



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 04:48 AM UTC

PDB ID : 8TEU / pdb_00008teu
EMDB ID : EMD-41202
Title : Human cytomegalovirus portal vertex, non-infectious enveloped particle (NIEP) configuration 2 - inverted (NC2-inv)
Authors : Jih, J.; Liu, Y.T.; Liu, W.; Zhou, H.
Deposited on : 2023-07-07
Resolution : 4.01 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:

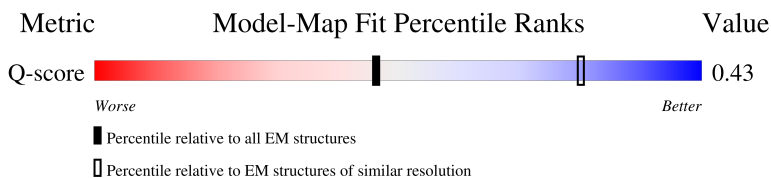
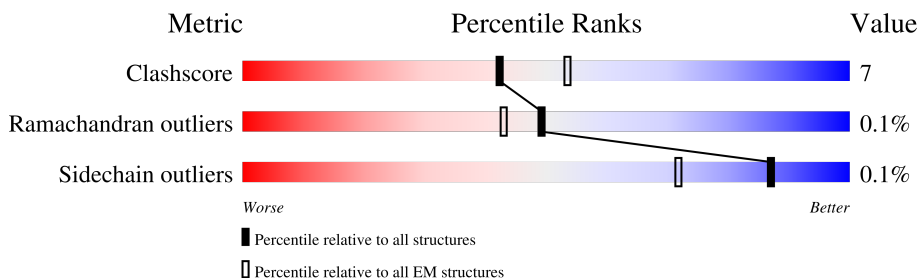
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.01 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	6765 (3.51 - 4.51)

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	A	2241	<p>32% (red), 23% (orange), 10% (yellow), 68% (grey)</p>
1	C	2241	<p>98% (grey)</p>
2	E	642	<p>76% (red), 52% (orange), 24% (yellow), 23% (grey)</p>
2	F	642	<p>13% (red), 11% (orange), 87% (grey)</p>

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Mol	Chain	Length	Quality of chain
3	G	594	
4	H	1370	
4	I	1370	
4	J	1370	
4	K	1370	
4	L	1370	
4	M	1370	
5	N	75	
5	O	75	
5	P	75	
5	Q	75	
5	R	75	
5	S	75	
6	T	290	
6	W	290	
7	U	306	
7	V	306	
7	X	306	
7	Y	306	
8	Z	1048	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 96759 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 Large tegument protein deneedylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	722	Total	C	N	O	S	0	0
			5830	3723	1027	1058	22		
1	C	40	Total	C	N	O	S	0	0
			332	213	60	58	1		

- Molecule 2 is a protein called Capsid vertex component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	495	Total	C	N	O	S	0	0
			3992	2559	706	715	12		
2	F	85	Total	C	N	O	S	0	0
			710	442	138	126	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	G	471	Total	C	N	O	S	0	0
			3862	2416	740	692	14		

- Molecule 4 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	H	1309	Total	C	N	O	S	0	0
			10391	6619	1800	1911	61		
4	I	1350	Total	C	N	O	S	0	0
			10693	6809	1853	1970	61		
4	J	1317	Total	C	N	O	S	0	0
			10433	6641	1814	1919	59		
4	K	1296	Total	C	N	O	S	0	0
			10259	6529	1787	1884	59		
4	L	1350	Total	C	N	O	S	0	0
			10693	6809	1853	1970	61		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	M	1350	10693	6809	1853	1970	61	0	0

- Molecule 5 is a protein called Small capsomere-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	N	63	513	321	97	91	4	0	0
5	O	63	513	321	97	91	4	0	0
5	P	63	513	321	97	91	4	0	0
5	Q	63	513	321	97	91	4	0	0
5	R	63	513	321	97	91	4	0	0
5	S	63	513	321	97	91	4	0	0

- Molecule 6 is a protein called Triplex capsid protein 1.

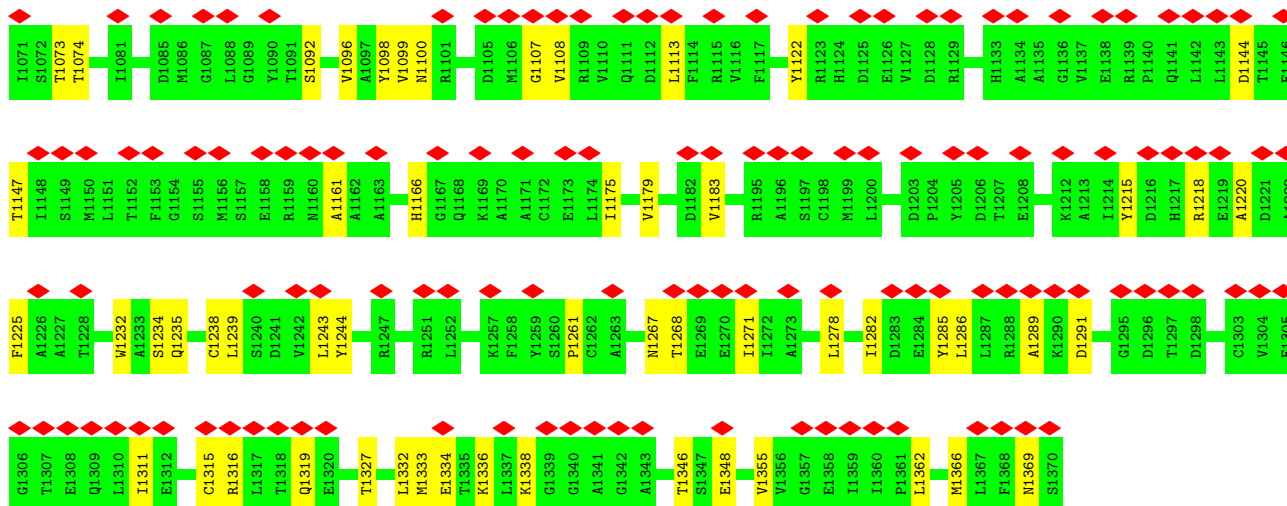
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	T	242	1939	1248	338	342	11	0	0
6	W	290	2325	1485	411	417	12	0	0

- Molecule 7 is a protein called Triplex capsid protein 2.

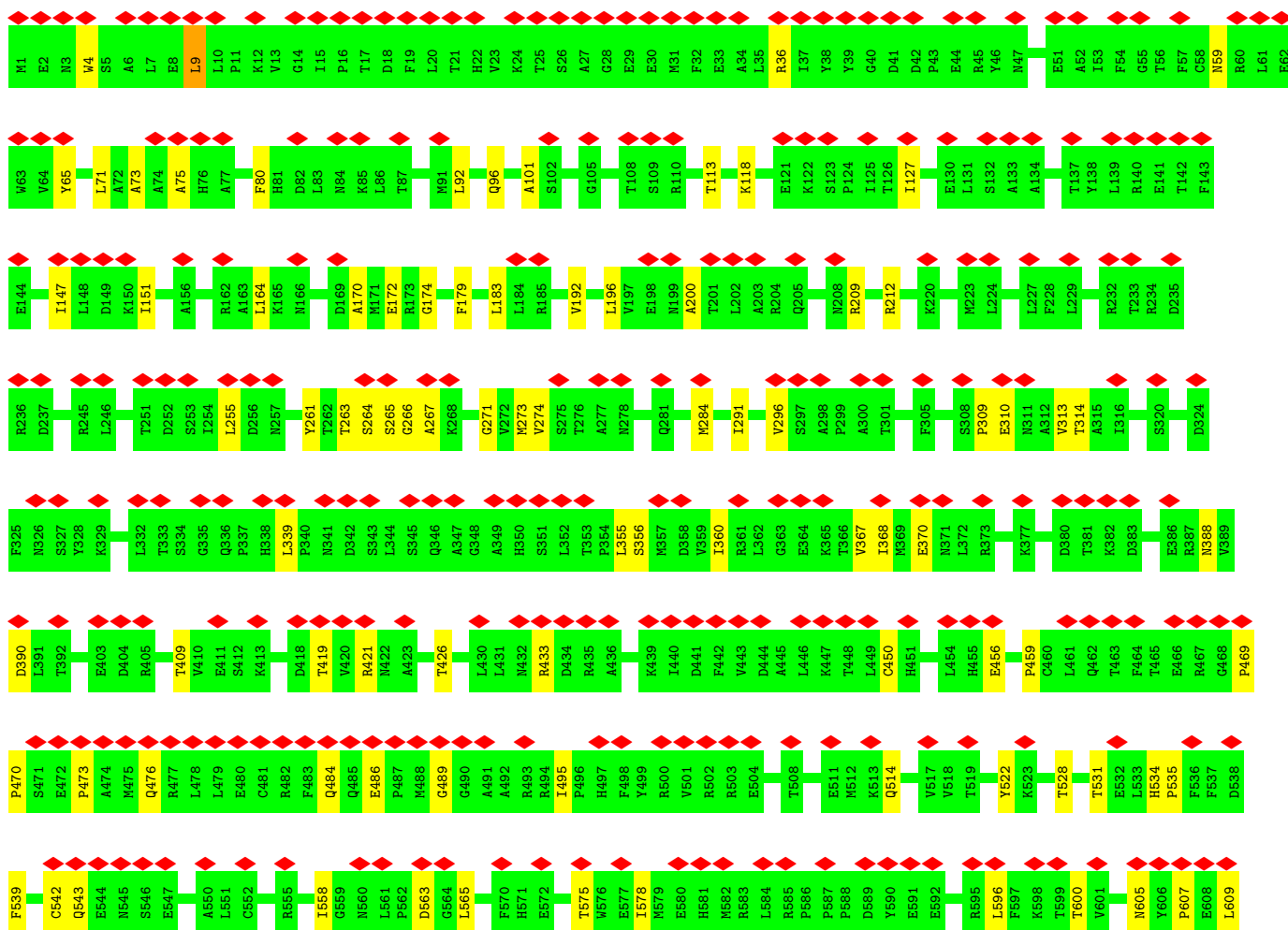
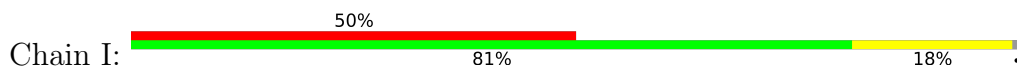
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	U	292	2317	1489	399	411	18	0	0
7	V	288	2292	1471	397	407	17	0	0
7	X	295	2334	1501	402	412	19	0	0
7	Y	285	2266	1456	387	405	18	0	0

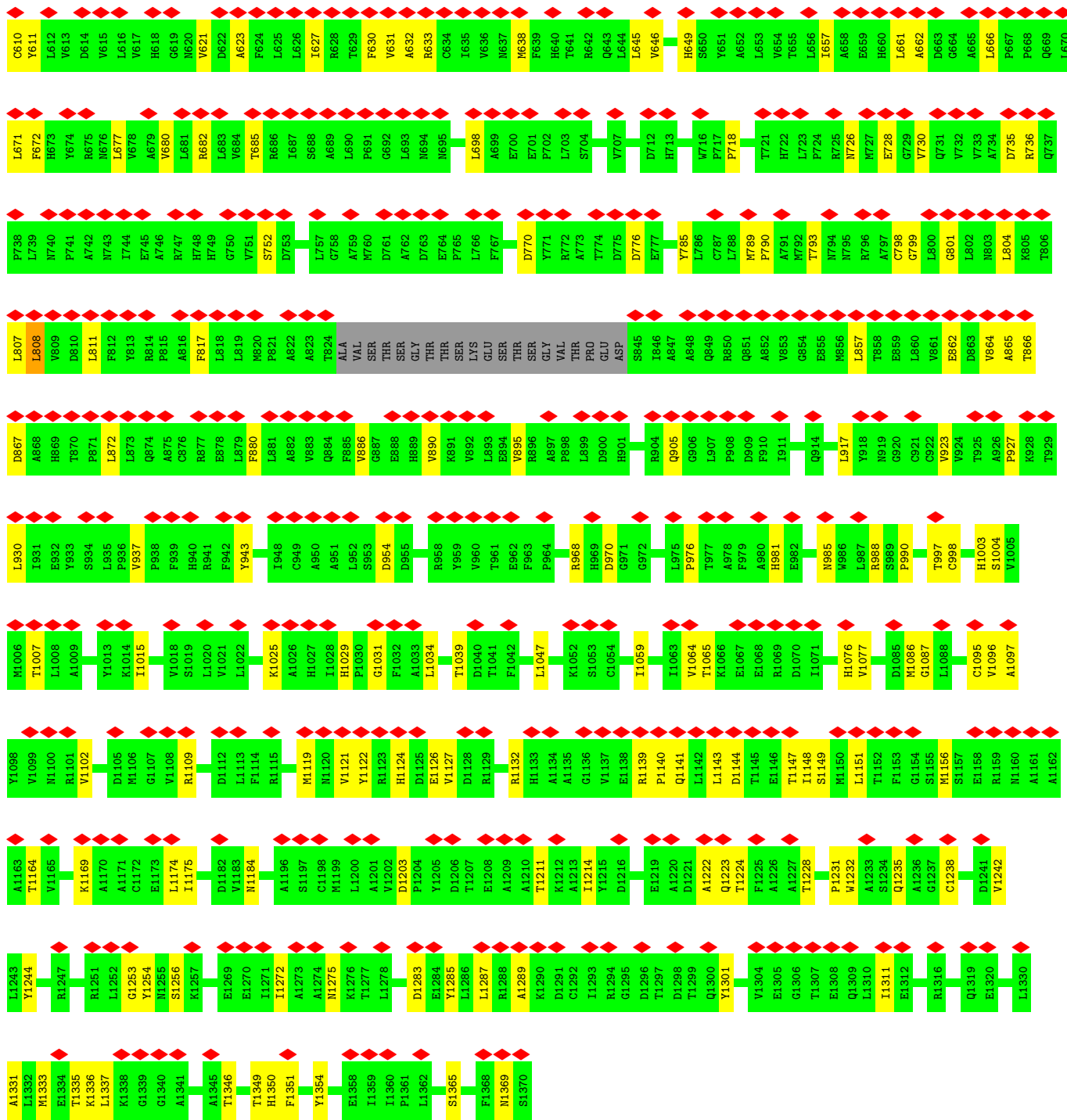
- Molecule 8 is a protein called Large structural phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	Z	284	2320	1463	425	420	12	0	0

