



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 09:14 AM UTC

PDB ID : 9R7V / pdb_00009r7v
EMDB ID : EMD-53794
Title : ssRNA-containing helical virus-like particle composed of PVA (isolate Datura)
coat protein
Authors : Koritnik, N.; Kezar, A.; Podobnik, M.
Deposited on : 2025-05-15
Resolution : 3.06 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

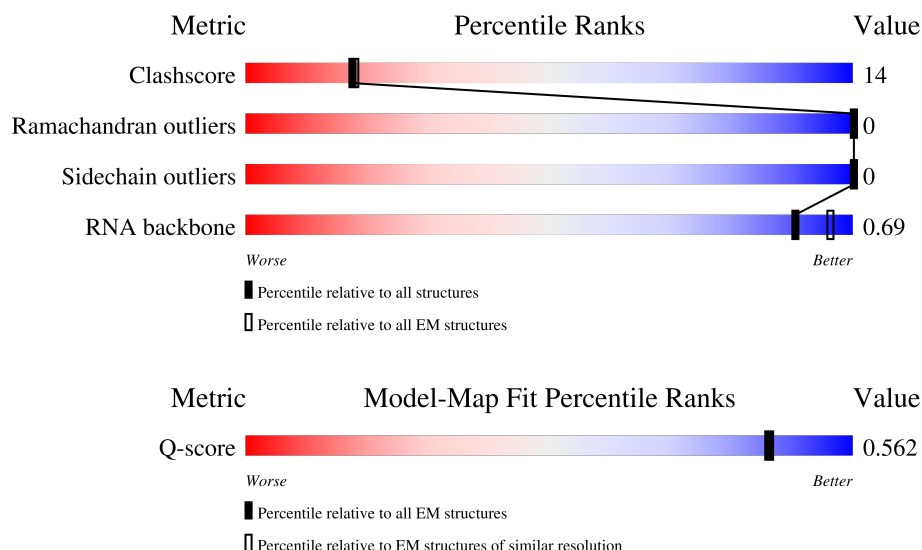
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.06 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.



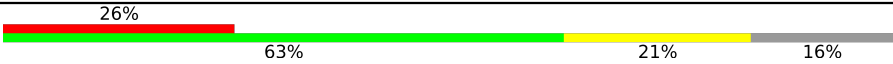
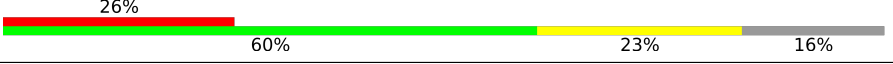
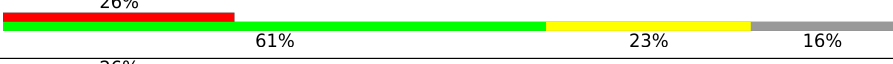
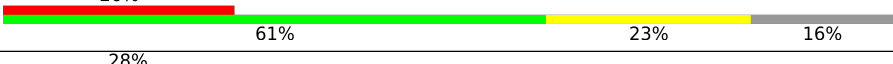
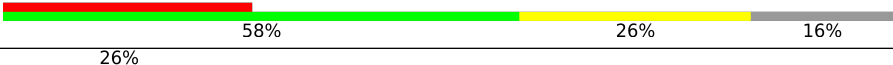
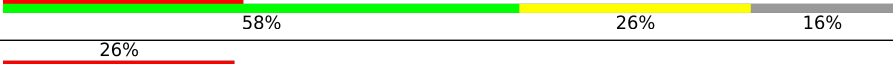
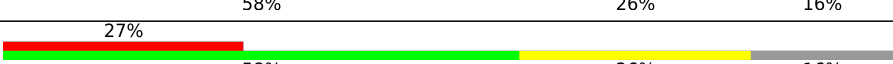
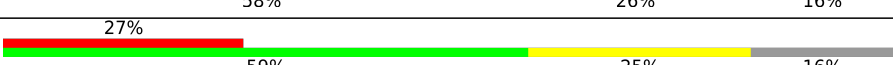
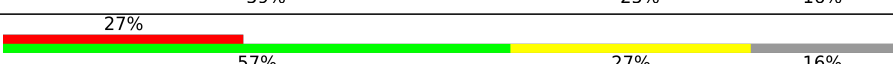
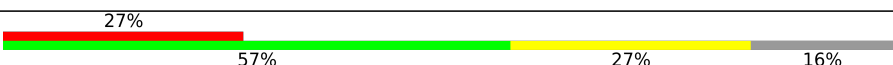
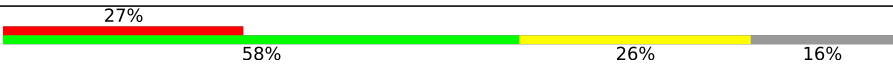
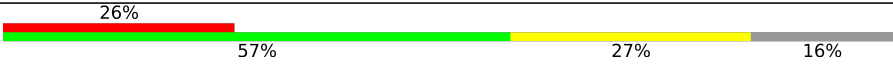
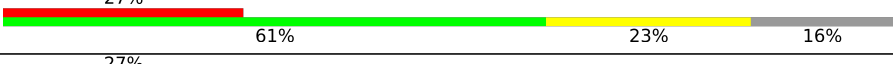
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13976 (2.56 - 3.56)

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	27% 59% 24% 16%
1	Ac	269	26% 59% 25% 16%
1	Ae	269	26% 58% 25% 16%

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Mol	Chain	Length	Quality of chain
1	Ag	269	
1	Ai	269	
1	Ak	269	
1	Am	269	
1	Ao	269	
1	Aq	269	
1	As	269	
1	Au	269	
1	Aw	269	
1	Ay	269	
1	Ba	269	
1	Bc	269	
1	Be	269	
1	Bg	269	
1	Bi	269	
1	Bk	269	
1	Bm	269	
1	Bo	269	
1	Bq	269	
1	Bs	269	
1	Bu	269	
1	Bw	269	
1	By	269	
1	Ca	269	
1	Cc	269	

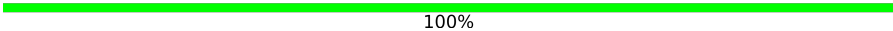
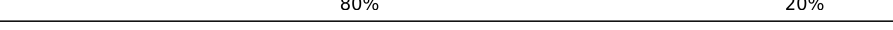
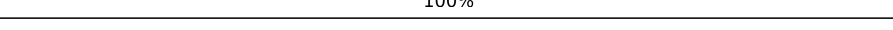
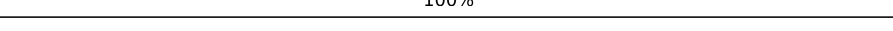
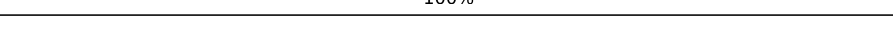
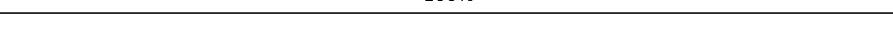
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Mol	Chain	Length	Quality of chain
1	Ce	269	
1	Cg	269	
1	Ci	269	
1	Ck	269	
1	Cm	269	
1	Co	269	
1	Cq	269	
1	Cs	269	
2	Ab	5	
2	Ad	5	
2	Af	5	
2	Ah	5	
2	Aj	5	
2	Al	5	
2	An	5	
2	Ap	5	
2	Ar	5	
2	At	5	
2	Av	5	
2	Ax	5	
2	Az	5	
2	Bb	5	
2	Bd	5	
2	Bf	5	
2	Bh	5	

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

2 Entry composition [i](#)

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 Genome polypeptide.

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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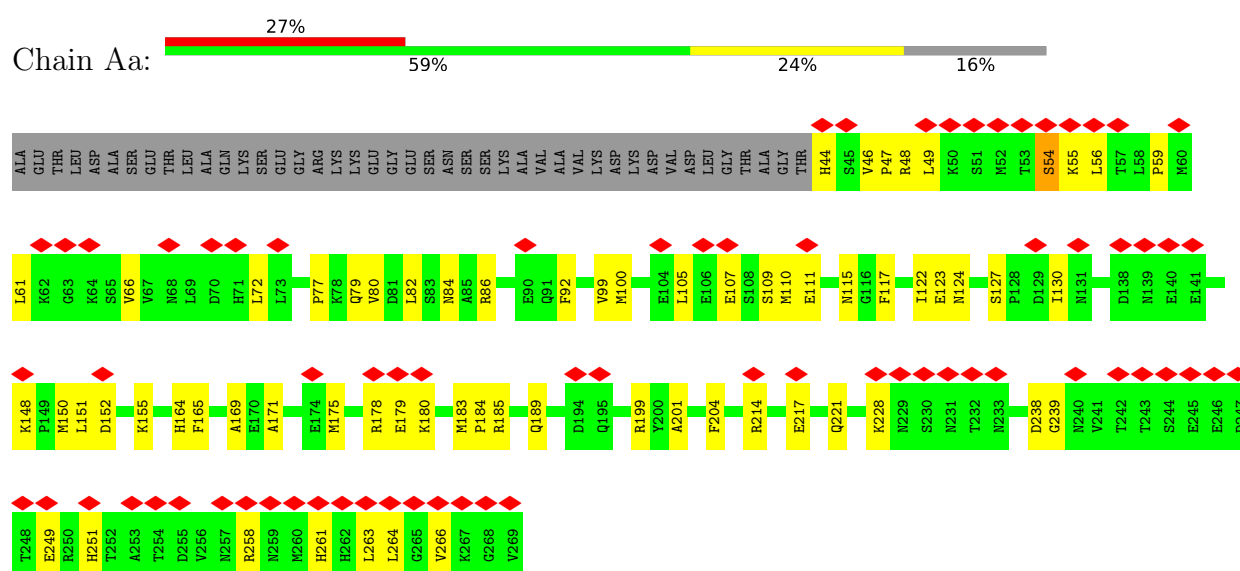
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Mol	Chain	Residues	Atoms					AltConf	Trace
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2	Bv	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bx	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Bz	5	Total 100	C 45	N 10	O 40	P 5	0	0
2	Cb	5	Total 100	C 45	N 10	O 40	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

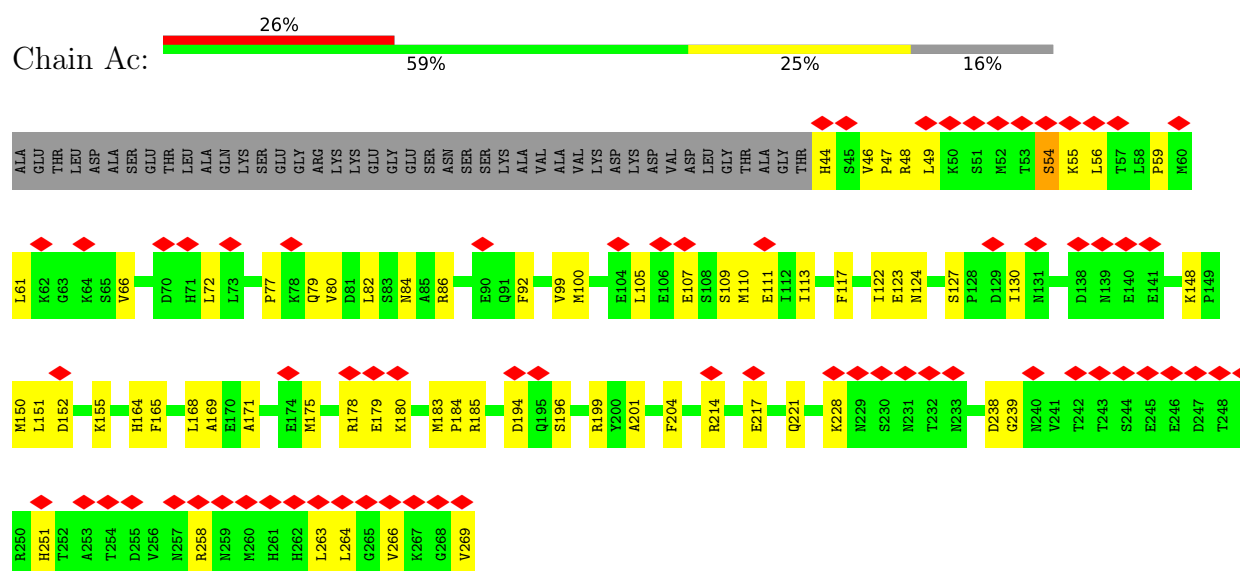
3 Residue-property plots

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.

