



## wwPDB EM Validation Summary Report ⓘ

Oct 26, 2024 – 01:07 PM EDT

PDB ID : 6MWV  
EMDB ID : EMD-9278  
Title : CryoEM structure of Chimeric Eastern Equine Encephalitis Virus with Fab of  
EEEV-58 Antibody  
Authors : Hasan, S.S.; Sun, C.; Kim, A.S.; Watanabe, Y.; Chen, C.L.; Klose, T.; Buda,  
G.; Crispin, M.; Diamond, M.S.; Klimstra, W.B.; Rossmann, M.G.  
Deposited on : 2018-10-30  
Resolution : 7.30 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

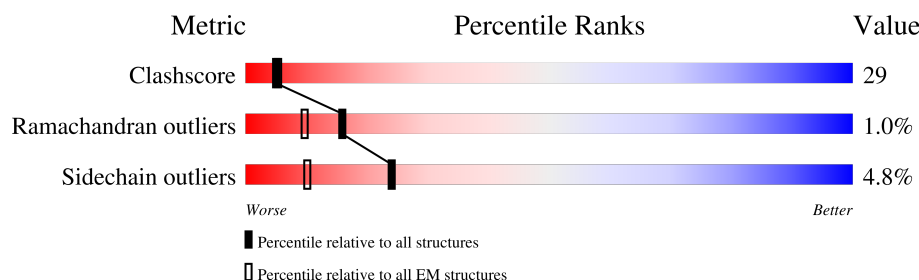
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 7.30 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	441	
1	E	441	
1	I	441	
1	M	441	
2	B	420	
2	F	420	
2	J	420	
2	N	420	

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Mol	Chain	Length	Quality of chain
3	C	218	
3	G	218	
3	K	218	
3	O	218	
4	D	214	
4	H	214	
4	L	214	
4	P	214	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 35528 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 E1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		
1	E	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		
1	I	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		
1	M	400	Total	C	N	O	S	0	0
			3063	1940	511	592	20		

- Molecule 2 is a protein called E2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		
2	F	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		
2	J	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		
2	N	325	Total	C	N	O	S	0	0
			2550	1601	471	462	16		

- Molecule 3 is a protein called EEEV-58 antibody heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		
3	G	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		
3	K	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		
3	O	218	Total	C	N	O	S	0	0
			1671	1066	272	326	7		

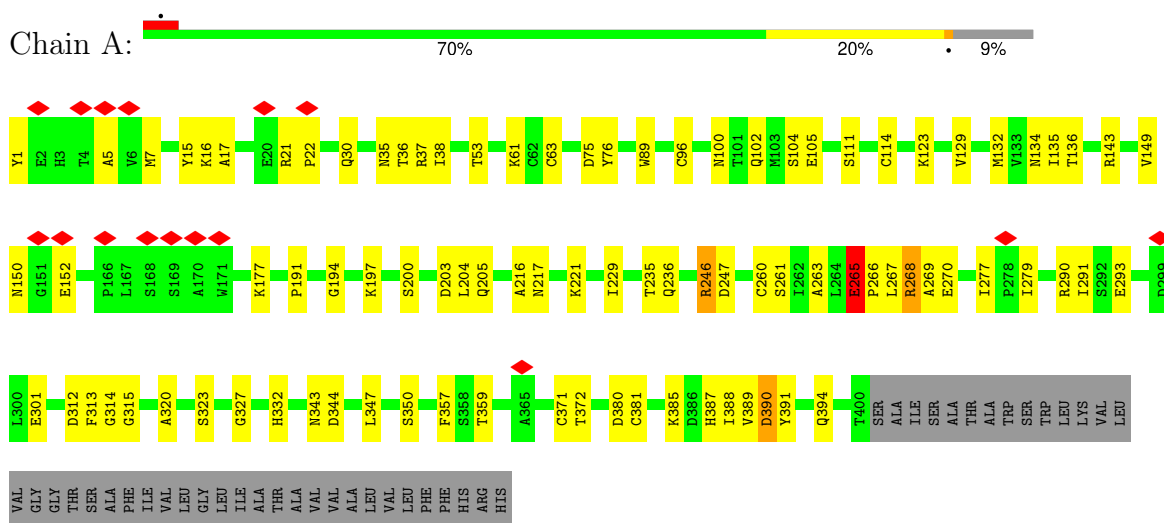
- Molecule 4 is a protein called EEEV-58 antibody light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		
4	H	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		
4	L	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		
4	P	211	Total	C	N	O	S	0	0
			1598	999	270	322	7		

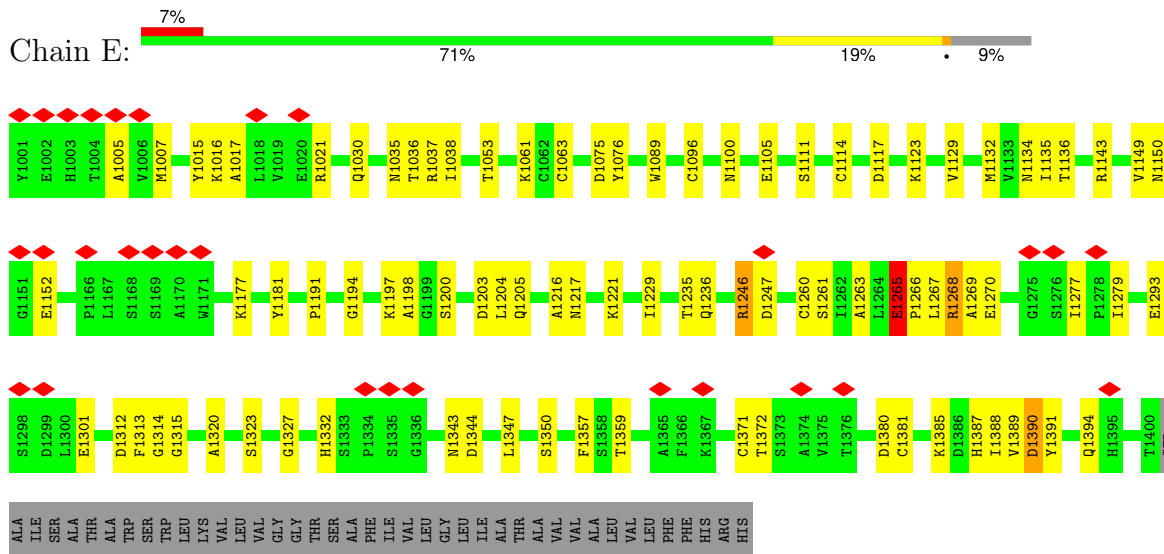
### 3 Residue-property plots

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: E1

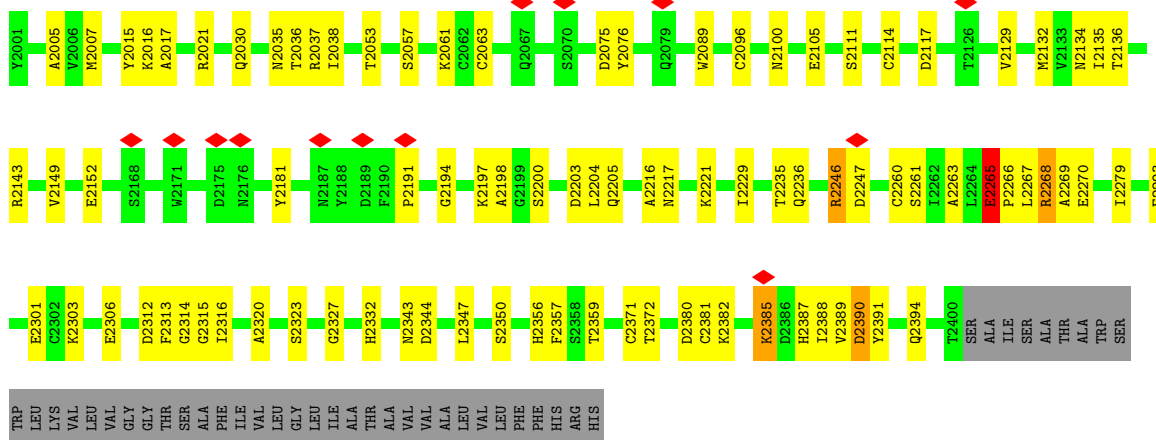


#### • Molecule 1: E1



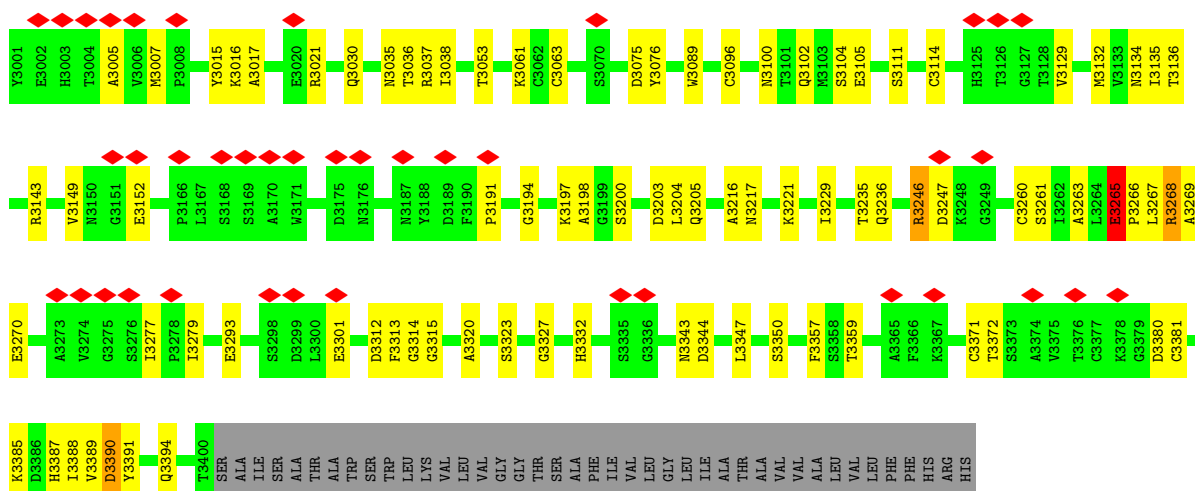
#### • Molecule 1: E1

Chain I: 



