



wwPDB EM Validation Summary Report ⓘ

Oct 5, 2024 – 01:55 pm BST

PDB ID : 4CKD
EMDB ID : EMD-2548
Title : Model of complex between the E.coli enzyme beta-galactosidase and four single chain Fv antibody domains scFv13R4.
Authors : Vinothkumar, K.R.; McMullan, G.; Henderson, R.
Deposited on : 2014-01-03
Resolution : 13.00 Å(reported)
Based on initial model : 1F4A

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.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

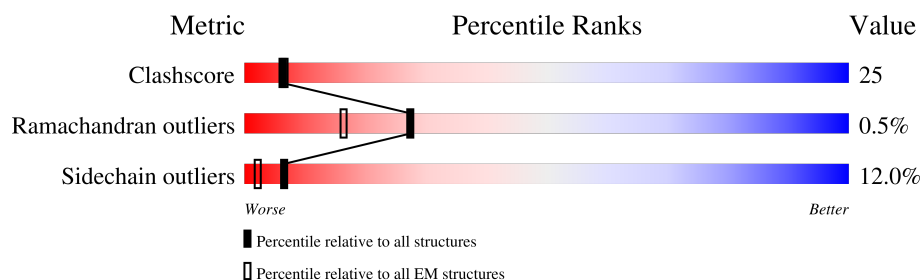
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 13.00 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.






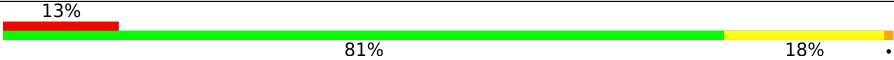
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1024	<div> <div>48%</div> <div>38%</div> <div>11%</div> <div>.</div> </div>
1	B	1024	<div> <div>49%</div> <div>38%</div> <div>11%</div> <div>.</div> </div>
1	C	1024	<div> <div>48%</div> <div>39%</div> <div>10%</div> <div>.</div> </div>
1	D	1024	<div> <div>48%</div> <div>39%</div> <div>11%</div> <div>.</div> </div>
2	H	114	<div> <div>19%</div> <div>75%</div> <div>25%</div> <div>.</div> </div>
2	I	114	<div> <div>18%</div> <div>73%</div> <div>26%</div> <div>.</div> </div>
2	J	114	<div> <div>18%</div> <div>75%</div> <div>25%</div> <div>.</div> </div>
2	K	114	<div> <div>19%</div> <div>76%</div> <div>23%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	L	107	 12% 83% 16% .
3	M	107	 12% 83% 16% .
3	N	107	 13% 81% 18% .
3	O	107	 13% 81% 18% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 39832 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 BETA-GALACTOSIDASE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1021	Total	C	N	O	S	7	0
			8238	5209	1466	1525	38		
1	B	1021	Total	C	N	O	S	7	0
			8238	5209	1466	1525	38		
1	C	1021	Total	C	N	O	S	7	0
			8238	5209	1466	1525	38		
1	D	1021	Total	C	N	O	S	7	0
			8238	5209	1466	1525	38		

- Molecule 2 is a protein called SCFV13R4 ANTIBODY FV HEAVY CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	114	Total	C	N	O	S	0	0
			902	567	144	188	3		
2	I	114	Total	C	N	O	S	0	0
			902	567	144	188	3		
2	J	114	Total	C	N	O	S	0	0
			902	567	144	188	3		
2	K	114	Total	C	N	O	S	0	0
			902	567	144	188	3		

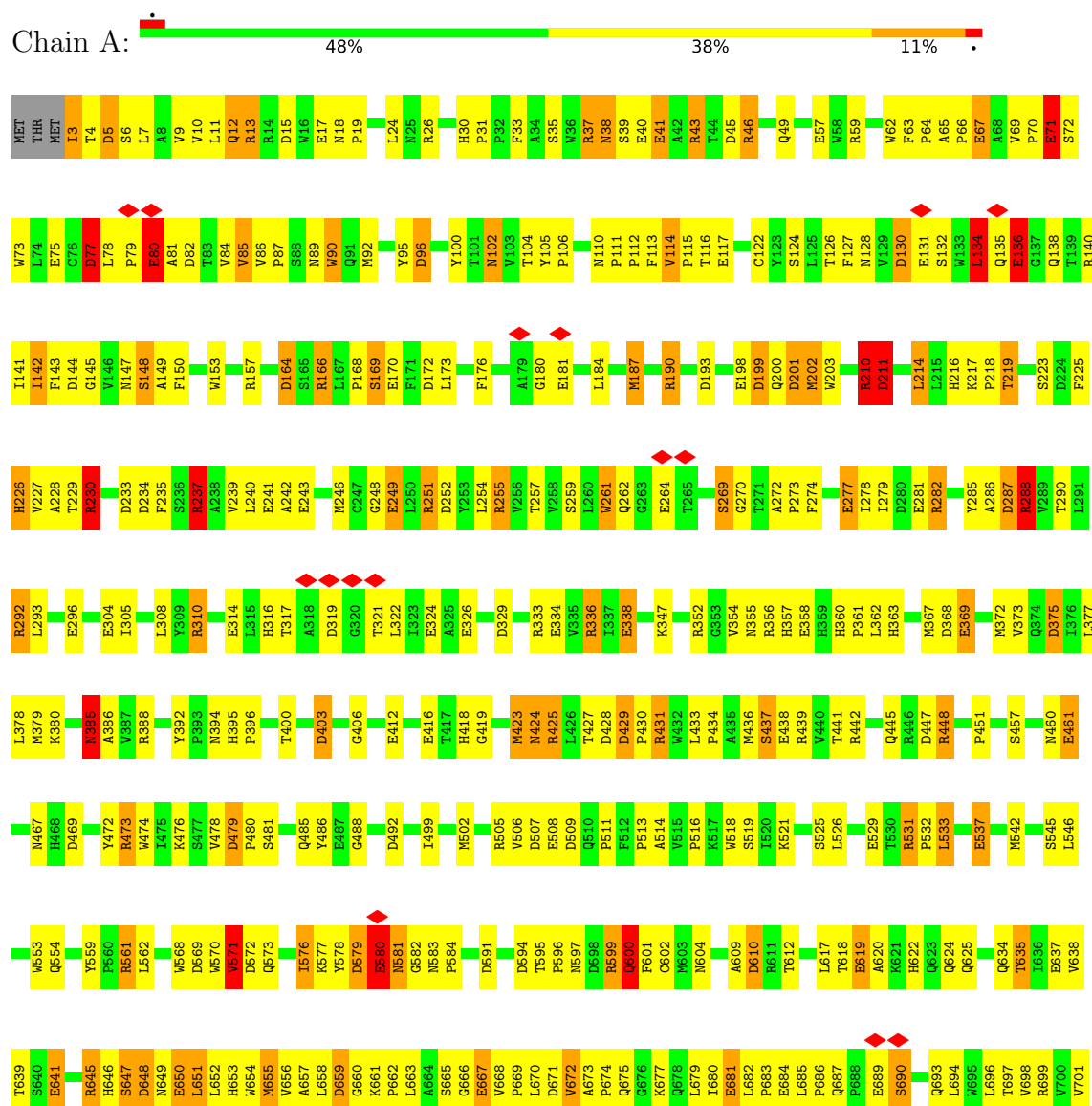
- Molecule 3 is a protein called SCFV13R4 ANTIBODY FV LIGHT CHAIN.

