



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:36 AM UTC

PDB ID : 5FXG / pdb_00005fxg
EMDB ID : EMD-3352
Title : GLUN1B-GLUN2B NMDA RECEPTOR IN ACTIVE CONFORMATION
Authors : Tajima, N.; Karakas, E.; Grant, T.; Simorowski, N.; Diaz-Avalos, R.; Grigorieff, N.; Furukawa, H.
Deposited on : 2016-03-02
Resolution : 6.80 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

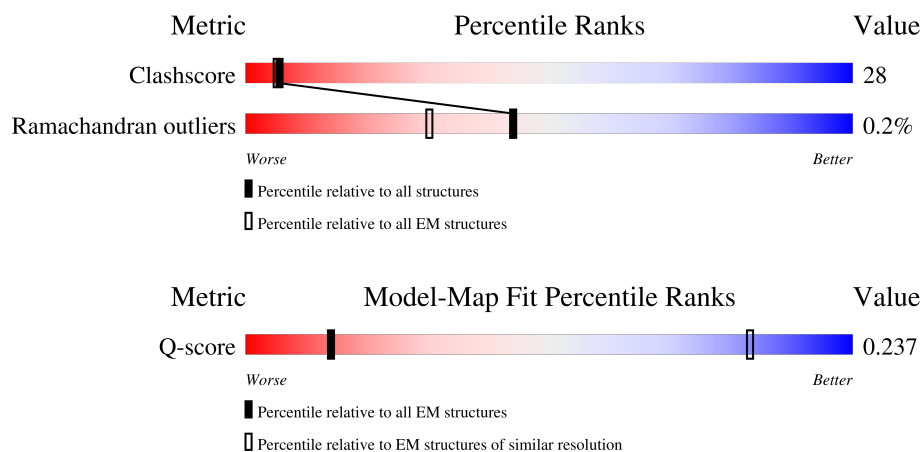
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.80 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	-
Q-score	-	25397	503 (6.30 - 7.30)

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	846	52% 24% 23%
1	C	846	52% 25% 23%
2	B	827	52% 25% 23%
2	D	827	52% 24% 23%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12648 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 N-METHYL-D-ASPARTATE RECEPTOR GLUN1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	648	Total	C	N	O	0	0
			3199	1903	648	648		
1	C	648	Total	C	N	O	0	0
			3199	1903	648	648		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	GLN	ASN	engineered mutation	UNP P35439
A	260	ASP	ASN	engineered mutation	UNP P35439
A	371	GLN	ASN	engineered mutation	UNP P35439
A	492	GLN	ASN	engineered mutation	UNP P35439
A	512	GLN	ASN	engineered mutation	UNP P35439
A	615	GLN	GLU	engineered mutation	UNP P35439
A	616	SER	GLU	engineered mutation	UNP P35439
A	618	SER	GLU	engineered mutation	UNP P35439
A	619	THR	GLU	engineered mutation	UNP P35439
A	792	GLN	ASN	engineered mutation	UNP P35439
A	831	CYS	PHE	engineered mutation	UNP P35439
A	865	ASN	ARG	engineered mutation	UNP P35439
A	866	GLY	ARG	engineered mutation	UNP P35439
A	867	ALA	LYS	engineered mutation	UNP P35439
C	61	GLN	ASN	engineered mutation	UNP P35439
C	260	ASP	ASN	engineered mutation	UNP P35439
C	371	GLN	ASN	engineered mutation	UNP P35439
C	492	GLN	ASN	engineered mutation	UNP P35439
C	512	GLN	ASN	engineered mutation	UNP P35439
C	615	GLN	GLU	engineered mutation	UNP P35439
C	616	SER	GLU	engineered mutation	UNP P35439
C	618	SER	GLU	engineered mutation	UNP P35439
C	619	THR	GLU	engineered mutation	UNP P35439
C	792	GLN	ASN	engineered mutation	UNP P35439
C	831	CYS	PHE	engineered mutation	UNP P35439
C	865	ASN	ARG	engineered mutation	UNP P35439

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Chain	Residue	Modelled	Actual	Comment	Reference
C	866	GLY	ARG	engineered mutation	UNP P35439
C	867	ALA	LYS	engineered mutation	UNP P35439

- Molecule 2 is a protein called N-METHYL-D-ASPARTATE RECEPTOR GLUN2B.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	634	Total 3125	C 1857	N 634	O 634	0	0
2	D	634	Total 3125	C 1857	N 634	O 634	0	0

