



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:12 PM UTC

PDB ID : 7RYC / pdb_00007ryc
EMDB ID : EMD-24733
Title : Oxytocin receptor (OTR) bound to oxytocin in complex with a heterotrimeric Gq protein
Authors : Meyerowitz, J.G.; Robertson, M.J.; Skiniotis, G.
Deposited on : 2021-08-24
Resolution : 2.90 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:

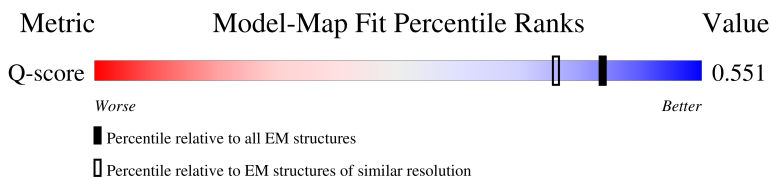
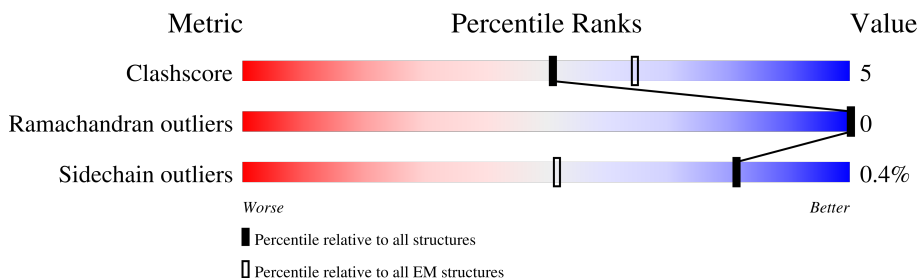
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 2.90 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	L	10	60% (green), 40% (yellow)
2	O	450	19% (red), 55% (green), 8% (yellow), 37% (grey)
3	D	326	19% (red), 74% (green), 7% (yellow), 19% (grey)
4	C	345	10% (red), 83% (green), 15% (yellow), 1% (grey)

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Mol	Chain	Length	Quality of chain
5	E	260	 <p>81% 8% 12%</p>

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 8277 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 Oxytocin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	L	10	69	43	12	12	2	0	1

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	10	NH2	-	amidation	UNP P01178

- Molecule 2 is a protein called Oxytocin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	O	285	2097	1414	335	331	17	0	0

There are 61 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-54	MET	-	initiating methionine	UNP P30559
O	-53	LYS	-	expression tag	UNP P30559
O	-52	THR	-	expression tag	UNP P30559
O	-51	ILE	-	expression tag	UNP P30559
O	-50	ILE	-	expression tag	UNP P30559
O	-49	ALA	-	expression tag	UNP P30559
O	-48	LEU	-	expression tag	UNP P30559
O	-47	SER	-	expression tag	UNP P30559
O	-46	TYR	-	expression tag	UNP P30559
O	-45	ILE	-	expression tag	UNP P30559
O	-44	PHE	-	expression tag	UNP P30559
O	-43	CYS	-	expression tag	UNP P30559
O	-42	LEU	-	expression tag	UNP P30559
O	-41	VAL	-	expression tag	UNP P30559
O	-40	PHE	-	expression tag	UNP P30559
O	-39	ALA	-	expression tag	UNP P30559

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-38	ASP	-	expression tag	UNP P30559
O	-37	TYR	-	expression tag	UNP P30559
O	-36	LYS	-	expression tag	UNP P30559
O	-35	ASP	-	expression tag	UNP P30559
O	-34	ASP	-	expression tag	UNP P30559
O	-33	ASP	-	expression tag	UNP P30559
O	-32	ASP	-	expression tag	UNP P30559
O	-31	ALA	-	expression tag	UNP P30559
O	-30	MET	-	expression tag	UNP P30559
O	-29	GLY	-	expression tag	UNP P30559
O	-28	GLN	-	expression tag	UNP P30559
O	-27	PRO	-	expression tag	UNP P30559
O	-26	GLY	-	expression tag	UNP P30559
O	-25	ASN	-	expression tag	UNP P30559
O	-24	GLY	-	expression tag	UNP P30559
O	-23	SER	-	expression tag	UNP P30559
O	-22	ALA	-	expression tag	UNP P30559
O	-21	PHE	-	expression tag	UNP P30559
O	-20	LEU	-	expression tag	UNP P30559
O	-19	LEU	-	expression tag	UNP P30559
O	-18	ALA	-	expression tag	UNP P30559
O	-17	PRO	-	expression tag	UNP P30559
O	-16	ASN	-	expression tag	UNP P30559
O	-15	ARG	-	expression tag	UNP P30559
O	-14	SER	-	expression tag	UNP P30559
O	-13	HIS	-	expression tag	UNP P30559
O	-12	ALA	-	expression tag	UNP P30559
O	-11	PRO	-	expression tag	UNP P30559
O	-10	ASP	-	expression tag	UNP P30559
O	-9	HIS	-	expression tag	UNP P30559
O	-8	ASP	-	expression tag	UNP P30559
O	-7	VAL	-	expression tag	UNP P30559
O	-6	GLU	-	expression tag	UNP P30559
O	-5	ASN	-	expression tag	UNP P30559
O	-4	LEU	-	expression tag	UNP P30559
O	-3	TYR	-	expression tag	UNP P30559
O	-2	PHE	-	expression tag	UNP P30559
O	-1	GLN	-	expression tag	UNP P30559
O	0	GLY	-	expression tag	UNP P30559
O	390	LEU	-	expression tag	UNP P30559
O	391	GLU	-	expression tag	UNP P30559
O	392	VAL	-	expression tag	UNP P30559