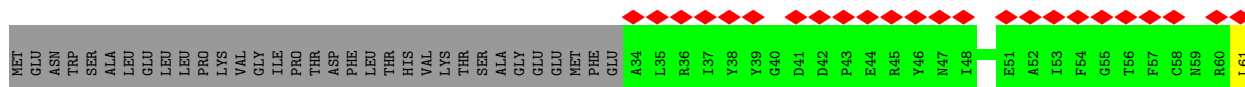
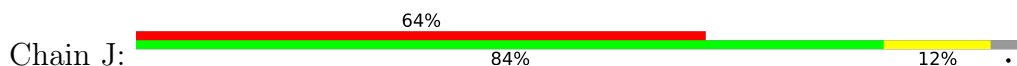


• Molecule 4: Major capsid protein

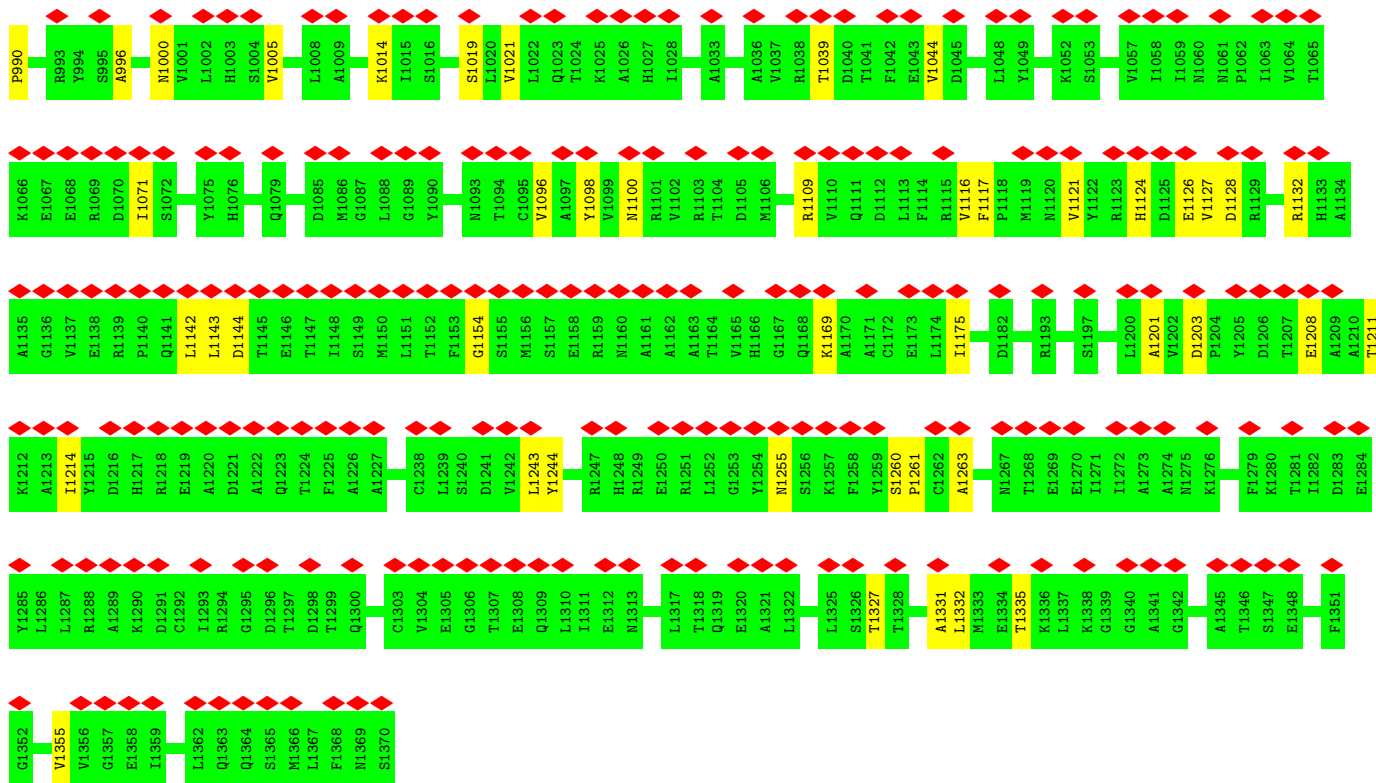




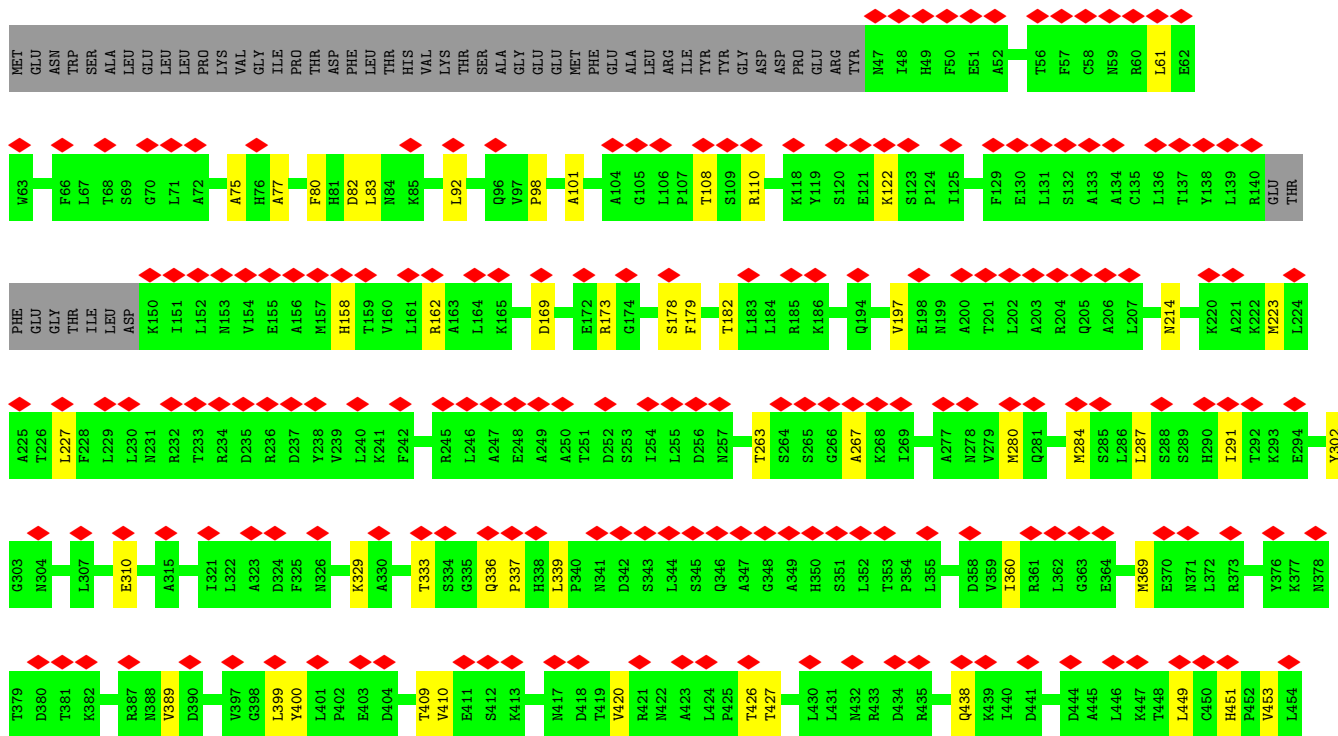
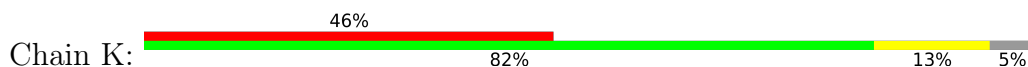
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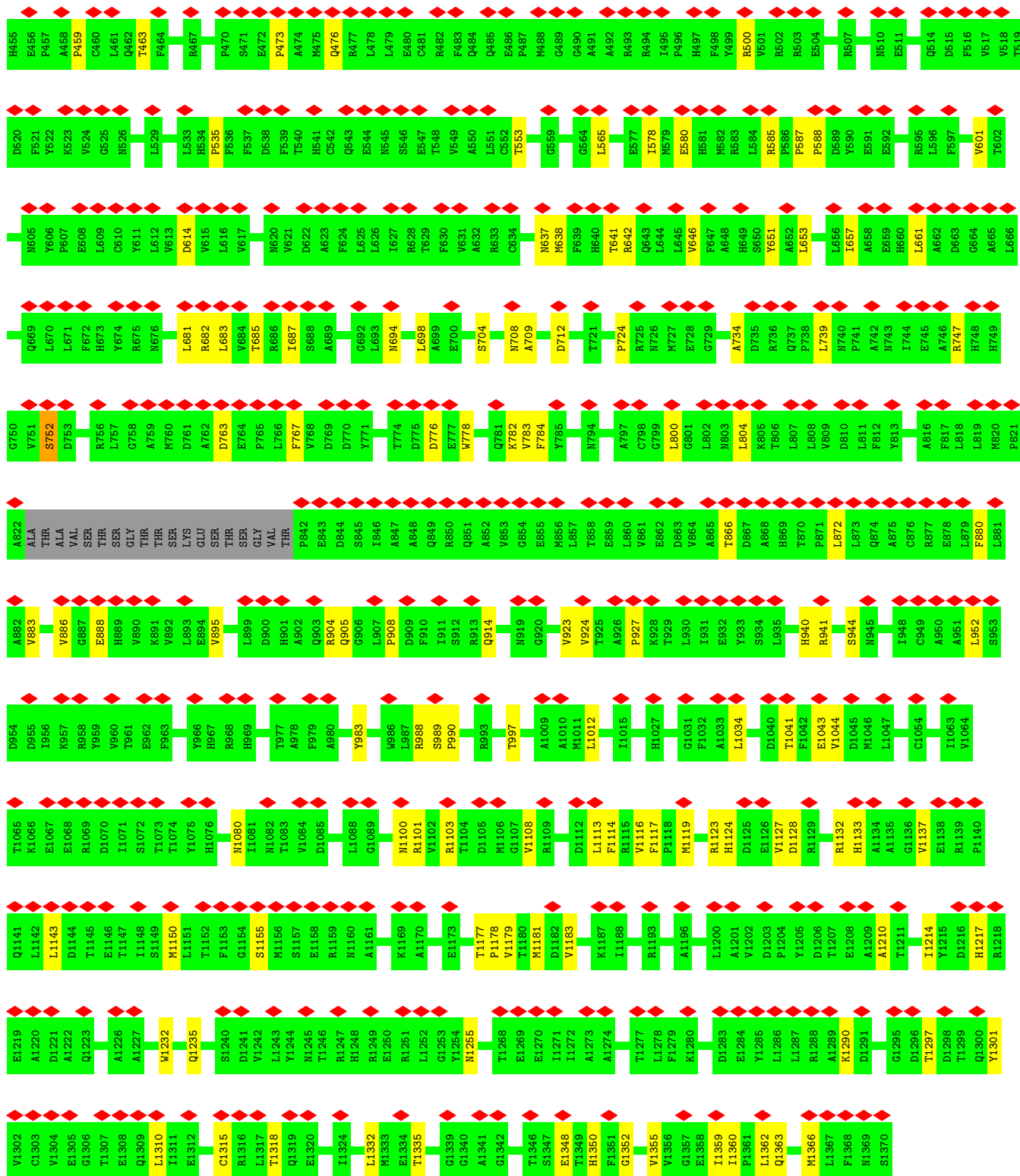


E62	W63	V64	Y65	F66	S69	G70	A74	H75	A77	H81	D82	L83	N84	K88	G89	L92	F93	H94	Y95	Q96	A101	A104	G105	L106	P107	T108	S109	R110	Q111	I114	M115	V116	V117	K118	E121	K122	S123	F124	F129	E130	L131	S132	A133	A134	L135	L136	T137	Y138																																																				
L139	R140	E141	T142	F143	E144	G145	T146	L147	H148	D149	K150	I151	L152	M153	V154	E155	A156	M157	H158	T159	V160	L161	R162	H94	A163	L164	K165	M166	T167	A168	D169	L243	L244	A170	M171	E172	R173	G174	L175	L176	H177	S178	F179	L180	Q181	T182	L183	L184	R185	K186	Q194	E198	M199	S265	A200	T201	G266	A267	L202	K268	M273	V274																																						
R209	Q211	Q212	I215	L216	Q217	S218	Q219	K220	A221	K222	M223	L224	A225	L229	L230	N231	R232	R233	R234	D235	R236	D237	Y238	V239	K241	F242	L243	L244	R245	L246	A247	E248	A249	A250	T251	S252	S253	L254	L255	L256	D256	K257	P258	T259	T260	T263	S264	N199	S265	A200	G266	A267	L202	K268	M273	V274																																												
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L431	N432	R433	D434	R435	A436	V437	Q438	K439	I440	D441	F442	V443	D444	A445	L446	K447	T448	L449	C450	H451	L454	H455	E456	P459	C460	Q462	T463	F464	T465	E466	R467	P469	P470	S471	E472	P473	A474	M475	Q476	R477	L478	L479	E480	C481	R482	F483	Q484	Q485	A486	P487	M488	G489	G490	A491	A492																																													
R493	R494	L495	P496	H497	F498	Y499	R500	V501	R502	R603	E504	V505	P506	R507	T508	V509	N510	E511	M512	K513	Q514	D515	F516	V517	V518	T519	D520	F521	Y522	K523	V524	L529	Y530	T531	E532	F536	F537	D538	F539	T540	H541	C542	O543	E544	M545	S546	E547	T548	V549	H549	H618	G619	L551	C552	R555	L556	F624	L625																																										
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H747	H748	H749	G750	V751	S752	D753	V754	P755	R756	L757	G758	A759	M760	D761	A762	D763	E764	F765	L766	F767	V768	D769	D770	Y771	R772	A773	T774	D775	D776	E777	H778	T779	L780	K782	V783	F784	Y785	Q849	L786	C787	L788	M789	F790	M792	T793	N794	R795	R796	A797	C798	G799	L800	G801	L802	M803	L804	K805	T806																																										
L807	L808	V809	D810	L811	F812	Y813	R814	P815	A816	F817	L818	L819	M820	P821	A822	A823	T824	ALA	VAL	SER	THR	SER	THR	GLY	THR	LYS	GLU	SER	THR	SER	GLY	VAL	THR	PRO	GLU	ASP	S845	I846	A847	A848	Q849	R850	Q851	A852	R853	G854	E855	M856	L857	T858	F859	V861	E862	D863	V864	A865	G866	C867	A868	C869	C870	N871	L872	R873	L874	I875	L876	L877	L878	L879	L880	L881	L882	L883	L884	A885	T886																							
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• Molecule 4: Major capsid protein





