



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 08:50 AM UTC

PDB ID : 5ZVT / pdb_00005zvt
EMDB ID : EMD-6969
Title : Structure of RNA polymerase complex and genome within a dsRNA virus provides insights into the mechanisms of transcription and assembly
Authors : Liu, H.; Fang, Q.; Cheng, L.
Deposited on : 2018-05-12
Resolution : 3.30 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:

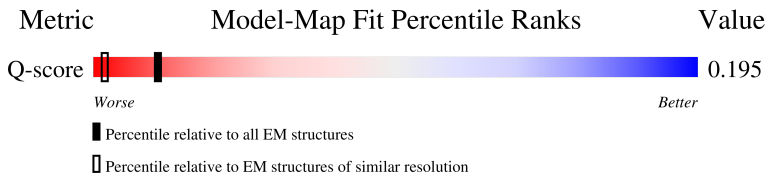
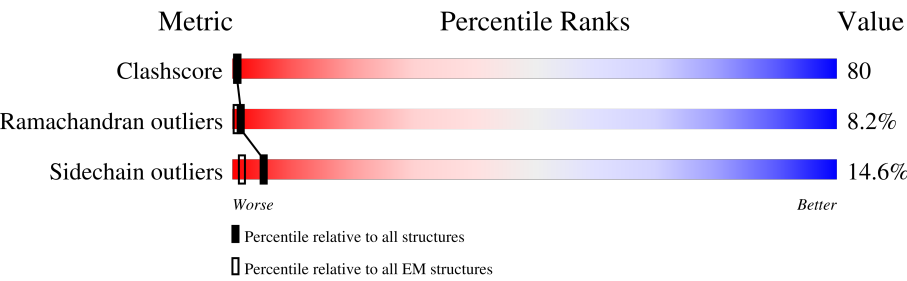
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.30 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	15087 (2.80 - 3.80)

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	b	276	8% 14%13%69%
1	d	276	13%15%69%
1	f	276	5% 14%13%69%
1	h	276	6% 16%12%69%

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Mol	Chain	Length	Quality of chain
1	j	276	
1	l	276	
1	n	276	
1	p	276	
1	r	276	
1	t	276	
2	A	42	
2	C	42	
2	E	42	
2	G	42	
2	I	42	
2	K	42	
2	M	42	
2	O	42	
2	Q	42	
2	S	42	
3	B	606	
3	D	606	
3	F	606	
3	H	606	
3	J	606	
3	L	606	
3	N	606	
3	P	606	
3	R	606	

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Mol	Chain	Length	Quality of chain
3	T	606	
4	U	412	
4	V	412	
5	W	1299	
6	X	1214	
6	Y	1214	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	MYR	A	101	-	-	X	-
7	MYR	C	101	-	-	X	-
7	MYR	E	101	-	-	X	-
7	MYR	G	101	-	-	X	-
7	MYR	I	101	-	-	X	-
7	MYR	K	101	-	-	X	-
7	MYR	M	101	-	-	X	-
7	MYR	O	101	-	-	X	-
7	MYR	Q	101	-	-	X	-
7	MYR	S	101	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 87645 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 Outer capsid VP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	l	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	b	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	f	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	d	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	h	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	j	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	n	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	p	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	r	86	Total 666	C 411	N 125	O 124	S 6	0	0
1	t	86	Total 666	C 411	N 125	O 124	S 6	0	0

- Molecule 2 is a protein called N-terminus of outer capsid protein VP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	41	Total 291	C 177	N 48	O 65	S 1	0	0
2	C	41	Total 291	C 177	N 48	O 65	S 1	0	0
2	E	41	Total 291	C 177	N 48	O 65	S 1	0	0
2	G	41	Total 284	C 174	N 46	O 63	S 1	0	0
2	I	41	Total 291	C 177	N 48	O 65	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	K	41	Total	C	N	O	S	0	0
			291	177	48	65	1		
2	M	41	Total	C	N	O	S	0	0
			284	174	46	63	1		
2	O	41	Total	C	N	O	S	0	0
			291	177	48	65	1		
2	Q	41	Total	C	N	O	S	0	0
			291	177	48	65	1		
2	S	41	Total	C	N	O	S	0	0
			284	174	46	63	1		

- Molecule 3 is a protein called C-terminus of outer capsid protein VP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	D	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	F	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	H	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	J	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	L	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	N	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	P	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	R	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		
3	T	604	Total	C	N	O	S	0	0
			4508	2858	761	872	17		

- Molecule 4 is a protein called Core protein VP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	411	Total	C	N	O	S	0	0
			3138	2008	544	571	15		
4	V	411	Total	C	N	O	S	0	0
			3138	2008	544	571	15		

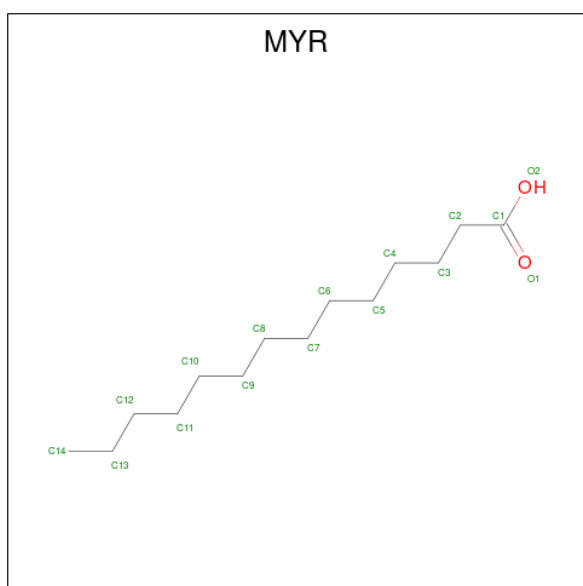
- Molecule 5 is a protein called VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	W	1284	Total	C	N	O	S	0	0
			9882	6335	1681	1839	27		

- Molecule 6 is a protein called VP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	X	1018	Total	C	N	O	S	0	0
			7873	5033	1347	1447	46		
6	Y	1154	Total	C	N	O	S	0	0
			8835	5604	1525	1656	50		

- Molecule 7 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).

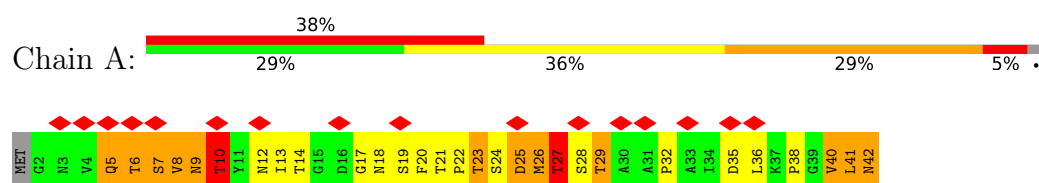


Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	C	O	0
			15	14	1	
7	C	1	Total	C	O	0
			15	14	1	
7	E	1	Total	C	O	0
			15	14	1	
7	G	1	Total	C	O	0
			15	14	1	
7	I	1	Total	C	O	0
			15	14	1	
7	K	1	Total	C	O	0
			15	14	1	

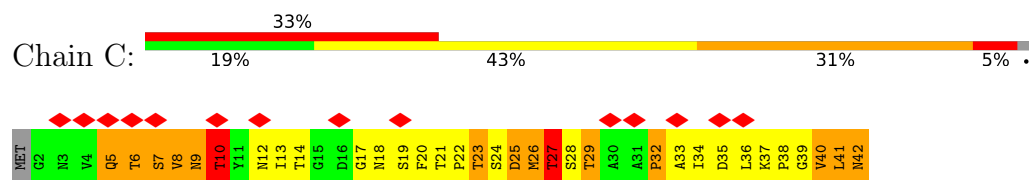
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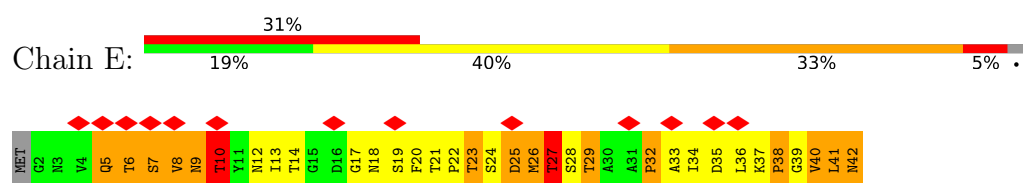
Mol	Chain	Residues	Atoms			AltConf
7	M	1	Total	C	O	0
			15	14	1	
7	O	1	Total	C	O	0
			15	14	1	
7	Q	1	Total	C	O	0
			15	14	1	
7	S	1	Total	C	O	0
			15	14	1	



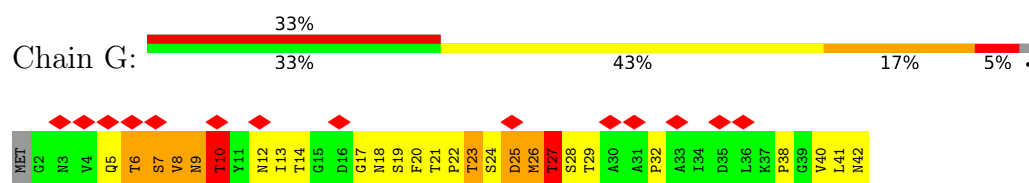
- Molecule 2: N-terminus of outer capsid protein VP5



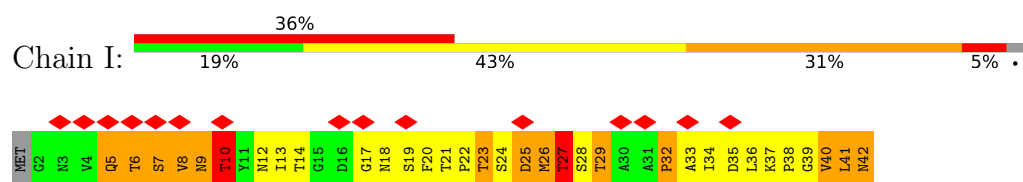
- Molecule 2: N-terminus of outer capsid protein VP5



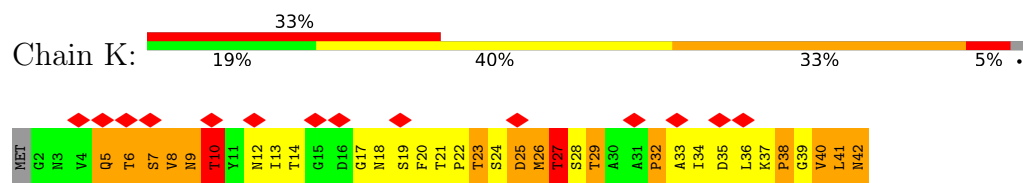
- Molecule 2: N-terminus of outer capsid protein VP5



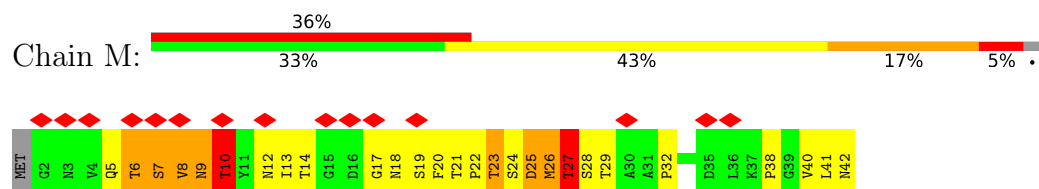
- Molecule 2: N-terminus of outer capsid protein VP5



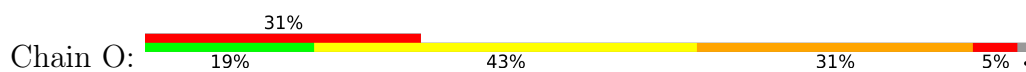
- Molecule 2: N-terminus of outer capsid protein VP5



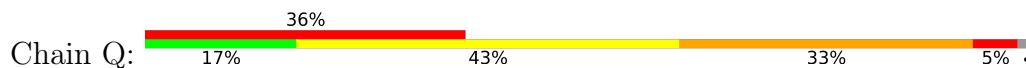
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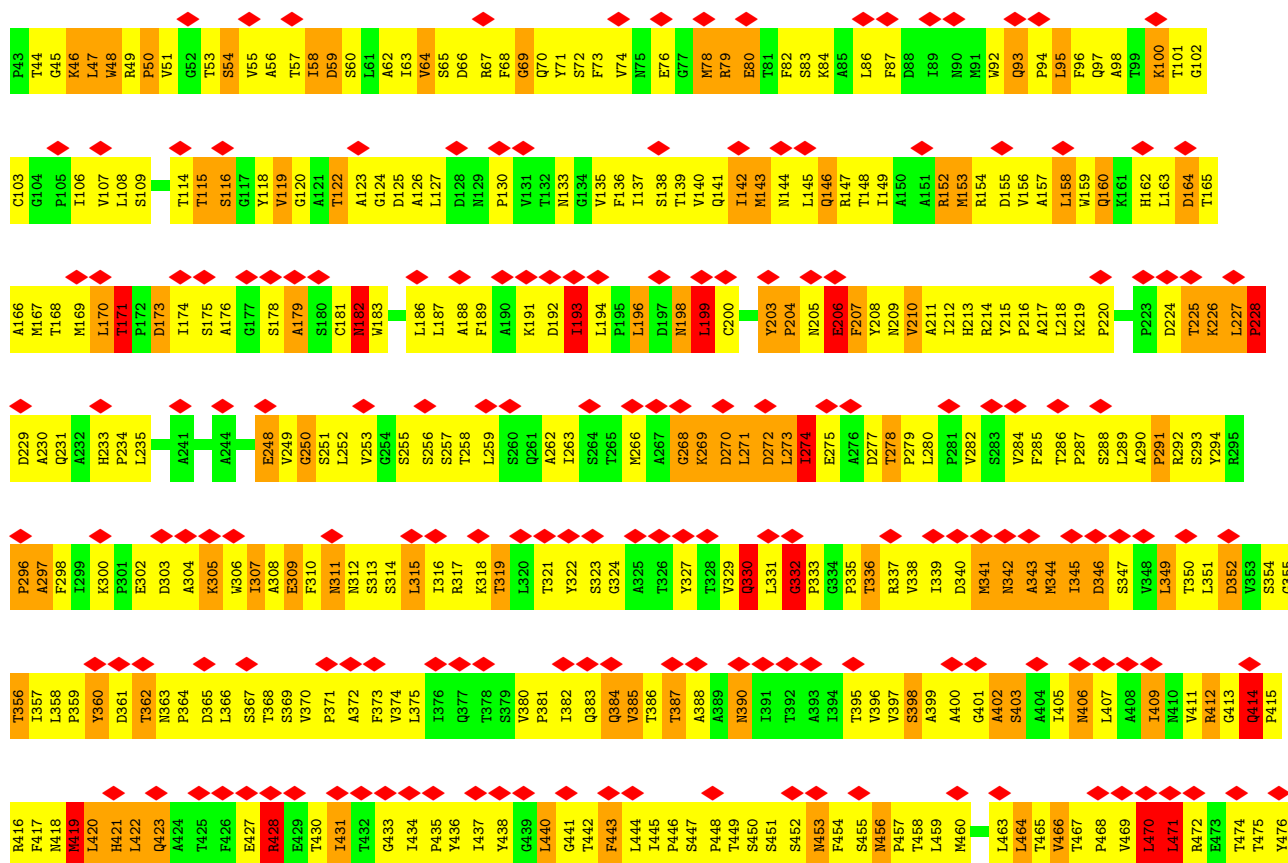
- Molecule 2: N-terminus of outer capsid protein VP5

