



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 11:25 PM UTC

PDB ID : 9H2A / pdb_00009h2a
EMDB ID : EMD-51791
Title : AcMNPV complete basal cap
Authors : Effantin, G.; Kandiah, E.; Pelosse, M.
Deposited on : 2024-10-11
Resolution : 5.20 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

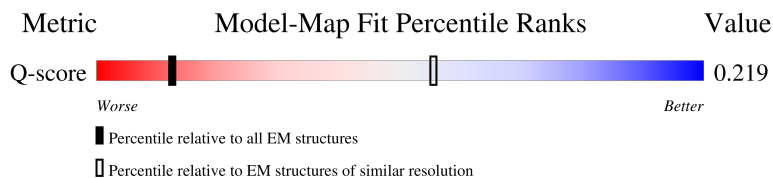
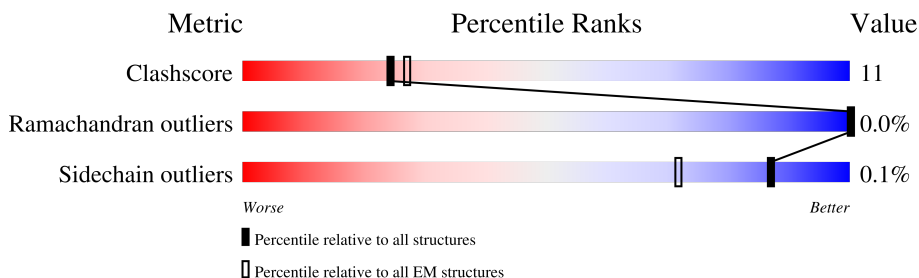
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.20 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.



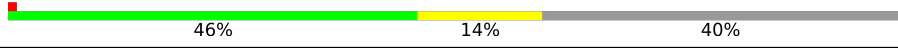
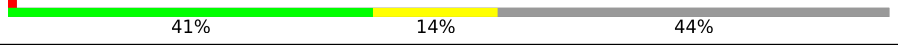
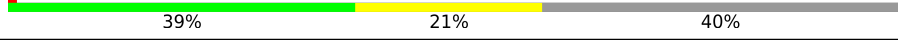
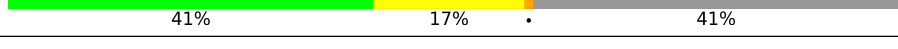
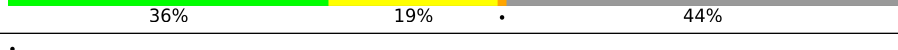
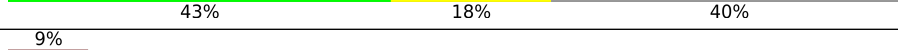
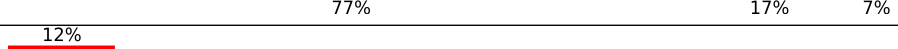
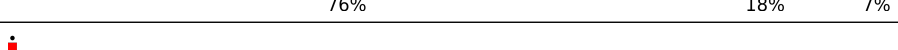
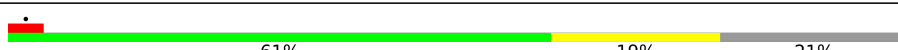
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	712 (4.70 - 5.70)

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	290	
1	B	290	
1	O	290	
1	P	290	

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Mol	Chain	Length	Quality of chain
1	Q	290	
1	R	290	
2	C	361	
2	D	361	
2	S	361	
2	T	361	
2	U	361	
2	V	361	
3	E	320	
3	W	320	
4	F	477	
4	X	477	
5	G	347	
5	H	347	
5	M	347	
5	N	347	
5	Y	347	
5	Z	347	
5	e	347	
5	f	347	
6	I	691	
6	J	691	
6	K	691	
6	a	691	
6	b	691	

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Mol	Chain	Length	Quality of chain
6	c	691	22% 75%
7	L	390	74% 17% 9%
7	d	390	77% 13% 9%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 66715 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 Occlusion-derived virus envelope protein E27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	246	Total	C	N	O	S	0	0
			1991	1276	324	382	9		
1	B	203	Total	C	N	O	S	0	0
			1649	1068	263	310	8		
1	O	246	Total	C	N	O	S	0	0
			1991	1276	324	382	9		
1	P	254	Total	C	N	O	S	0	0
			2056	1320	331	396	9		
1	Q	203	Total	C	N	O	S	0	0
			1649	1068	263	310	8		
1	R	192	Total	C	N	O	S	0	0
			1560	1009	244	299	8		

- Molecule 2 is a protein called Protein C42.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	216	Total	C	N	O	S	0	0
			1790	1135	305	334	16		
2	D	201	Total	C	N	O	S	0	0
			1677	1065	286	312	14		
2	S	216	Total	C	N	O	S	0	0
			1790	1135	305	334	16		
2	T	212	Total	C	N	O	S	0	0
			1764	1121	301	326	16		
2	U	201	Total	C	N	O	S	0	0
			1677	1065	286	312	14		
2	V	218	Total	C	N	O	S	0	0
			1811	1148	311	337	15		

- Molecule 3 is a protein called Uncharacterized 38.0 kDa protein in P143-LEF5 intergenic region.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	299	Total	C	N	O	S	0	0
			2526	1648	413	451	14		
3	W	299	Total	C	N	O	S	0	0
			2526	1648	413	451	14		

- Molecule 4 is a protein called Protein AC142.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	461	Total	C	N	O	S	0	0
			3792	2468	619	682	23		
4	X	461	Total	C	N	O	S	0	0
			3792	2468	619	682	23		

- Molecule 5 is a protein called Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	275	Total	C	N	O	S	0	0
			2213	1397	388	413	15		
5	H	283	Total	C	N	O	S	0	0
			2274	1434	398	427	15		
5	M	248	Total	C	N	O	S	0	0
			2008	1280	337	379	12		
5	N	275	Total	C	N	O	S	0	0
			2226	1413	384	417	12		
5	Y	275	Total	C	N	O	S	0	0
			2213	1397	388	413	15		
5	Z	283	Total	C	N	O	S	0	0
			2274	1434	398	427	15		
5	e	248	Total	C	N	O	S	0	0
			2008	1280	337	379	12		
5	f	275	Total	C	N	O	S	0	0
			2226	1413	384	417	12		

- Molecule 6 is a protein called Capsid-associated protein VP80.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	215	Total	C	N	O	S	0	0
			1802	1168	301	319	14		
6	J	176	Total	C	N	O	S	0	0
			1462	947	242	261	12		
6	K	176	Total	C	N	O	S	0	0
			1468	956	243	257	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	215	Total	C	N	O	S	0	0
			1802	1168	301	319	14		
6	b	176	Total	C	N	O	S	0	0
			1462	947	242	261	12		
6	c	176	Total	C	N	O	S	0	0
			1468	956	243	257	12		

- Molecule 7 is a protein called Protein AC109.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	353	Total	C	N	O	S	0	0
			2880	1861	480	523	16		
7	d	353	Total	C	N	O	S	0	0
			2880	1861	480	523	16		

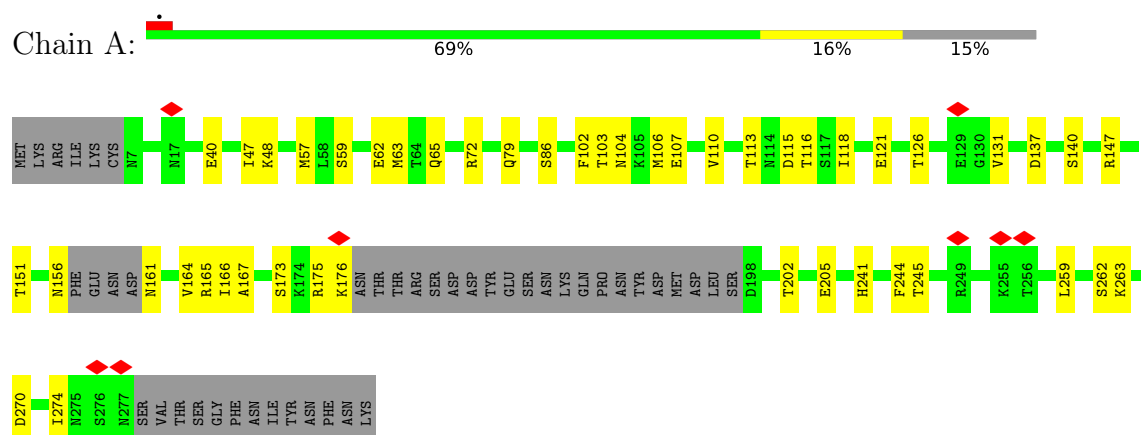
- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
8	G	1	Total	Zn	0
			1	1	
8	H	1	Total	Zn	0
			1	1	
8	M	1	Total	Zn	0
			1	1	
8	N	1	Total	Zn	0
			1	1	
8	Y	1	Total	Zn	0
			1	1	
8	Z	1	Total	Zn	0
			1	1	
8	e	1	Total	Zn	0
			1	1	
8	f	1	Total	Zn	0
			1	1	

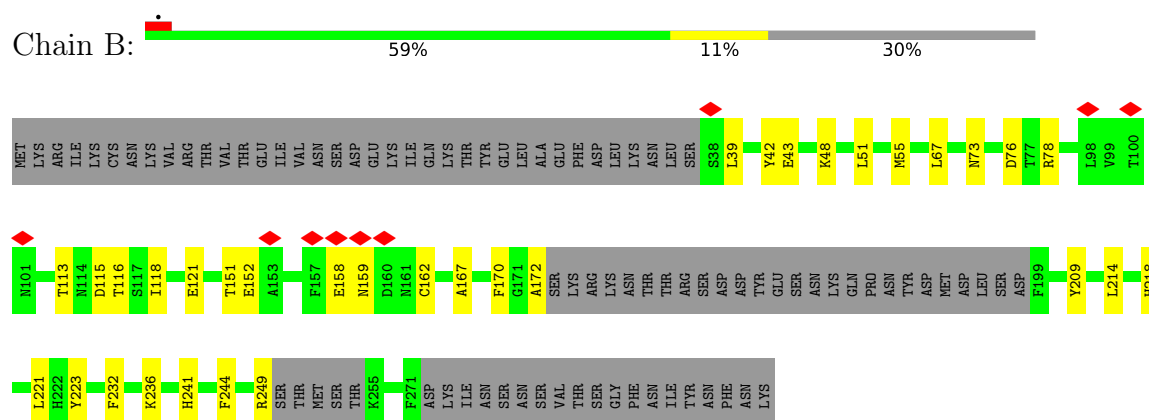
3 Residue-property plots

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.

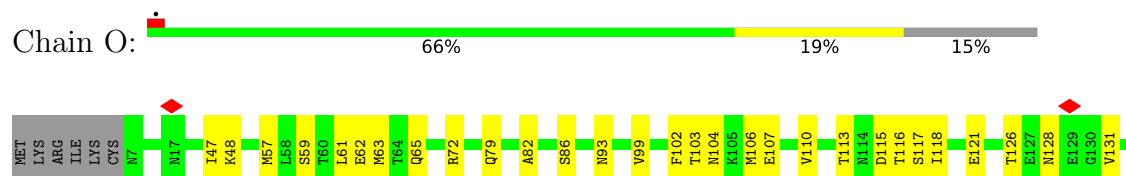
• Molecule 1: Occlusion-derived virus envelope protein E27

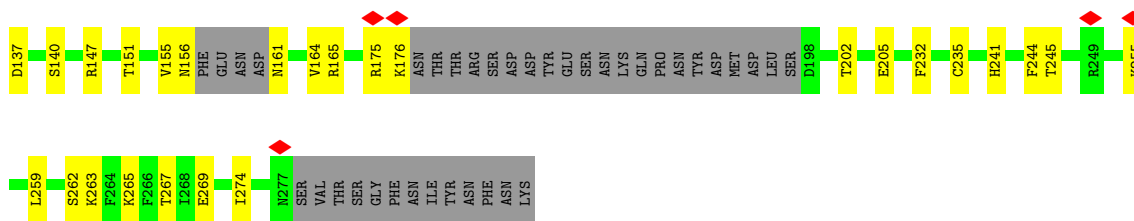


• Molecule 1: Occlusion-derived virus envelope protein E27

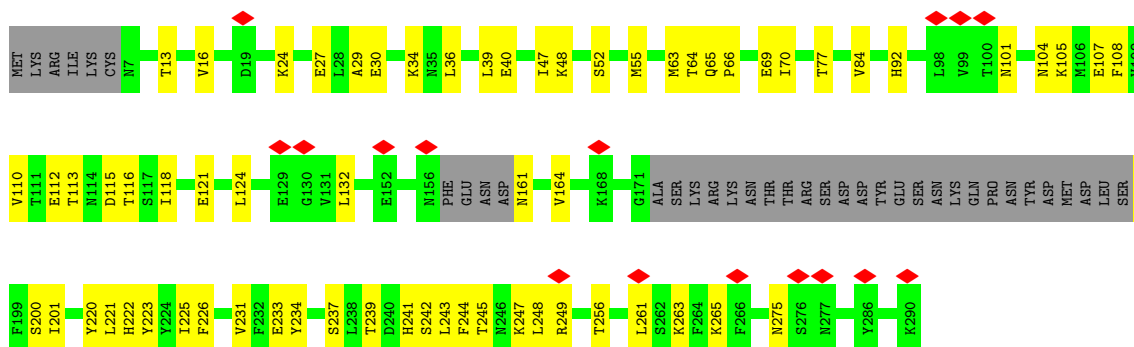


• Molecule 1: Occlusion-derived virus envelope protein E27

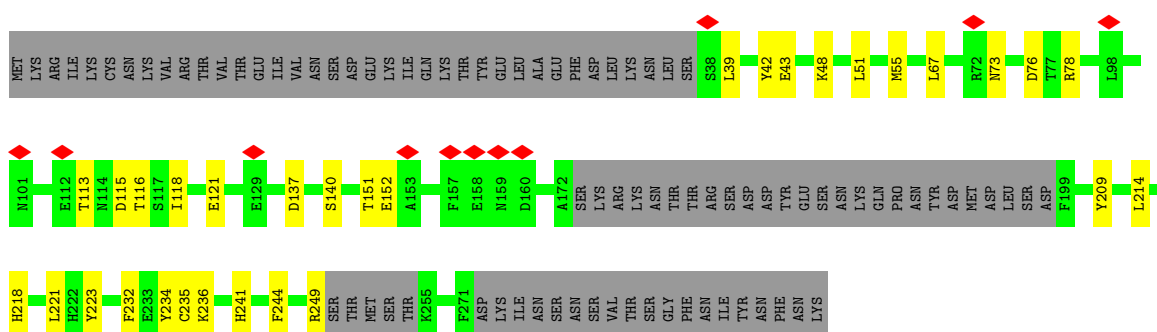




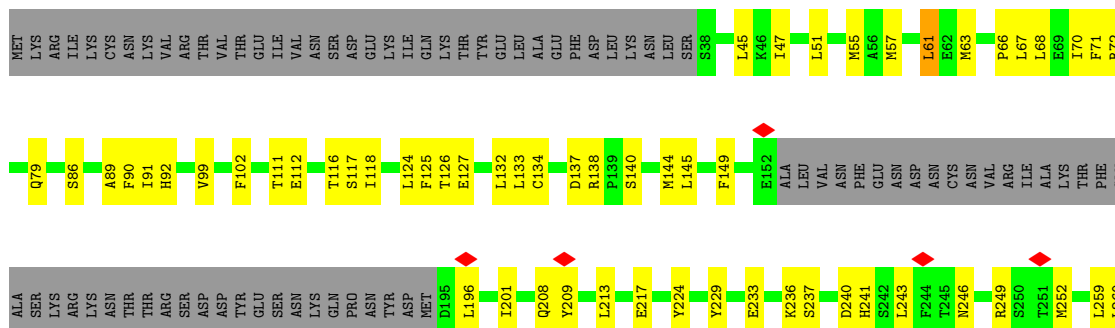
• Molecule 1: Occlusion-derived virus envelope protein E27

