



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 05:48 AM UTC

PDB ID : 9R7R / pdb_00009r7r
EMDB ID : EMD-53790
Title : Potato virus A (PVA)
Authors : Koritnik, N.; Kezar, A.; Podobnik, M.
Deposited on : 2025-05-15
Resolution : 2.39 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

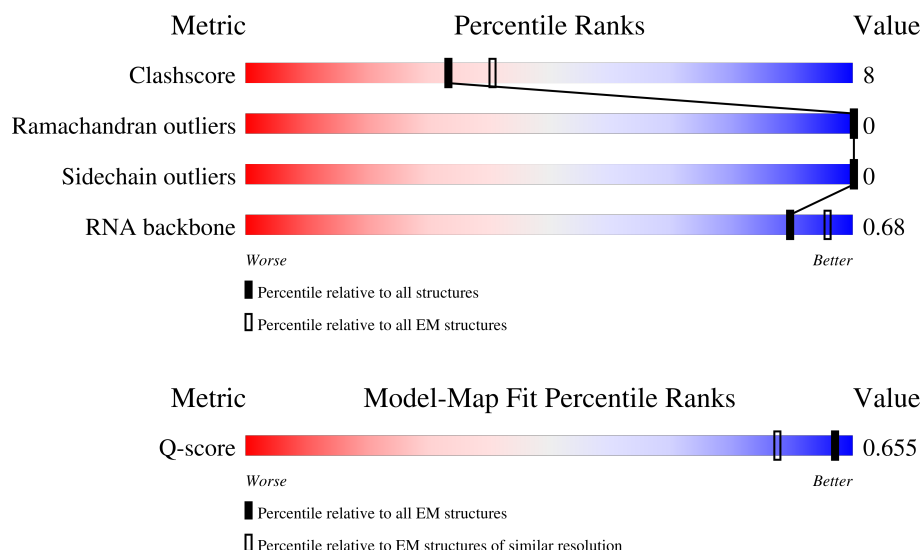
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.39 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	4884 (1.90 - 2.89)

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	Aa	269	23% 71% 13% 16%
1	Ac	269	22% 69% 15% 16%
1	Ae	269	21% 69% 15% 16%

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Mol	Chain	Length	Quality of chain			
1	Ag	269	22%	69%	15%	16%
1	Ai	269	21%	68%	16%	16%
1	Ak	269	21%	68%	16%	16%
1	Am	269	22%	70%	14%	16%
1	Ao	269	22%	68%	16%	16%
1	Aq	269	22%	68%	16%	16%
1	As	269	23%	66%	18%	16%
1	Au	269	20%	64%	20%	16%
1	Aw	269	23%	65%	19%	16%
1	Ay	269	21%	66%	18%	16%
1	Ba	269	21%	65%	19%	16%
1	Bc	269	22%	66%	18%	16%
1	Be	269	22%	65%	19%	16%
1	Bg	269	22%	65%	19%	16%
1	Bi	269	21%	65%	19%	16%
1	Bk	269	22%	67%	17%	16%
1	Bm	269	22%	65%	19%	16%
1	Bo	269	23%	65%	19%	16%
1	Bq	269	22%	65%	19%	16%
1	Bs	269	22%	65%	19%	16%
1	Bu	269	21%	65%	19%	16%
1	Bw	269	22%	65%	19%	16%
1	By	269	21%	65%	19%	16%
1	Ca	269	23%	67%	17%	16%
1	Cc	269	21%	68%	16%	16%

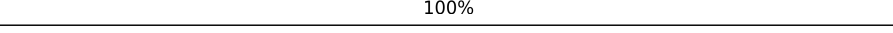
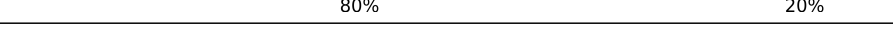
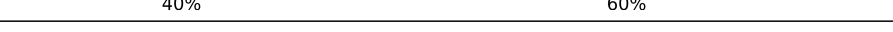
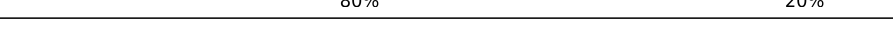
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Mol	Chain	Length	Quality of chain
1	Ce	269	21% 68% 16% 16%
1	Cg	269	22% 69% 15% 16%
1	Ci	269	22% 67% 17% 16%
1	Ck	269	23% 68% 16% 16%
1	Cm	269	23% 68% 16% 16%
1	Co	269	22% 69% 15% 16%
1	Cq	269	21% 68% 16% 16%
1	Cs	269	23% 69% 15% 16%
2	Ab	5	80% 20%
2	Ad	5	80% 20%
2	Af	5	80% 20%
2	Ah	5	60% 40%
2	Aj	5	60% 40%
2	Al	5	80% 20%
2	An	5	80% 20%
2	Ap	5	40% 60%
2	Ar	5	40% 60%
2	At	5	40% 60%
2	Av	5	100%
2	Ax	5	80% 20%
2	Az	5	80% 20%
2	Bb	5	60% 40%
2	Bd	5	60% 40%
2	Bf	5	20% 80%
2	Bh	5	60% 40%

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Mol	Chain	Length	Quality of chain
2	Bj	5	 80%20%
2	Bl	5	 60%40%
2	Bn	5	 40%60%
2	Bp	5	 40%60%
2	Br	5	 60%40%
2	Bt	5	 80%20%
2	Bv	5	 40%60%
2	Bx	5	 60%40%
2	Bz	5	 60%40%
2	Cb	5	 60%40%
2	Cd	5	 80%20%
2	Cf	5	 100%
2	Ch	5	 80%20%
2	Cj	5	 40%60%
2	Cl	5	 40%60%
2	Cn	5	 80%20%
2	Cp	5	 80%20%
2	Cr	5	 40%60%
2	Ct	5	 80%20%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 68940 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	Aa	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ac	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ae	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ag	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ai	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ak	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Am	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ao	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Aq	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	As	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Au	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Aw	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ay	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ba	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bc	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Be	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bg	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Bi	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bk	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bm	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bo	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bq	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bs	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bu	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Bw	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	By	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ca	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Cc	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ce	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Cg	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ci	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Ck	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Cm	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Co	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Cq	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		
1	Cs	226	Total	C	N	O	S	0	0
			1815	1136	321	343	15		

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ad	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Af	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ah	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Aj	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Al	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	An	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ap	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ar	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	At	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Av	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ax	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Az	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bb	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bd	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bf	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bh	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bj	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bl	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bn	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bp	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Br	5	Total 100	C 45	N 10	O 40	P 5	0	0

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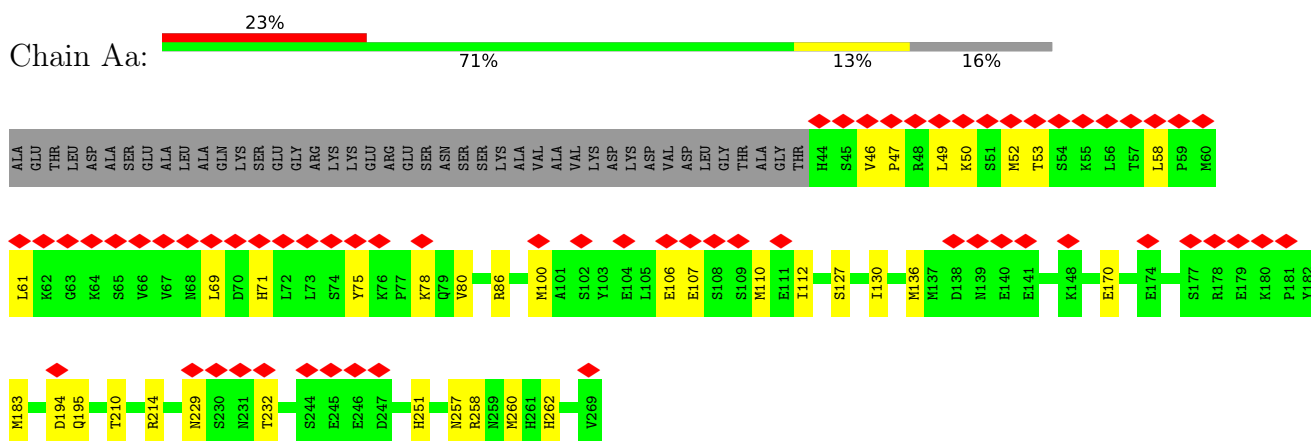
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Bt	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bv	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bx	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bz	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cb	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cd	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cf	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ch	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cj	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cl	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cn	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cp	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cr	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Ct	5	Total 100	C 45	N 10	O 40	P 5	0	0

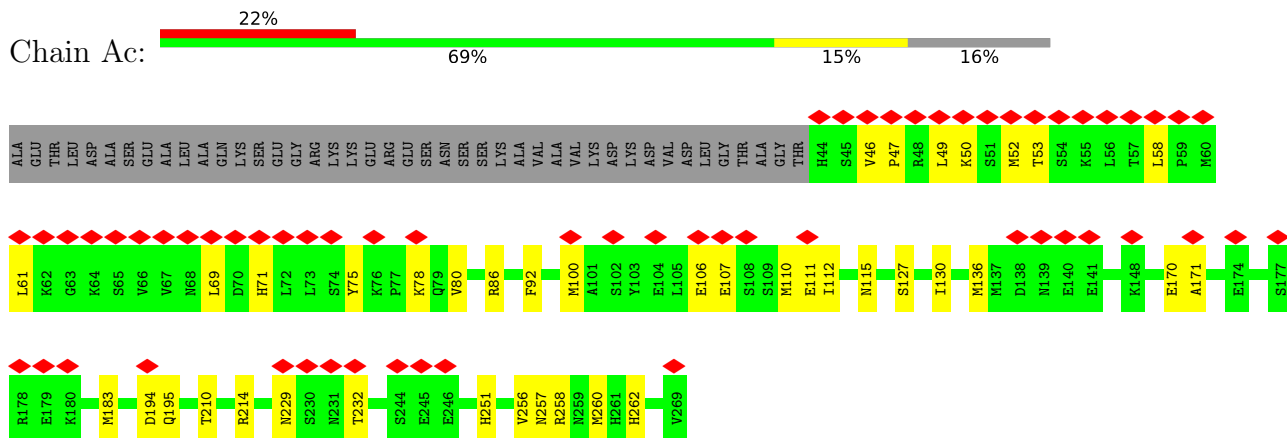
3 Residue-property plots

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

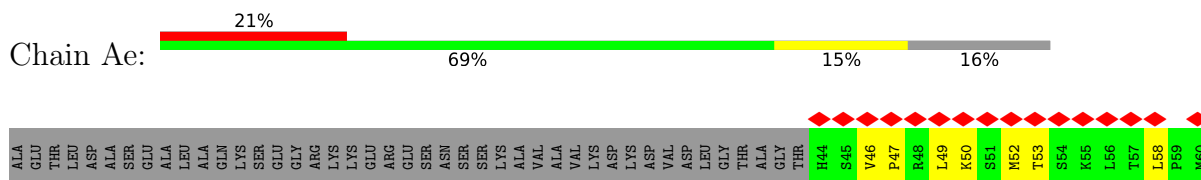
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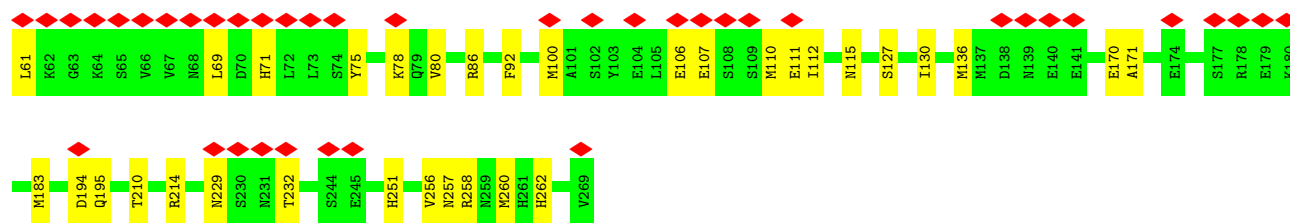


- Molecule 1: Capsid protein

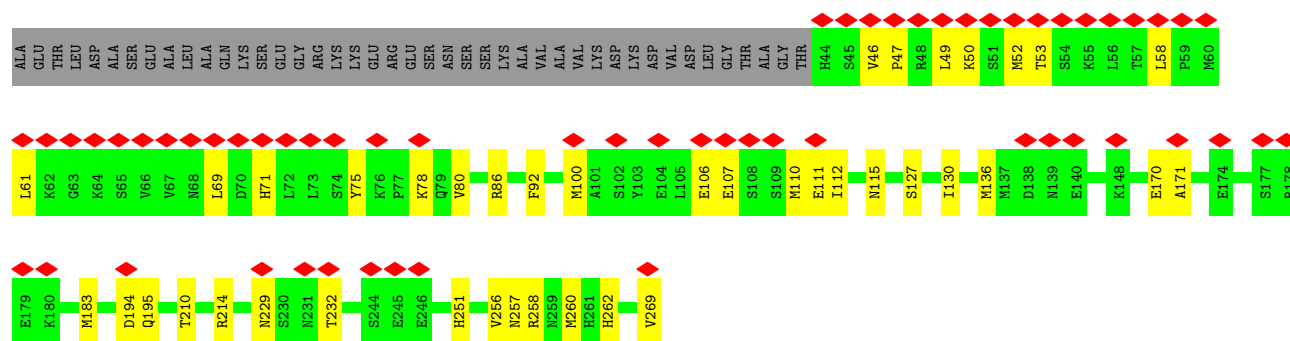
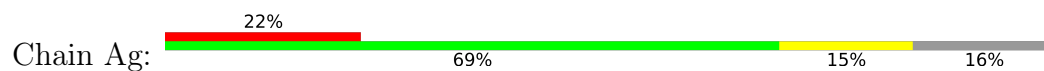


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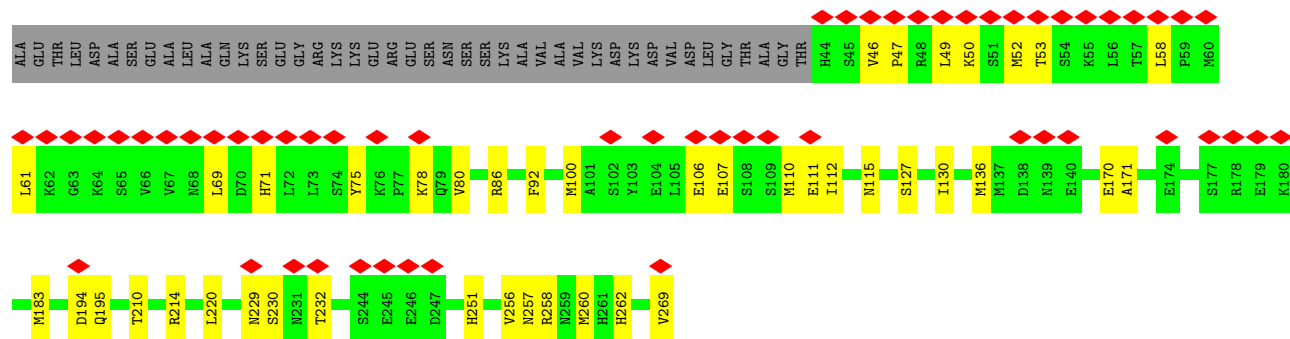




