



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:52 PM UTC

PDB ID : 7WY5 / pdb_00007wy5
EMDB ID : EMD-32884
Title : ADGRL3/Gq complex
Authors : He, Y.; Qian, Y.
Deposited on : 2022-02-15
Resolution : 2.83 Å(reported)
Based on initial model : 6VMS

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

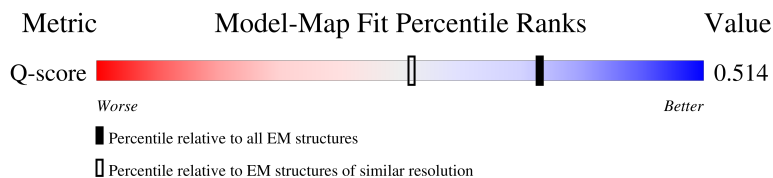
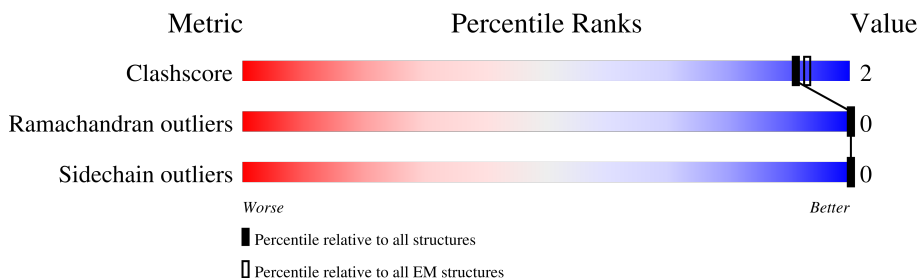
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.83 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	11847 (2.33 - 3.33)

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	362	 62% 37%
2	B	345	 94%
3	G	71	 11% 79% 20%
4	N	161	 73% 7% 20%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	R	1543	16% 83%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8009 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 engineered mini G alpha q subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	228	Total	C	N	O	S	0	0
			1877	1186	334	349	8		

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	338	Total	C	N	O	S	0	0
			2600	1604	467	508	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	initiating methionine	UNP P62873
B	-3	GLY	-	expression tag	UNP P62873
B	-2	SER	-	expression tag	UNP P62873
B	-1	LEU	-	expression tag	UNP P62873
B	0	LEU	-	expression tag	UNP P62873
B	1	GLN	-	expression tag	UNP P62873

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	57	Total	C	N	O	S	0	0
			436	273	77	83	3		

- Molecule 4 is a protein called NB35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	128	Total	C	N	O	S	0	0
			973	605	170	192	6		

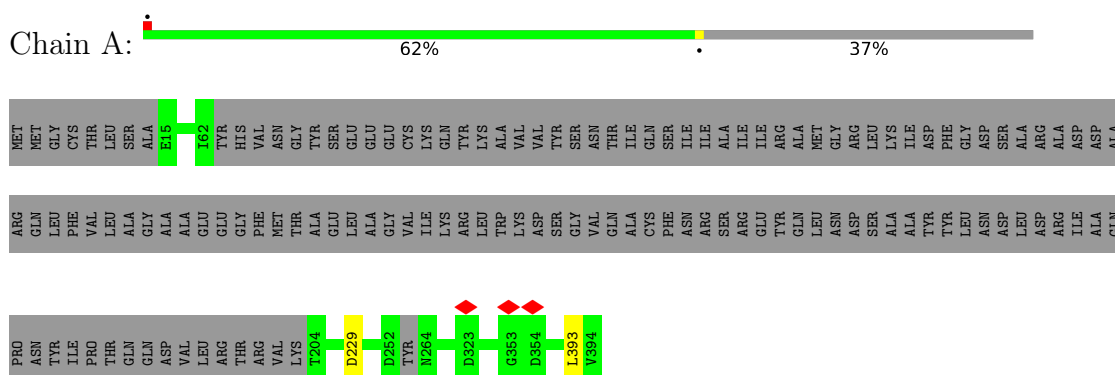
- Molecule 5 is a protein called Isoform 3 of Adhesion G protein-coupled receptor L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	R	262	2123	1429	334	342	18	0	0

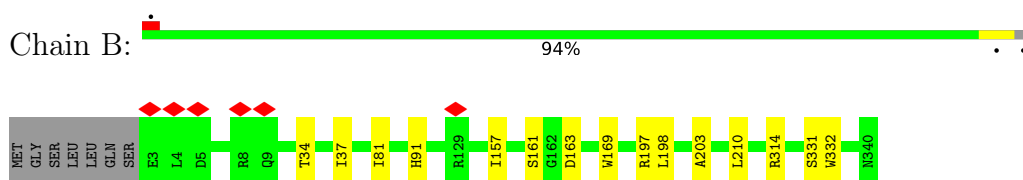
3 Residue-property plots [i](#)

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.

