



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:33 PM UTC

PDB ID : 8COA / pdb_00008coa
EMDB ID : EMD-16774
Title : in situ Subtomogram average of Immature Rotavirus TLP spike
Authors : Shah, P.N.M.; Stuart, D.I.
Deposited on : 2023-02-27
Resolution : 4.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

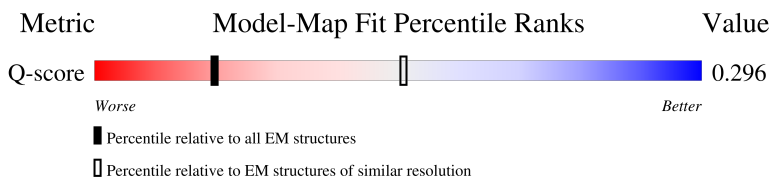
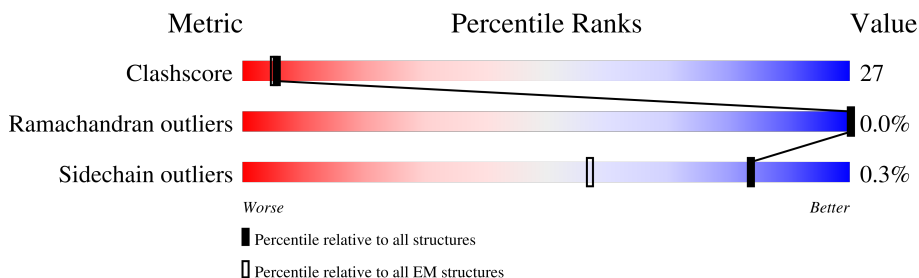
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	776	
1	B	776	
1	C	776	
2	D	326	

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Mol	Chain	Length	Quality of chain
2	E	326	
2	F	326	
2	G	326	
2	H	326	
2	I	326	
2	J	326	
2	K	326	
2	L	326	
2	M	326	
2	N	326	
2	O	326	
2	P	326	
3	d	397	
3	e	397	
3	f	397	
3	g	397	
3	h	397	
3	i	397	
3	j	397	
3	k	397	
3	l	397	
3	m	397	
3	n	397	
3	o	397	
3	p	397	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 84883 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Outer capsid protein VP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	726	Total	C	N	O	S	0	0
			5715	3616	952	1128	19		
1	B	744	Total	C	N	O	S	0	0
			5860	3703	977	1160	20		
1	C	692	Total	C	N	O	S	0	0
			5478	3472	911	1075	20		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	185	THR	ARG	conflict	UNP A0A1Q2TSK9
A	323	MET	VAL	conflict	UNP A0A1Q2TSK9
A	737	SER	THR	conflict	UNP A0A1Q2TSK9
A	738	ARG	LYS	conflict	UNP A0A1Q2TSK9
B	185	THR	ARG	conflict	UNP A0A1Q2TSK9
B	323	MET	VAL	conflict	UNP A0A1Q2TSK9
B	737	SER	THR	conflict	UNP A0A1Q2TSK9
B	738	ARG	LYS	conflict	UNP A0A1Q2TSK9
C	185	THR	ARG	conflict	UNP A0A1Q2TSK9
C	323	MET	VAL	conflict	UNP A0A1Q2TSK9
C	737	SER	THR	conflict	UNP A0A1Q2TSK9
C	738	ARG	LYS	conflict	UNP A0A1Q2TSK9

- Molecule 2 is a protein called Outer capsid glycoprotein VP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	262	Total	C	N	O	S	0	0
			2077	1324	329	408	16		
2	E	244	Total	C	N	O	S	0	0
			1928	1227	304	381	16		
2	F	267	Total	C	N	O	S	0	0
			2118	1348	337	417	16		
2	G	268	Total	C	N	O	S	0	0
			2126	1354	338	418	16		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	242	Total	C	N	O	S	0	0
			1913	1217	302	378	16		
2	I	264	Total	C	N	O	S	0	0
			2096	1333	334	413	16		
2	J	265	Total	C	N	O	S	0	0
			2101	1336	335	414	16		
2	K	256	Total	C	N	O	S	0	0
			2031	1293	323	399	16		
2	L	265	Total	C	N	O	S	0	0
			2101	1336	335	414	16		
2	M	267	Total	C	N	O	S	0	0
			2118	1348	337	417	16		
2	N	263	Total	C	N	O	S	0	0
			2088	1329	333	410	16		
2	O	265	Total	C	N	O	S	0	0
			2101	1336	335	414	16		
2	P	242	Total	C	N	O	S	0	0
			1913	1217	302	378	16		

- Molecule 3 is a protein called Intermediate capsid protein VP6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	e	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	f	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	g	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	h	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	i	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	j	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	k	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	l	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	m	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	n	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	o	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		
3	p	397	Total	C	N	O	S	0	0
			3163	2007	550	592	14		

3 Residue-property plots

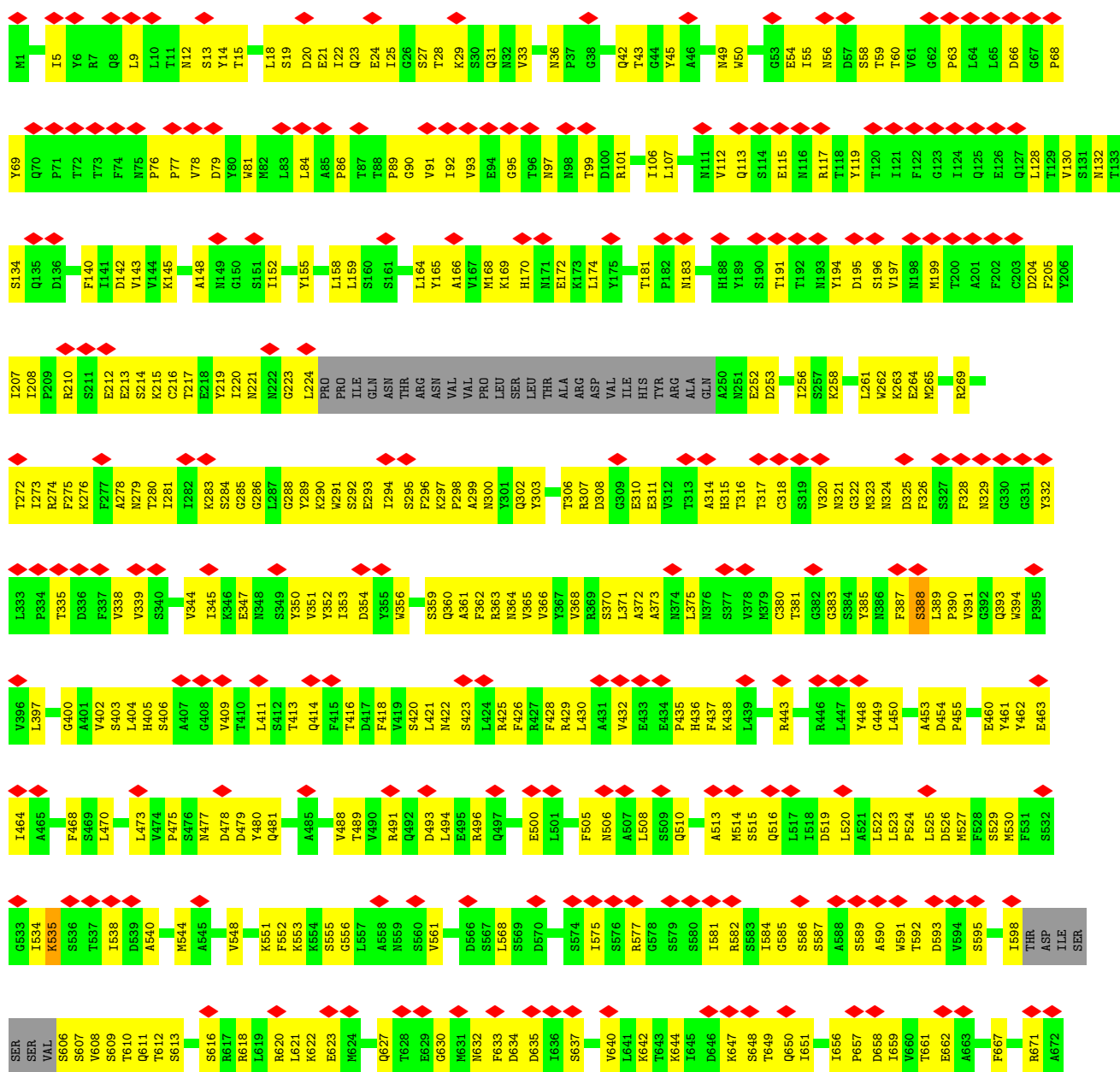
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

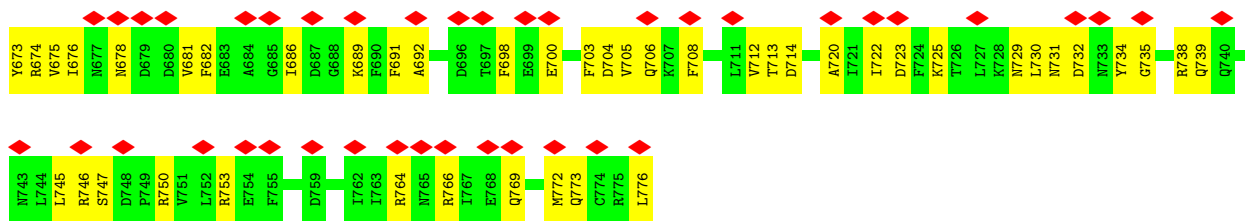
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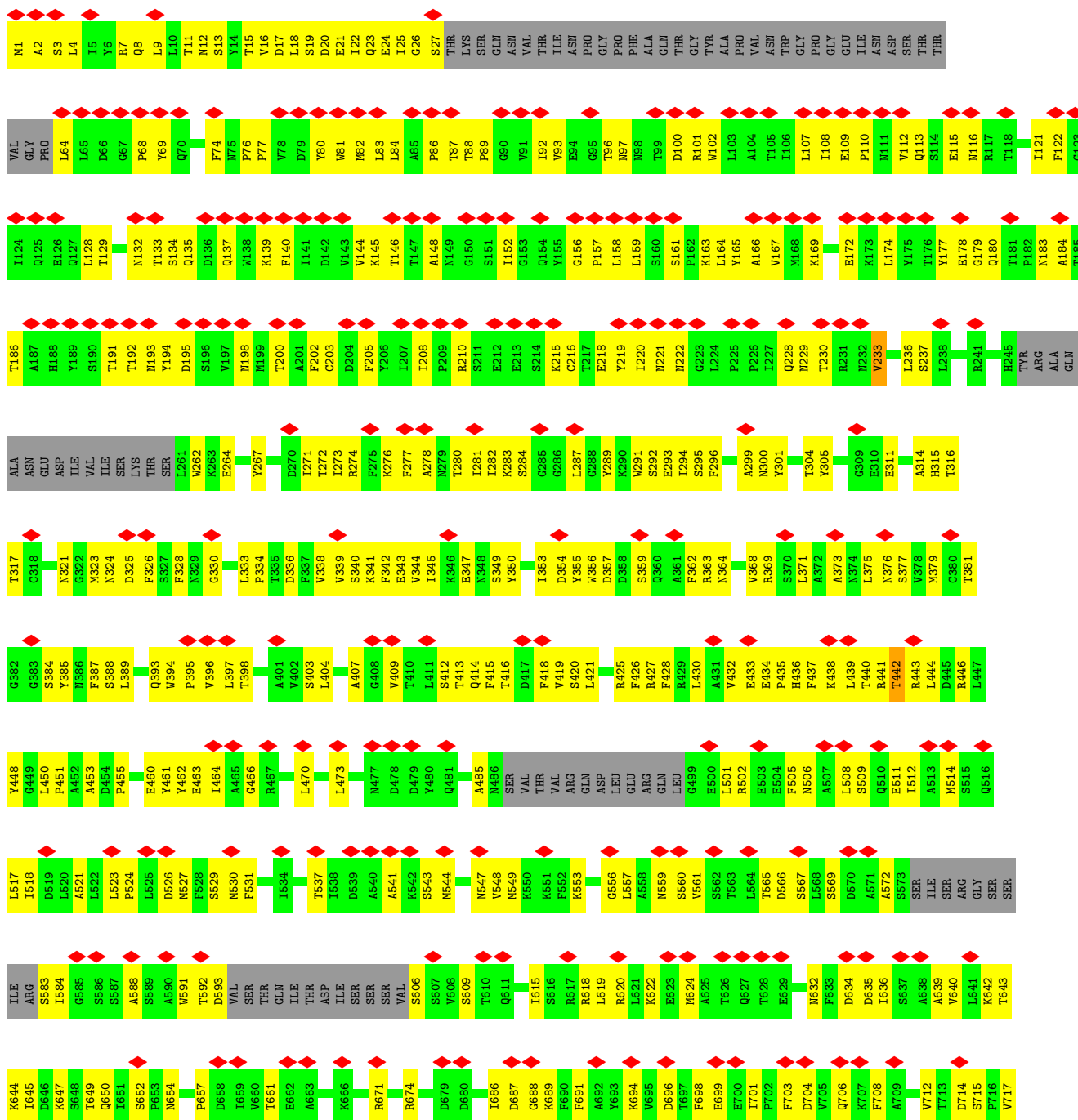