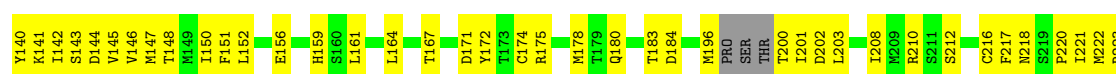


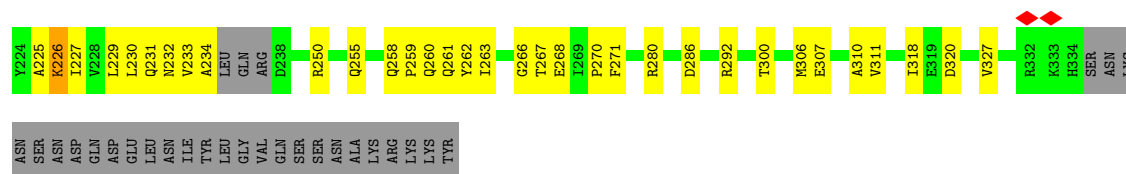
• Molecule 1: Occlusion-derived virus envelope protein E27



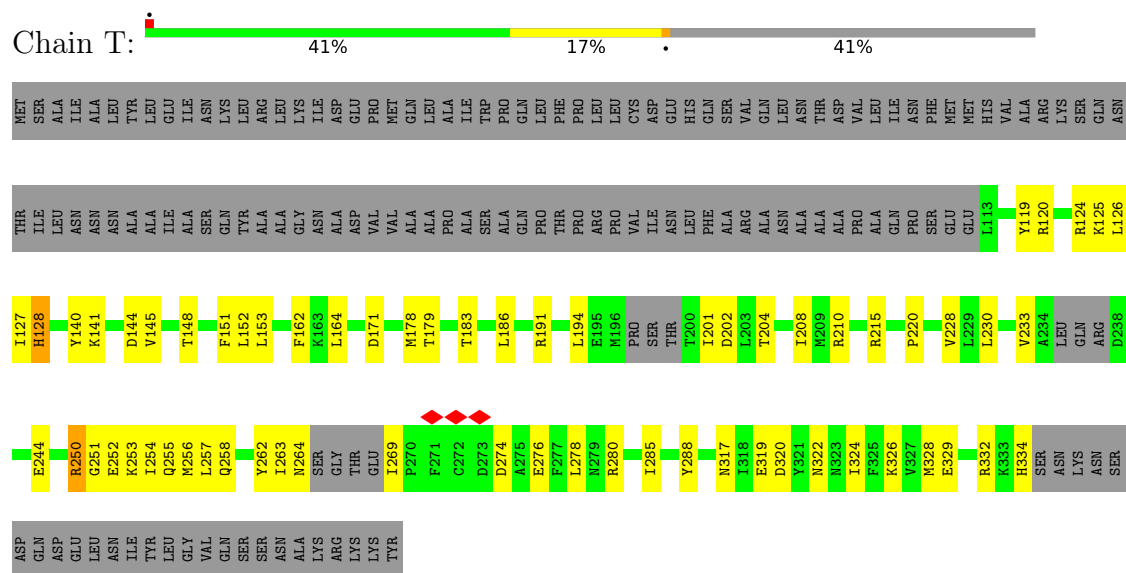
• Molecule 1: Occlusion-derived virus envelope protein E27



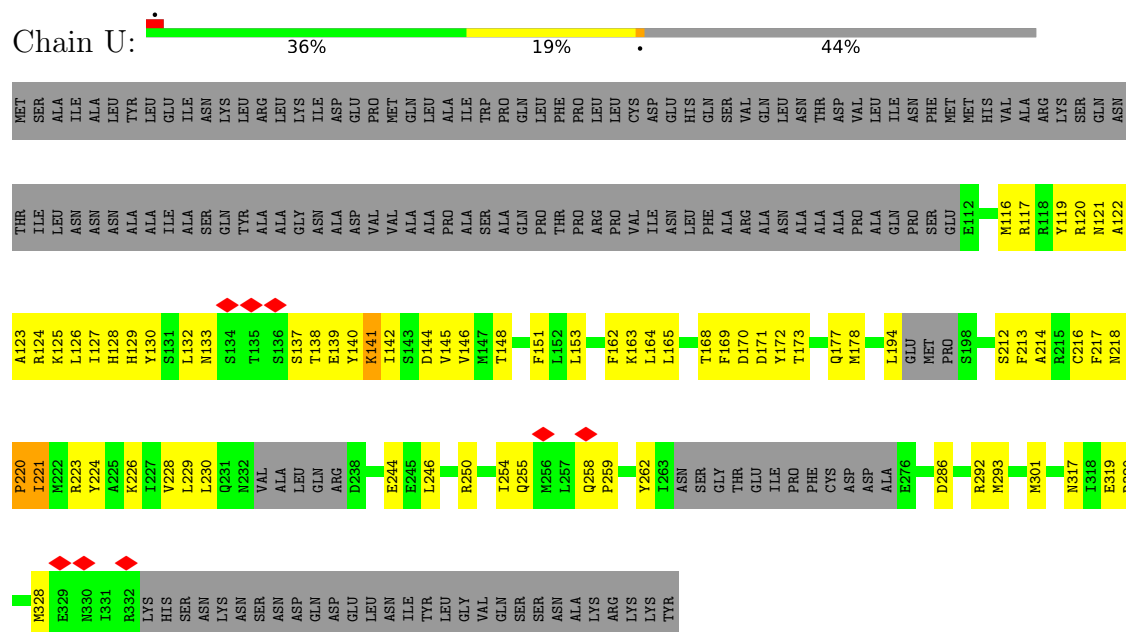




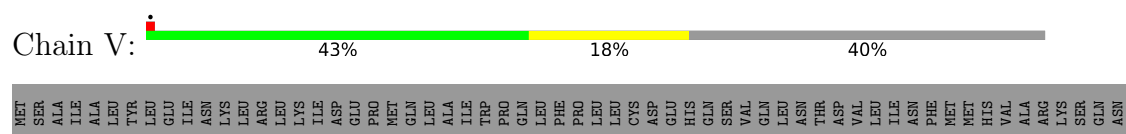
• Molecule 2: Protein C42

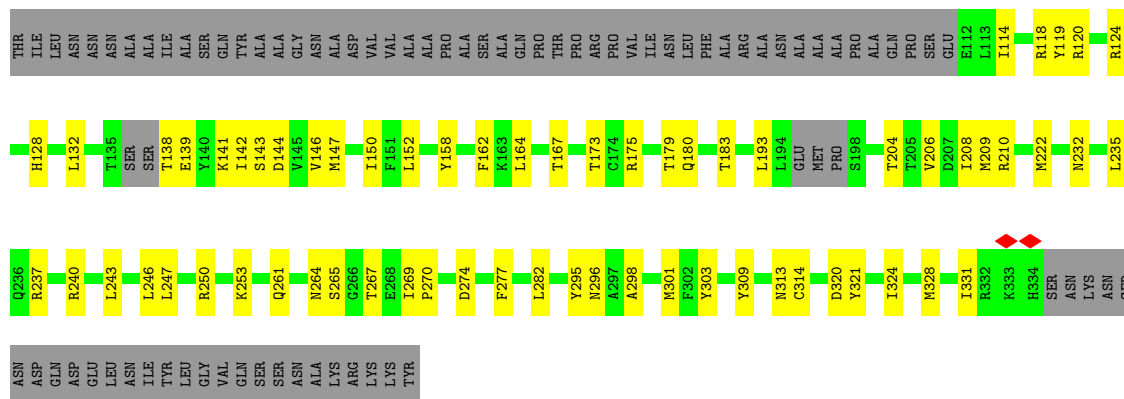


• Molecule 2: Protein C42

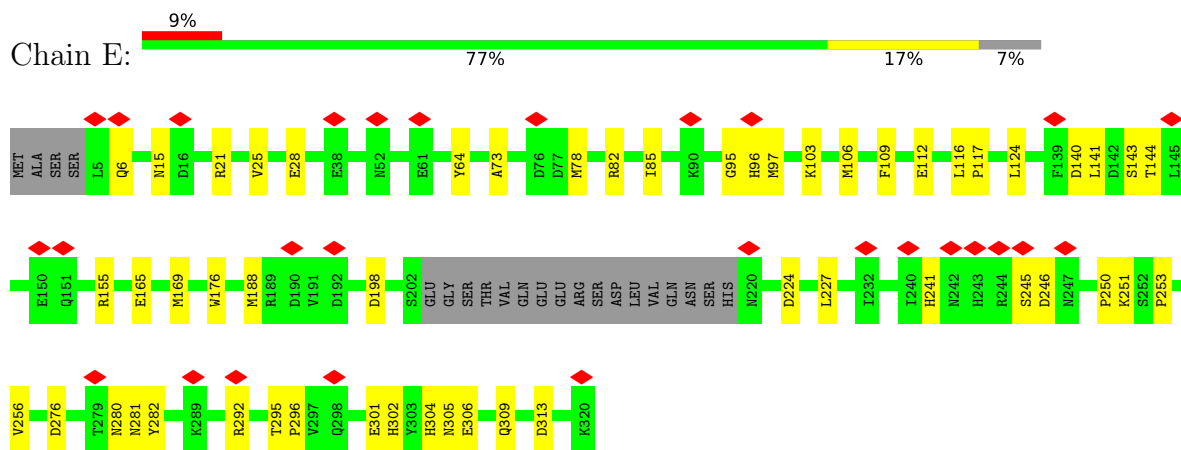


• Molecule 2: Protein C42

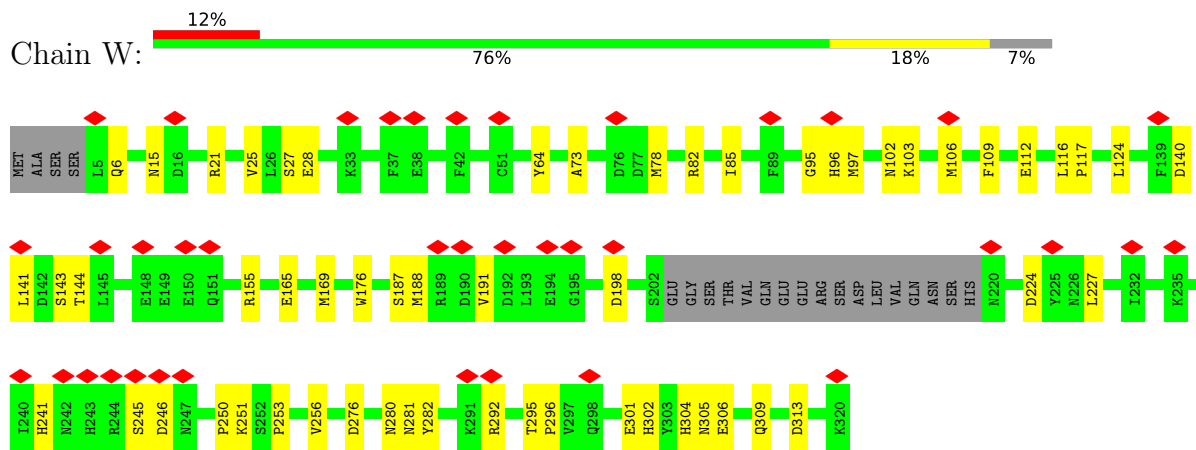




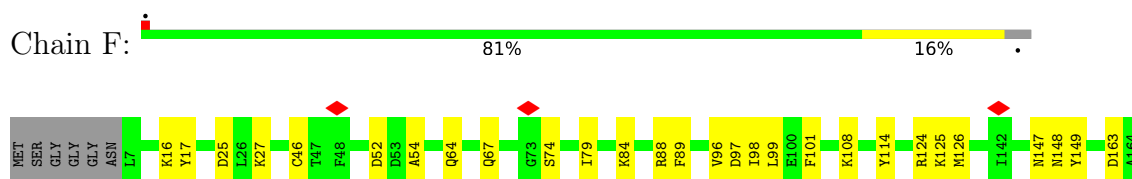
- Molecule 3: Uncharacterized 38.0 kDa protein in P143-LEF5 intergenic region