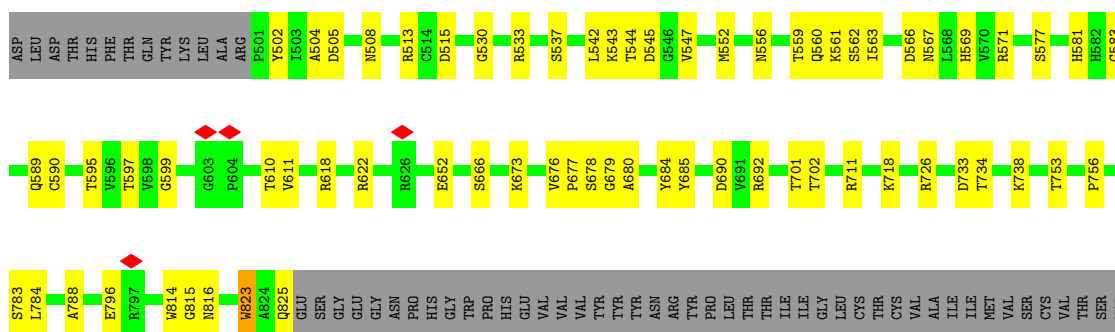
• Molecule 1: E1

Chain M: 



• Molecule 2: E2

Chain B: 



TRP  
LEU  
LEU  
CYS  
THR  
ARG  
THR  
ARG  
ASN  
LEU  
CYS  
ILE  
THR  
PRO  
TYR  
LYS  
LEU  
ALA  
ALA  
ASN  
ALA  
GLN  
VAL  
PRO  
ILE  
LEU  
LEU  
ALA  
CYS  
ILE  
LYS  
PRO  
THR  
ARG  
ALA

• Molecule 2: E2

Chain F:  58% 19% 23%

ASP  
LEU  
ASP  
THR  
HIS  
PHE  
THR  
GLN  
TYR  
CYS  
LEU  
ILE  
THR  
PRO  
ARG  
P1501  
Y1502  
D1505  
G1506  
P1507  
N1508  
R1513  
C1514  
D1515  
G1530  
R1533  
S1537  
L1542  
K1543  
T1544  
D1545  
G1546  
V1547  
M1552  
N1556  
T1559  
Q1560  
K1561  
S1562  
I1563  
D1566  
N1567  
L1568  
H1569  
V1570  
R1571  
T1572  
S1573  
S1577  
H1581

H1582  
G1583  
Q1589  
C1590  
D1594  
T1595  
V1596  
T1597  
W1598  
G1599  
P1604  
N1605  
R1606  
T1610  
V1611  
K1614  
R1618  
R1622  
R1626  
H1627  
E1630  
C1637  
E1652  
D1661  
H1662  
S1663  
S1666  
K1673  
V1676  
P1677  
S1678  
G1679  
Q1681  
Y1684  
Y1685  
D1690  
V1691  
R1692  
T1701  
T1702

R1711  
D1716  
N1717  
K1718  
R1726  
D1733  
T1734  
K1738  
C1750  
T1753  
P1756  
L1759  
T1780  
T1781  
S1782  
S1783  
L1784  
G1785  
S1786  
D1787  
A1788  
T1791  
R1792  
E1796  
R1797  
T1804  
W1814  
G1815  
N1816  
W1823  
A1824  
Q1825  
GLU  
SER  
GLY  
GLY  
GLY  
ASN  
PRO  
HIS  
GLY  
TRP  
HIS  
GLU  
VAL

VAL  
VAL  
TYR  
TYR  
ASN  
ARG  
TYR  
PRO  
TYR  
THR  
LEU  
THR  
ILE  
ILE  
GLY  
LEU  
CYS  
CYS  
THR  
CYS  
VAL  
ALA  
ILE  
ILE  
MET  
VAL  
SER  
CYS  
VAL  
THR  
SER  
VAL  
TRP  
LEU  
LEU  
CYS  
CYS  
ARG  
THR  
ARG  
ASN  
LEU  
CYS  
ILE  
THR  
PRO  
TYR  
LYS  
LEU  
ALA  
PRO  
ASN  
ALA  
GLN  
VAL  
VAL  
ILE  
LEU  
LEU  
ALA  
LEU  
LEU  
LEU

CYS  
CYS  
ILE  
LYS  
PRO  
THR  
ARG  
ALA

• Molecule 2: E2

Chain J:  60% 17% 23%

ASP  
LEU  
ASP  
THR  
HIS  
PHE  
THR  
GLN  
TYR  
CYS  
LEU  
ALA  
ARG  
P2501  
Y2502  
I2503  
A2504  
D2505  
C2506  
P2507  
N2508  
R2513  
C2514  
D2515  
G2530  
R2533  
S2537  
L2542  
D2545  
G2546  
V2547  
W2552  
N2556  
G2557  
K2558  
S2562  
I2563  
D2566  
N2567  
L2568  
H2569  
V2570  
R2571  
T2572  
S2573  
S2577  
H2581  
H2582

Q2583  
Q2589  
C2590  
D2594  
T2595  
V2596  
T2597  
W2598  
G2599  
P2604  
T2610  
V2611  
K2614  
V2615  
E2616  
F2617  
R2618  
R2622  
R2626  
H2627  
E2630  
C2637  
E2652  
S2666  
K2673  
P2677  
S2678  
G2679  
A2680  
Y2684  
Y2685  
D2690  
V2691  
R2692  
T2701  
T2702  
R2711  
W2720  
S2724  
G2725  
R2726

D2733  
T2734  
K2738  
C2750  
T2763  
P2766  
L2759  
R2782  
S2783  
L2784  
D2787  
A2788  
E2796  
R2797  
W2814  
G2815  
N2816  
V2823  
A2824  
Q2825  
GLU  
SER  
GLY  
GLY  
GLY  
ASN  
PRO  
HIS  
GLY  
TRP  
PRO  
HIS  
GLU  
VAL  
VAL  
VAL  
TYR  
TYR  
TYR  
ASN  
ARG  
PRO  
LEU  
LEU  
CYS  
ILE  
LYS  
PRO  
THR  
ARG  
ALA

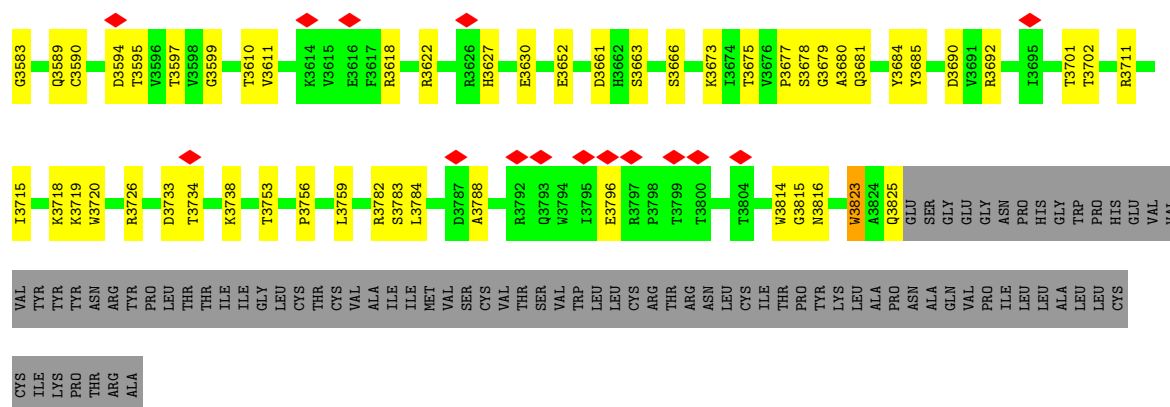
LEU  
CYS  
THR  
CYS  
VAL  
ALA  
ILE  
ILE  
MET  
VAL  
VAL  
SER  
CYS  
VAL  
THR  
SER  
VAL  
TRP  
LEU  
LEU  
CYS  
ARG  
THR  
ARG  
ASN  
LEU  
CYS  
ILE  
THR  
PRO  
TYR  
LYS  
LEU  
ALA  
PRO  
ASN  
ALA  
GLN  
VAL  
PRO  
ILE  
LEU  
LEU  
ALA  
LEU  
LEU  
CYS  
CYS  
VAL  
ILE  
LYS  
PRO  
THR  
THR  
ARG  
ALA

• Molecule 2: E2

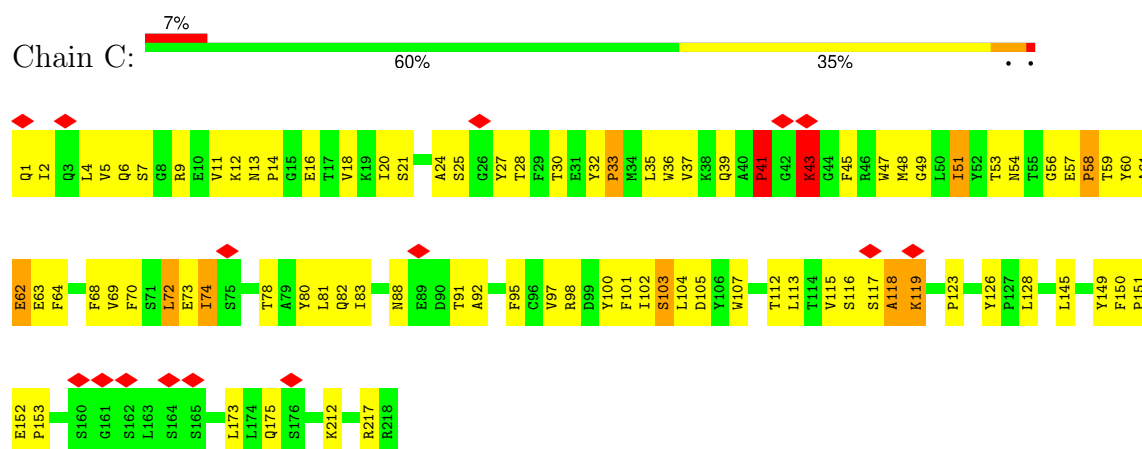
Chain N:  59% 18% 23%

ASP  
LEU  
ASP  
THR  
HIS  
PHE  
THR  
GLN  
TYR  
CYS  
LEU  
LEU  
ARG  
P3501  
Y3502  
I3503  
A3504  
D3505  
C3506  
P3507  
N3508  
R3513  
C3514  
D3515  
G3530  
R3533  
S3537  
L3542  
D3545  
M3552  
N3556  
G3557  
K3558  
T3559  
Q3560  
K3561  
S3562  
I3563  
D3566  
N3567  
L3568  
H3569  
V3570  
R3571  
T3572  
S3573  
S3577  
H3581  
H3582

