



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 03:59 PM UTC

PDB ID : 9YR6 / pdb_00009yr6
EMDB ID : EMD-73361
Title : Structure of HTTQ23-HAP40 complex bound to a small molecule ligand
Authors : Balakrishnan, S.; Deme, J.; Lea, S.M.; Harding, R.J.
Deposited on : 2025-10-16
Resolution : 2.30 Å(reported)
Based on initial model : 6X90

This is a Full wwPDB EM Validation 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
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

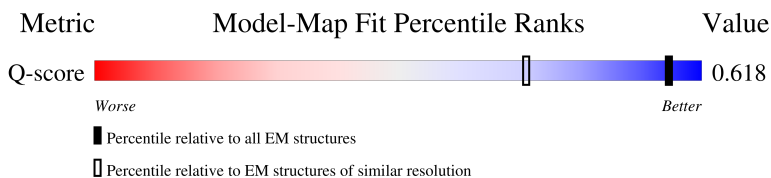
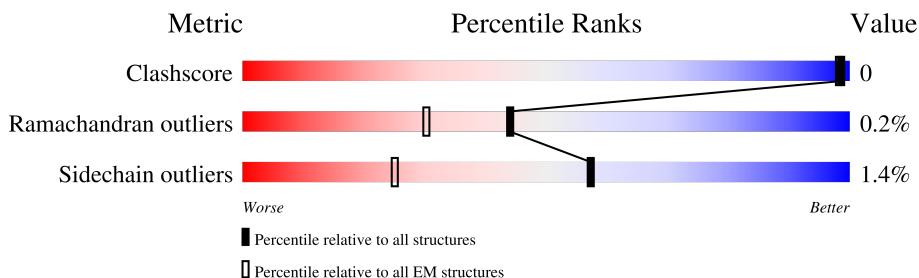
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.30 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	4254 (1.80 - 2.80)

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	3156	
2	B	389	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 42907 atoms, of which 21699 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 Huntingtin.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2429	Total	C	H	N	O	S	0	0
			38627	12219	19551	3283	3452	122		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	39	GLN	-	insertion	UNP P42858
A	40	GLN	-	insertion	UNP P42858
A	2311	HIS	TYR	conflict	UNP P42858
A	2788	ILE	VAL	conflict	UNP P42858
A	3145	GLY	-	expression tag	UNP P42858
A	3146	GLY	-	expression tag	UNP P42858
A	3147	SER	-	expression tag	UNP P42858
A	3148	GLY	-	expression tag	UNP P42858
A	3149	ASP	-	expression tag	UNP P42858
A	3150	TYR	-	expression tag	UNP P42858
A	3151	LYS	-	expression tag	UNP P42858
A	3152	ASP	-	expression tag	UNP P42858
A	3153	ASP	-	expression tag	UNP P42858
A	3154	ASP	-	expression tag	UNP P42858
A	3155	ASP	-	expression tag	UNP P42858
A	3156	LYS	-	expression tag	UNP P42858

- Molecule 2 is a protein called 40-kDa huntingtin-associated protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	280	Total	C	H	N	O	S	0	0
			4257	1334	2148	380	385	10		

There are 18 discrepancies between the modelled and reference sequences:

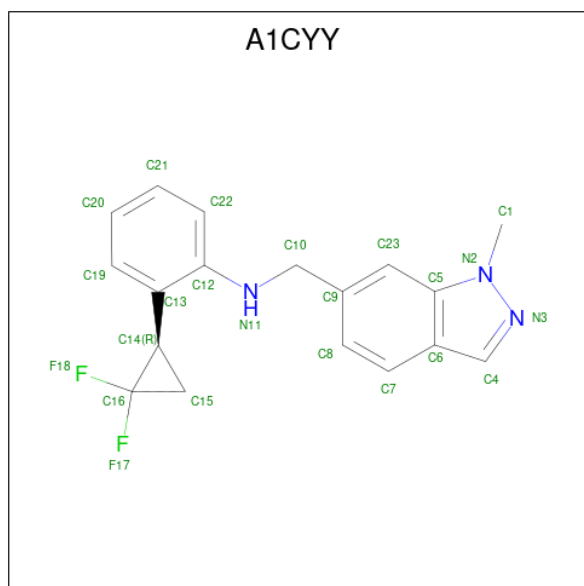
Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	expression tag	UNP P23610

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	expression tag	UNP P23610
B	-15	HIS	-	expression tag	UNP P23610
B	-14	HIS	-	expression tag	UNP P23610
B	-13	HIS	-	expression tag	UNP P23610
B	-12	HIS	-	expression tag	UNP P23610
B	-11	HIS	-	expression tag	UNP P23610
B	-10	SER	-	expression tag	UNP P23610
B	-9	SER	-	expression tag	UNP P23610
B	-8	GLY	-	expression tag	UNP P23610
B	-7	ARG	-	expression tag	UNP P23610
B	-6	GLU	-	expression tag	UNP P23610
B	-5	ASN	-	expression tag	UNP P23610
B	-4	LEU	-	expression tag	UNP P23610
B	-3	TYR	-	expression tag	UNP P23610
B	-2	PHE	-	expression tag	UNP P23610
B	-1	GLN	-	expression tag	UNP P23610
B	0	GLY	-	expression tag	UNP P23610

- Molecule 3 is 2-[(1R)-2,2-difluorocyclopropyl]-N-[(1-methyl-1H-indazol-6-yl)methyl]aniline (CCD ID: A1CYY) (formula: C₁₈H₁₇F₂N₃) (labeled as "Ligand of Interest" by depositor).