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Chain	Residue	Modelled	Actual	Comment	Reference
O	393	LEU	-	expression tag	UNP P30559
O	394	PHE	-	expression tag	UNP P30559
O	395	GLN	-	expression tag	UNP P30559

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2, Guanine nucleotide-binding protein G(i) subunit alpha-2, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	263	1973	1263	339	362	9	0	0

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	338	2442	1520	436	468	18	0	0

There are 6 discrepancies between the modelled and reference sequences:

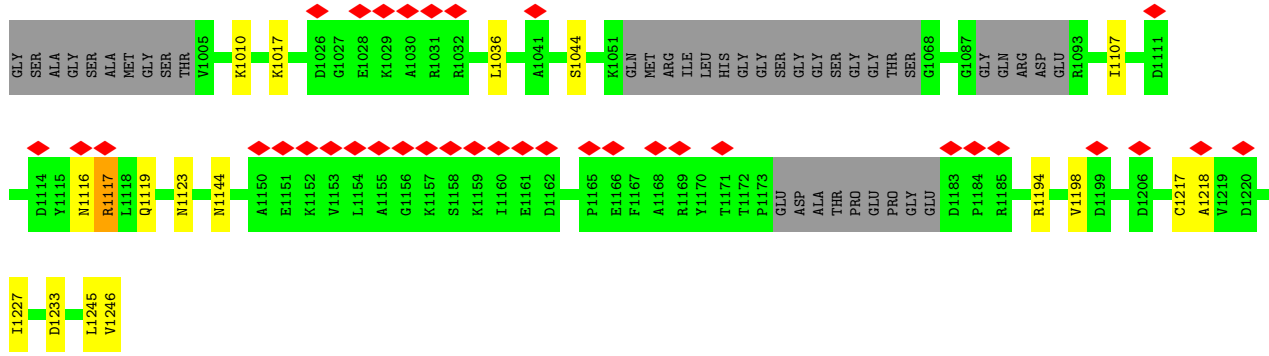
Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	GLY	-	expression tag	UNP P62873
C	-3	PRO	-	expression tag	UNP P62873
C	-2	GLY	-	expression tag	UNP P62873
C	-1	SER	-	expression tag	UNP P62873
C	0	SER	-	expression tag	UNP P62873
C	1	GLY	-	expression tag	UNP P62873

- Molecule 5 is a protein called scFv16.

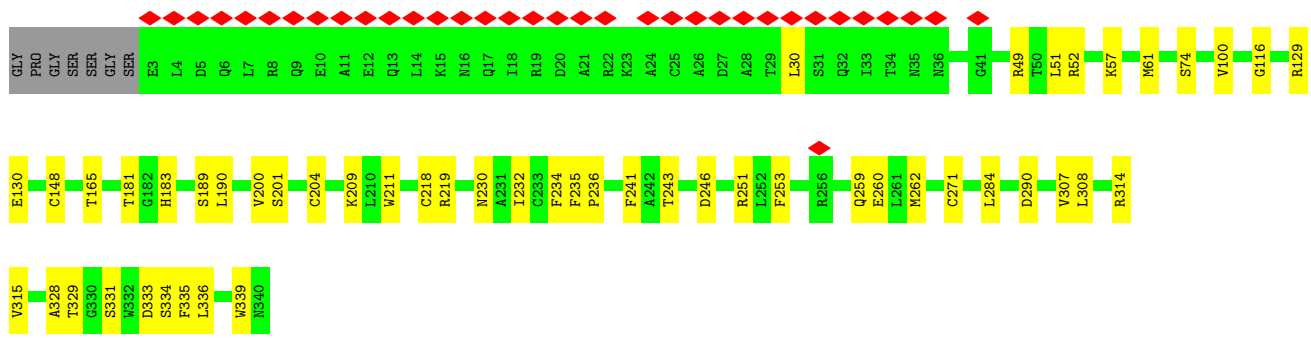
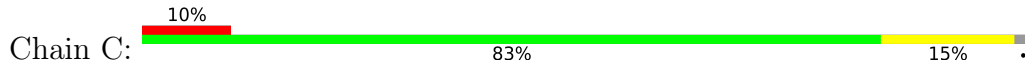
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	230	1695	1081	287	318	9	0	0