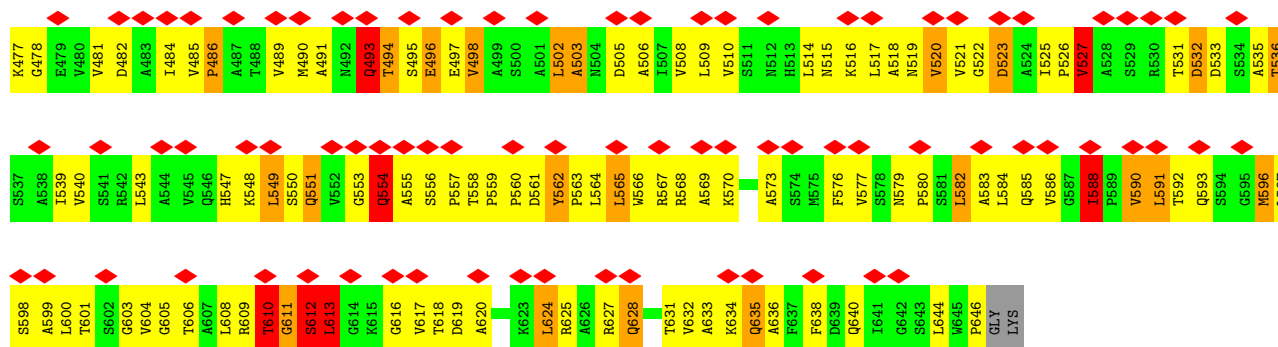


- Molecule 2: N-terminus of outer capsid protein VP5

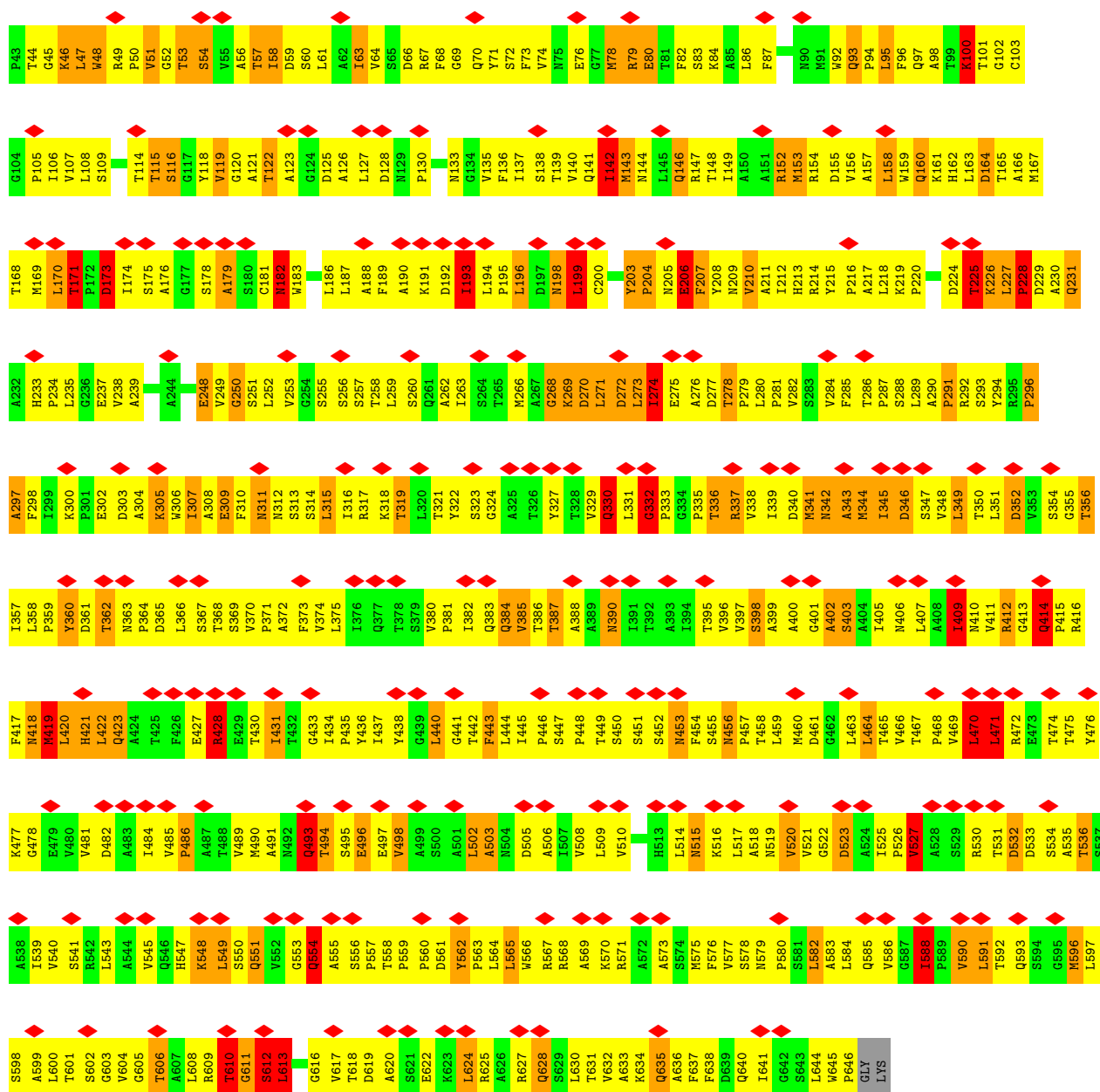


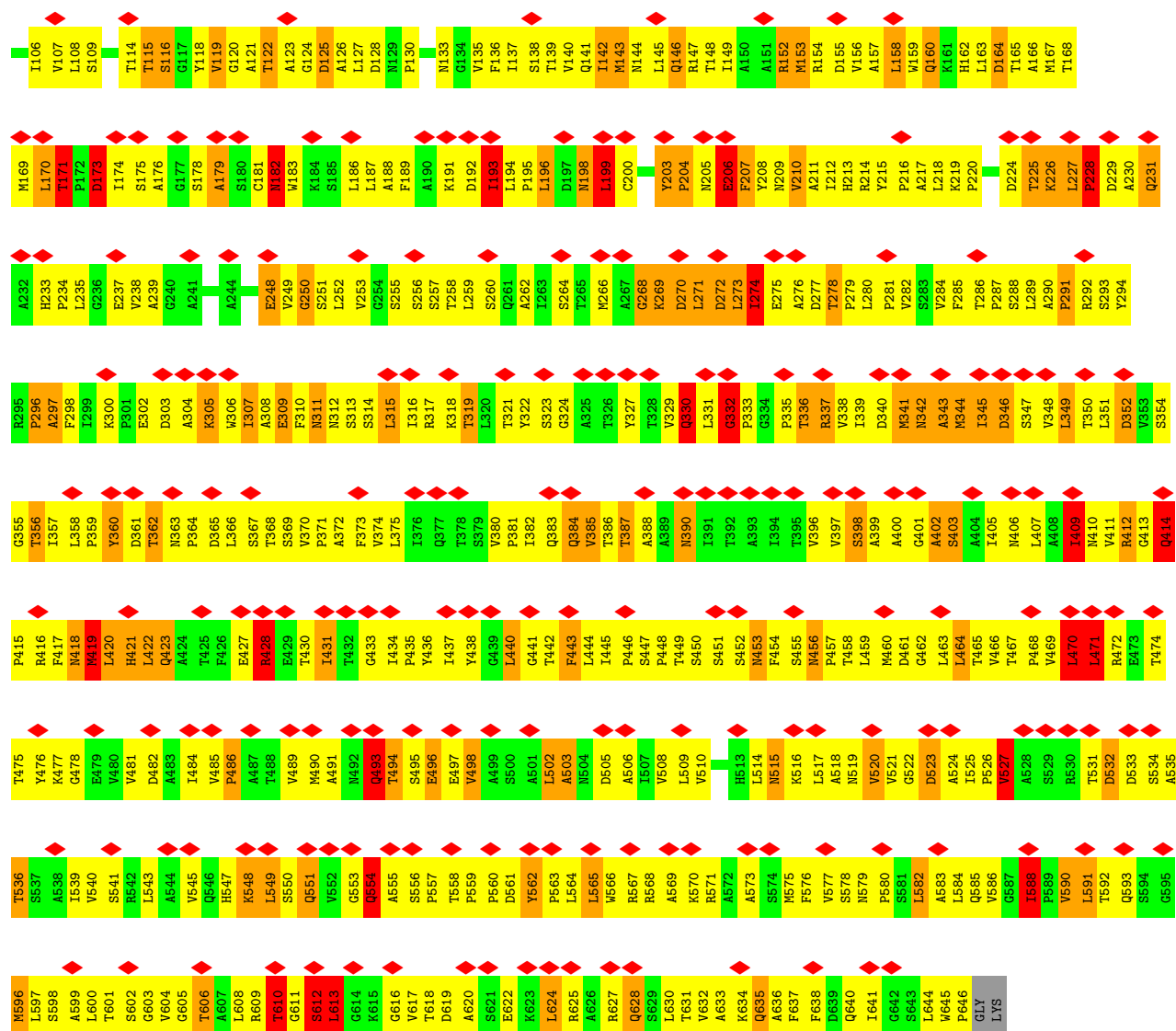
- Molecule 3: C-terminus of outer capsid protein VP5



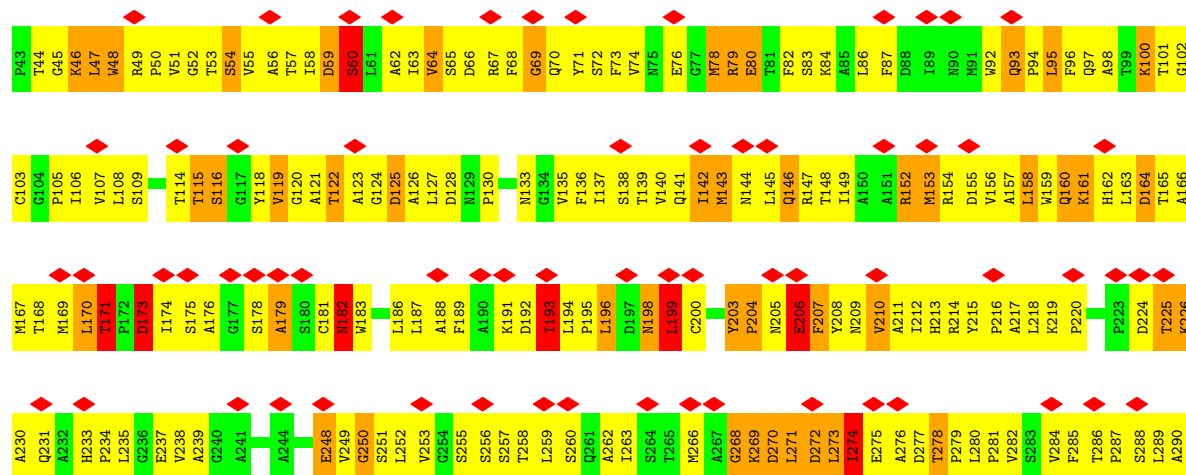


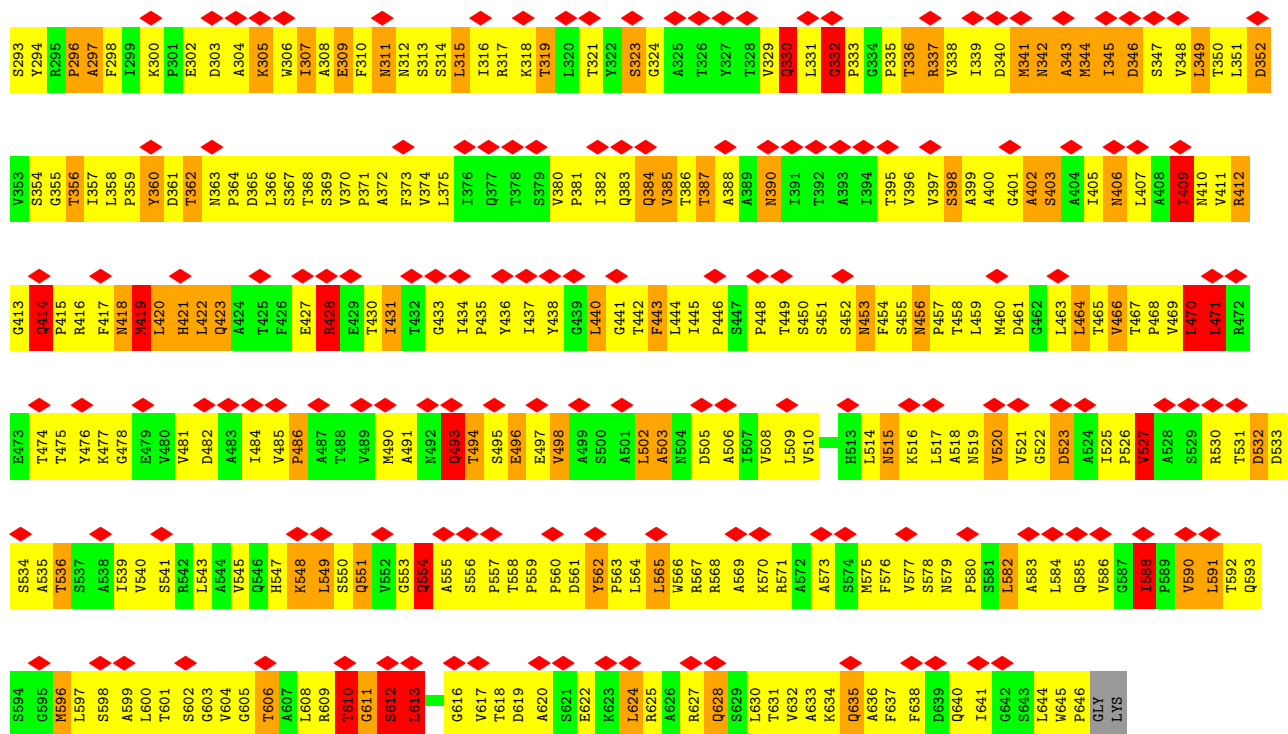
• Molecule 3: C-terminus of outer capsid protein VP5