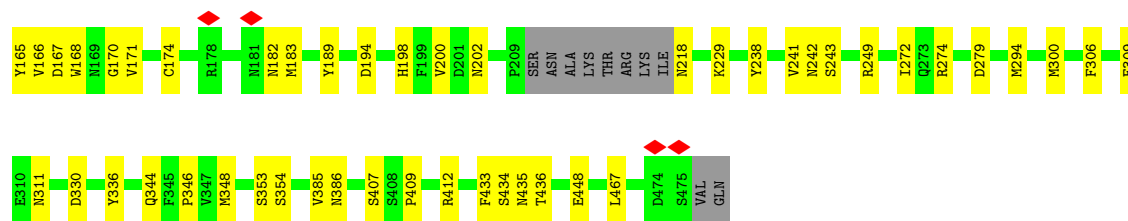


- Molecule 3: Uncharacterized 38.0 kDa protein in P143-LEF5 intergenic region



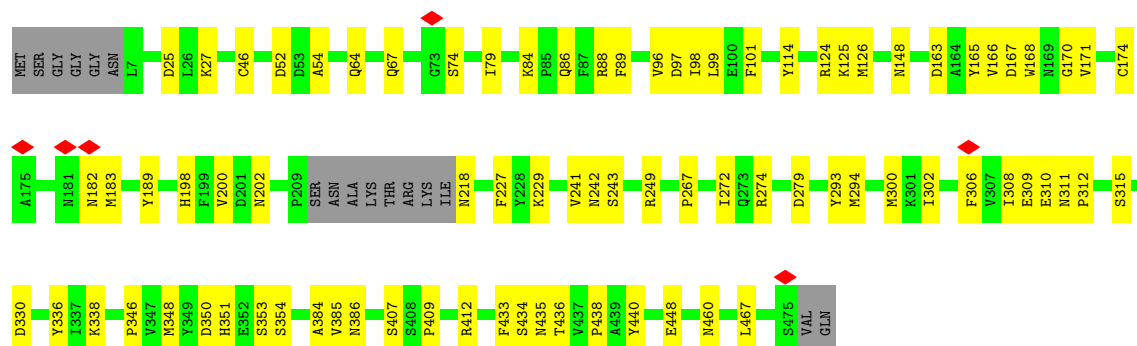
- Molecule 4: Protein AC142





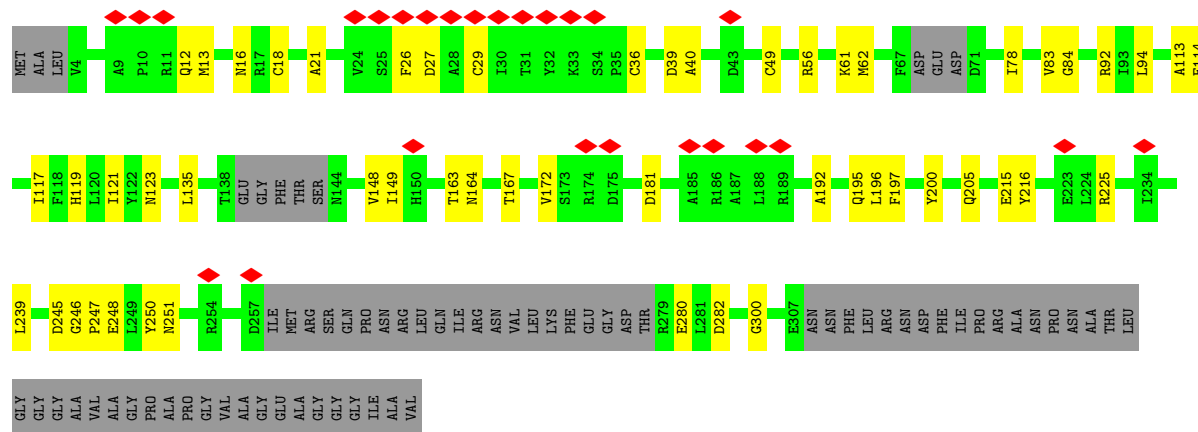
• Molecule 4: Protein AC142

Chain X: 79% 17%



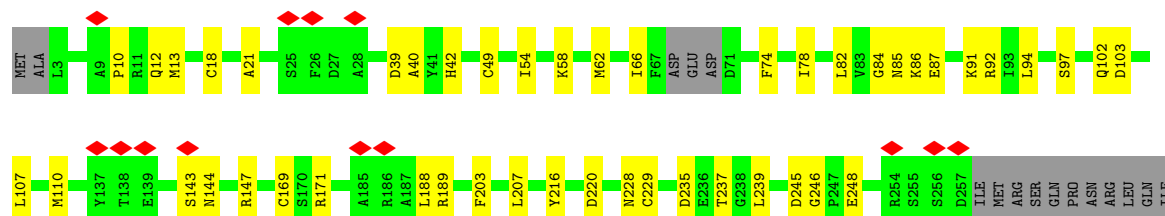
• Molecule 5: Major capsid protein

Chain G: 7% 64% 15% 21%

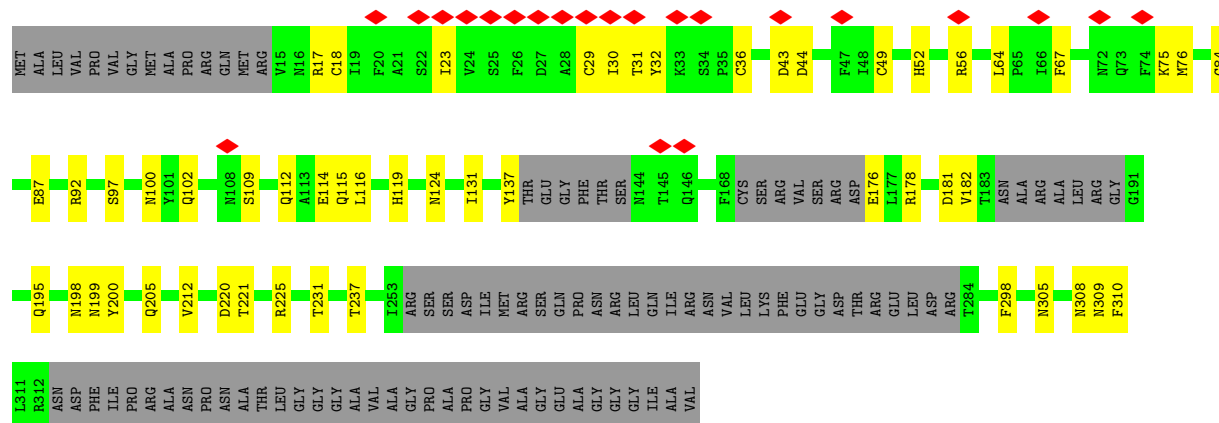


• Molecule 5: Major capsid protein

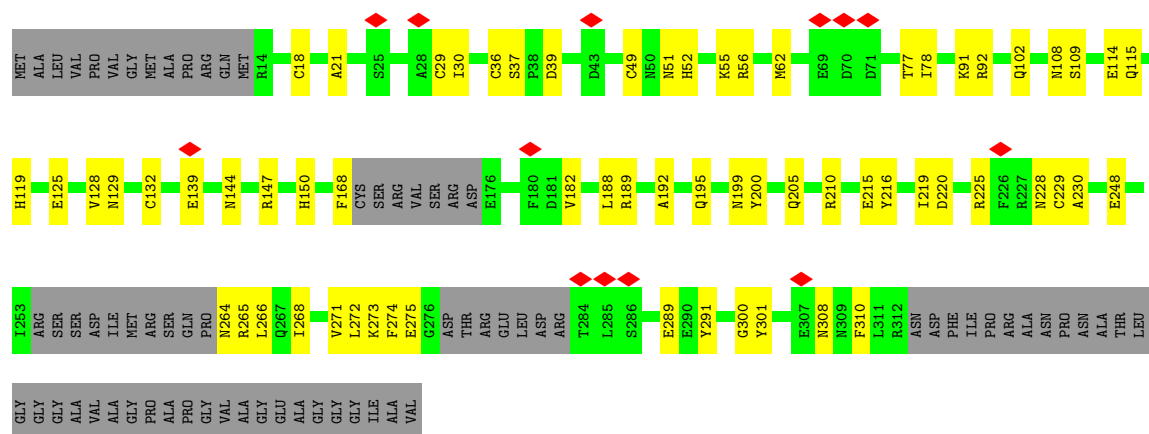
Chain H: 5% 66% 15% 18%



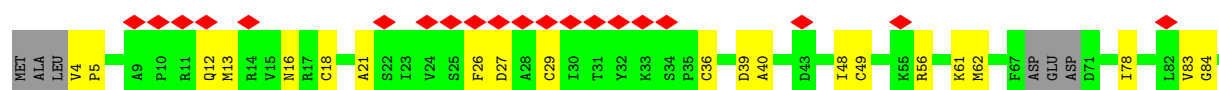
- Molecule 5: Major capsid protein

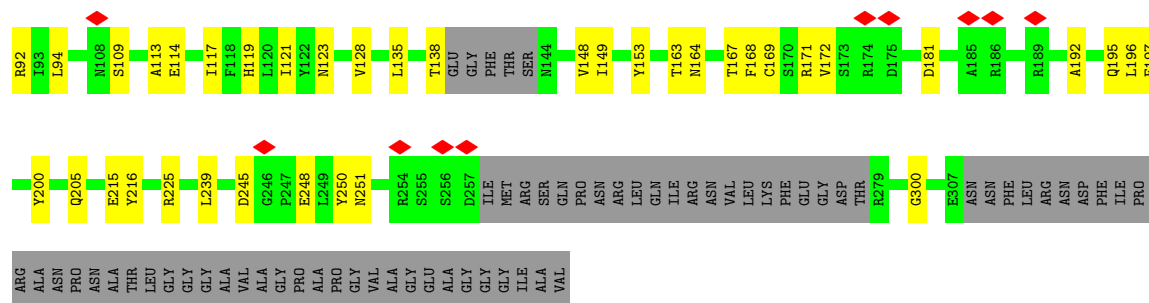


- Molecule 5: Major capsid protein

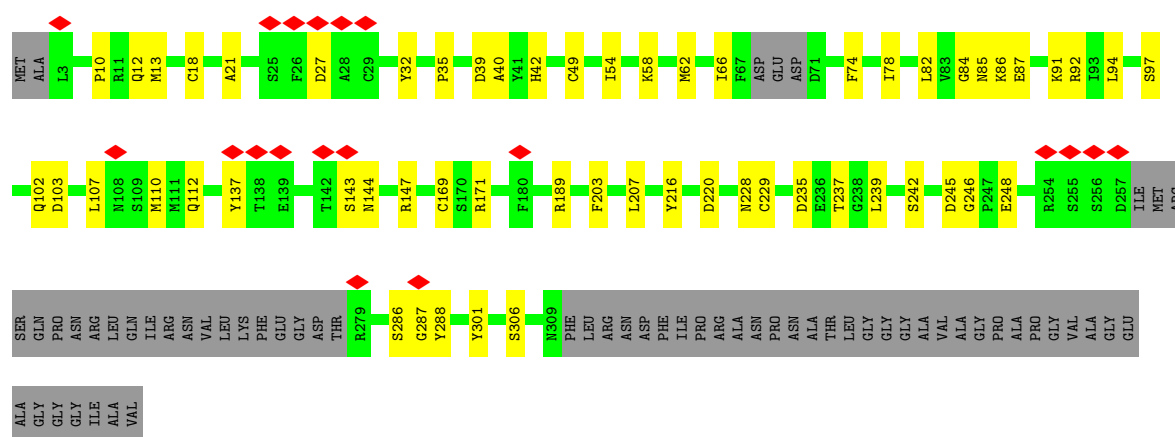


- Molecule 5: Major capsid protein

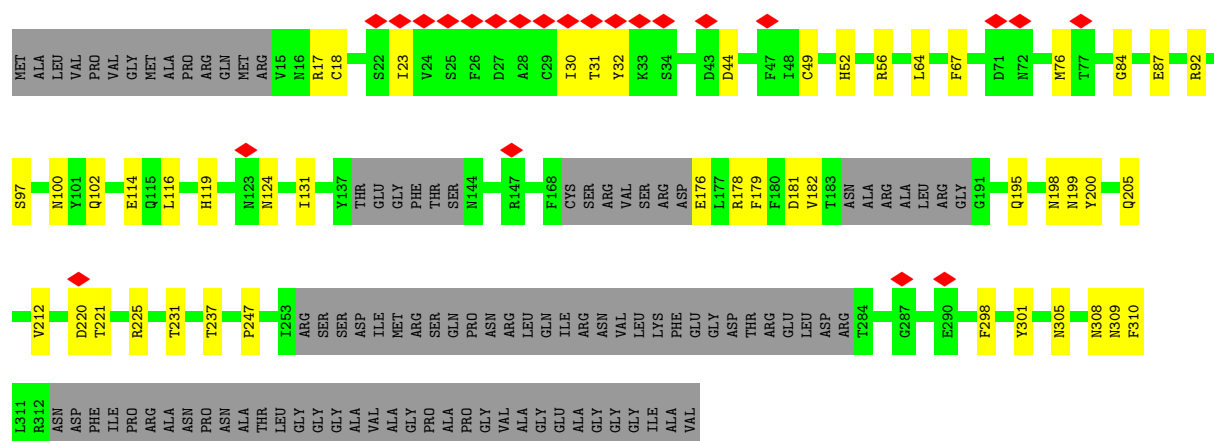




• Molecule 5: Major capsid protein

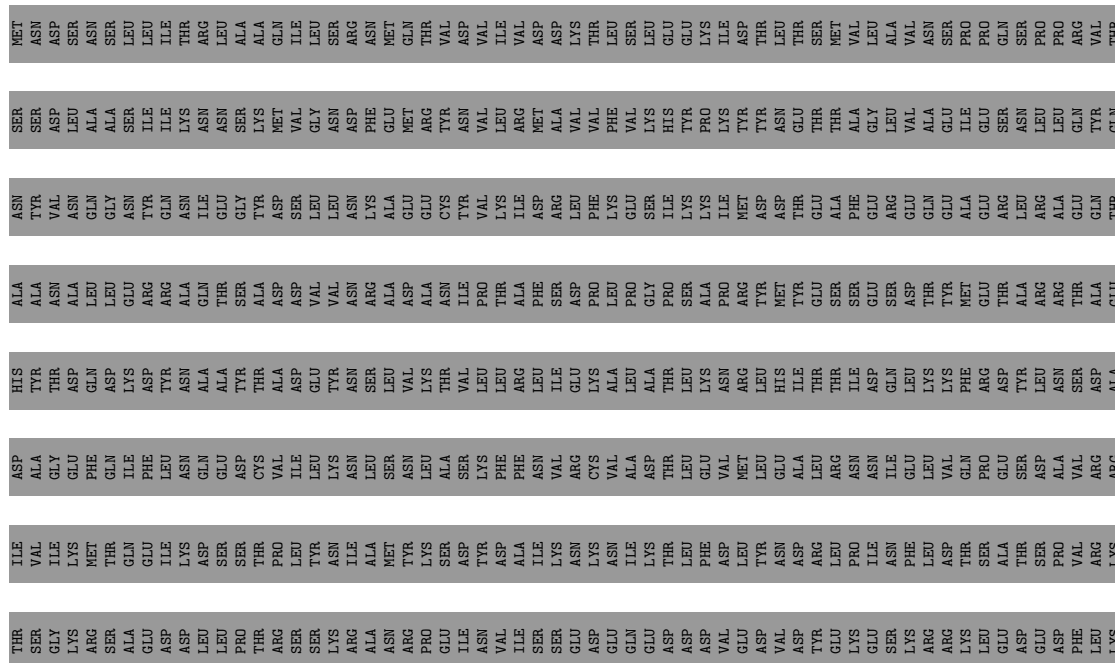
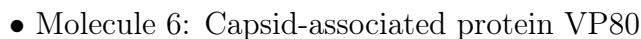