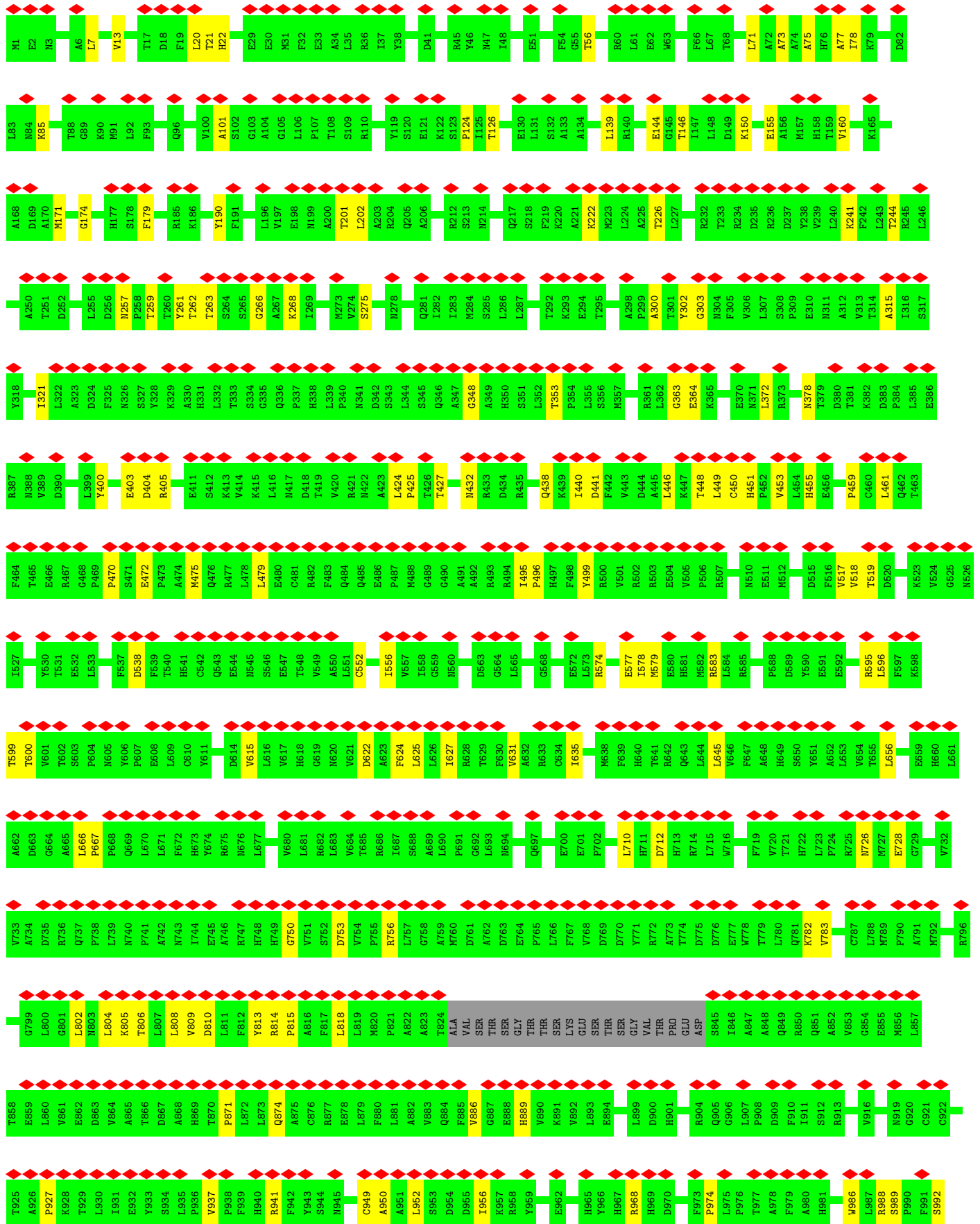
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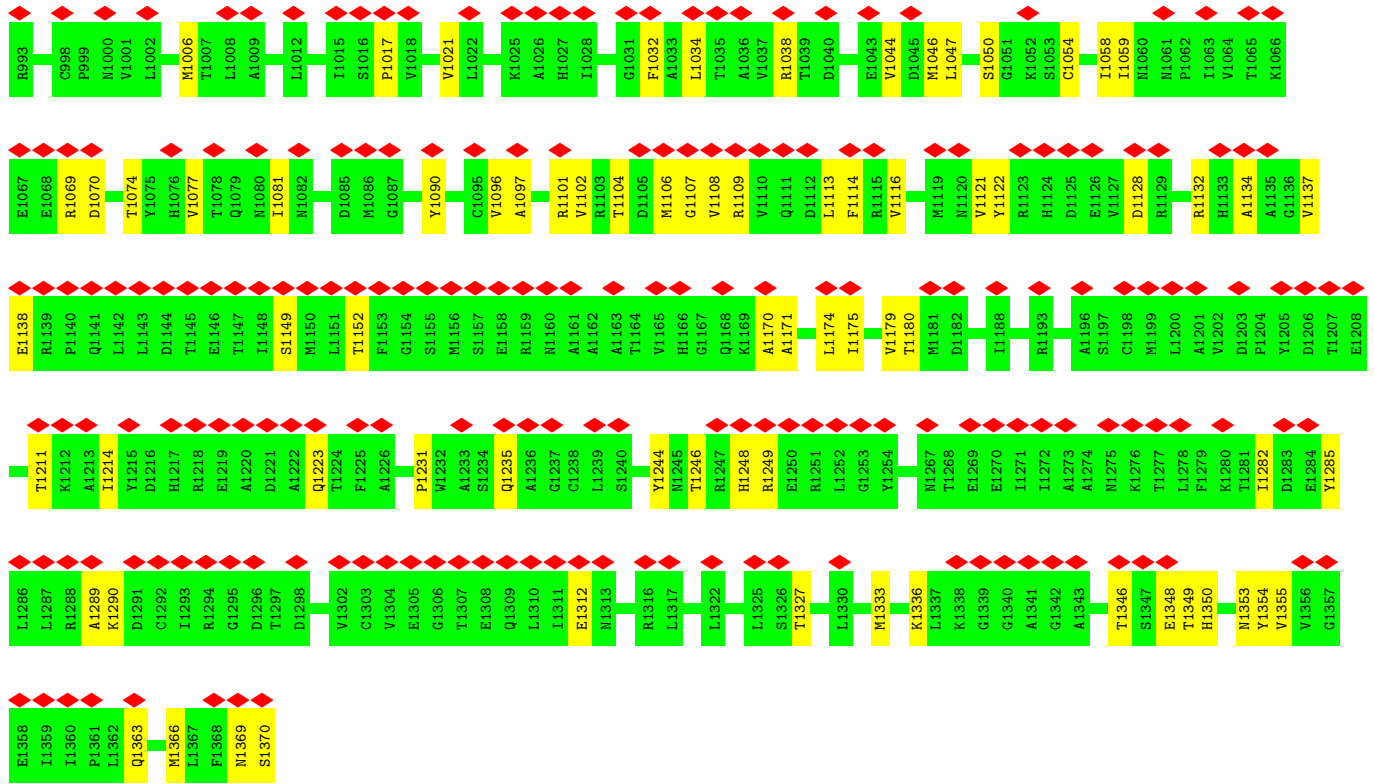
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Chain L:

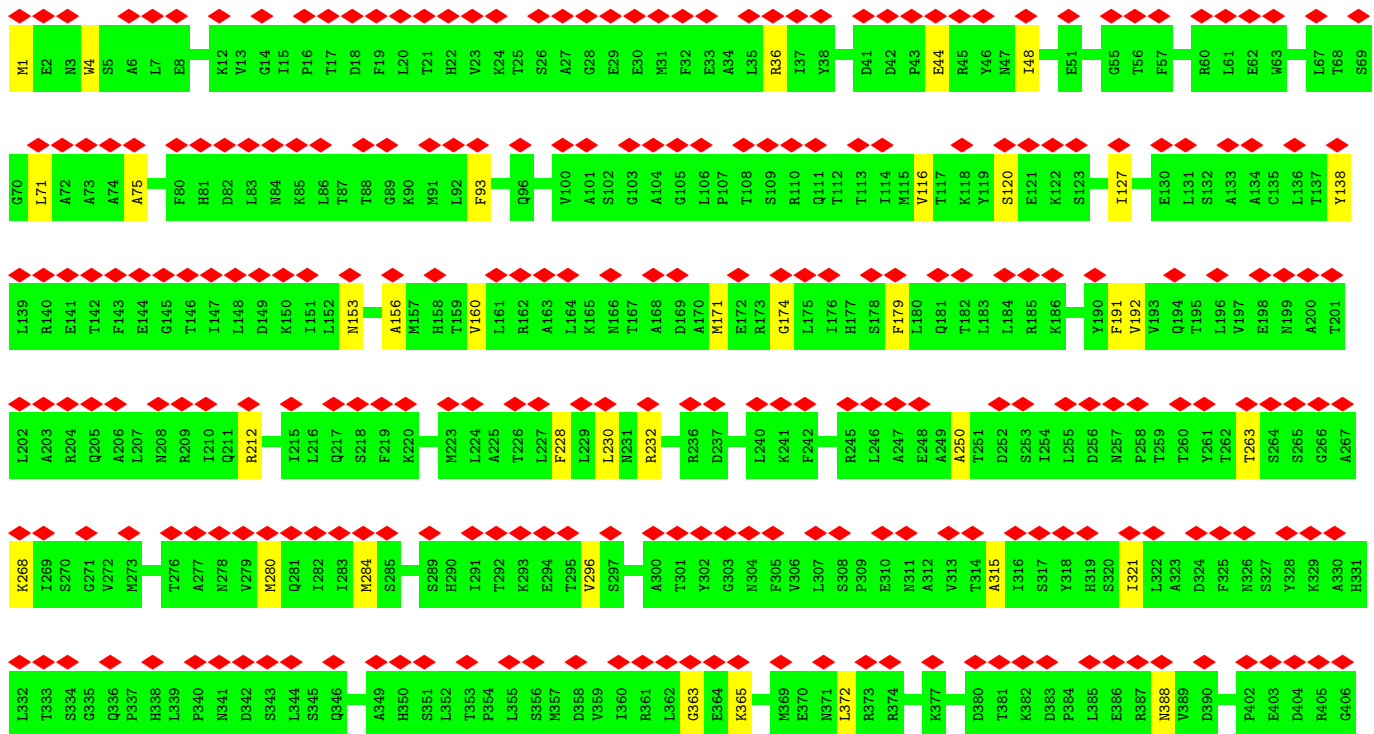
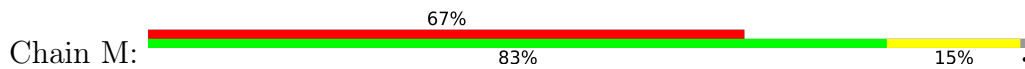
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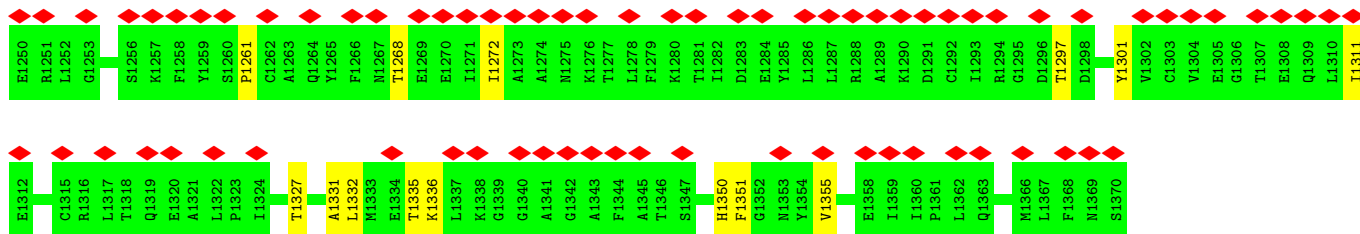
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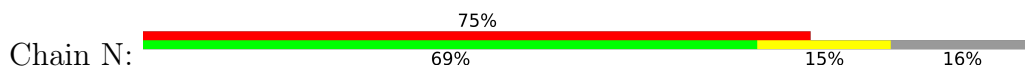


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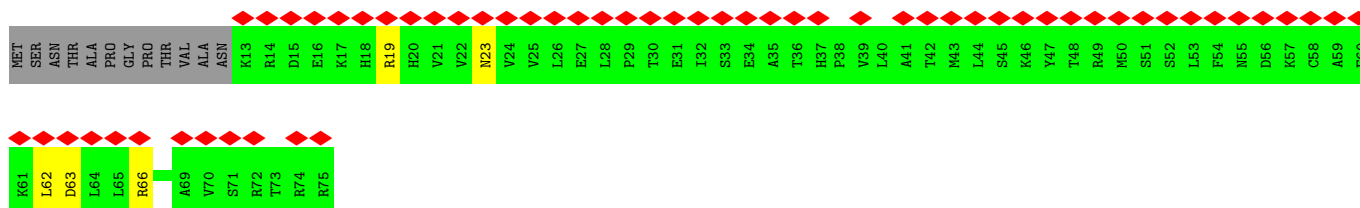
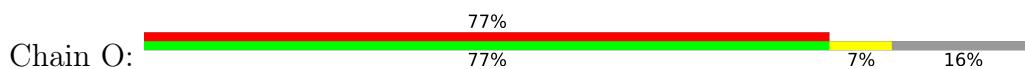




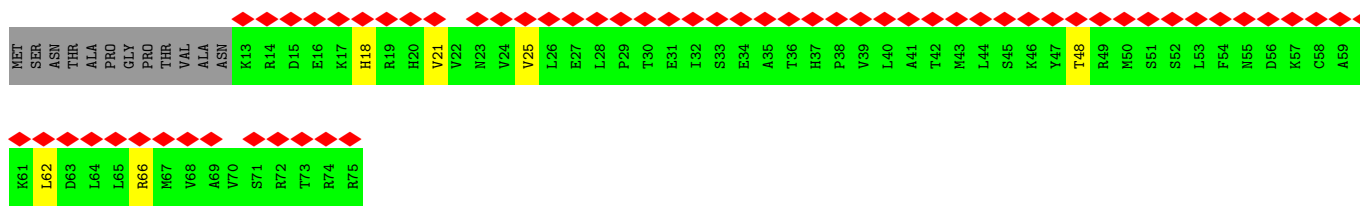
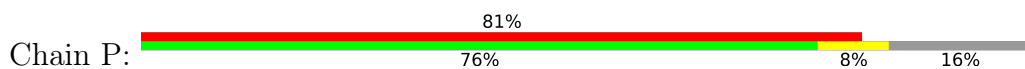
• Molecule 5: Small capsomere-interacting protein



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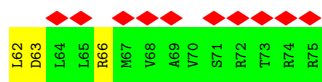


