



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:57 AM UTC

PDB ID : 9QXL / pdb_00009qxl
EMDB ID : EMD-53437
Title : The structure of ADGRL4 in the active-state
Authors : Chen, Q.; Favara, D.M.
Deposited on : 2025-04-15
Resolution : 3.14 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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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

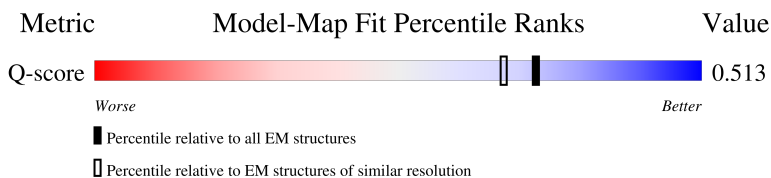
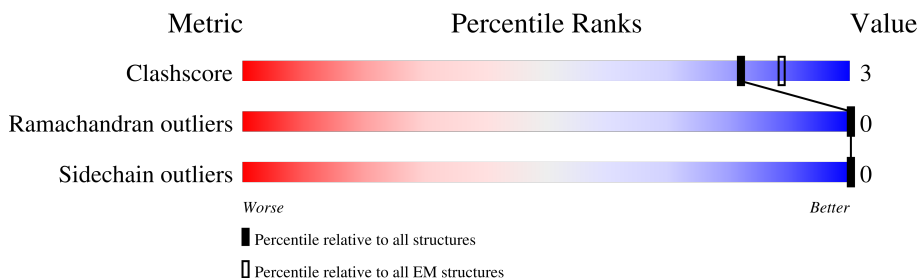
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.14 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	14483 (2.64 - 3.64)

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	628	
2	B	268	
3	C	348	
4	E	71	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6947 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 Green fluorescent protein, Adhesion G protein-coupled receptor L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	272	2170	1461	342	353	14	0	0

There are 111 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	MET	-	initiating methionine	UNP P42212
A	64	LYS	-	expression tag	UNP P42212
A	65	ARG	-	expression tag	UNP P42212
A	66	LEU	-	expression tag	UNP P42212
A	67	PRO	-	expression tag	UNP P42212
A	68	LEU	-	expression tag	UNP P42212
A	69	LEU	-	expression tag	UNP P42212
A	70	VAL	-	expression tag	UNP P42212
A	71	VAL	-	expression tag	UNP P42212
A	72	PHE	-	expression tag	UNP P42212
A	73	SER	-	expression tag	UNP P42212
A	74	THR	-	expression tag	UNP P42212
A	75	LEU	-	expression tag	UNP P42212
A	76	LEU	-	expression tag	UNP P42212
A	77	ASN	-	expression tag	UNP P42212
A	78	CYS	-	expression tag	UNP P42212
A	79	SER	-	expression tag	UNP P42212
A	80	TYR	-	expression tag	UNP P42212
A	81	THR	-	expression tag	UNP P42212
A	82	GLN	-	expression tag	UNP P42212
A	83	TYR	-	expression tag	UNP P42212
A	84	PRO	-	expression tag	UNP P42212
A	85	TYR	-	expression tag	UNP P42212
A	86	ASP	-	expression tag	UNP P42212
A	87	VAL	-	expression tag	UNP P42212
A	88	PRO	-	expression tag	UNP P42212
A	89	ASP	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	90	TYR	-	expression tag	UNP P42212
A	91	ALA	-	expression tag	UNP P42212
A	92	GLY	-	expression tag	UNP P42212
A	93	SER	-	expression tag	UNP P42212
A	94	GLY	-	expression tag	UNP P42212
A	95	GLY	-	expression tag	UNP P42212
A	96	SER	-	expression tag	UNP P42212
A	97	ALA	-	expression tag	UNP P42212
A	98	TRP	-	expression tag	UNP P42212
A	99	SER	-	expression tag	UNP P42212
A	100	HIS	-	expression tag	UNP P42212
A	101	PRO	-	expression tag	UNP P42212
A	102	GLN	-	expression tag	UNP P42212
A	103	PHE	-	expression tag	UNP P42212
A	104	GLU	-	expression tag	UNP P42212
A	105	LYS	-	expression tag	UNP P42212
A	106	GLY	-	expression tag	UNP P42212
A	107	GLY	-	expression tag	UNP P42212
A	108	GLY	-	expression tag	UNP P42212
A	109	SER	-	expression tag	UNP P42212
A	110	GLY	-	expression tag	UNP P42212
A	111	GLY	-	expression tag	UNP P42212
A	112	GLY	-	expression tag	UNP P42212
A	113	SER	-	expression tag	UNP P42212
A	114	GLY	-	expression tag	UNP P42212
A	115	GLY	-	expression tag	UNP P42212
A	116	SER	-	expression tag	UNP P42212
A	117	ALA	-	expression tag	UNP P42212
A	118	TRP	-	expression tag	UNP P42212
A	119	SER	-	expression tag	UNP P42212
A	120	HIS	-	expression tag	UNP P42212
A	121	PRO	-	expression tag	UNP P42212
A	122	GLN	-	expression tag	UNP P42212
A	123	PHE	-	expression tag	UNP P42212
A	124	GLU	-	expression tag	UNP P42212
A	125	LYS	-	expression tag	UNP P42212
A	126	GLY	-	expression tag	UNP P42212
A	127	SER	-	expression tag	UNP P42212
A	128	GLY	-	expression tag	UNP P42212
A	129	HIS	-	expression tag	UNP P42212
A	130	HIS	-	expression tag	UNP P42212
A	131	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	132	HIS	-	expression tag	UNP P42212
A	133	HIS	-	expression tag	UNP P42212
A	134	HIS	-	expression tag	UNP P42212
A	135	HIS	-	expression tag	UNP P42212
A	136	HIS	-	expression tag	UNP P42212
A	137	HIS	-	expression tag	UNP P42212
A	138	HIS	-	expression tag	UNP P42212
A	139	GLY	-	expression tag	UNP P42212
A	140	SER	-	expression tag	UNP P42212
A	141	GLY	-	expression tag	UNP P42212
A	142	LEU	-	expression tag	UNP P42212
A	143	GLU	-	expression tag	UNP P42212
A	144	VAL	-	expression tag	UNP P42212
A	145	LEU	-	expression tag	UNP P42212
A	146	PHE	-	expression tag	UNP P42212
A	147	GLN	-	expression tag	UNP P42212
A	148	GLY	-	expression tag	UNP P42212
A	149	PRO	-	expression tag	UNP P42212
A	150	GLY	-	expression tag	UNP P42212
A	151	SER	-	expression tag	UNP P42212
A	152	GLY	-	expression tag	UNP P42212
A	153	VAL	-	expression tag	UNP P42212
A	216	LEU	PHE	conflict	UNP P42212
A	217	THR	SER	conflict	UNP P42212
A	358	LYS	ALA	conflict	UNP P42212
A	383	LEU	HIS	conflict	UNP P42212
A	391	GLY	-	linker	UNP P42212
A	392	SER	-	linker	UNP P42212
A	393	GLY	-	linker	UNP P42212
A	394	GLU	-	linker	UNP P42212
A	395	ASN	-	linker	UNP P42212
A	396	LEU	-	linker	UNP P42212
A	397	TYR	-	linker	UNP P42212
A	398	PHE	-	linker	UNP P42212
A	399	GLN	-	linker	UNP P42212
A	400	SER	-	linker	UNP P42212
A	401	GLY	-	linker	UNP P42212
A	402	SER	-	linker	UNP P42212
A	403	GLY	-	linker	UNP P42212
A	404	GLY	-	linker	UNP P42212
A	405	SER	-	linker	UNP P42212
A	406	GLY	-	linker	UNP P42212