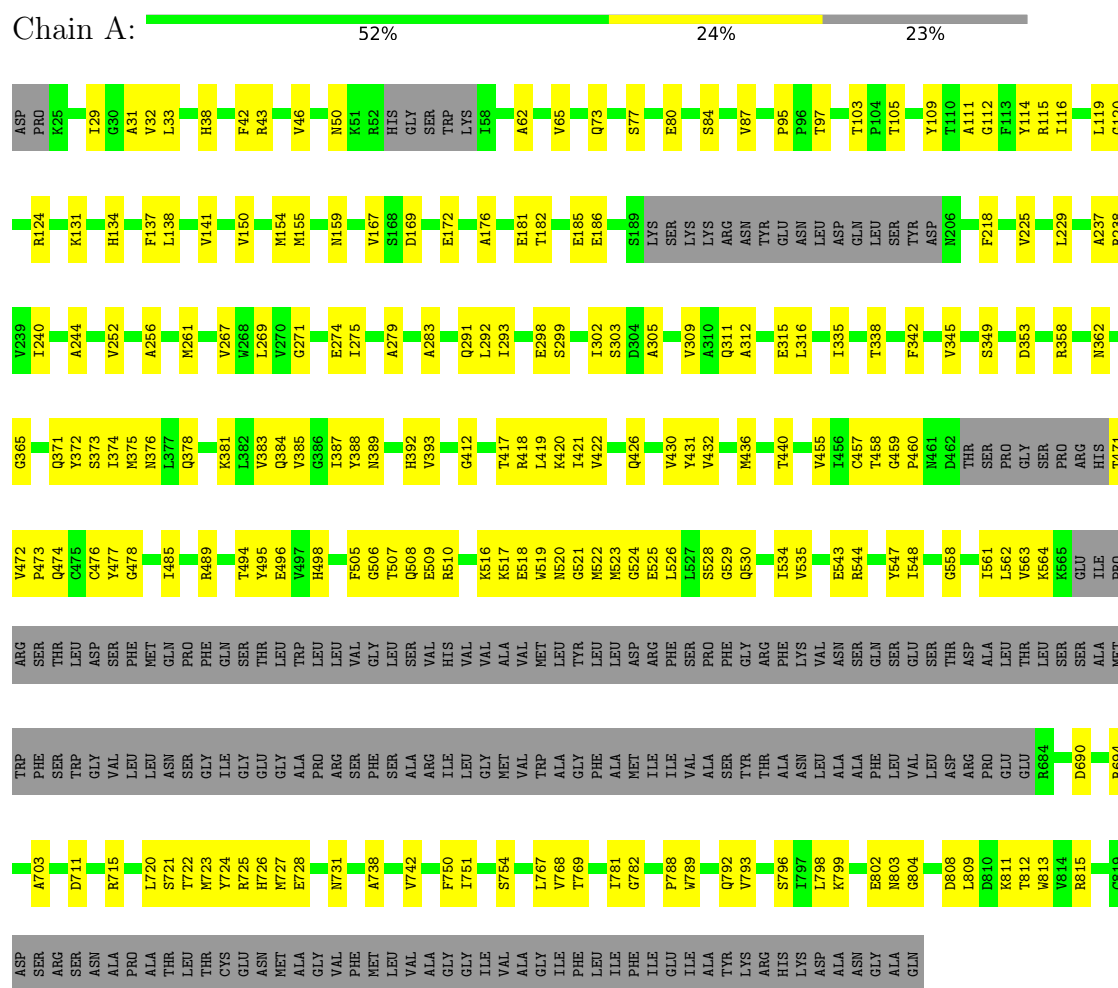
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	26	GLY	-	expression tag	UNP Q00960
B	348	ASP	ASN	engineered mutation	UNP Q00960
B	557	CYS	ASP	engineered mutation	UNP Q00960
B	588	SER	CYS	engineered mutation	UNP Q00960
B	838	SER	CYS	engineered mutation	UNP Q00960
B	849	SER	CYS	engineered mutation	UNP Q00960
D	26	GLY	-	expression tag	UNP Q00960
D	348	ASP	ASN	engineered mutation	UNP Q00960
D	557	CYS	ASP	engineered mutation	UNP Q00960
D	588	SER	CYS	engineered mutation	UNP Q00960
D	838	SER	CYS	engineered mutation	UNP Q00960
D	849	SER	CYS	engineered mutation	UNP Q00960

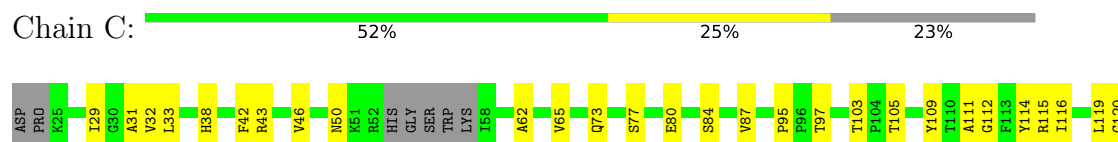
3 Residue-property plots

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: N-METHYL-D-ASPARTATE RECEPTOR GLUN1