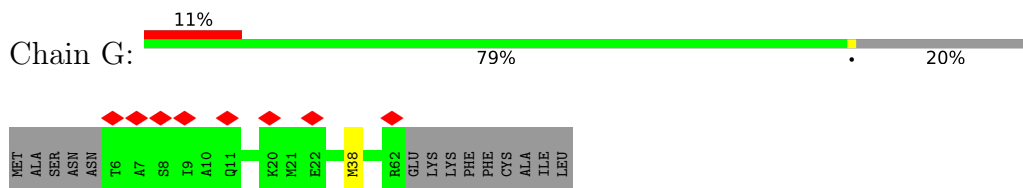
- Molecule 1: engineered mini G alpha q subunit



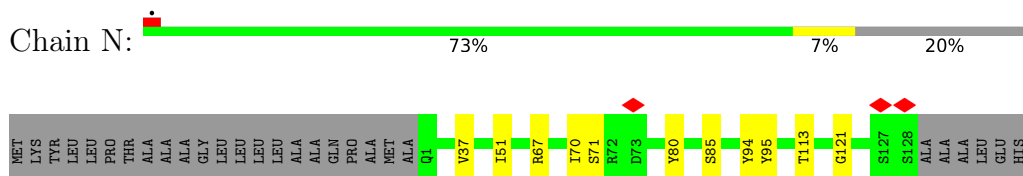
- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



- Molecule 4: NB35



- Molecule 5: Isoform 3 of Adhesion G protein-coupled receptor L3

83%



MET	PHE	GLU	SER
PRO	PHE	ASP	ASN
ASN	PRO	ASP	CYS
LEU	LEU	ALA	VAL
GLY	THR	ILE	GLN
SER	ASP	VAL	ILE
ARG	ASP	LEU	ILE
ASN	GLU	ASP	ASP
HIS	HIS	ASP	ARG
VAL	THR	ALA	GLY
HIS	GLU	ALA	TYR
PRO	ASP	SER	ASN
LEU	LEU	PHE	HIS
HIS	GLN	ASN	ASN
ALA	SER	HIS	GLU
TYR	PRO	GLU	THR
TYR	HIS	GLU	ALA
GLN	ARG	SER	LEU
LEU	ASP	LEU	GLU
GLY	SER	GLY	LYS
ARG	LEU	LEU	LYS
GLY	TYR	GLU	ILE
SER	THR	LEU	LEU
SER	SER	ILE	LYS
ASP	MET	HIS	GLU
GLY	PRO	GLU	LEU
PHE	ALA	GLU	THR
ILE	LEU	SER	SER
VAL	ALA	ASP	ASN
VAL	GLY	ALA	TYR
PRO	VAL	ALA	ILE
PRO	VAL	PRO	PRO
ASN	PRO	LEU	LEU
LYS	ALA	LEU	SER
ASP	ALA	PRO	TYR
GLY	ASP	PRO	LEU
ALA	SER	ARG	ASN
SER	VAL	VAL	ASN
PRO	THR	TYR	HIS
GLU	THR	SER	GLU
GLY	SER	THR	ARG
THR	THR	ASP	SER
SER	GLN	ASN	SER
LYS	THR	HIS	GLU
PRO	GLU	GLN	GLN
PRO	ALA	PRO	ASN
HIS	ALA	HIS	ARG
LEU	ALA	TYR	ASN
VAL	ALA	THR	MET
THR	LYS	SER	MET
SER	GLY	ARG	ASN
LEU	ASP	ARG	LYS
	ALA	ARG	LEU
	GLU	PHE	VAL
	ASP	PRO	ASN
	VAL	GLN	ASN
	VAL	ASP	LEU
	TYR	HIS	GLY
	TYR	SER	SER
	LYS	GLU	GLY
	SER	SER	SER

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	370000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.947	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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	0.22	0/1909	0.40	0/2567
2	B	0.25	0/2647	0.50	1/3589 (0.0%)
3	G	0.17	0/442	0.29	0/597
4	N	0.22	0/993	0.53	0/1345
5	R	0.24	0/2181	0.46	1/2960 (0.0%)
All	All	0.23	0/8172	0.46	2/11058 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	203	ALA	N-CA-C	6.02	117.51	110.41
5	R	1165	ILE	N-CA-C	5.55	116.00	111.62

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	1877	0	1874	2	0
2	B	2600	0	2505	9	0
3	G	436	0	448	1	0
4	N	973	0	942	6	0
5	R	2123	0	2172	10	0
All	All	8009	0	7941	25	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 2.