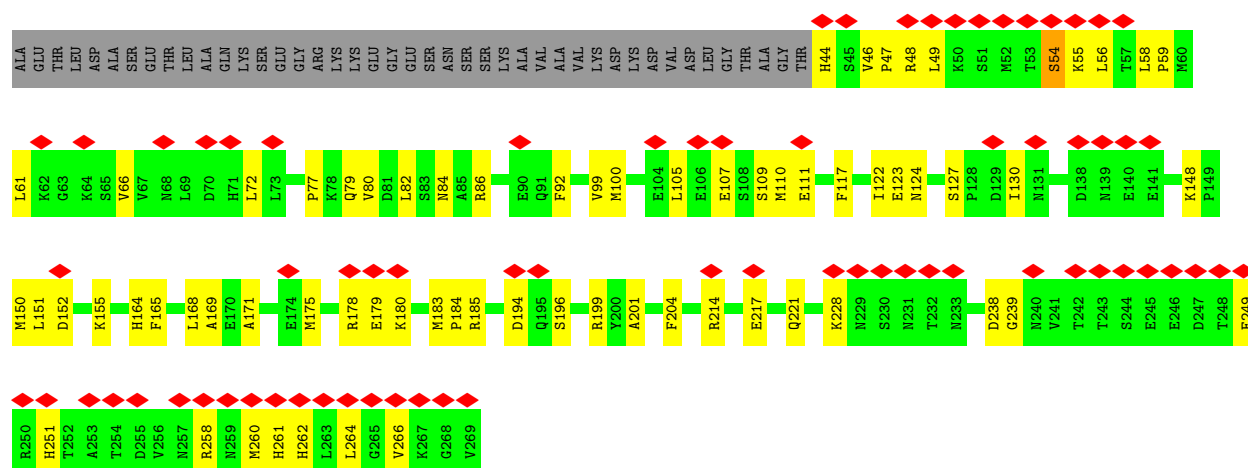
• Molecule 1: Genome polyprotein



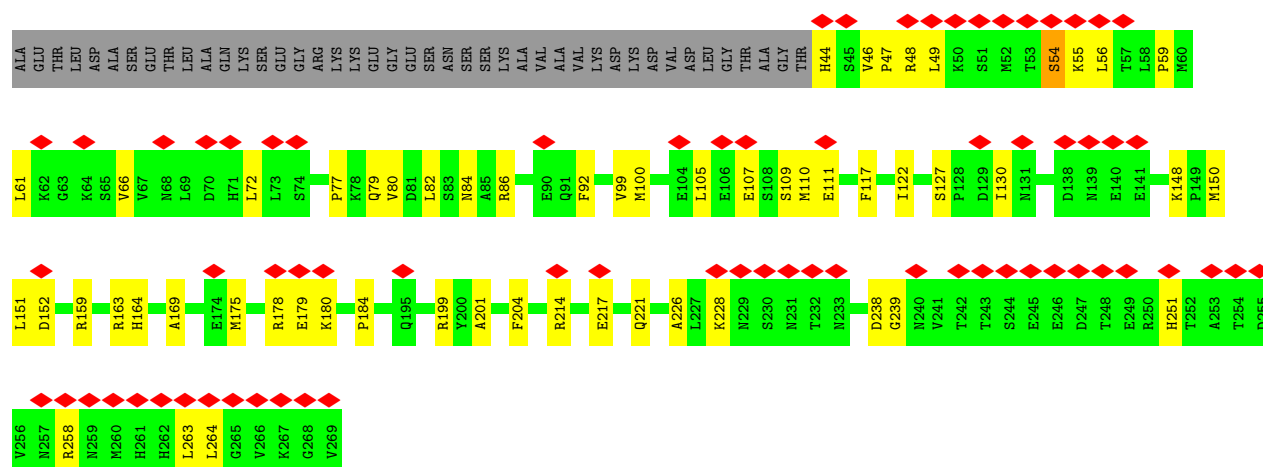
• Molecule 1: Genome polyprotein



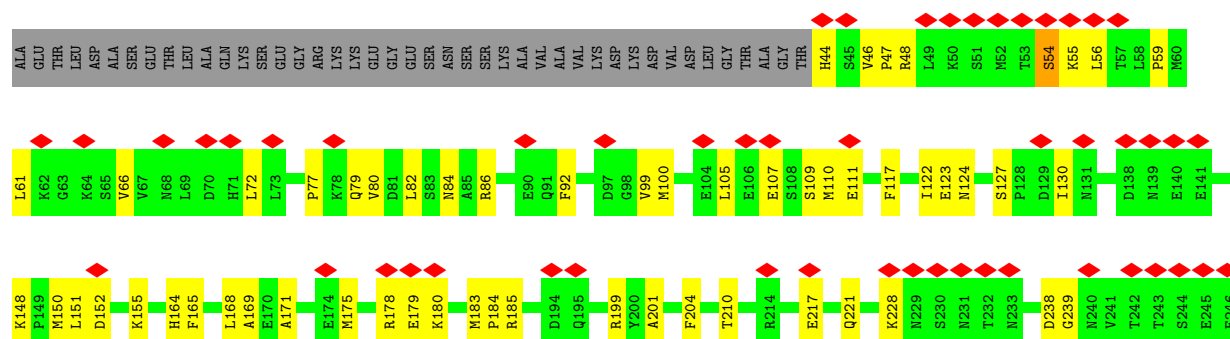
• Molecule 1: Genome polyprotein

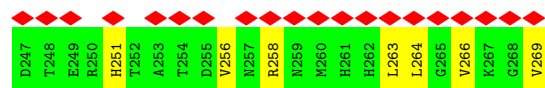


• Molecule 1: Genome polypeptide

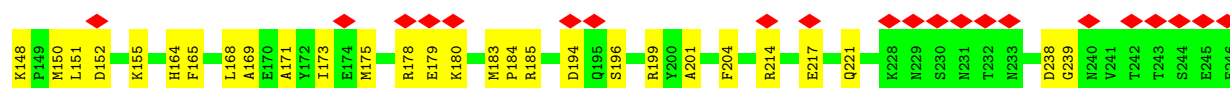
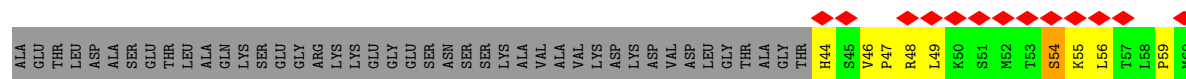


• Molecule 1: Genome polypeptide

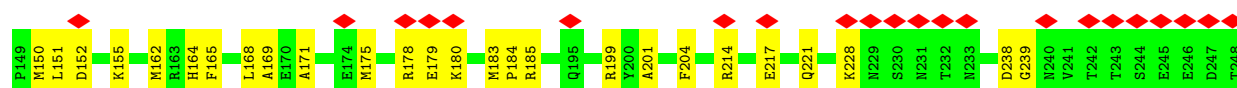
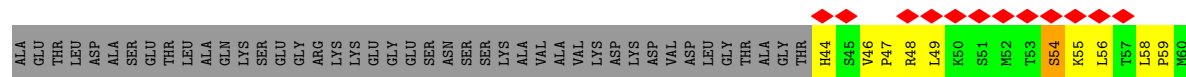




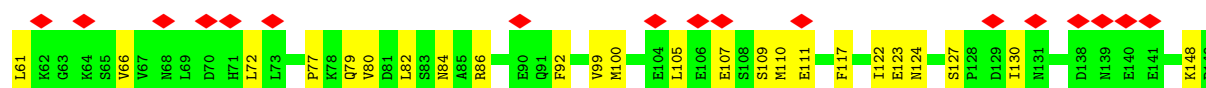
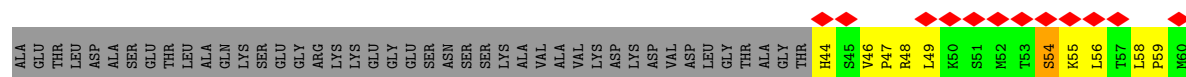
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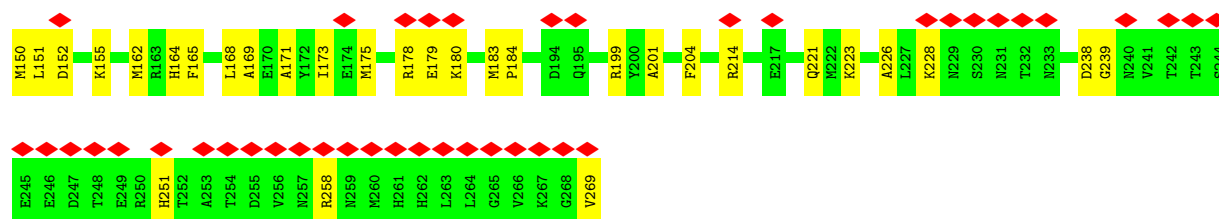


• Molecule 1: Genome polyprotein

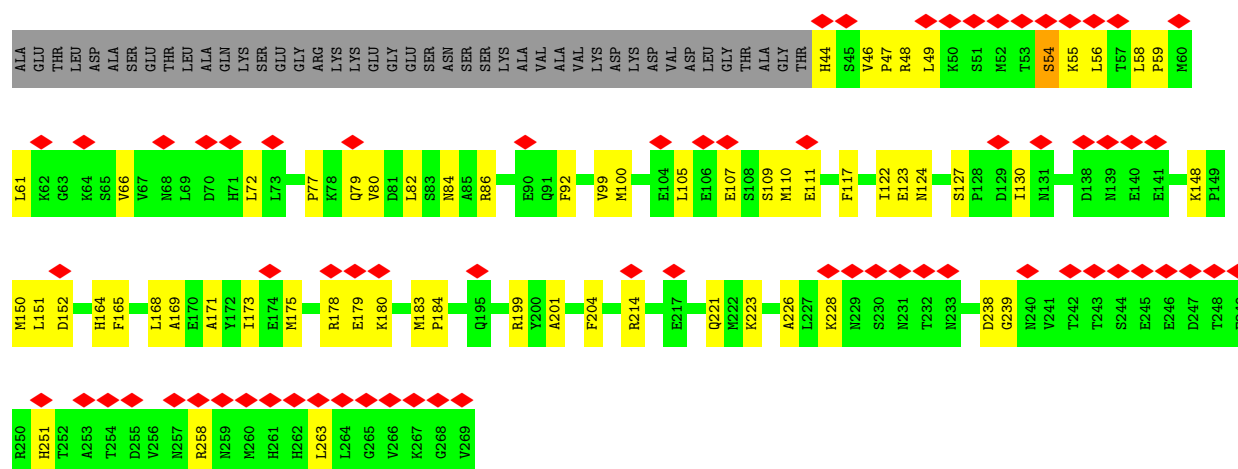


• Molecule 1: Genome polyprotein

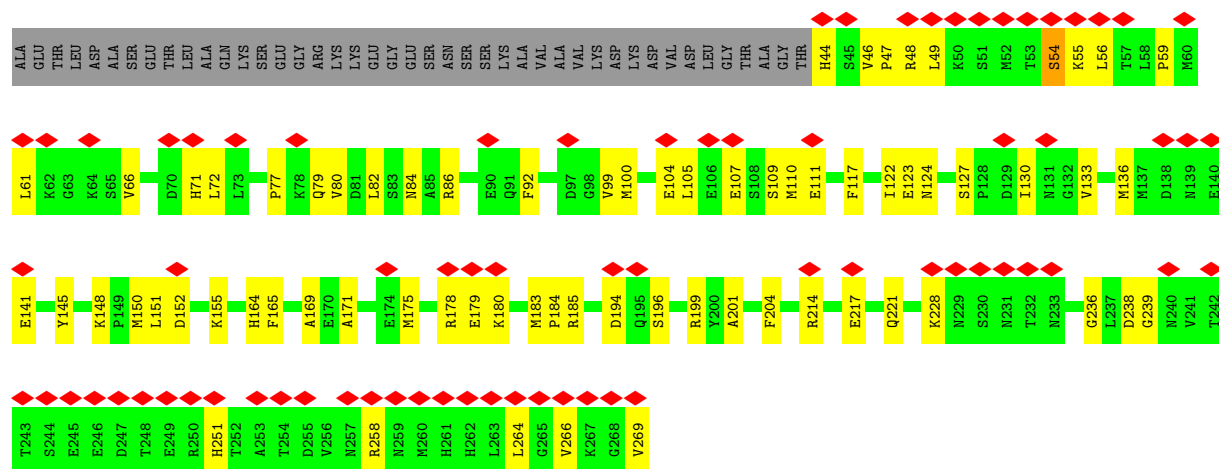




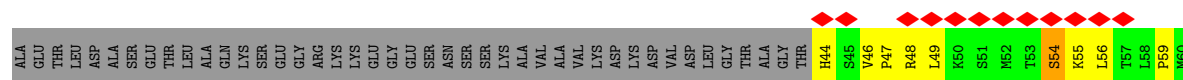
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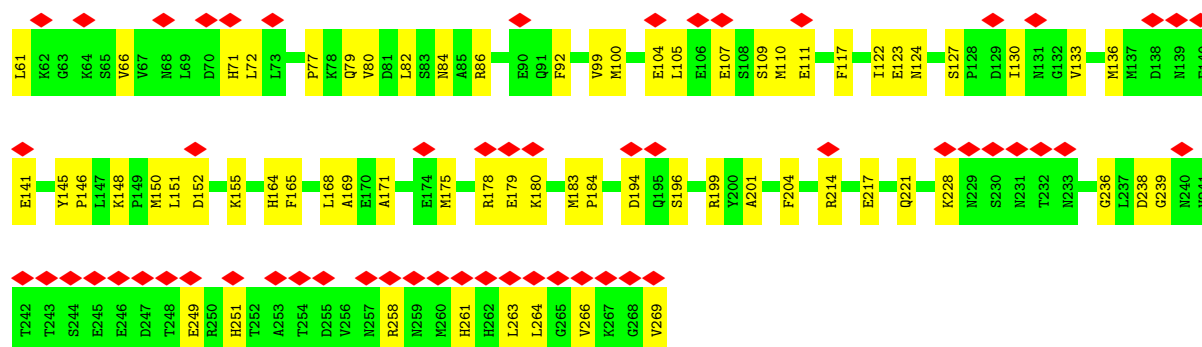