• Molecule 5: Small capsomere-interacting protein

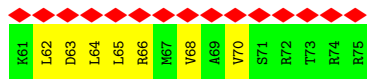
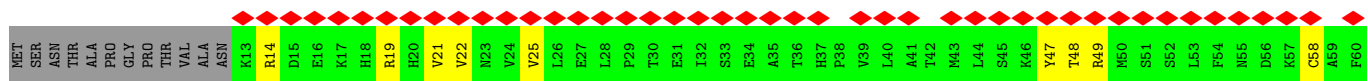
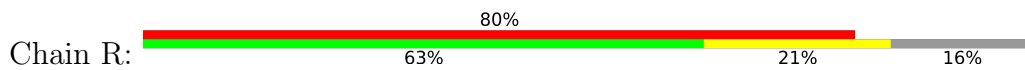


• Molecule 5: Small capsomere-interacting protein

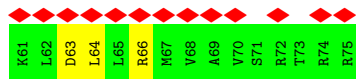
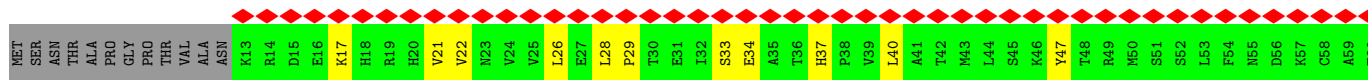
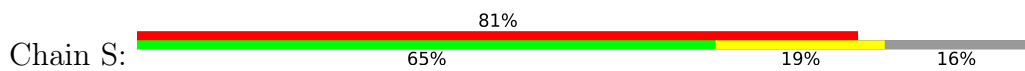




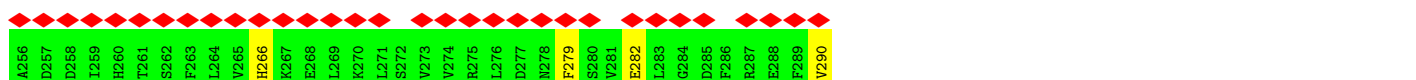
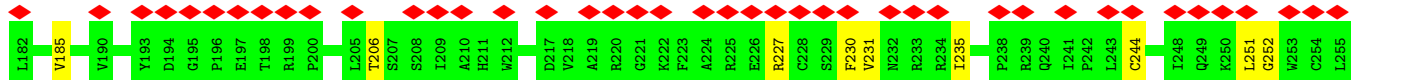
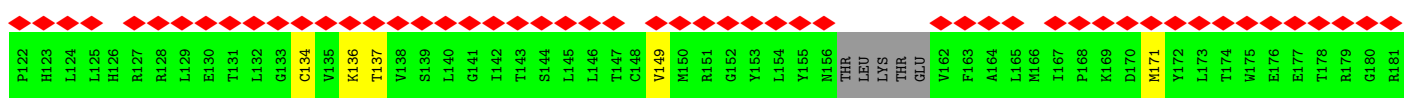
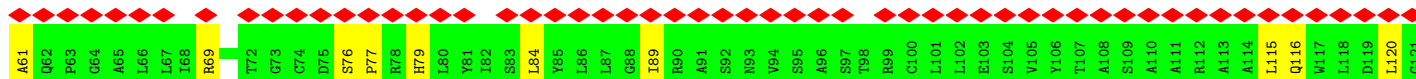
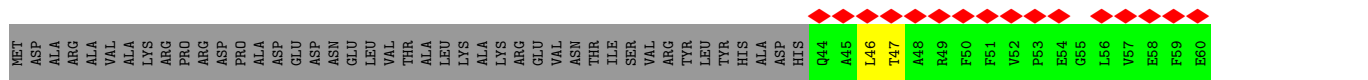
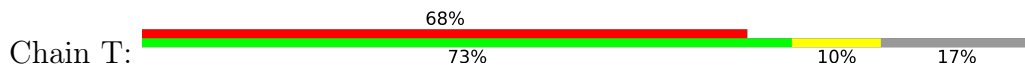
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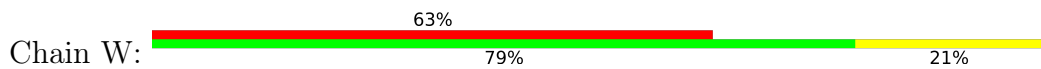
• Molecule 5: Small capsomere-interacting protein

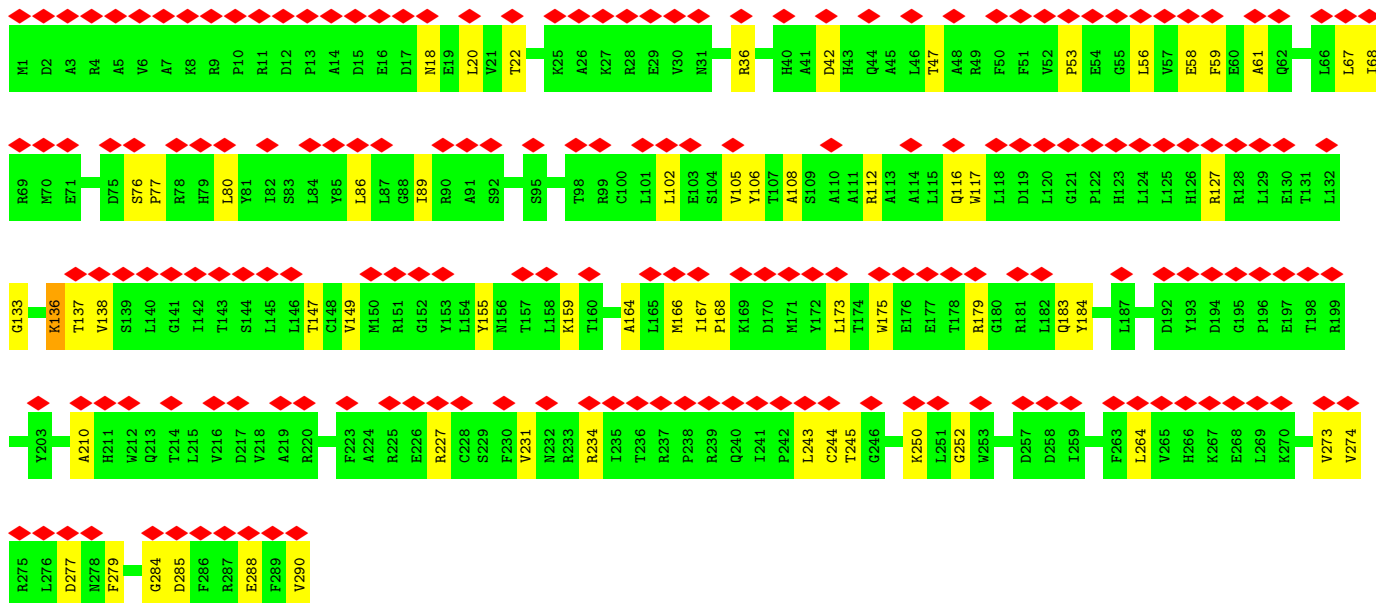


• Molecule 6: Triplex capsid protein 1

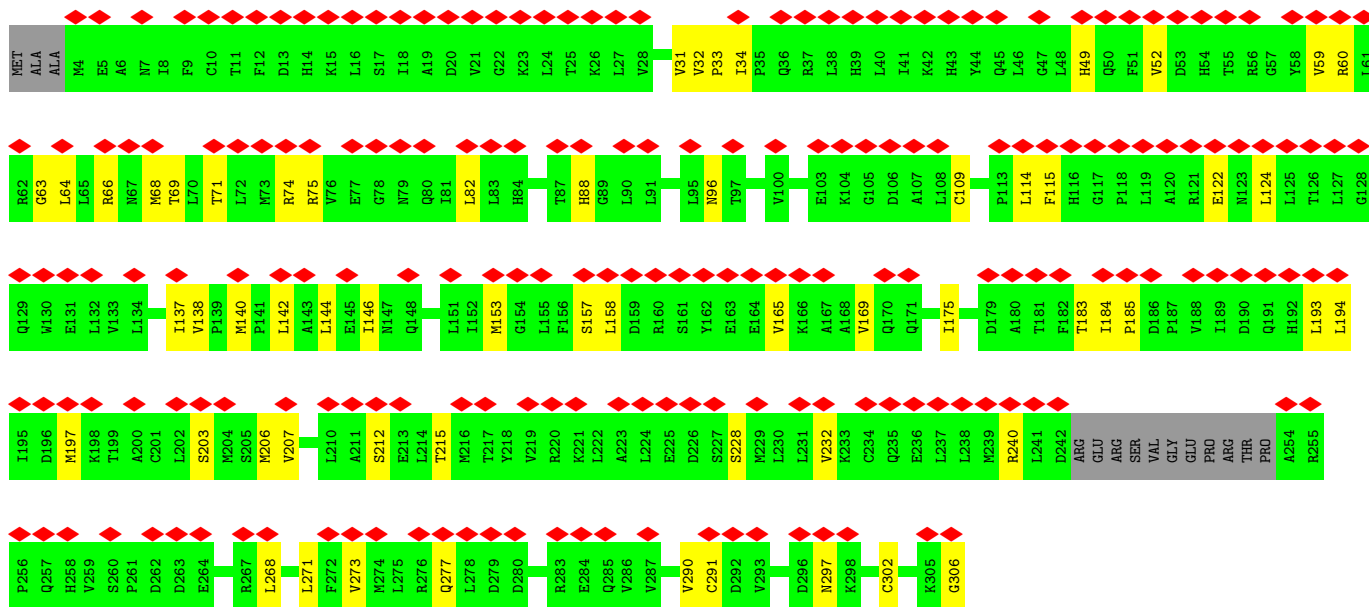
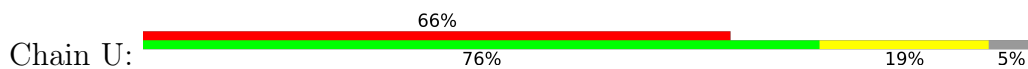


• Molecule 6: Triplex capsid protein 1

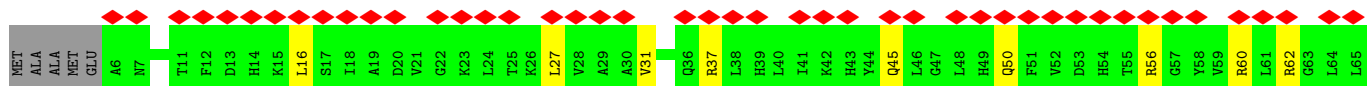
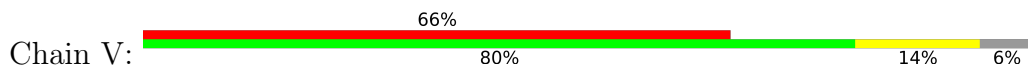


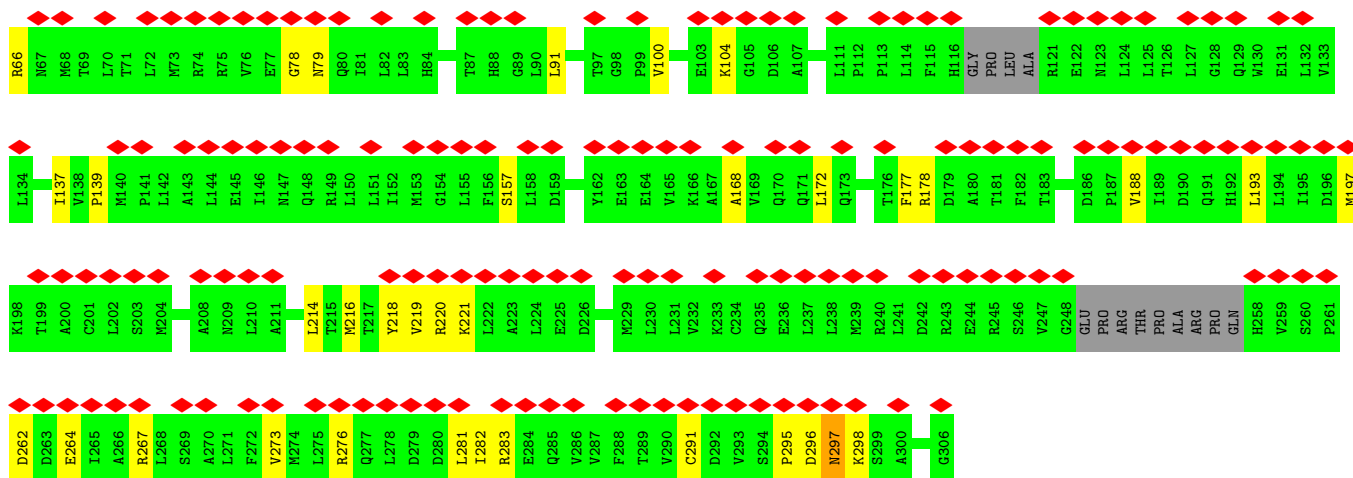


• Molecule 7: Triplex capsid protein 2

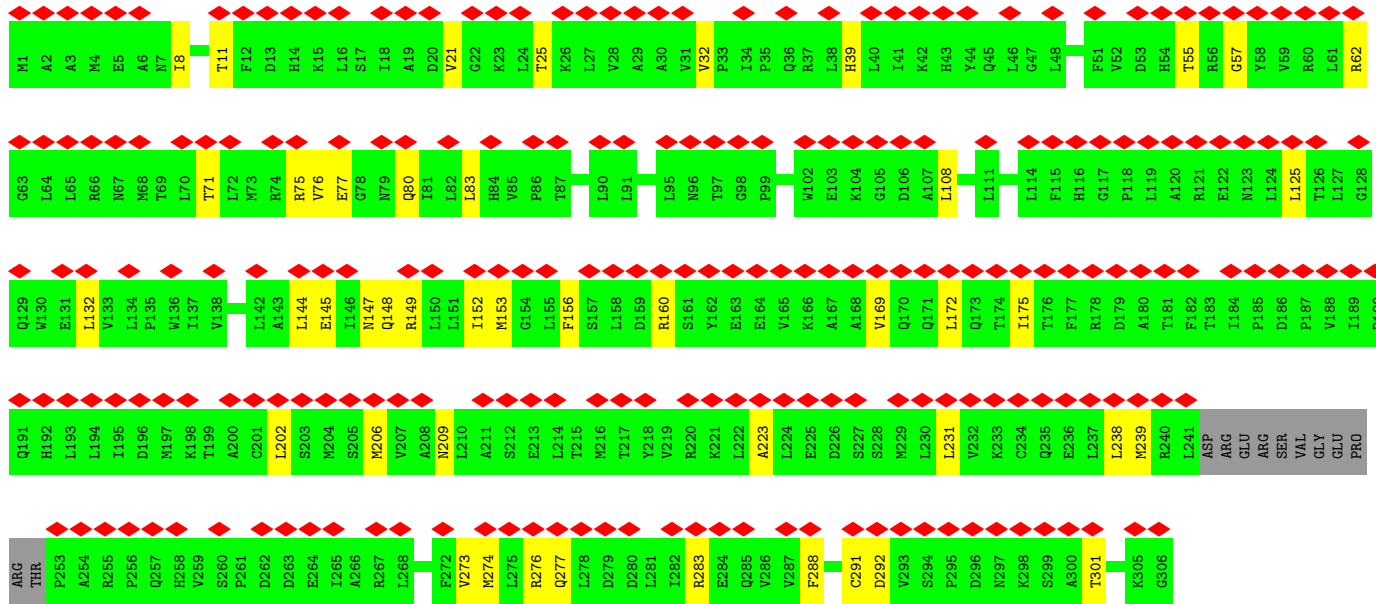
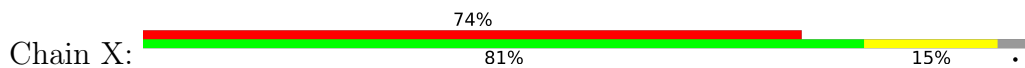