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

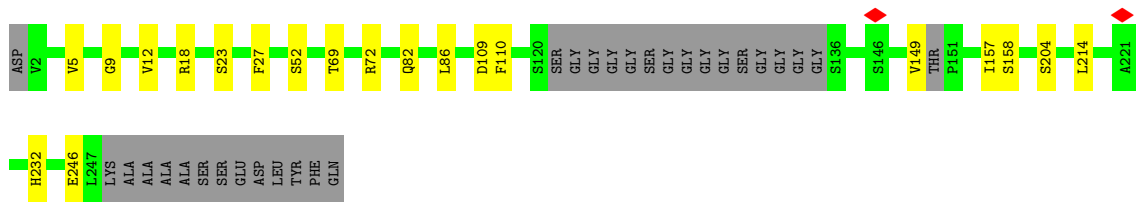
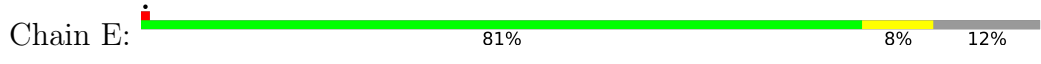
Mol	Chain	Residues	Atoms		AltConf
6	O	1	Total	Mg	0
			1	1	



• Molecule 4: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



• Molecule 5: scFv16



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	423703	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54.8	Depositor
Minimum defocus (nm)	-0.8	Depositor
Maximum defocus (nm)	-1.8	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	13.391	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	1	Depositor
Map size (Å)	272.672, 272.672, 272.672	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8521, 0.8521, 0.8521	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, NH2

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	L	0.67	0/69	1.26	0/93
2	O	0.57	4/2152 (0.2%)	0.75	1/2958 (0.0%)
3	D	0.31	1/2008 (0.0%)	0.44	0/2725
4	C	0.42	1/2487 (0.0%)	0.59	0/3389
5	E	0.24	0/1738	0.45	0/2362
All	All	0.42	6/8454 (0.1%)	0.59	1/11527 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	203	TRP	C-N	-6.14	1.26	1.33
2	O	139	LEU	C-N	5.94	1.42	1.33
2	O	157	VAL	C-N	-5.79	1.26	1.33
3	D	1117	ARG	C-N	-5.59	1.26	1.33
2	O	270	LYS	C-N	-5.49	1.26	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	101	ILE	N-CA-C	-5.14	105.48	110.42

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	L	69	0	65	3	0
2	O	2097	0	2051	28	0
3	D	1973	0	1854	19	0
4	C	2442	0	2232	35	0
5	E	1695	0	1562	12	0
6	O	1	0	0	0	0
All	All	8277	0	7764	88	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 88 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)
2:O:192:ILE:HG22	2:O:194:PRO:HD2	1.73	0.71
5:E:52:SER:O	5:E:72:ARG:NH1	2.30	0.65
4:C:183:HIS:CE1	4:C:211:TRP:HZ2	2.15	0.64
2:O:201:ILE:HG22	2:O:296:MET:SD	2.37	0.63
4:C:230:ASN:ND2	4:C:246:ASP:OD1	2.32	0.63

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	L	8/10 (80%)	7 (88%)	1 (12%)	0	100	100
2	O	279/450 (62%)	265 (95%)	14 (5%)	0	100	100
3	D	253/326 (78%)	242 (96%)	11 (4%)	0	100	100
4	C	336/345 (97%)	319 (95%)	17 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	224/260 (86%)	213 (95%)	11 (5%)	0	100	100
All	All	1100/1391 (79%)	1046 (95%)	54 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	L	8/8 (100%)	7 (88%)	1 (12%)	4	15
2	O	198/369 (54%)	197 (100%)	1 (0%)	81	93
3	D	191/274 (70%)	191 (100%)	0	100	100
4	C	234/285 (82%)	233 (100%)	1 (0%)	84	94
5	E	169/209 (81%)	169 (100%)	0	100	100
All	All	800/1145 (70%)	797 (100%)	3 (0%)	81	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	6	CYS
2	O	41	VAL
4	C	234	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
4	C	183	HIS
4	C	220	GLN
2	O	321	ASN
3	D	18	GLN
3	D	1244	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

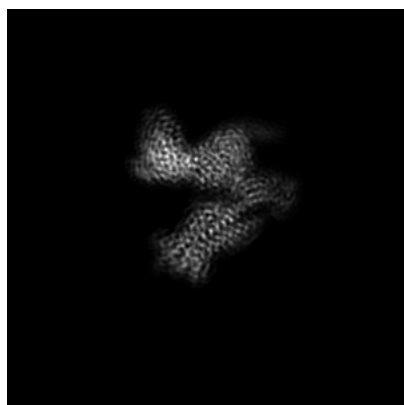
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24733. These allow visual inspection of the internal detail of the map and identification of artifacts.