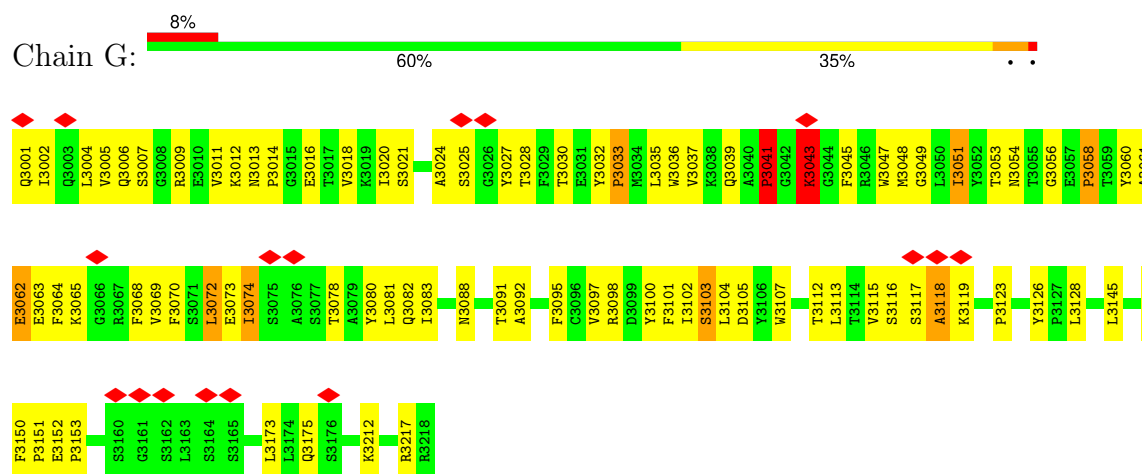




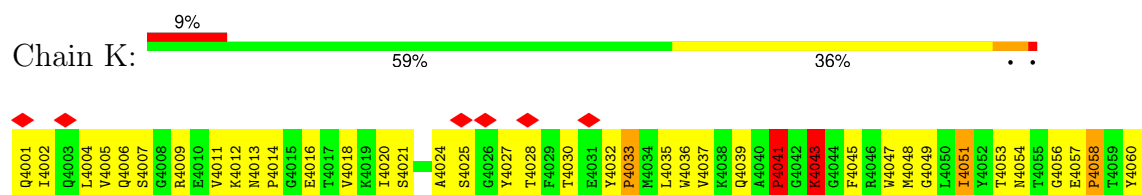
- Molecule 3: EEEV-58 antibody heavy chain

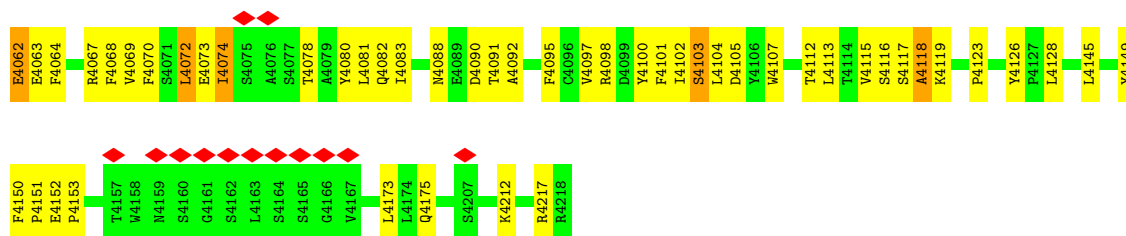


- Molecule 3: EEEV-58 antibody heavy chain

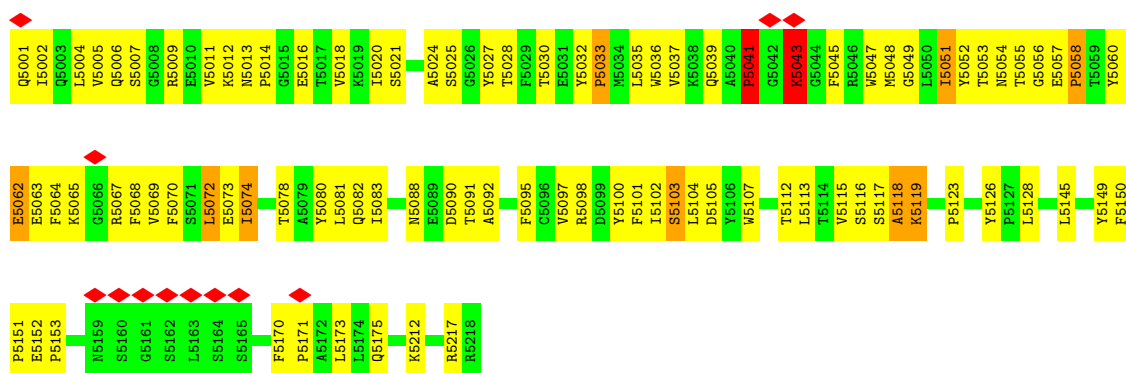


- Molecule 3: EEEV-58 antibody heavy chain

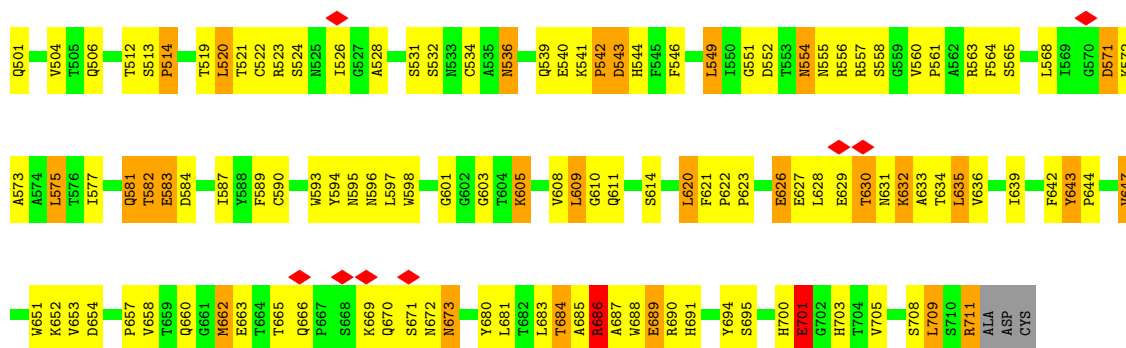




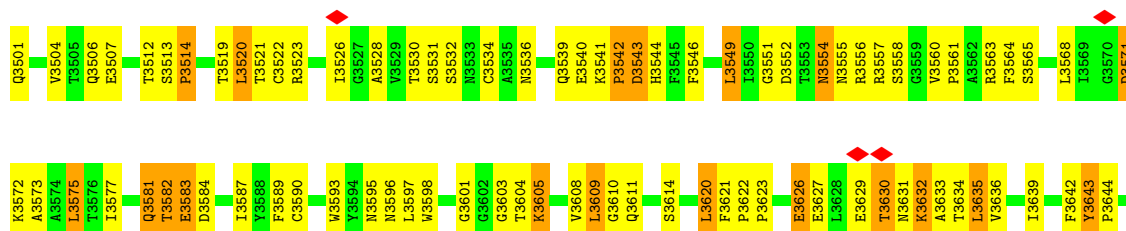
• Molecule 3: EEEV-58 antibody heavy chain

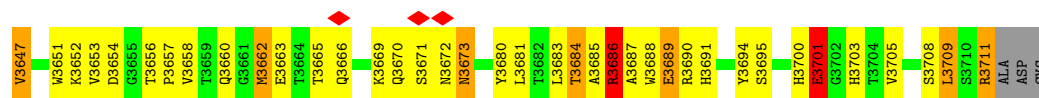


• Molecule 4: EEEV-58 antibody light chain

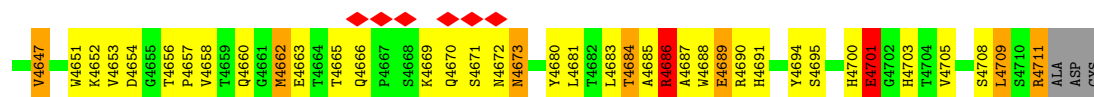
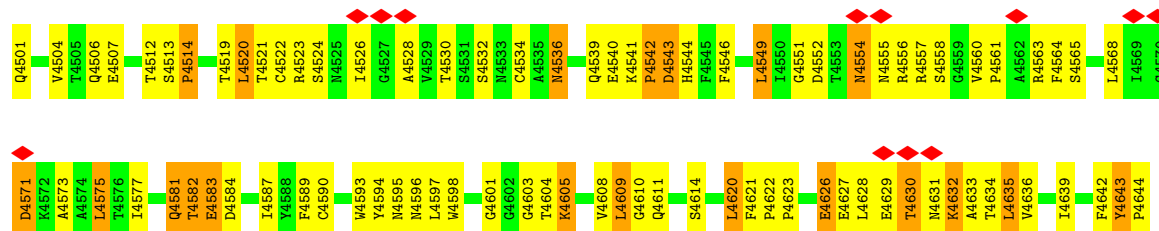


• Molecule 4: EEEV-58 antibody light chain

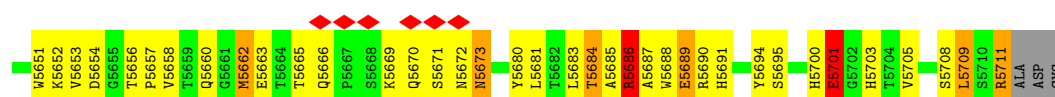
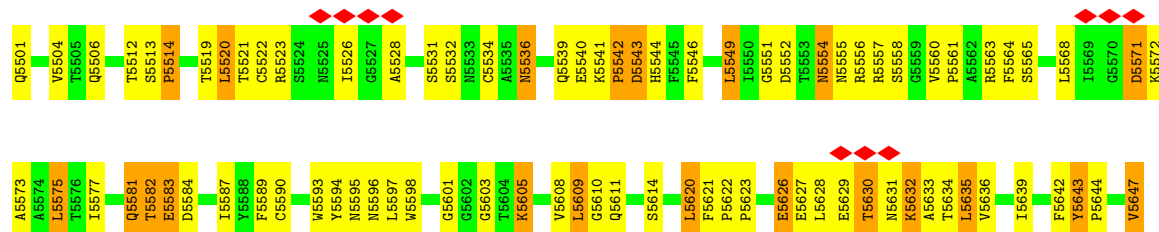




