



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 12:35 AM UTC

PDB ID : 9IZ0 / pdb_00009iz0
EMDB ID : EMD-61006
Title : ATM/Tel1 bound to CHK2 peptide
Authors : Wang, P.
Deposited on : 2024-07-31
Resolution : 3.63 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
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

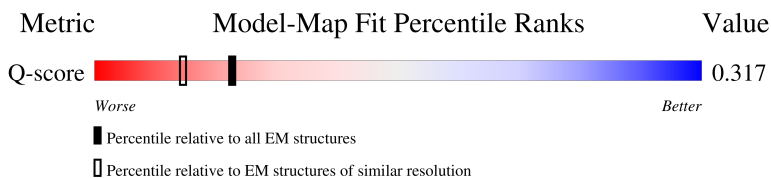
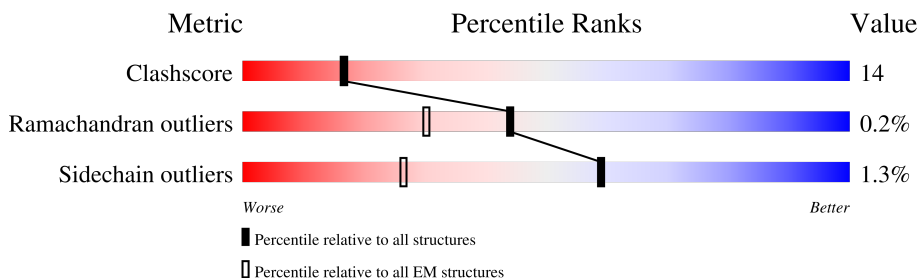
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.63 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	11696 (3.13 - 4.13)

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	F	8	
2	A	2812	
2	B	2812	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 32048 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.

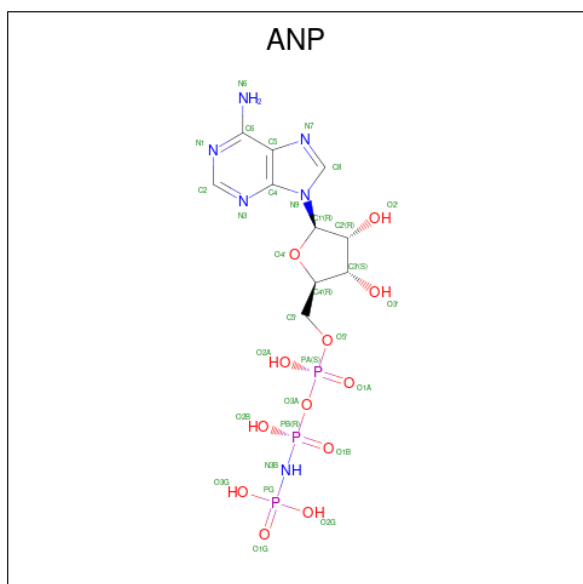
- Molecule 1 is a protein called VAL-SER-THR-GLN-GLU-LEU-TYR-SER.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	F	8	Total	C	N	O	0	0
			64	40	9	15		

- Molecule 2 is a protein called Serine/threonine-protein kinase tel1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	2430	Total	C	N	O	S	0	0
			15929	10030	2839	3040	20		
2	B	2424	Total	C	N	O	S	0	0
			15993	10091	2847	3035	20		

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	10	6	12	3	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	B	1	31	10	6	12	3	0

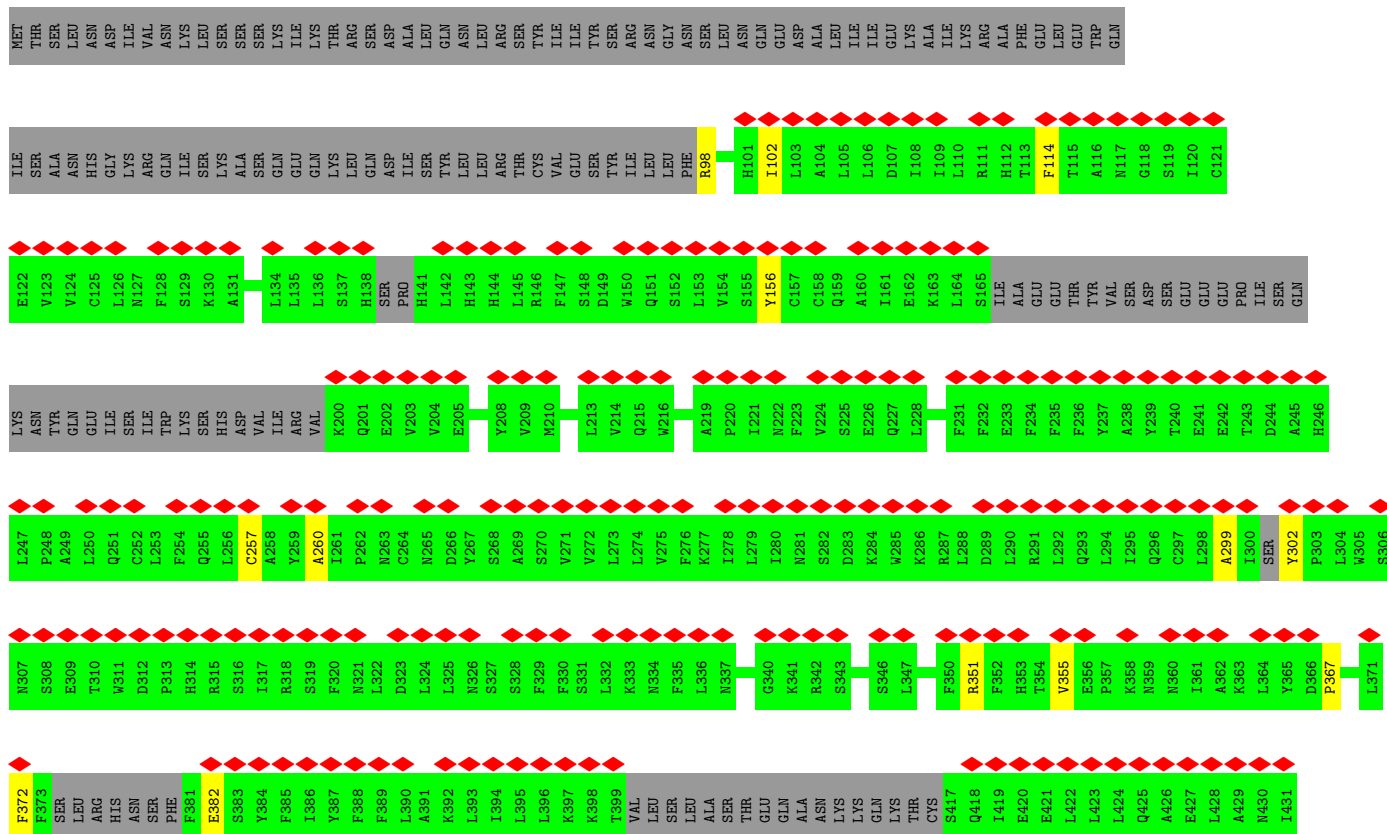
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: VAL-SER-THR-GLN-GLU-LEU-TYR-SER