- Molecule 2 is a protein called GNAS complex locus, Guanine nucleotide-binding protein G(s) subunit alpha isoforms short.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	244	Total	C	N	O	S	0	0
			1995	1254	361	373	7		

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	127	GLY	-	expression tag	UNP Q5JWD1
B	128	GLY	-	expression tag	UNP Q5JWD1
B	129	SER	-	expression tag	UNP Q5JWD1
B	130	GLY	-	expression tag	UNP Q5JWD1
B	131	SER	-	expression tag	UNP Q5JWD1
B	132	GLY	-	expression tag	UNP Q5JWD1
B	133	ASP	-	expression tag	UNP Q5JWD1
B	134	TYR	-	expression tag	UNP Q5JWD1
B	135	LYS	-	expression tag	UNP Q5JWD1
B	136	ASP	-	expression tag	UNP Q5JWD1
B	137	ASP	-	expression tag	UNP Q5JWD1
B	138	ASP	-	expression tag	UNP Q5JWD1
B	139	ASP	-	expression tag	UNP Q5JWD1
B	140	LYS	-	expression tag	UNP Q5JWD1
B	141	GLY	-	expression tag	UNP Q5JWD1
B	142	GLY	-	expression tag	UNP Q5JWD1
B	143	SER	-	expression tag	UNP Q5JWD1
B	144	GLY	-	expression tag	UNP Q5JWD1
B	145	SER	-	expression tag	UNP Q5JWD1
B	190	ASP	GLY	conflict	UNP Q5JWD1
B	191	ASN	GLU	conflict	UNP Q5JWD1
B	206	GLY	-	linker	UNP Q5JWD1
B	207	GLY	-	linker	UNP Q5JWD1
B	208	SER	-	linker	UNP Q5JWD1
B	209	GLY	-	linker	UNP Q5JWD1
B	210	GLY	-	linker	UNP Q5JWD1
B	211	SER	-	linker	UNP Q5JWD1
B	212	GLY	-	linker	UNP Q5JWD1
B	213	GLY	-	linker	UNP Q5JWD1
B	259	ASP	ALA	conflict	UNP P63092
B	262	ASP	SER	conflict	UNP P63092
B	?	-	ASN	deletion	UNP P63092
B	?	-	MET	deletion	UNP P63092
B	?	-	VAL	deletion	UNP P63092
B	?	-	ILE	deletion	UNP P63092

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ARG	deletion	UNP P63092
B	?	-	GLU	deletion	UNP P63092
B	?	-	ASP	deletion	UNP P63092
B	?	-	ASN	deletion	UNP P63092
B	?	-	GLN	deletion	UNP P63092
B	?	-	THR	deletion	UNP P63092
B	372	ALA	ILE	conflict	UNP P63092
B	375	ILE	VAL	conflict	UNP P63092
B	380	LYS	ARG	conflict	UNP P63092
B	384	LEU	GLN	conflict	UNP P63092
B	385	GLN	ARG	conflict	UNP P63092
B	387	ASN	HIS	conflict	UNP P63092
B	390	GLU	GLN	conflict	UNP P63092
B	392	ASN	GLU	conflict	UNP P63092
B	394	VAL	LEU	conflict	UNP P63092

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	325	Total	C	N	O	S	0	0
			2489	1537	447	484	21		

There are 9 discrepancies between the modelled and reference sequences:

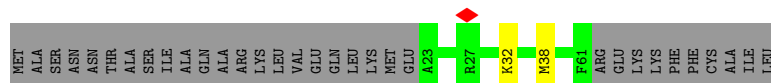
Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	MET	-	initiating methionine	UNP P62873
C	-7	HIS	-	expression tag	UNP P62873
C	-6	HIS	-	expression tag	UNP P62873
C	-5	HIS	-	expression tag	UNP P62873
C	-4	HIS	-	expression tag	UNP P62873
C	-3	HIS	-	expression tag	UNP P62873
C	-2	HIS	-	expression tag	UNP P62873
C	-1	HIS	-	expression tag	UNP P62873
C	0	HIS	-	expression tag	UNP P62873

- Molecule 4 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	39	Total	C	N	O	S	0	0
			293	185	49	57	2		



Chain E: 52% 45%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	339728	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.121	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	268.0, 268.0, 268.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.67, 0.67, 0.67	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	0.25	0/2231	0.55	0/3033
2	B	0.22	0/2033	0.46	0/2735
3	C	0.19	0/2536	0.49	0/3441
4	E	0.19	0/299	0.49	0/407
All	All	0.22	0/7099	0.50	0/9616

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	2170	0	2221	10	0
2	B	1995	0	1967	11	0
3	C	2489	0	2395	19	0
4	E	293	0	290	2	0
All	All	6947	0	6873	35	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 3.

