



wwPDB EM Validation Summary Report ⓘ

Mar 4, 2026 – 05:11 PM UTC

PDB ID : 9QFH / pdb_00009qfh
EMDB ID : EMD-53109
Title : The composite map of of the AMPAR complex GluA3- TARP gamma2 in the apo state.
Authors : Pokharna, A.; Krieger, J.; Greger, I.; Singh, B.
Deposited on : 2025-03-11
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

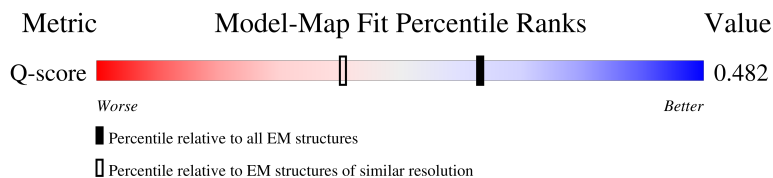
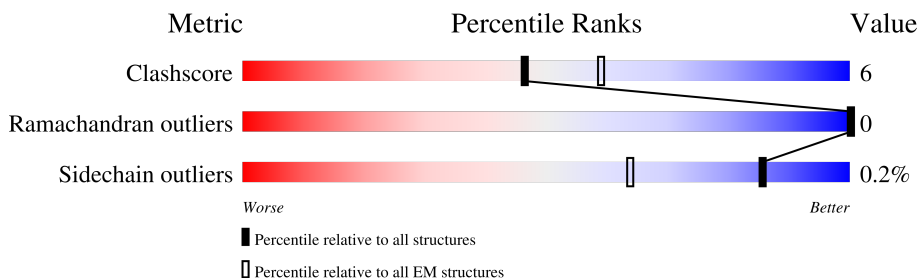
1 Overall quality at a glance

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	A	1170	
1	B	1170	
1	C	1170	
1	D	1170	

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Mol	Chain	Length	Quality of chain
1	W	1170	 12% 86%
1	X	1170	 12% 86%
1	Y	1170	 12% 86%
1	Z	1170	 13% 86%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 29625 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 Isoform Flip of Glutamate receptor 3, Voltage-dependent calcium channel gamma-2 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	774	Total	C	N	O	S	2	0
			6127	3950	1024	1119	34		
1	B	776	Total	C	N	O	S	1	0
			6134	3954	1027	1119	34		
1	C	777	Total	C	N	O	S	0	0
			6100	3939	1022	1105	34		
1	D	772	Total	C	N	O	S	1	0
			6100	3936	1021	1110	33		
1	W	165	Total	C	N	O	S	0	0
			1292	856	212	214	10		
1	X	165	Total	C	N	O	S	0	0
			1295	857	212	216	10		
1	Y	164	Total	C	N	O	S	0	0
			1290	854	211	215	10		
1	Z	166	Total	C	N	O	S	0	0
			1287	848	212	217	10		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	844	GLY	-	linker	UNP P19492
A	845	GLY	-	linker	UNP P19492
A	846	SER	-	linker	UNP P19492
