



wwPDB EM Validation Summary Report ⓘ

Sep 26, 2024 – 04:23 PM EDT

PDB ID : 8VH2
EMDB ID : EMD-43232
Title : CH235.12 Fab bound to the HIV-1 CH505.M5 SOSIP
Authors : Henderson, R.; Acharya, P.
Deposited on : 2023-12-30
Resolution : 4.31 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.dev112
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) : 2.38.3

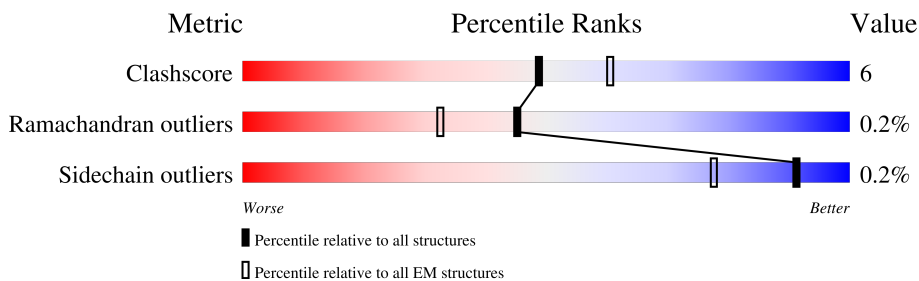
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.31 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.




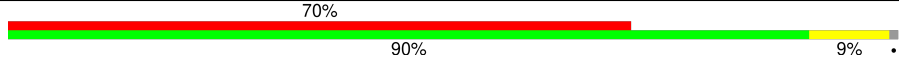


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 ≥ 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	464	35% (Poor fit) 81% (0 outliers), 14% (1 outlier), 5% (2+ outliers)
1	E	464	36% (Poor fit) 81% (0 outliers), 15% (1 outlier), 5% (2+ outliers)
1	I	464	37% (Poor fit) 83% (0 outliers), 12% (1 outlier), 5% (2+ outliers)
2	B	159	43% (Poor fit) 64% (0 outliers), 13% (1 outlier), 23% (2+ outliers)
2	F	159	44% (Poor fit) 67% (0 outliers), 9% (1 outlier), 23% (2+ outliers)
2	J	159	48% (Poor fit) 66% (0 outliers), 10% (1 outlier), 23% (2+ outliers)
3	C	225	49% (Poor fit) 85% (0 outliers), 12% (1 outlier)
3	G	225	49% (Poor fit) 84% (0 outliers), 14% (1 outlier)

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Mol	Chain	Length	Quality of chain
3	K	225	
4	D	213	
4	H	213	
4	L	213	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 46227 atoms, of which 22914 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 CH505.M5.G458Y SOSIP gp120.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	443	6959	2194	3469	610	658	28	0	0
1	E	443	6959	2194	3469	610	658	28	0	0
1	I	443	6959	2194	3469	610	658	28	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	ALA	-	expression tag	UNP M4M5H1
A	32	GLU	-	expression tag	UNP M4M5H1
A	33	ASN	-	expression tag	UNP M4M5H1
A	34	LEU	MET	conflict	UNP M4M5H1
A	64	LYS	GLU	conflict	UNP M4M5H1
A	279	LYS	ASN	conflict	UNP M4M5H1
A	316	TRP	ALA	conflict	UNP M4M5H1
A	458	TYR	GLY	conflict	UNP M4M5H1
A	488	LYS	GLU	conflict	UNP M4M5H1
A	489	ILE	VAL	conflict	UNP M4M5H1
A	490	GLU	LYS	conflict	UNP M4M5H1
A	498	ARG	ASN	conflict	UNP M4M5H1
A	499	CYS	ALA	conflict	UNP M4M5H1
A	500	LYS	ARG	conflict	UNP M4M5H1
E	31	ALA	-	expression tag	UNP M4M5H1
E	32	GLU	-	expression tag	UNP M4M5H1
E	33	ASN	-	expression tag	UNP M4M5H1
E	34	LEU	MET	conflict	UNP M4M5H1
E	64	LYS	GLU	conflict	UNP M4M5H1
E	279	LYS	ASN	conflict	UNP M4M5H1
E	316	TRP	ALA	conflict	UNP M4M5H1
E	458	TYR	GLY	conflict	UNP M4M5H1
E	488	LYS	GLU	conflict	UNP M4M5H1
E	489	ILE	VAL	conflict	UNP M4M5H1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	490	GLU	LYS	conflict	UNP M4M5H1
E	498	ARG	ASN	conflict	UNP M4M5H1
E	499	CYS	ALA	conflict	UNP M4M5H1
E	500	LYS	ARG	conflict	UNP M4M5H1
I	31	ALA	-	expression tag	UNP M4M5H1
I	32	GLU	-	expression tag	UNP M4M5H1
I	33	ASN	-	expression tag	UNP M4M5H1
I	34	LEU	MET	conflict	UNP M4M5H1
I	64	LYS	GLU	conflict	UNP M4M5H1
I	279	LYS	ASN	conflict	UNP M4M5H1
I	316	TRP	ALA	conflict	UNP M4M5H1
I	458	TYR	GLY	conflict	UNP M4M5H1
I	488	LYS	GLU	conflict	UNP M4M5H1
I	489	ILE	VAL	conflict	UNP M4M5H1
I	490	GLU	LYS	conflict	UNP M4M5H1
I	498	ARG	ASN	conflict	UNP M4M5H1
I	499	CYS	ALA	conflict	UNP M4M5H1
I	500	LYS	ARG	conflict	UNP M4M5H1

- Molecule 2 is a protein called Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	B	122	1920	611	951	167	185	6	0	0
2	F	122	1920	611	951	167	185	6	0	0
2	J	122	1920	611	951	167	185	6	0	0

There are 75 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	506	ARG	VAL	conflict	UNP M4M5H1
B	507	ARG	GLY	conflict	UNP M4M5H1
B	509	ARG	GLU	conflict	UNP M4M5H1
B	510	ARG	LYS	conflict	UNP M4M5H1
B	515	ILE	MET	conflict	UNP M4M5H1
B	535	MET	ILE	conflict	UNP M4M5H1
B	543	ASN	GLN	conflict	UNP M4M5H1
B	557	ARG	LYS	conflict	UNP M4M5H1
B	559	PRO	ILE	conflict	UNP M4M5H1
B	565	LEU	MET	conflict	UNP M4M5H1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	583	VAL	LEU	conflict	UNP M4M5H1
B	588	ARG	LYS	conflict	UNP M4M5H1
B	595	ILE	MET	conflict	UNP M4M5H1
B	605	CYS	THR	conflict	UNP M4M5H1
B	609	PRO	TYR	conflict	UNP M4M5H1
B	617	ARG	LYS	conflict	UNP M4M5H1
B	618	ASN	THR	conflict	UNP M4M5H1
B	619	LEU	TYR	conflict	UNP M4M5H1
B	620	SER	GLY	conflict	UNP M4M5H1
B	621	GLU	ASP	conflict	UNP M4M5H1
B	629	LEU	MET	conflict	UNP M4M5H1
B	632	ASP	GLU	conflict	UNP M4M5H1
B	633	LYS	ARG	conflict	UNP M4M5H1
B	640	GLN	GLU	conflict	UNP M4M5H1
B	644	GLY	GLU	conflict	UNP M4M5H1
F	506	ARG	VAL	conflict	UNP M4M5H1
F	507	ARG	GLY	conflict	UNP M4M5H1
F	509	ARG	GLU	conflict	UNP M4M5H1
F	510	ARG	LYS	conflict	UNP M4M5H1
F	515	ILE	MET	conflict	UNP M4M5H1
F	535	MET	ILE	conflict	UNP M4M5H1
F	543	ASN	GLN	conflict	UNP M4M5H1
F	557	ARG	LYS	conflict	UNP M4M5H1
F	559	PRO	ILE	conflict	UNP M4M5H1
F	565	LEU	MET	conflict	UNP M4M5H1
F	583	VAL	LEU	conflict	UNP M4M5H1
F	588	ARG	LYS	conflict	UNP M4M5H1
F	595	ILE	MET	conflict	UNP M4M5H1
F	605	CYS	THR	conflict	UNP M4M5H1
F	609	PRO	TYR	conflict	UNP M4M5H1
F	617	ARG	LYS	conflict	UNP M4M5H1
F	618	ASN	THR	conflict	UNP M4M5H1
F	619	LEU	TYR	conflict	UNP M4M5H1
F	620	SER	GLY	conflict	UNP M4M5H1
F	621	GLU	ASP	conflict	UNP M4M5H1
F	629	LEU	MET	conflict	UNP M4M5H1
F	632	ASP	GLU	conflict	UNP M4M5H1
F	633	LYS	ARG	conflict	UNP M4M5H1
F	640	GLN	GLU	conflict	UNP M4M5H1
F	644	GLY	GLU	conflict	UNP M4M5H1
J	506	ARG	VAL	conflict	UNP M4M5H1
J	507	ARG	GLY	conflict	UNP M4M5H1

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Chain	Residue	Modelled	Actual	Comment	Reference
J	509	ARG	GLU	conflict	UNP M4M5H1
J	510	ARG	LYS	conflict	UNP M4M5H1
J	515	ILE	MET	conflict	UNP M4M5H1
J	535	MET	ILE	conflict	UNP M4M5H1
J	543	ASN	GLN	conflict	UNP M4M5H1
J	557	ARG	LYS	conflict	UNP M4M5H1
J	559	PRO	ILE	conflict	UNP M4M5H1
J	565	LEU	MET	conflict	UNP M4M5H1
J	583	VAL	LEU	conflict	UNP M4M5H1
J	588	ARG	LYS	conflict	UNP M4M5H1
J	595	ILE	MET	conflict	UNP M4M5H1
J	605	CYS	THR	conflict	UNP M4M5H1
J	609	PRO	TYR	conflict	UNP M4M5H1
J	617	ARG	LYS	conflict	UNP M4M5H1
J	618	ASN	THR	conflict	UNP M4M5H1
J	619	LEU	TYR	conflict	UNP M4M5H1
J	620	SER	GLY	conflict	UNP M4M5H1
J	621	GLU	ASP	conflict	UNP M4M5H1
J	629	LEU	MET	conflict	UNP M4M5H1
J	632	ASP	GLU	conflict	UNP M4M5H1
J	633	LYS	ARG	conflict	UNP M4M5H1
J	640	GLN	GLU	conflict	UNP M4M5H1
J	644	GLY	GLU	conflict	UNP M4M5H1