• Molecule 4: EEEV-58 antibody light chain



• Molecule 4: EEEV-58 antibody light chain



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7335	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	31	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	7.238	Depositor
Minimum map value	-8.327	Depositor
Average map value	0.069	Depositor
Map value standard deviation	1.011	Depositor
Recommended contour level	0.7	Depositor
Map size (Å)	907.2, 907.2, 907.2	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.62, 1.62, 1.62	Depositor

## 5 Model quality

### 5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.51	0/3147	0.69	1/4294 (0.0%)
1	E	0.51	0/3147	0.69	1/4294 (0.0%)
1	I	0.51	0/3147	0.69	1/4294 (0.0%)
1	M	0.51	0/3147	0.69	1/4294 (0.0%)
2	B	0.50	1/2624 (0.0%)	0.74	2/3571 (0.1%)
2	F	0.50	1/2624 (0.0%)	0.74	2/3571 (0.1%)
2	J	0.50	1/2624 (0.0%)	0.74	3/3571 (0.1%)
2	N	0.50	1/2624 (0.0%)	0.74	3/3571 (0.1%)
3	C	0.73	4/1714 (0.2%)	0.86	3/2340 (0.1%)
3	G	0.73	4/1714 (0.2%)	0.86	3/2340 (0.1%)
3	K	0.73	4/1714 (0.2%)	0.86	3/2340 (0.1%)
3	O	0.73	4/1714 (0.2%)	0.86	3/2340 (0.1%)
4	D	0.91	3/1634 (0.2%)	1.44	12/2232 (0.5%)
4	H	0.91	3/1634 (0.2%)	1.44	12/2232 (0.5%)
4	L	0.91	3/1634 (0.2%)	1.44	12/2232 (0.5%)
4	P	0.91	3/1634 (0.2%)	1.44	12/2232 (0.5%)
All	All	0.64	32/36476 (0.1%)	0.91	74/49748 (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	A	0	1
1	E	0	1
1	I	0	1
1	M	0	1
All	All	0	4

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	58	PRO	N-CD	17.43	1.72	1.47
3	O	5058	PRO	N-CD	17.43	1.72	1.47
3	G	3058	PRO	N-CD	17.40	1.72	1.47
3	K	4058	PRO	N-CD	17.39	1.72	1.47
3	G	3041	PRO	N-CD	14.00	1.67	1.47

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	4686	ARG	NE-CZ-NH1	10.11	125.36	120.30
4	P	5686	ARG	NE-CZ-NH1	10.03	125.32	120.30
4	H	3686	ARG	NE-CZ-NH1	10.02	125.31	120.30
4	D	686	ARG	NE-CZ-NH1	9.99	125.29	120.30
4	P	5635	LEU	CA-CB-CG	9.69	137.60	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	385	LYS	Peptide
1	E	1385	LYS	Peptide
1	I	2385	LYS	Peptide
1	M	3385	LYS	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	3063	0	2950	84	0
1	E	3063	0	2947	66	0
1	I	3063	0	2945	76	0
1	M	3063	0	2947	56	0
2	B	2550	0	2488	156	0
2	F	2550	0	2490	128	0
2	J	2550	0	2490	89	0
2	N	2550	0	2487	142	0
3	C	1671	0	1640	257	0
3	G	1671	0	1638	228	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	1671	0	1638	247	0
3	O	1671	0	1634	259	0
4	D	1598	0	1524	252	0
4	H	1598	0	1524	238	0
4	L	1598	0	1522	189	0
4	P	1598	0	1524	207	0
All	All	35528	0	34388	2004	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 29.

The worst 5 of 2004 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:O:5032:TYR:HE1	3:O:5100:TYR:CD1	1.00	1.69
3:O:5118:ALA:HB3	3:O:5150:PHE:CE2	1.17	1.69
2:B:543:LYS:HE2	4:D:534:CYS:SG	1.34	1.67
3:G:3118:ALA:HB3	3:G:3150:PHE:CE2	1.17	1.65
3:G:3032:TYR:HE1	3:G:3100:TYR:CD1	1.00	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	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	13	49
1	E	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	13	49
1	I	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	13	49
1	M	398/441 (90%)	322 (81%)	72 (18%)	4 (1%)	13	49
2	B	323/420 (77%)	258 (80%)	65 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	F	323/420 (77%)	259 (80%)	64 (20%)	0	100	100
2	J	323/420 (77%)	259 (80%)	64 (20%)	0	100	100
2	N	323/420 (77%)	259 (80%)	64 (20%)	0	100	100
3	C	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
3	G	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
3	K	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
3	O	216/218 (99%)	196 (91%)	15 (7%)	5 (2%)	5	28
4	D	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	13	49
4	H	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	13	49
4	L	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	13	49
4	P	209/214 (98%)	188 (90%)	19 (9%)	2 (1%)	13	49
All	All	4584/5172 (89%)	3859 (84%)	681 (15%)	44 (1%)	16	49

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	390	ASP
3	C	43	LYS
4	D	543	ASP
1	E	1390	ASP
3	G	3043	LYS

### 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	339/370 (92%)	334 (98%)	5 (2%)	60	75
1	E	339/370 (92%)	334 (98%)	5 (2%)	60	75
1	I	339/370 (92%)	334 (98%)	5 (2%)	60	75
1	M	339/370 (92%)	334 (98%)	5 (2%)	60	75
2	B	282/367 (77%)	279 (99%)	3 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	282/367 (77%)	279 (99%)	3 (1%)	70	80
2	J	282/367 (77%)	279 (99%)	3 (1%)	70	80
2	N	282/367 (77%)	279 (99%)	3 (1%)	70	80
3	C	188/188 (100%)	178 (95%)	10 (5%)	19	40
3	G	188/188 (100%)	178 (95%)	10 (5%)	19	40
3	K	188/188 (100%)	178 (95%)	10 (5%)	19	40
3	O	188/188 (100%)	178 (95%)	10 (5%)	19	40
4	D	178/183 (97%)	149 (84%)	29 (16%)	2	10
4	H	178/183 (97%)	149 (84%)	29 (16%)	2	10
4	L	178/183 (97%)	149 (84%)	29 (16%)	2	10
4	P	178/183 (97%)	149 (84%)	29 (16%)	2	10
All	All	3948/4432 (89%)	3760 (95%)	188 (5%)	24	43

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	L	4554	ASN
1	M	3217	ASN
4	L	4582	THR
4	L	4662	MET
3	O	5005	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
4	H	3555	ASN
3	O	5082	GLN
2	J	2816	ASN
3	O	5054	ASN
4	P	5554	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

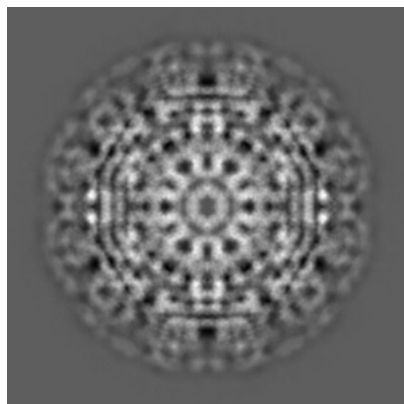
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9278. These allow visual inspection of the internal detail of the map and identification of artifacts.

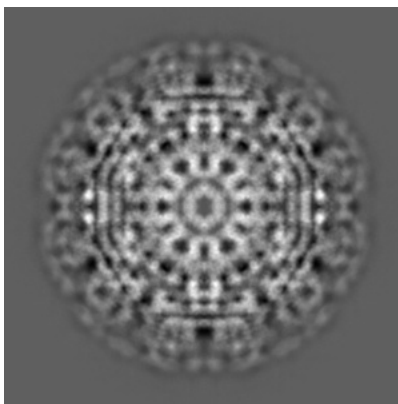
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

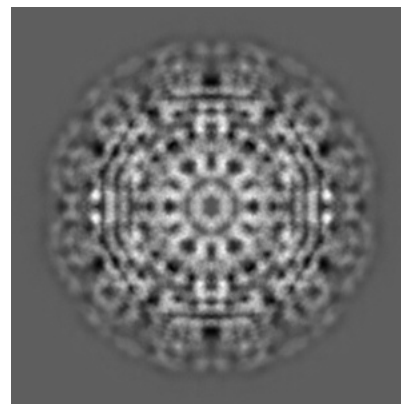
#### 6.1.1 Primary map



X

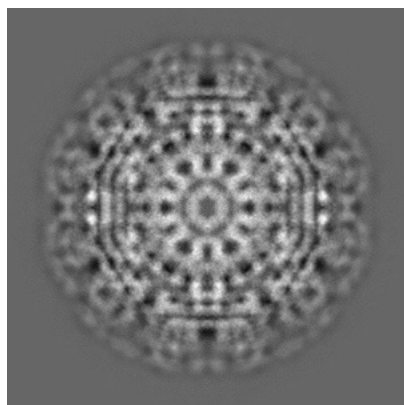


Y

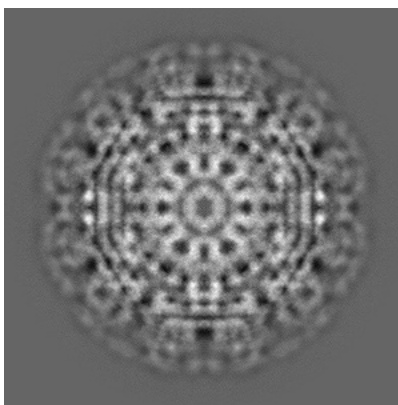


Z

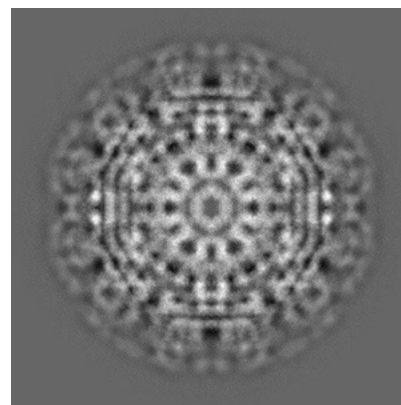
#### 6.1.2 Raw map



X



Y

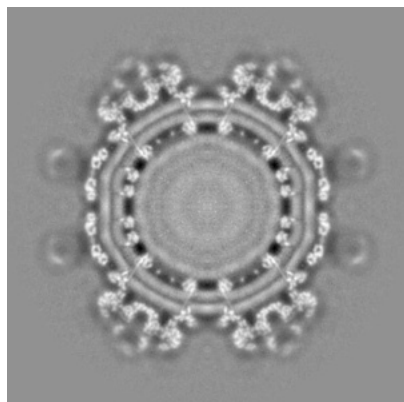


Z

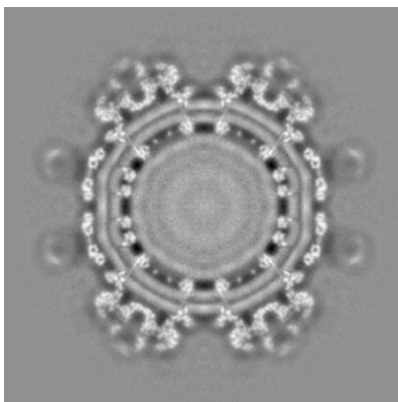
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