• Molecule 1: N-METHYL-D-ASPARTATE RECEPTOR GLUN1





TRP	LEU	C457	K377	I228	T121	GLY
	LEU	K458	K378	I229	P122	ARG
	ALA	C461	K379	L230	I123	SER
	PHE		K380	Y231	L124	GLN
	LEU	I464	S383	A237	G125	LYS
	GLU		K384	A238	I126	SER
	PRO	I468			F241	H127
	PHE	S469	G128	G128	G36	
	ASN	A473	K391	A244	I37	ASN
	ALA		P392	S130	A38	
	SER	D477	K393	G248	S141	V39
	VAL		K394	T255	M142	V39
	PRO	VAL	C395	P259	F143	L41
	GLN	VAL	PRO		F144	L41
	MET	VAL	Y479	GLU	D52	
	ASN	MET	H486	THR	G147	
	PHE	PHE		K487	F148	K66
	LYS	VAL	K488	GLU	S149	
	GLY	THR	K489	GLU	F59	
	THR	LEU	I494	ASP	Q153	V64
SER	ILE	ASP		L277	V65	
LYS	VAL	K495	D404	I160		
ILE	SER	K496	D404	M161		
MET	ALA	K497	I408	V71		
VAL	VAL	I498	V409	A72		
SER	ALA	K499	G499	M73		
VAL	VAL	E500	E413			
TRP	PHE	V501	V501	F169	I81	
ALA	VAL	V502	F416	S170	I82	
PHE	PHE	M503	V417	I171	R83	
PHE	GLU	K504	K504	V172	R84	
ALA	ALA	R505	L418	T173	I85	
VAL	PHE	A506	D423	T174	C86	
ILE	SER	Y507	D427	Y175	D87	
PHE	PRO	M508		L339	L88	
LEU	VAL	A509	I340	Q180		
ALA	GLY	M516	V434	D181	D91	
SER	TYR		P435	F182		
ASN	ASN	C436	V183	I94		
THR	ARG	K437	L349	M184	O95	
ALA	SER	K438	S352	K185	G96	
ASN	LEU	R439		I186		
LEU	ALA	D524	ILE	N192	A100	
ALA	ASP	F529	SER	D101	D102	
PHE	ARG	I534	GLU	L199		
MET	GLU		ASN	E200	I108	
ILE	PRO	S536	LYS	E201	A109	
GLN	GLY	V536	THR	V202	Q110	
GLY	GLY	M537	ASP	I364	I111	
PRO	PRO	V538	GLU	L204	L112	
SER	SER	S539	GLU	L205	D113	
PHE	PHE	R540	PRO	L367	F114	
THR	THR	SER	GLY	N368	I115	
ILE	ILE	ASN	V452		S116	
GLY	GLY	THR	I453	K372	A117	
LYS	LYS	VAL	K454	W373	Q118	
ALA	ALA	VAL	K455	E374	A177	
ILE	ILE	SER	C456	P226	T119	
				F257	I120	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	12000	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	38168	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.021	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	335.36, 335.36, 335.36	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.31, 1.31, 1.31	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	0.20	0/3194	0.45	0/4439
1	C	0.20	0/3194	0.45	0/4439
2	B	0.20	0/3121	0.41	0/4336
2	D	0.20	0/3121	0.41	0/4336
All	All	0.20	0/12630	0.43	0/17550

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	3199	0	1427	126	0
1	C	3199	0	1427	130	0
2	B	3125	0	1379	125	0
2	D	3125	0	1379	124	0
All	All	12648	0	5612	503	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 28.

The worst 5 of 503 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:B:736:LEU:O	2:B:740:ALA:HB2	1.55	1.06
2:D:736:LEU:O	2:D:740:ALA:HB2	1.55	1.04
1:A:388:TYR:HA	1:A:393:VAL:HA	1.57	0.87
1:C:388:TYR:HA	1:C:393:VAL:HA	1.57	0.86
2:B:343:THR:HA	2:B:349:LEU:H	1.42	0.83

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	638/846 (75%)	563 (88%)	75 (12%)	0	100	100
1	C	638/846 (75%)	563 (88%)	75 (12%)	0	100	100
2	B	626/827 (76%)	554 (88%)	69 (11%)	3 (0%)	24	63
2	D	626/827 (76%)	554 (88%)	69 (11%)	3 (0%)	24	63
All	All	2528/3346 (76%)	2234 (88%)	288 (11%)	6 (0%)	44	78

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	660	VAL
2	D	660	VAL
2	B	523	VAL
2	D	523	VAL
2	B	468	ILE

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

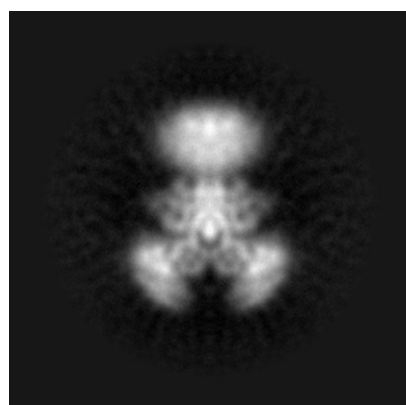
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3352. These allow visual inspection of the internal detail of the map and identification of artifacts.

