



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 05:52 pm GMT

PDB ID : 2YEW  
EMDB ID : EMD-1886  
Title : Modeling Barmah Forest virus structural proteins  
Authors : Kostyuchenko, V.A.; Jakana, J.; Liu, X.; Haddow, A.D.; Aung, M.; Weaver, S.C.; Chiu, W.; Lok, S.M.  
Deposited on : 2011-03-31  
Resolution : 5.00 Å (reported)  
Based on initial models : 2XFB, 1SVP, 2ALA

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

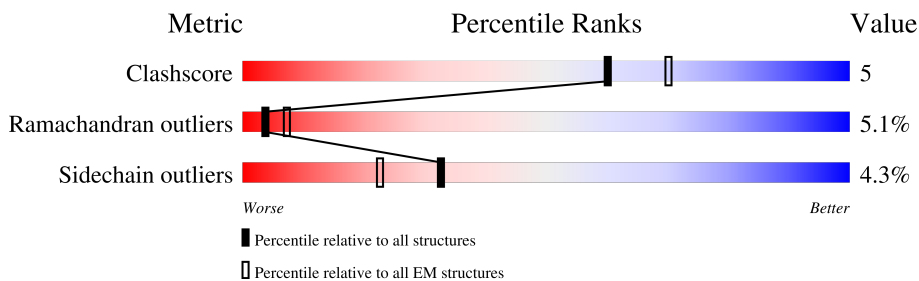
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.00 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.



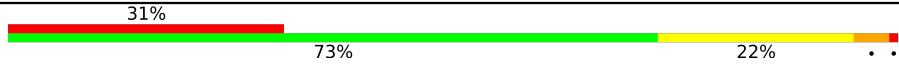

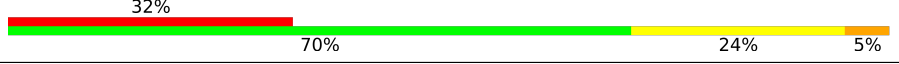
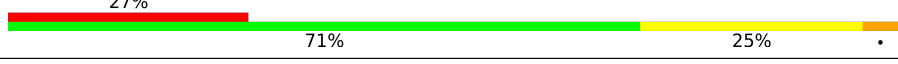
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	253	17% (Poor fit), 49% (0 outliers), 15% (1 outlier), 32% (2+ outliers)
1	D	253	23% (Poor fit), 49% (0 outliers), 15% (1 outlier), 32% (2+ outliers)
1	G	253	22% (Poor fit), 46% (0 outliers), 18% (1 outlier), 32% (2+ outliers)
1	J	253	24% (Poor fit), 49% (0 outliers), 14% (1 outlier), 32% (2+ outliers)
2	B	427	20% (Poor fit), 67% (0 outliers), 25% (1 outlier), 6% (2+ outliers)
2	E	427	24% (Poor fit), 69% (0 outliers), 25% (1 outlier), 5% (2+ outliers)
2	H	427	28% (Poor fit), 74% (0 outliers), 20% (1 outlier), 5% (2+ outliers)
2	K	427	23% (Poor fit), 70% (0 outliers), 24% (1 outlier), 5% (2+ outliers)

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Mol	Chain	Length	Quality of chain
3	C	421	
3	F	421	
3	I	421	
3	L	421	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 31120 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called CAPSID PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	171	1316	827	234	244	11	0	0
1	D	171	1316	827	234	244	11	0	0
1	G	171	1316	827	234	244	11	0	0
1	J	171	1316	827	234	244	11	0	0

- Molecule 2 is a protein called E1 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	426	3225	2045	526	631	23	0	1
2	E	426	3225	2045	526	631	23	0	1
2	H	426	3225	2045	526	631	23	0	1
2	K	426	3225	2045	526	631	23	0	1

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
B	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
E	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
H	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946
K	?	-	HIS	deletion	UNP P89946

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Chain	Residue	Modelled	Actual	Comment	Reference
K	?	-	HIS	deletion	UNP P89946

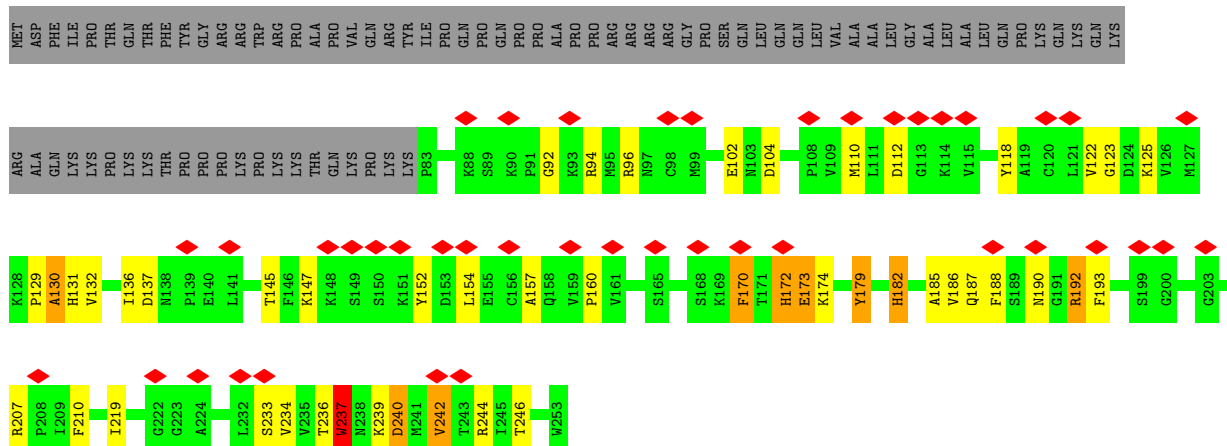
- Molecule 3 is a protein called E2 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	421	3239	2054	552	610	23	0	0
3	F	421	3239	2054	552	610	23	0	0
3	I	421	3239	2054	552	610	23	0	0
3	L	421	3239	2054	552	610	23	0	0