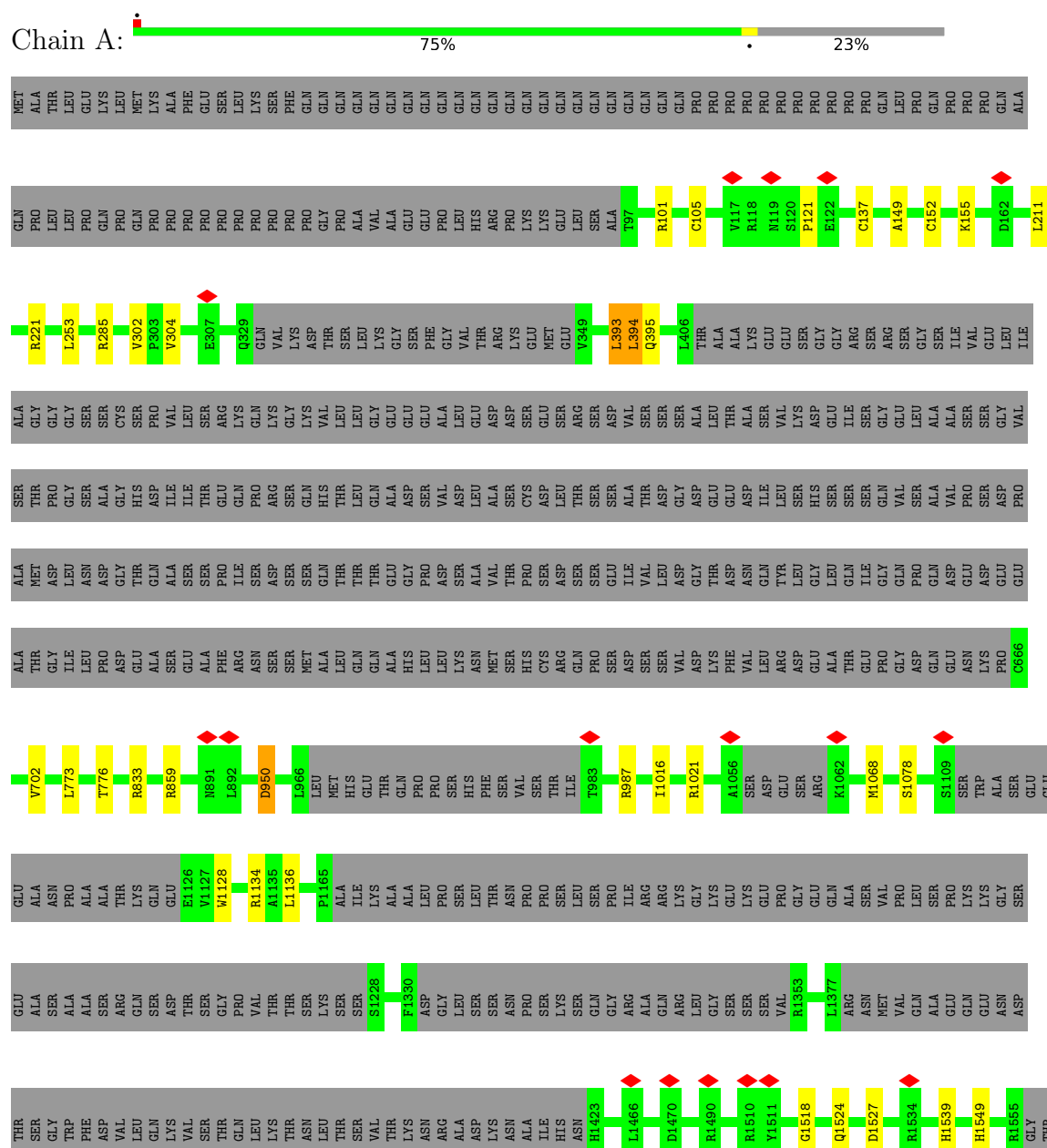


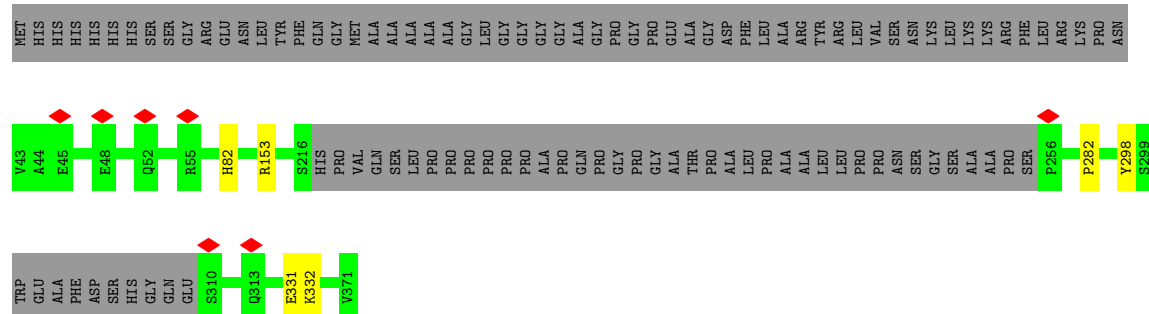
Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	F	N	0
			23	18	2	3	

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: Huntingtin





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	387879	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 ($e^-/\text{\AA}^2$)	51.1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	165000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.717	Depositor
Minimum map value	-0.112	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.07	Depositor
Map size (\AA)	374.784, 374.784, 374.784	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.732, 0.732, 0.732	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A1CYY

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	0.74	2/19449 (0.0%)	1.35	35/26413 (0.1%)
2	B	0.74	0/2145	1.36	3/2913 (0.1%)
All	All	0.74	2/21594 (0.0%)	1.35	38/29326 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1962	ARG	CZ-NH2	-9.72	1.20	1.33
1	A	1962	ARG	CZ-NH1	-7.70	1.22	1.32

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	302	VAL	CB-CA-C	-9.76	104.43	113.70
1	A	302	VAL	N-CA-CB	8.24	116.04	110.52
1	A	2210	LEU	CB-CG-CD1	8.18	135.24	110.70
1	A	2797	LEU	CB-CG-CD1	7.01	131.73	110.70
1	A	1996	ASP	CA-CB-CG	6.85	119.45	112.60
1	A	393	LEU	CB-CG-CD1	6.46	130.08	110.70
1	A	950	ASP	CA-CB-CG	6.31	118.91	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2600	LEU	CB-CG-CD1	6.29	129.56	110.70
1	A	1134	ARG	NE-CZ-NH2	6.24	124.81	119.20
1	A	1518	GLY	CA-C-N	6.19	124.14	120.24
1	A	1518	GLY	C-N-CA	6.19	124.14	120.24
1	A	2792	LEU	CB-CG-CD1	5.94	128.51	110.70
1	A	1962	ARG	NE-CZ-NH2	5.79	124.41	119.20
1	A	1136	LEU	CA-C-N	5.72	123.85	120.24
1	A	1136	LEU	C-N-CA	5.72	123.85	120.24
1	A	221	ARG	NE-CZ-NH2	5.71	124.33	119.20
1	A	1527	ASP	CA-CB-CG	5.65	118.25	112.60
2	B	282	PRO	N-CA-CB	5.51	106.28	103.19
1	A	1021	ARG	NE-CZ-NH2	5.47	124.12	119.20
1	A	2916	ARG	NE-CZ-NH2	5.42	124.08	119.20
1	A	2040	ARG	NE-CZ-NH2	5.38	124.04	119.20
1	A	394	LEU	CB-CG-CD1	5.33	126.70	110.70
2	B	82	HIS	CA-C-N	5.31	125.00	121.13
2	B	82	HIS	C-N-CA	5.31	125.00	121.13
1	A	1539	HIS	CB-CG-CD2	-5.30	124.31	131.20
1	A	3136	ARG	NE-CZ-NH2	5.28	123.95	119.20
1	A	1637	ASN	CA-CB-CG	5.26	117.86	112.60
1	A	285	ARG	NE-CZ-NH2	5.21	123.89	119.20
1	A	2017	ARG	NE-CZ-NH2	5.20	123.88	119.20
1	A	833	ARG	NE-CZ-NH2	5.15	123.84	119.20
1	A	1893	ARG	NE-CZ-NH2	5.13	123.82	119.20
1	A	859	ARG	NE-CZ-NH2	5.12	123.81	119.20
1	A	101	ARG	NE-CZ-NH2	5.08	123.77	119.20
1	A	1857	GLN	OE1-CD-NE2	-5.07	117.53	122.60
1	A	2664	HIS	CB-CG-CD2	-5.03	124.66	131.20
1	A	2662	ARG	NE-CZ-NH2	5.02	123.72	119.20
1	A	1128	TRP	CB-CA-C	5.02	115.37	111.00
1	A	1652	ASP	CA-CB-CG	5.00	117.60	112.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	987	ARG	Sidechain
2	B	153	ARG	Sidechain
2	B	298	TYR	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	19076	19551	19535	8	0
2	B	2109	2148	2146	0	0
3	A	23	0	0	2	0
All	All	21208	21699	21681	8	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 0.

