



wwPDB EM Validation Summary Report ⓘ

May 6, 2025 – 10:57 AM EDT

PDB ID : 7L6I / pdb_00007l6i
EMDB ID : EMD-23205
Title : The empty AAV13 capsid
Authors : Mietzsch, M.; Agbandje-McKenna, M.
Deposited on : 2020-12-23
Resolution : 2.76 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

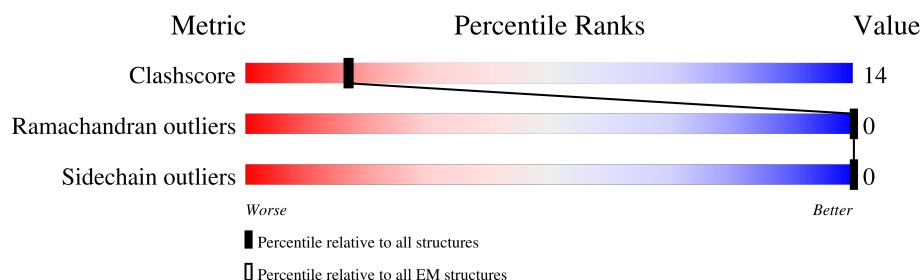
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.76 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.



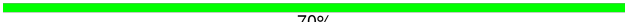
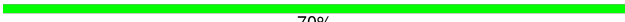
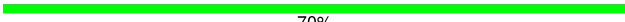
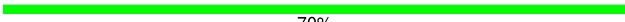
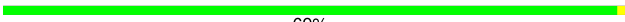
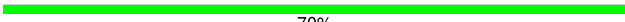
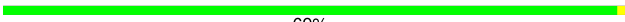
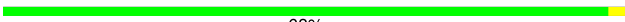
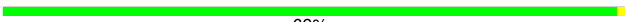
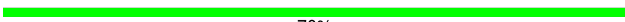















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1	517	69% 31%
1	2	517	69% 31%
1	3	517	69% 31%
1	4	517	70% 30%
1	5	517	68% 32%
1	6	517	69% 31%
1	7	517	69% 31%
1	8	517	69% 31%

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Mol	Chain	Length	Quality of chain	
1	A	517		30%
1	B	517		30%
1	C	517		30%
1	D	517		30%
1	E	517		31%
1	F	517		30%
1	G	517		31%
1	H	517		32%
1	I	517		31%
1	J	517		30%
1	K	517		30%
1	L	517		30%
1	M	517		30%
1	N	517		31%
1	O	517		30%
1	P	517		30%
1	Q	517		31%
1	R	517		31%
1	S	517		30%
1	T	517		31%
1	U	517		30%
1	V	517		31%
1	W	517		32%
1	X	517		31%
1	Y	517		31%



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Mol	Chain	Length	Quality of chain	
1	Z	517	<div><div></div></div>	69% 31%
1	a	517	<div><div></div></div>	70% 30%
1	b	517	<div><div></div></div>	70% 30%
1	c	517	<div><div></div></div>	69% 31%
1	d	517	<div><div></div></div>	69% 31%
1	e	517	<div><div></div></div>	69% 31%
1	f	517	<div><div></div></div>	70% 30%
1	g	517	<div><div></div></div>	70% 30%
1	h	517	<div><div></div></div>	69% 31%
1	i	517	<div><div></div></div>	69% 31%
1	j	517	<div><div></div></div>	70% 30%
1	k	517	<div><div></div></div>	69% 31%
1	l	517	<div><div></div></div>	70% 30%
1	m	517	<div><div></div></div>	69% 31%
1	n	517	<div><div></div></div>	69% 31%
1	o	517	<div><div></div></div>	69% 31%
1	p	517	<div><div></div></div>	70% 30%
1	q	517	<div><div></div></div>	69% 31%
1	r	517	<div><div></div></div>	70% 30%
1	s	517	<div><div></div></div>	69% 31%
1	t	517	<div><div></div></div>	69% 31%
1	u	517	<div><div></div></div>	70% 30%
1	v	517	<div><div></div></div>	70% 30%
1	w	517	<div><div></div></div>	69% 31%
1	x	517	<div><div></div></div>	69% 31%

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Mol	Chain	Length	Quality of chain	
1	y	517		
1	z	517		

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 248820 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 Capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	B	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	C	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	D	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	E	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	F	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	G	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	H	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	I	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	J	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	K	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	L	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	M	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	N	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	O	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	P	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	Q	517	Total 4147	C 2615	N 727	O 790	S 15	1	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	S	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	T	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	U	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	V	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	W	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	X	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	Y	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	Z	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	a	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	b	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	c	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	d	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	e	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	f	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	g	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	h	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	i	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	j	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	k	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	l	517	Total 4147	C 2615	N 727	O 790	S 15	1	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	n	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	o	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	p	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	q	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	r	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	s	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	t	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	u	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	v	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	w	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	x	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	y	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	z	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	1	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	2	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	3	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	4	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	5	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	6	517	Total 4147	C 2615	N 727	O 790	S 15	1	0
1	7	517	Total 4147	C 2615	N 727	O 790	S 15	1	0

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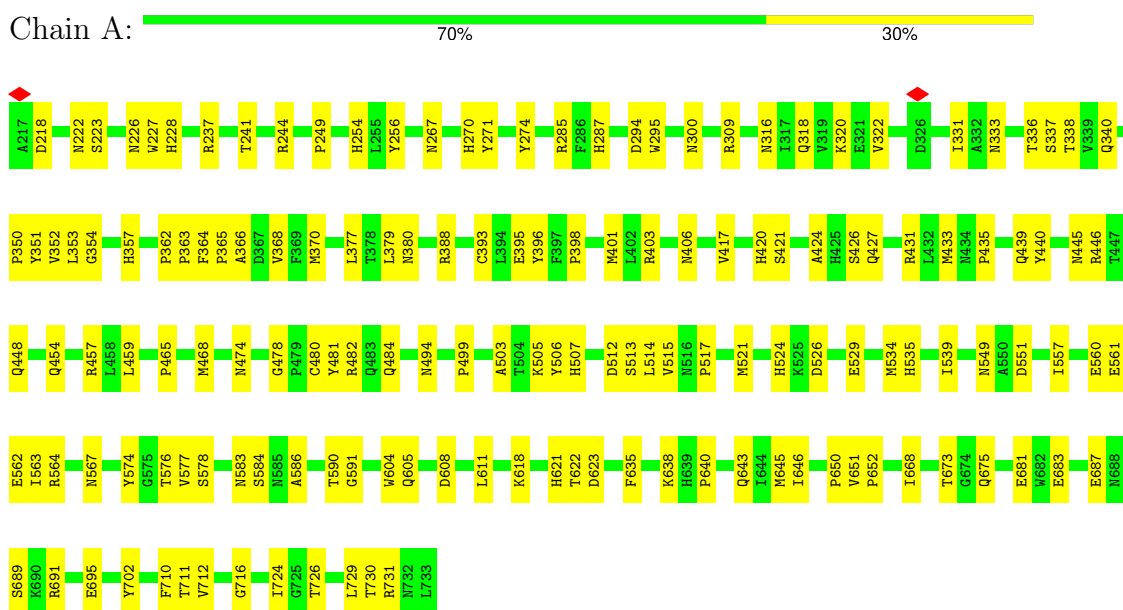
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	517	Total	C	N	O	S	1	0
			4147	2615	727	790	15		

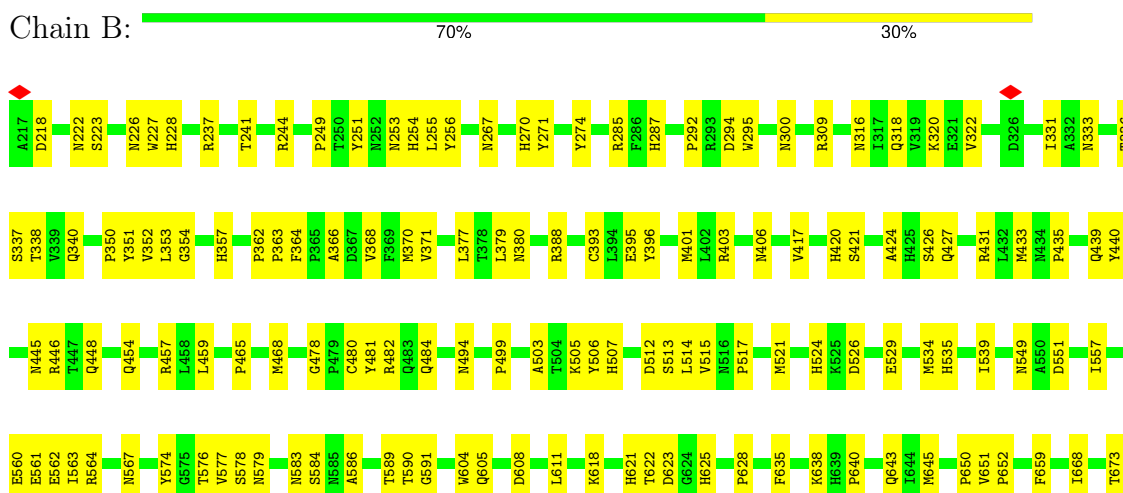
3 Residue-property plots

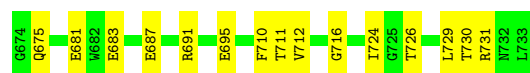
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Capsid protein