• Molecule 7: Triplex capsid protein 2

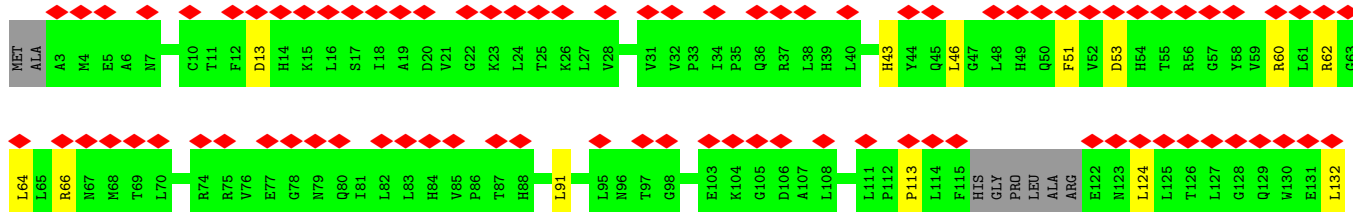
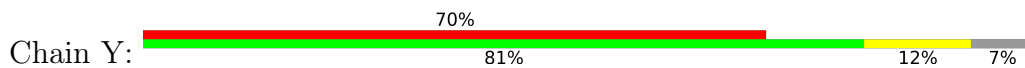


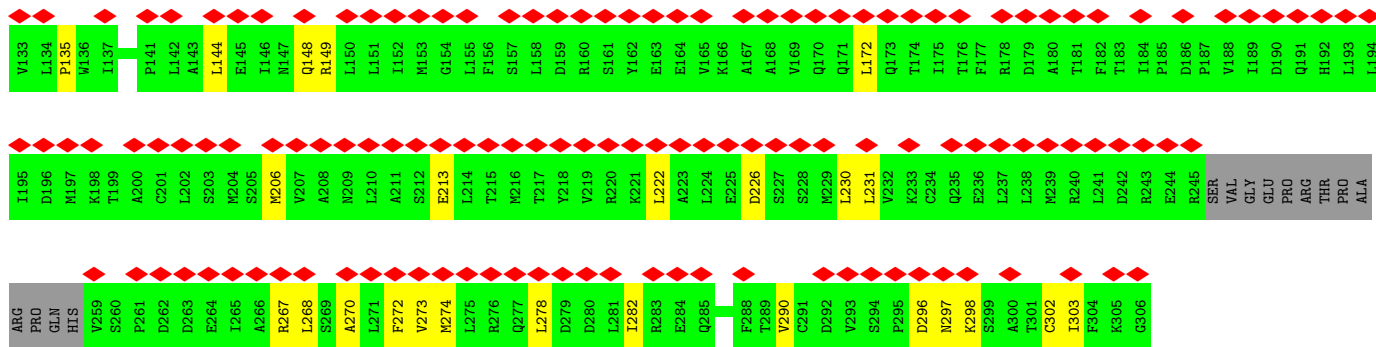


• Molecule 7: Triplex capsid protein 2

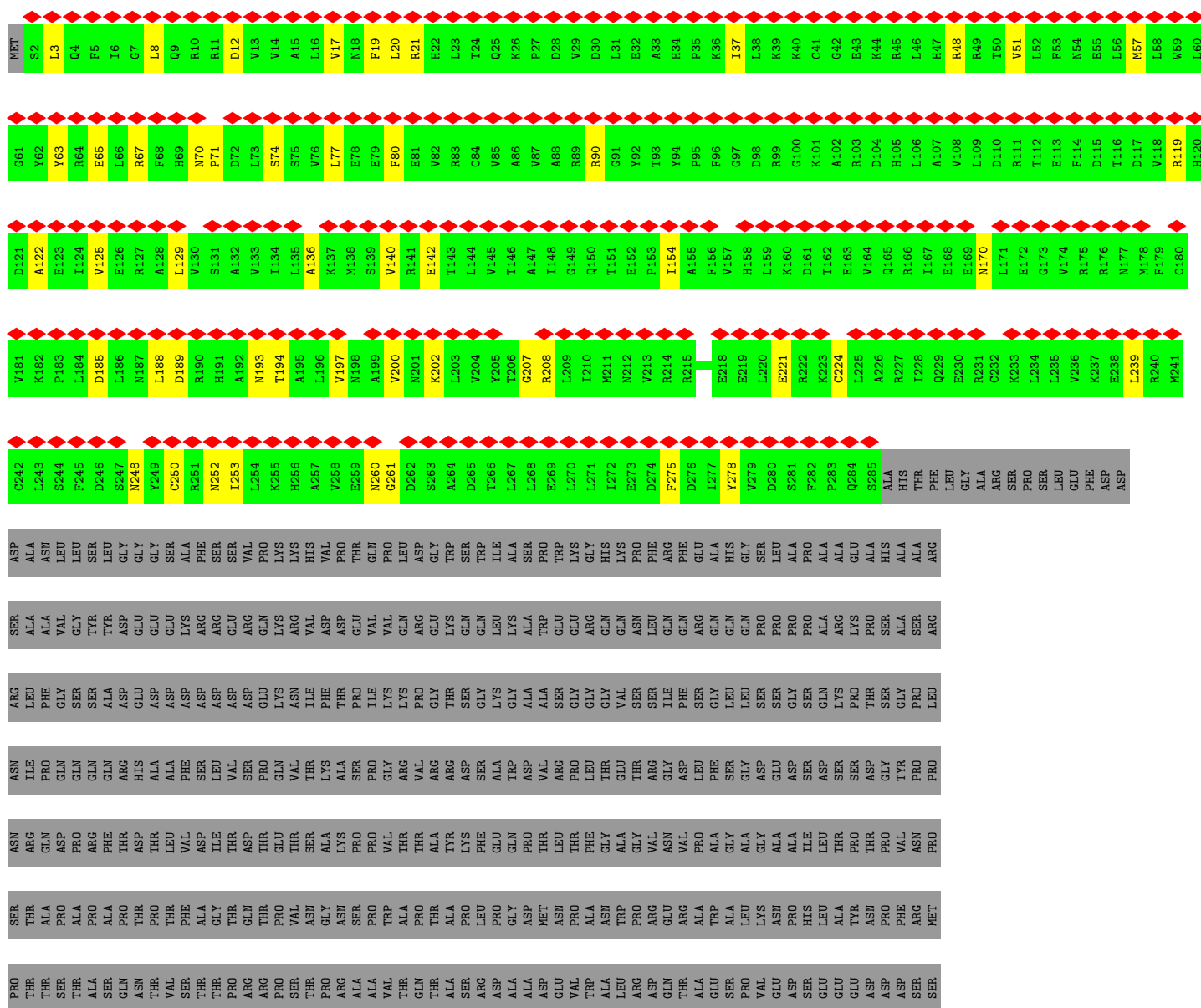


• Molecule 7: Triplex capsid protein 2





• Molecule 8: Large structural phosphoprotein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	16225	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 ($e^-/\text{\AA}^2$)	47.2	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.063	Depositor
Minimum map value	-0.049	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.019	Depositor
Map size (\AA)	489.6, 489.6, 489.6	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.36, 1.36, 1.36	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	A	0.13	0/5969	0.37	0/8139
1	C	0.17	0/334	0.36	0/450
2	E	0.16	0/4094	0.42	1/5558 (0.0%)
2	F	0.14	0/721	0.38	0/969
3	G	0.13	0/3951	0.36	0/5357
4	H	0.13	0/10638	0.39	0/14487
4	I	0.13	0/10949	0.39	0/14916
4	J	0.14	0/10682	0.38	0/14553
4	K	0.13	0/10503	0.37	2/14307 (0.0%)
4	L	0.14	0/10949	0.37	2/14916 (0.0%)
4	M	0.13	0/10949	0.38	2/14916 (0.0%)
5	N	0.10	0/520	0.32	0/697
5	O	0.09	0/520	0.28	0/697
5	P	0.12	0/520	0.32	0/697
5	Q	0.11	0/520	0.31	0/697
5	R	0.11	0/520	0.33	0/697
5	S	0.10	0/520	0.29	0/697
6	T	0.16	0/1981	0.44	0/2687
6	W	0.15	0/2374	0.43	0/3221
7	U	0.16	0/2361	0.41	0/3206
7	V	0.18	0/2333	0.45	0/3164
7	X	0.15	0/2379	0.41	2/3230 (0.1%)
7	Y	0.15	0/2305	0.43	0/3126
8	Z	0.15	0/2358	0.41	0/3182
All	All	0.14	0/98950	0.39	9/134566 (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
3	G	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	H	0	2
4	I	0	1
4	J	0	1
4	K	0	2
4	M	0	1
6	W	0	1
All	All	0	9

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	270	TYR	N-CA-C	-8.96	102.50	112.72
4	M	753	ASP	CA-C-N	6.52	124.35	120.24
4	M	753	ASP	C-N-CA	6.52	124.35	120.24
4	K	752	SER	CA-C-N	6.19	133.37	121.54
4	K	752	SER	C-N-CA	6.19	133.37	121.54

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	312	SER	Peptide
4	H	1100	ASN	Peptide
4	H	265	SER	Peptide
4	I	1143	LEU	Peptide
4	J	794	ASN	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	A	5830	0	5830	164	0
1	C	332	0	358	15	0
2	E	3992	0	3913	142	0
2	F	710	0	711	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	3862	0	3779	46	0
4	H	10391	0	10342	128	0
4	I	10693	0	10635	153	0
4	J	10433	0	10379	103	0
4	K	10259	0	10216	103	0
4	L	10693	0	10635	135	0
4	M	10693	0	10635	124	0
5	N	513	0	539	7	0
5	O	513	0	539	3	0
5	P	513	0	539	5	0
5	Q	513	0	539	12	0
5	R	513	0	539	11	0
5	S	513	0	539	10	0
6	T	1939	0	1972	20	0
6	W	2325	0	2363	44	0
7	U	2317	0	2405	36	0
7	V	2292	0	2379	27	0
7	X	2334	0	2431	29	0
7	Y	2266	0	2355	24	0
8	Z	2320	0	2351	30	0
All	All	96759	0	96923	1289	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 7.

The worst 5 of 1289 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:E:267:TYR:HE1	2:E:270:TYR:HB3	1.35	0.90
4:J:795:ASN:ND2	4:J:969:HIS:O	2.09	0.84
7:U:240:ARG:HB2	7:V:267:ARG:HH21	1.43	0.84
2:E:267:TYR:CE1	2:E:270:TYR:HB3	2.15	0.81
2:E:371:PHE:HB3	2:E:376:VAL:HB	1.64	0.80

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	710/2241 (32%)	695 (98%)	15 (2%)	0	100	100
1	C	38/2241 (2%)	38 (100%)	0	0	100	100
2	E	483/642 (75%)	459 (95%)	22 (5%)	2 (0%)	30	65
2	F	81/642 (13%)	80 (99%)	1 (1%)	0	100	100
3	G	467/594 (79%)	451 (97%)	16 (3%)	0	100	100
4	H	1303/1370 (95%)	1241 (95%)	61 (5%)	1 (0%)	48	81
4	I	1346/1370 (98%)	1281 (95%)	64 (5%)	1 (0%)	48	81
4	J	1313/1370 (96%)	1251 (95%)	61 (5%)	1 (0%)	48	81
4	K	1290/1370 (94%)	1235 (96%)	55 (4%)	0	100	100
4	L	1346/1370 (98%)	1290 (96%)	55 (4%)	1 (0%)	48	81
4	M	1346/1370 (98%)	1288 (96%)	55 (4%)	3 (0%)	43	75
5	N	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
5	O	61/75 (81%)	59 (97%)	2 (3%)	0	100	100
5	P	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
5	Q	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
5	R	61/75 (81%)	60 (98%)	1 (2%)	0	100	100
5	S	61/75 (81%)	61 (100%)	0	0	100	100
6	T	238/290 (82%)	228 (96%)	10 (4%)	0	100	100
6	W	288/290 (99%)	277 (96%)	11 (4%)	0	100	100
7	U	288/306 (94%)	270 (94%)	17 (6%)	1 (0%)	36	70
7	V	282/306 (92%)	265 (94%)	15 (5%)	2 (1%)	18	54
7	X	291/306 (95%)	275 (94%)	16 (6%)	0	100	100
7	Y	279/306 (91%)	268 (96%)	10 (4%)	1 (0%)	30	65
8	Z	282/1048 (27%)	275 (98%)	6 (2%)	1 (0%)	30	65
All	All	12037/17882 (67%)	11527 (96%)	496 (4%)	14 (0%)	49	81

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	H	266	GLY
4	I	266	GLY
4	M	760	MET
4	M	886	VAL
7	Y	297	ASN

5.3.2 Protein sidechains [i](#)

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	A	647/1941 (33%)	647 (100%)	0	100	100
1	C	38/1941 (2%)	38 (100%)	0	100	100
2	E	422/526 (80%)	417 (99%)	5 (1%)	63	73
2	F	76/526 (14%)	76 (100%)	0	100	100
3	G	397/500 (79%)	397 (100%)	0	100	100
4	H	1142/1192 (96%)	1139 (100%)	3 (0%)	86	85
4	I	1175/1192 (99%)	1171 (100%)	4 (0%)	86	85
4	J	1146/1192 (96%)	1146 (100%)	0	100	100
4	K	1129/1192 (95%)	1129 (100%)	0	100	100
4	L	1175/1192 (99%)	1175 (100%)	0	100	100
4	M	1175/1192 (99%)	1175 (100%)	0	100	100
5	N	59/68 (87%)	59 (100%)	0	100	100
5	O	59/68 (87%)	59 (100%)	0	100	100
5	P	59/68 (87%)	59 (100%)	0	100	100
5	Q	59/68 (87%)	59 (100%)	0	100	100
5	R	59/68 (87%)	59 (100%)	0	100	100
5	S	59/68 (87%)	59 (100%)	0	100	100
6	T	211/252 (84%)	211 (100%)	0	100	100
6	W	252/252 (100%)	252 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	U	262/273 (96%)	262 (100%)	0	100	100
7	V	260/273 (95%)	260 (100%)	0	100	100
7	X	263/273 (96%)	263 (100%)	0	100	100
7	Y	257/273 (94%)	257 (100%)	0	100	100
8	Z	255/883 (29%)	255 (100%)	0	100	100
All	All	10636/15473 (69%)	10624 (100%)	12 (0%)	87	89

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	677	LEU
4	I	9	LEU
4	I	886	VAL
4	I	621	VAL
2	E	275	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
4	K	217	GLN
4	L	620	ASN
7	V	88	HIS
4	K	319	HIS
4	K	1184	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 [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.

