



## wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 10:12 PM EST

PDB ID : 6OJ3  
EMDB ID : EMD-20086  
Title : In situ structure of rotavirus VP1 RNA-dependent RNA polymerase (TLP)  
Authors : Jenni, S.; Salgado, E.N.; Herrmann, T.; Li, Z.; Grant, T.; Grigorieff, N.;  
Trapani, S.; Estrozi, L.F.; Harrison, S.C.  
Deposited on : 2019-04-10  
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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

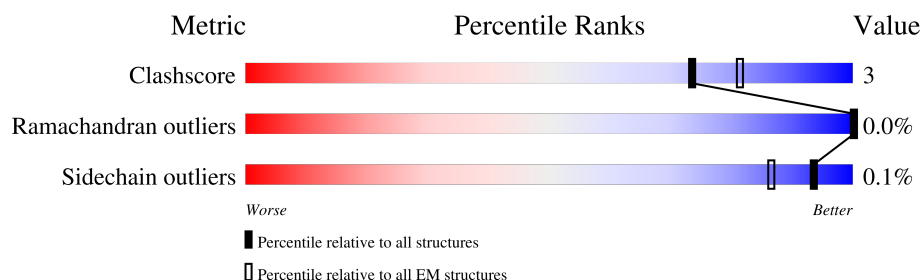
# 1 Overall quality at a glance

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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	887	<div> <div>13%</div> <div>77%</div> <div>10%</div> <div>12%</div> </div>
1	B	887	<div> <div>16%</div> <div>77%</div> <div>11%</div> <div>12%</div> </div>
1	C	887	<div> <div>15%</div> <div>78%</div> <div>10%</div> <div>12%</div> </div>
1	D	887	<div> <div>20%</div> <div>80%</div> <div>12%</div> <div>7%</div> </div>
1	E	887	<div> <div>16%</div> <div>80%</div> <div>9%</div> <div>10%</div> </div>
1	F	887	<div> <div>16%</div> <div>82%</div> <div>8%</div> <div>10%</div> </div>
1	G	887	<div> <div>15%</div> <div>80%</div> <div>10%</div> <div>10%</div> </div>
1	H	887	<div> <div>16%</div> <div>83%</div> <div>8%</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
1	I	887	<div><div></div><div>16%</div><div>82%</div><div>8%</div><div>10%</div></div>
1	J	887	<div><div></div><div>15%</div><div>82%</div><div>10%</div><div>8%</div></div>
2	P	1088	<div><div></div><div>18%</div><div>87%</div><div>13%</div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 148557 atoms, of which 74462 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 Inner capsid protein VP2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	781	Total	C	H	N	O	S	0	0
			12787	4052	6408	1101	1190	36		
1	B	781	Total	C	H	N	O	S	0	0
			12787	4052	6408	1101	1190	36		
1	C	780	Total	C	H	N	O	S	0	0
			12772	4047	6400	1100	1189	36		
1	D	827	Total	C	H	N	O	S	0	0
			13574	4297	6809	1163	1269	36		
1	E	795	Total	C	H	N	O	S	0	0
			13028	4132	6529	1118	1213	36		
1	F	802	Total	C	H	N	O	S	0	0
			13151	4170	6588	1130	1227	36		
1	G	802	Total	C	H	N	O	S	0	0
			13151	4170	6588	1130	1227	36		
1	H	802	Total	C	H	N	O	S	0	0
			13151	4170	6588	1130	1227	36		
1	I	800	Total	C	H	N	O	S	0	0
			13114	4159	6569	1127	1223	36		
1	J	816	Total	C	H	N	O	S	0	0
			13391	4242	6713	1149	1251	36		

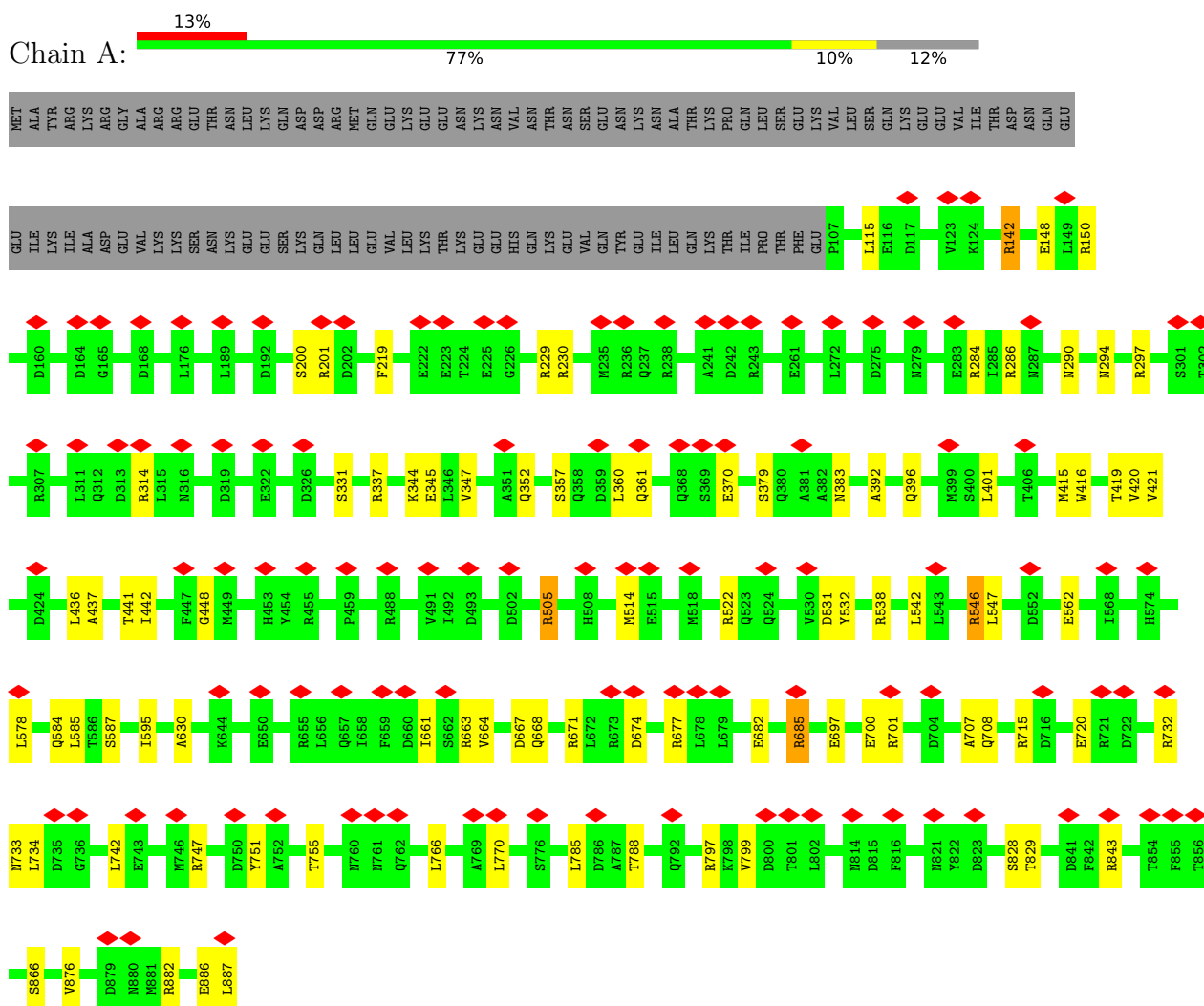
- Molecule 2 is a protein called RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	P	1086	Total	C	H	N	O	S	0	0
			17651	5633	8862	1455	1662	39		

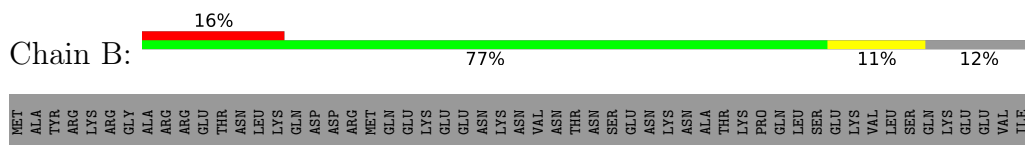
### 3 Residue-property plots

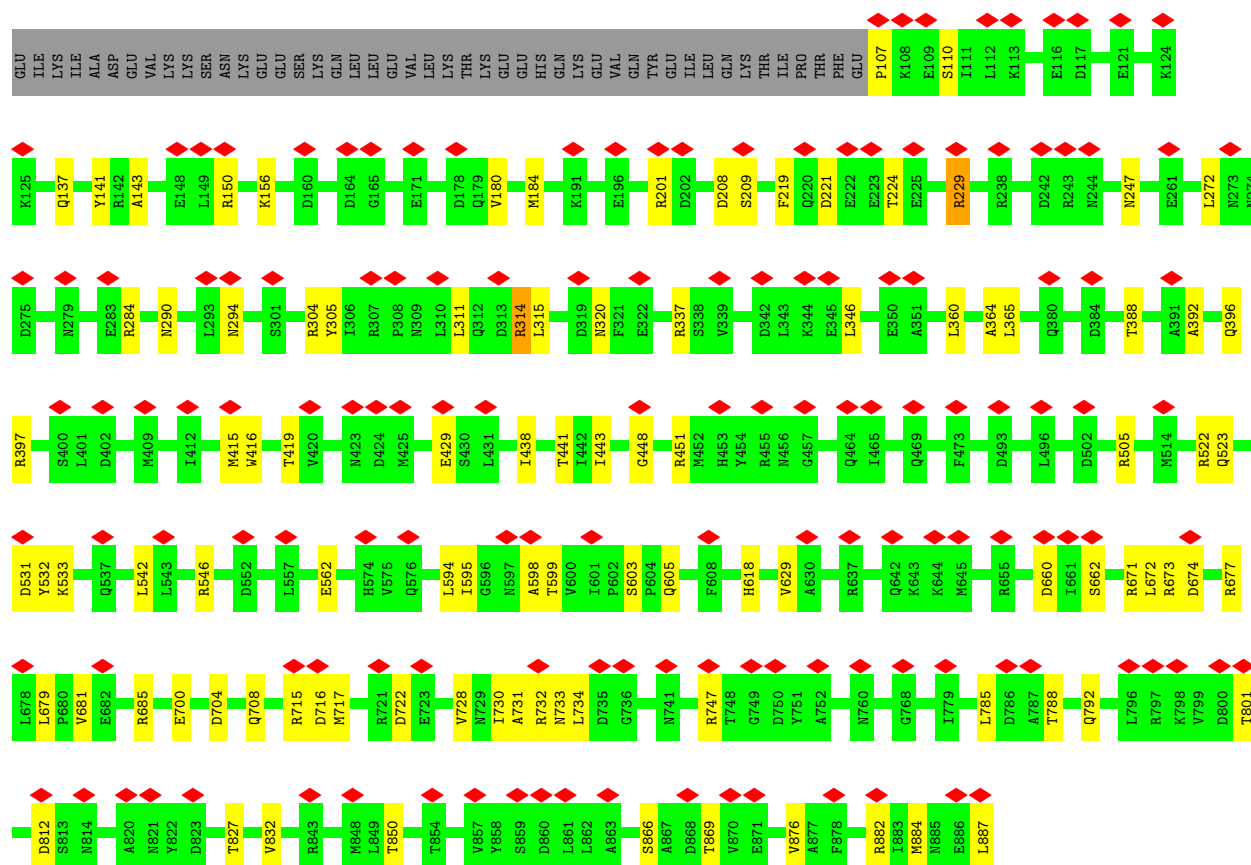
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Inner capsid protein VP2