A	847	GLY	-	linker	UNP P19492
A	848	SER	-	linker	UNP P19492
A	849	GLY	-	linker	UNP P19492
B	844	GLY	-	linker	UNP P19492
B	845	GLY	-	linker	UNP P19492
B	846	SER	-	linker	UNP P19492
B	847	GLY	-	linker	UNP P19492
B	848	SER	-	linker	UNP P19492
B	849	GLY	-	linker	UNP P19492
C	844	GLY	-	linker	UNP P19492

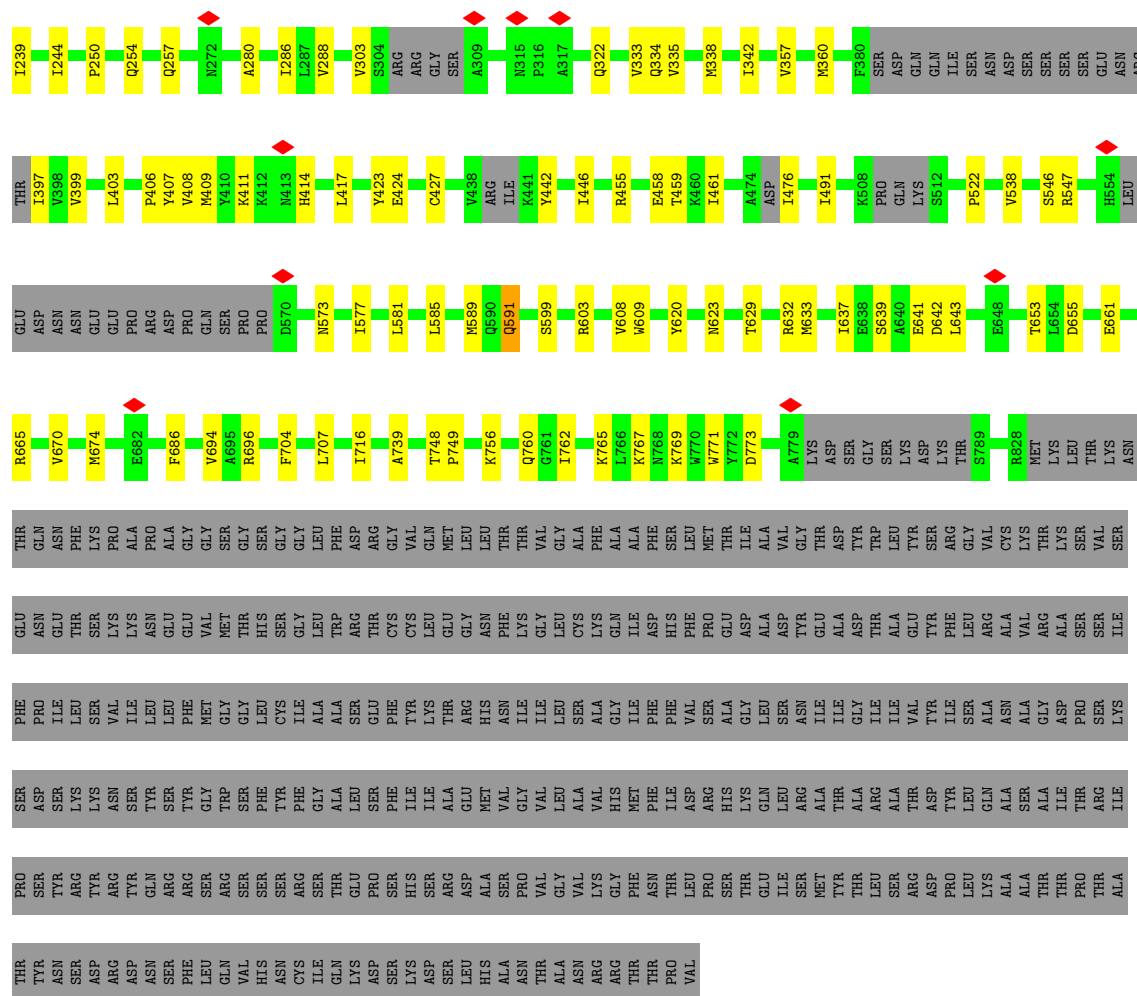
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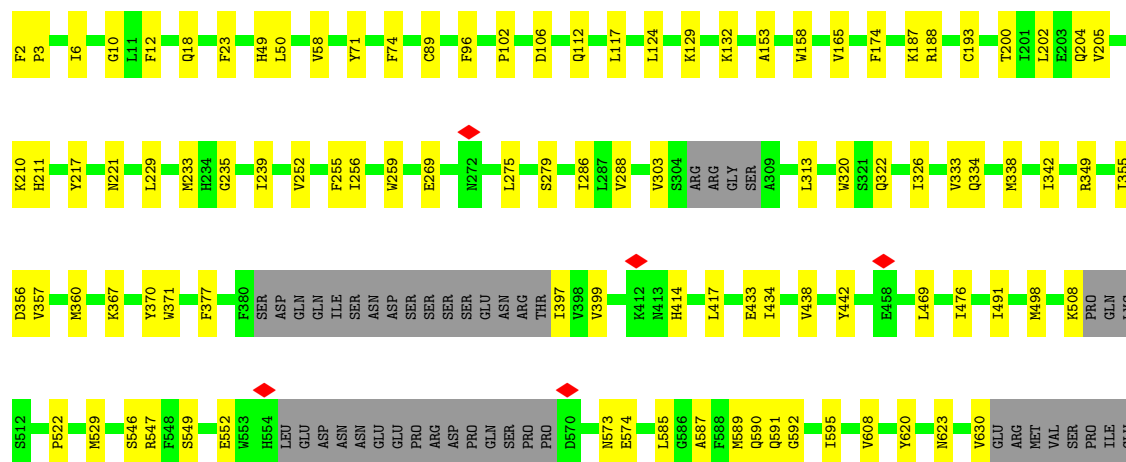
Chain	Residue	Modelled	Actual	Comment	Reference
C	845	GLY	-	linker	UNP P19492
C	846	SER	-	linker	UNP P19492
C	847	GLY	-	linker	UNP P19492
C	848	SER	-	linker	UNP P19492
C	849	GLY	-	linker	UNP P19492
D	844	GLY	-	linker	UNP P19492
D	845	GLY	-	linker	UNP P19492
D	846	SER	-	linker	UNP P19492
D	847	GLY	-	linker	UNP P19492
D	848	SER	-	linker	UNP P19492
D	849	GLY	-	linker	UNP P19492
W	-4	GLY	-	linker	UNP P19492
W	-3	GLY	-	linker	UNP P19492
W	-2	SER	-	linker	UNP P19492
W	-1	GLY	-	linker	UNP P19492
W	0	SER	-	linker	UNP P19492
W	1	GLY	-	linker	UNP P19492
X	-4	GLY	-	linker	UNP P19492
X	-3	GLY	-	linker	UNP P19492
X	-2	SER	-	linker	UNP P19492
X	-1	GLY	-	linker	UNP P19492
X	0	SER	-	linker	UNP P19492
X	1	GLY	-	linker	UNP P19492
Y	-4	GLY	-	linker	UNP P19492
Y	-3	GLY	-	linker	UNP P19492
Y	-2	SER	-	linker	UNP P19492
Y	-1	GLY	-	linker	UNP P19492
Y	0	SER	-	linker	UNP P19492
Y	1	GLY	-	linker	UNP P19492
Z	-4	GLY	-	linker	UNP P19492
Z	-3	GLY	-	linker	UNP P19492
Z	-2	SER	-	linker	UNP P19492
Z	-1	GLY	-	linker	UNP P19492
Z	0	SER	-	linker	UNP P19492
Z	1	GLY	-	linker	UNP P19492

