



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:03 PM UTC

PDB ID : 7Q60 / pdb_00007q60
EMDB ID : EMD-13848
Title : Structure of TEV cleaved A2ML1 (A2ML1-TE)
Authors : Nielsen, N.S.; Zarantonello, A.; Andersen, G.R.
Deposited on : 2021-11-05
Resolution : 3.13 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

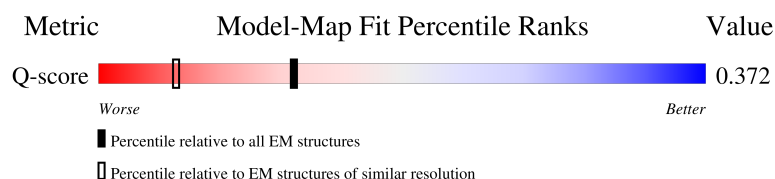
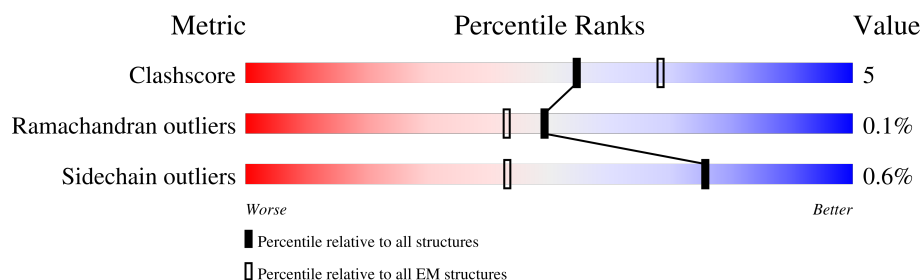
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.13 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	14478 (2.63 - 3.63)

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	1436	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9450 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.

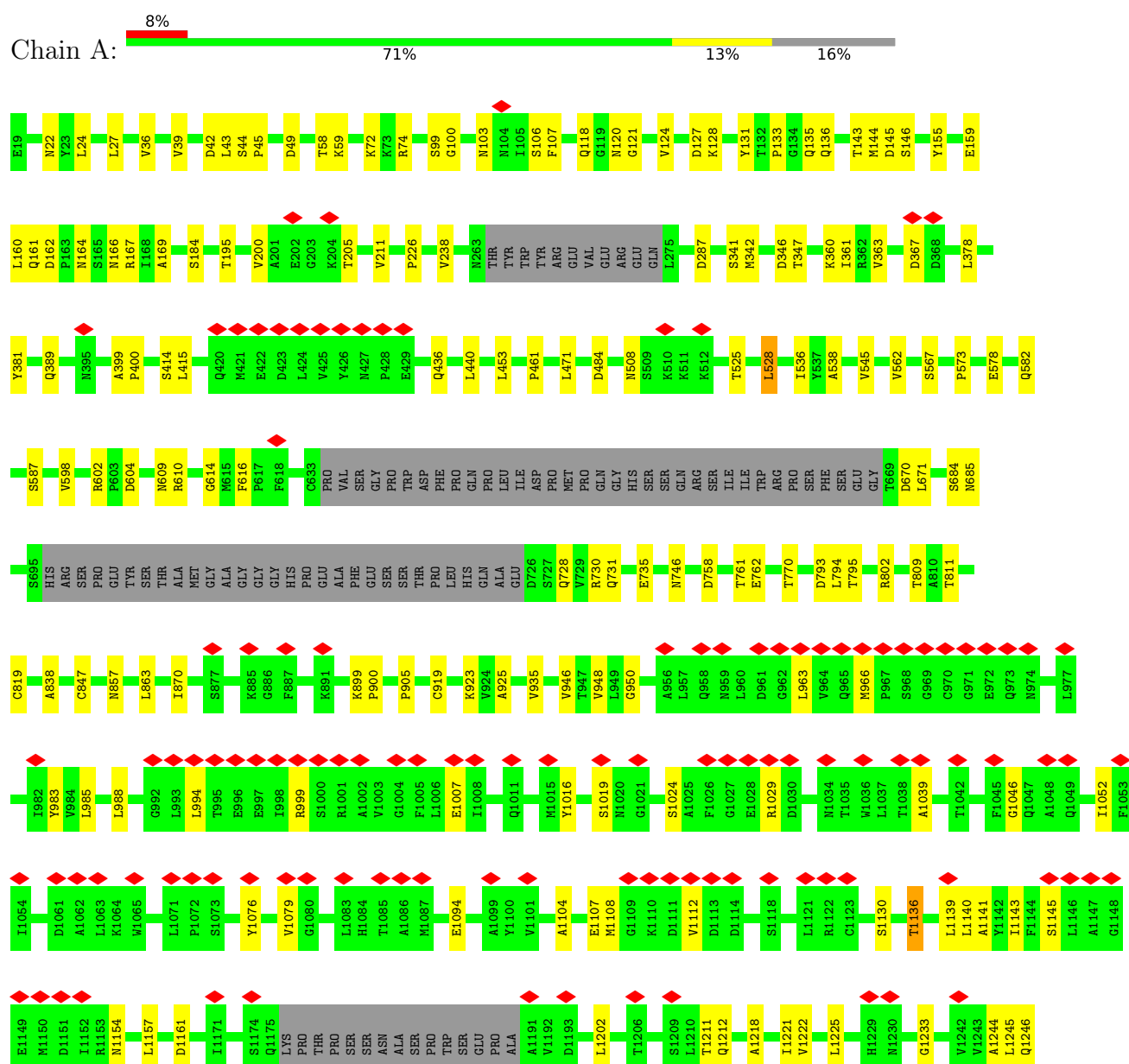
- Molecule 1 is a protein called Alpha-2-macroglobulin-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1212	9450	6047	1554	1803	46	0	0