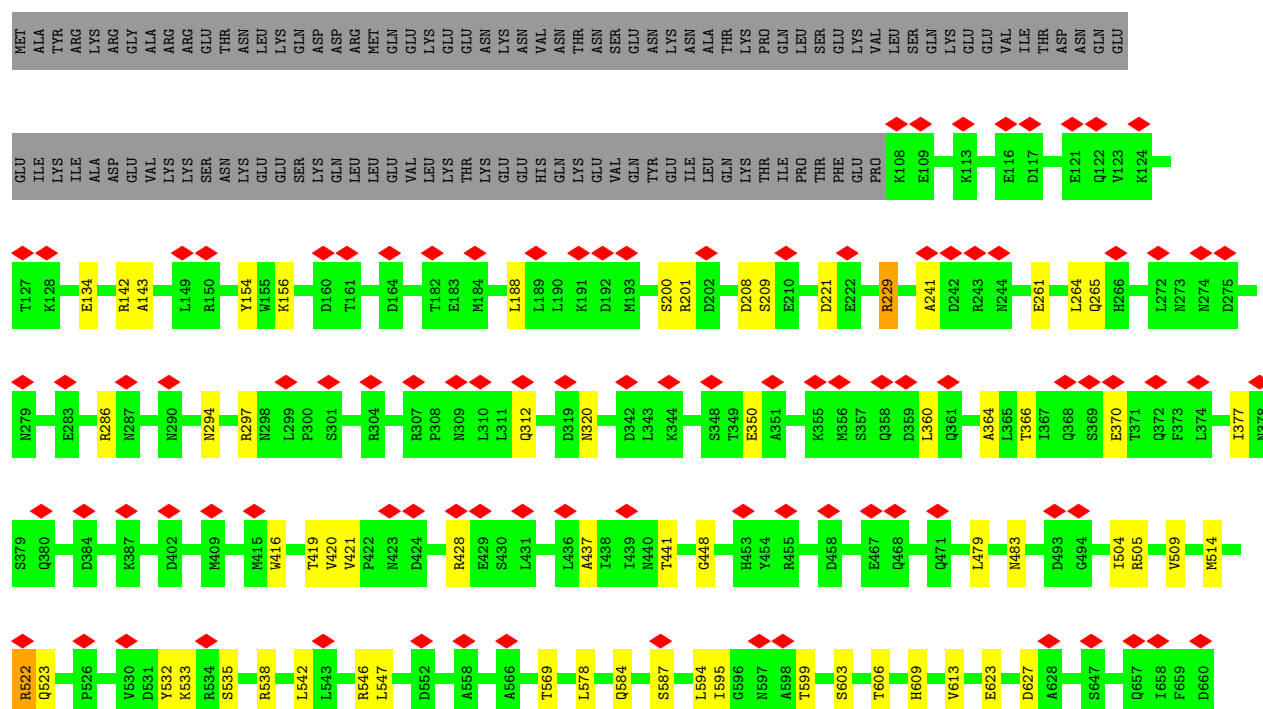
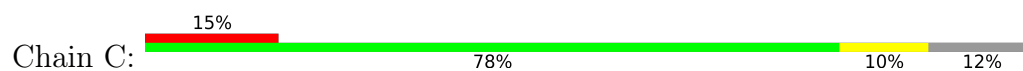


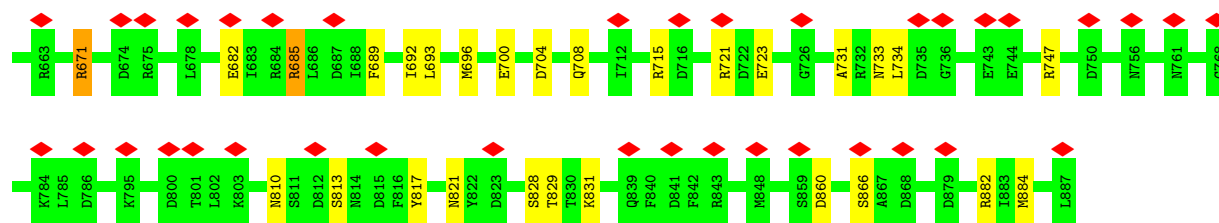
#### • Molecule 1: Inner capsid protein VP2



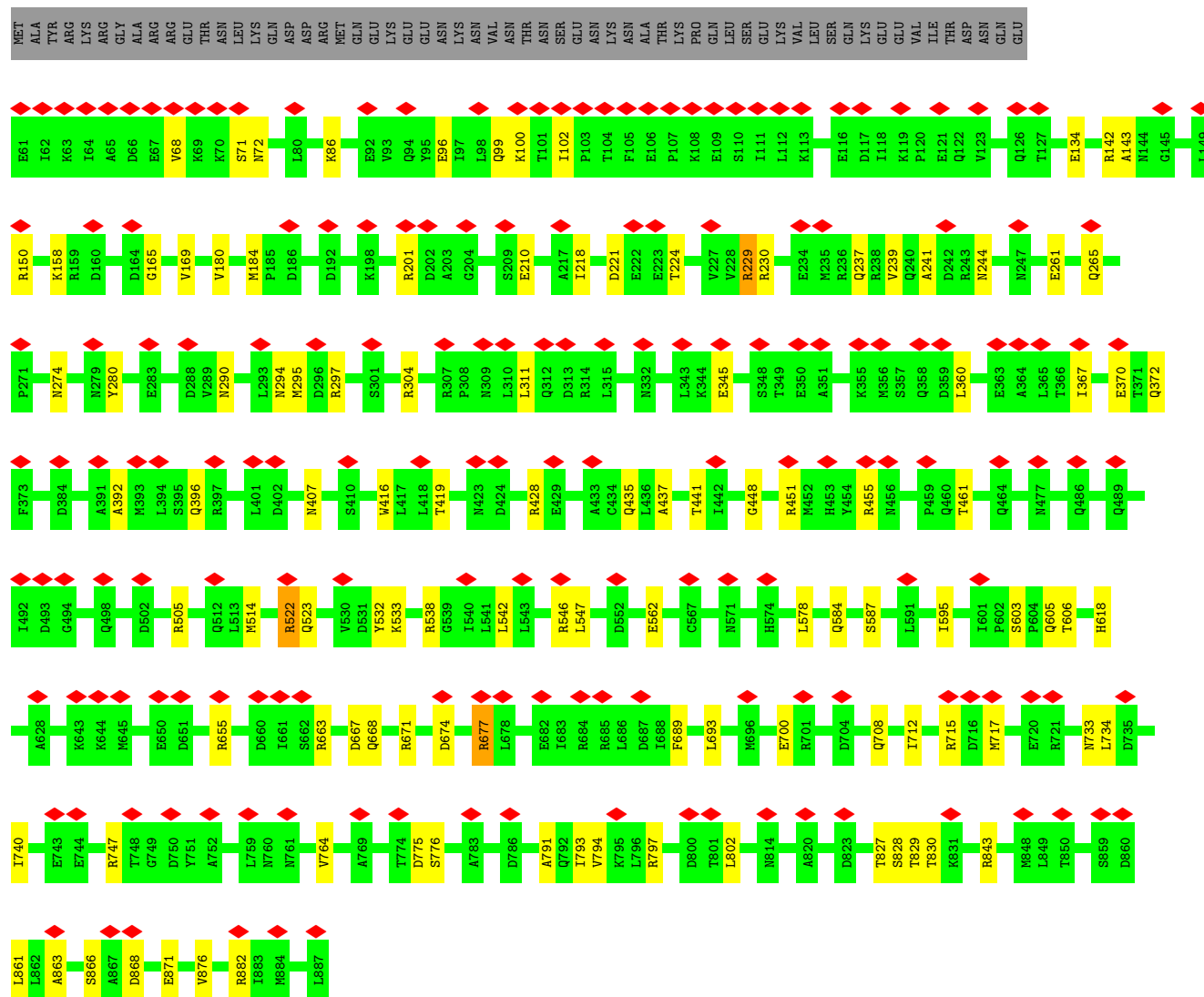
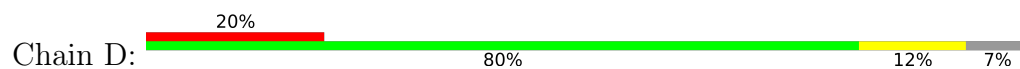


• Molecule 1: Inner capsid protein VP2

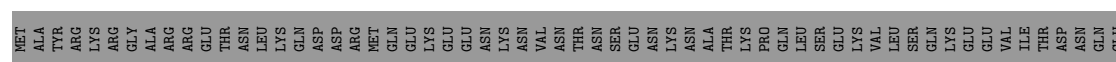
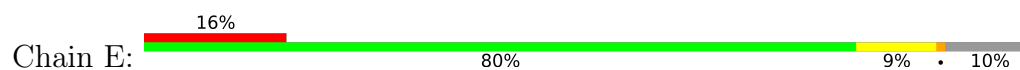