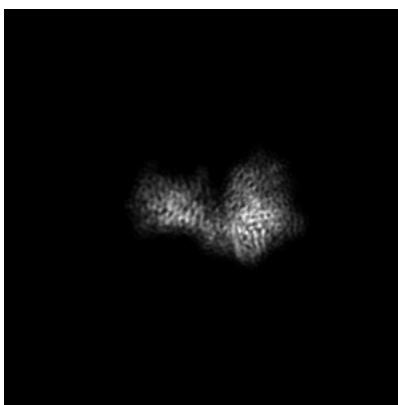
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

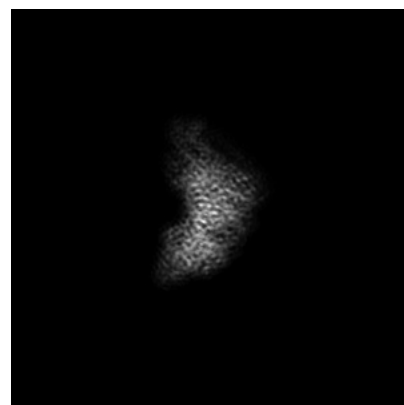
6.1.1 Primary map



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: 160



Y Index: 160



Z Index: 160

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: 151



Y Index: 156

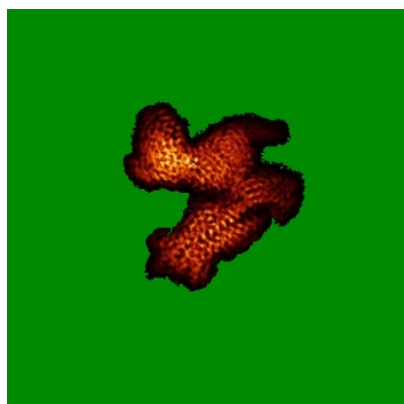


Z Index: 197

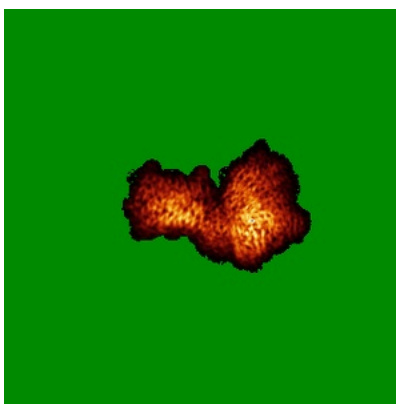
The images above show the largest variance slices of the map in three orthogonal directions.