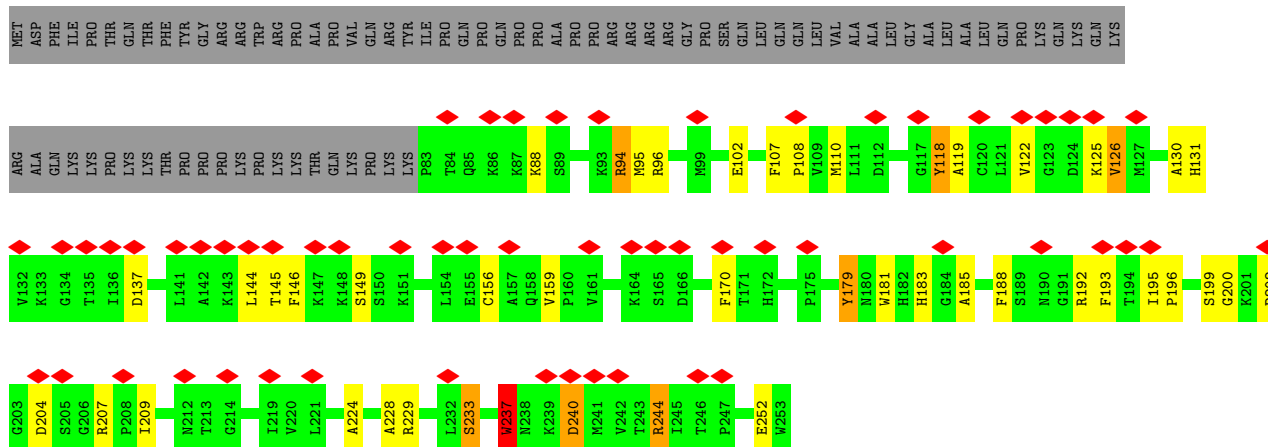
### 3 Residue-property plots

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

#### • Molecule 1: CAPSID PROTEIN

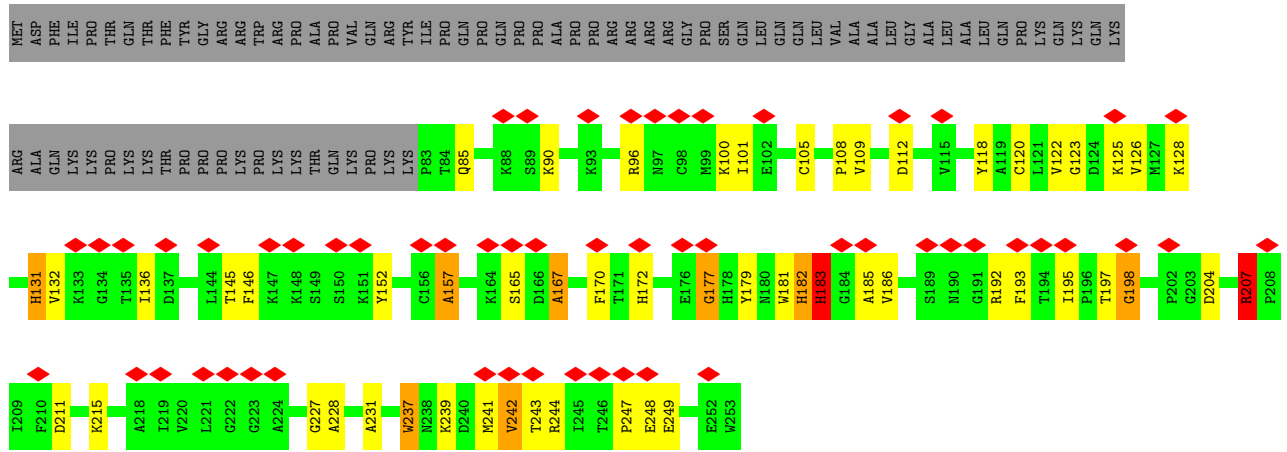


#### • Molecule 1: CAPSID PROTEIN

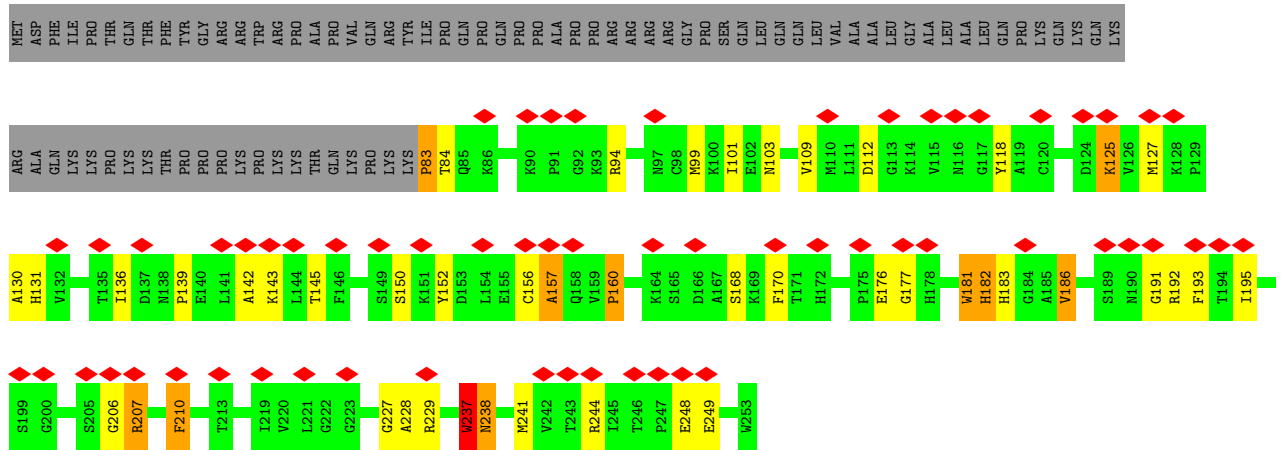


#### • Molecule 1: CAPSID PROTEIN

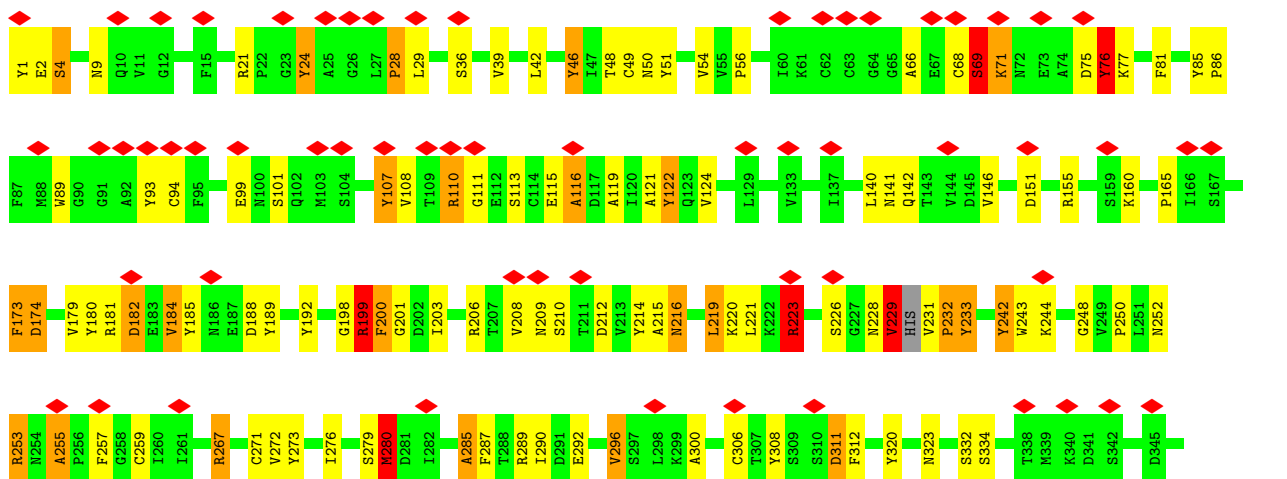




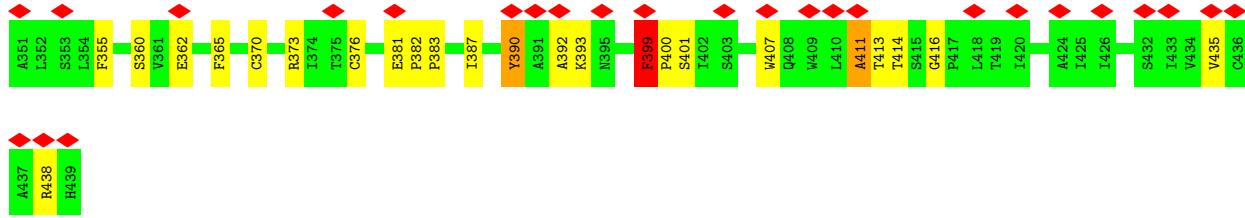
• Molecule 1: CAPSID PROTEIN



• Molecule 2: E1 ENVELOPE GLYCOPROTEIN



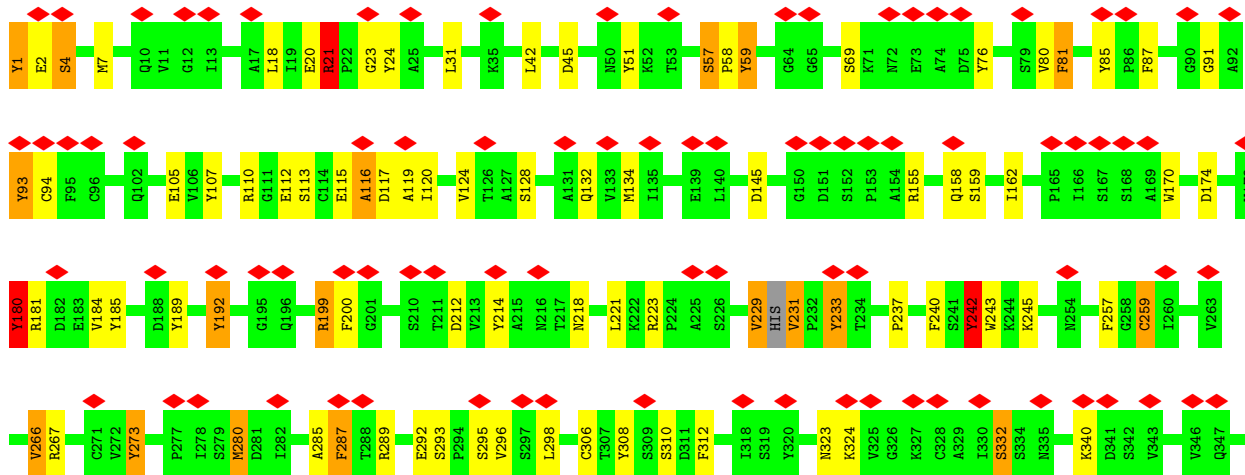
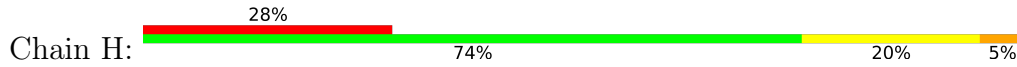