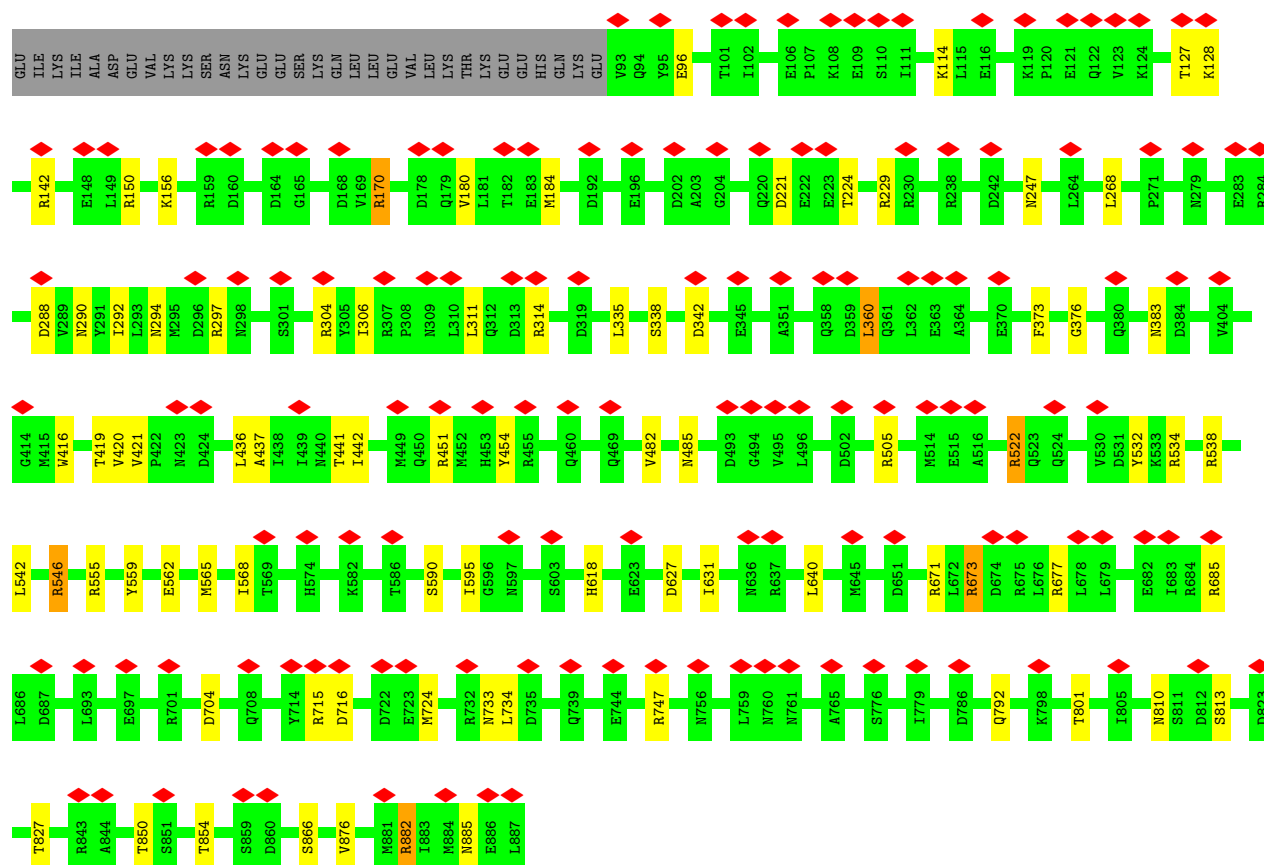


• Molecule 1: Inner capsid protein VP2

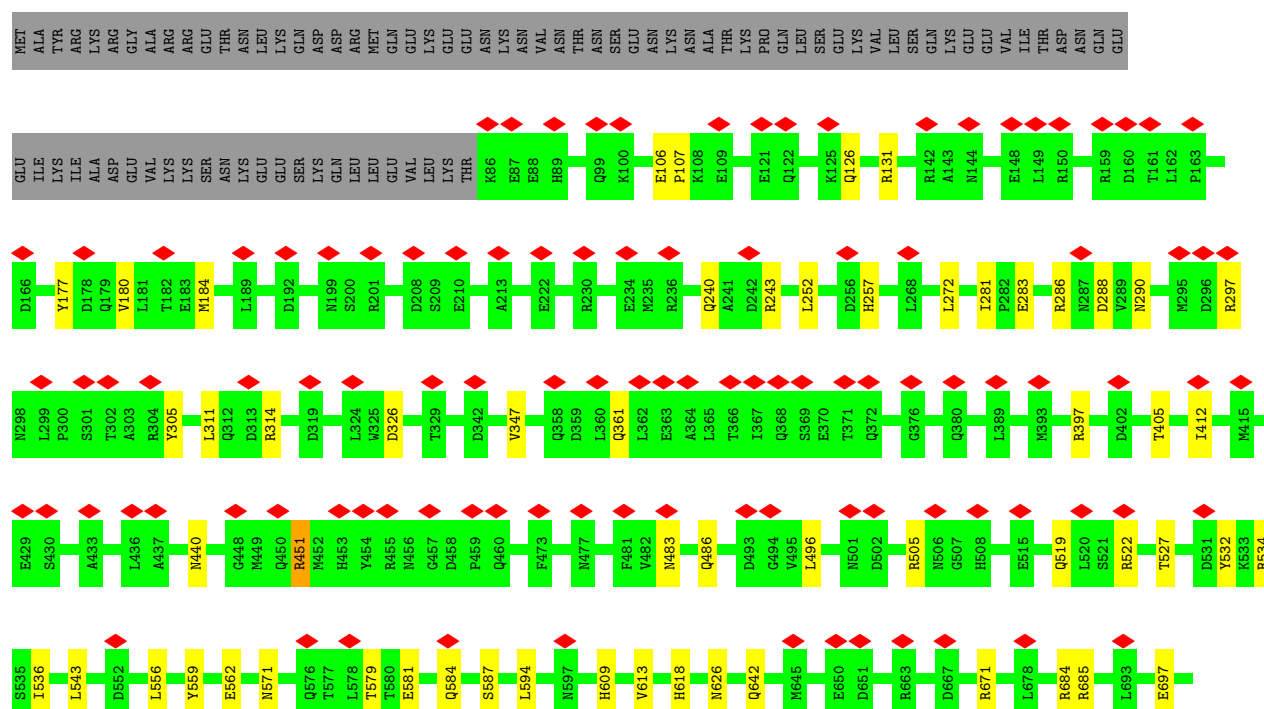
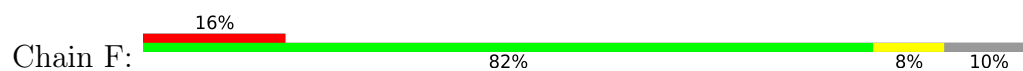


• Molecule 1: Inner capsid protein VP2

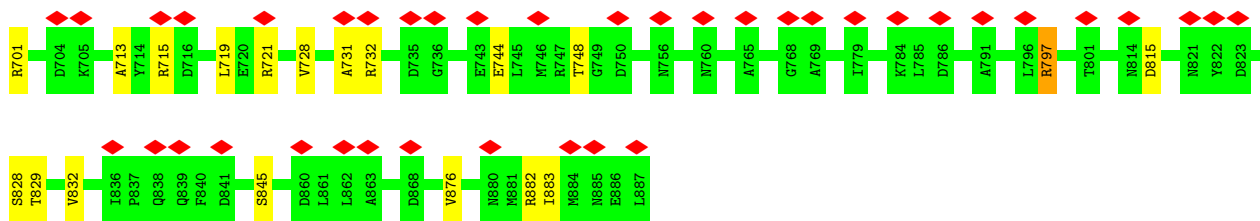




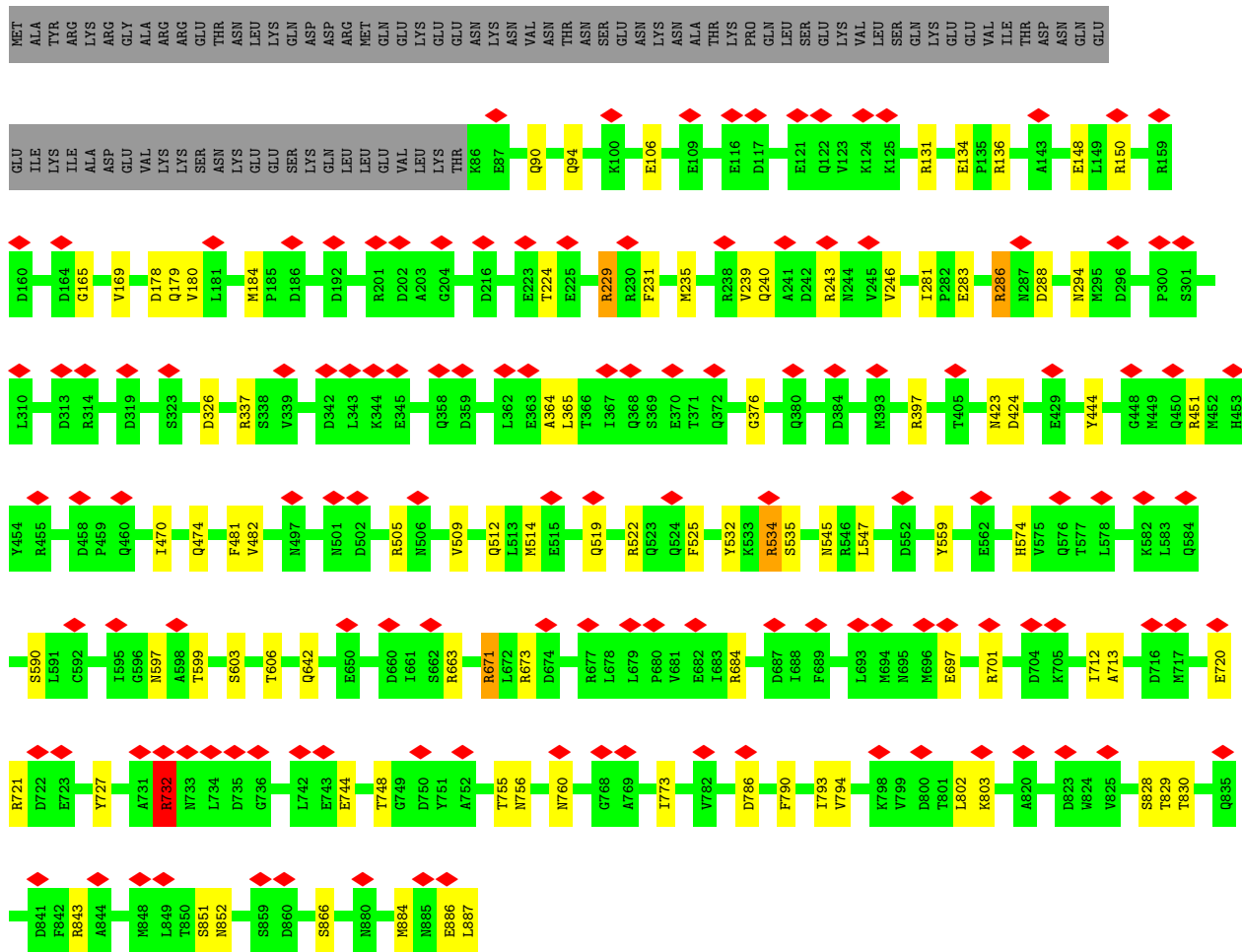
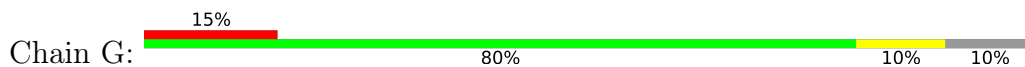
• Molecule 1: Inner capsid protein VP2