3 Residue-property plots

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

• Molecule 1: Alpha-2-macroglobulin-like protein 1



Protein	Gene	Accession	Length	Weight	PI	Charge	Score	Rank
THR	IL247	IL247	1247	1247	1247	1247	1247	1247
ILE	IL248	IL248	1248	1248	1248	1248	1248	1248
HIS	IL249	IL249	1249	1249	1249	1249	1249	1249
THR	IL250	IL250	1250	1250	1250	1250	1250	1250
THR	IL251	IL251	1251	1251	1251	1251	1251	1251
TYR	IL252	IL252	1252	1252	1252	1252	1252	1252
THR	IL253	IL253	1253	1253	1253	1253	1253	1253
PHE	IL254	IL254	1254	1254	1254	1254	1254	1254
THR	IL255	IL255	1255	1255	1255	1255	1255	1255
ILE	IL256	IL256	1256	1256	1256	1256	1256	1256
ILE	IL257	IL257	1257	1257	1257	1257	1257	1257
THR	IL258	IL258	1258	1258	1258	1258	1258	1258
THR	IL259	IL259	1259	1259	1259	1259	1259	1259
GLN	IL260	IL260	1260	1260	1260	1260	1260	1260
THR	IL261	IL261	1261	1261	1261	1261	1261	1261
VAL	IL262	IL262	1262	1262	1262	1262	1262	1262
VAL	IL263	IL263	1263	1263	1263	1263	1263	1263
THR	IL264	IL264	1264	1264	1264	1264	1264	1264
THR	IL265	IL265	1265	1265	1265	1265	1265	1265
THR	IL266	IL266	1266	1266	1266	1266	1266	1266
THR	IL267	IL267	1267	1267	1267	1267	1267	1267
THR	IL268	IL268	1268	1268	1268	1268	1268	1268
THR	IL269	IL269	1269	1269	1269	1269	1269	1269
THR	IL270	IL270	1270	1270	1270	1270	1270	1270
THR	IL271	IL271	1271	1271	1271	1271	1271	1271
THR	IL272	IL272	1272	1272	1272	1272	1272	1272
THR	IL273	IL273	1273	1273	1273	1273	1273	1273
THR	IL274	IL274	1274	1274	1274	1274	1274	1274
THR	IL275	IL275	1275	1275	1275	1275	1275	1275
THR	IL276	IL276	1276	1276	1276	1276	1276	1276
THR	IL277	IL277	1277	1277	1277	1277	1277	1277
THR	IL278	IL278	1278	1278	1278	1278	1278	1278
THR	IL279	IL279	1279	1279	1279	1279	1279	1279
THR	IL280	IL280	1280	1280	1280	1280	1280	1280
THR	IL281	IL281	1281	1281	1281	1281	1281	1281
THR	IL282	IL282	1282	1282	1282	1282	1282	1282
THR	IL283	IL283	1283	1283	1283	1283	1283	1283
THR	IL284	IL284	1284	1284	1284	1284	1284	1284
THR	IL285	IL285	1285	1285	1285	1285	1285	1285
THR	IL286	IL286	1286	1286	1286	1286	1286	1286
THR	IL287	IL287	1287	1287	1287	1287	1287	1287
THR	IL288	IL288	1288	1288	1288	1288	1288	1288
THR	IL289	IL289	1289	1289	1289</			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	291904	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; cryoSPARK	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.750	Depositor
Minimum map value	-0.344	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.085	Depositor
Map size (Å)	331.264, 331.264, 331.264	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1042134, 1.1042134, 1.1042134	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	0.29	1/9663 (0.0%)	0.70	21/13130 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	133	PRO	CG-CD	-5.84	1.30	1.50

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	PRO	CA-N-CD	-12.94	93.89	112.00
1	A	966	MET	CB-CG-SD	8.34	137.72	112.70
1	A	133	PRO	N-CD-CG	-8.18	90.93	103.20
1	A	400	PRO	CA-N-CD	-6.53	102.86	112.00
1	A	1112	VAL	CA-C-N	6.46	136.32	124.82