• Molecule 1: Genome polyprotein

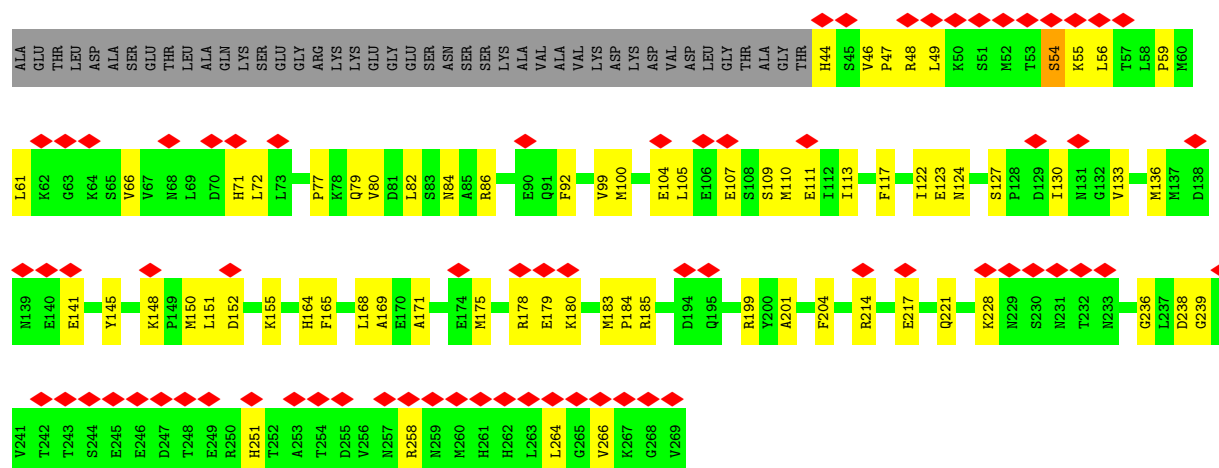


• Molecule 1: Genome polyprotein

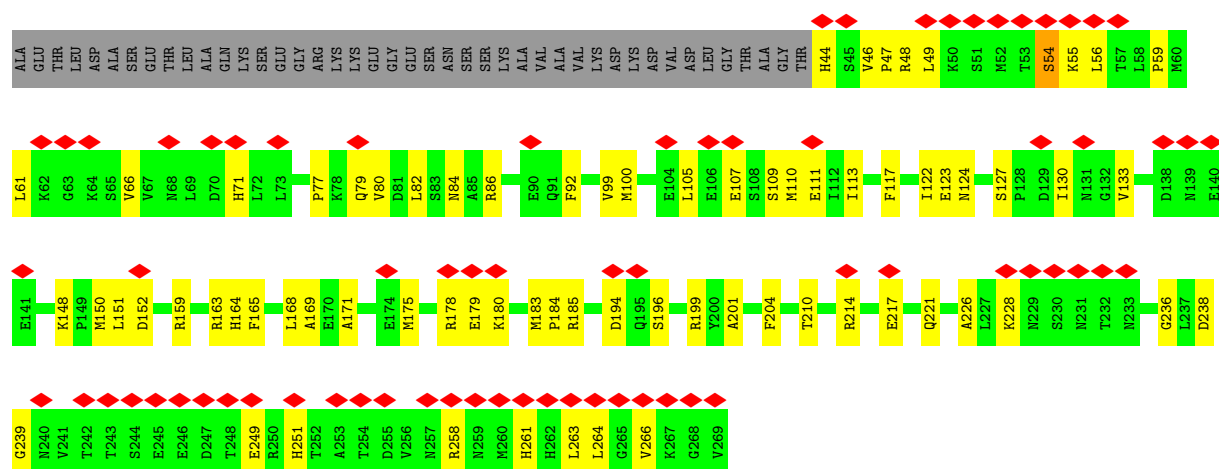




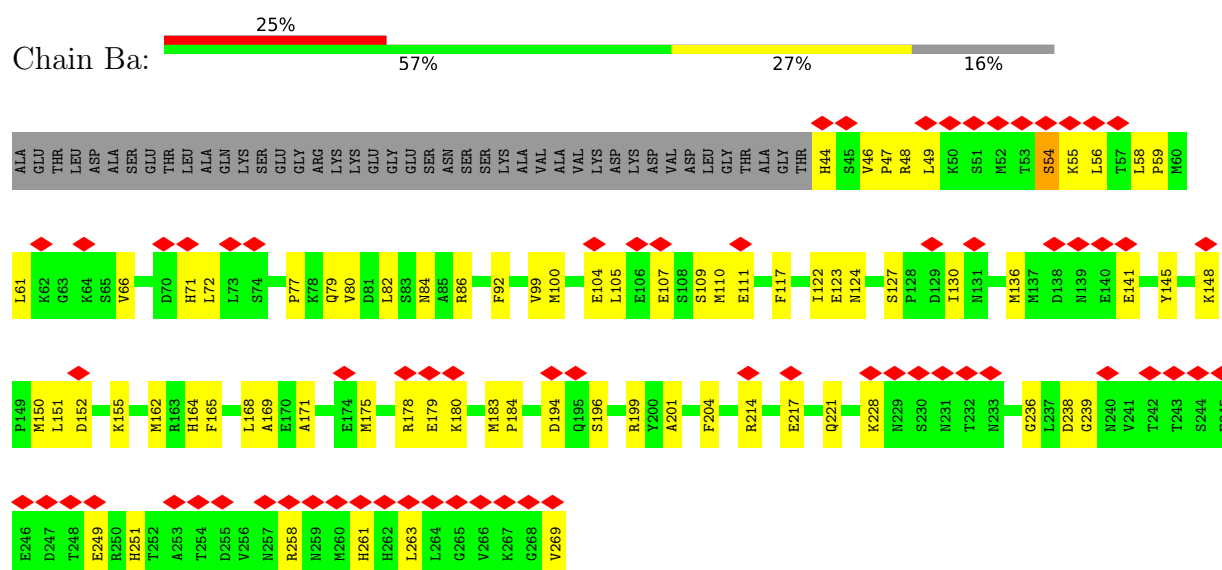
• Molecule 1: Genome polyprotein



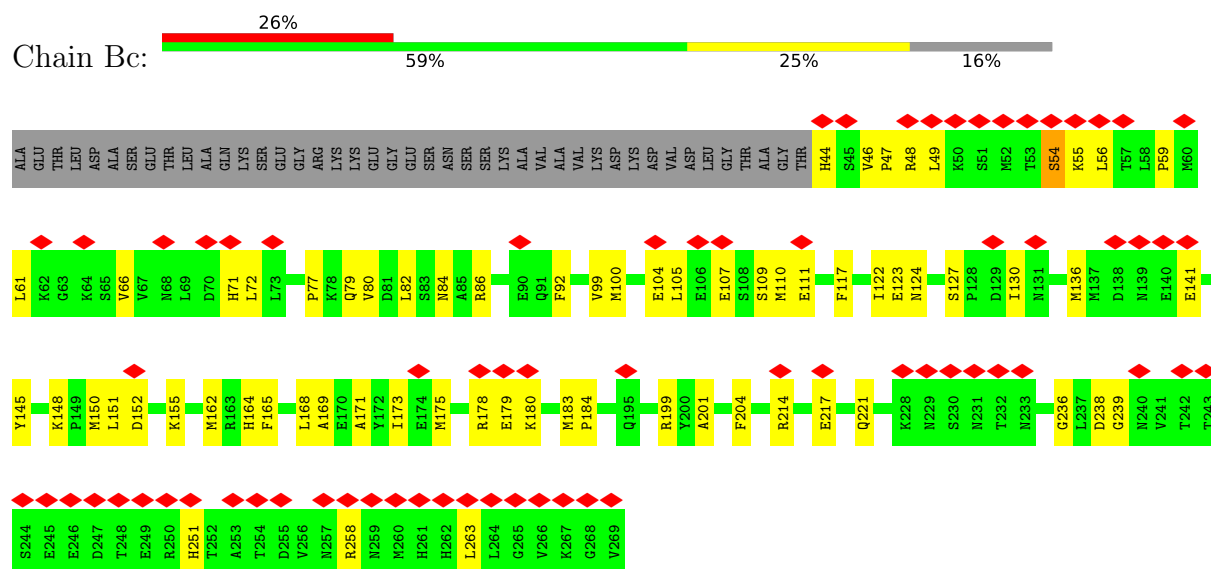
• Molecule 1: Genome polyprotein



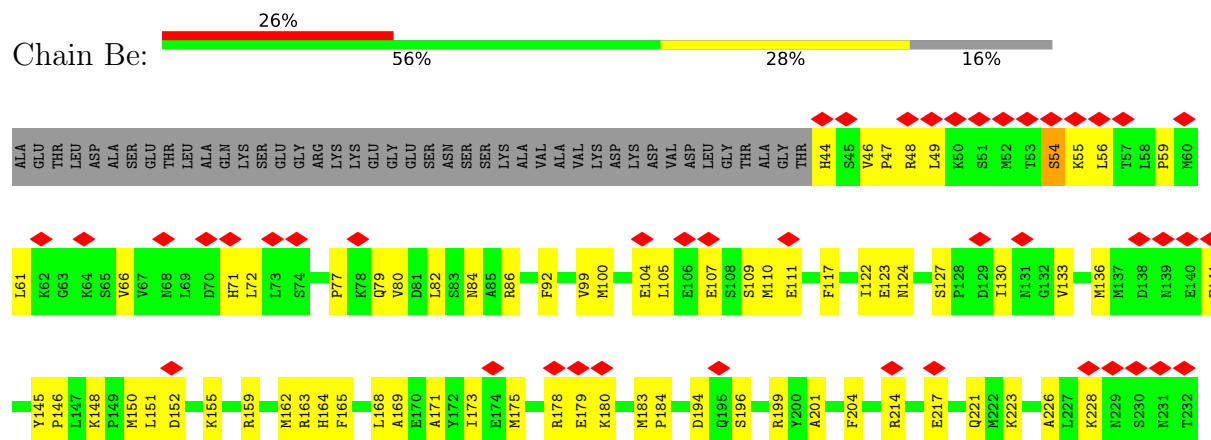
• Molecule 1: Genome polyprotein



• Molecule 1: Genome polyprotein

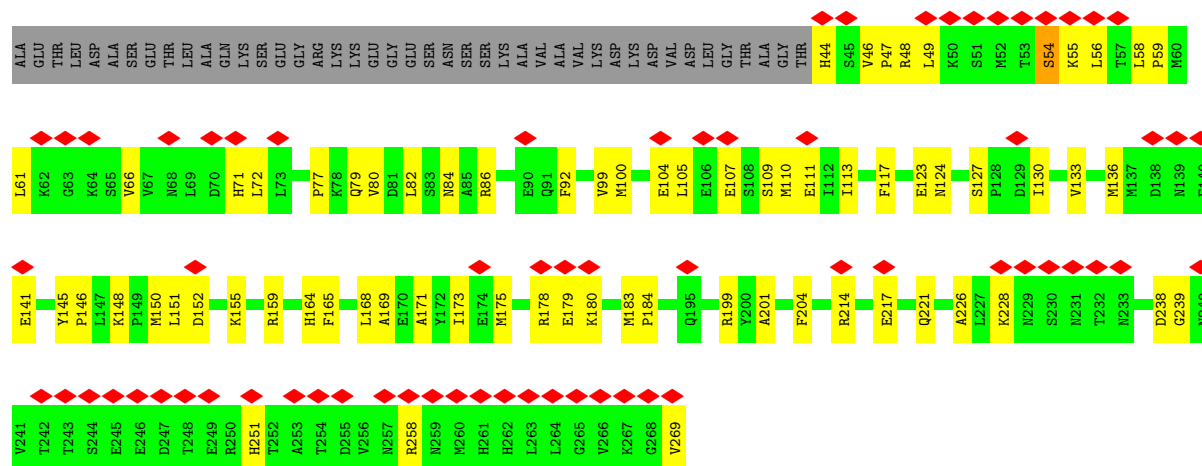


• Molecule 1: Genome polyprotein

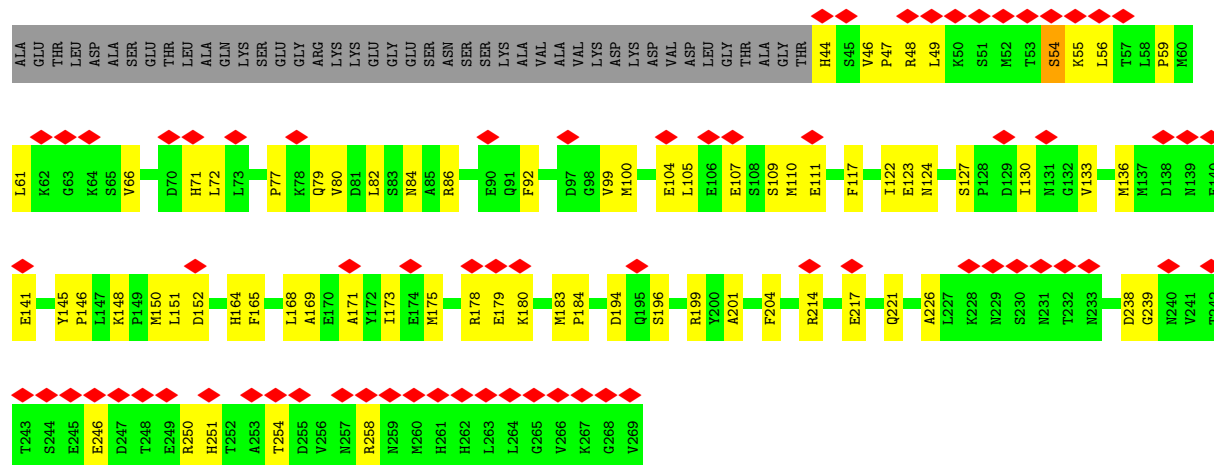




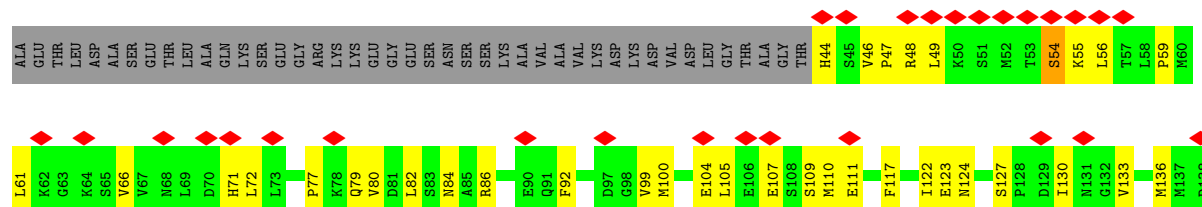
• Molecule 1: Genome polyprotein

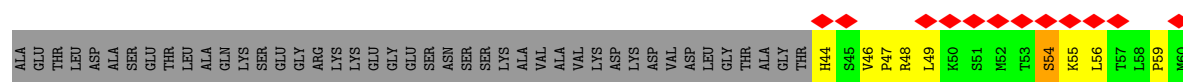


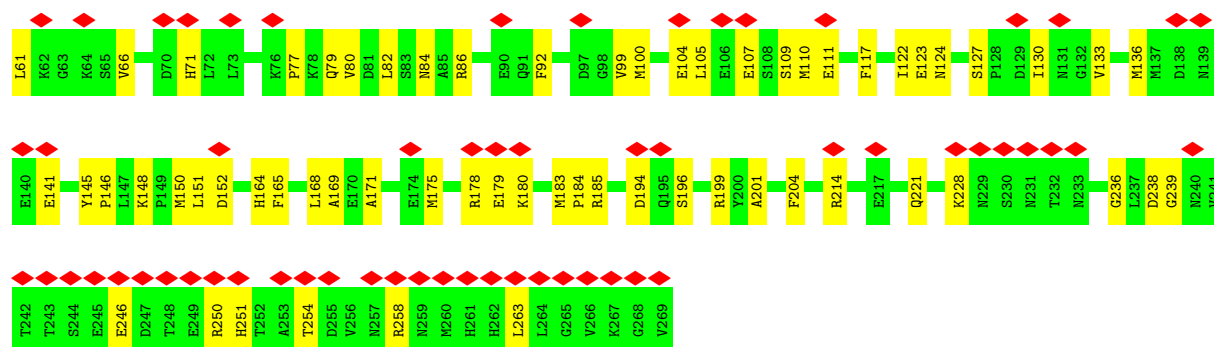
• Molecule 1: Genome polyprotein



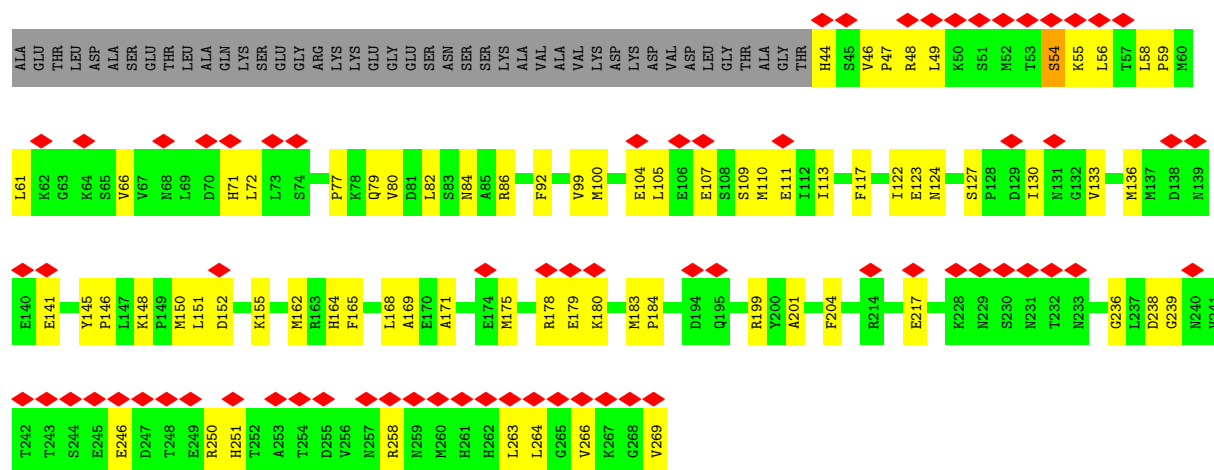
• Molecule 1: Genome polyprotein



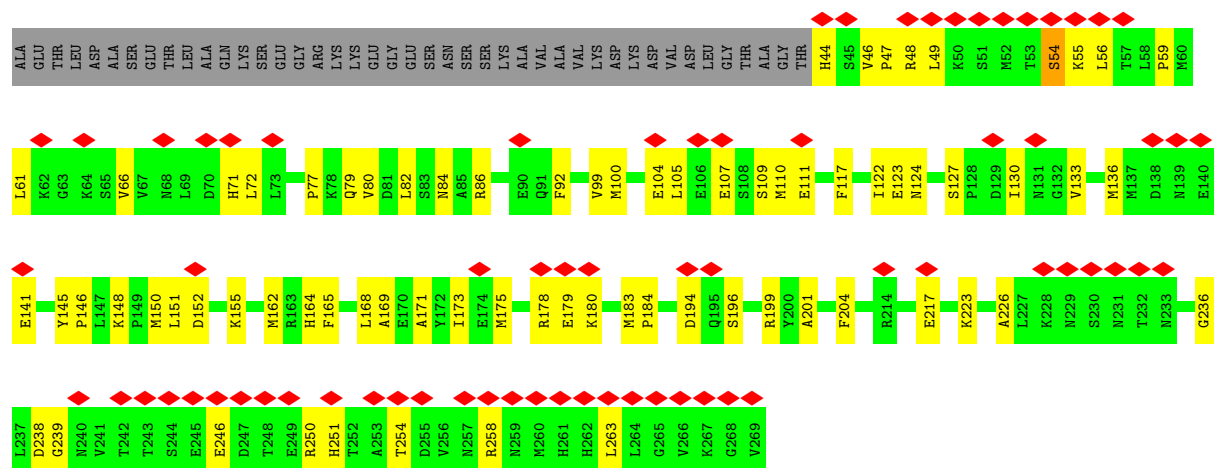




• Molecule 1: Genome polyprotein

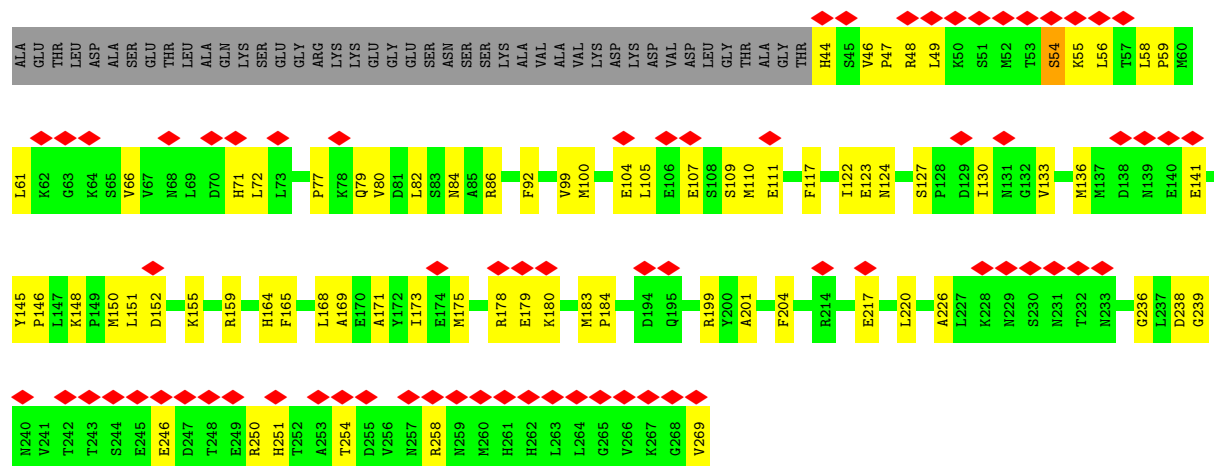


• Molecule 1: Genome polyprotein

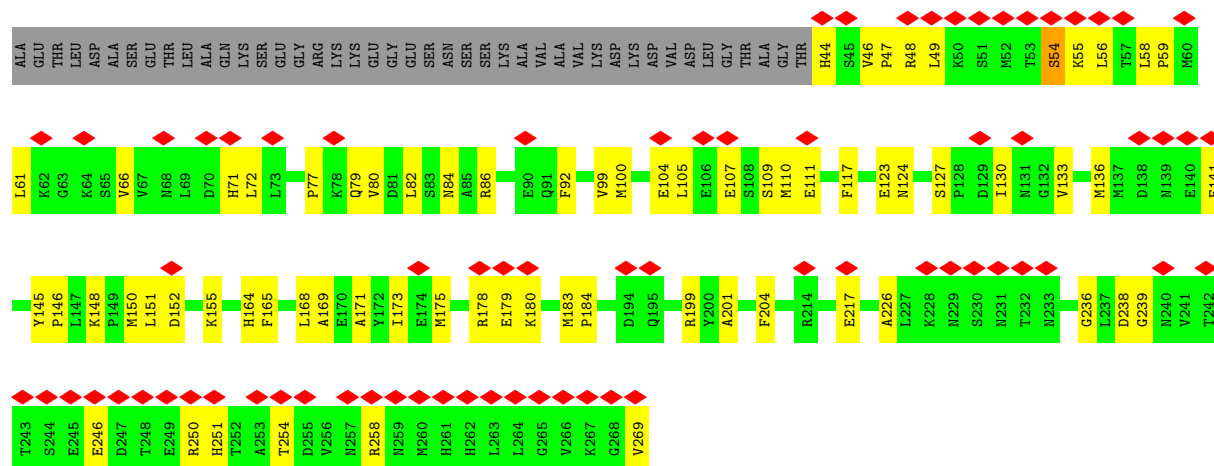


• Molecule 1: Genome polyprotein

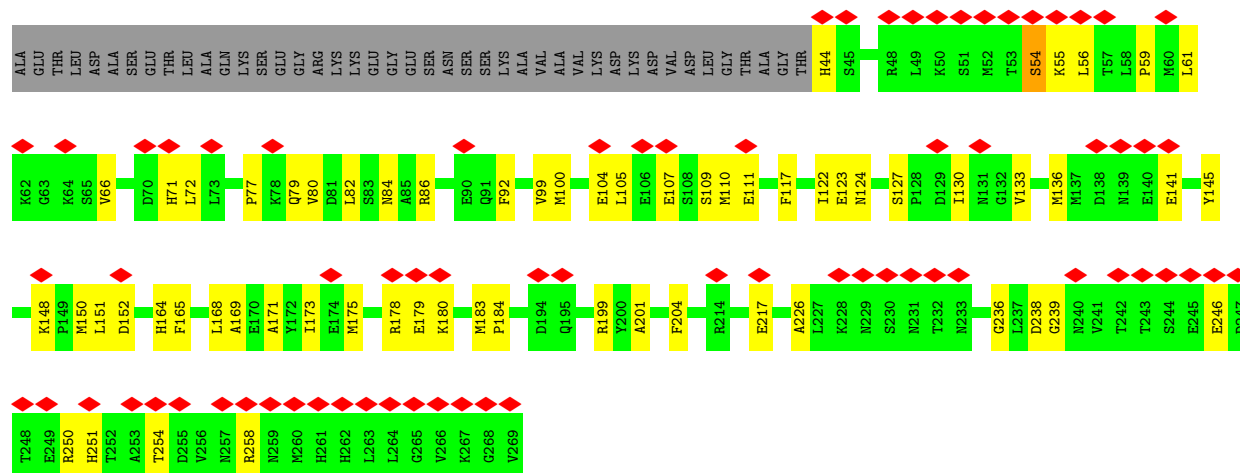




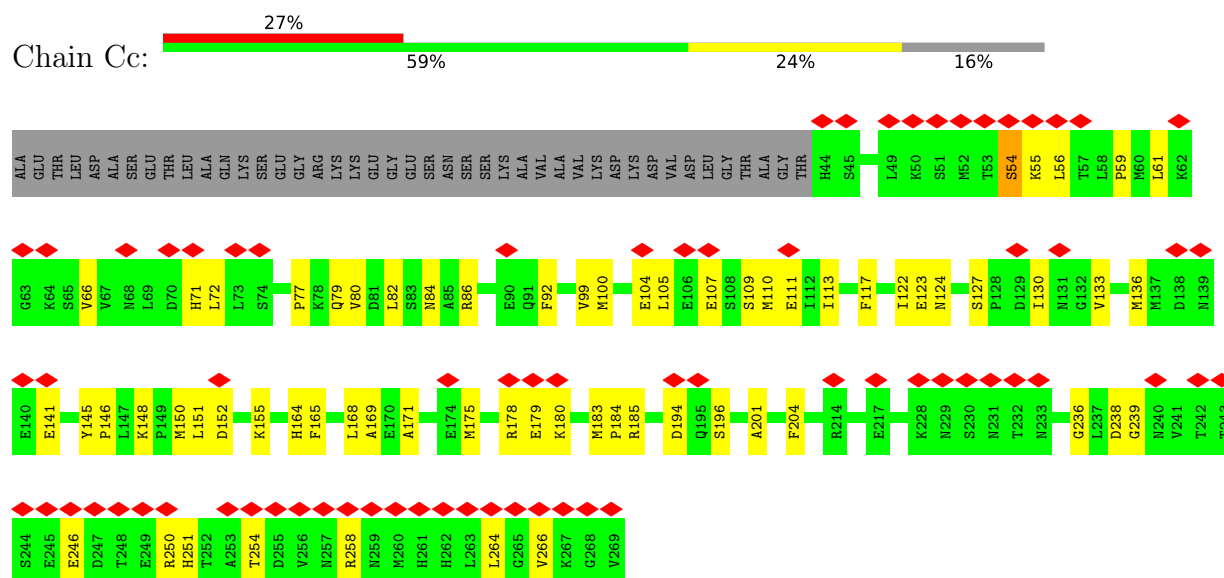
• Molecule 1: Genome polyprotein



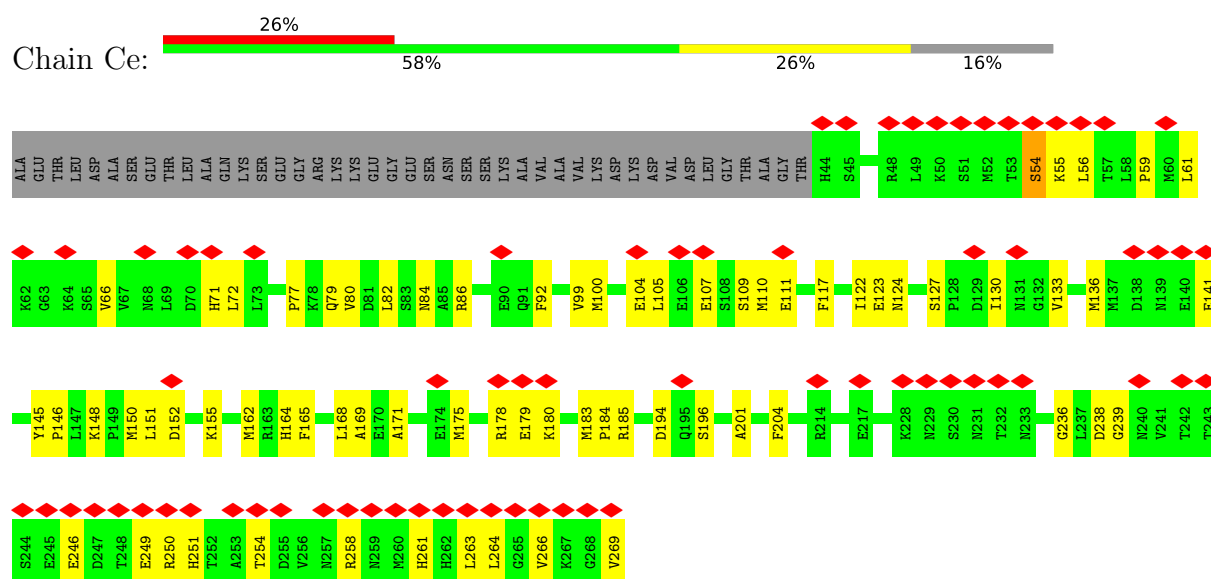
• Molecule 1: Genome polyprotein



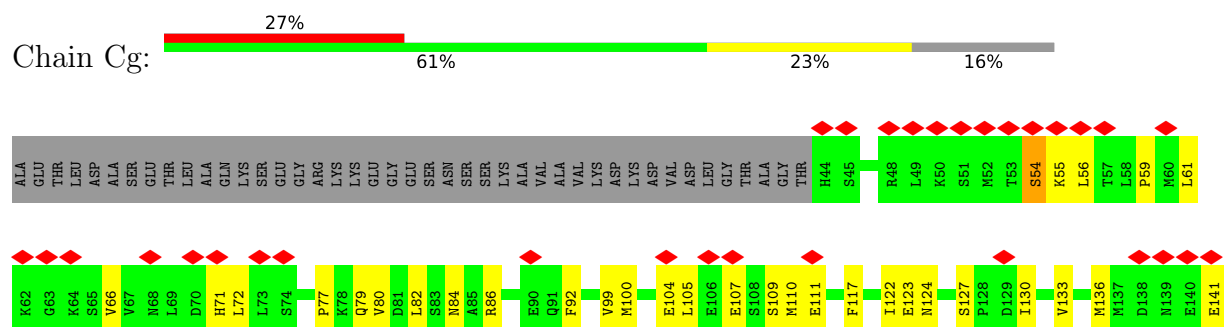
- Molecule 1: Genome polyprotein

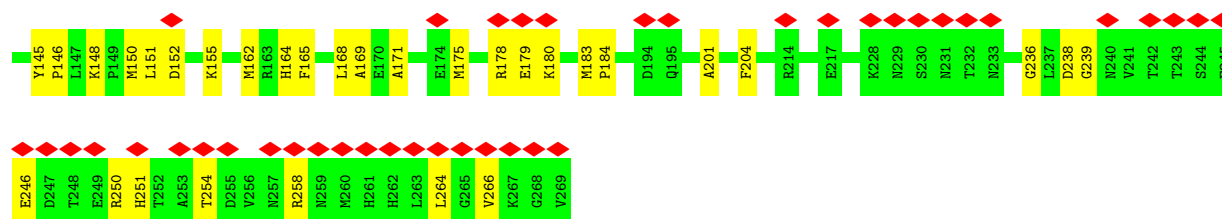


- Molecule 1: Genome polyprotein

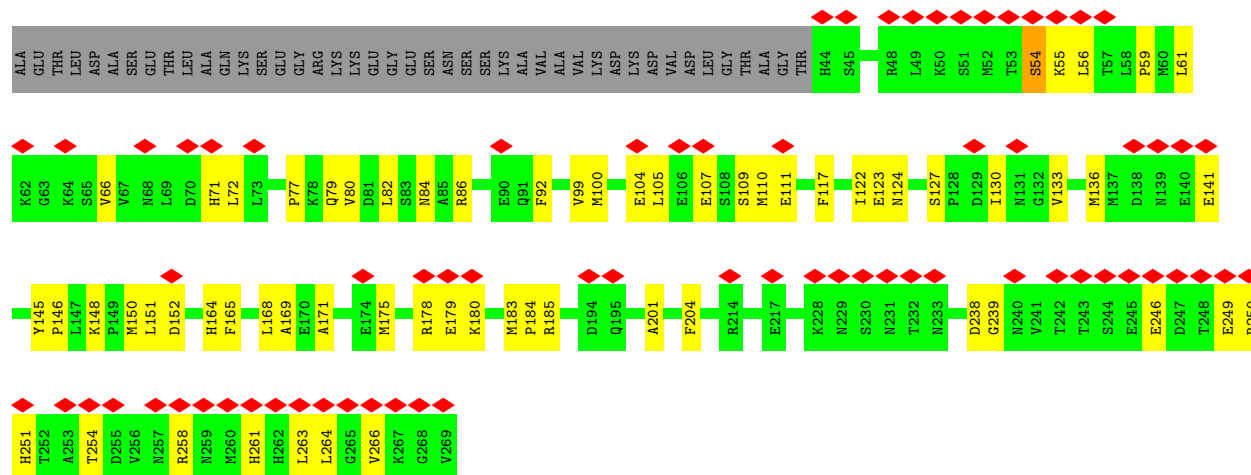


- Molecule 1: Genome polyprotein

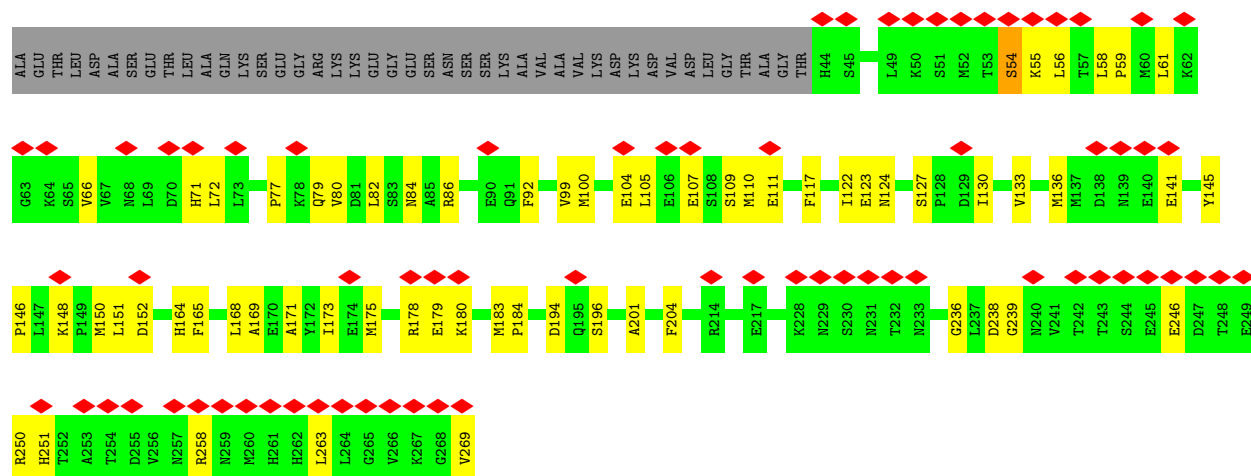




• Molecule 1: Genome polyprotein

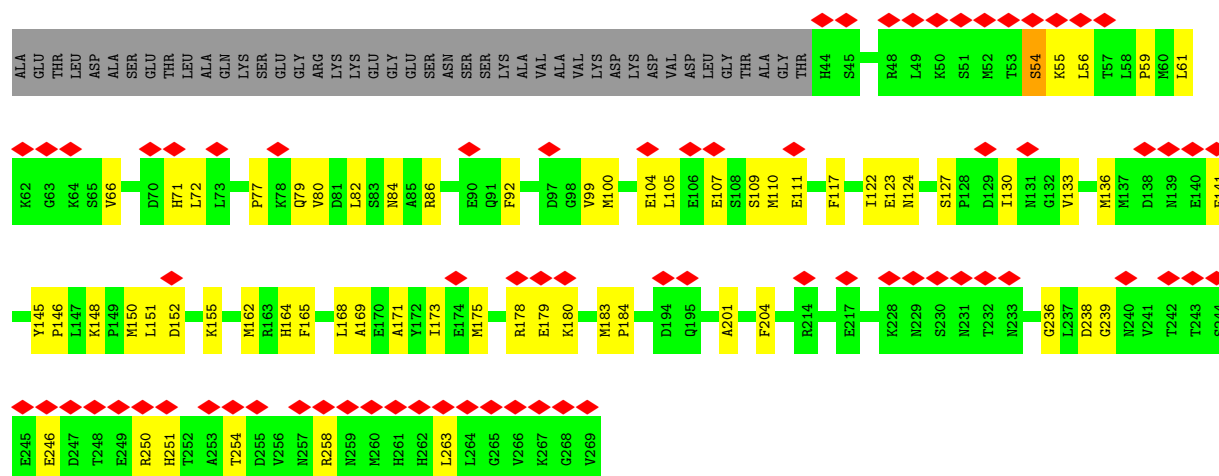


• Molecule 1: Genome polyprotein

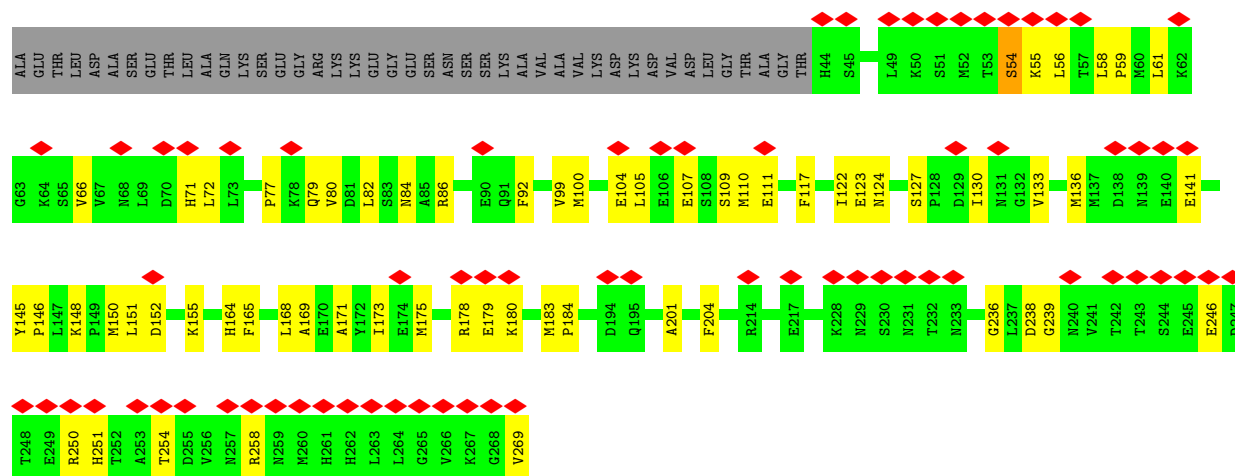


• Molecule 1: Genome polyprotein

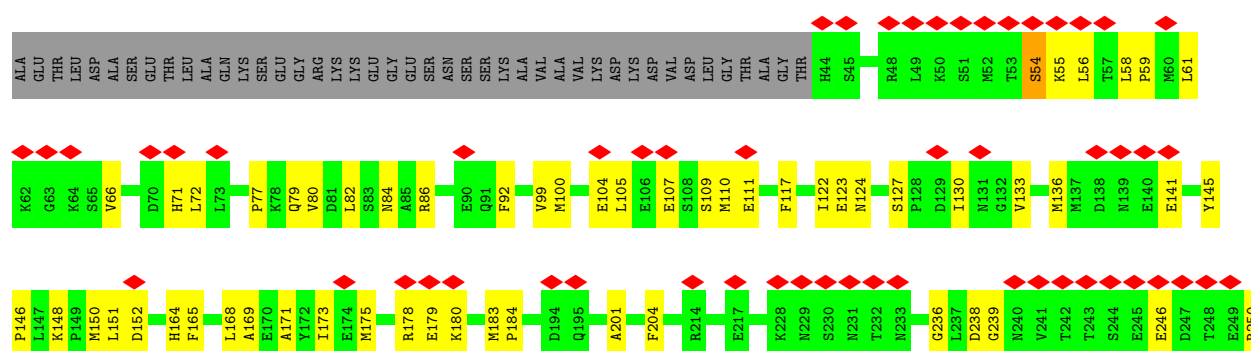


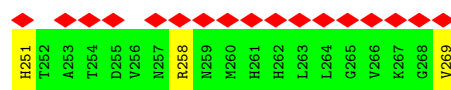


• Molecule 1: Genome polyprotein

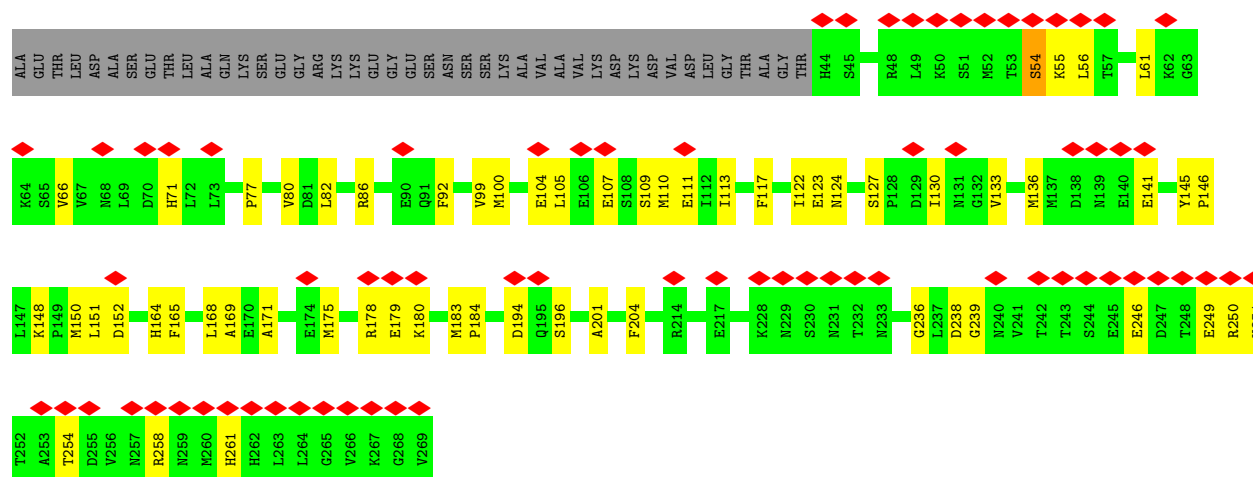


• Molecule 1: Genome polyprotein

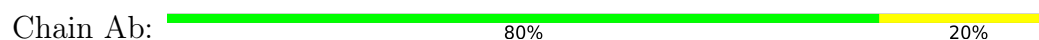




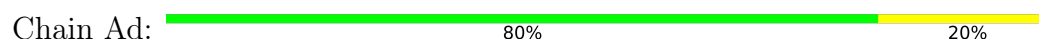
- Molecule 1: Genome polyprotein



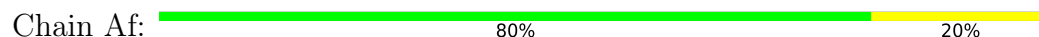
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



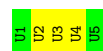
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- 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 Aj:  80% 20%



- 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:  80% 20%



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

Chain Ar:  80% 20%



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

Chain At:  80% 20%



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

Chain Av:  100%