All (8) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:ILE:HD12	3:A:3201:A1CYY:C15	2.11	0.81
1:A:2518:VAL:HG11	1:A:2593:LEU:HD21	1.90	0.54
1:A:1078:SER:OG	3:A:3201:A1CYY:C20	2.56	0.53
1:A:2788:ILE:O	1:A:2792:LEU:HG	2.11	0.50
1:A:152:CYS:HA	1:A:155:LYS:HZ2	1.79	0.46
1:A:1592:LEU:HD23	1:A:1592:LEU:C	2.44	0.43
1:A:137:CYS:HB3	1:A:149:ALA:HB2	2.03	0.41
1:A:773:LEU:HA	1:A:776:THR:HG22	2.04	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	2391/3156 (76%)	2335 (98%)	51 (2%)	5 (0%)	43 55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	274/389 (70%)	270 (98%)	3 (1%)	1 (0%)	30	38
All	All	2665/3545 (75%)	2605 (98%)	54 (2%)	6 (0%)	44	55

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	PRO
1	A	2574	HIS
2	B	331	GLU
1	A	2355	PRO
1	A	2518	VAL
1	A	304	VAL

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	2145/2778 (77%)	2113 (98%)	32 (2%)	57	75
2	B	211/290 (73%)	210 (100%)	1 (0%)	81	90
All	All	2356/3068 (77%)	2323 (99%)	33 (1%)	57	76

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	CYS
1	A	211	LEU
1	A	253	LEU
1	A	393	LEU
1	A	394	LEU
1	A	395	GLN
1	A	702	VAL
1	A	950	ASP
1	A	1068	MET
1	A	1524	GLN

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Mol	Chain	Res	Type
1	A	1549	HIS
1	A	1600	GLU
1	A	1610	ARG
1	A	1652	ASP
1	A	1740	GLU
1	A	1741	THR
1	A	1763	LYS
1	A	1982	ILE
1	A	2052	GLN
1	A	2138	MET
1	A	2139	ASN
1	A	2270	GLN
1	A	2308	SER
1	A	2327	GLN
1	A	2370	GLU
1	A	2564	VAL
1	A	2573	HIS
1	A	2597	GLU
1	A	2803	GLN
1	A	2849	VAL
1	A	3042	LEU
1	A	3048	ARG
2	B	332	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	169	GLN
1	A	246	ASN
1	A	260	ASN
1	A	287	GLN
1	A	295	ASN
1	A	308	HIS
1	A	355	GLN
1	A	365	HIS
1	A	701	ASN
1	A	757	ASN
1	A	911	ASN
1	A	1089	GLN
1	A	1315	GLN
1	A	1423	HIS
1	A	1437	GLN

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Mol	Chain	Res	Type
1	A	1447	GLN
1	A	1449	GLN
1	A	1480	GLN
1	A	1488	GLN
1	A	1569	GLN
1	A	1624	GLN
1	A	1770	GLN
1	A	1776	GLN
1	A	1840	GLN
1	A	1846	ASN
1	A	1892	ASN
1	A	1924	ASN
1	A	1927	GLN
1	A	2025	ASN
1	A	2134	ASN
1	A	2270	GLN
1	A	2278	GLN
1	A	2289	GLN
1	A	2396	ASN
1	A	2777	HIS
1	A	2859	GLN
2	B	175	GLN
2	B	354	HIS
2	B	361	GLN

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 ⓘ

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	$\# Z > 2$
3	A1CYY	A	3201	-	26,26,26	0.47	0	37,39,39	0.68	1 (2%)

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
3	A1CYY	A	3201	-	-	4/9/17/17	0/4/4/4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	3201	A1CYY	C15-C14-C16	2.51	59.53	57.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3201	A1CYY	C12-C13-C14-C15
3	A	3201	A1CYY	C19-C13-C14-C15
3	A	3201	A1CYY	C12-C13-C14-C16
3	A	3201	A1CYY	C19-C13-C14-C16

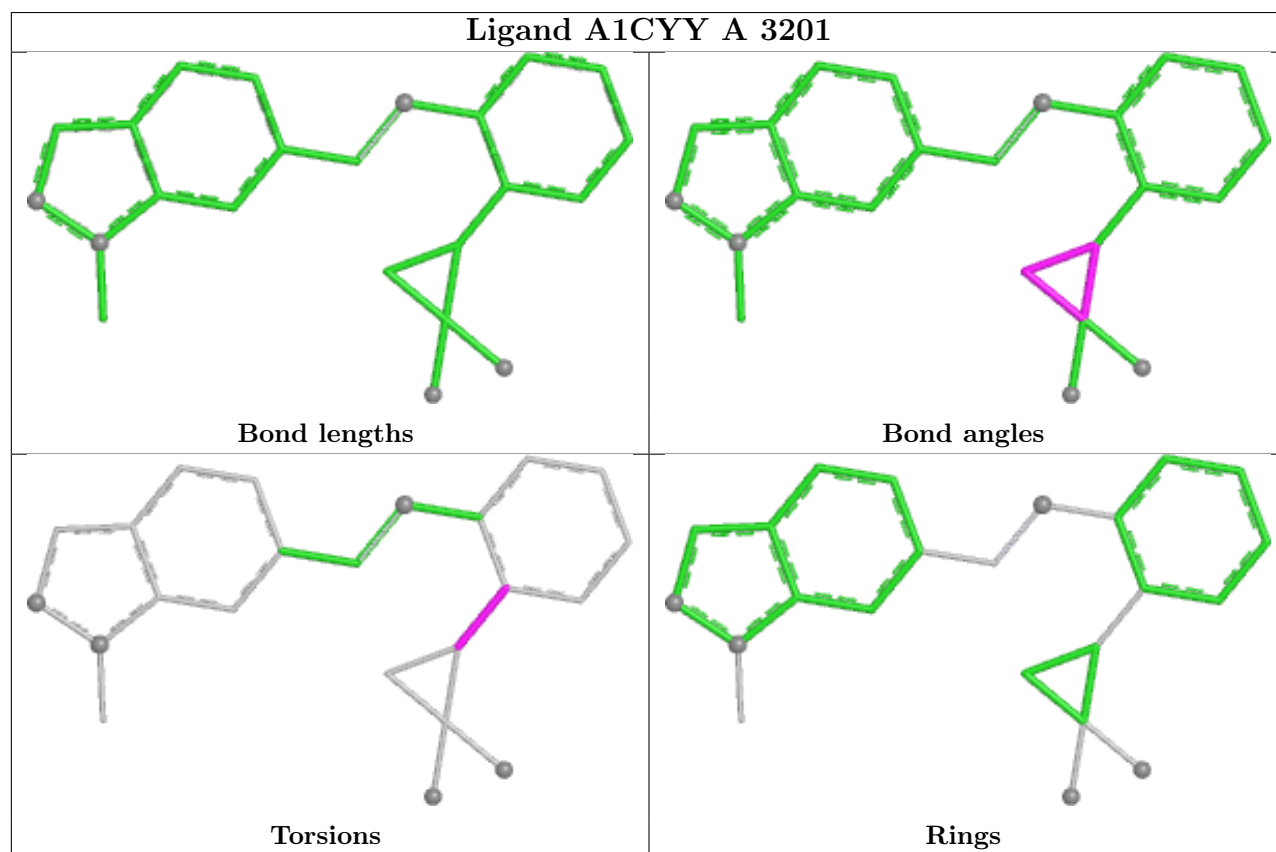
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3201	A1CYY	2	0

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.

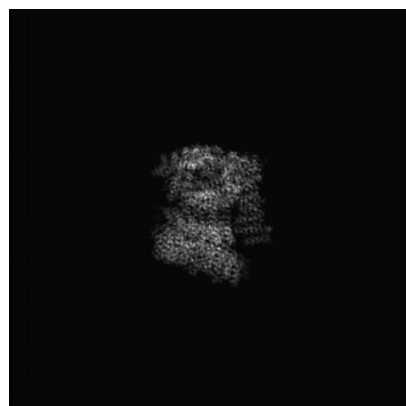
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73361. These allow visual inspection of the internal detail of the map and identification of artifacts.