All (35) 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)
3:C:48:ARG:NH1	3:C:49:THR:O	2.34	0.61
3:C:270:CYS:HB3	3:C:289:ASP:HB2	1.86	0.57
2:B:186:LEU:HD21	2:B:194:LYS:HB2	1.87	0.57
1:A:439:LEU:HA	1:A:442:LEU:HB2	1.89	0.55
2:B:242:ARG:HE	2:B:243:LYS:HE2	1.71	0.54
1:A:605:PRO:HD2	2:B:358:TYR:HD2	1.74	0.53
2:B:339:TYR:HD1	2:B:342:ARG:HH21	1.58	0.51
1:A:619:GLY:HA3	2:B:393:LEU:HD23	1.92	0.51
3:C:114:GLY:HA3	3:C:145:LEU:HD23	1.94	0.49
2:B:160:GLN:HG2	3:C:87:ASN:HD22	1.78	0.48
3:C:251:LEU:HD21	4:E:38:MET:HE1	1.95	0.48
2:B:283:ARG:O	2:B:357:HIS:ND1	2.47	0.48
3:C:21:ARG:NH1	3:C:257:ASP:O	2.47	0.47
2:B:190:ASP:HB3	2:B:265:ARG:HH12	1.79	0.47
3:C:94:LEU:HD13	3:C:99:VAL:HG21	1.96	0.47
3:C:27:ALA:O	4:E:32:LYS:NZ	2.47	0.47
1:A:441:CYS:HA	1:A:444:ILE:HB	1.98	0.46
3:C:41:ARG:NH1	3:C:303:ARG:O	2.47	0.46
1:A:569:ASN:O	1:A:572:TRP:HB2	2.16	0.45
3:C:330:SER:OG	3:C:331:TRP:N	2.50	0.45
3:C:47:ARG:HE	3:C:339:ASN:HB3	1.83	0.44
1:A:610:PHE:HE2	1:A:614:ARG:HH21	1.66	0.44
2:B:261:SER:O	2:B:300:LYS:NZ	2.42	0.44
1:A:442:LEU:HD23	1:A:442:LEU:HA	1.89	0.43
3:C:244:SER:OG	3:C:245:ASP:N	2.51	0.43
3:C:223:GLY:O	3:C:250:ARG:NH1	2.50	0.43
1:A:596:VAL:HG11	2:B:393:LEU:HB3	2.01	0.43
3:C:170:ILE:HD13	3:C:170:ILE:HA	1.92	0.42
3:C:159:SER:HB3	3:C:189:LEU:HD23	2.01	0.42
3:C:145:LEU:HD11	3:C:158:THR:HB	2.01	0.42
3:C:127:THR:HG22	3:C:129:GLU:H	1.83	0.41
3:C:285:LEU:HD22	3:C:326:VAL:HG21	2.02	0.41
3:C:319:VAL:HG22	3:C:326:VAL:HG23	2.02	0.41
1:A:524:TYR:HB2	1:A:529:LEU:HD23	2.03	0.40
1:A:596:VAL:HG21	2:B:393:LEU:HD13	2.03	0.40

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	270/628 (43%)	266 (98%)	4 (2%)	0	100	100
2	B	242/268 (90%)	235 (97%)	7 (3%)	0	100	100
3	C	323/348 (93%)	313 (97%)	10 (3%)	0	100	100
4	E	37/71 (52%)	34 (92%)	3 (8%)	0	100	100
All	All	872/1315 (66%)	848 (97%)	24 (3%)	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	234/533 (44%)	234 (100%)	0	100	100
2	B	215/231 (93%)	215 (100%)	0	100	100
3	C	269/291 (92%)	269 (100%)	0	100	100
4	E	31/58 (53%)	31 (100%)	0	100	100
All	All	749/1113 (67%)	749 (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. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	465	ASN
1	A	484	ASN
1	A	599	HIS
2	B	164	ASN
2	B	228	ASN
3	C	31	GLN
3	C	35	ASN
3	C	87	ASN
3	C	219	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.

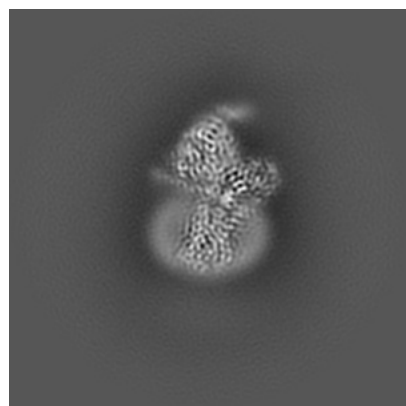
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53437. These allow visual inspection of the internal detail of the map and identification of artifacts.

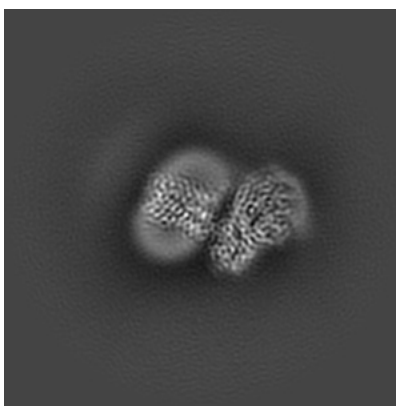
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

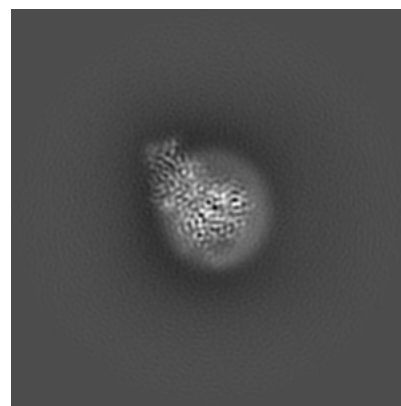
6.1.1 Primary map



X

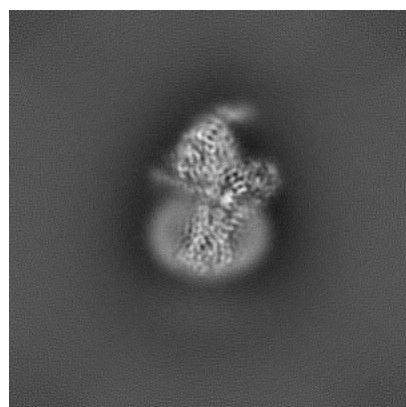


Y

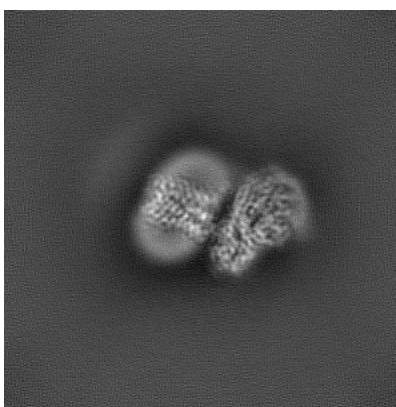


Z

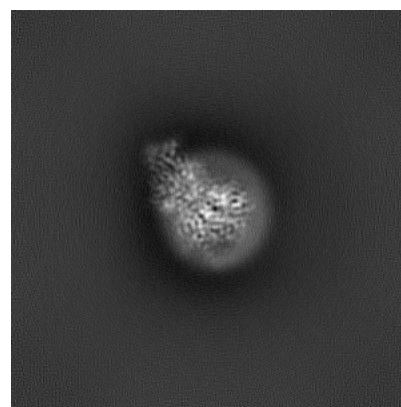
6.1.2 Raw map



X



Y

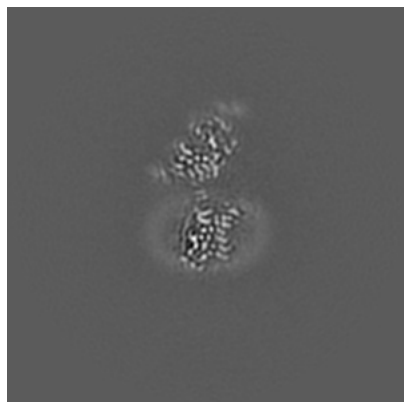


Z

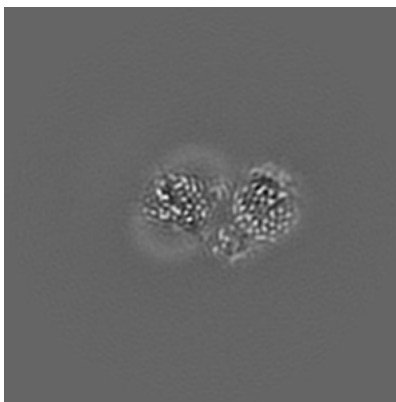
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