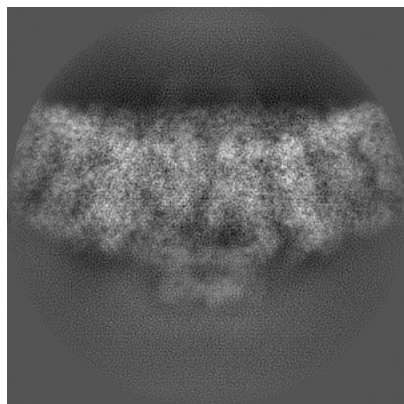
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41202. These allow visual inspection of the internal detail of the map and identification of artifacts.

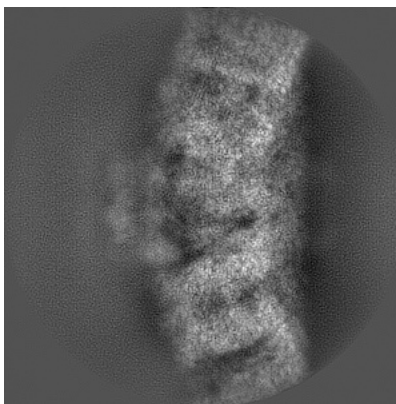
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

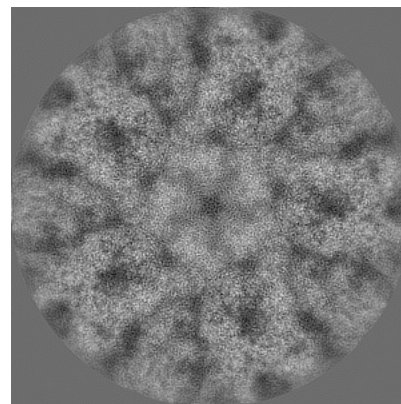
6.1.1 Primary map



X

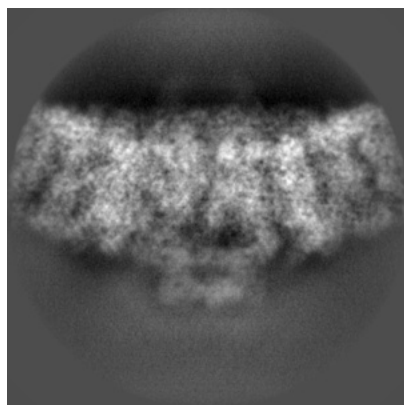


Y

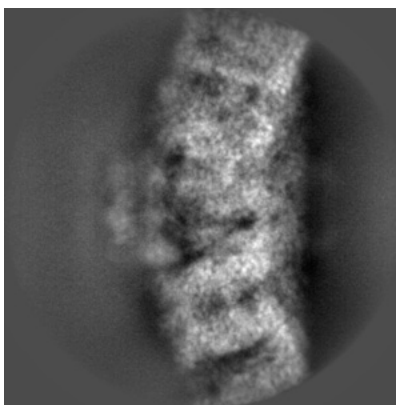


Z

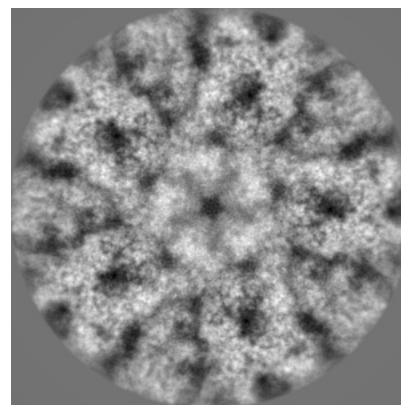
6.1.2 Raw map



X



Y

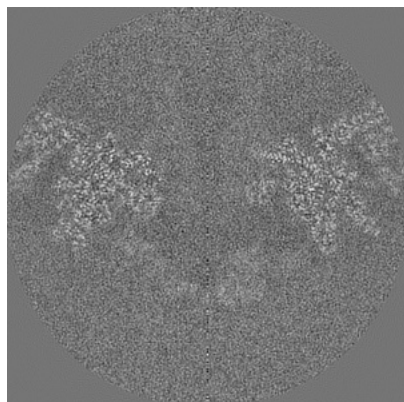


Z

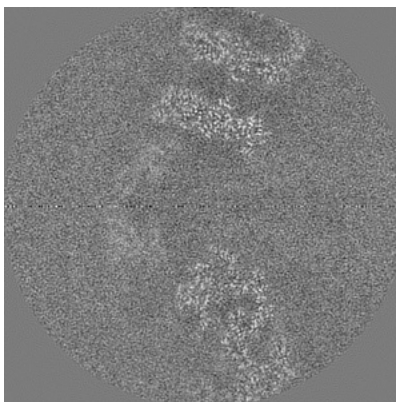
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

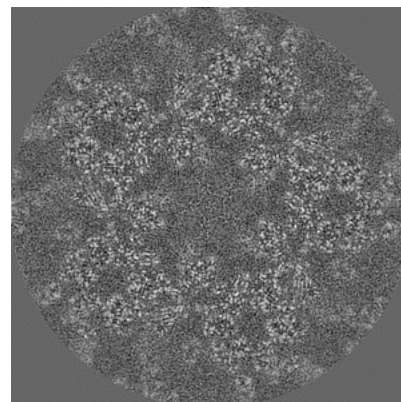
6.2.1 Primary map



X Index: 180

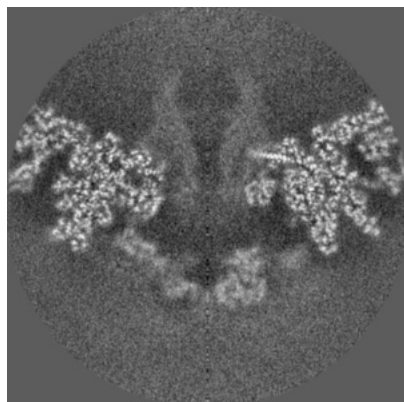


Y Index: 180

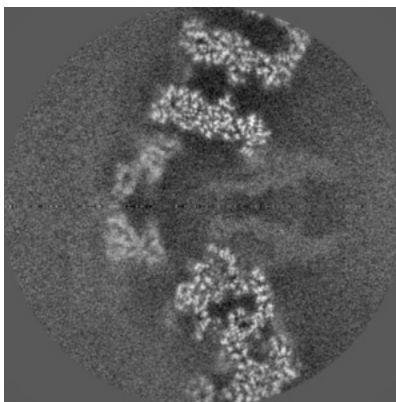


Z Index: 180

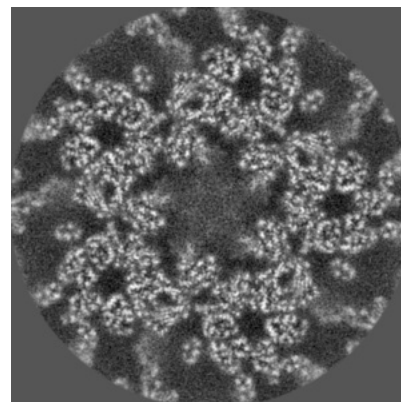
6.2.2 Raw map



X Index: 180



Y Index: 180

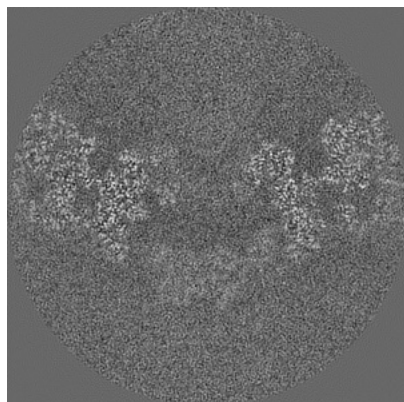


Z Index: 180

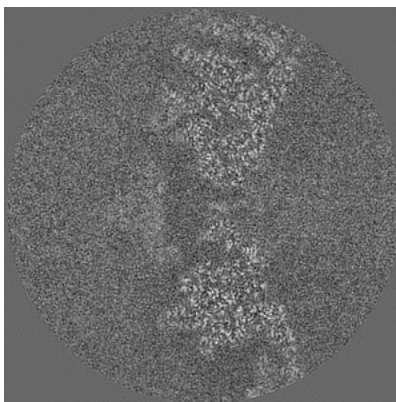
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

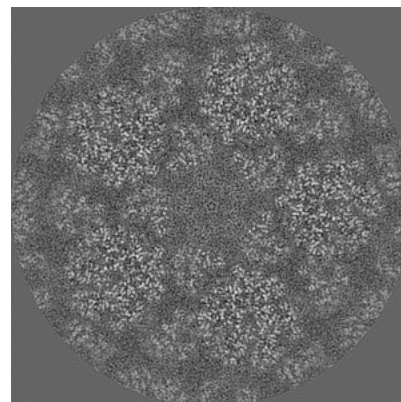
6.3.1 Primary map



X Index: 204

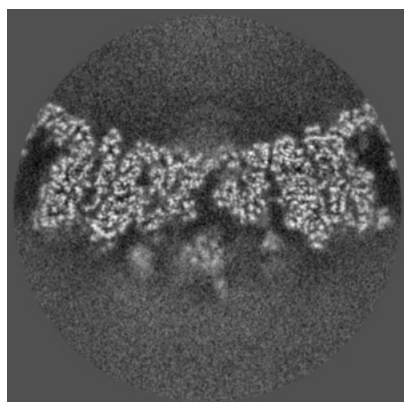


Y Index: 217

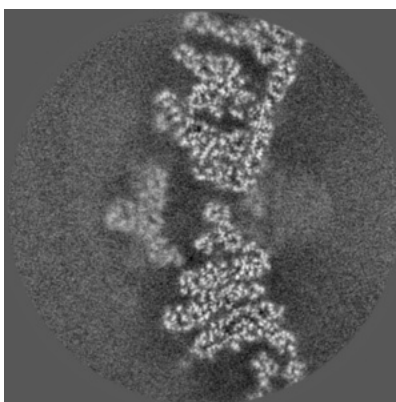


Z Index: 203

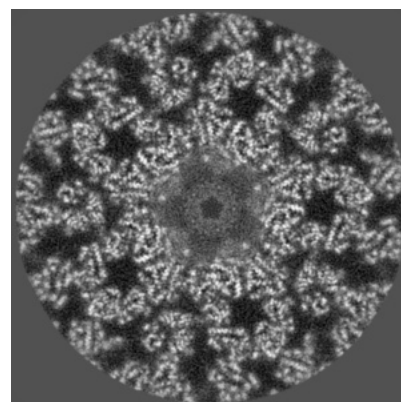
6.3.2 Raw map



X Index: 230



Y Index: 220

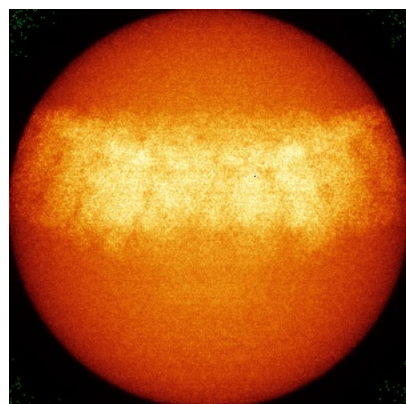


Z Index: 223

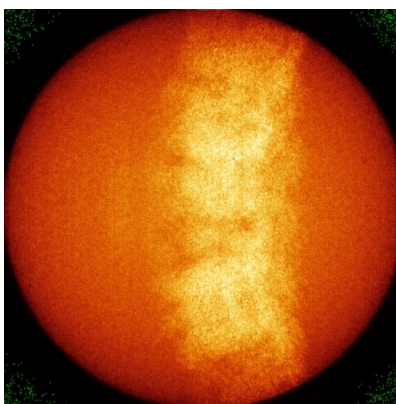
The images above show the largest variance slices of the map in three orthogonal directions.