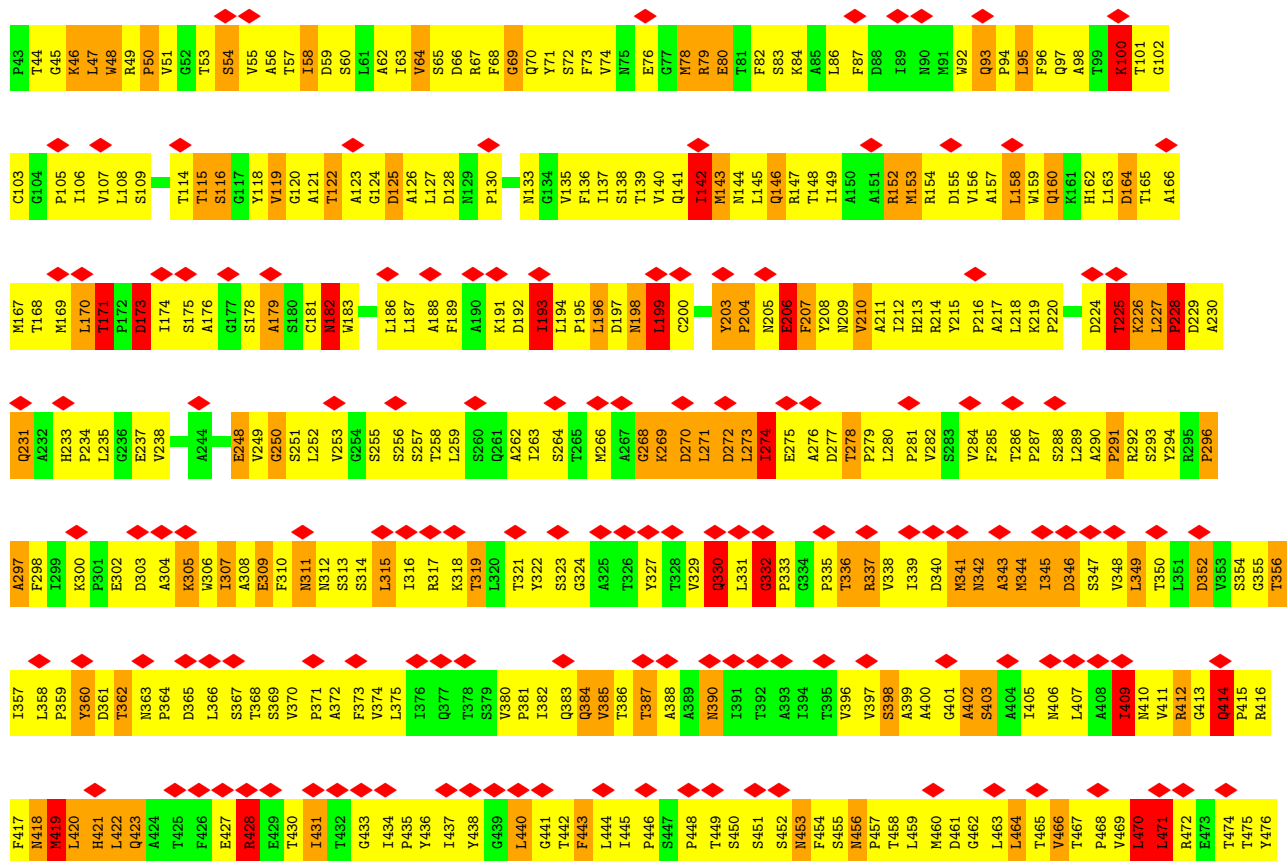


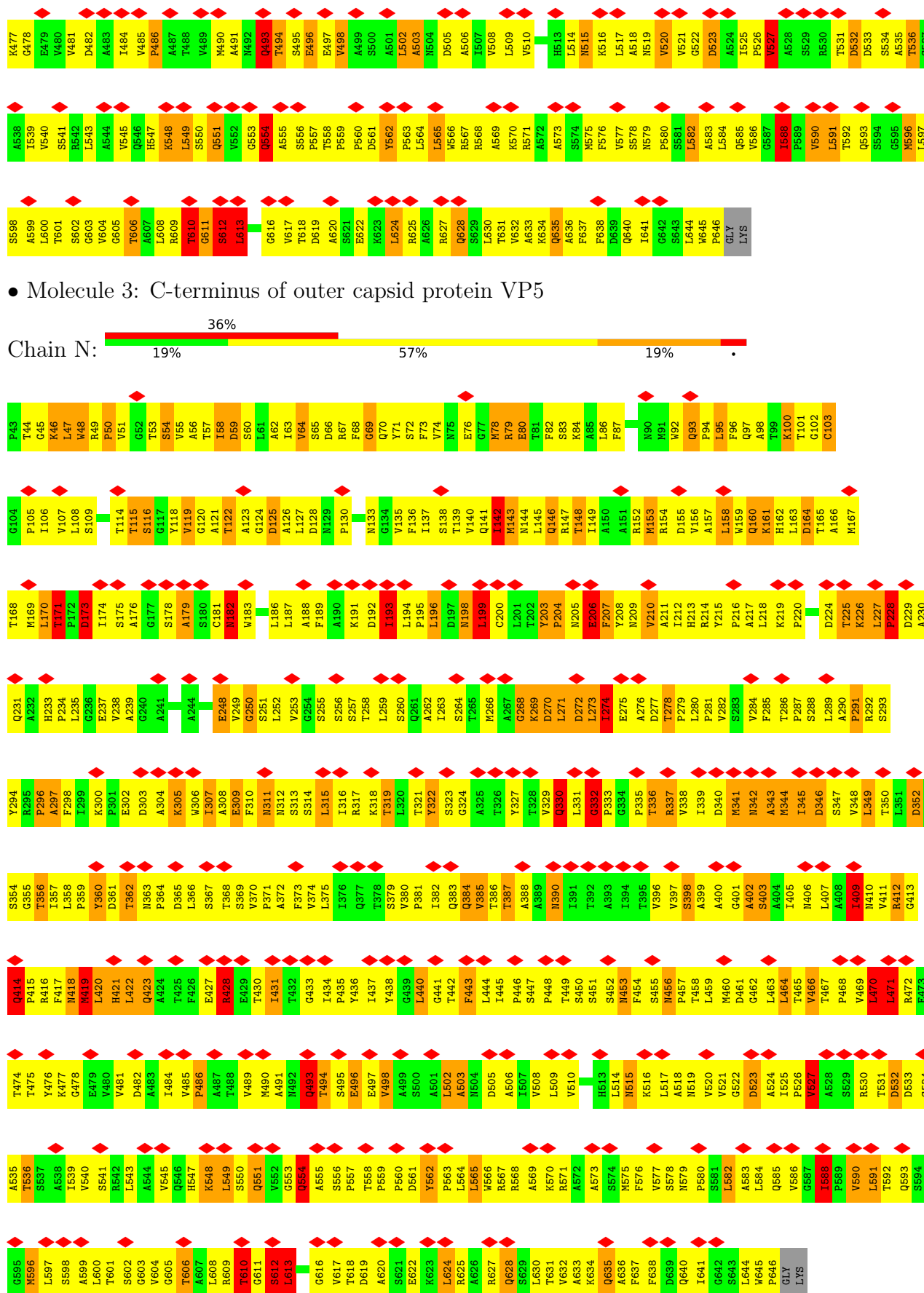
• Molecule 3: C-terminus of outer capsid protein VP5





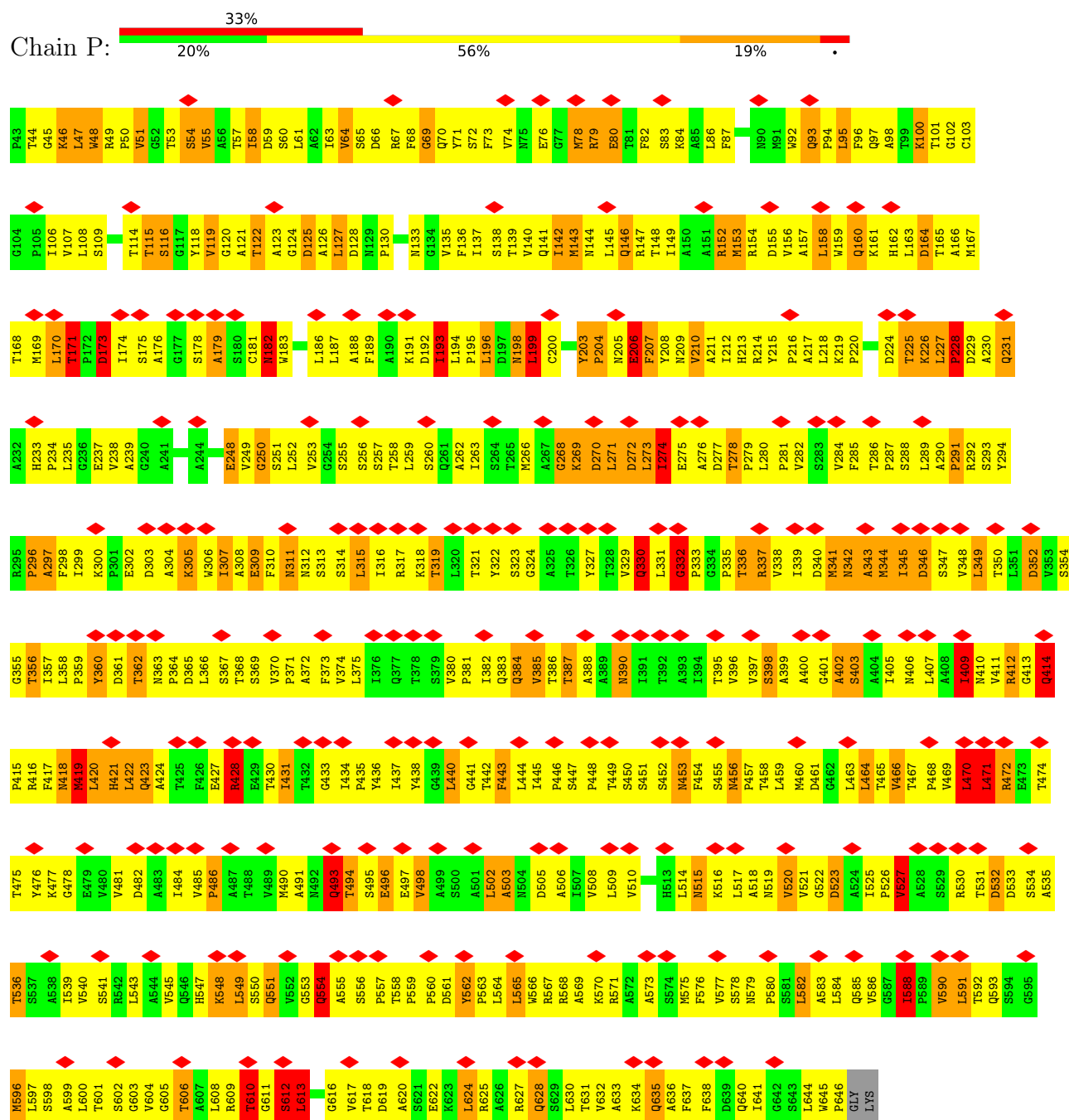
• Molecule 3: C-terminus of outer capsid protein VP5



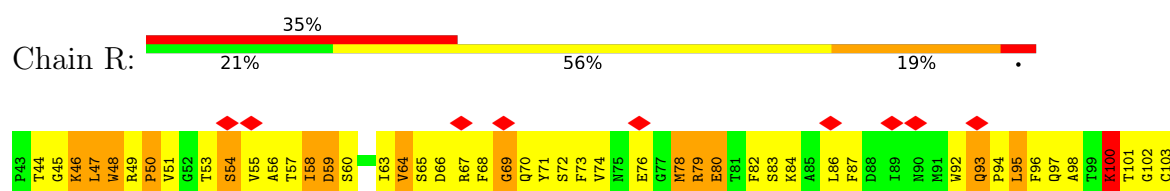


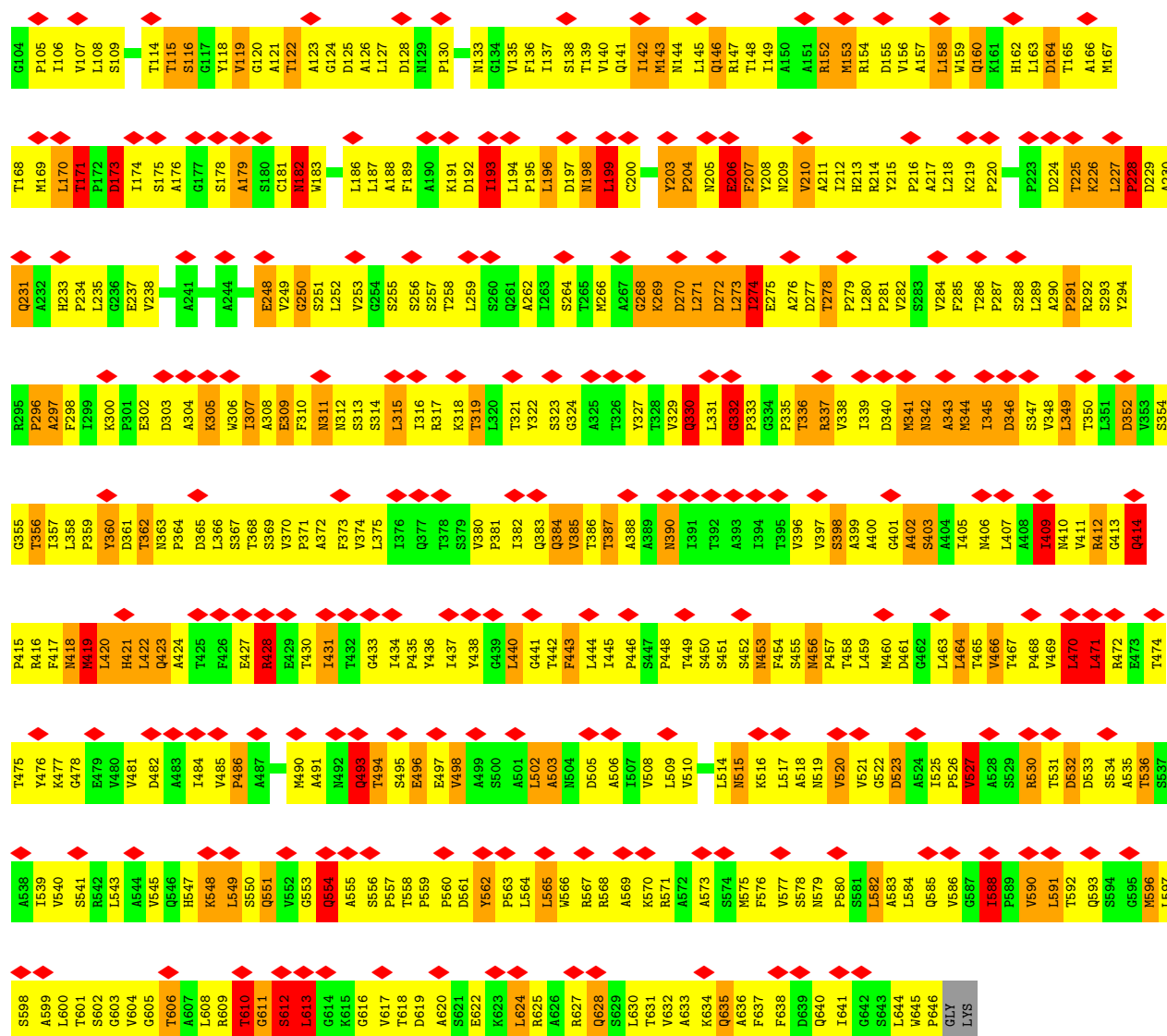
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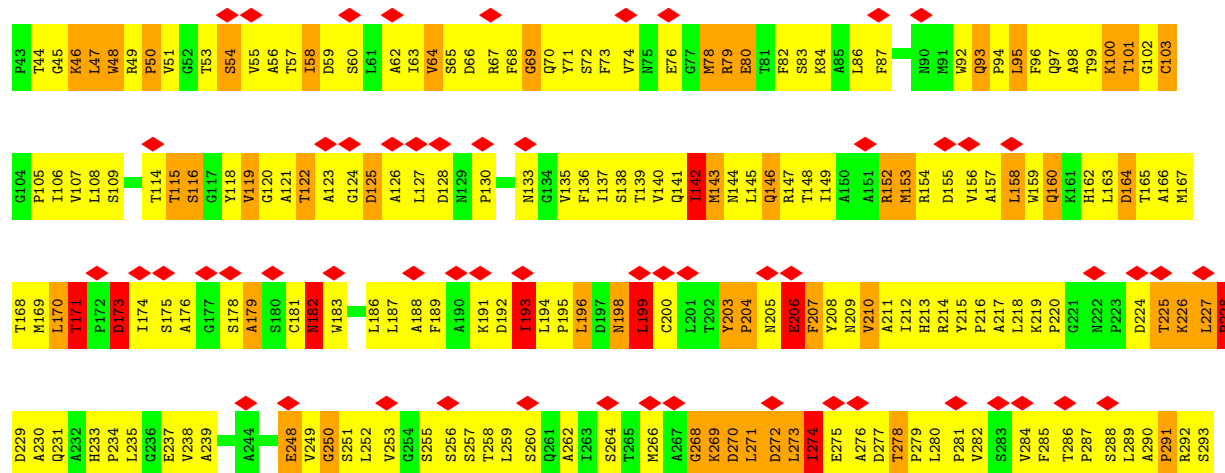


