



wwPDB EM Validation Summary Report ⓘ

Apr 5, 2026 – 08:47 PM UTC

PDB ID : 9LLI / pdb_00009lli
EMDB ID : EMD-63203
Title : Cryo-EM structure of D1R in complex with de novo designed GEM targeting TM1/2/4 and GEM targeting TM3/4/5, and negative allosteric GEM targeting TM5/6/7
Authors : Guo, J.; Zhou, Y.; Cheng, S.; Zhang, Y.
Deposited on : 2025-01-17
Resolution : 3.00 Å(reported)

This is a wwPDB EM Validation Summary 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

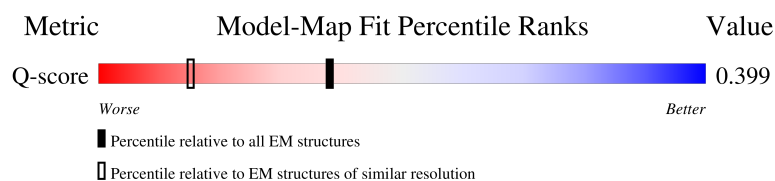
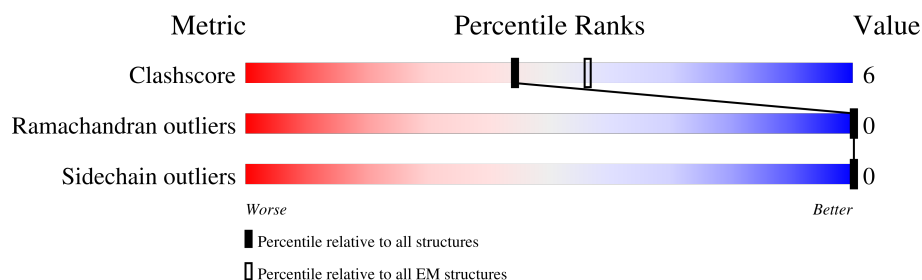
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	R	519	
2	O	97	
3	P	77	
4	Q	95	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4466 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 D(1A) dopamine receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	343	Total	C	N	O	S	0	0
			2723	1798	442	468	15		

There are 130 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	163	ASN	TRP	conflict	UNP P21728
R	1001	LEU	-	linker	UNP P21728
R	1002	LYS	-	linker	UNP P21728
R	1003	LYS	-	linker	UNP P21728
R	1004	GLU	-	linker	UNP P21728
R	1005	LEU	-	linker	UNP P21728
R	1006	ASP	-	linker	UNP P21728
R	1007	ALA	-	linker	UNP P21728
R	1008	LEU	-	linker	UNP P21728
R	1009	ASN	-	linker	UNP P21728
R	1010	ASP	-	linker	UNP P21728
R	1011	ASN	-	linker	UNP P21728
R	1012	TRP	-	linker	UNP P21728
R	1013	GLU	-	linker	UNP P21728
R	1014	THR	-	linker	UNP P21728
R	1015	LEU	-	linker	UNP P21728
R	1016	ASN	-	linker	UNP P21728
R	1017	ASP	-	linker	UNP P21728
R	1018	ASN	-	linker	UNP P21728
R	1019	LEU	-	linker	UNP P21728
R	1020	LYS	-	linker	UNP P21728
R	1021	VAL	-	linker	UNP P21728
R	1022	ILE	-	linker	UNP P21728
R	1023	GLU	-	linker	UNP P21728
R	1024	LYS	-	linker	UNP P21728
R	1025	ALA	-	linker	UNP P21728
R	1026	ASP	-	linker	UNP P21728

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Chain	Residue	Modelled	Actual	Comment	Reference
R	1027	ASN	-	linker	UNP P21728
R	1028	ALA	-	linker	UNP P21728
R	1029	ALA	-	linker	UNP P21728
R	1030	GLN	-	linker	UNP P21728
R	1031	VAL	-	linker	UNP P21728
R	1032	LYS	-	linker	UNP P21728
R	1033	ASP	-	linker	UNP P21728
R	1034	ALA	-	linker	UNP P21728
R	1035	LEU	-	linker	UNP P21728
R	1036	THR	-	linker	UNP P21728
R	1037	LYS	-	linker	UNP P21728
R	1038	MET	-	linker	UNP P21728
R	1039	ARG	-	linker	UNP P21728
R	1040	ALA	-	linker	UNP P21728
R	1041	ALA	-	linker	UNP P21728
R	1042	ALA	-	linker	UNP P21728
R	1043	LEU	-	linker	UNP P21728
R	1044	ASP	-	linker	UNP P21728
R	1045	ALA	-	linker	UNP P21728
R	1046	GLN	-	linker	UNP P21728
R	1047	LYS	-	linker	UNP P21728
R	1048	ALA	-	linker	UNP P21728
R	1049	THR	-	linker	UNP P21728
R	1050	PRO	-	linker	UNP P21728
R	1051	PRO	-	linker	UNP P21728
R	1052	LYS	-	linker	UNP P21728
R	1053	LEU	-	linker	UNP P21728
R	1054	GLU	-	linker	UNP P21728
R	1055	ASP	-	linker	UNP P21728
R	1056	LYS	-	linker	UNP P21728
R	1057	SER	-	linker	UNP P21728
R	1058	PRO	-	linker	UNP P21728
R	1059	ASP	-	linker	UNP P21728
R	1060	SER	-	linker	UNP P21728
R	1061	PRO	-	linker	UNP P21728
R	1062	GLU	-	linker	UNP P21728
R	1063	MET	-	linker	UNP P21728
R	1064	LYS	-	linker	UNP P21728
R	1065	ASP	-	linker	UNP P21728
R	1066	PHE	-	linker	UNP P21728
R	1067	ARG	-	linker	UNP P21728
R	1068	HIS	-	linker	UNP P21728

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Chain	Residue	Modelled	Actual	Comment	Reference
R	1069	GLY	-	linker	UNP P21728
R	1070	PHE	-	linker	UNP P21728
R	1071	ASP	-	linker	UNP P21728
R	1072	ILE	-	linker	UNP P21728
R	1073	LEU	-	linker	UNP P21728
R	1074	VAL	-	linker	UNP P21728
R	1075	GLY	-	linker	UNP P21728
R	1076	GLN	-	linker	UNP P21728
R	1077	ILE	-	linker	UNP P21728
R	1078	ASP	-	linker	UNP P21728
R	1079	ASP	-	linker	UNP P21728
R	1080	ALA	-	linker	UNP P21728
R	1081	LEU	-	linker	UNP P21728
R	1082	LYS	-	linker	UNP P21728
R	1083	LEU	-	linker	UNP P21728
R	1084	ALA	-	linker	UNP P21728
R	1085	ASN	-	linker	UNP P21728
R	1086	GLU	-	linker	UNP P21728
R	1087	GLY	-	linker	UNP P21728
R	1088	LYS	-	linker	UNP P21728
R	1089	VAL	-	linker	UNP P21728
R	1090	LYS	-	linker	UNP P21728
R	1091	GLU	-	linker	UNP P21728
R	1092	ALA	-	linker	UNP P21728
R	1093	GLN	-	linker	UNP P21728
R	1094	ALA	-	linker	UNP P21728
R	1095	ALA	-	linker	UNP P21728
R	1096	ALA	-	linker	UNP P21728
R	1097	GLU	-	linker	UNP P21728
R	1098	GLN	-	linker	UNP P21728
R	1099	LEU	-	linker	UNP P21728
R	1100	LYS	-	linker	UNP P21728
R	1101	THR	-	linker	UNP P21728
R	1102	THR	-	linker	UNP P21728
R	1103	ARG	-	linker	UNP P21728
R	1104	ASP	-	linker	UNP P21728
R	1105	ALA	-	linker	UNP P21728
R	1106	ILE	-	linker	UNP P21728
R	1107	LEU	-	linker	UNP P21728
R	1108	LYS	-	linker	UNP P21728
R	1109	PRO	-	linker	UNP P21728
R	1110	PHE	-	linker	UNP P21728