- Molecule 2: Serine/threonine-protein kinase tell









MET	THR	SER	LEU	ASN	ASP	ILE	VAL	GLN	ASN	GLN	LEU	SER	THR	ARG	SER	ASP	ALA	LEU	GLN	THR	LEU	ARG	SER	THR	ILE	GLY	ASN	LEU	ASN	SER	LEU	GLN	ASP	ALA	LEU	ILE	GLY	LEU	ALA	ILE	LYS	ARG	ALA	PHE	GLU	LEU	TRP	GLN											
ILE	SER	ALA	ASN	HIS	GLY	LYS	ARG	GLN	ASN	GLN	LEU	SER	THR	ILE	GLY	LEU	ALA	LEU	ILE	GLY	LEU	ARG	SER	THR	ILE	GLY	LEU	ASN	LEU	PHE	R98	E99	P100	GLU	H101	H102	L103	A104	L105	L106	D107	I108	I109	L110	R111	H112	T113	F114	T115	A116	N117	G118	S119	I120					
C121	E122	V123	V124	C125	L126	N127	F128	S129	K130	A131	R132	L133	L134	L135	S139	P140	H141	L142	H143	H144	L145	R146	F147	S148	D149	W150	Q151	V154	C157	C158	Q159	ALA	I161	E162	K163	L164	S165	ILE	ALA	GLU	GLU	THR	VAL	SER	ASP	GLU	GLU	PRO	ILE	GLN	LYS	ASN							
TYR	GLN	GLU	ILE	ILE	TRP	LYS	HIS	VAL	ILE	ARG	K200	Q201	E202	V203	V204	E205	L206	I207	Y208	Y209	W210	R211	S212	L213	D149	V214	Q215	W216	Y217	A218	A219	P220	F223	V224	S225	E226	F231	F232	E233	F234	F235	F236	Y237	A238	Y239	T240	E241	E242	T243	L247	L250	Q251							
A258	Y259	A260	I261	F262	N263	C264	N265	D266	Y267	S268	A269	S270	V271	V272	L273	L274	V275	F276	K277	L278	L279	S282	D283	K284	W285	K286	R287	L288	L290	R291	L292	Q293	L294	T295	Q296	C297	LEU	A299	I300	SER	Y302	F303	L304	K305	E309	T310	K311	D312	F313	H314	R315	S316	T317	R318	S319				
F320	N321	L322	D323	L324	L325	S326	S327	S328	F329	F330	S331	L332	K333	N334	F335	L336	F338	F339	R342	S343	S344	L345	S346	L347	F350	H353	T354	V355	E356	I361	A362	K363	F373	SER	LEU	ARG	HIS	ASN	SER	PHE	F381	E382	S383	Y384	F385	I386	Y387	PHE	F389	K392	L393	I394							
L395	L396	K397	K398	T399	VAL	LEU	SER	LEU	ALA	SER	THR	GLN	GLN	ALA	ASN	LYS	LYS	GLN	LYS	THR	S417	Q418	I419	E420	F421	L422	L423	L424	Q425	T431	S434	S437	L438	Q439	V442	L443	A446	I447	S448	L451	T452	N453	L457	T467	K468	K469	K470	N471	E472	L473									
Q474	S475	F478	F482	S491	SER	H493	L503	A504	A505	S507	R508	ALA	S511	N512	S513	V514	T515	SER	F517	L523	N527	P531	R542	I546	P553	H554	L570	L574	F575	G577	Q578	S579	V588	H592	L596	F597	S598	K599	E600	G601	E602	L603																	
P604	S607	F608	I613	H620	H621	F623	S628	T633	T634	E635	L636	R637	S638	P639	F640	E641	L644	F645	H646	L647	K648	F649	A650	V651	SER	P653	T655	D663	GLU	ILE	CYS	LYS	GLN	THR	GLU	GLY	CYS	TYR	PRO	PHE	ASN	S678	M679	H680	T681	F682	I688	D699											
GLU	I701	D707	L711	D712	K713	P716	SER	PHE	GLU	ALA	VAL	MET	ILE	PHE	SER	GLN	ILE	SER	PHE	GLN	LYS	ASN	CYS	ILE	HIS	ASN	VAL	THR	PRO	ASN	ASN	ASN	LEU	VAL	ILE	PHE	LYS	THR	GLU	GLY	CYS	TYR	PRO	PHE	ASN	S678	M679	H680	T681	F682	I688	D699							
N768	H769	S770	Y771	D772	F773	I774	I775	N776	Q783	F784	T785	D788	GLU	PRO	K791	H792	L793	R794	TYR	GLU	ILE	GLY	PHE	LEU	ASN	D800	L801	R802	R803	S804	T805	H806	F807	R808	D809	V810	L813	K814	T815	L816	V817	L818	Y819	I820	M821	D822	M823	A824	S825	K826	N827	V828	F829	I830	LYS	PRO	GLN	GLU	
PHE	ASP	HIS	ASP	GLU	TYR	PHE	SER	GLN	GLU	GLU	GLU	ASP	ILE	TYR	ARG	PRO	GLU	ASN	LEU	I855	R856	N857	H858	Q859	I860	L861	G862	L863	M864	E865	G866	S867	L868	E869	Q870	I871	R872	R873	T874	D875	L876	F877	I878	L879	Q880	K881	Y882	I883	D884	Y885	PHE	SER	SER	HIS	PRO	H891	D892	S893	L894
I895	N896	I897	L898	H899	L900	Y901	I903	E904	T905	F906	C907	F908	G909	M910	S911	A912	I913	G914	A915	Y916	F917	I918	D919	V920	A921	R922	T923	S924	E925	P926	I927	F928	Y929	K930	C931	L932	E933	I934	L935	A936	Q937	K938	I939	L940	M941	N942	Y943	D944	Y945	E946	R947	D948	E949	V950	I954	K961			





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64713	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.494	Depositor
Minimum map value	-1.293	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.27	Depositor
Map size (Å)	308.16, 308.16, 308.16	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: ANP

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	F	0.67	0/64	0.74	0/86
2	A	0.20	1/16139 (0.0%)	0.43	10/22100 (0.0%)
2	B	0.15	0/16185	0.36	3/22124 (0.0%)
All	All	0.18	1/32388 (0.0%)	0.39	13/44310 (0.0%)

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
2	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2658	LYS	CA-C	-12.38	1.36	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2334	PRO	CA-N-CD	-9.86	98.20	112.00
2	A	2661	PRO	N-CA-C	-6.93	103.89	113.53
2	B	2334	PRO	CA-N-CD	-6.40	103.04	112.00
2	B	2458	GLY	N-CA-C	-5.92	104.83	113.48
2	A	2457	SER	N-CA-C	5.72	117.84	108.52

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	2657	GLY	Mainchain

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	F	64	0	59	6	0
2	A	15929	0	12395	416	0
2	B	15993	0	12577	381	0
3	A	31	0	13	3	0
3	B	31	0	13	4	0
All	All	32048	0	25057	799	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 14.