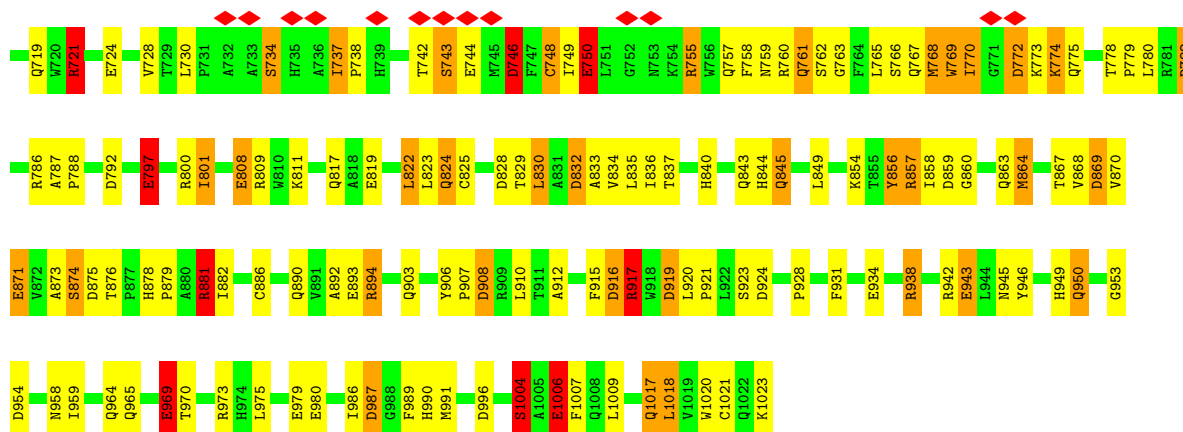
Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	107	Total	C	N	O	S	0	0
			818	511	137	167	3		
3	M	107	Total	C	N	O	S	0	0
			818	511	137	167	3		
3	N	107	Total	C	N	O	S	0	0
			818	511	137	167	3		
3	O	107	Total	C	N	O	S	0	0
			818	511	137	167	3		

3 Residue-property plots

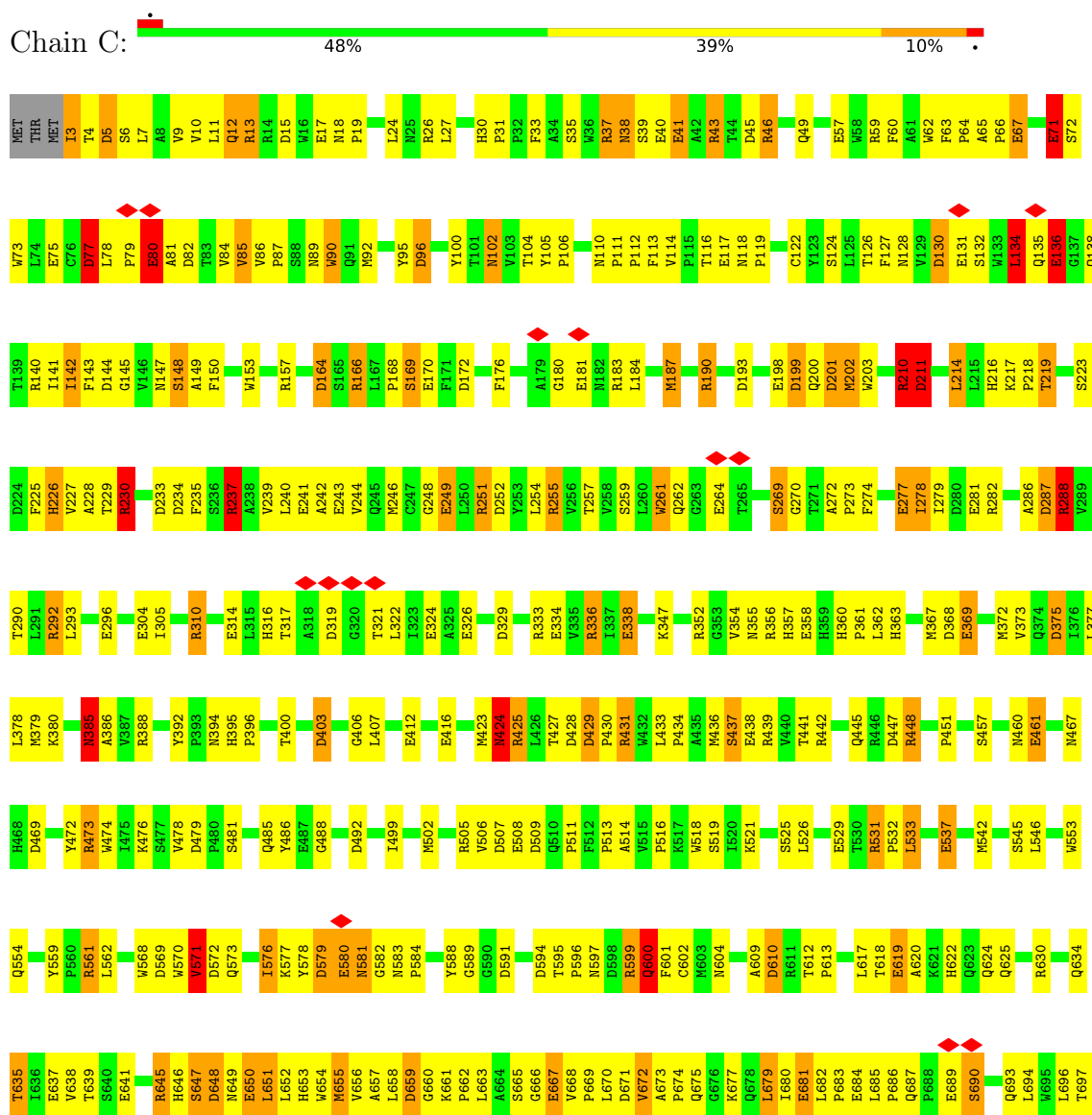
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