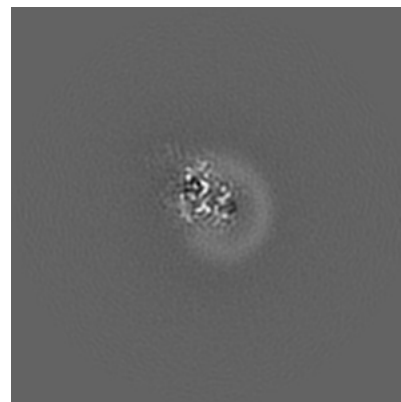
6.2.1 Primary map



X Index: 200

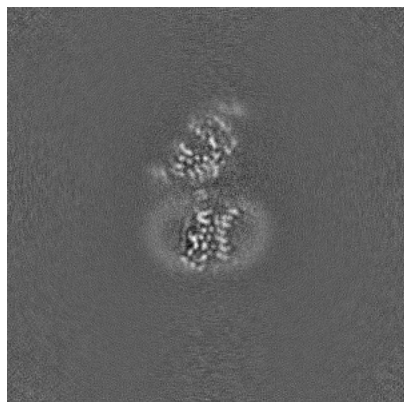


Y Index: 200

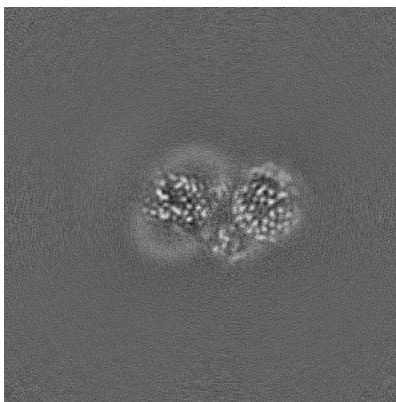


Z Index: 200

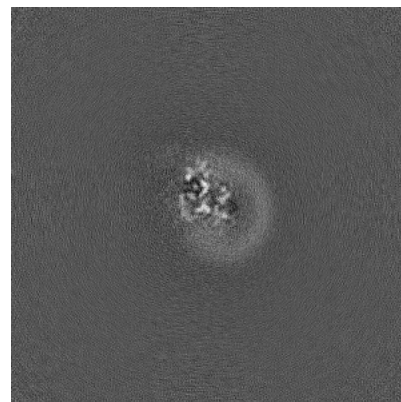
6.2.2 Raw map



X Index: 200



Y Index: 200

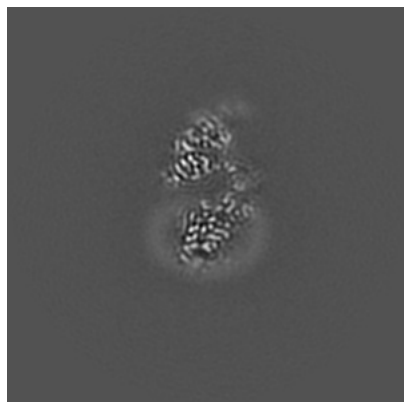


Z Index: 200

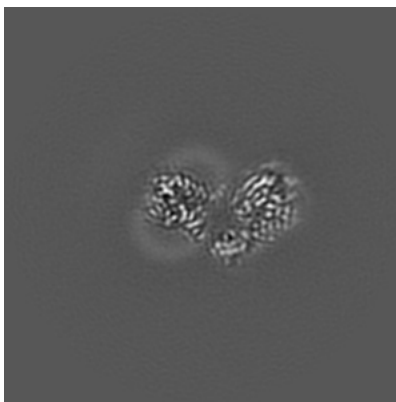
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