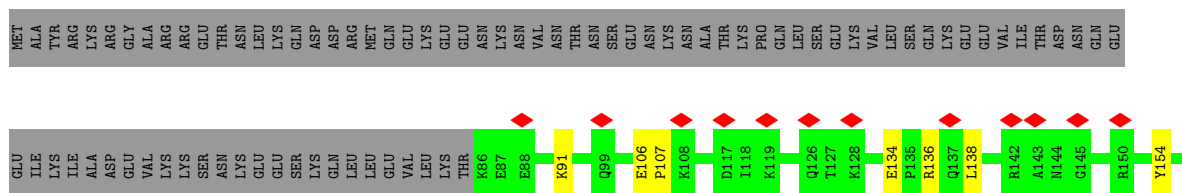
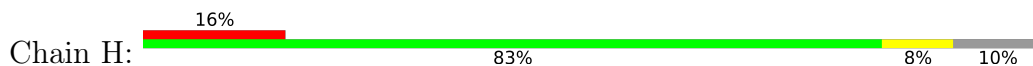


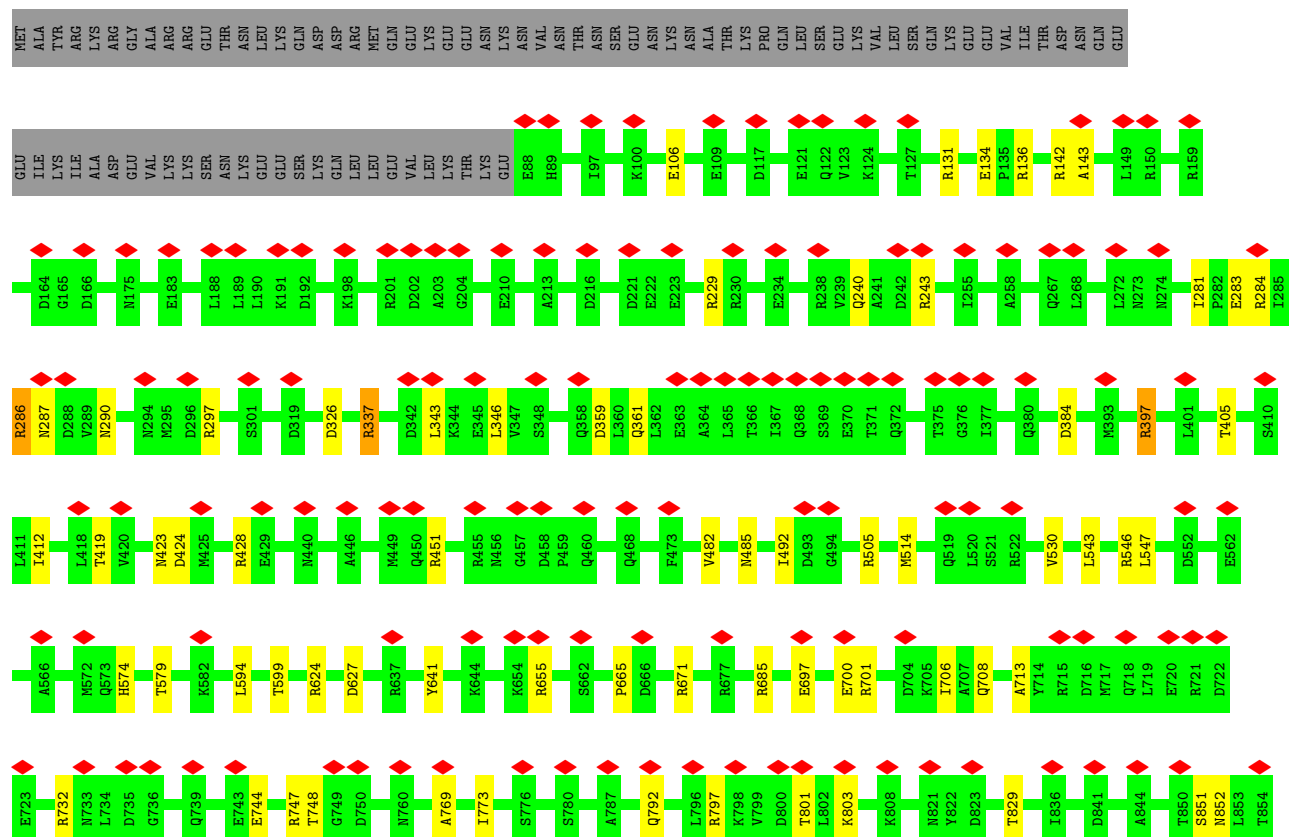


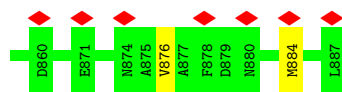
• Molecule 1: Inner capsid protein VP2



• Molecule 1: Inner capsid protein VP2







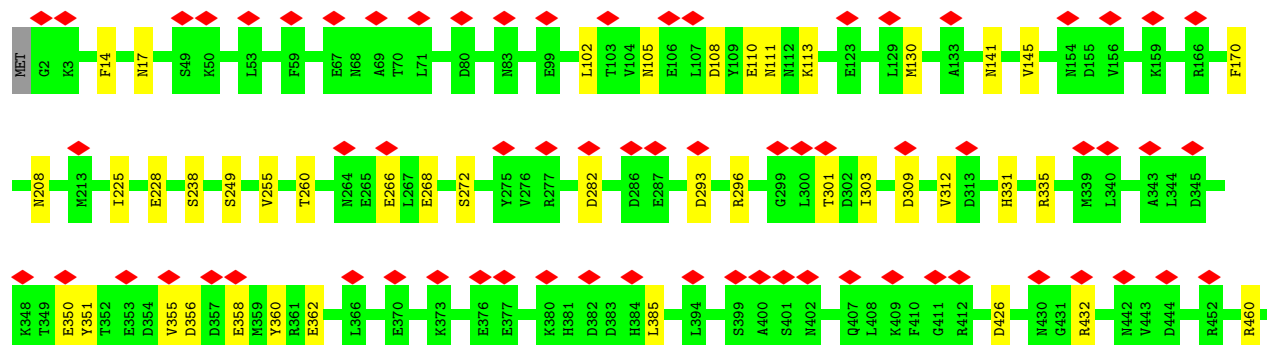
• Molecule 1: Inner capsid protein VP2

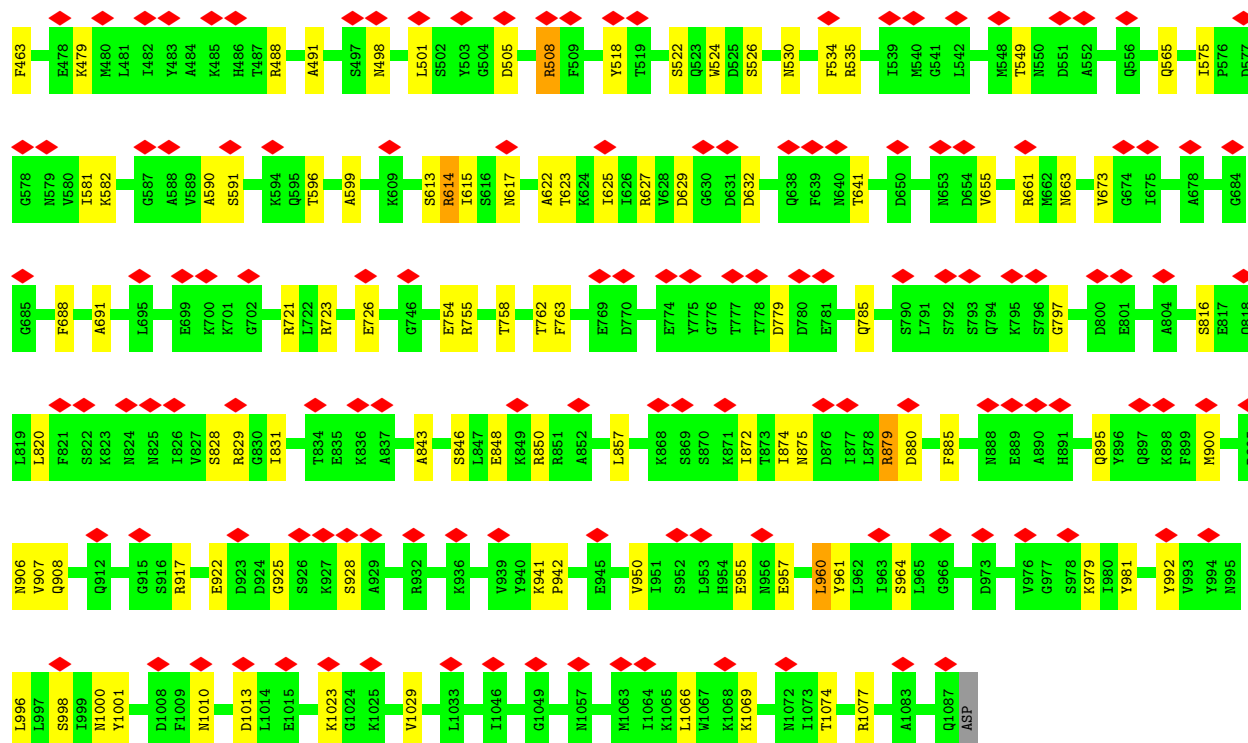
Chain J: 15% 82% 10% 8%



• Molecule 2: RNA-directed RNA polymerase

Chain P: 18% 87% 13%





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30606	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	9.960	Depositor
Minimum map value	-6.111	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.425	Depositor
Recommended contour level	2.0	Depositor
Map size (Å)	369.0, 369.0, 369.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	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	0.47	0/6495	0.87	20/8810 (0.2%)
1	B	0.46	0/6495	0.85	13/8810 (0.1%)
1	C	0.46	0/6487	0.86	12/8799 (0.1%)
1	D	0.45	0/6885	0.85	19/9332 (0.2%)
1	E	0.47	0/6618	0.87	18/8979 (0.2%)
1	F	0.45	0/6683	0.84	9/9064 (0.1%)
1	G	0.45	0/6683	0.84	12/9064 (0.1%)
1	H	0.45	0/6683	0.83	9/9064 (0.1%)
1	I	0.45	0/6665	0.85	15/9041 (0.2%)
1	J	0.46	0/6798	0.85	15/9217 (0.2%)
2	P	0.45	0/8963	0.81	9/12120 (0.1%)
All	All	0.46	0/75455	0.85	151/102300 (0.1%)

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
1	C	0	1
1	D	0	3
1	F	0	1
1	G	0	2
1	H	0	1
1	I	0	3
1	J	0	4
2	P	0	1
All	All	0	17

There are no bond length outliers.