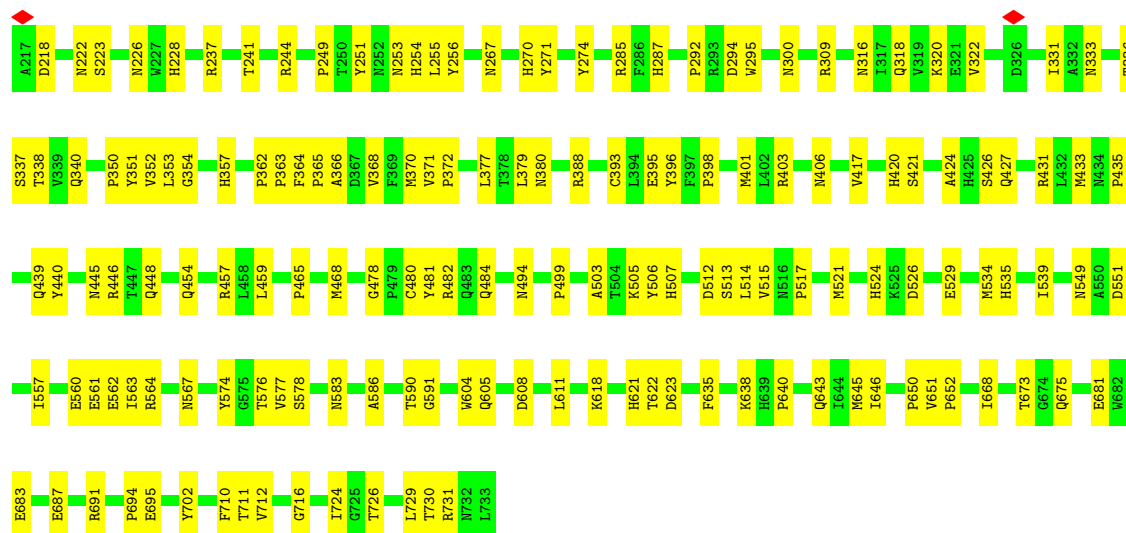
• Molecule 1: Capsid protein





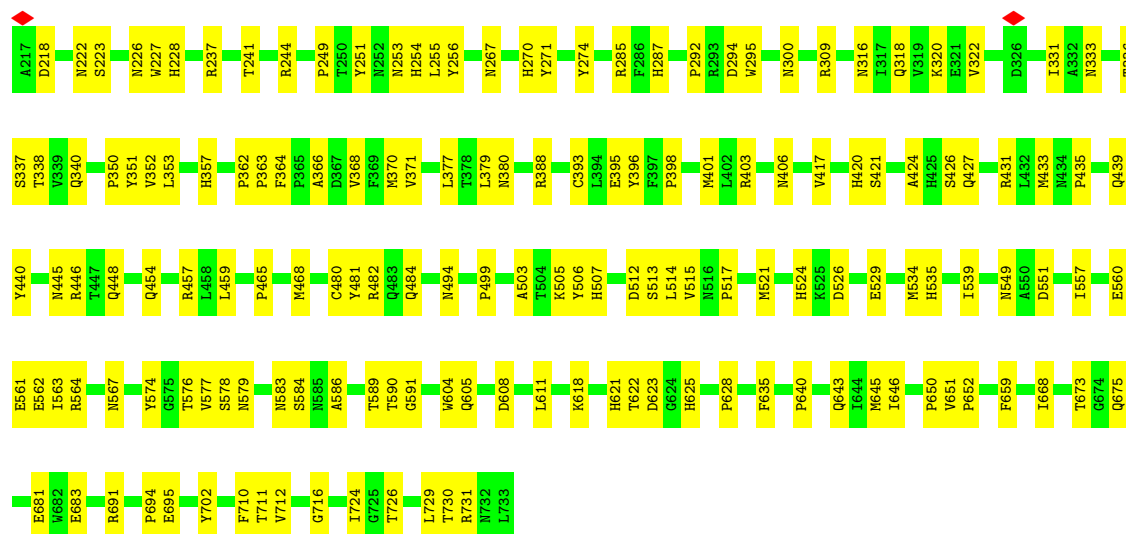
• Molecule 1: Capsid protein

Chain C: 70% 30%



• Molecule 1: Capsid protein

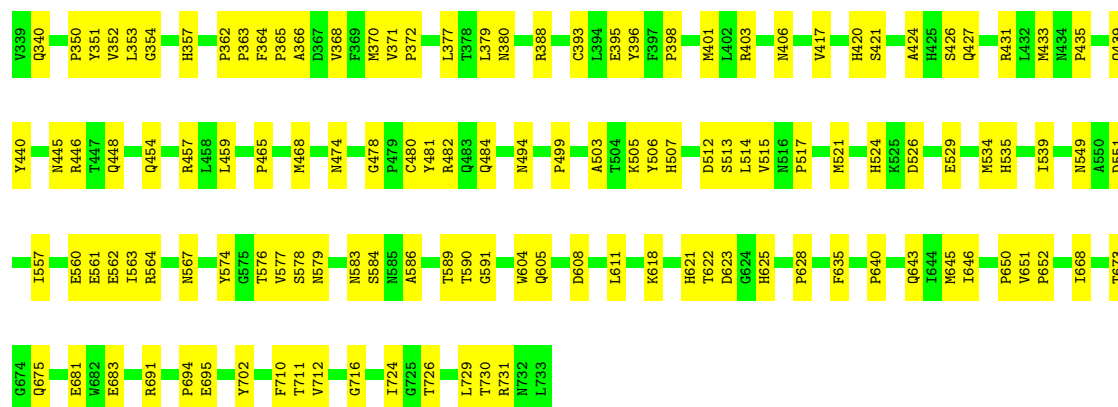
Chain D: 70% 30%



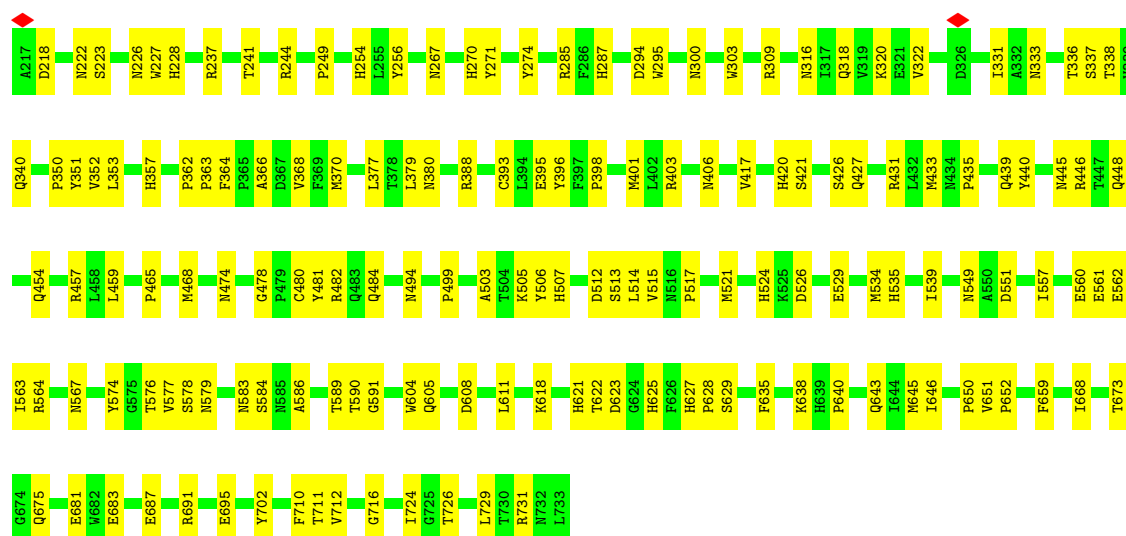
• Molecule 1: Capsid protein

Chain E: 69% 31%

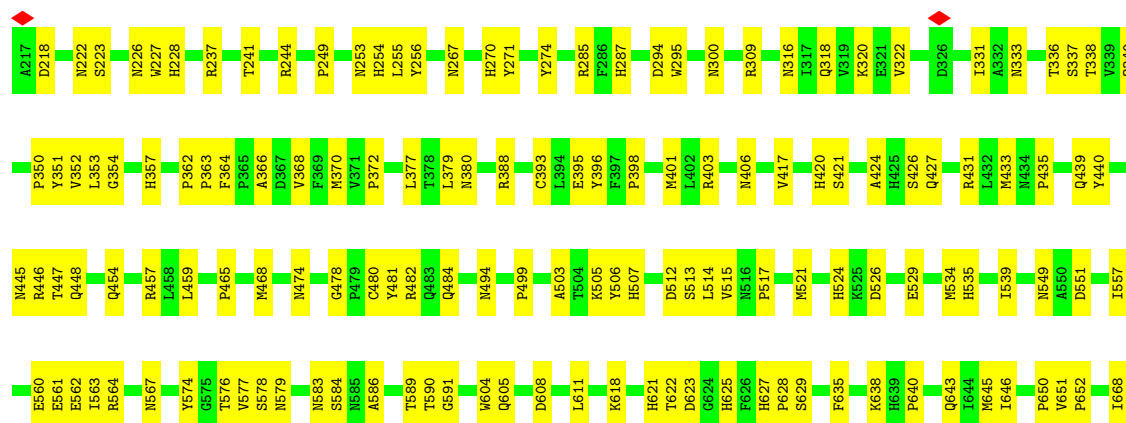




• Molecule 1: Capsid protein



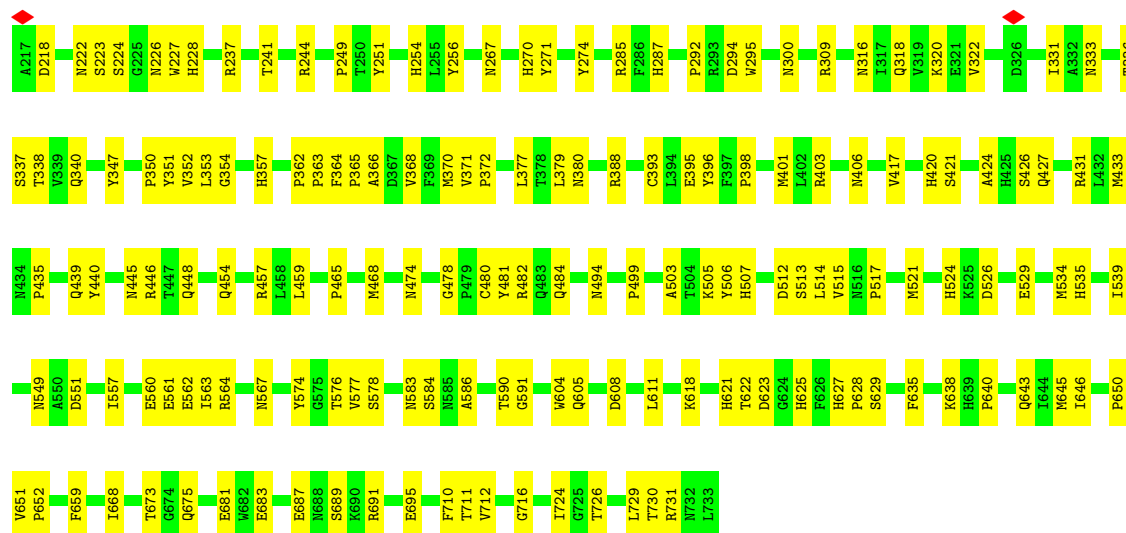
• Molecule 1: Capsid protein





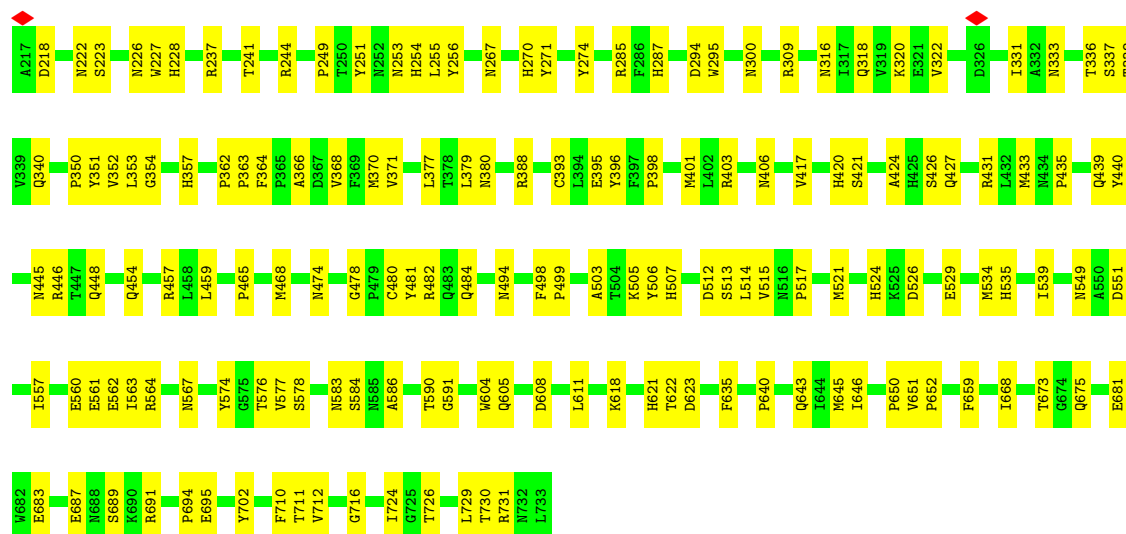
• Molecule 1: Capsid protein

Chain H: 68% 32%



• Molecule 1: Capsid protein

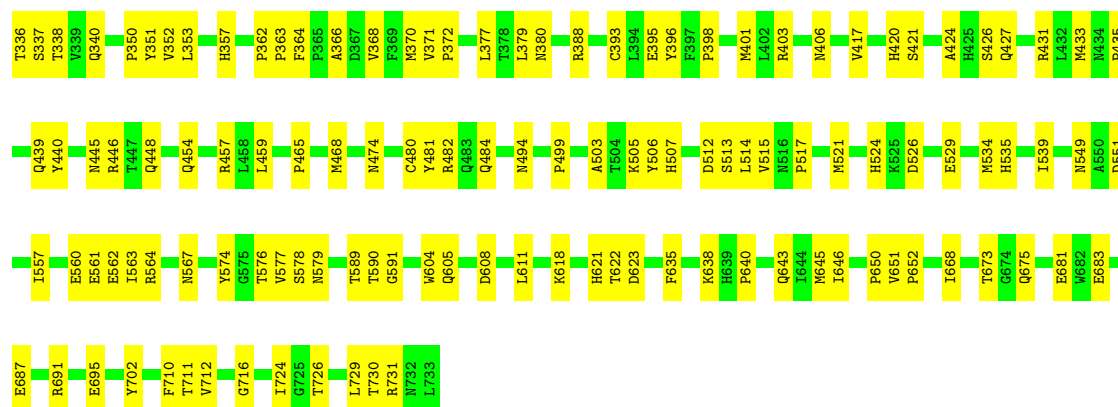
Chain I: 69% 31%



• Molecule 1: Capsid protein

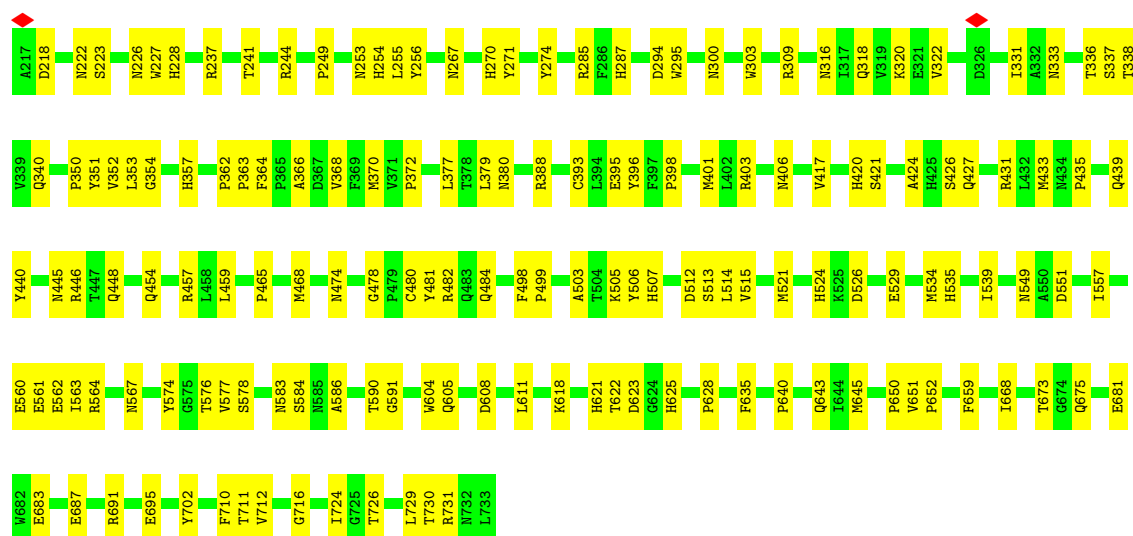
Chain J: 70% 30%





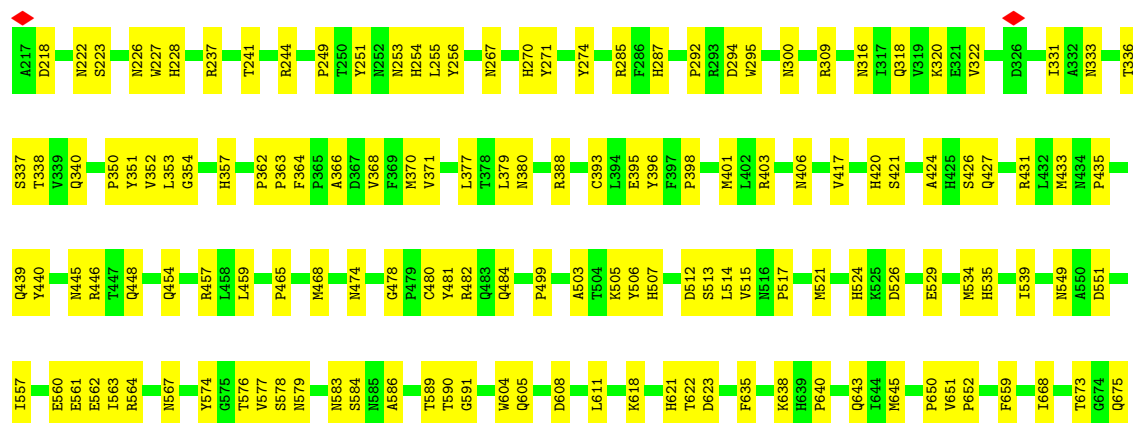
• Molecule 1: Capsid protein

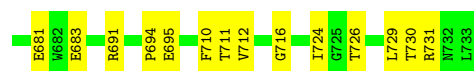
Chain K: 70% 30%



• Molecule 1: Capsid protein

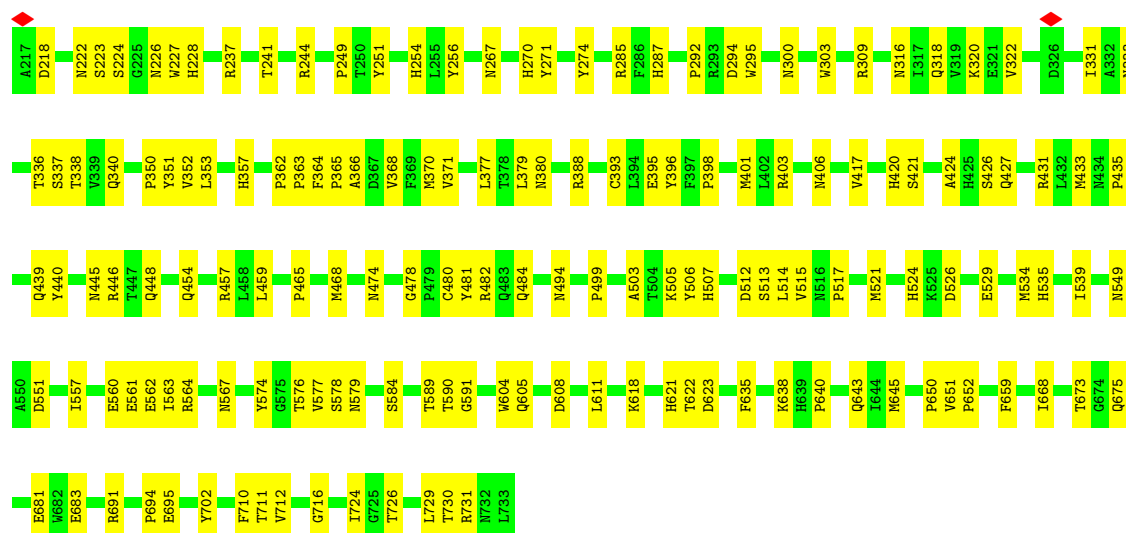
Chain L: 70% 30%





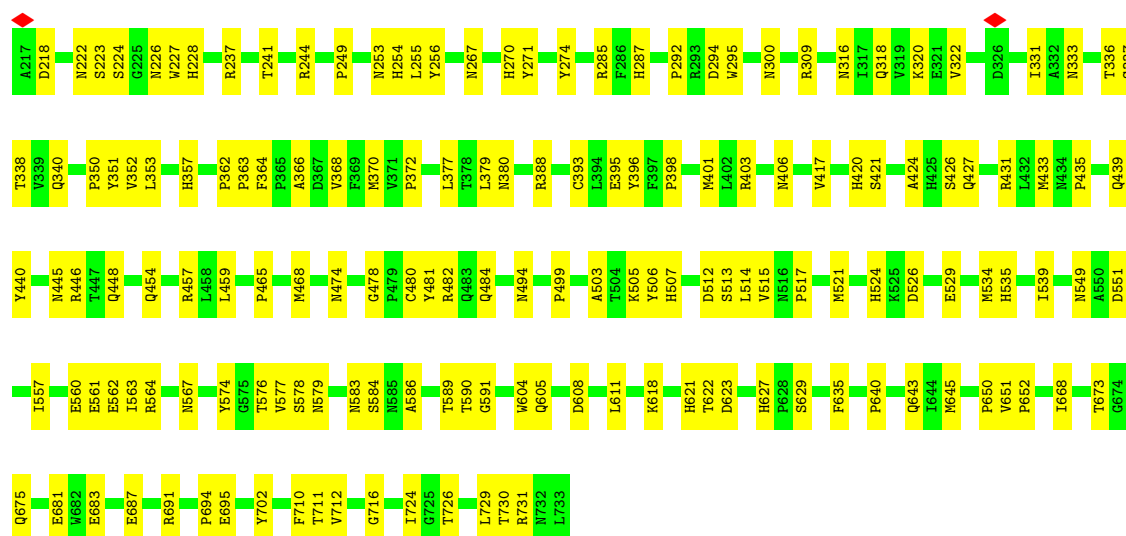
• Molecule 1: Capsid protein

Chain M: 70% 30%



• Molecule 1: Capsid protein

Chain N: 69% 31%



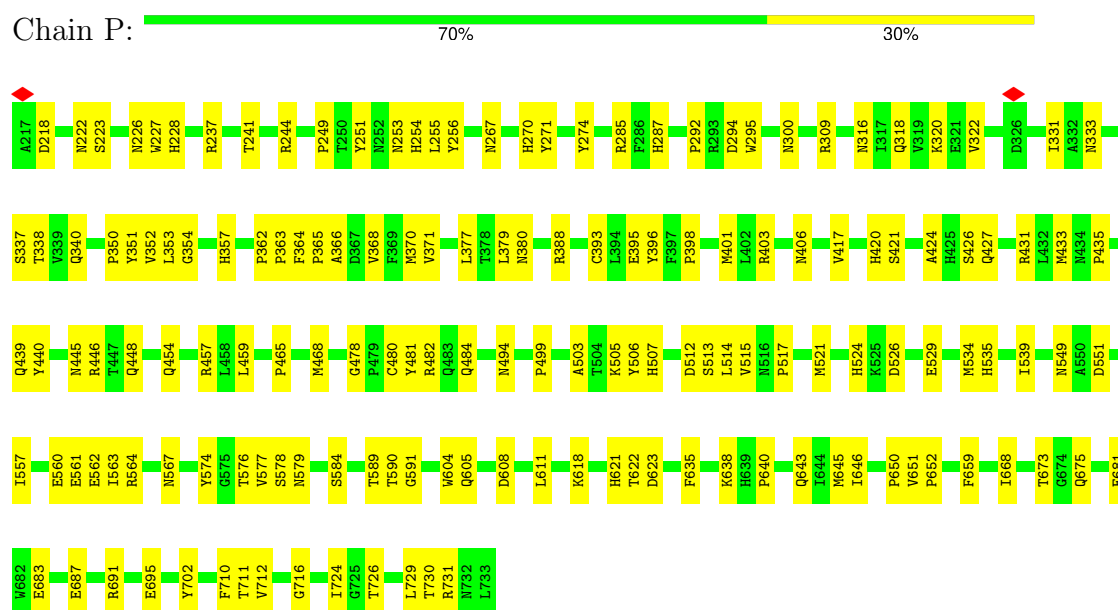
• Molecule 1: Capsid protein

Chain O: 70% 30%

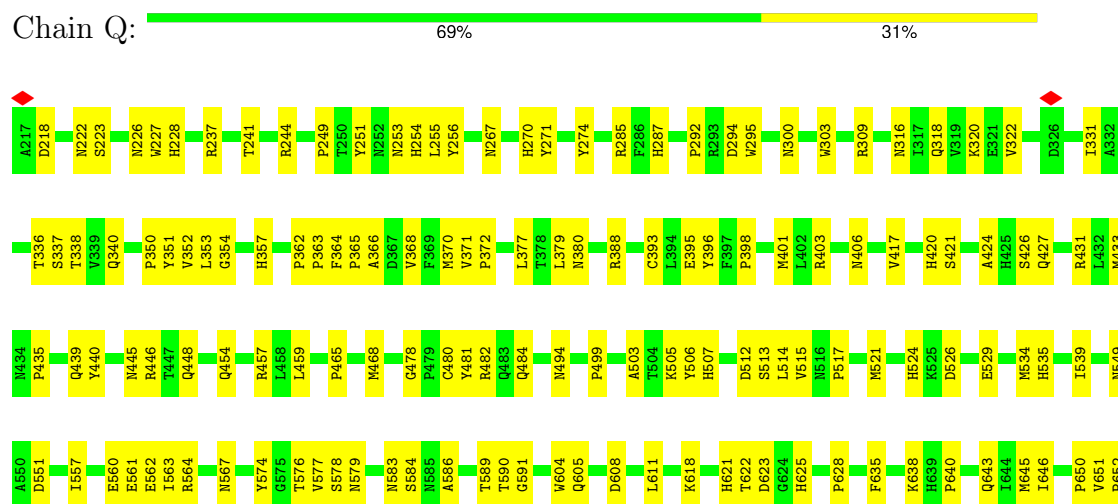




- Molecule 1: Capsid protein



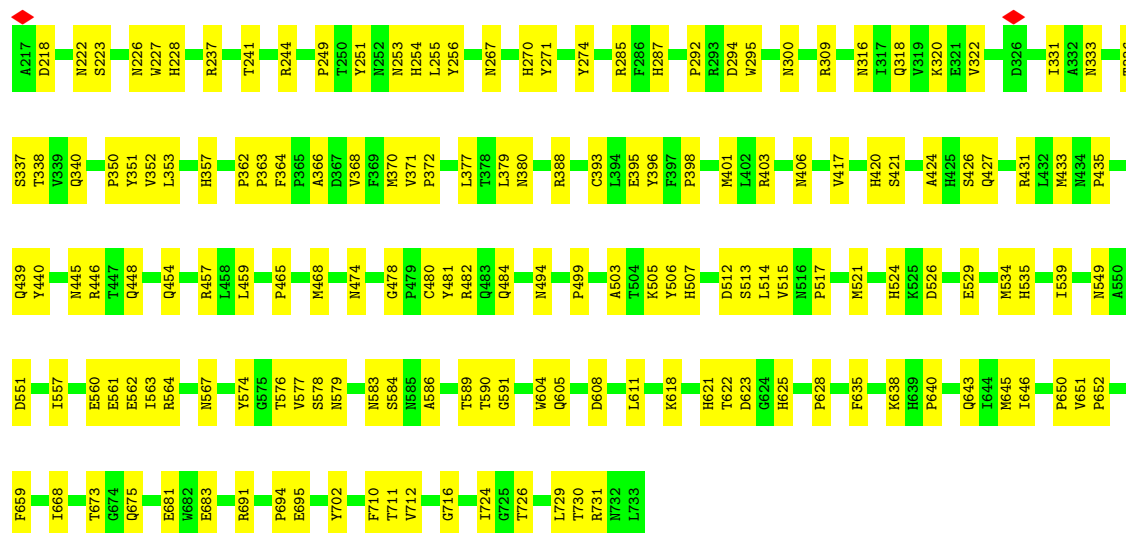
- Molecule 1: Capsid protein





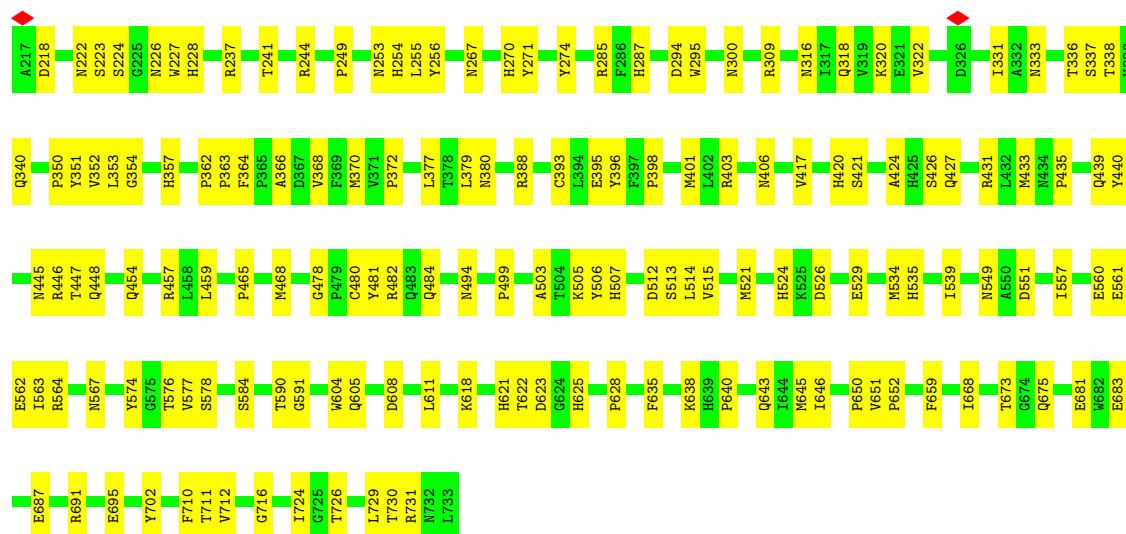
• Molecule 1: Capsid protein

Chain R: 69% 31%



• Molecule 1: Capsid protein

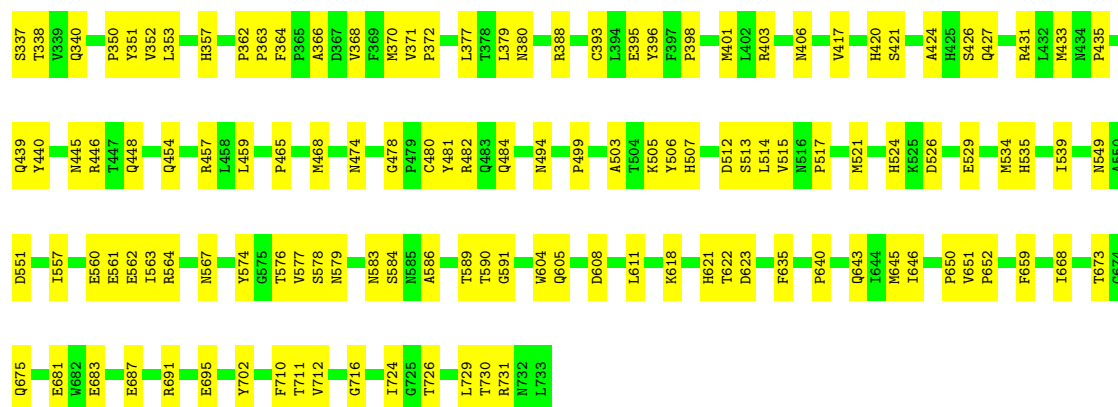
Chain S: 70% 30%



• Molecule 1: Capsid protein

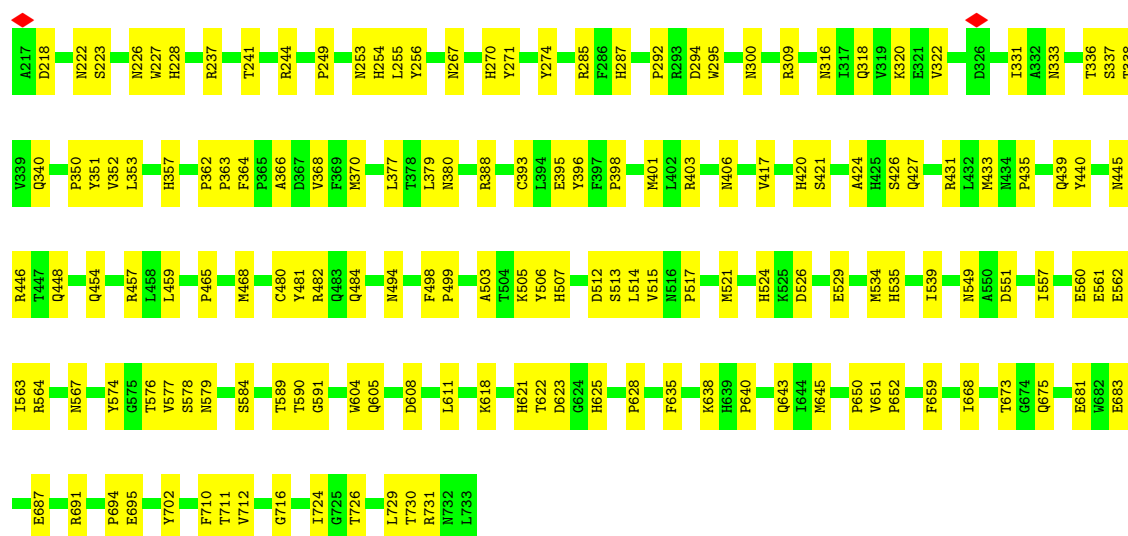
Chain T: 69% 31%





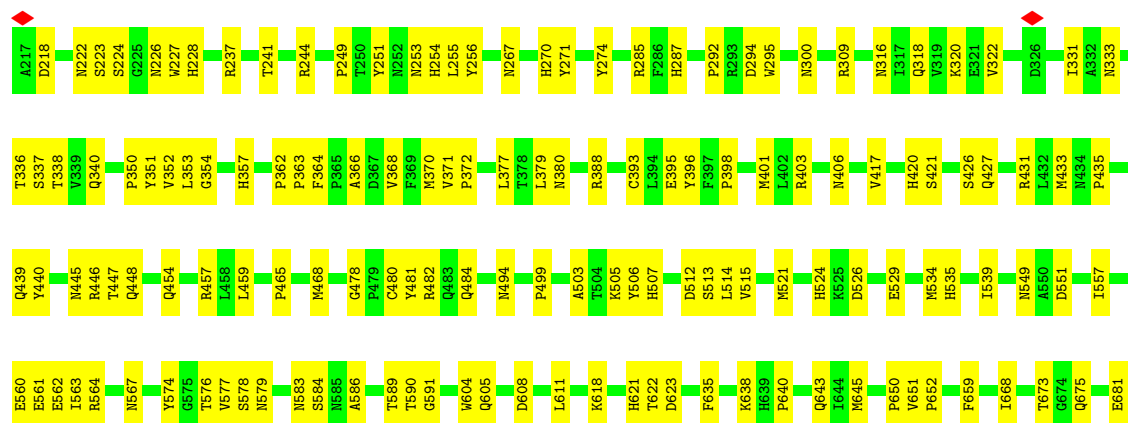
• Molecule 1: Capsid protein

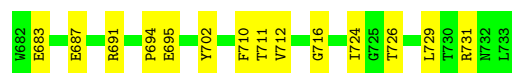