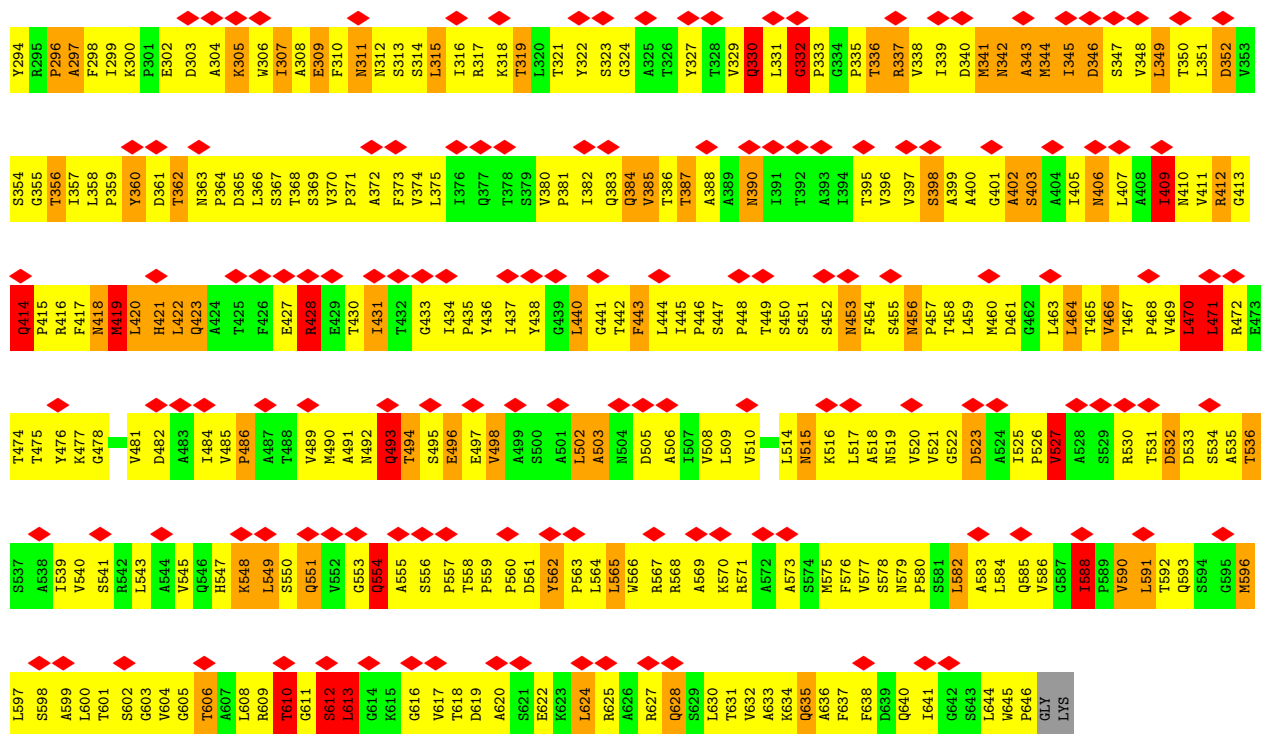
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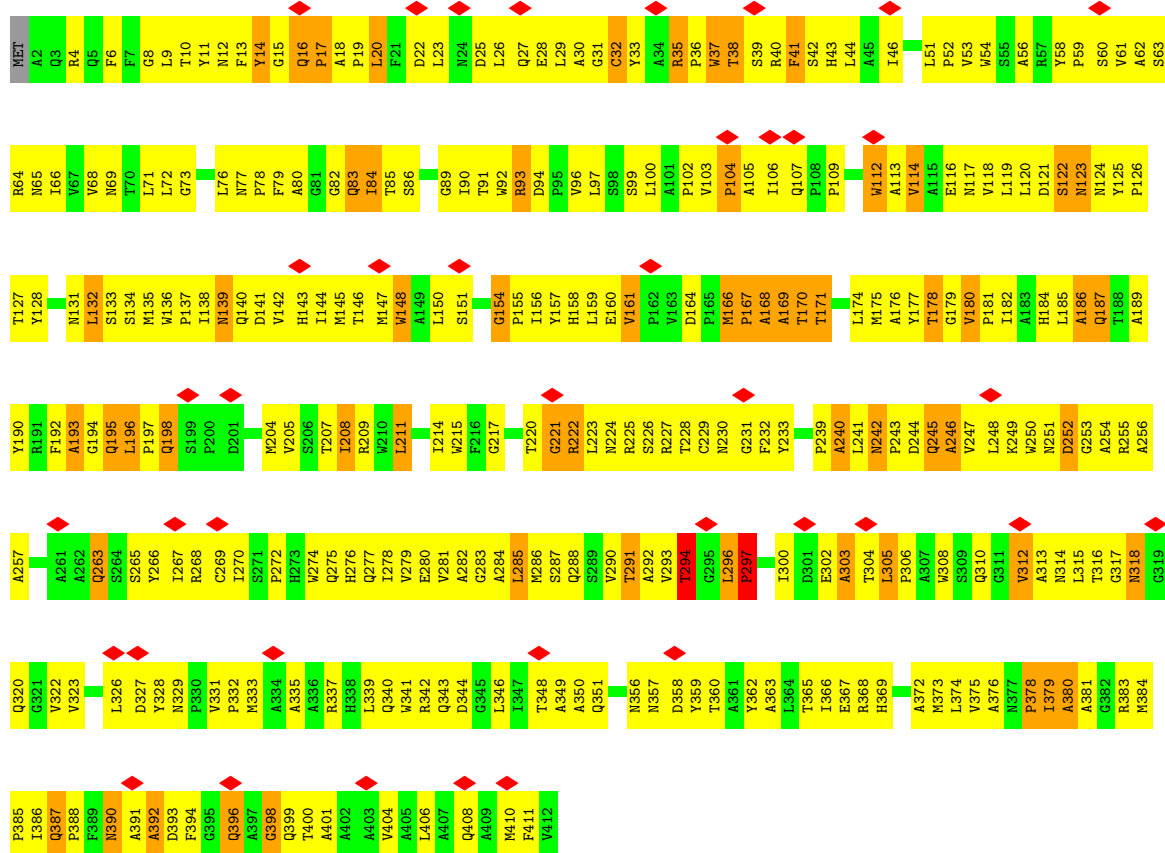


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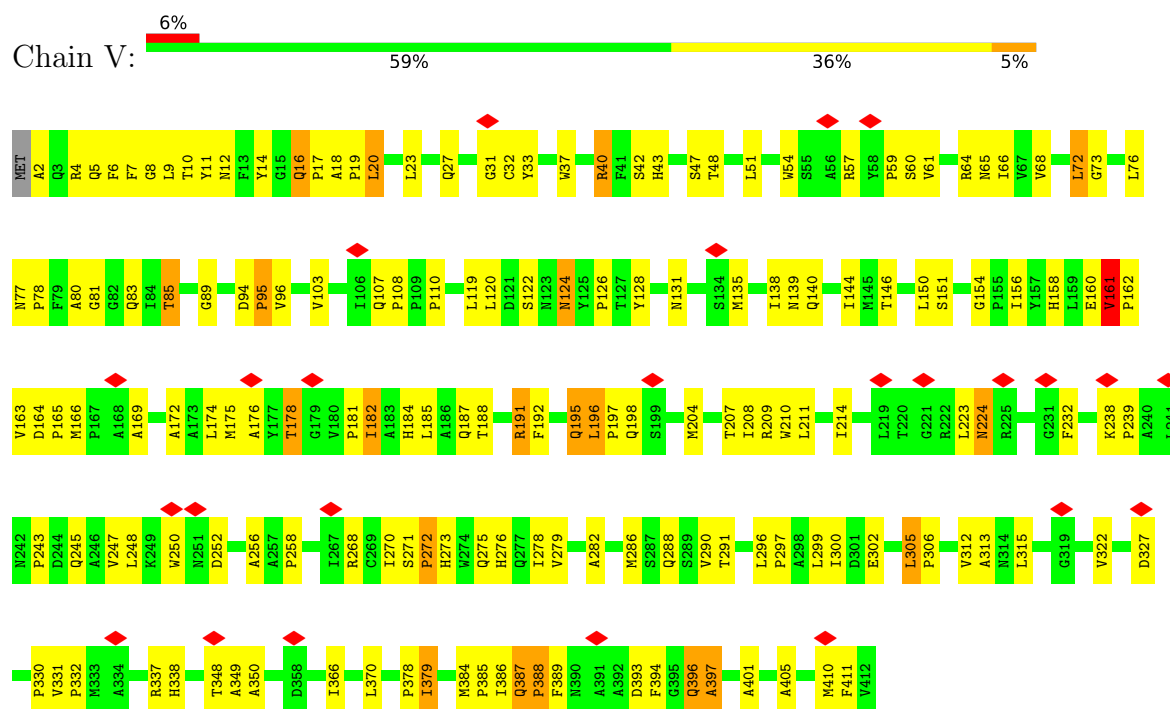