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1320	PRO	Peptide
1	A	602	ARG	Sidechain
1	A	616	PHE	Peptide
1	A	731	GLN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9450	0	9346	96	0
All	All	9450	0	9346	96	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 96 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:A:43:LEU:O	1:A:74:ARG:HA	1.77	0.83
1:A:562:VAL:HA	1:A:582:GLN:O	1.87	0.74
1:A:162:ASP:HB2	1:A:166:ASN:H	1.60	0.66
1:A:1141:ALA:O	1:A:1145:SER:HB2	2.00	0.62
1:A:131:TYR:HB2	1:A:211:VAL:HG22	1.85	0.59

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	1202/1436 (84%)	1139 (95%)	62 (5%)	1 (0%)	48 76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1079	VAL

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	1051/1253 (84%)	1045 (99%)	6 (1%)	78 80

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	LEU
1	A	528	LEU
1	A	1136	THR
1	A	124	VAL
1	A	36	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1060	GLN
1	A	1081	ASN
1	A	1277	ASN
1	A	1246	GLN
1	A	1273	GLN

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](#)

There are no chain breaks in this entry.

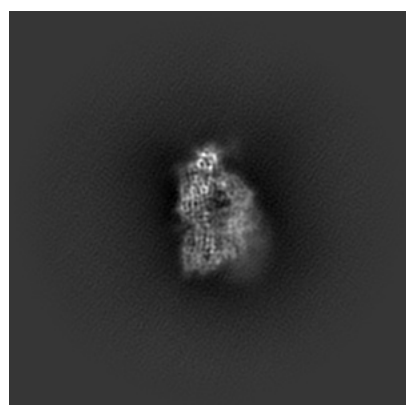
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13848. These allow visual inspection of the internal detail of the map and identification of artifacts.

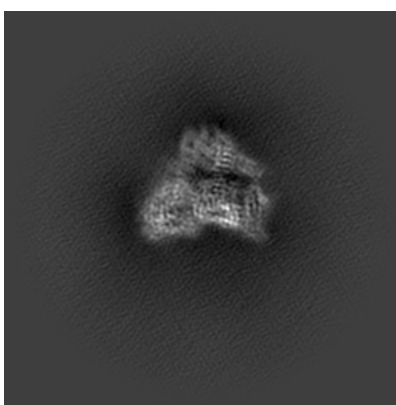
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

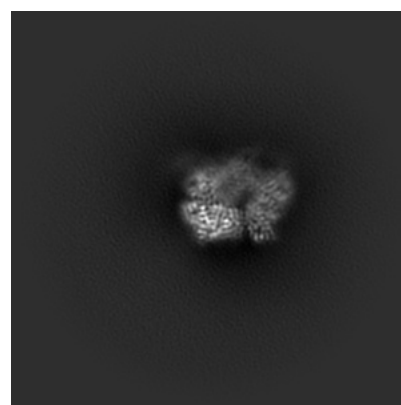
6.1.1 Primary map



X



Y

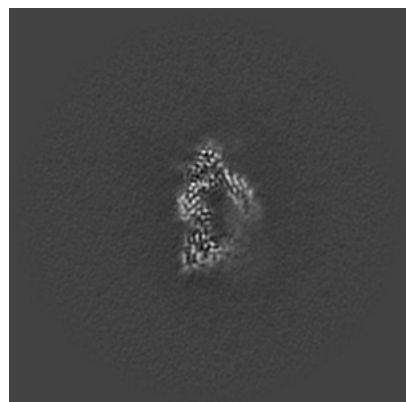


Z

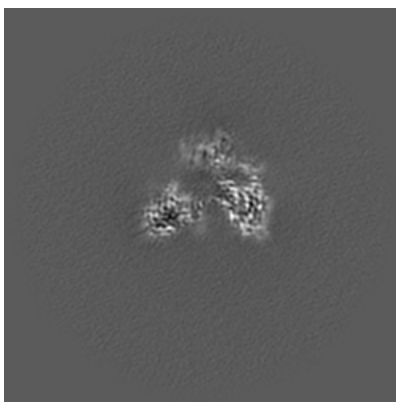
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