- Molecule 3 is a protein called CH235.12 Fab Heavy Chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	220	Total	C	H	N	O	S	0	0
			3310	1061	1633	287	320	9		
3	G	220	Total	C	H	N	O	S	0	0
			3310	1061	1633	287	320	9		
3	K	220	Total	C	H	N	O	S	0	0
			3310	1061	1633	287	320	9		

- Molecule 4 is a protein called CH235.12 Fab Light Chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	211	Total	C	H	N	O	S	0	0
			3220	1022	1585	285	324	4		
4	H	211	Total	C	H	N	O	S	0	0
			3220	1022	1585	285	324	4		

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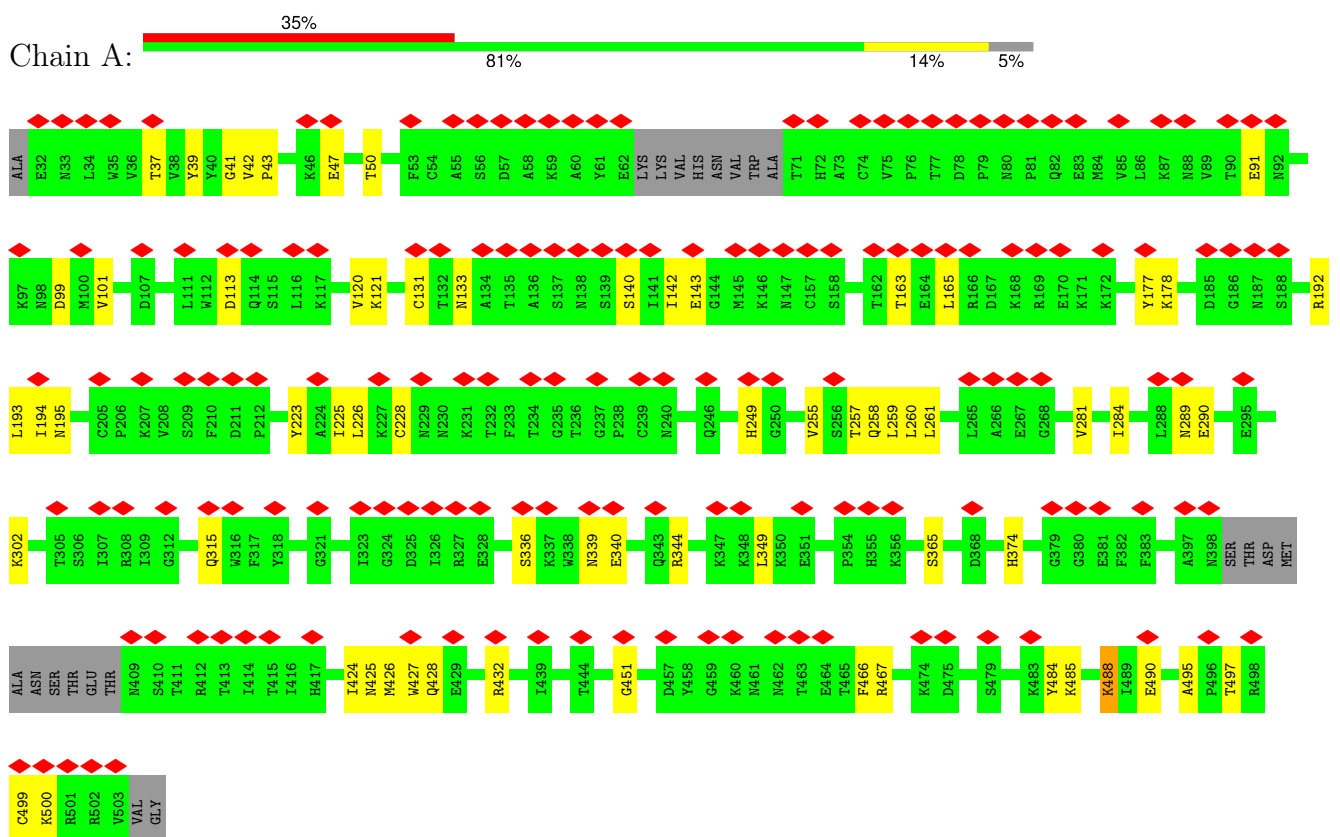
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Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
4	L	211	3220	1022	1585	285	324	4	0	0

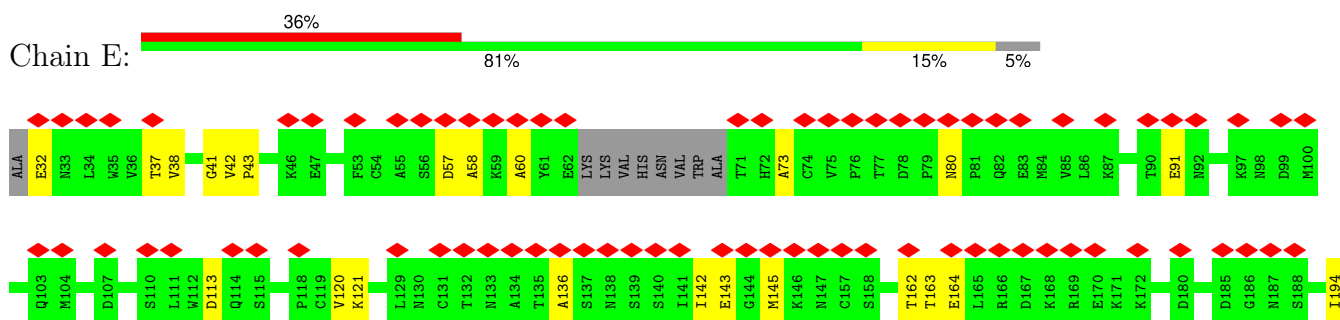
3 Residue-property plots [i](#)

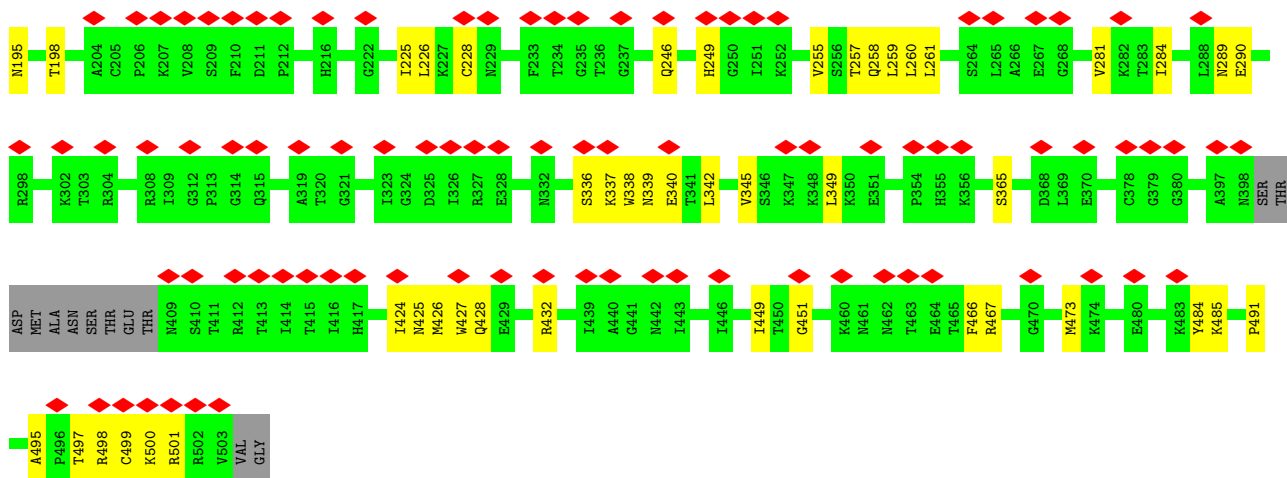
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: CH505.M5.G458Y SOSIP gp120

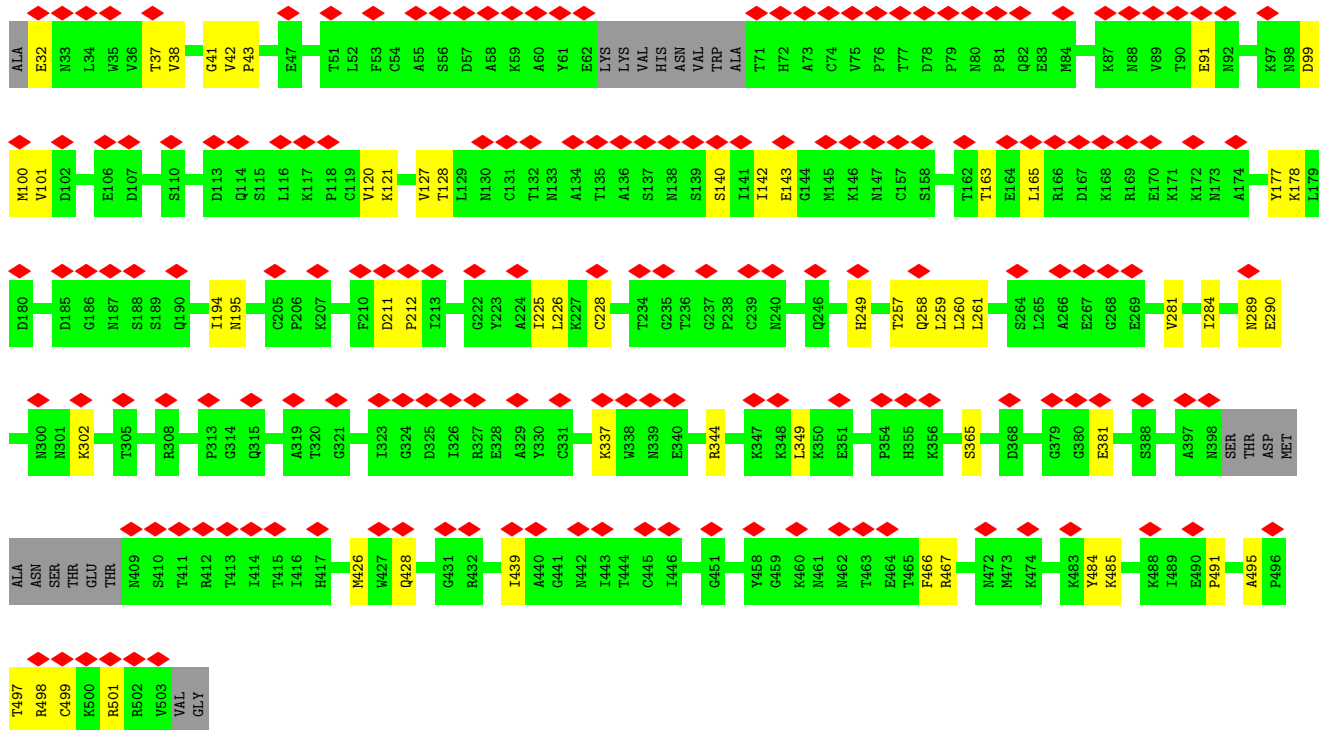
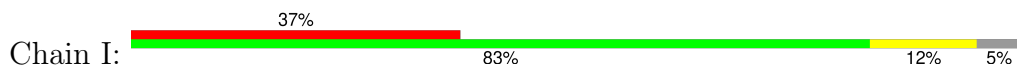