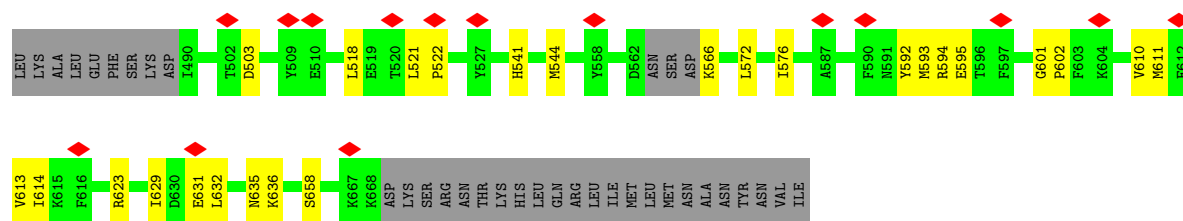
• Molecule 5: Major capsid protein



• Molecule 5: Major capsid protein

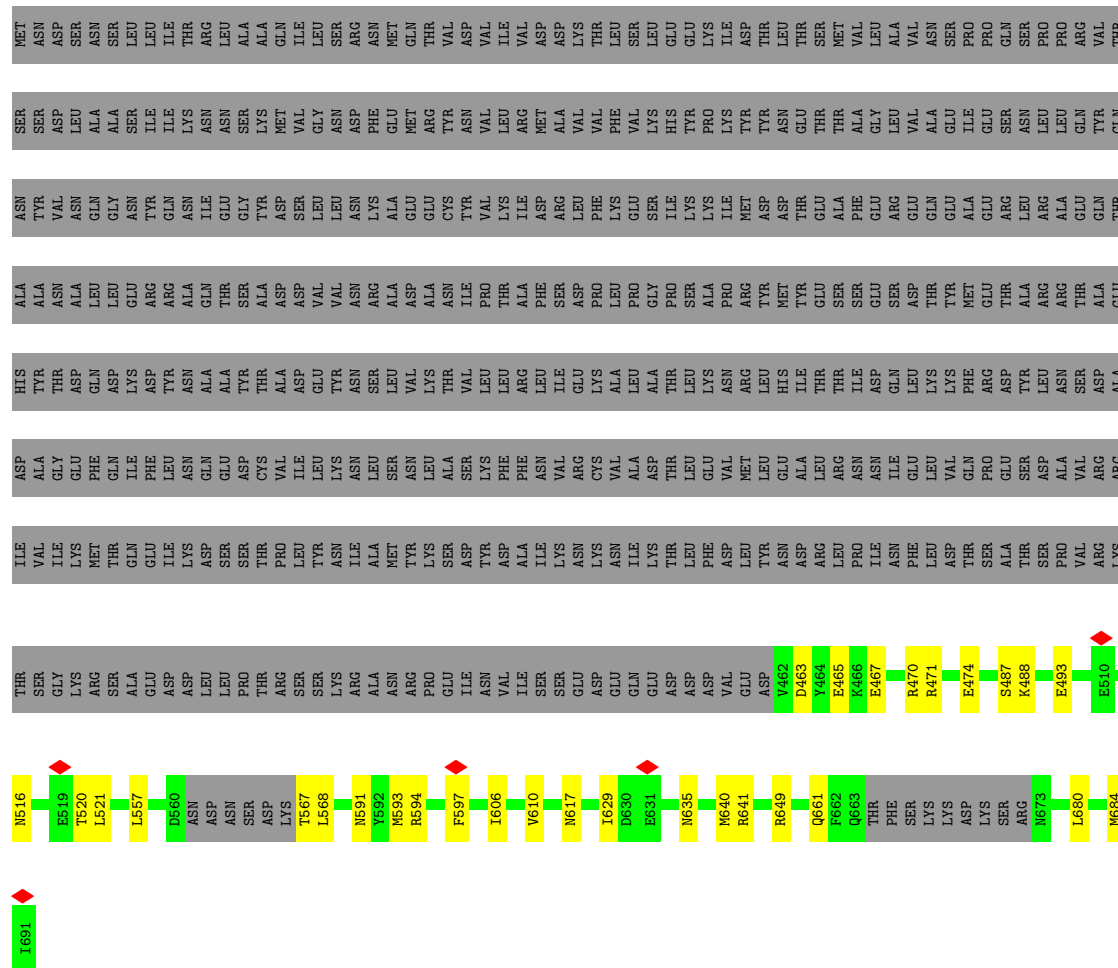






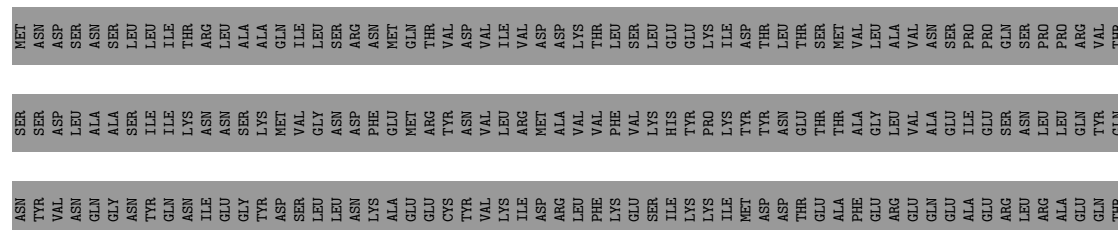
• Molecule 6: Capsid-associated protein VP80

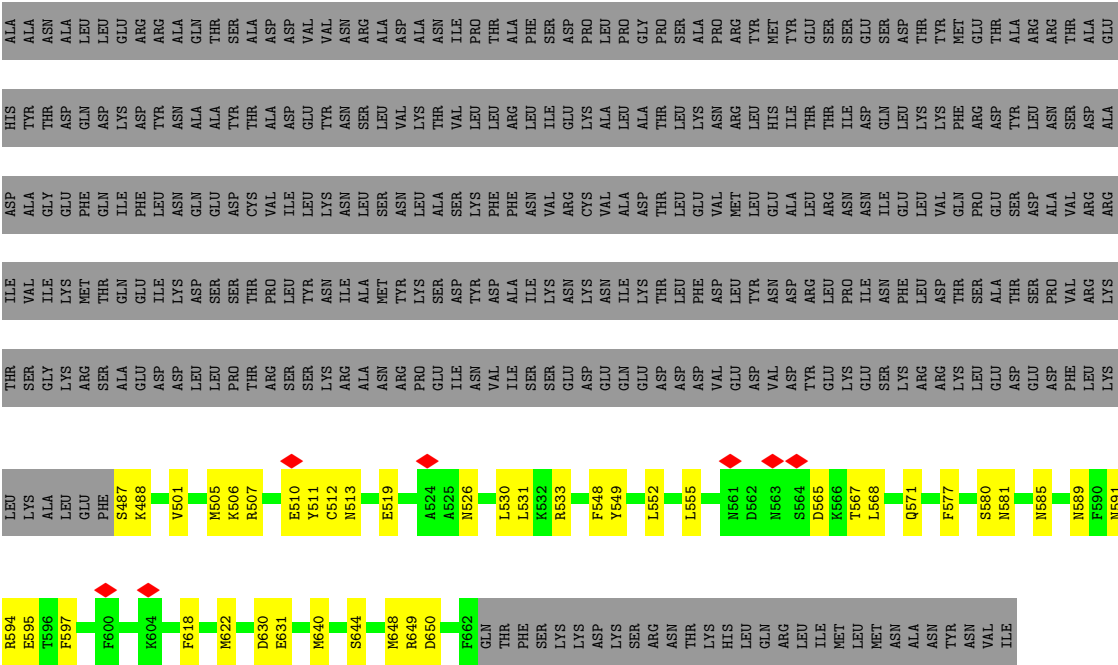
Chain a: 27% 69%



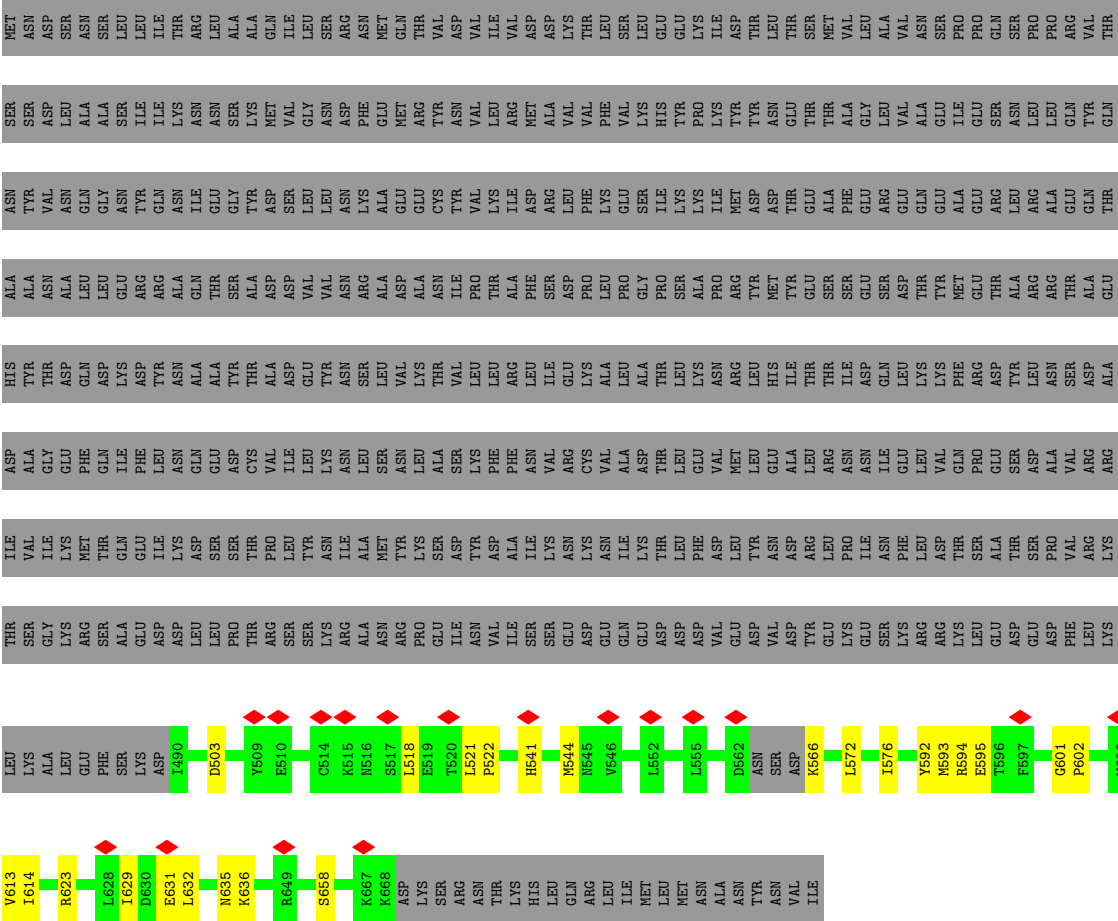
• Molecule 6: Capsid-associated protein VP80

Chain b: 20% 6% 75%

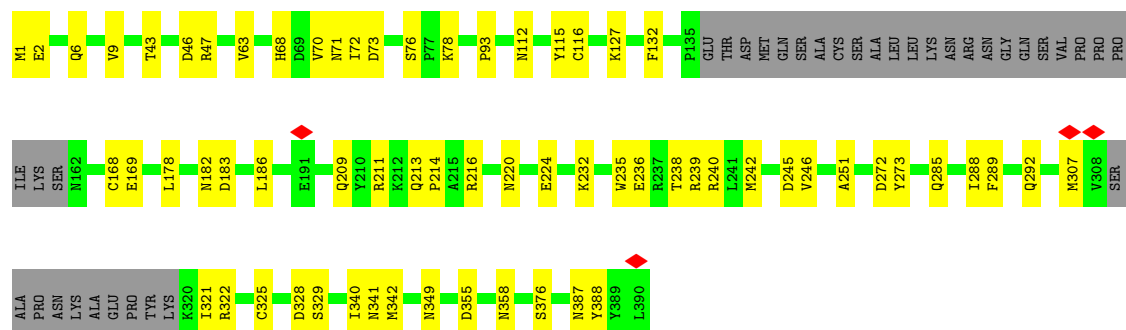




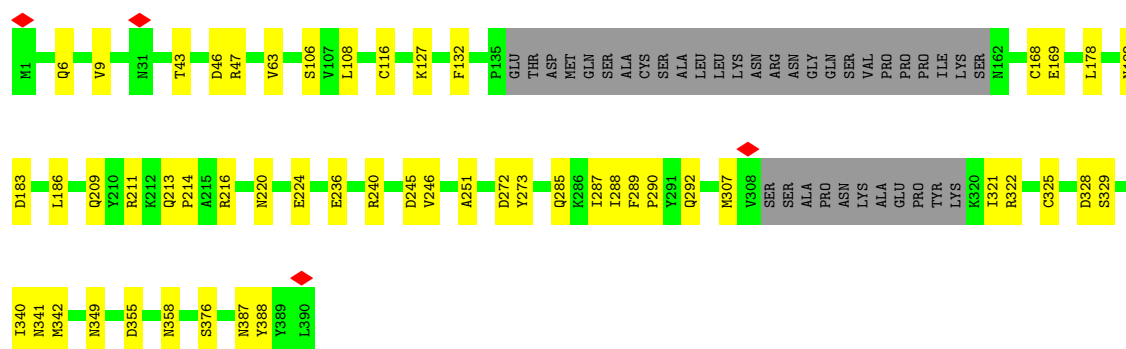
• Molecule 6: Capsid-associated protein VP80