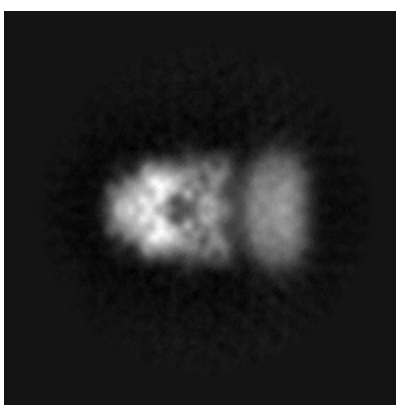
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

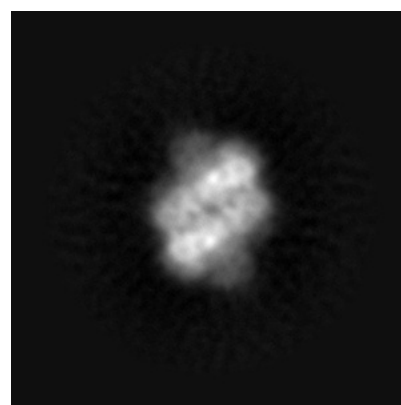
6.1.1 Primary map



X



Y

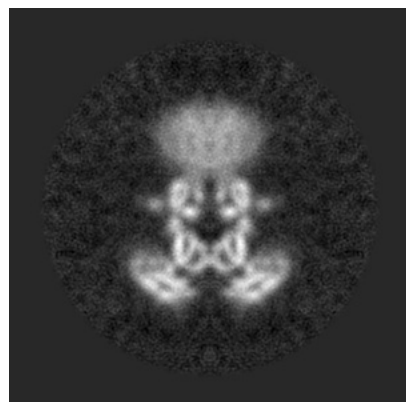


Z

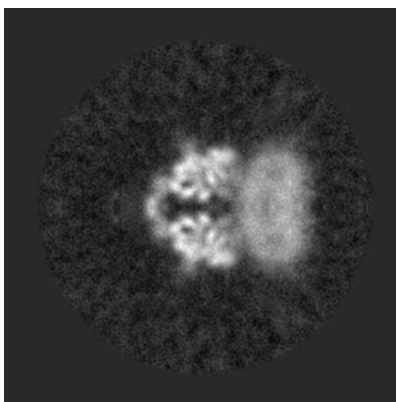
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

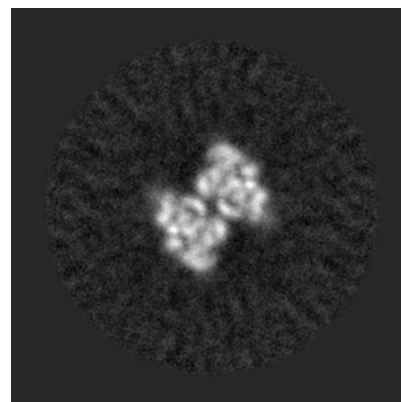
6.2.1 Primary map



X Index: 128



Y Index: 128

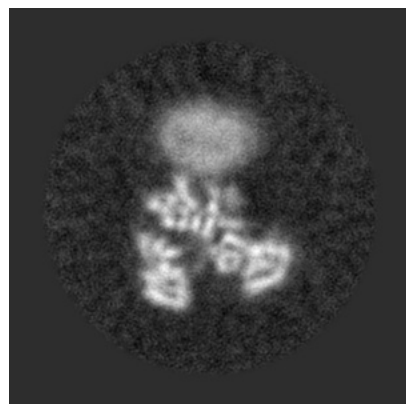


Z Index: 128

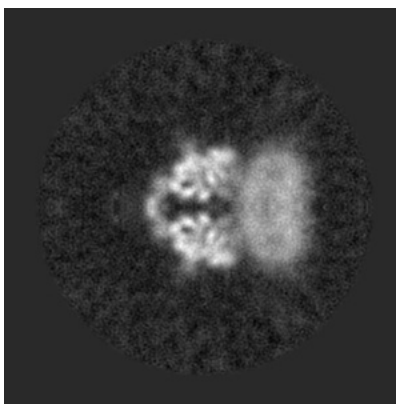
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