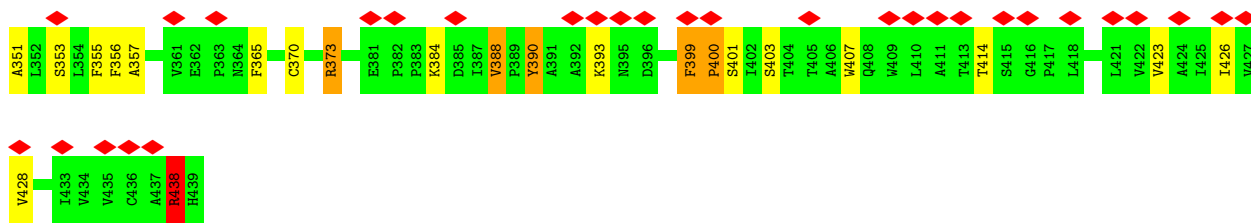


• Molecule 2: E1 ENVELOPE GLYCOPROTEIN

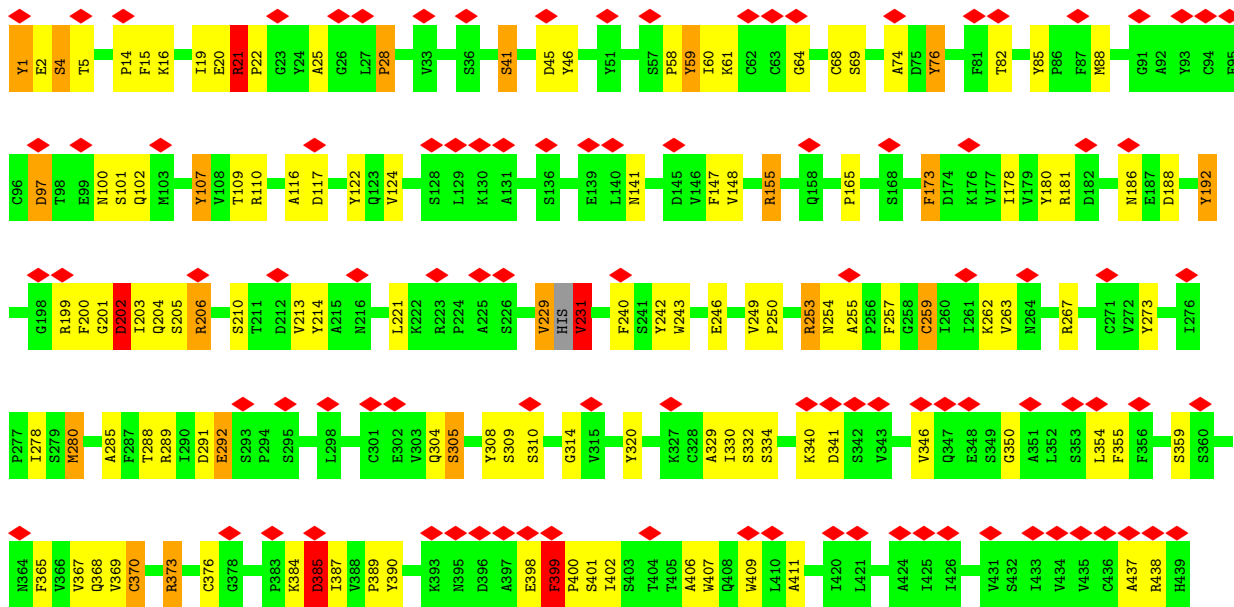


• Molecule 2: E1 ENVELOPE GLYCOPROTEIN

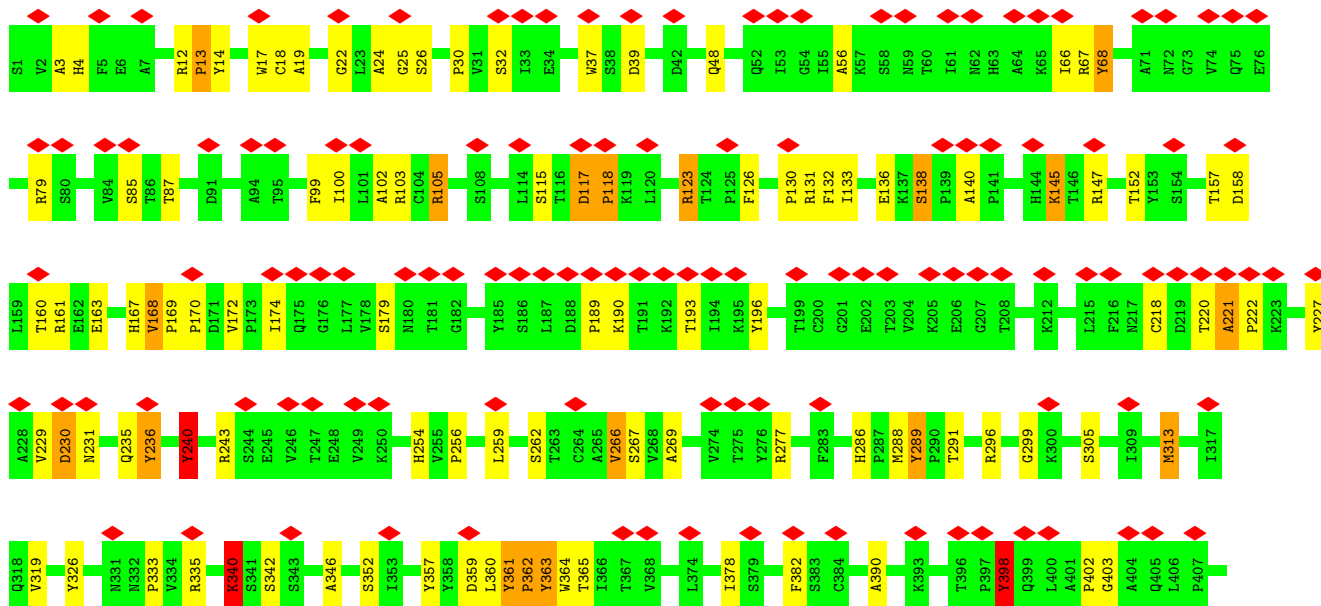


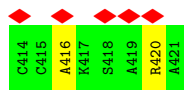


• Molecule 2: E1 ENVELOPE GLYCOPROTEIN

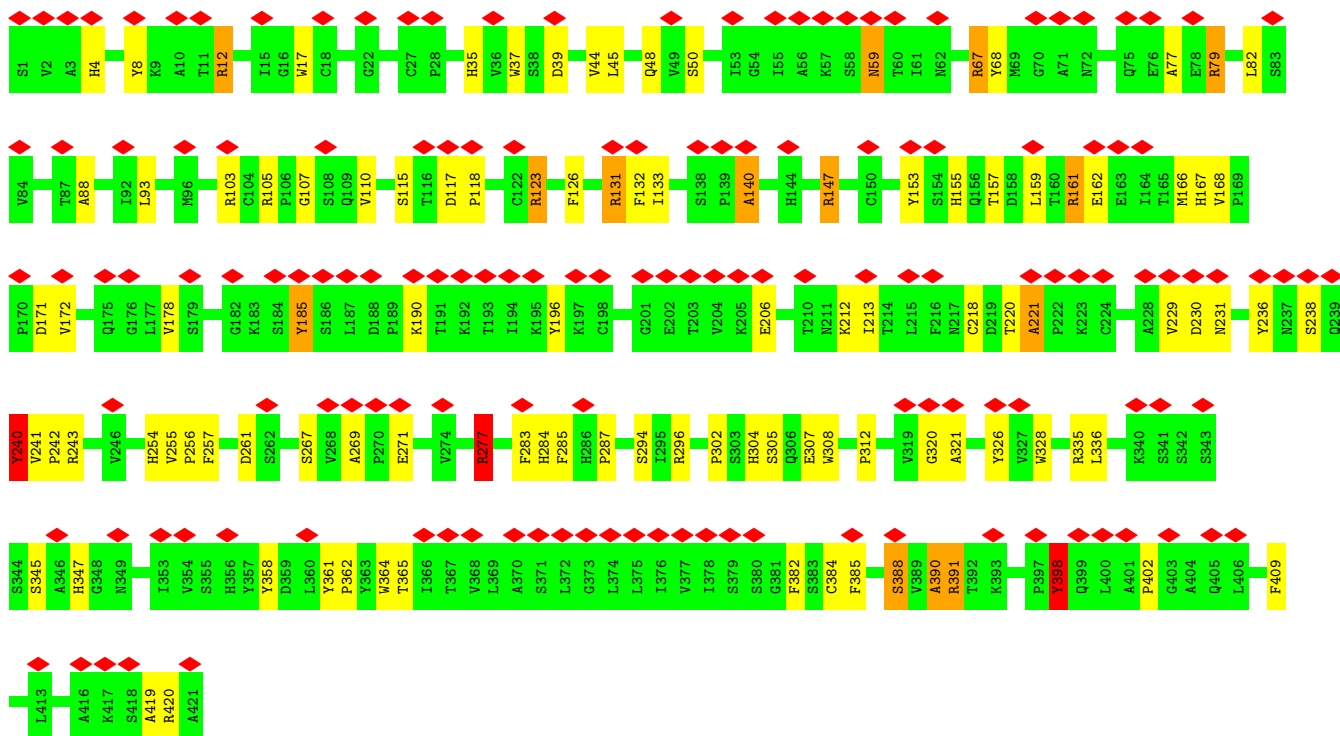
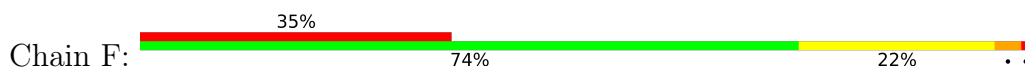