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

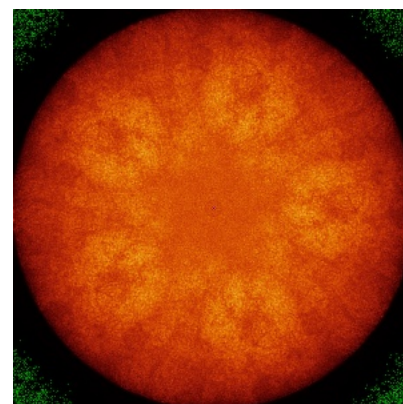
6.4.1 Primary map



X

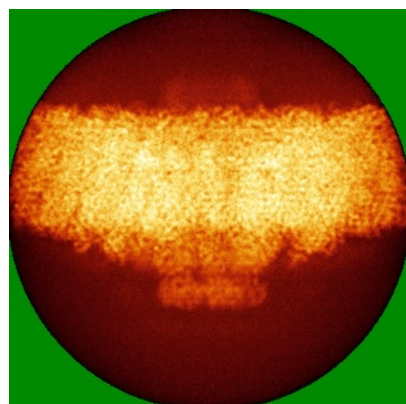


Y

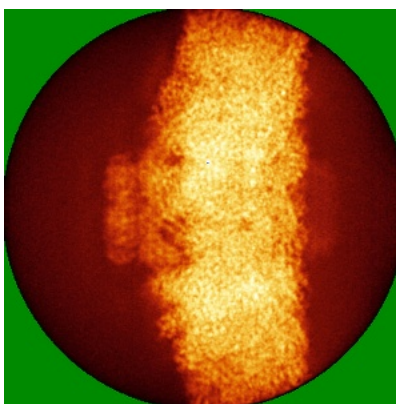


Z

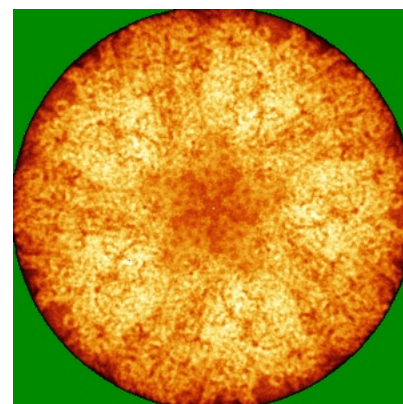
6.4.2 Raw map



X



Y

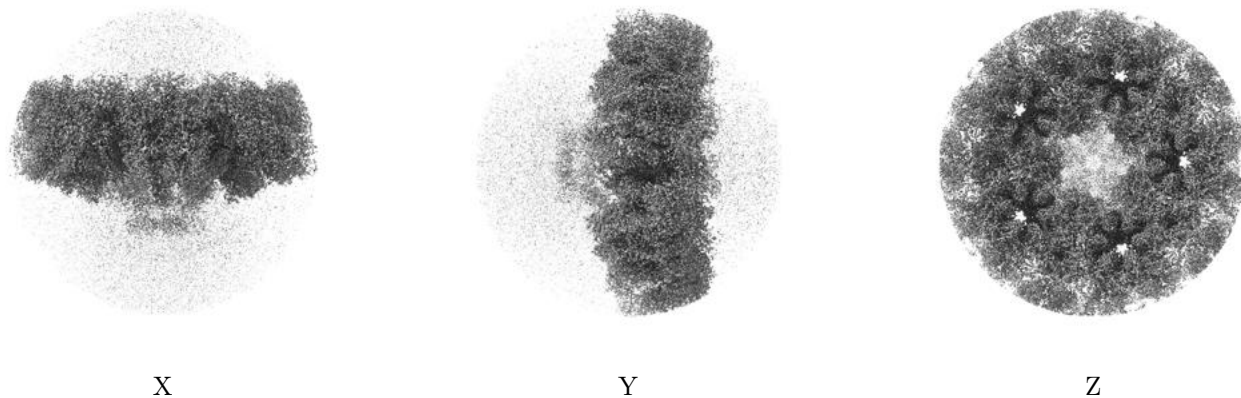


Z

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.

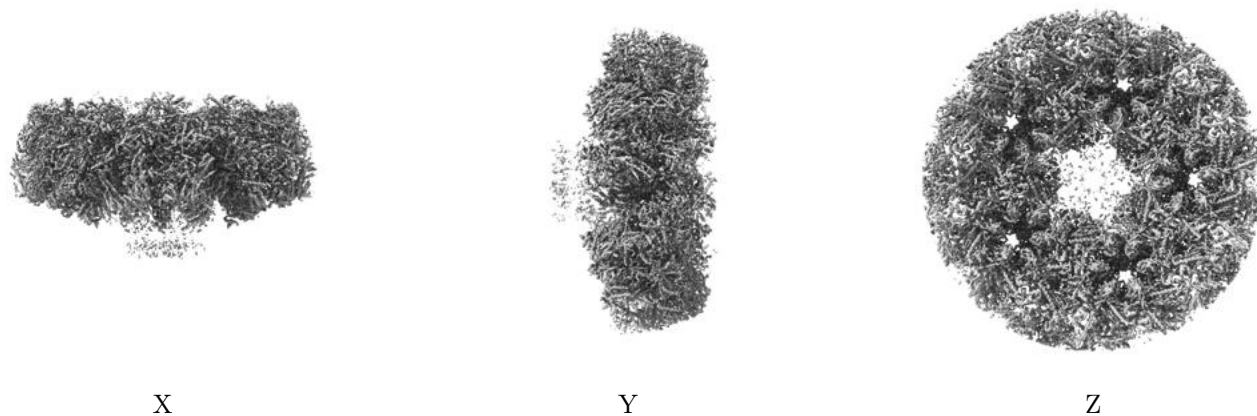
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.019. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

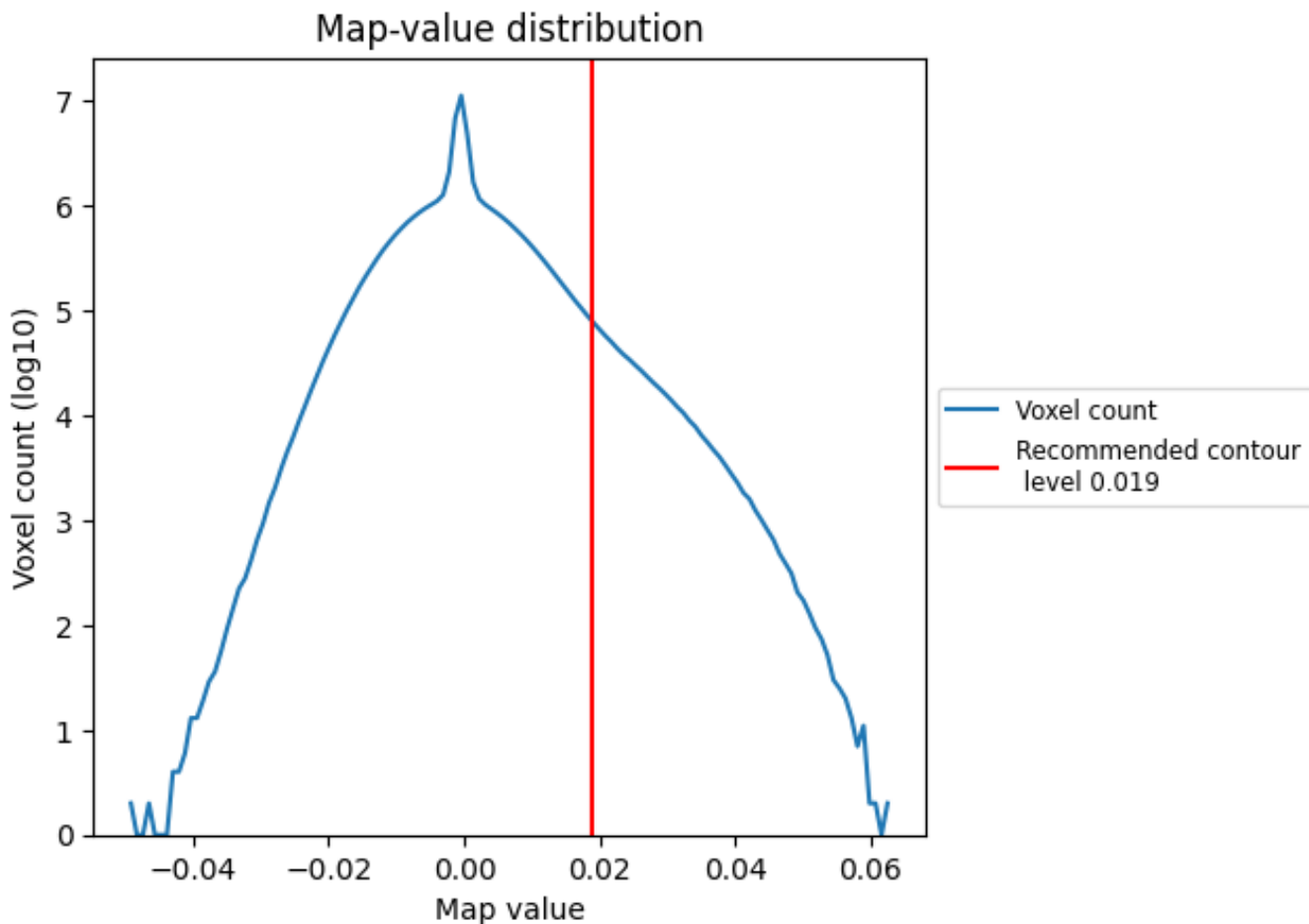
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

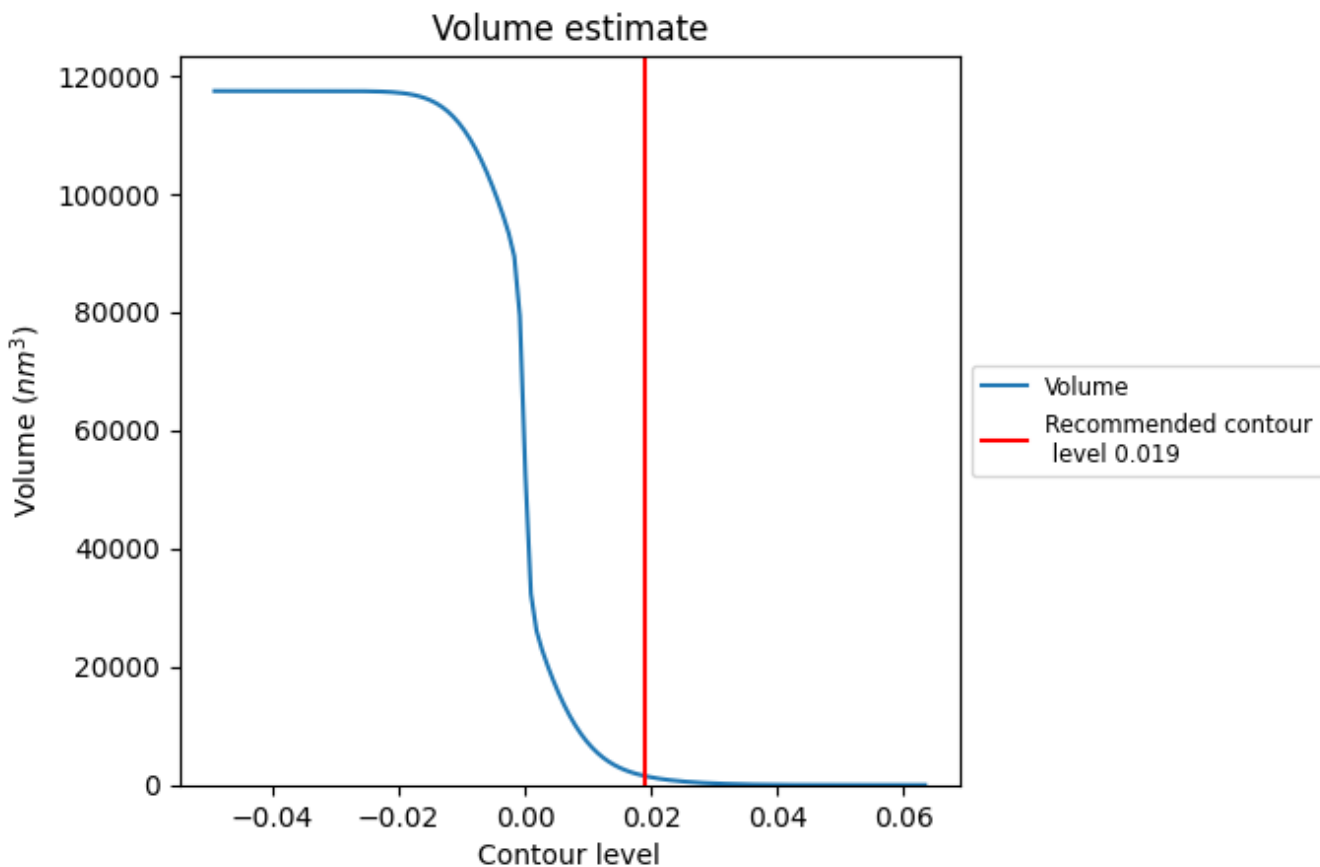
This section contains the results of statistical analysis of the map.

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.

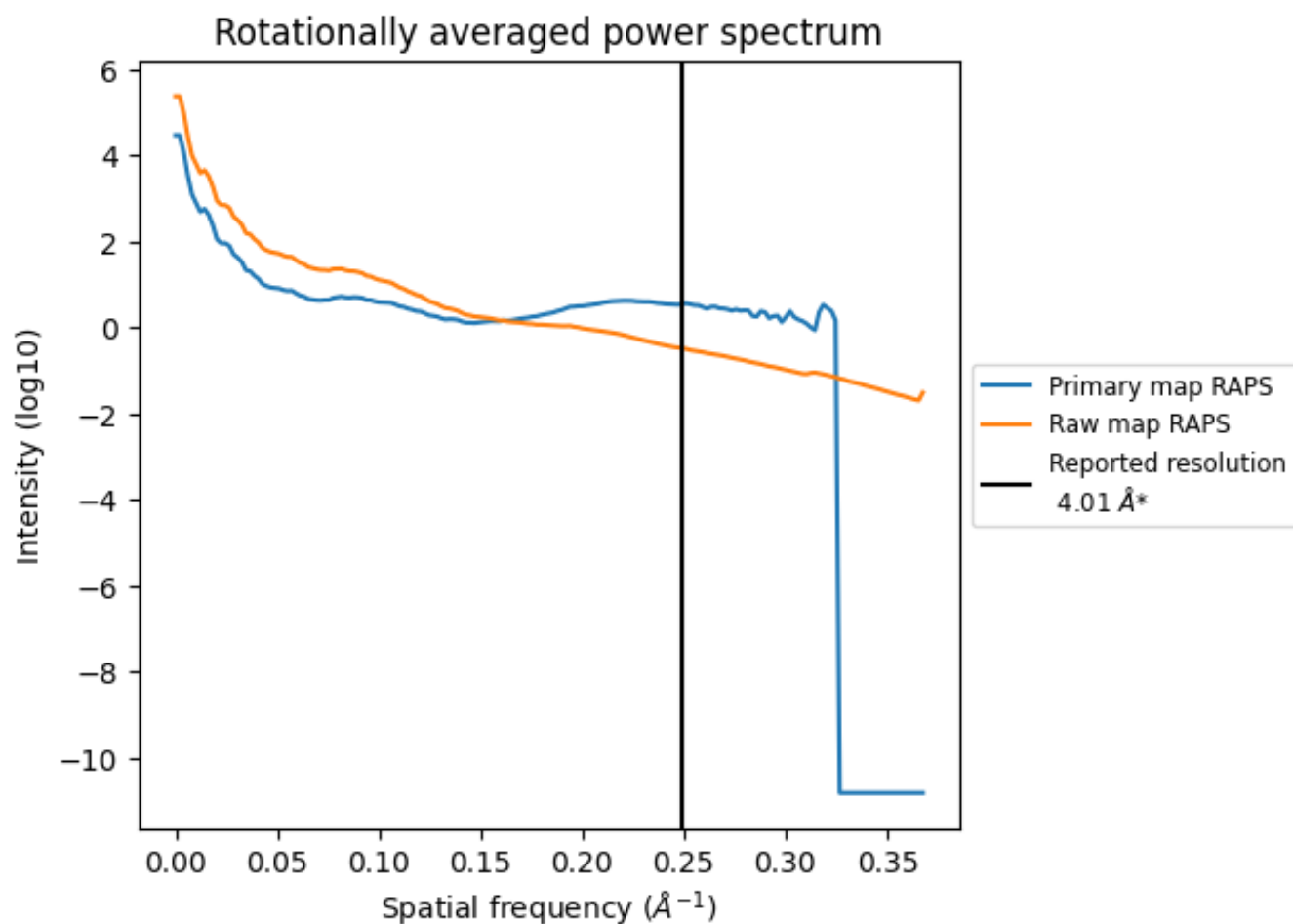
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1523 nm³; this corresponds to an approximate mass of 1376 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](#)