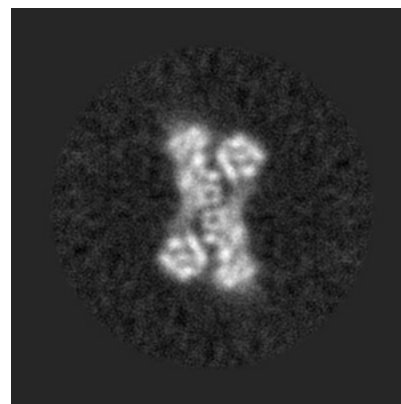
6.3.1 Primary map



X Index: 118



Y Index: 128

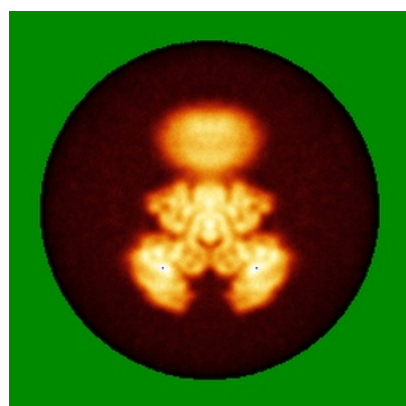


Z Index: 99

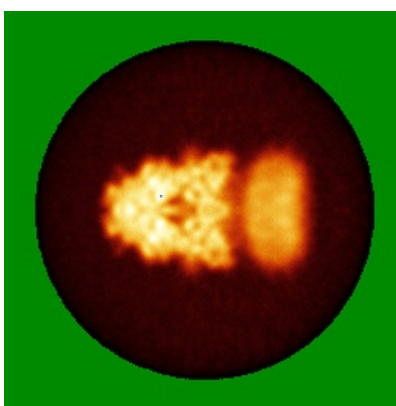
The images above show the largest variance slices of the map in three orthogonal directions.

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

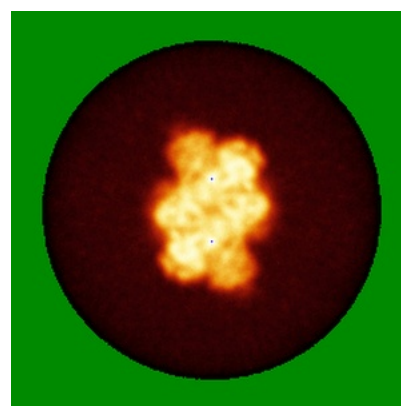
6.4.1 Primary map



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

This section was not generated.