● Molecule 7: Protein AC109

Chain L:  74% 17% 9%

● Molecule 7: Protein AC109

Chain d:  77% 13% 9%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35066	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	675.0, 675.0, 675.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	0.19	0/2024	0.29	0/2732
1	B	0.22	0/1681	0.31	0/2273
1	O	0.19	0/2024	0.29	0/2732
1	P	0.14	0/2092	0.37	0/2827
1	Q	0.22	0/1681	0.32	0/2273
1	R	0.18	0/1591	0.40	0/2153
2	C	0.24	0/1821	0.38	0/2455
2	D	0.30	0/1704	0.55	1/2295 (0.0%)
2	S	0.25	0/1821	0.37	0/2455
2	T	0.20	0/1794	0.47	1/2417 (0.0%)
2	U	0.44	2/1704 (0.1%)	0.60	1/2295 (0.0%)
2	V	0.16	0/1842	0.36	0/2484
3	E	0.15	0/2598	0.31	0/3518
3	W	0.15	0/2598	0.31	0/3518
4	F	0.18	0/3890	0.31	0/5268
4	X	0.18	0/3890	0.31	0/5268
5	G	0.14	0/2257	0.29	0/3056
5	H	0.15	0/2320	0.28	0/3143
5	M	0.13	0/2050	0.29	0/2779
5	N	0.16	0/2271	0.30	0/3075
5	Y	0.15	0/2257	0.29	0/3056
5	Z	0.15	0/2320	0.28	0/3143
5	e	0.13	0/2050	0.28	0/2779
5	f	0.16	0/2271	0.30	0/3075
6	I	0.15	0/1836	0.28	0/2467
6	J	0.16	0/1493	0.33	0/2013
6	K	0.15	0/1499	0.32	0/2018
6	a	0.16	0/1836	0.28	0/2467
6	b	0.16	0/1493	0.33	0/2013
6	c	0.15	0/1499	0.32	0/2018
7	L	0.17	0/2952	0.27	0/4012
7	d	0.18	0/2952	0.27	0/4012

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.19	2/68111 (0.0%)	0.33	3/92089 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	U	212	SER	C-N	6.65	1.43	1.33
2	U	141	LYS	C-N	-5.98	1.26	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	250	ARG	N-CA-C	-6.96	103.69	111.28
2	D	131	SER	N-CA-C	-5.47	106.11	112.89
2	U	220	PRO	CB-CA-C	-5.11	103.13	111.56

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	A	1991	0	2012	48	0
1	B	1649	0	1652	35	0
1	O	1991	0	2012	70	0
1	P	2056	0	2061	83	0
1	Q	1649	0	1652	30	0
1	R	1560	0	1562	53	0
2	C	1790	0	1789	69	0
2	D	1677	0	1685	82	0
2	S	1790	0	1789	118	0
2	T	1764	0	1767	73	0
2	U	1677	0	1685	137	0
2	V	1811	0	1814	64	0
3	E	2526	0	2476	34	0
3	W	2526	0	2476	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	3792	0	3777	61	0
4	X	3792	0	3777	116	0
5	G	2213	0	2169	34	0
5	H	2274	0	2222	44	0
5	M	2008	0	1944	47	0
5	N	2226	0	2170	97	0
5	Y	2213	0	2169	77	0
5	Z	2274	0	2222	57	0
5	e	2008	0	1944	32	0
5	f	2226	0	2170	38	0
6	I	1802	0	1821	21	0
6	J	1462	0	1462	34	0
6	K	1468	0	1481	19	0
6	a	1802	0	1821	20	0
6	b	1462	0	1462	32	0
6	c	1468	0	1481	18	0
7	L	2880	0	2878	90	0
7	d	2880	0	2878	39	0
8	G	1	0	0	0	0
8	H	1	0	0	0	0
8	M	1	0	0	0	0
8	N	1	0	0	0	0
8	Y	1	0	0	0	0
8	Z	1	0	0	0	0
8	e	1	0	0	0	0
8	f	1	0	0	0	0
All	All	66715	0	66280	1428	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 11.

The worst 5 of 1428 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)
4:X:101:PHE:CE1	4:X:171:VAL:CG2	1.75	1.64
4:F:101:PHE:CE1	4:F:171:VAL:CG2	1.75	1.56
4:F:101:PHE:CE1	4:F:171:VAL:HG21	1.02	1.51
4:X:101:PHE:CE1	4:X:171:VAL:HG21	1.02	1.51
2:U:128:HIS:CE1	2:U:132:LEU:HD11	1.47	1.50

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	240/290 (83%)	230 (96%)	10 (4%)	0	100	100
1	B	197/290 (68%)	187 (95%)	10 (5%)	0	100	100
1	O	240/290 (83%)	230 (96%)	10 (4%)	0	100	100
1	P	248/290 (86%)	235 (95%)	13 (5%)	0	100	100
1	Q	197/290 (68%)	188 (95%)	9 (5%)	0	100	100
1	R	188/290 (65%)	185 (98%)	3 (2%)	0	100	100
2	C	210/361 (58%)	203 (97%)	7 (3%)	0	100	100
2	D	193/361 (54%)	179 (93%)	14 (7%)	0	100	100
2	S	210/361 (58%)	205 (98%)	5 (2%)	0	100	100
2	T	204/361 (56%)	191 (94%)	13 (6%)	0	100	100
2	U	193/361 (54%)	174 (90%)	19 (10%)	0	100	100
2	V	212/361 (59%)	208 (98%)	4 (2%)	0	100	100
3	E	295/320 (92%)	258 (88%)	37 (12%)	0	100	100
3	W	295/320 (92%)	259 (88%)	36 (12%)	0	100	100
4	F	457/477 (96%)	433 (95%)	24 (5%)	0	100	100
4	X	457/477 (96%)	433 (95%)	24 (5%)	0	100	100
5	G	267/347 (77%)	243 (91%)	24 (9%)	0	100	100
5	H	277/347 (80%)	254 (92%)	23 (8%)	0	100	100
5	M	238/347 (69%)	215 (90%)	22 (9%)	1 (0%)	30	67
5	N	267/347 (77%)	228 (85%)	39 (15%)	0	100	100
5	Y	267/347 (77%)	244 (91%)	23 (9%)	0	100	100
5	Z	277/347 (80%)	255 (92%)	22 (8%)	0	100	100
5	e	238/347 (69%)	215 (90%)	22 (9%)	1 (0%)	30	67
5	f	267/347 (77%)	228 (85%)	39 (15%)	0	100	100
6	I	209/691 (30%)	197 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	J	174/691 (25%)	163 (94%)	11 (6%)	0	100	100
6	K	172/691 (25%)	160 (93%)	12 (7%)	0	100	100
6	a	209/691 (30%)	197 (94%)	12 (6%)	0	100	100
6	b	174/691 (25%)	163 (94%)	11 (6%)	0	100	100
6	c	172/691 (25%)	160 (93%)	12 (7%)	0	100	100
7	L	347/390 (89%)	334 (96%)	13 (4%)	0	100	100
7	d	347/390 (89%)	334 (96%)	13 (4%)	0	100	100
All	All	7938/13202 (60%)	7388 (93%)	548 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	M	309	ASN
5	e	309	ASN

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	230/273 (84%)	230 (100%)	0	100	100
1	B	188/273 (69%)	186 (99%)	2 (1%)	65	74
1	O	230/273 (84%)	230 (100%)	0	100	100
1	P	238/273 (87%)	237 (100%)	1 (0%)	84	83
1	Q	188/273 (69%)	188 (100%)	0	100	100
1	R	181/273 (66%)	180 (99%)	1 (1%)	78	81
2	C	204/326 (63%)	204 (100%)	0	100	100
2	D	192/326 (59%)	192 (100%)	0	100	100
2	S	204/326 (63%)	203 (100%)	1 (0%)	81	82
2	T	201/326 (62%)	200 (100%)	1 (0%)	81	82
2	U	192/326 (59%)	191 (100%)	1 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	V	206/326 (63%)	206 (100%)	0	100	100
3	E	285/304 (94%)	285 (100%)	0	100	100
3	W	285/304 (94%)	285 (100%)	0	100	100
4	F	428/440 (97%)	428 (100%)	0	100	100
4	X	428/440 (97%)	428 (100%)	0	100	100
5	G	247/299 (83%)	247 (100%)	0	100	100
5	H	254/299 (85%)	254 (100%)	0	100	100
5	M	225/299 (75%)	225 (100%)	0	100	100
5	N	247/299 (83%)	247 (100%)	0	100	100
5	Y	247/299 (83%)	247 (100%)	0	100	100
5	Z	254/299 (85%)	254 (100%)	0	100	100
5	e	225/299 (75%)	225 (100%)	0	100	100
5	f	247/299 (83%)	247 (100%)	0	100	100
6	I	204/634 (32%)	204 (100%)	0	100	100
6	J	167/634 (26%)	167 (100%)	0	100	100
6	K	167/634 (26%)	167 (100%)	0	100	100
6	a	204/634 (32%)	204 (100%)	0	100	100
6	b	167/634 (26%)	167 (100%)	0	100	100
6	c	167/634 (26%)	167 (100%)	0	100	100
7	L	334/366 (91%)	334 (100%)	0	100	100
7	d	334/366 (91%)	334 (100%)	0	100	100
All	All	7570/12010 (63%)	7563 (100%)	7 (0%)	87	88

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	61	LEU
2	S	226	LYS
2	U	221	ILE
2	T	128	HIS
1	P	256	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
3	W	241	HIS
6	c	581	ASN
3	W	298	GLN
5	Z	112	GLN
5	H	42	HIS

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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

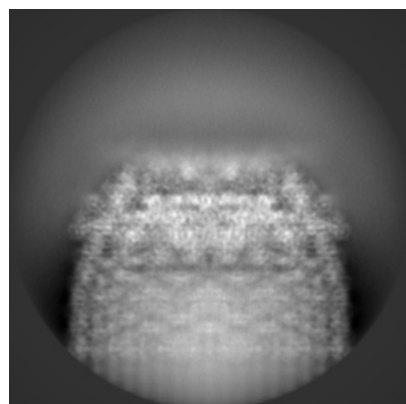
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51791. These allow visual inspection of the internal detail of the map and identification of artifacts.

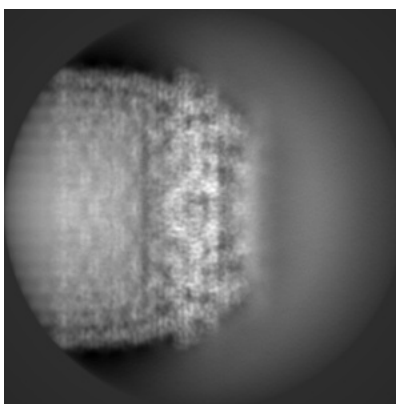
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

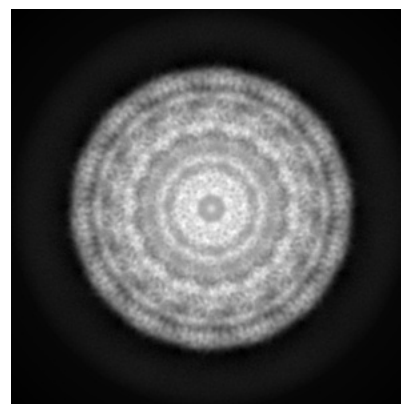
6.1.1 Primary map



X

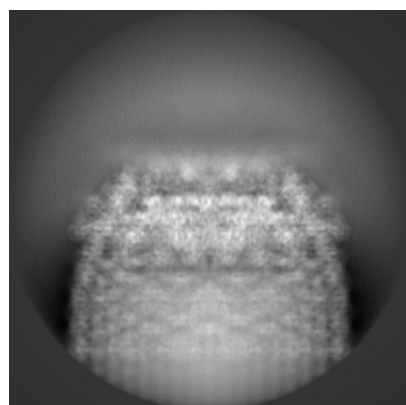


Y

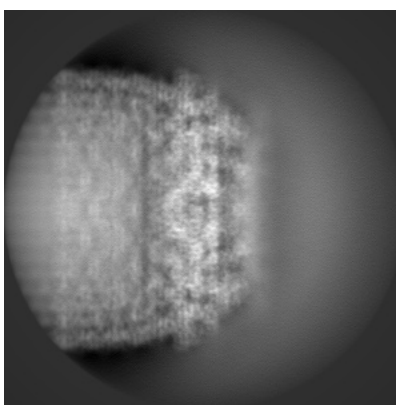


Z

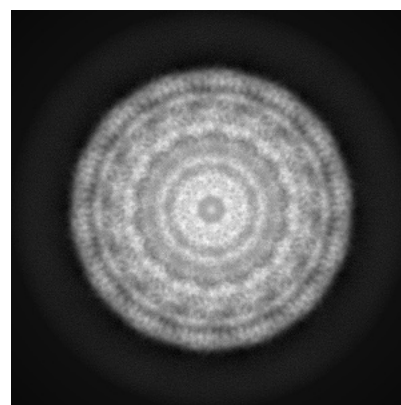
6.1.2 Raw map



X



Y

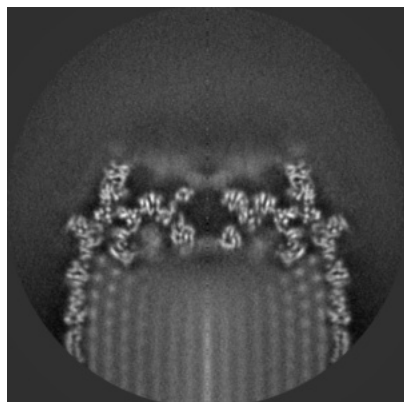


Z

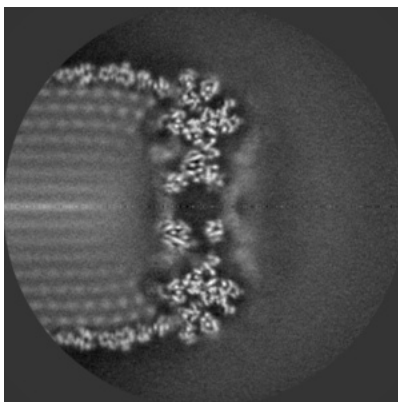
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