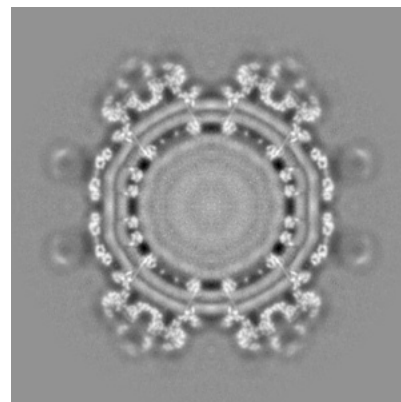
### 6.2.1 Primary map



X Index: 280

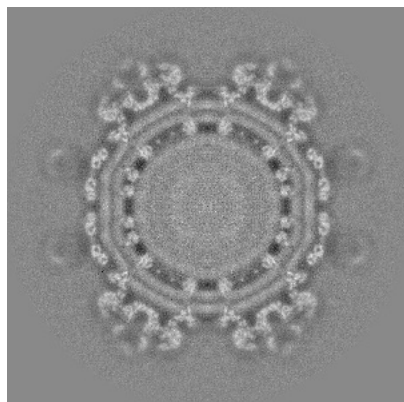


Y Index: 280

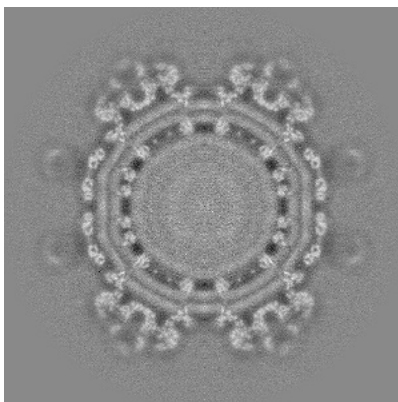


Z Index: 280

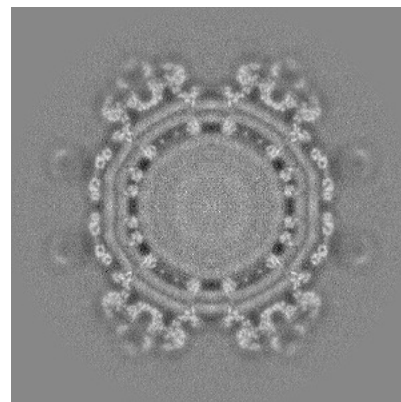
### 6.2.2 Raw map



X Index: 280



Y Index: 280

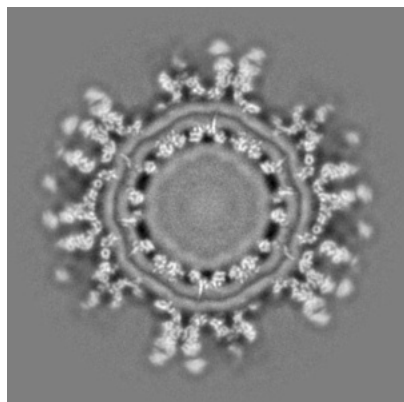


Z Index: 280

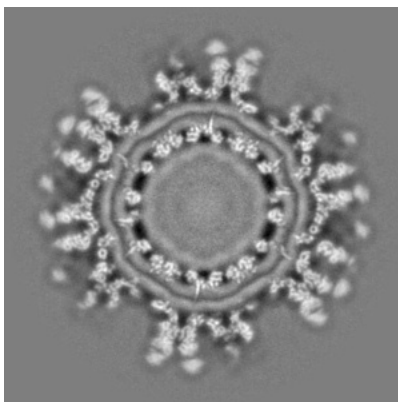
The images above show central slices of the map in three orthogonal directions.