Chain U: 70% 30%



• Molecule 1: Capsid protein

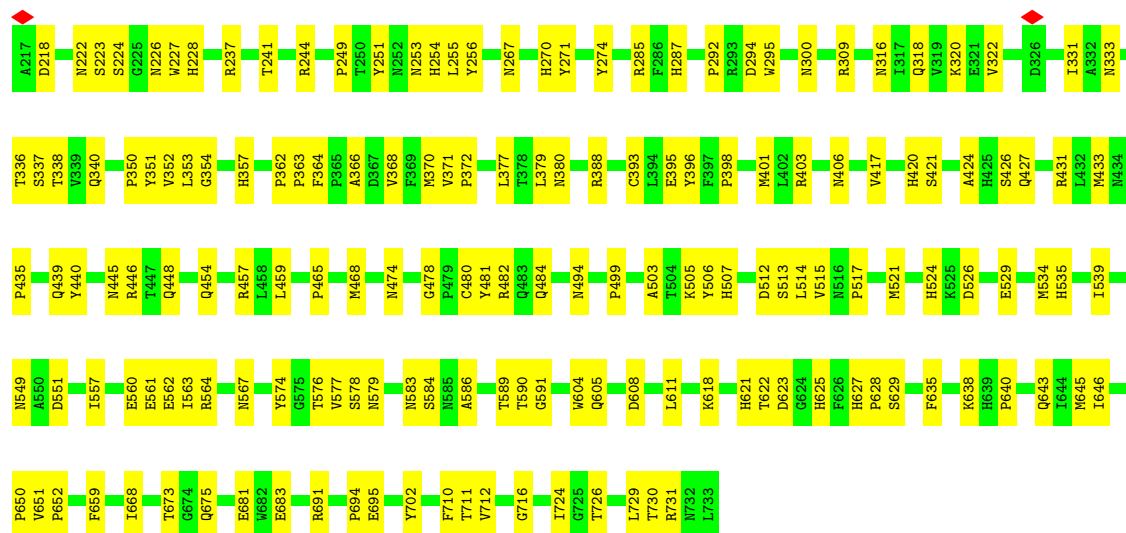
Chain V: 69% 31%





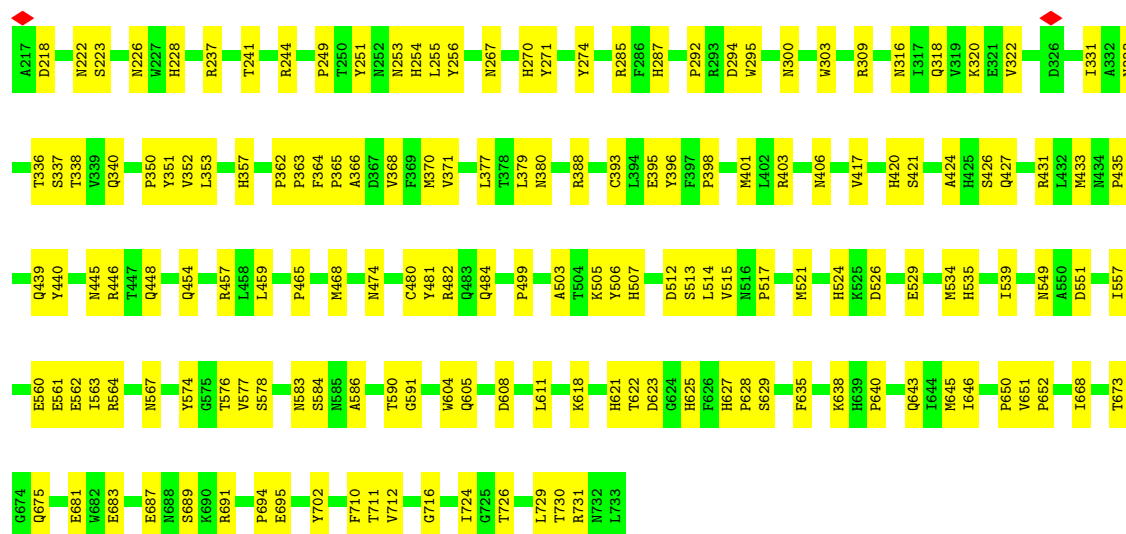
• Molecule 1: Capsid protein

Chain W: 68% 32%



• Molecule 1: Capsid protein

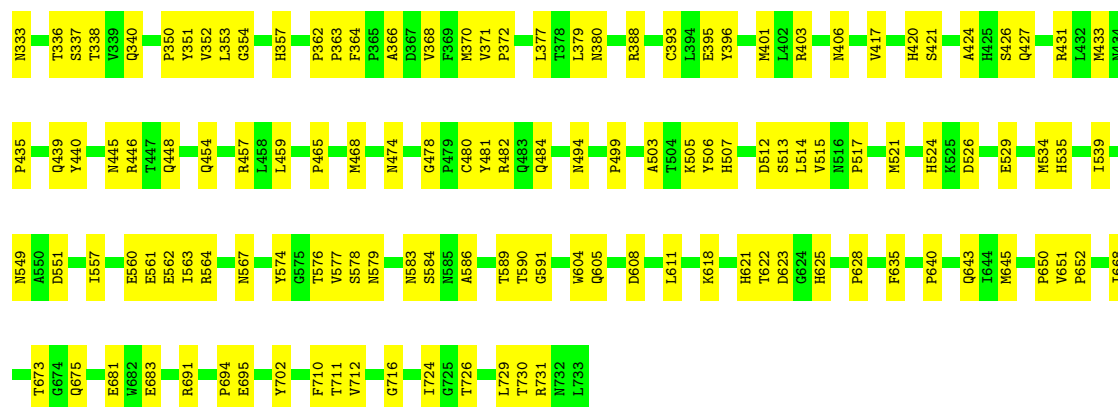
Chain X: 69% 31%



• Molecule 1: Capsid protein

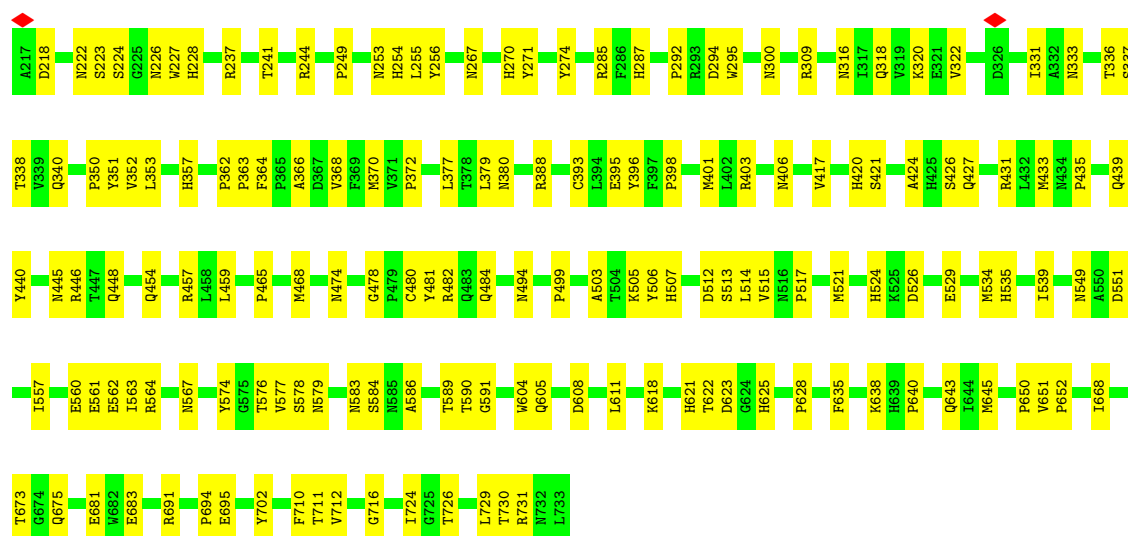
Chain Y: 69% 31%





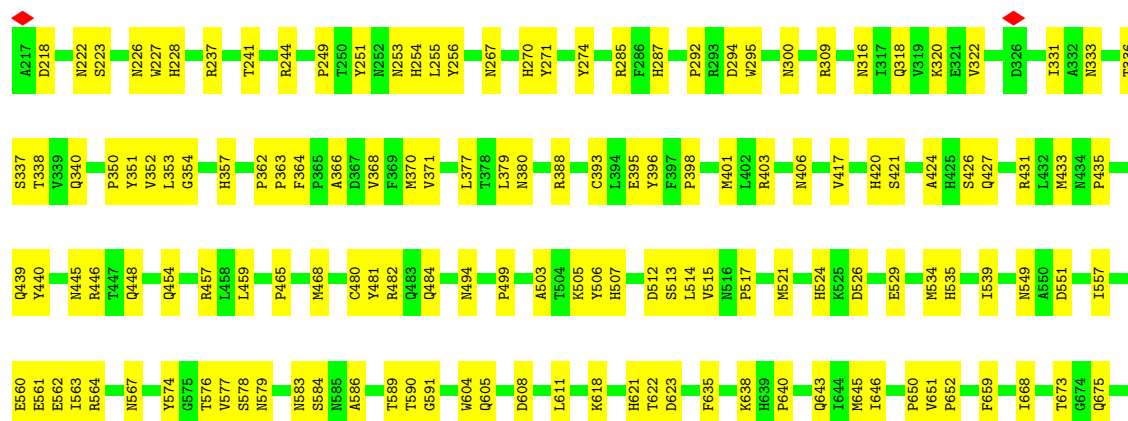
• Molecule 1: Capsid protein

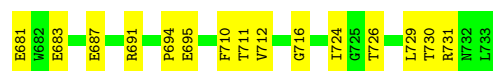
Chain Z: 69% 31%



• Molecule 1: Capsid protein

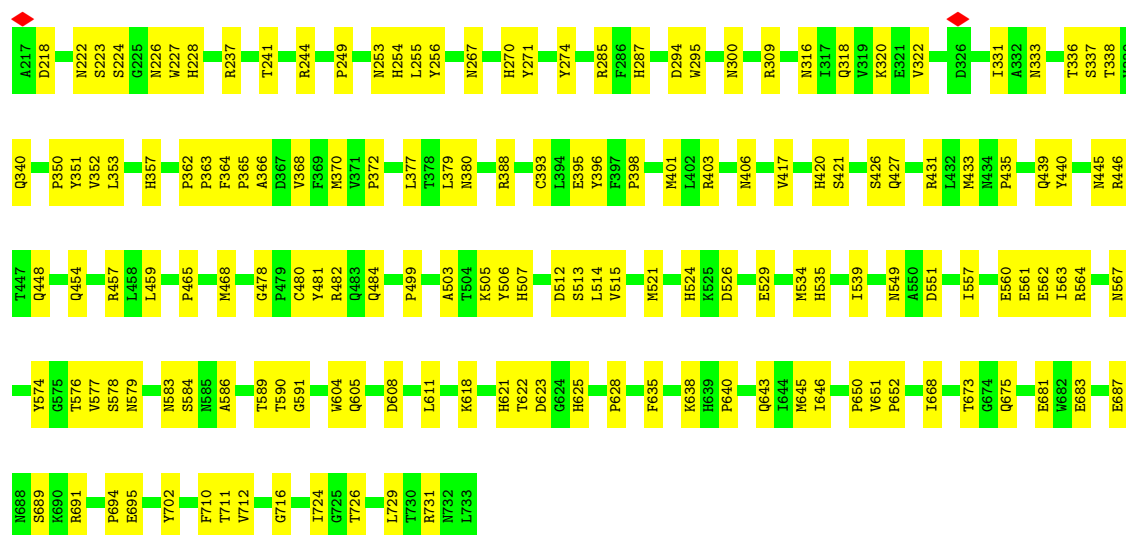
Chain a: 70% 30%





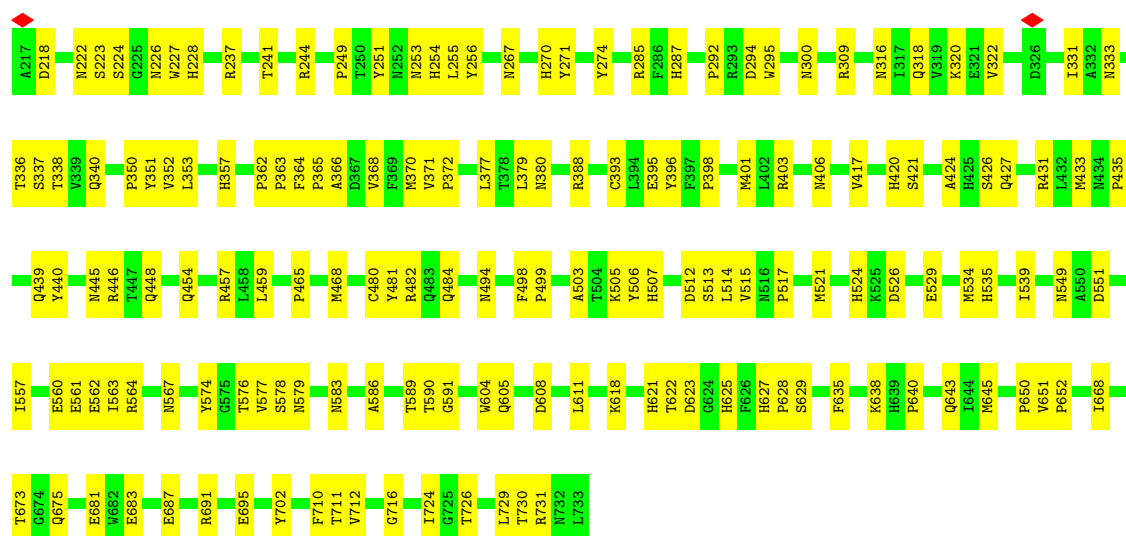
• Molecule 1: Capsid protein

Chain b: 70% 30%



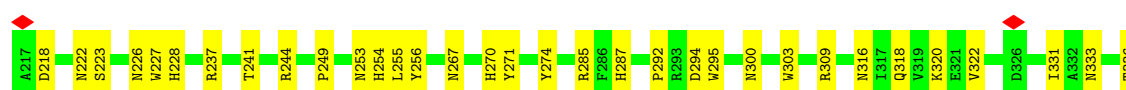
• Molecule 1: Capsid protein

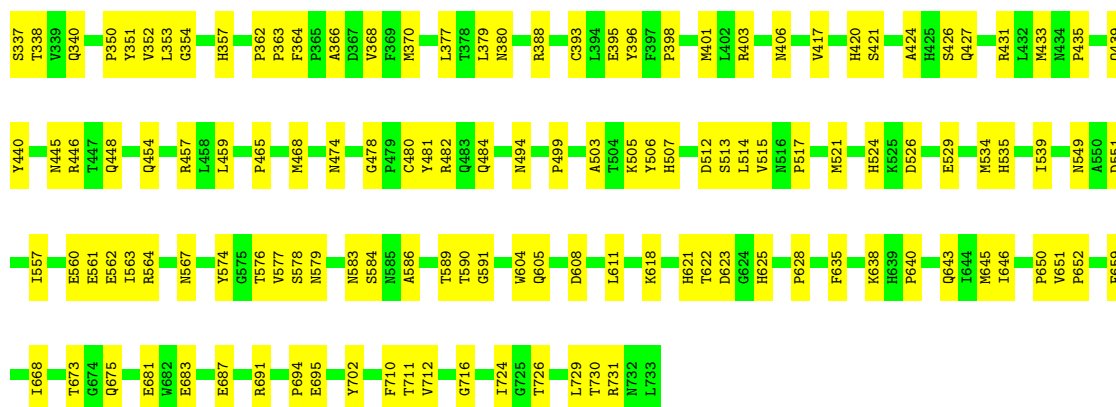
Chain c: 69% 31%



• Molecule 1: Capsid protein

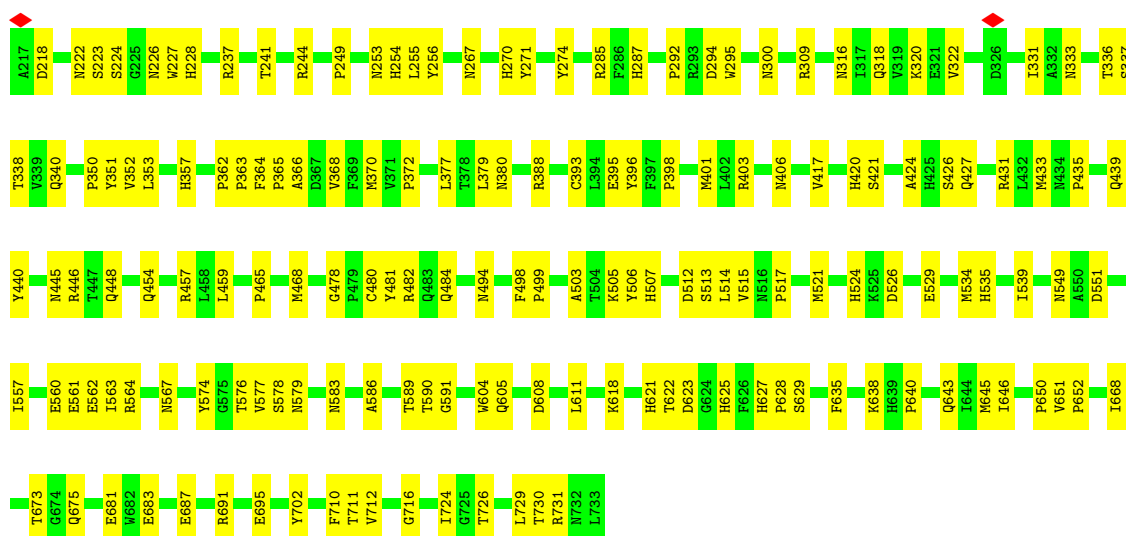
Chain d: 69% 31%





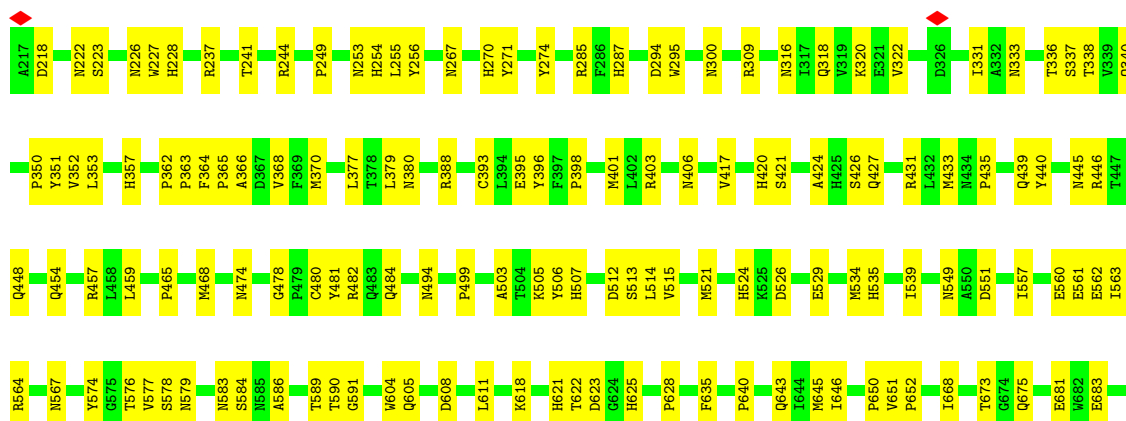
• Molecule 1: Capsid protein

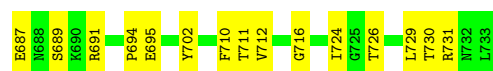
Chain e: 69% 31%



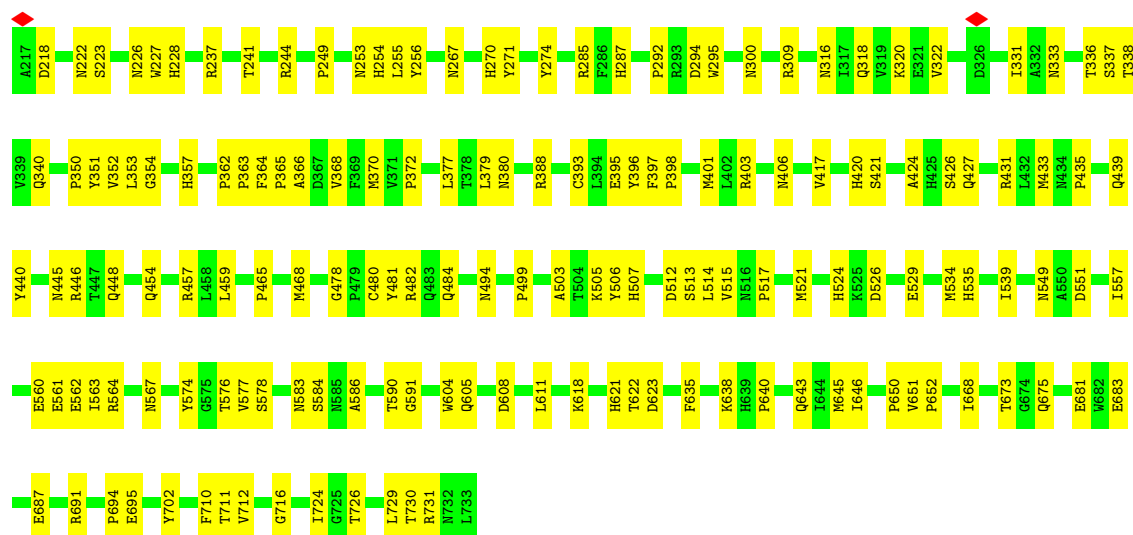
• Molecule 1: Capsid protein

Chain f: 70% 30%

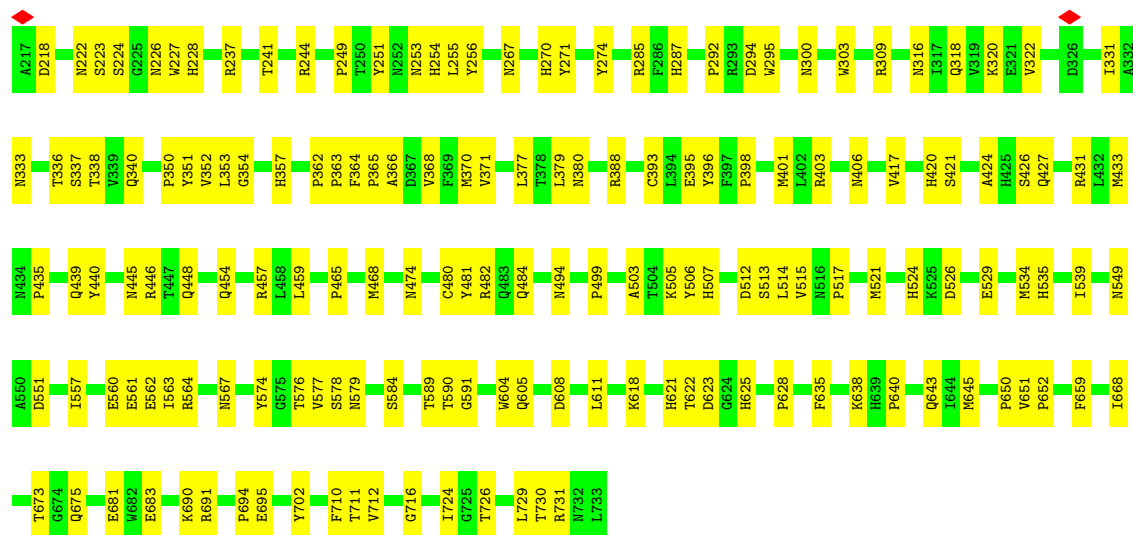




• Molecule 1: Capsid protein

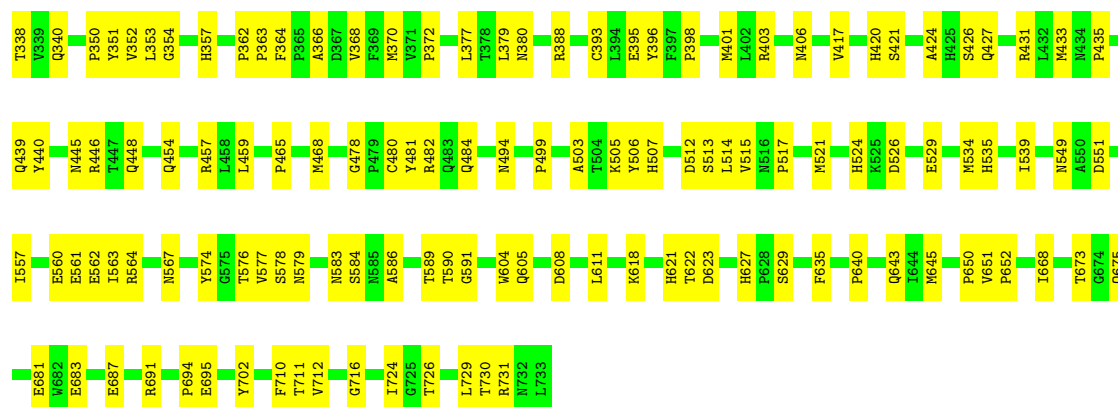


• Molecule 1: Capsid protein

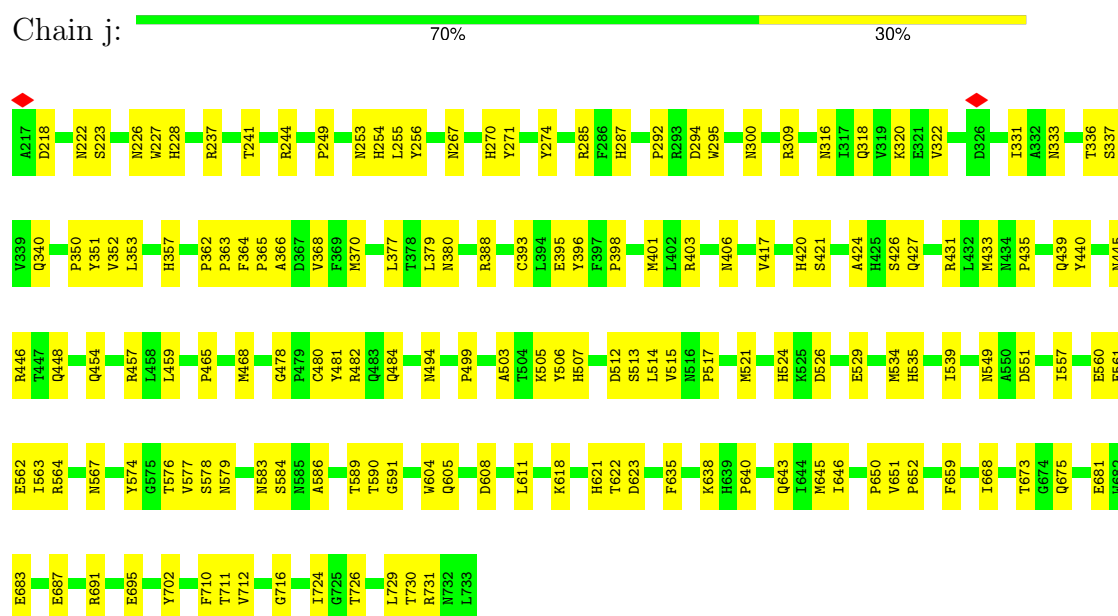


• Molecule 1: Capsid protein

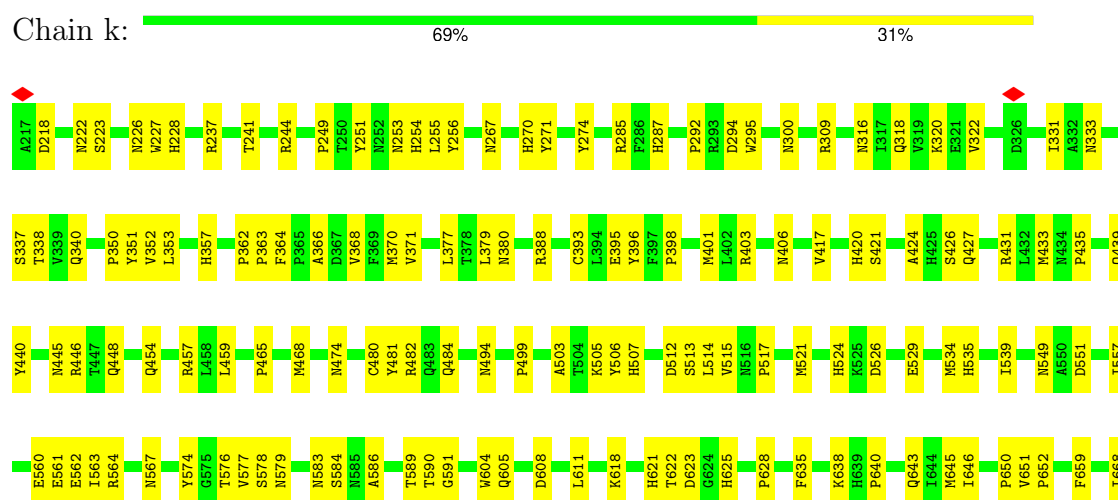




• Molecule 1: Capsid protein

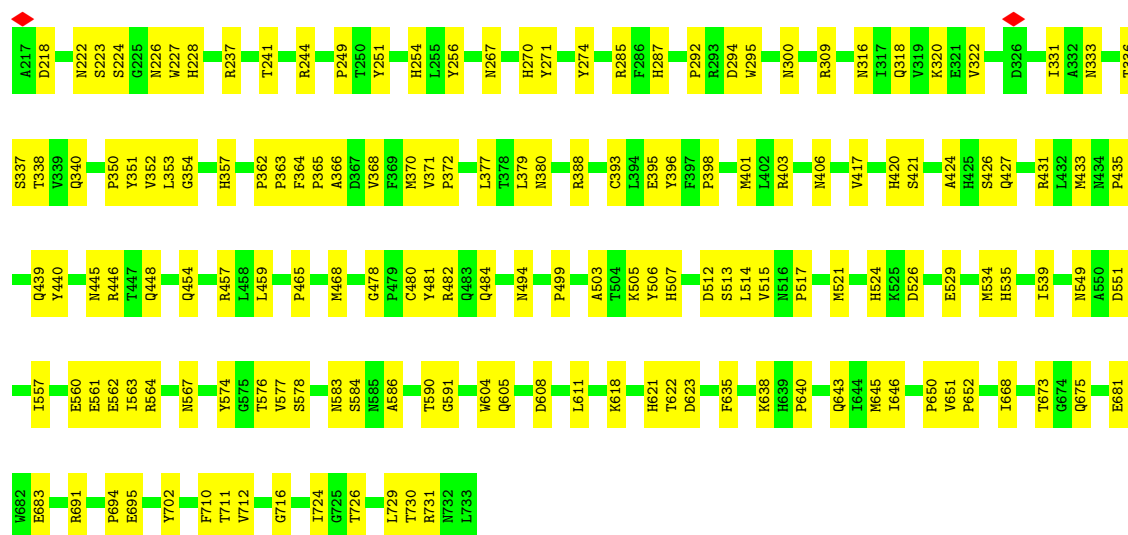


• Molecule 1: Capsid protein

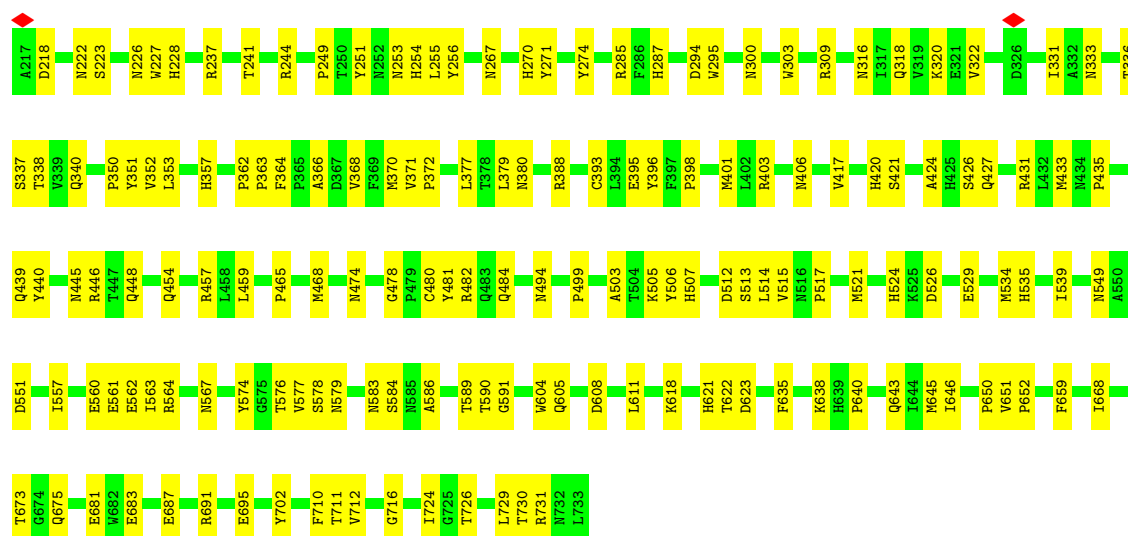




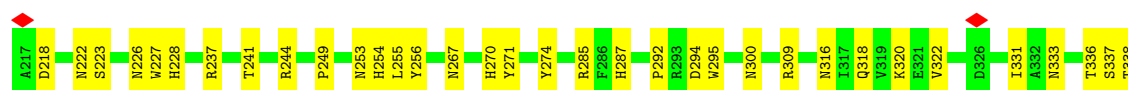
• Molecule 1: Capsid protein

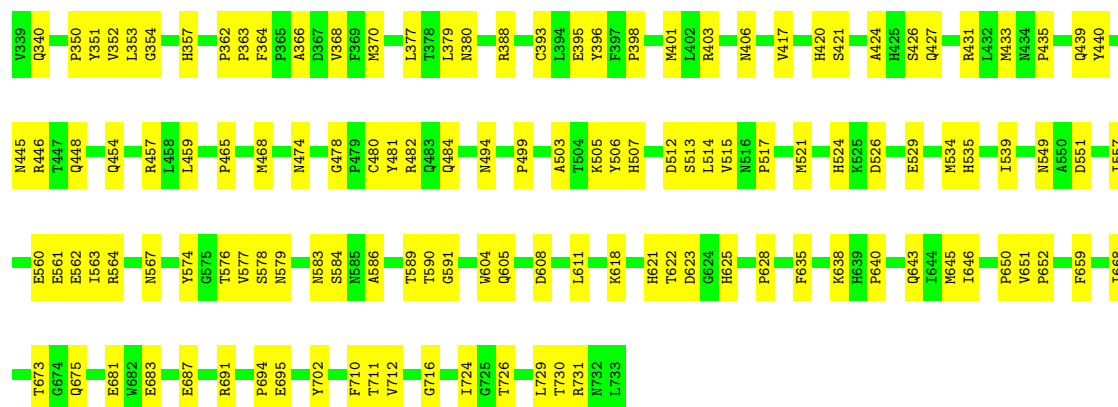


• Molecule 1: Capsid protein