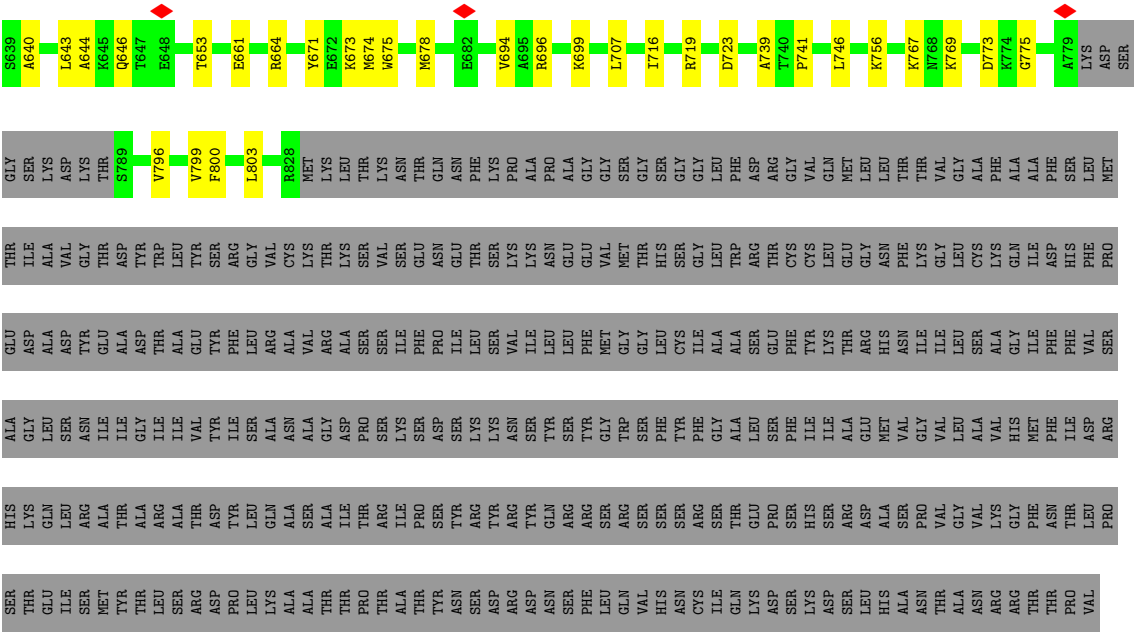
THR
ALA
ASN
ARG
ARG
THR
THR
PRO
VAL

F2	I6	L11	T16	E19	F23	F41	L50	V58	F62	C63	F88	C89	F96	M113	R114	P115	A116	L117	L124	V165	F174	E180	M181	L190	V205	V206	K210	H211	L219	A220	R221	L222	L227	L228	L229	G235
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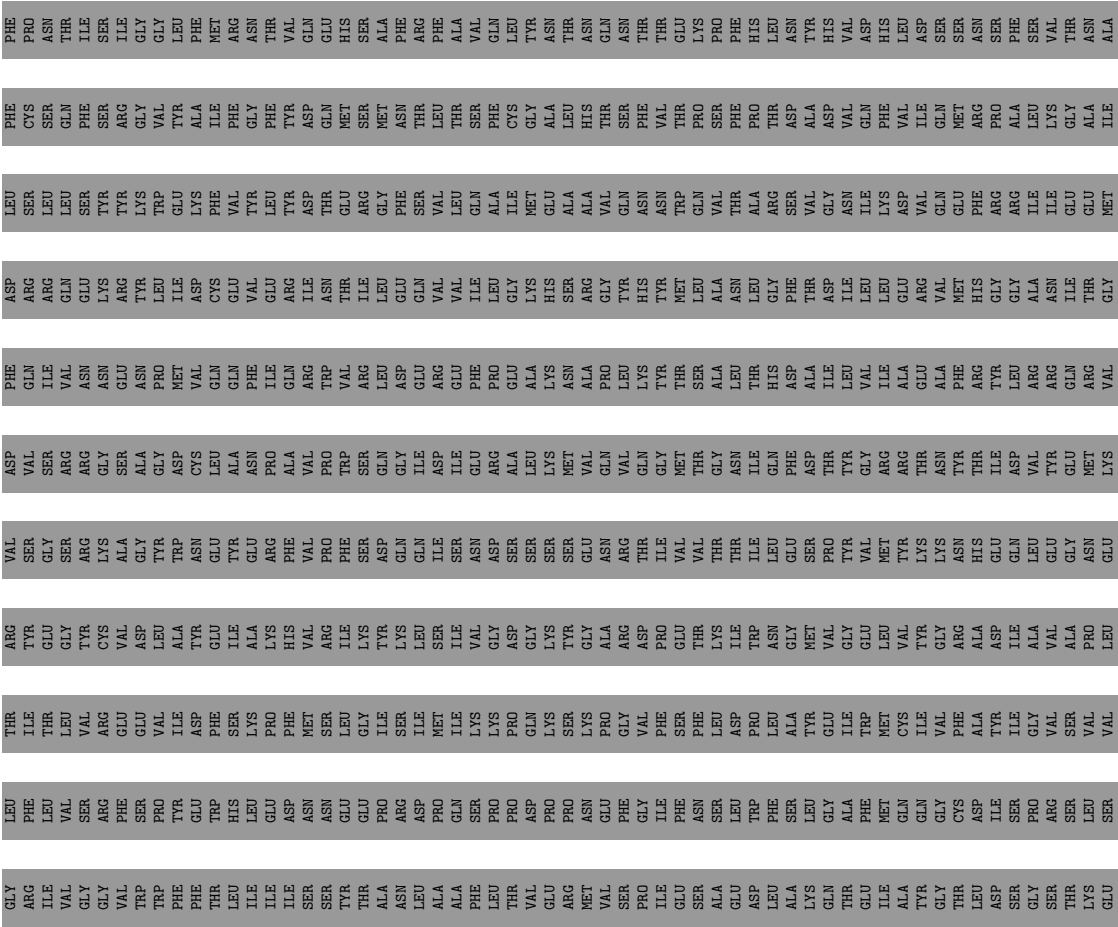
- Molecule 1: Isoform Flip of Glutamate receptor 3, Voltage-dependent calcium channel gamma-2 subunit





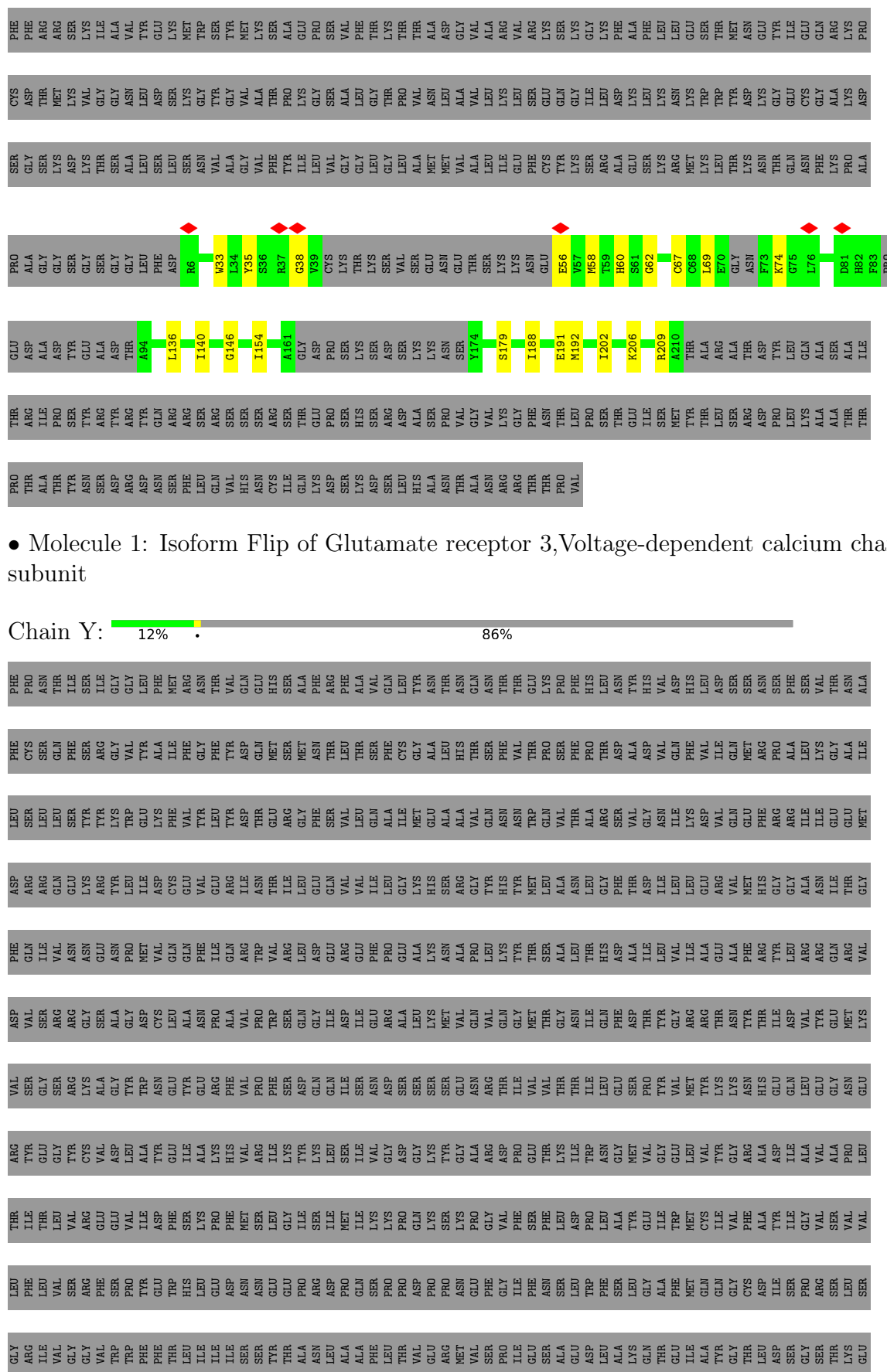
- Molecule 1: Isoform Flip of Glutamate receptor 3,Voltage-dependent calcium channel gamma-2 subunit