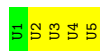
There are no outlier residues recorded for this chain.

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

Chain Ax:  80% 20%



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

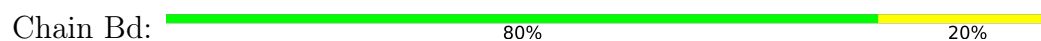


- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')

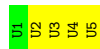


There are no outlier residues recorded for this chain.

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



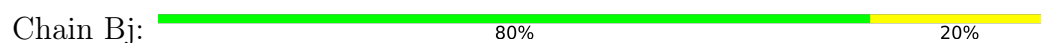
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



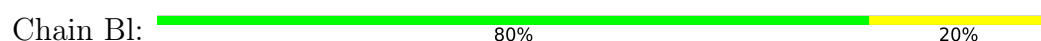
- Molecule 2: RNA (5'-R(P*UP*UP*UP*UP*U)-3')



- 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 Bn:  100%

There are no outlier residues recorded for this chain.

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

Chain Bp:  80% 20%



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

Chain Br:  80% 20%



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

Chain Bt:  100%

There are no outlier residues recorded for this chain.

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

Chain Bv:  60% 40%



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

Chain Bx:  40% 60%



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

Chain Bz:  80% 20%



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

Chain Cb:  80% 20%



- 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:  80% 20%



- 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:  80% 20%



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

Chain Cl:  80% 20%



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

Chain Cn:  100%

There are no outlier residues recorded for this chain.

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

Chain Cp:  100%

There are no outlier residues recorded for this chain.

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

Chain Cr:  100%

There are no outlier residues recorded for this chain.

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

Chain Ct:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-40.95°, rise=3.91 Å, axial sym=C1	Depositor
Number of segments used	6503	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	3.489	Depositor
Minimum map value	-1.841	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.213	Depositor
Recommended contour level	1.13	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 ⓘ

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	Aa	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ac	0.54	0/1854	0.71	1/2503 (0.0%)