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Chain	Residue	Modelled	Actual	Comment	Reference
R	1111	ILE	-	linker	UNP P21728
R	1112	GLU	-	linker	UNP P21728
R	1113	GLU	-	linker	UNP P21728
R	1114	LEU	-	linker	UNP P21728
R	1115	LYS	-	linker	UNP P21728
R	1116	GLU	-	linker	UNP P21728
R	1117	LEU	-	linker	UNP P21728
R	1118	LYS	-	linker	UNP P21728
R	1119	GLY	-	linker	UNP P21728
R	1120	LYS	-	linker	UNP P21728
R	1121	PRO	-	linker	UNP P21728
R	1122	PHE	-	linker	UNP P21728
R	1123	LEU	-	linker	UNP P21728
R	1124	ILE	-	linker	UNP P21728
R	1125	ASP	-	linker	UNP P21728
R	1126	ALA	-	linker	UNP P21728
R	447	GLY	-	expression tag	UNP P21728
R	448	GLY	-	expression tag	UNP P21728
R	449	SER	-	expression tag	UNP P21728

- Molecule 2 is a protein called De novo designed GPCR exoframe modulator targeting TM1/2/4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	68	Total	C	N	O	S	0	0
			582	409	91	80	2		

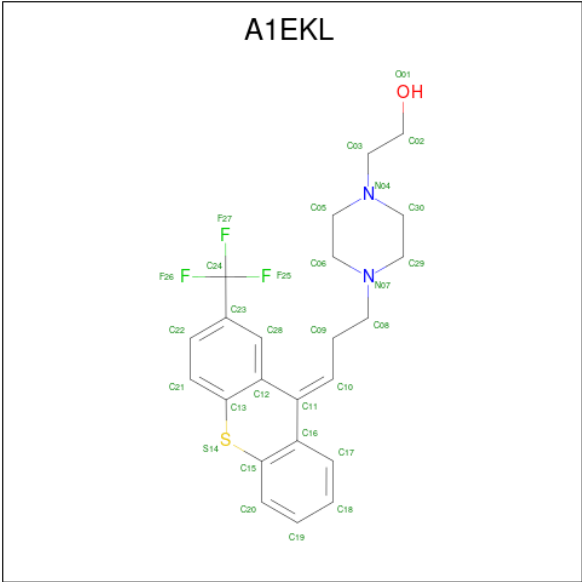
- Molecule 3 is a protein called De novo designed GPCR exoframe modulator targeting TM3/4/5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	66	Total	C	N	O	S	0	0
			550	394	72	82	2		

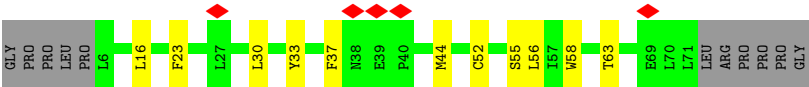
- Molecule 4 is a protein called De novo designed negative allosteric GPCR exoframe modulator targeting TM5/6/7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Q	66	Total	C	N	O		0	0
			581	420	83	78			

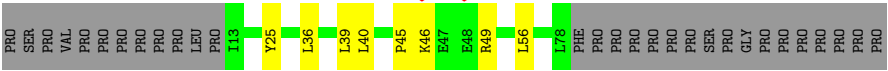
- Molecule 5 is Flupentixol (CCD ID: A1EKL) (formula: C₂₃H₂₅F₃N₂OS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	F	N	O	S	
5	R	1	30	23	3	2	1	1	0



- Molecule 4: De novo designed negative allosteric GPCR exoframe modulator targeting TM5/6/7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	314295	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	7.896	Depositor
Minimum map value	-7.027	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.349	Depositor
Map size (\AA)	297.6, 297.6, 297.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.93, 0.93, 0.93	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: A1EKL

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	R	0.17	0/2785	0.34	0/3782
2	O	0.12	0/595	0.27	0/803
3	P	0.11	0/562	0.22	0/767
4	Q	0.15	0/598	0.31	0/810
All	All	0.16	0/4540	0.32	0/6162

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	R	2723	0	2805	49	0
2	O	582	0	658	7	0
3	P	550	0	638	13	0
4	Q	581	0	657	7	0
5	R	30	0	0	0	0
All	All	4466	0	4758	59	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 59 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:R:1035:LEU:HB3	1:R:1081:LEU:HD11	1.55	0.89
1:R:1035:LEU:HB3	1:R:1081:LEU:CD1	2.03	0.88
1:R:1077:ILE:O	1:R:1081:LEU:HD13	1.77	0.83
1:R:1039:ARG:NH1	1:R:1078:ASP:OD1	2.18	0.76
3:P:23:PHE:HZ	3:P:52:CYS:HB3	1.51	0.75

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	R	335/519 (64%)	332 (99%)	3 (1%)	0	100	100
2	O	66/97 (68%)	66 (100%)	0	0	100	100
3	P	64/77 (83%)	64 (100%)	0	0	100	100
4	Q	64/95 (67%)	64 (100%)	0	0	100	100
All	All	529/788 (67%)	526 (99%)	3 (1%)	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	R	295/446 (66%)	295 (100%)	0	100	100
2	O	66/91 (72%)	66 (100%)	0	100	100
3	P	66/75 (88%)	66 (100%)	0	100	100
4	Q	64/92 (70%)	64 (100%)	0	100	100
All	All	491/704 (70%)	491 (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. There are no such sidechains identified.

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	A1EKL	R	601	-	33,33,33	3.13	12 (36%)	46,47,47	1.51	6 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	A1EKL	R	601	-	-	4/15/37/37	0/4/4/4

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	601	A1EKL	C03-N04	-8.49	1.28	1.47
5	R	601	A1EKL	C08-N07	-8.18	1.28	1.47
5	R	601	A1EKL	C16-C11	6.41	1.61	1.47
5	R	601	A1EKL	C12-C11	6.32	1.61	1.47
5	R	601	A1EKL	C29-N07	-3.77	1.36	1.46

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	601	A1EKL	C29-N07-C06	4.18	117.85	108.84
5	R	601	A1EKL	C21-C13-C12	3.39	123.37	119.16
5	R	601	A1EKL	C20-C15-C16	2.51	122.28	119.16
5	R	601	A1EKL	C12-C28-C23	-2.46	118.18	121.98
5	R	601	A1EKL	F25-C24-C23	-2.14	108.32	112.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