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

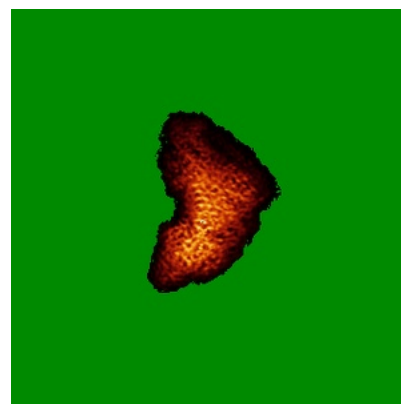
6.4.1 Primary map



X



Y

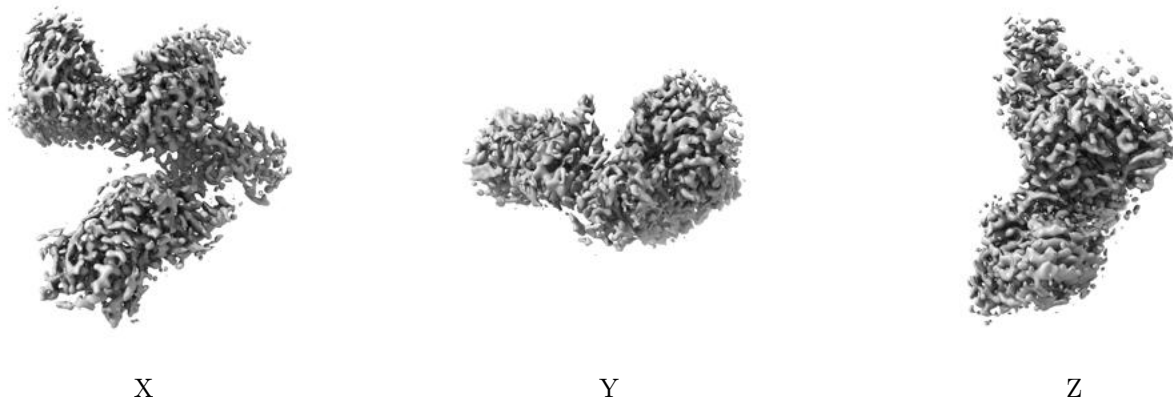


Z

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

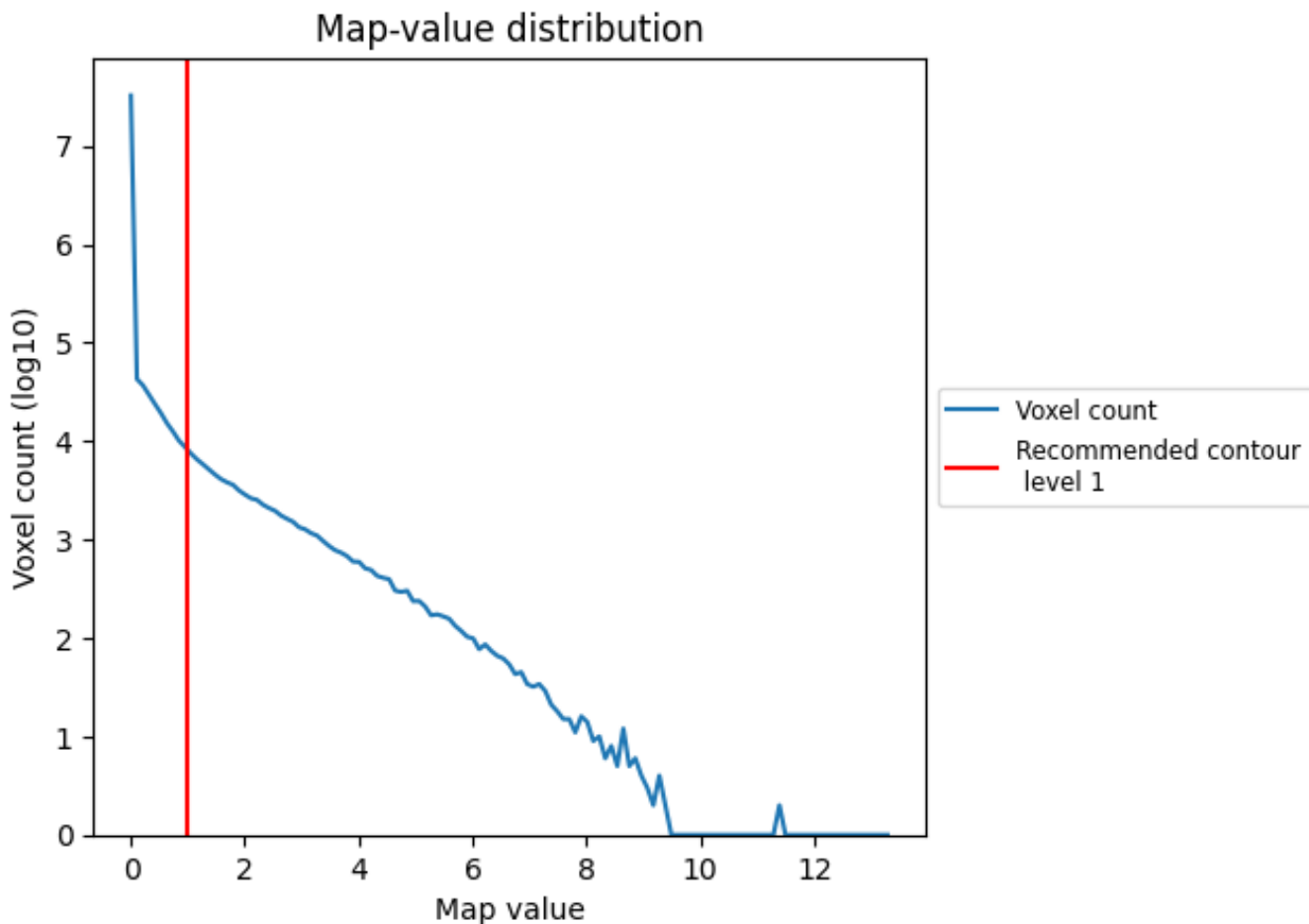
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

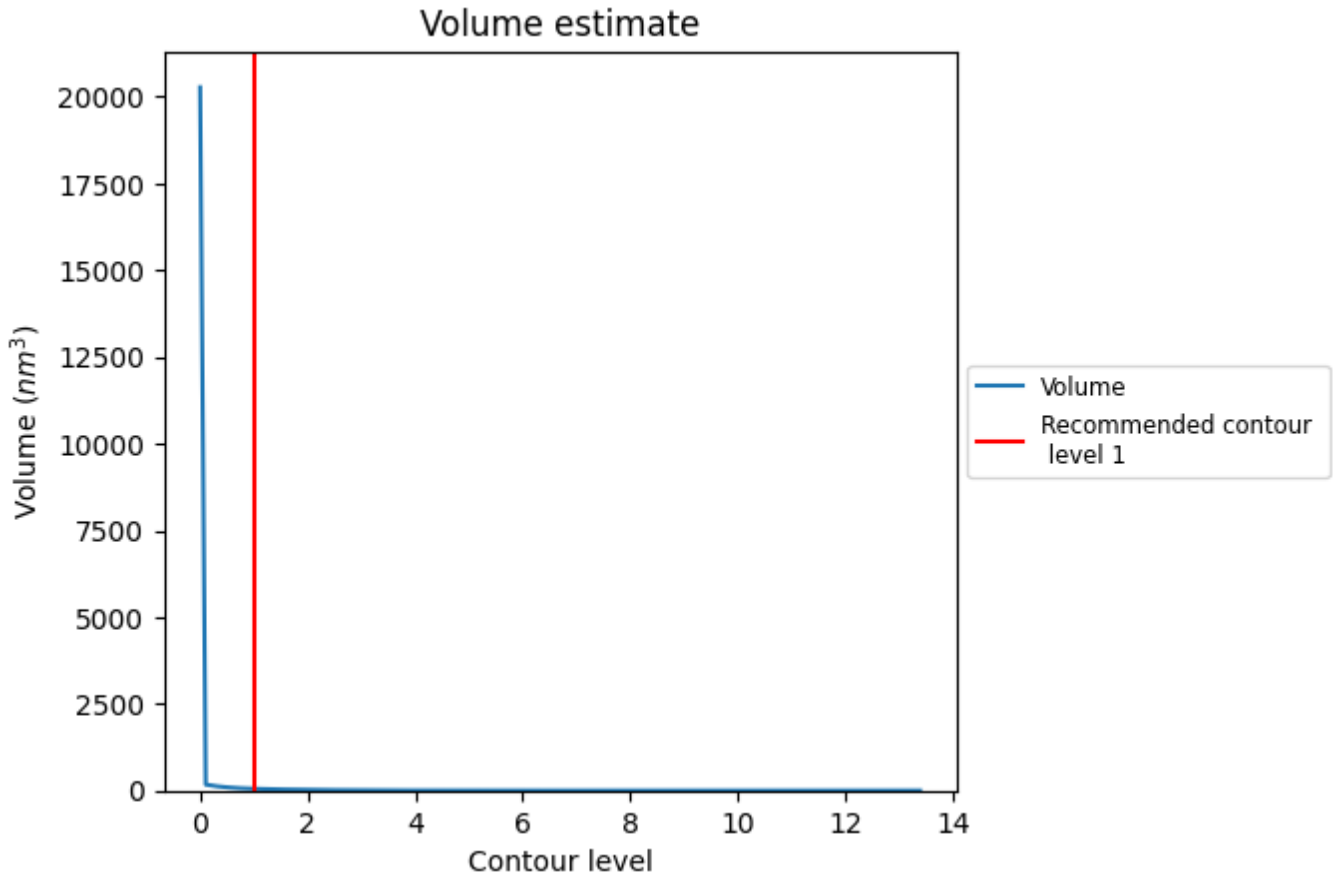
This section contains the results of statistical analysis of the map.