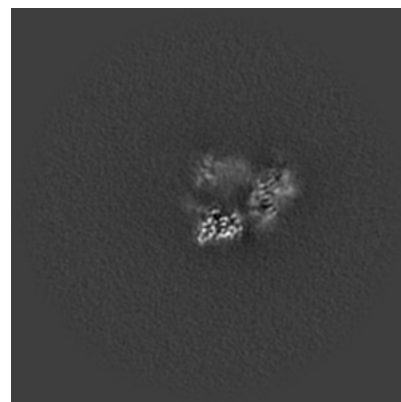
6.2.1 Primary map



X Index: 150



Y Index: 150

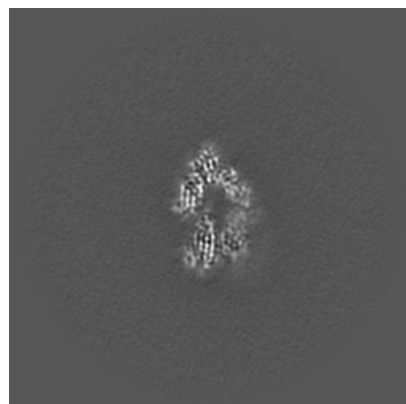


Z Index: 150

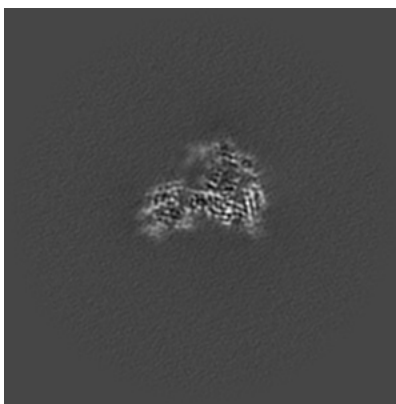
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

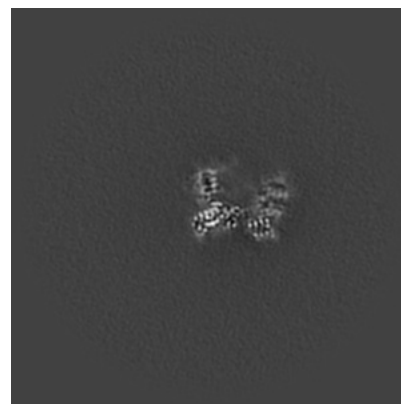
6.3.1 Primary map



X Index: 143



Y Index: 142



Z Index: 167

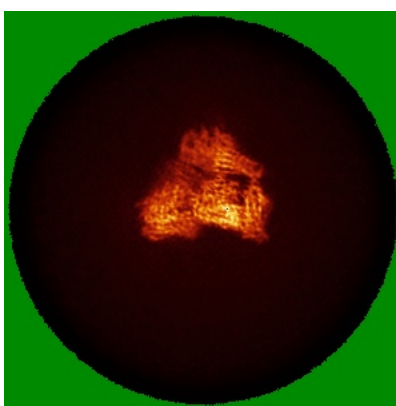
The images above show the largest variance slices of the map in three orthogonal directions.