• Molecule 1: Outer capsid protein VP4



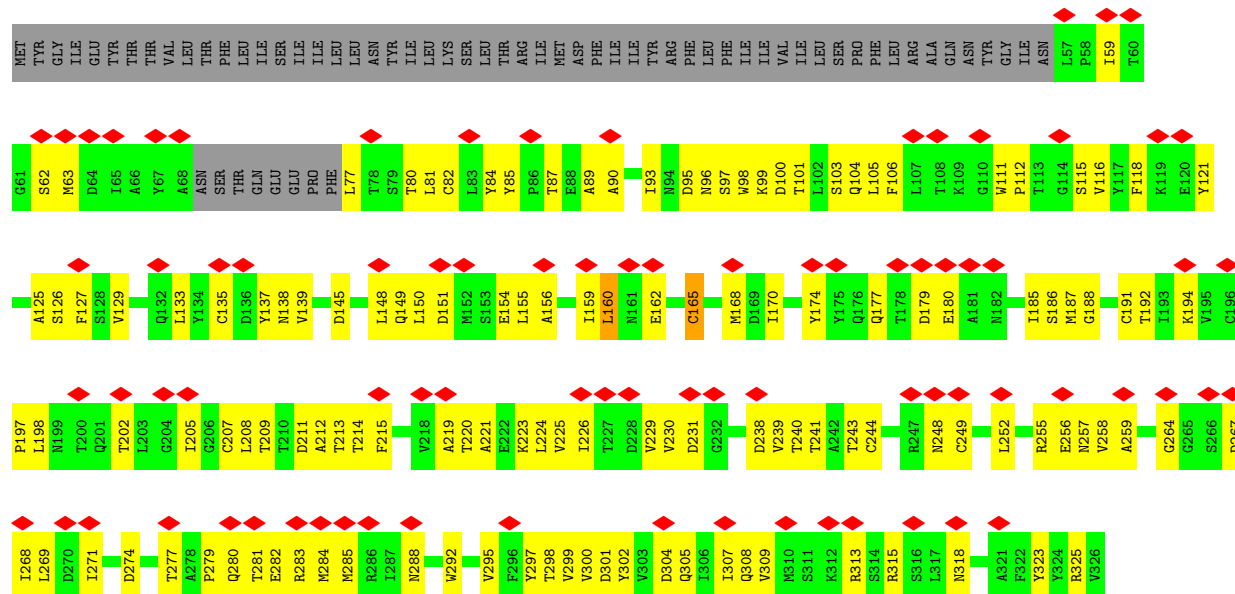


• Molecule 1: Outer capsid protein VP4

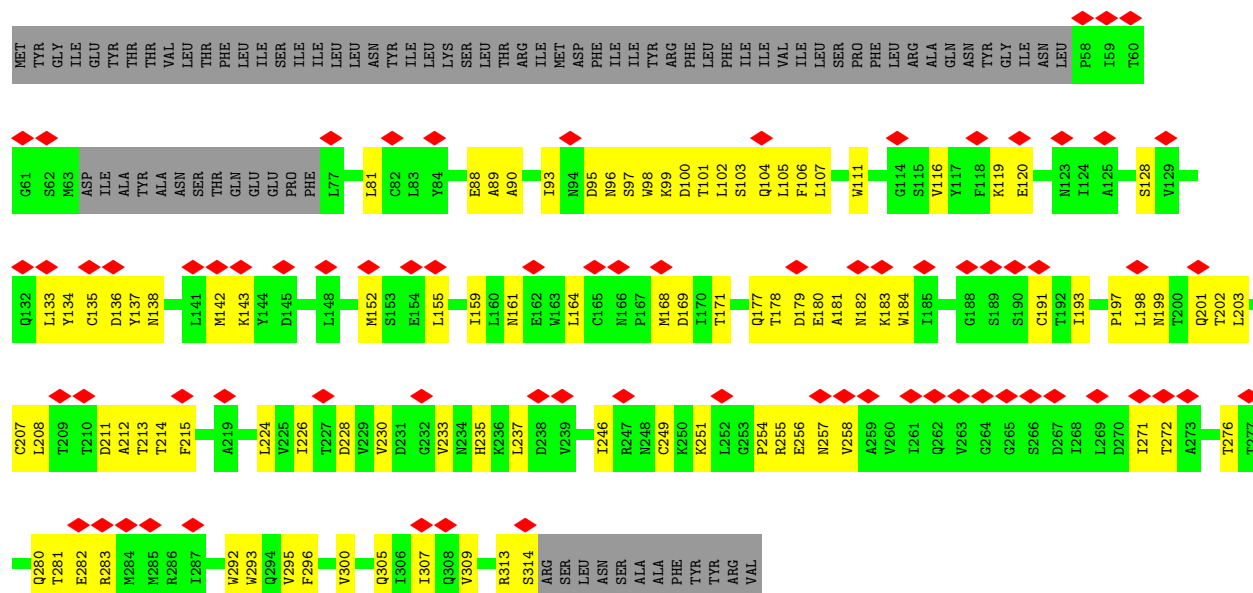




• Molecule 2: Outer capsid glycoprotein VP7

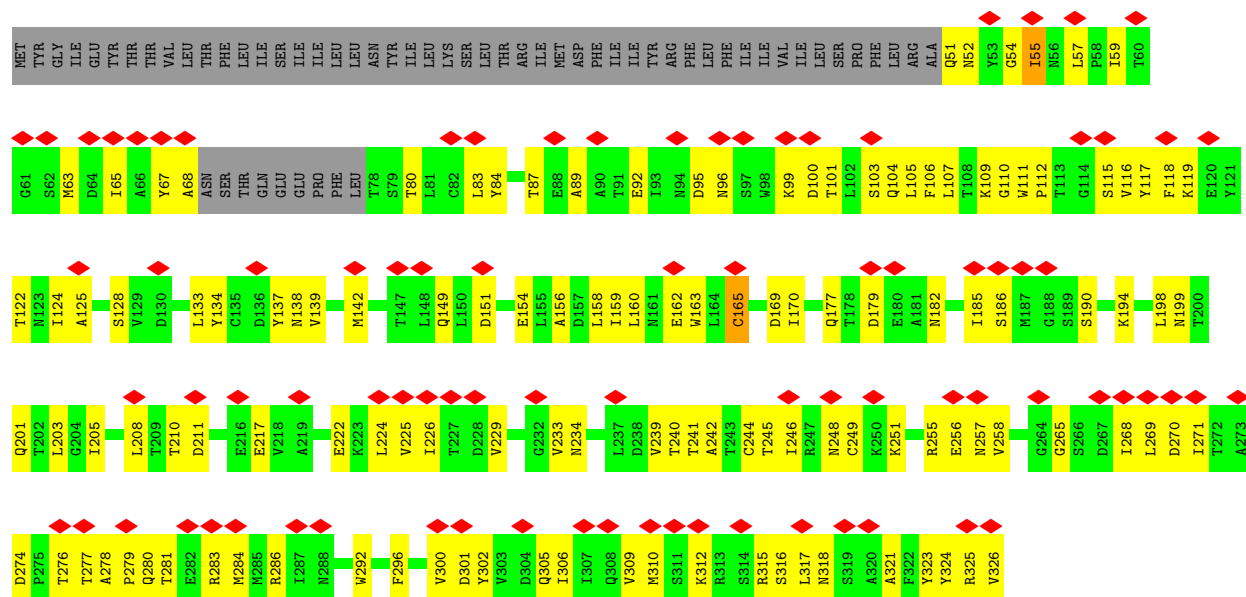


• Molecule 2: Outer capsid glycoprotein VP7

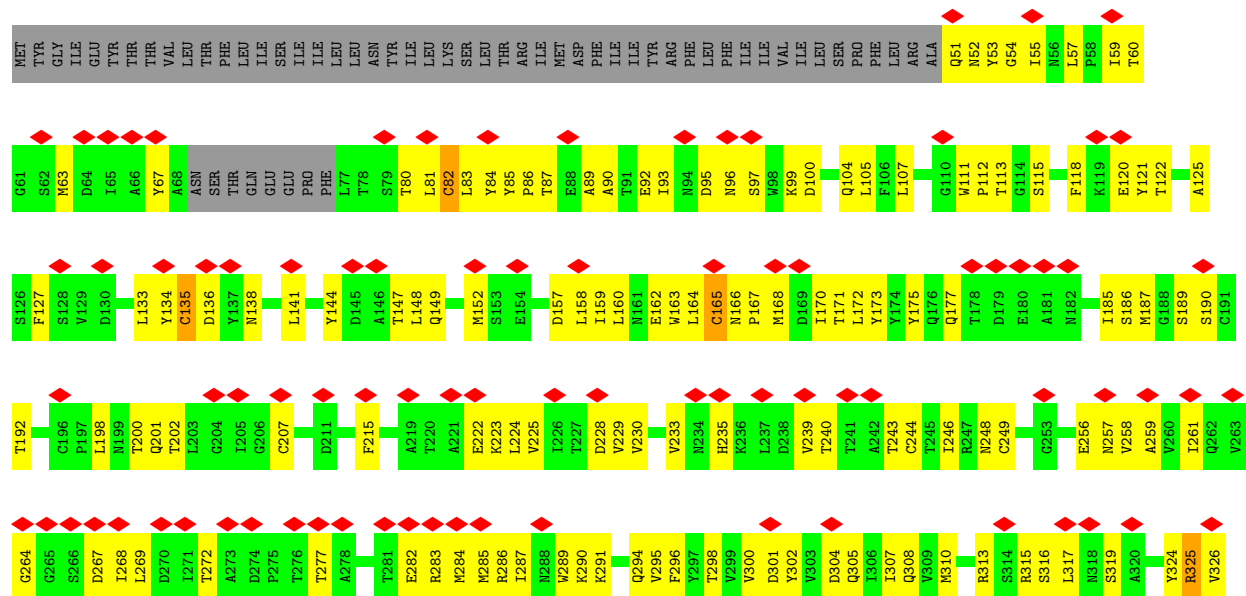
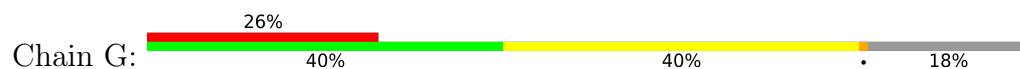


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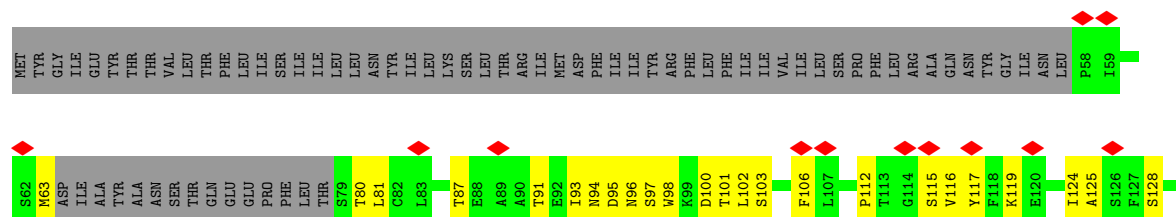


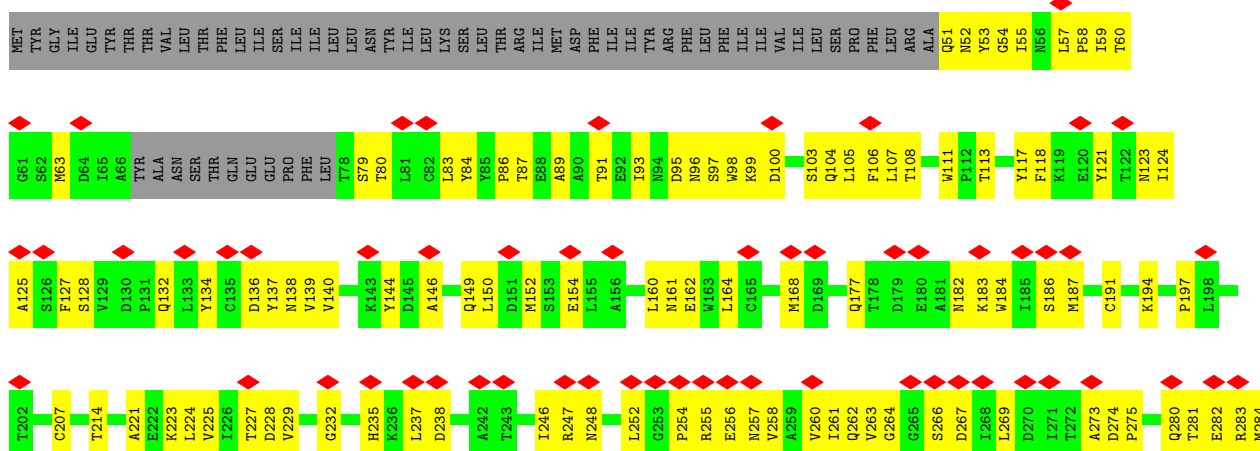


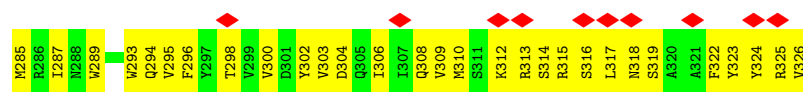
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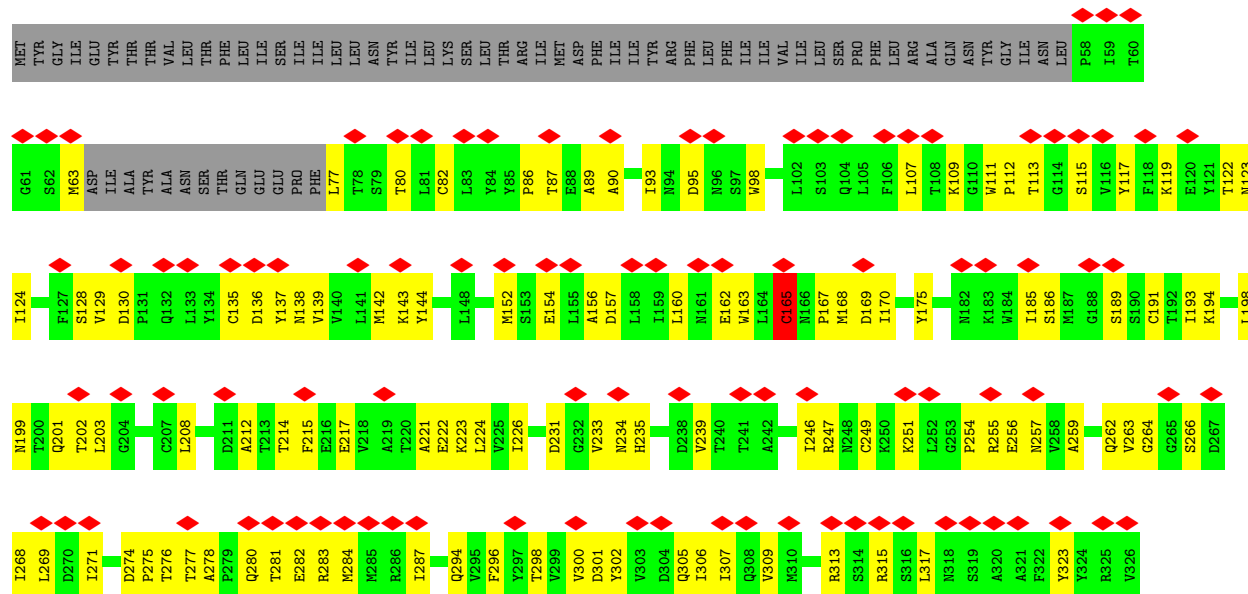
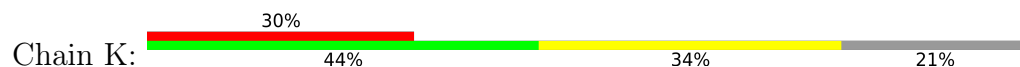
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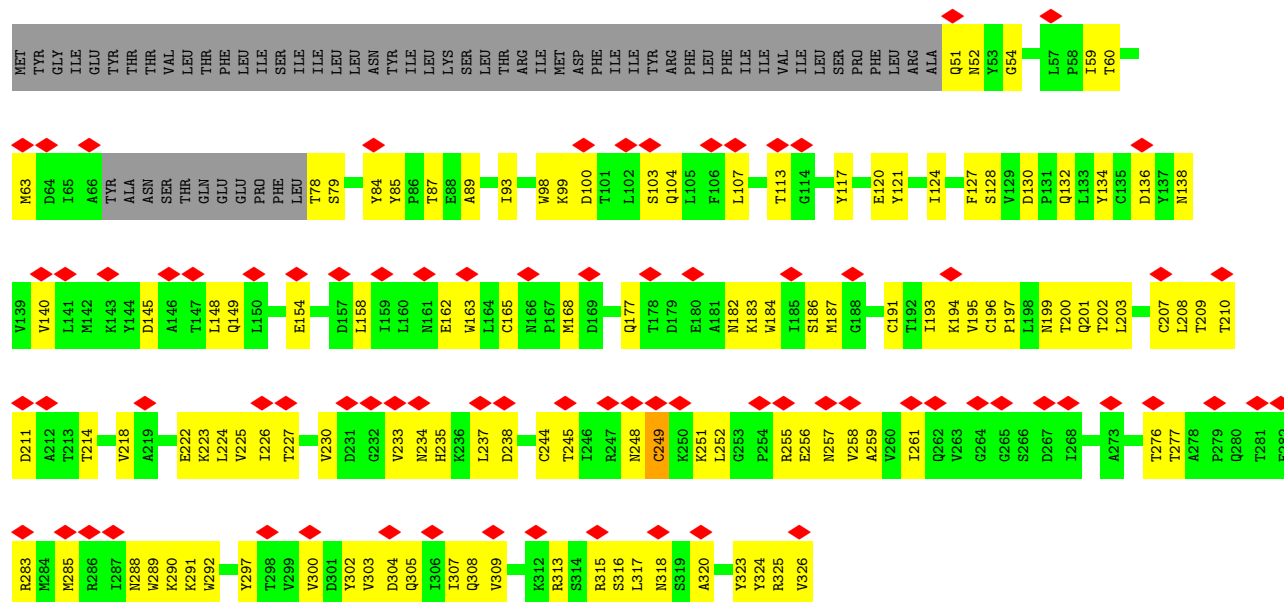
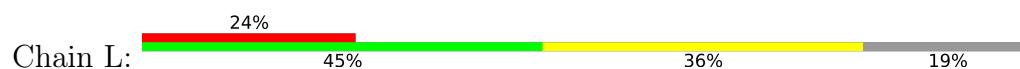