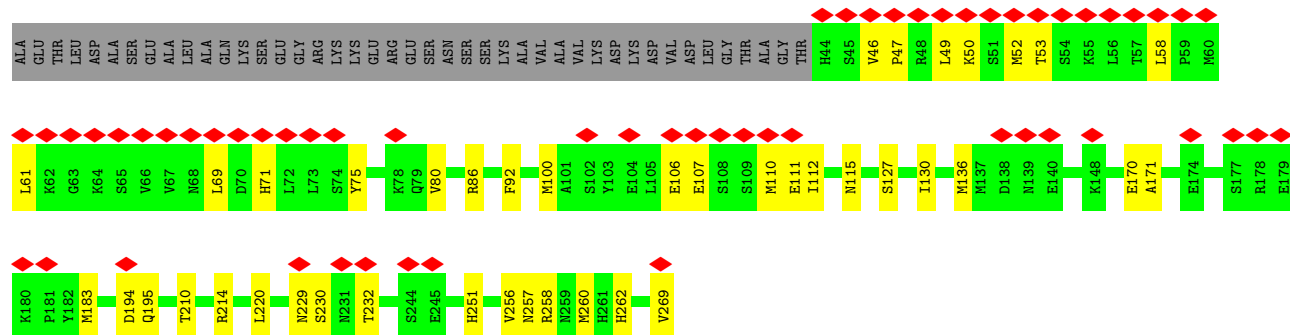
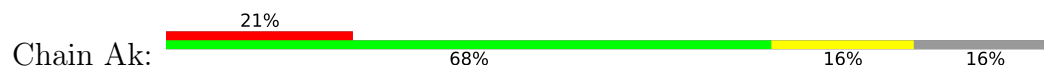
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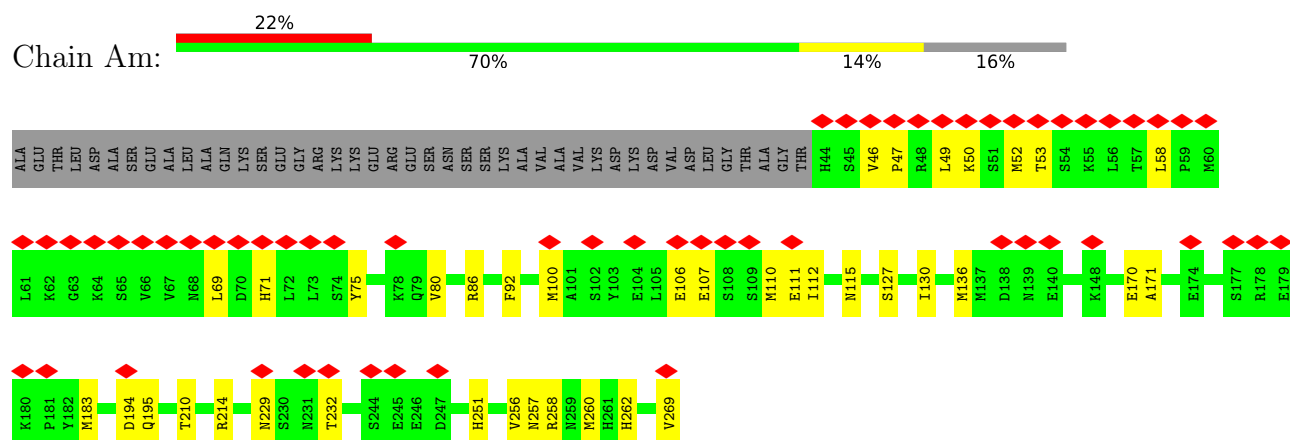
• Molecule 1: Capsid protein



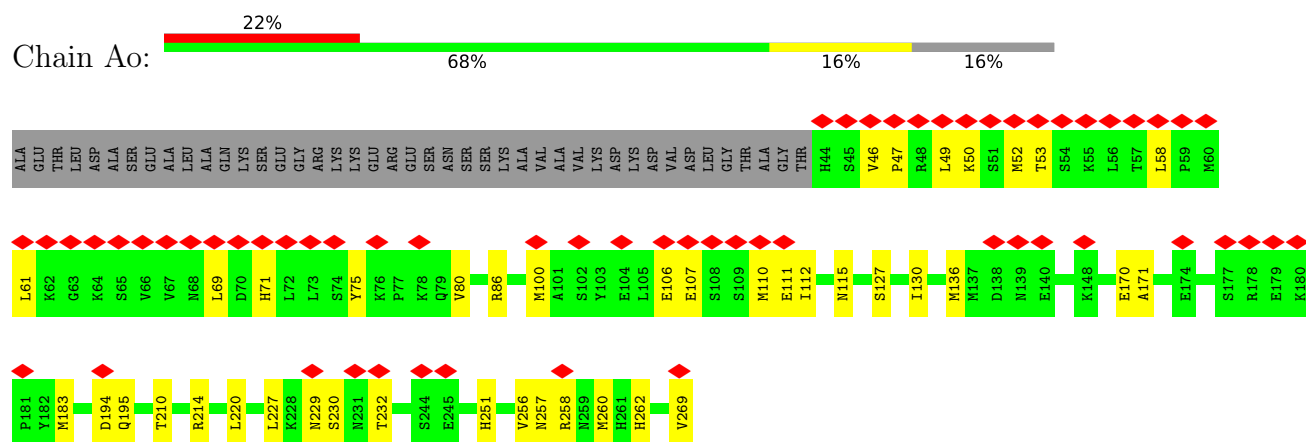
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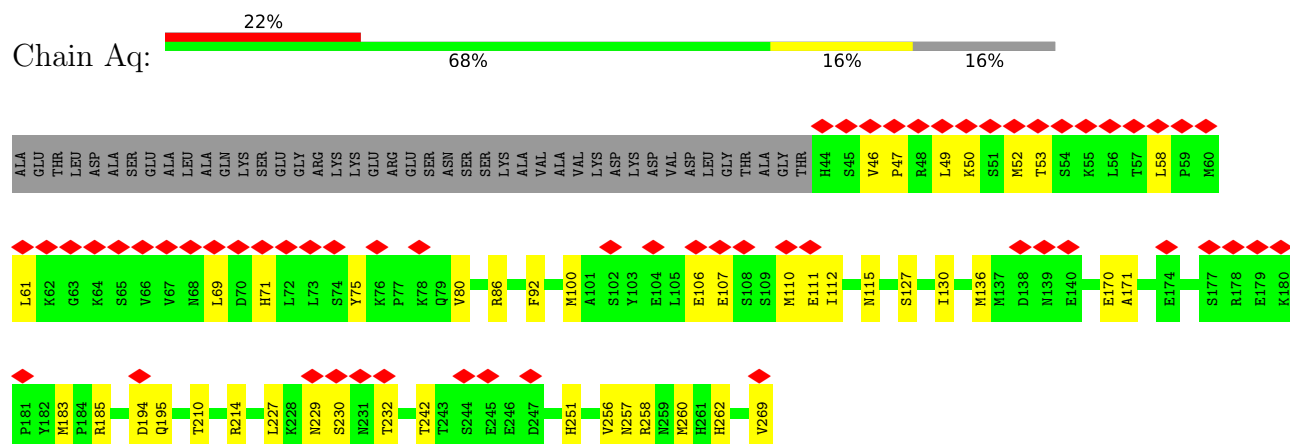
• Molecule 1: Capsid protein



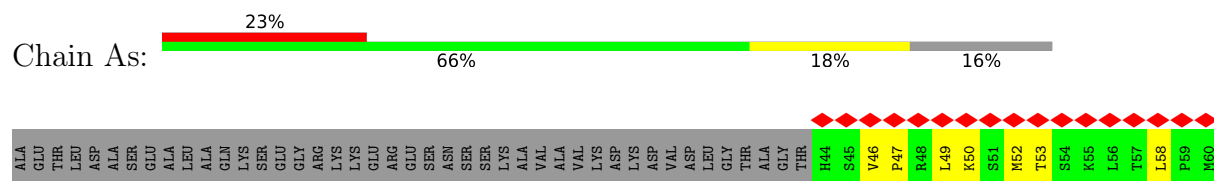
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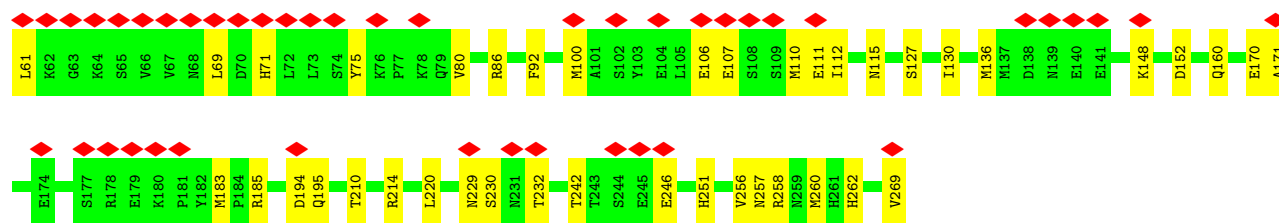


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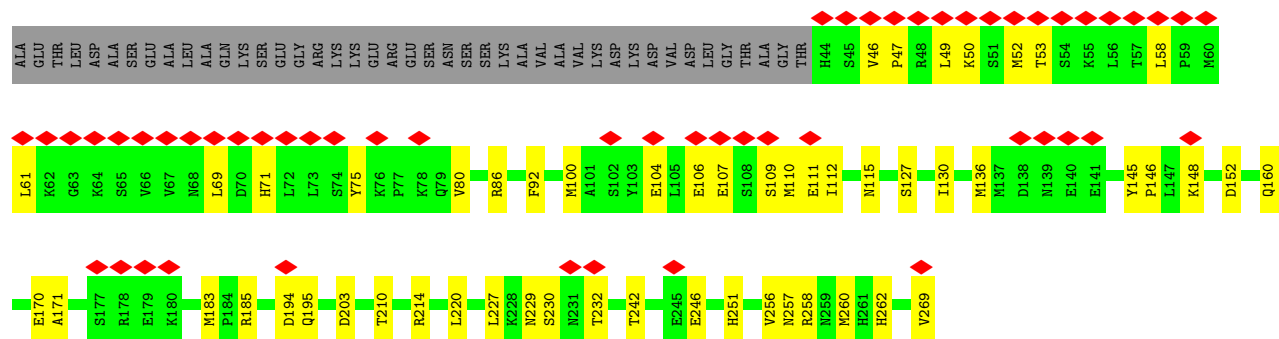


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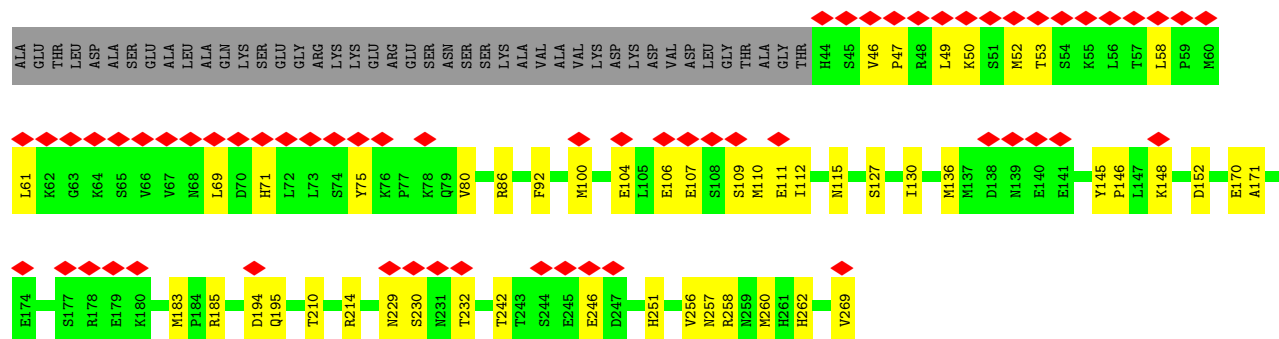