The worst 5 of 25 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)
5:R:1076:THR:OG1	5:R:1079:VAL:O	1.99	0.81
4:N:67:ARG:NH1	4:N:85:SER:O	2.18	0.76
2:B:34:THR:HB	2:B:37:ILE:HD12	1.71	0.71
5:R:1076:THR:HG22	5:R:1083:ARG:HG2	1.75	0.68
4:N:71:SER:HB3	4:N:80:TYR:HB2	1.81	0.62

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	222/362 (61%)	215 (97%)	7 (3%)	0	100	100
2	B	336/345 (97%)	319 (95%)	17 (5%)	0	100	100
3	G	55/71 (78%)	53 (96%)	2 (4%)	0	100	100
4	N	126/161 (78%)	118 (94%)	8 (6%)	0	100	100
5	R	258/1543 (17%)	238 (92%)	20 (8%)	0	100	100
All	All	997/2482 (40%)	943 (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	A	207/317 (65%)	207 (100%)	0	100	100
2	B	281/287 (98%)	281 (100%)	0	100	100
3	G	46/58 (79%)	46 (100%)	0	100	100
4	N	106/128 (83%)	106 (100%)	0	100	100
5	R	228/1331 (17%)	228 (100%)	0	100	100
All	All	868/2121 (41%)	868 (100%)	0	100	100

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

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

Mol	Chain	Res	Type
5	R	978	ASN
5	R	1191	HIS
2	B	156	GLN
3	G	44	HIS
4	N	31	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

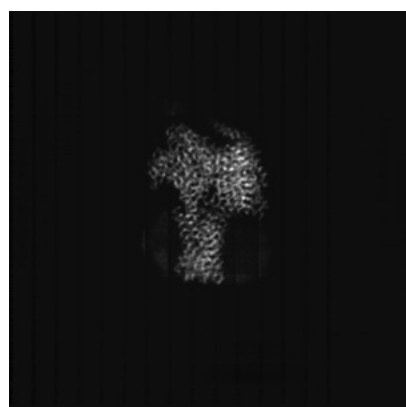
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32884. These allow visual inspection of the internal detail of the map and identification of artifacts.

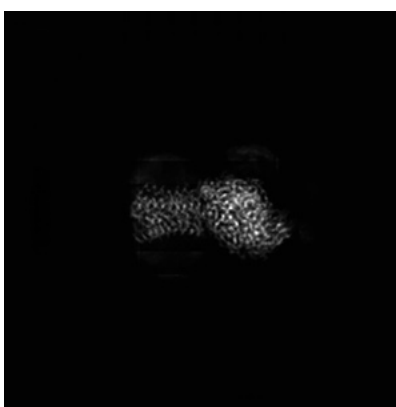
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

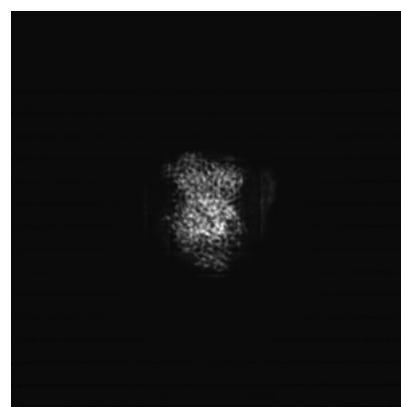
6.1.1 Primary map



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

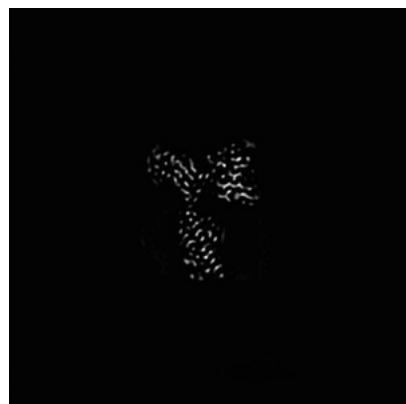


Z Index: 128

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: 133



Y Index: 115



Z Index: 147

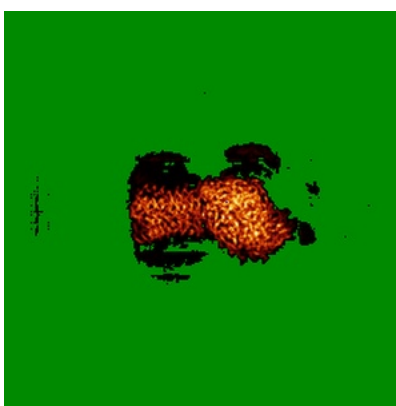
The images above show the largest variance slices of the map in three orthogonal directions.