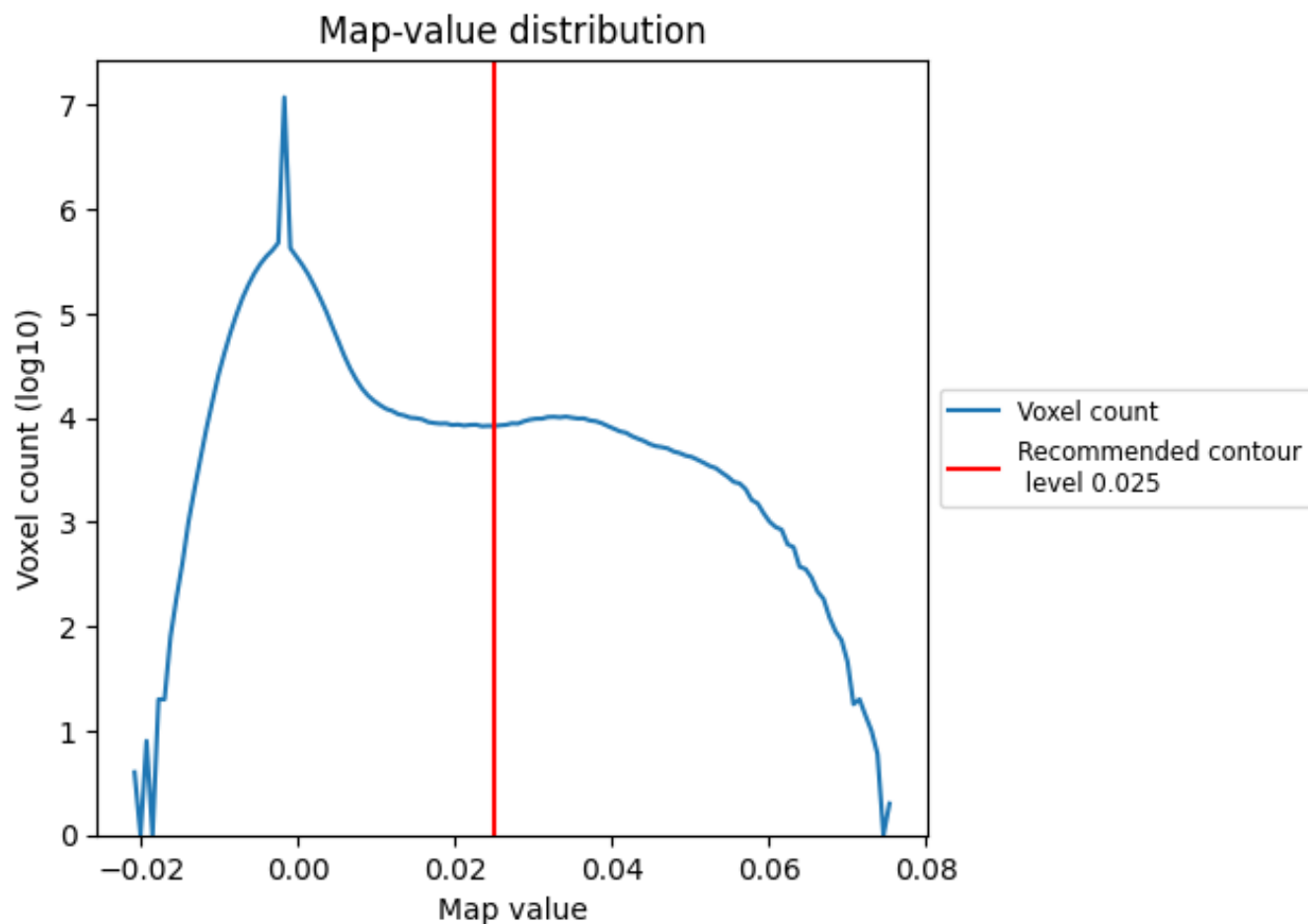
6.6 Mask visualisation

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

7 Map analysis [i](#)

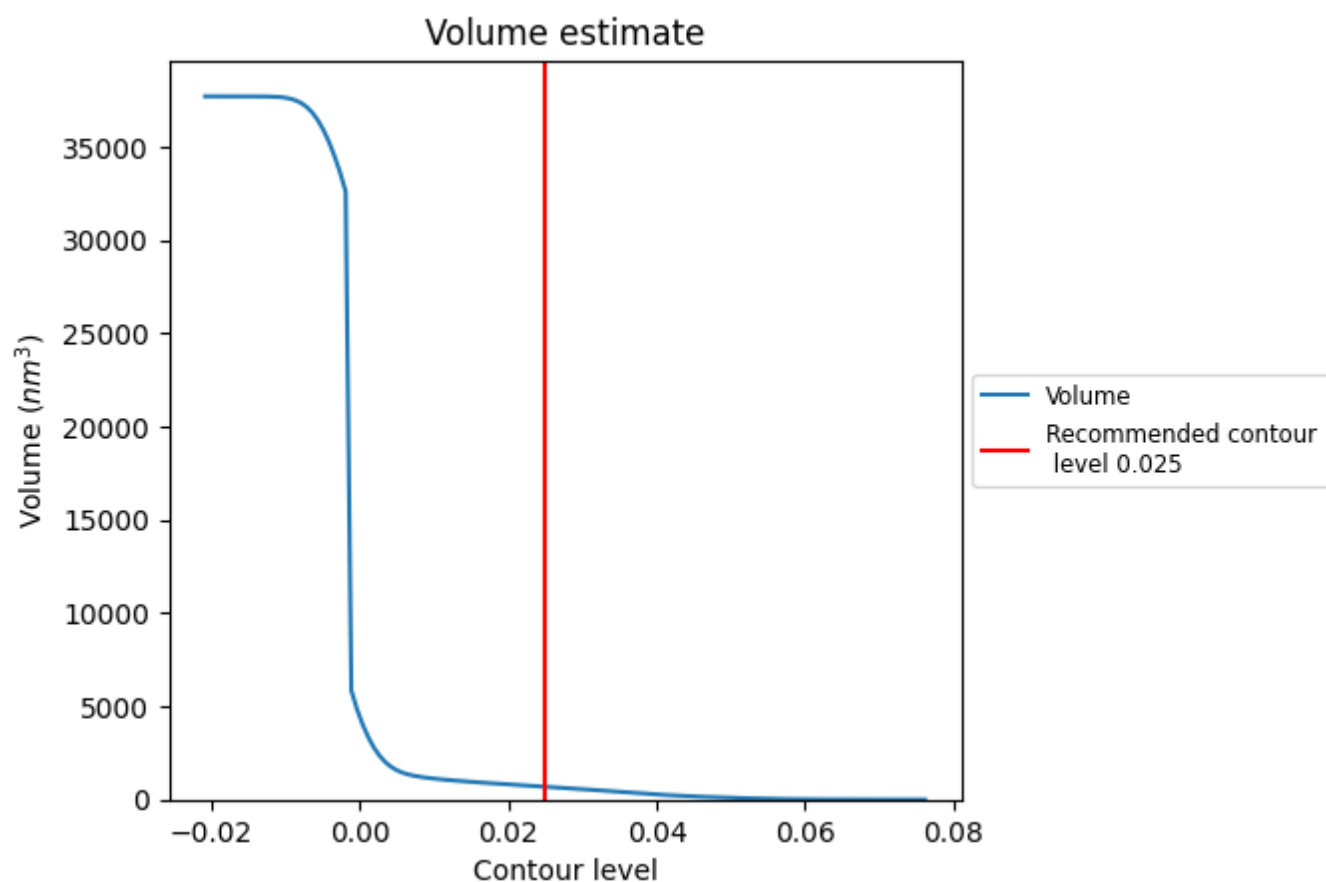
This section contains the results of statistical analysis of the map.

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.