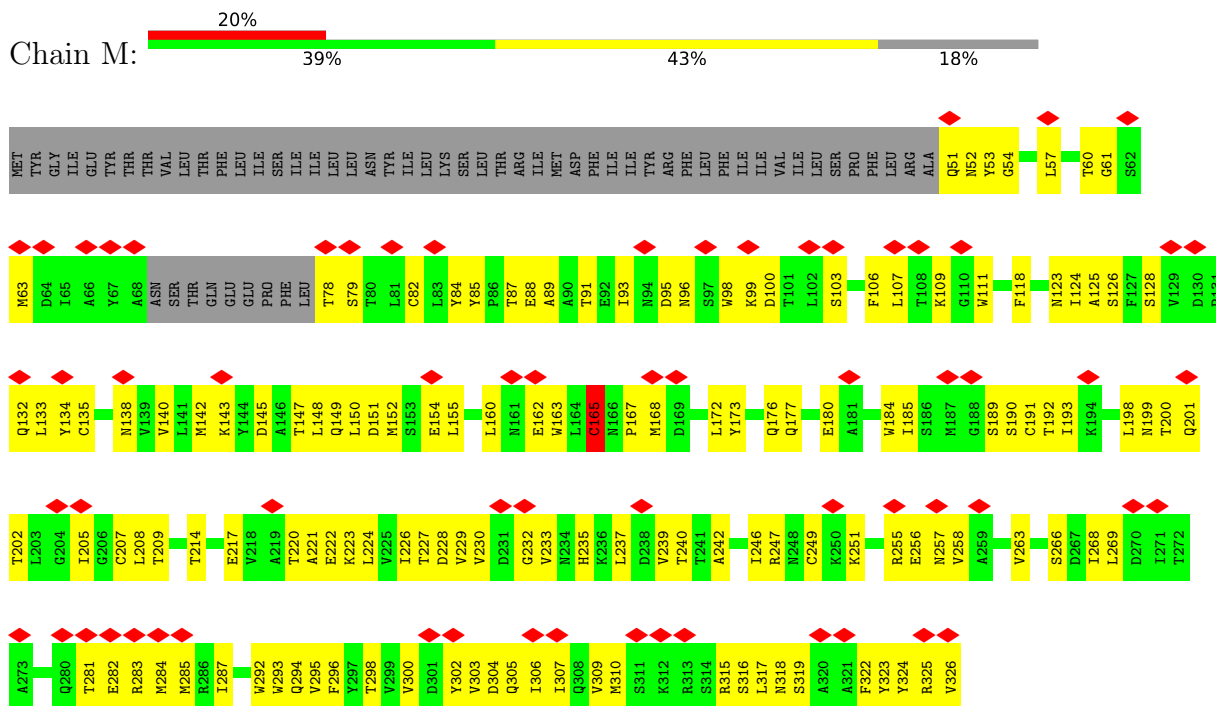
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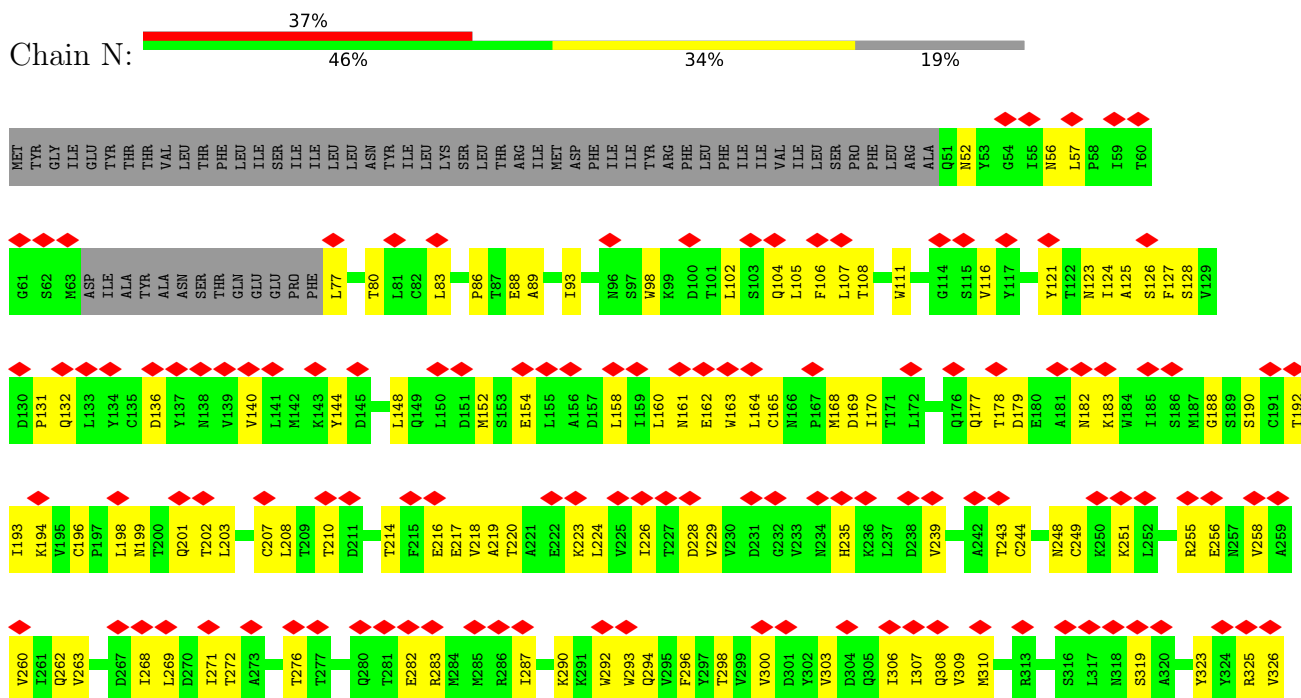
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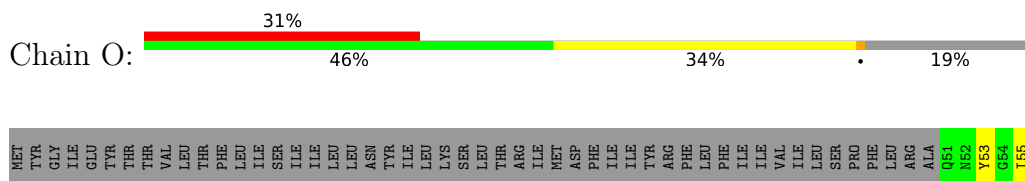
• Molecule 2: Outer capsid glycoprotein VP7