The worst 5 of 799 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2195:LYS:HD3	2:A:2229:PHE:HB2	1.56	0.88
2:A:2018:LEU:HB3	2:A:2037:ARG:HH22	1.38	0.88
2:B:2459:ILE:HG22	2:B:2459:ILE:O	1.73	0.86
2:A:1399:LYS:HG3	2:A:1400:PRO:HD3	1.59	0.84
2:A:1492:MET:HE3	2:A:1492:MET:H	1.41	0.84

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	F	6/8 (75%)	5 (83%)	1 (17%)	0	100	100
2	A	2372/2812 (84%)	2222 (94%)	142 (6%)	8 (0%)	36	64
2	B	2330/2812 (83%)	2190 (94%)	137 (6%)	3 (0%)	48	78
All	All	4708/5632 (84%)	4417 (94%)	280 (6%)	11 (0%)	44	71

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	1571	LYS
2	A	2640	LYS
2	A	2658	LYS
2	A	2462	PRO
2	A	2562	ARG

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	F	8/8 (100%)	8 (100%)	0	100	100
2	A	1106/2621 (42%)	1090 (99%)	16 (1%)	59	68
2	B	1126/2621 (43%)	1113 (99%)	13 (1%)	63	70
All	All	2240/5250 (43%)	2211 (99%)	29 (1%)	59	69

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	2660	LEU
2	B	2730	LYS
2	B	1599	LEU
2	B	2726	ARG
2	B	1456	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1744	ASN
2	B	1957	ASN
2	B	1879	ASN
2	B	1996	ASN
2	A	2332	ASN

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](#)

2 ligands are 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	ANP	A	2901	-	33,33,33	0.93	4 (12%)	45,52,52	0.58	0
3	ANP	B	2901	-	33,33,33	0.93	4 (12%)	45,52,52	0.55	0

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	ANP	A	2901	-	-	5/18/38/38	0/3/3/3
3	ANP	B	2901	-	-	9/18/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2901	ANP	PG-O1G	2.54	1.50	1.46
3	A	2901	ANP	PG-O1G	2.48	1.49	1.46
3	B	2901	ANP	PG-N3B	2.47	1.69	1.63
3	A	2901	ANP	PG-N3B	2.44	1.69	1.63
3	A	2901	ANP	PB-O3A	-2.40	1.56	1.59

There are no bond angle outliers.

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

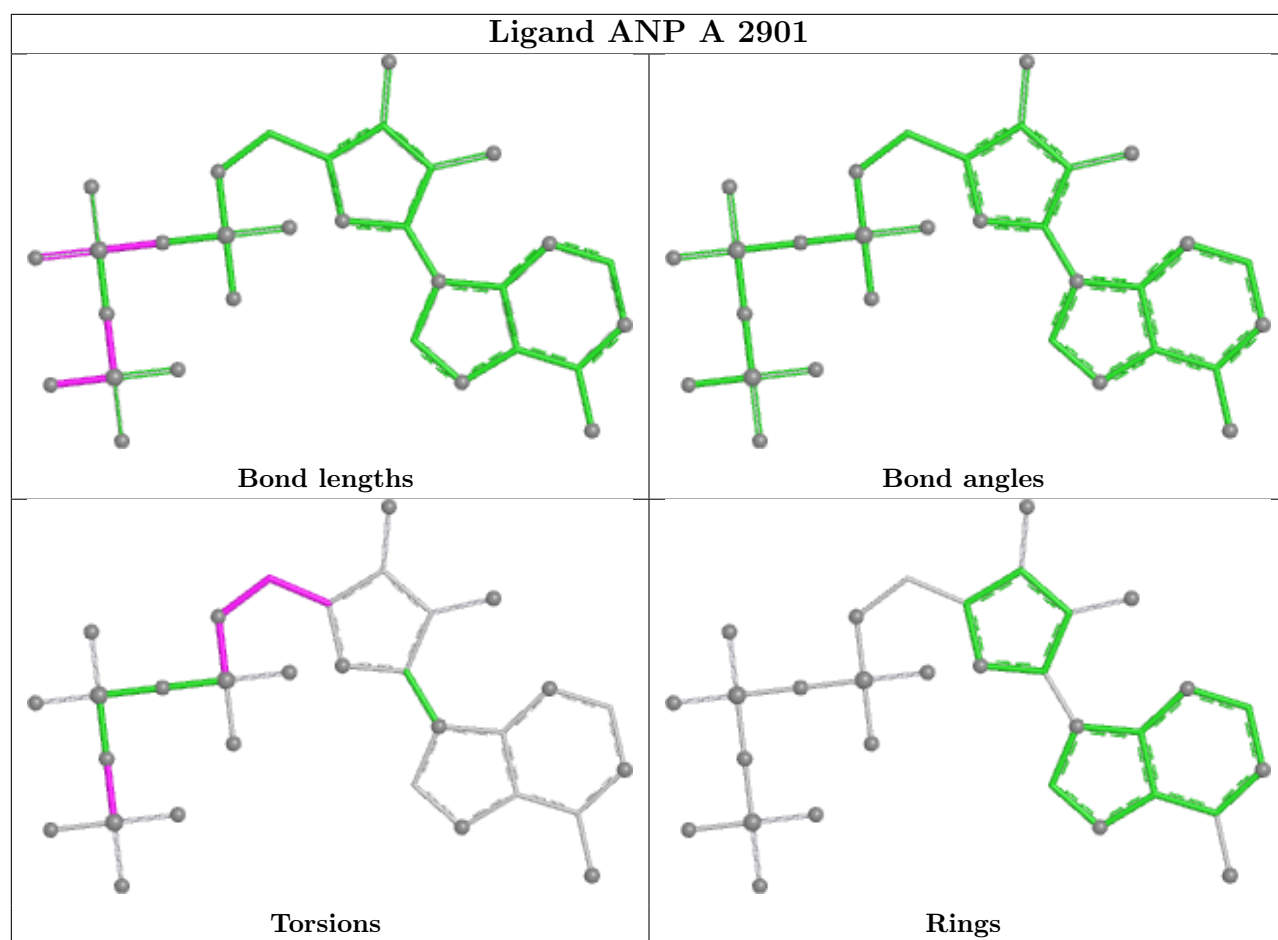
Mol	Chain	Res	Type	Atoms
3	A	2901	ANP	PB-N3B-PG-O1G
3	B	2901	ANP	PB-N3B-PG-O1G
3	B	2901	ANP	C5'-O5'-PA-O3A
3	A	2901	ANP	O4'-C4'-C5'-O5'
3	A	2901	ANP	C3'-C4'-C5'-O5'

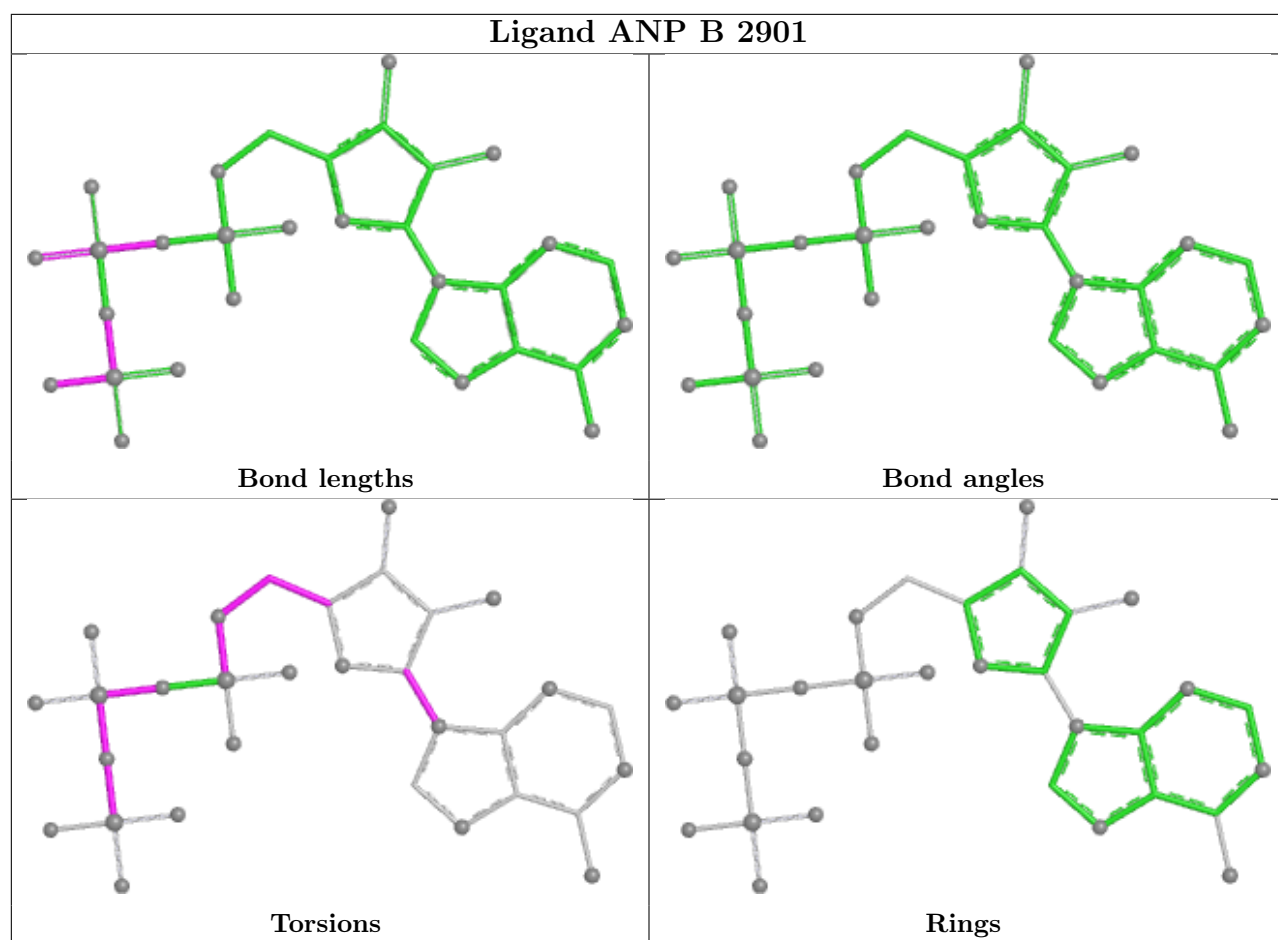
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2901	ANP	3	0
3	B	2901	ANP	4	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.