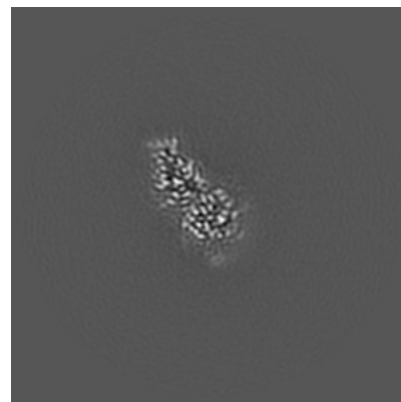
6.3.1 Primary map



X Index: 190

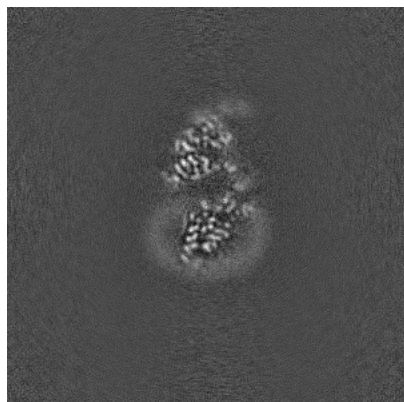


Y Index: 204

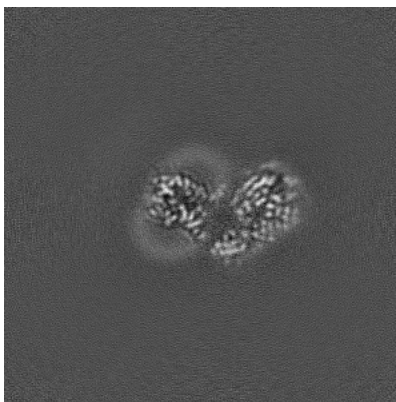


Z Index: 239

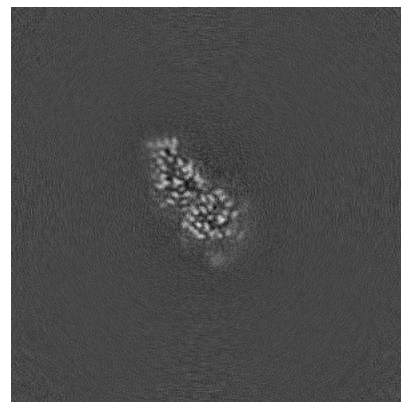
6.3.2 Raw map



X Index: 190



Y Index: 204

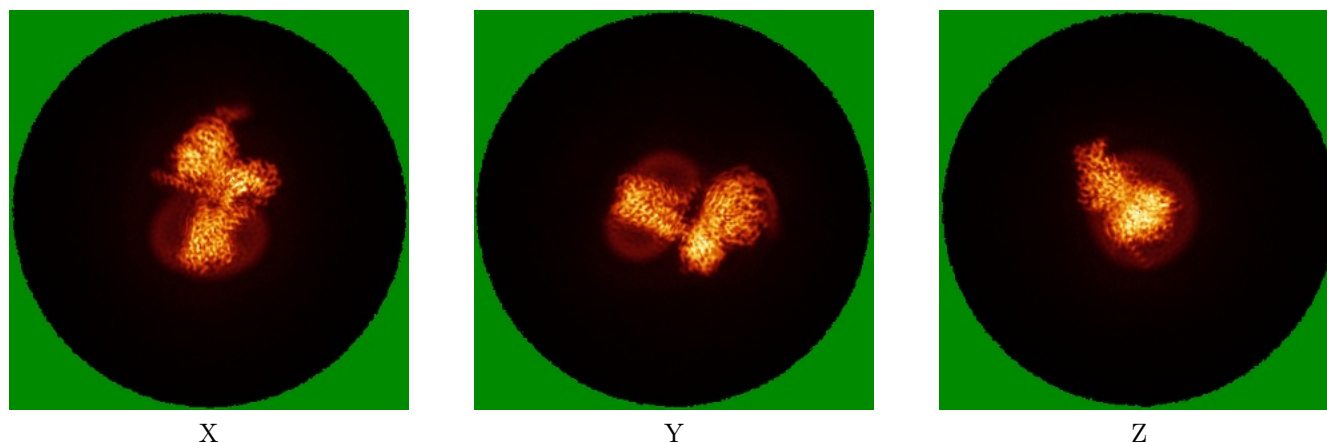


Z Index: 239

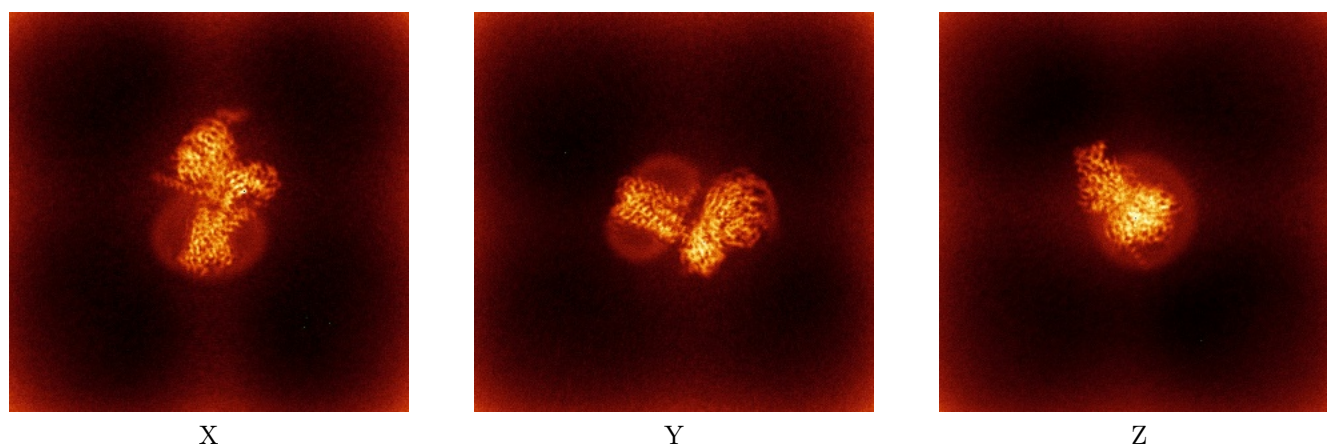
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

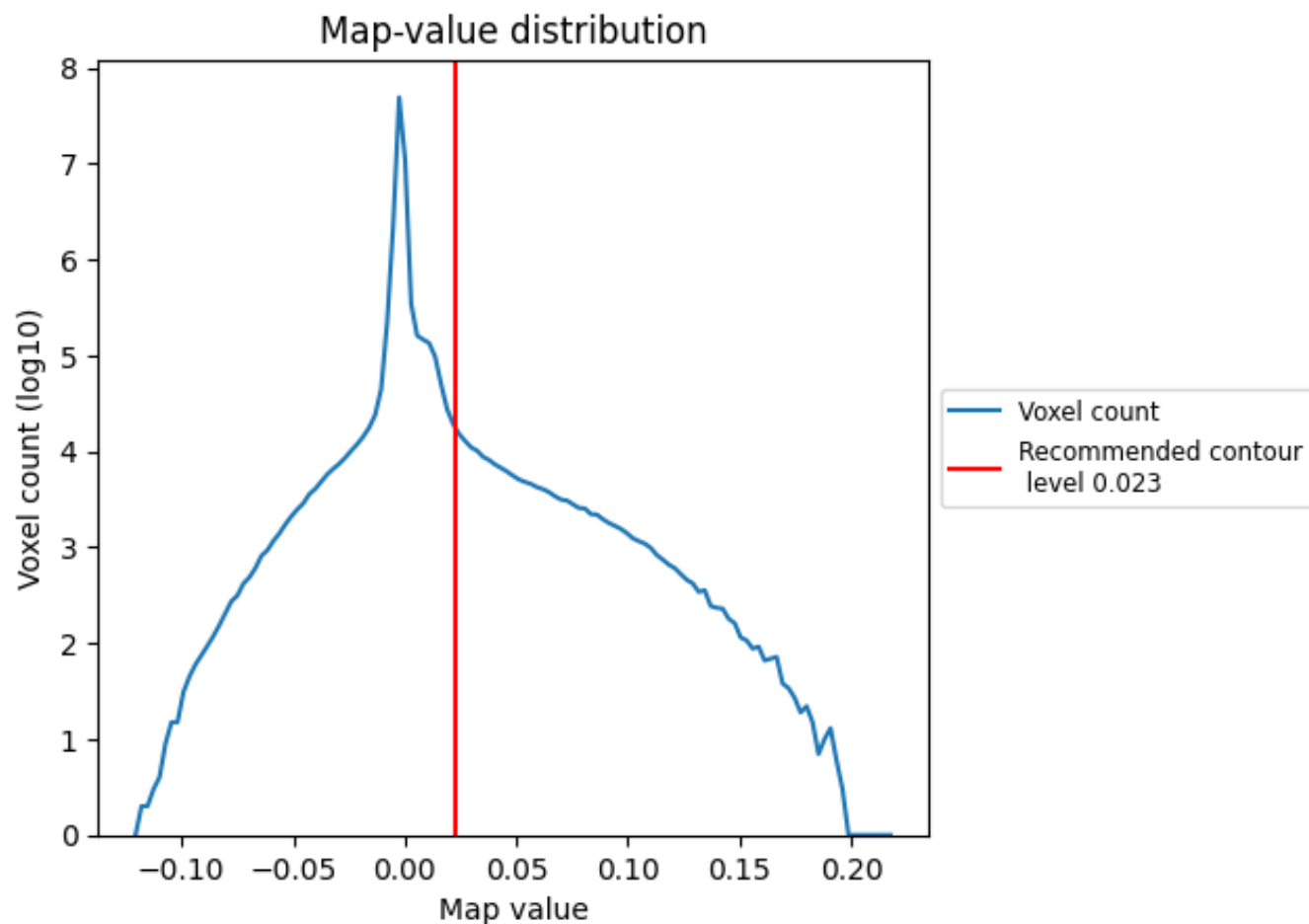
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