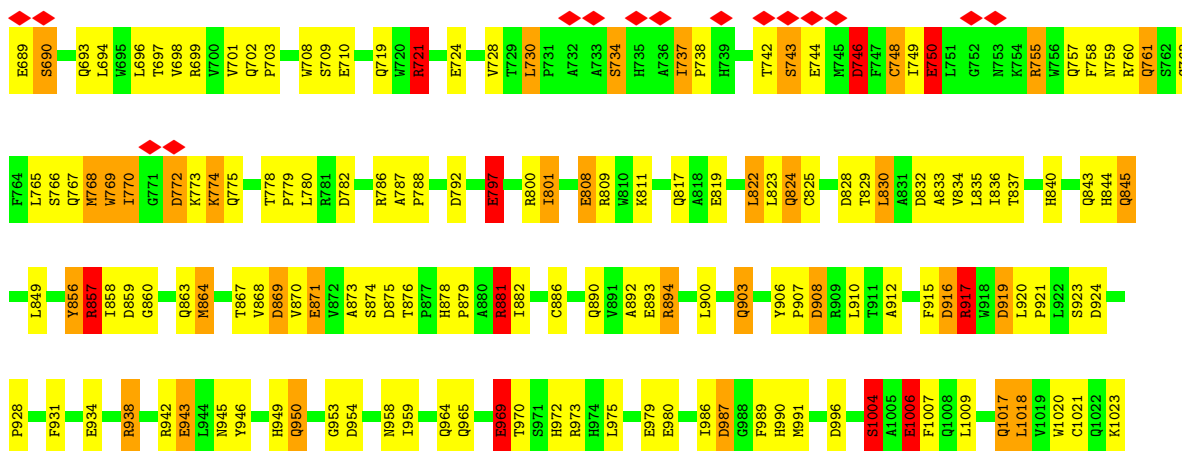
• Molecule 1: BETA-GALACTOSIDASE



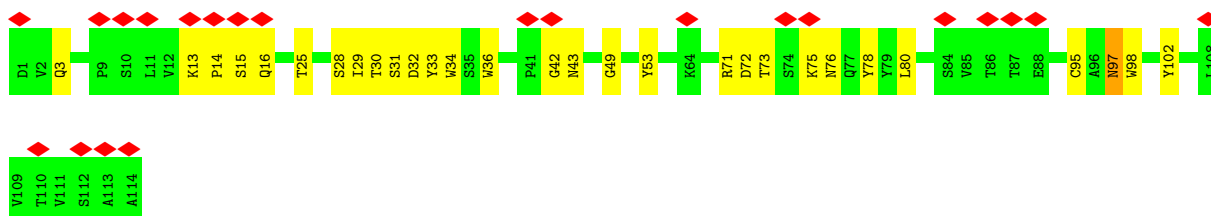
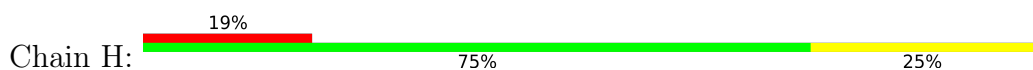


• Molecule 1: BETA-GALACTOSIDASE

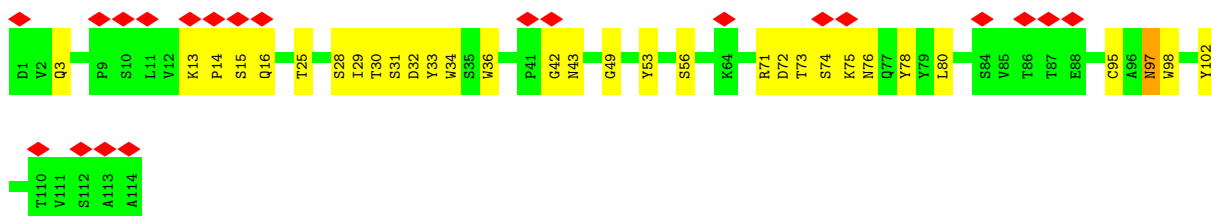




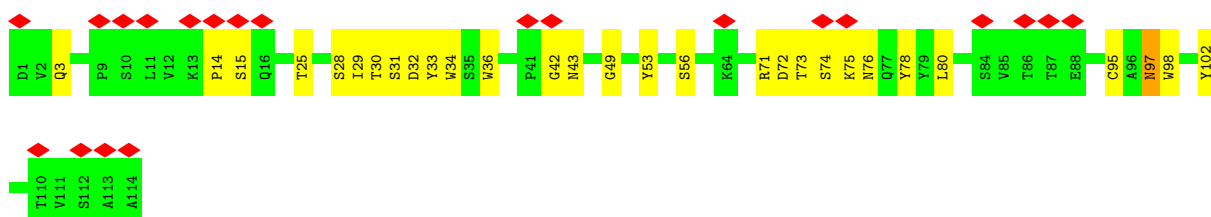
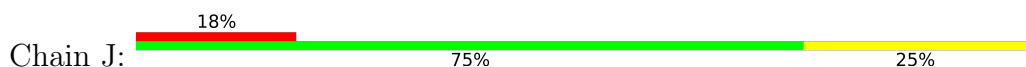
• Molecule 2: SCFV13R4 ANTIBODY FV HEAVY CHAIN



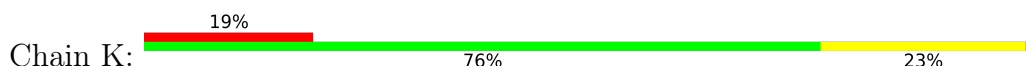
• Molecule 2: SCFV13R4 ANTIBODY FV HEAVY CHAIN

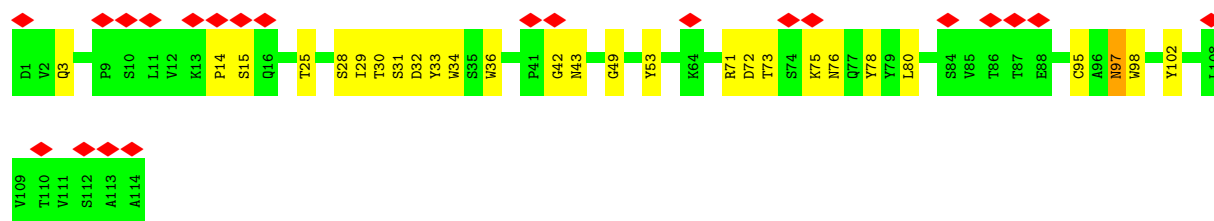


• Molecule 2: SCFV13R4 ANTIBODY FV HEAVY CHAIN

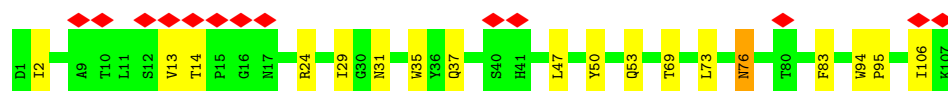
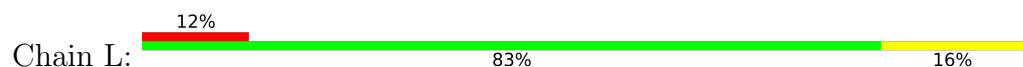


• Molecule 2: SCFV13R4 ANTIBODY FV HEAVY CHAIN

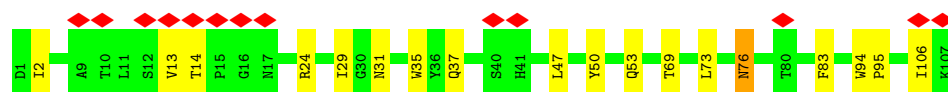
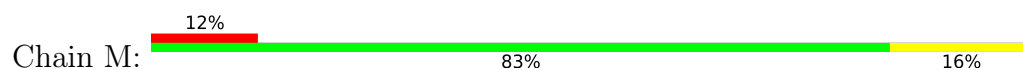