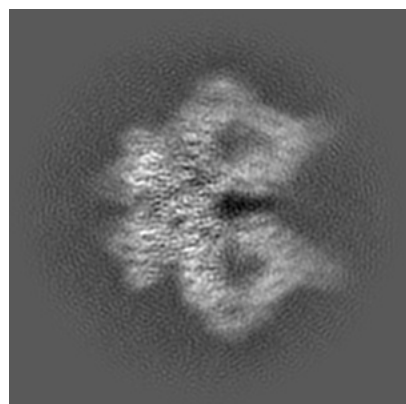
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61006. These allow visual inspection of the internal detail of the map and identification of artifacts.

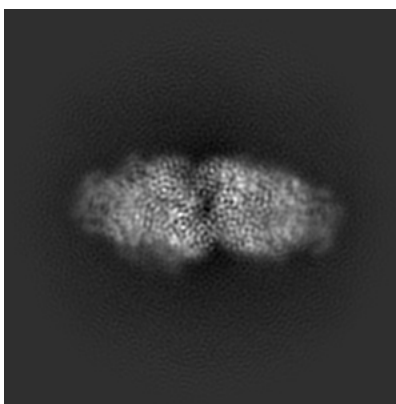
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

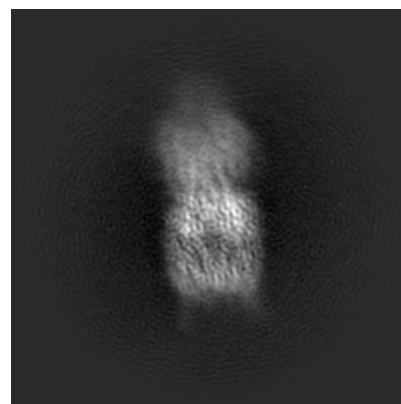
6.1.1 Primary map



X

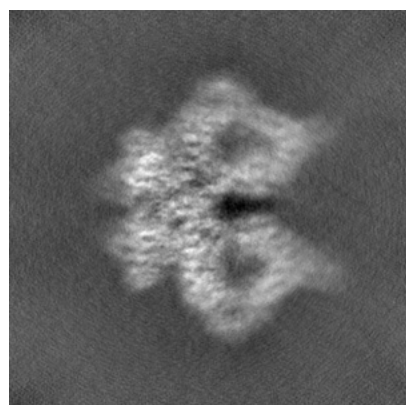


Y

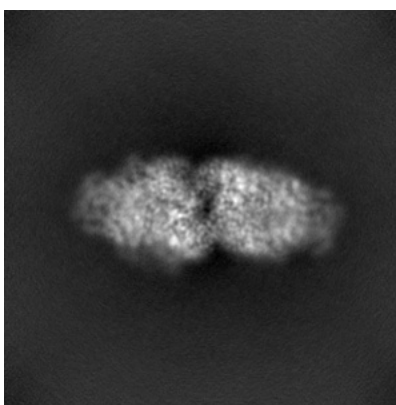


Z

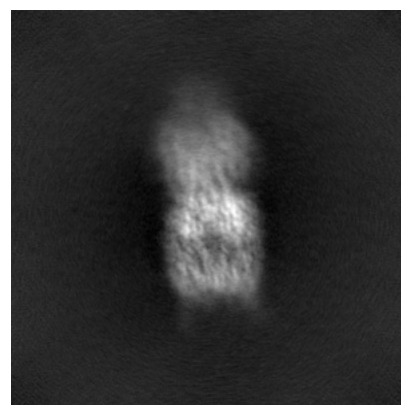
6.1.2 Raw map



X



Y

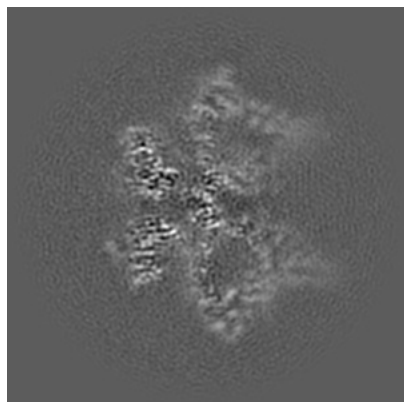


Z

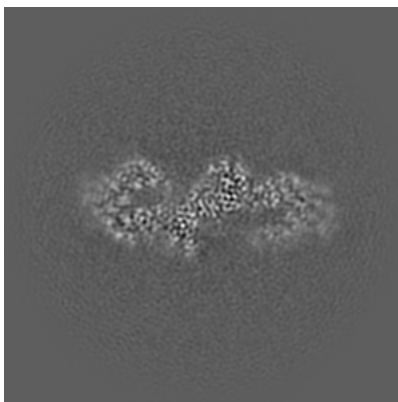
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