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

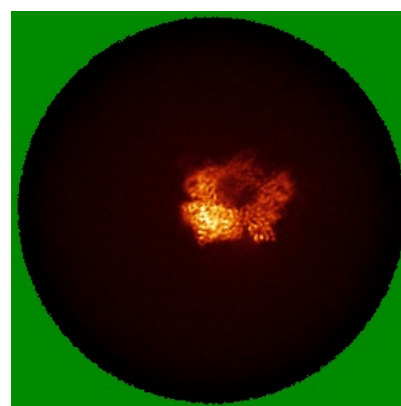
6.4.1 Primary map



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

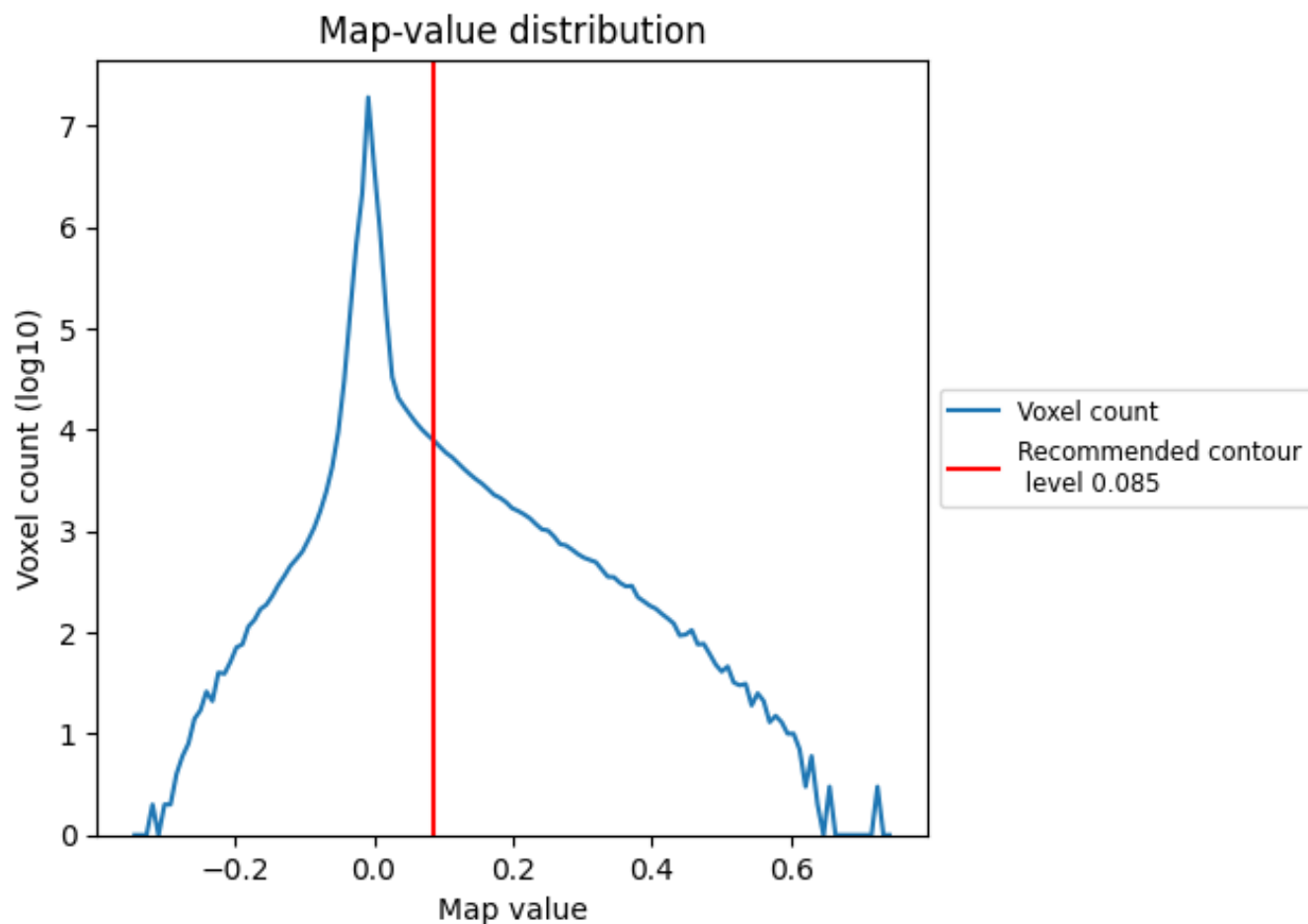
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

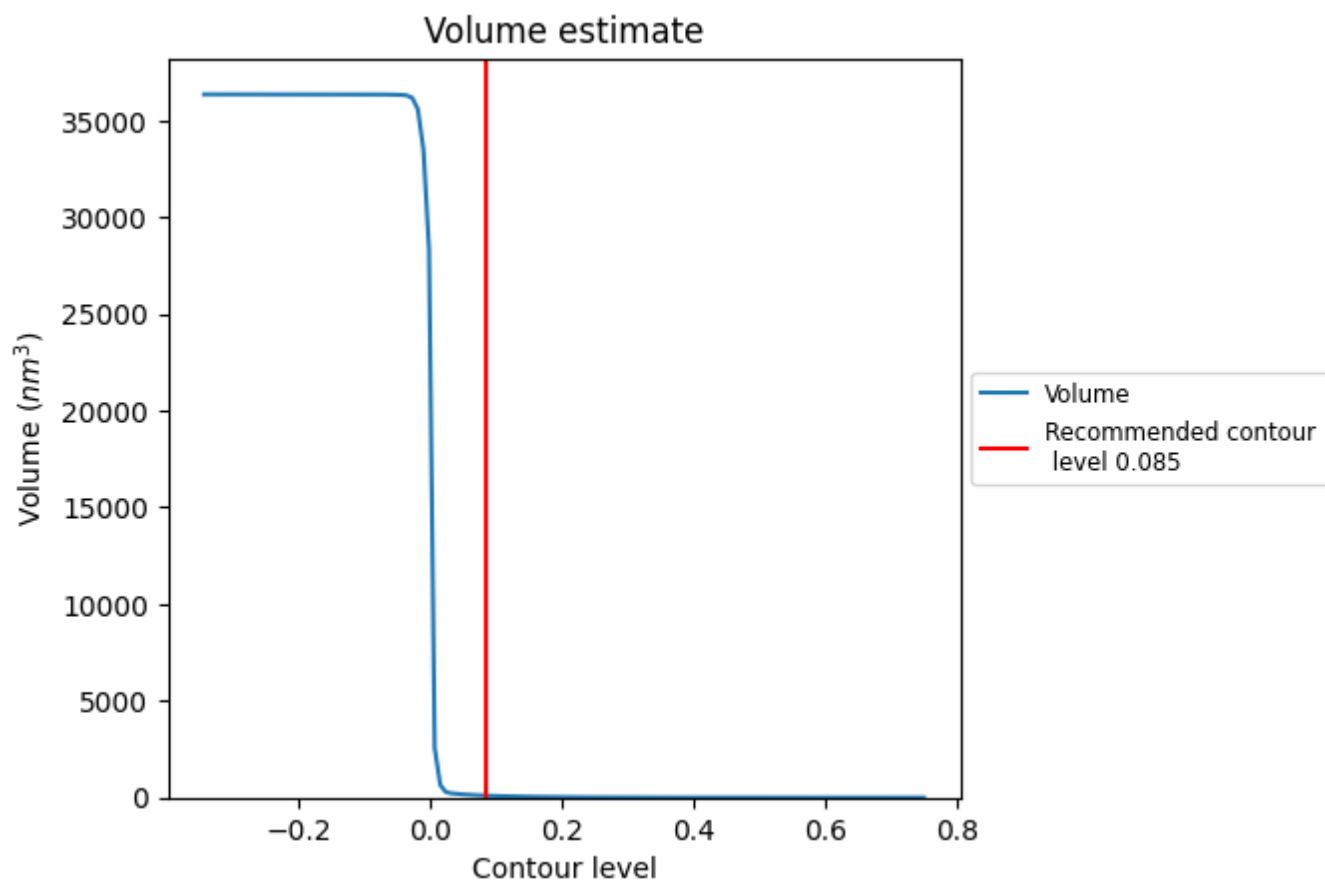
This section contains the results of statistical analysis of the map.