Chain W: 12% . 86%

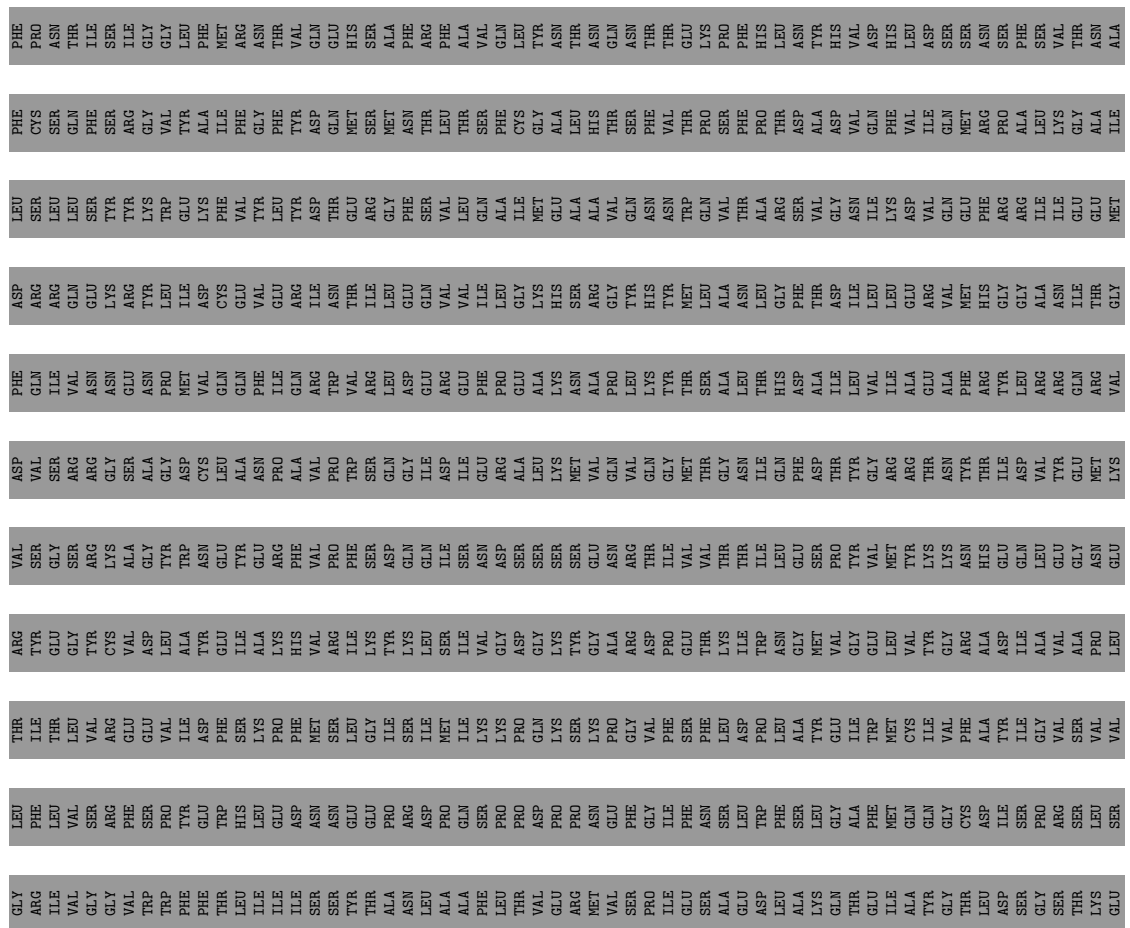


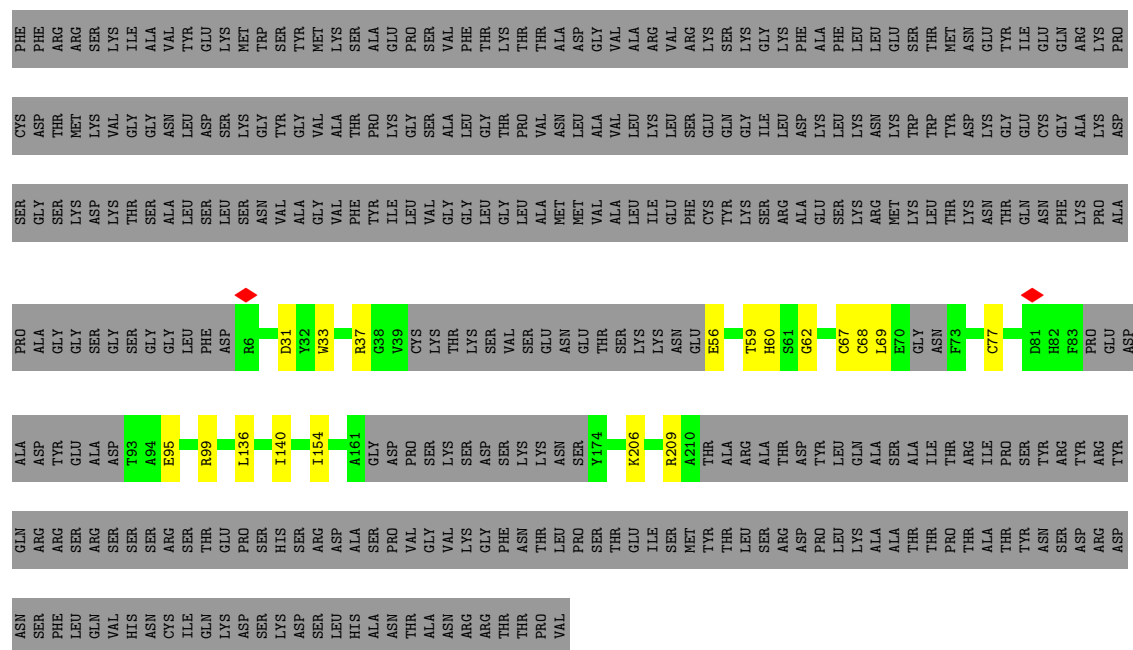


Chain X: 12% 86%



- Molecule 1: Isoform Flip of Glutamate receptor 3, Voltage-dependent calcium channel gamma-2 subunit





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1184304	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	66.084	Depositor
Minimum map value	-0.766	Depositor
Average map value	1.744	Depositor
Map value standard deviation	1.309	Depositor
Recommended contour level	9	Depositor
Map size (Å)	422.912, 422.912, 422.912	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	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	0.21	0/6269	0.39	2/8488 (0.0%)
1	B	0.25	0/6275	0.43	0/8495
1	C	0.20	0/6242	0.37	0/8456
1	D	0.21	0/6242	0.40	4/8451 (0.0%)
1	W	0.19	0/1321	0.29	0/1780
1	X	0.16	0/1324	0.30	0/1784
1	Y	0.24	0/1319	0.41	1/1777 (0.1%)
1	Z	0.15	0/1315	0.32	0/1774
All	All	0.21	0/30307	0.39	7/41005 (0.0%)

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

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

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	587	ALA	N-CA-C	-8.15	100.73	111.24
1	Y	28	VAL	N-CA-C	-7.52	105.68	112.90
1	D	592	GLY	N-CA-C	5.55	118.51	111.85
1	A	576	GLY	CA-C-O	-5.39	116.65	122.47
1	D	433	GLU	O-C-N	-5.34	115.97	122.22

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	598	ARG	Sidechain

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	6127	0	5970	94	0
1	B	6134	0	5997	87	0
1	C	6100	0	5945	79	0
1	D	6100	0	5975	79	0
1	W	1292	0	1305	12	0
1	X	1295	0	1307	15	0
1	Y	1290	0	1302	11	0
1	Z	1287	0	1282	11	0
All	All	29625	0	29083	358	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 358 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:554:HIS:CE1	1:X:209:ARG:HE	2.00	0.80
1:X:38:GLY:O	1:X:56:GLU:HA	1.87	0.74
1:B:640:ALA:HB1	1:B:674:MET:HE1	1.69	0.72
1:D:640:ALA:HB1	1:D:674:MET:HE1	1.72	0.72
1:C:653:THR:HG22	1:C:707:LEU:HB2	1.74	0.69

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	760/1170 (65%)	742 (98%)	18 (2%)	0	100	100
1	B	761/1170 (65%)	743 (98%)	18 (2%)	0	100	100
1	C	761/1170 (65%)	745 (98%)	16 (2%)	0	100	100
1	D	759/1170 (65%)	745 (98%)	14 (2%)	0	100	100
1	W	155/1170 (13%)	152 (98%)	3 (2%)	0	100	100
1	X	155/1170 (13%)	153 (99%)	2 (1%)	0	100	100
1	Y	154/1170 (13%)	151 (98%)	3 (2%)	0	100	100
1	Z	156/1170 (13%)	153 (98%)	3 (2%)	0	100	100
All	All	3661/9360 (39%)	3584 (98%)	77 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	644/1005 (64%)	642 (100%)	2 (0%)	86	96
1	B	647/1005 (64%)	647 (100%)	0	100	100
1	C	636/1005 (63%)	635 (100%)	1 (0%)	87	96
1	D	643/1005 (64%)	641 (100%)	2 (0%)	86	96
1	W	133/1005 (13%)	133 (100%)	0	100	100
1	X	134/1005 (13%)	134 (100%)	0	100	100
1	Y	134/1005 (13%)	133 (99%)	1 (1%)	76	92
1	Z	131/1005 (13%)	131 (100%)	0	100	100
All	All	3102/8040 (39%)	3096 (100%)	6 (0%)	85	96

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

Mol	Chain	Res	Type
1	D	434	ILE
1	D	590	GLN
1	Y	23	LEU
1	A	595	ILE
1	A	574	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	341	ASN
1	Z	149	ASN
1	D	760	GLN
1	W	205	HIS
1	B	221	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](#)

There are no chain breaks in this entry.