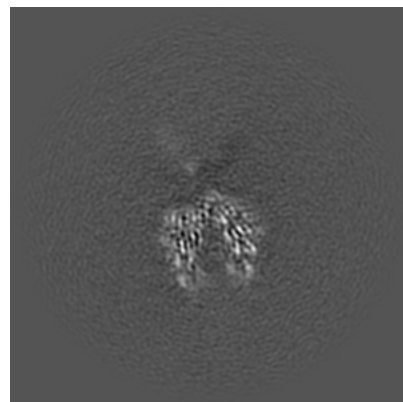
6.2.1 Primary map



X Index: 144

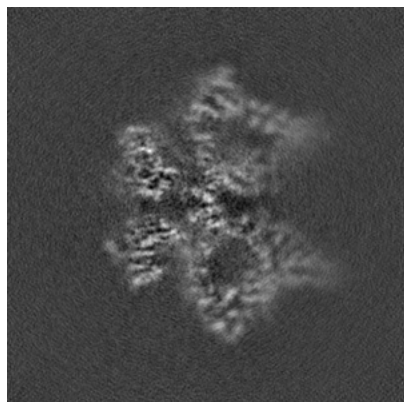


Y Index: 144

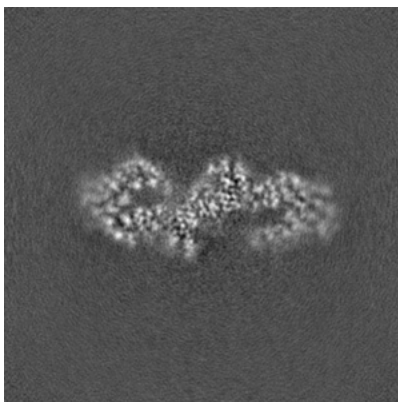


Z Index: 144

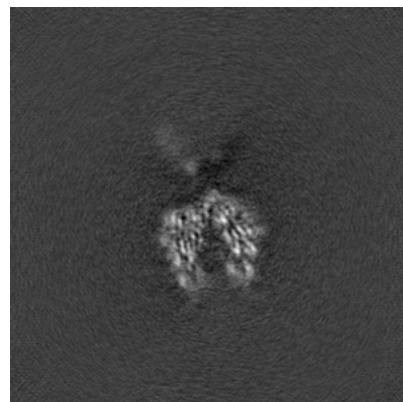
6.2.2 Raw map



X Index: 144



Y Index: 144

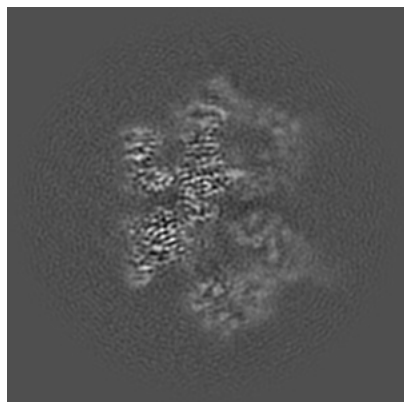


Z Index: 144

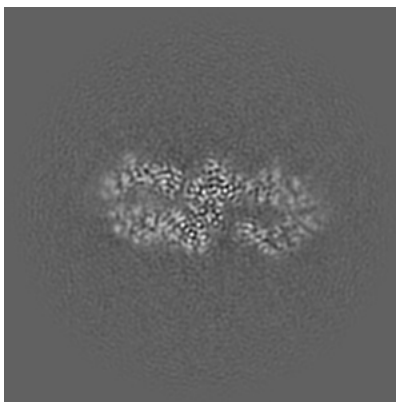
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

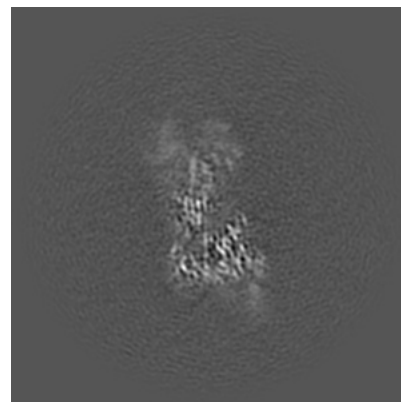
6.3.1 Primary map



X Index: 152

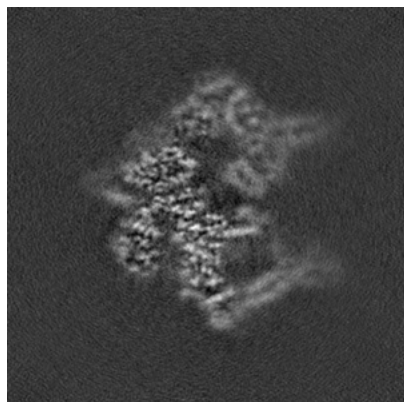


Y Index: 133

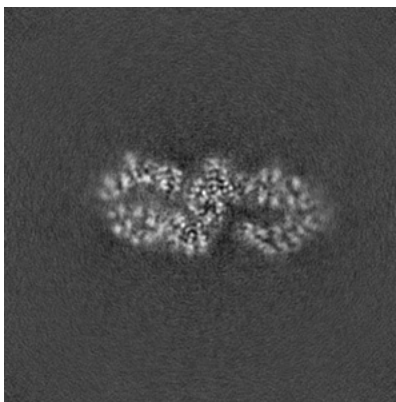


Z Index: 127

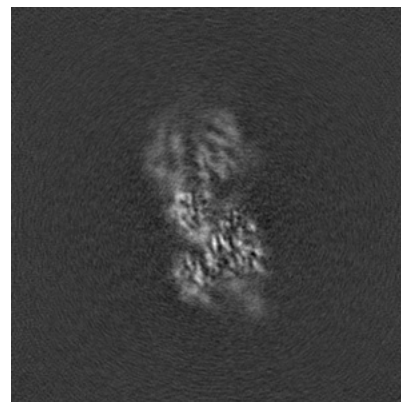
6.3.2 Raw map



X Index: 131



Y Index: 134

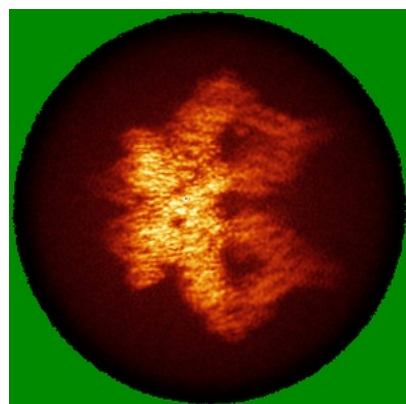


Z Index: 120

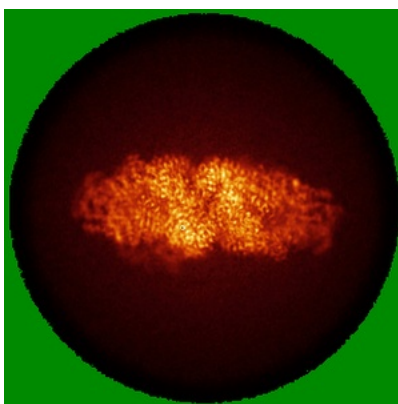
The images above show the largest variance slices of the map in three orthogonal directions.