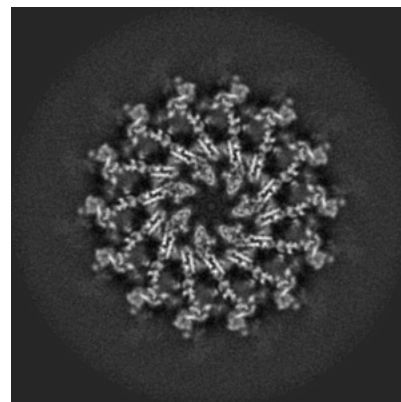
6.2.1 Primary map



X Index: 250

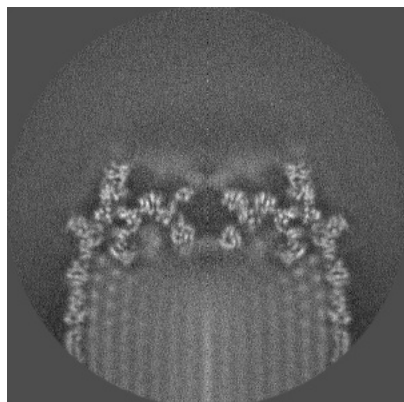


Y Index: 250

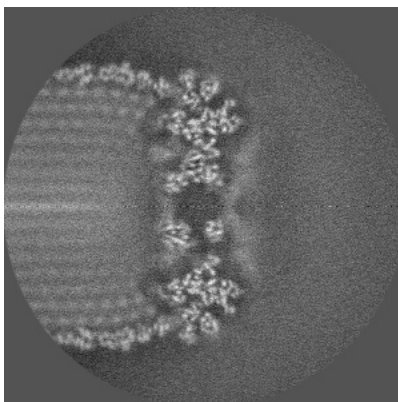


Z Index: 250

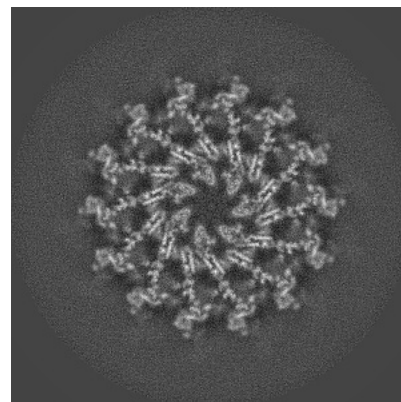
6.2.2 Raw map



X Index: 250



Y Index: 250

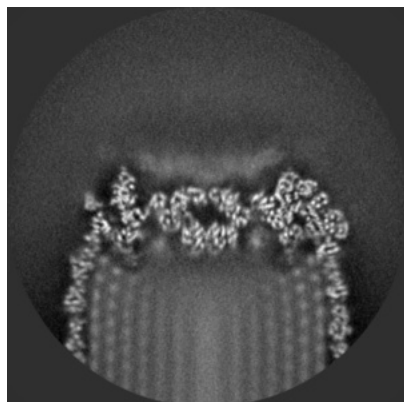


Z Index: 250

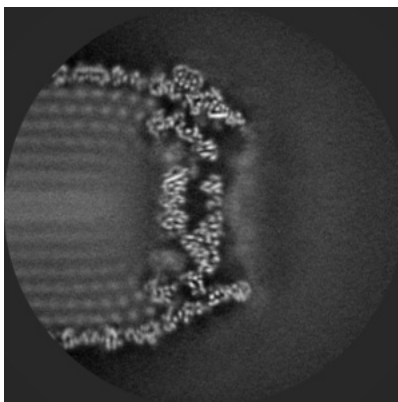
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

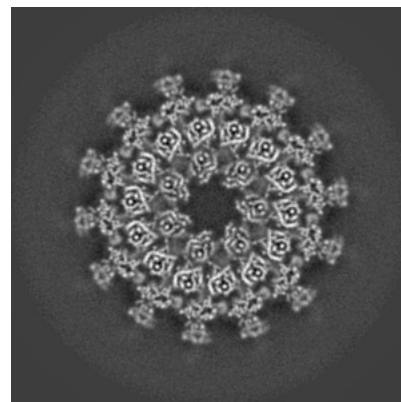
6.3.1 Primary map



X Index: 273

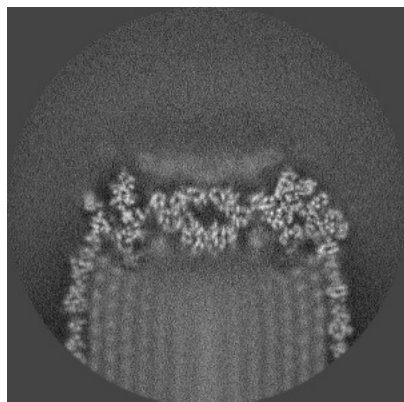


Y Index: 269

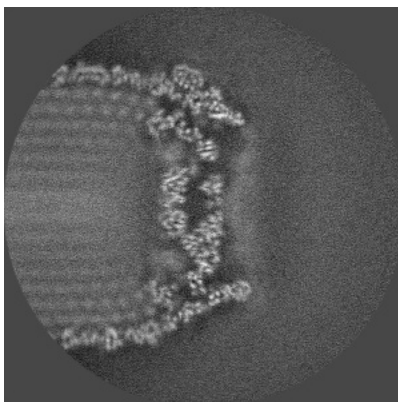


Z Index: 240

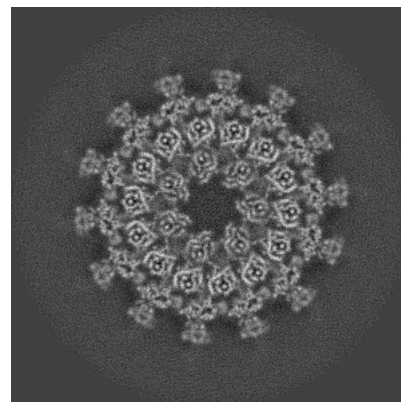
6.3.2 Raw map



X Index: 274



Y Index: 268

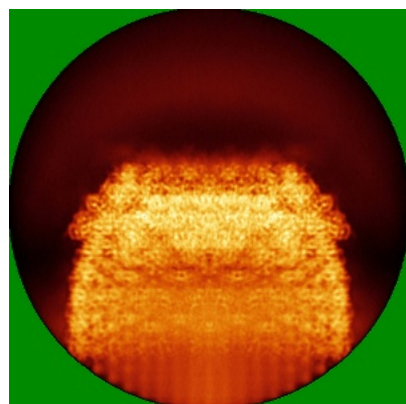


Z Index: 240

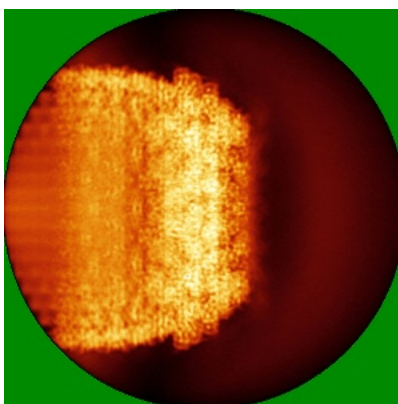
The images above show the largest variance slices of the map in three orthogonal directions.

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

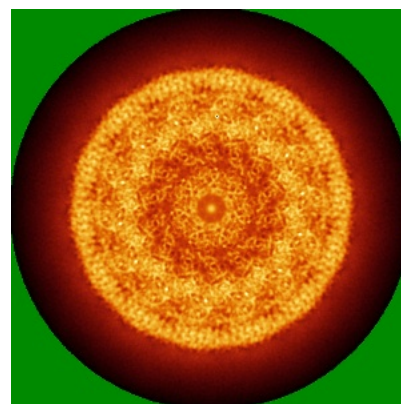
6.4.1 Primary map



X

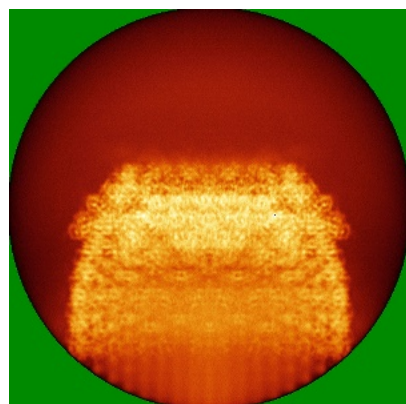


Y

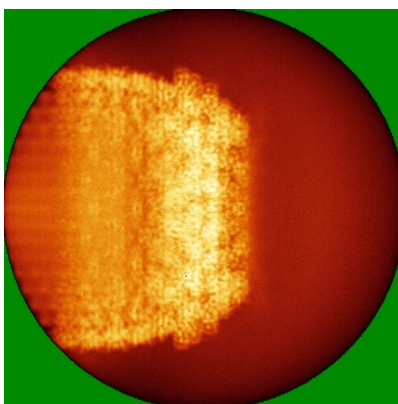


Z

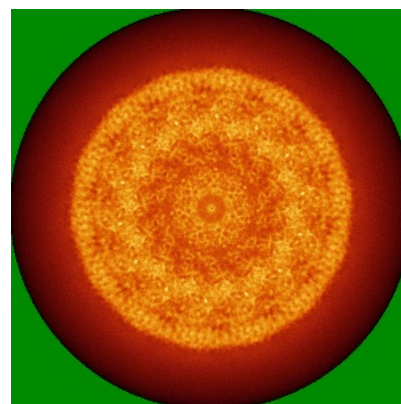
6.4.2 Raw map



X



Y

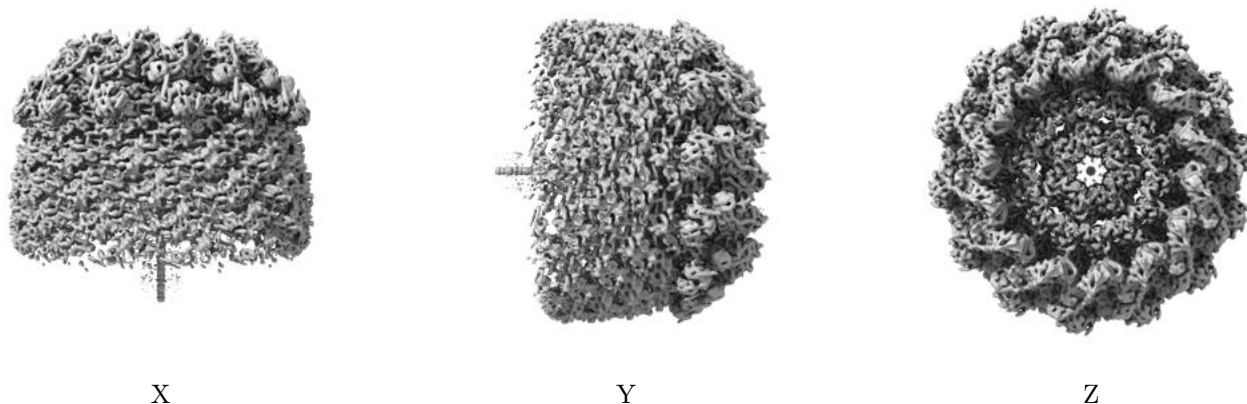


Z

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.

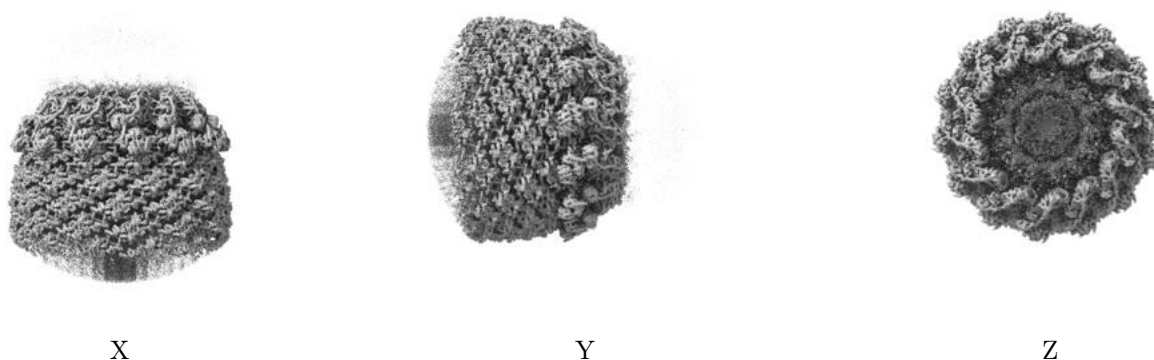
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. 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.