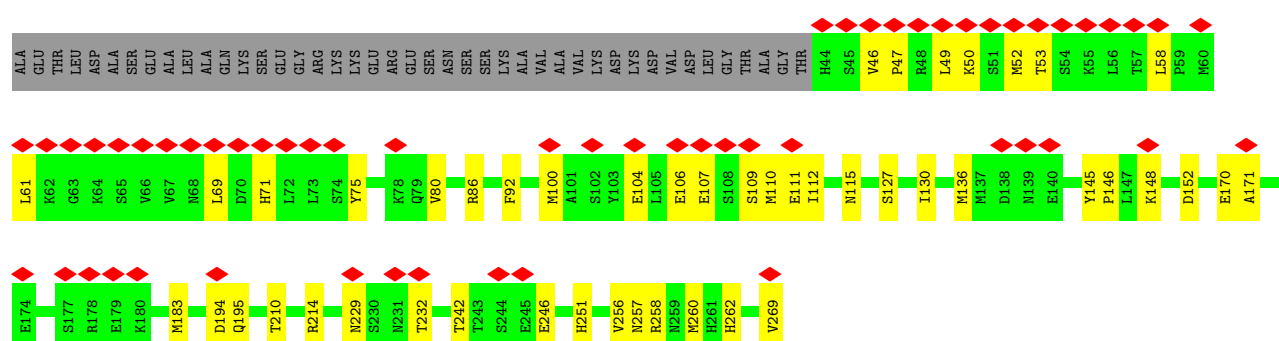
• Molecule 1: Capsid protein



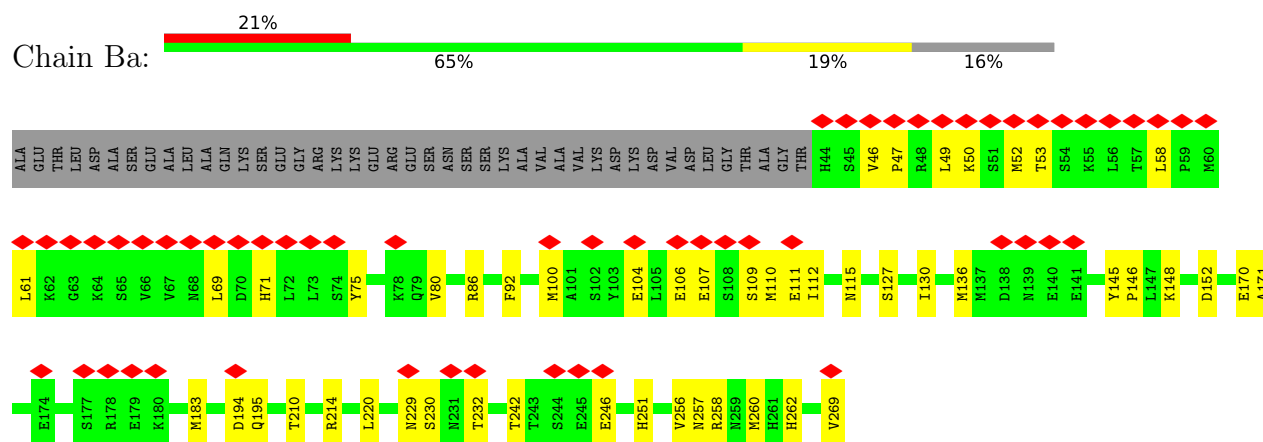
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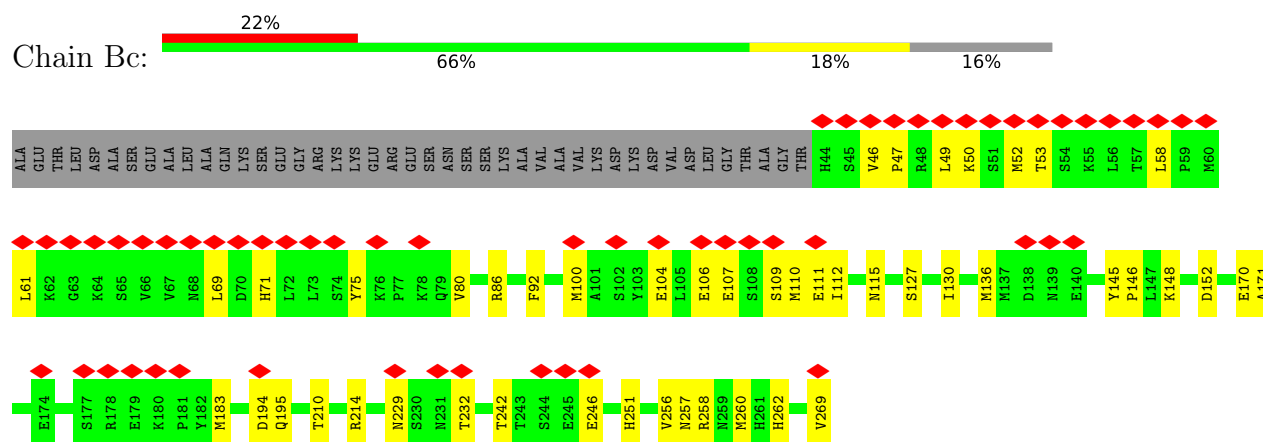
• Molecule 1: Capsid protein



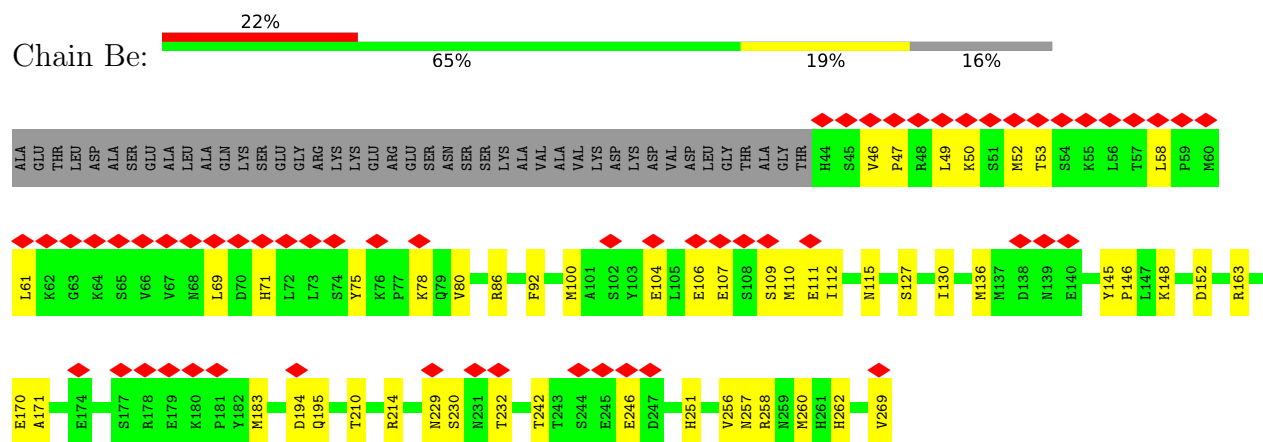
- Molecule 1: Capsid protein



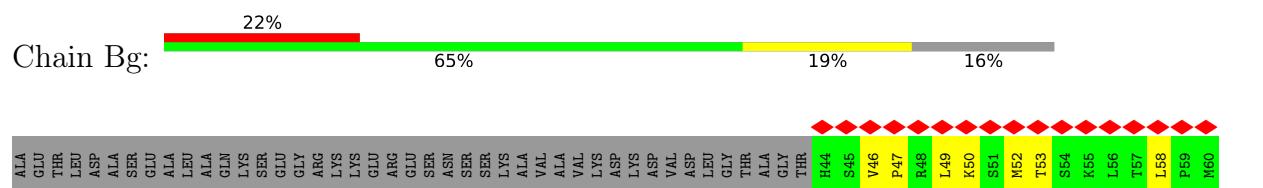
- Molecule 1: Capsid protein

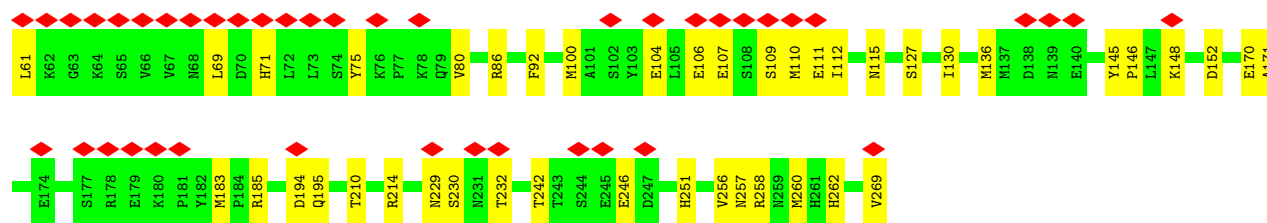


- Molecule 1: Capsid protein

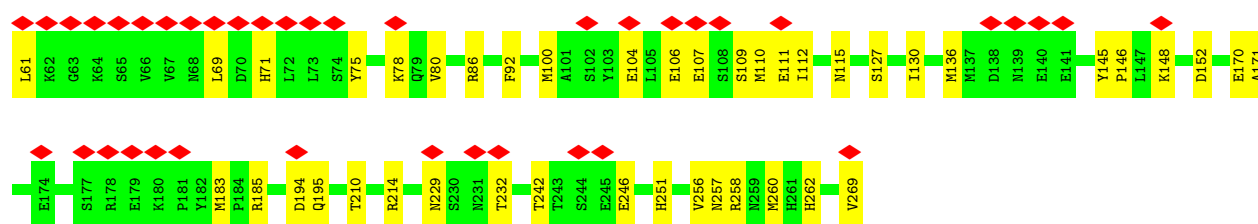
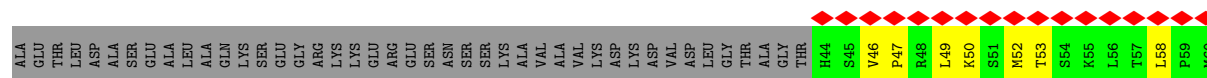


- Molecule 1: Capsid protein

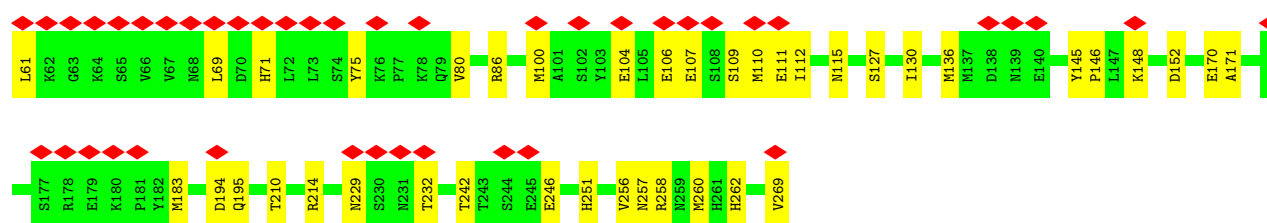
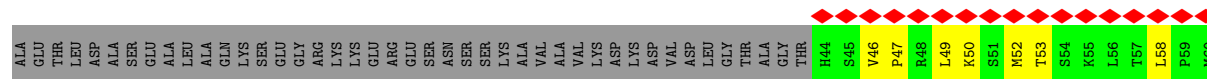




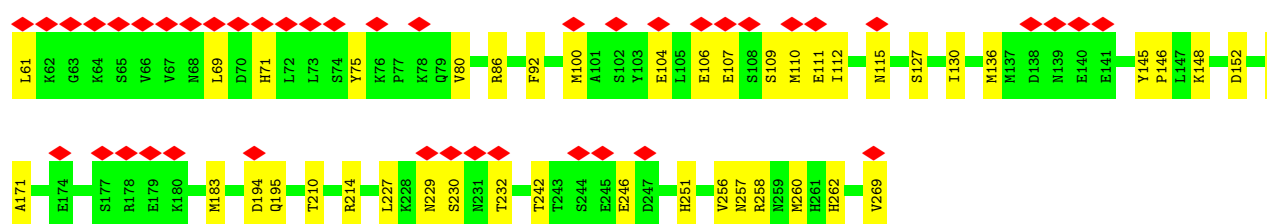
• Molecule 1: Capsid protein



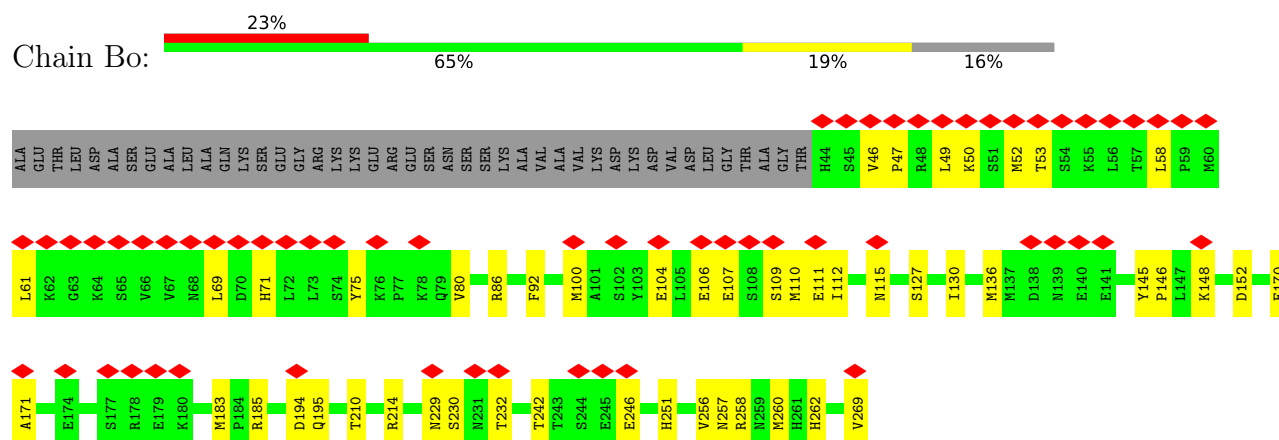
• Molecule 1: Capsid protein



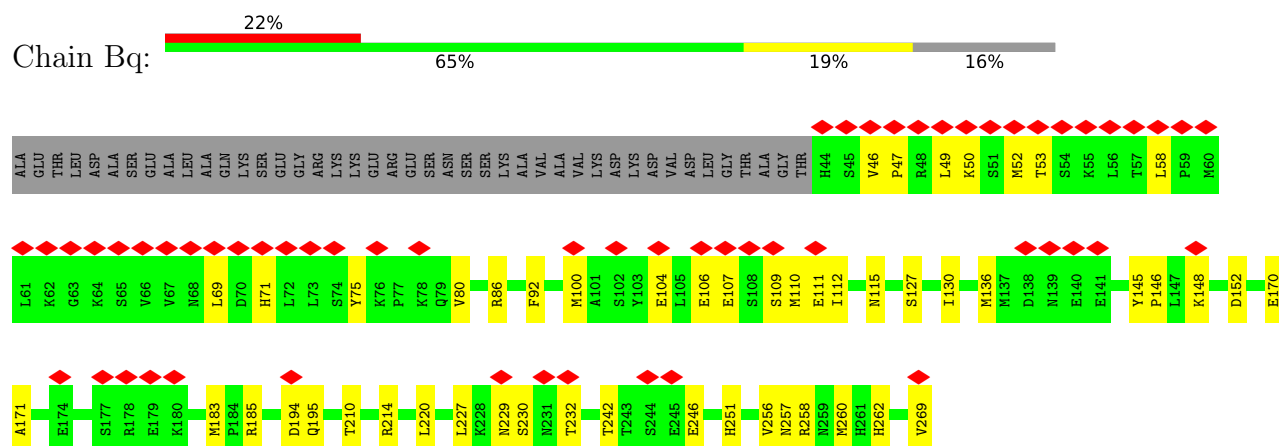
• Molecule 1: Capsid protein



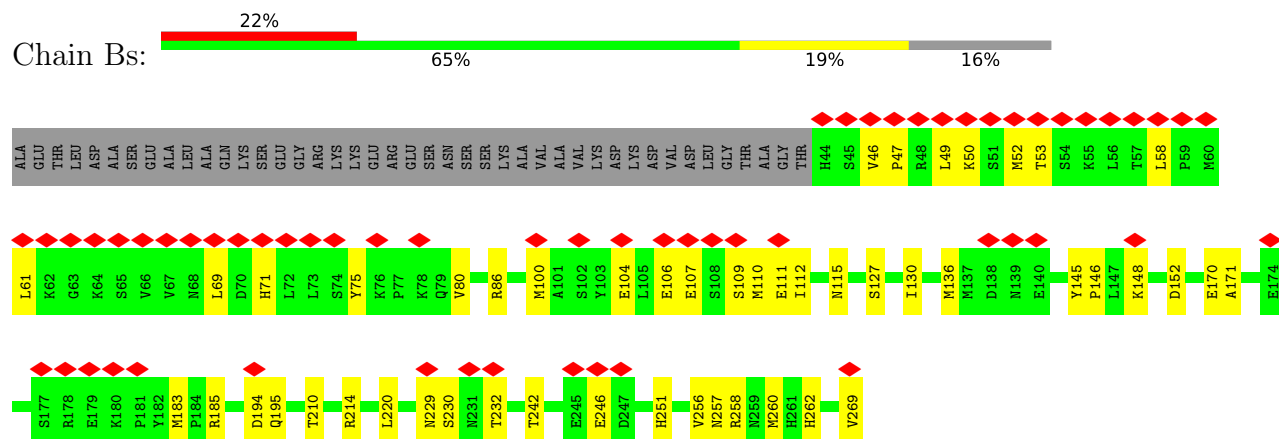
- Molecule 1: Capsid protein



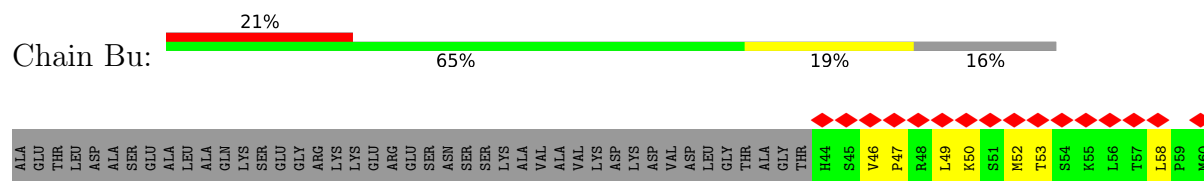
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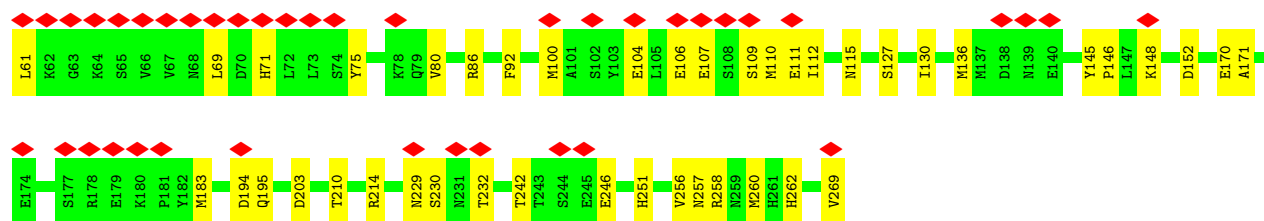