- Molecule 1: CH505.M5.G458Y SOSIP gp120

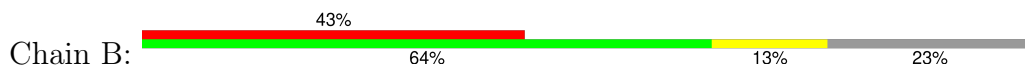


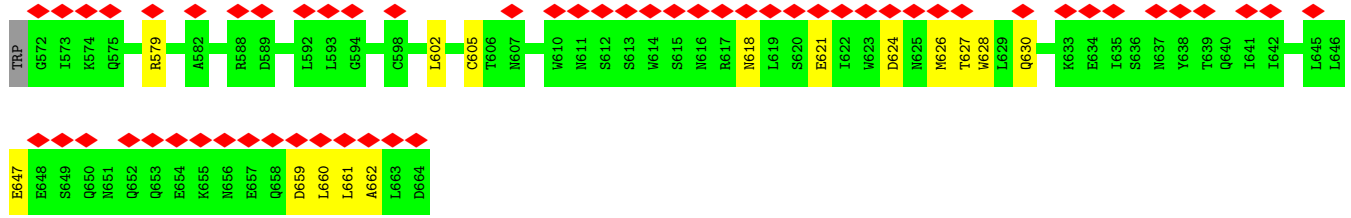


• Molecule 1: CH505.M5.G458Y SOSIP gp120

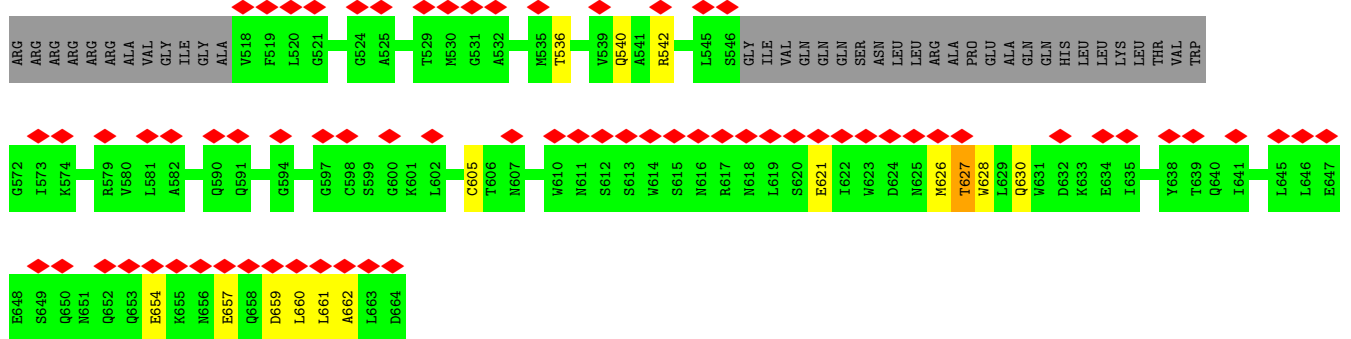
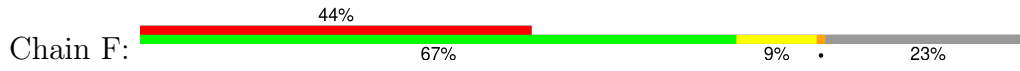


• Molecule 2: Envelope glycoprotein gp160

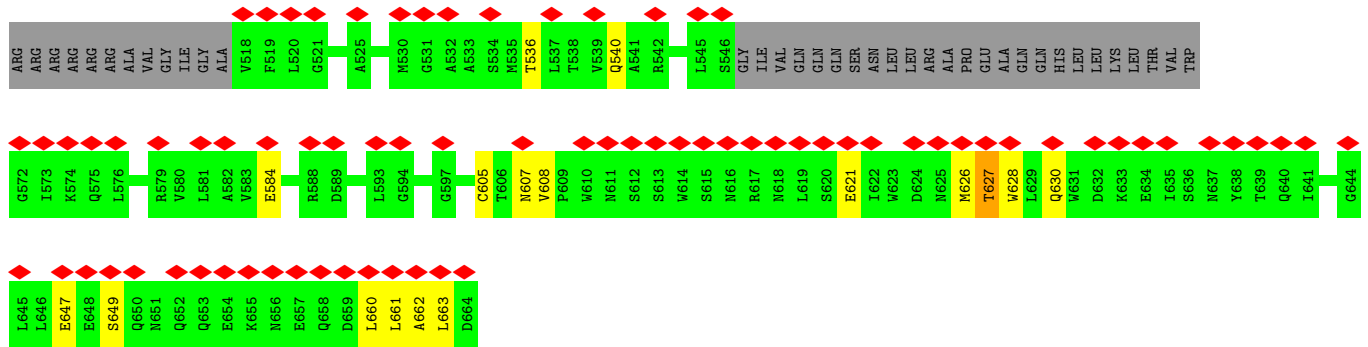




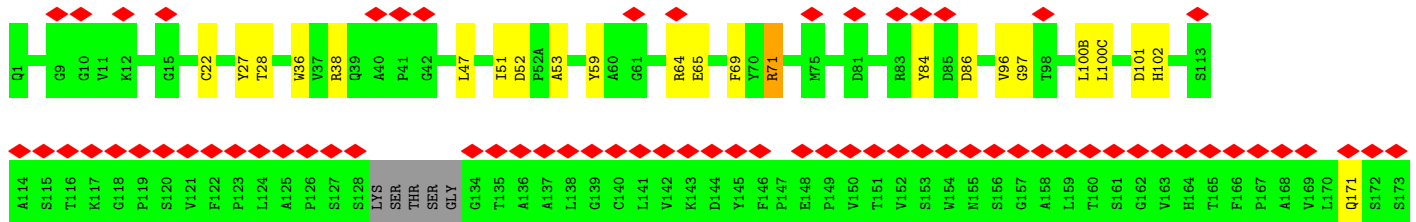
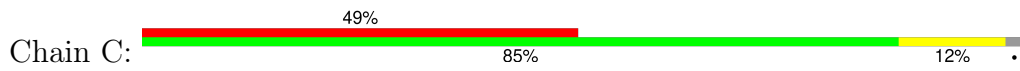
• Molecule 2: Envelope glycoprotein gp160

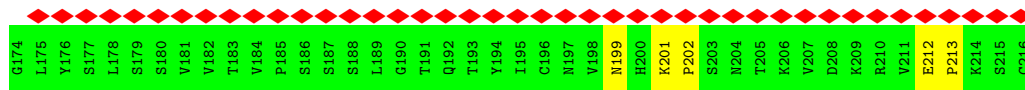


• Molecule 2: Envelope glycoprotein gp160

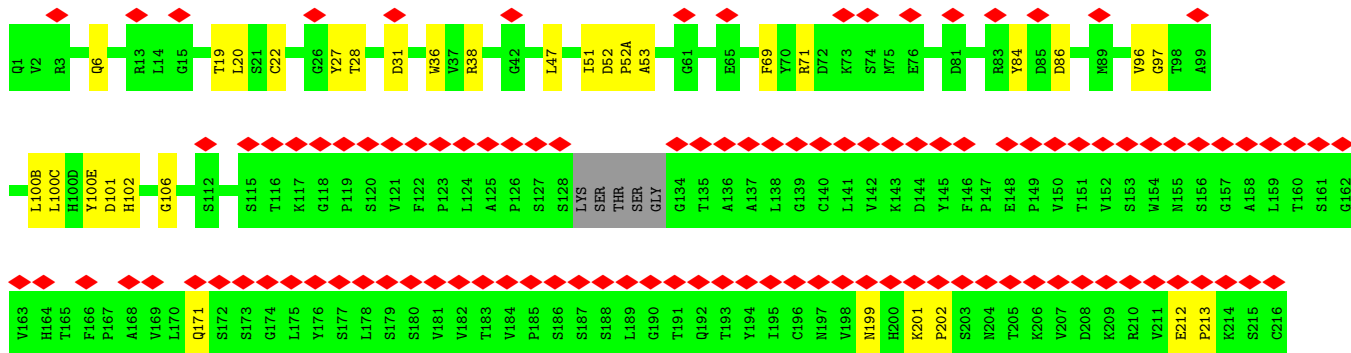
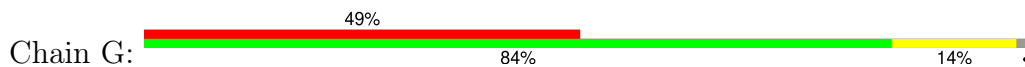


• Molecule 3: CH235.12 Fab Heavy Chain

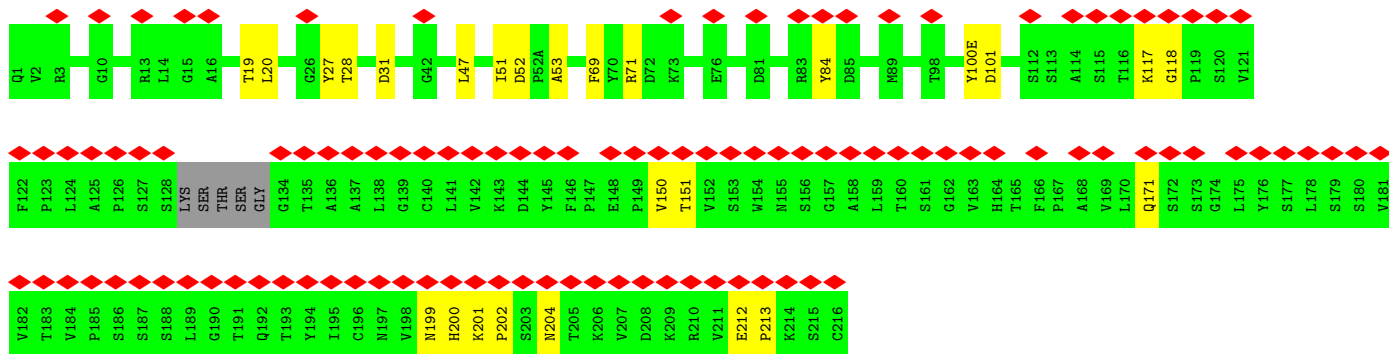
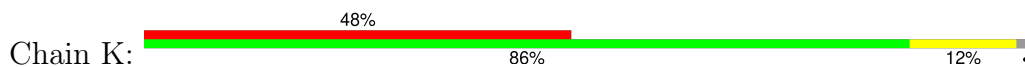