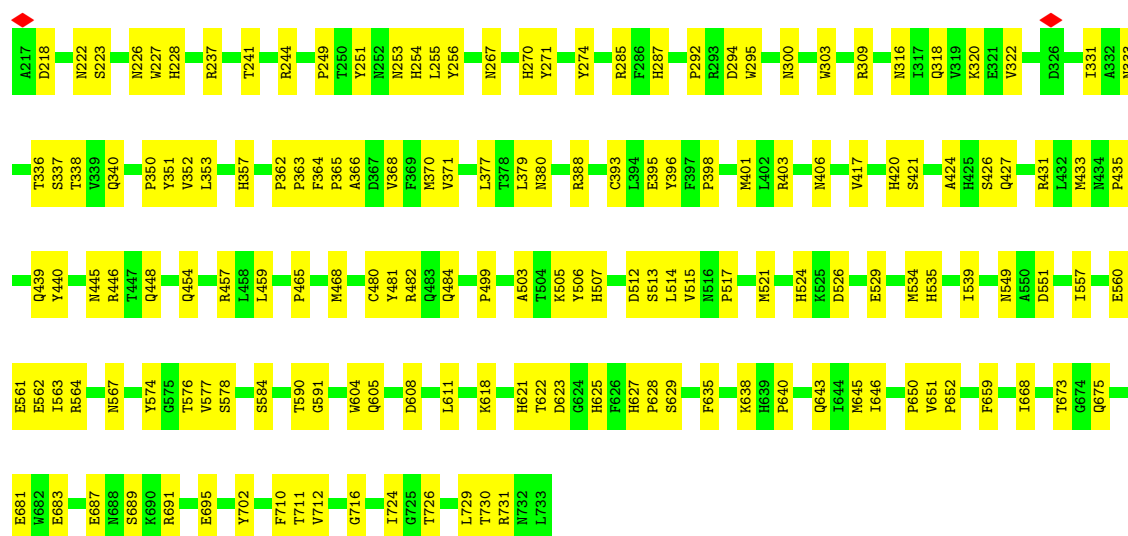
• Molecule 1: Capsid protein





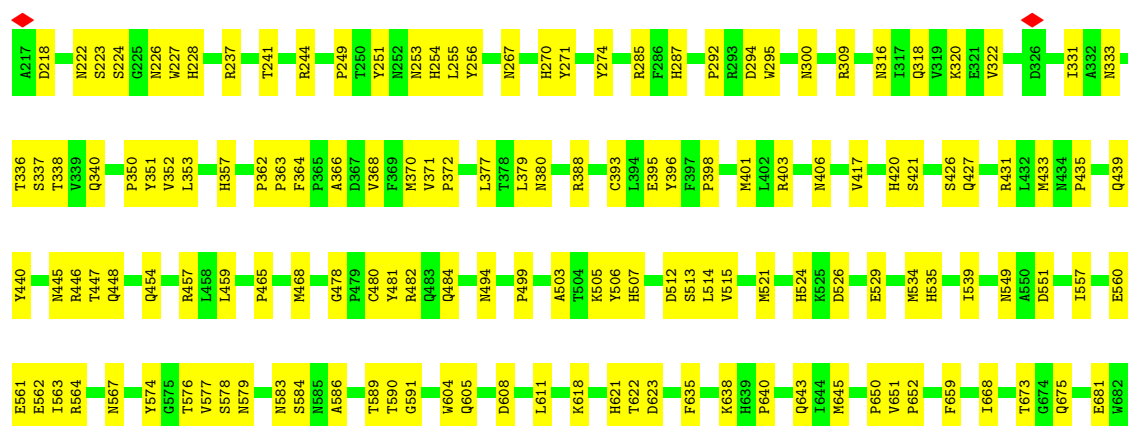
• Molecule 1: Capsid protein

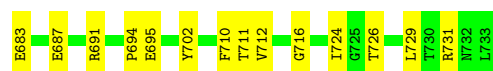
Chain o: 69% 31%



• Molecule 1: Capsid protein

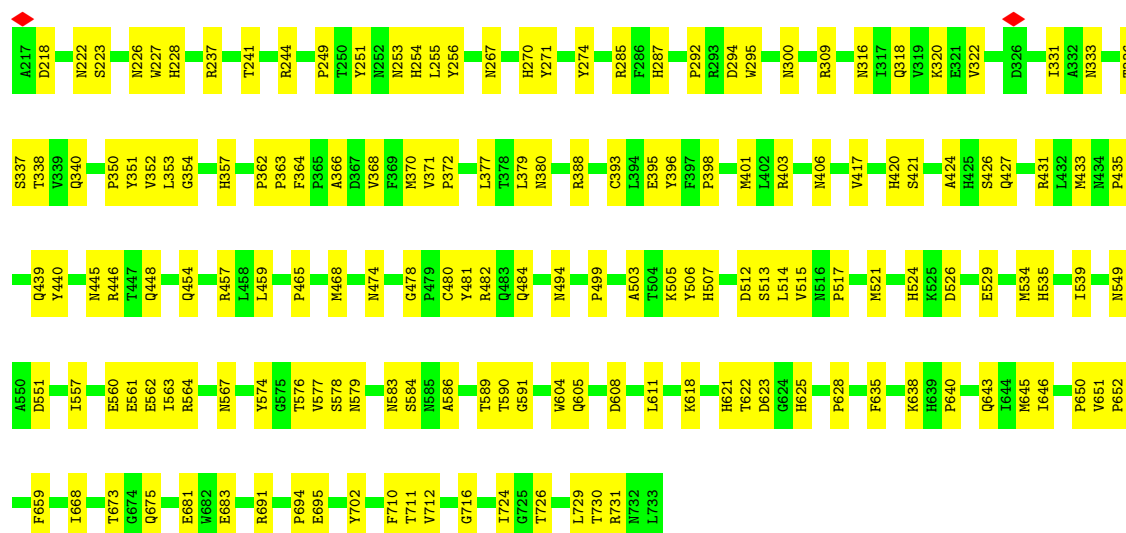
Chain p: 70% 30%





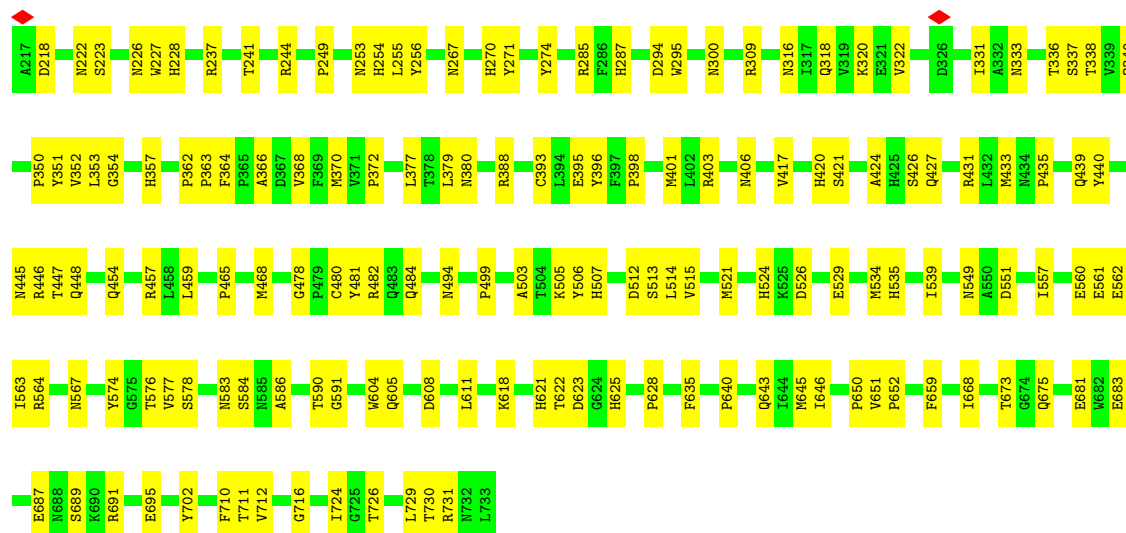
• Molecule 1: Capsid protein

Chain q: 69% 31%



• Molecule 1: Capsid protein

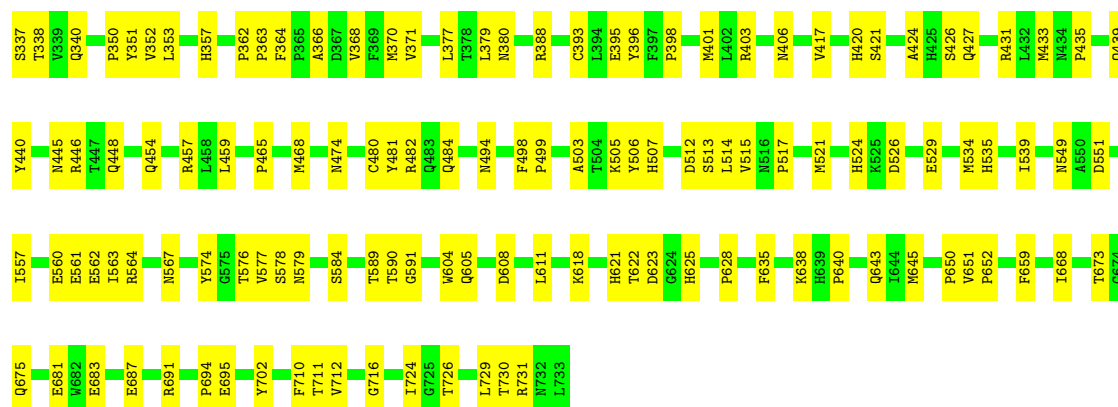
Chain r: 70% 30%



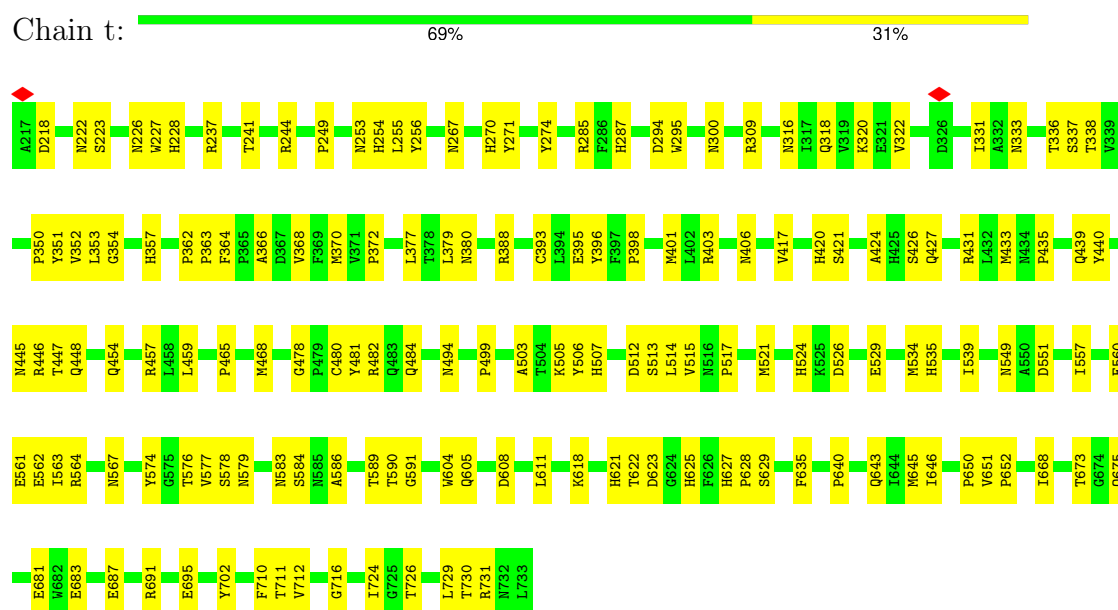
• Molecule 1: Capsid protein

Chain s: 69% 31%

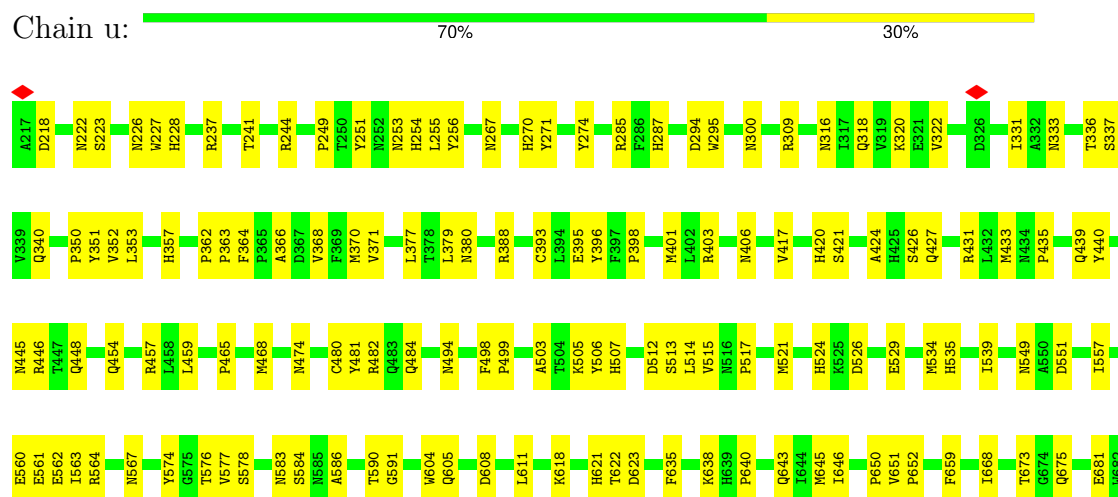


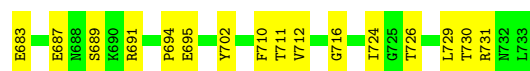


• Molecule 1: Capsid protein



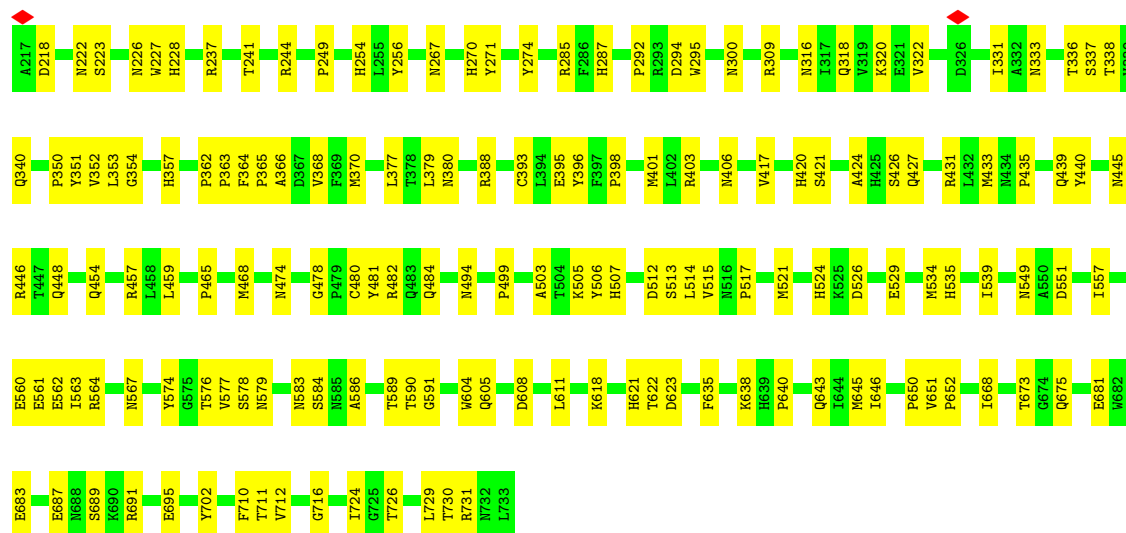
• Molecule 1: Capsid protein





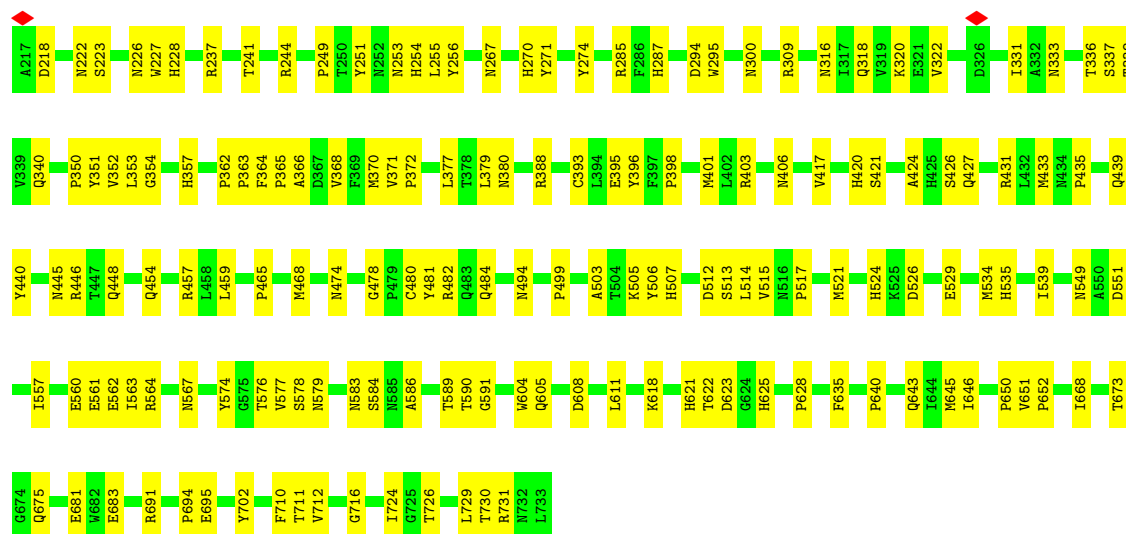
• Molecule 1: Capsid protein

Chain v: 70% 30%



• Molecule 1: Capsid protein

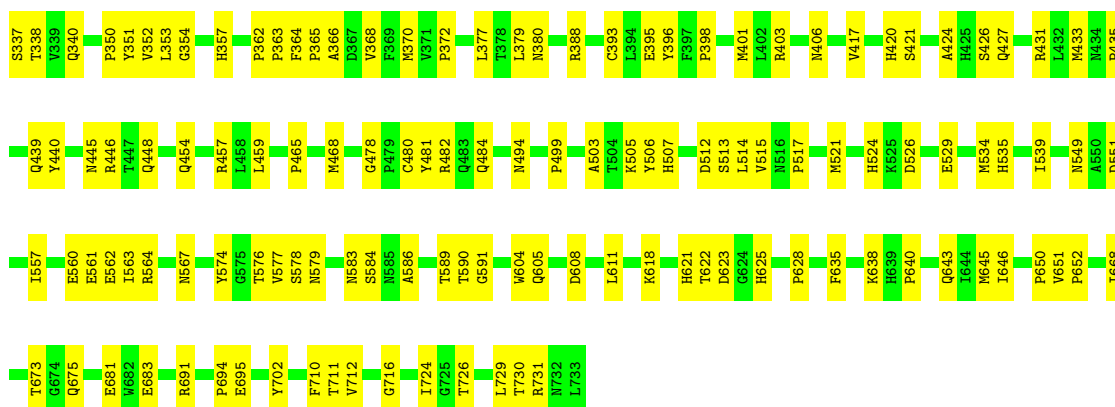
Chain w: 69% 31%



• Molecule 1: Capsid protein

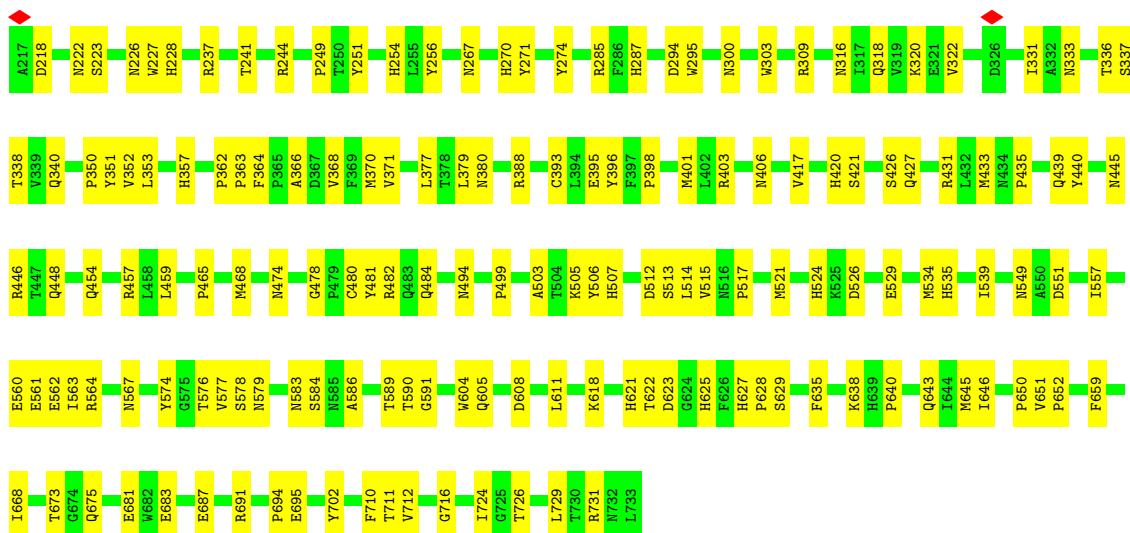
Chain x: 69% 31%





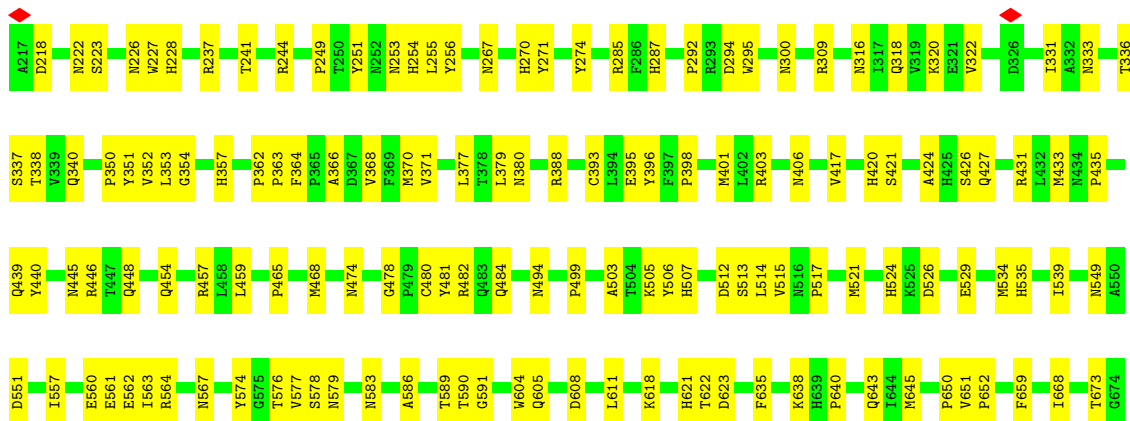
• Molecule 1: Capsid protein

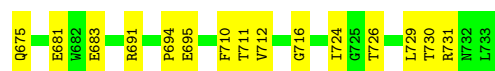
Chain y: 69% 31%



• Molecule 1: Capsid protein

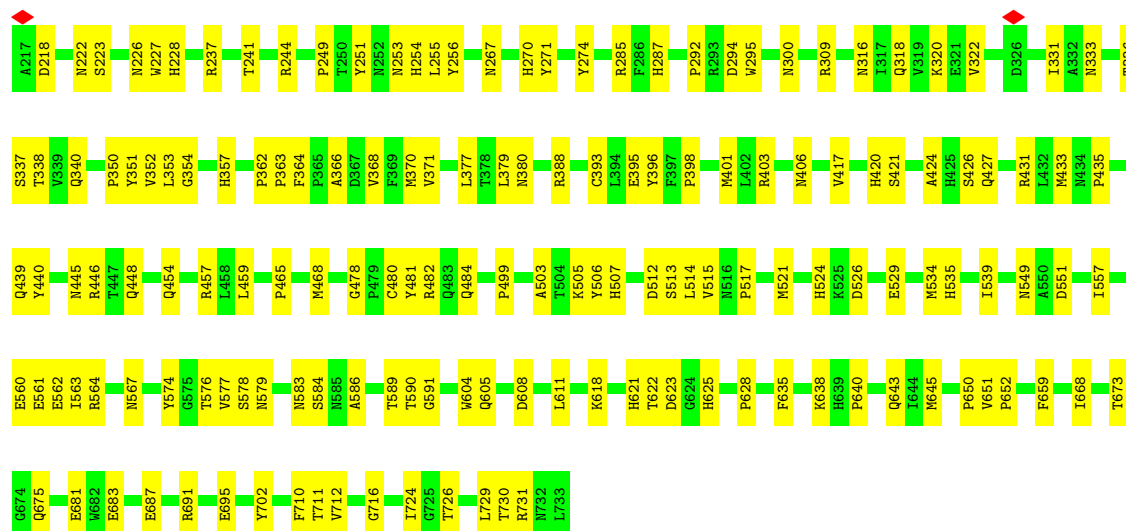
Chain z: 70% 30%





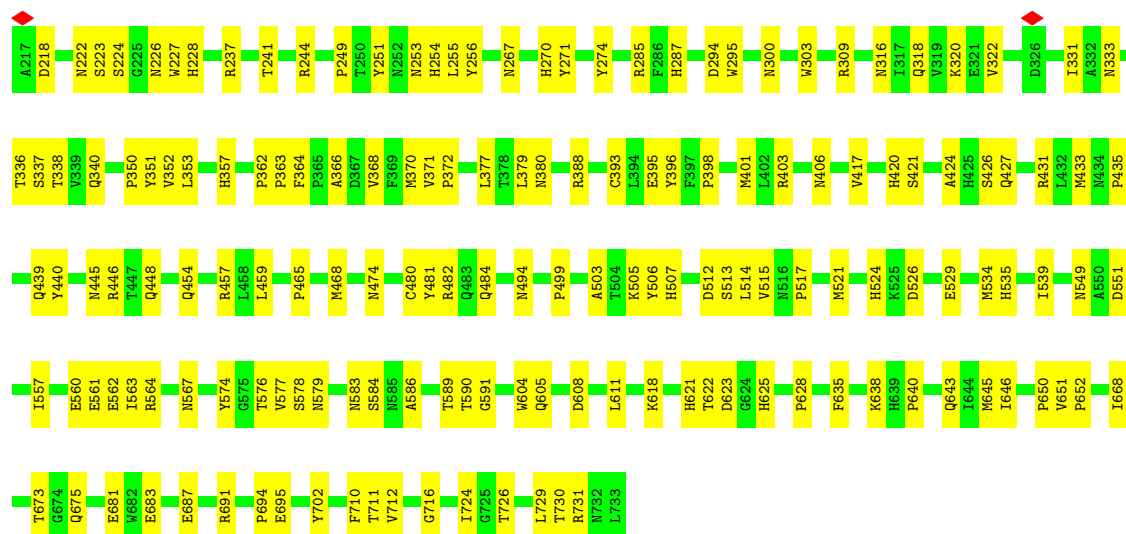
• Molecule 1: Capsid protein

Chain 1: 69% 31%



• Molecule 1: Capsid protein

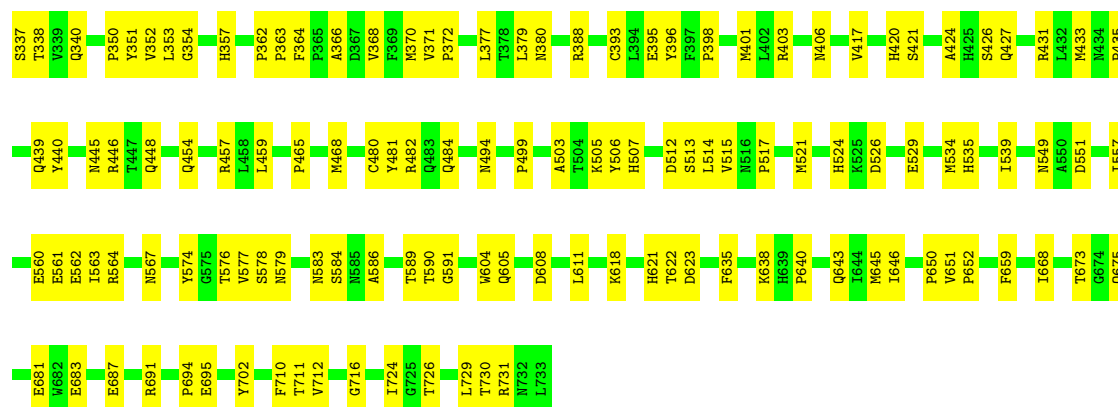
Chain 2: 69% 31%



• Molecule 1: Capsid protein

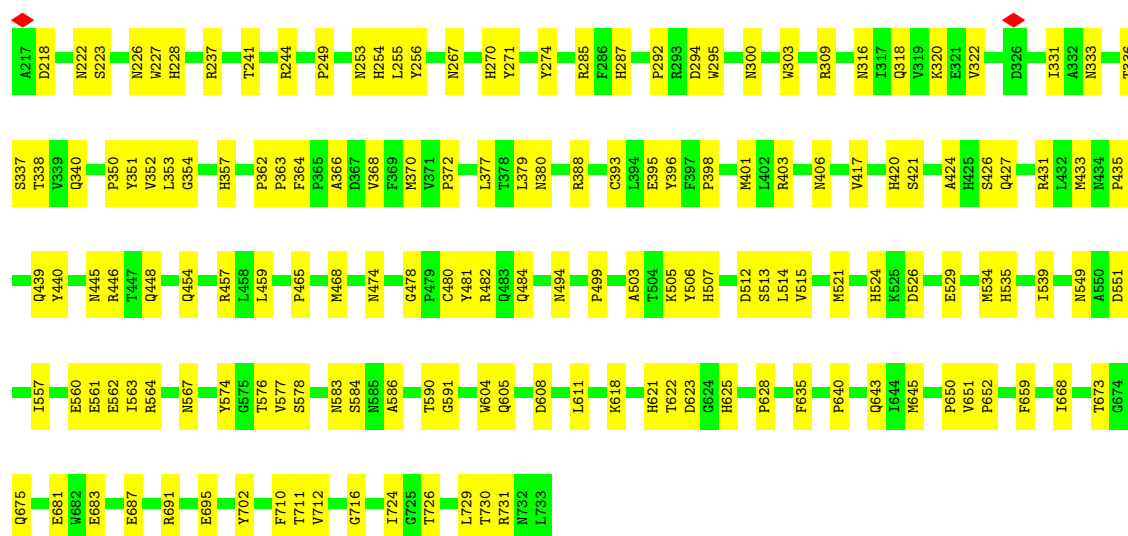
Chain 3: 69% 31%





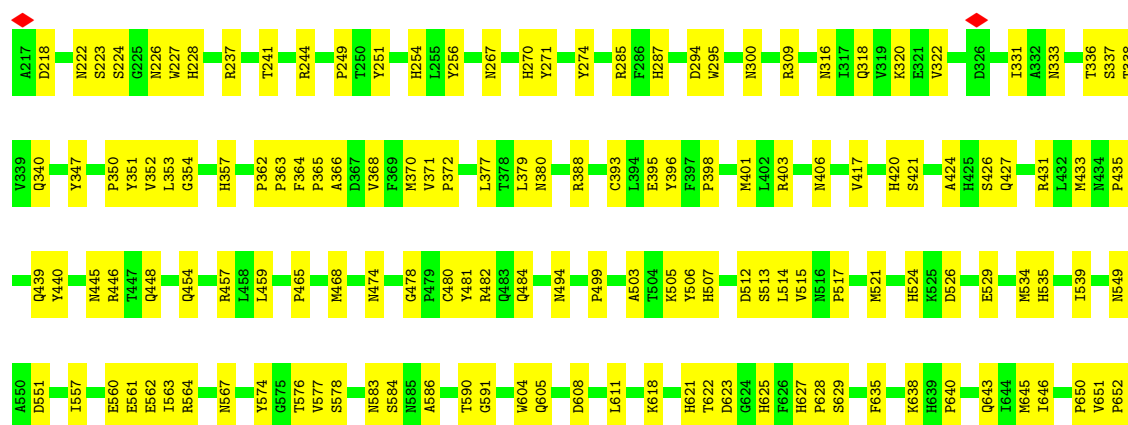
• Molecule 1: Capsid protein

Chain 4: 70% 30%



• Molecule 1: Capsid protein

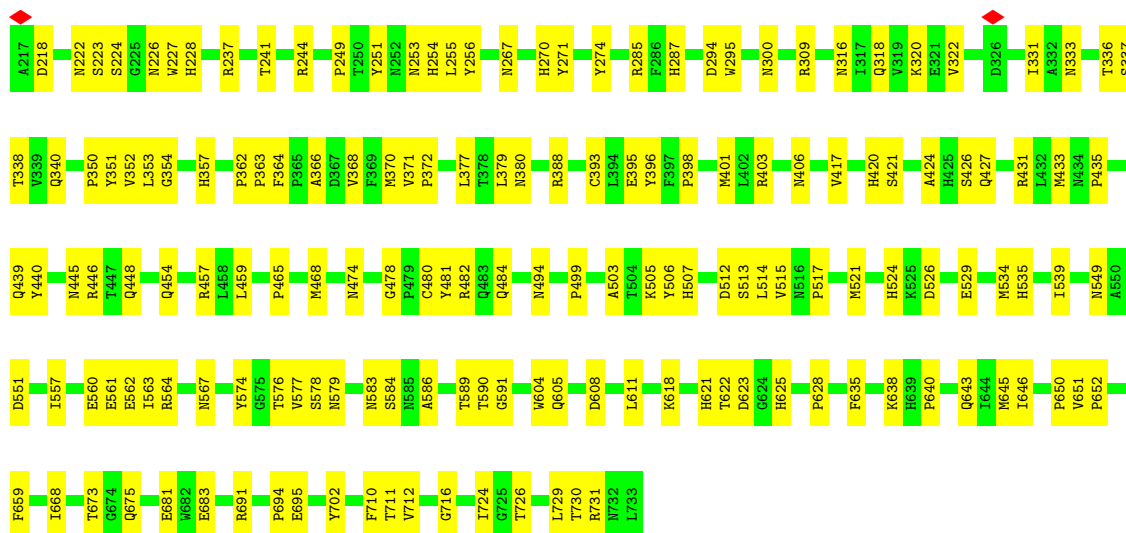
Chain 5: 68% 32%





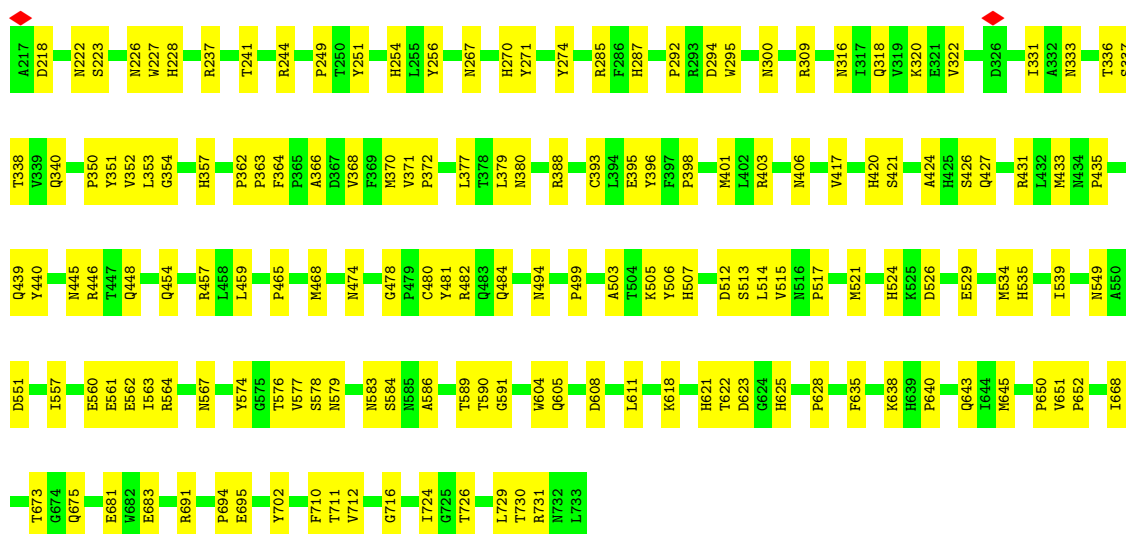