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

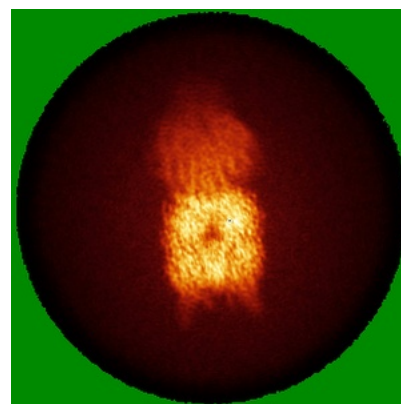
6.4.1 Primary map



X

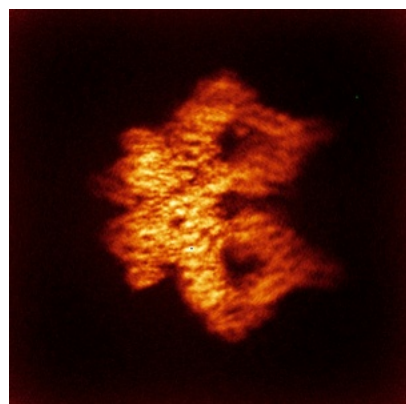


Y

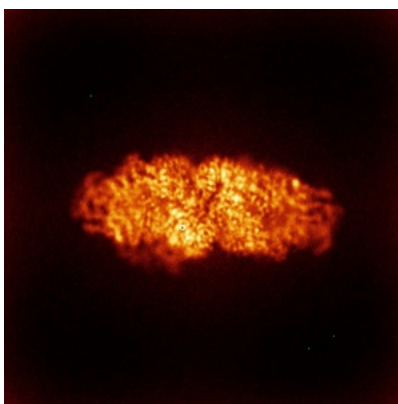


Z

6.4.2 Raw map



X



Y

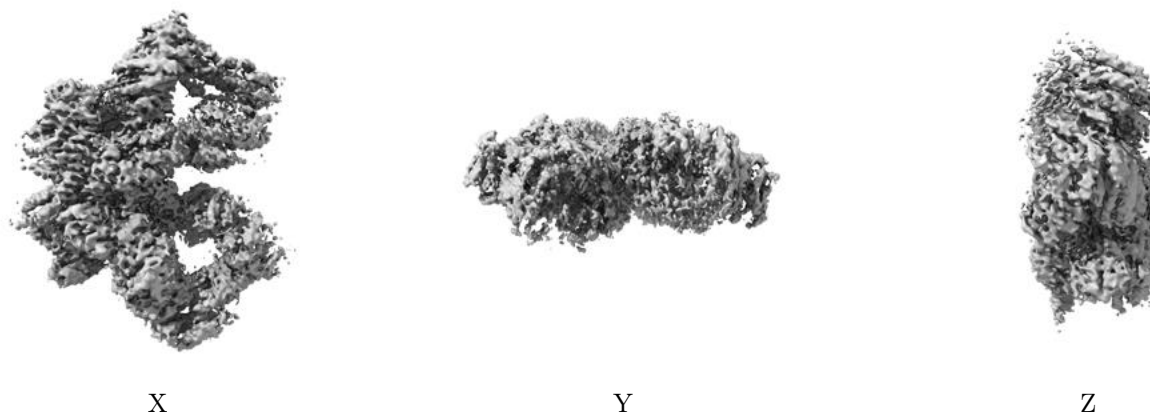


Z

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.

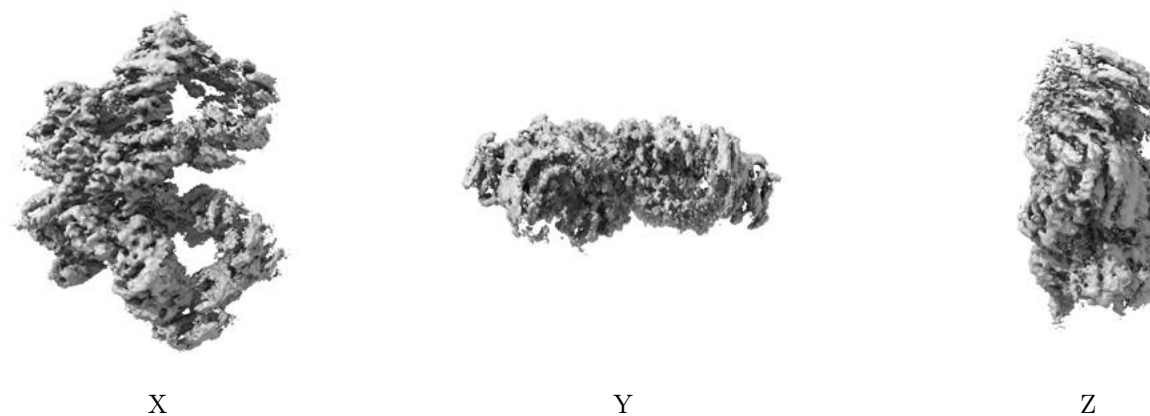
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.27. 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.

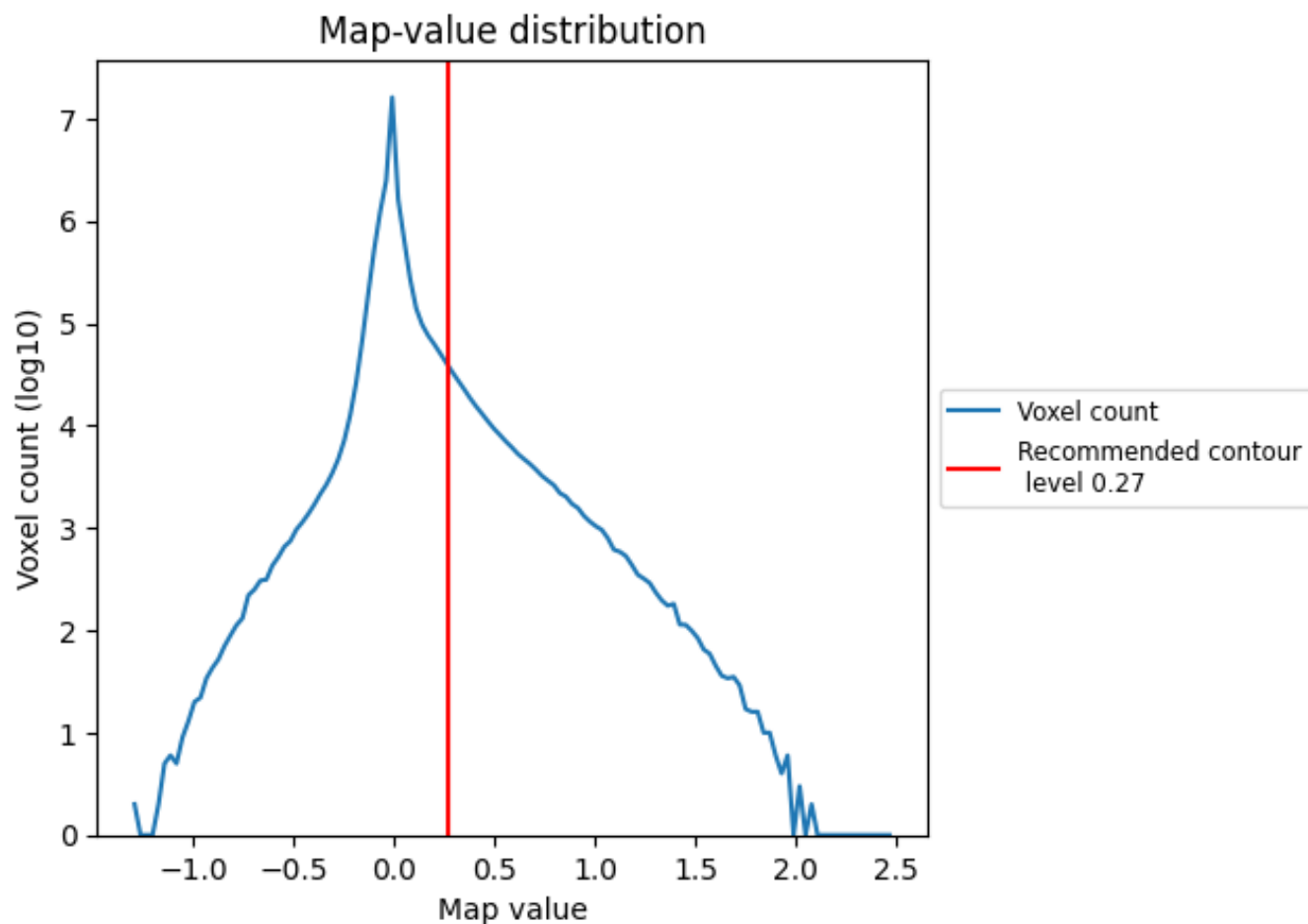
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