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.

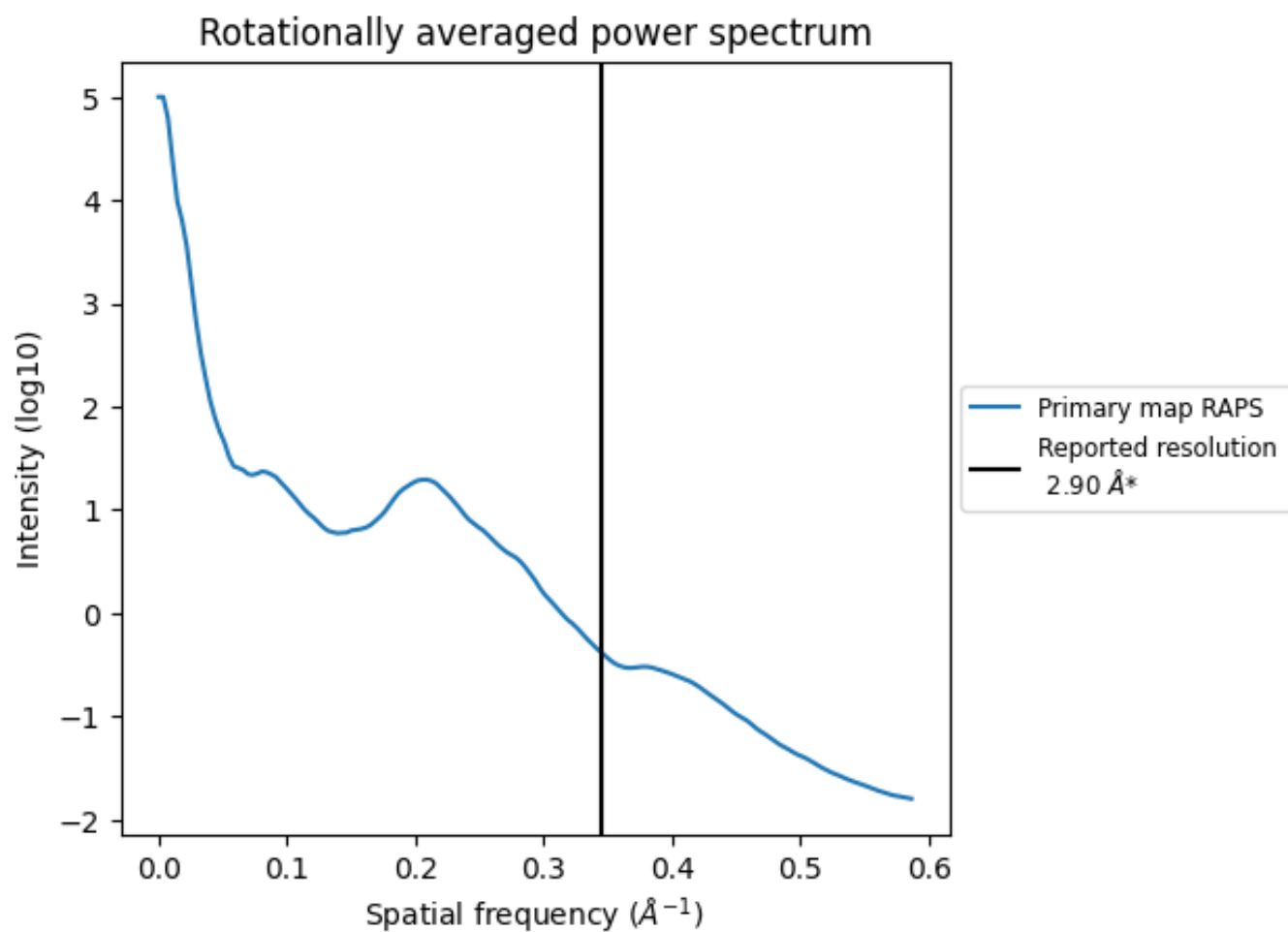
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 52 nm^3 ; this corresponds to an approximate mass of 47 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 0.345\AA^{-1}