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.

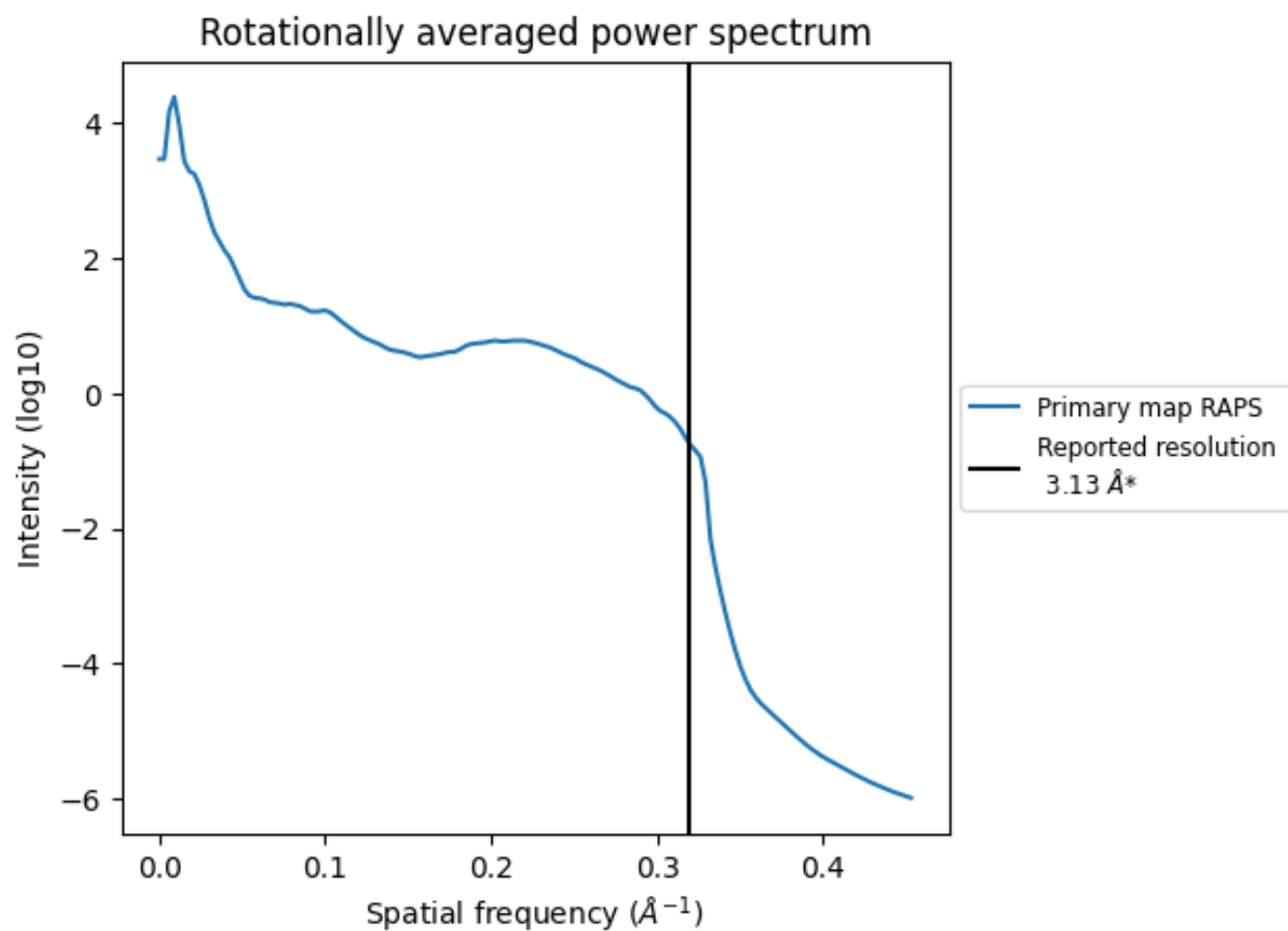
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 99 nm^3 ; this corresponds to an approximate mass of 89 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 0.319 Å⁻¹