The worst 5 of 151 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	671	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	D	671	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	B	671	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	J	79	LEU	CA-CB-CG	6.50	130.25	115.30
1	E	747	ARG	NE-CZ-NH1	6.48	123.54	120.30

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	143	ALA	Peptide
1	C	143	ALA	Peptide
1	D	102	ILE	Peptide
1	D	143	ALA	Peptide
1	D	99	GLN	Peptide

## 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	6379	6408	6408	49	0
1	B	6379	6408	6408	55	0
1	C	6372	6400	6400	54	0
1	D	6765	6809	6809	58	0
1	E	6499	6529	6529	45	0
1	F	6563	6588	6588	42	0
1	G	6563	6588	6588	49	0
1	H	6563	6588	6588	37	0
1	I	6545	6569	6569	33	0
1	J	6678	6713	6713	49	0
2	P	8789	8862	8861	79	0
All	All	74095	74462	74461	493	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 3.

The worst 5 of 493 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:E:360:LEU:HD21	1:E:542:LEU:HD11	1.61	0.81
2:P:874:ILE:HD11	2:P:996:LEU:HD13	1.70	0.73
1:F:744:GLU:O	1:F:748:THR:OG1	2.06	0.72
1:A:344:LYS:O	2:P:508:ARG:NH1	2.23	0.71
1:D:523:GLN:O	1:D:533:LYS:NZ	2.22	0.71

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	A	779/887 (88%)	714 (92%)	65 (8%)	0	100	100
1	B	779/887 (88%)	717 (92%)	62 (8%)	0	100	100
1	C	778/887 (88%)	708 (91%)	70 (9%)	0	100	100
1	D	825/887 (93%)	756 (92%)	69 (8%)	0	100	100
1	E	793/887 (89%)	723 (91%)	70 (9%)	0	100	100
1	F	800/887 (90%)	717 (90%)	82 (10%)	1 (0%)	51	85
1	G	800/887 (90%)	727 (91%)	73 (9%)	0	100	100
1	H	800/887 (90%)	717 (90%)	82 (10%)	1 (0%)	51	85
1	I	798/887 (90%)	725 (91%)	73 (9%)	0	100	100
1	J	814/887 (92%)	741 (91%)	72 (9%)	1 (0%)	51	85
2	P	1084/1088 (100%)	986 (91%)	97 (9%)	1 (0%)	51	85
All	All	9050/9958 (91%)	8231 (91%)	815 (9%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	P	942	PRO
1	H	107	PRO

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Mol	Chain	Res	Type
1	F	107	PRO
1	J	367	ILE

### 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	717/818 (88%)	715 (100%)	2 (0%)	92	95
1	B	717/818 (88%)	717 (100%)	0	100	100
1	C	716/818 (88%)	716 (100%)	0	100	100
1	D	762/818 (93%)	762 (100%)	0	100	100
1	E	731/818 (89%)	730 (100%)	1 (0%)	93	96
1	F	738/818 (90%)	737 (100%)	1 (0%)	93	96
1	G	738/818 (90%)	737 (100%)	1 (0%)	93	96
1	H	738/818 (90%)	737 (100%)	1 (0%)	93	96
1	I	736/818 (90%)	735 (100%)	1 (0%)	93	96
1	J	752/818 (92%)	751 (100%)	1 (0%)	93	96
2	P	986/989 (100%)	985 (100%)	1 (0%)	93	96
All	All	8331/9169 (91%)	8322 (100%)	9 (0%)	93	96

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	732	ARG
2	P	130	MET
1	F	732	ARG
1	G	732	ARG
1	H	732	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	P	530	ASN
2	P	663	ASN
2	P	908	GLN
1	D	560	ASN
1	C	614	ASN

### 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 monosaccharides 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.

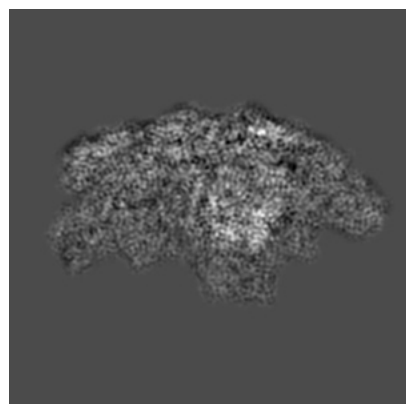
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20086. These allow visual inspection of the internal detail of the map and identification of artifacts.

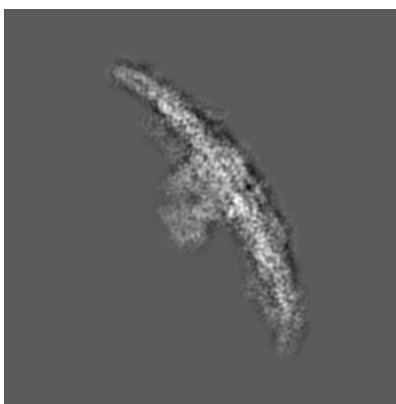
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

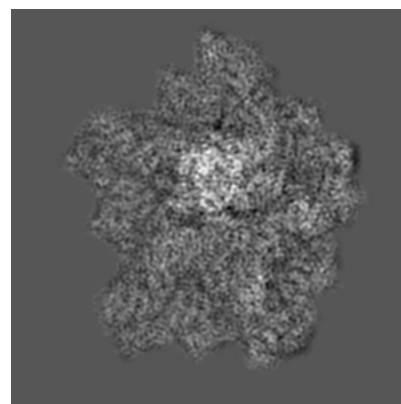
#### 6.1.1 Primary map



X

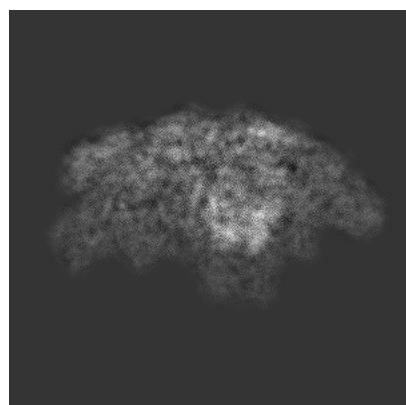


Y

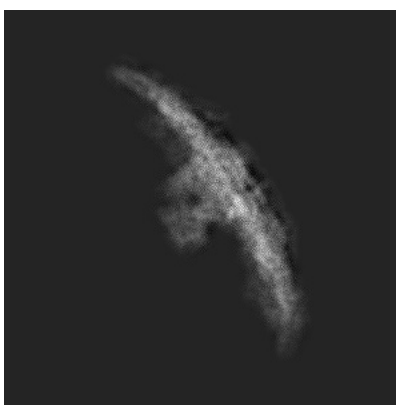


Z

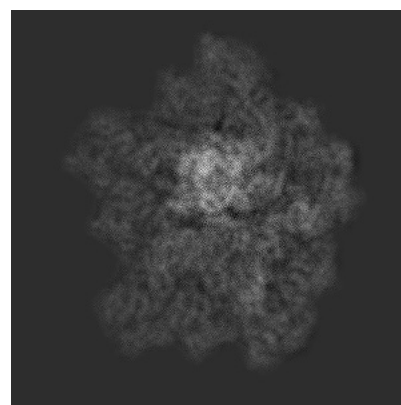
#### 6.1.2 Raw map



X



Y

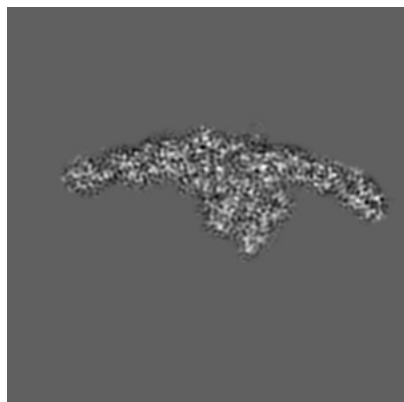


Z

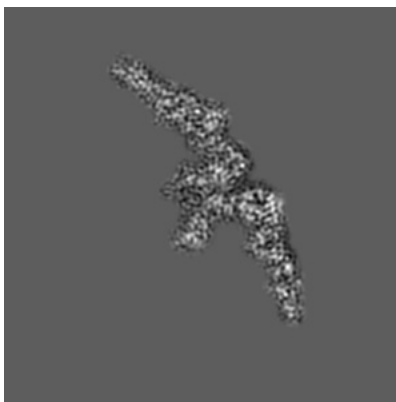
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

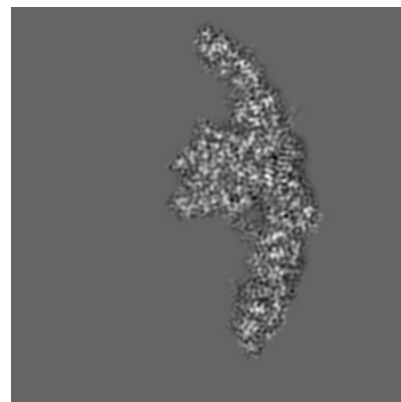
### 6.2.1 Primary map



X Index: 150

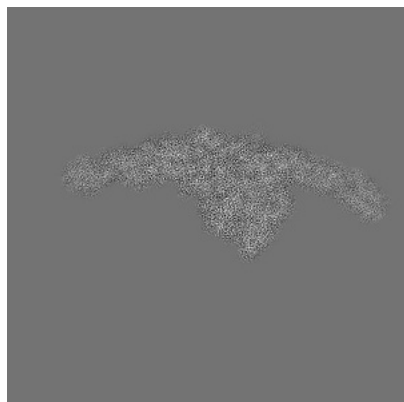


Y Index: 150

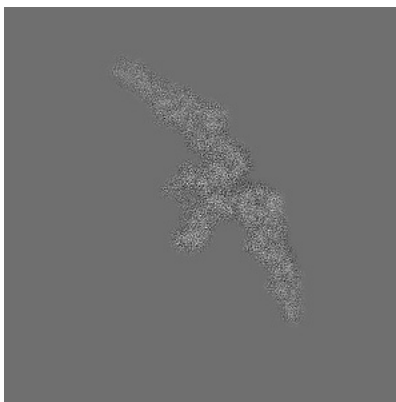


Z Index: 150

### 6.2.2 Raw map



X Index: 150



Y Index: 150



Z Index: 150

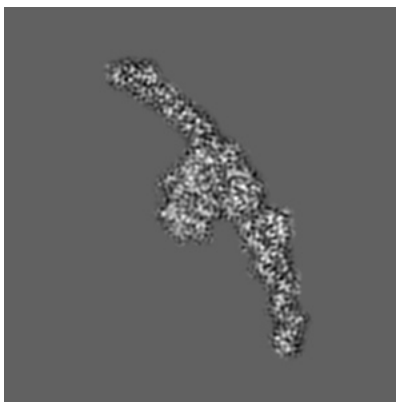
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