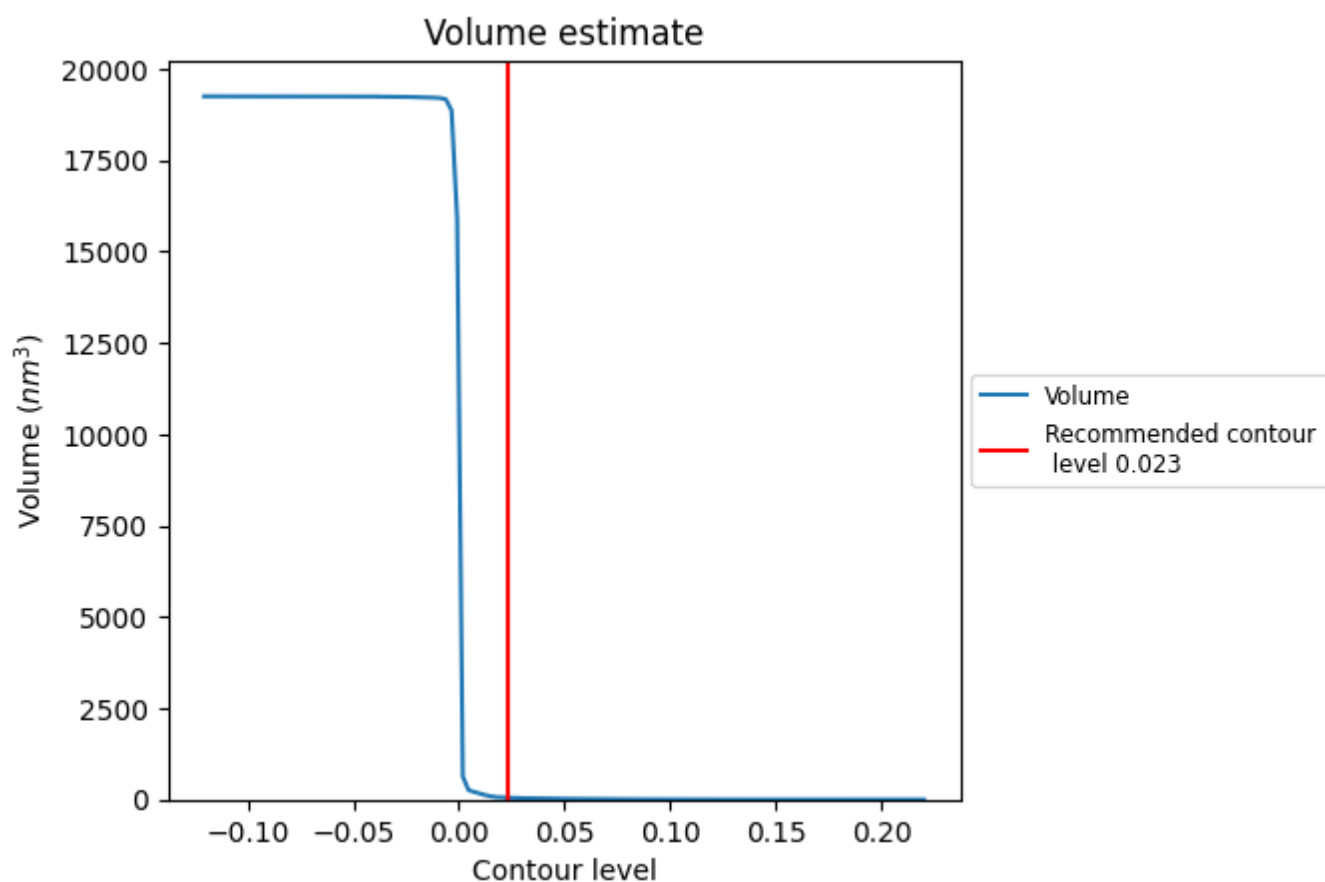
This section contains the results of statistical analysis of the map.

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.

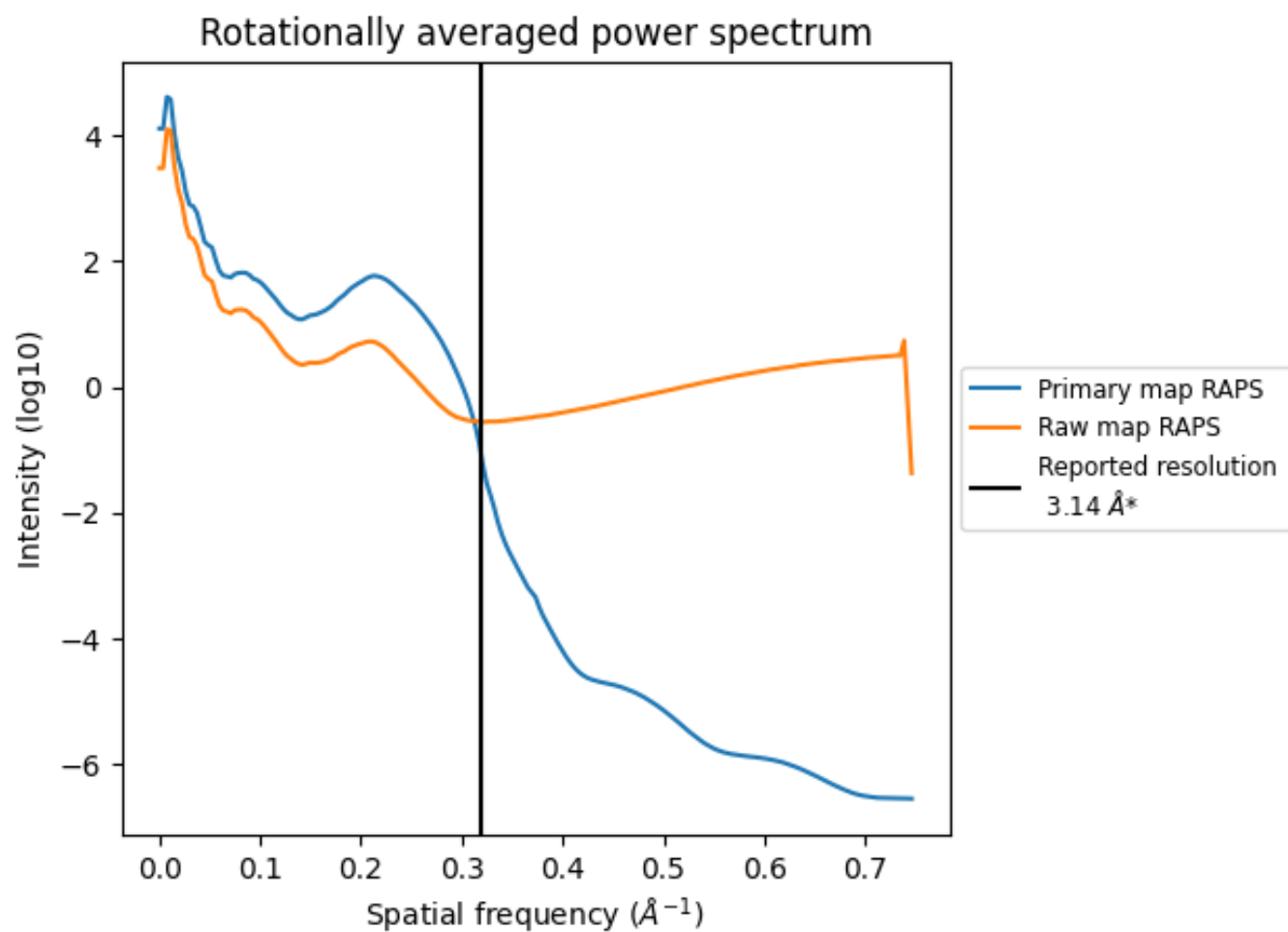
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 51 nm^3 ; this corresponds to an approximate mass of 46 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 ⓘ