• Molecule 1: Capsid protein

Chain 6: 69% 31%



• Molecule 1: Capsid protein

Chain 7: 69% 31%



• Molecule 1: Capsid protein

Chain 8: 69% 31%



T336	Q439	A550	I668
S337	Y440	D551	
T338		I557	T673
V339	N445	E560	G674
Q340	R446	E561	Q675
P350	T447	E562	E681
Y351	Q448	I563	W682
V352		R564	E683
L353	Q454		
		N567	R691
H357	R457		
	L468	Y574	P694
P362	L459	G575	E695
P363		T576	
F364	P465	V577	Y702
P365	M468	S578	
A366		N579	F710
D367			T711
V368	N474	N583	V712
F369			
M370	G478	A586	G716
V371	P479	T589	
P372	C480	T590	I724
	Y481	G591	G725
L377	R482		T726
T378	Q483	W604	
L379	Q484	Q605	L729
N380		D608	T730
	N494		R731
R388			
	P499	L611	H732
C393		K618	L733
L394	A503	H621	
E395	T504	T622	
Y396	K505	D623	
F397	Y506	G624	
P398	H507	H625	
		P628	
	D512	F635	
M401	S513	K638	
L402	L514	H639	
R403	V515	P640	
		Q643	
M406	N516	I644	
	P517	M645	
V417			
	M521	P650	
		V651	
H420	H524	P652	
S421	K525	F659	
	D526		
A424			
H425	E529		
S426			
Q427			
	M534		
R431	H535		
L432			
H433	I539		
N434			
P435	N549		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	56962	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	17.134	Depositor
Minimum map value	-9.775	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (\AA)	452.34, 452.34, 452.34	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.077, 1.077, 1.077	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.45	0/4276	0.57	1/5833 (0.0%)
1	2	0.45	0/4276	0.57	1/5833 (0.0%)
1	3	0.45	0/4276	0.57	1/5833 (0.0%)
1	4	0.45	0/4276	0.57	0/5833
1	5	0.45	0/4276	0.57	1/5833 (0.0%)
1	6	0.45	0/4276	0.57	1/5833 (0.0%)
1	7	0.45	0/4276	0.57	1/5833 (0.0%)
1	8	0.45	0/4276	0.57	1/5833 (0.0%)
1	A	0.45	0/4276	0.57	1/5833 (0.0%)
1	B	0.45	0/4276	0.57	1/5833 (0.0%)
1	C	0.45	0/4276	0.57	1/5833 (0.0%)