- Molecule 1: Capsid protein

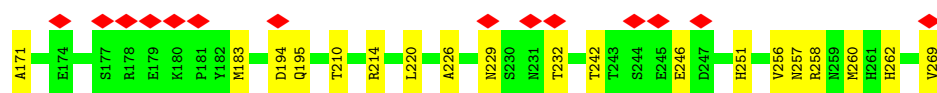
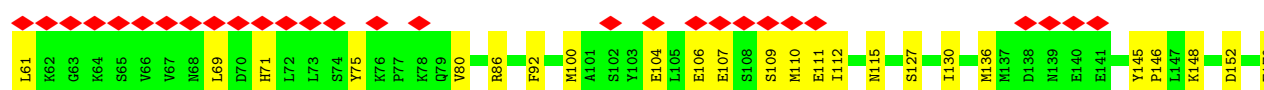
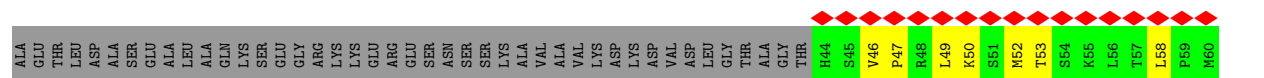


- Molecule 1: Capsid protein

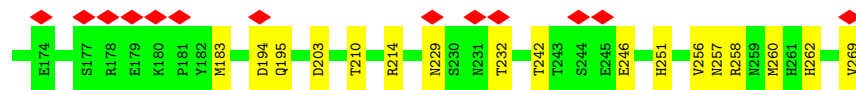
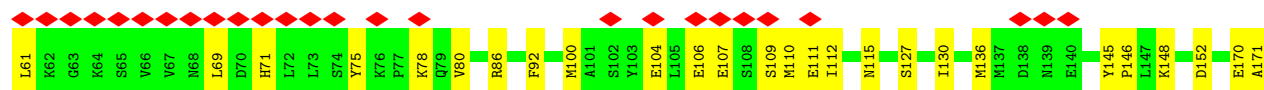
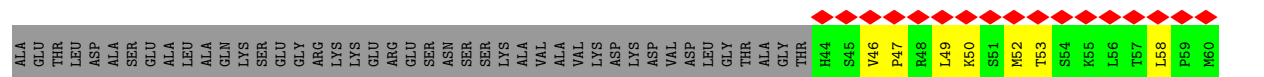




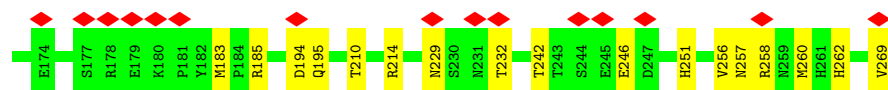
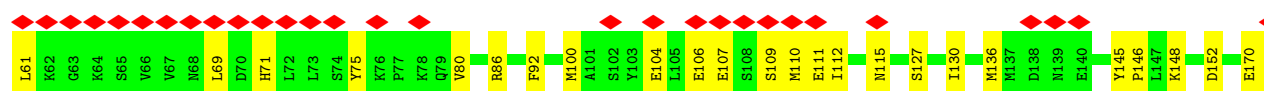
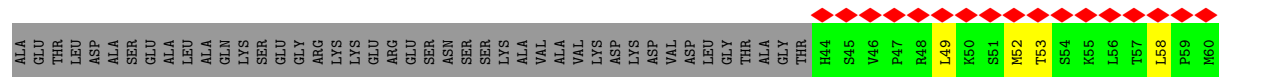
• Molecule 1: Capsid protein



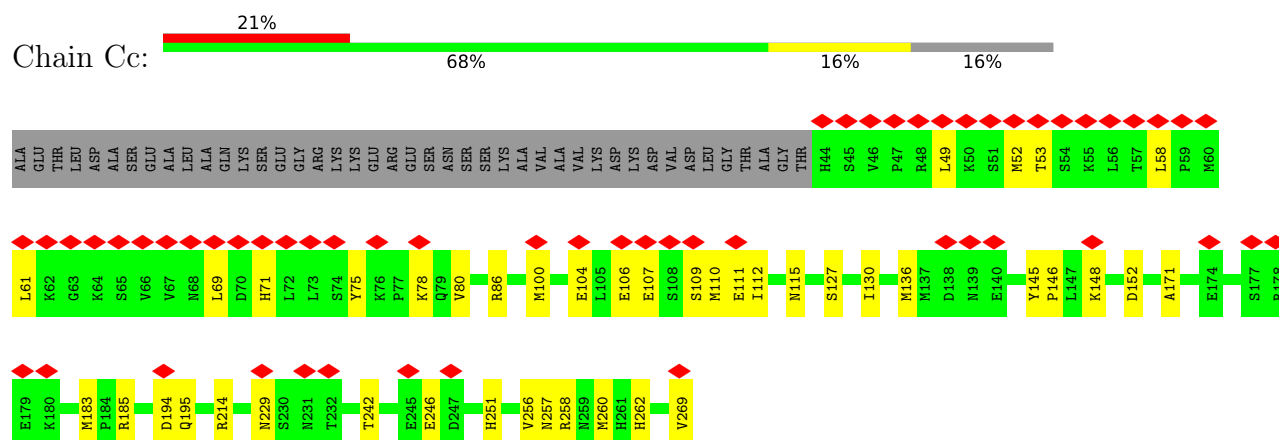
• Molecule 1: Capsid protein



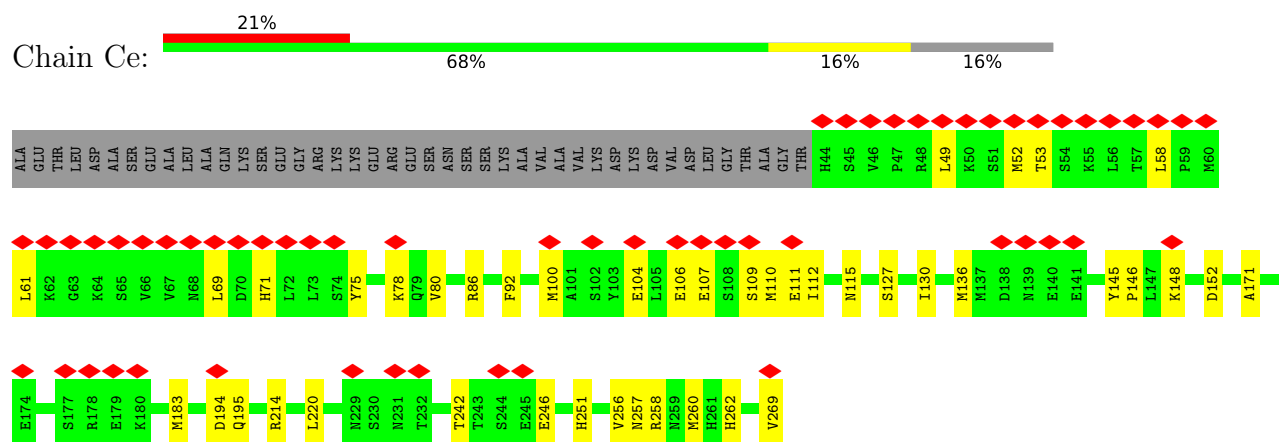
• Molecule 1: Capsid protein



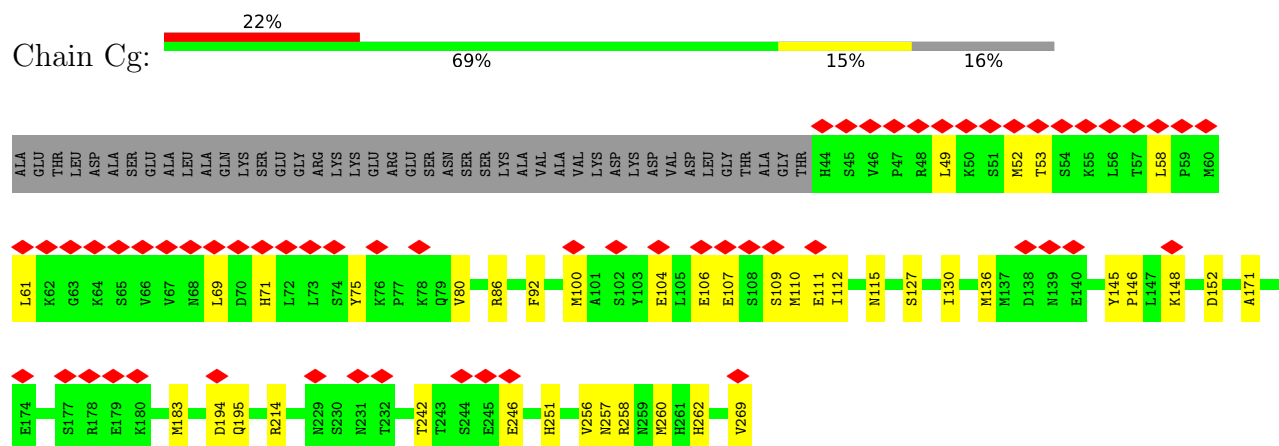
• Molecule 1: Capsid protein



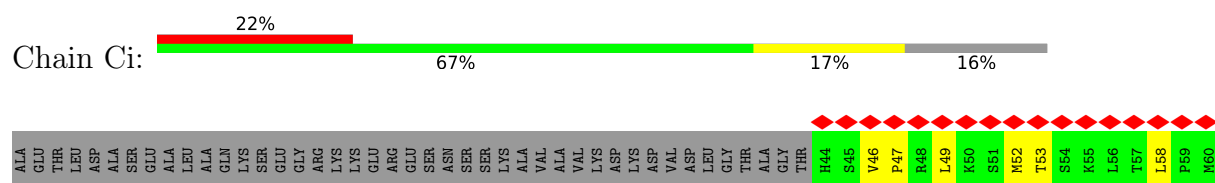
• Molecule 1: Capsid protein

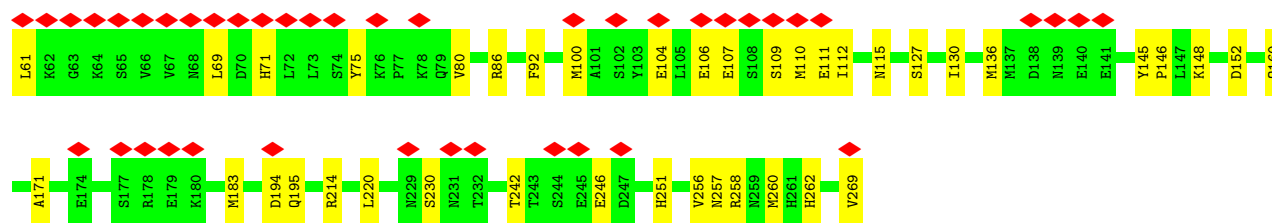


• Molecule 1: Capsid protein

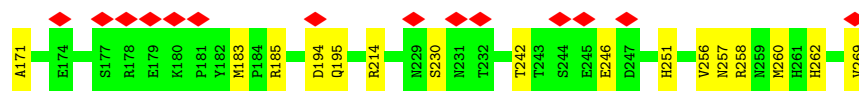
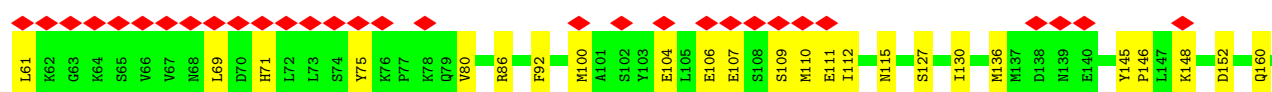
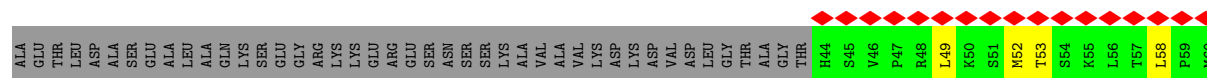


• Molecule 1: Capsid protein

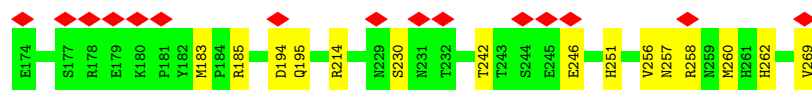
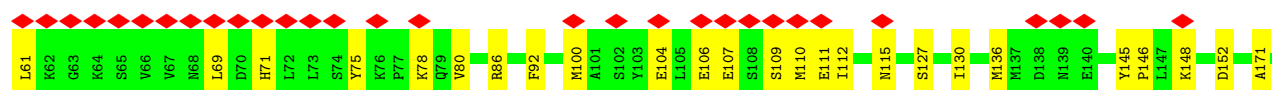
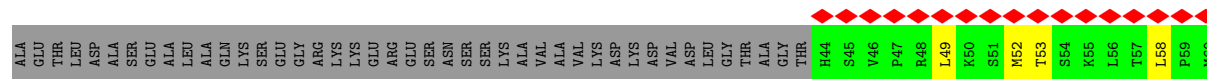
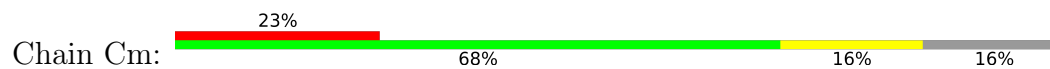