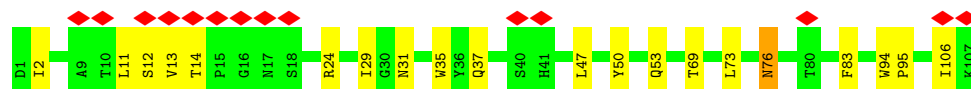
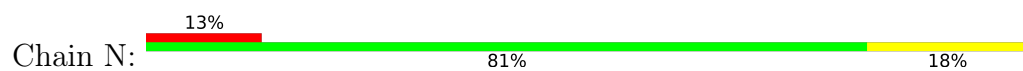
• Molecule 3: SCFV13R4 ANTIBODY FV LIGHT CHAIN



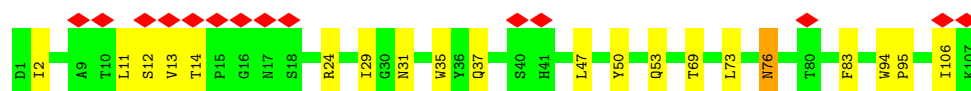
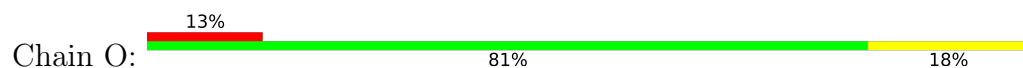
• Molecule 3: SCFV13R4 ANTIBODY FV LIGHT CHAIN



• Molecule 3: SCFV13R4 ANTIBODY FV LIGHT CHAIN



• Molecule 3: SCFV13R4 ANTIBODY FV LIGHT CHAIN



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	2965	Depositor
Resolution determination method	Not provided	
CTF correction method	DONE INSIDE FREALIGN	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	67	Depositor
Minimum defocus (nm)	2678	Depositor
Maximum defocus (nm)	4027	Depositor
Magnification	81600	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.322	Depositor
Minimum map value	-0.057	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.13	Depositor
Map size (\AA)	300.0, 300.0, 300.0	wwPDB
Map dimensions	100, 100, 100	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3.0, 3.0, 3.0	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	1.08	52/8515 (0.6%)	1.61	174/11615 (1.5%)
1	B	1.08	52/8515 (0.6%)	1.61	175/11615 (1.5%)
1	C	1.08	52/8515 (0.6%)	1.61	173/11615 (1.5%)
1	D	1.08	53/8515 (0.6%)	1.61	180/11615 (1.5%)
2	H	0.31	0/925	0.65	0/1263
2	I	0.31	0/925	0.65	0/1263
2	J	0.31	0/925	0.65	0/1263
2	K	0.31	0/925	0.65	0/1263
3	L	0.32	0/837	0.58	0/1133
3	M	0.32	0/837	0.58	0/1133
3	N	0.32	0/837	0.58	0/1133
3	O	0.32	0/837	0.59	0/1133
All	All	1.00	209/41108 (0.5%)	1.49	702/56044 (1.3%)

The worst 5 of 209 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	75	GLU	CD-OE2	9.50	1.36	1.25
1	A	75	GLU	CD-OE2	9.50	1.36	1.25
1	D	75	GLU	CD-OE2	9.48	1.36	1.25
1	C	75	GLU	CD-OE2	9.41	1.36	1.25
1	B	710	GLU	CD-OE1	7.65	1.34	1.25

The worst 5 of 702 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	809[A]	ARG	NE-CZ-NH1	11.67	126.14	120.30
1	B	809[B]	ARG	NE-CZ-NH1	11.67	126.14	120.30
1	D	809[A]	ARG	NE-CZ-NH1	11.59	126.09	120.30
1	D	809[B]	ARG	NE-CZ-NH1	11.59	126.09	120.30
1	A	809[A]	ARG	NE-CZ-NH1	11.58	126.09	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8238	0	7821	477	0
1	B	8238	0	7822	458	0
1	C	8238	0	7821	460	0
1	D	8238	0	7821	471	0
2	H	902	0	838	111	0
2	I	902	0	838	110	0
2	J	902	0	839	108	0
2	K	902	0	839	109	0
3	L	818	0	780	12	0
3	M	818	0	780	12	0
3	N	818	0	780	13	0
3	O	818	0	780	13	0
All	All	39832	0	37759	1937	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 25.

The worst 5 of 1937 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:C:584:PRO:CB	2:H:30:THR:HG22	1.48	1.42
1:A:584:PRO:CB	2:J:30:THR:HG22	1.50	1.40
1:B:609:ALA:CB	2:K:53:TYR:OH	1.70	1.40
1:B:584:PRO:CB	2:K:30:THR:HG22	1.50	1.38
1:D:584:PRO:CB	2:I:30:THR:HG22	1.50	1.38

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1026/1024 (100%)	954 (93%)	66 (6%)	6 (1%)	22	60
1	B	1026/1024 (100%)	953 (93%)	67 (6%)	6 (1%)	22	60
1	C	1026/1024 (100%)	953 (93%)	67 (6%)	6 (1%)	22	60
1	D	1026/1024 (100%)	953 (93%)	67 (6%)	6 (1%)	22	60
2	H	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
2	I	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
2	J	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
2	K	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
3	L	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
3	M	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
3	N	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
3	O	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
All	All	4972/4980 (100%)	4657 (94%)	291 (6%)	24 (0%)	27	64

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	647	SER
1	B	647	SER
1	C	647	SER
1	D	647	SER
1	A	77	ASP

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	880/876 (100%)	754 (86%)	126 (14%)	2	12
1	B	880/876 (100%)	754 (86%)	126 (14%)	2	12
1	C	880/876 (100%)	754 (86%)	126 (14%)	2	12
1	D	880/876 (100%)	754 (86%)	126 (14%)	2	12
2	H	102/102 (100%)	101 (99%)	1 (1%)	73	82
2	I	102/102 (100%)	101 (99%)	1 (1%)	73	82
2	J	102/102 (100%)	101 (99%)	1 (1%)	73	82
2	K	102/102 (100%)	101 (99%)	1 (1%)	73	82
3	L	94/94 (100%)	93 (99%)	1 (1%)	70	80
3	M	94/94 (100%)	93 (99%)	1 (1%)	70	80
3	N	94/94 (100%)	93 (99%)	1 (1%)	70	80
3	O	94/94 (100%)	93 (99%)	1 (1%)	70	80
All	All	4304/4288 (100%)	3792 (88%)	512 (12%)	6	16

5 of 512 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	743	SER
1	D	800	ARG
1	D	737	ILE
1	B	581	ASN
1	B	546	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	394	ASN
3	L	53	GLN
1	D	38	ASN
2	K	97	ASN
2	I	76	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.

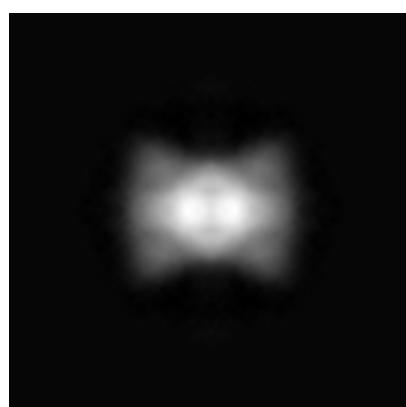
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2548. These allow visual inspection of the internal detail of the map and identification of artifacts.