1	Ae	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ag	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ai	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ak	0.54	0/1854	0.72	1/2503 (0.0%)
1	Am	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ao	0.54	0/1854	0.72	1/2503 (0.0%)
1	Aq	0.54	0/1854	0.72	1/2503 (0.0%)
1	As	0.54	0/1854	0.72	1/2503 (0.0%)
1	Au	0.54	0/1854	0.72	1/2503 (0.0%)
1	Aw	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ay	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ba	0.54	0/1854	0.71	1/2503 (0.0%)
1	Bc	0.54	0/1854	0.72	1/2503 (0.0%)
1	Be	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bg	0.54	0/1854	0.71	1/2503 (0.0%)
1	Bi	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bk	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bm	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bo	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bq	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bs	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bu	0.54	0/1854	0.72	1/2503 (0.0%)
1	Bw	0.54	0/1854	0.72	1/2503 (0.0%)
1	By	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ca	0.54	0/1854	0.71	1/2503 (0.0%)
1	Cc	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ce	0.54	0/1854	0.71	1/2503 (0.0%)
1	Cg	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ci	0.54	0/1854	0.72	1/2503 (0.0%)
1	Ck	0.54	0/1854	0.71	1/2503 (0.0%)
1	Cm	0.54	0/1854	0.72	1/2503 (0.0%)
1	Co	0.54	0/1854	0.72	1/2503 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	Cq	0.54	0/1854	0.72	1/2503 (0.0%)
1	Cs	0.54	0/1854	0.72	1/2503 (0.0%)
2	Ab	0.27	0/109	0.23	0/166
2	Ad	0.27	0/109	0.22	0/166
2	Af	0.27	0/109	0.22	0/166
2	Ah	0.27	0/109	0.23	0/166
2	Aj	0.27	0/109	0.23	0/166
2	Al	0.27	0/109	0.22	0/166
2	An	0.27	0/109	0.22	0/166
2	Ap	0.27	0/109	0.23	0/166
2	Ar	0.27	0/109	0.23	0/166
2	At	0.27	0/109	0.23	0/166
2	Av	0.27	0/109	0.23	0/166
2	Ax	0.27	0/109	0.23	0/166
2	Az	0.27	0/109	0.22	0/166
2	Bb	0.27	0/109	0.23	0/166
2	Bd	0.27	0/109	0.22	0/166
2	Bf	0.27	0/109	0.23	0/166
2	Bh	0.27	0/109	0.23	0/166
2	Bj	0.27	0/109	0.23	0/166
2	Bl	0.27	0/109	0.23	0/166
2	Bn	0.27	0/109	0.22	0/166
2	Bp	0.27	0/109	0.23	0/166
2	Br	0.27	0/109	0.23	0/166
2	Bt	0.27	0/109	0.23	0/166
2	Bv	0.27	0/109	0.23	0/166
2	Bx	0.27	0/109	0.22	0/166
2	Bz	0.27	0/109	0.22	0/166
2	Cb	0.27	0/109	0.23	0/166
2	Cd	0.27	0/109	0.23	0/166
2	Cf	0.27	0/109	0.22	0/166
2	Ch	0.27	0/109	0.23	0/166
2	Cj	0.27	0/109	0.23	0/166
2	Cl	0.27	0/109	0.23	0/166
2	Cn	0.27	0/109	0.22	0/166
2	Cp	0.27	0/109	0.23	0/166
2	Cr	0.27	0/109	0.22	0/166
2	Ct	0.26	0/109	0.23	0/166
All	All	0.53	0/70668	0.70	36/96084 (0.0%)