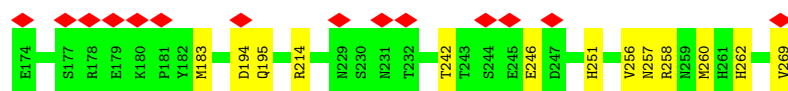
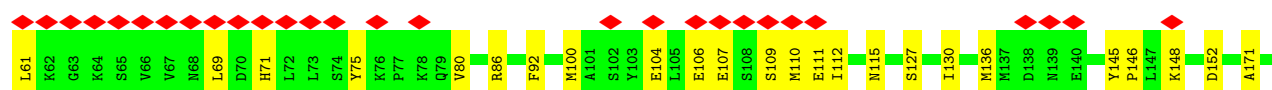
• Molecule 1: Capsid protein



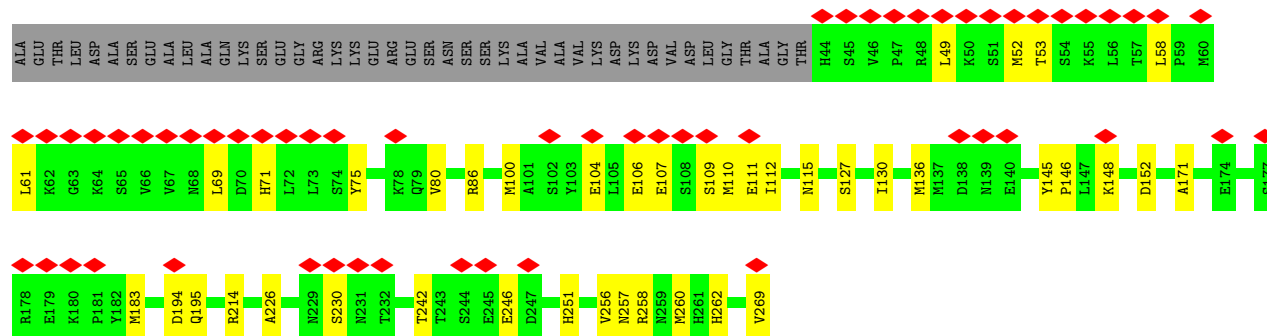
• Molecule 1: Capsid protein



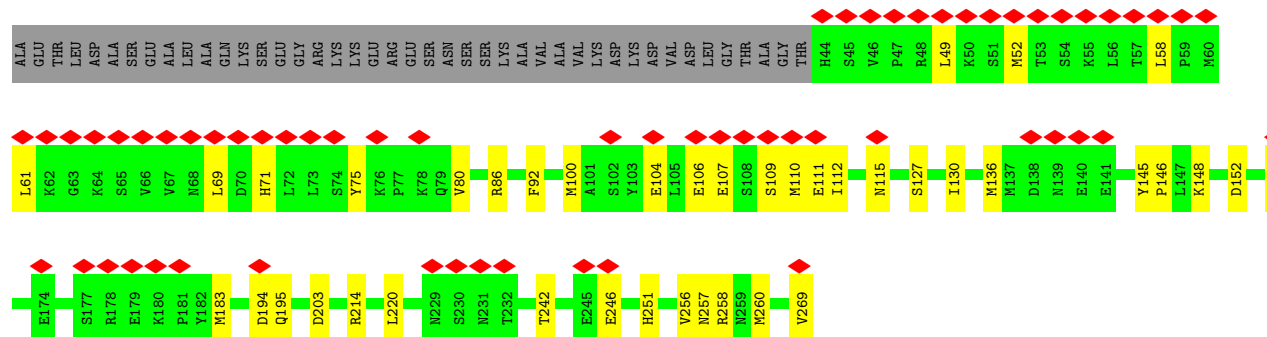
• Molecule 1: Capsid protein



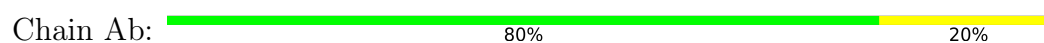
- Molecule 1: Capsid protein



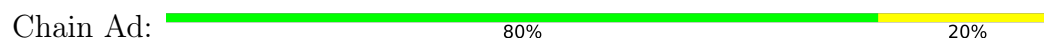
- Molecule 1: Capsid protein



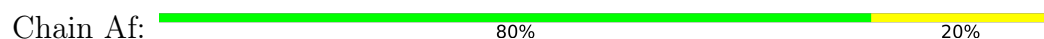
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ah:  60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Aj:  60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Al:  80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain An:  80% 20%

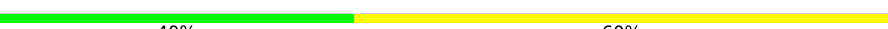


- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ap:  40% 60%



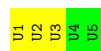
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ar:  40% 60%



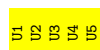
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain At:  40% 60%

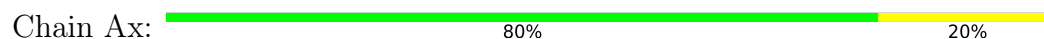


- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

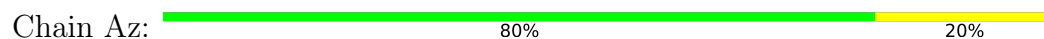
Chain Av:  100%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



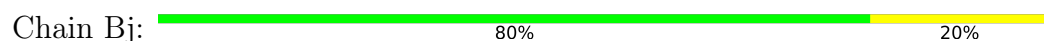
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bl:  60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bn:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bp:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Br:  60% 40%



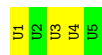
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bt:  80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bv:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bx:  60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Bz:  60% 40%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cb:  60% 40%

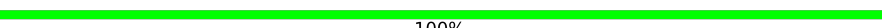


- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cd:  80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cf:  100%

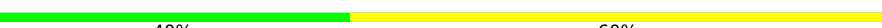
There are no outlier residues recorded for this chain.

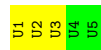
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ch:  80% 20%



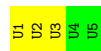
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cj:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cl:  40% 60%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cn:  80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cp:  80% 20%



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Cr: 



- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

Chain Ct: 



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-40.90°, rise=3.89 Å, axial sym=C1	Depositor
Number of segments used	481088	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{Å}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	150000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	12.524	Depositor
Minimum map value	-7.729	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.478	Depositor
Recommended contour level	2.11	Depositor
Map size (Å)	331.1, 331.1, 331.1	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.94600004, 0.94600004, 0.94600004	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	Aa	0.47	0/1854	0.64	0/2503
1	Ac	0.47	0/1854	0.64	0/2503
1	Ae	0.47	0/1854	0.64	0/2503
1	Ag	0.47	0/1854	0.64	0/2503
1	Ai	0.47	0/1854	0.64	0/2503
1	Ak	0.47	0/1854	0.64	0/2503
1	Am	0.47	0/1854	0.64	0/2503
1	Ao	0.47	0/1854	0.64	0/2503
1	Aq	0.47	0/1854	0.64	0/2503
1	As	0.47	0/1854	0.64	0/2503
1	Au	0.47	0/1854	0.64	0/2503
1	Aw	0.47	0/1854	0.64	0/2503
1	Ay	0.47	0/1854	0.64	0/2503
1	Ba	0.47	0/1854	0.64	0/2503
1	Bc	0.47	0/1854	0.64	0/2503
1	Be	0.47	0/1854	0.64	0/2503
1	Bg	0.47	0/1854	0.64	0/2503
1	Bi	0.47	0/1854	0.64	0/2503
1	Bk	0.47	0/1854	0.64	0/2503
1	Bm	0.47	0/1854	0.64	0/2503
1	Bo	0.47	0/1854	0.64	0/2503
1	Bq	0.47	0/1854	0.64	0/2503
1	Bs	0.47	0/1854	0.64	0/2503
1	Bu	0.47	0/1854	0.65	0/2503
1	Bw	0.47	0/1854	0.64	0/2503
1	By	0.47	0/1854	0.64	0/2503
1	Ca	0.47	0/1854	0.65	0/2503
1	Cc	0.47	0/1854	0.64	0/2503
1	Ce	0.47	0/1854	0.64	0/2503
1	Cg	0.47	0/1854	0.64	0/2503
1	Ci	0.47	0/1854	0.64	0/2503
1	Ck	0.47	0/1854	0.64	0/2503
1	Cm	0.47	0/1854	0.64	0/2503
1	Co	0.47	0/1854	0.64	0/2503

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Cq	0.47	0/1854	0.64	0/2503
1	Cs	0.47	0/1854	0.64	0/2503
2	Ab	0.36	0/109	0.36	0/166
2	Ad	0.36	0/109	0.36	0/166
2	Af	0.36	0/109	0.36	0/166
2	Ah	0.36	0/109	0.36	0/166
2	Aj	0.37	0/109	0.36	0/166
2	Al	0.37	0/109	0.36	0/166
2	An	0.36	0/109	0.36	0/166
2	Ap	0.36	0/109	0.36	0/166
2	Ar	0.36	0/109	0.36	0/166
2	At	0.36	0/109	0.36	0/166
2	Av	0.36	0/109	0.36	0/166
2	Ax	0.36	0/109	0.36	0/166
2	Az	0.36	0/109	0.36	0/166
2	Bb	0.37	0/109	0.36	0/166
2	Bd	0.37	0/109	0.36	0/166
2	Bf	0.36	0/109	0.36	0/166
2	Bh	0.36	0/109	0.36	0/166
2	Bj	0.36	0/109	0.36	0/166
2	Bl	0.36	0/109	0.36	0/166
2	Bn	0.36	0/109	0.36	0/166
2	Bp	0.36	0/109	0.36	0/166
2	Br	0.36	0/109	0.36	0/166
2	Bt	0.36	0/109	0.36	0/166
2	Bv	0.36	0/109	0.36	0/166
2	Bx	0.36	0/109	0.36	0/166
2	Bz	0.36	0/109	0.36	0/166
2	Cb	0.36	0/109	0.36	0/166
2	Cd	0.36	0/109	0.36	0/166
2	Cf	0.36	0/109	0.36	0/166
2	Ch	0.36	0/109	0.36	0/166
2	Cj	0.36	0/109	0.36	0/166
2	Cl	0.36	0/109	0.36	0/166
2	Cn	0.37	0/109	0.36	0/166
2	Cp	0.36	0/109	0.36	0/166
2	Cr	0.36	0/109	0.36	0/166
2	Ct	0.36	0/109	0.36	0/166
All	All	0.46	0/70668	0.63	0/96084

There are no bond length outliers.

There are no bond angle outliers.

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	Aa	1815	0	1785	32	0
1	Ac	1815	0	1785	36	0
1	Ae	1815	0	1785	37	0
1	Ag	1815	0	1785	36	0
1	Ai	1815	0	1785	38	0
1	Ak	1815	0	1785	36	0
1	Am	1815	0	1785	33	0
1	Ao	1815	0	1785	37	0
1	Aq	1815	0	1785	40	0
1	As	1815	0	1785	43	0
1	Au	1815	0	1785	55	0
1	Aw	1815	0	1785	46	0
1	Ay	1815	0	1785	47	0
1	Ba	1815	0	1785	48	0
1	Bc	1815	0	1785	47	0
1	Be	1815	0	1785	48	0
1	Bg	1815	0	1785	49	0
1	Bi	1815	0	1785	47	0
1	Bk	1815	0	1785	45	0
1	Bm	1815	0	1785	49	0
1	Bo	1815	0	1785	46	0
1	Bq	1815	0	1785	49	0
1	Bs	1815	0	1785	48	0
1	Bu	1815	0	1785	47	0
1	Bw	1815	0	1785	47	0
1	By	1815	0	1785	48	0
1	Ca	1815	0	1785	39	0
1	Cc	1815	0	1785	37	0
1	Ce	1815	0	1785	37	0
1	Cg	1815	0	1785	36	0
1	Ci	1815	0	1785	41	0
1	Ck	1815	0	1785	40	0
1	Cm	1815	0	1785	38	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Co	1815	0	1785	33	0
1	Cq	1815	0	1785	36	0
1	Cs	1815	0	1785	33	0
2	Ab	100	0	51	1	0
2	Ad	100	0	51	1	0
2	Af	100	0	51	1	0
2	Ah	100	0	51	3	0
2	Aj	100	0	51	3	0
2	Al	100	0	51	1	0
2	An	100	0	51	1	0
2	Ap	100	0	51	10	0
2	Ar	100	0	51	8	0
2	At	100	0	51	4	0
2	Av	100	0	51	8	0
2	Ax	100	0	51	1	0
2	Az	100	0	51	1	0
2	Bb	100	0	51	2	0
2	Bd	100	0	51	2	0
2	Bf	100	0	51	4	0
2	Bh	100	0	51	2	0
2	Bj	100	0	51	1	0
2	Bl	100	0	51	3	0
2	Bn	100	0	51	8	0
2	Bp	100	0	51	5	0
2	Br	100	0	51	3	0
2	Bt	100	0	51	1	0
2	Bv	100	0	51	3	0
2	Bx	100	0	51	2	0
2	Bz	100	0	51	3	0
2	Cb	100	0	51	2	0
2	Cd	100	0	51	1	0
2	Cf	100	0	51	0	0
2	Ch	100	0	51	1	0
2	Cj	100	0	51	4	0
2	Cl	100	0	51	4	0
2	Cn	100	0	51	1	0
2	Cp	100	0	51	2	0
2	Cr	100	0	51	5	0
2	Ct	100	0	51	1	0
All	All	68940	0	66096	1116	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1116 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:Av:1:U:P	1:Aw:185:ARG:HH12	2.05	0.79
1:Aq:230:SER:HB2	2:Ar:3:U:O2'	1.87	0.75
1:Bm:230:SER:HB2	2:Bn:3:U:O2'	1.86	0.74
1:Ao:230:SER:HB2	2:Ap:3:U:O2'	1.87	0.74
1:Bq:230:SER:HB2	2:Br:3:U:O2'	1.88	0.73