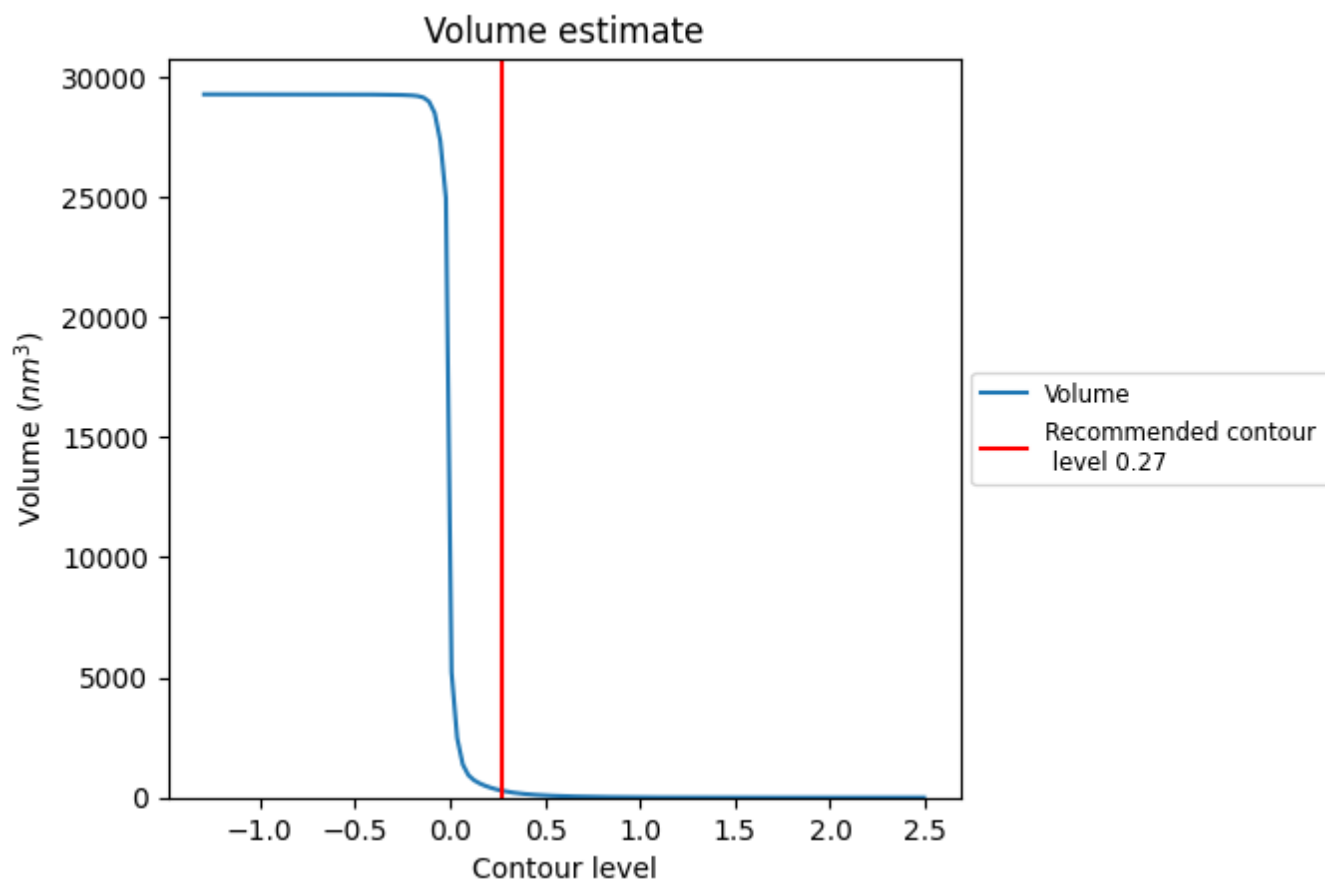
This section contains the results of statistical analysis of the map.

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.

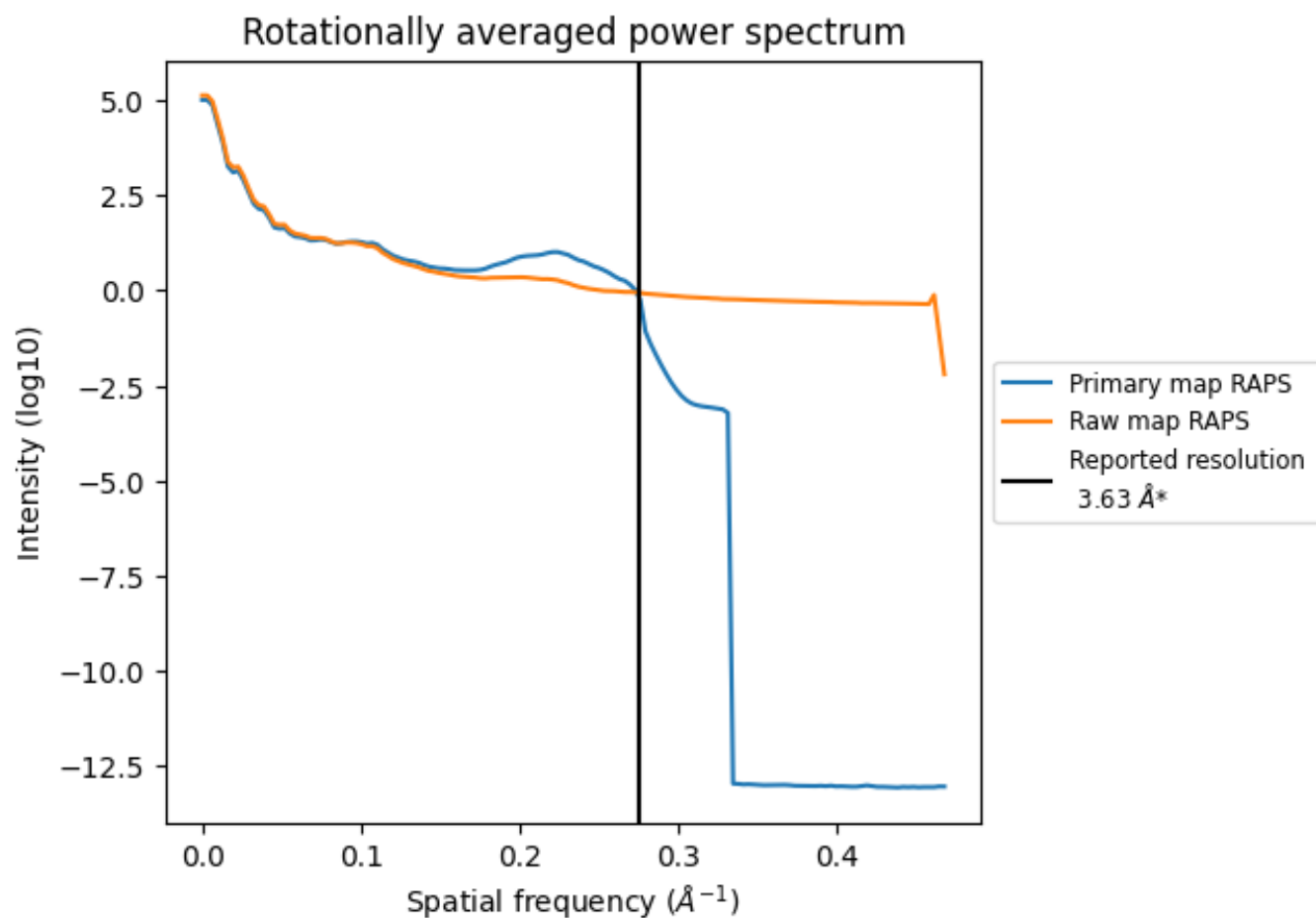
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 294 nm^3 ; this corresponds to an approximate mass of 265 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 ⓘ