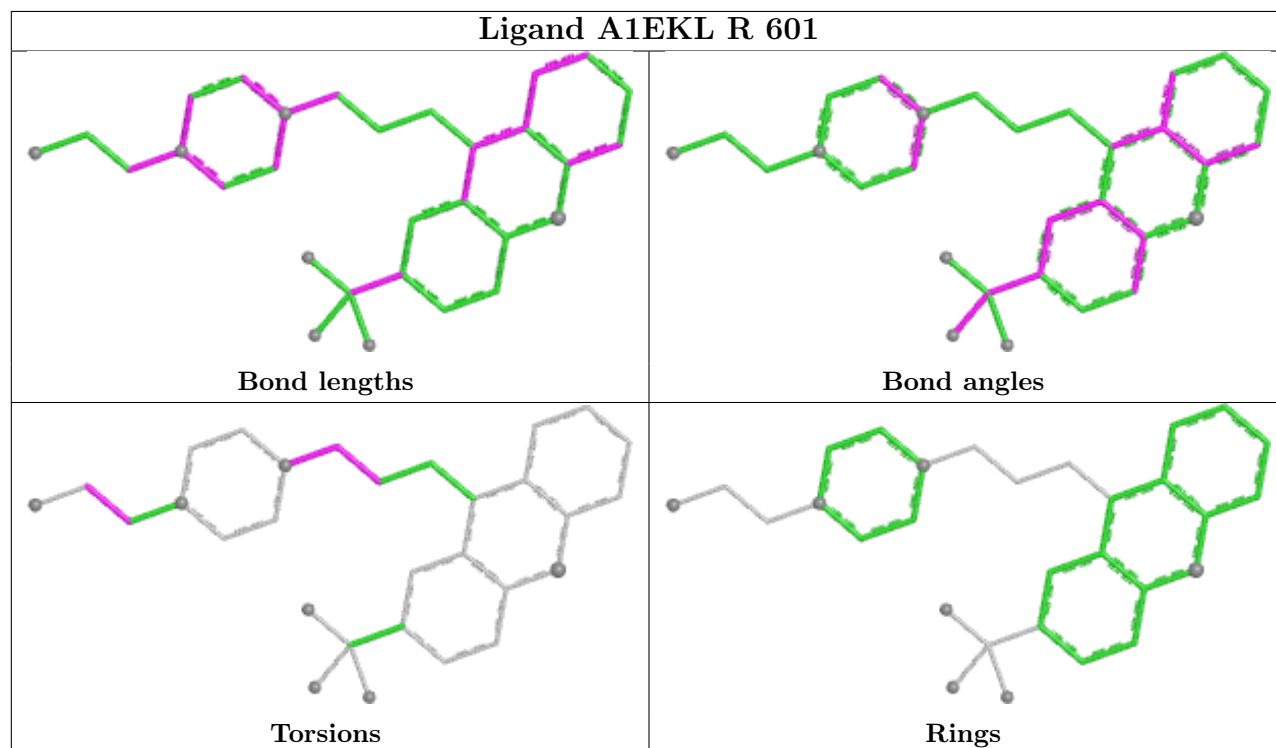
Mol	Chain	Res	Type	Atoms
5	R	601	A1EKL	N07-C08-C09-C10
5	R	601	A1EKL	O01-C02-C03-N04
5	R	601	A1EKL	C09-C08-N07-C06
5	R	601	A1EKL	C09-C08-N07-C29

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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-63203. These allow visual inspection of the internal detail of the map and identification of artifacts.

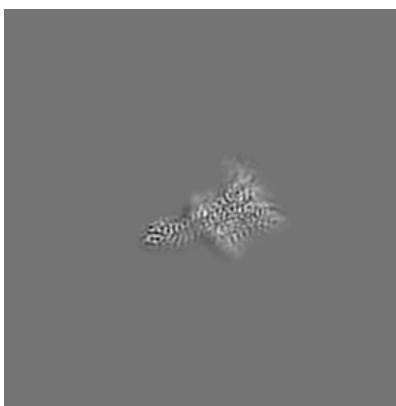
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