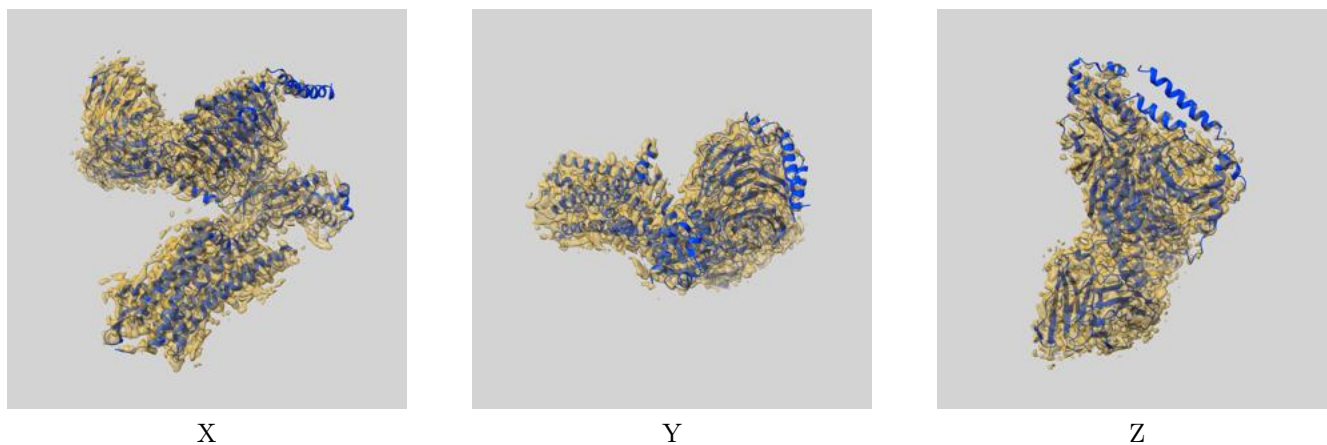
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

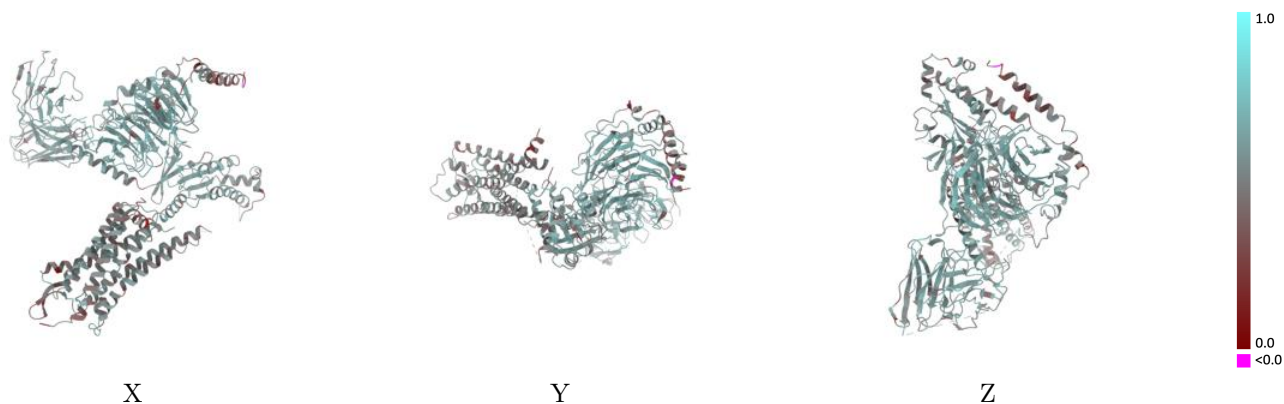
This section contains information regarding the fit between EMDB map EMD-24733 and PDB model 7RYC. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