1	D	0.45	0/4276	0.57	0/5833
1	E	0.45	0/4276	0.57	0/5833
1	F	0.45	0/4276	0.57	1/5833 (0.0%)
1	G	0.45	0/4276	0.57	1/5833 (0.0%)
1	H	0.45	0/4276	0.57	1/5833 (0.0%)
1	I	0.45	0/4276	0.57	0/5833
1	J	0.45	0/4276	0.57	1/5833 (0.0%)
1	K	0.45	0/4276	0.57	0/5833
1	L	0.45	0/4276	0.57	1/5833 (0.0%)
1	M	0.45	0/4276	0.57	1/5833 (0.0%)
1	N	0.45	0/4276	0.57	0/5833
1	O	0.45	0/4276	0.57	1/5833 (0.0%)
1	P	0.45	0/4276	0.57	1/5833 (0.0%)
1	Q	0.45	0/4276	0.57	1/5833 (0.0%)
1	R	0.45	0/4276	0.57	1/5833 (0.0%)
1	S	0.45	0/4276	0.57	1/5833 (0.0%)
1	T	0.45	0/4276	0.57	0/5833
1	U	0.45	0/4276	0.57	1/5833 (0.0%)
1	V	0.45	0/4276	0.57	1/5833 (0.0%)
1	W	0.45	0/4276	0.57	1/5833 (0.0%)
1	X	0.45	0/4276	0.57	1/5833 (0.0%)
1	Y	0.45	0/4276	0.57	0/5833
1	Z	0.45	0/4276	0.57	1/5833 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.45	0/4276	0.57	1/5833 (0.0%)
1	b	0.45	0/4276	0.57	1/5833 (0.0%)
1	c	0.45	0/4276	0.57	1/5833 (0.0%)
1	d	0.45	0/4276	0.57	1/5833 (0.0%)
1	e	0.45	0/4276	0.57	1/5833 (0.0%)
1	f	0.45	0/4276	0.57	0/5833
1	g	0.45	0/4276	0.57	1/5833 (0.0%)
1	h	0.45	0/4276	0.57	1/5833 (0.0%)
1	i	0.45	0/4276	0.57	0/5833
1	j	0.45	0/4276	0.57	1/5833 (0.0%)
1	k	0.45	0/4276	0.57	1/5833 (0.0%)
1	l	0.45	0/4276	0.57	1/5833 (0.0%)
1	m	0.45	0/4276	0.57	1/5833 (0.0%)
1	n	0.45	0/4276	0.57	1/5833 (0.0%)
1	o	0.45	0/4276	0.57	1/5833 (0.0%)
1	p	0.45	0/4276	0.57	1/5833 (0.0%)
1	q	0.45	0/4276	0.57	1/5833 (0.0%)
1	r	0.45	0/4276	0.57	0/5833
1	s	0.45	0/4276	0.57	1/5833 (0.0%)
1	t	0.45	0/4276	0.57	0/5833
1	u	0.45	0/4276	0.57	1/5833 (0.0%)
1	v	0.45	0/4276	0.57	1/5833 (0.0%)
1	w	0.45	0/4276	0.57	0/5833
1	x	0.45	0/4276	0.57	1/5833 (0.0%)
1	y	0.45	0/4276	0.57	1/5833 (0.0%)
1	z	0.45	0/4276	0.57	1/5833 (0.0%)
All	All	0.45	0/256560	0.57	47/349980 (0.0%)

There are no bond length outliers.