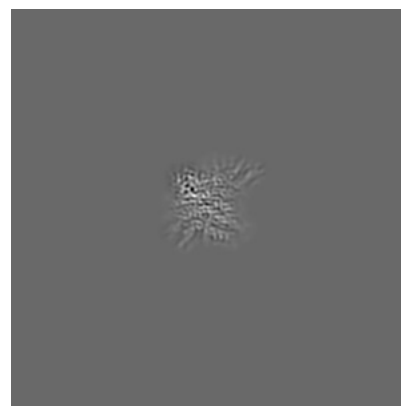
6.1.1 Primary map



X

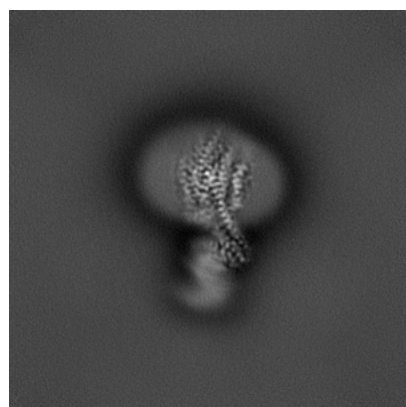


Y

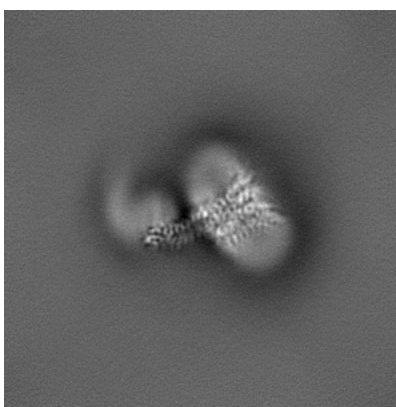


Z

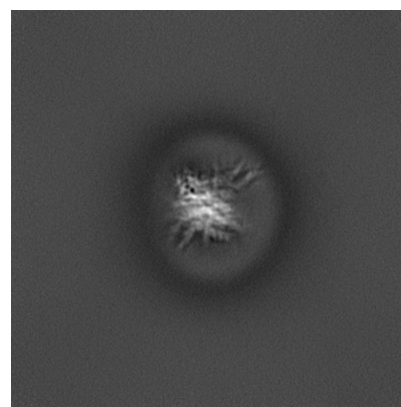
6.1.2 Raw map



X



Y

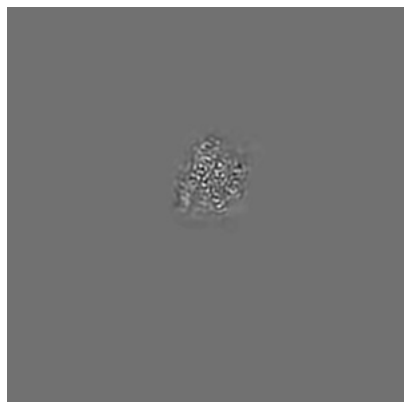


Z

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

6.2 Central slices [i](#)

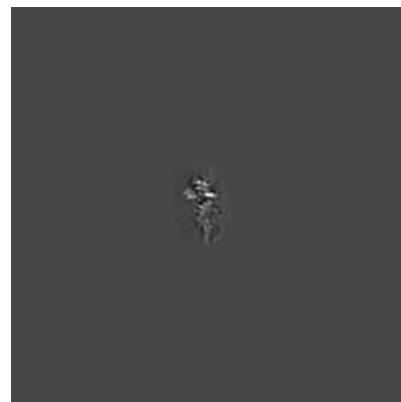
6.2.1 Primary map



X Index: 160

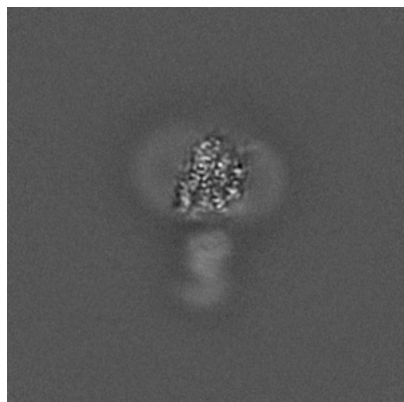


Y Index: 160

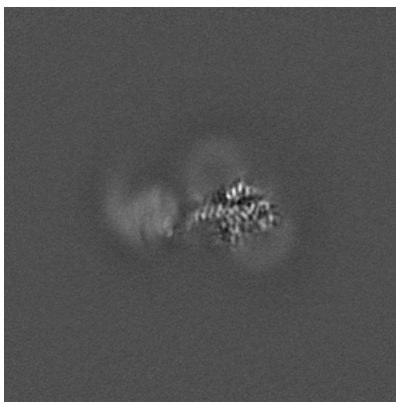


Z Index: 160

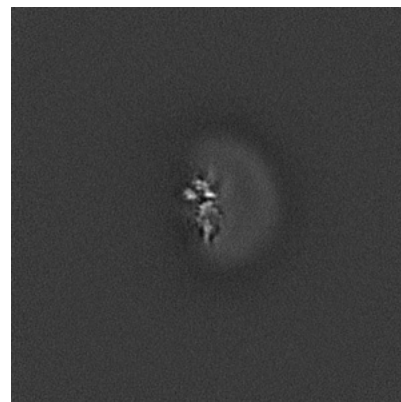
6.2.2 Raw map



X Index: 160



Y Index: 160

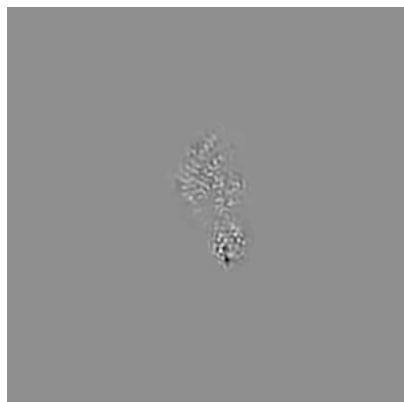


Z Index: 160

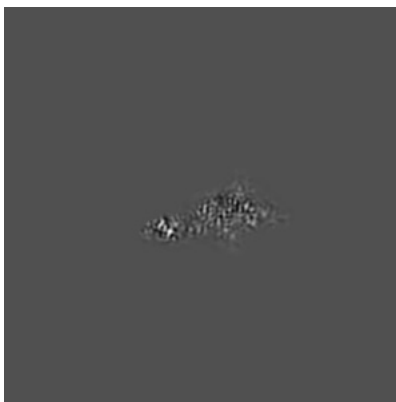
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

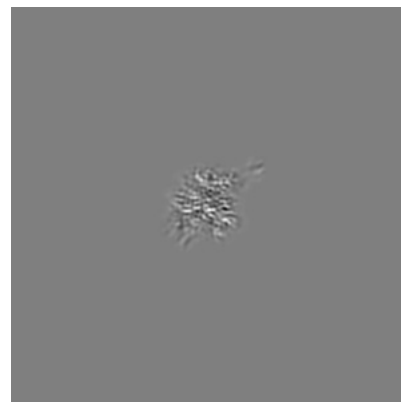
6.3.1 Primary map



X Index: 145

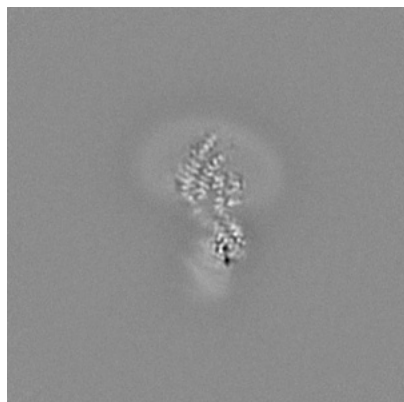


Y Index: 170

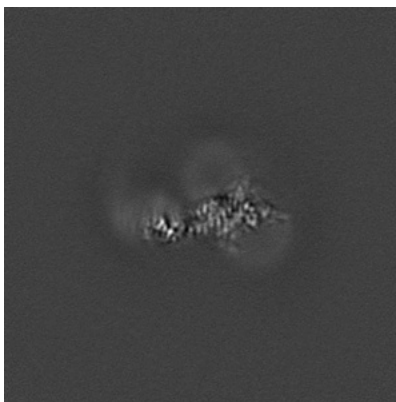


Z Index: 182

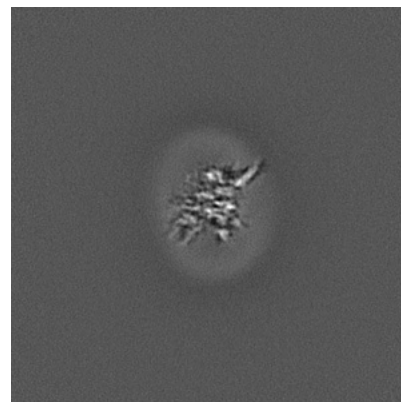
6.3.2 Raw map



X Index: 145



Y Index: 170

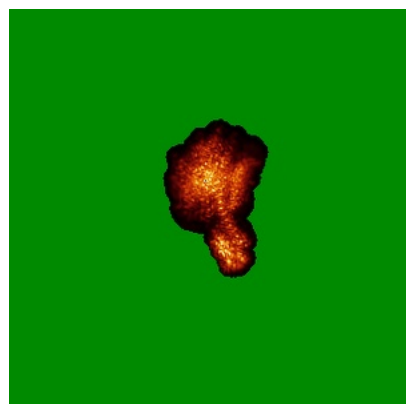


Z Index: 188

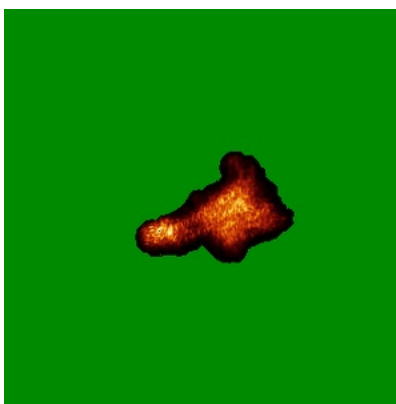
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