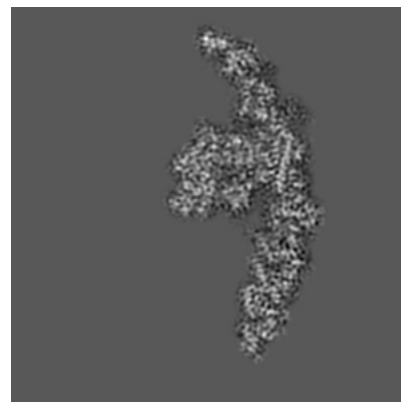
### 6.3.1 Primary map



X Index: 145

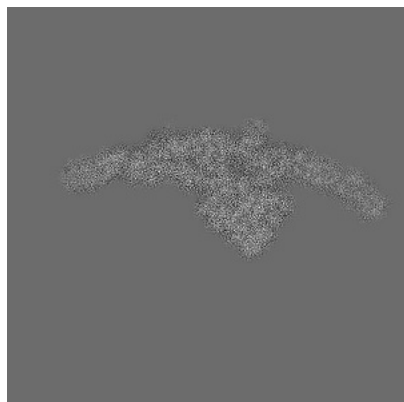


Y Index: 189

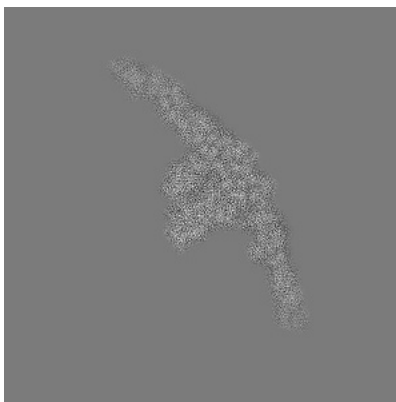


Z Index: 146

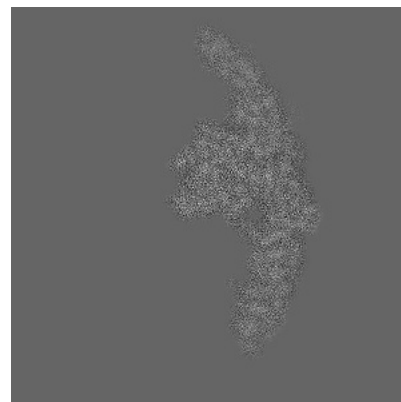
### 6.3.2 Raw map



X Index: 146



Y Index: 167

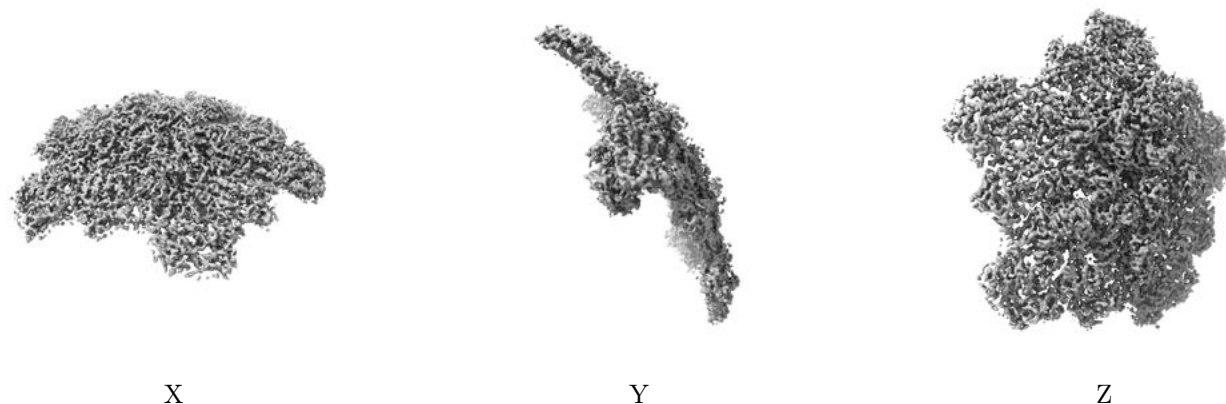


Z Index: 150

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

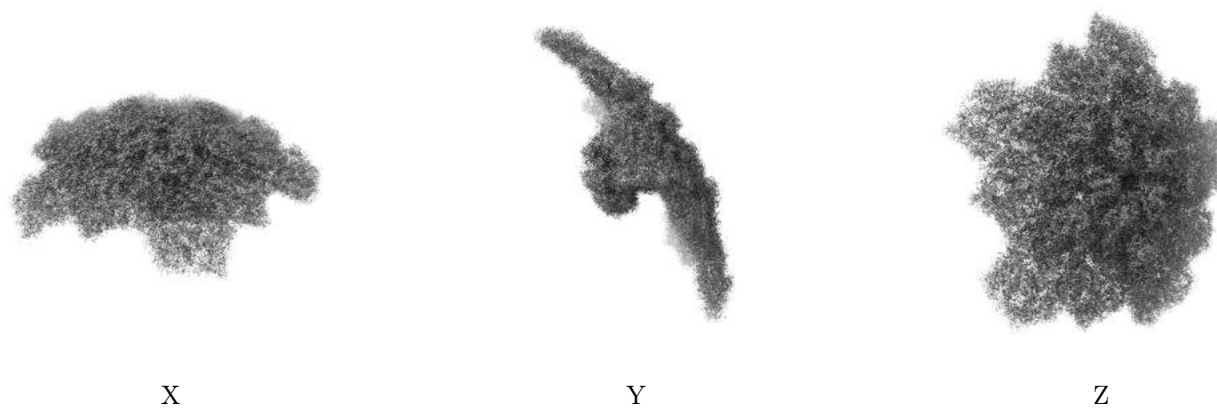
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



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

### 6.4.2 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.

## 6.5 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

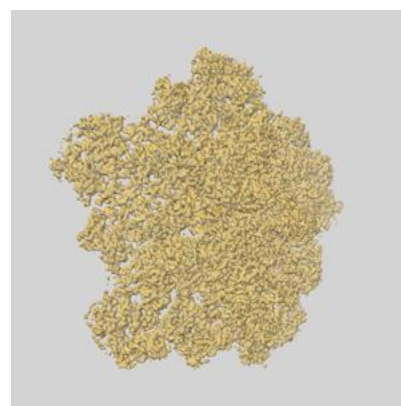
### 6.5.1 emd\_20086\_msk\_1.map [i](#)