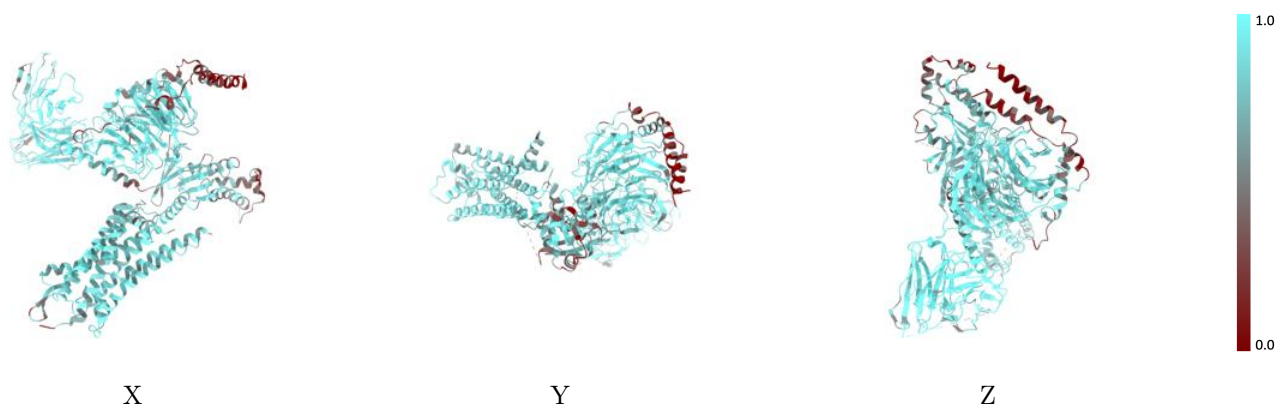
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



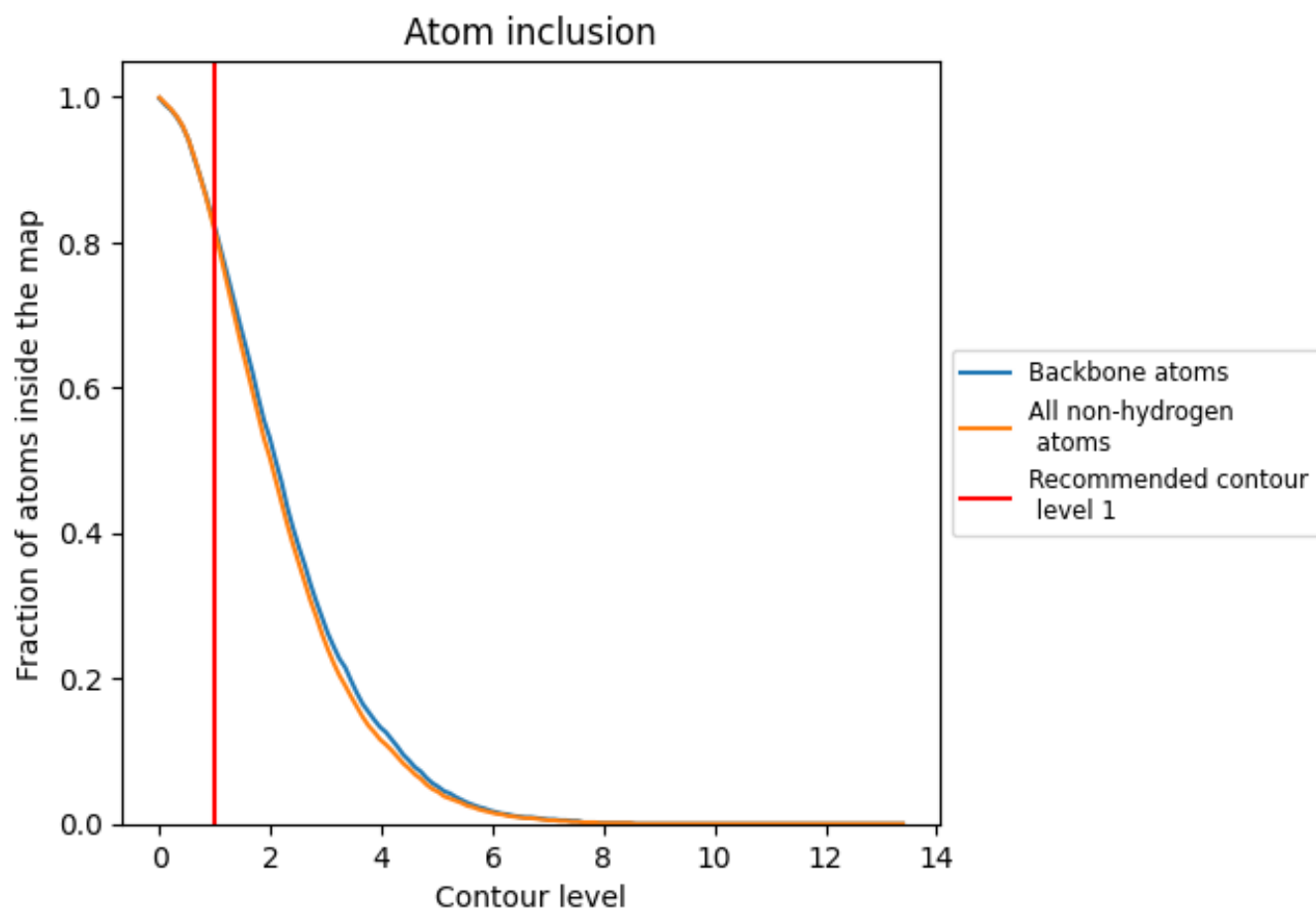
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 82% of all backbone atoms, 81% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8140	 0.5510
C	 0.8380	 0.5960
D	 0.6760	 0.5460
E	 0.9280	 0.5680
L	 0.8530	 0.5190
O	 0.8230	 0.4900