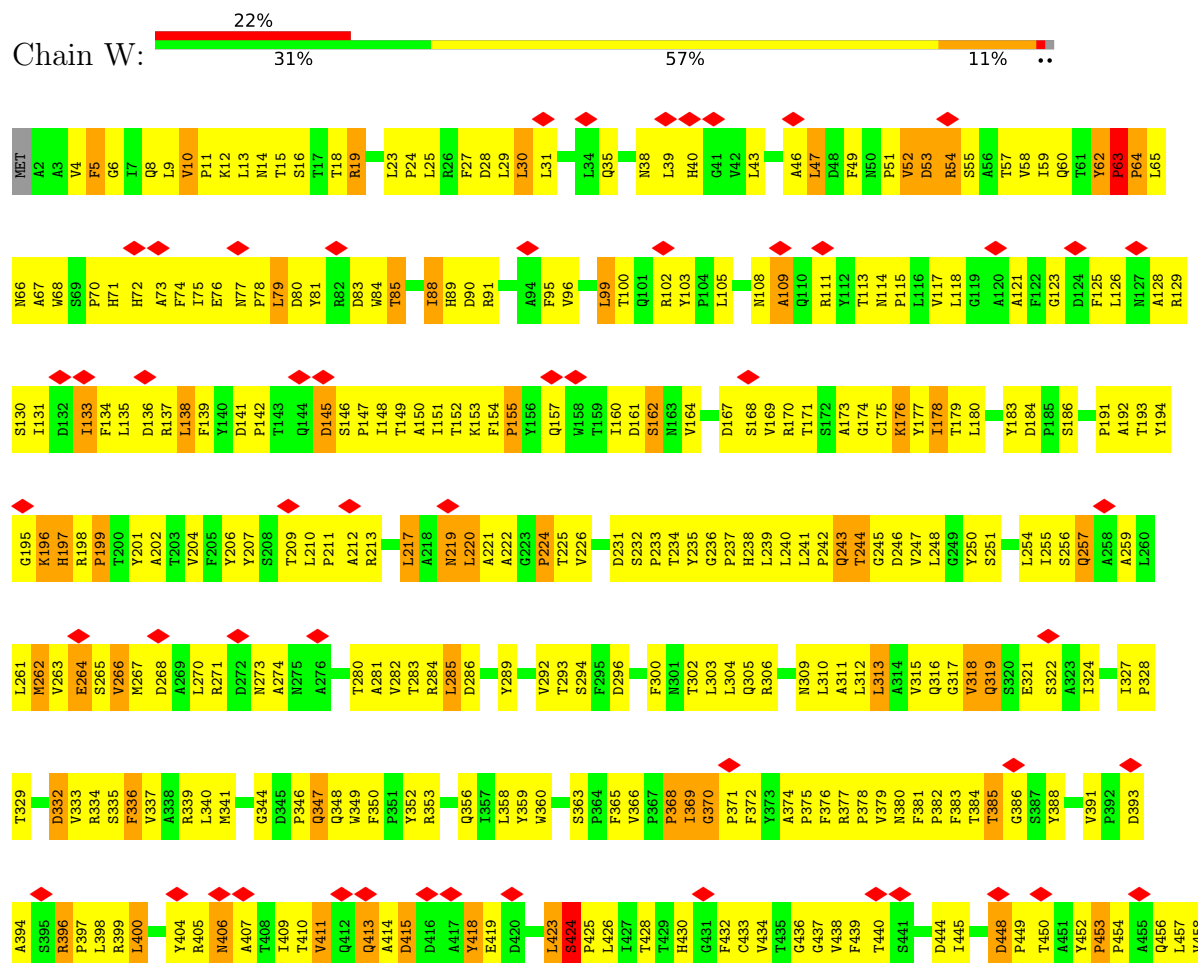
• Molecule 4: Core protein VP6



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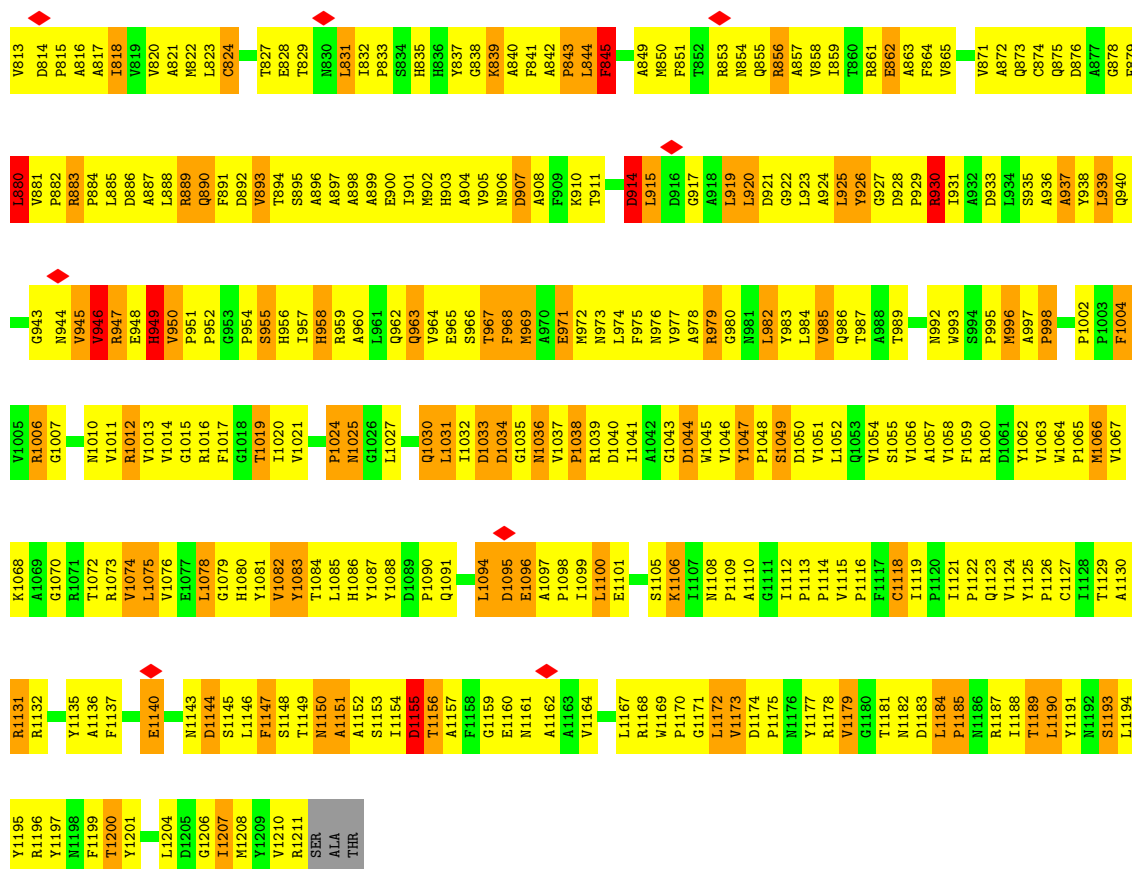
• Molecule 5: VP1



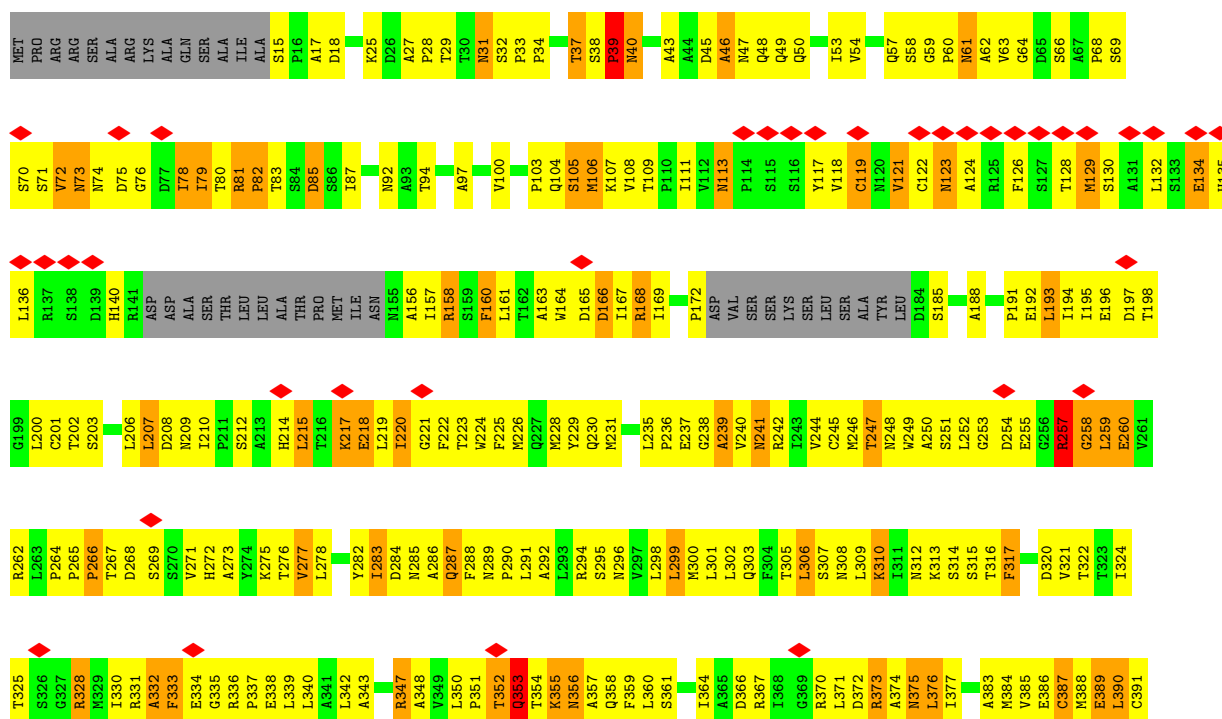
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G520	A521	S522	SER	ALA	HIS	ALA	ASN	ALA	D529	E530	P531	V532	I533	L534	A535	I537	G540	S541	I542	P543	T551	V552	Q553	F554	D557	V558	V559	H560	G561	S562	L563	L564	D565	L566	V570	P571	T572	G573	T574	F575	G576	L577	V578	Y579	A580	D581	L582	N507	P508	V509	L510	P647	Q584	D583	V585	GLU	ASP	ALA	GLY		
THR	D591	M592	P593	N596	R597	A598	A601	M602	L603	G604	T605	A606	L607	Q608	M609	T610	T611	G614	V615	S616	L618	Q619	V620	F622	P623	T624	R625	A626	D627	L628	T629	Q630	V631	F632	Y635	A636	T637	H638	A639	T640	T641	L642	H643	L644	G645	K646	R647	T648	I649	V650	N651	E654									
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L781	T782	T783	T784	L785	V786	H787	Q788	R789	R790	F791	T792	T793	P794	F797	T798	L799	F800	S801	S802	E803	A804	V805	T809	L810	V811	A812	A813	G814	Y815	N816	S817	F818	L819	S820	E821	Q822	T823	R824	N825	P826	A829	H830	L831	L832	D833	L834	G835	T836	G837	P838	E839	C840	R841	T842	L843	S844					
L846	P847	P848	T849	L850	Q851	V852	T853	H854	S855	D856	S857	R858	P859	C860	A861	E862	L863	H864	A865	S866	F867	D868	P869	A870	L871	T872	A873	Y874	H875	Q876	G877	D878	Y879	S880	T881	A882	A883	F884	W885	N886	G887	L888	R889	C890	D891	S892	A893	T894	A895	G896	G961	F897	T898	A901	A904	A905					
G907	T908	P909	L910	V914	Q915	Q916	L917	I918	P919	R920	I921	V922	A923	A924	G925	G926	T927	R928	Y929	W930	L931	D932	L933	N934	T935	P936	L937	Y938	E939	V940	S941	S942	L943	L946	P947	Y949	E948	I949	D950	L951	R952	D953	H954	Y955	Y956	R957	F958	N959	G960	L961	R962	R963	Y964	E965	P966	Y967	A968				
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T1031	P1034	L1035	R1036	L1037	M1038	P1039	V1040	P1041	T1042	P1043	L1044	Q1045	Q1046	Q1047	C1048	A1049	I1052	T1053	S1054	L1055	D1056	P1057	A1058	A1059	V1060	L1061	S1062	V1063	H1064	H1065	M1066	G1067	V1068	E1069	V1070	I1071	G1072	G1073	T1074	P1075	G1076	N1077	V1078	I1079	D1080	T1081	A1082	G1083	A1084	A1085	I1025	A1086	L1087	G1088	Y1089	D1029	L1091	A1092			
M1093	Q1094	E1095	F1096	L1097	L1098	Q1099	F1100	T1101	P1102	T1103	L1104	P1105	G1106	I1107	F1108	D1109	F1110	F1111	T1112	T1113	T1114	L1115	G1116	Q1117	P1118	P1119	V1120	S1124	F1125	T1126	I1127	P1130	P1131	V1134	L1135	L1136	N1137	M1138	P1139	P1140	P1141	R1142	Q1143	L1144	D1145	F1146	T1147	D1148	V1149	G1150	M1151	D1152	A1153	R1154	T1155	T1156					
C1157	D1158	P1159	Y1160	Y1161	Q1162	L1163	A1164	V1165	C1166	I1167	F1168	K1169	D1170	G1171	Q1172	V1173	V1174	R1175	V1176	M1177	P1178	E1179	K1180	A1181	S1182	V1183	V1184	T1185	N1186	A1187	P1188	M1189	R1190	L1191	L1192	V1195	L1196	D1197	L1198	A1199	H1202	V1203	L1204	L1205	Y1206	L1207	C1208	L1209	S1213	G1214	L1215	P1216	T1217	R1218	I1219	A1220					
F1221	P1222	I1223	V1224	D1225	I1226	V1227	A1228	I1229	A1230	R1233	T1235	P1236	V1237	R1238	A1239	S1240	L1241	R1242	Y1243	T1244	G1245	H1249	L1250	T1251	G1254	N1255	P1256	F1257	M1258	L1259	L1260	T1261	T1262	P1263	P1264	A1265	V1266	P1268	L1273	A1274	L1275	L1276	S1277	T1278	S1279	V1280	A1281	Q1283	L1284	P1285	T1286	Y1287									

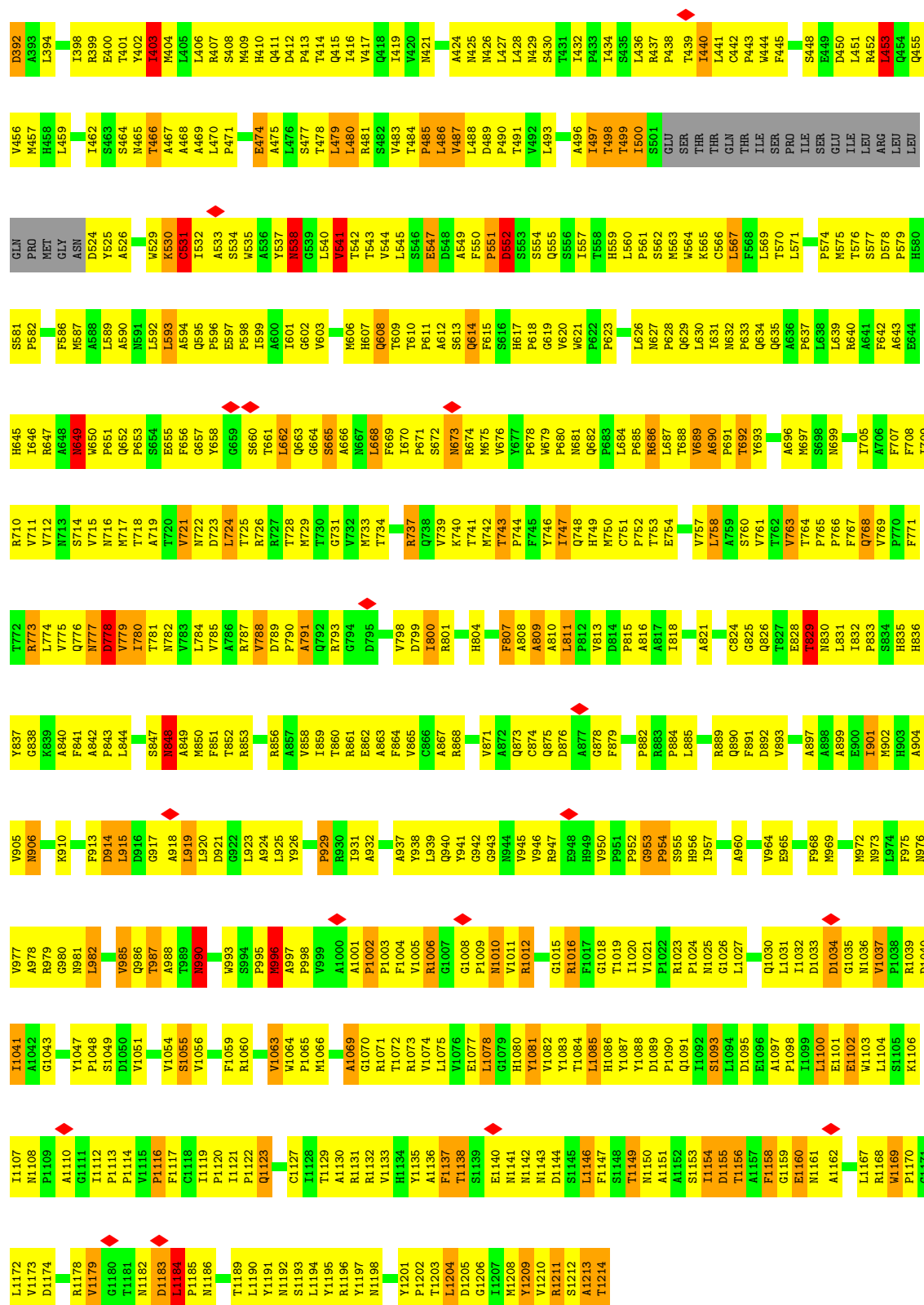
Chain X: 19% 47% 17% • 16%





• Molecule 6: VP3





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	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 II (4k x 4k)	Depositor
Maximum map value	134.413	Depositor
Minimum map value	-88.945	Depositor
Average map value	0.680	Depositor
Map value standard deviation	8.761	Depositor
Recommended contour level	9	Depositor
Map size (Å)	838.8, 838.8, 838.8	wwPDB
Map dimensions	900, 900, 900	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.932, 0.932, 0.932	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MYR