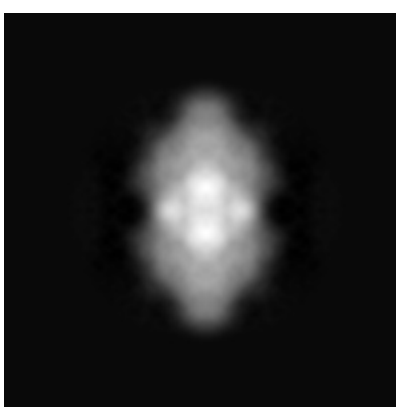
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

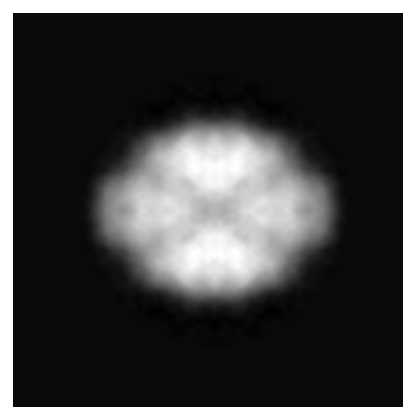
6.1.1 Primary map



X



Y

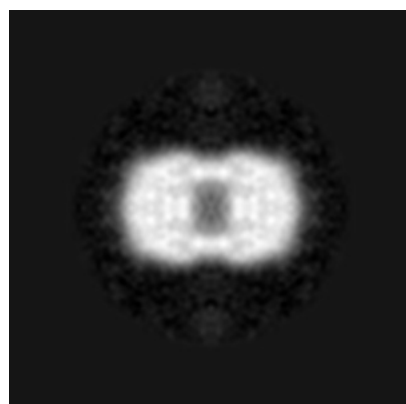


Z

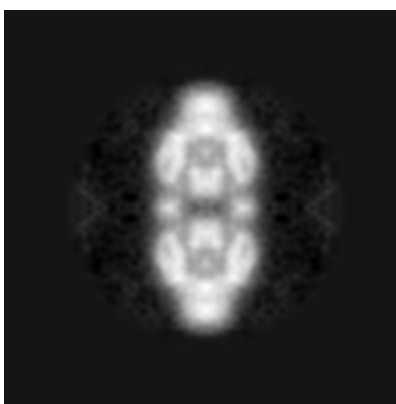
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 50



Y Index: 50

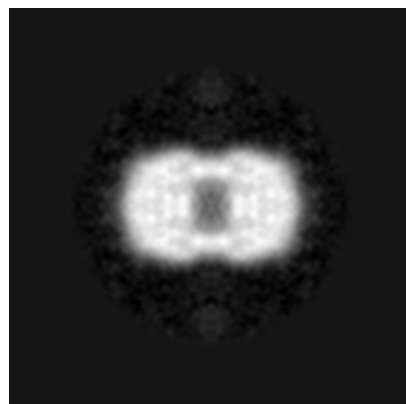


Z Index: 50

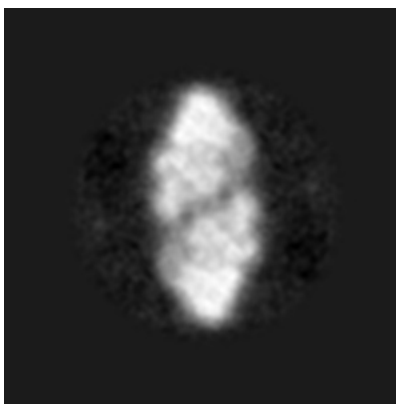
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

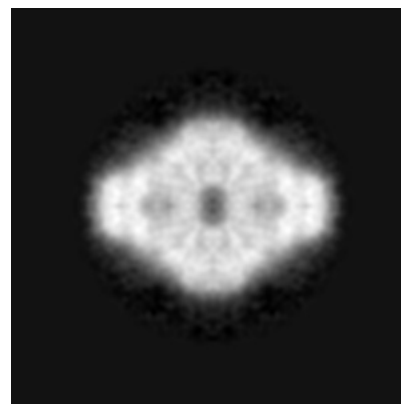
6.3.1 Primary map



X Index: 50



Y Index: 54



Z Index: 50

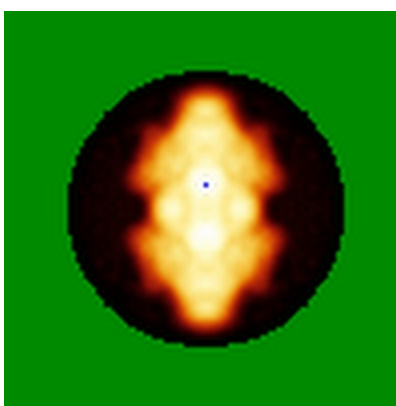
The images above show the largest variance slices of the map in three orthogonal directions.

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

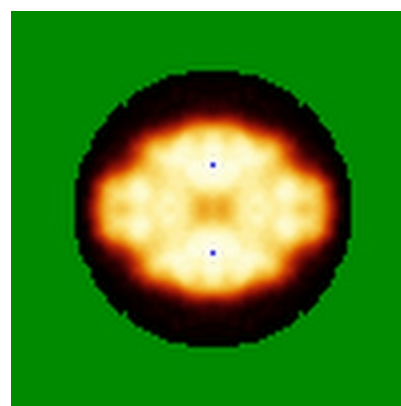
6.4.1 Primary map



X



Y

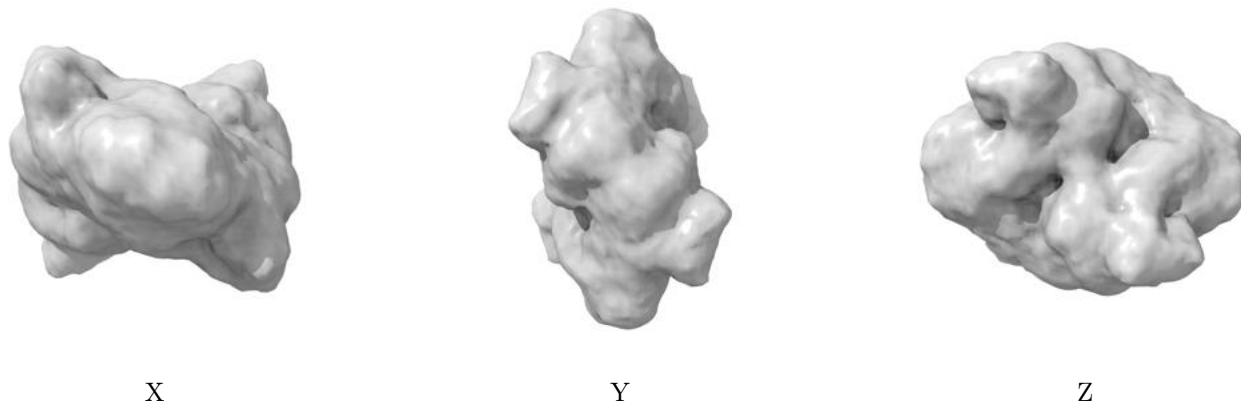


Z

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 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