• Molecule 3: E2 ENVELOPE GLYCOPROTEIN

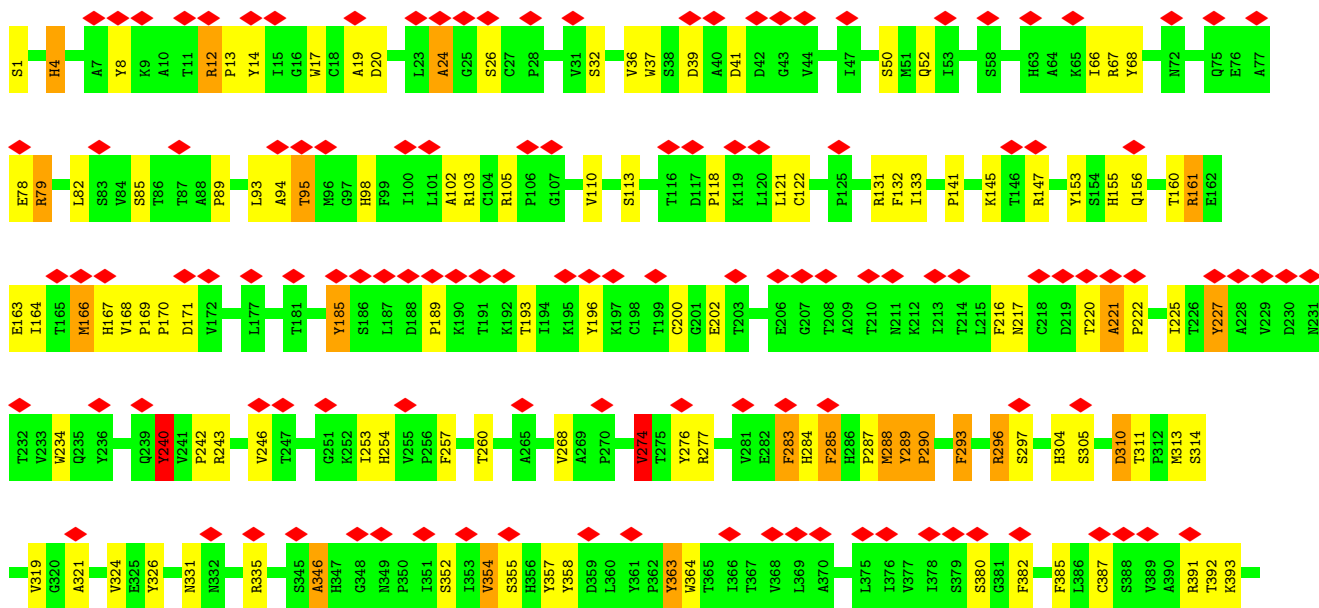


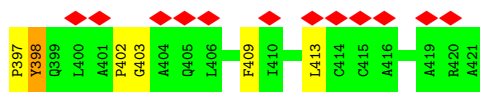


• Molecule 3: E2 ENVELOPE GLYCOPROTEIN

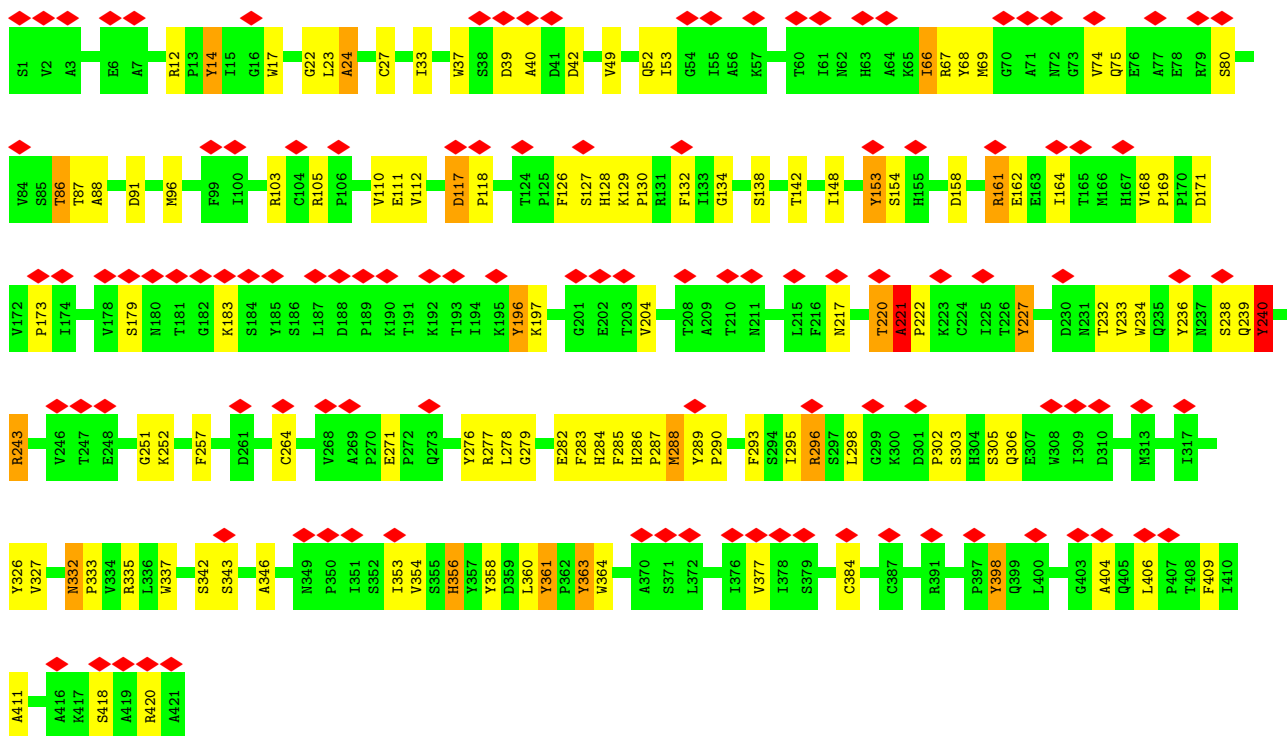


• Molecule 3: E2 ENVELOPE GLYCOPROTEIN





• Molecule 3: E2 ENVELOPE GLYCOPROTEIN



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	5169	Depositor
Resolution determination method	Not provided	
CTF correction method	INDIVIDUAL PARTICLES	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	50000	Depositor
Image detector	GENERIC GATAN	Depositor
Maximum map value	29.373	Depositor
Minimum map value	-20.788	Depositor
Average map value	0.000	Depositor
Map value standard deviation	2.501	Depositor
Recommended contour level	5.0	Depositor
Map size ( $\text{\AA}$ )	817.92, 817.92, 817.92	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.42, 1.42, 1.42	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	3.19	16/1346 (1.2%)	2.07	35/1812 (1.9%)
1	D	3.19	11/1346 (0.8%)	2.09	43/1812 (2.4%)
1	G	3.16	17/1346 (1.3%)	2.03	33/1812 (1.8%)
1	J	3.19	18/1346 (1.3%)	2.09	31/1812 (1.7%)
2	B	1.75	29/3296 (0.9%)	2.05	102/4494 (2.3%)
2	E	1.75	28/3296 (0.8%)	1.98	84/4494 (1.9%)
2	H	1.74	26/3296 (0.8%)	2.05	93/4494 (2.1%)
2	K	1.78	29/3296 (0.9%)	1.99	83/4494 (1.8%)
3	C	2.79	40/3326 (1.2%)	1.94	75/4537 (1.7%)
3	F	2.71	44/3326 (1.3%)	1.99	82/4537 (1.8%)
3	I	2.80	48/3326 (1.4%)	2.00	80/4537 (1.8%)
3	L	2.77	35/3326 (1.1%)	2.01	95/4537 (2.1%)
All	All	2.49	341/31872 (1.1%)	2.01	836/43372 (1.9%)

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	A	0	4
1	D	0	7
1	G	0	8
1	J	0	4
2	B	0	20
2	E	0	21
2	H	0	19
2	K	0	20
3	C	0	11
3	F	0	6
3	I	0	11
3	L	0	9
All	All	0	140

The worst 5 of 341 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	237	TRP	CE2-CZ2	91.21	2.94	1.39
1	J	237	TRP	CE2-CZ2	88.72	2.90	1.39
1	G	237	TRP	CE2-CZ2	87.75	2.88	1.39
1	A	237	TRP	CE2-CZ2	87.70	2.88	1.39
3	I	398	TYR	CD2-CE2	78.02	2.56	1.39

The worst 5 of 836 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	105	ARG	NE-CZ-NH1	19.59	130.09	120.30
3	C	398	TYR	CB-CG-CD2	-18.30	110.02	121.00
1	G	237	TRP	NE1-CE2-CZ2	17.45	149.59	130.40
3	L	398	TYR	CG-CD2-CE2	-16.81	107.85	121.30
3	F	398	TYR	CG-CD2-CE2	-15.85	108.62	121.30

There are no chirality outliers.