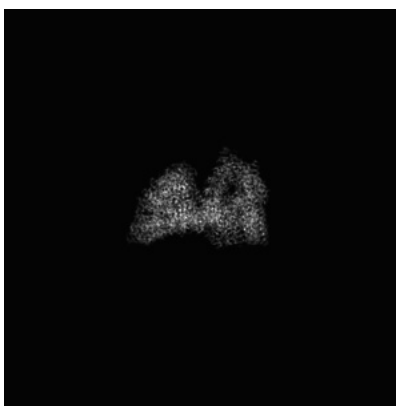
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

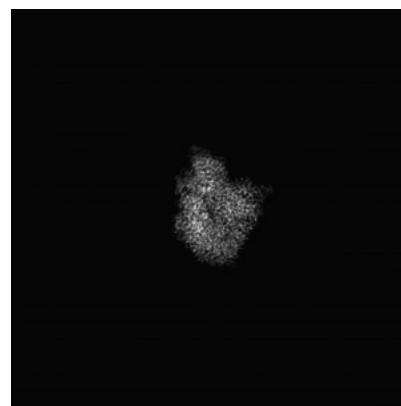
6.1.1 Primary map



X

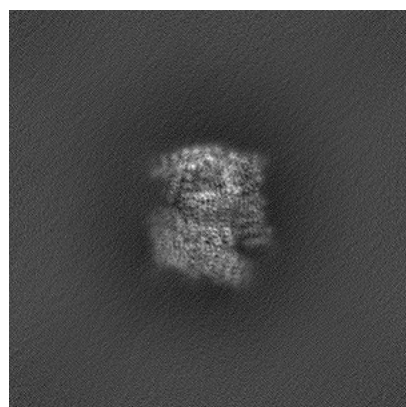


Y

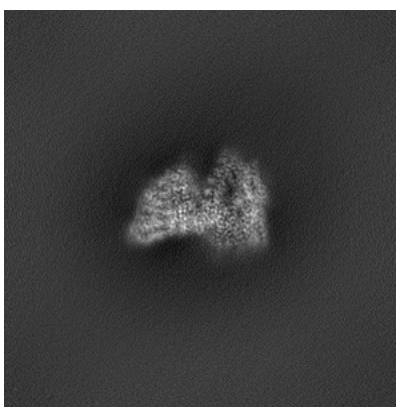


Z

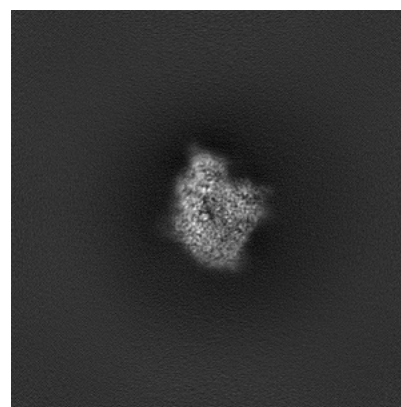
6.1.2 Raw map



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: 256

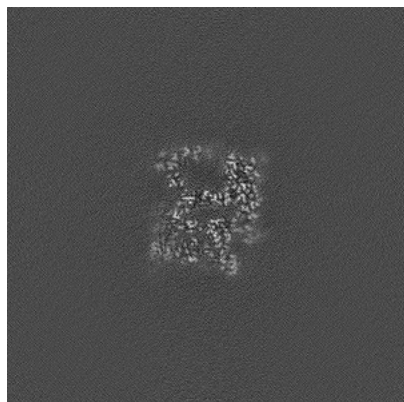


Y Index: 256

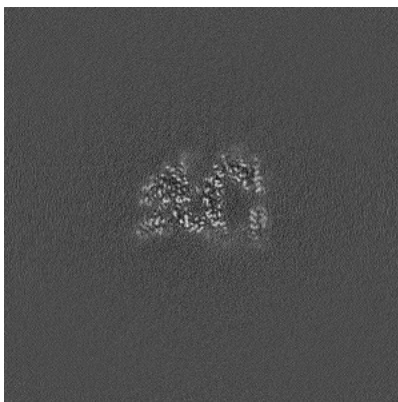


Z Index: 256

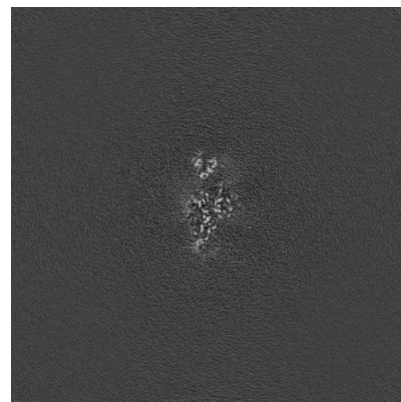
6.2.2 Raw map



X Index: 256



Y Index: 256

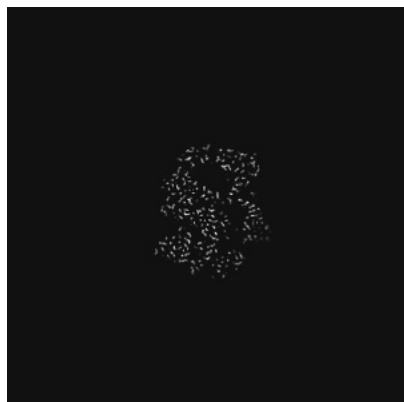


Z Index: 256

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

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 239

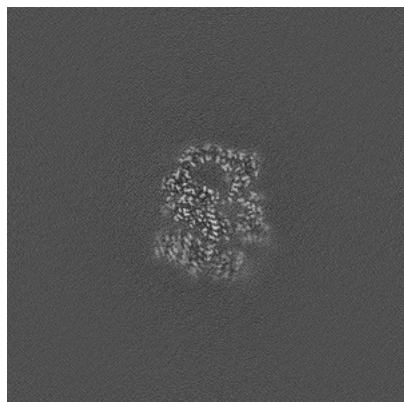


Y Index: 257

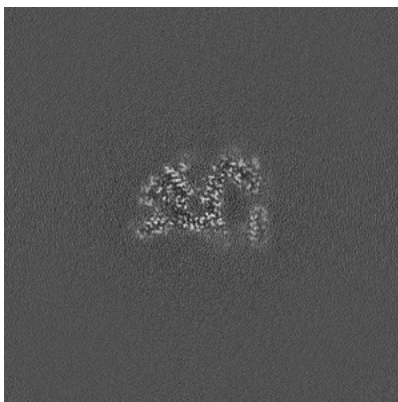


Z Index: 230

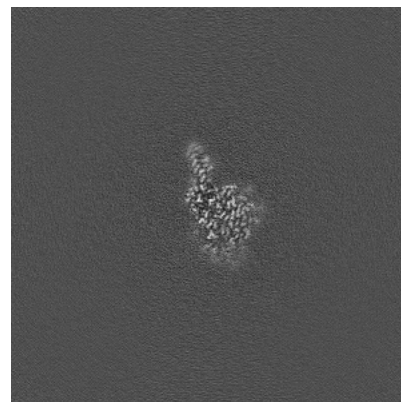
6.3.2 Raw map



X Index: 240



Y Index: 258

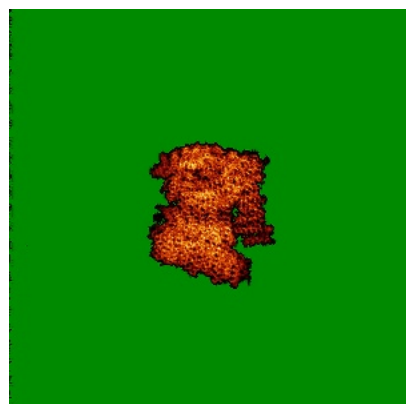


Z Index: 230

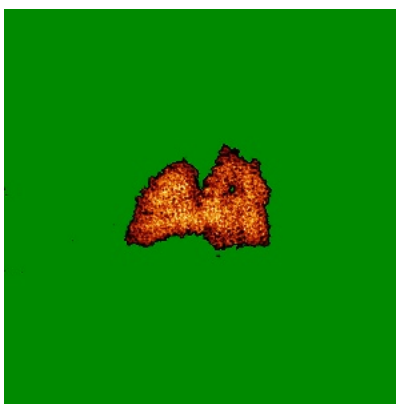
The images above show the largest variance slices of the map in three orthogonal directions.