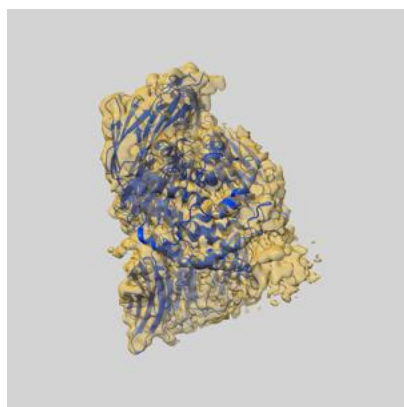
8 Fourier-Shell correlation ⓘ

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

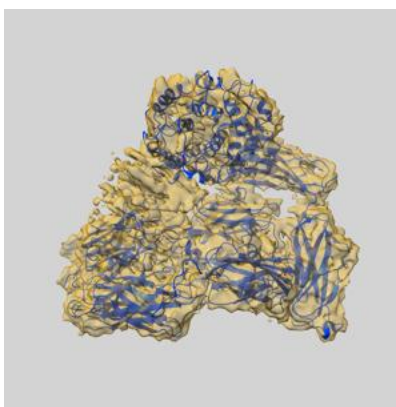
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13848 and PDB model 7Q60. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

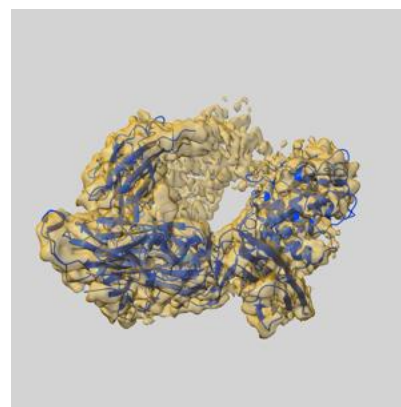
9.1 Map-model overlay [i](#)