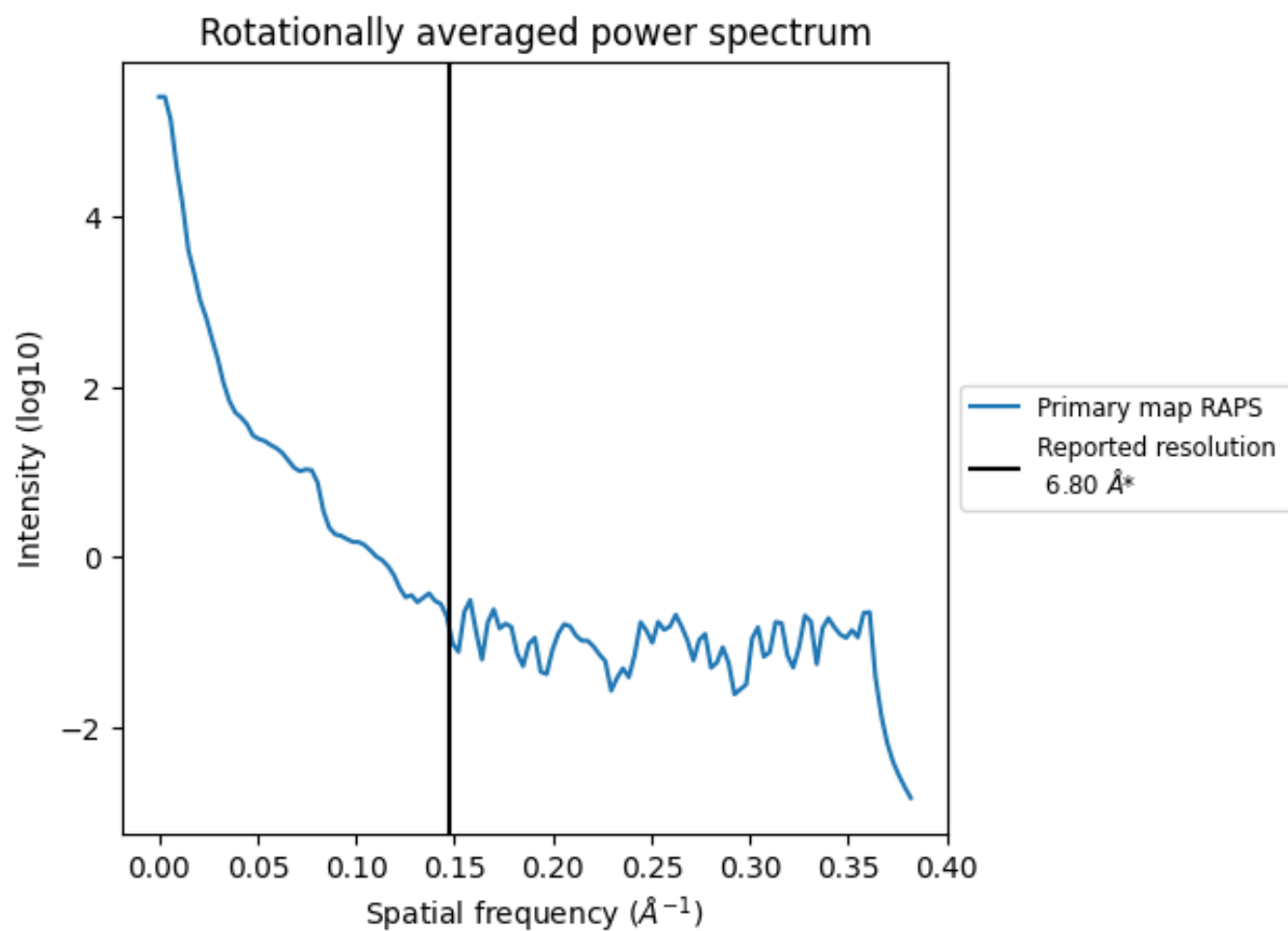
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 690 nm³; this corresponds to an approximate mass of 623 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 0.147 Å⁻¹

8 Fourier-Shell correlation

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

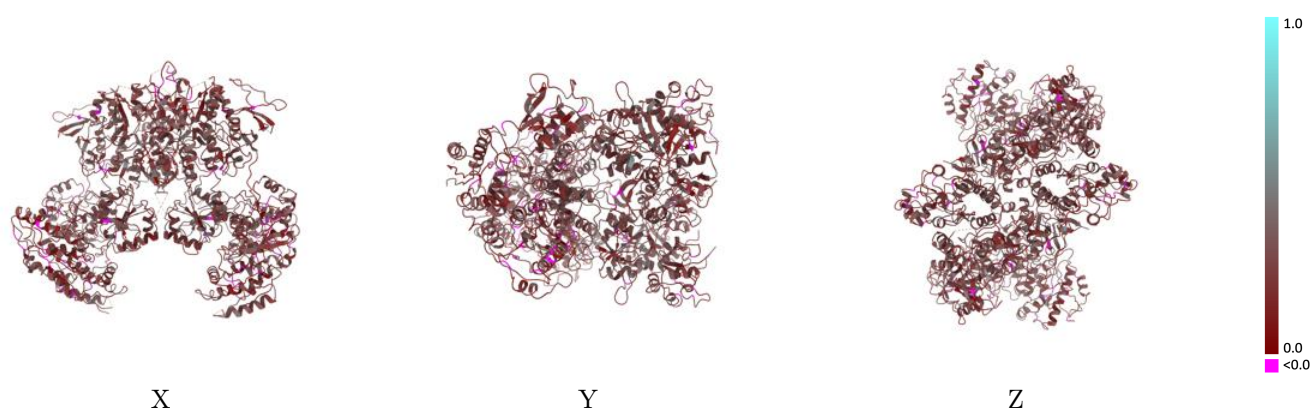
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3352 and PDB model 5FXG. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