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

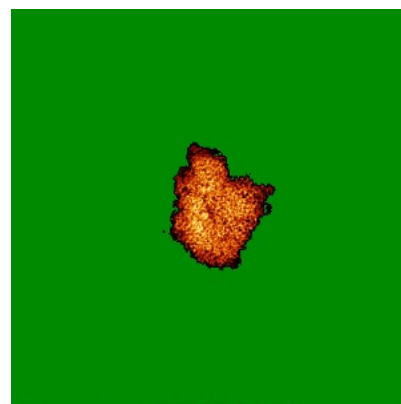
6.4.1 Primary map



X

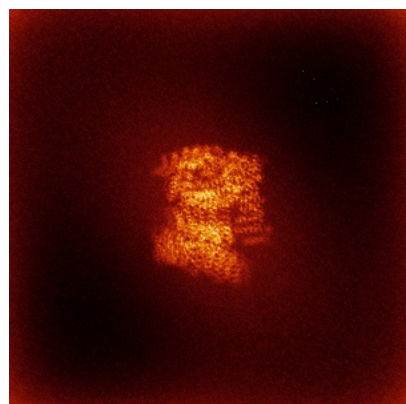


Y

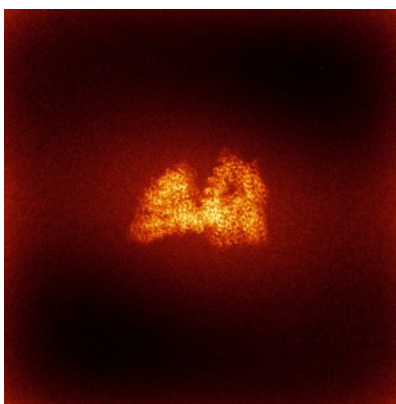


Z

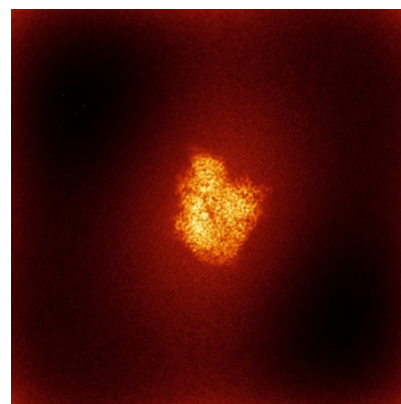
6.4.2 Raw map



X



Y

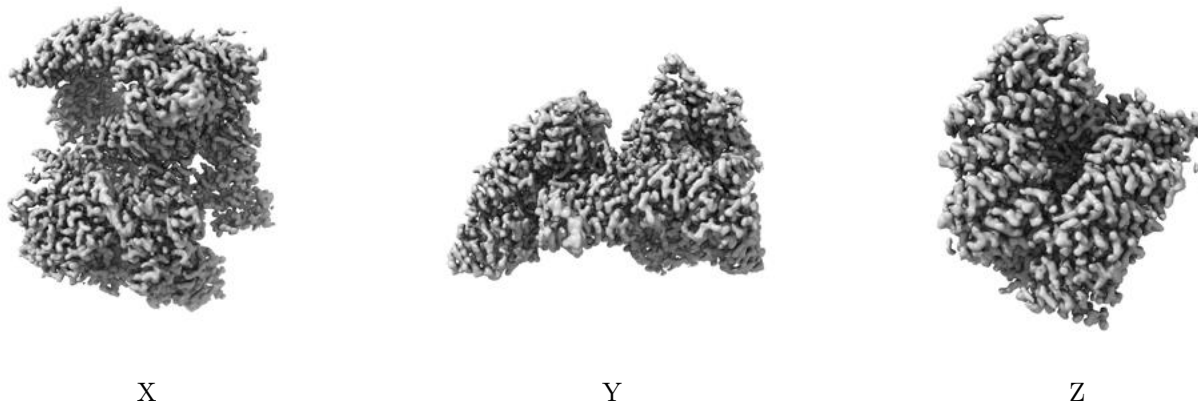


Z

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.

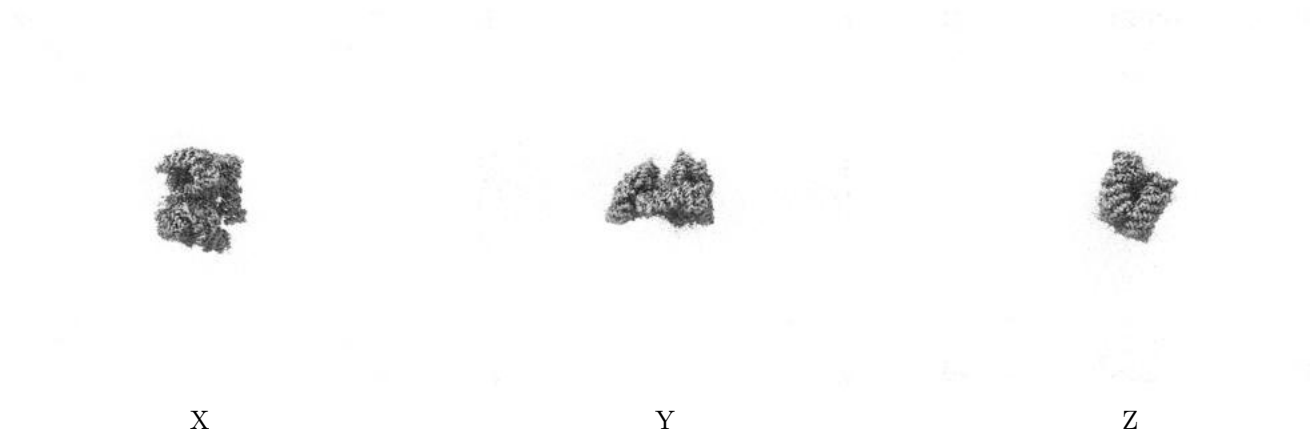
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