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ci	54	SER	CA-C-O	-5.99	115.16	121.99
1	Ca	54	SER	CA-C-O	-5.97	115.19	121.99
1	Ag	54	SER	CA-C-O	-5.96	115.19	121.99
1	Ba	54	SER	CA-C-O	-5.96	115.19	121.99
1	Ck	54	SER	CA-C-O	-5.96	115.20	121.99

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	68	0
1	Ac	1815	0	1785	67	0
1	Ae	1815	0	1785	69	0
1	Ag	1815	0	1785	54	0
1	Ai	1815	0	1785	70	0
1	Ak	1815	0	1785	67	0
1	Am	1815	0	1785	71	0
1	Ao	1815	0	1785	71	0
1	Aq	1815	0	1785	68	0
1	As	1815	0	1785	77	0
1	Au	1815	0	1785	80	0
1	Aw	1815	0	1785	79	0
1	Ay	1815	0	1785	78	0
1	Ba	1815	0	1785	82	0
1	Bc	1815	0	1785	77	0
1	Be	1815	0	1785	88	0
1	Bg	1815	0	1785	80	0
1	Bi	1815	0	1785	82	0
1	Bk	1815	0	1785	75	0
1	Bm	1815	0	1785	80	0
1	Bo	1815	0	1785	80	0
1	Bq	1815	0	1785	81	0
1	Bs	1815	0	1785	83	0
1	Bu	1815	0	1785	87	0
1	Bw	1815	0	1785	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	By	1815	0	1785	80	0
1	Ca	1815	0	1785	70	0
1	Cc	1815	0	1785	67	0
1	Ce	1815	0	1785	70	0
1	Cg	1815	0	1785	65	0
1	Ci	1815	0	1785	64	0
1	Ck	1815	0	1785	67	0
1	Cm	1815	0	1785	69	0
1	Co	1815	0	1785	67	0
1	Cq	1815	0	1785	66	0
1	Cs	1815	0	1785	56	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	4	0
2	Aj	100	0	51	1	0
2	Al	100	0	51	1	0
2	An	100	0	51	1	0
2	Ap	100	0	51	3	0
2	Ar	100	0	51	3	0
2	At	100	0	51	1	0
2	Av	100	0	51	0	0
2	Ax	100	0	51	1	0
2	Az	100	0	51	4	0
2	Bb	100	0	51	0	0
2	Bd	100	0	51	5	0
2	Bf	100	0	51	10	0
2	Bh	100	0	51	3	0
2	Bj	100	0	51	2	0
2	Bl	100	0	51	1	0
2	Bn	100	0	51	0	0
2	Bp	100	0	51	1	0
2	Br	100	0	51	1	0
2	Bt	100	0	51	0	0
2	Bv	100	0	51	5	0
2	Bx	100	0	51	5	0
2	Bz	100	0	51	1	0
2	Cb	100	0	51	1	0
2	Cd	100	0	51	1	0
2	Cf	100	0	51	1	0
2	Ch	100	0	51	1	0
2	Cj	100	0	51	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Cl	100	0	51	1	0
2	Cn	100	0	51	0	0
2	Cp	100	0	51	0	0
2	Cr	100	0	51	0	0
2	Ct	100	0	51	0	0
All	All	68940	0	66096	1827	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 1827 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:Be:226:ALA:HB1	2:Bf:4:U:H1'	1.68	0.74
1:Ag:226:ALA:HB1	2:Ah:4:U:H1'	1.68	0.74
2:Bd:1:U:P	2:Bf:5:U:H3'	2.36	0.66
2:Bv:1:U:P	2:Bx:5:U:H3'	2.38	0.63
1:Ag:148:LYS:O	1:Ag:152:ASP:HB2	1.99	0.63

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%)	216 (96%)	8 (4%)	0	100	100
1	Ac	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ae	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ag	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ai	224/269 (83%)	216 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ak	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Am	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ao	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Aq	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	As	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Au	165/269 (61%)	160 (97%)	5 (3%)	0	100	100
1	Aw	148/269 (55%)	142 (96%)	6 (4%)	0	100	100
1	Ay	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ba	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bc	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Be	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bg	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bi	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bk	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bm	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bo	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bq	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bs	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bu	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Bw	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	By	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ca	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Cc	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ce	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Cg	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ci	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Ck	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Cm	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Co	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Cq	224/269 (83%)	216 (96%)	8 (4%)	0	100	100
1	Cs	224/269 (83%)	216 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7929/9684 (82%)	7646 (96%)	283 (4%)	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	101/233 (43%)	101 (100%)	0	100	100
1	Am	35/233 (15%)	35 (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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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	6736/8155 (83%)	6736 (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 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	Bs	115	ASN
1	Ca	115	ASN
1	Bs	189	GLN
1	Bw	115	ASN
1	Ce	115	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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
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
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 ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

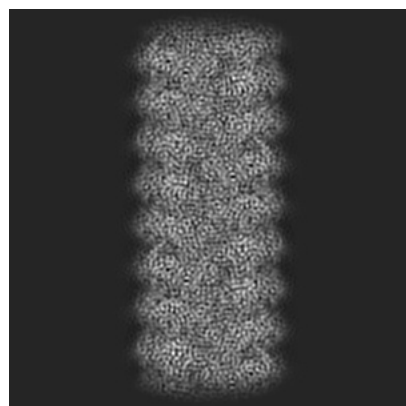
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53794. These allow visual inspection of the internal detail of the map and identification of artifacts.

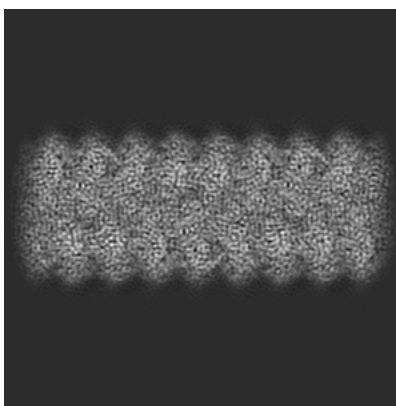
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

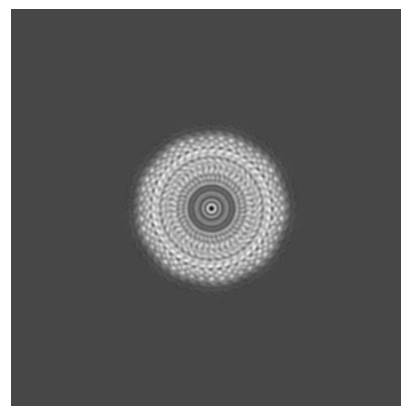
6.1.1 Primary map



X

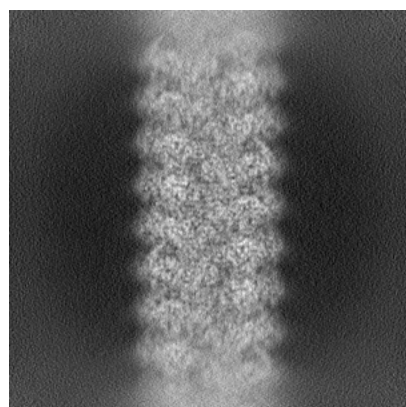


Y

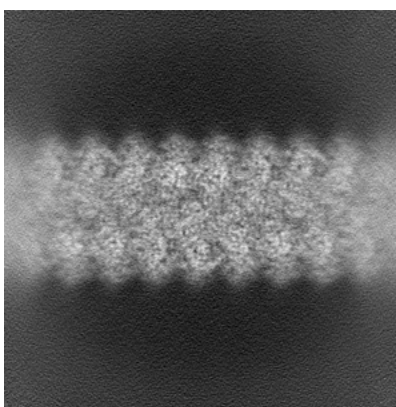


Z

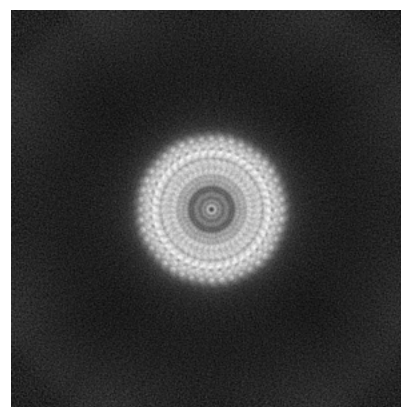
6.1.2 Raw map



X



Y

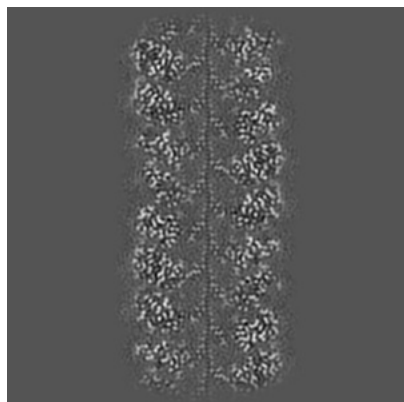


Z

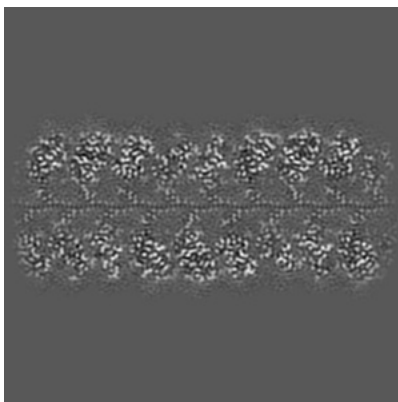
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

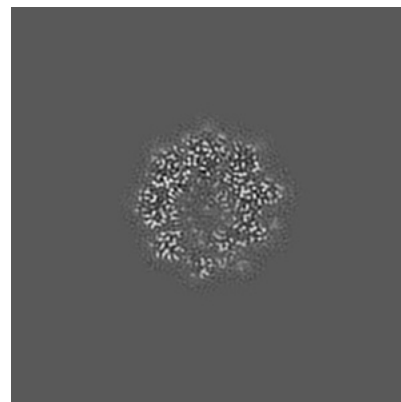
6.2.1 Primary map



X Index: 175

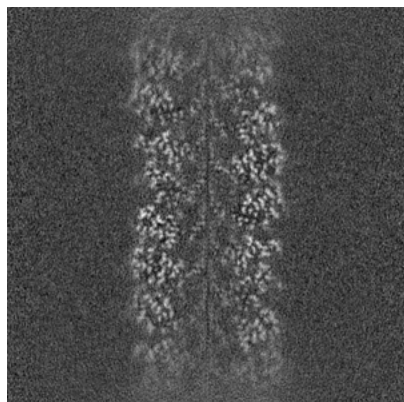


Y Index: 175

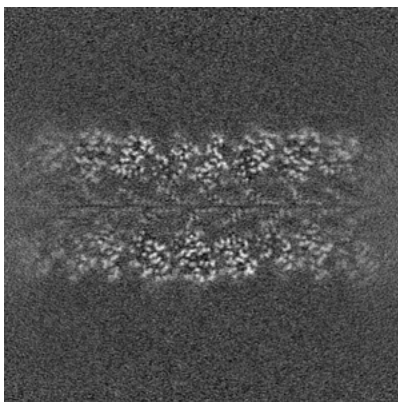


Z Index: 175

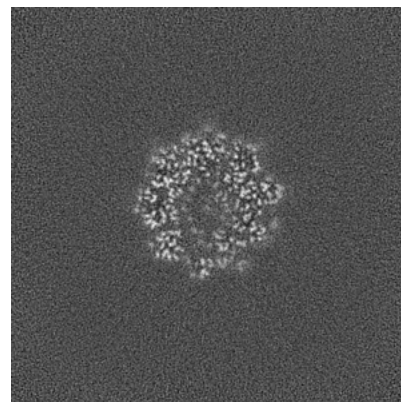
6.2.2 Raw map



X Index: 175



Y Index: 175

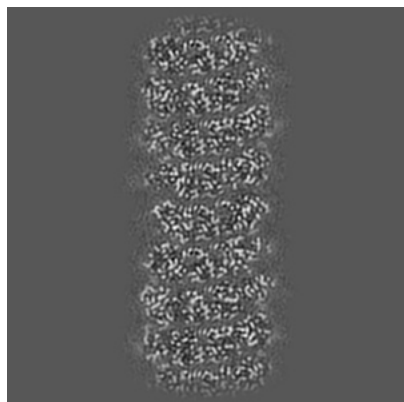


Z Index: 175

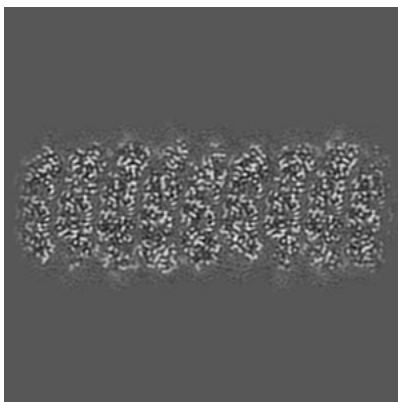
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

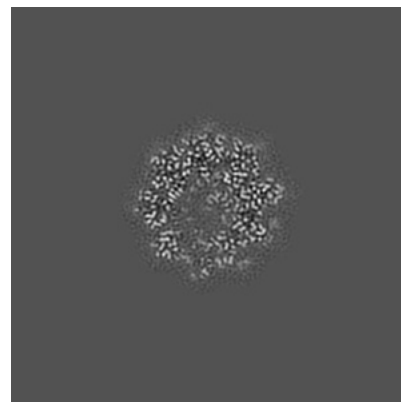
6.3.1 Primary map



X Index: 143

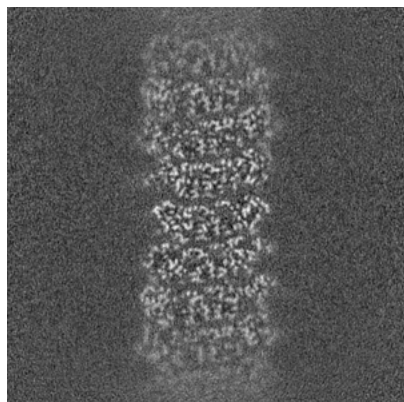


Y Index: 207

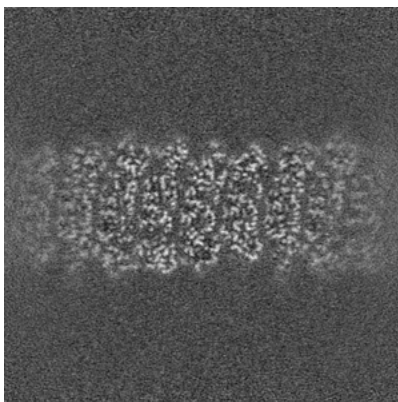


Z Index: 176

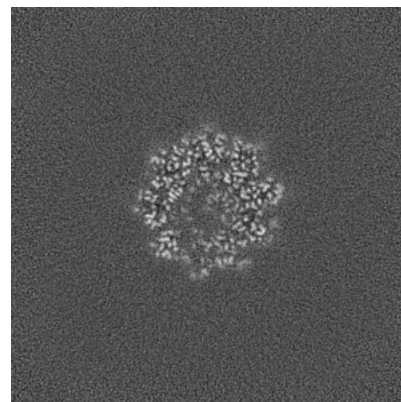
6.3.2 Raw map



X Index: 143



Y Index: 207

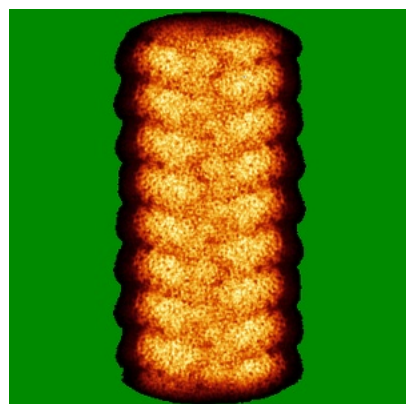


Z Index: 176

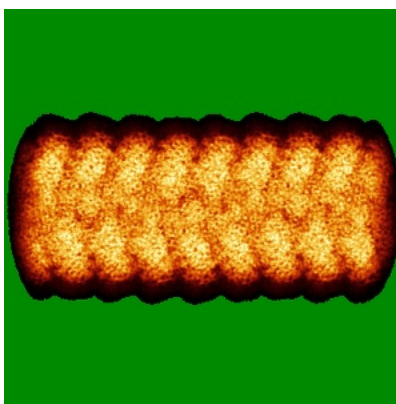
The images above show the largest variance slices of the map in three orthogonal directions.