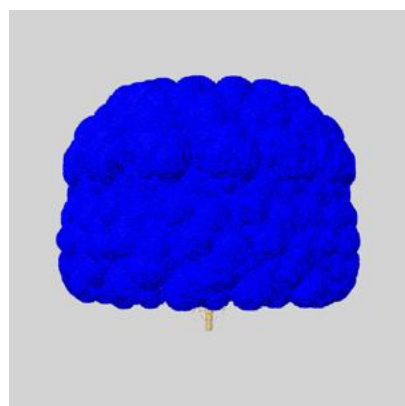
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

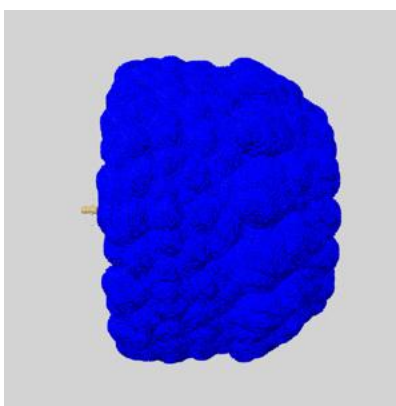
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

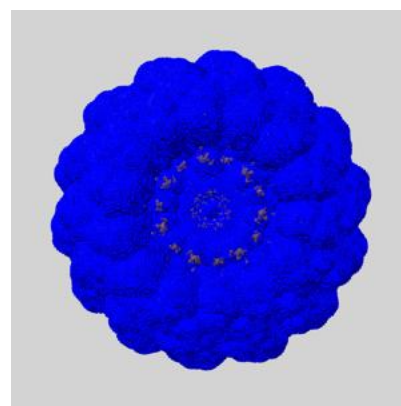
6.6.1 emd_51791_msk_1.map [i](#)



X



Y

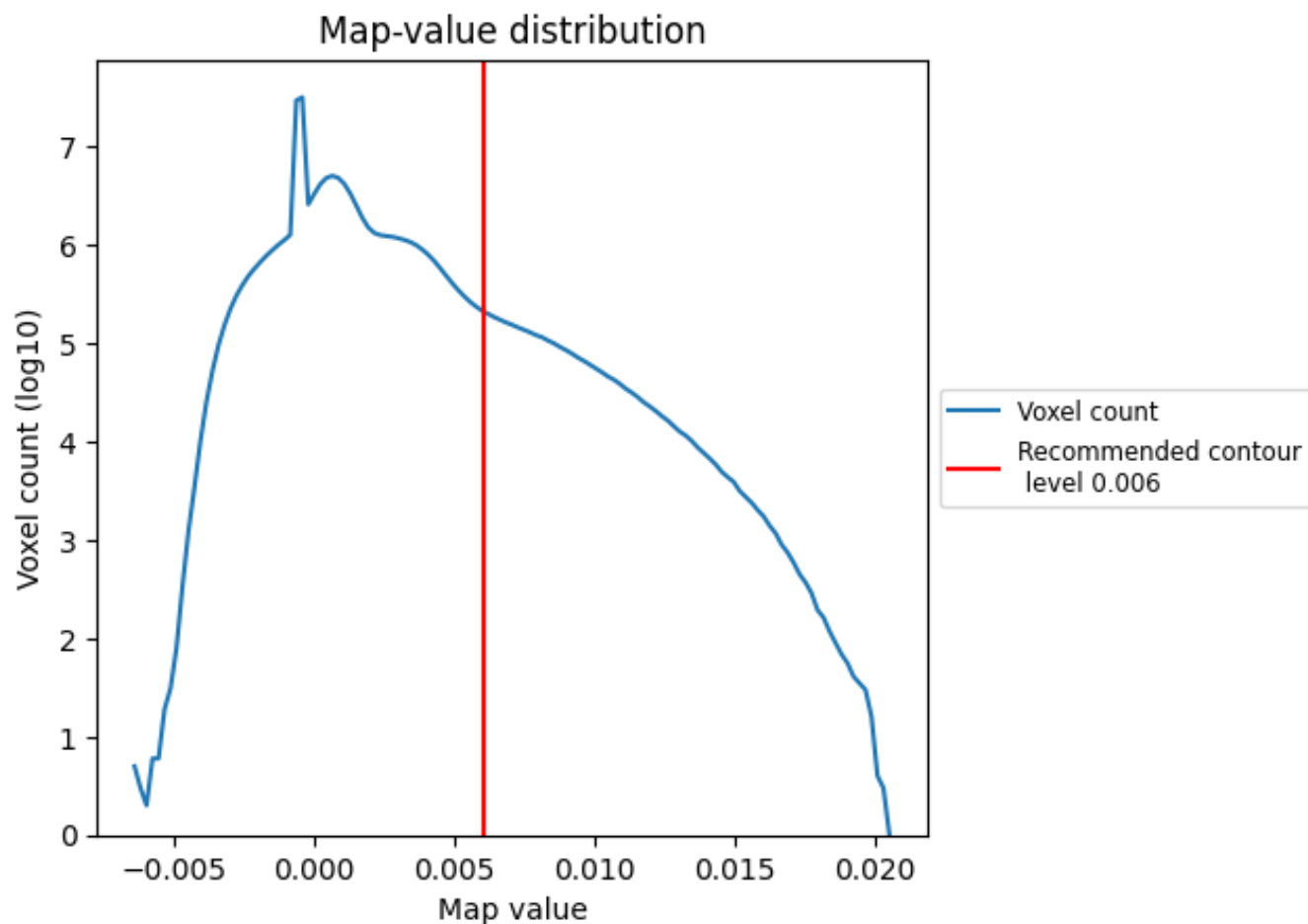


Z

7 Map analysis [i](#)

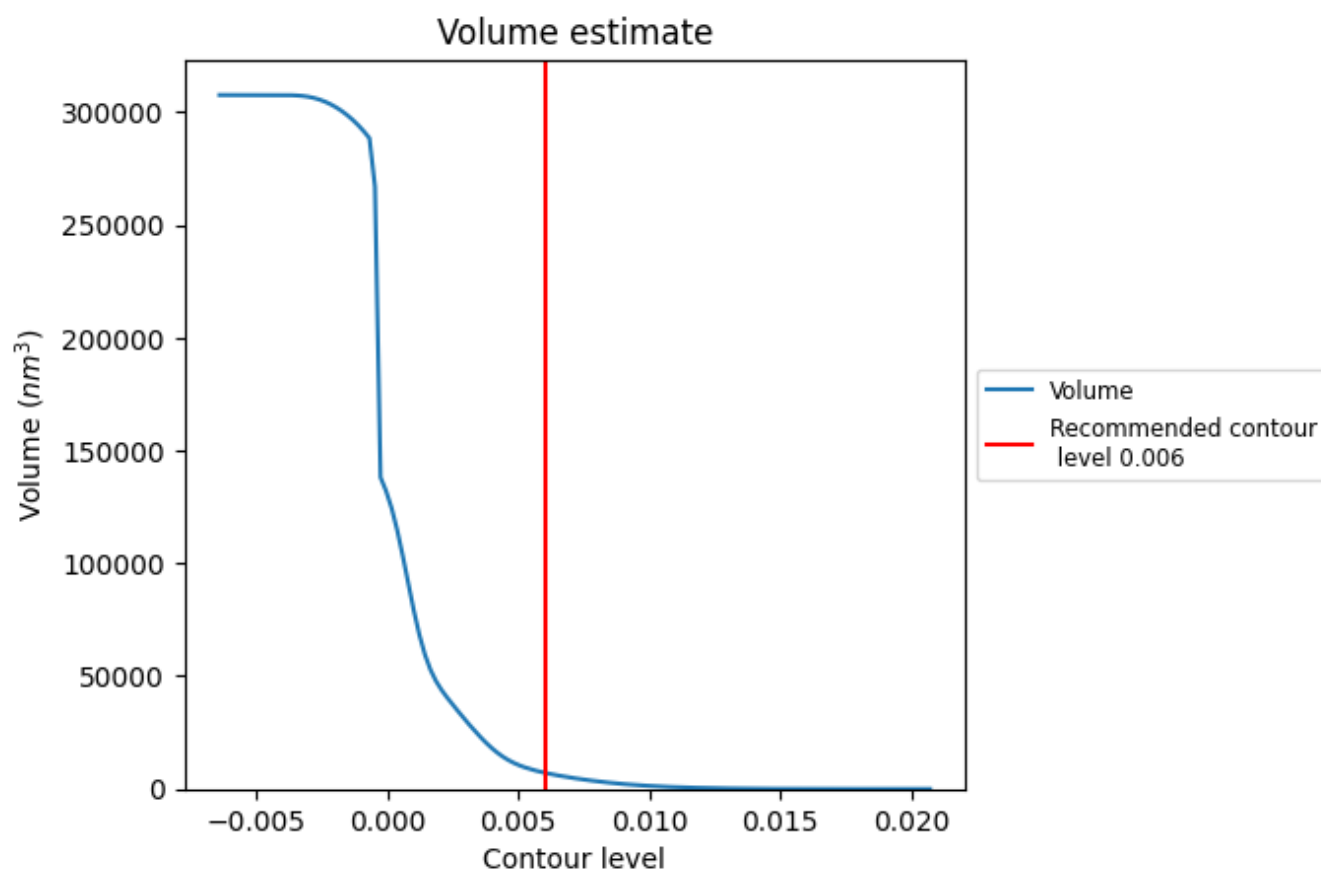
This section contains the results of statistical analysis of the map.

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.

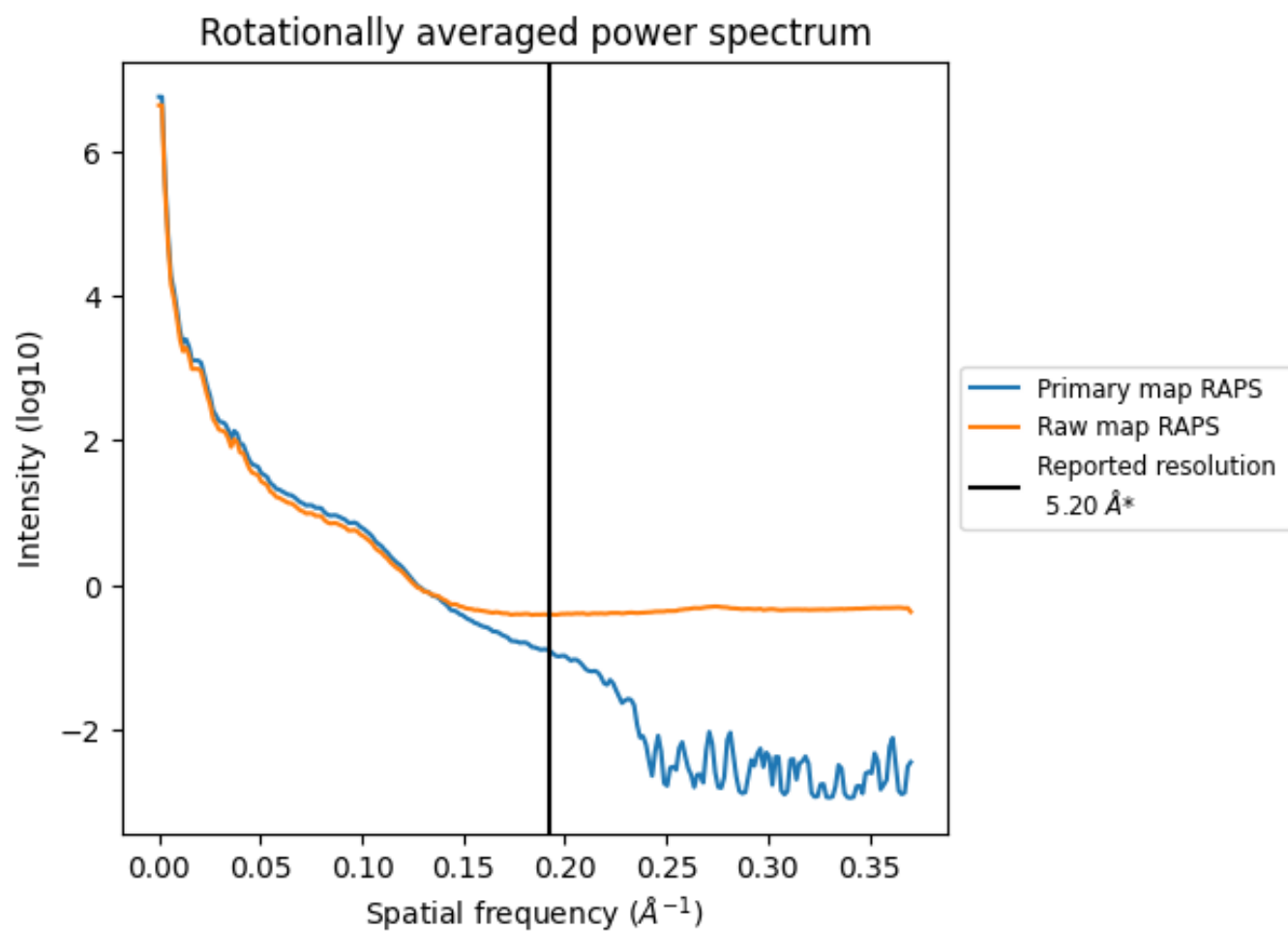
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 7187 nm^3 ; this corresponds to an approximate mass of 6492 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](#)

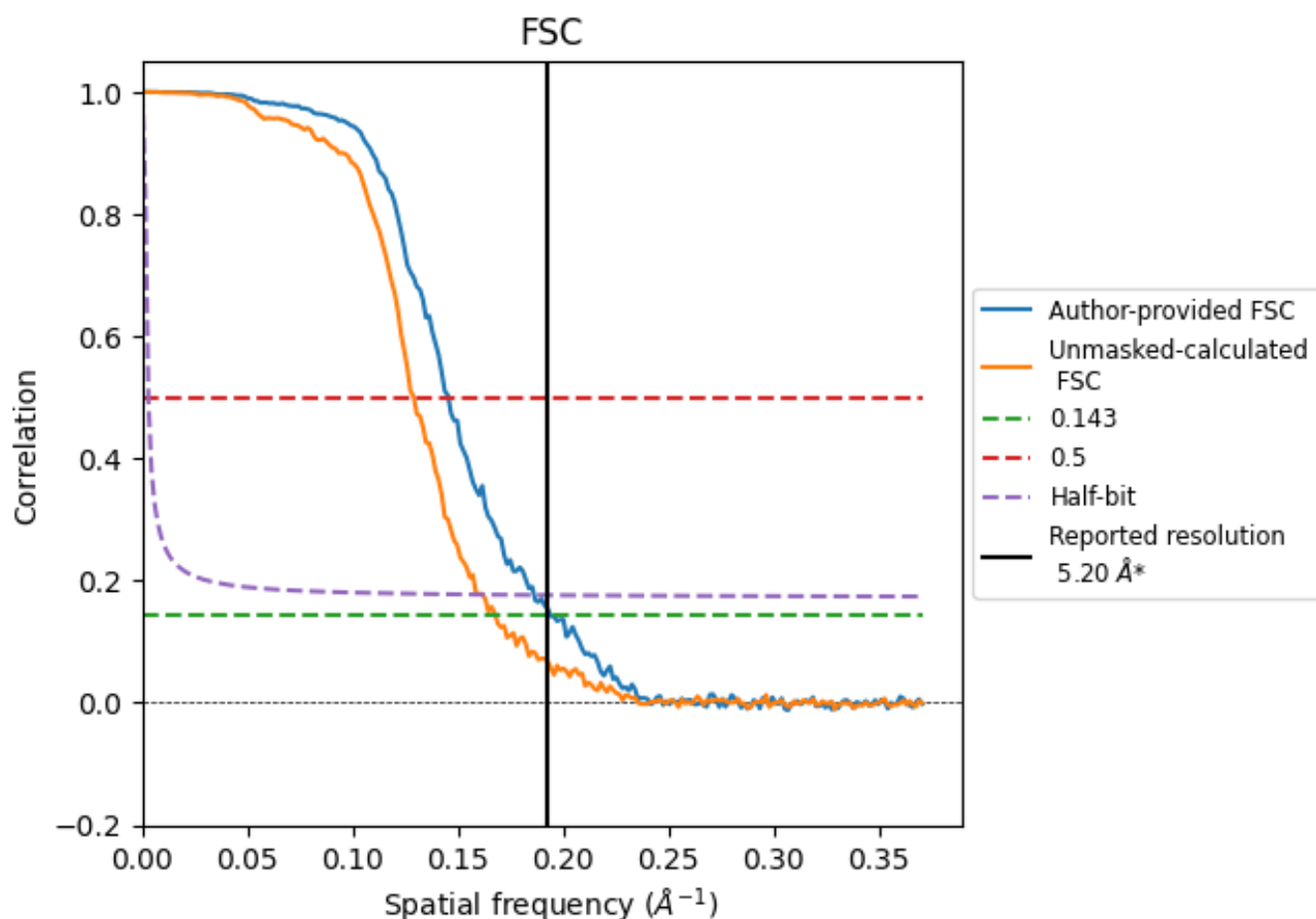


*Reported resolution corresponds to spatial frequency of 0.192 Å⁻¹

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 0.192 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.20	-	-
Author-provided FSC curve	5.16	6.88	5.37
Unmasked-calculated*	5.96	7.75	6.18