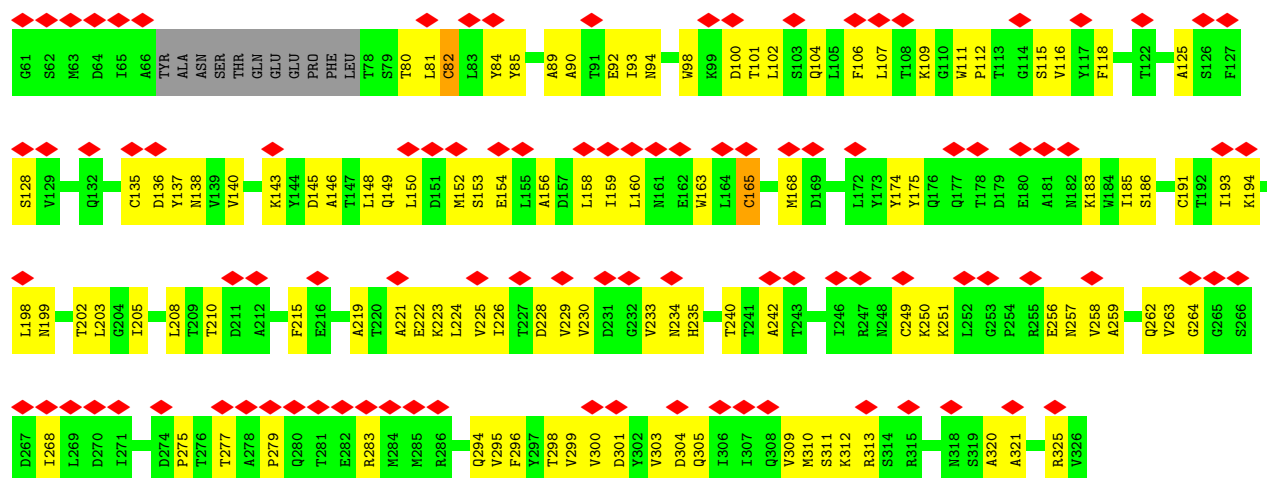


- Molecule 2: Outer capsid glycoprotein VP7

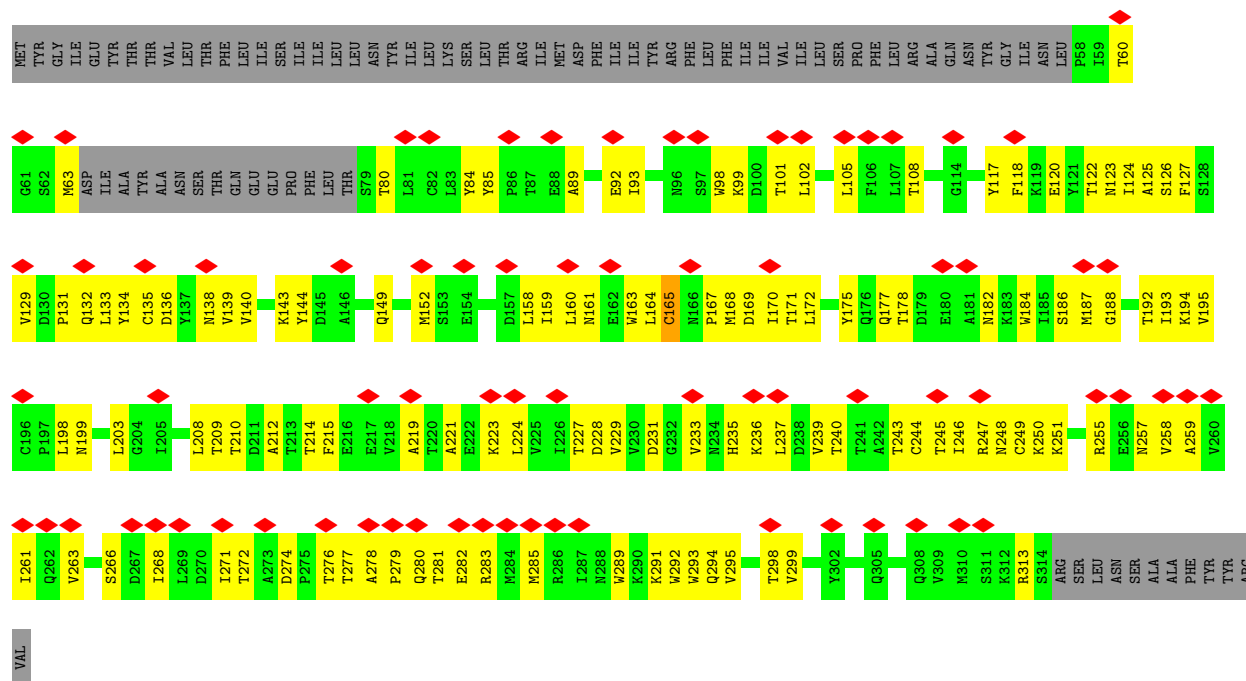


- Molecule 2: Outer capsid glycoprotein VP7

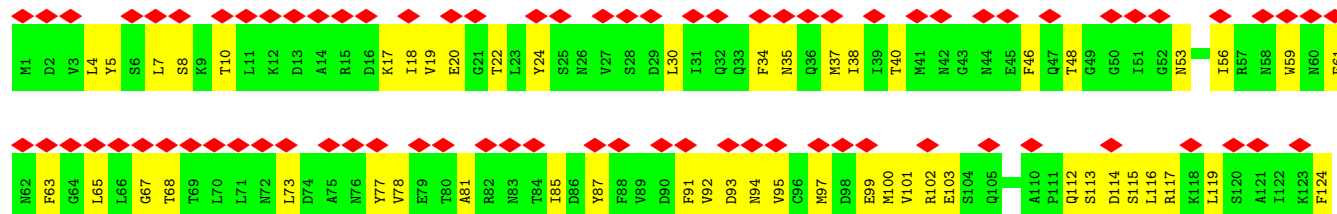


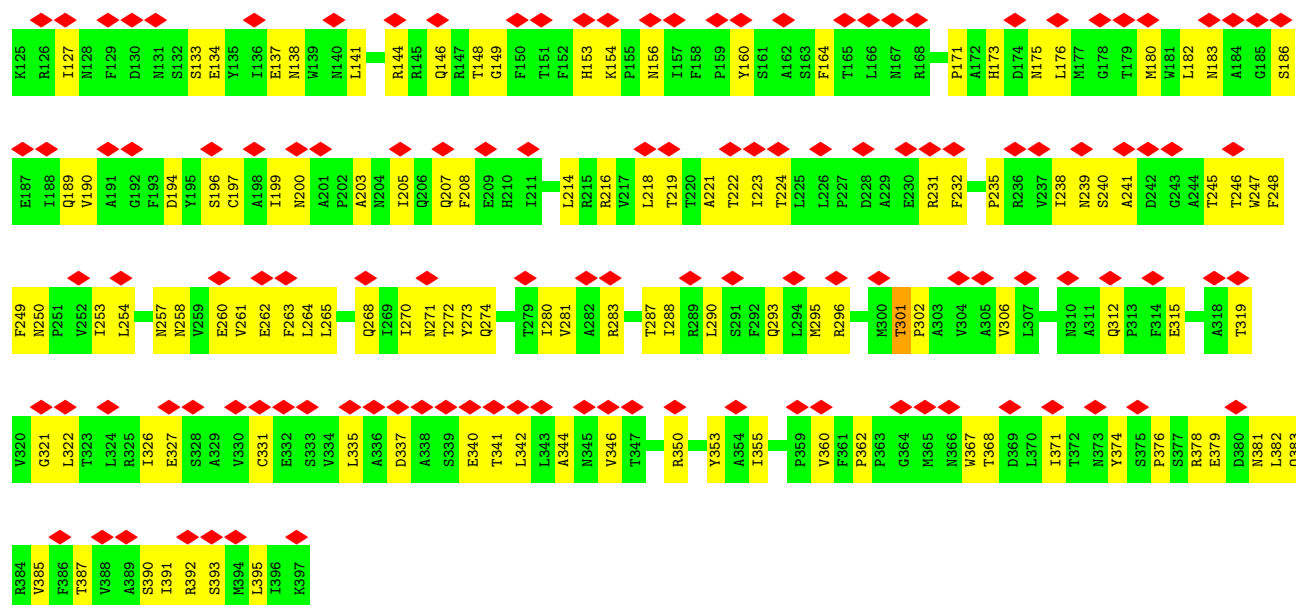


• Molecule 2: Outer capsid glycoprotein VP7

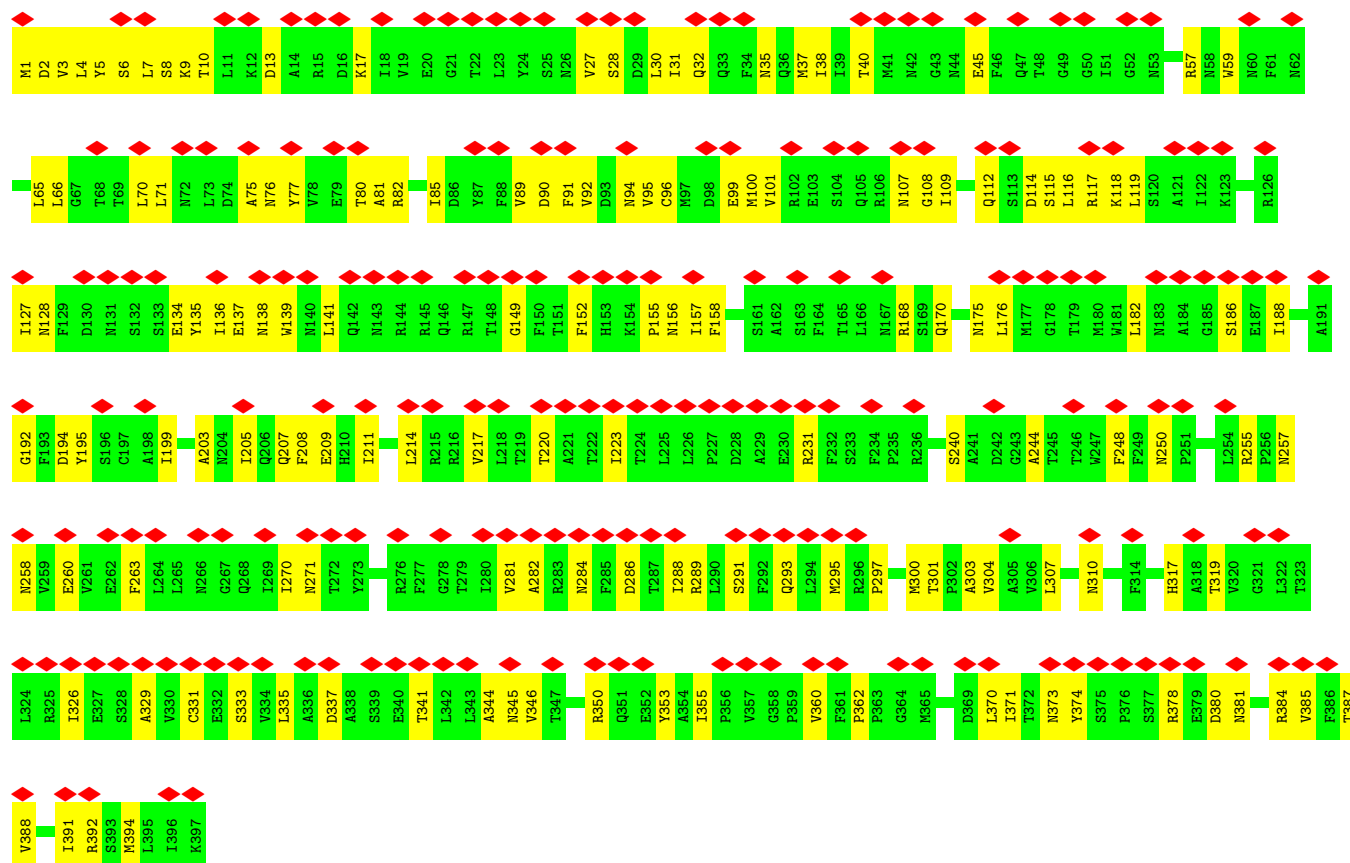


• Molecule 3: Intermediate capsid protein VP6

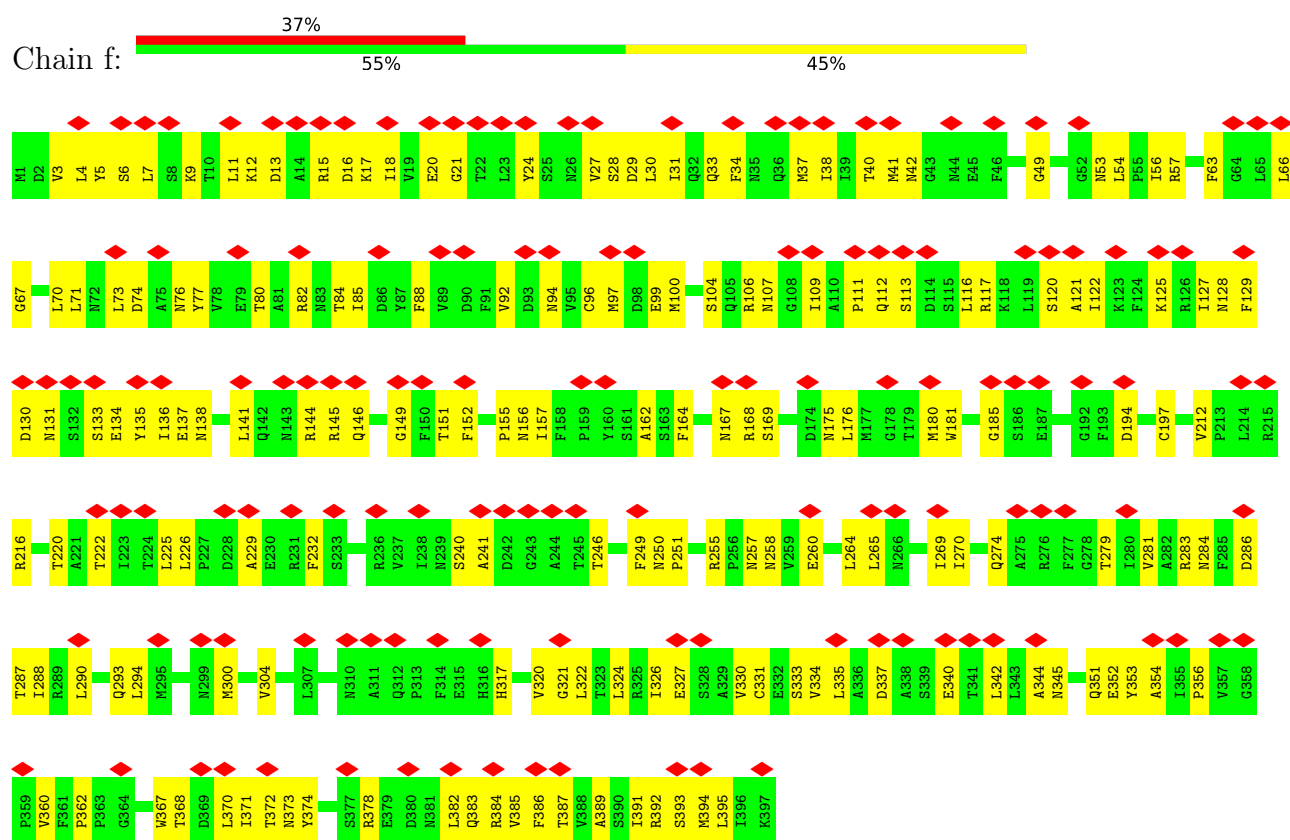




• Molecule 3: Intermediate capsid protein VP6



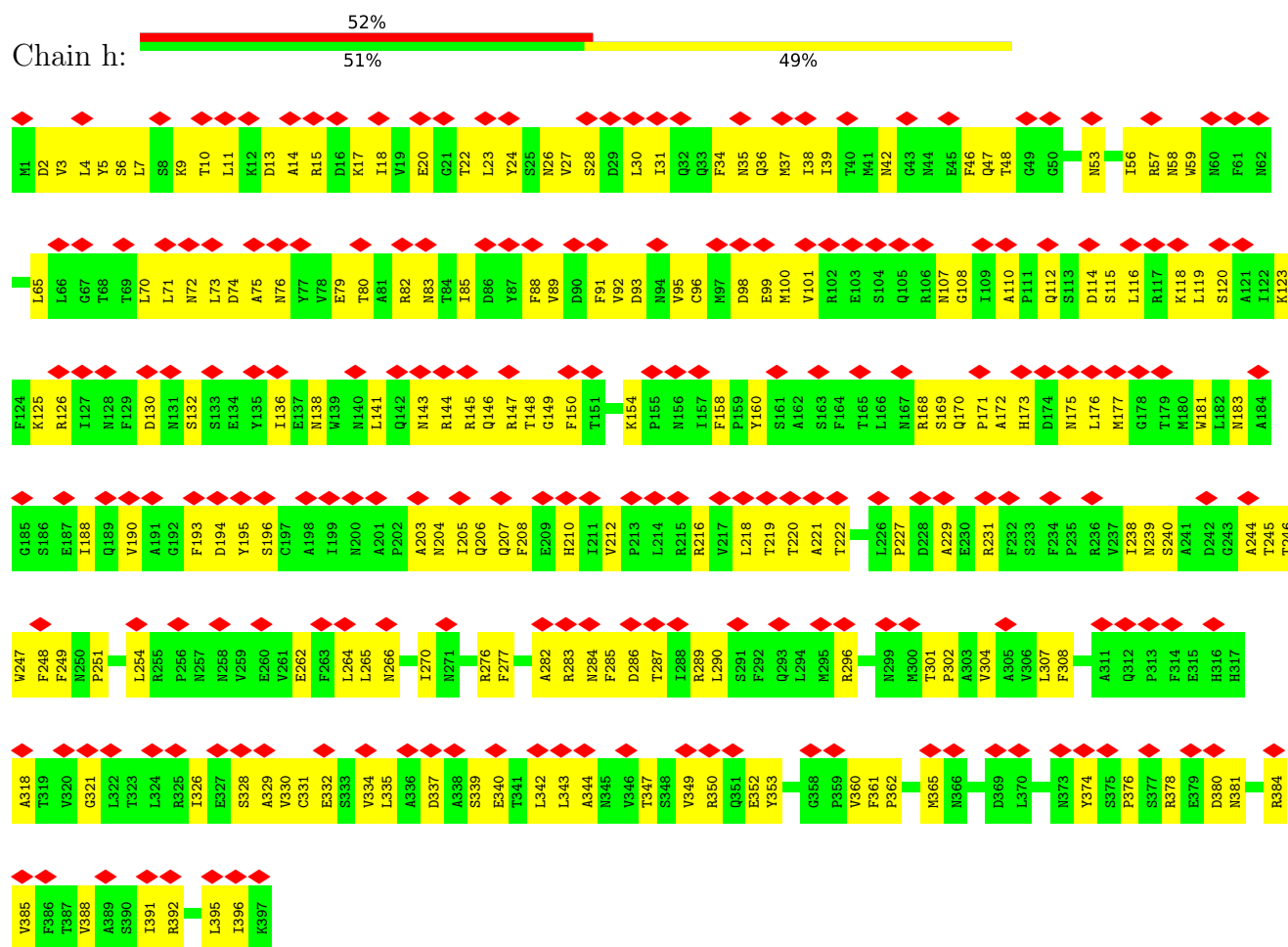
• Molecule 3: Intermediate capsid protein VP6



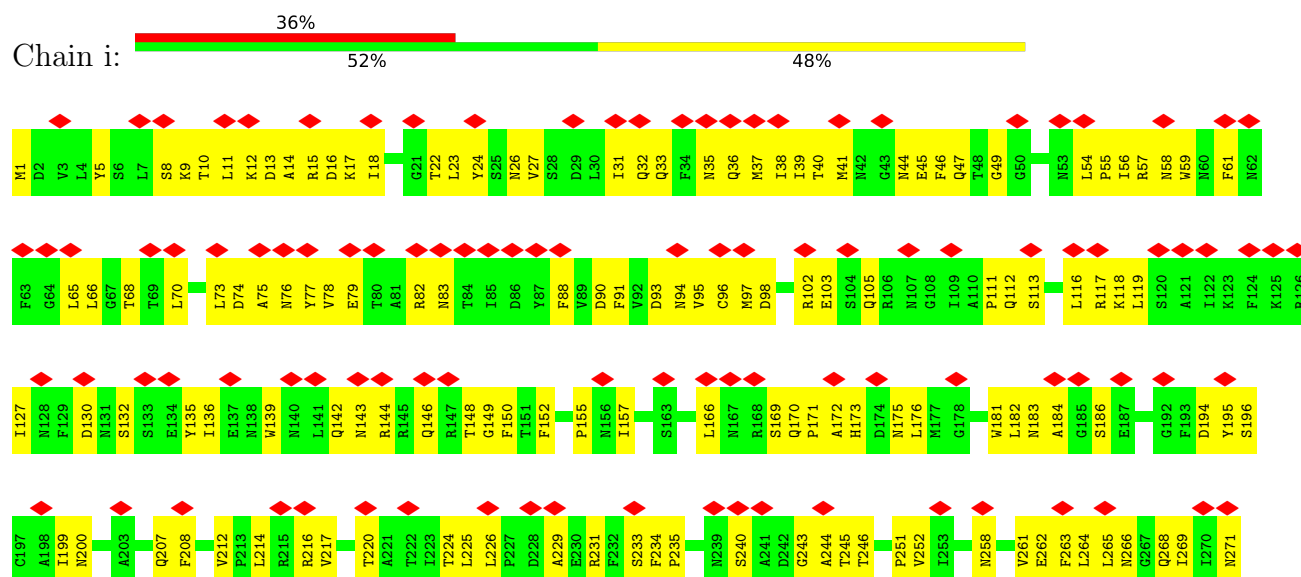
- Molecule 3: Intermediate capsid protein VP6

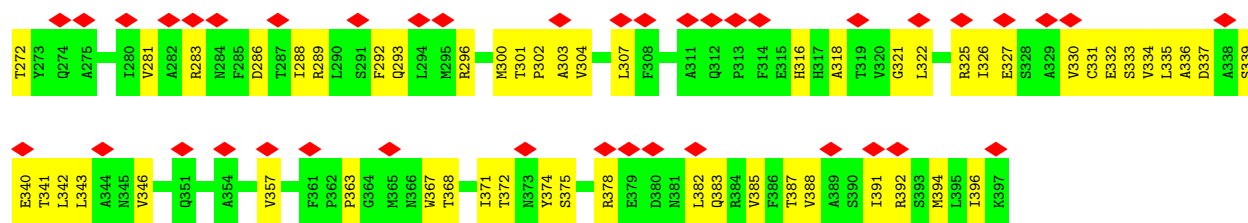


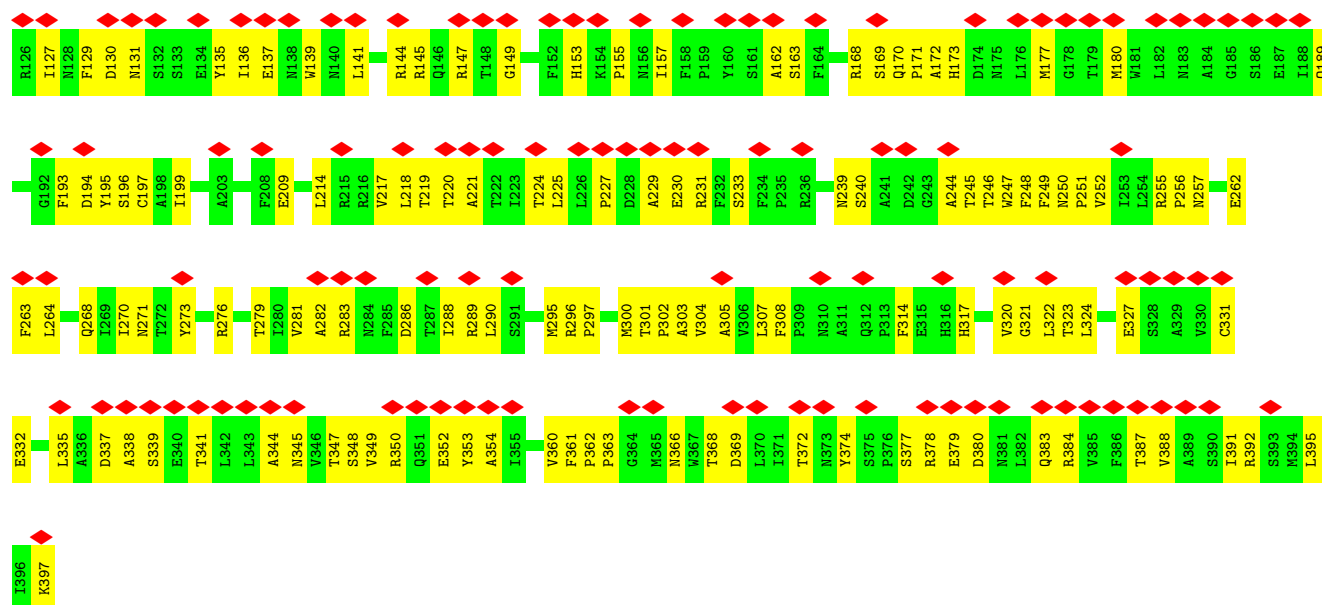
- Molecule 3: Intermediate capsid protein VP6



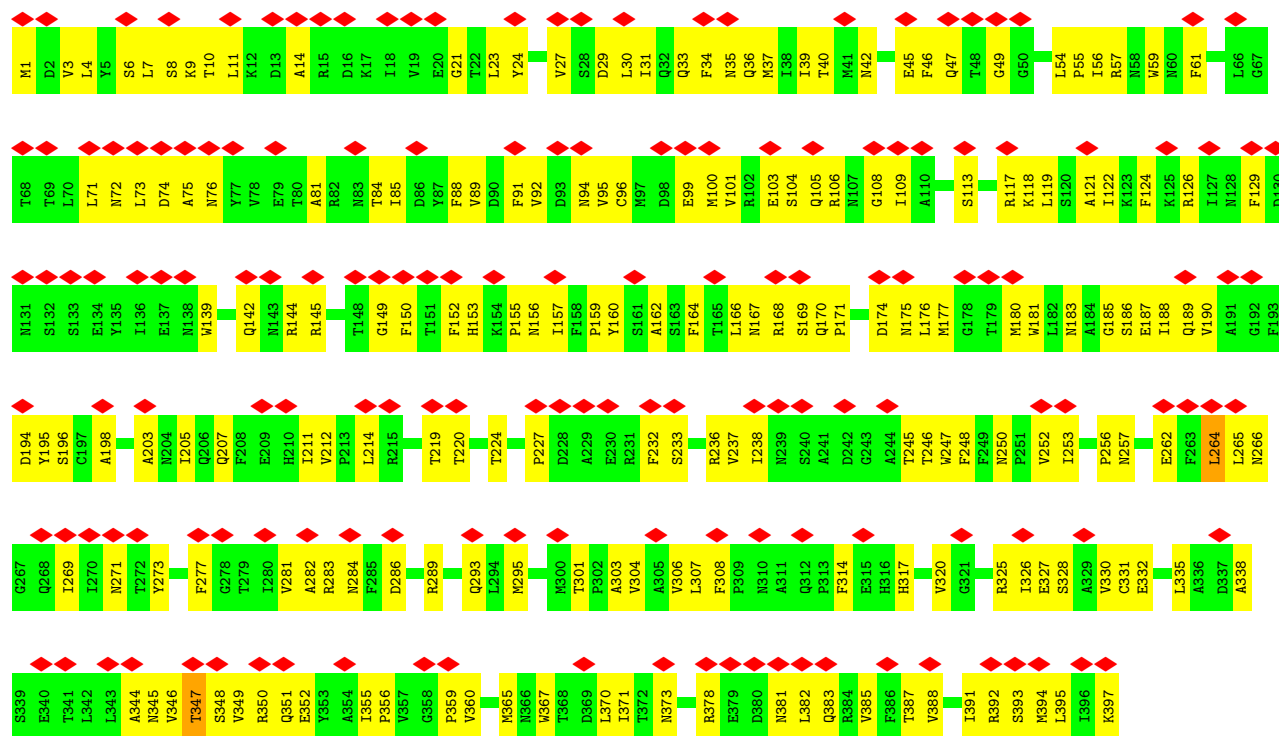
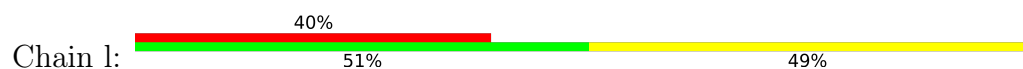
- Molecule 3: Intermediate capsid protein VP6