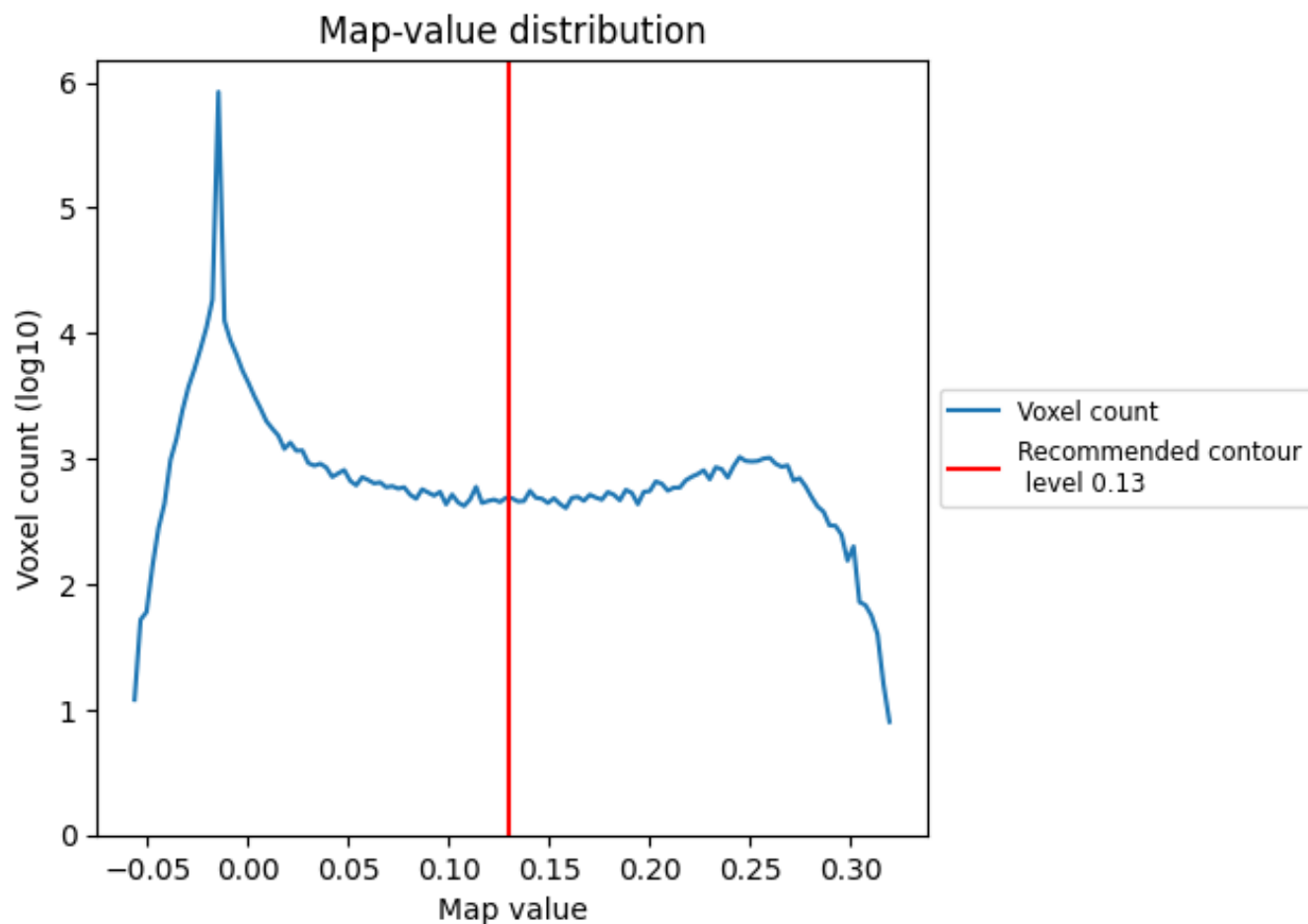
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

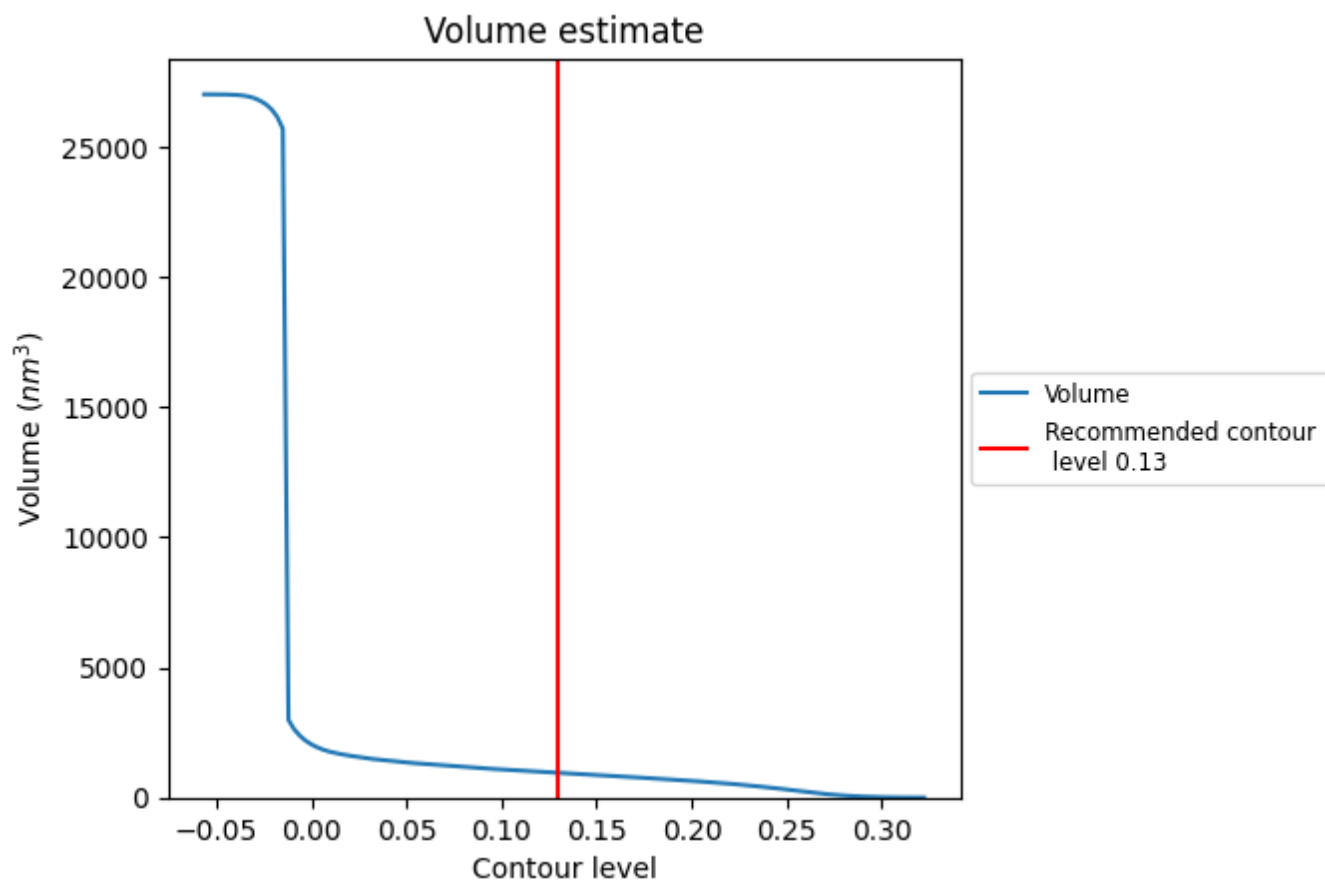
This section contains the results of statistical analysis of the map.