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

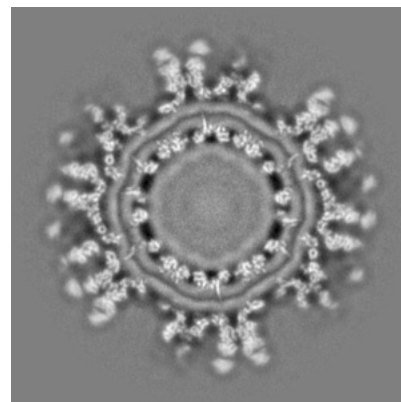
### 6.3.1 Primary map



X Index: 228

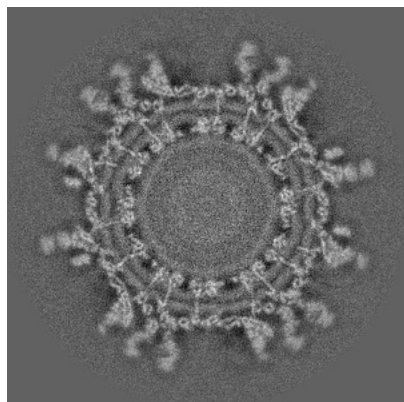


Y Index: 228

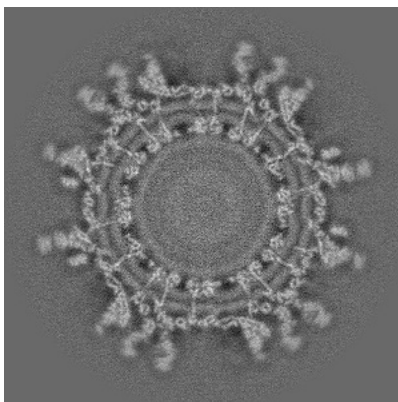


Z Index: 332

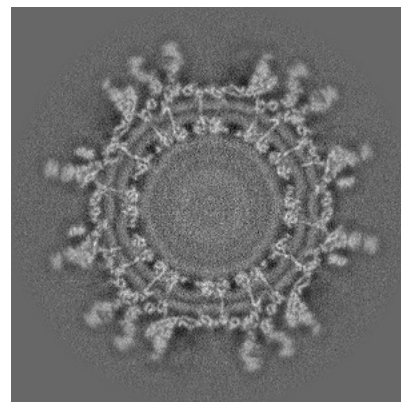
### 6.3.2 Raw map



X Index: 262



Y Index: 262



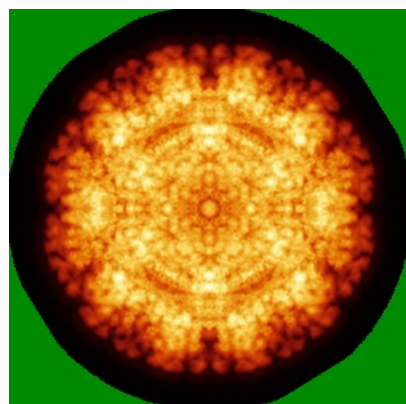
Z Index: 298

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

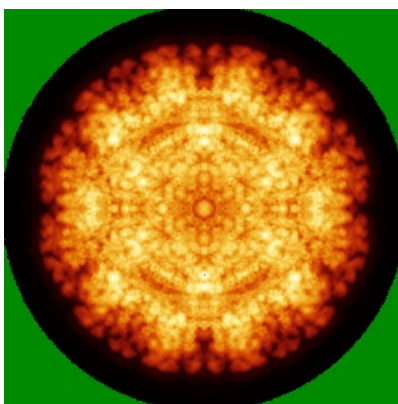


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

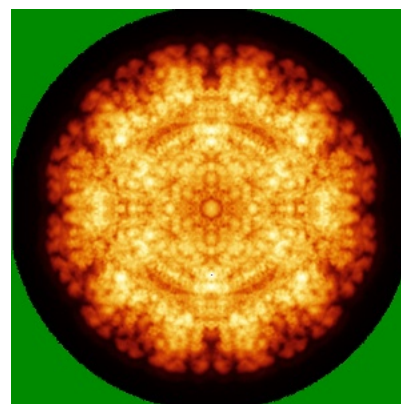
### 6.4.1 Primary map



X

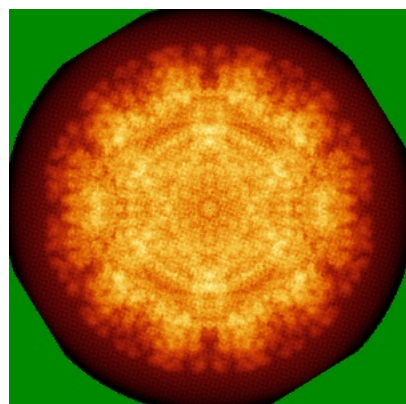


Y

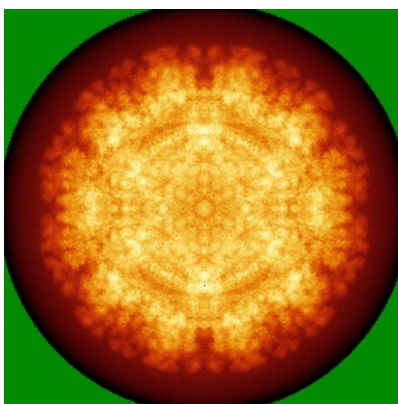


Z

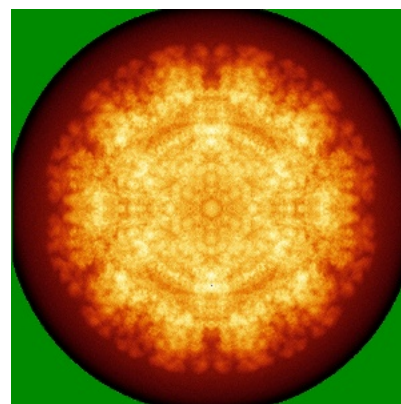
### 6.4.2 Raw map



X



Y

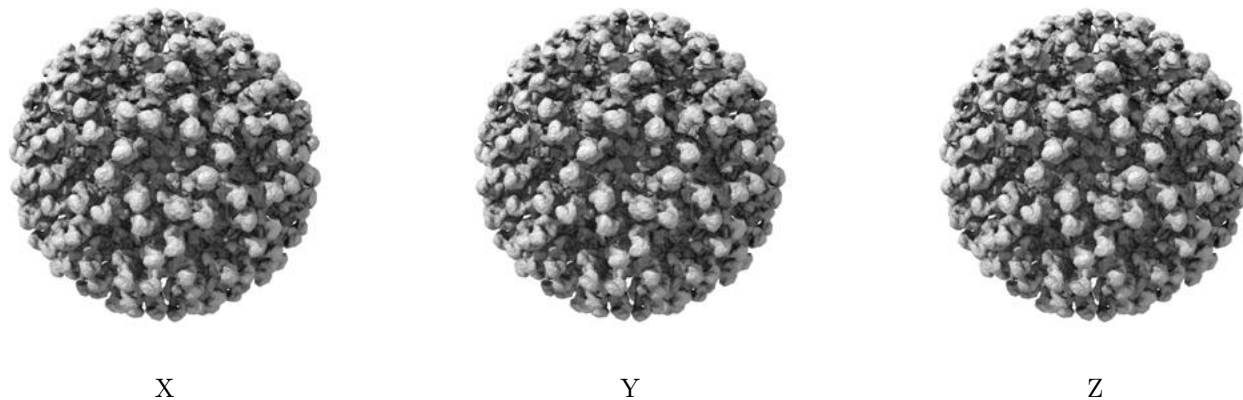


Z

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.

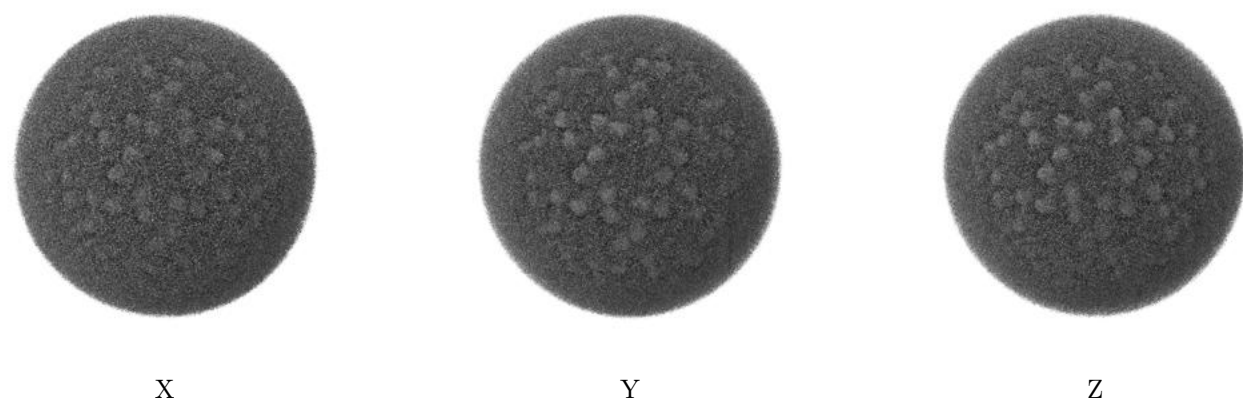
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

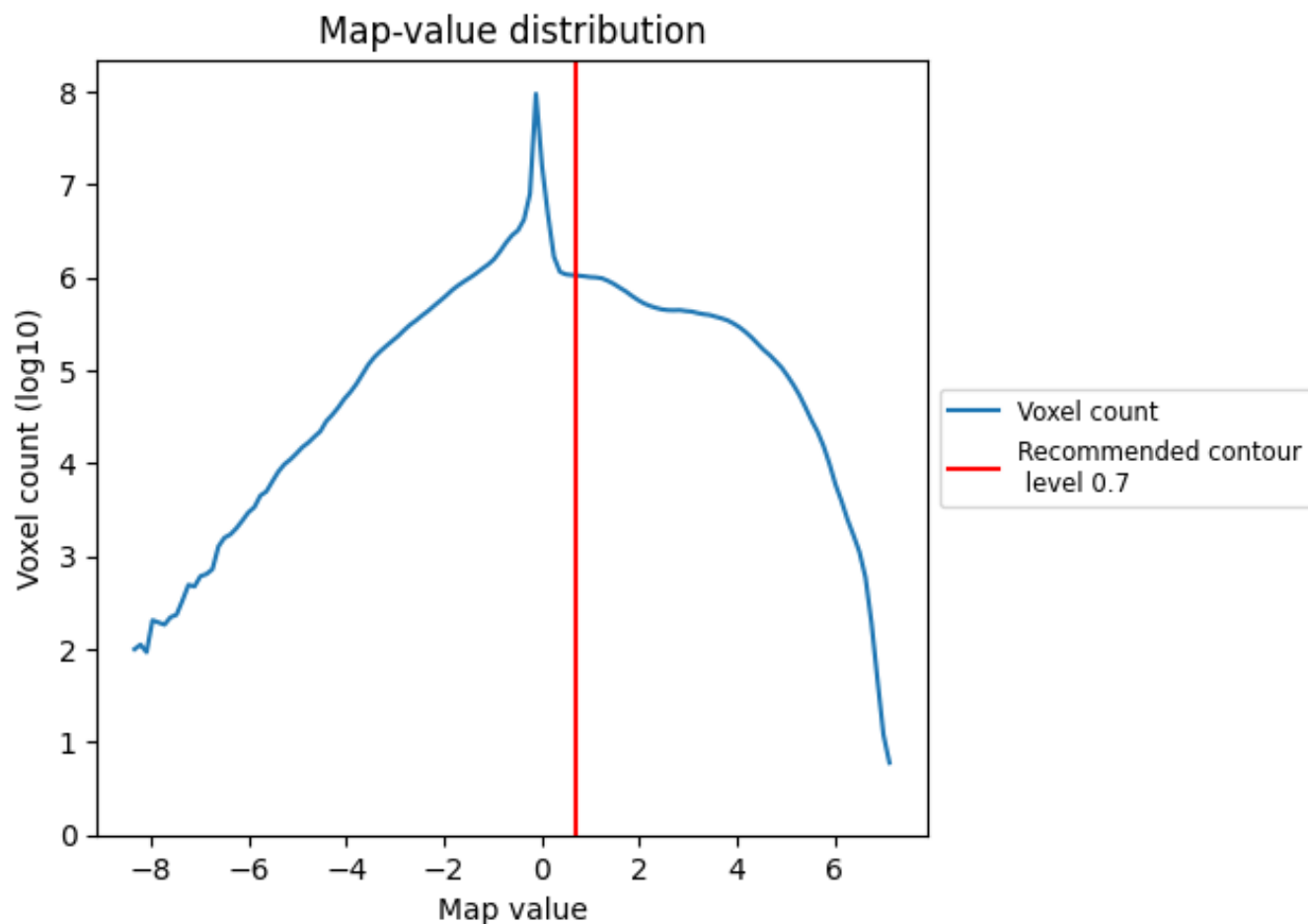
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

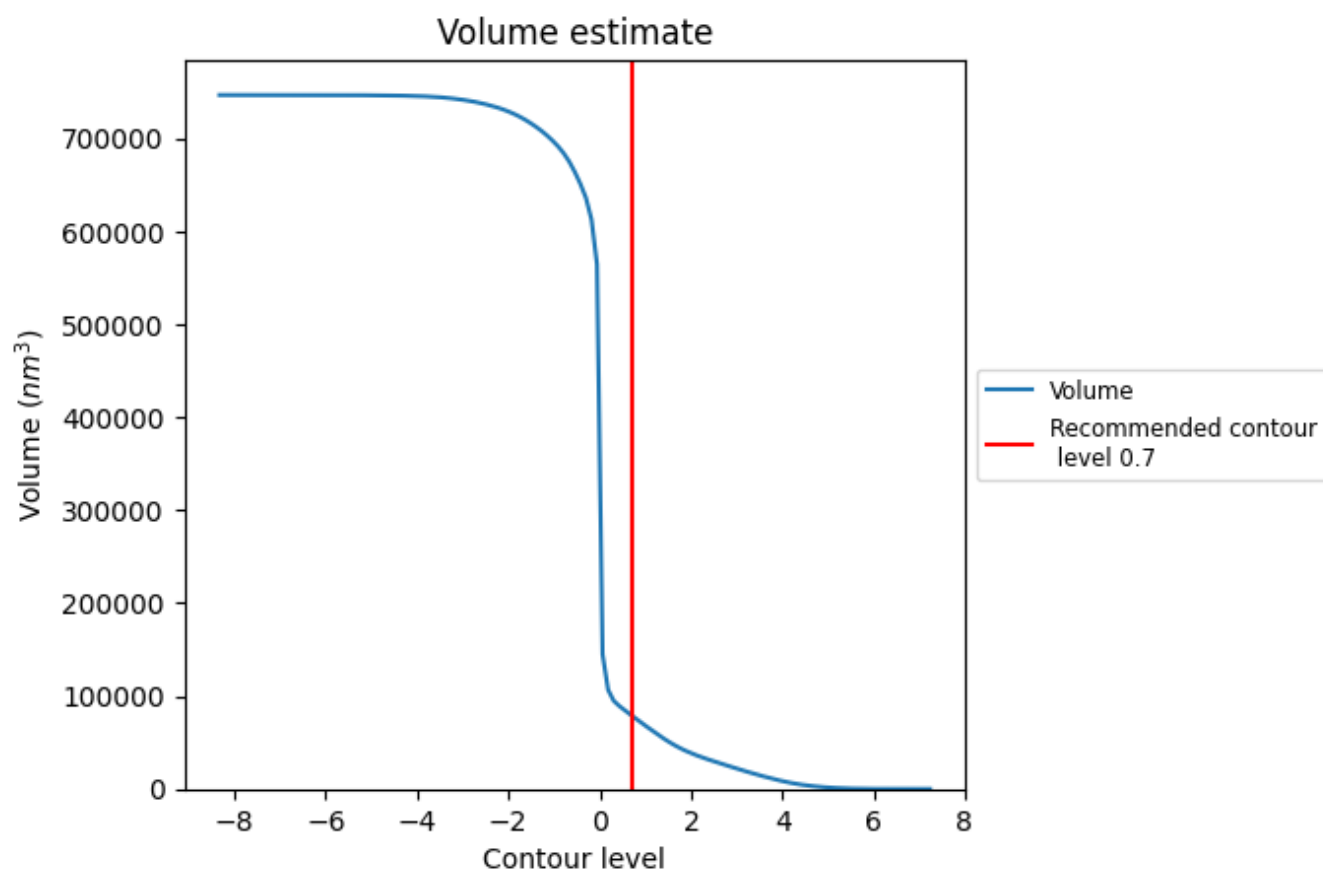
### 7.1 Map-value distribution [i](#)