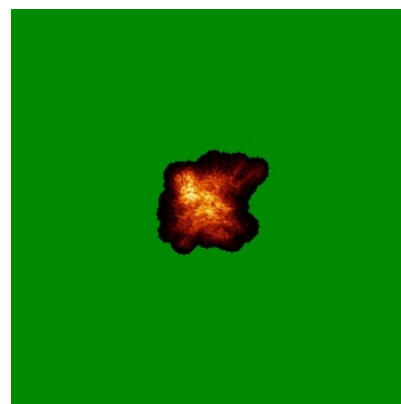
6.4.1 Primary map



X

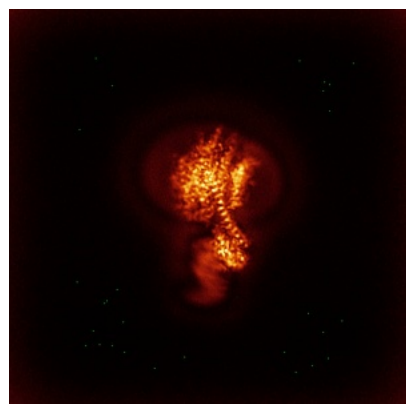


Y

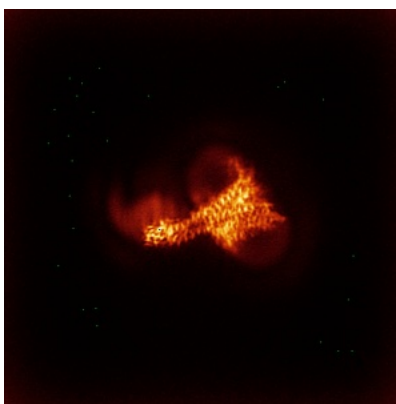


Z

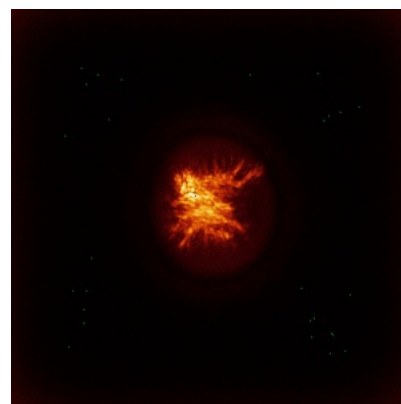
6.4.2 Raw map



X



Y

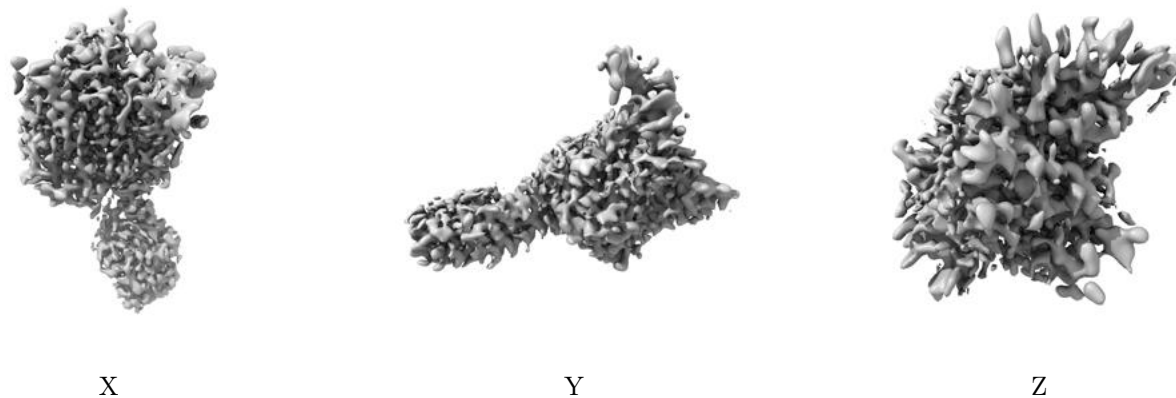


Z

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.

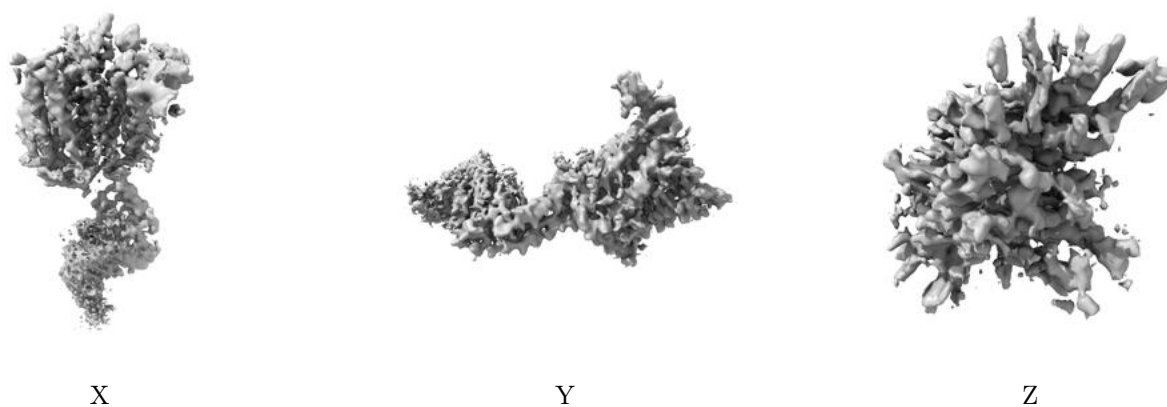
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.349. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

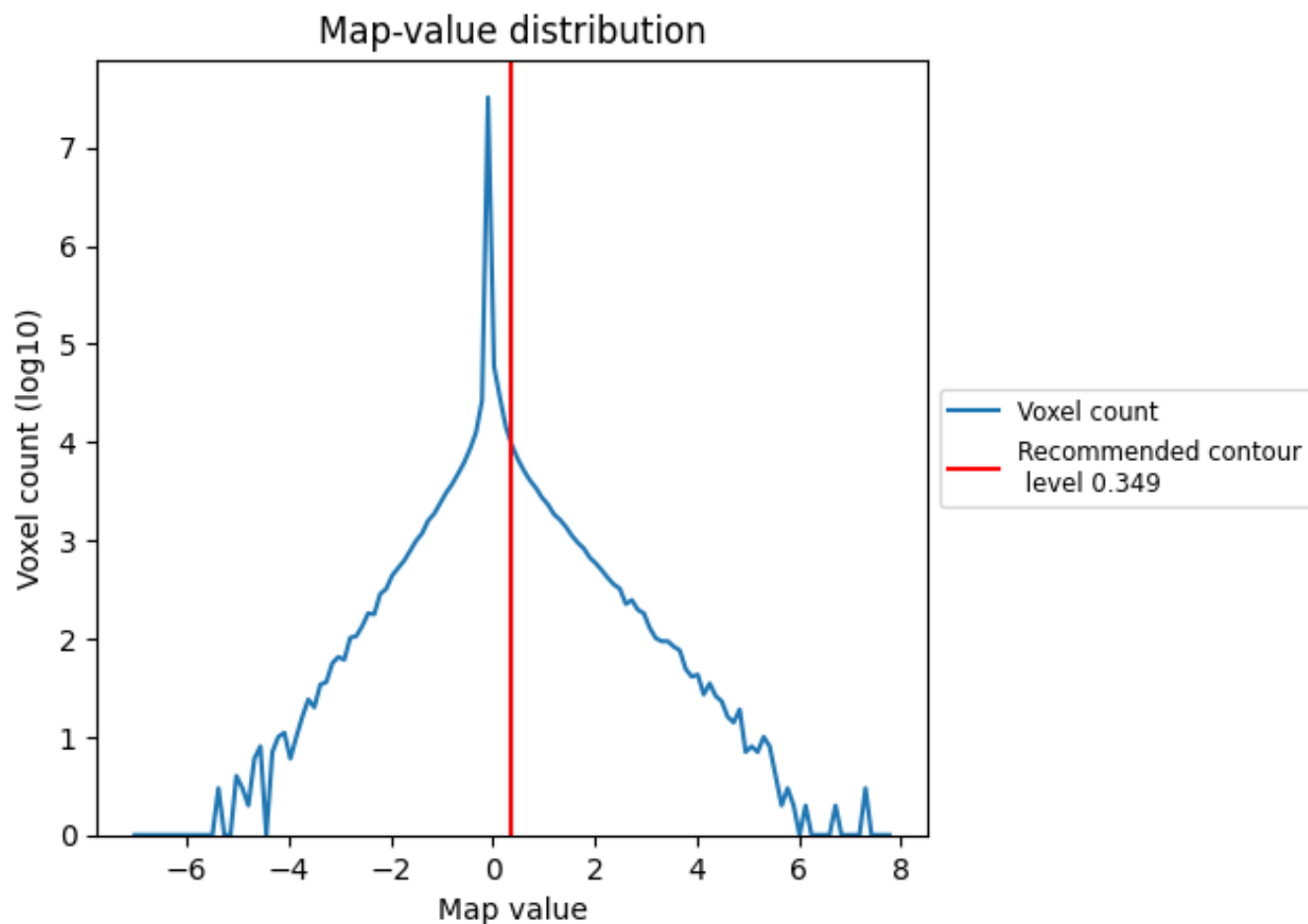
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