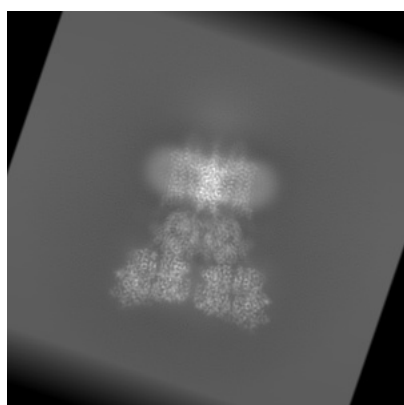
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53109. These allow visual inspection of the internal detail of the map and identification of artifacts.

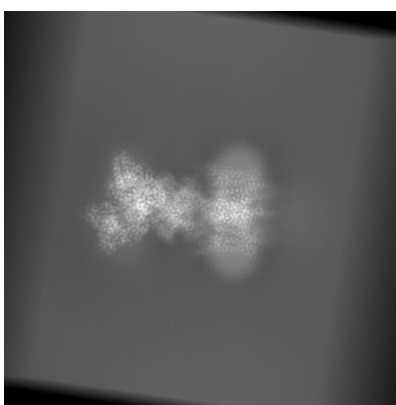
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

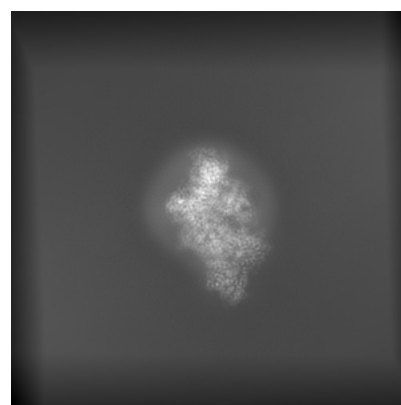
6.1.1 Primary map



X



Y

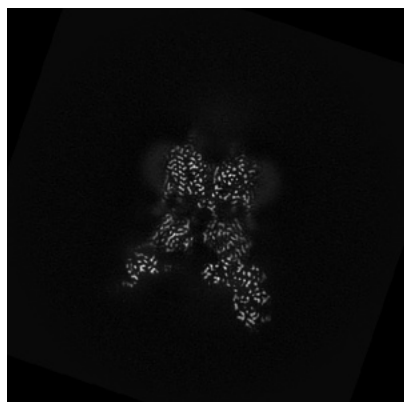


Z

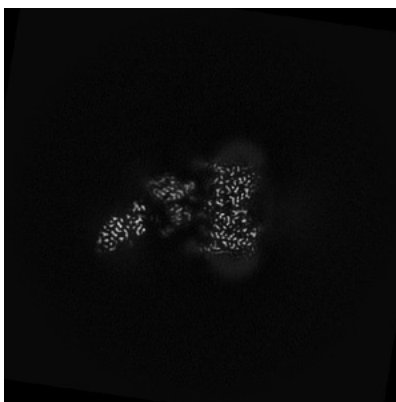
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

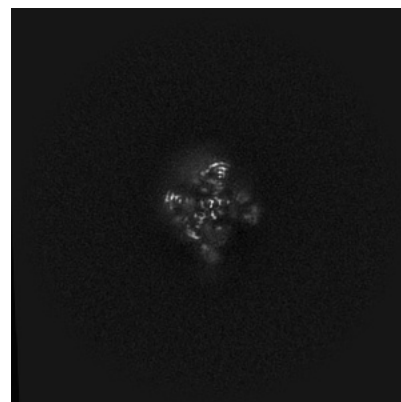
6.2.1 Primary map



X Index: 256



Y Index: 256

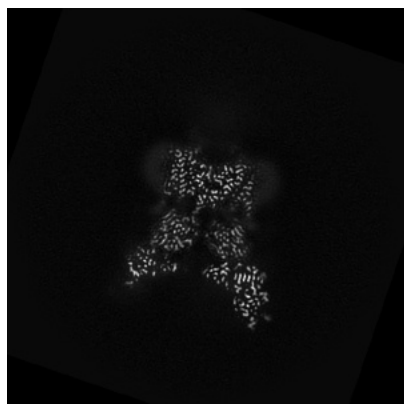


Z Index: 256

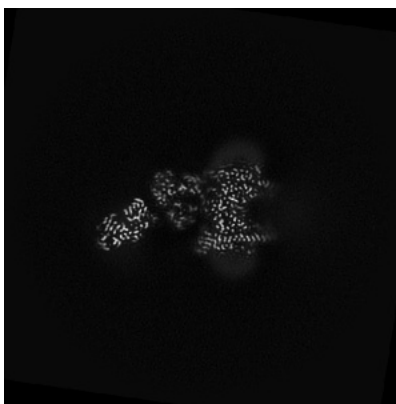
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 259



Y Index: 267



Z Index: 171

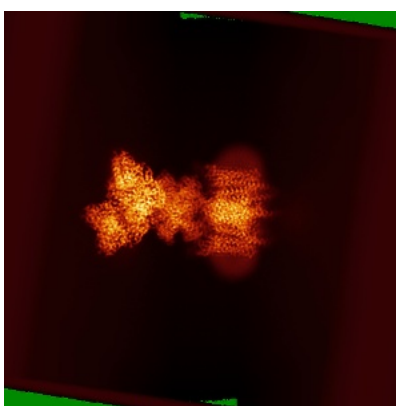
The images above show the largest variance slices of the map in three orthogonal directions.