X



Y

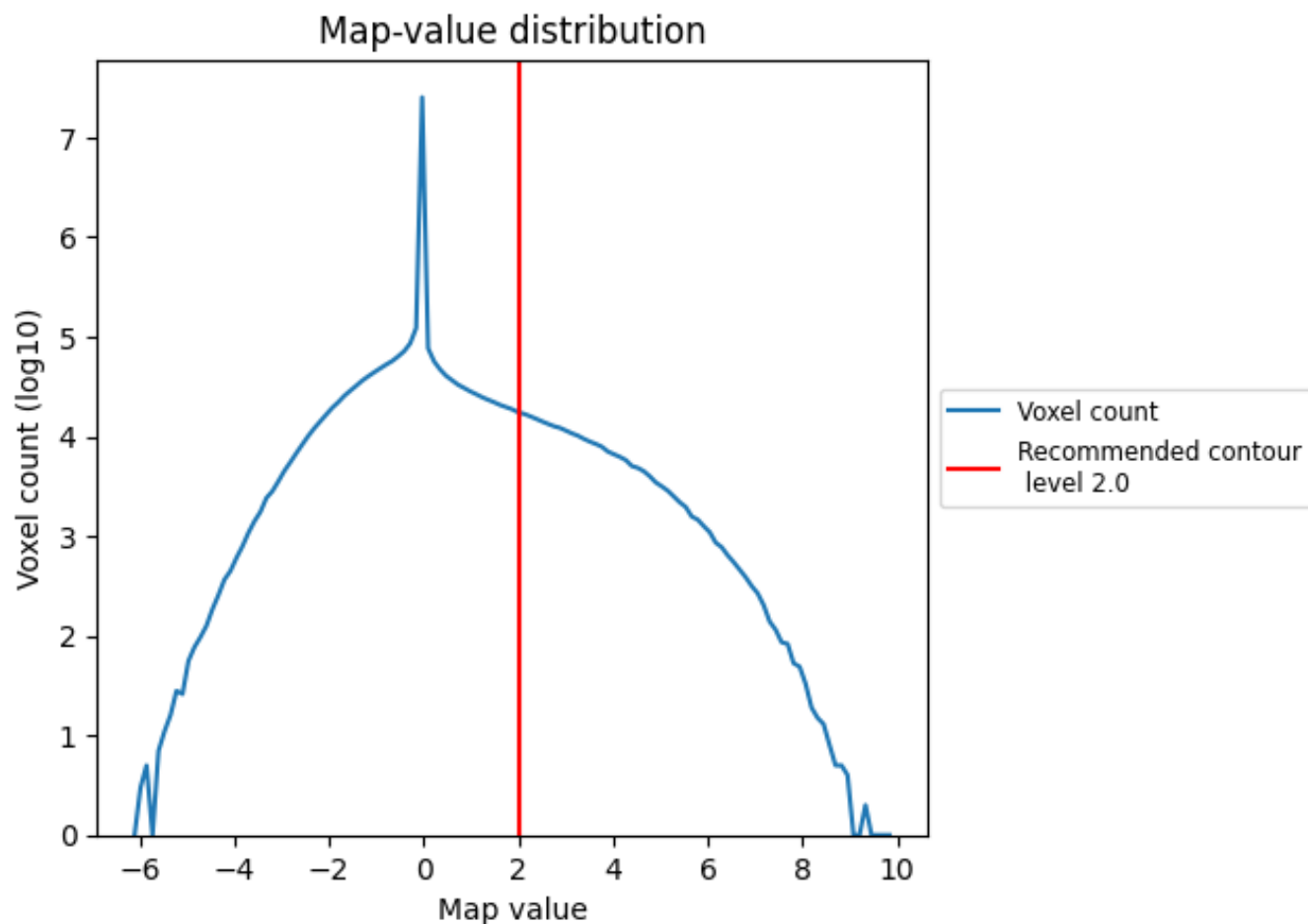


Z

## 7 Map analysis [i](#)

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

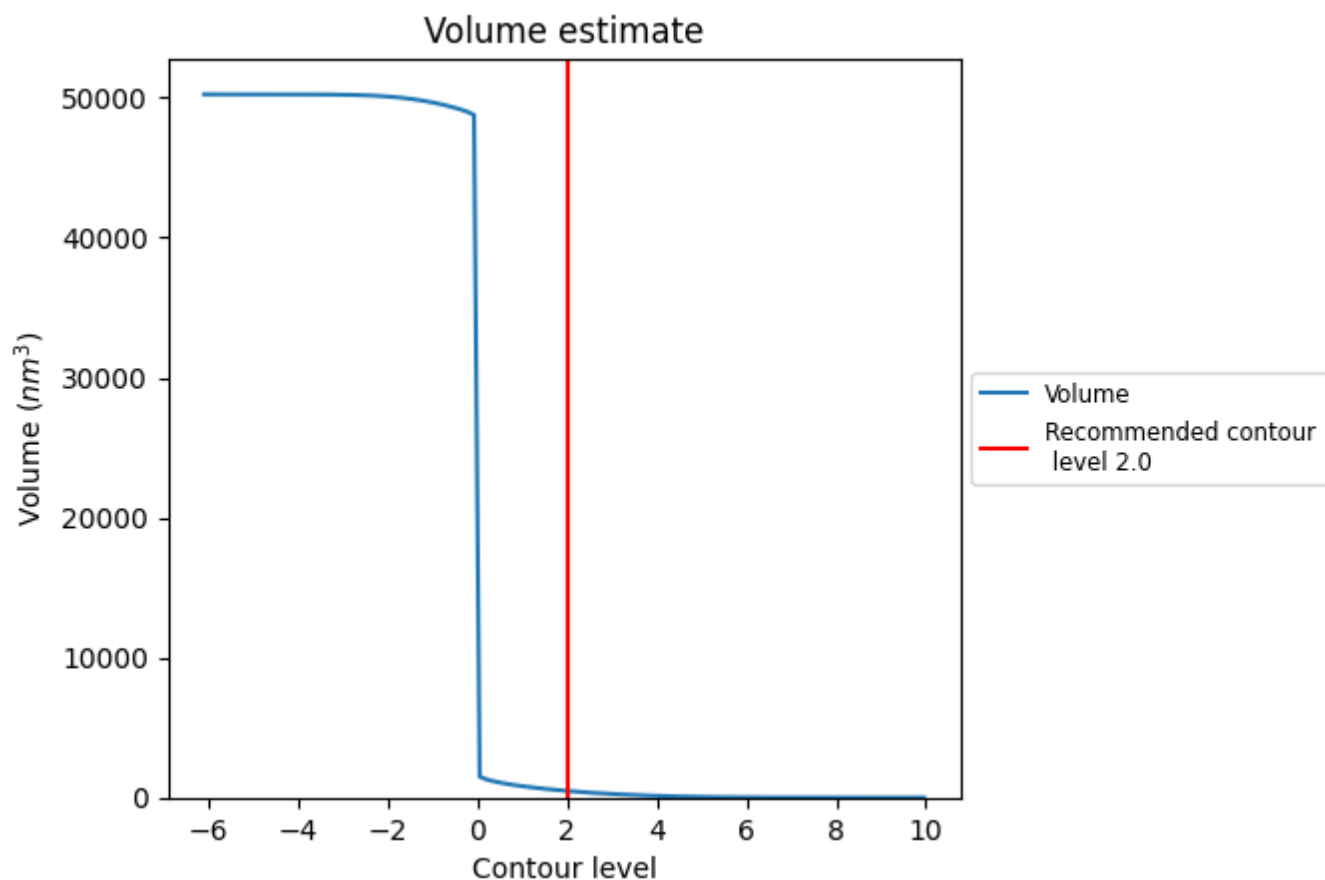
### 7.1 Map-value distribution [i](#)



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.



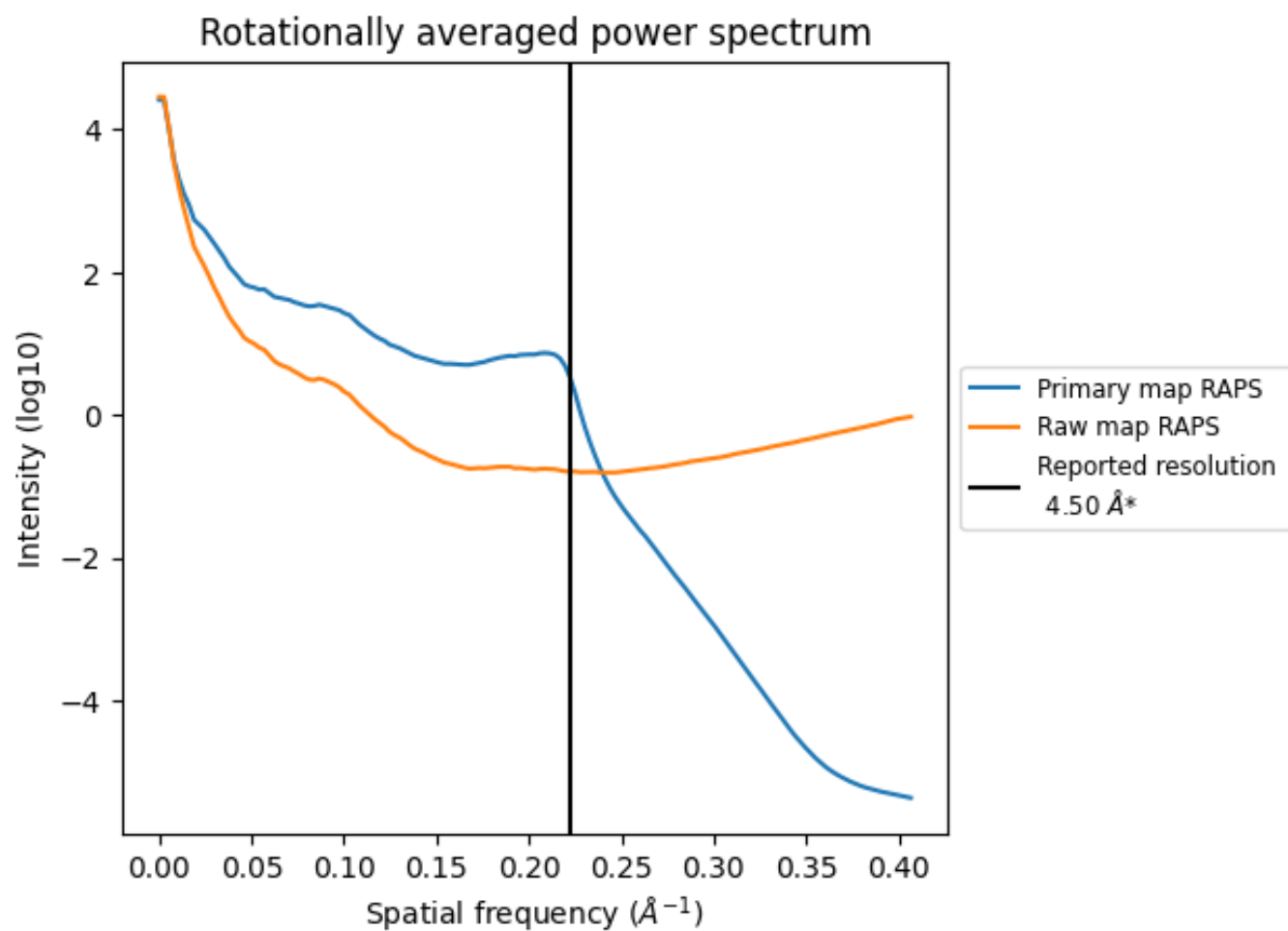
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 473 nm<sup>3</sup>; this corresponds to an approximate mass of 427 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 ⓘ