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.

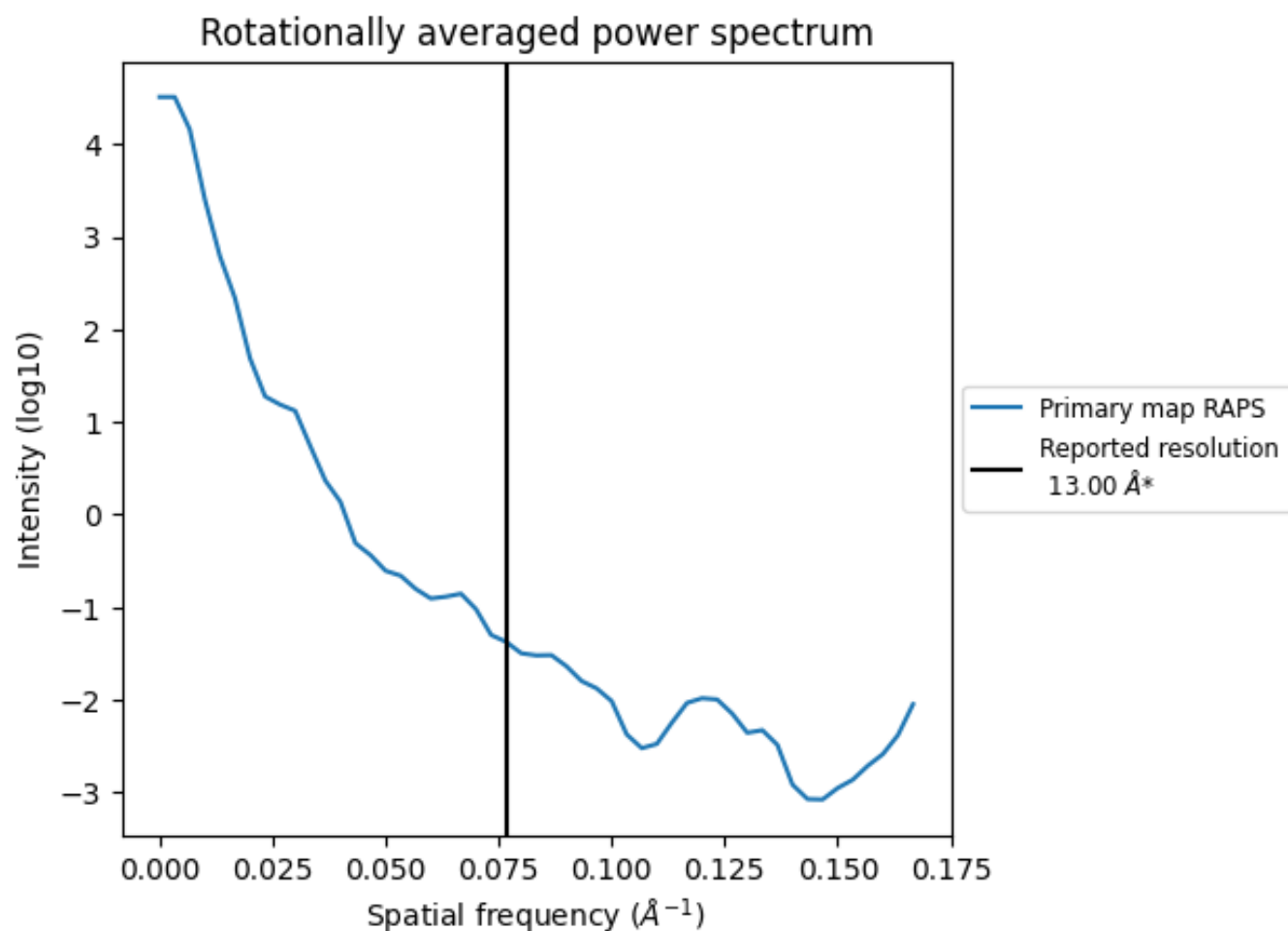
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 950 nm³; this corresponds to an approximate mass of 859 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 0.077 Å⁻¹

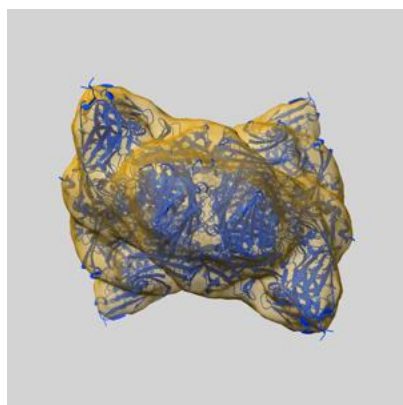
8 Fourier-Shell correlation

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

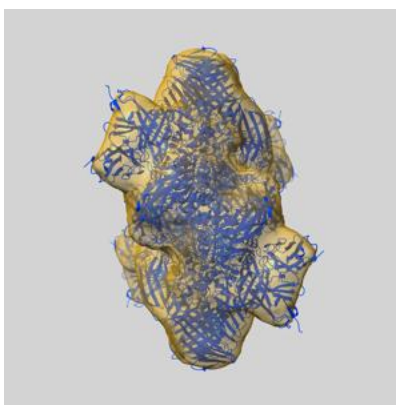
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2548 and PDB model 4CKD. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

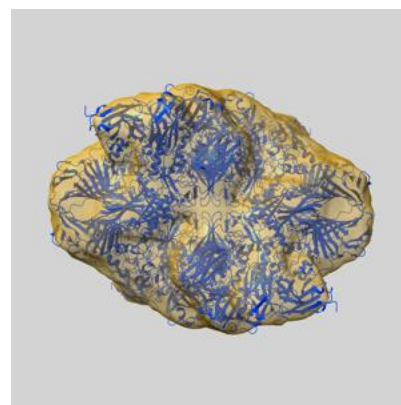
9.1 Map-model overlay [i](#)