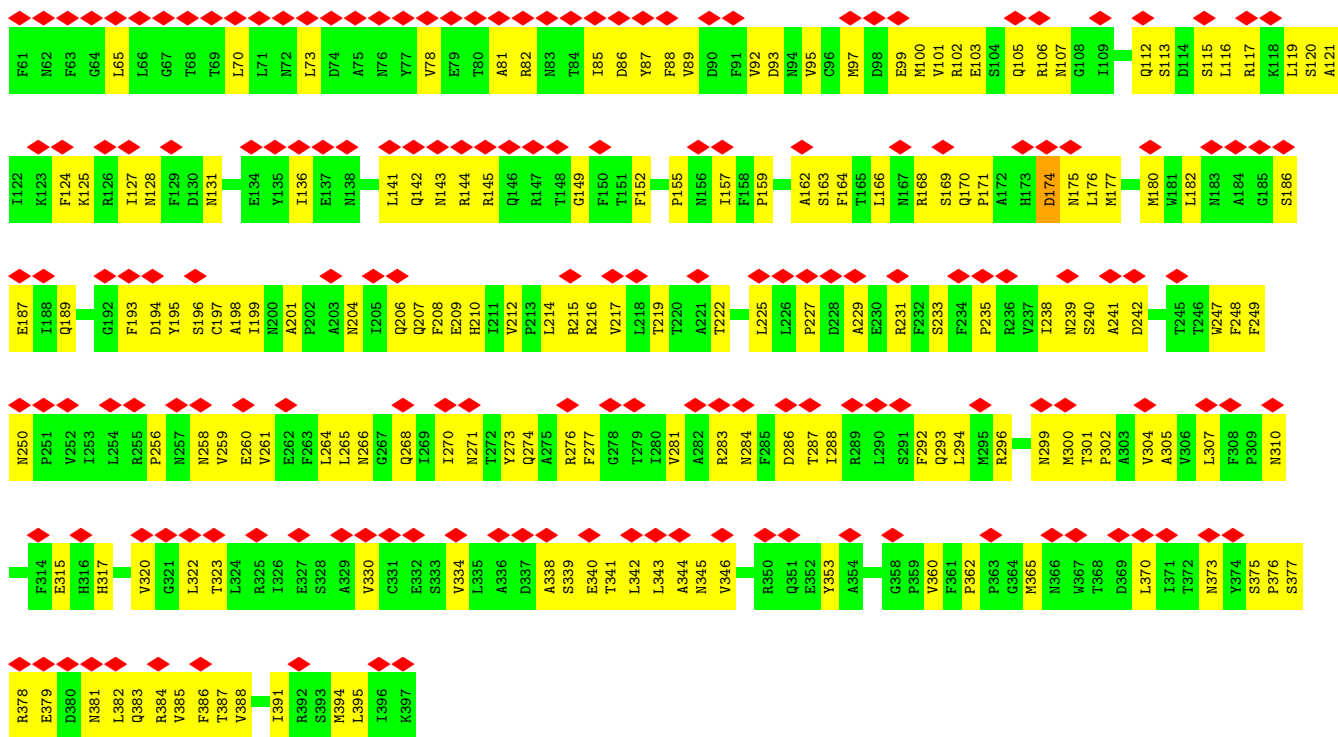


- Molecule 3: Intermediate capsid protein VP6

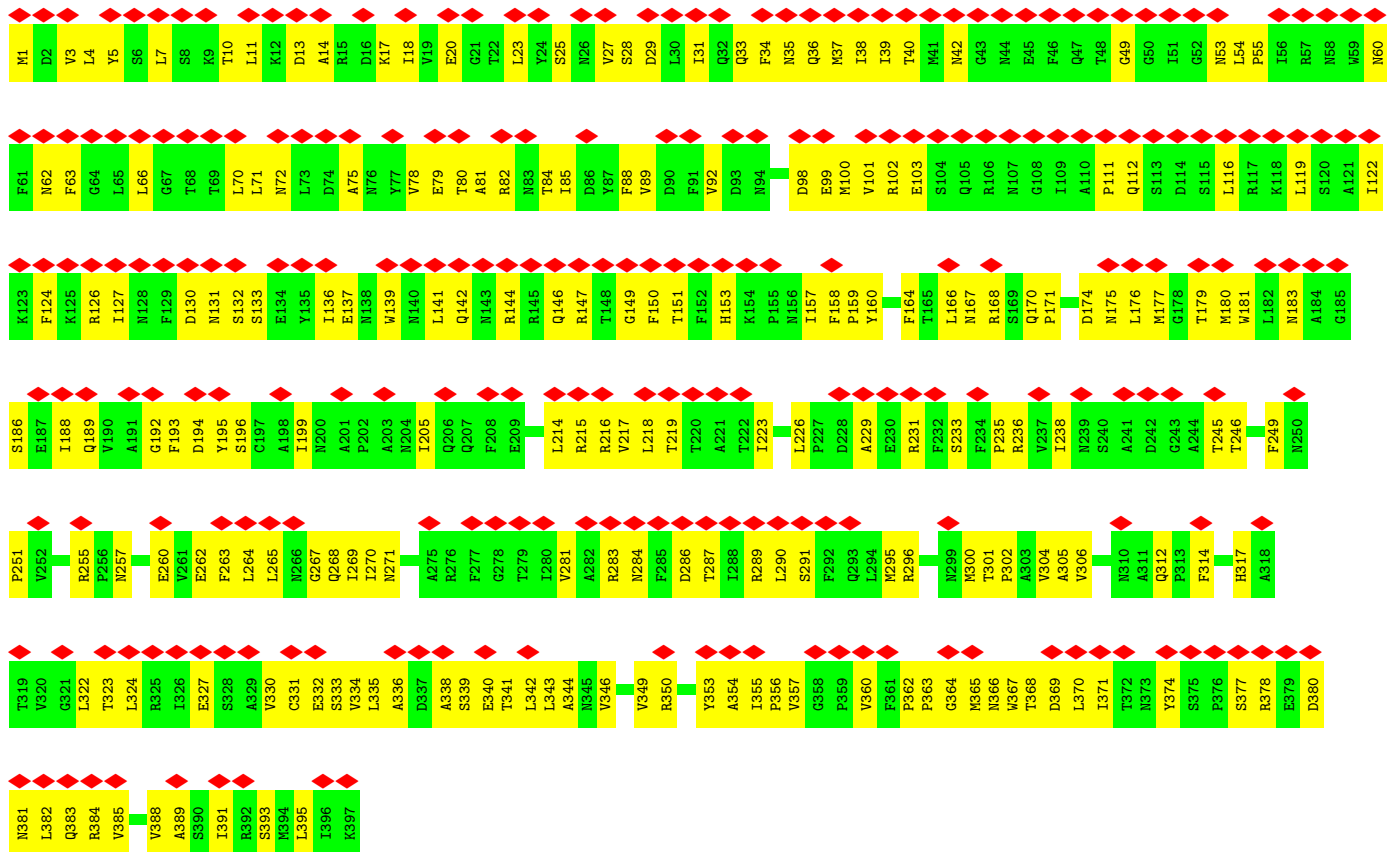


- Molecule 3: Intermediate capsid protein VP6

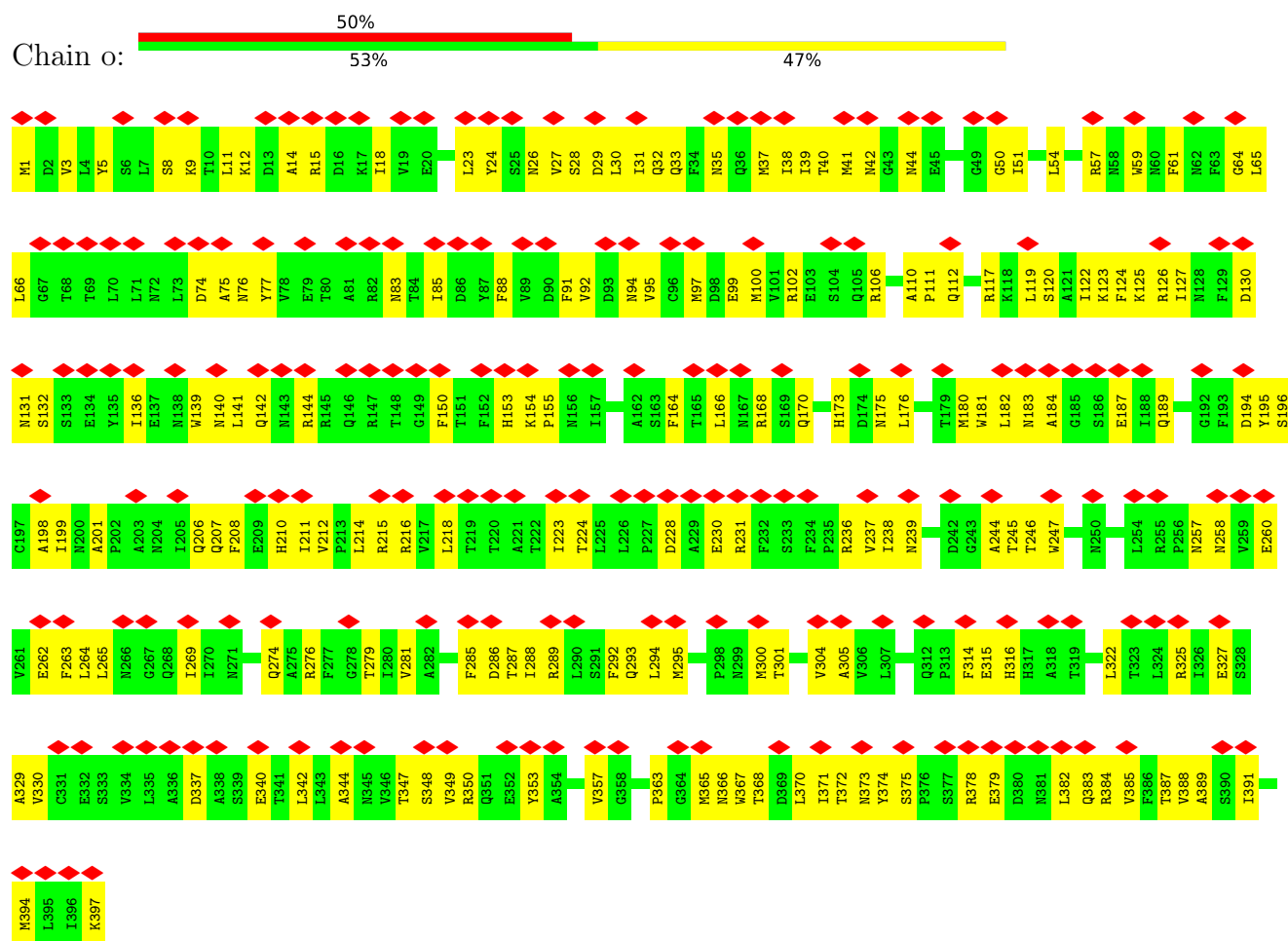




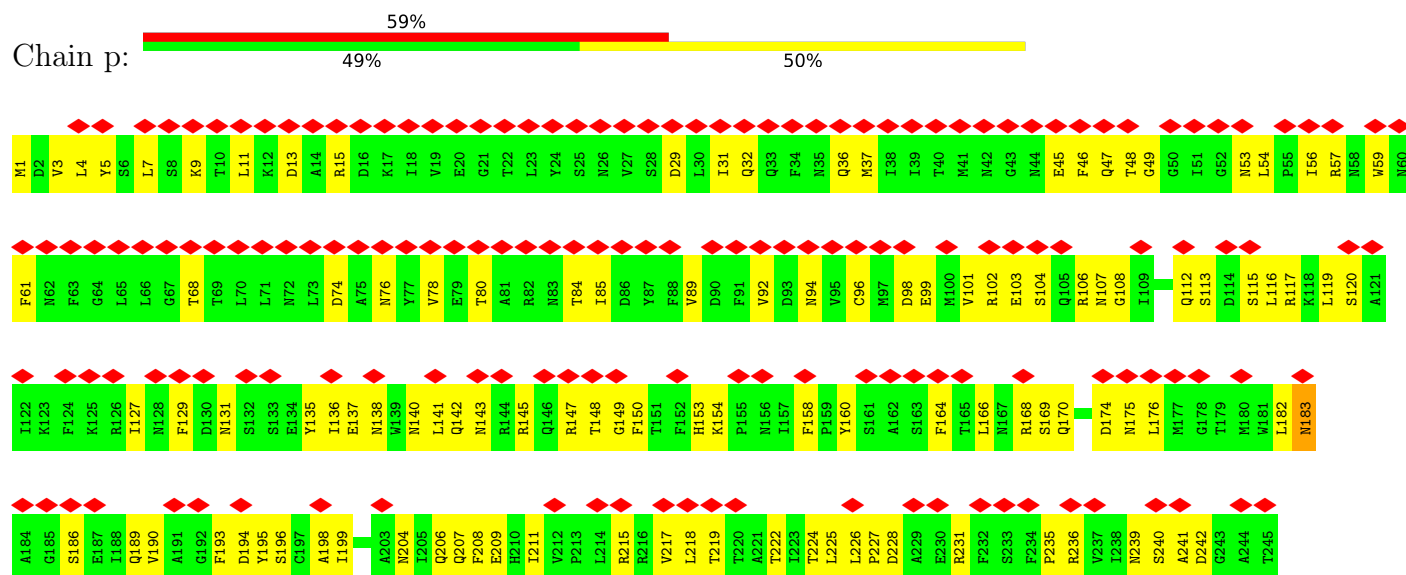
- Molecule 3: Intermediate capsid protein VP6