5 of 140 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	125	LYS	Peptide
1	A	145	THR	Peptide
1	A	192	ARG	Sidechain
1	A	207	ARG	Sidechain
2	B	2	GLU	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	1316	0	1322	30	0
1	D	1316	0	1322	23	0
1	G	1316	0	1322	28	0
1	J	1316	0	1322	26	0
2	B	3225	0	3161	34	0
2	E	3225	0	3161	33	0
2	H	3225	0	3161	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	3225	0	3161	32	0
3	C	3239	0	3208	57	0
3	F	3239	0	3208	58	0
3	I	3239	0	3208	58	0
3	L	3239	0	3208	58	0
All	All	31120	0	30764	289	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 5.

The worst 5 of 289 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:I:240:TYR:CE1	3:I:240:TYR:CD1	1.81	1.68
3:I:240:TYR:CE2	3:I:240:TYR:CD2	1.80	1.67
3:F:240:TYR:CD2	3:F:240:TYR:CE2	1.79	1.65
1:A:237:TRP:CE3	1:A:237:TRP:CD2	1.82	1.64
1:G:237:TRP:CE3	1:G:237:TRP:CD2	1.74	1.64

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	169/253 (67%)	136 (80%)	24 (14%)	9 (5%)	2	21
1	D	169/253 (67%)	148 (88%)	15 (9%)	6 (4%)	3	28
1	G	169/253 (67%)	133 (79%)	21 (12%)	15 (9%)	1	12
1	J	169/253 (67%)	132 (78%)	22 (13%)	15 (9%)	1	12
2	B	422/427 (99%)	354 (84%)	47 (11%)	21 (5%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	422/427 (99%)	352 (83%)	42 (10%)	28 (7%)	1	17
2	H	422/427 (99%)	362 (86%)	47 (11%)	13 (3%)	4	30
2	K	422/427 (99%)	366 (87%)	33 (8%)	23 (6%)	2	21
3	C	419/421 (100%)	359 (86%)	36 (9%)	24 (6%)	1	20
3	F	419/421 (100%)	365 (87%)	38 (9%)	16 (4%)	3	26
3	I	419/421 (100%)	364 (87%)	38 (9%)	17 (4%)	3	25
3	L	419/421 (100%)	360 (86%)	40 (10%)	19 (4%)	2	24
All	All	4040/4404 (92%)	3431 (85%)	403 (10%)	206 (5%)	4	21

5 of 206 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	ILE
1	A	182	HIS
2	B	69	SER
2	B	86	PRO
2	B	89	TRP

### 5.3.2 Protein sidechains [i](#)

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	145/217 (67%)	140 (97%)	5 (3%)	37	60
1	D	145/217 (67%)	140 (97%)	5 (3%)	37	60
1	G	145/217 (67%)	142 (98%)	3 (2%)	53	72
1	J	145/217 (67%)	138 (95%)	7 (5%)	25	51
2	B	364/366 (100%)	338 (93%)	26 (7%)	14	41
2	E	364/366 (100%)	355 (98%)	9 (2%)	47	68
2	H	364/366 (100%)	350 (96%)	14 (4%)	33	57
2	K	364/366 (100%)	346 (95%)	18 (5%)	25	51
3	C	366/366 (100%)	352 (96%)	14 (4%)	33	57

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	366/366 (100%)	353 (96%)	13 (4%)	35	59
3	I	366/366 (100%)	343 (94%)	23 (6%)	18	44
3	L	366/366 (100%)	351 (96%)	15 (4%)	30	55
All	All	3500/3796 (92%)	3348 (96%)	152 (4%)	33	54

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	160	PRO
3	L	158	ASP
2	K	1	TYR
2	K	280	MET
3	L	343	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	204	GLN
2	K	344	GLN
3	L	109	GLN
2	E	335	ASN
2	E	254	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.

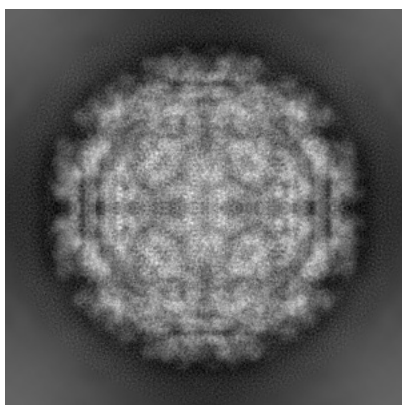
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1886. These allow visual inspection of the internal detail of the map and identification of artifacts.

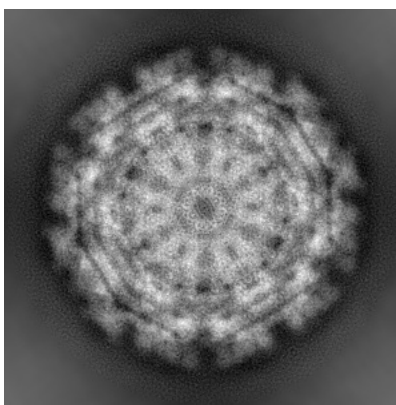
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

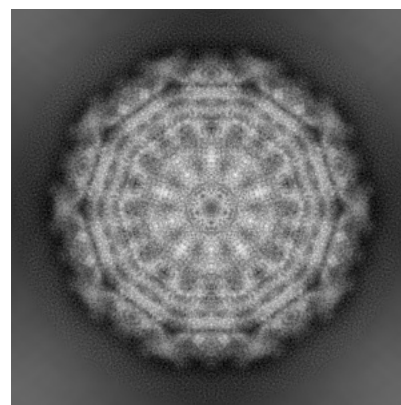
#### 6.1.1 Primary map



X



Y

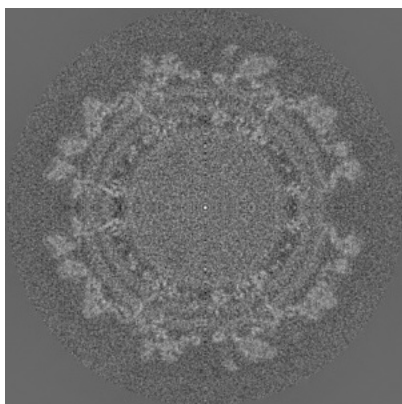


Z

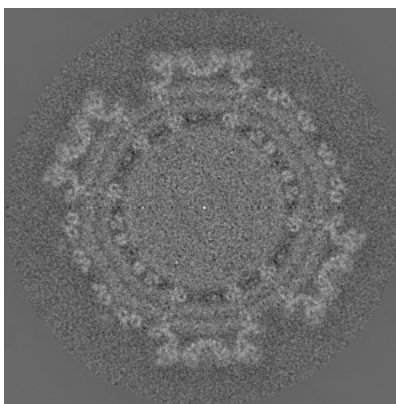
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

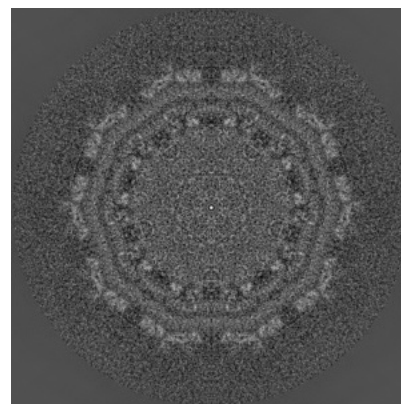
#### 6.2.1 Primary map



X Index: 288



Y Index: 288

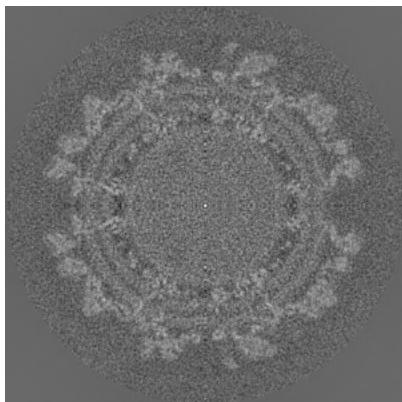


Z Index: 288

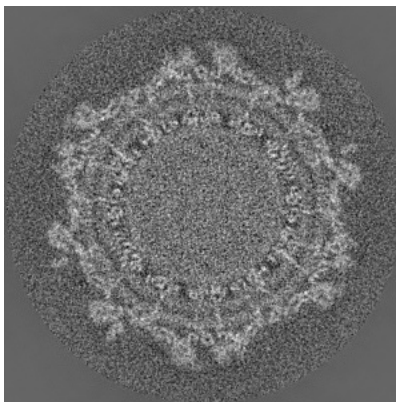
The images above show central slices of the map in three orthogonal directions.