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	b	0.81	2/678 (0.3%)	1.50	8/922 (0.9%)
1	d	0.55	0/678	1.05	3/922 (0.3%)
1	f	0.55	0/678	1.39	16/922 (1.7%)
1	h	0.57	0/678	1.03	3/922 (0.3%)
1	j	0.56	0/678	1.08	11/922 (1.2%)
1	l	0.51	0/678	1.13	10/922 (1.1%)
1	n	0.53	0/678	1.01	3/922 (0.3%)
1	p	0.56	0/678	1.01	5/922 (0.5%)
1	r	0.51	0/678	1.10	7/922 (0.8%)
1	t	0.54	0/678	0.96	2/922 (0.2%)
2	A	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	C	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	E	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	G	0.89	2/286 (0.7%)	1.38	3/391 (0.8%)
2	I	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	K	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	M	0.89	2/286 (0.7%)	1.38	3/391 (0.8%)
2	O	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	Q	0.90	2/295 (0.7%)	1.53	6/405 (1.5%)
2	S	0.89	2/286 (0.7%)	1.38	3/391 (0.8%)
3	B	0.70	1/4601 (0.0%)	1.28	52/6295 (0.8%)
3	D	0.70	1/4601 (0.0%)	1.30	54/6295 (0.9%)
3	F	0.70	1/4601 (0.0%)	1.28	52/6295 (0.8%)
3	H	0.70	1/4601 (0.0%)	1.28	53/6295 (0.8%)
3	J	0.69	1/4601 (0.0%)	1.28	53/6295 (0.8%)
3	L	0.70	1/4601 (0.0%)	1.28	52/6295 (0.8%)
3	N	0.70	1/4601 (0.0%)	1.28	52/6295 (0.8%)
3	P	0.70	1/4601 (0.0%)	1.28	52/6295 (0.8%)
3	R	0.70	1/4601 (0.0%)	1.28	52/6295 (0.8%)
3	T	0.70	1/4601 (0.0%)	1.28	51/6295 (0.8%)
4	U	0.38	0/3233	0.93	16/4443 (0.4%)
4	V	0.41	0/3233	0.88	5/4443 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	W	0.38	0/10148	1.00	52/13935 (0.4%)
6	X	0.65	5/8078 (0.1%)	1.16	69/11071 (0.6%)
6	Y	0.45	1/9056 (0.0%)	1.04	52/12412 (0.4%)
All	All	0.62	38/89461 (0.0%)	1.19	836/122482 (0.7%)

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	b	0	4
1	d	0	3
1	f	0	2
1	h	0	2
1	j	0	2
1	l	0	2
1	n	0	3
1	p	0	3
1	r	0	2
1	t	0	2
3	B	0	1
3	D	0	1
3	F	0	1
3	H	0	1
3	J	0	1
3	L	0	1
3	N	0	1
3	P	0	1
3	R	0	1
3	T	0	1
6	X	0	3
6	Y	0	2
All	All	0	40

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	b	74	GLN	C-N	14.77	1.68	1.33
3	N	227	LEU	N-CA	7.64	1.52	1.45
3	H	227	LEU	N-CA	7.64	1.52	1.45
3	R	227	LEU	N-CA	7.63	1.52	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	227	LEU	N-CA	7.60	1.52	1.45

The worst 5 of 836 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	b	73	ARG	O-C-N	-31.64	90.78	121.79
3	D	51	VAL	N-CA-C	17.02	126.53	110.53
1	f	73	ARG	N-CA-C	13.44	125.93	111.28
6	X	526	ALA	N-CA-C	-11.80	98.50	111.36
5	W	63	PRO	N-CA-C	11.78	125.07	110.70

There are no chirality outliers.

5 of 40 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	b	43	CYS	Peptide
1	b	73	ARG	Mainchain,Peptide
1	b	75	PRO	Peptide
1	l	43	CYS	Peptide
1	l	75	PRO	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	b	666	0	660	204	0
1	d	666	0	660	172	0
1	f	666	0	657	151	0
1	h	666	0	655	167	0
1	j	666	0	659	188	0
1	l	666	0	656	194	0
1	n	666	0	658	170	0
1	p	666	0	659	224	0
1	r	666	0	657	171	0
1	t	666	0	659	230	0
2	A	291	0	277	57	0
2	C	291	0	277	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	291	0	277	80	0
2	G	284	0	267	58	0
2	I	291	0	277	84	0
2	K	291	0	277	81	0
2	M	284	0	267	60	0
2	O	291	0	277	78	0
2	Q	291	0	277	88	0
2	S	284	0	267	60	0
3	B	4508	0	4555	785	0
3	D	4508	0	4554	1045	0
3	F	4508	0	4554	1002	0
3	H	4508	0	4554	1005	0
3	J	4508	0	4553	1049	0
3	L	4508	0	4555	1031	0
3	N	4508	0	4555	1023	0
3	P	4508	0	4555	1083	0
3	R	4508	0	4554	1006	0
3	T	4508	0	4555	1053	0
4	U	3138	0	3061	471	0
4	V	3138	0	3061	181	0
5	W	9882	0	9821	1088	0
6	X	7873	0	7851	1319	0
6	Y	8835	0	8748	1111	0
7	A	15	0	27	27	0
7	C	15	0	27	31	0
7	E	15	0	27	27	0
7	G	15	0	27	28	0
7	I	15	0	27	29	0
7	K	15	0	27	27	0
7	M	15	0	27	26	0
7	O	15	0	27	28	0
7	Q	15	0	27	27	0
7	S	15	0	27	30	0
All	All	87645	0	87676	14002	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 80.

The worst 5 of 14002 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:p:8:GLN:HG2	3:R:302:GLU:CG	1.26	1.59
1:h:23:THR:CB	3:H:323:SER:HA	1.11	1.58
1:b:45:ARG:CG	3:B:400:ALA:HA	1.27	1.57
1:t:59:HIS:HB3	3:T:398:SER:CB	1.32	1.56
1:p:59:HIS:CB	3:P:398:SER:HA	1.35	1.55

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	b	84/276 (30%)	70 (83%)	9 (11%)	5 (6%)	1	9
1	d	84/276 (30%)	70 (83%)	11 (13%)	3 (4%)	2	17
1	f	84/276 (30%)	68 (81%)	12 (14%)	4 (5%)	2	12
1	h	84/276 (30%)	71 (84%)	10 (12%)	3 (4%)	2	17
1	j	84/276 (30%)	72 (86%)	9 (11%)	3 (4%)	2	17
1	l	84/276 (30%)	70 (83%)	13 (16%)	1 (1%)	10	37
1	n	84/276 (30%)	69 (82%)	12 (14%)	3 (4%)	2	17
1	p	84/276 (30%)	74 (88%)	7 (8%)	3 (4%)	2	17
1	r	84/276 (30%)	71 (84%)	11 (13%)	2 (2%)	4	24
1	t	84/276 (30%)	72 (86%)	10 (12%)	2 (2%)	4	24
2	A	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1
2	C	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1
2	E	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1
2	G	37/42 (88%)	24 (65%)	8 (22%)	5 (14%)	0	1
2	I	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1
2	K	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	M	37/42 (88%)	24 (65%)	8 (22%)	5 (14%)	0	1
2	O	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1
2	Q	39/42 (93%)	25 (64%)	9 (23%)	5 (13%)	0	1
2	S	37/42 (88%)	24 (65%)	8 (22%)	5 (14%)	0	1
3	B	602/606 (99%)	407 (68%)	134 (22%)	61 (10%)	0	3
3	D	602/606 (99%)	416 (69%)	129 (21%)	57 (10%)	0	3
3	F	602/606 (99%)	408 (68%)	133 (22%)	61 (10%)	0	3
3	H	602/606 (99%)	409 (68%)	132 (22%)	61 (10%)	0	3
3	J	602/606 (99%)	411 (68%)	132 (22%)	59 (10%)	0	3
3	L	602/606 (99%)	409 (68%)	132 (22%)	61 (10%)	0	3
3	N	602/606 (99%)	408 (68%)	133 (22%)	61 (10%)	0	3
3	P	602/606 (99%)	410 (68%)	132 (22%)	60 (10%)	0	3
3	R	602/606 (99%)	406 (67%)	135 (22%)	61 (10%)	0	3
3	T	602/606 (99%)	406 (67%)	135 (22%)	61 (10%)	0	3
4	U	409/412 (99%)	283 (69%)	81 (20%)	45 (11%)	0	2
4	V	409/412 (99%)	330 (81%)	60 (15%)	19 (5%)	2	13
5	W	1276/1299 (98%)	1063 (83%)	173 (14%)	40 (3%)	3	20
6	X	1012/1214 (83%)	714 (71%)	219 (22%)	79 (8%)	1	5
6	Y	1146/1214 (94%)	860 (75%)	204 (18%)	82 (7%)	1	6
All	All	11496/13791 (83%)	8294 (72%)	2255 (20%)	947 (8%)	1	5

5 of 947 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	l	19	ALA
1	b	62	VAL
1	b	75	PRO
1	f	75	PRO
1	d	22	LEU

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	b	72/228 (32%)	66 (92%)	6 (8%)	10	34
1	d	72/228 (32%)	68 (94%)	4 (6%)	19	47
1	f	72/228 (32%)	69 (96%)	3 (4%)	26	55
1	h	72/228 (32%)	66 (92%)	6 (8%)	10	34
1	j	72/228 (32%)	68 (94%)	4 (6%)	19	47
1	l	72/228 (32%)	67 (93%)	5 (7%)	14	41
1	n	72/228 (32%)	69 (96%)	3 (4%)	26	55
1	p	72/228 (32%)	67 (93%)	5 (7%)	14	41
1	r	72/228 (32%)	67 (93%)	5 (7%)	14	41
1	t	72/228 (32%)	69 (96%)	3 (4%)	26	55
2	A	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	C	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	E	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	G	32/35 (91%)	23 (72%)	9 (28%)	0	2
2	I	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	K	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	M	32/35 (91%)	23 (72%)	9 (28%)	0	2
2	O	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	Q	34/35 (97%)	25 (74%)	9 (26%)	0	2
2	S	32/35 (91%)	23 (72%)	9 (28%)	0	2
3	B	499/501 (100%)	412 (83%)	87 (17%)	2	9
3	D	499/501 (100%)	410 (82%)	89 (18%)	2	8
3	F	499/501 (100%)	413 (83%)	86 (17%)	2	10
3	H	499/501 (100%)	413 (83%)	86 (17%)	2	10
3	J	499/501 (100%)	410 (82%)	89 (18%)	2	8
3	L	499/501 (100%)	412 (83%)	87 (17%)	2	9
3	N	499/501 (100%)	410 (82%)	89 (18%)	2	8
3	P	499/501 (100%)	410 (82%)	89 (18%)	2	8
3	R	499/501 (100%)	412 (83%)	87 (17%)	2	9
3	T	499/501 (100%)	410 (82%)	89 (18%)	2	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	U	325/326 (100%)	305 (94%)	20 (6%)	16	45
4	V	325/326 (100%)	306 (94%)	19 (6%)	18	47
5	W	1082/1092 (99%)	979 (90%)	103 (10%)	8	29
6	X	869/1030 (84%)	726 (84%)	143 (16%)	2	11
6	Y	976/1030 (95%)	865 (89%)	111 (11%)	5	21
All	All	9621/11444 (84%)	8213 (85%)	1408 (15%)	5	14

5 of 1408 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	T	51	VAL
5	W	1146	PHE
3	T	225	THR
3	T	48	TRP
4	V	124	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 433 such sidechains are listed below:

Mol	Chain	Res	Type
3	R	312	ASN
4	U	251	ASN
6	Y	356	ASN
3	R	453	ASN
3	T	418	ASN

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

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	MYR	A	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	C	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	E	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	O	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	S	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	I	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	M	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	G	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	K	101	2	13,14,15	0.44	0	12,13,15	0.49	0
7	MYR	Q	101	2	13,14,15	0.45	0	12,13,15	0.49	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MYR	A	101	2	-	8/12/12/13	-
7	MYR	C	101	2	-	8/12/12/13	-
7	MYR	E	101	2	-	8/12/12/13	-
7	MYR	O	101	2	-	8/12/12/13	-
7	MYR	S	101	2	-	8/12/12/13	-
7	MYR	I	101	2	-	8/12/12/13	-
7	MYR	M	101	2	-	8/12/12/13	-
7	MYR	G	101	2	-	8/12/12/13	-
7	MYR	K	101	2	-	8/12/12/13	-
7	MYR	Q	101	2	-	8/12/12/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 80 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	101	MYR	C3-C4-C5-C6
7	K	101	MYR	C3-C4-C5-C6
7	Q	101	MYR	C3-C4-C5-C6
7	A	101	MYR	C3-C4-C5-C6
7	C	101	MYR	C3-C4-C5-C6

There are no ring outliers.

10 monomers are involved in 280 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	101	MYR	27	0
7	C	101	MYR	31	0
7	E	101	MYR	27	0
7	O	101	MYR	28	0
7	S	101	MYR	30	0
7	I	101	MYR	29	0
7	M	101	MYR	26	0
7	G	101	MYR	28	0
7	K	101	MYR	27	0
7	Q	101	MYR	27	0

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	b	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	b	74:GLN	C	75:PRO	N	1.68

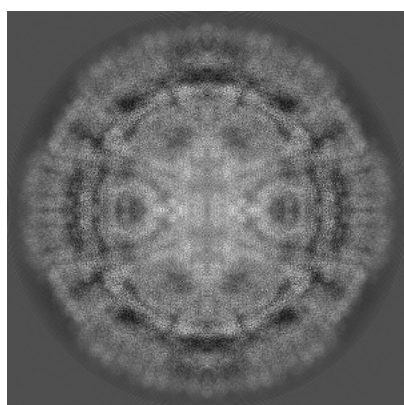
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6969. These allow visual inspection of the internal detail of the map and identification of artifacts.