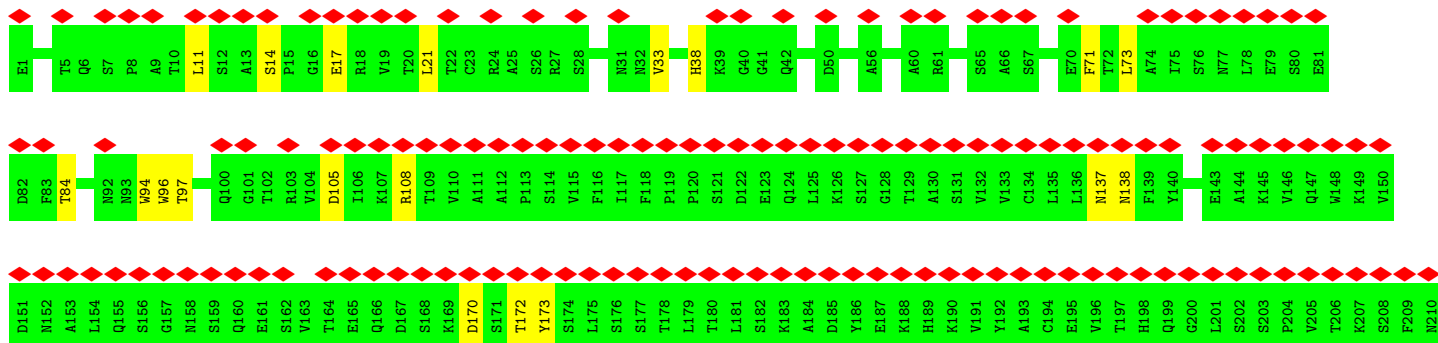
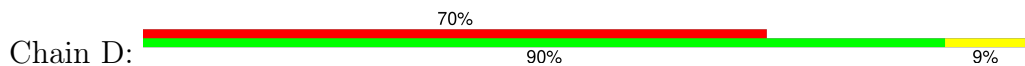
• Molecule 3: CH235.12 Fab Heavy Chain



• Molecule 3: CH235.12 Fab Heavy Chain

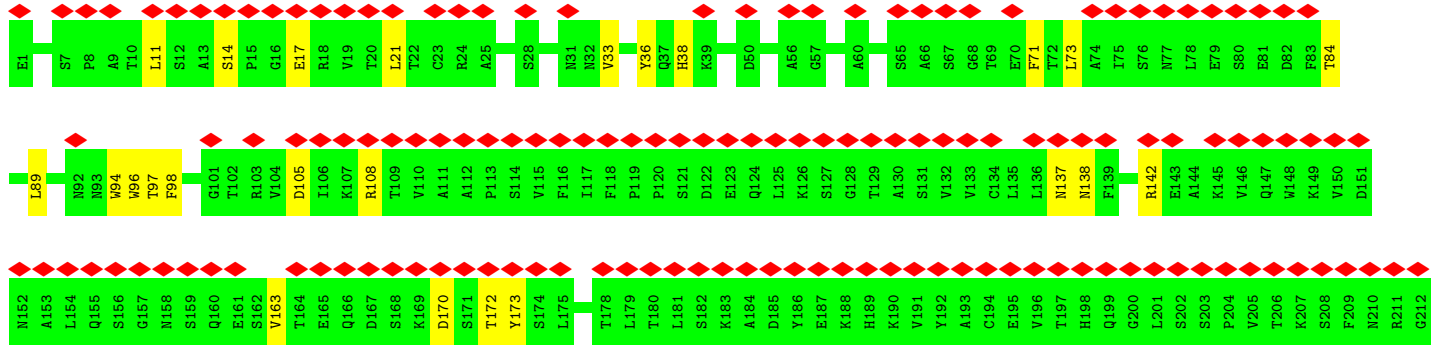
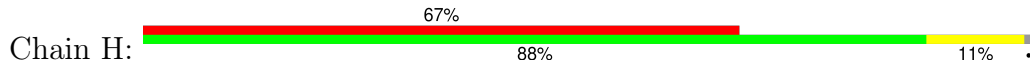


• Molecule 4: CH235.12 Fab Light Chain

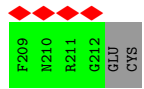
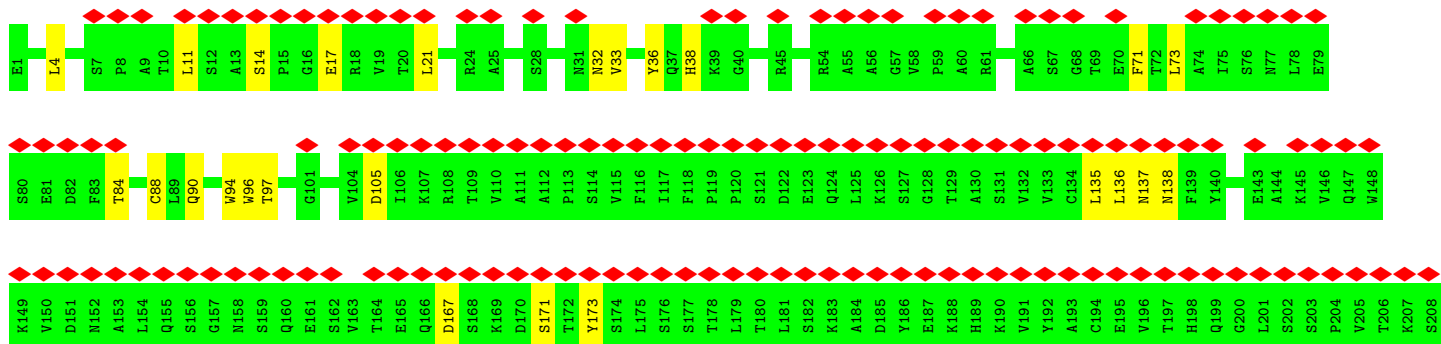
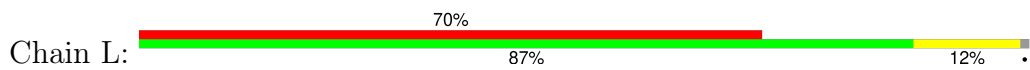




• Molecule 4: CH235.12 Fab Light Chain



• Molecule 4: CH235.12 Fab Light Chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	148858	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 ($e^-/\text{\AA}^2$)	59.7	Depositor
Minimum defocus (nm)	100	Depositor
Maximum defocus (nm)	3400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.973	Depositor
Minimum map value	-5.599	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.124	Depositor
Recommended contour level	1	Depositor
Map size (\AA)	324.0, 324.0, 324.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/3558	0.50	0/4822
1	E	0.26	0/3558	0.51	0/4822
1	I	0.26	0/3558	0.51	0/4822
2	B	0.25	0/985	0.49	0/1334
2	F	0.25	0/985	0.50	0/1334
2	J	0.25	0/985	0.46	0/1334
3	C	0.31	0/1720	0.53	0/2341
3	G	0.30	0/1720	0.53	0/2341
3	K	0.30	0/1720	0.53	0/2341
4	D	0.27	0/1671	0.50	0/2272
4	H	0.26	0/1671	0.50	0/2272
4	L	0.26	0/1671	0.50	0/2272
All	All	0.27	0/23802	0.51	0/32307

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3490	3469	3462	49	0
1	E	3490	3469	3462	49	0
1	I	3490	3469	3462	40	0
2	B	969	951	949	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	969	951	949	19	0
2	J	969	951	949	19	0
3	C	1677	1633	1632	17	0
3	G	1677	1633	1632	19	0
3	K	1677	1633	1632	16	0
4	D	1635	1585	1585	13	0
4	H	1635	1585	1585	16	0
4	L	1635	1585	1585	17	0
All	All	23313	22914	22884	260	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 6.

The worst 5 of 260 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:41:GLY:O	2:F:540:GLN:NE2	1.96	0.99
1:I:41:GLY:O	2:J:540:GLN:NE2	1.95	0.97
4:D:108:ARG:NH1	4:D:170:ASP:O	2.01	0.91
4:H:108:ARG:NH1	4:H:170:ASP:O	2.06	0.87
1:A:41:GLY:O	2:B:540:GLN:NE2	2.07	0.87

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	433/464 (93%)	388 (90%)	44 (10%)	1 (0%)	44 78
1	E	433/464 (93%)	395 (91%)	37 (8%)	1 (0%)	44 78
1	I	433/464 (93%)	398 (92%)	34 (8%)	1 (0%)	44 78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	118/159 (74%)	109 (92%)	9 (8%)	0	100	100
2	F	118/159 (74%)	110 (93%)	7 (6%)	1 (1%)	16	53
2	J	118/159 (74%)	106 (90%)	11 (9%)	1 (1%)	16	53
3	C	216/225 (96%)	193 (89%)	23 (11%)	0	100	100
3	G	216/225 (96%)	196 (91%)	20 (9%)	0	100	100
3	K	216/225 (96%)	198 (92%)	18 (8%)	0	100	100
4	D	209/213 (98%)	200 (96%)	9 (4%)	0	100	100
4	H	209/213 (98%)	200 (96%)	9 (4%)	0	100	100
4	L	209/213 (98%)	201 (96%)	8 (4%)	0	100	100
All	All	2928/3183 (92%)	2694 (92%)	229 (8%)	5 (0%)	45	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	J	627	THR
1	A	228	CYS
1	E	228	CYS
2	F	627	THR
1	I	228	CYS