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Aa	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ac	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ae	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ag	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ai	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ak	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Am	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ao	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Aq	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	As	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Au	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Aw	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ay	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ba	224/269 (83%)	219 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Bc	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Be	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bg	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bi	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bk	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bm	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bo	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bq	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bs	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bu	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Bw	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	By	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ca	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Cc	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ce	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Cg	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ci	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Ck	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Cm	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Co	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Cq	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
1	Cs	224/269 (83%)	219 (98%)	5 (2%)	0	100	100
All	All	8064/9684 (83%)	7884 (98%)	180 (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	Aa	200/233 (86%)	200 (100%)	0	100	100
1	Ac	200/233 (86%)	200 (100%)	0	100	100
1	Ae	200/233 (86%)	200 (100%)	0	100	100
1	Ag	200/233 (86%)	200 (100%)	0	100	100
1	Ai	200/233 (86%)	200 (100%)	0	100	100
1	Ak	200/233 (86%)	200 (100%)	0	100	100
1	Am	200/233 (86%)	200 (100%)	0	100	100
1	Ao	200/233 (86%)	200 (100%)	0	100	100
1	Aq	200/233 (86%)	200 (100%)	0	100	100
1	As	200/233 (86%)	200 (100%)	0	100	100
1	Au	200/233 (86%)	200 (100%)	0	100	100
1	Aw	200/233 (86%)	200 (100%)	0	100	100
1	Ay	200/233 (86%)	200 (100%)	0	100	100
1	Ba	200/233 (86%)	200 (100%)	0	100	100
1	Bc	200/233 (86%)	200 (100%)	0	100	100
1	Be	200/233 (86%)	200 (100%)	0	100	100
1	Bg	200/233 (86%)	200 (100%)	0	100	100
1	Bi	200/233 (86%)	200 (100%)	0	100	100
1	Bk	200/233 (86%)	200 (100%)	0	100	100
1	Bm	200/233 (86%)	200 (100%)	0	100	100
1	Bo	200/233 (86%)	200 (100%)	0	100	100
1	Bq	200/233 (86%)	200 (100%)	0	100	100
1	Bs	200/233 (86%)	200 (100%)	0	100	100
1	Bu	200/233 (86%)	200 (100%)	0	100	100
1	Bw	200/233 (86%)	200 (100%)	0	100	100
1	By	200/233 (86%)	200 (100%)	0	100	100
1	Ca	200/233 (86%)	200 (100%)	0	100	100
1	Cc	200/233 (86%)	200 (100%)	0	100	100
1	Ce	200/233 (86%)	200 (100%)	0	100	100
1	Cg	200/233 (86%)	200 (100%)	0	100	100
1	Ci	200/233 (86%)	200 (100%)	0	100	100
1	Ck	200/233 (86%)	200 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Cm	200/233 (86%)	200 (100%)	0	100	100
1	Co	200/233 (86%)	200 (100%)	0	100	100
1	Cq	200/233 (86%)	200 (100%)	0	100	100
1	Cs	200/233 (86%)	200 (100%)	0	100	100
All	All	7200/8388 (86%)	7200 (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 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	Ca	240	ASN
1	Cq	240	ASN
1	Cc	79	GLN
1	Ck	240	ASN
1	Aq	240	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Ab	4/5 (80%)	0	0
2	Ad	4/5 (80%)	0	0
2	Af	4/5 (80%)	0	0
2	Ah	4/5 (80%)	0	0
2	Aj	4/5 (80%)	0	0
2	Al	4/5 (80%)	0	0
2	An	4/5 (80%)	0	0
2	Ap	4/5 (80%)	0	0
2	Ar	4/5 (80%)	0	0
2	At	4/5 (80%)	0	0
2	Av	4/5 (80%)	0	0
2	Ax	4/5 (80%)	0	0
2	Az	4/5 (80%)	0	0
2	Bb	4/5 (80%)	0	0
2	Bd	4/5 (80%)	0	0
2	Bf	4/5 (80%)	0	0
2	Bh	4/5 (80%)	0	0
2	Bj	4/5 (80%)	0	0
2	Bl	4/5 (80%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Bn	4/5 (80%)	0	0
2	Bp	4/5 (80%)	0	0
2	Br	4/5 (80%)	0	0
2	Bt	4/5 (80%)	0	0
2	Bv	4/5 (80%)	0	0
2	Bx	4/5 (80%)	0	0
2	Bz	4/5 (80%)	0	0
2	Cb	4/5 (80%)	0	0
2	Cd	4/5 (80%)	0	0
2	Cf	4/5 (80%)	0	0
2	Ch	4/5 (80%)	0	0
2	Cj	4/5 (80%)	0	0
2	Cl	4/5 (80%)	0	0
2	Cn	4/5 (80%)	0	0
2	Cp	4/5 (80%)	0	0
2	Cr	4/5 (80%)	0	0
2	Ct	4/5 (80%)	0	0
All	All	144/180 (80%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 ⓘ

There are no chain breaks in this entry.

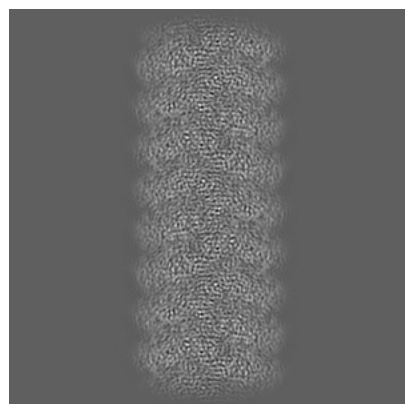
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53790. These allow visual inspection of the internal detail of the map and identification of artifacts.

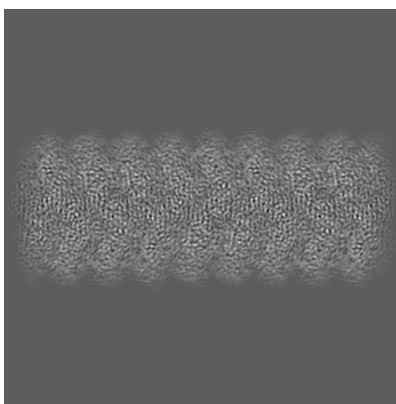
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

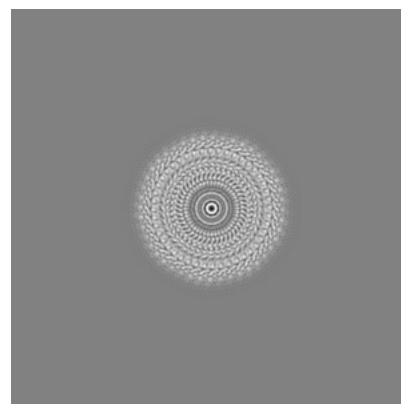
6.1.1 Primary map



X

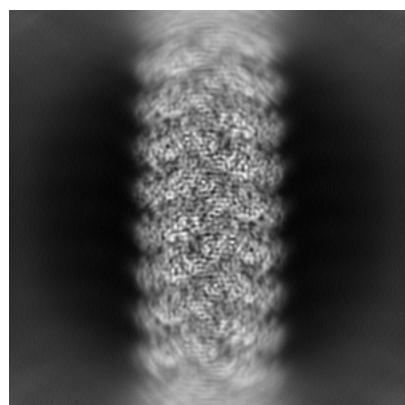


Y

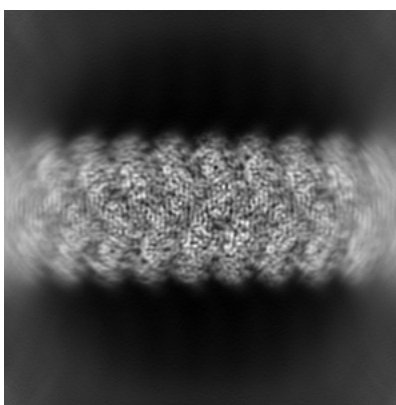


Z

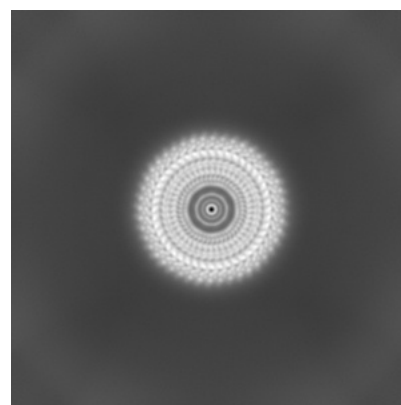
6.1.2 Raw map



X



Y

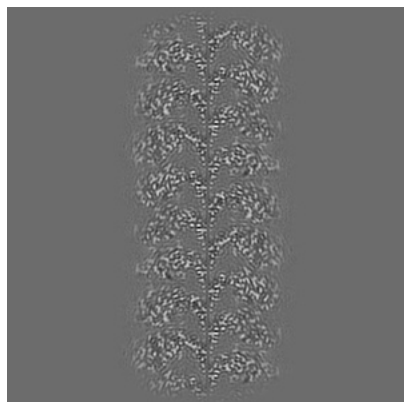


Z

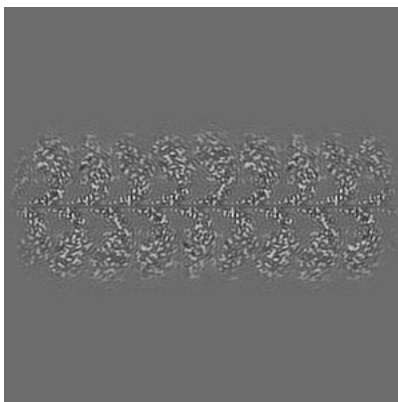
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

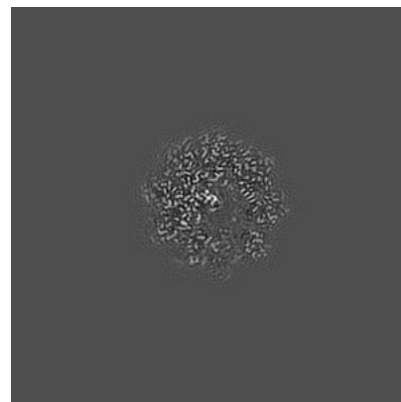
6.2.1 Primary map



X Index: 175

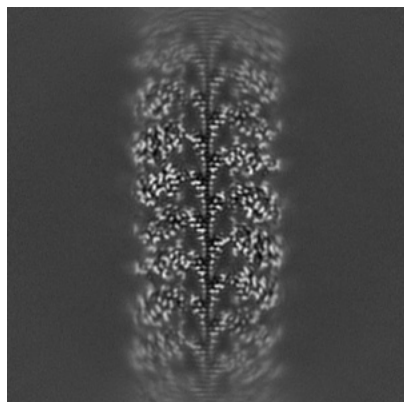


Y Index: 175

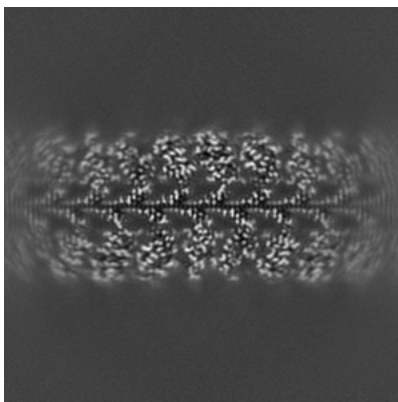


Z Index: 175

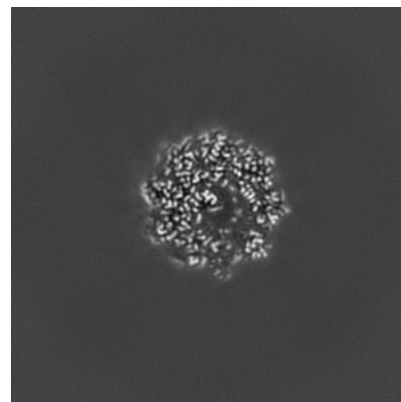
6.2.2 Raw map



X Index: 175



Y Index: 175

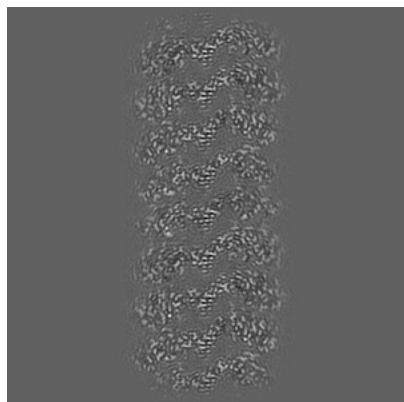


Z Index: 175

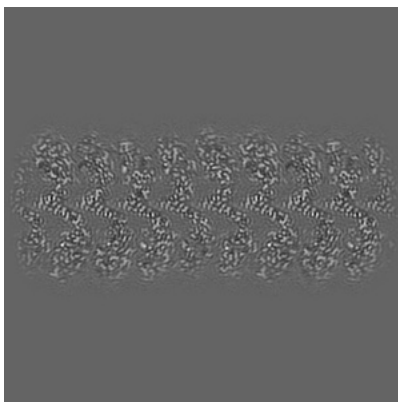
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

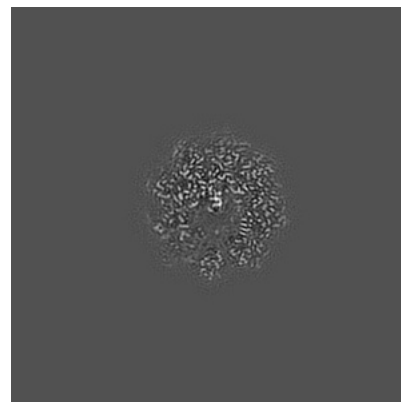
6.3.1 Primary map



X Index: 168

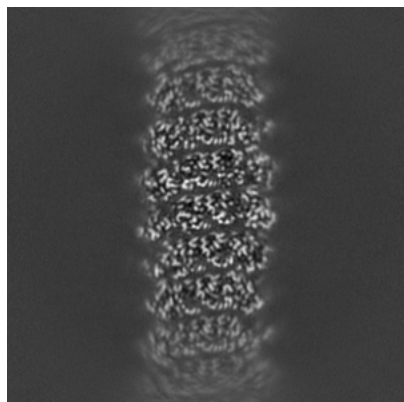


Y Index: 172

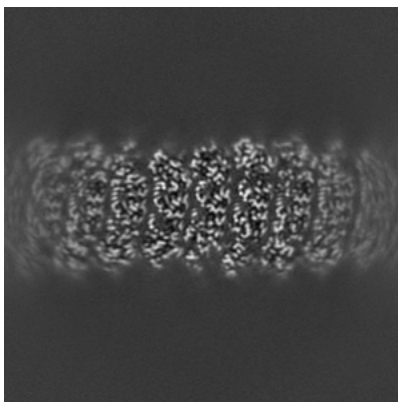


Z Index: 216

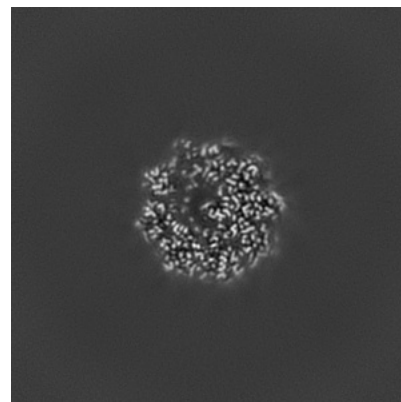
6.3.2 Raw map



X Index: 143



Y Index: 207

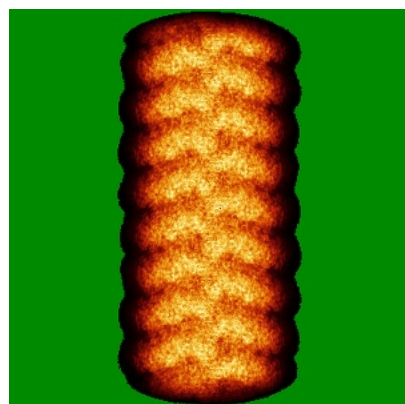


Z Index: 192

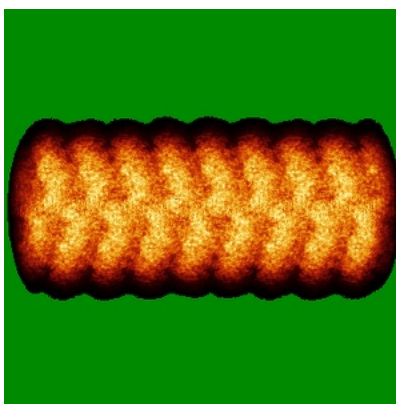
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