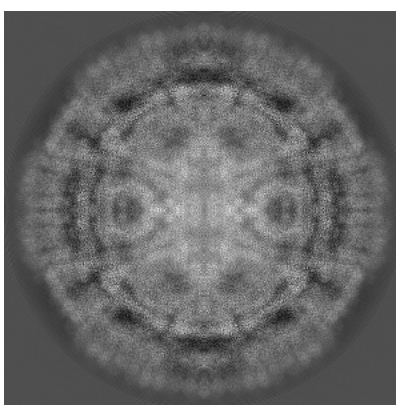
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

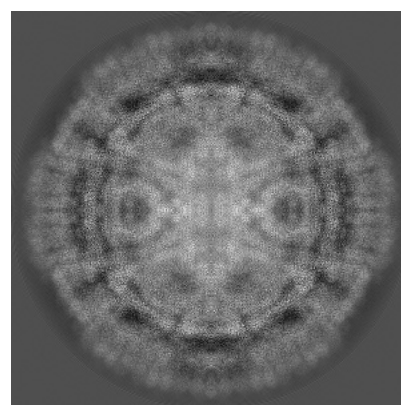
6.1.1 Primary map



X



Y

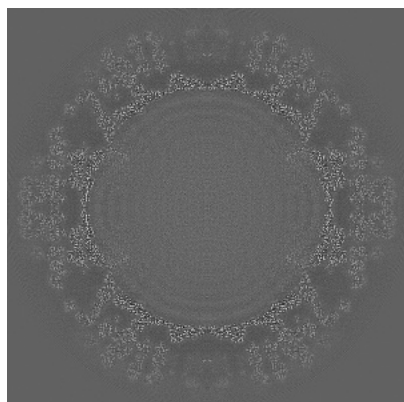


Z

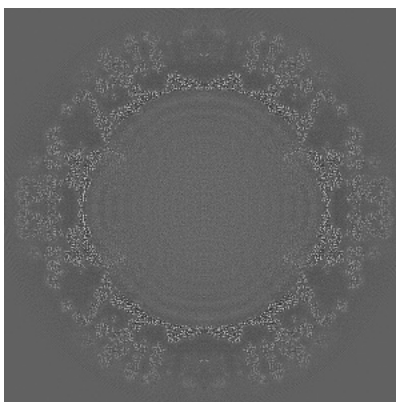
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

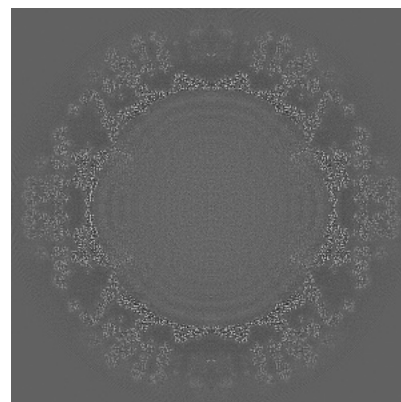
6.2.1 Primary map



X Index: 450



Y Index: 450

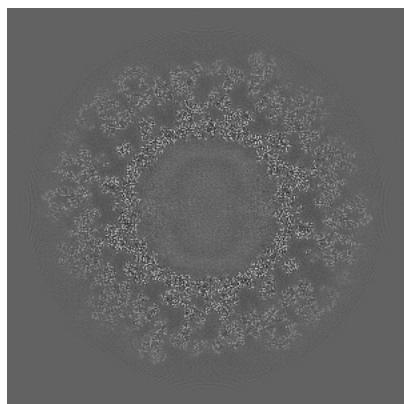


Z Index: 450

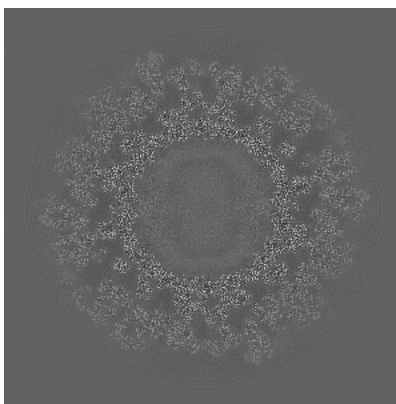
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

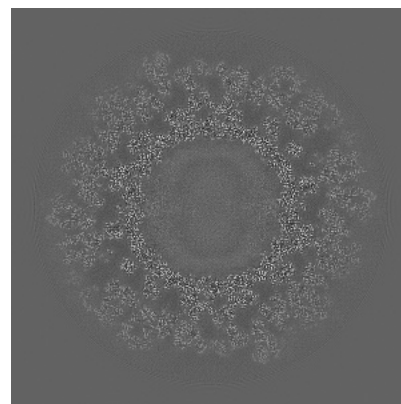
6.3.1 Primary map



X Index: 241



Y Index: 659

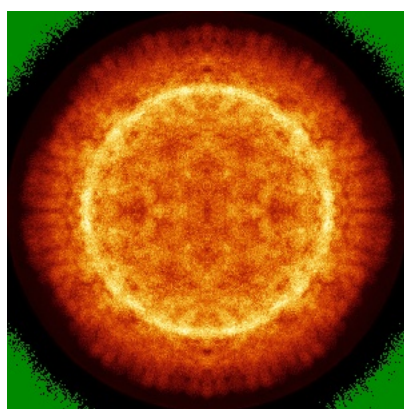


Z Index: 659

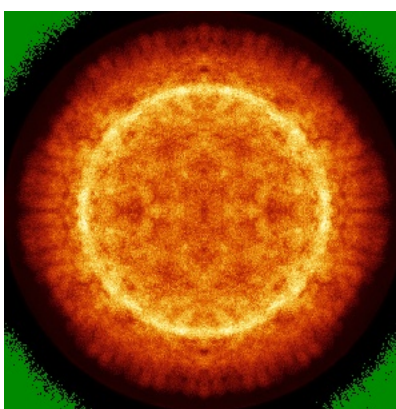
The images above show the largest variance slices of the map in three orthogonal directions.

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

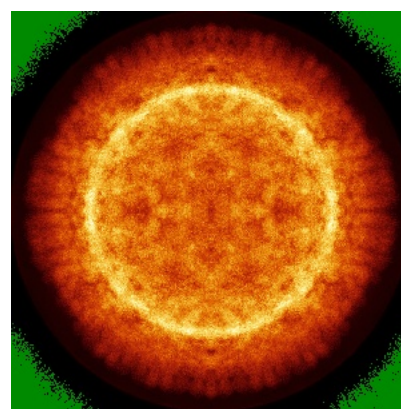
6.4.1 Primary map



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](#)

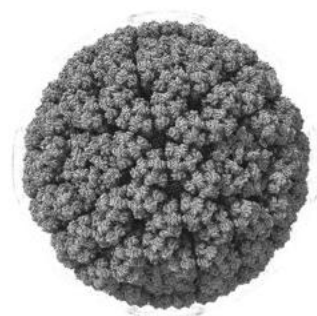
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 9.0. 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 shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

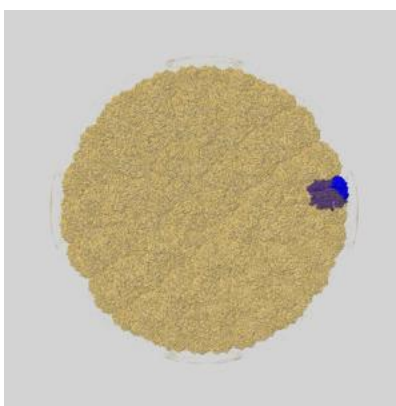
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

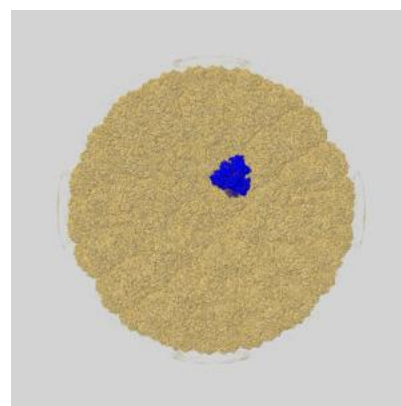
6.6.1 emd_6969_msk_1.map [i](#)



X



Y

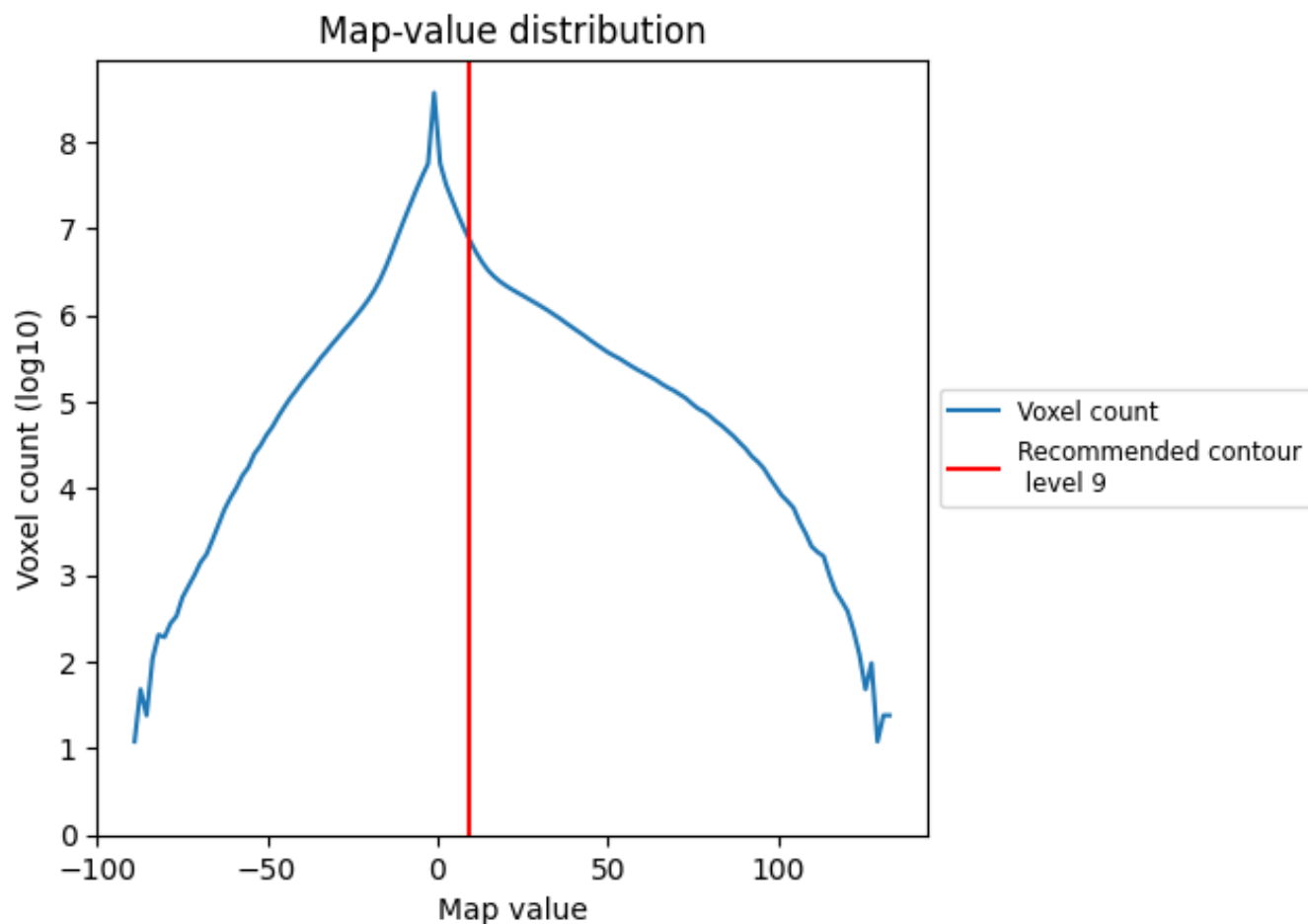


Z

7 Map analysis [i](#)

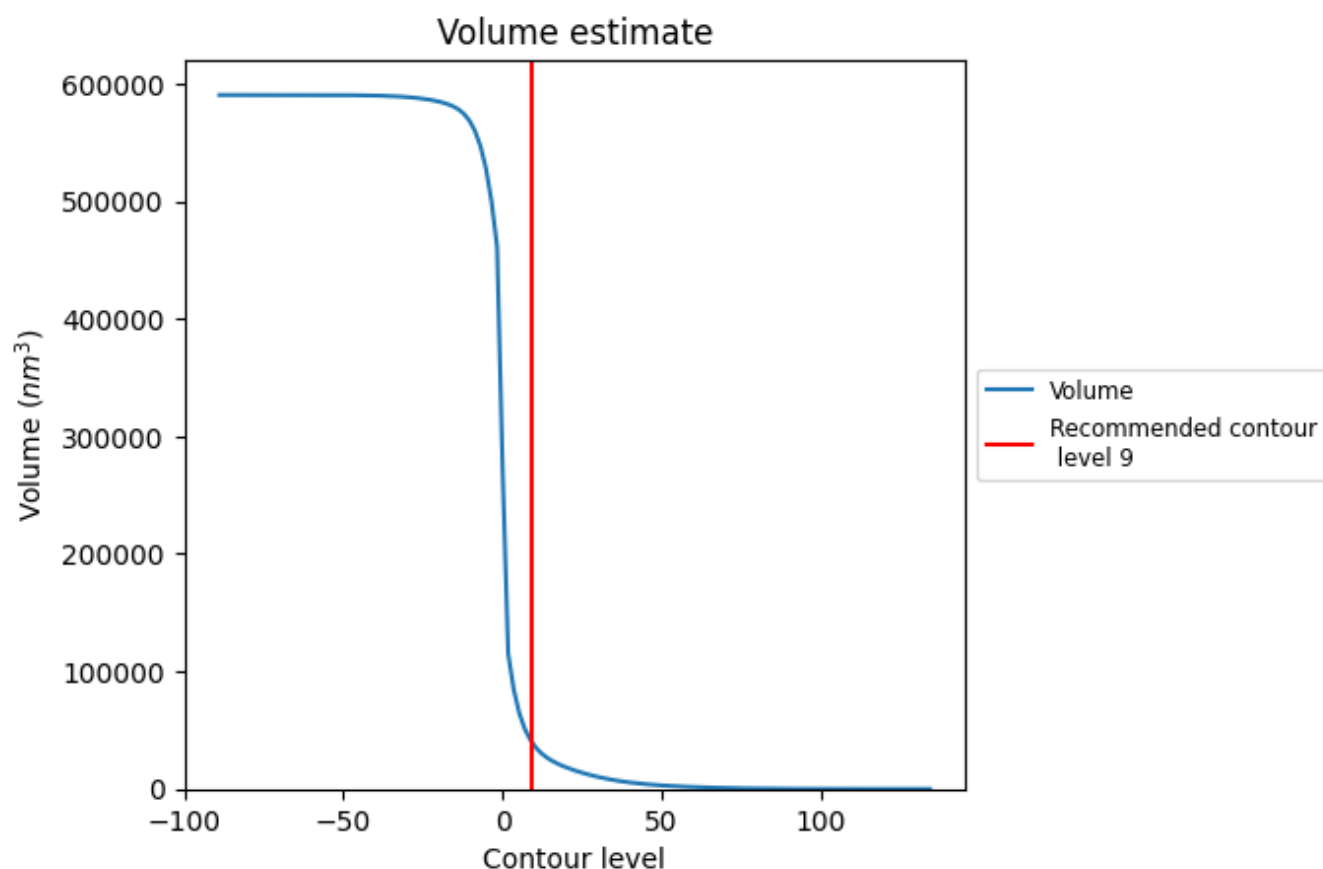
This section contains the results of statistical analysis of the map.

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.