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	638	LYS	N-CA-C	-5.04	105.87	111.36
1	V	638	LYS	N-CA-C	-5.04	105.87	111.36
1	x	638	LYS	N-CA-C	-5.04	105.87	111.36
1	7	638	LYS	N-CA-C	-5.04	105.87	111.36
1	O	638	LYS	N-CA-C	-5.04	105.87	111.36

There are no chirality outliers.

There are no planarity outliers.

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	1	4147	0	3890	143	0
1	2	4147	0	3890	147	0
1	3	4147	0	3890	145	0
1	4	4147	0	3890	143	0
1	5	4147	0	3890	150	0
1	6	4147	0	3890	150	0
1	7	4147	0	3890	145	0
1	8	4147	0	3890	148	0
1	A	4147	0	3890	140	0
1	B	4147	0	3890	143	0
1	C	4147	0	3890	144	0
1	D	4147	0	3890	144	0
1	E	4147	0	3890	146	0
1	F	4147	0	3890	145	0
1	G	4147	0	3890	148	0
1	H	4147	0	3890	150	0
1	I	4147	0	3890	146	0
1	J	4147	0	3890	144	0
1	K	4147	0	3890	142	0
1	L	4147	0	3890	144	0
1	M	4147	0	3890	145	0
1	N	4147	0	3890	143	0
1	O	4147	0	3890	144	0
1	P	4147	0	3890	146	0
1	Q	4147	0	3890	147	0
1	R	4147	0	3890	146	0
1	S	4147	0	3890	144	0
1	T	4147	0	3890	149	0
1	U	4147	0	3890	140	0
1	V	4147	0	3890	148	0
1	W	4147	0	3890	151	0
1	X	4147	0	3890	148	0
1	Y	4147	0	3890	148	0
1	Z	4147	0	3890	146	0
1	a	4147	0	3890	144	0
1	b	4147	0	3890	144	0
1	c	4147	0	3890	145	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	d	4147	0	3890	149	0
1	e	4147	0	3890	148	0
1	f	4147	0	3890	147	0
1	g	4147	0	3890	149	0
1	h	4147	0	3890	150	0
1	i	4147	0	3890	145	0
1	j	4147	0	3890	145	0
1	k	4147	0	3890	146	0
1	l	4147	0	3890	146	0
1	m	4147	0	3890	149	0
1	n	4147	0	3890	149	0
1	o	4147	0	3890	144	0
1	p	4147	0	3890	147	0
1	q	4147	0	3890	148	0
1	r	4147	0	3890	145	0
1	s	4147	0	3890	143	0
1	t	4147	0	3890	148	0
1	u	4147	0	3890	145	0
1	v	4147	0	3890	143	0
1	w	4147	0	3890	146	0
1	x	4147	0	3890	146	0
1	y	4147	0	3890	146	0
1	z	4147	0	3890	144	0
All	All	248820	0	233400	6625	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 14.

The worst 5 of 6625 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:F:563:ILE:HD12	1:F:567:ASN:HD22	1.36	0.91
1:a:563:ILE:HD12	1:a:567:ASN:HD22	1.36	0.91
1:y:563:ILE:HD12	1:y:567:ASN:HD22	1.36	0.91
1:M:563:ILE:HD12	1:M:567:ASN:HD22	1.36	0.91
1:2:563:ILE:HD12	1:2:567:ASN:HD22	1.36	0.91

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	1	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	2	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	3	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	4	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	5	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	6	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	7	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	8	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	A	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	B	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	C	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	D	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	E	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	F	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	G	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	H	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	I	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	J	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	K	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	L	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	M	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	N	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	O	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	P	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	Q	516/517 (100%)	505 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	S	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	T	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	U	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	V	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	W	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	X	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	Y	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	Z	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	a	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	b	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	c	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	d	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	e	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	f	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	g	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	h	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	i	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	j	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	k	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	l	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	m	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	n	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	o	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	p	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	q	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	r	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	s	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	t	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	u	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	v	516/517 (100%)	505 (98%)	11 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	x	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	y	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
1	z	516/517 (100%)	505 (98%)	11 (2%)	0	100	100
All	All	30960/31020 (100%)	30300 (98%)	660 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	1	456/455 (100%)	456 (100%)	0	100	100
1	2	456/455 (100%)	456 (100%)	0	100	100
1	3	456/455 (100%)	456 (100%)	0	100	100
1	4	456/455 (100%)	456 (100%)	0	100	100
1	5	456/455 (100%)	456 (100%)	0	100	100
1	6	456/455 (100%)	456 (100%)	0	100	100
1	7	456/455 (100%)	456 (100%)	0	100	100
1	8	456/455 (100%)	456 (100%)	0	100	100
1	A	456/455 (100%)	456 (100%)	0	100	100
1	B	456/455 (100%)	456 (100%)	0	100	100
1	C	456/455 (100%)	456 (100%)	0	100	100
1	D	456/455 (100%)	456 (100%)	0	100	100
1	E	456/455 (100%)	456 (100%)	0	100	100
1	F	456/455 (100%)	456 (100%)	0	100	100
1	G	456/455 (100%)	456 (100%)	0	100	100
1	H	456/455 (100%)	456 (100%)	0	100	100
1	I	456/455 (100%)	456 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	456/455 (100%)	456 (100%)	0	100	100
1	K	456/455 (100%)	456 (100%)	0	100	100
1	L	456/455 (100%)	456 (100%)	0	100	100
1	M	456/455 (100%)	456 (100%)	0	100	100
1	N	456/455 (100%)	456 (100%)	0	100	100
1	O	456/455 (100%)	456 (100%)	0	100	100
1	P	456/455 (100%)	456 (100%)	0	100	100
1	Q	456/455 (100%)	456 (100%)	0	100	100
1	R	456/455 (100%)	456 (100%)	0	100	100
1	S	456/455 (100%)	456 (100%)	0	100	100
1	T	456/455 (100%)	456 (100%)	0	100	100
1	U	456/455 (100%)	456 (100%)	0	100	100
1	V	456/455 (100%)	456 (100%)	0	100	100
1	W	456/455 (100%)	456 (100%)	0	100	100
1	X	456/455 (100%)	456 (100%)	0	100	100
1	Y	456/455 (100%)	456 (100%)	0	100	100
1	Z	456/455 (100%)	456 (100%)	0	100	100
1	a	456/455 (100%)	456 (100%)	0	100	100
1	b	456/455 (100%)	456 (100%)	0	100	100
1	c	456/455 (100%)	456 (100%)	0	100	100
1	d	456/455 (100%)	456 (100%)	0	100	100
1	e	456/455 (100%)	456 (100%)	0	100	100
1	f	456/455 (100%)	456 (100%)	0	100	100
1	g	456/455 (100%)	456 (100%)	0	100	100
1	h	456/455 (100%)	456 (100%)	0	100	100
1	i	456/455 (100%)	456 (100%)	0	100	100
1	j	456/455 (100%)	456 (100%)	0	100	100
1	k	456/455 (100%)	456 (100%)	0	100	100
1	l	456/455 (100%)	456 (100%)	0	100	100
1	m	456/455 (100%)	456 (100%)	0	100	100
1	n	456/455 (100%)	456 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	o	456/455 (100%)	456 (100%)	0	100	100
1	p	456/455 (100%)	456 (100%)	0	100	100
1	q	456/455 (100%)	456 (100%)	0	100	100
1	r	456/455 (100%)	456 (100%)	0	100	100
1	s	456/455 (100%)	456 (100%)	0	100	100
1	t	456/455 (100%)	456 (100%)	0	100	100
1	u	456/455 (100%)	456 (100%)	0	100	100
1	v	456/455 (100%)	456 (100%)	0	100	100
1	w	456/455 (100%)	456 (100%)	0	100	100
1	x	456/455 (100%)	456 (100%)	0	100	100
1	y	456/455 (100%)	456 (100%)	0	100	100
1	z	456/455 (100%)	456 (100%)	0	100	100
All	All	27360/27300 (100%)	27360 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1055 such sidechains are listed below:

Mol	Chain	Res	Type
1	1	625	HIS
1	3	325	ASN
1	1	605	GLN
1	8	318	GLN
1	W	254	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

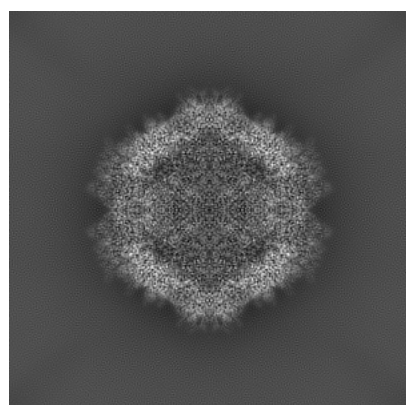
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23205. These allow visual inspection of the internal detail of the map and identification of artifacts.

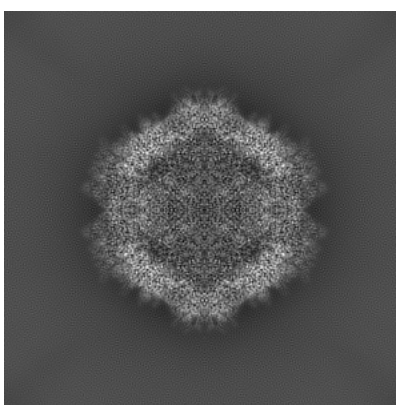
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

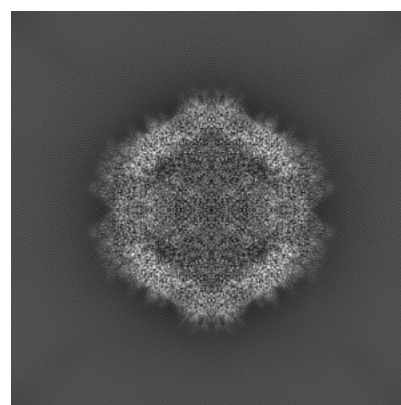
6.1.1 Primary map



X



Y

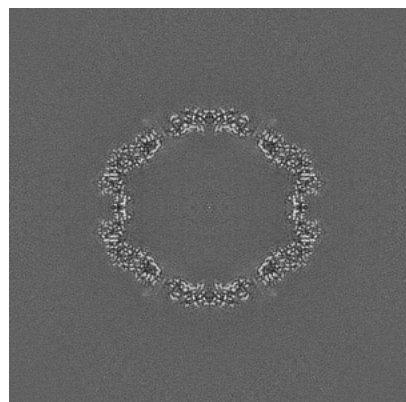


Z

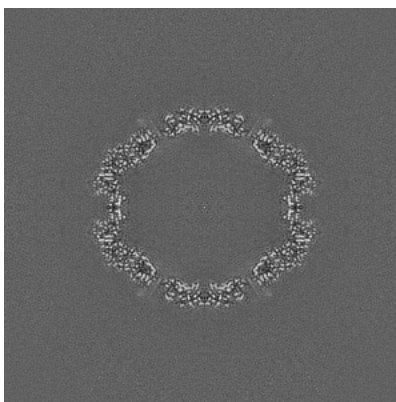
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

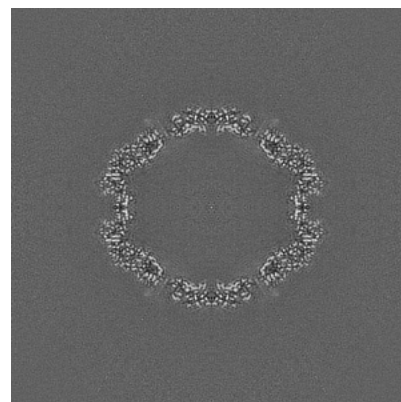
6.2.1 Primary map



X Index: 210



Y Index: 210

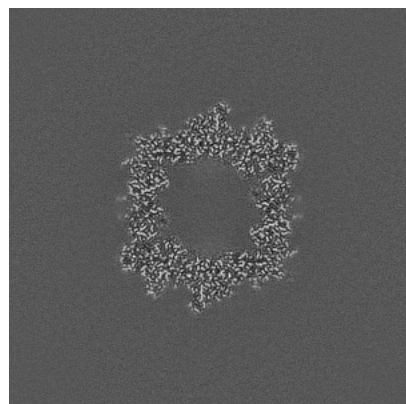


Z Index: 210

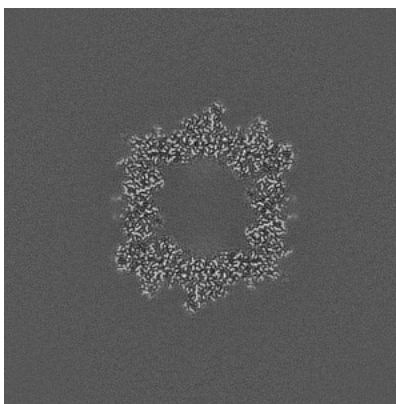
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

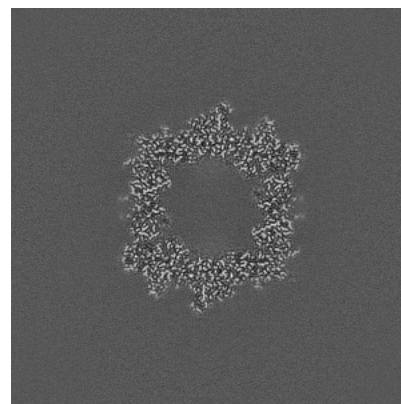
6.3.1 Primary map



X Index: 271



Y Index: 271

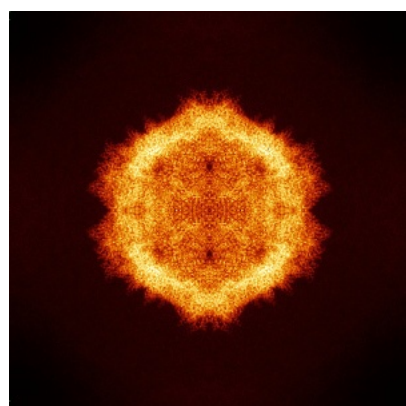


Z Index: 271

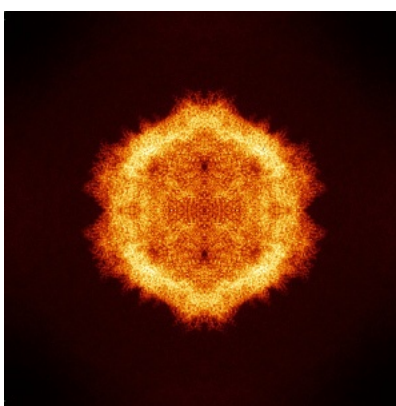
The images above show the largest variance slices of the map in three orthogonal directions.

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

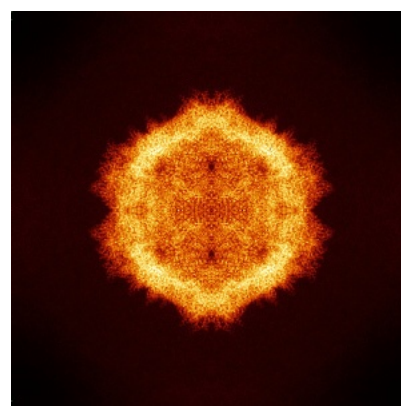
6.4.1 Primary map



X



Y

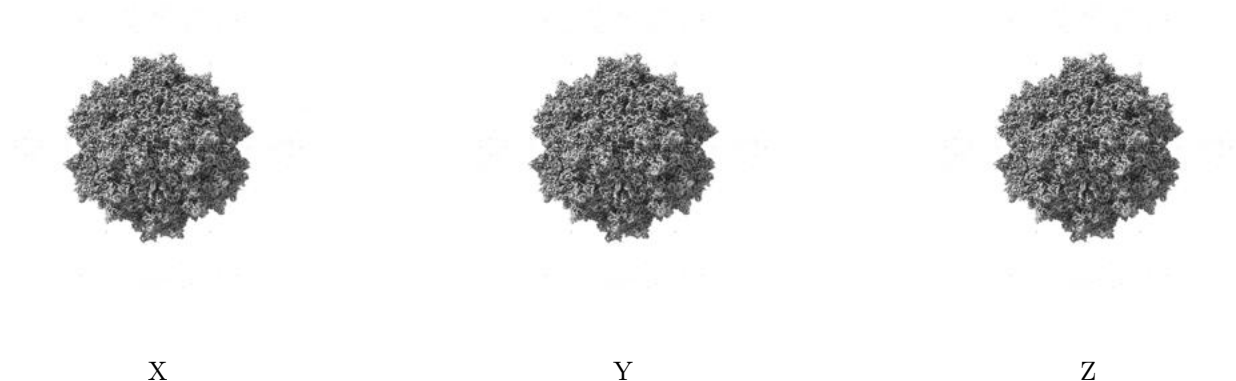


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

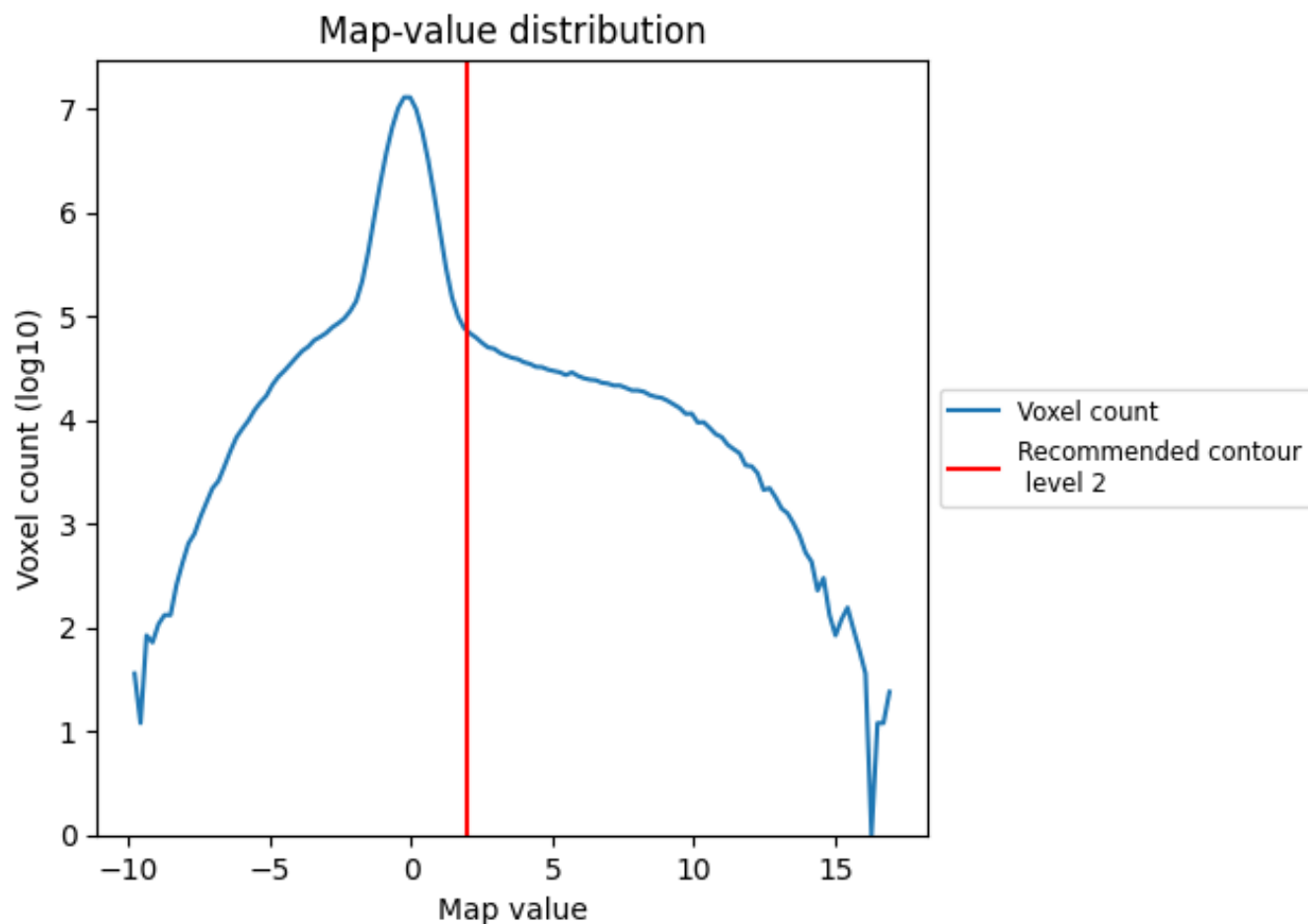
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