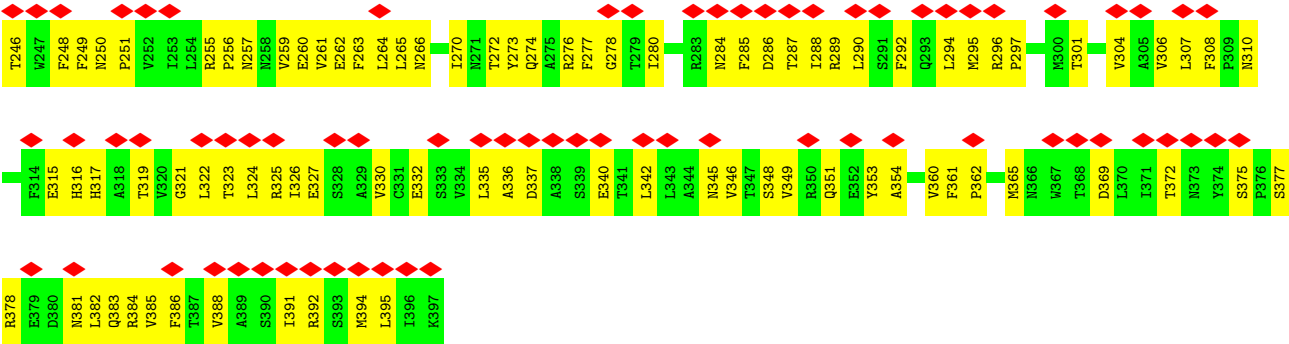


• Molecule 3: Intermediate capsid protein VP6



• Molecule 3: Intermediate capsid protein VP6





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	16740	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	90.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.006	Depositor
Minimum map value	-0.004	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.001	Depositor
Map size (Å)	315.2, 315.2, 315.2	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.97, 1.97, 1.97	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/5833	0.53	1/7925 (0.0%)
1	B	0.25	0/5981	0.52	2/8129 (0.0%)
1	C	0.28	0/5591	0.53	0/7594
2	D	0.31	0/2120	0.53	2/2893 (0.1%)
2	E	0.30	0/1967	0.55	0/2685
2	F	0.30	0/2162	0.55	1/2950 (0.0%)
2	G	0.31	0/2170	0.57	0/2961
2	H	0.31	0/1952	0.52	0/2664
2	I	0.31	0/2139	0.54	0/2918
2	J	0.29	0/2144	0.52	0/2925
2	K	0.30	0/2073	0.54	1/2827 (0.0%)
2	L	0.29	0/2144	0.52	0/2925
2	M	0.31	0/2162	0.55	1/2950 (0.0%)
2	N	0.24	0/2131	0.51	0/2907
2	O	0.28	0/2144	0.56	2/2925 (0.1%)
2	P	0.28	0/1952	0.52	0/2664
3	d	0.27	0/3234	0.53	2/4402 (0.0%)
3	e	0.26	0/3234	0.52	0/4402
3	f	0.28	0/3234	0.51	0/4402
3	g	0.28	0/3234	0.51	0/4402
3	h	0.28	0/3234	0.53	0/4402
3	i	0.30	0/3234	0.54	0/4402
3	j	0.28	0/3234	0.53	0/4402
3	k	0.26	0/3234	0.51	1/4402 (0.0%)
3	l	0.28	0/3234	0.55	0/4402
3	m	0.26	0/3234	0.56	0/4402
3	n	0.24	0/3234	0.48	0/4402
3	o	0.27	0/3234	0.51	0/4402
3	p	0.24	0/3234	0.50	0/4402
All	All	0.28	0/86707	0.53	13/118068 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
2	G	0	1
2	M	0	1
3	e	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	55	ILE	N-CA-C	-7.50	106.58	113.71
2	D	165	CYS	N-CA-C	6.59	116.94	108.24
3	d	254	LEU	CA-C-N	-6.46	112.15	121.20
3	d	254	LEU	C-N-CA	-6.46	112.15	121.20
2	O	165	CYS	N-CA-C	6.43	117.99	108.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	535	LYS	Peptide
2	G	325	ARG	Peptide
2	M	322	PHE	Peptide
3	e	108	GLY	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5715	0	5598	349	0
1	B	5860	0	5737	351	0
1	C	5478	0	5365	304	0
2	D	2077	0	2035	125	0
2	E	1928	0	1892	80	0
2	F	2118	0	2067	198	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	2126	0	2078	195	0
2	H	1913	0	1874	125	0
2	I	2096	0	2048	182	0
2	J	2101	0	2053	202	0
2	K	2031	0	1991	114	0
2	L	2101	0	2053	150	0
2	M	2118	0	2067	189	0
2	N	2088	0	2044	94	0
2	O	2101	0	2053	97	0
2	P	1913	0	1874	118	0
3	d	3163	0	3114	143	0
3	e	3163	0	3114	121	0
3	f	3163	0	3114	179	0
3	g	3163	0	3114	177	0
3	h	3163	0	3114	224	0
3	i	3163	0	3114	201	0
3	j	3163	0	3114	250	0
3	k	3163	0	3114	225	0
3	l	3163	0	3114	242	0
3	m	3163	0	3114	233	0
3	n	3163	0	3114	190	0
3	o	3163	0	3114	228	0
3	p	3163	0	3114	196	0
All	All	84883	0	83311	4618	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 27.

The worst 5 of 4618 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)
3:m:304:VAL:HG21	3:o:246:THR:CG2	1.40	1.52
3:m:304:VAL:CG2	3:o:246:THR:HG23	1.42	1.48
3:m:29:ASP:CG	3:o:26:ASN:HD22	1.28	1.39
2:K:63:MET:HE3	3:k:162:ALA:O	1.19	1.35
3:n:245:THR:OG1	3:o:301:THR:CG2	1.75	1.32

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	718/776 (92%)	648 (90%)	70 (10%)	0	100	100
1	B	738/776 (95%)	667 (90%)	71 (10%)	0	100	100
1	C	680/776 (88%)	598 (88%)	82 (12%)	0	100	100
2	D	258/326 (79%)	229 (89%)	29 (11%)	0	100	100
2	E	240/326 (74%)	216 (90%)	23 (10%)	1 (0%)	30	67
2	F	263/326 (81%)	241 (92%)	22 (8%)	0	100	100
2	G	264/326 (81%)	235 (89%)	29 (11%)	0	100	100
2	H	238/326 (73%)	219 (92%)	19 (8%)	0	100	100
2	I	260/326 (80%)	233 (90%)	27 (10%)	0	100	100
2	J	261/326 (80%)	230 (88%)	31 (12%)	0	100	100
2	K	252/326 (77%)	231 (92%)	21 (8%)	0	100	100
2	L	261/326 (80%)	237 (91%)	24 (9%)	0	100	100
2	M	263/326 (81%)	237 (90%)	26 (10%)	0	100	100
2	N	259/326 (79%)	234 (90%)	25 (10%)	0	100	100
2	O	261/326 (80%)	236 (90%)	24 (9%)	1 (0%)	30	67
2	P	238/326 (73%)	224 (94%)	14 (6%)	0	100	100
3	d	395/397 (100%)	369 (93%)	26 (7%)	0	100	100
3	e	395/397 (100%)	366 (93%)	29 (7%)	0	100	100
3	f	395/397 (100%)	369 (93%)	26 (7%)	0	100	100
3	g	395/397 (100%)	370 (94%)	25 (6%)	0	100	100
3	h	395/397 (100%)	359 (91%)	36 (9%)	0	100	100
3	i	395/397 (100%)	364 (92%)	31 (8%)	0	100	100
3	j	395/397 (100%)	370 (94%)	25 (6%)	0	100	100
3	k	395/397 (100%)	361 (91%)	34 (9%)	0	100	100
3	l	395/397 (100%)	358 (91%)	37 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	m	395/397 (100%)	365 (92%)	30 (8%)	0	100	100
3	n	395/397 (100%)	373 (94%)	22 (6%)	0	100	100
3	o	395/397 (100%)	366 (93%)	29 (7%)	0	100	100
3	p	395/397 (100%)	365 (92%)	30 (8%)	0	100	100
All	All	10589/11727 (90%)	9670 (91%)	917 (9%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	O	136	ASP
2	E	136	ASP

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	A	642/689 (93%)	640 (100%)	2 (0%)	86	84
1	B	659/689 (96%)	659 (100%)	0	100	100
1	C	615/689 (89%)	613 (100%)	2 (0%)	86	84
2	D	235/296 (79%)	234 (100%)	1 (0%)	84	82
2	E	221/296 (75%)	221 (100%)	0	100	100
2	F	239/296 (81%)	238 (100%)	1 (0%)	84	82
2	G	240/296 (81%)	235 (98%)	5 (2%)	47	65
2	H	219/296 (74%)	219 (100%)	0	100	100
2	I	238/296 (80%)	236 (99%)	2 (1%)	73	77
2	J	238/296 (80%)	238 (100%)	0	100	100
2	K	231/296 (78%)	230 (100%)	1 (0%)	84	82
2	L	238/296 (80%)	237 (100%)	1 (0%)	84	82
2	M	239/296 (81%)	238 (100%)	1 (0%)	84	82
2	N	237/296 (80%)	237 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	O	238/296 (80%)	237 (100%)	1 (0%)	84	82
2	P	219/296 (74%)	218 (100%)	1 (0%)	81	81
3	d	351/351 (100%)	350 (100%)	1 (0%)	86	84
3	e	351/351 (100%)	351 (100%)	0	100	100
3	f	351/351 (100%)	351 (100%)	0	100	100
3	g	351/351 (100%)	351 (100%)	0	100	100
3	h	351/351 (100%)	349 (99%)	2 (1%)	78	80
3	i	351/351 (100%)	351 (100%)	0	100	100
3	j	351/351 (100%)	351 (100%)	0	100	100
3	k	351/351 (100%)	351 (100%)	0	100	100
3	l	351/351 (100%)	349 (99%)	2 (1%)	78	80
3	m	351/351 (100%)	350 (100%)	1 (0%)	86	84
3	n	351/351 (100%)	351 (100%)	0	100	100
3	o	351/351 (100%)	351 (100%)	0	100	100
3	p	351/351 (100%)	350 (100%)	1 (0%)	86	84
All	All	9511/10478 (91%)	9486 (100%)	25 (0%)	84	84

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	249	CYS
2	P	165	CYS
3	p	183	ASN
2	O	82	CYS
3	d	301	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 270 such sidechains are listed below:

Mol	Chain	Res	Type
3	n	42	ASN
3	o	33	GLN
3	p	175	ASN
2	M	123	ASN
2	L	201	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

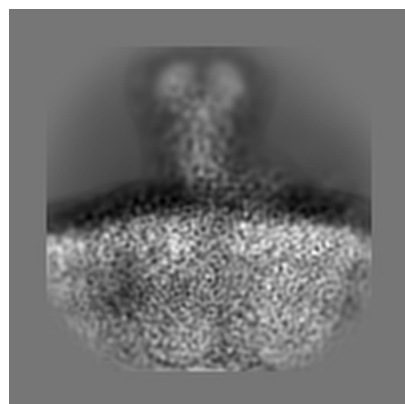
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16774. These allow visual inspection of the internal detail of the map and identification of artifacts.

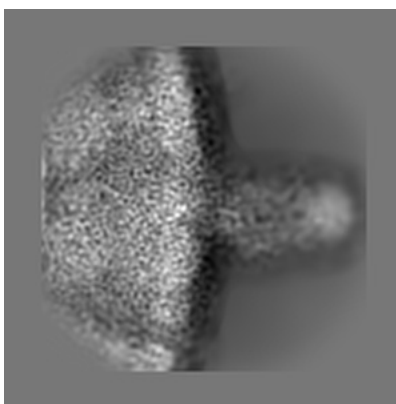
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

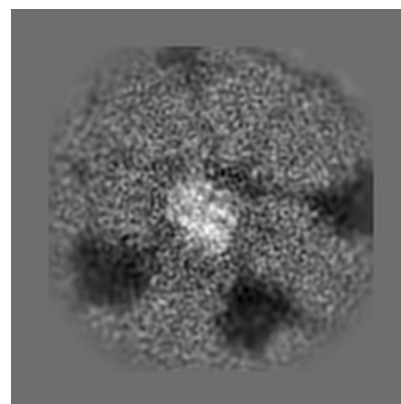
6.1.1 Primary map



X

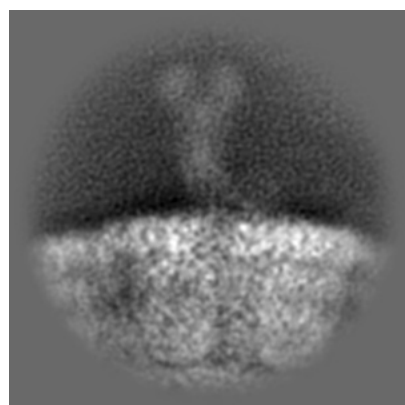


Y

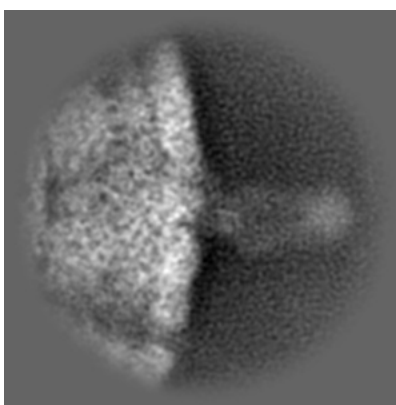


Z

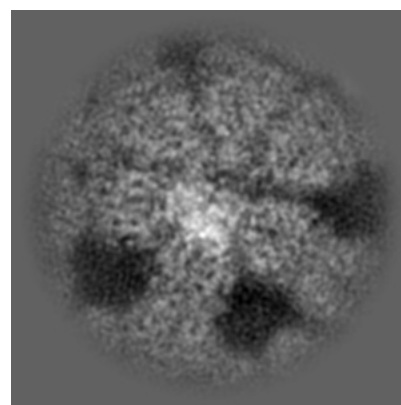
6.1.2 Raw map



X



Y



Z

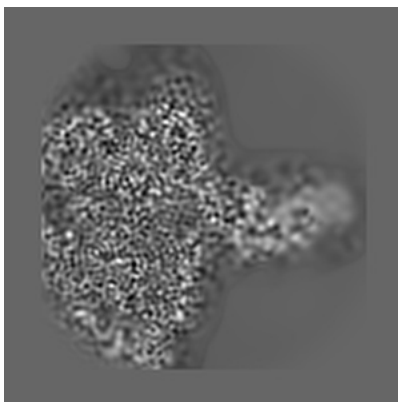
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

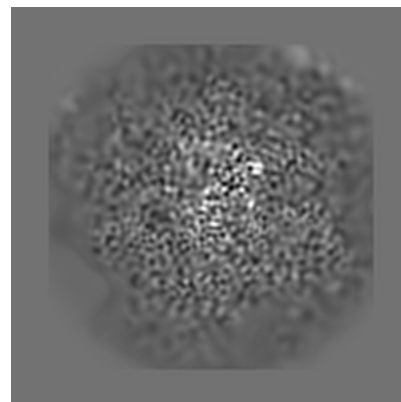
6.2.1 Primary map



X Index: 80

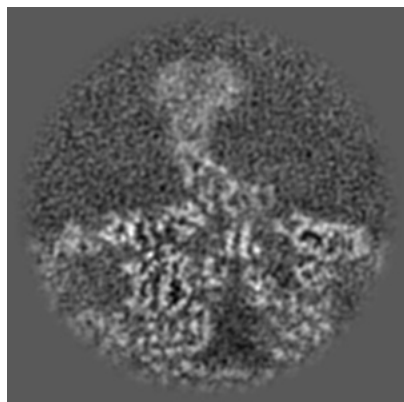


Y Index: 80

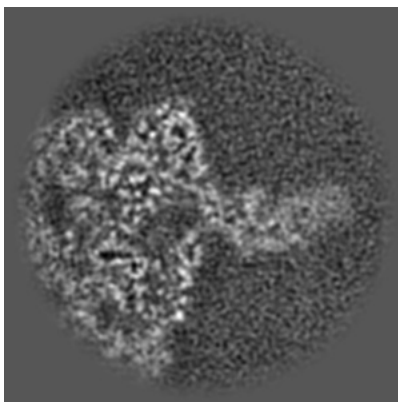


Z Index: 80

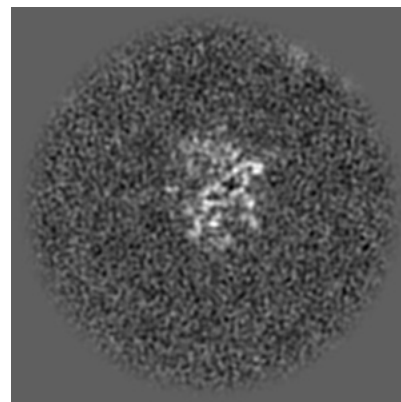
6.2.2 Raw map



X Index: 80



Y Index: 80



Z Index: 80

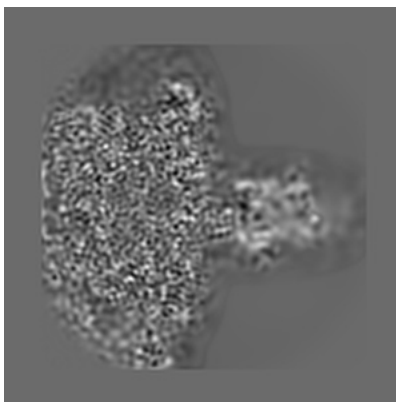
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

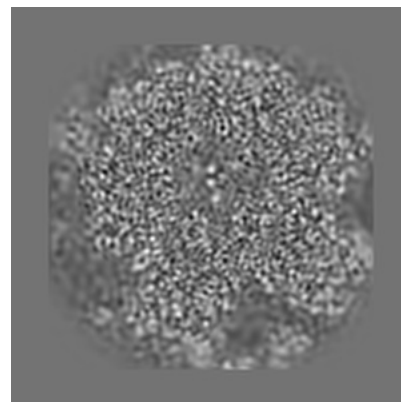
6.3.1 Primary map



X Index: 80

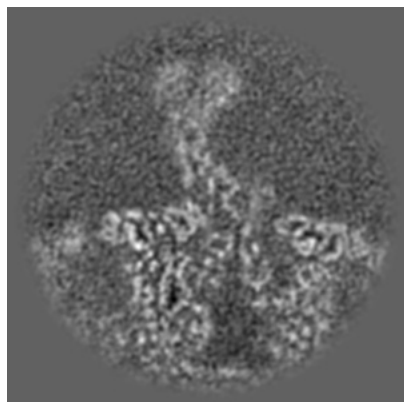


Y Index: 75

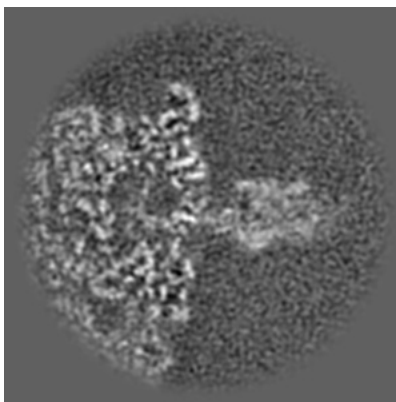


Z Index: 68

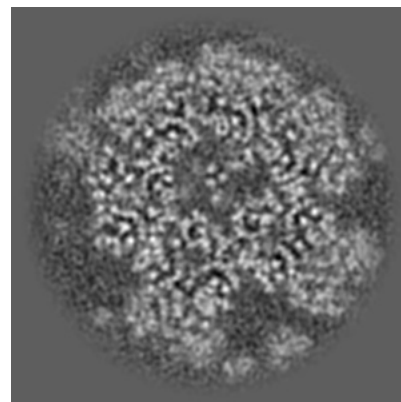
6.3.2 Raw map



X Index: 81



Y Index: 75

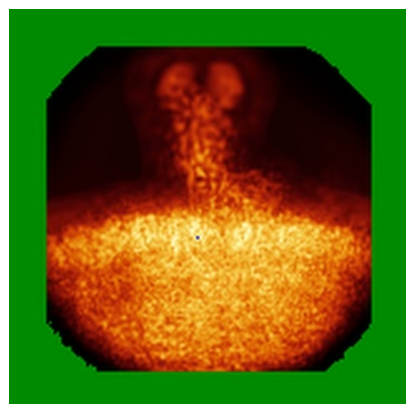


Z Index: 68

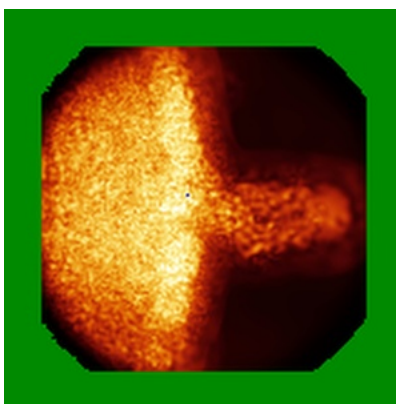
The images above show the largest variance slices of the map in three orthogonal directions.