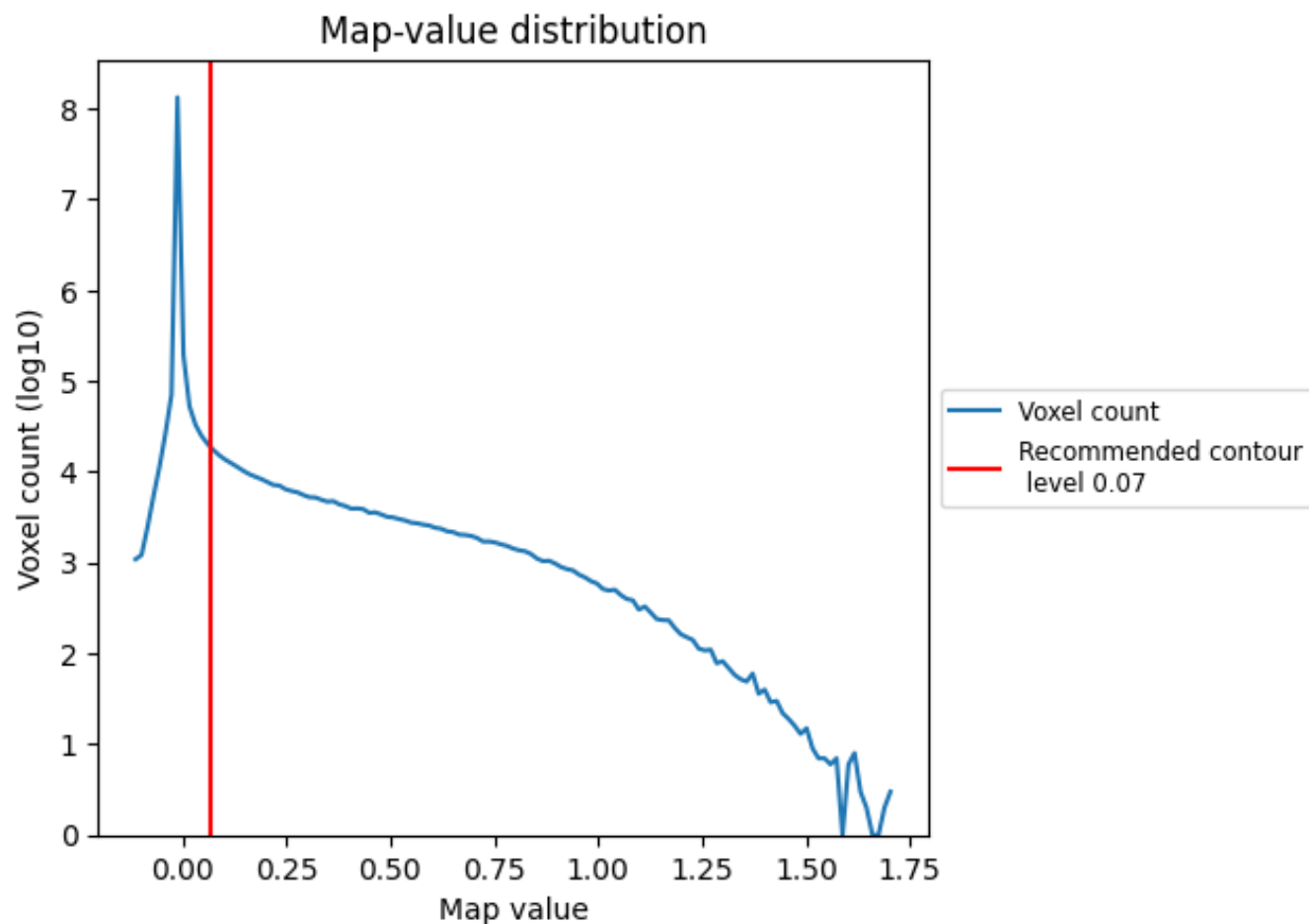
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

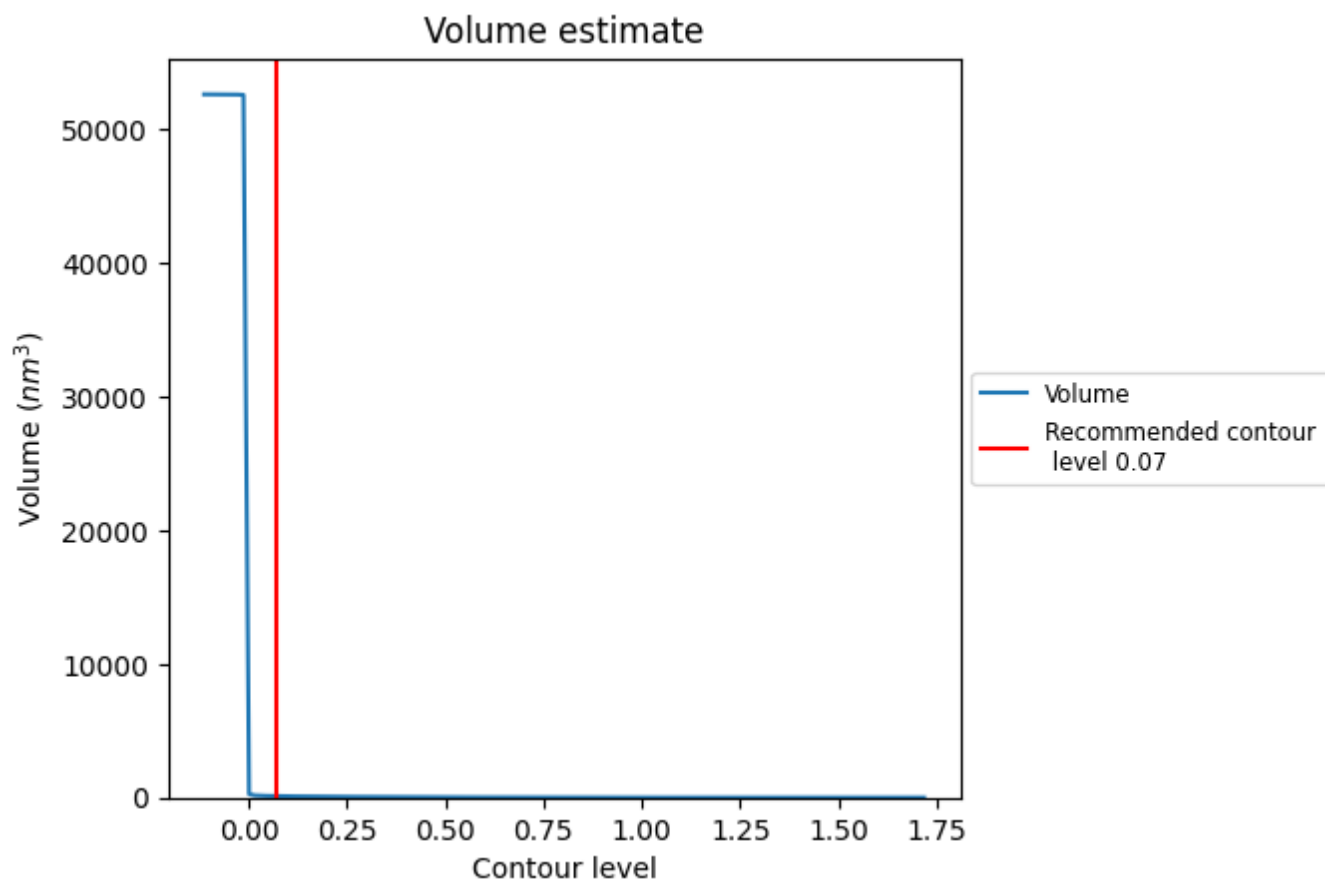
This section contains the results of statistical analysis of the map.

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.