This section was not generated.

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

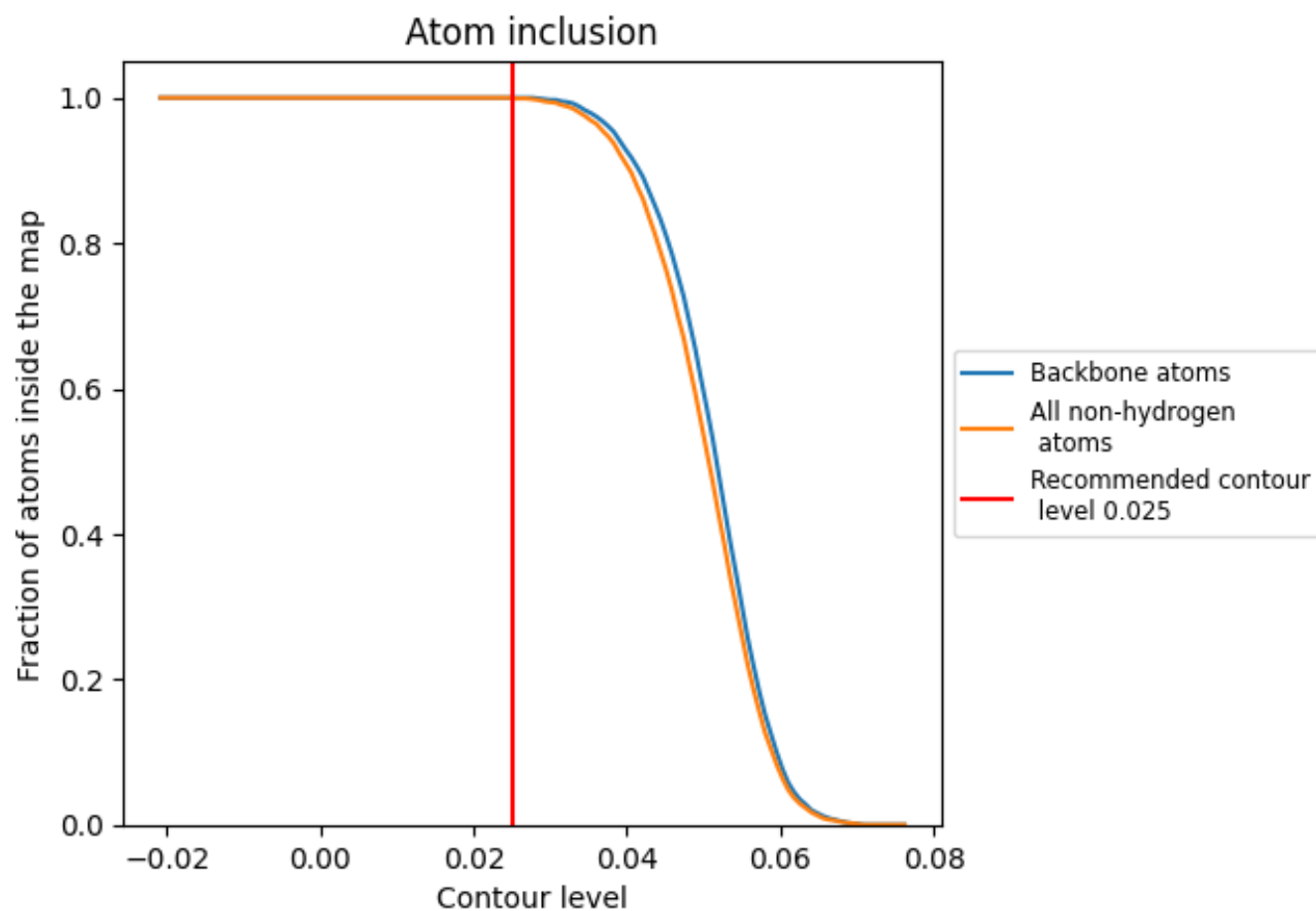


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	1.0000	0.2370
A	1.0000	0.2370
B	1.0000	0.2370
C	1.0000	0.2370
D	1.0000	0.2380