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



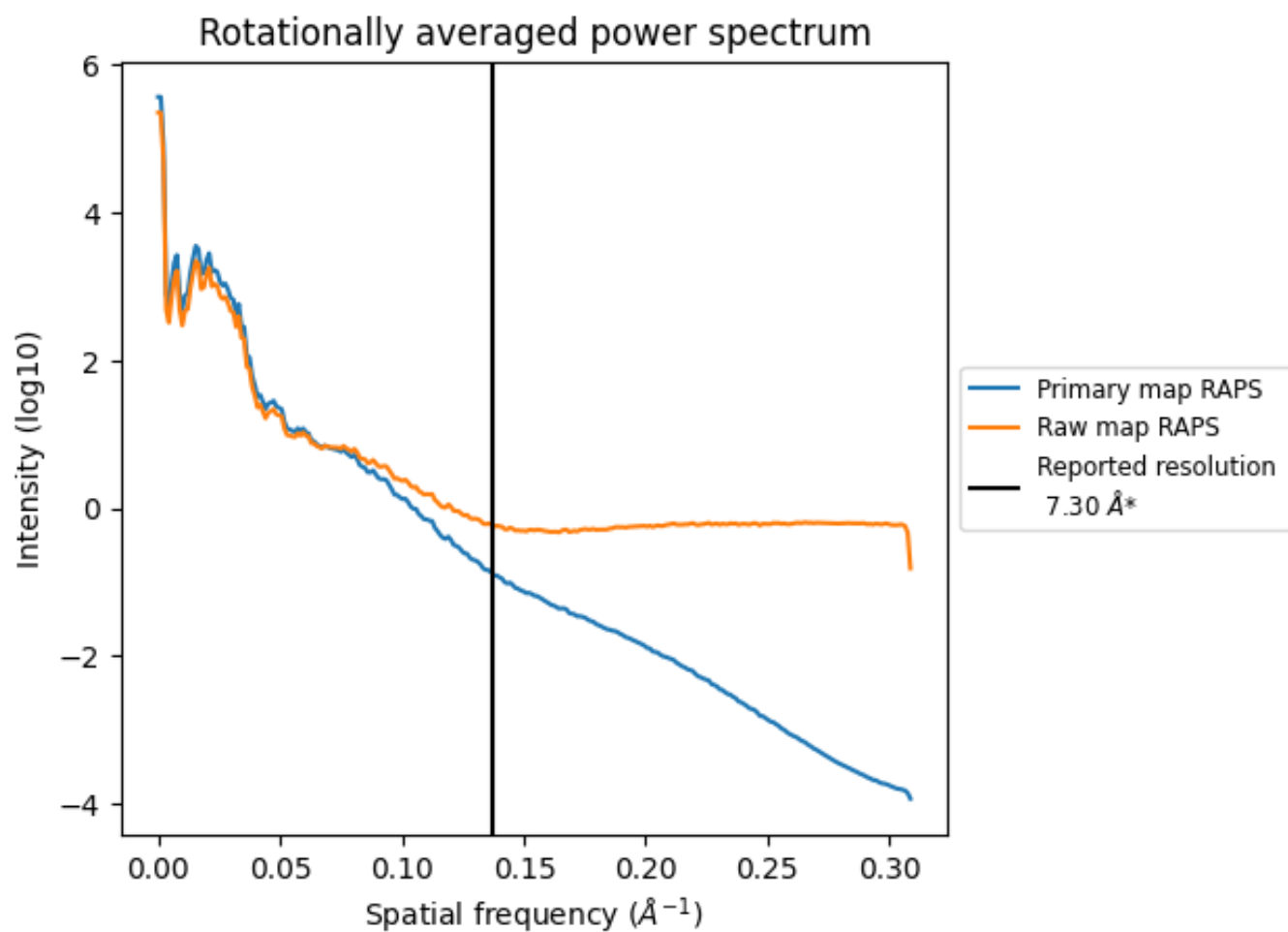
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 79048  $\text{nm}^3$ ; this corresponds to an approximate mass of 71406 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 ⓘ

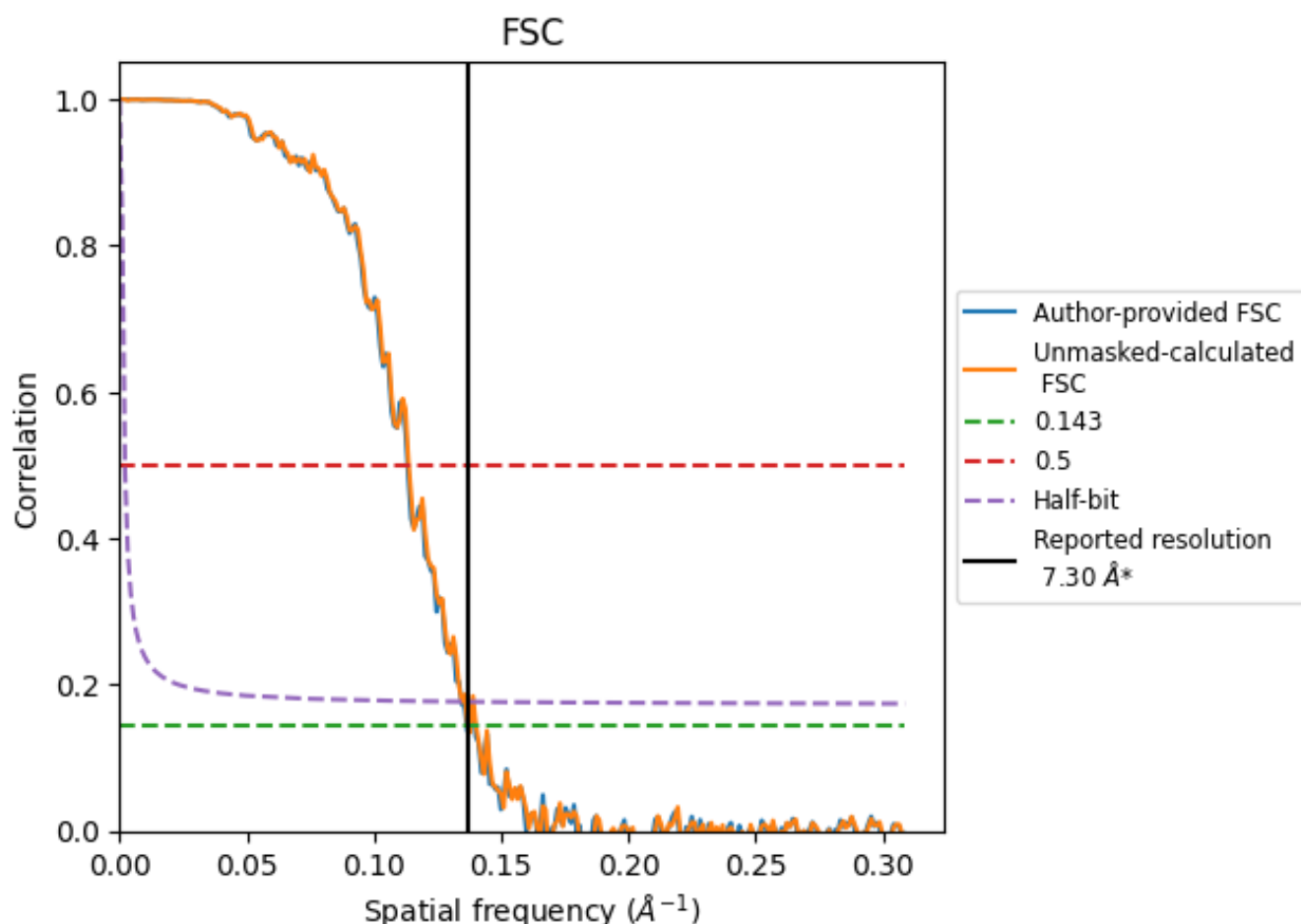


\*Reported resolution corresponds to spatial frequency of 0.137 Å<sup>-1</sup>

## 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 0.137 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.30	-	-
Author-provided FSC curve	7.33	8.83	7.44
Unmasked-calculated*	7.29	8.80	7.36

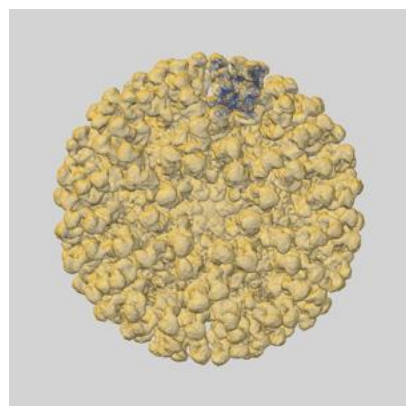
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

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

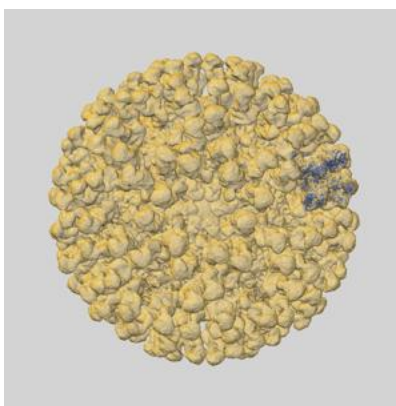
This section contains information regarding the fit between EMDB map EMD-9278 and PDB model 6MWV. Per-residue inclusion information can be found in section 3 on page 6.