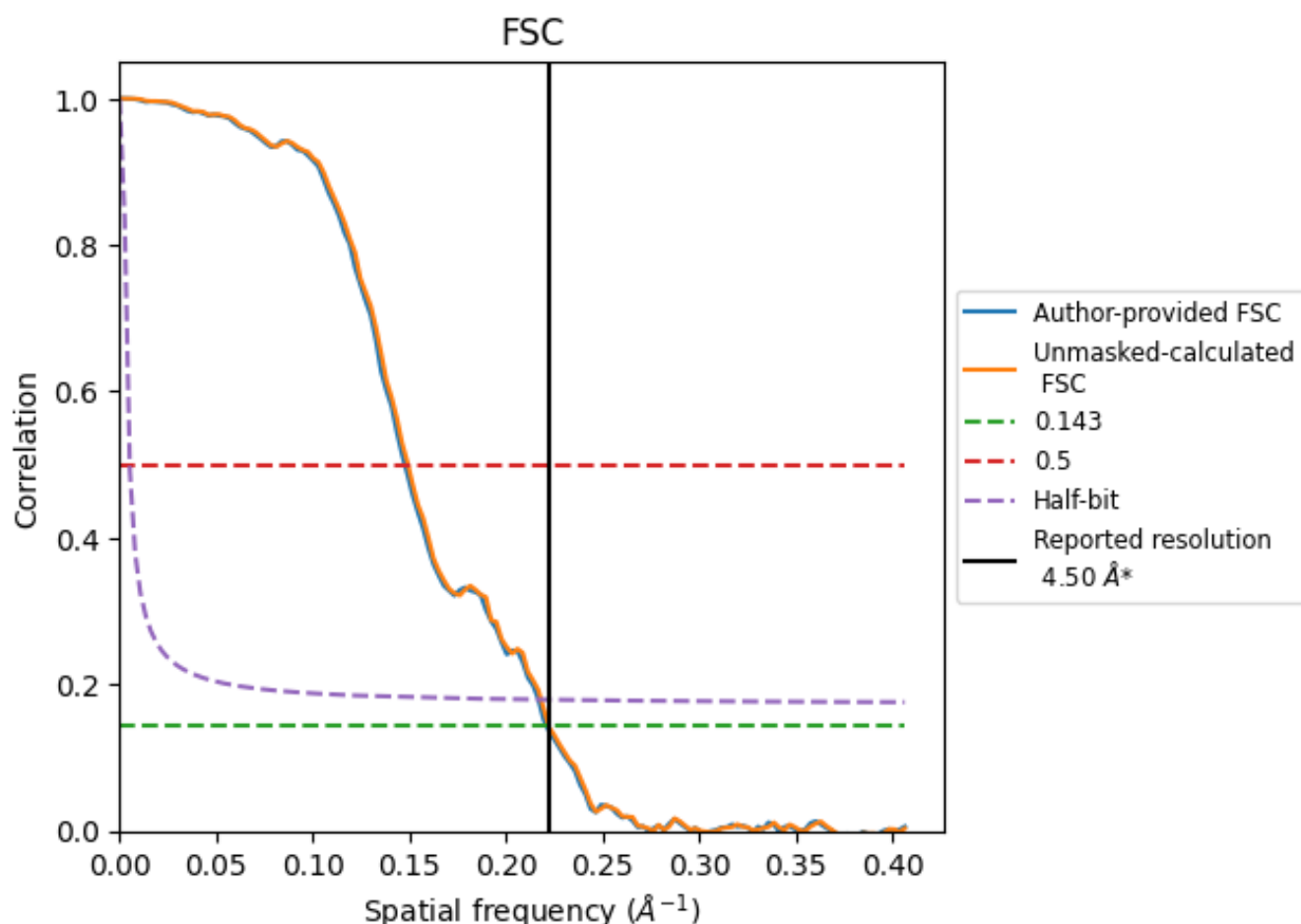


\*Reported resolution corresponds to spatial frequency of 0.222 Å<sup>-1</sup>

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

## 8.2 Resolution estimates [i](#)

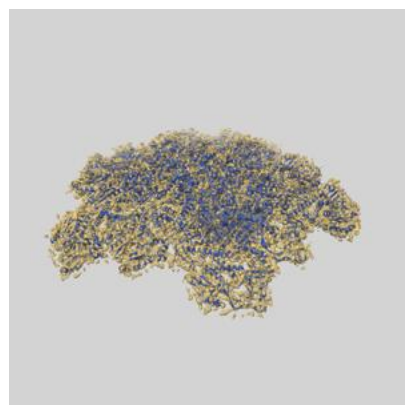
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.52	6.77	4.61
Unmasked-calculated*	4.50	6.70	4.58

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

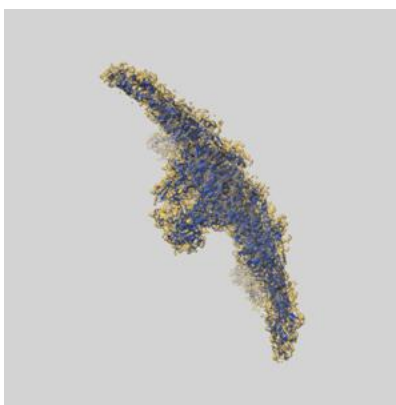
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20086 and PDB model 6OJ3. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

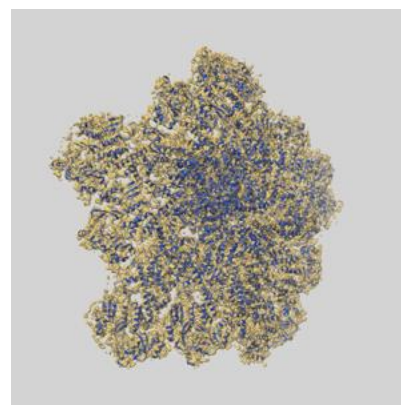
### 9.1 Map-model overlay [i](#)



X



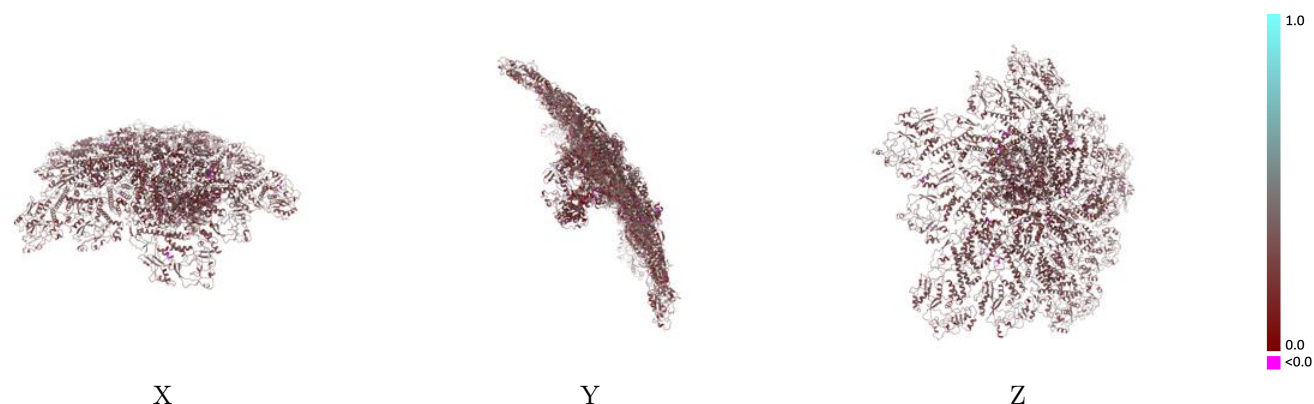
Y



Z

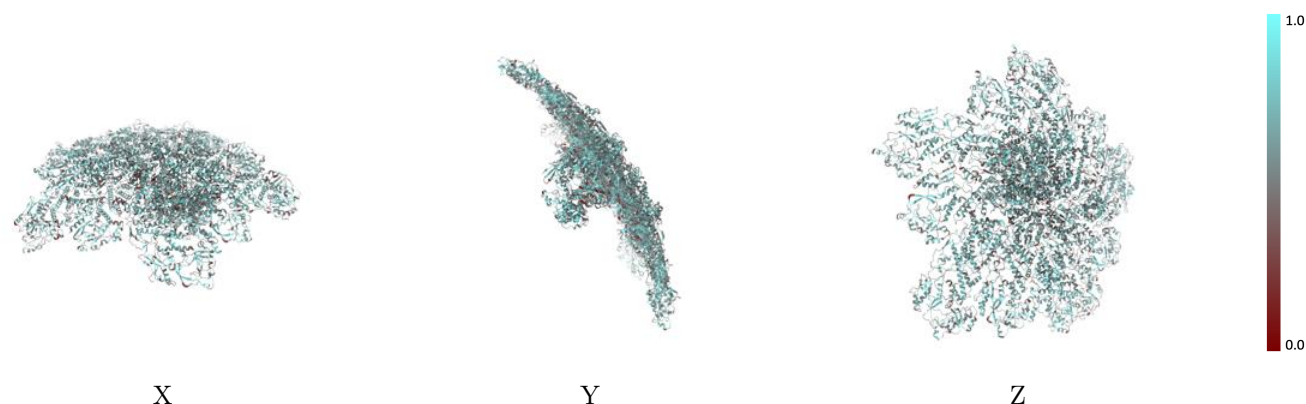
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



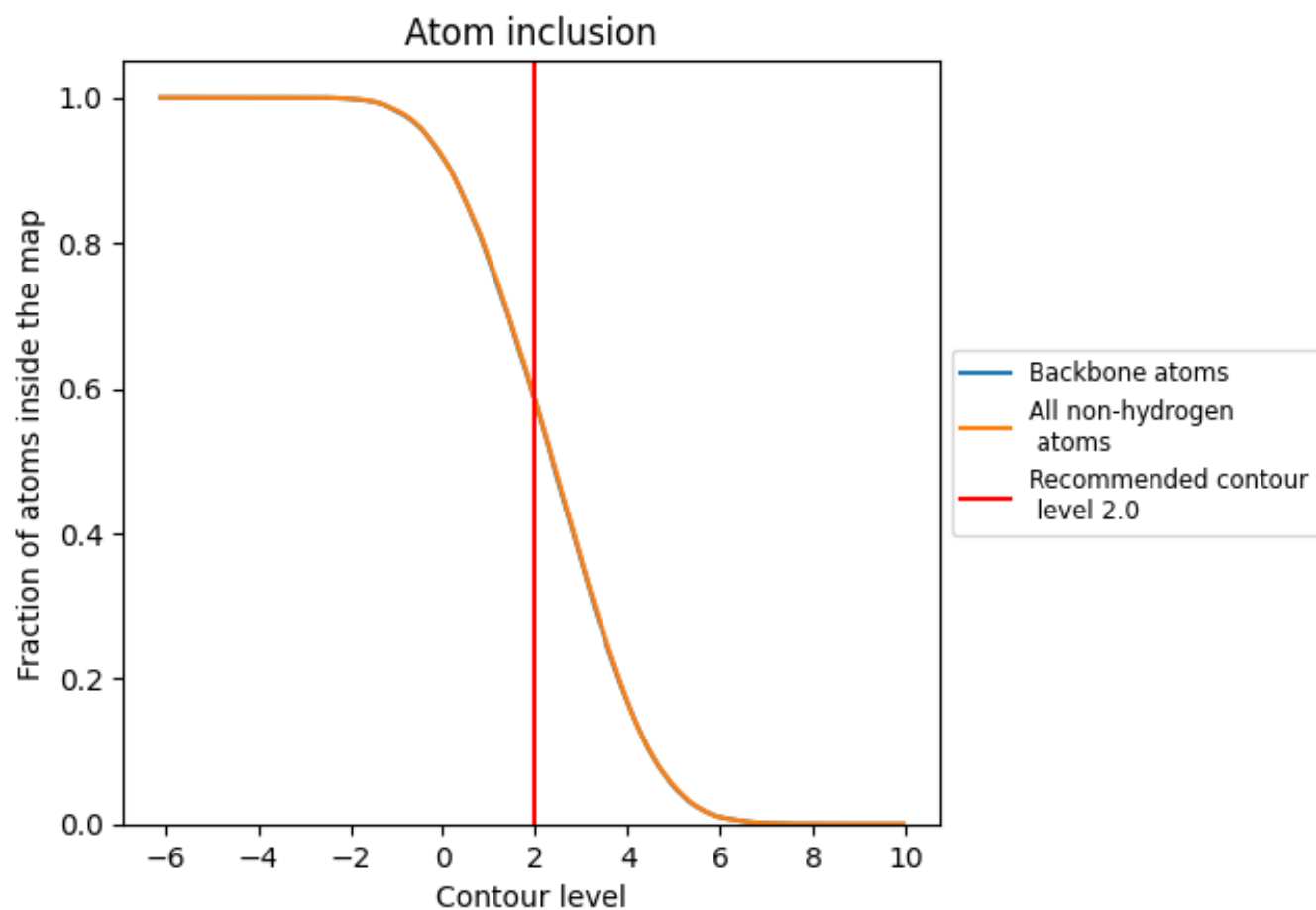
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.0).

























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (2.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5844	 0.3000
A	 0.6020	 0.3060
B	 0.5840	 0.3030
C	 0.5912	 0.3090
D	 0.5688	 0.3040
E	 0.5869	 0.3040
F	 0.5898	 0.3020
G	 0.6089	 0.3080
H	 0.5957	 0.3060
I	 0.5891	 0.3010
J	 0.6008	 0.3040
P	 0.6009	 0.2640