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

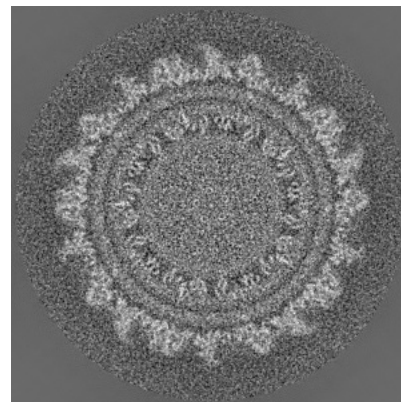
### 6.3.1 Primary map



X Index: 288



Y Index: 268

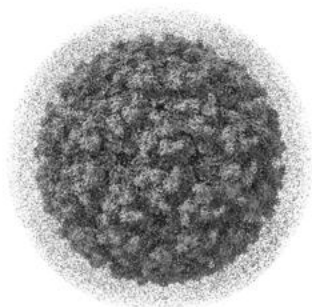


Z Index: 338

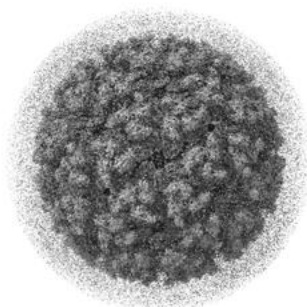
The images above show the largest variance slices of the map in three orthogonal directions.

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

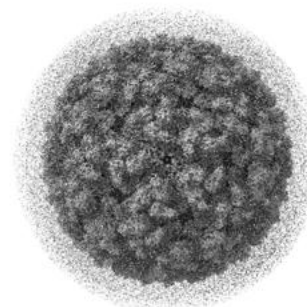
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

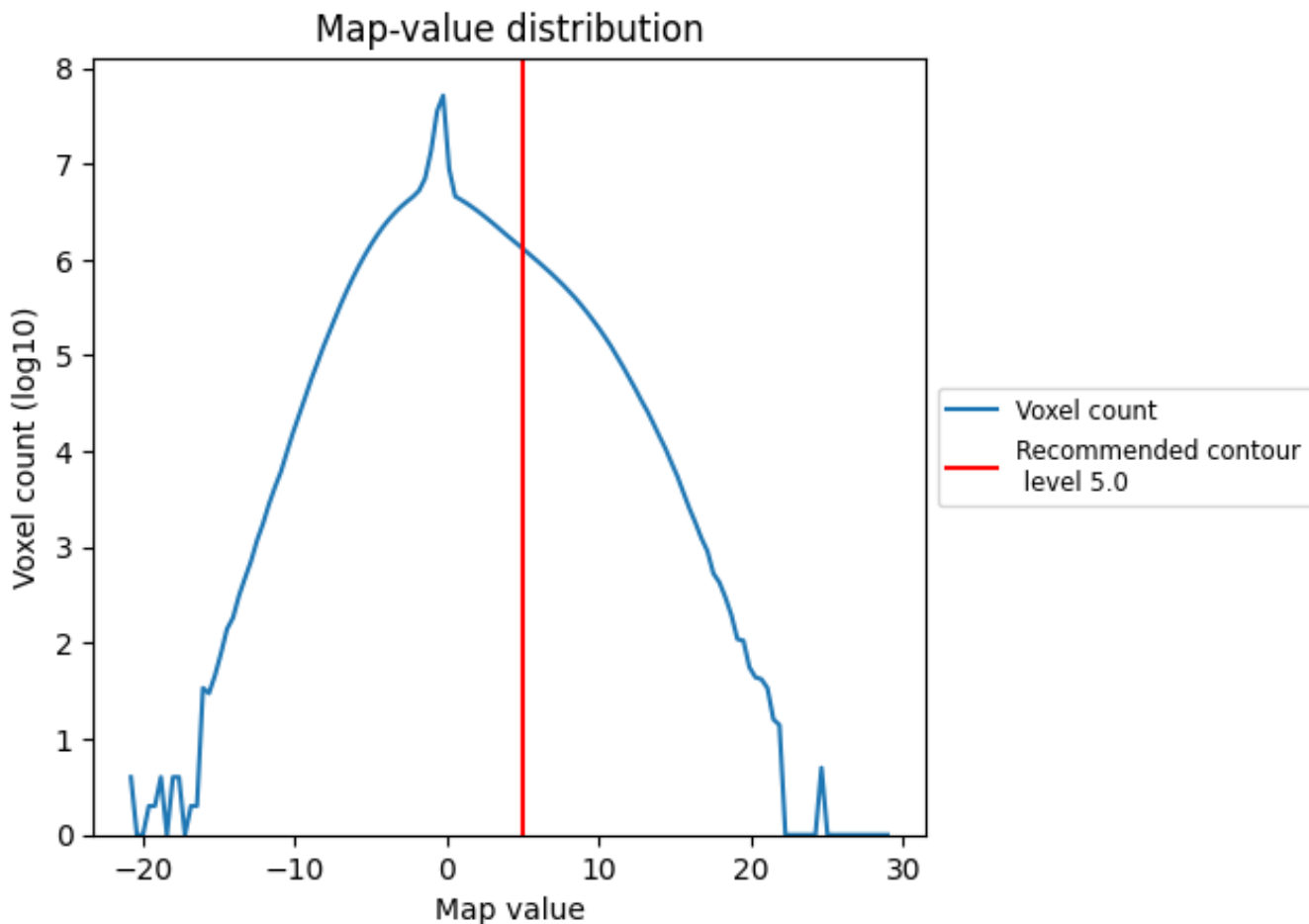
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

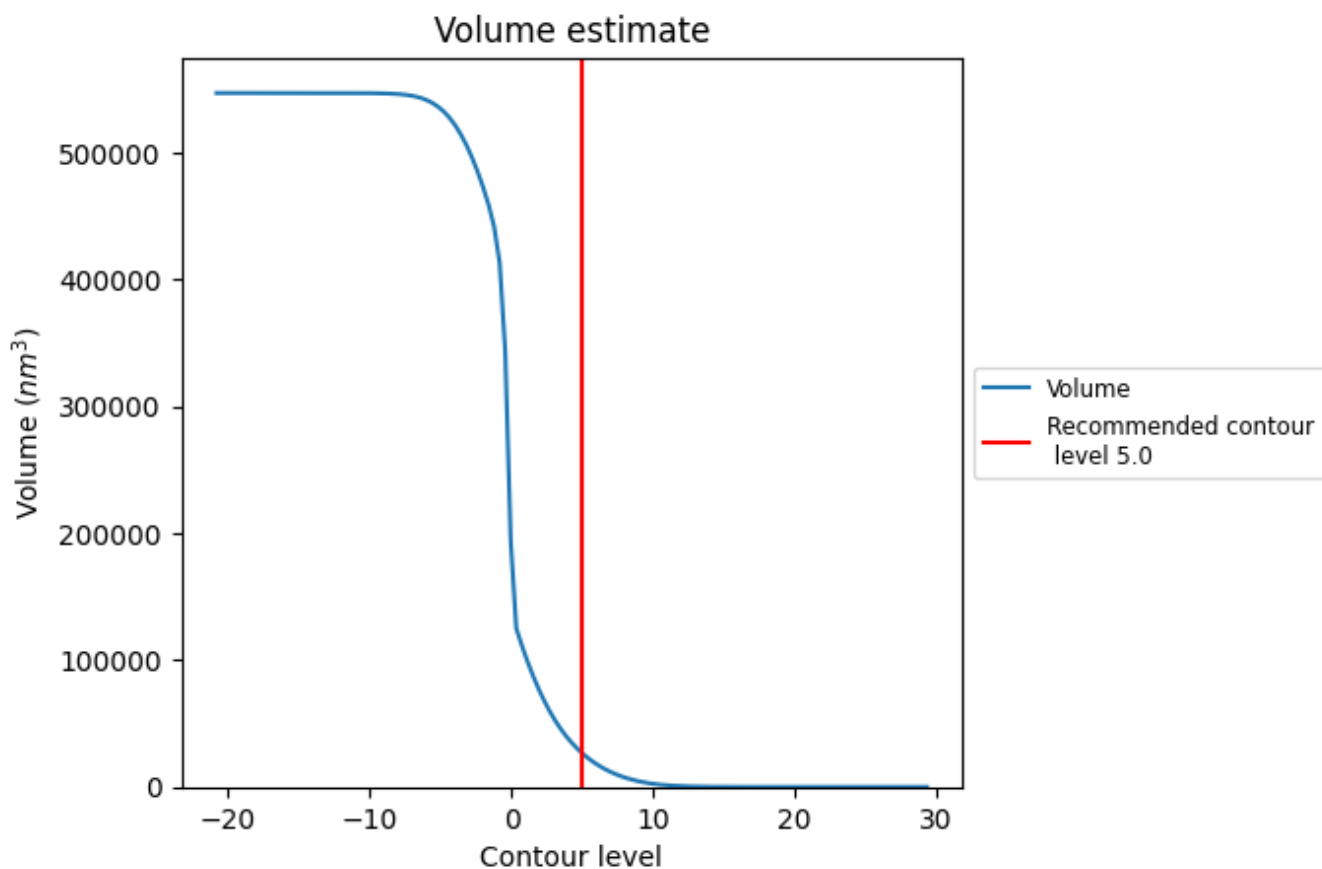
This section contains the results of statistical analysis of the map.