X



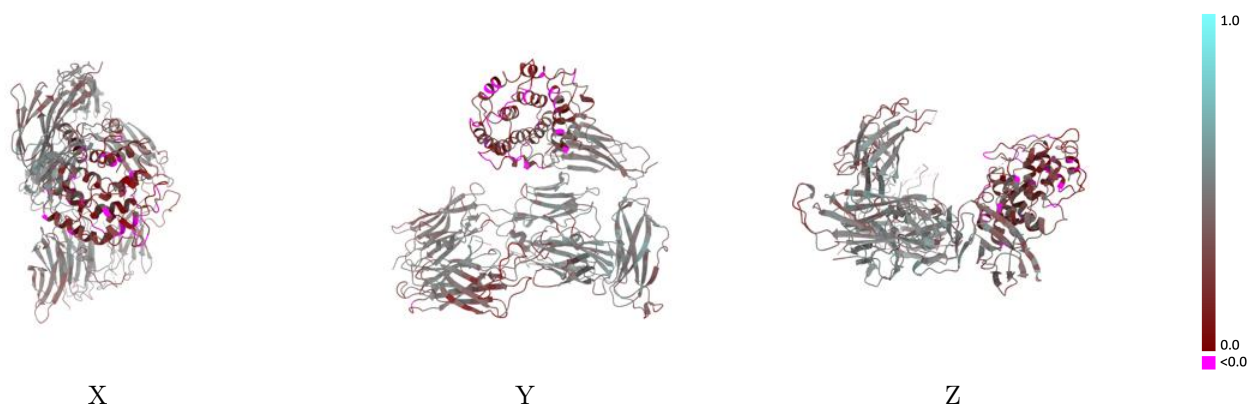
Y



Z

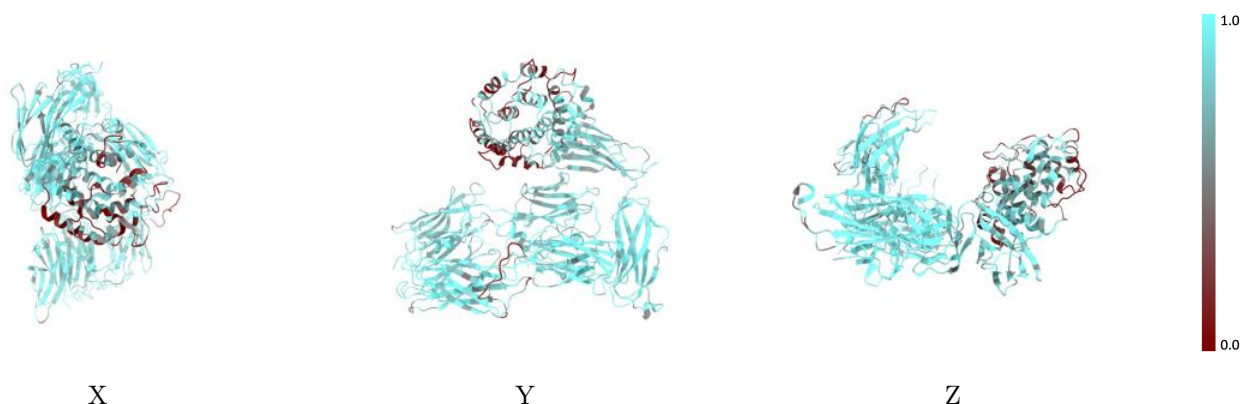
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



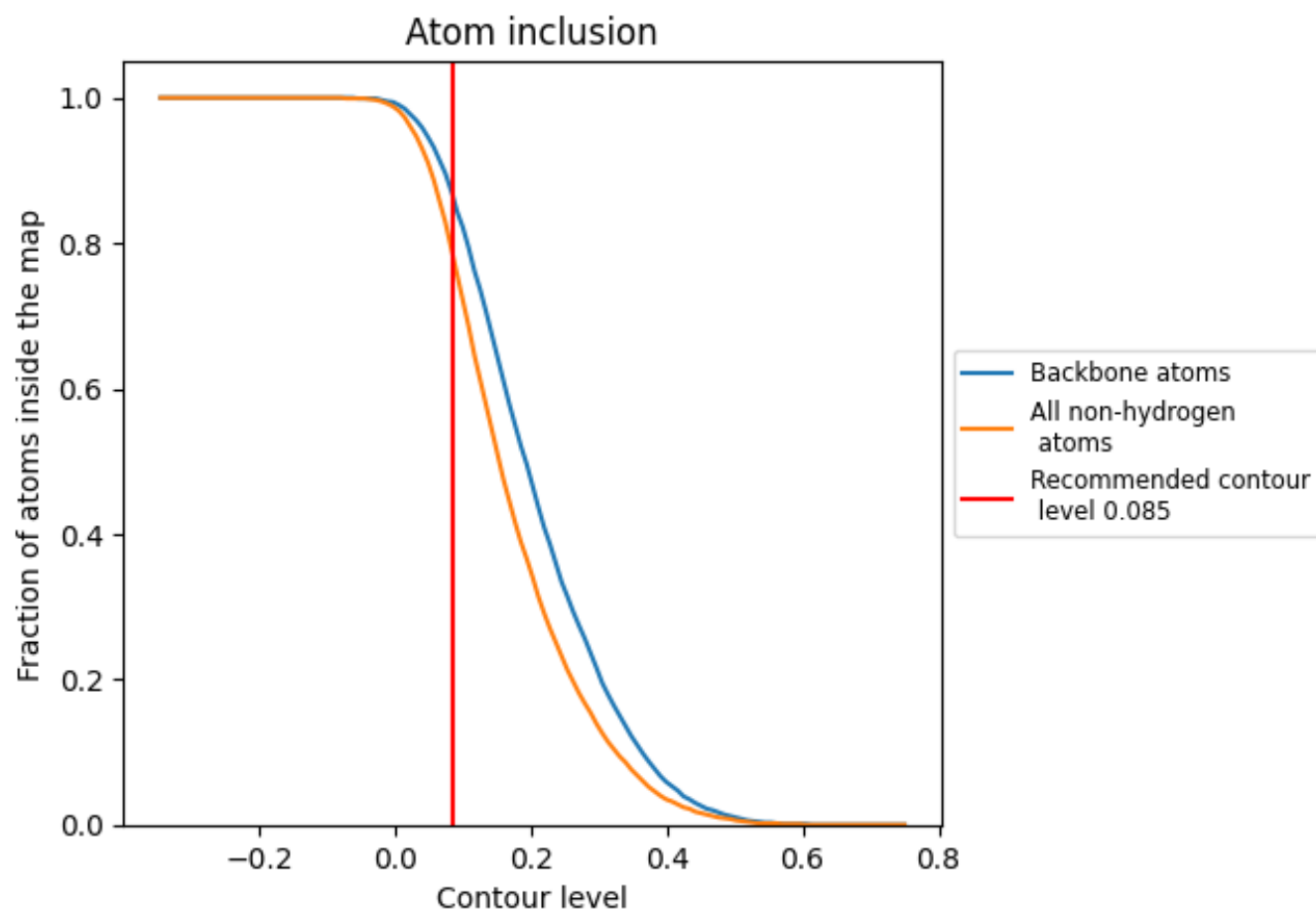
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.085).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 79% 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 (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7860	0.3720
A	0.7860	0.3720