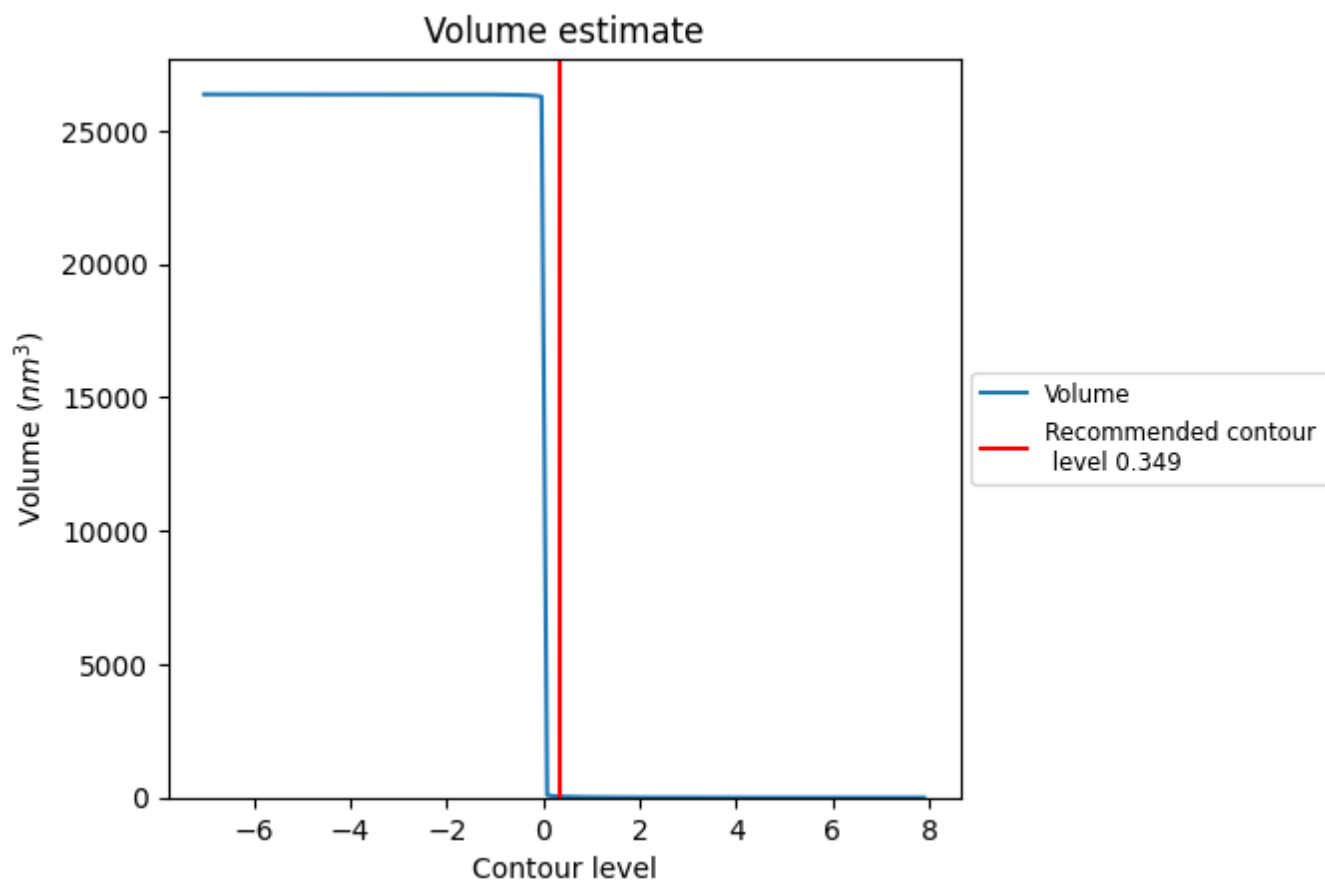
This section contains the results of statistical analysis of the map.

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.

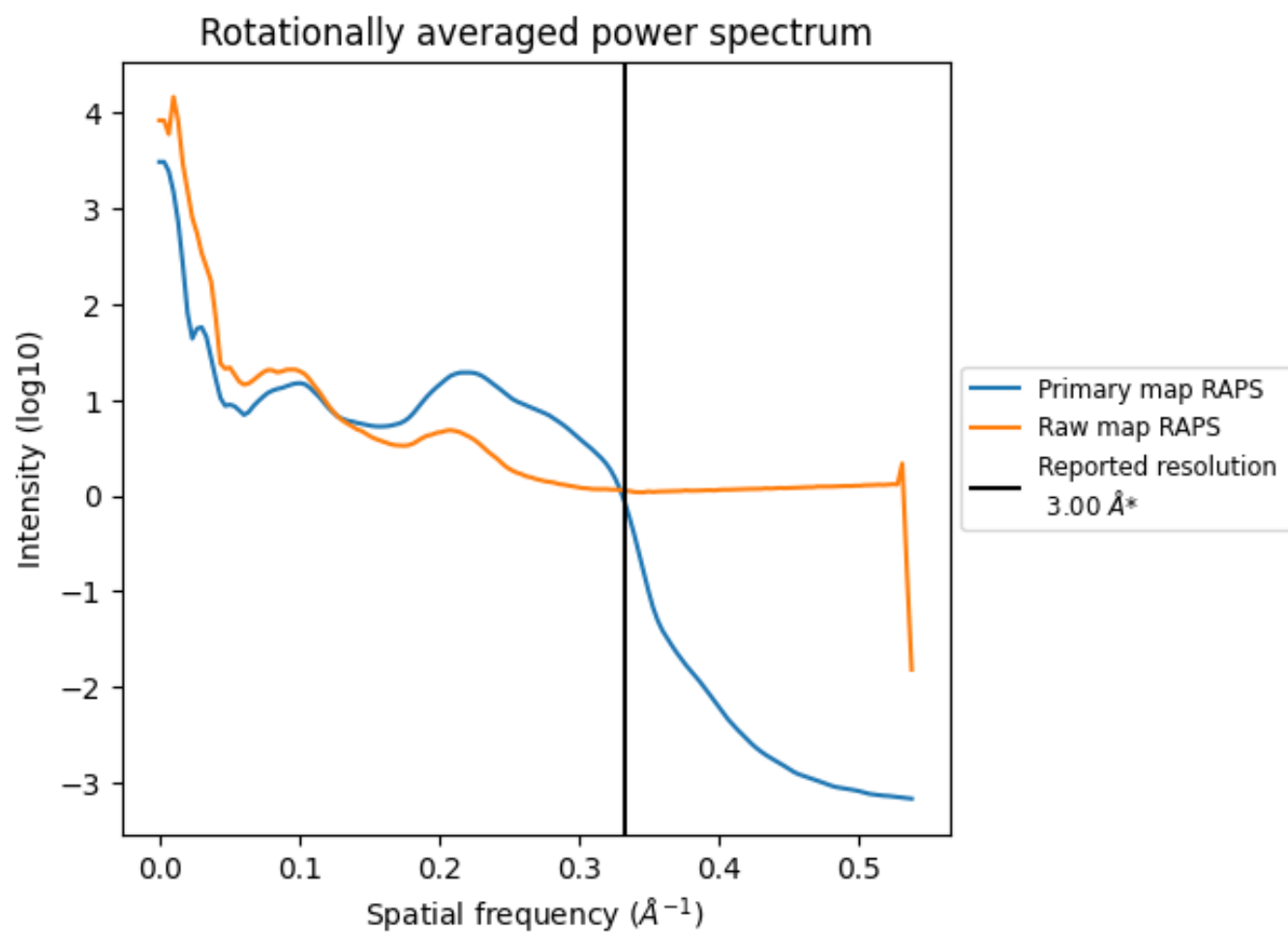
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 39 nm^3 ; this corresponds to an approximate mass of 36 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 ⓘ