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

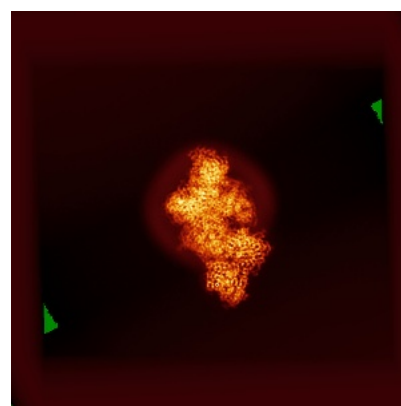
6.4.1 Primary map



X



Y

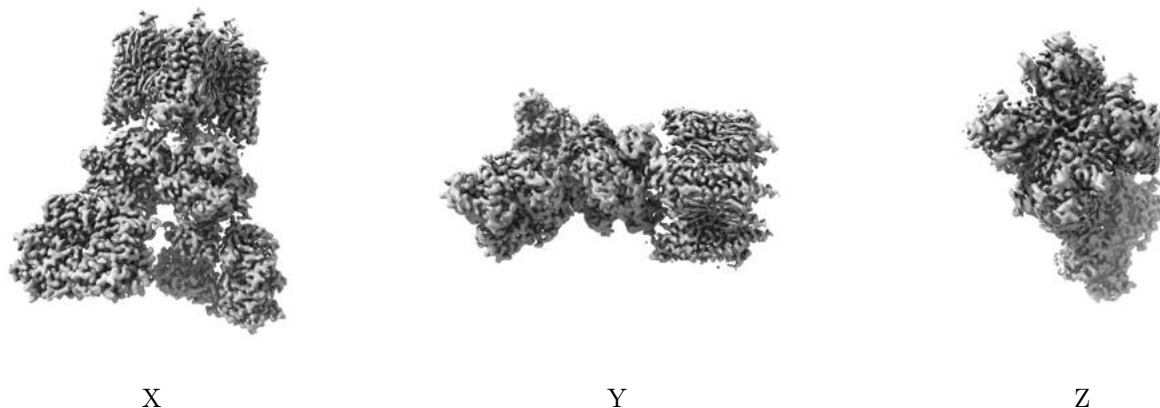


Z

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

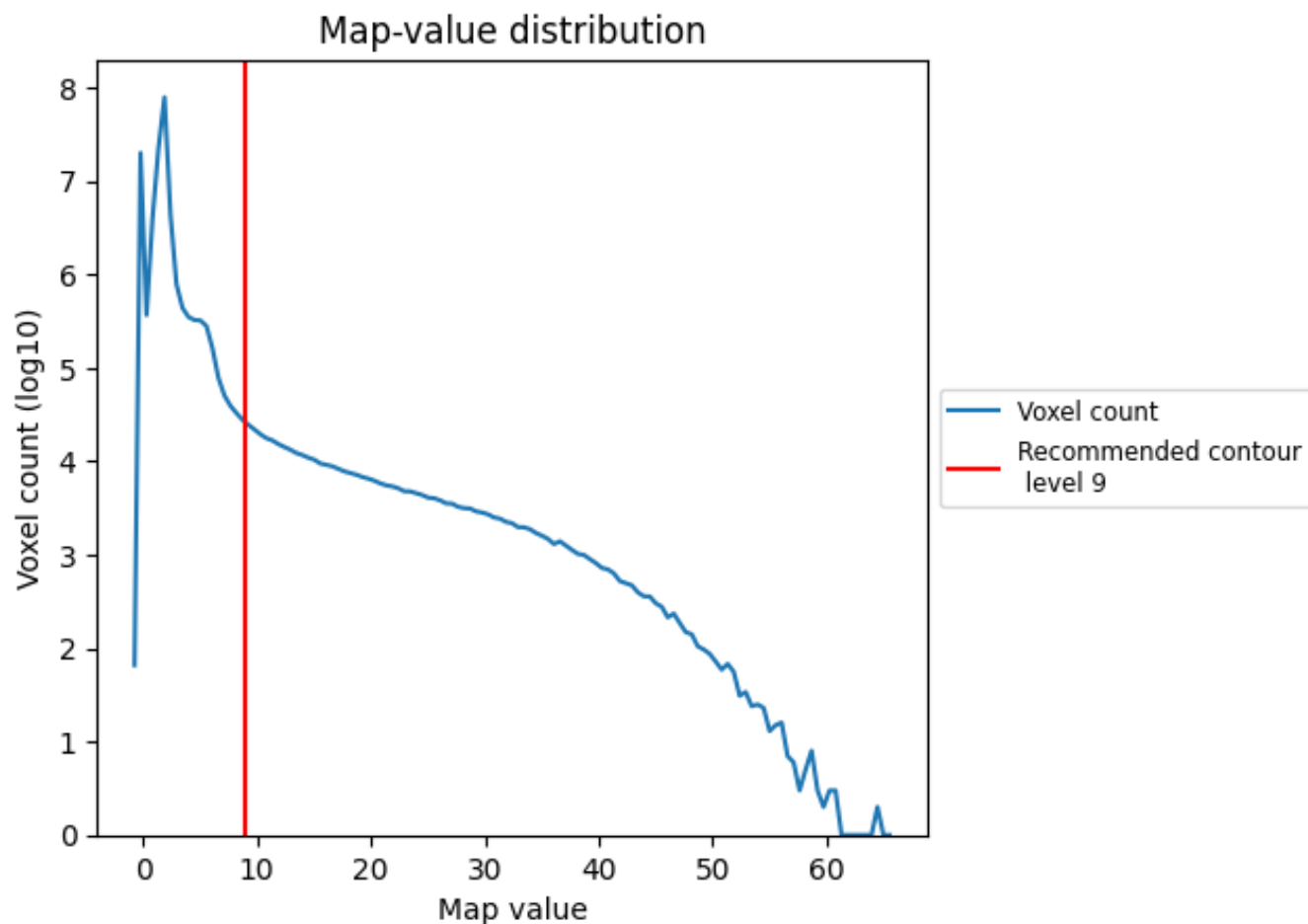
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

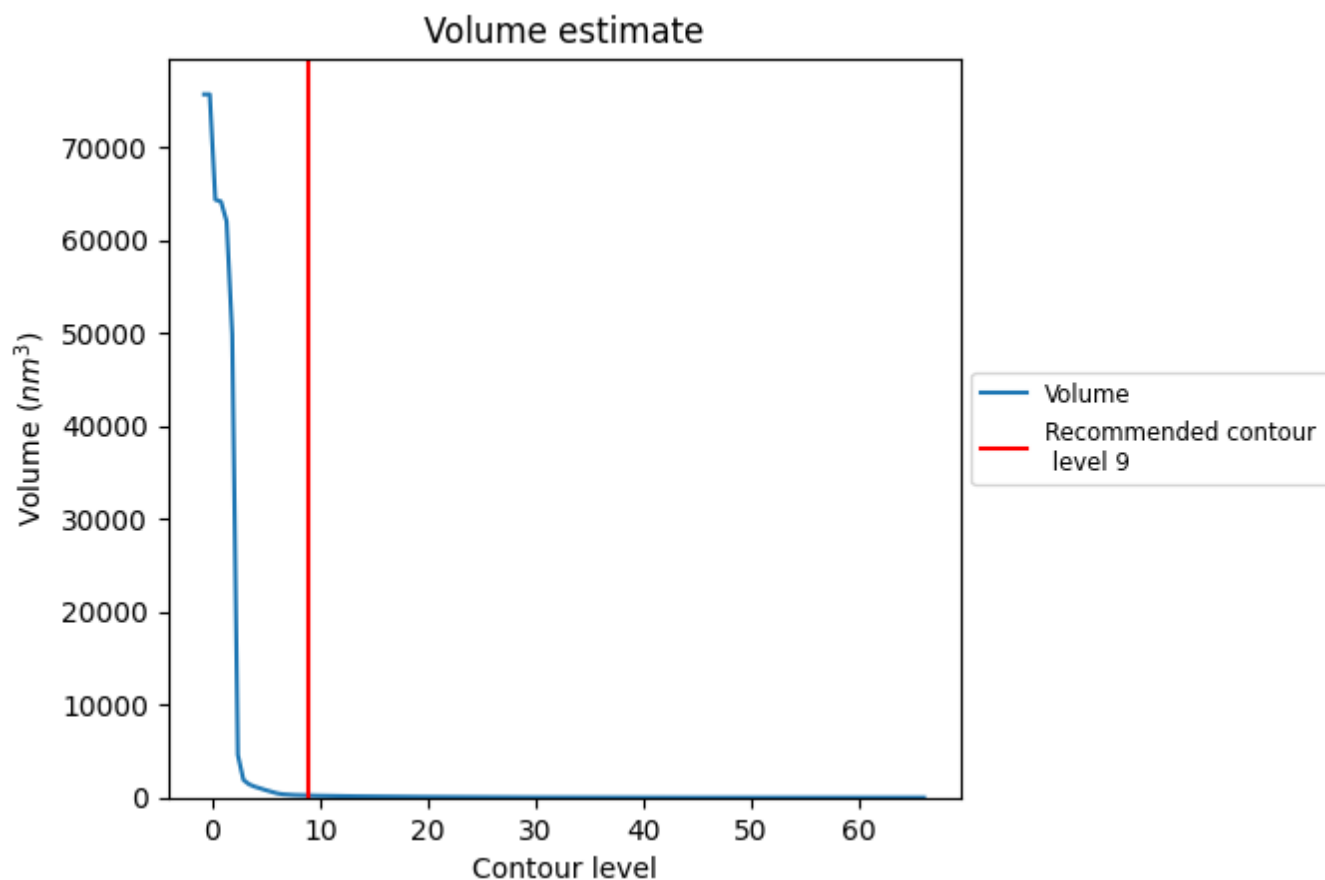
This section contains the results of statistical analysis of the map.