### 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](#)

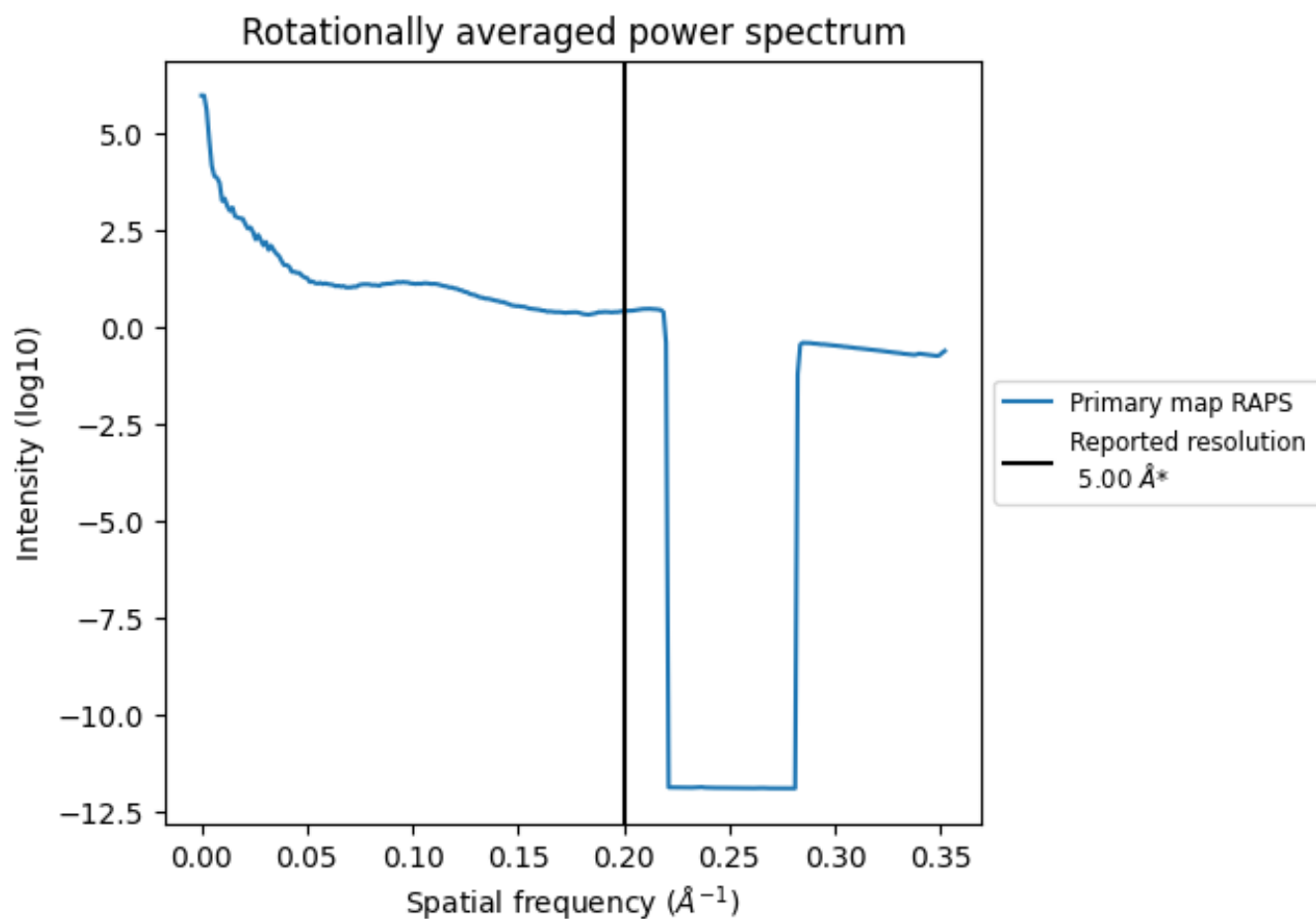


The volume at the recommended contour level is 26924  $\text{nm}^3$ ; this corresponds to an approximate mass of 24321 kDa.

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  $0.200 \text{\AA}^{-1}$

## 8 Fourier-Shell correlation

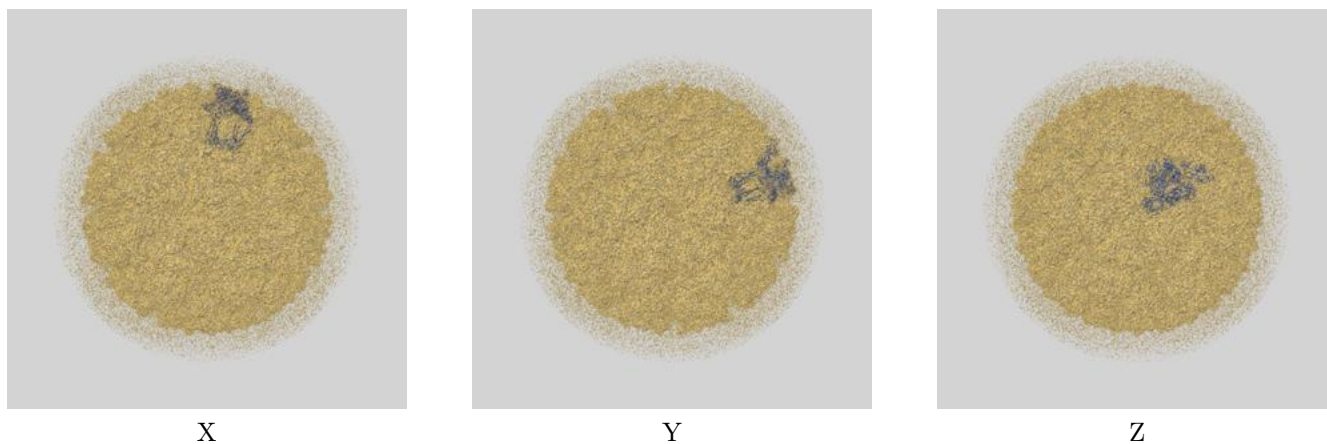
This section was not generated. No FSC curve or half-maps provided.

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

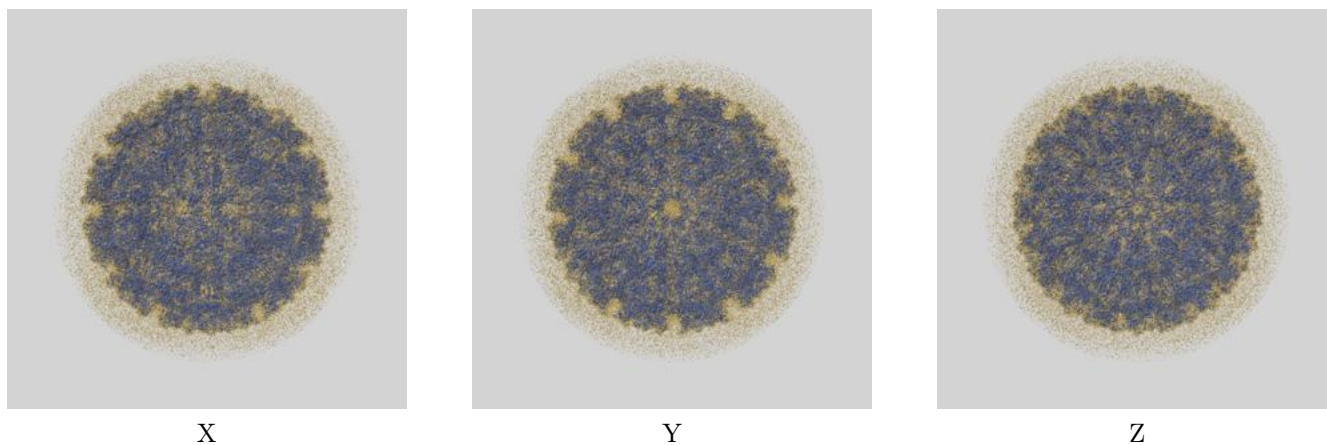
This section contains information regarding the fit between EMDB map EMD-1886 and PDB model 2YEW. Per-residue inclusion information can be found in section 3 on page 7.