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

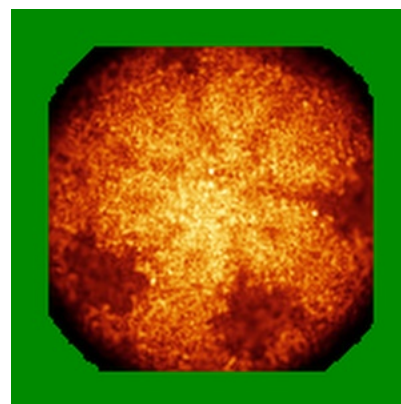
6.4.1 Primary map



X

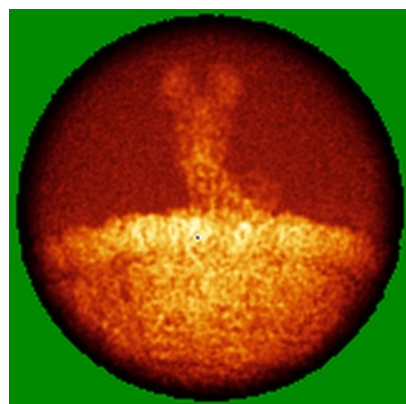


Y

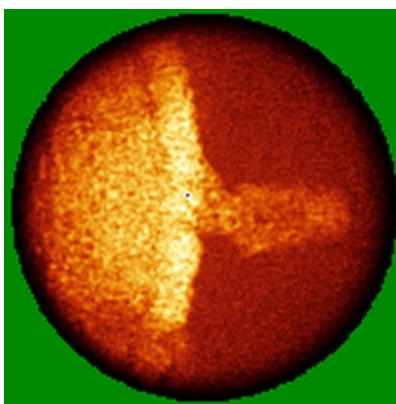


Z

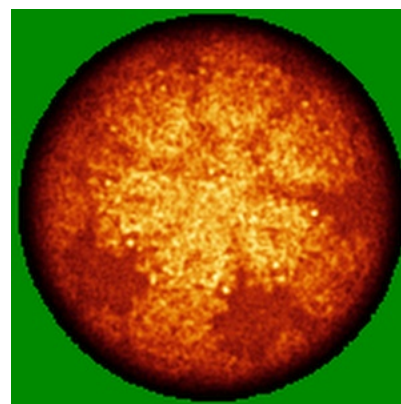
6.4.2 Raw map



X



Y

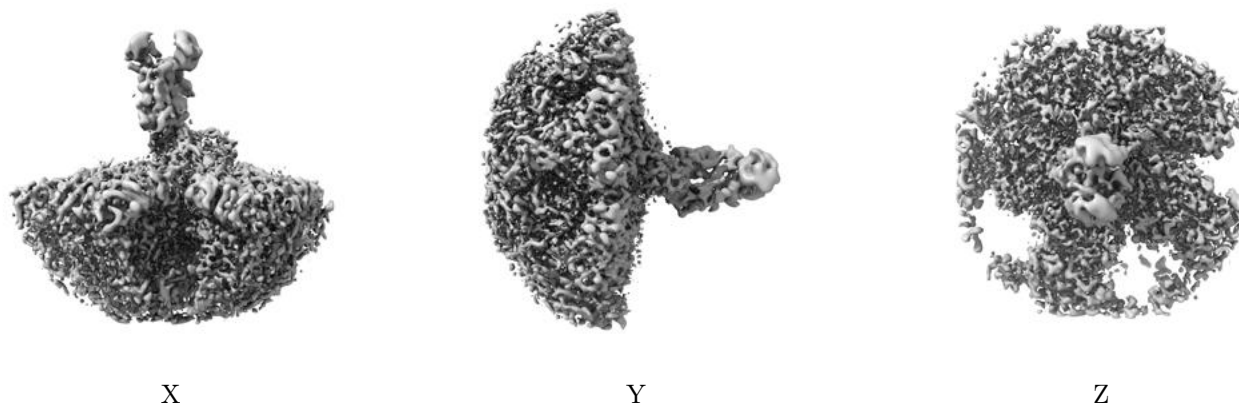


Z

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

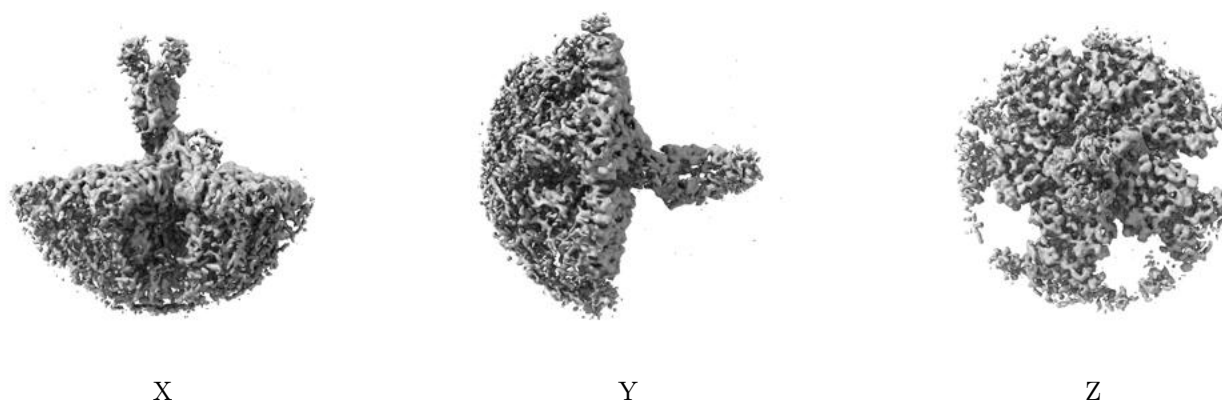
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.001. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

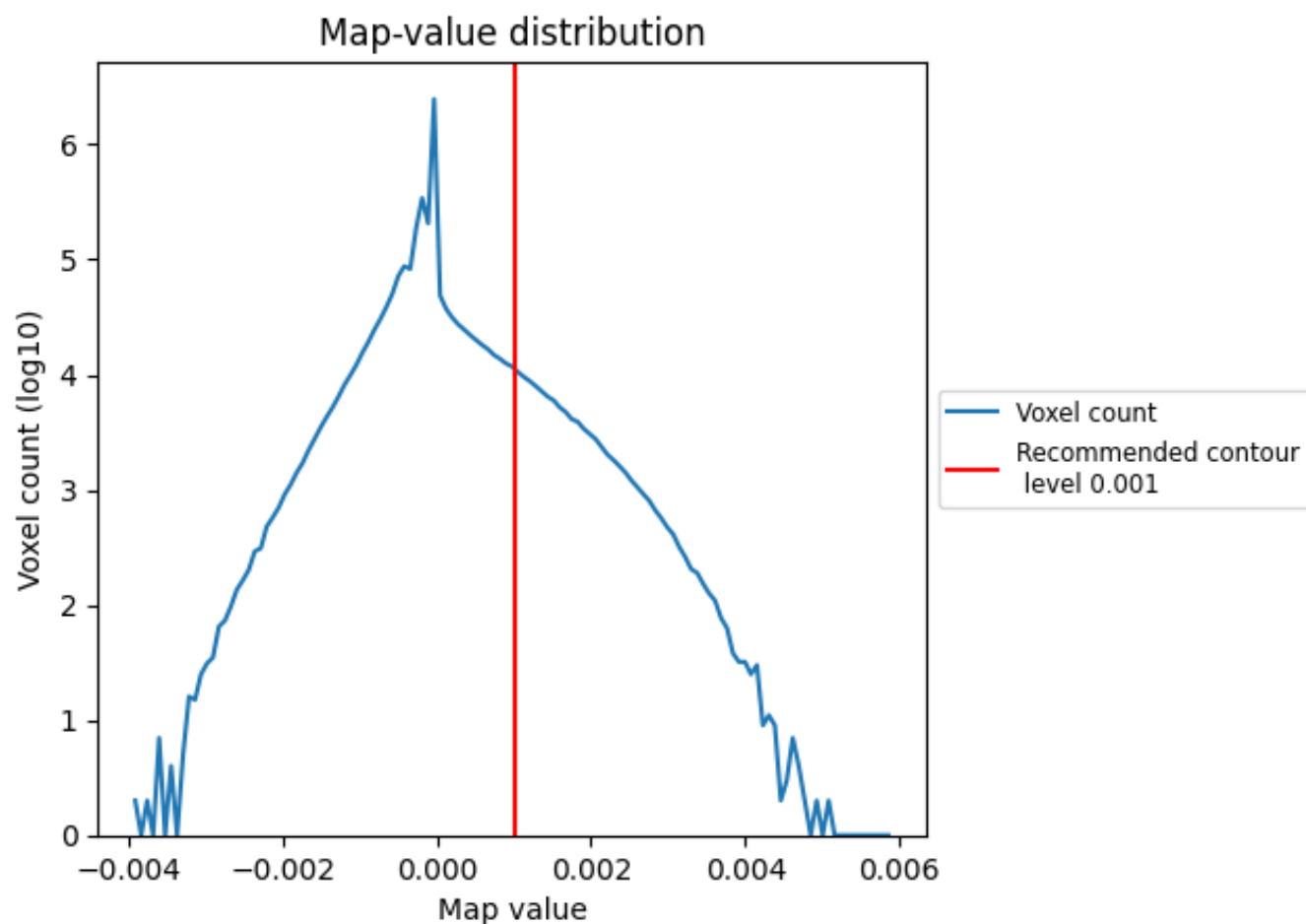
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

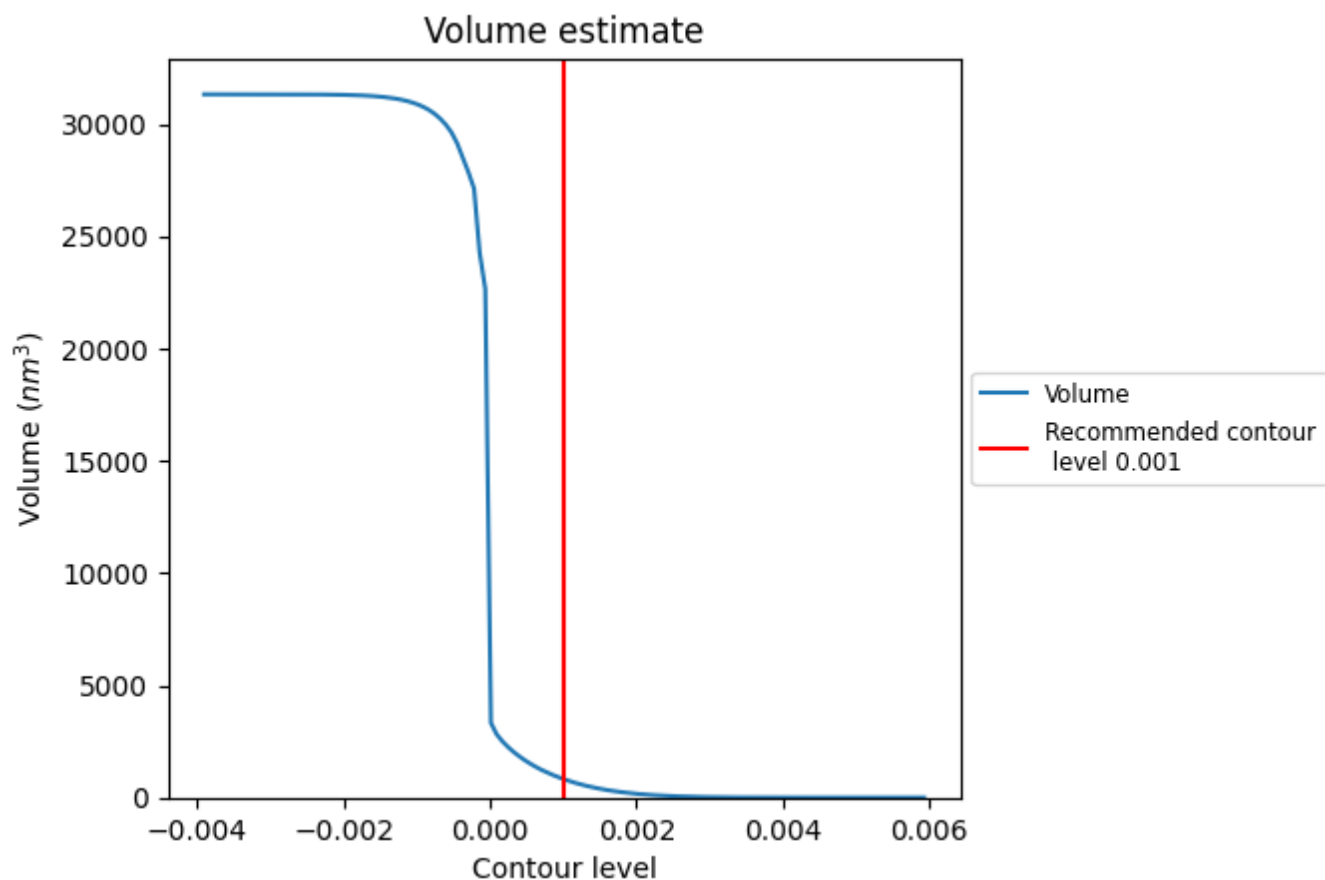
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