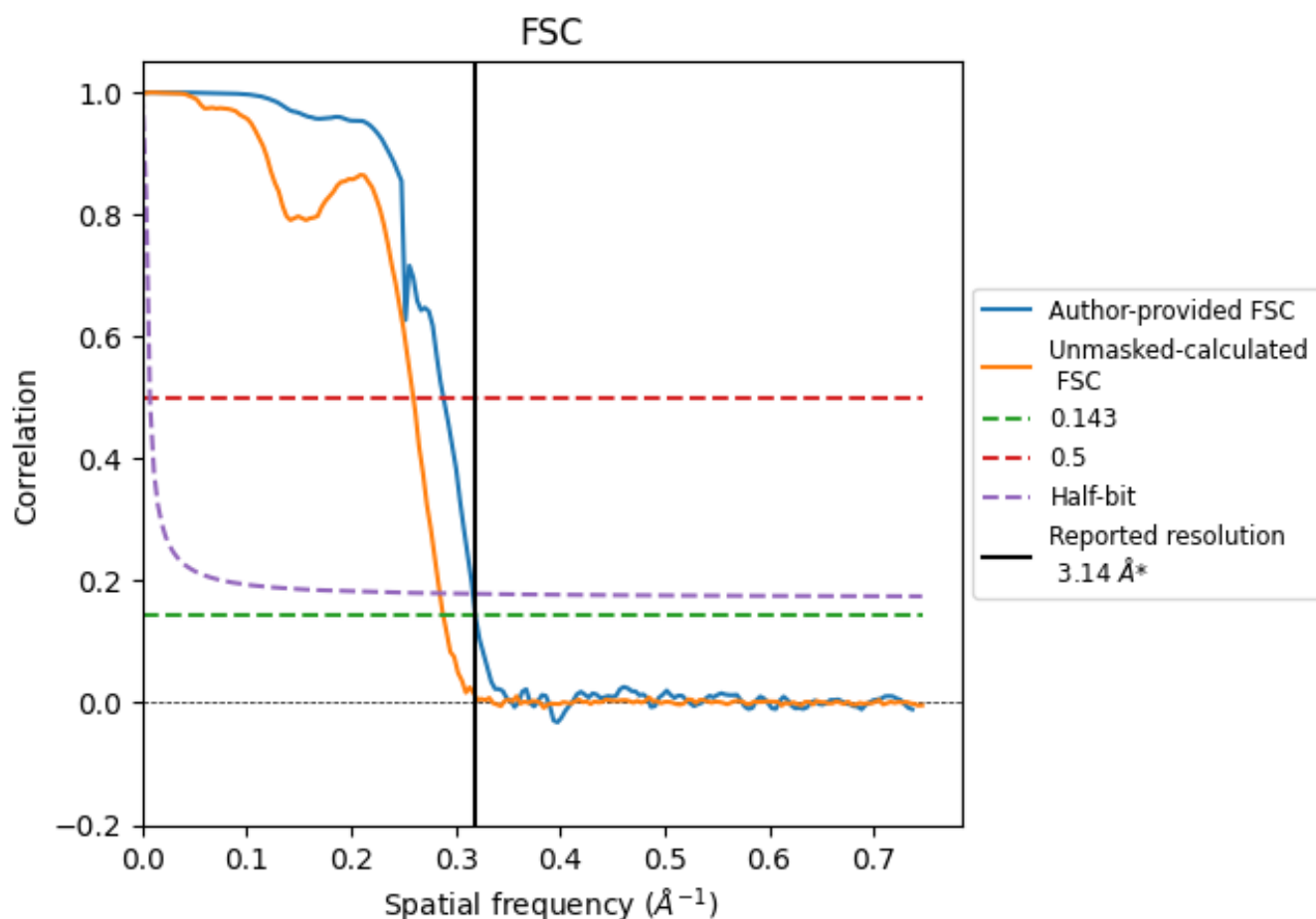


*Reported resolution corresponds to spatial frequency of 0.318 $\text{\AA}^{-1}$

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 $0.318 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

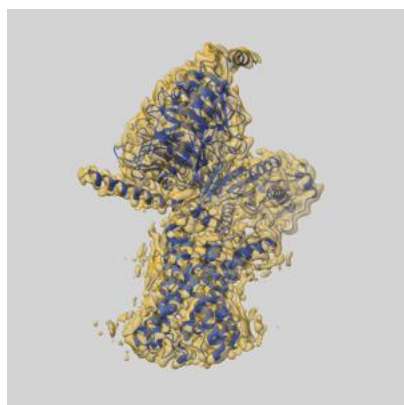
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.14	3.47	3.16
Unmasked-calculated*	3.47	3.85	3.51

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.47 differs from the reported value 3.14 by more than 10 %

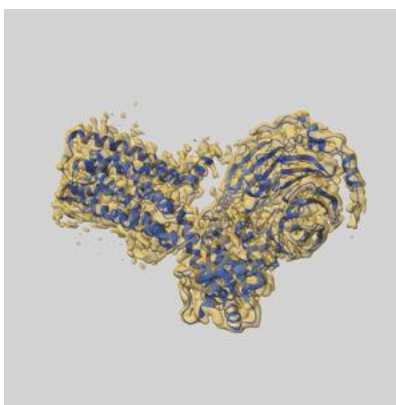
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53437 and PDB model 9QXL. Per-residue inclusion information can be found in section 3 on page 8.