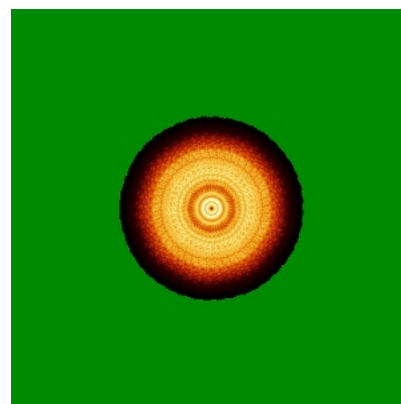
6.4.1 Primary map



X

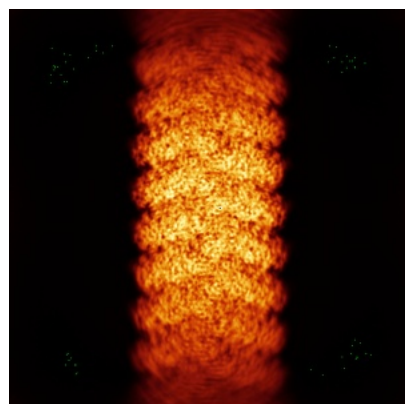


Y

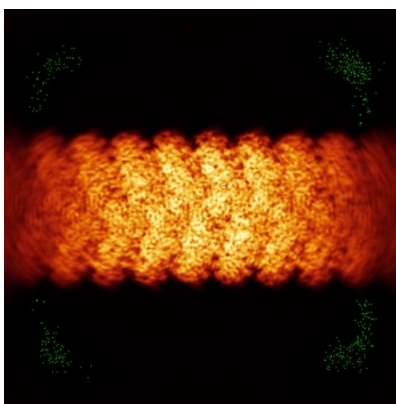


Z

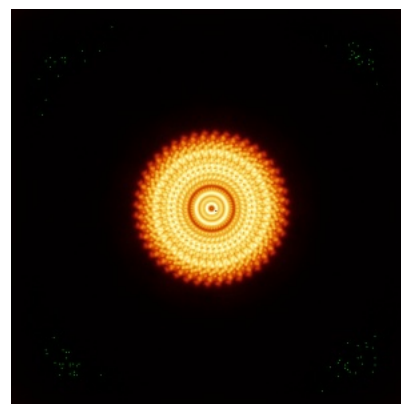
6.4.2 Raw map



X



Y

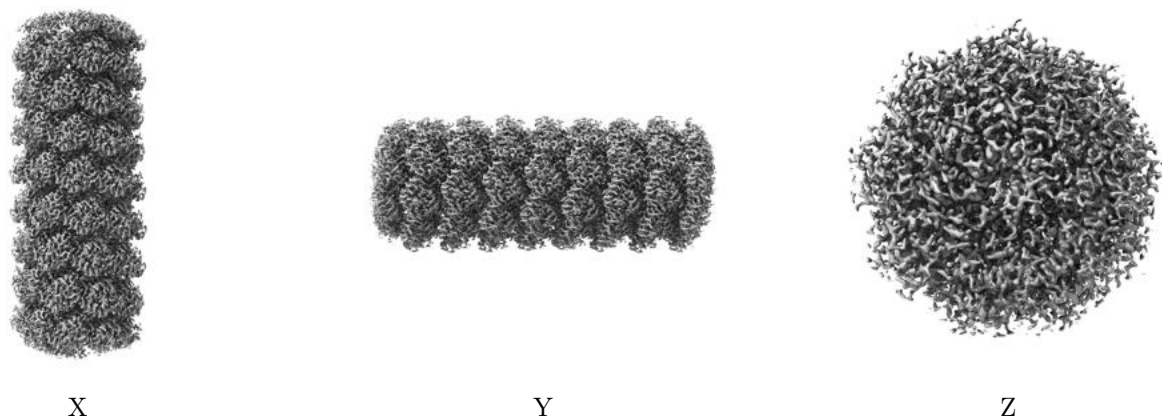


Z

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 2.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

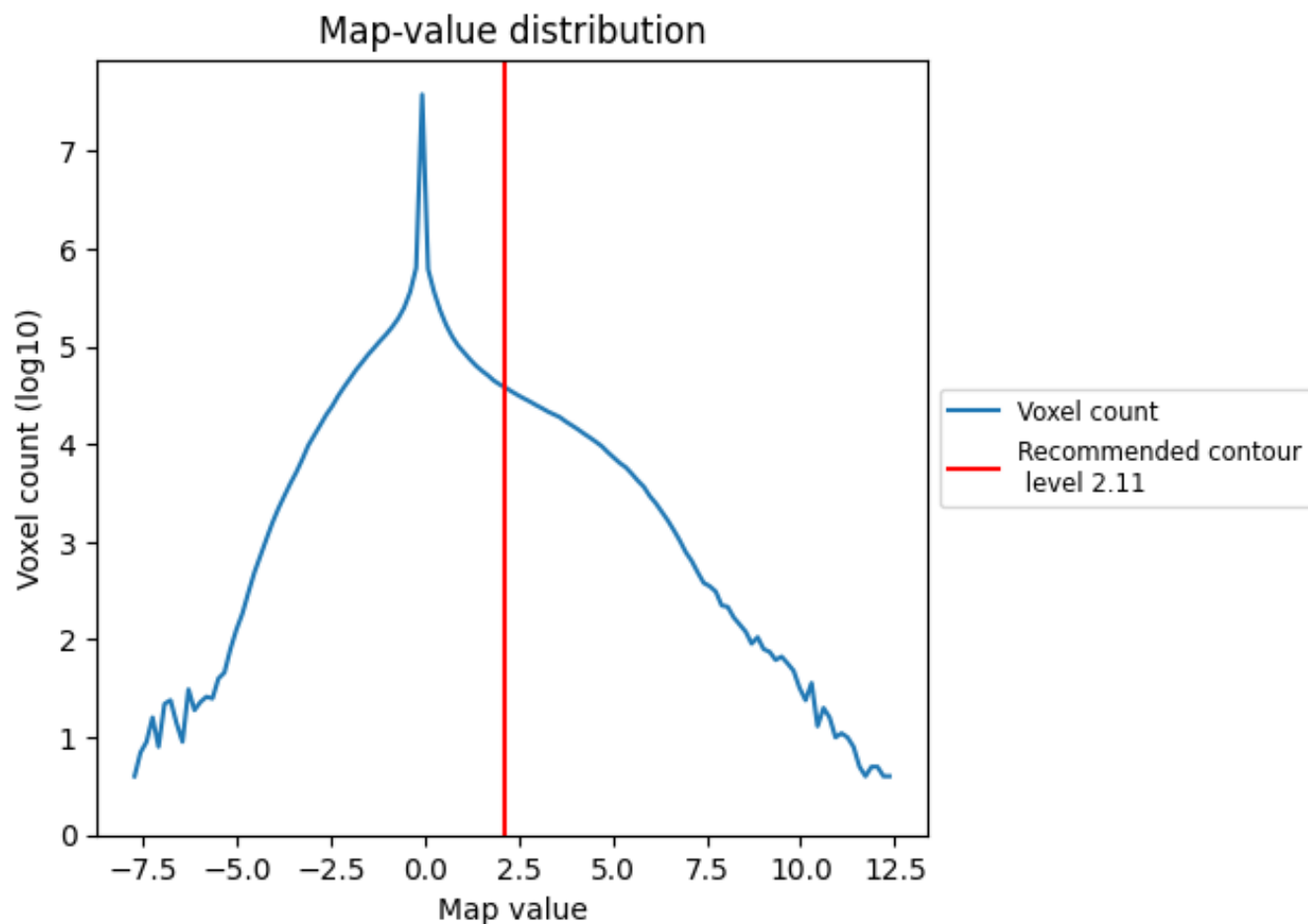
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

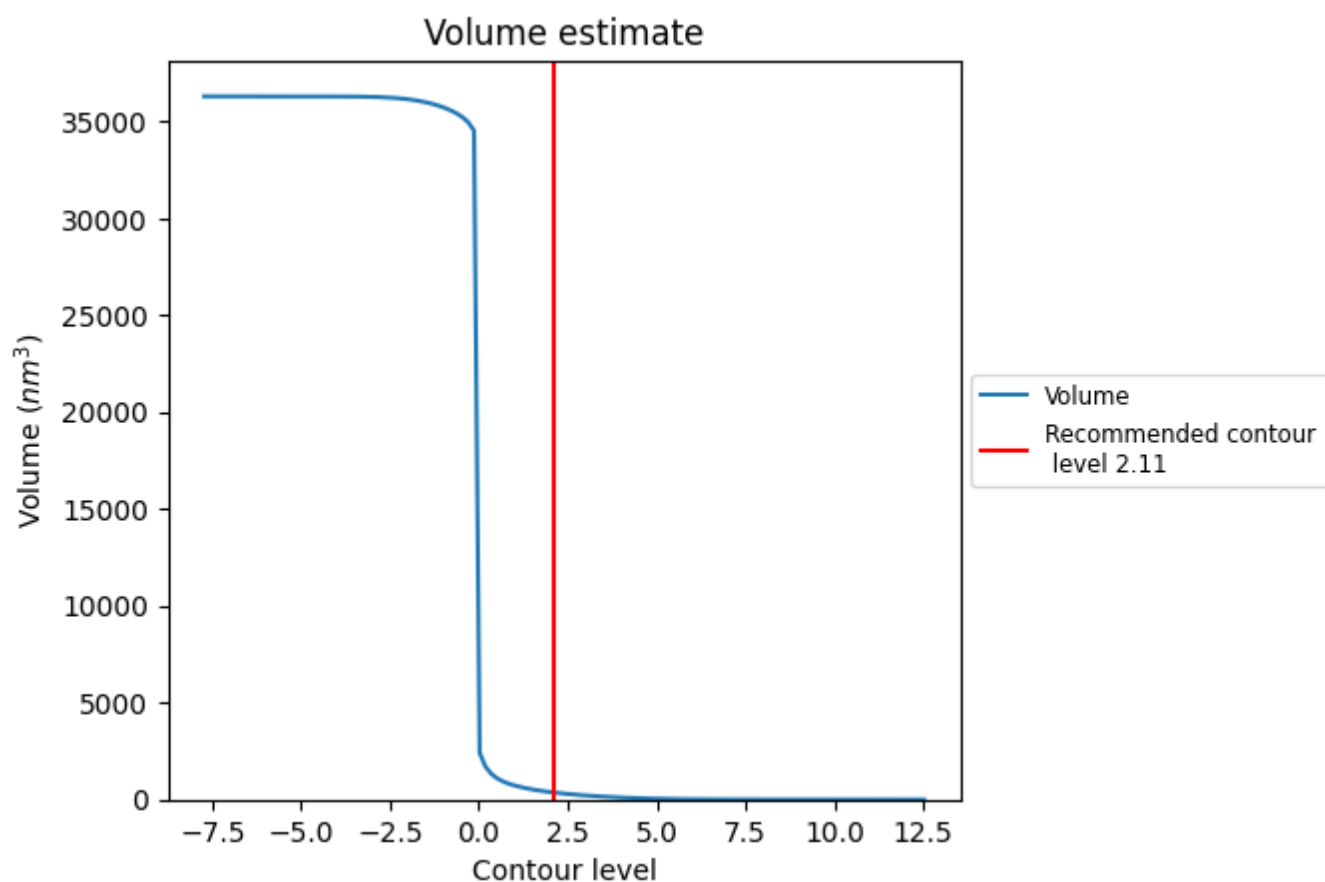
This section contains the results of statistical analysis of the map.

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.

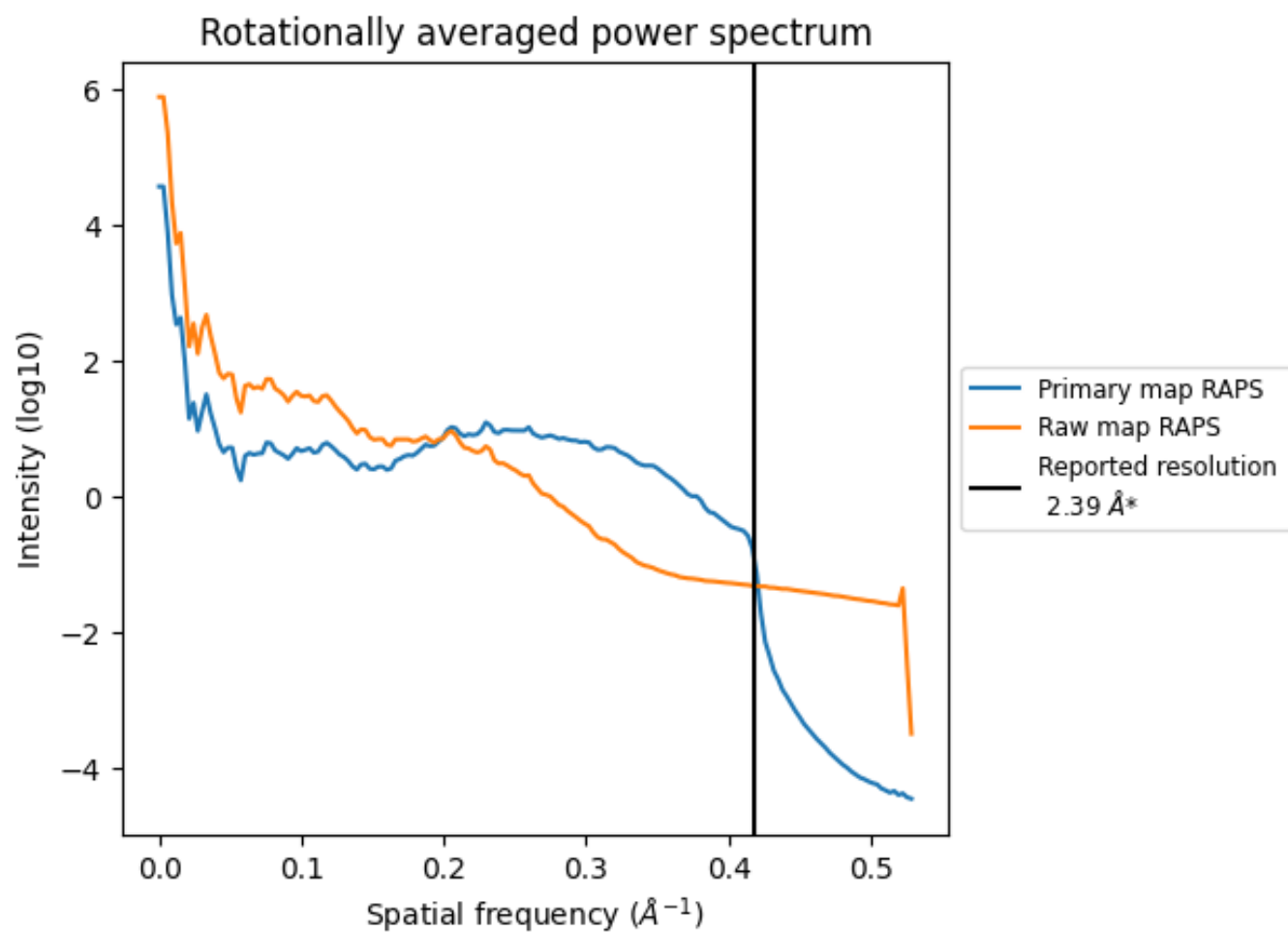
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 364 nm³; this corresponds to an approximate mass of 329 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 ⓘ