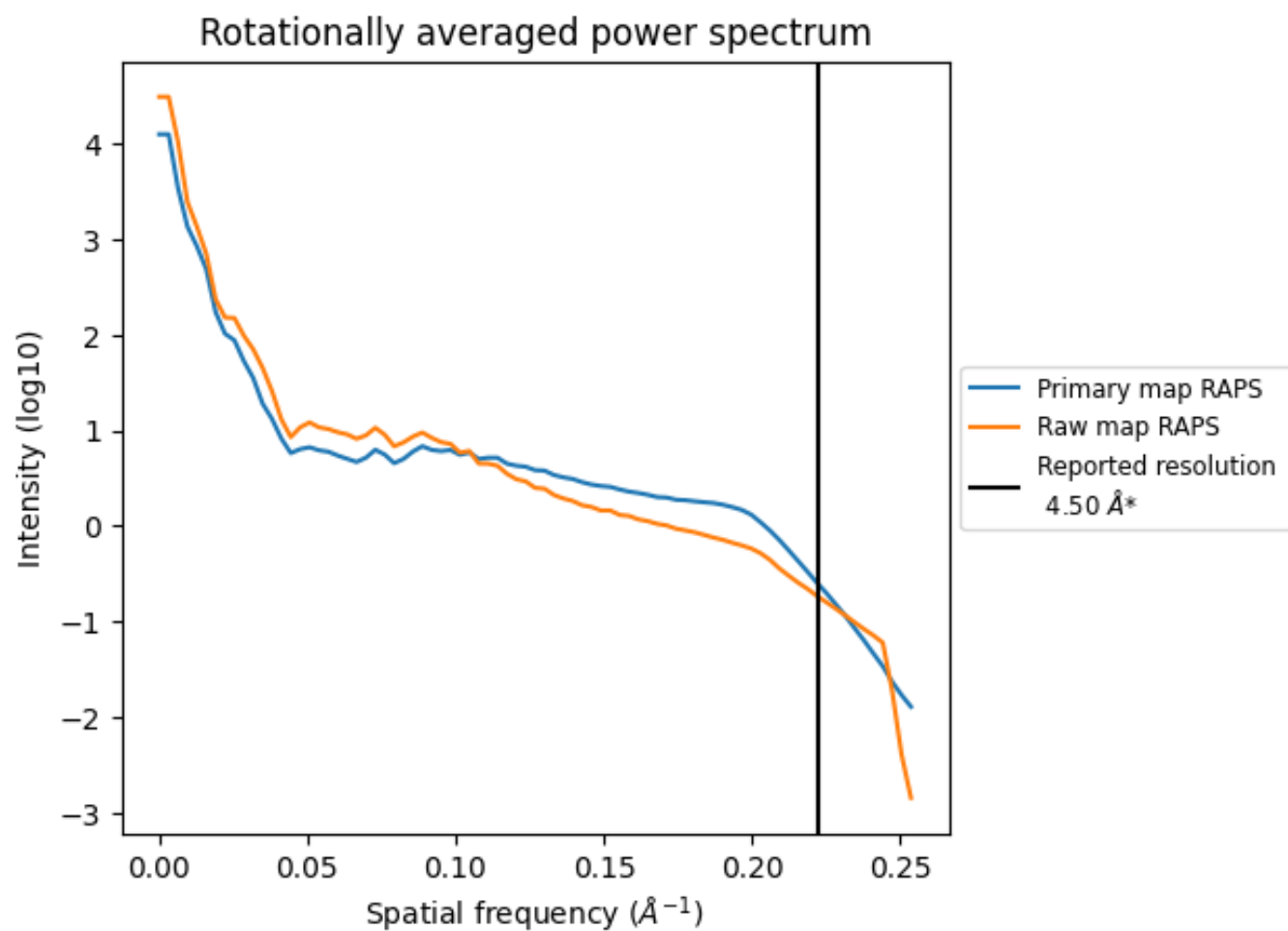
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 829 nm³; this corresponds to an approximate mass of 748 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)

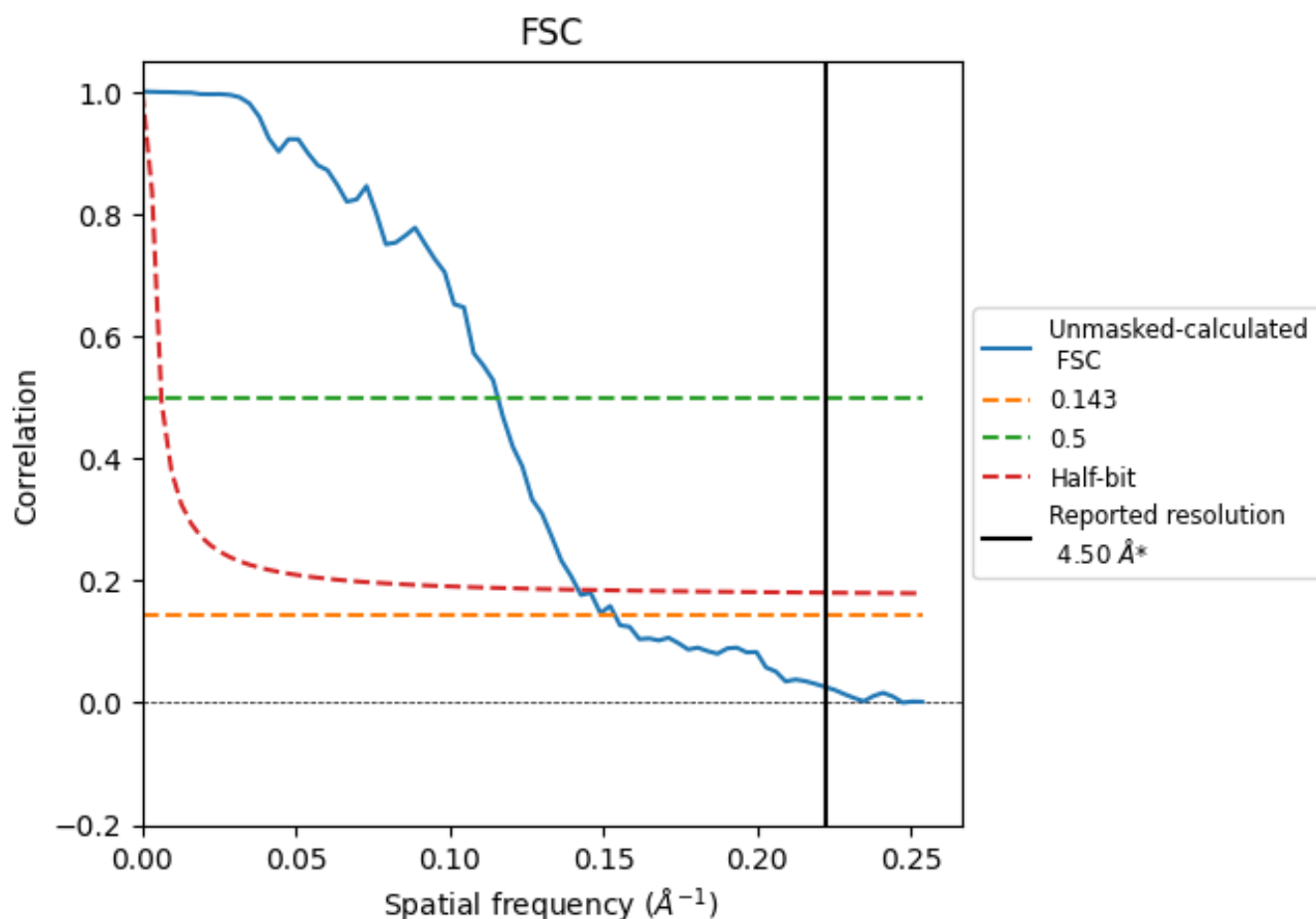


*Reported resolution corresponds to spatial frequency of 0.222 $\text{\AA}^{-1}$

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

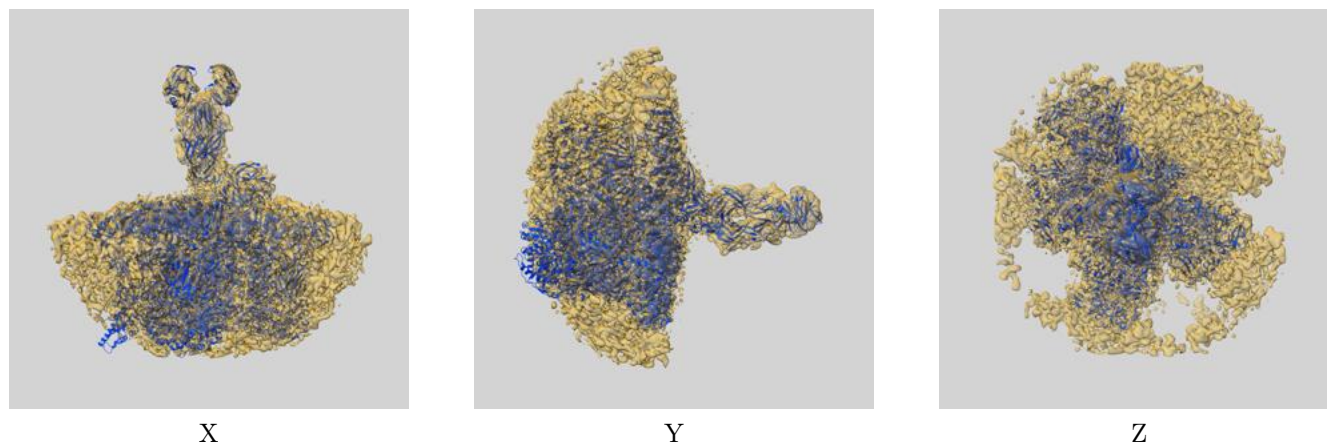
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.50	8.64	7.05

*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 6.50 differs from the reported value 4.5 by more than 10 %

9 Map-model fit [i](#)

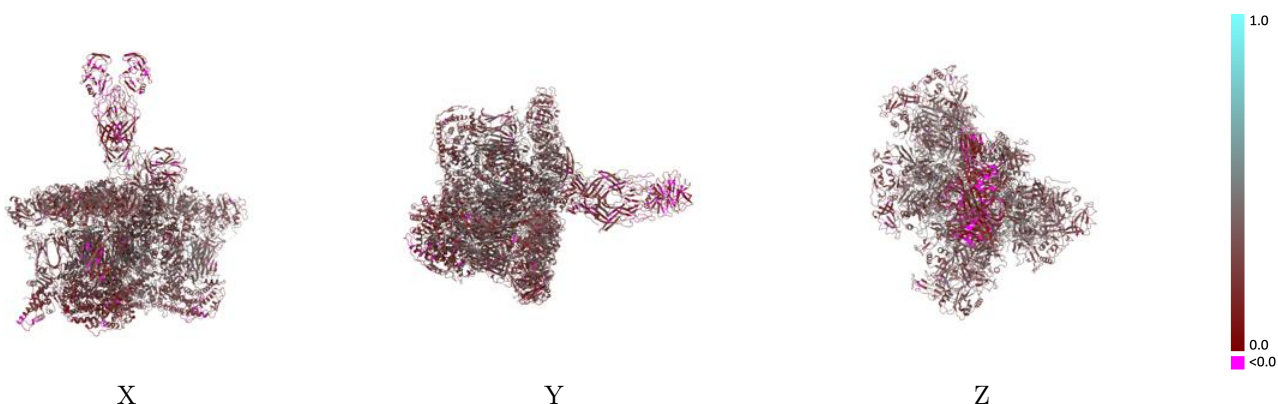
This section contains information regarding the fit between EMDB map EMD-16774 and PDB model 8COA. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



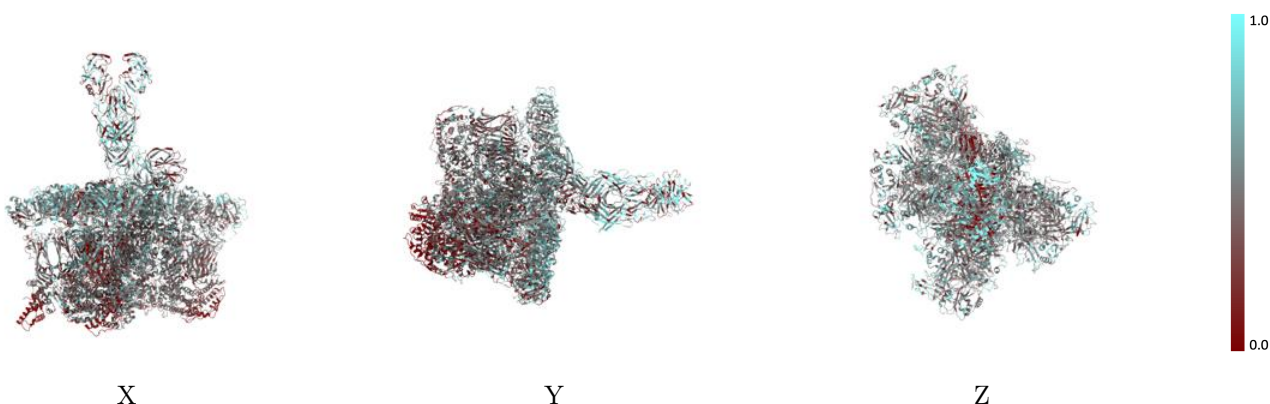
The images above show the 3D surface view of the map at the recommended contour level 0.001 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



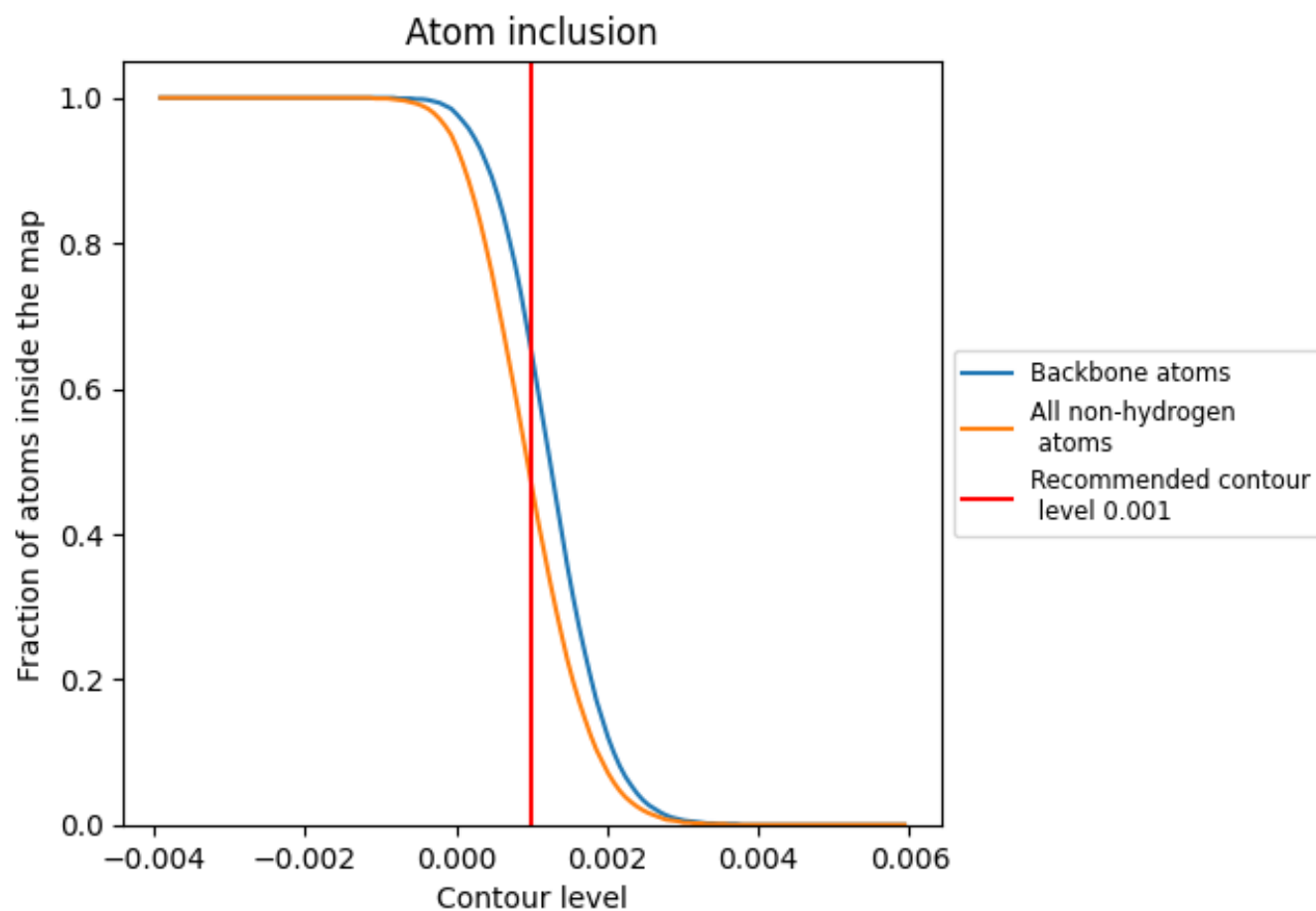
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.001).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 47% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.001) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4670	 0.2960
A	 0.5100	 0.2320
B	 0.5300	 0.2370
C	 0.4830	 0.2830
D	 0.5230	 0.3060
E	 0.5330	 0.2820
F	 0.5050	 0.3330
G	 0.5230	 0.3570
H	 0.5440	 0.3120
I	 0.5360	 0.3480
J	 0.5380	 0.3550
K	 0.4830	 0.2410
L	 0.5370	 0.3430
M	 0.5570	 0.3370
N	 0.4270	 0.2530
O	 0.4900	 0.3020
P	 0.5330	 0.3000
d	 0.4150	 0.2950
e	 0.4000	 0.2500
f	 0.4780	 0.3500
g	 0.4970	 0.3450
h	 0.3980	 0.2450
i	 0.4810	 0.3400
j	 0.4390	 0.3190
k	 0.4050	 0.3190
l	 0.4690	 0.3380
m	 0.3680	 0.2760
n	 0.3040	 0.2860
o	 0.4080	 0.3210
p	 0.3510	 0.2590