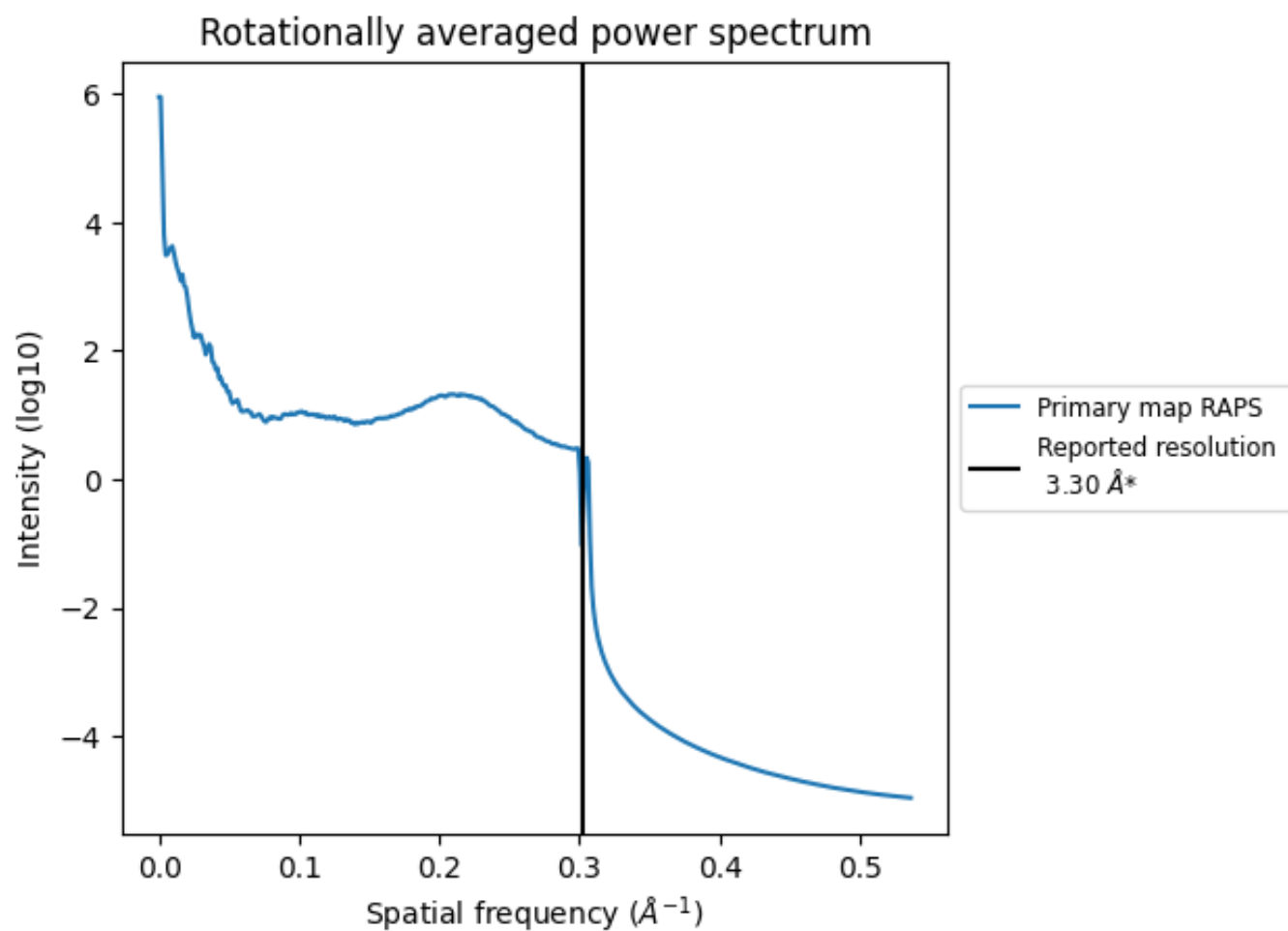
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 40818 nm³; this corresponds to an approximate mass of 36872 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 0.303 Å⁻¹

8 Fourier-Shell correlation

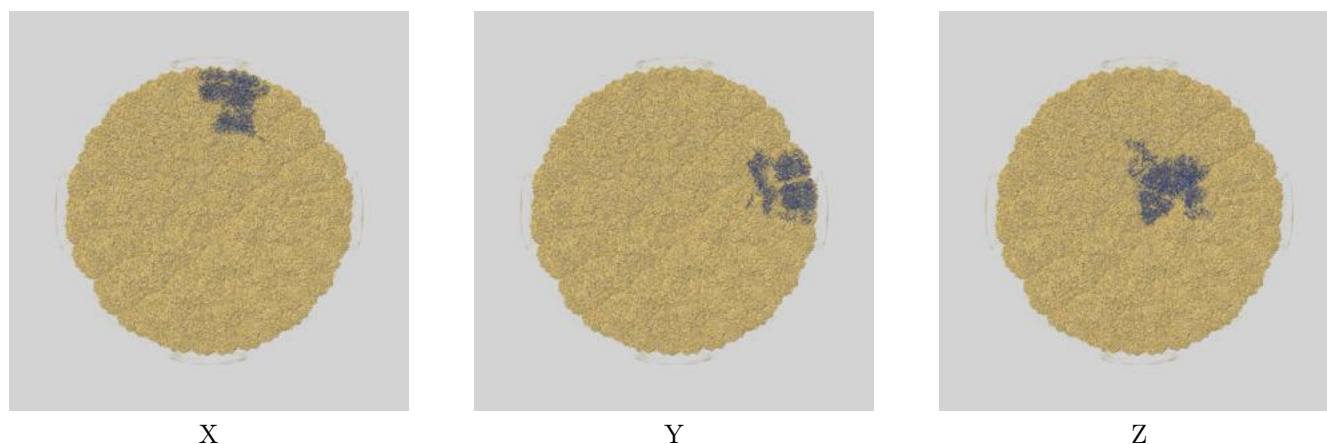
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

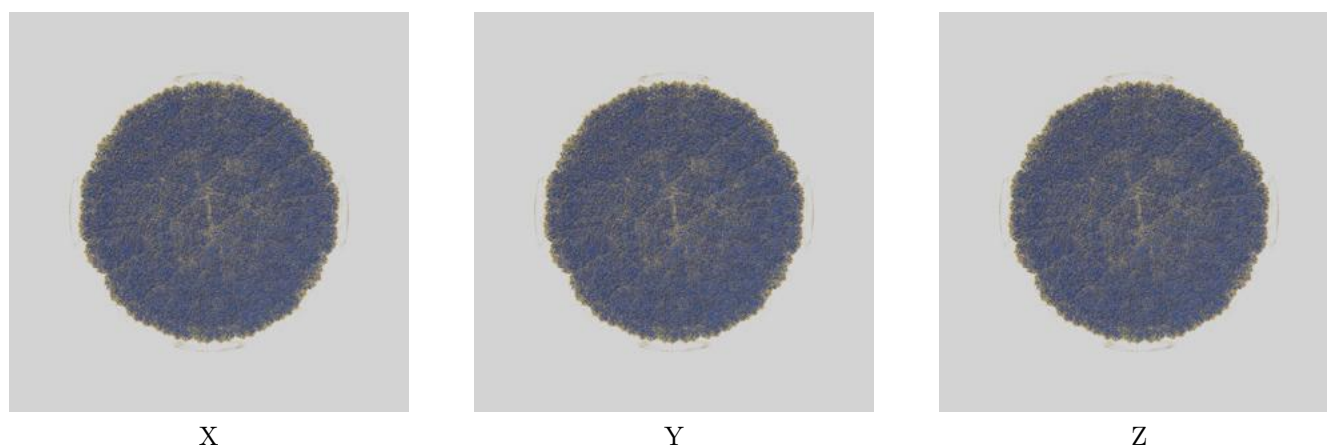
This section contains information regarding the fit between EMDB map EMD-6969 and PDB model 5ZVT. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

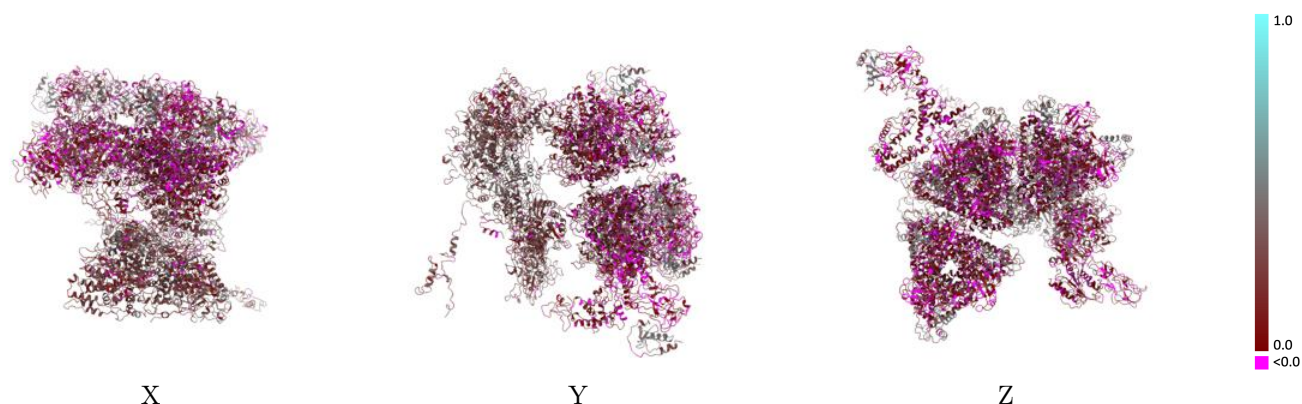


9.1.2 Map-model assembly overlay [i](#)



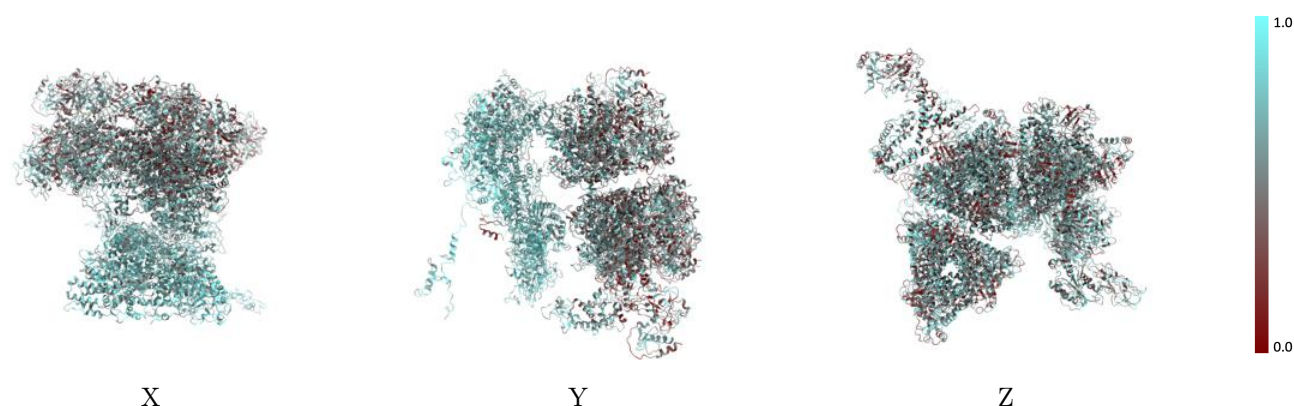
The images above show the 3D surface view of the map at the recommended contour level 9.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



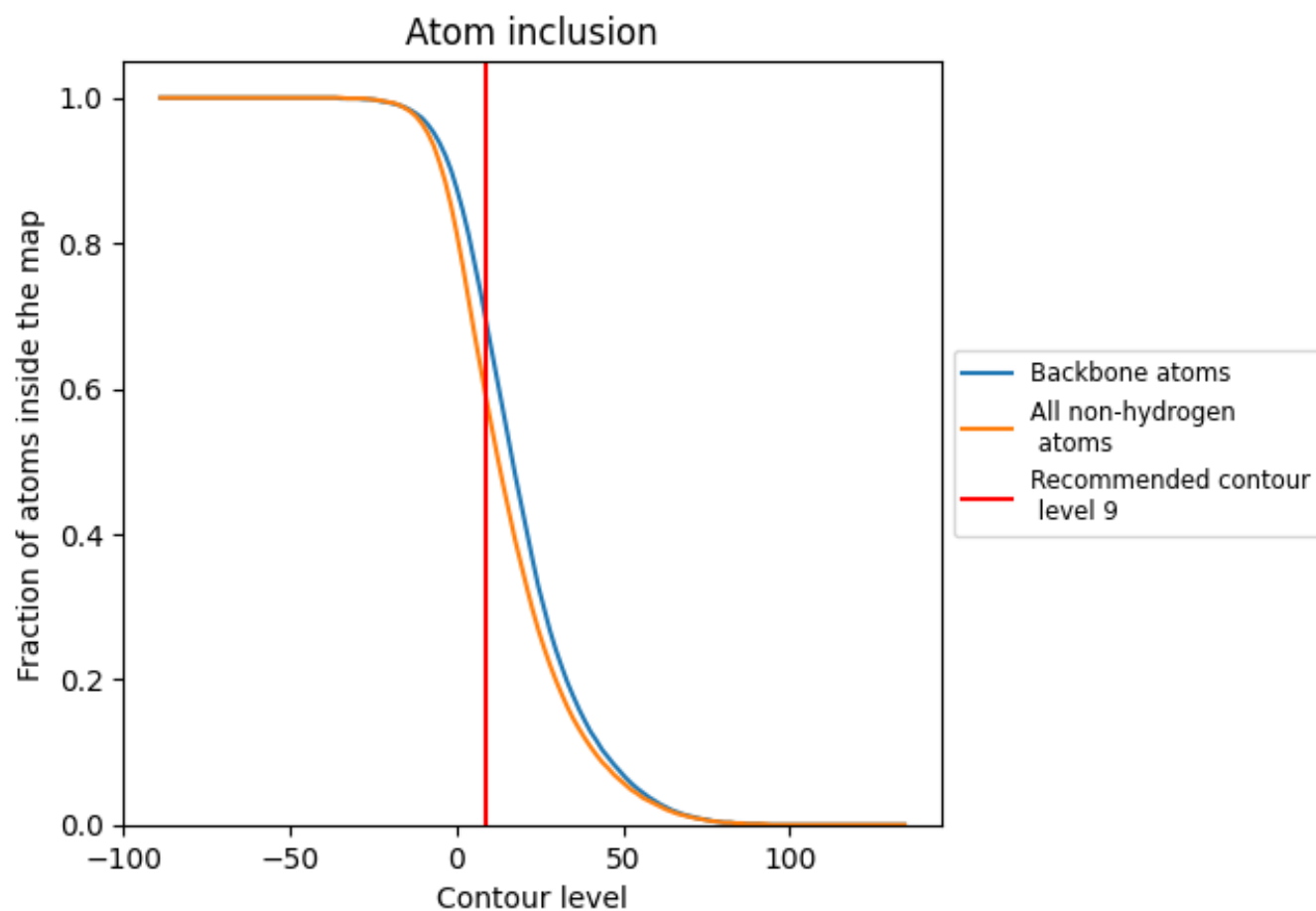
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% 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 (9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5820	 0.1950
A	 0.5020	 0.1370
B	 0.4820	 0.1040
C	 0.5180	 0.1540
D	 0.5200	 0.1290
E	 0.5180	 0.1500
F	 0.5270	 0.1390
G	 0.5300	 0.1670
H	 0.5220	 0.1340
I	 0.5050	 0.1360
J	 0.5110	 0.1220
K	 0.5280	 0.1550
L	 0.5070	 0.1240
M	 0.4800	 0.1230
N	 0.5110	 0.1200
O	 0.5340	 0.1600
P	 0.5200	 0.1270
Q	 0.5210	 0.1220
R	 0.5070	 0.1210
S	 0.5600	 0.1760
T	 0.5240	 0.1310
U	 0.6810	 0.2370
V	 0.7020	 0.2490
W	 0.5820	 0.1600
X	 0.7510	 0.3170
Y	 0.7450	 0.3150
b	 0.5450	 0.3850
d	 0.6160	 0.3980
f	 0.5960	 0.4170
h	 0.5810	 0.4070
j	 0.5810	 0.4010
l	 0.5640	 0.3930
n	 0.6380	 0.4120
p	 0.5380	 0.4020
r	 0.5670	 0.4080
t	 0.4410	 0.3620