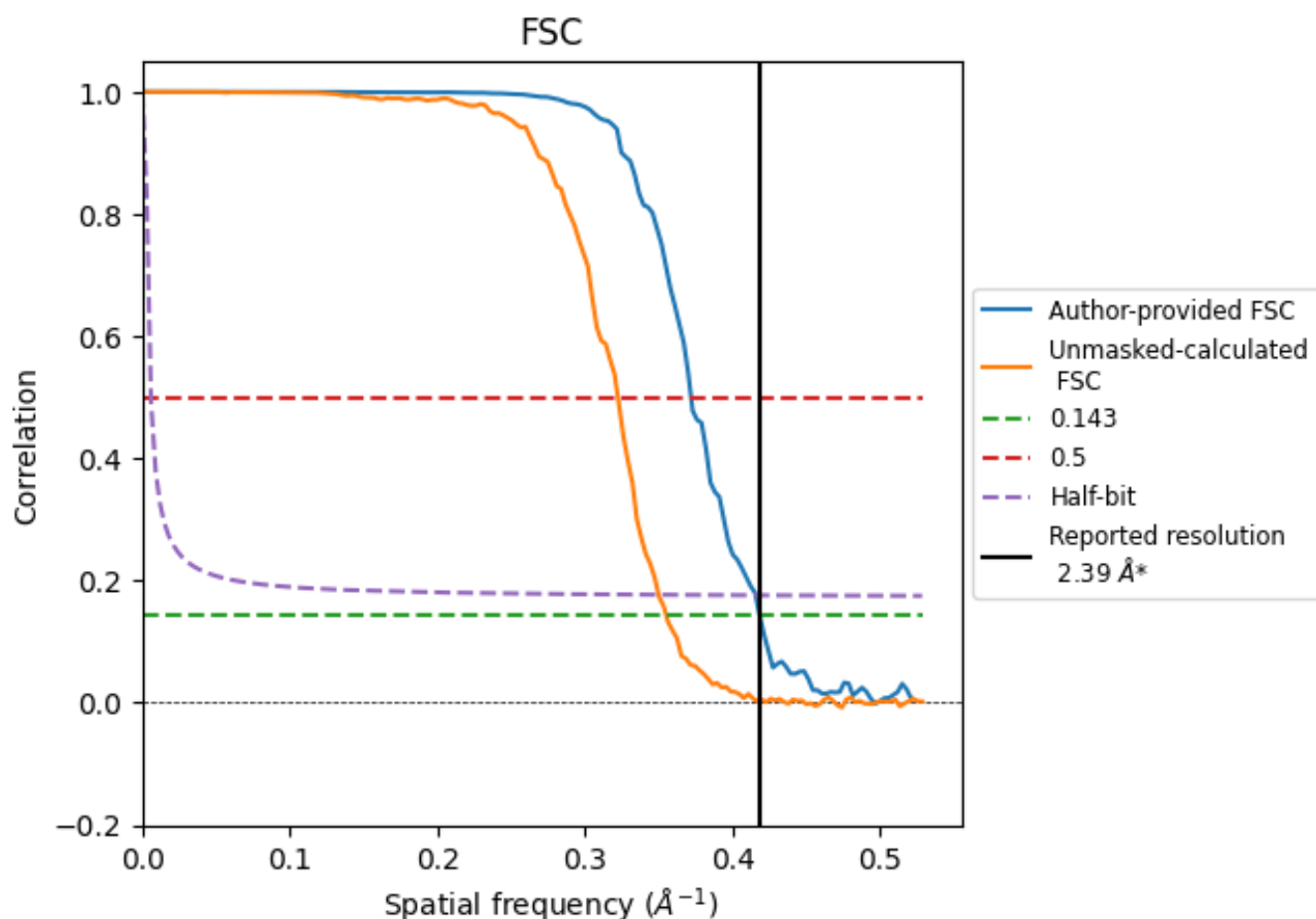


*Reported resolution corresponds to spatial frequency of 0.418 $\text{\AA}^{-1}$

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 0.418 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.39	-	-
Author-provided FSC curve	2.39	2.69	2.41
Unmasked-calculated*	2.82	3.10	2.86

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.82 differs from the reported value 2.39 by more than 10 %

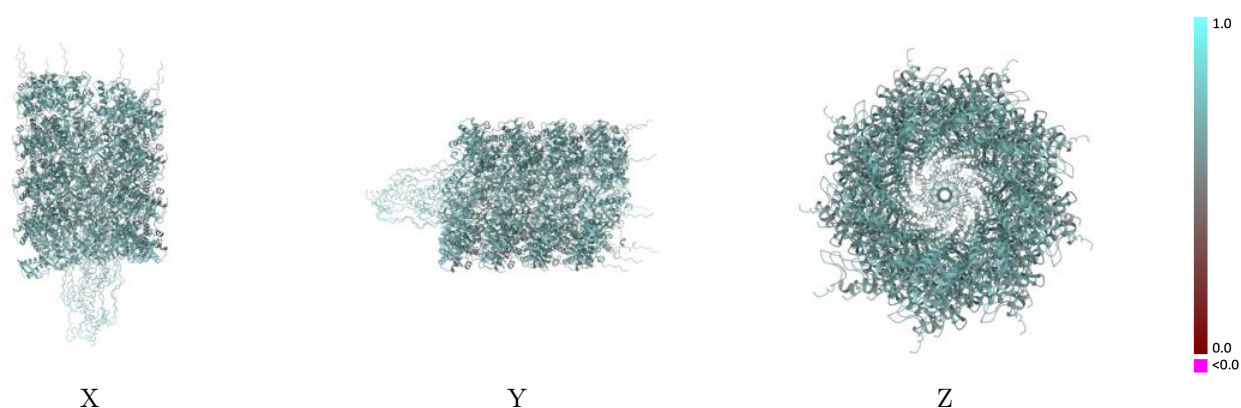
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53790 and PDB model 9R7R. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

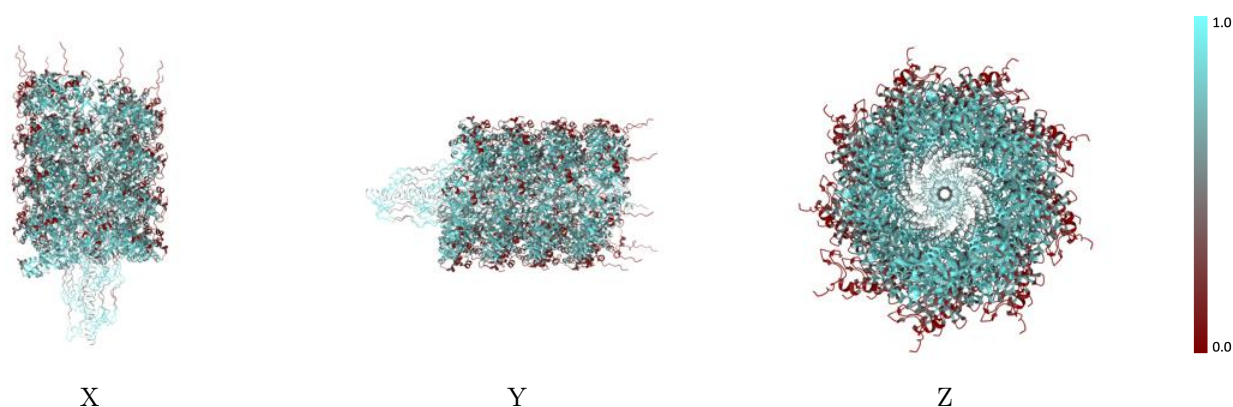
This section was not generated.

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



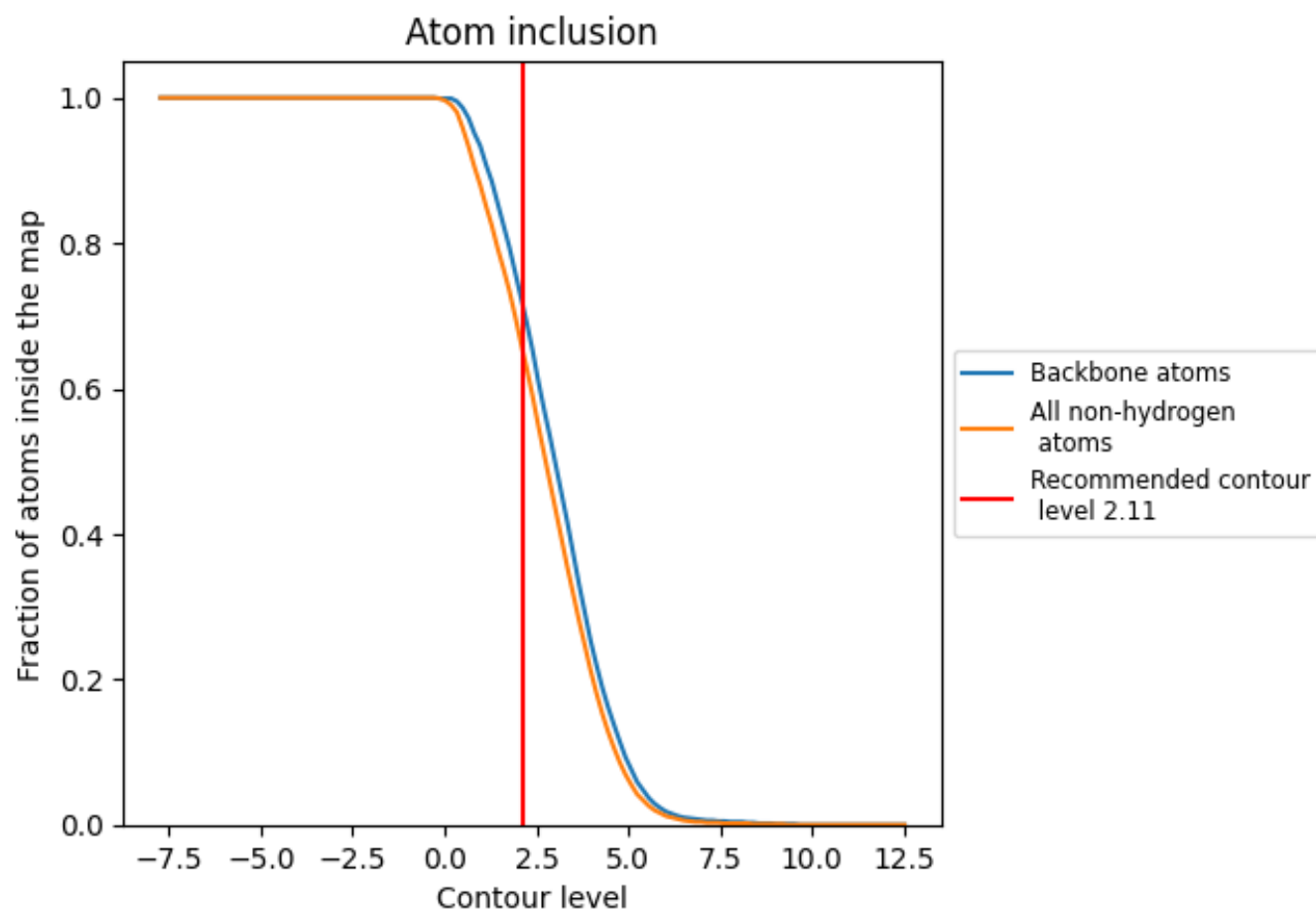
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 66% 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 (2.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6560	 0.6550
Aa	 0.6420	 0.6550
Ab	 0.9300	 0.6550
Ac	 0.6390	 0.6540
Ad	 0.9000	 0.6610
Ae	 0.6520	 0.6550
Af	 0.9100	 0.6690
Ag	 0.6450	 0.6540
Ah	 0.8700	 0.6590
Ai	 0.6410	 0.6560
Aj	 0.8900	 0.6550
Ak	 0.6430	 0.6550
Al	 0.8700	 0.6620
Am	 0.6430	 0.6550
An	 0.9300	 0.6670
Ao	 0.6400	 0.6540
Ap	 0.8600	 0.6420
Aq	 0.6450	 0.6550
Ar	 0.8800	 0.6360
As	 0.6430	 0.6550
At	 0.8800	 0.6420
Au	 0.6480	 0.6550
Av	 0.9100	 0.6500
Aw	 0.6430	 0.6550
Ax	 0.8500	 0.6610
Ay	 0.6440	 0.6540
Az	 0.8900	 0.6550
Ba	 0.6480	 0.6550
Bb	 0.9000	 0.6590
Bc	 0.6450	 0.6550
Bd	 0.8900	 0.6640
Be	 0.6320	 0.6560
Bf	 0.9300	 0.6470
Bg	 0.6450	 0.6550
Bh	 0.9000	 0.6600



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Chain	Atom inclusion	Q-score
Bi	 0.6430	 0.6550
Bj	 0.9300	 0.6650
Bk	 0.6400	 0.6550
Bl	 0.8800	 0.6420
Bm	 0.6440	 0.6540
Bn	 0.8800	 0.6440
Bo	 0.6430	 0.6550
Bp	 0.8500	 0.6470
Bq	 0.6400	 0.6540
Br	 0.8700	 0.6370
Bs	 0.6430	 0.6550
Bt	 0.8700	 0.6610
Bu	 0.6450	 0.6540
Bv	 0.9200	 0.6520
Bw	 0.6380	 0.6550
Bx	 0.9000	 0.6590
By	 0.6460	 0.6560
Bz	 0.9400	 0.6620
Ca	 0.6350	 0.6550
Cb	 0.9600	 0.6670
Cc	 0.6470	 0.6550
Cd	 0.8800	 0.6600
Ce	 0.6440	 0.6540
Cf	 0.9200	 0.6660
Cg	 0.6400	 0.6540
Ch	 0.8800	 0.6540
Ci	 0.6440	 0.6540
Cj	 0.8800	 0.6410
Ck	 0.6390	 0.6550
Cl	 0.8700	 0.6380
Cm	 0.6390	 0.6540
Cn	 0.9000	 0.6610
Co	 0.6410	 0.6550
Cp	 0.9200	 0.6610
Cq	 0.6470	 0.6560
Cr	 0.8900	 0.6470
Cs	 0.6440	 0.6550
Ct	 0.9300	 0.6620