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

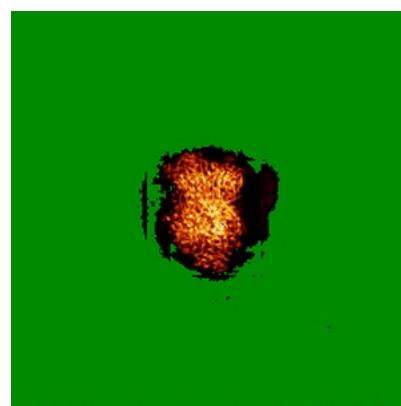
6.4.1 Primary map



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.

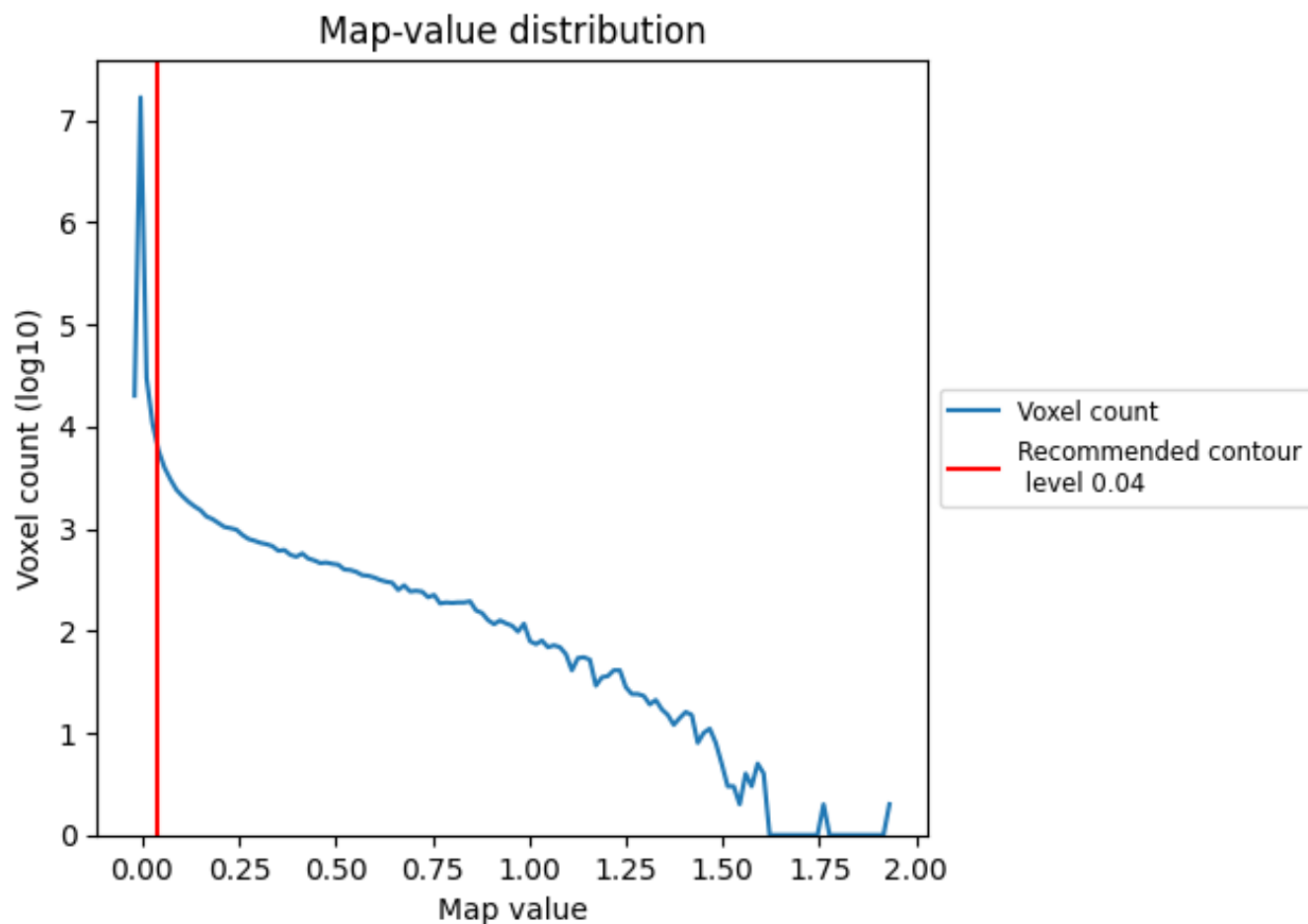
6.6 Mask visualisation