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.

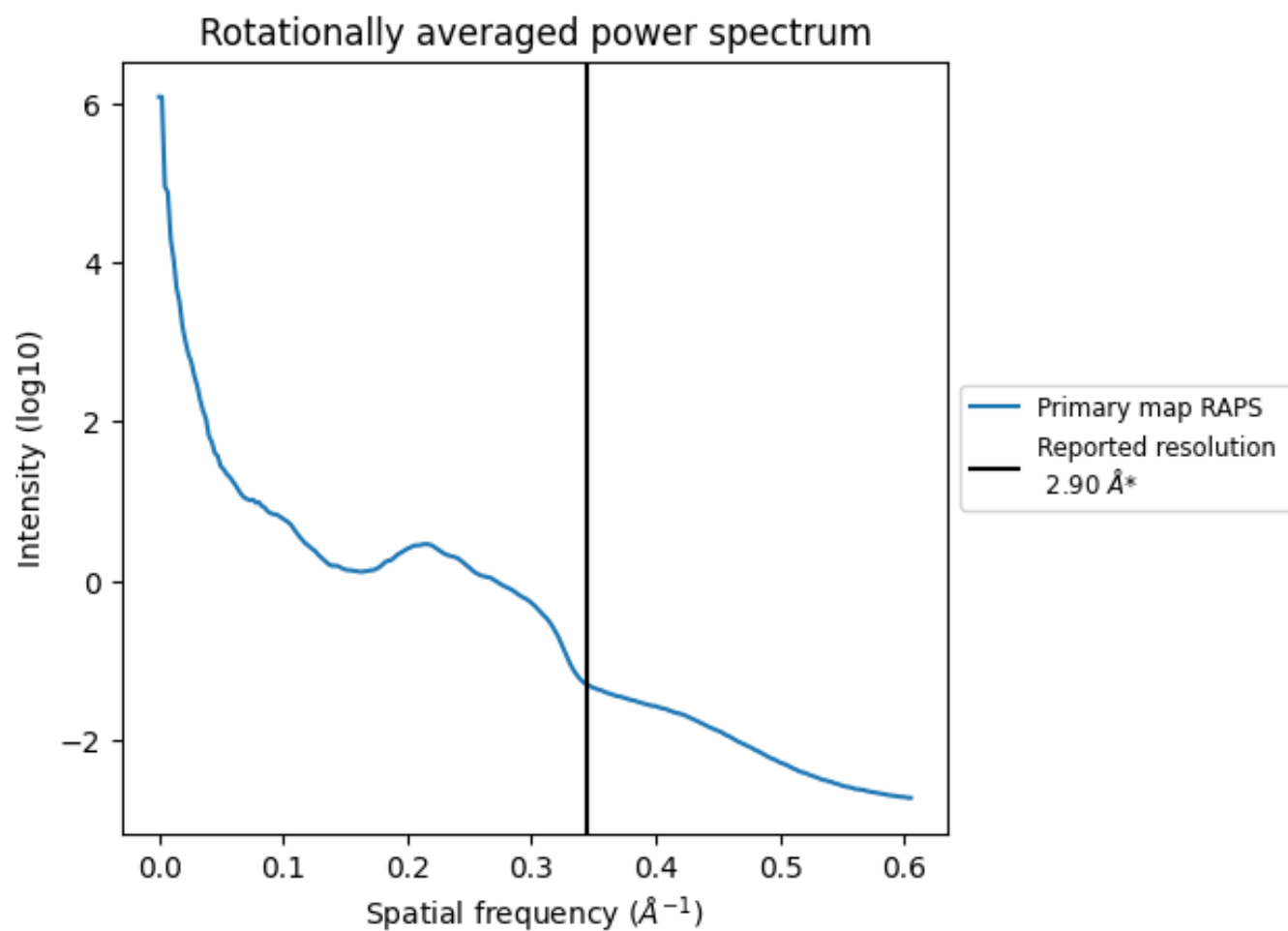
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 222 nm^3 ; this corresponds to an approximate mass of 200 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 0.345 Å⁻¹

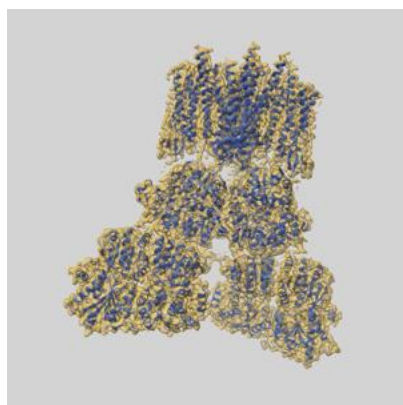
8 Fourier-Shell correlation

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

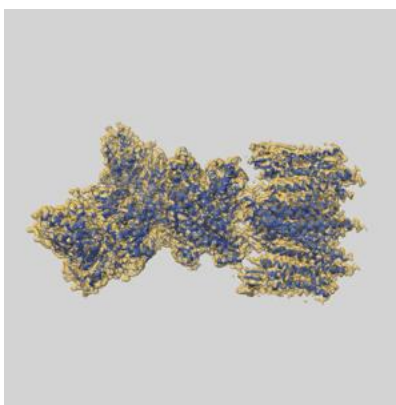
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53109 and PDB model 9QFH. Per-residue inclusion information can be found in section [3](#) on page [6](#).