### 9.1 Map-model overlays

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

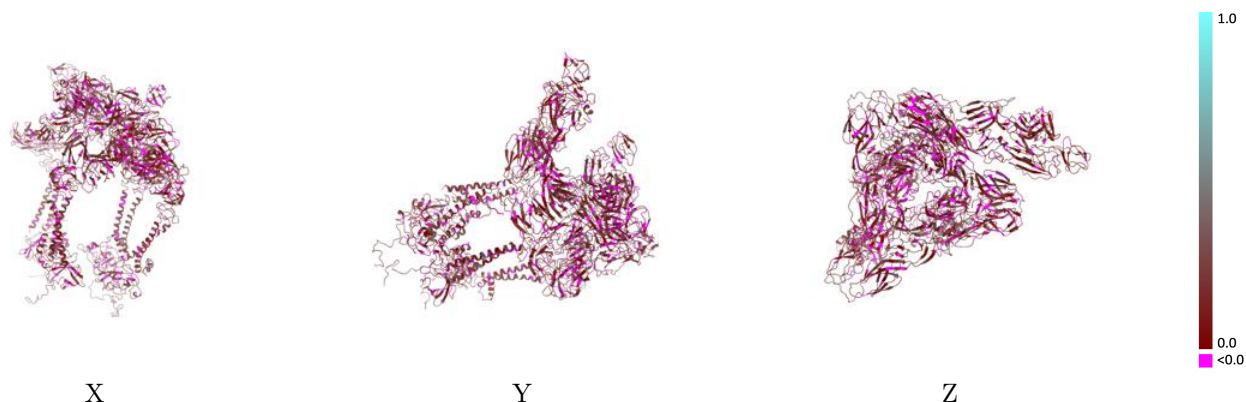


#### 9.1.2 Map-model assembly overlay [i](#)



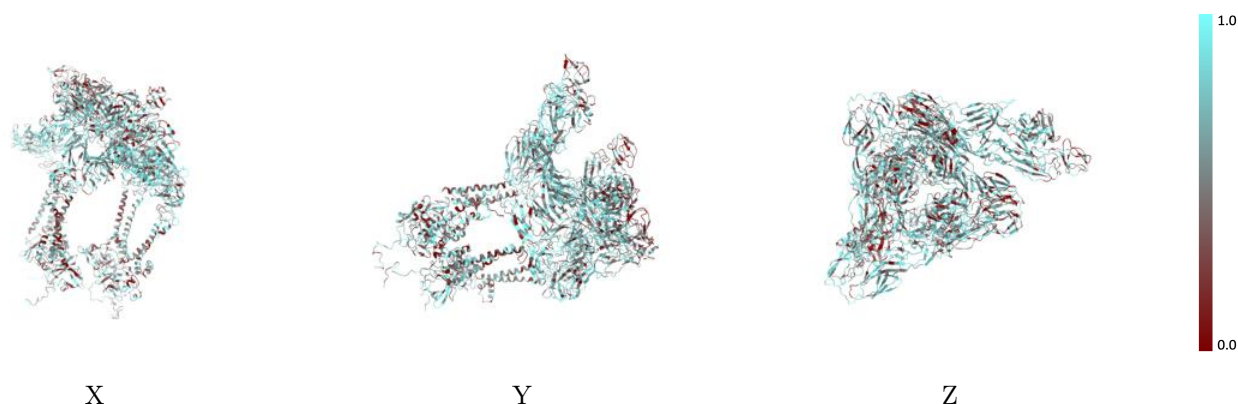
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



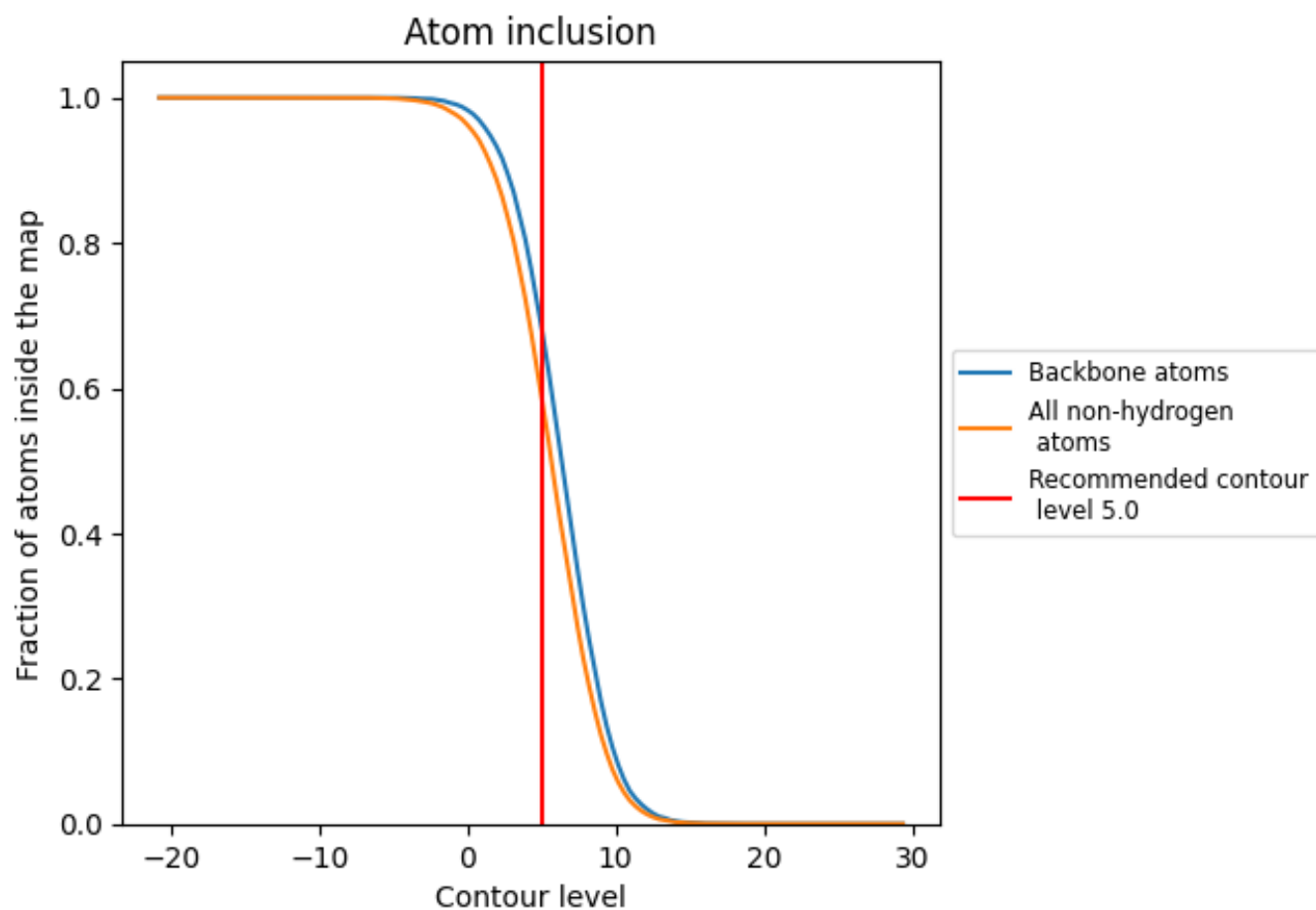
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.0).



























## 9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (5.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5877	 0.1540
A	 0.5940	 0.1610
B	 0.6517	 0.1800
C	 0.5771	 0.1520
D	 0.5431	 0.1610
E	 0.6202	 0.1580
F	 0.5410	 0.1270
G	 0.5455	 0.1880
H	 0.5981	 0.1490
I	 0.5548	 0.1360
J	 0.5470	 0.1750
K	 0.6202	 0.1480
L	 0.5884	 0.1490