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

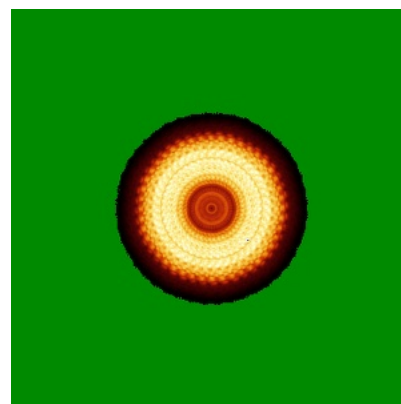
6.4.1 Primary map



X

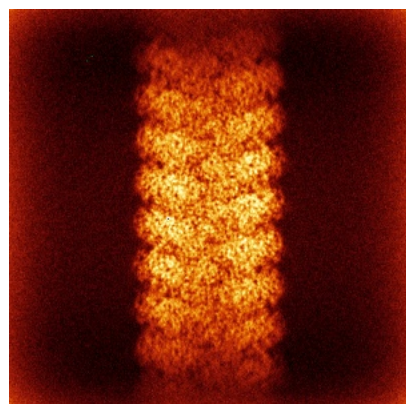


Y

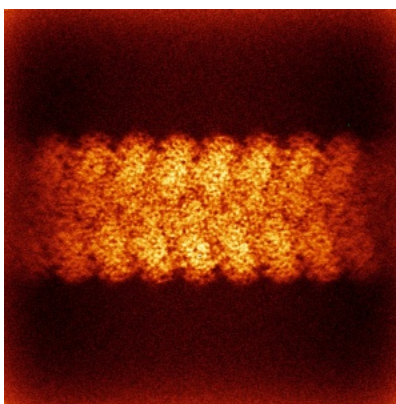


Z

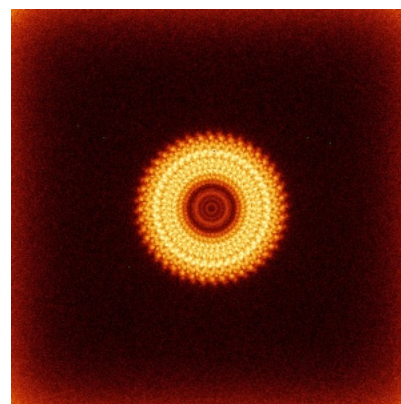
6.4.2 Raw map



X



Y

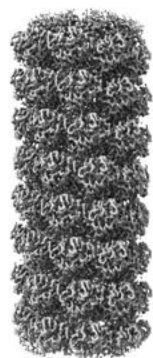


Z

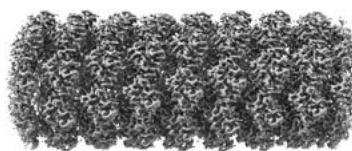
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

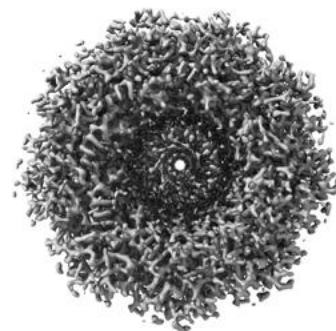
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

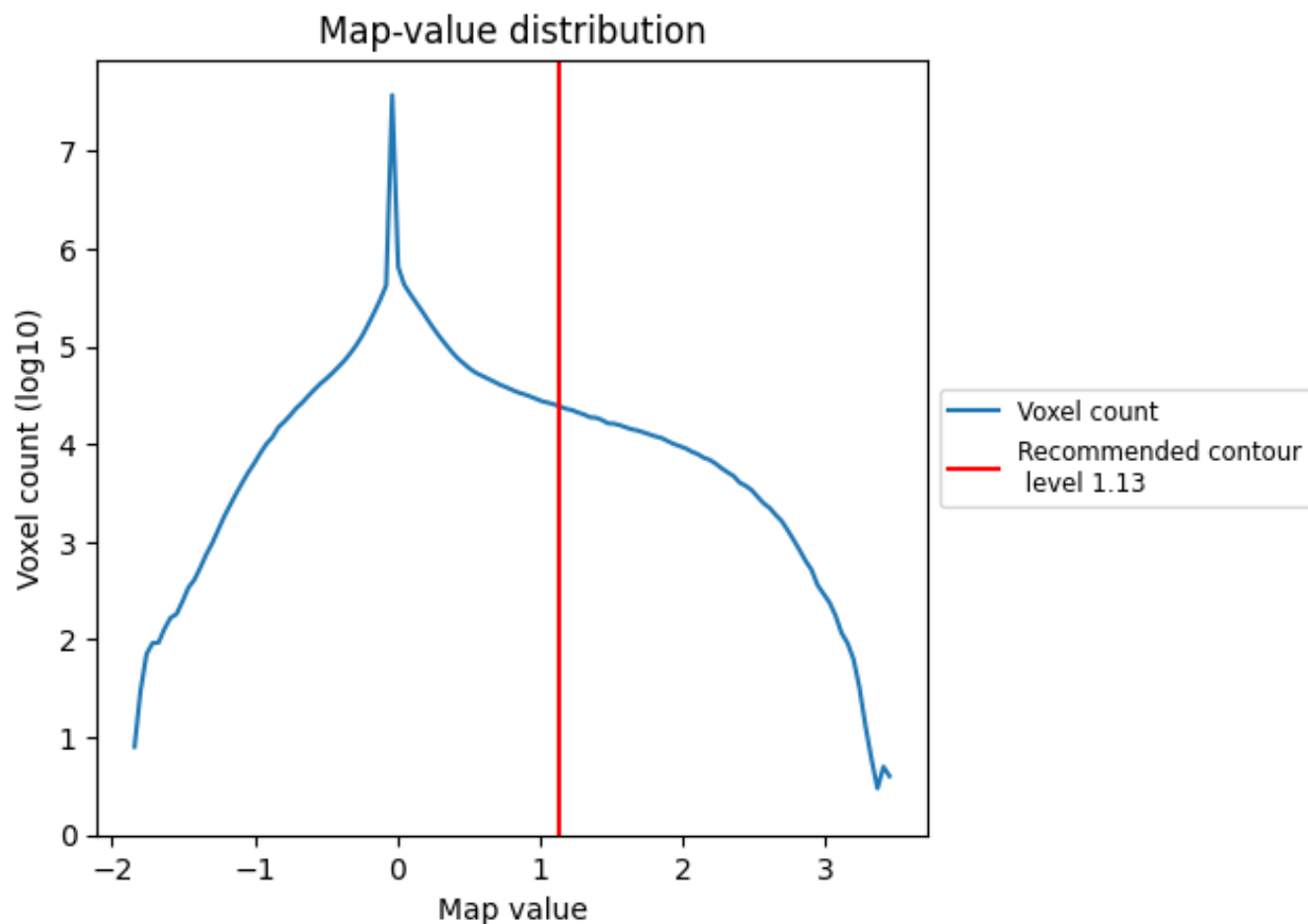
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

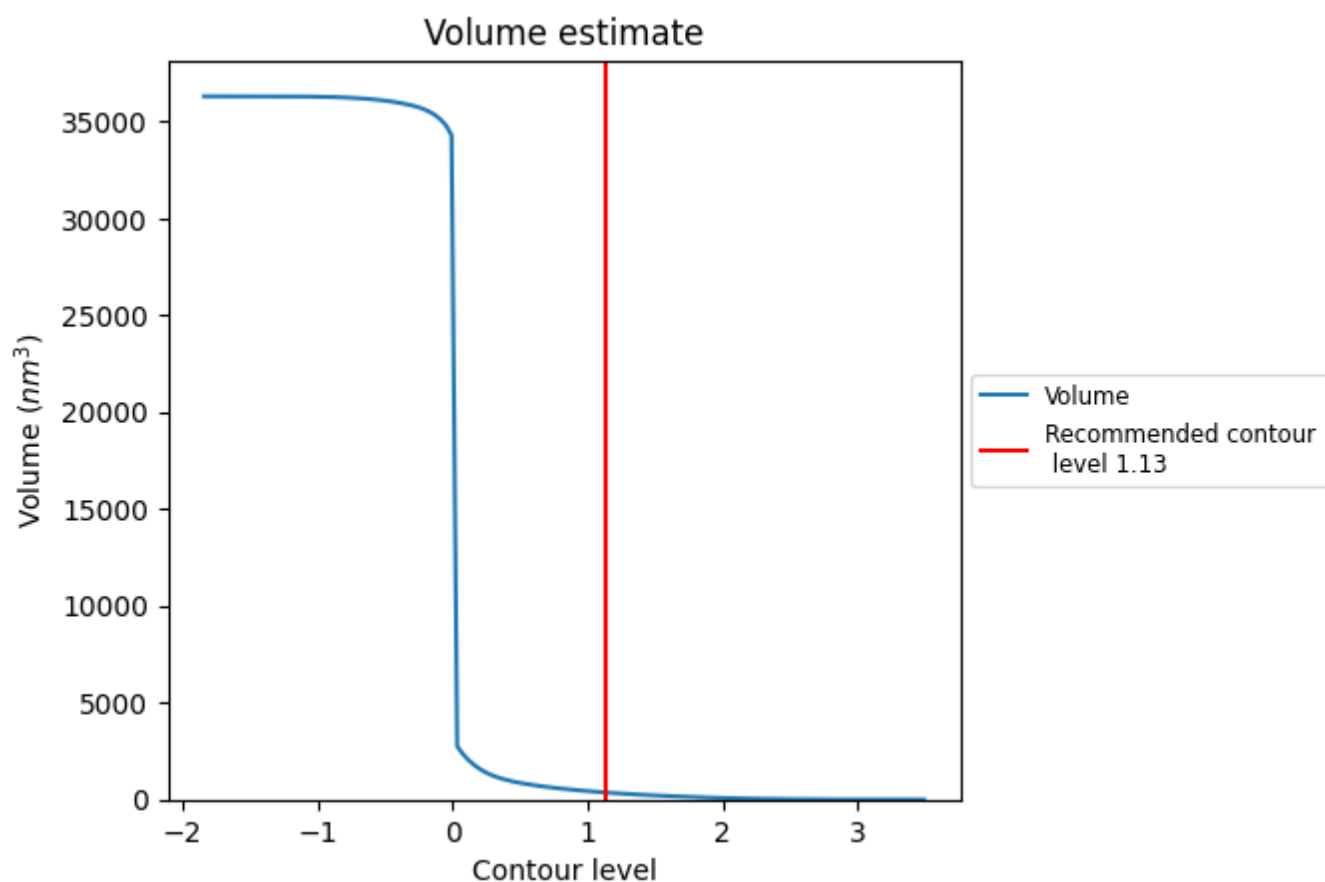
This section contains the results of statistical analysis of the map.

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.

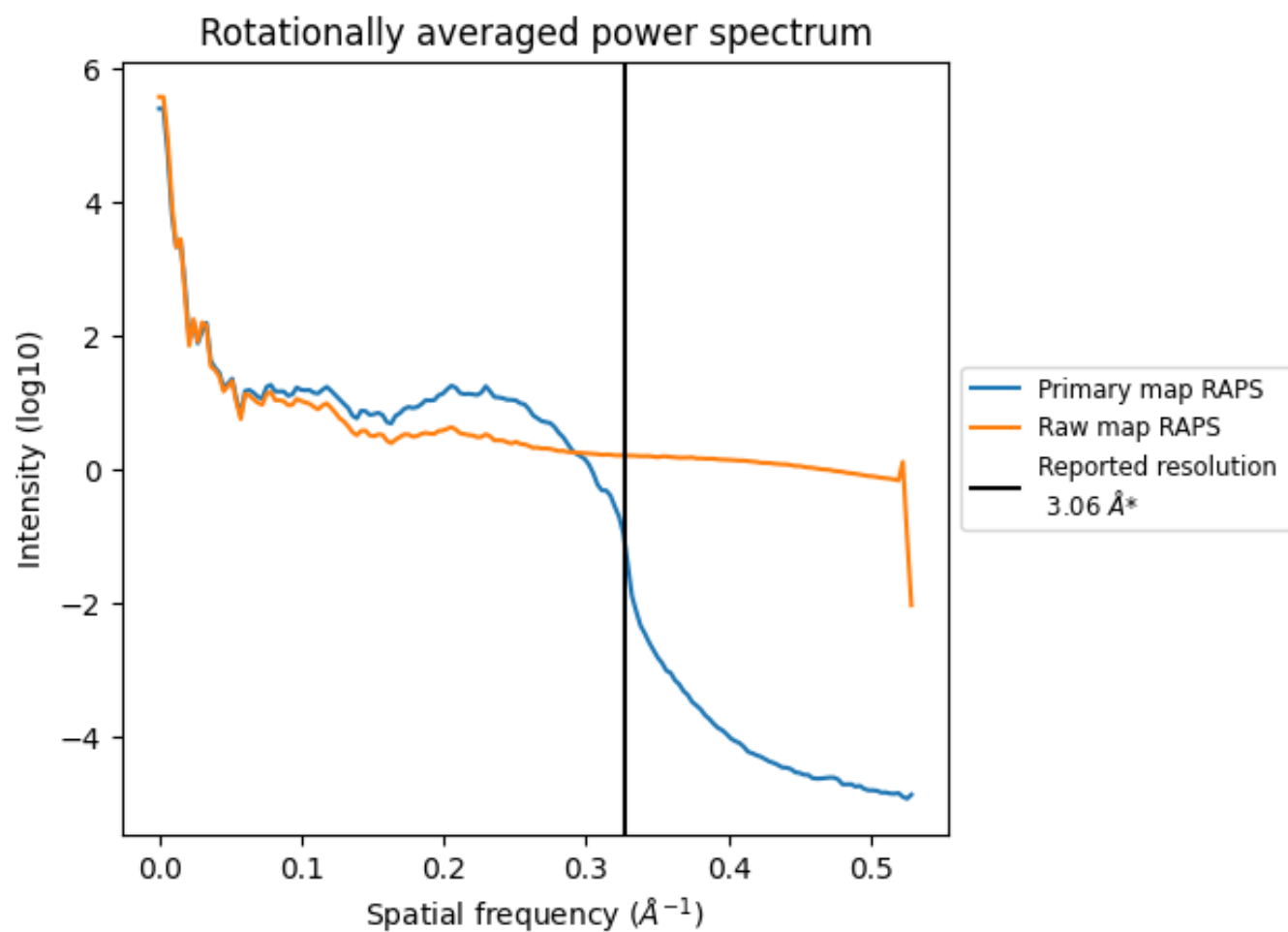
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 365 nm³; this corresponds to an approximate mass of 330 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 ⓘ