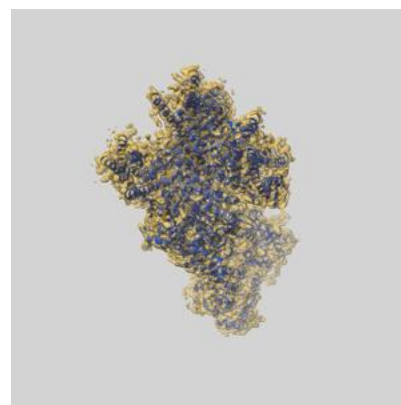
9.1 Map-model overlay [i](#)



X



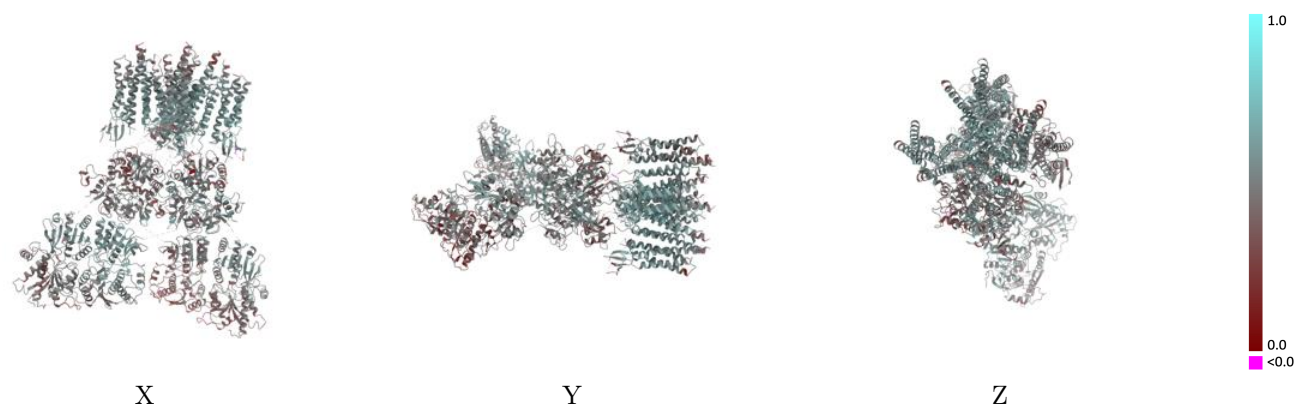
Y



Z

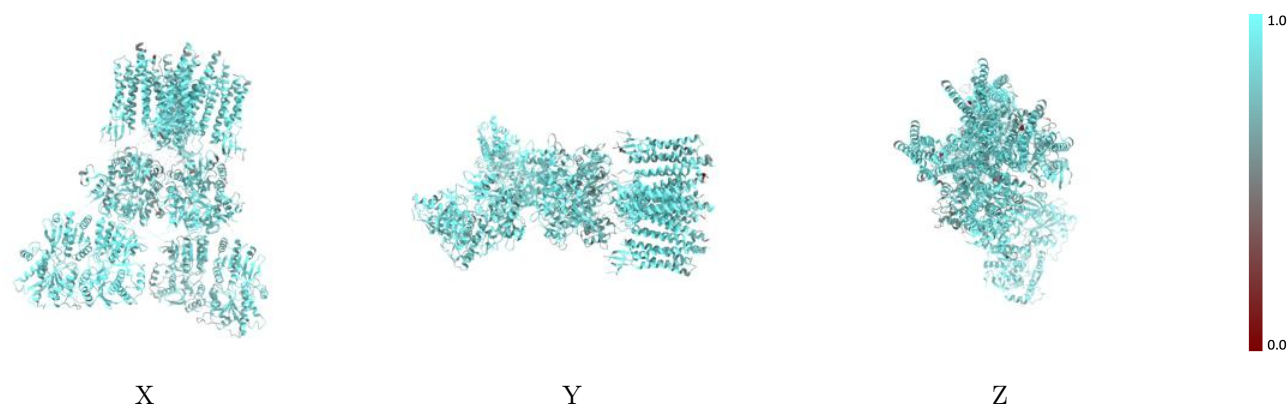
The images above show the 3D surface view of the map at the recommended contour level 9.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



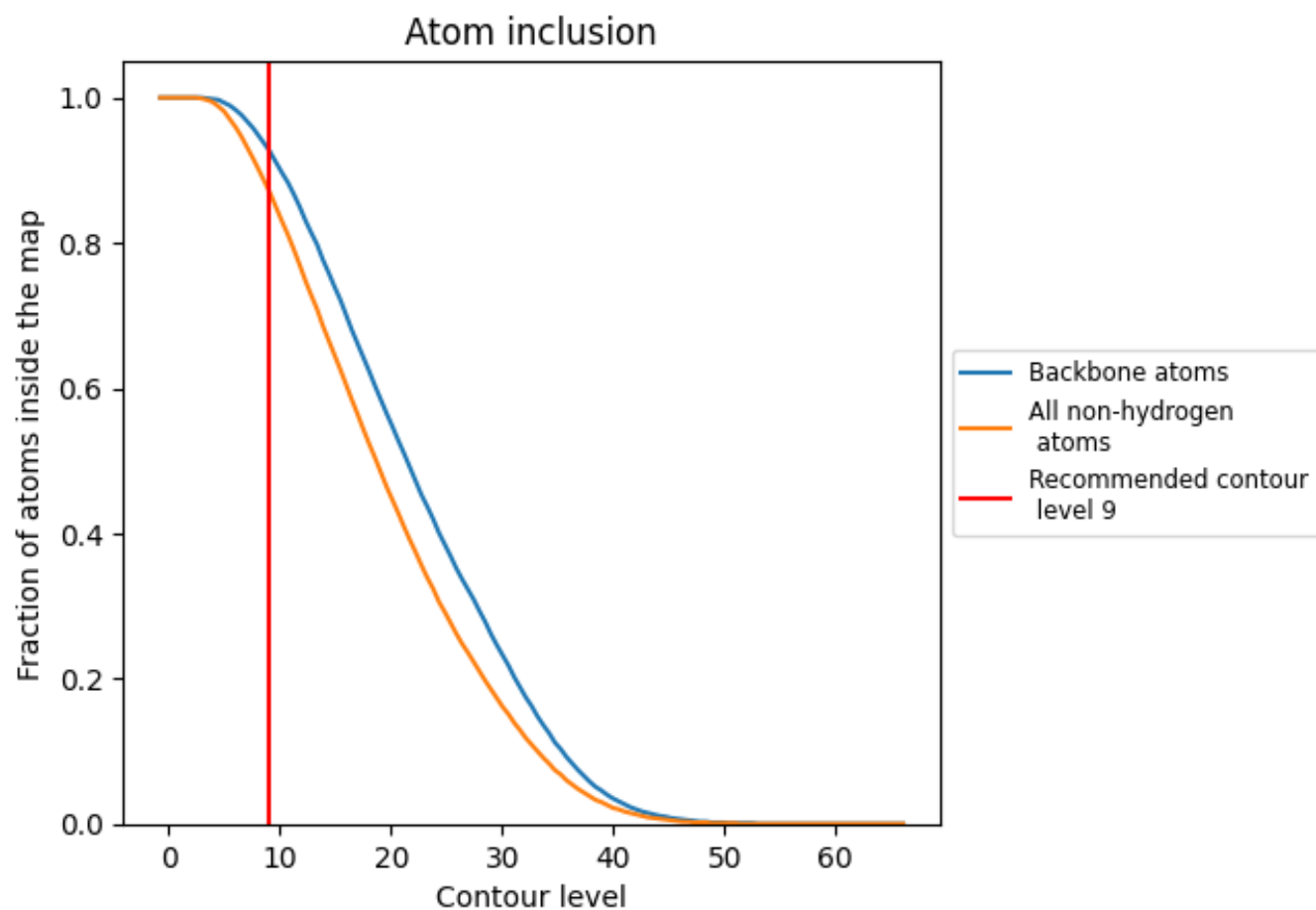
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 87% 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 (9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8720	0.4820
A	0.8800	0.4750
B	0.8940	0.5110
C	0.8690	0.4920
D	0.8380	0.4220
W	0.8810	0.5090
X	0.8440	0.4650
Y	0.9080	0.5500
Z	0.8990	0.5420

1.0

0.0

<0.0