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

7 Map analysis [i](#)

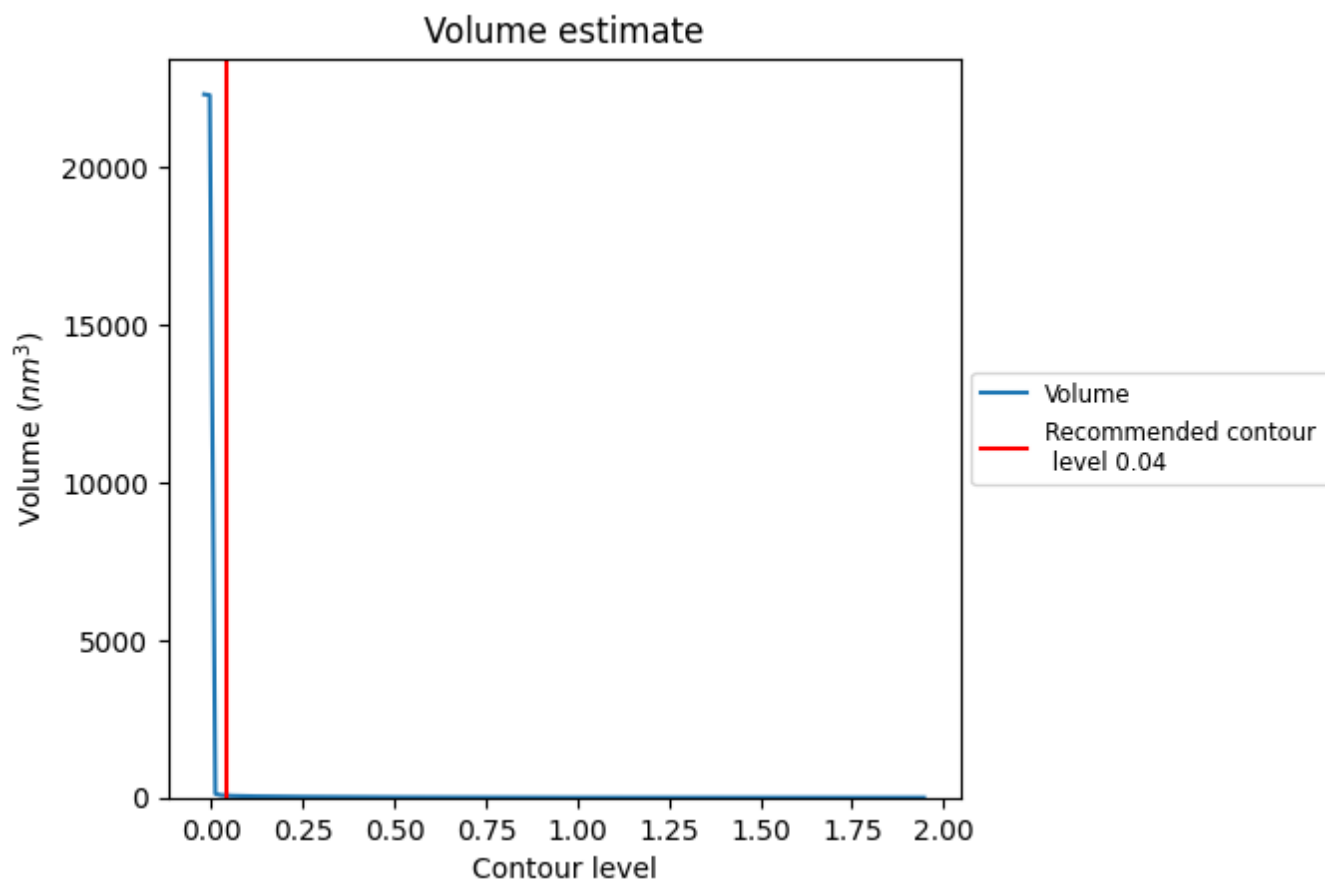
This section contains the results of statistical analysis of the map.

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.