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	397/415 (96%)	396 (100%)	1 (0%)	91	92
1	E	397/415 (96%)	397 (100%)	0	100	100
1	I	397/415 (96%)	396 (100%)	1 (0%)	91	92
2	B	105/135 (78%)	105 (100%)	0	100	100
2	F	105/135 (78%)	105 (100%)	0	100	100
2	J	105/135 (78%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	184/188 (98%)	183 (100%)	1 (0%)	86	90
3	G	184/188 (98%)	183 (100%)	1 (0%)	86	90
3	K	184/188 (98%)	183 (100%)	1 (0%)	86	90
4	D	182/184 (99%)	182 (100%)	0	100	100
4	H	182/184 (99%)	182 (100%)	0	100	100
4	L	182/184 (99%)	182 (100%)	0	100	100
All	All	2604/2766 (94%)	2599 (100%)	5 (0%)	91	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	488	LYS
3	C	71	ARG
3	G	71	ARG
1	I	100	MET
3	K	71	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	J	651	ASN
3	K	171	GLN
4	L	138	ASN
4	L	137	ASN
4	H	137	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	E	2
1	A	2
1	I	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	147:ASN	C	157:CYS	N	6.47
1	A	147:ASN	C	157:CYS	N	6.33
1	I	147:ASN	C	157:CYS	N	4.32
1	E	309:ILE	C	312:GLY	N	3.35
1	A	309:ILE	C	312:GLY	N	3.08

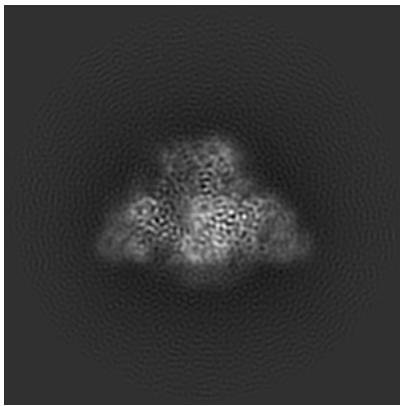
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43232. These allow visual inspection of the internal detail of the map and identification of artifacts.

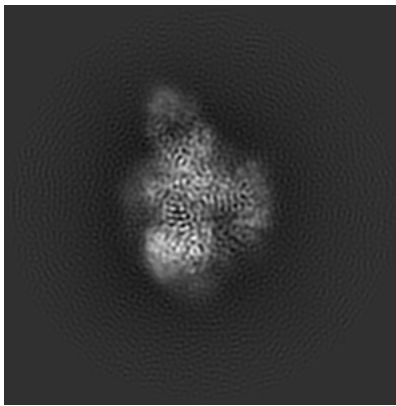
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

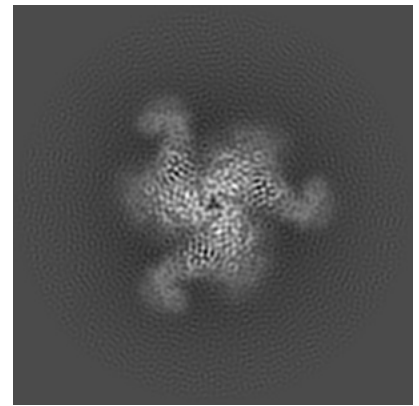
6.1.1 Primary map



X

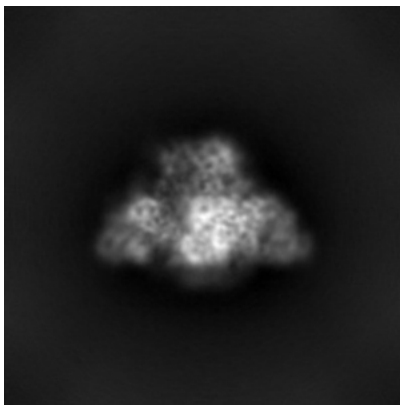


Y

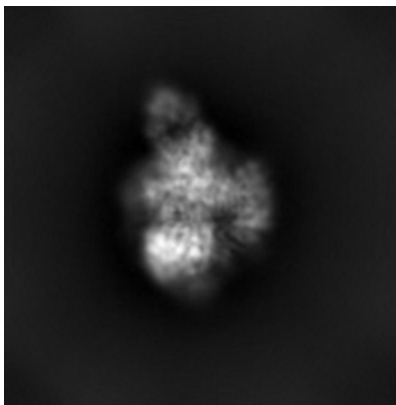


Z

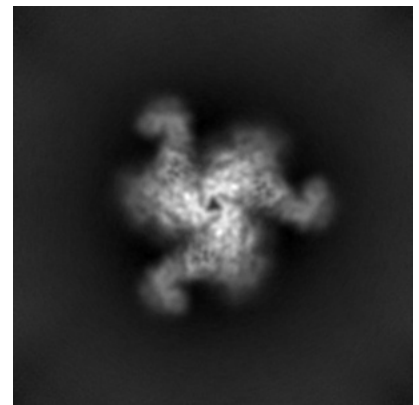
6.1.2 Raw map



X



Y

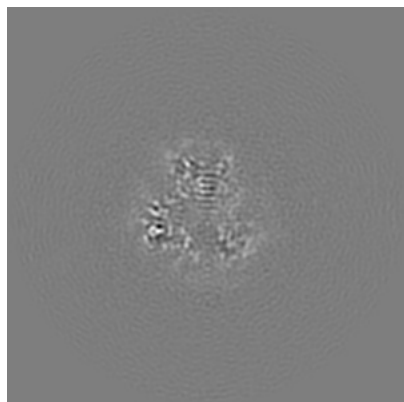


Z

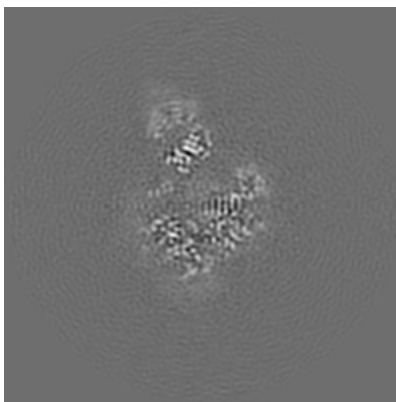
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

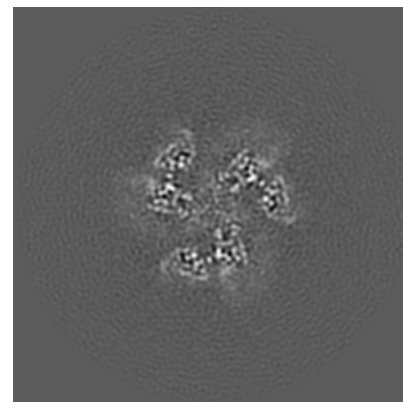
6.2.1 Primary map



X Index: 150

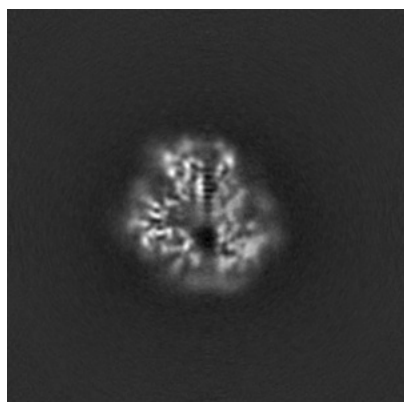


Y Index: 150

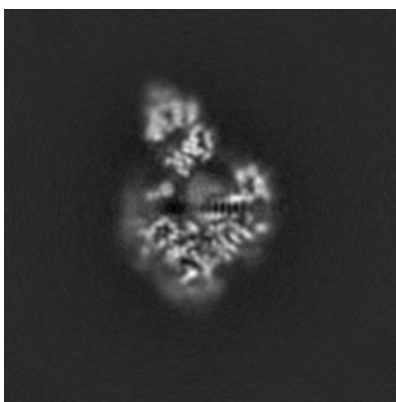


Z Index: 150

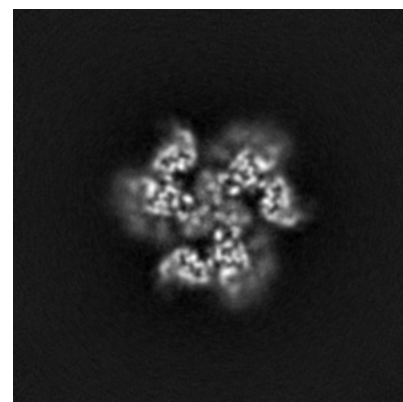
6.2.2 Raw map



X Index: 150



Y Index: 150

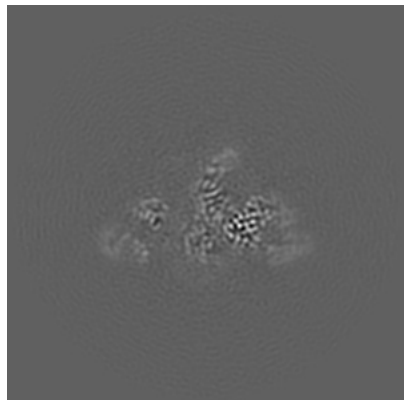


Z Index: 150

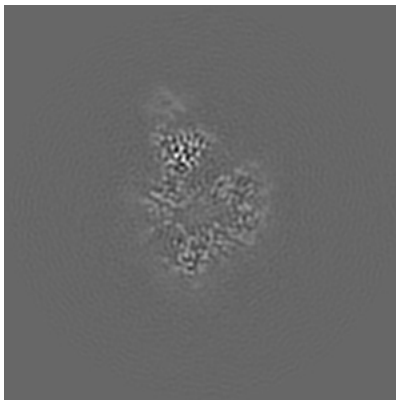
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