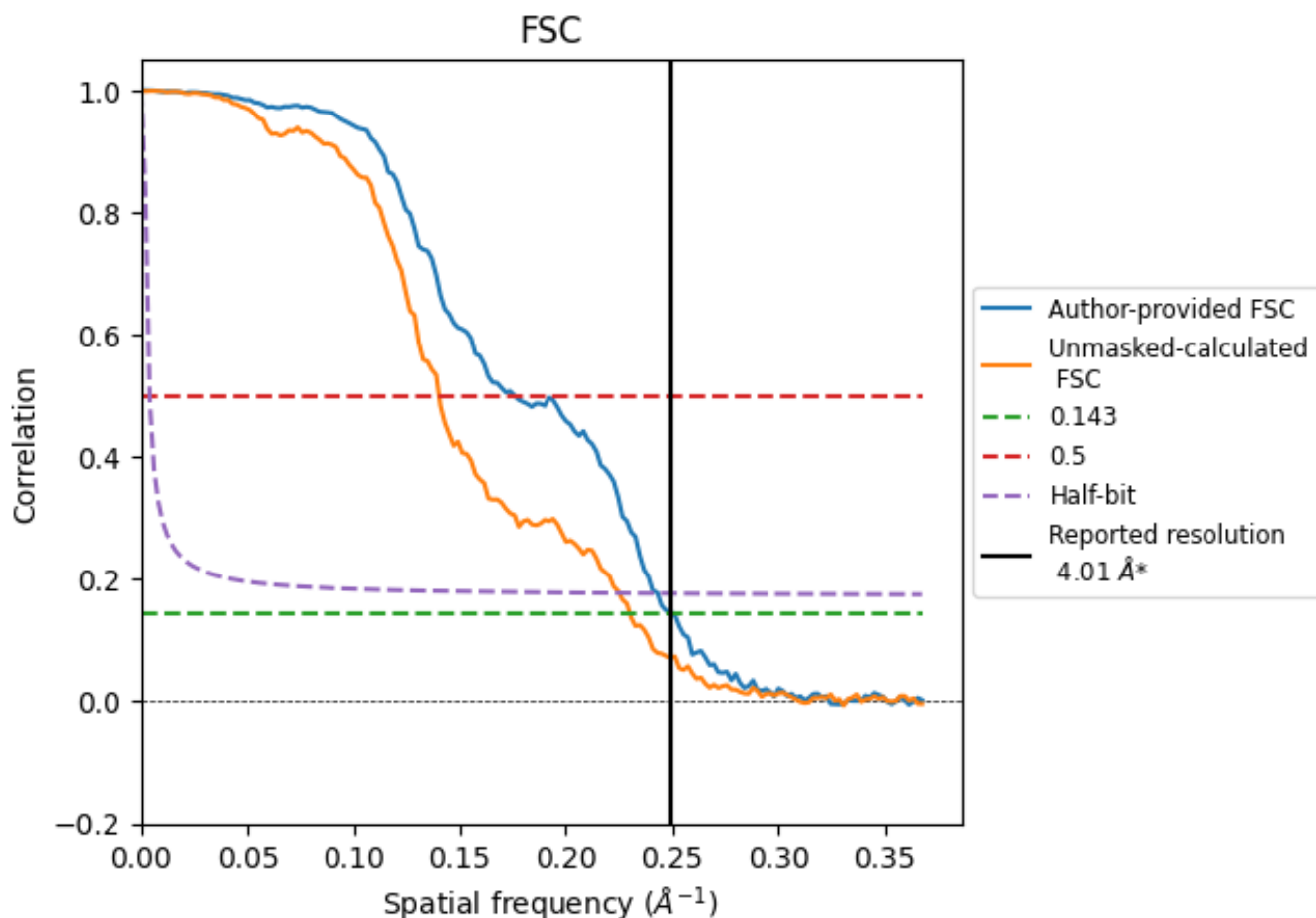


*Reported resolution corresponds to spatial frequency of 0.249 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.249 Å⁻¹

8.2 Resolution estimates [i](#)

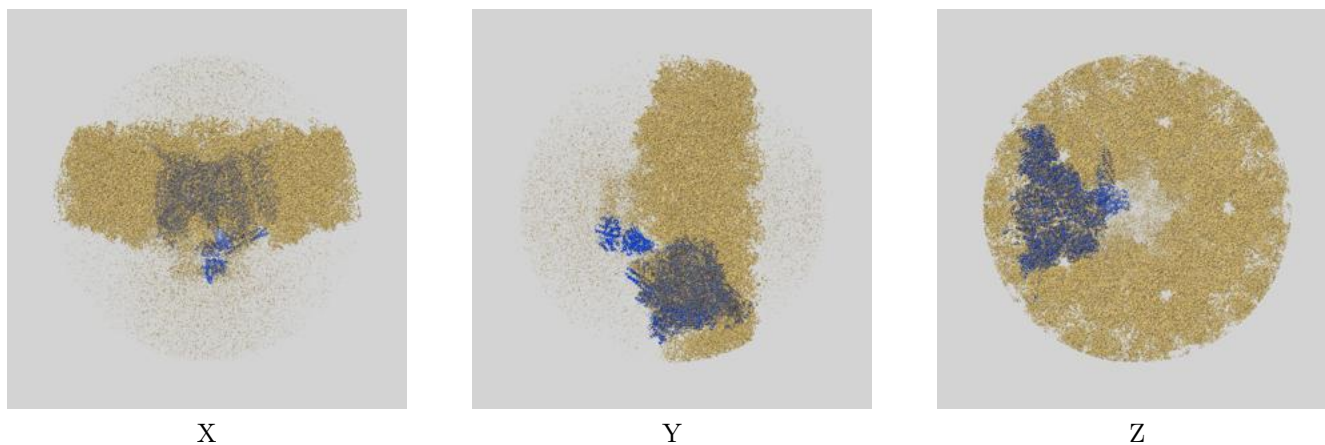
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.01	-	-
Author-provided FSC curve	3.99	5.69	4.11
Unmasked-calculated*	4.34	7.13	4.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

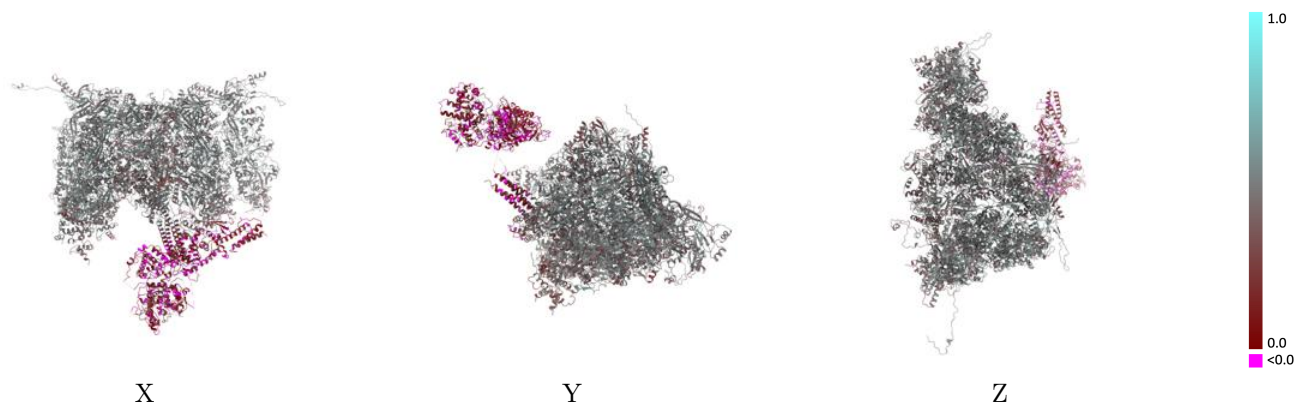
This section contains information regarding the fit between EMDB map EMD-41202 and PDB model 8TEU. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



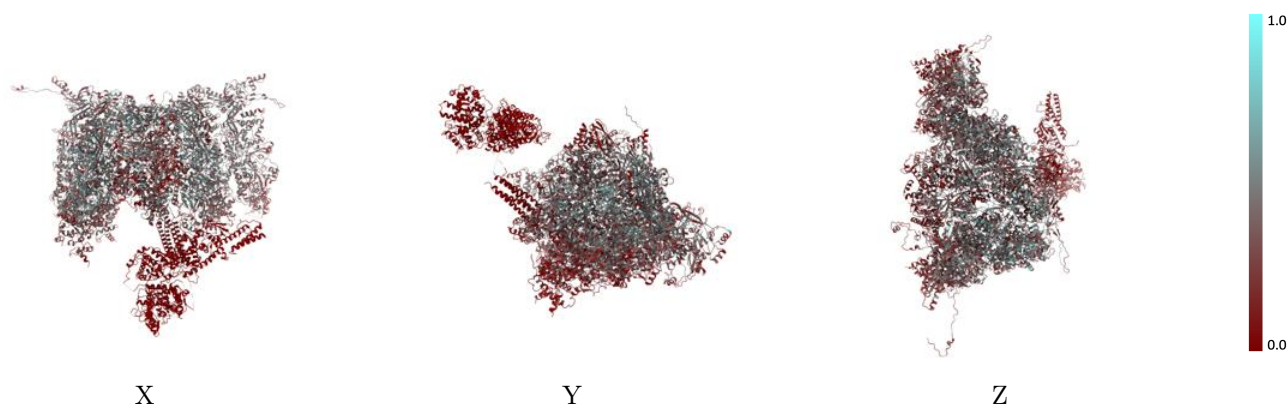
The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



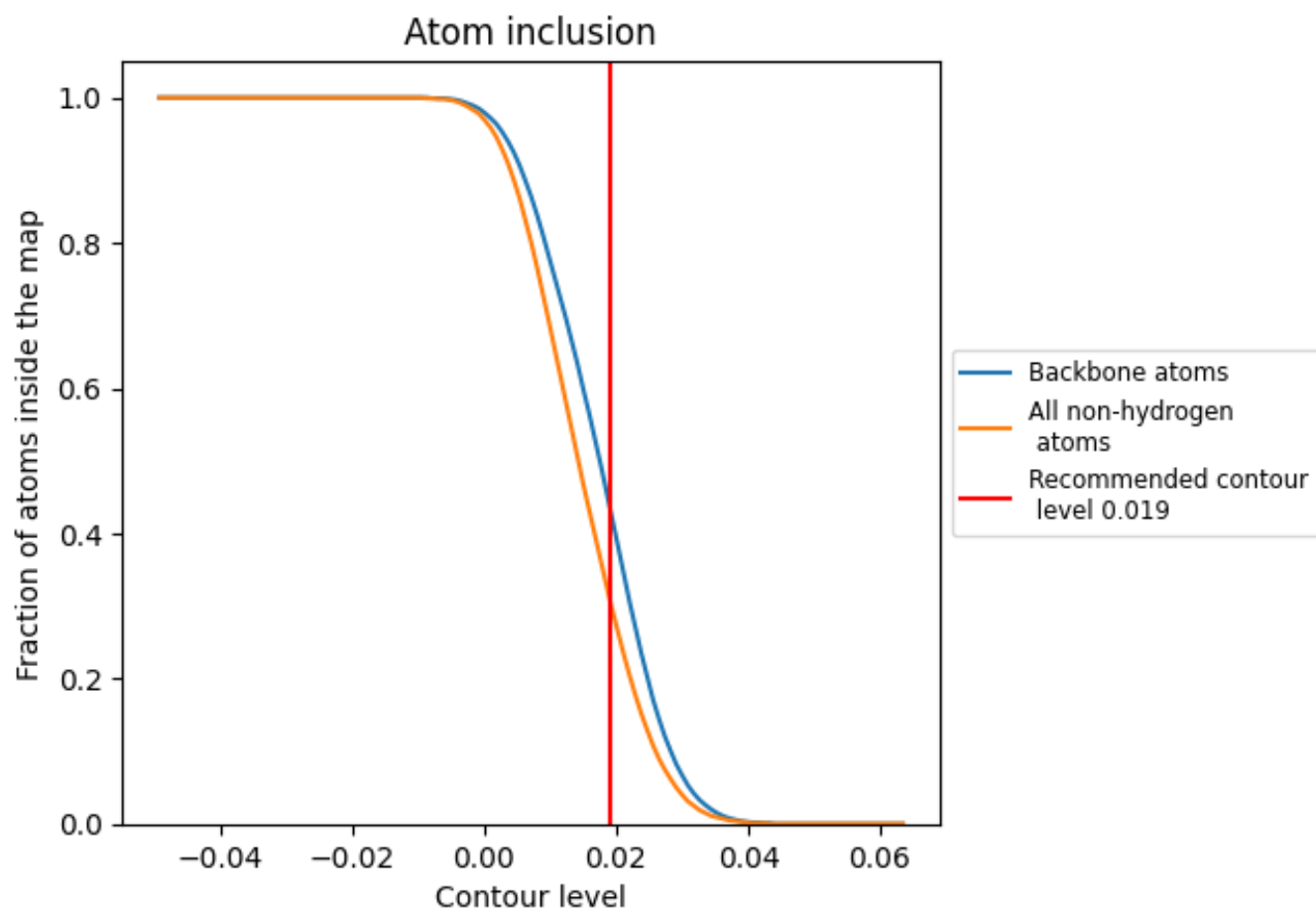
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.019).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 44% of all backbone atoms, 31% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3100	 0.4300
A	 0.0170	 0.1030
C	 0.0190	 0.1850
E	 0.0350	 0.1650
F	 0.1000	 0.3010
G	 0.3070	 0.4630
H	 0.4230	 0.4860
I	 0.4030	 0.4820
J	 0.3360	 0.4690
K	 0.4120	 0.4810
L	 0.3660	 0.4750
M	 0.3180	 0.4690
N	 0.1870	 0.3950
O	 0.1990	 0.3710
P	 0.1270	 0.3470
Q	 0.1950	 0.3570
R	 0.1290	 0.3740
S	 0.1120	 0.3710
T	 0.2090	 0.4150
U	 0.3140	 0.4590
V	 0.3100	 0.4470
W	 0.3340	 0.4730
X	 0.2610	 0.4490
Y	 0.2850	 0.4550
Z	 0.1620	 0.4000