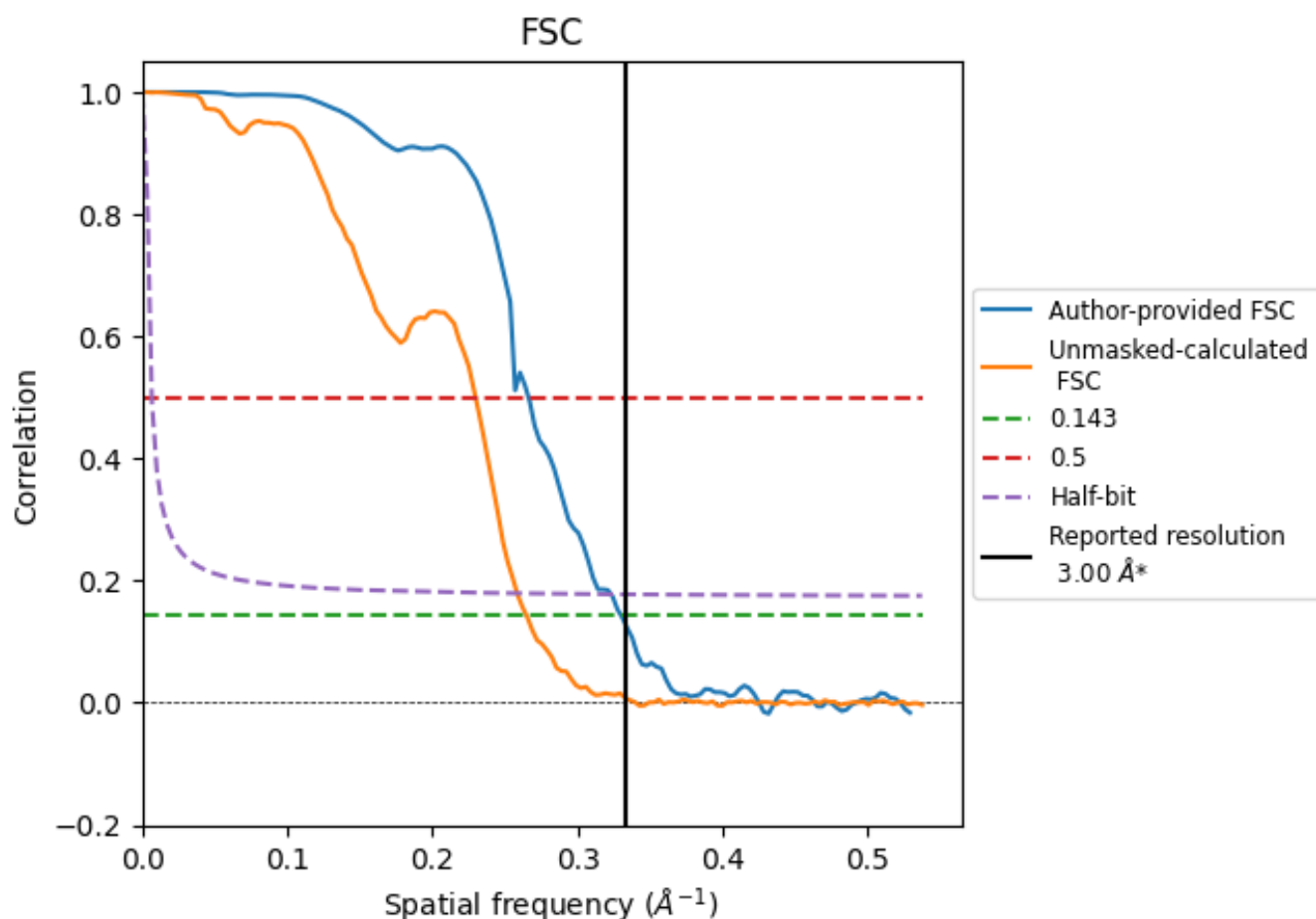


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

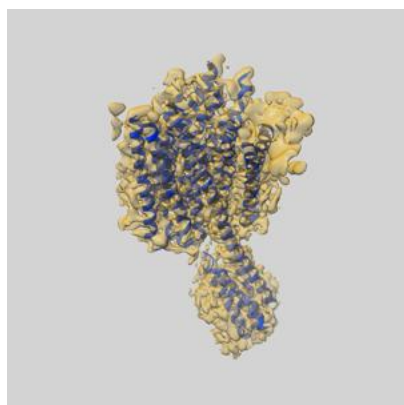
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.03	3.76	3.10
Unmasked-calculated*	3.78	4.35	3.87

*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 3.78 differs from the reported value 3.0 by more than 10 %

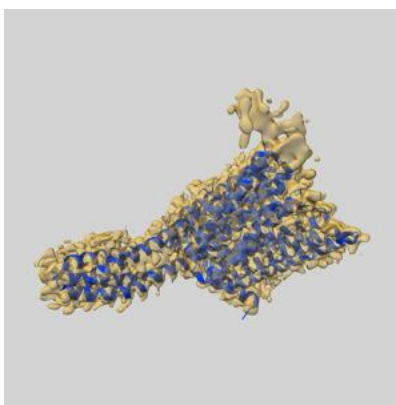
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-63203 and PDB model 9LLI. Per-residue inclusion information can be found in section 3 on page 8.