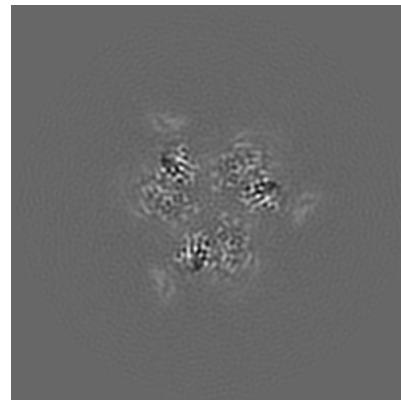
6.3.1 Primary map



X Index: 125

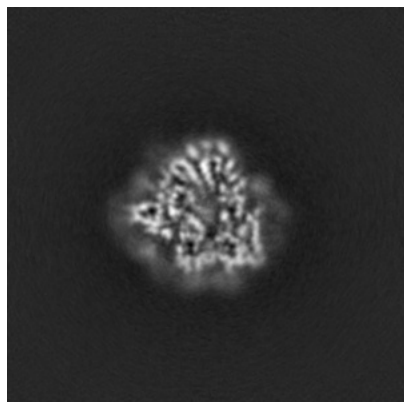


Y Index: 160

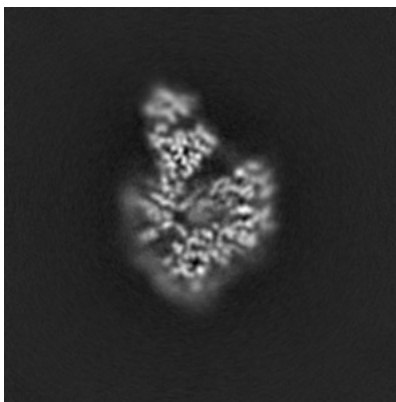


Z Index: 137

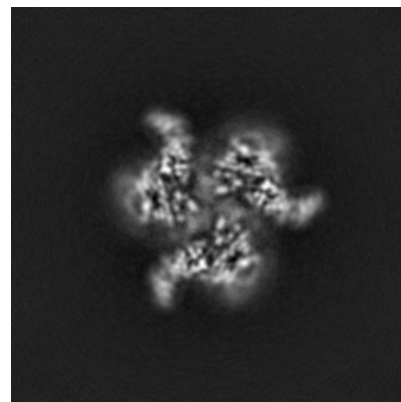
6.3.2 Raw map



X Index: 159



Y Index: 159

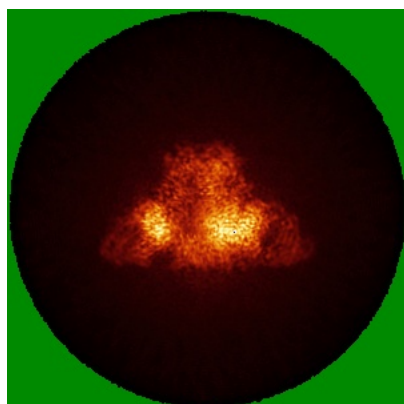


Z Index: 141

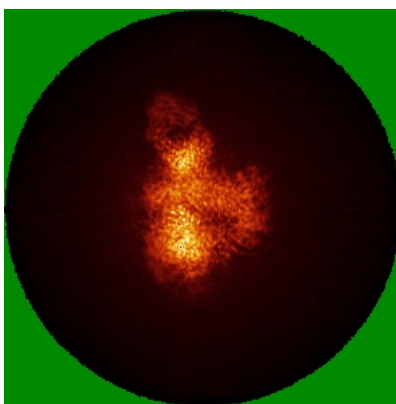
The images above show the largest variance slices of the map in three orthogonal directions.

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

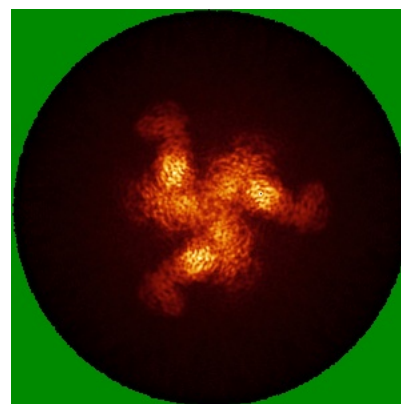
6.4.1 Primary map



X

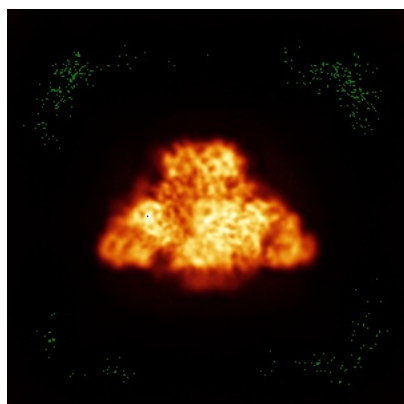


Y

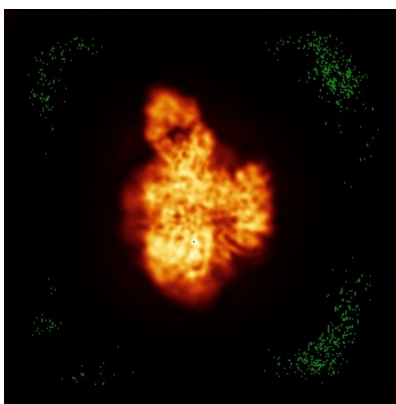


Z

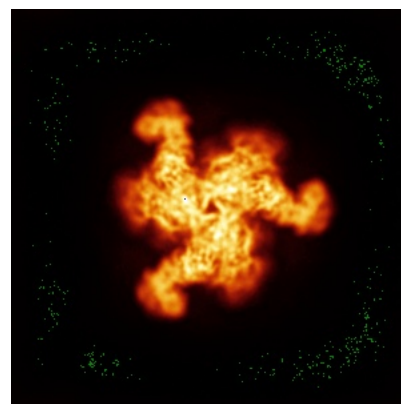
6.4.2 Raw map



X



Y

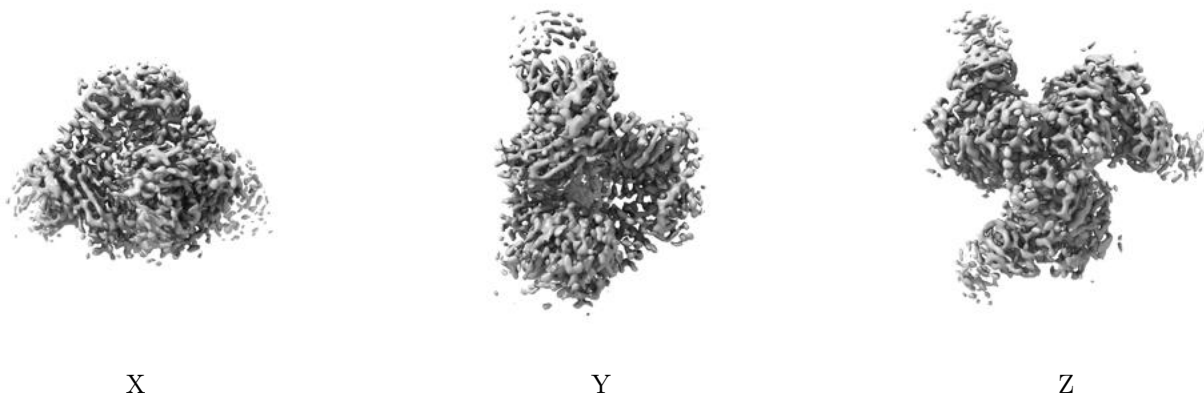


Z

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.

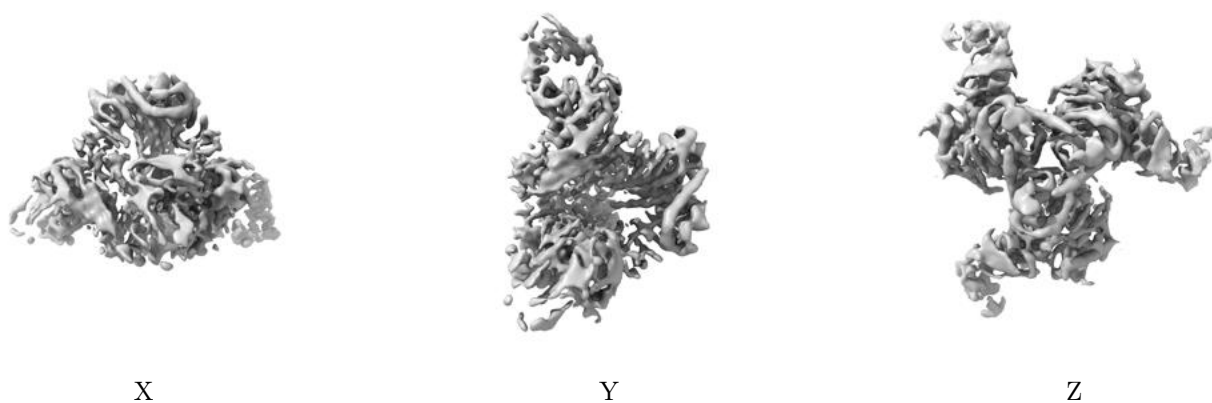
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. 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.

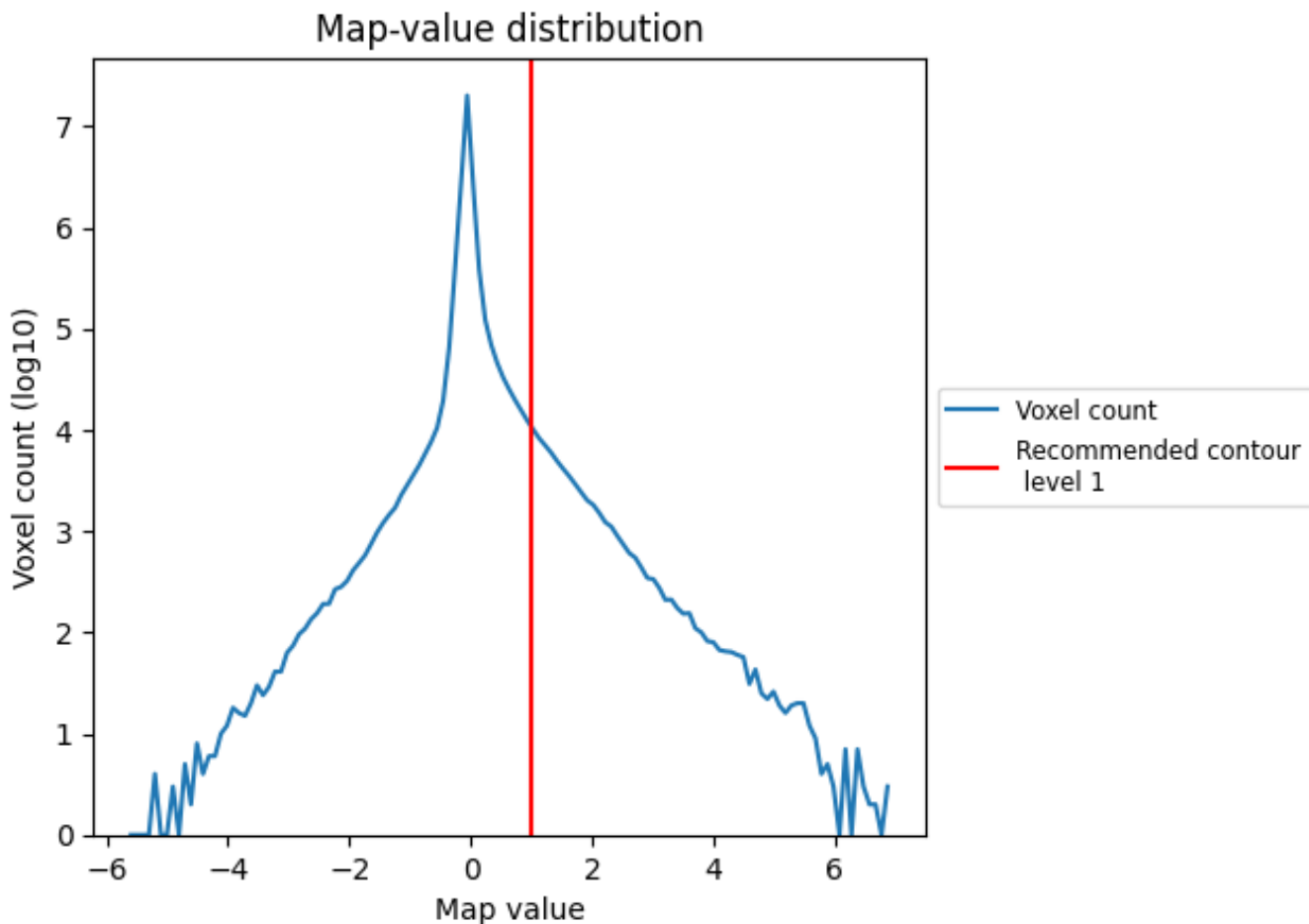
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