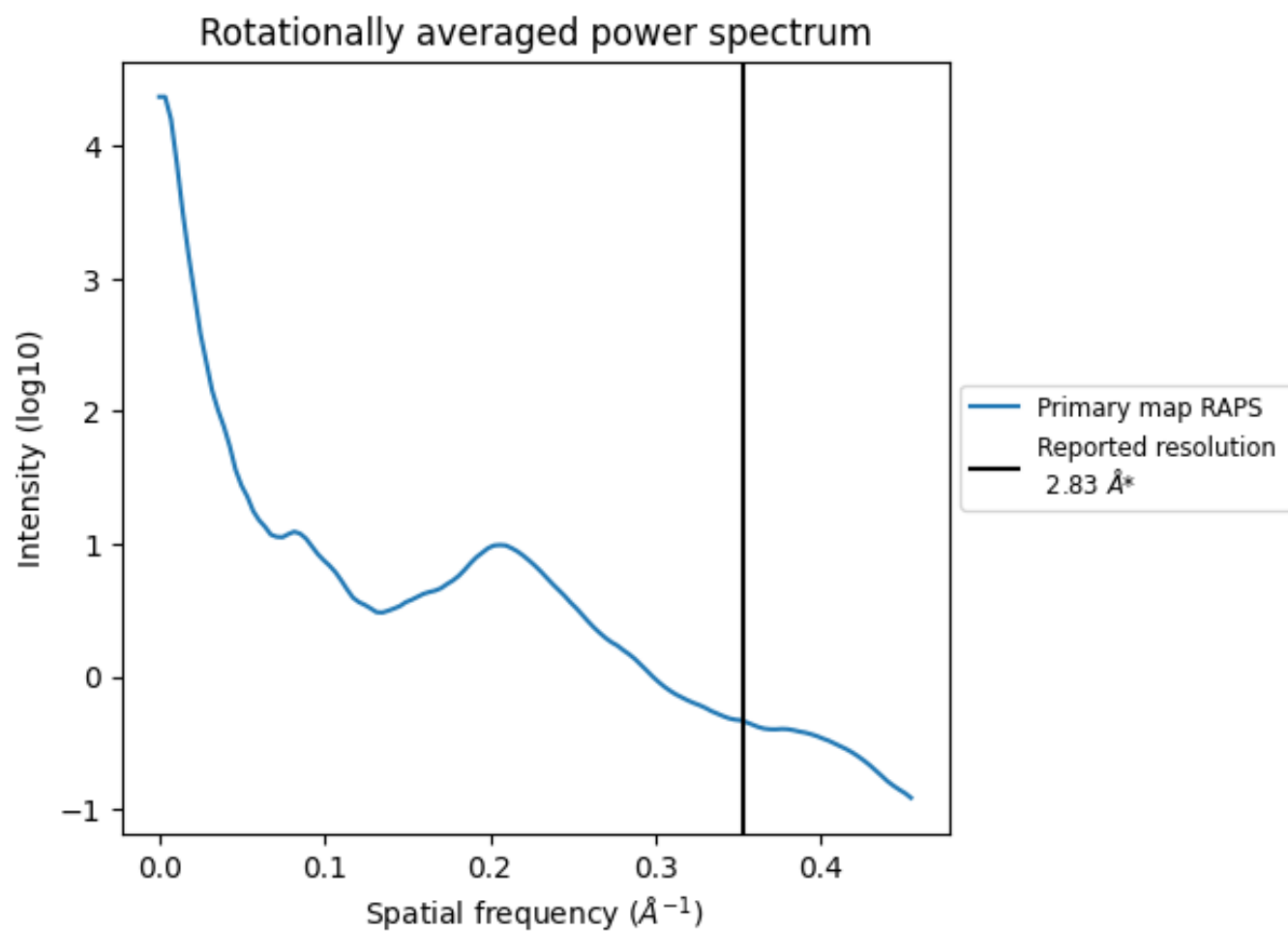
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 65 nm^3 ; this corresponds to an approximate mass of 58 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 ⓘ

