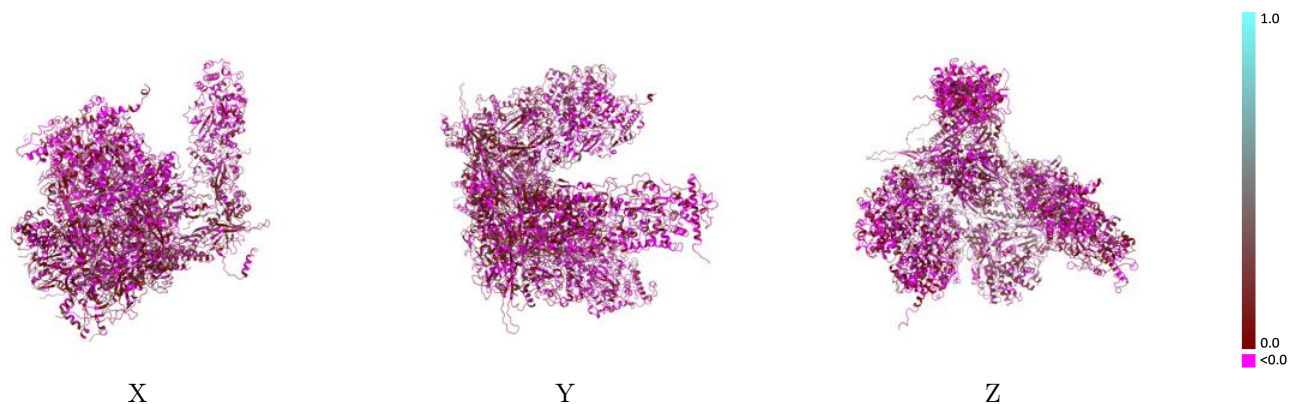
9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)



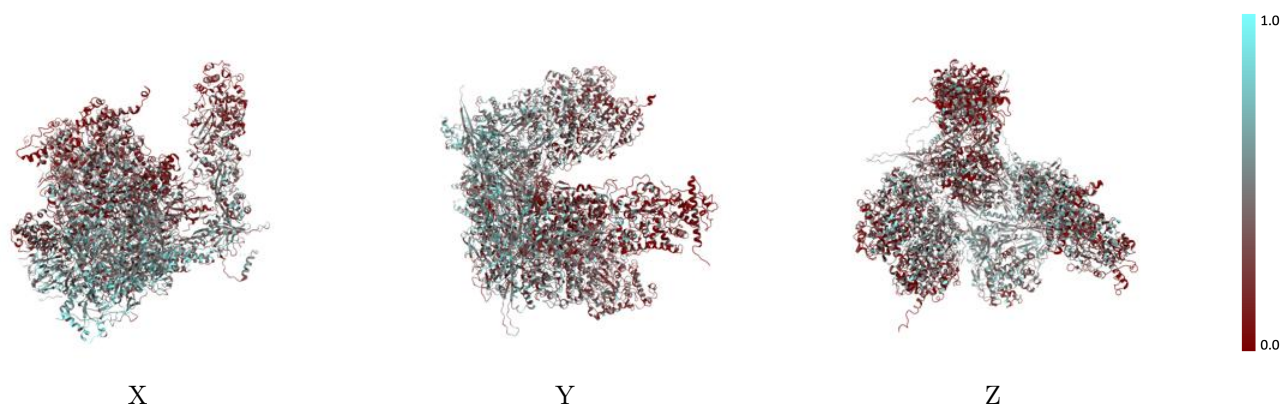
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



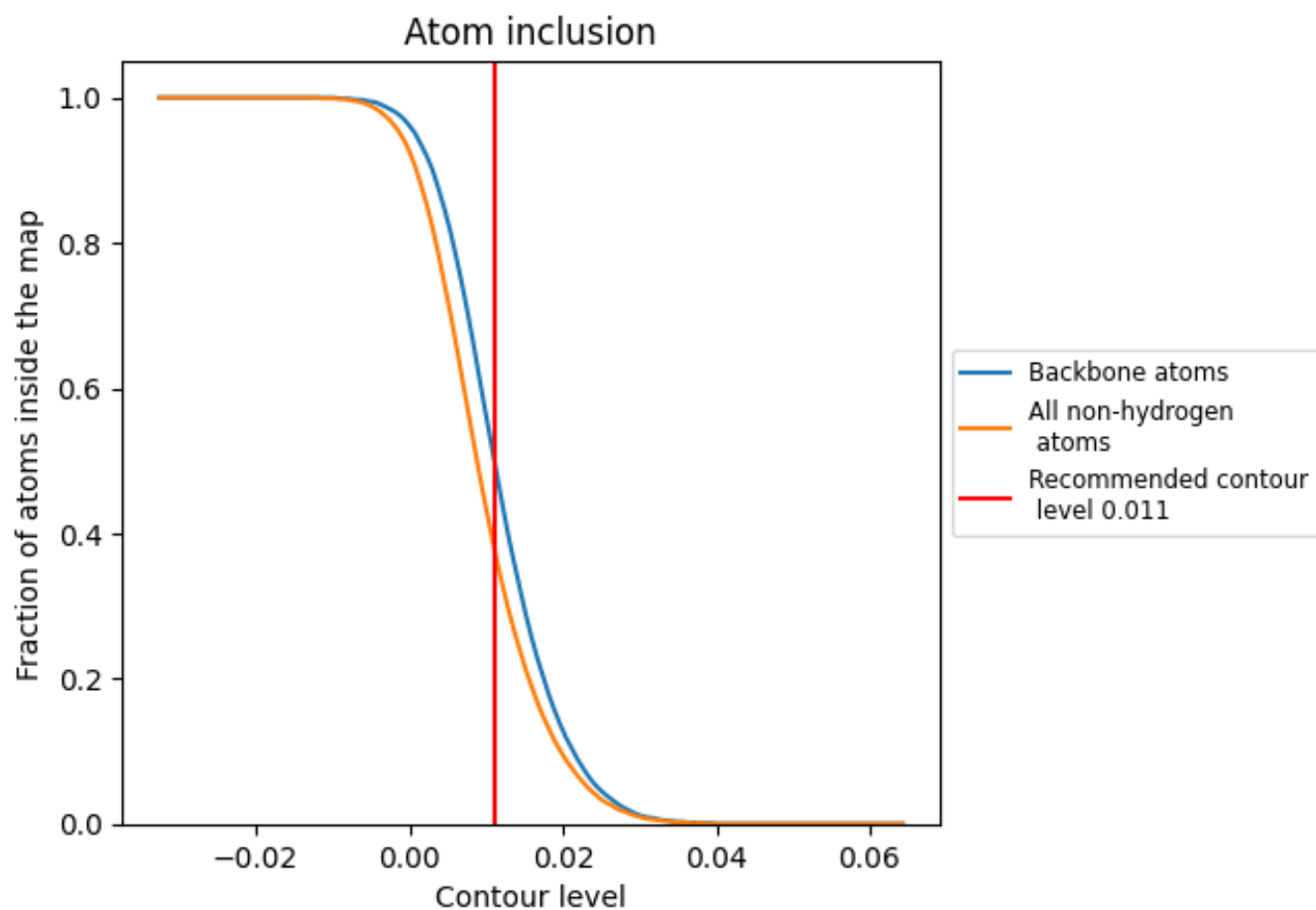
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.011).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 38% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3840	 0.0390
2	 0.0900	 0.0040
5	 0.3400	 0.0580
6	 0.2570	 0.0380
7	 0.2150	 0.0200
S	 0.3920	 0.0270
T	 0.4150	 0.0250
W	 0.4590	 0.0620
Y	 0.1880	 -0.0060
Z	 0.1430	 -0.0060
e	 0.4820	 0.0630
f	 0.4460	 0.0640
g	 0.4600	 0.0620
l	 0.3240	 0.0360
m	 0.0830	 -0.0260
x	 0.4190	 0.0370
y	 0.1570	 0.0320