X



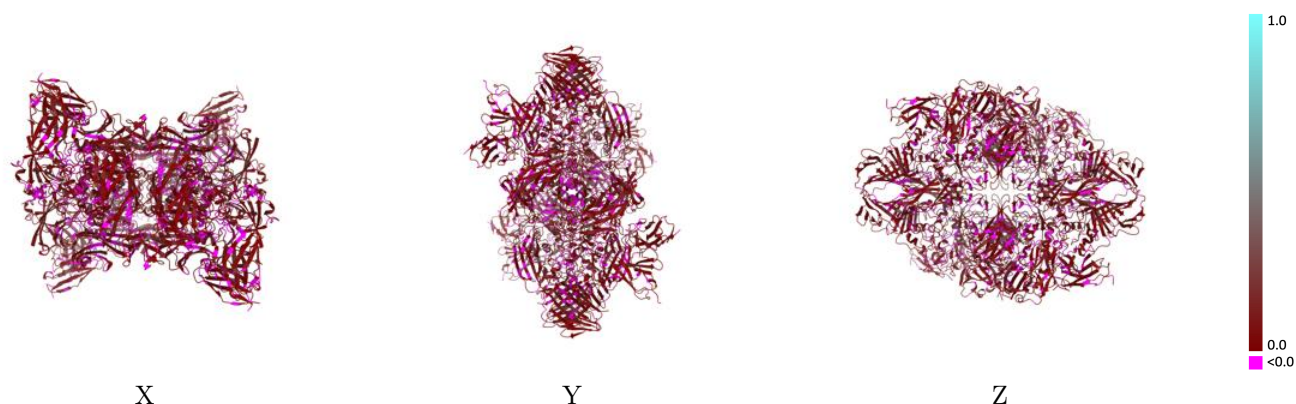
Y



Z

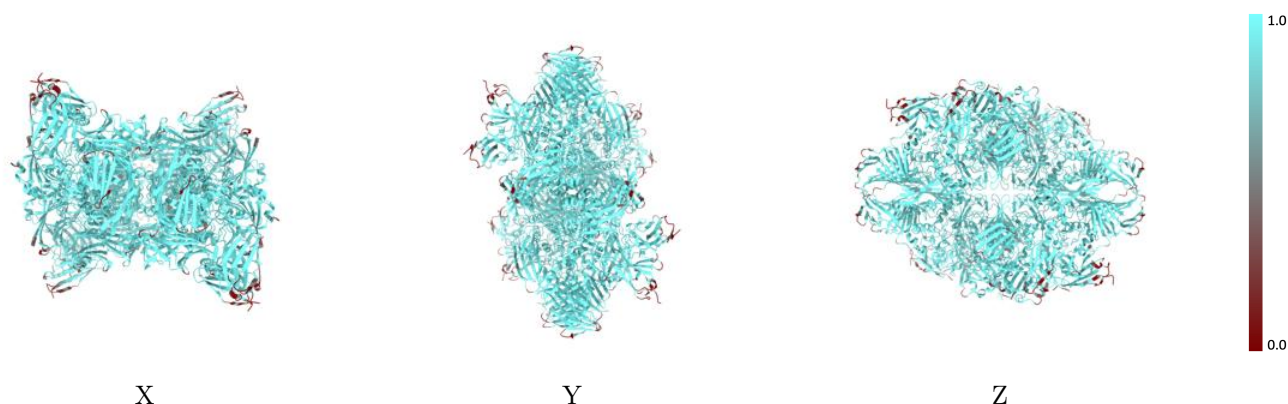
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



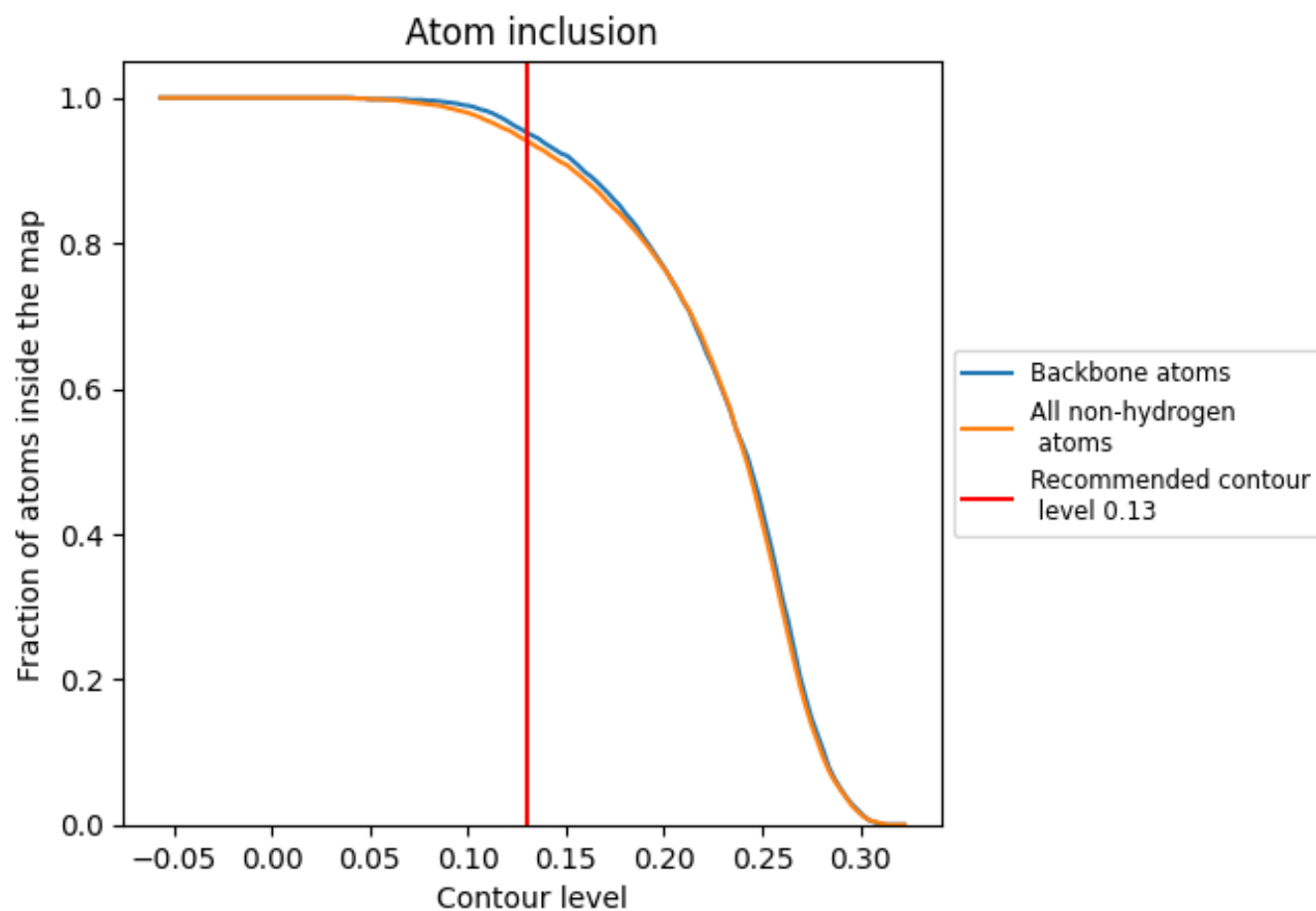
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9410	<div></div> 0.0750
A	<div></div> 0.9660	<div></div> 0.0760
B	<div></div> 0.9660	<div></div> 0.0790
C	<div></div> 0.9660	<div></div> 0.0750
D	<div></div> 0.9660	<div></div> 0.0790
H	<div></div> 0.7920	<div></div> 0.0510
I	<div></div> 0.7970	<div></div> 0.0590
J	<div></div> 0.7960	<div></div> 0.0580
K	<div></div> 0.7950	<div></div> 0.0660
L	<div></div> 0.8520	<div></div> 0.0580
M	<div></div> 0.8520	<div></div> 0.0740
N	<div></div> 0.8510	<div></div> 0.0590
O	<div></div> 0.8510	<div></div> 0.0700