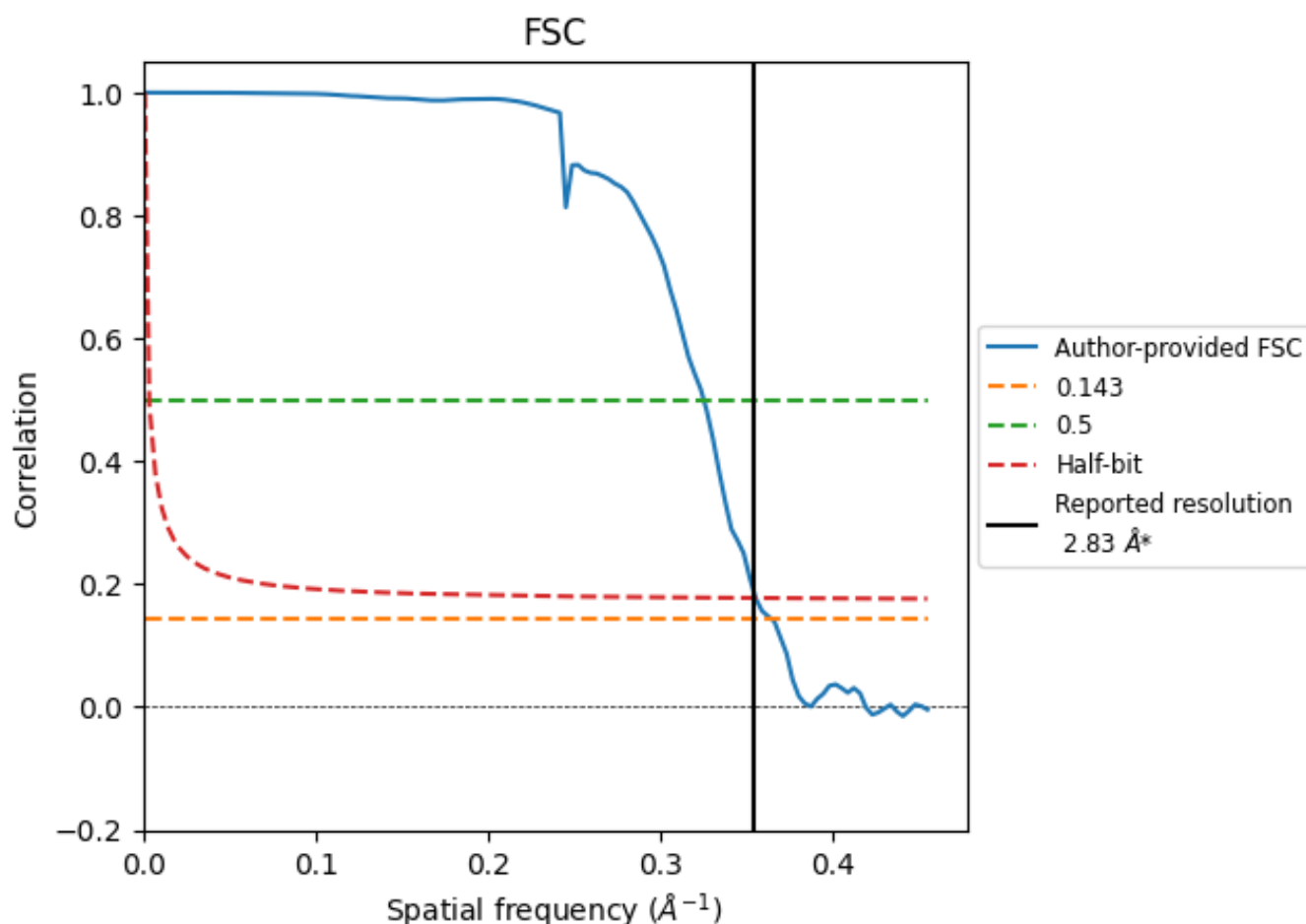


*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.353 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.83	-	-
Author-provided FSC curve	2.75	3.08	2.82
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32884 and PDB model 7WY5. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)

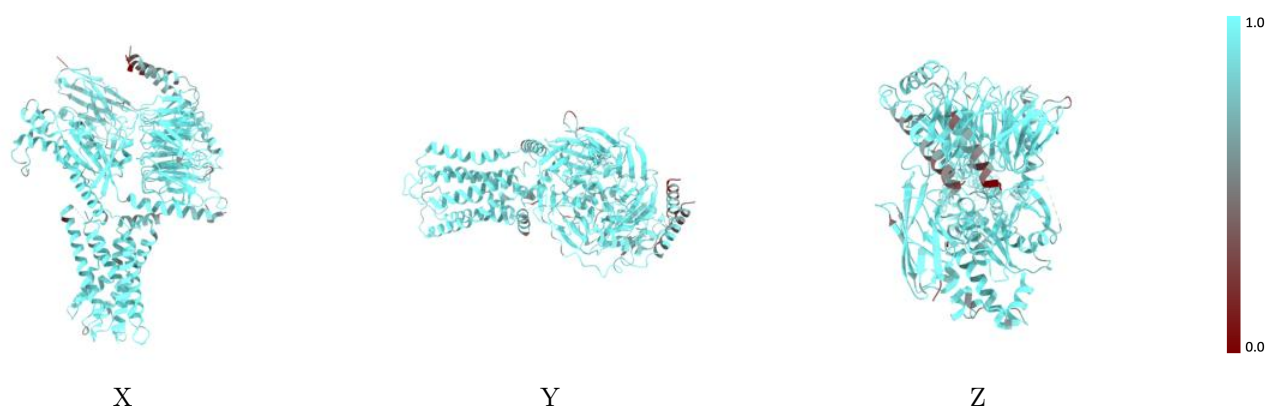
This section was not generated.