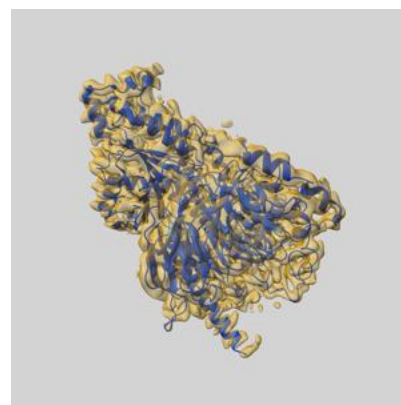
9.1 Map-model overlay [i](#)



X



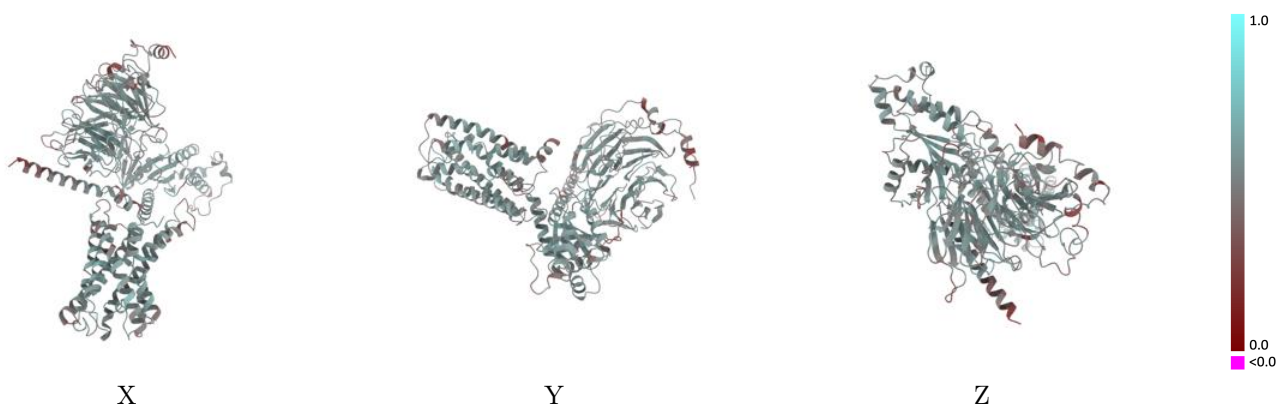
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.023 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](#)

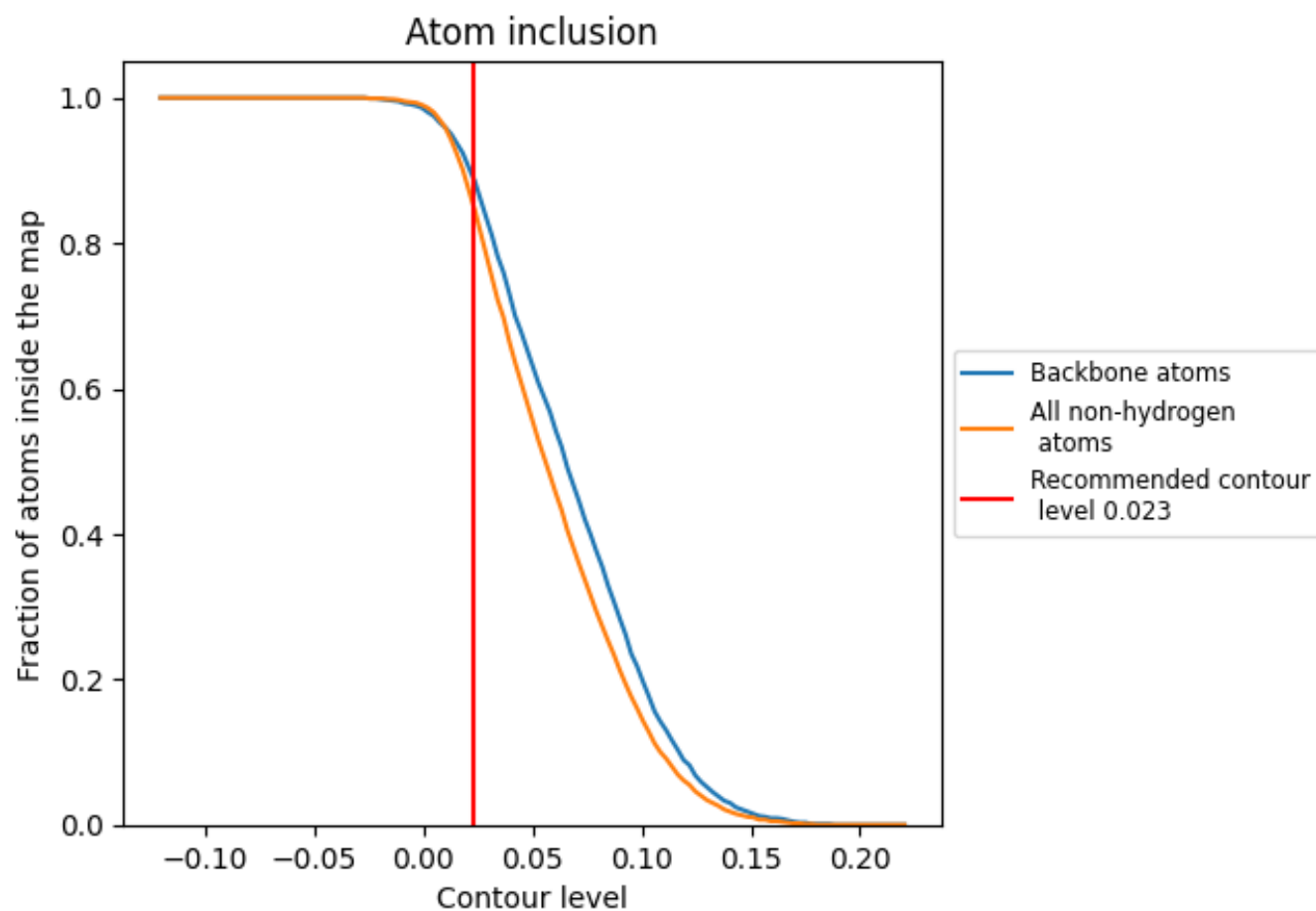


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 89% of all backbone atoms, 85% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8490	0.5130
A	0.8640	0.5200
B	0.8400	0.5100
C	0.8570	0.5180
E	0.7380	0.4400