### 9.1 Map-model overlays

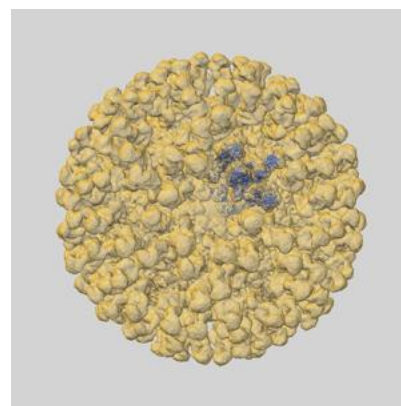
#### 9.1.1 Map-model overlay [i](#)



X

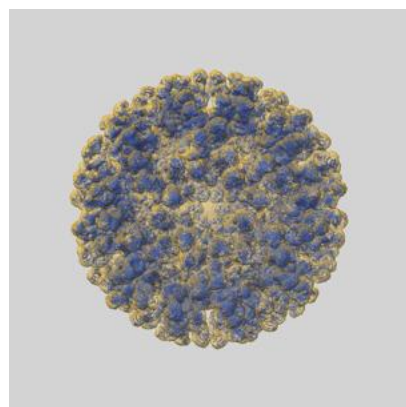


Y

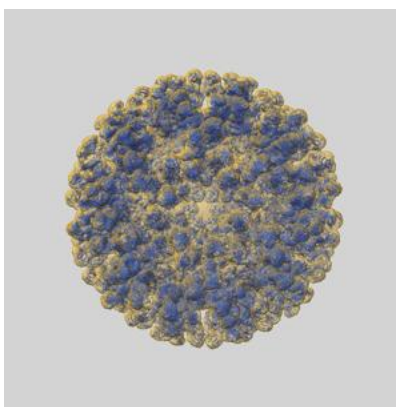


Z

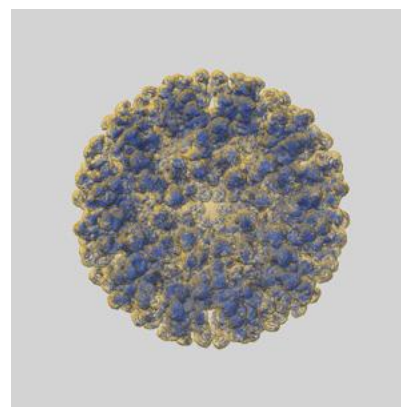
#### 9.1.2 Map-model assembly overlay [i](#)



X



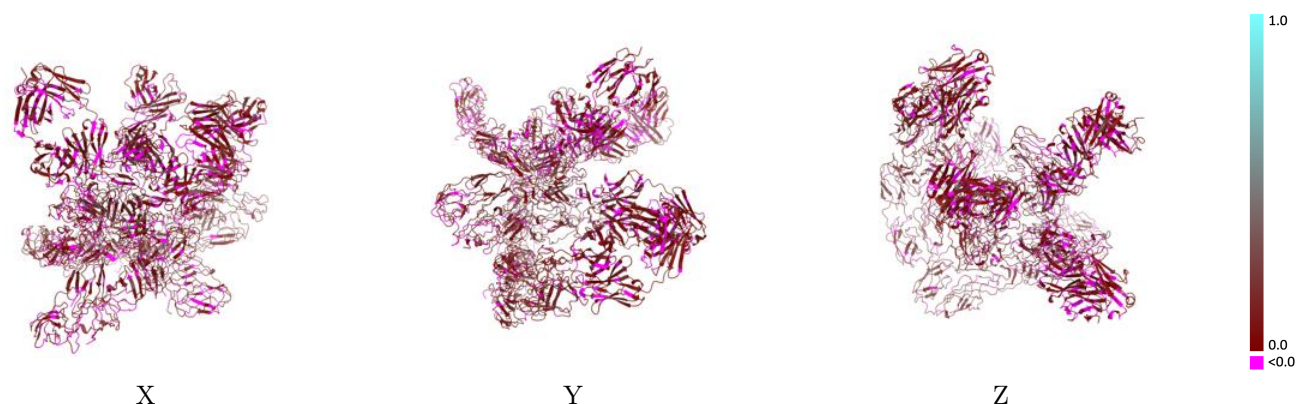
Y



Z

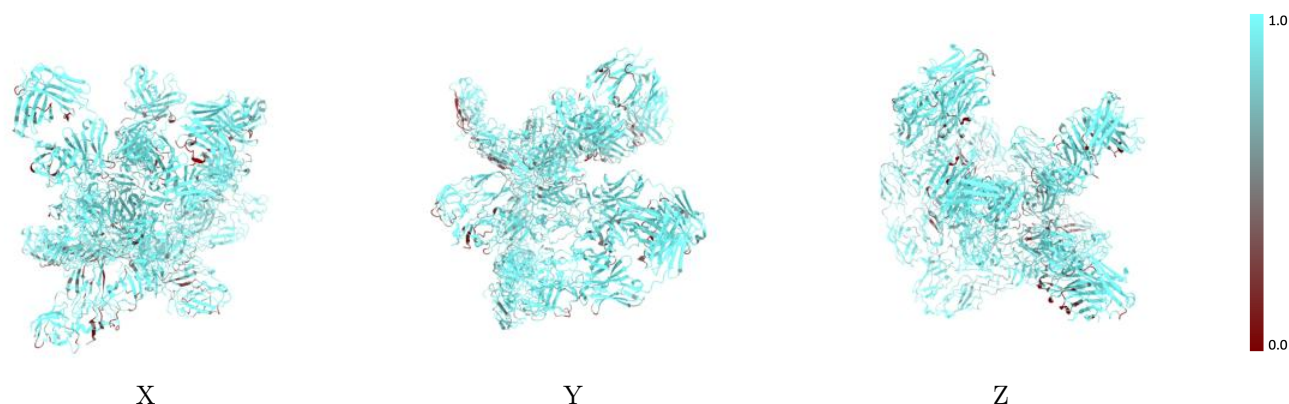
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



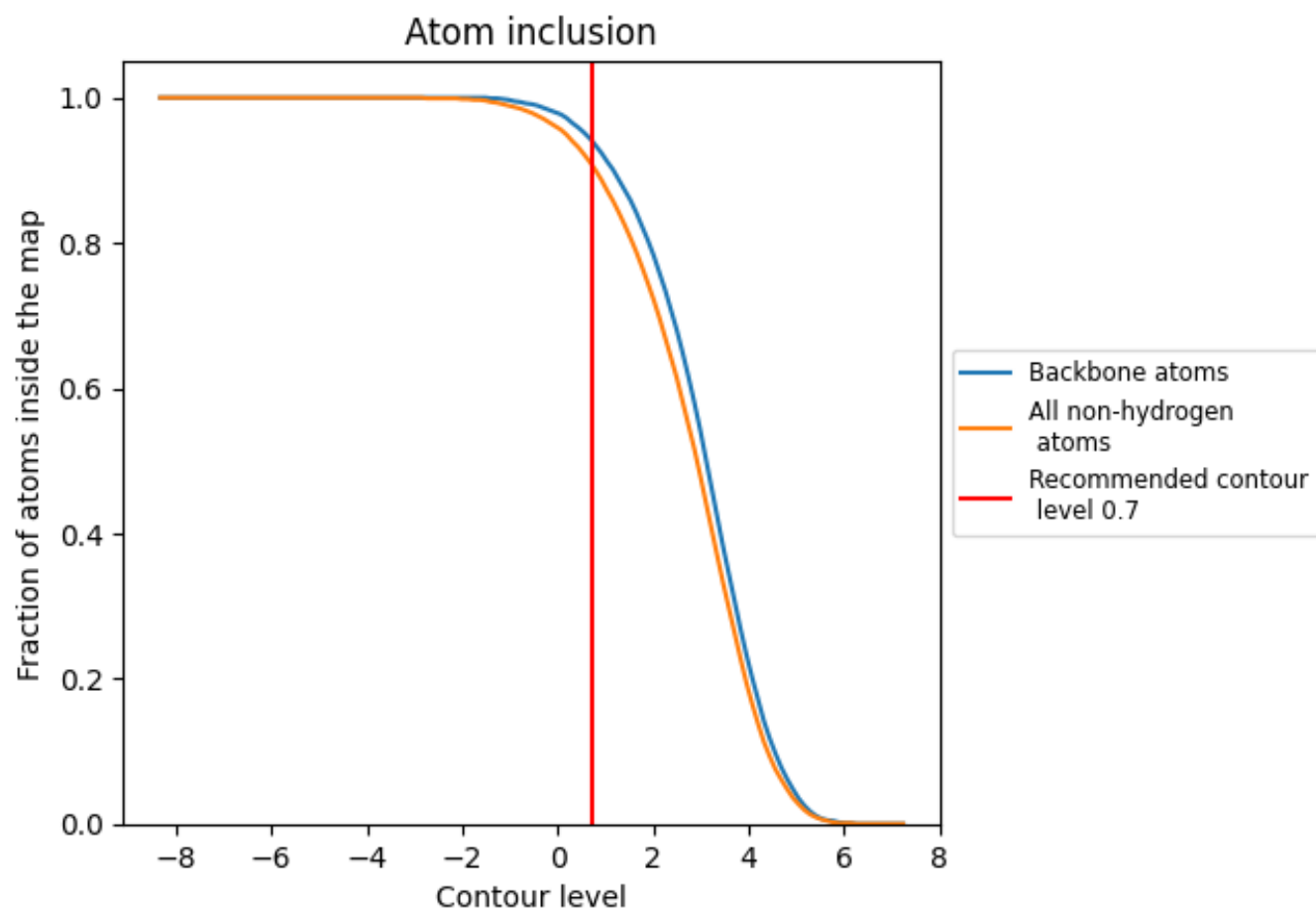
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.7).



































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 91% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.0920
A	 0.9200	 0.1260
B	 0.9250	 0.1360
C	 0.9300	 0.0710
D	 0.9330	 0.0740
E	 0.8810	 0.1080
F	 0.9210	 0.1170
G	 0.9170	 0.0700
H	 0.9450	 0.0640
I	 0.9210	 0.1200
J	 0.9160	 0.0900
K	 0.8870	 0.0600
L	 0.9100	 0.0580
M	 0.8650	 0.0880
N	 0.8850	 0.0780
O	 0.9090	 0.0600
P	 0.9100	 0.0630