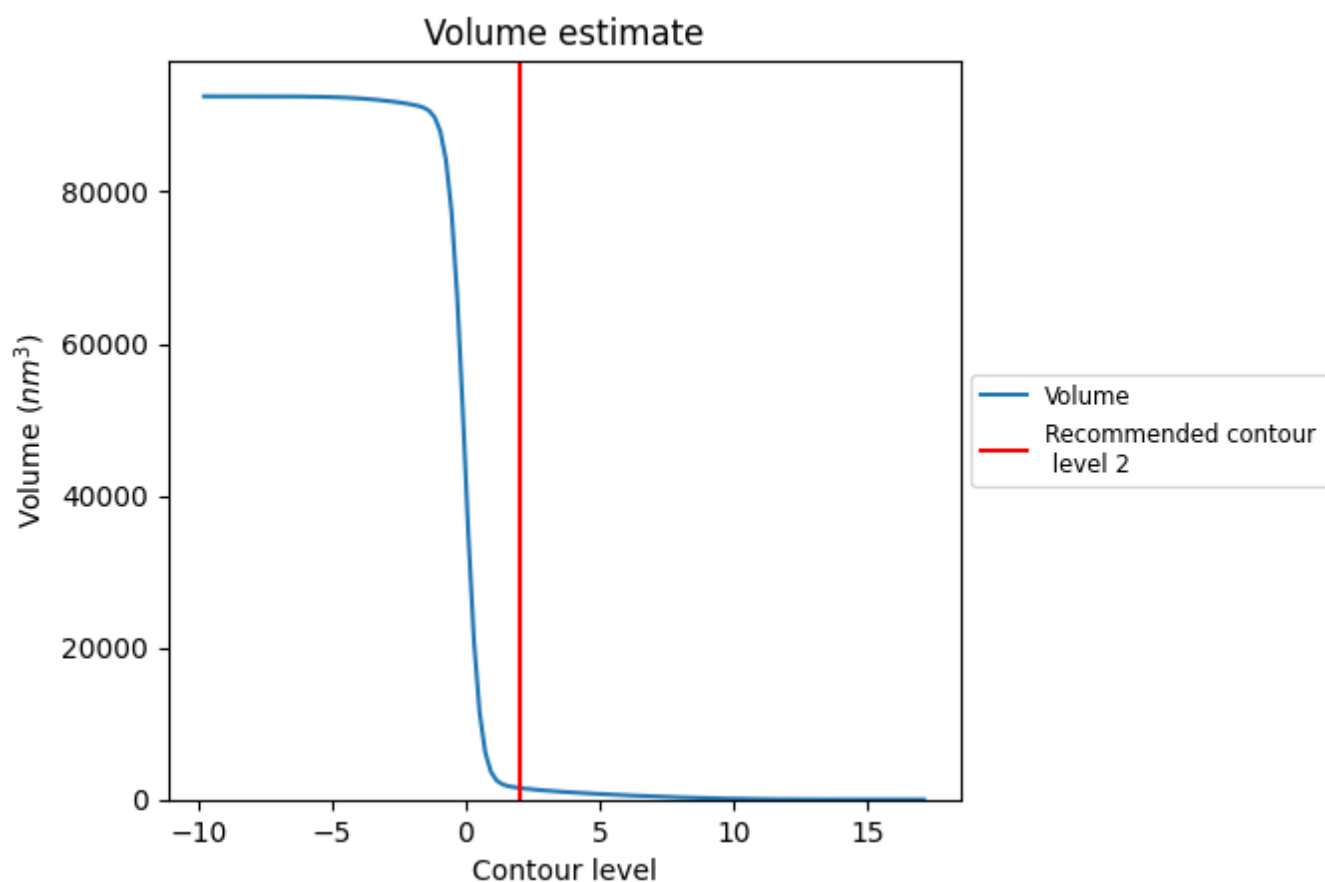
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

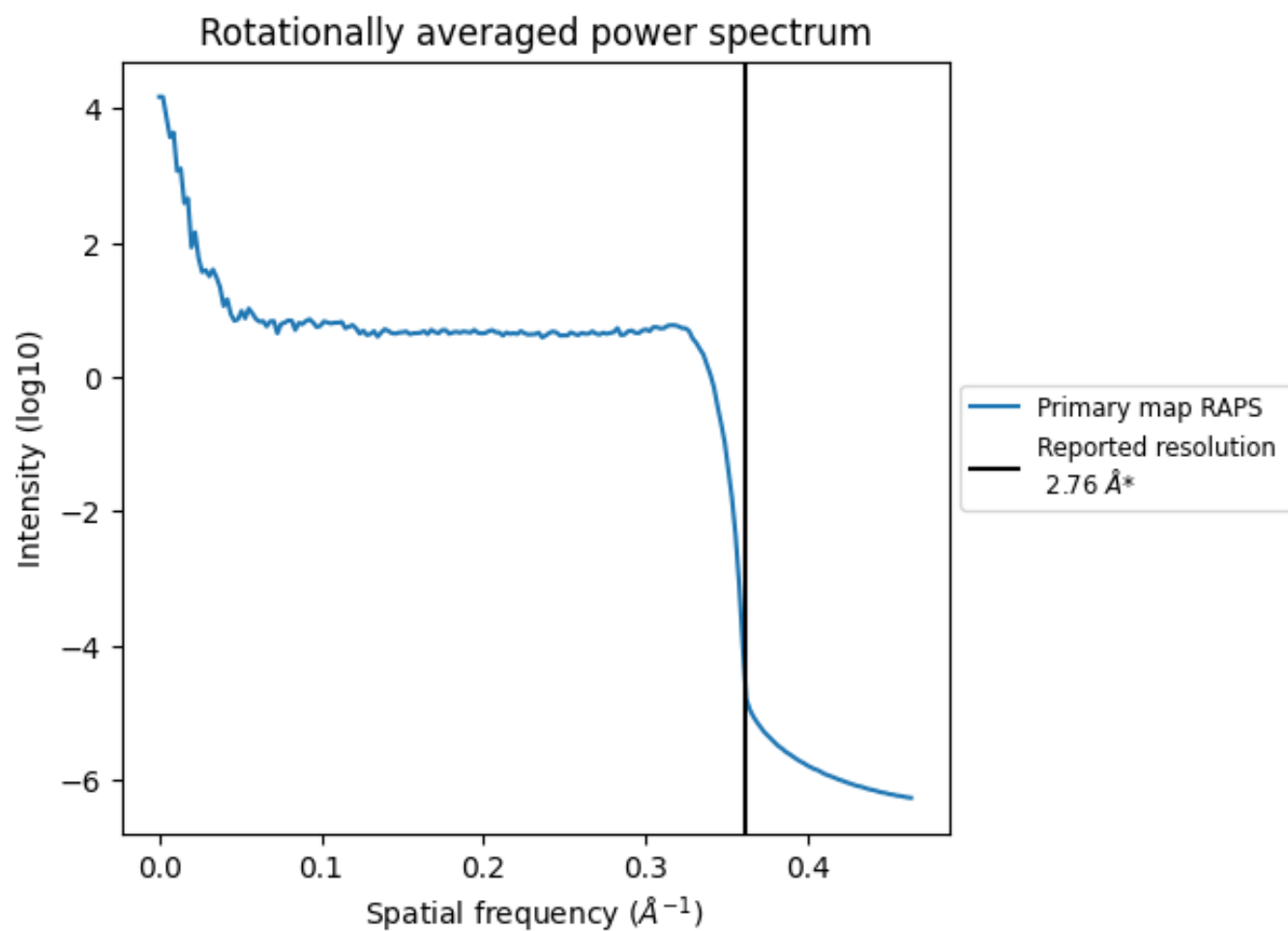
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1534 nm³; this corresponds to an approximate mass of 1385 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 0.362 Å⁻¹

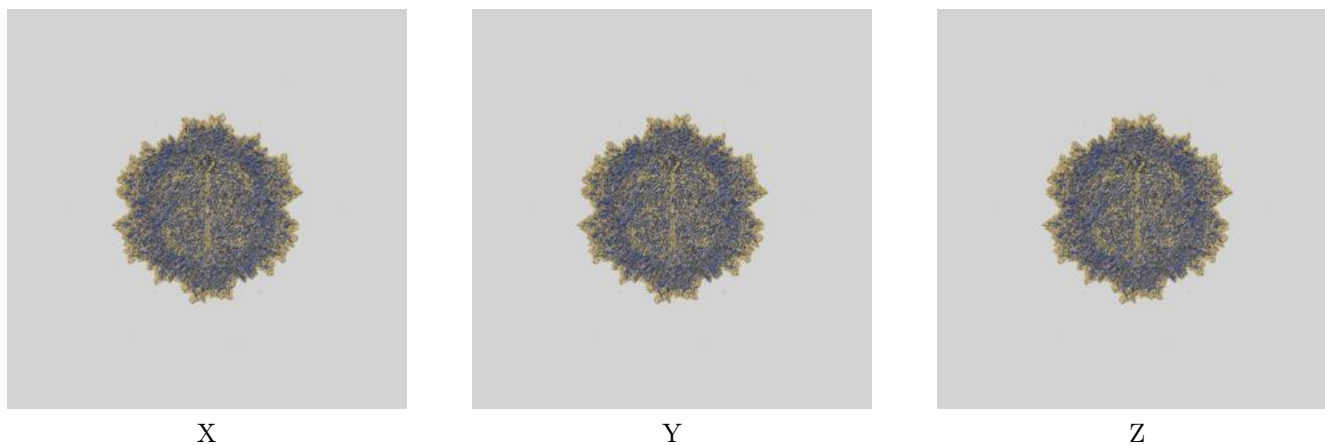
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

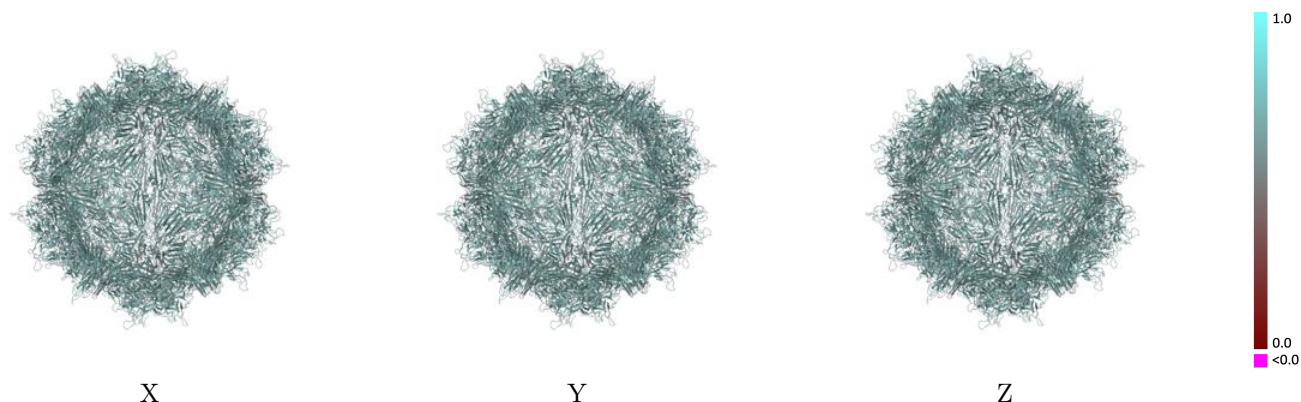
This section contains information regarding the fit between EMDB map EMD-23205 and PDB model 7L6I. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



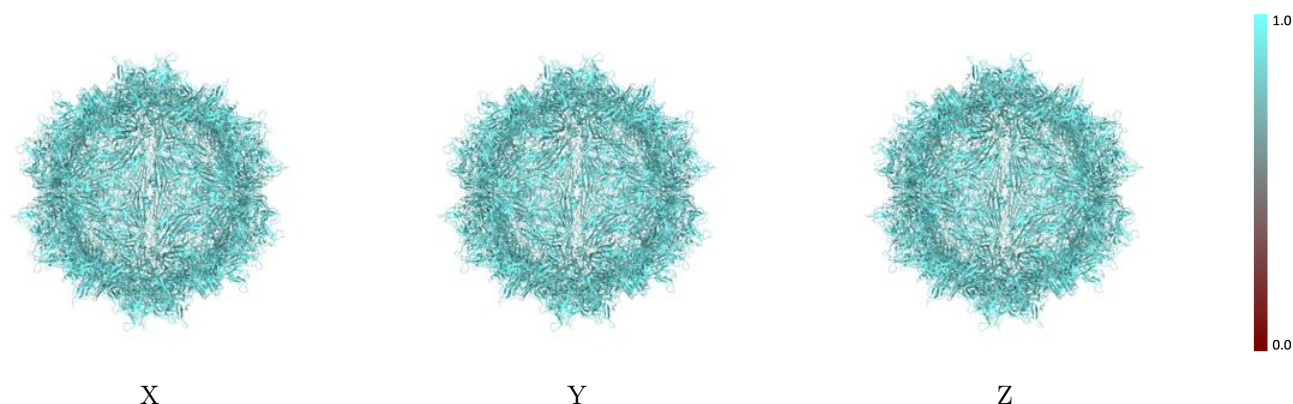
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



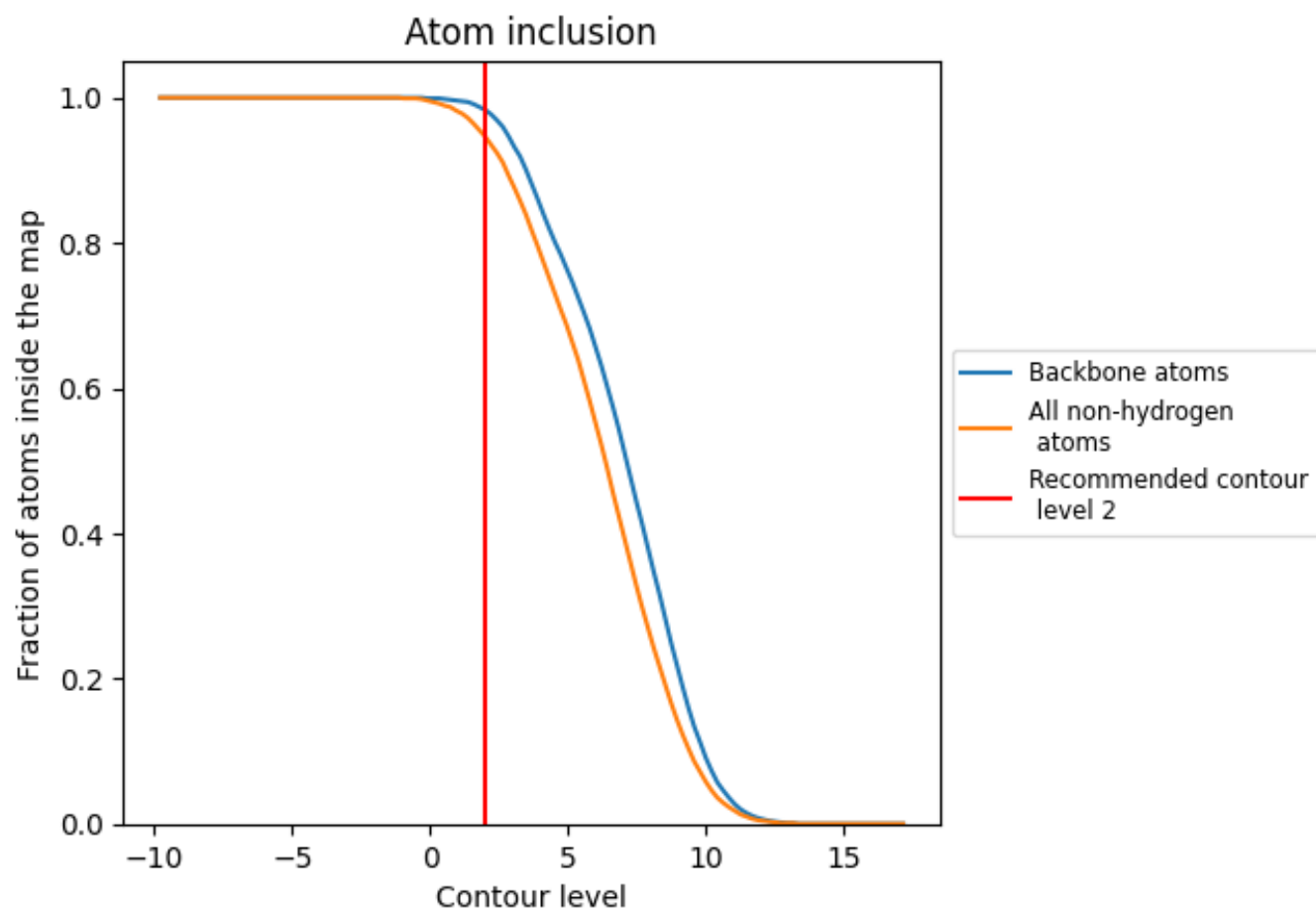
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































The table lists the average atom inclusion at the recommended contour level (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.6250
1	 0.9470	 0.6250
2	 0.9460	 0.6240
3	 0.9460	 0.6250
4	 0.9470	 0.6260
5	 0.9480	 0.6250
6	 0.9480	 0.6240
7	 0.9480	 0.6250
8	 0.9460	 0.6260
A	 0.9460	 0.6250
B	 0.9470	 0.6250
C	 0.9460	 0.6250
D	 0.9480	 0.6250
E	 0.9460	 0.6250
F	 0.9460	 0.6250
G	 0.9460	 0.6240
H	 0.9480	 0.6250
I	 0.9470	 0.6250
J	 0.9460	 0.6250
K	 0.9470	 0.6250
L	 0.9460	 0.6250
M	 0.9460	 0.6260
N	 0.9480	 0.6250
O	 0.9460	 0.6250
P	 0.9480	 0.6250
Q	 0.9470	 0.6250
R	 0.9470	 0.6250
S	 0.9460	 0.6250
T	 0.9470	 0.6260
U	 0.9460	 0.6260
V	 0.9460	 0.6250
W	 0.9480	 0.6250
X	 0.9460	 0.6250
Y	 0.9480	 0.6250
Z	 0.9460	 0.6250



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Chain	Atom inclusion	Q-score
a	 0.9460	 0.6250
b	 0.9460	 0.6260
c	 0.9460	 0.6250
d	 0.9460	 0.6250
e	 0.9460	 0.6250
f	 0.9460	 0.6250
g	 0.9470	 0.6240
h	 0.9450	 0.6250
i	 0.9480	 0.6250
j	 0.9480	 0.6260
k	 0.9480	 0.6250
l	 0.9460	 0.6250
m	 0.9470	 0.6260
n	 0.9460	 0.6250
o	 0.9460	 0.6250
p	 0.9460	 0.6250
q	 0.9470	 0.6250
r	 0.9460	 0.6250
s	 0.9460	 0.6250
t	 0.9460	 0.6240
u	 0.9470	 0.6240
v	 0.9460	 0.6250
w	 0.9460	 0.6240
x	 0.9470	 0.6250
y	 0.9460	 0.6250
z	 0.9460	 0.6250