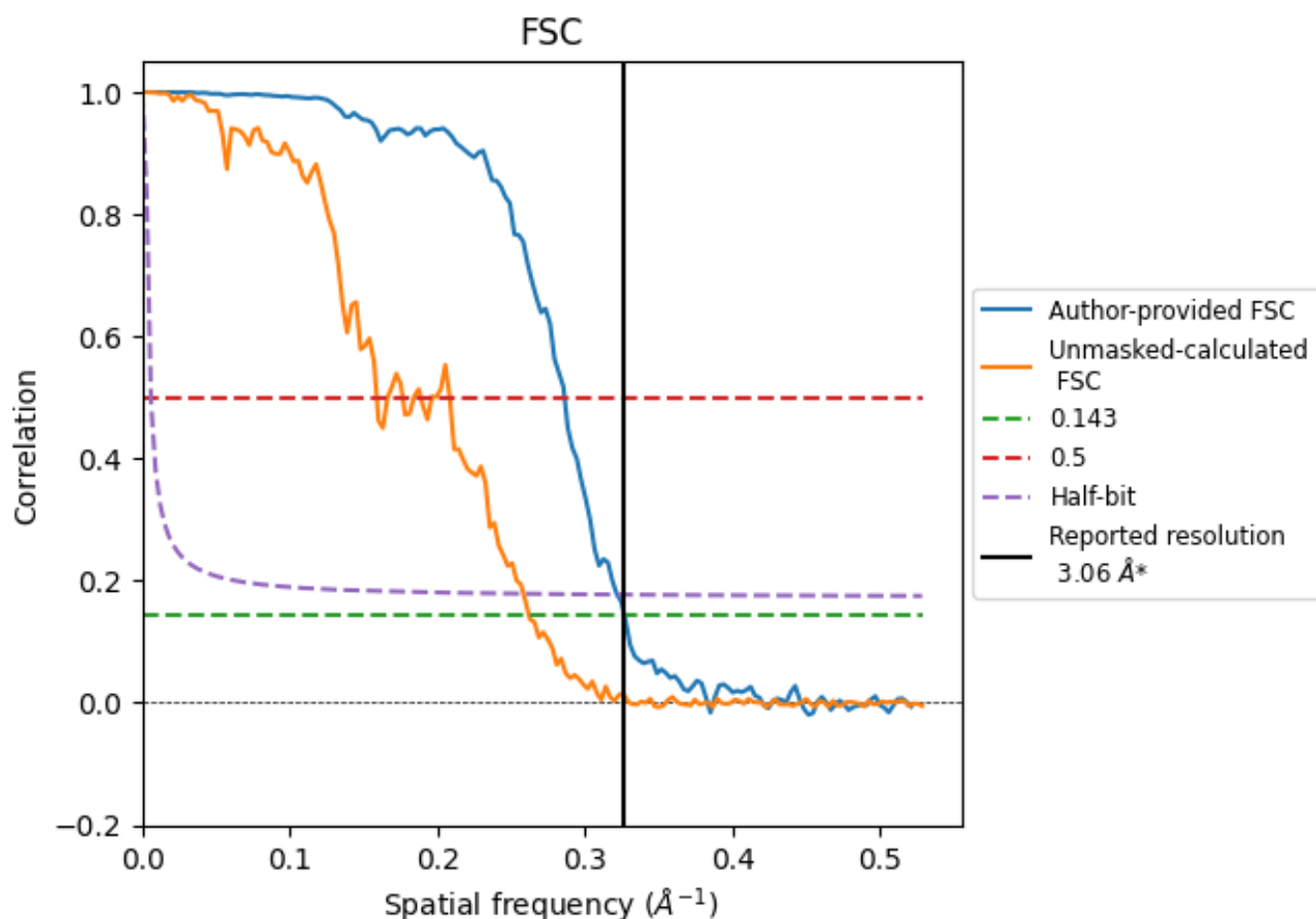


*Reported resolution corresponds to spatial frequency of 0.327 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.327 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.06	-	-
Author-provided FSC curve	3.06	3.49	3.11
Unmasked-calculated*	3.82	6.29	3.87

*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 3.82 differs from the reported value 3.06 by more than 10 %

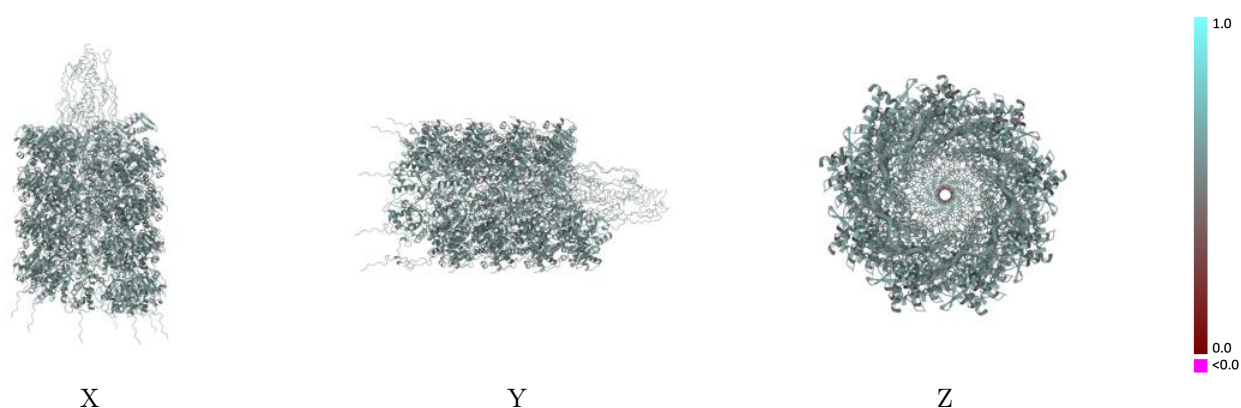
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53794 and PDB model 9R7V. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

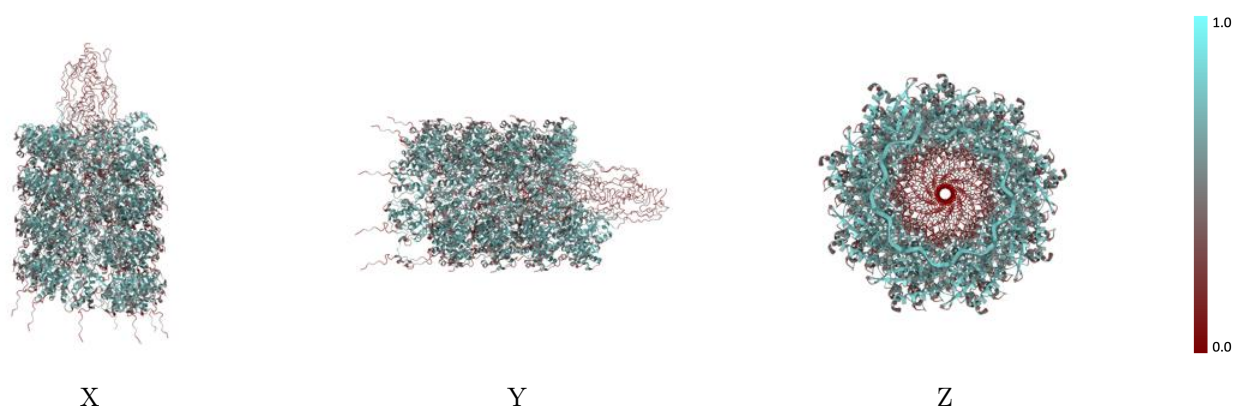
This section was not generated.

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



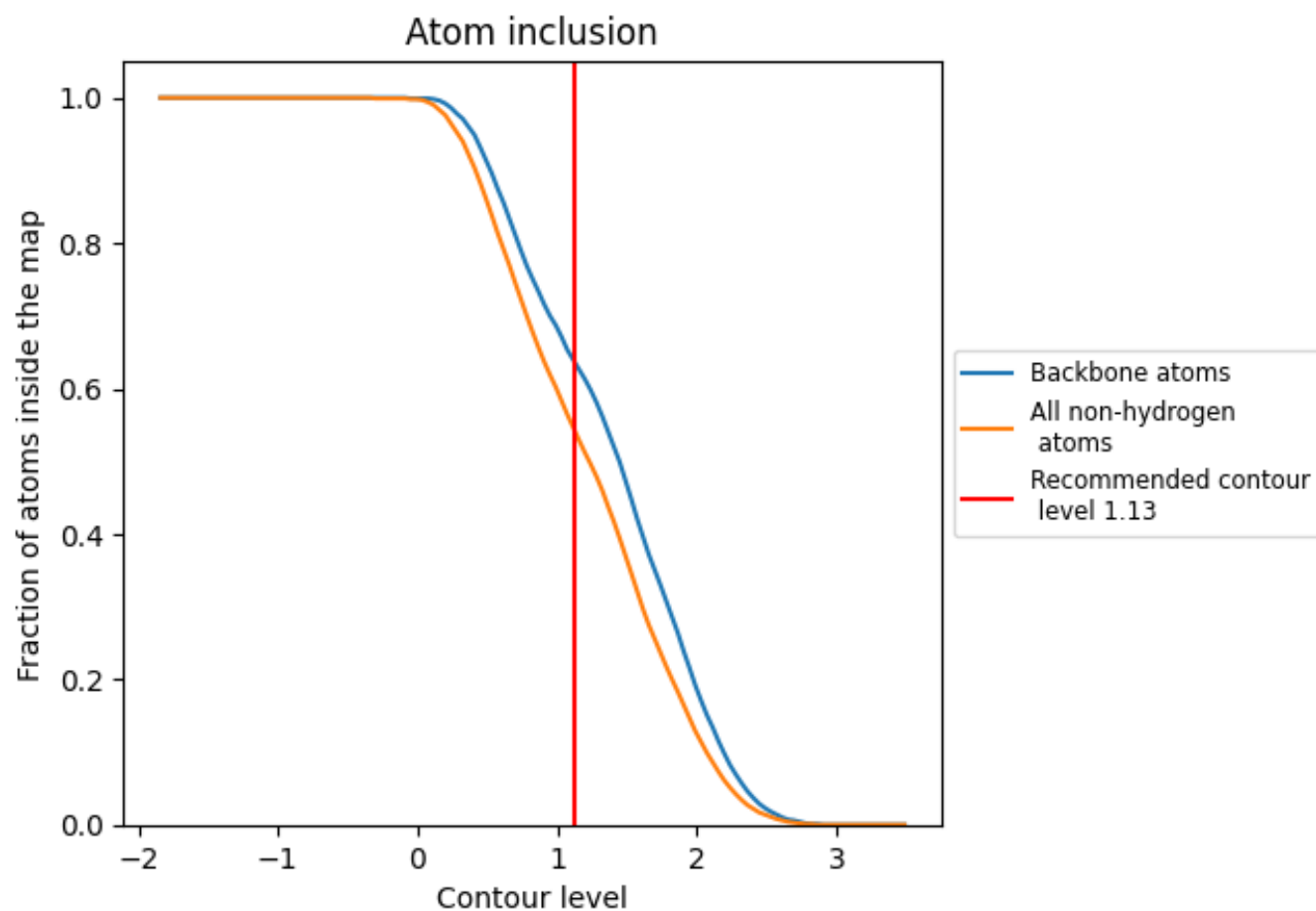
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 54% 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 (1.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5400	 0.5620
Aa	 0.5280	 0.5620
Ab	 0.7800	 0.5770
Ac	 0.5290	 0.5610
Ad	 0.8100	 0.5860
Ae	 0.5260	 0.5590
Af	 0.8300	 0.5850
Ag	 0.5270	 0.5620
Ah	 0.7500	 0.5500
Ai	 0.5270	 0.5610
Aj	 0.8100	 0.5840
Ak	 0.5260	 0.5610
Al	 0.8300	 0.5910
Am	 0.5250	 0.5620
An	 0.8300	 0.5830
Ao	 0.5260	 0.5610
Ap	 0.7900	 0.5550
Aq	 0.5230	 0.5610
Ar	 0.7900	 0.5570
As	 0.5220	 0.5610
At	 0.8000	 0.5760
Au	 0.5280	 0.5620
Av	 0.8300	 0.5940
Aw	 0.5280	 0.5600
Ax	 0.8100	 0.5870
Ay	 0.5250	 0.5620
Az	 0.7800	 0.5630
Ba	 0.5260	 0.5630
Bb	 0.7800	 0.5800
Bc	 0.5270	 0.5610
Bd	 0.7900	 0.5790
Be	 0.5250	 0.5610
Bf	 0.7700	 0.5460
Bg	 0.5250	 0.5620
Bh	 0.7800	 0.5680



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Chain	Atom inclusion	Q-score
Bi	 0.5220	 0.5610
Bj	 0.7900	 0.5720
Bk	 0.5220	 0.5610
Bl	 0.8000	 0.5840
Bm	 0.5250	 0.5630
Bn	 0.8100	 0.5920
Bo	 0.5230	 0.5600
Bp	 0.8100	 0.5880
Bq	 0.5270	 0.5630
Br	 0.8000	 0.5860
Bs	 0.5310	 0.5620
Bt	 0.7900	 0.5860
Bu	 0.5280	 0.5600
Bv	 0.7600	 0.5570
Bw	 0.5230	 0.5620
Bx	 0.7900	 0.5610
By	 0.5260	 0.5630
Bz	 0.8200	 0.5810
Ca	 0.5260	 0.5610
Cb	 0.7700	 0.5670
Cc	 0.5260	 0.5600
Cd	 0.8300	 0.5820
Ce	 0.5240	 0.5620
Cf	 0.8100	 0.5840
Cg	 0.5250	 0.5600
Ch	 0.8100	 0.5830
Ci	 0.5260	 0.5630
Cj	 0.8100	 0.5880
Ck	 0.5240	 0.5600
Cl	 0.8100	 0.5780
Cm	 0.5230	 0.5610
Cn	 0.8100	 0.5850
Co	 0.5260	 0.5620
Cp	 0.8200	 0.5910
Cq	 0.5270	 0.5630
Cr	 0.7900	 0.5780
Cs	 0.5260	 0.5620
Ct	 0.7700	 0.5750