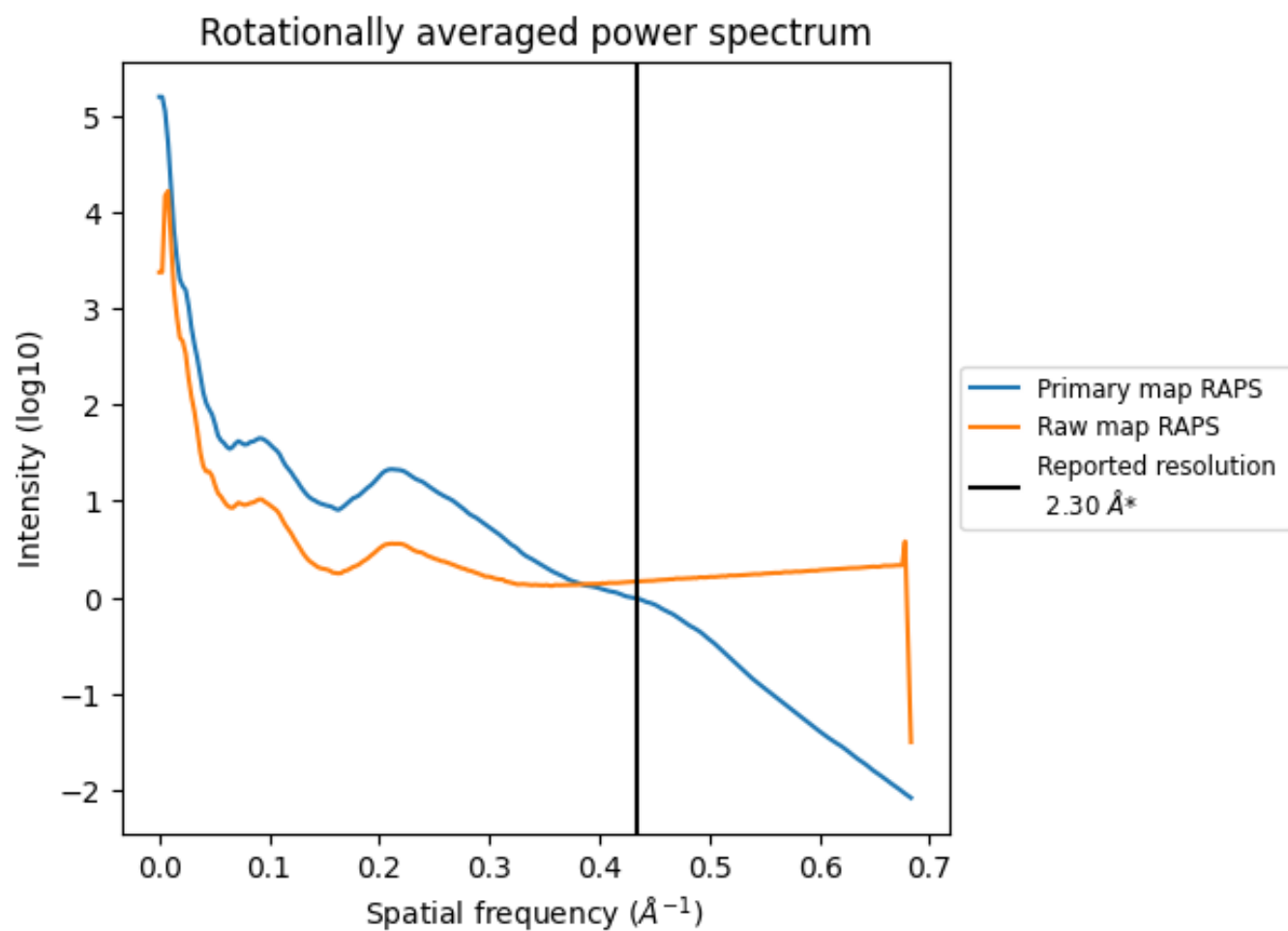
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 112 nm^3 ; this corresponds to an approximate mass of 101 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 ⓘ

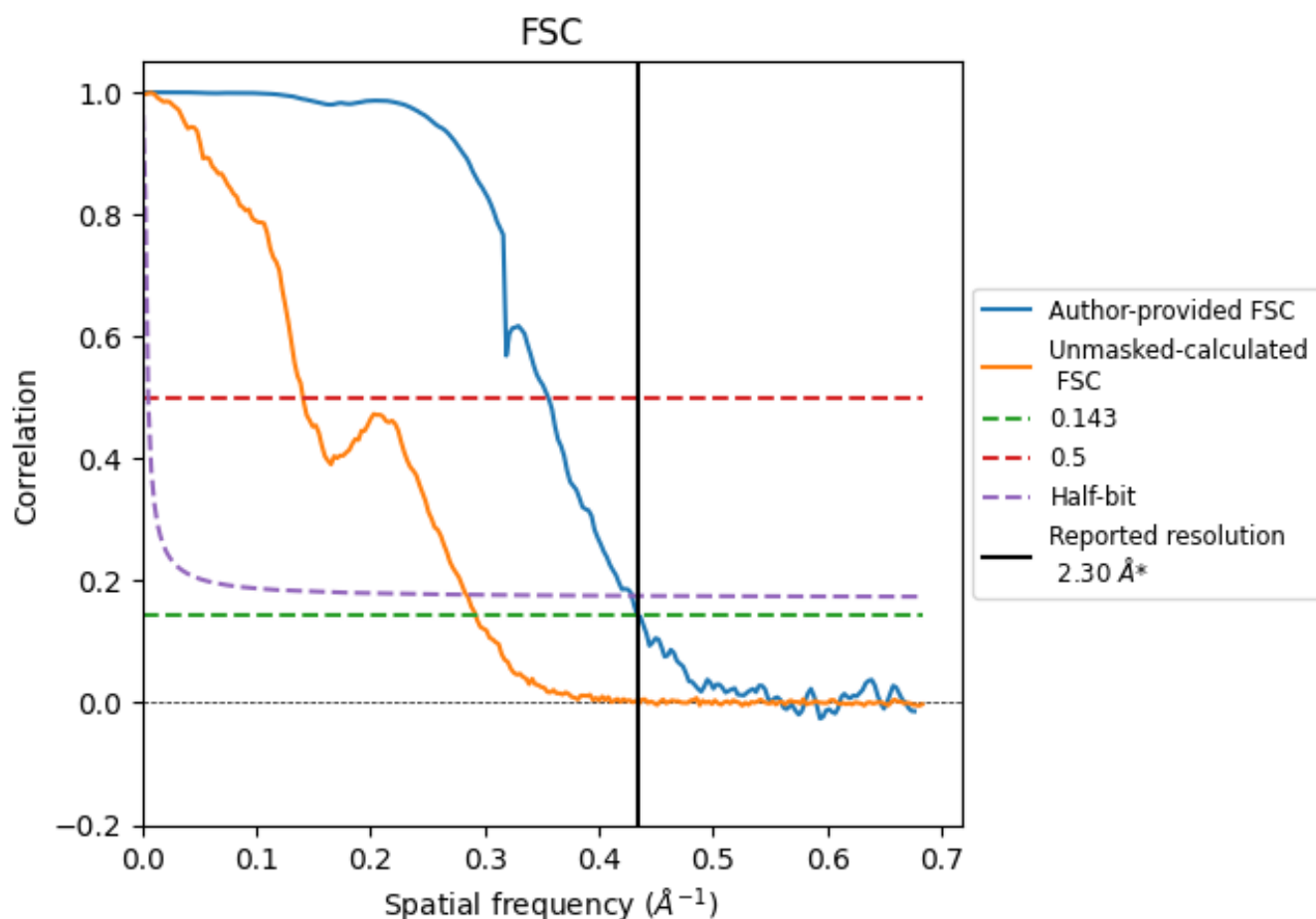


*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

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 0.435 \AA^{-1}

8.2 Resolution estimates [i](#)

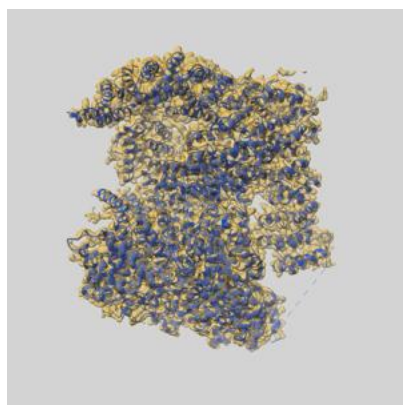
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	2.30	2.81	2.33
Unmasked-calculated*	3.42	7.10	3.52

*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 3.42 differs from the reported value 2.3 by more than 10 %

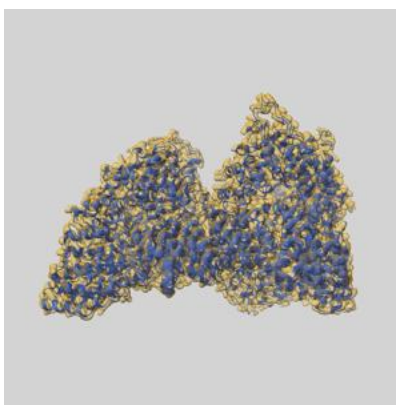
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73361 and PDB model 9YR6. Per-residue inclusion information can be found in section [3](#) on page [5](#).