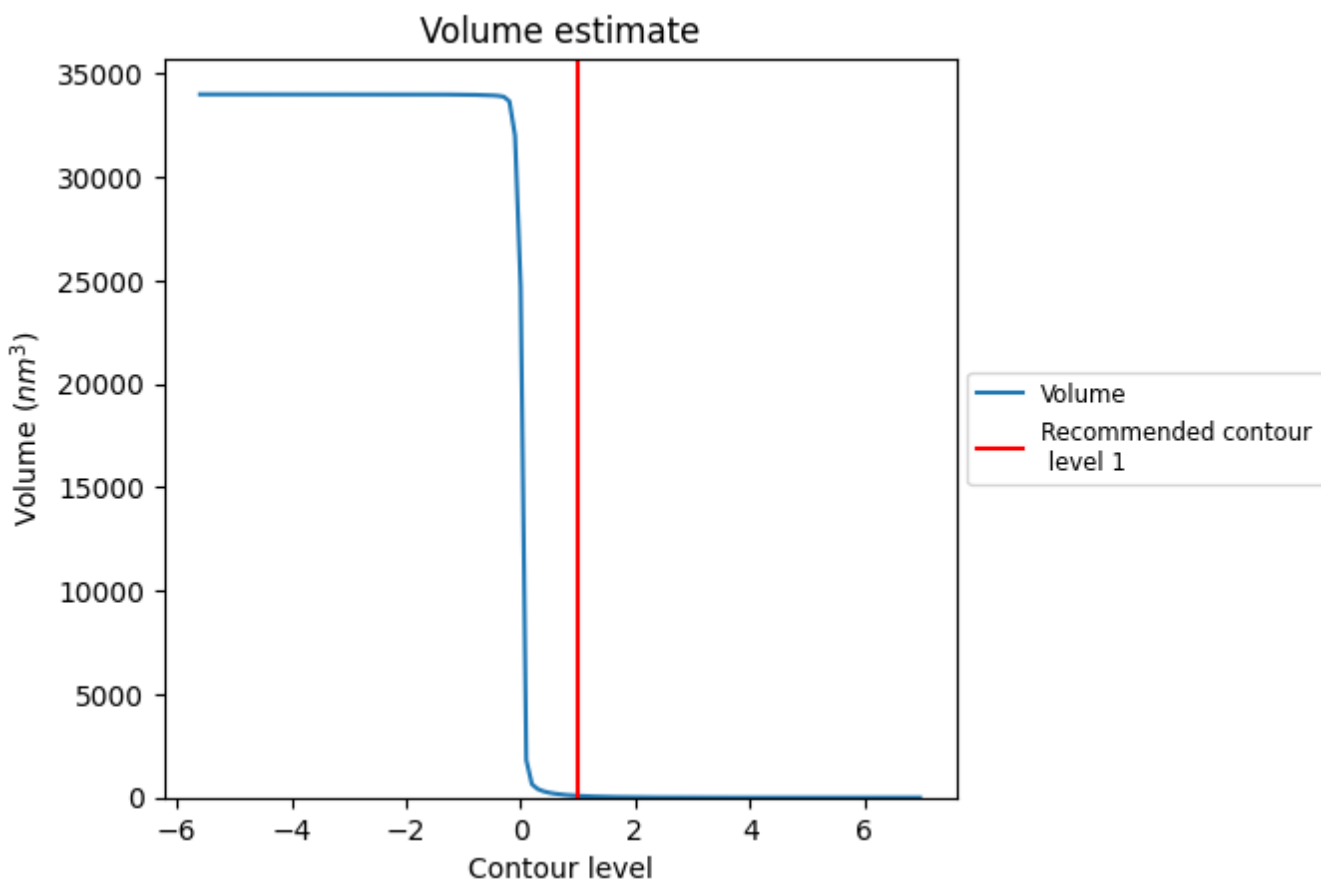
This section contains the results of statistical analysis of the map.

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.

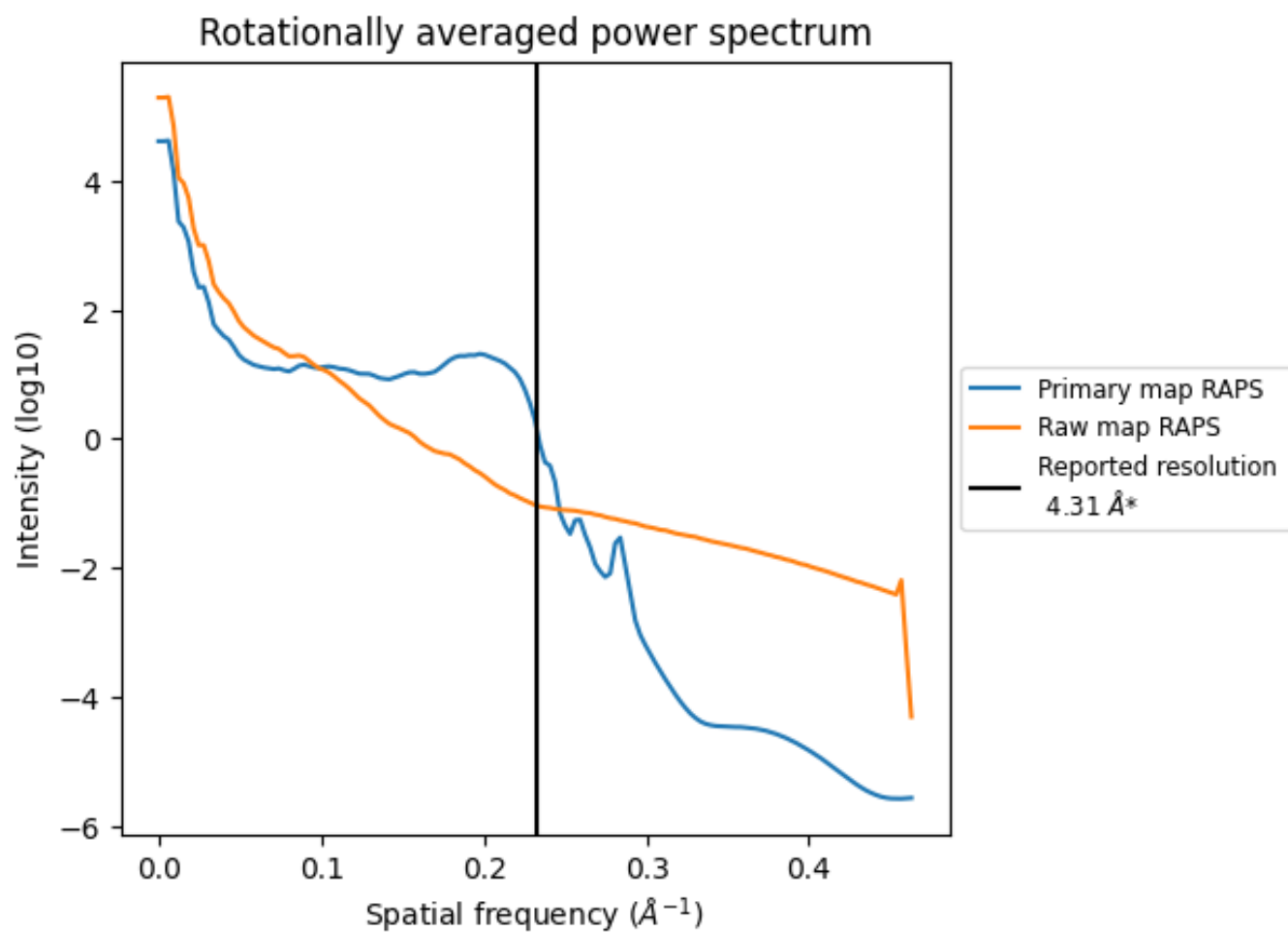
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 84 nm³; this corresponds to an approximate mass of 76 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