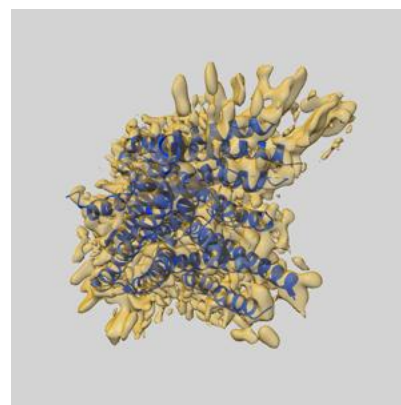
9.1 Map-model overlay [i](#)



X



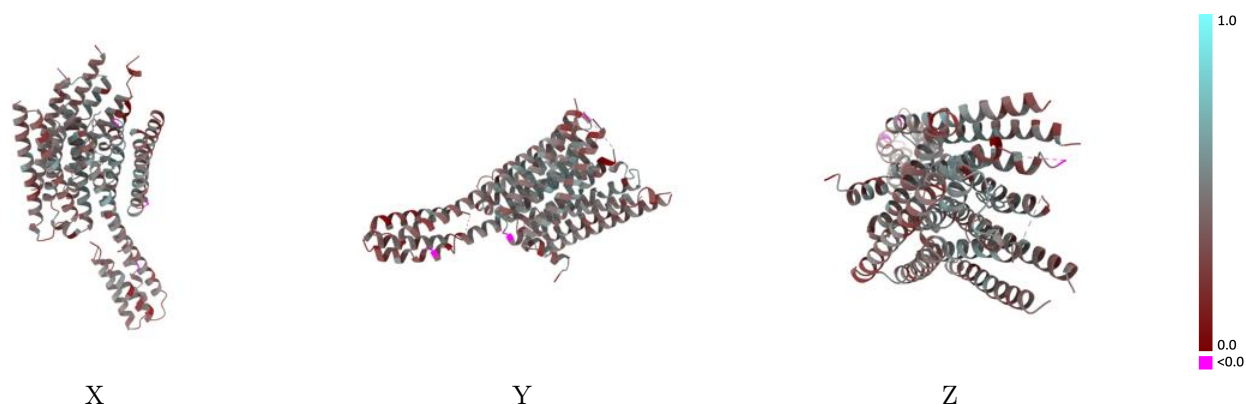
Y



Z

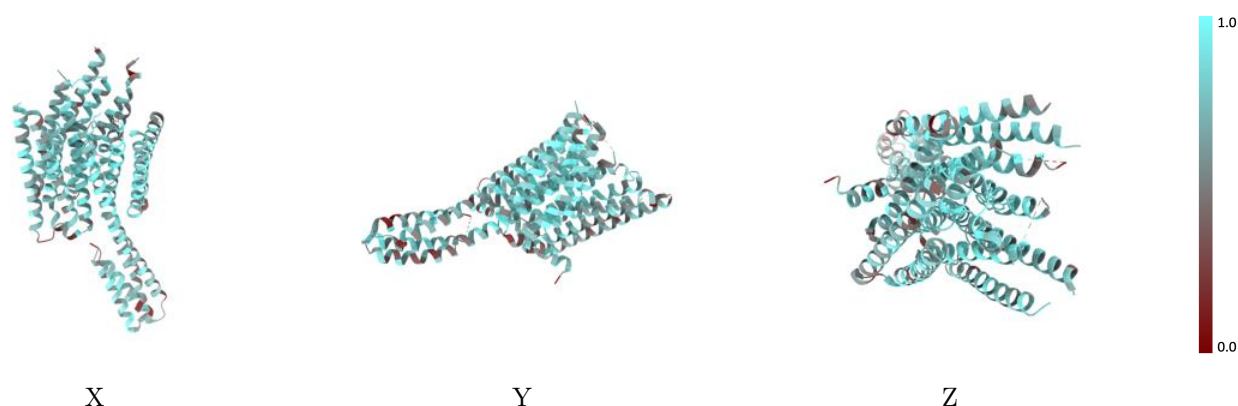
The images above show the 3D surface view of the map at the recommended contour level 0.349 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



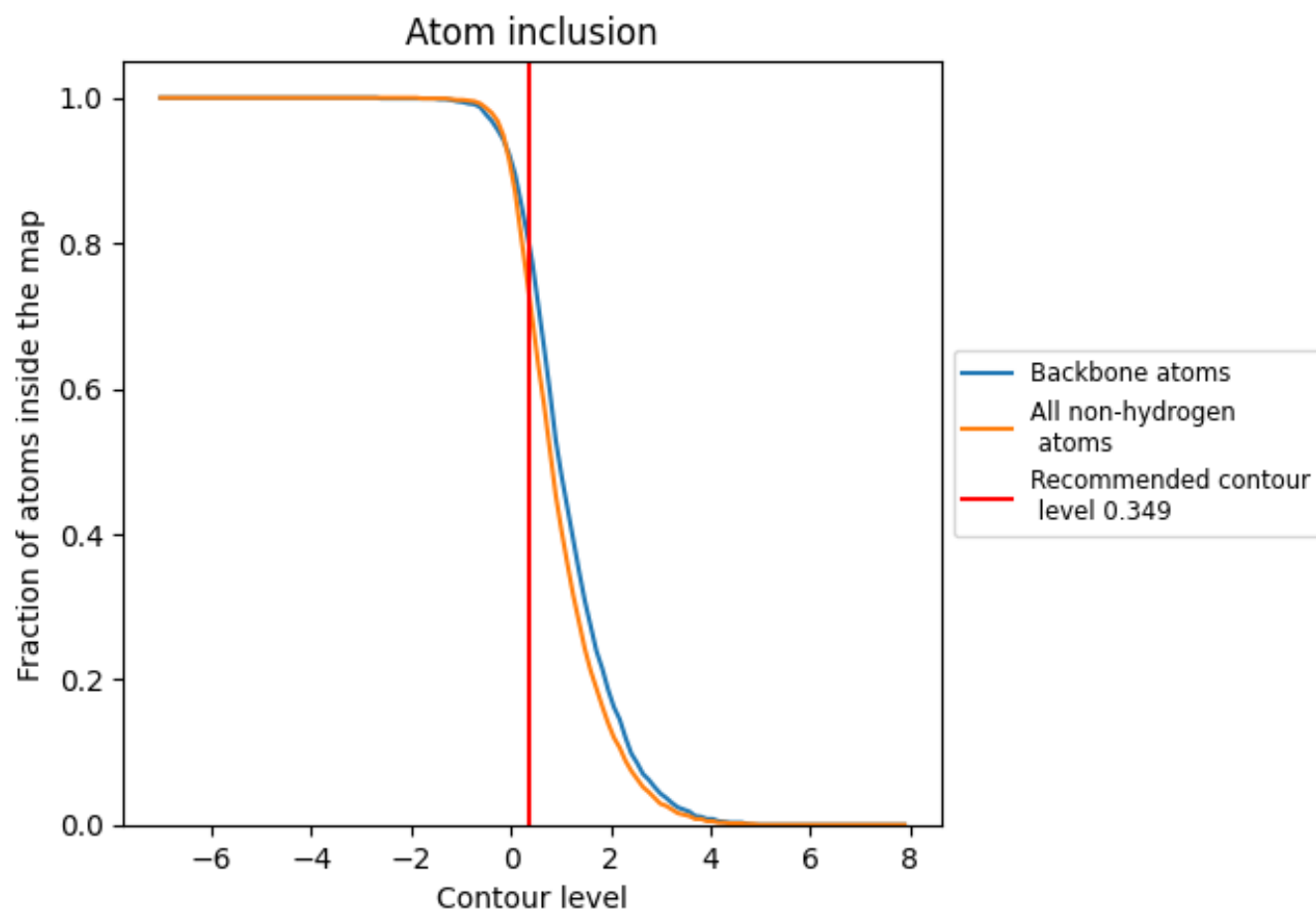
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.349).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 74% 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 (0.349) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7360	<div></div> 0.3990
O	<div></div> 0.6890	<div></div> 0.3680
P	<div></div> 0.6860	<div></div> 0.3750
Q	<div></div> 0.7800	<div></div> 0.4130
R	<div></div> 0.7460	<div></div> 0.4080