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



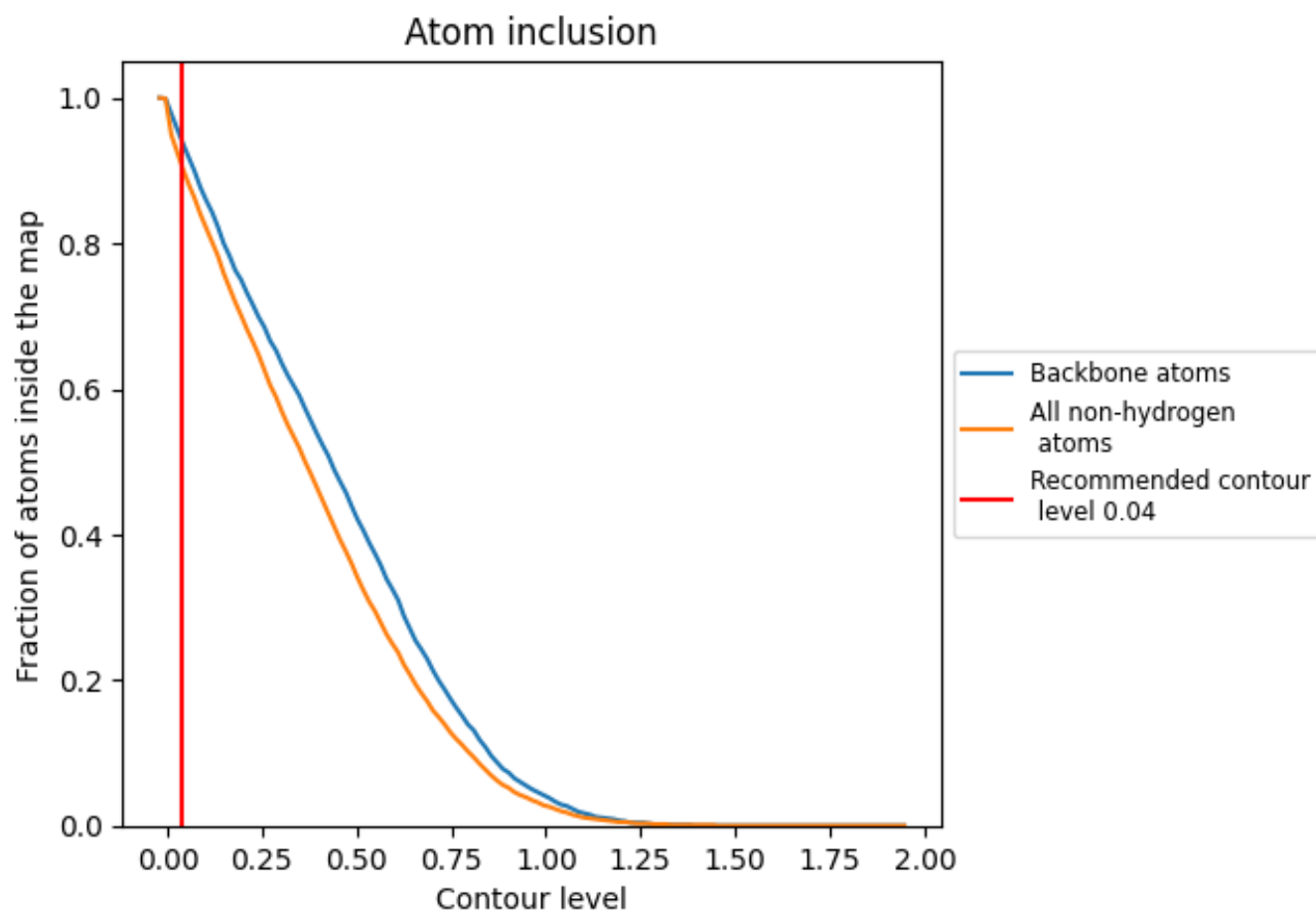
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9040	0.5140
A	0.9090	0.5240
B	0.9240	0.5430
G	0.7200	0.3750
N	0.8920	0.4780
R	0.9200	0.5150