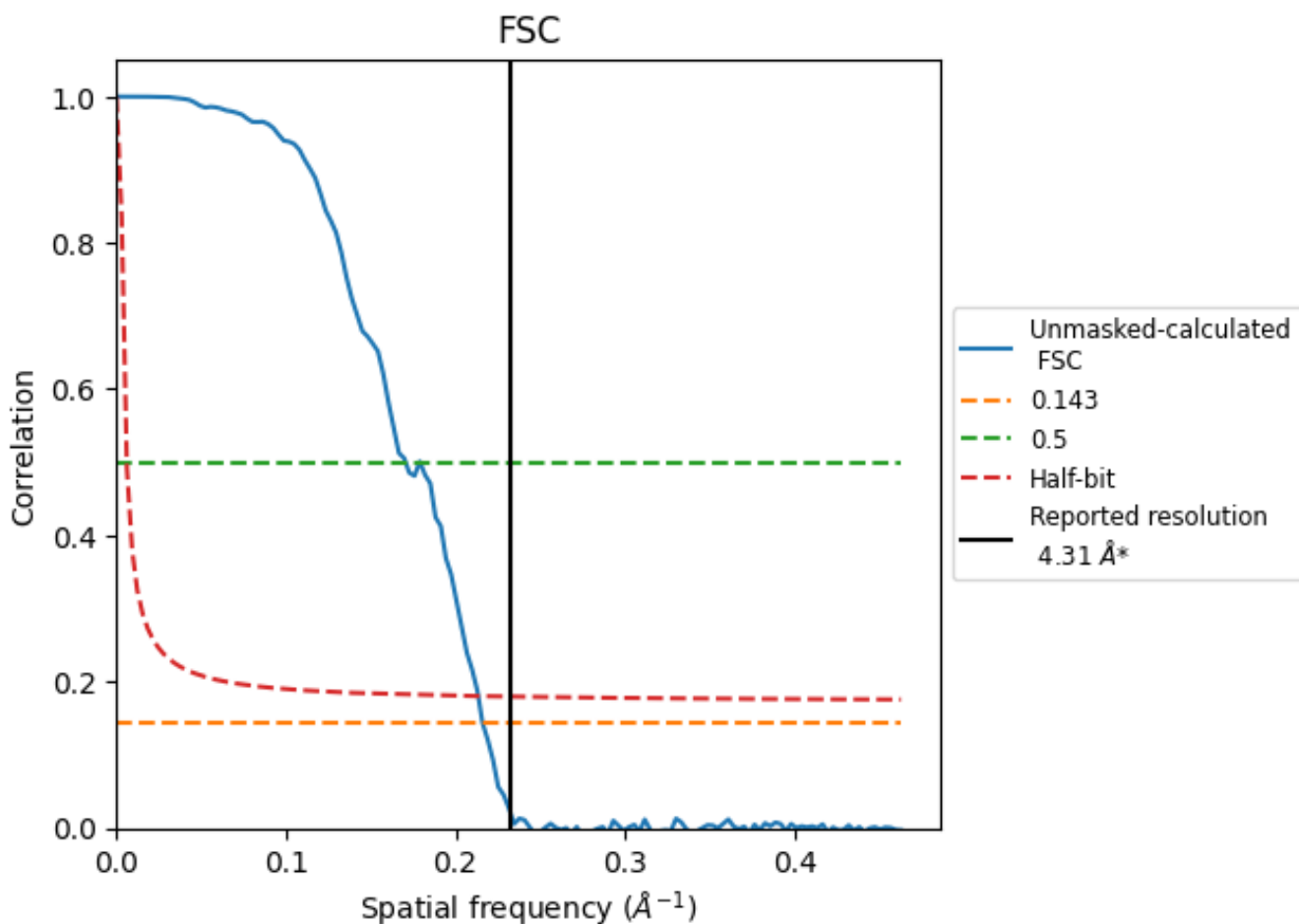


*Reported resolution corresponds to spatial frequency of 0.232 Å⁻¹

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 0.232 Å⁻¹

8.2 Resolution estimates [i](#)

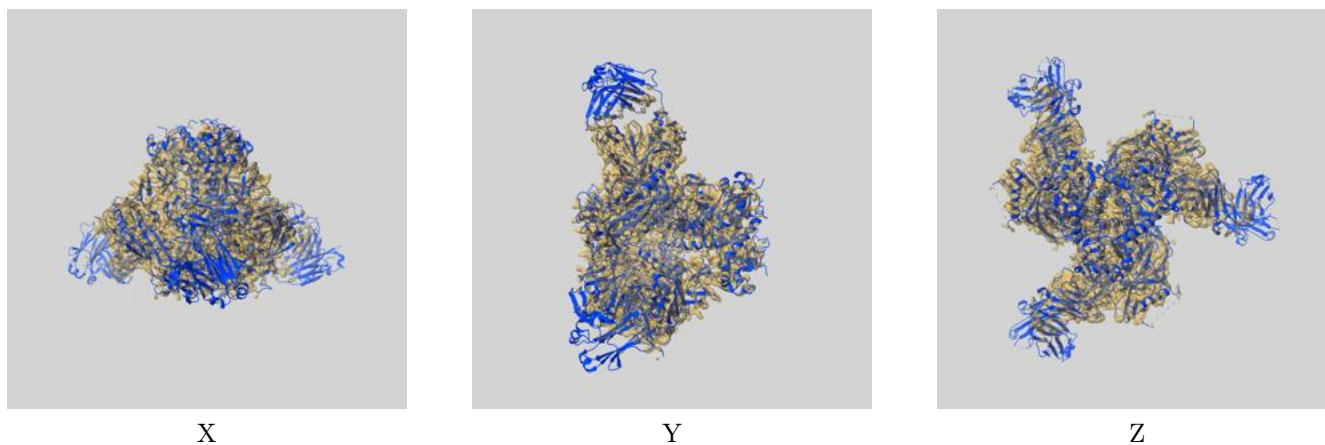
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.31	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.63	5.86	4.68

*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-43232 and PDB model 8VH2. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)



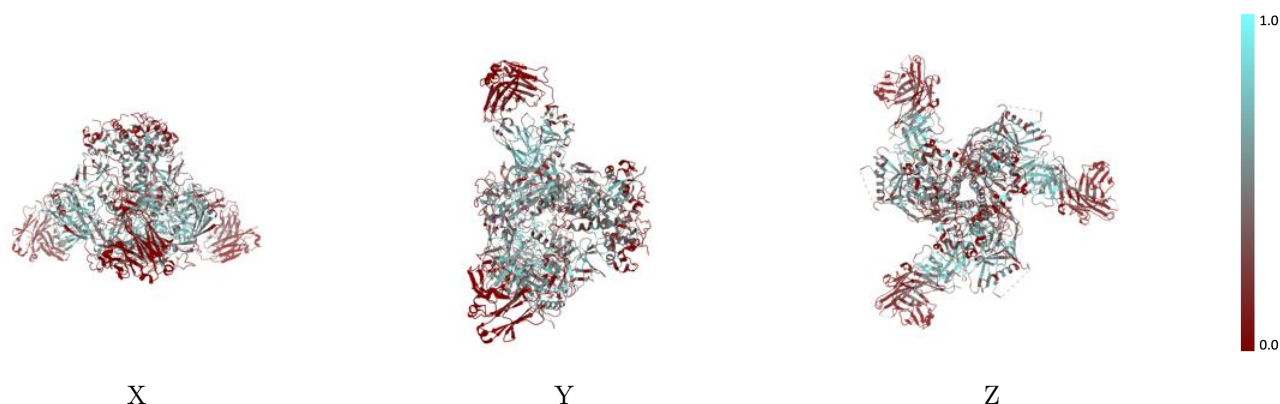
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



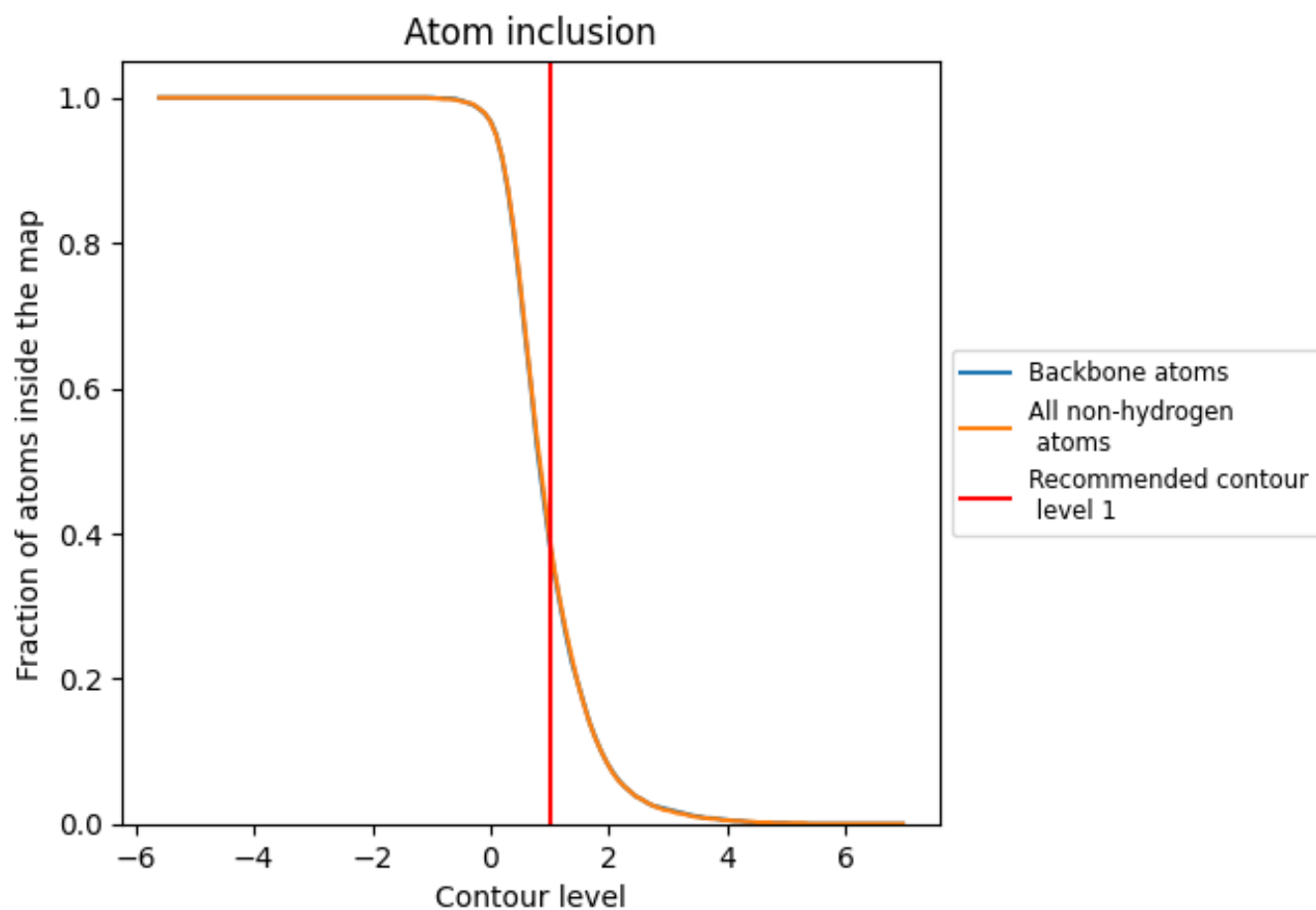
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 39% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3930	0.3200
A	0.4620	0.3300
B	0.3430	0.2830
C	0.3960	0.3270
D	0.2640	0.2800
E	0.4650	0.3350
F	0.3430	0.2870
G	0.4270	0.3410
H	0.2790	0.3040
I	0.4670	0.3440
J	0.3430	0.2790
K	0.4020	0.3340
L	0.2700	0.2920