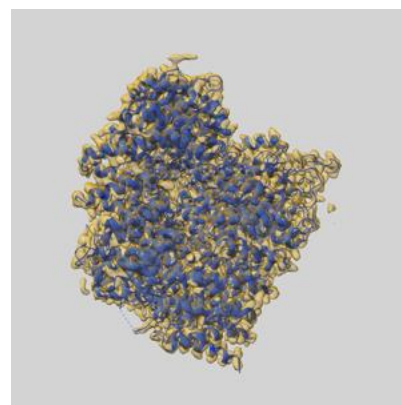
9.1 Map-model overlay [i](#)



X



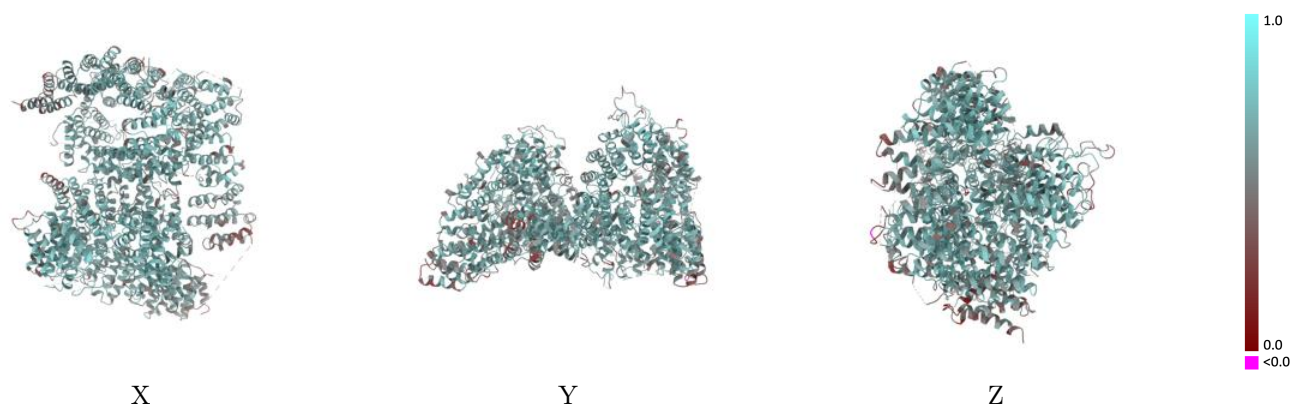
Y



Z

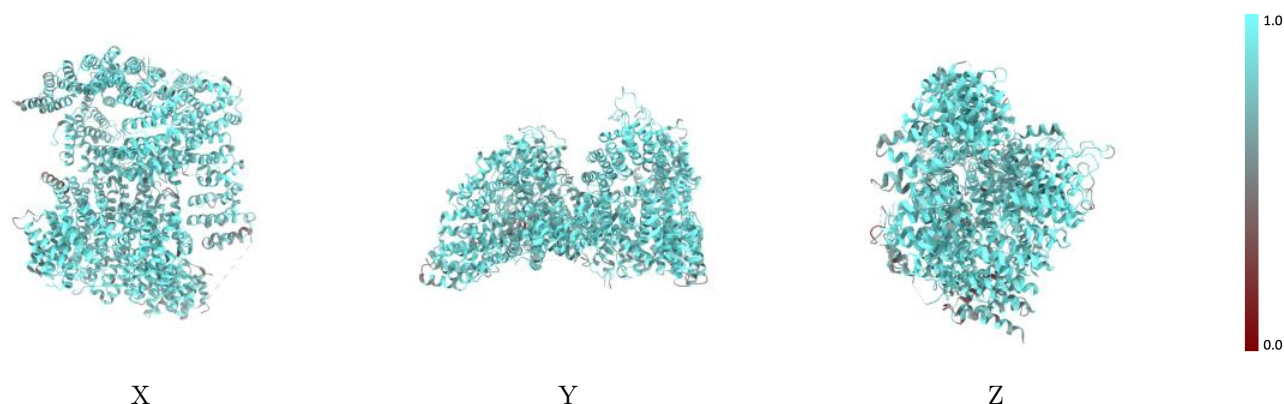
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



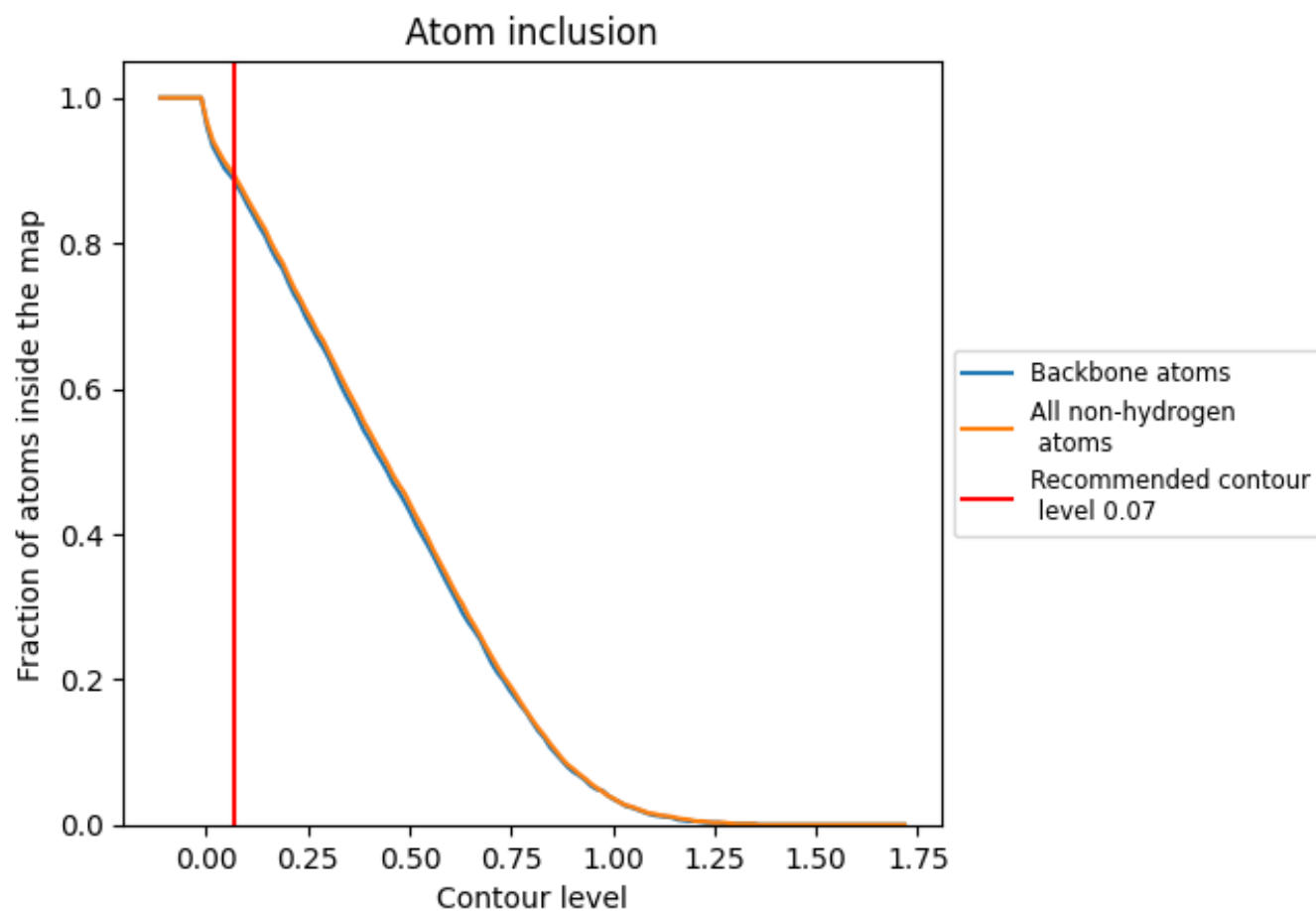
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8930	<div></div> 0.6180
A	<div></div> 0.8930	<div></div> 0.6140
B	<div></div> 0.9000	<div></div> 0.6500