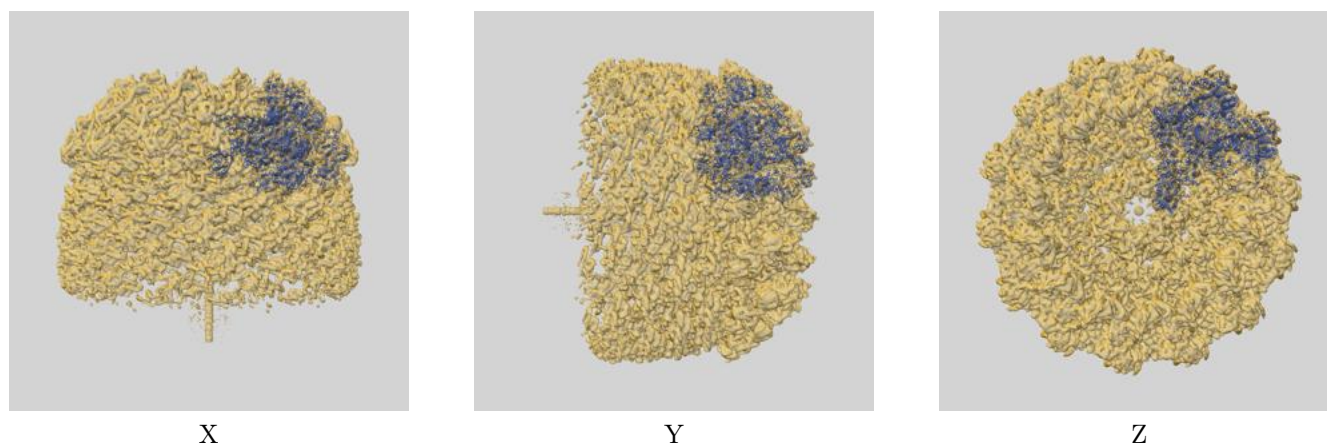
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.96 differs from the reported value 5.2 by more than 10 %

9 Map-model fit [i](#)

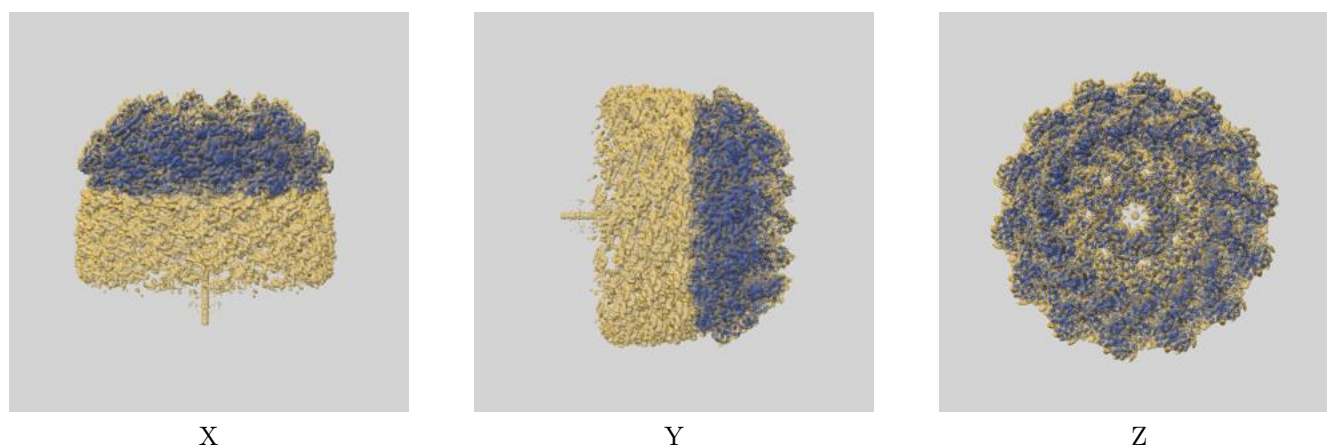
This section contains information regarding the fit between EMDB map EMD-51791 and PDB model 9H2A. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

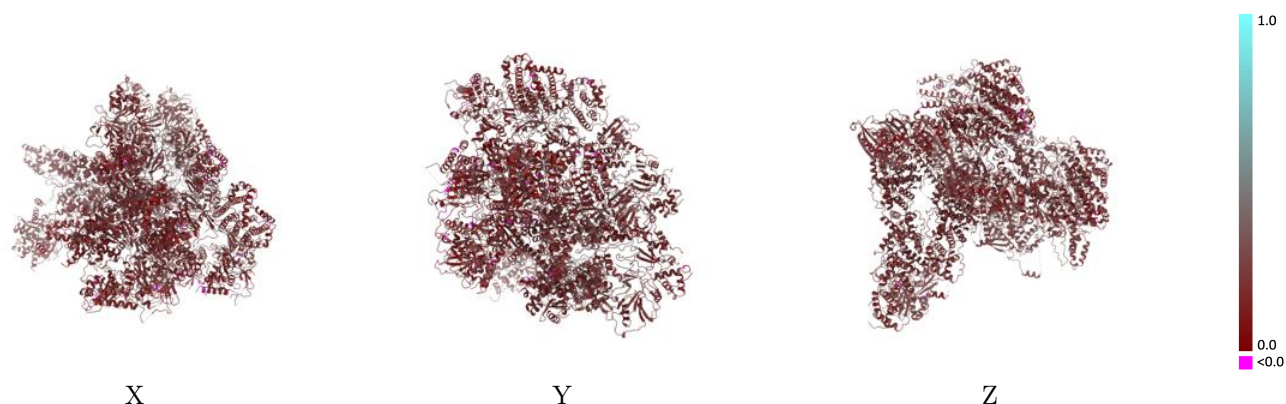


9.1.2 Map-model assembly overlay [i](#)



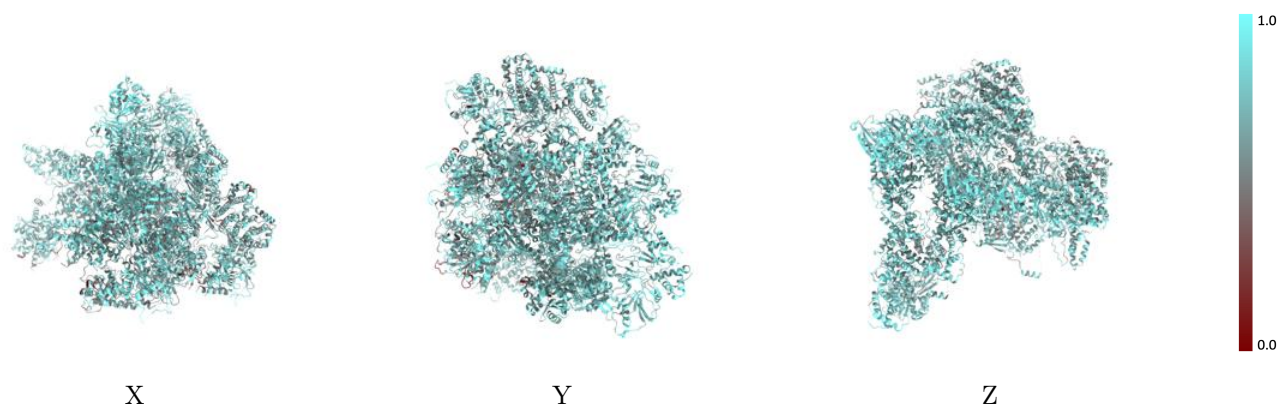
The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



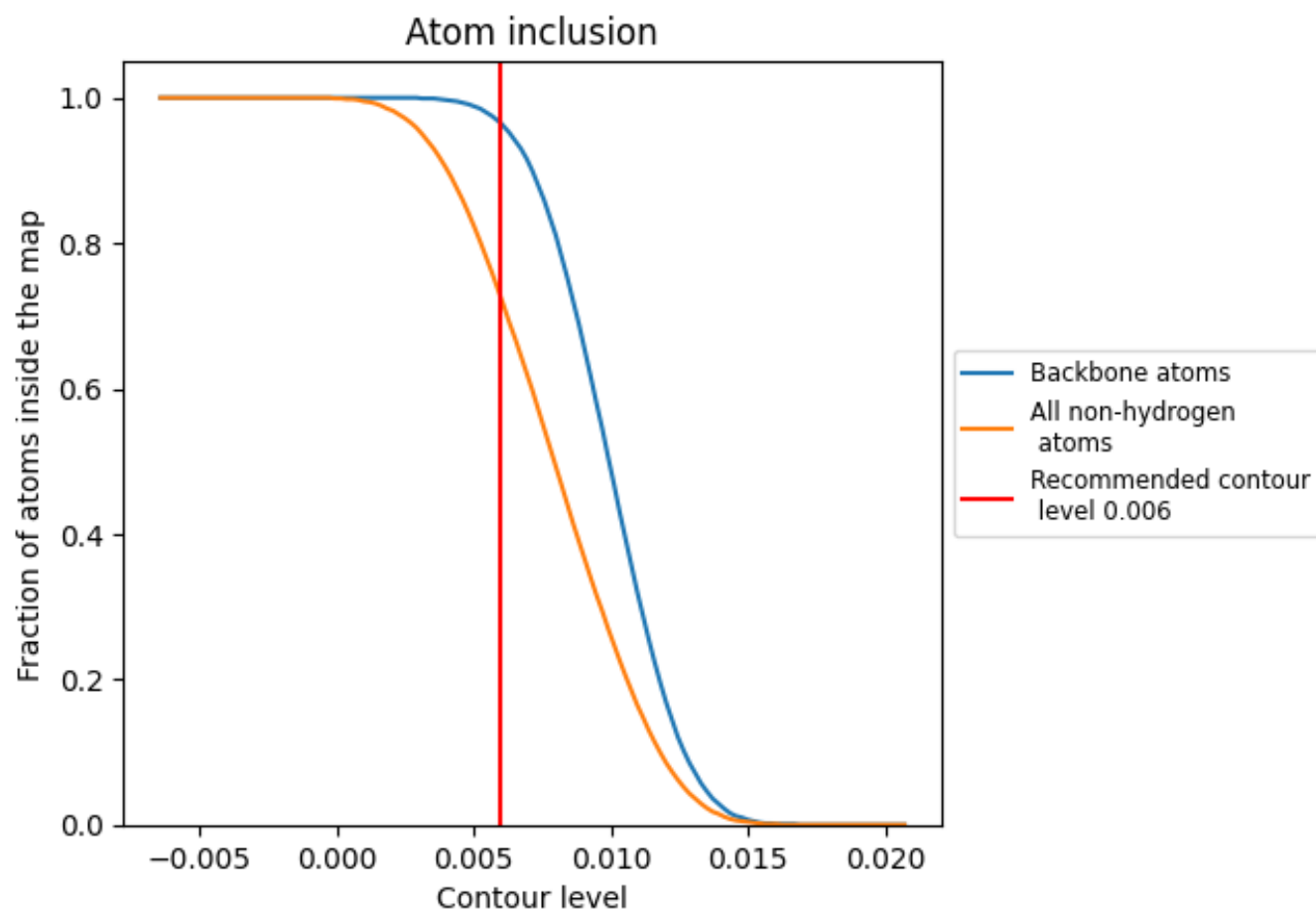
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.006).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 72% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7250	 0.2190
A	 0.7130	 0.2330
B	 0.6690	 0.2140
C	 0.7780	 0.2300
D	 0.7720	 0.2220
E	 0.6320	 0.2010
F	 0.7880	 0.2400
G	 0.6760	 0.2110
H	 0.7200	 0.2300
I	 0.7420	 0.1940
J	 0.6700	 0.1870
K	 0.6700	 0.1880
L	 0.7890	 0.2550
M	 0.7160	 0.1990
N	 0.7360	 0.2330
O	 0.7090	 0.2280
P	 0.6610	 0.2030
Q	 0.6820	 0.2160
R	 0.7350	 0.2090
S	 0.7610	 0.2230
T	 0.7700	 0.2120
U	 0.7550	 0.2200
V	 0.7740	 0.2100
W	 0.6330	 0.2010
X	 0.7880	 0.2390
Y	 0.6780	 0.2120
Z	 0.7200	 0.2370
a	 0.7420	 0.1910
b	 0.6850	 0.1960
c	 0.6490	 0.1930
d	 0.7930	 0.2570
e	 0.7130	 0.1990
f	 0.7390	 0.2370