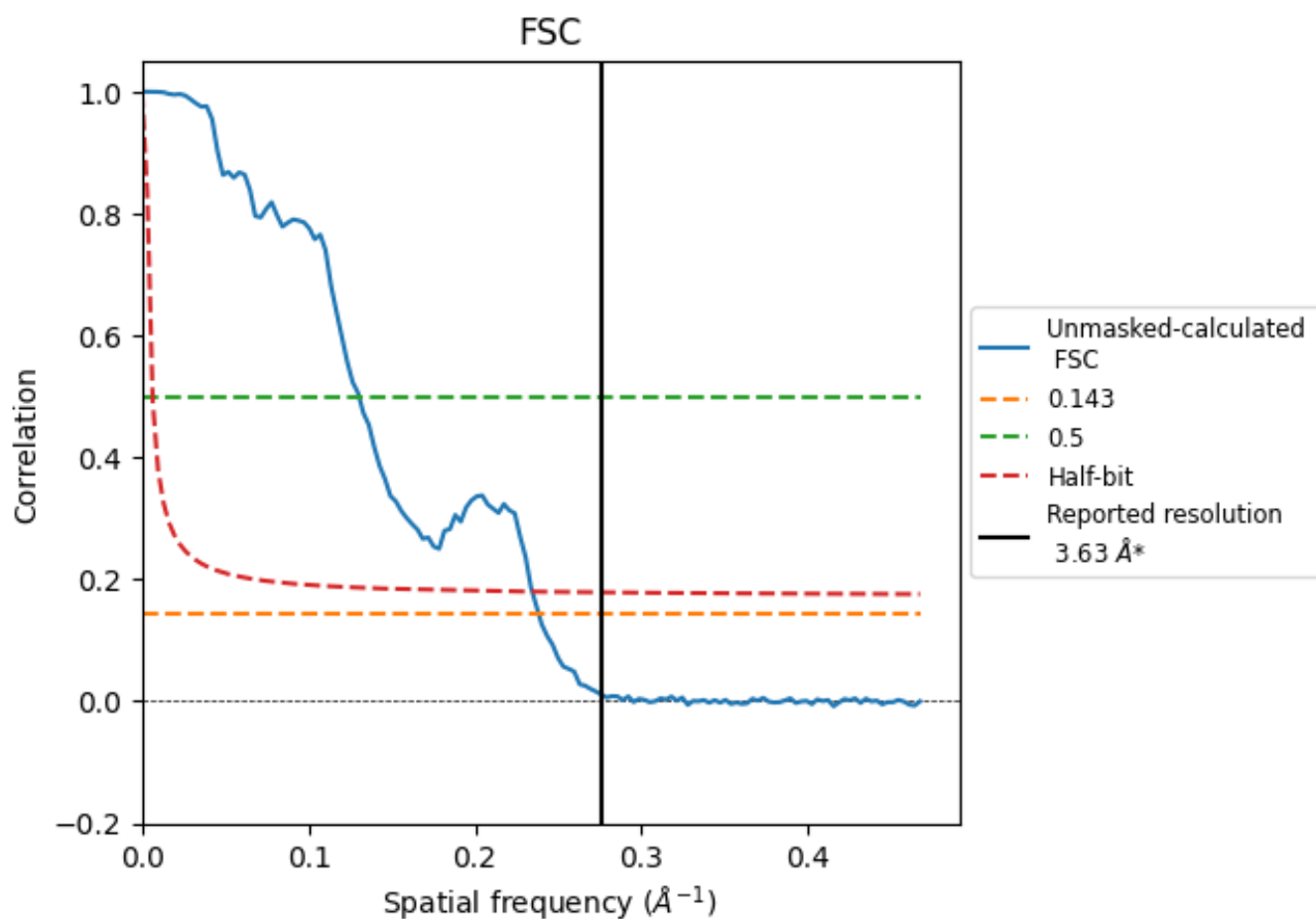


*Reported resolution corresponds to spatial frequency of 0.275 Å⁻¹

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 $0.275 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

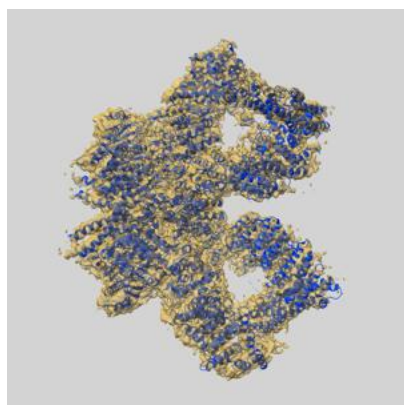
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.63	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.20	7.67	4.27

*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 4.20 differs from the reported value 3.63 by more than 10 %

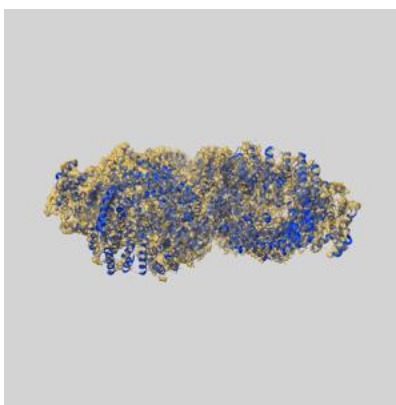
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-61006 and PDB model 9IZ0. Per-residue inclusion information can be found in section [3](#) on page [5](#).

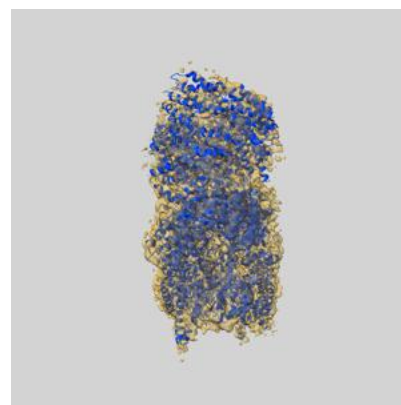
9.1 Map-model overlay [i](#)



X



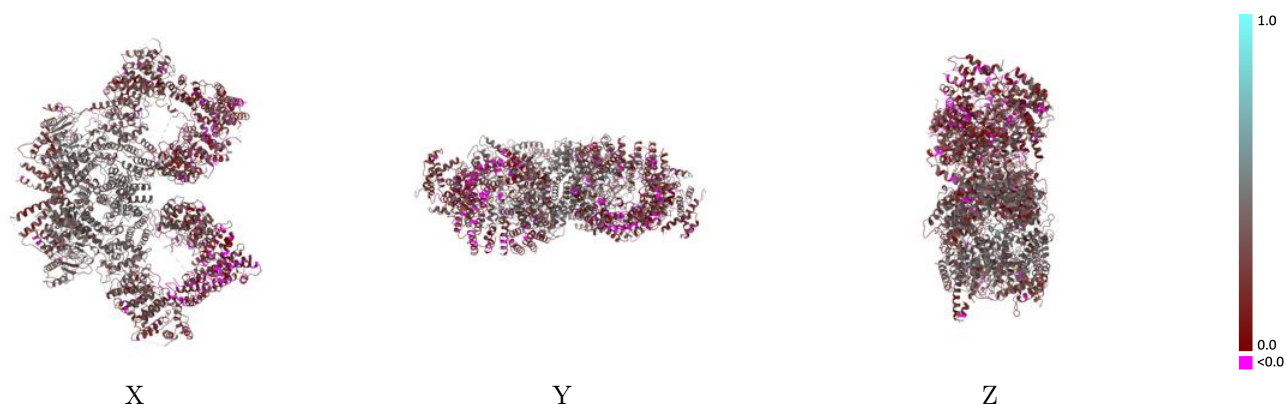
Y



Z

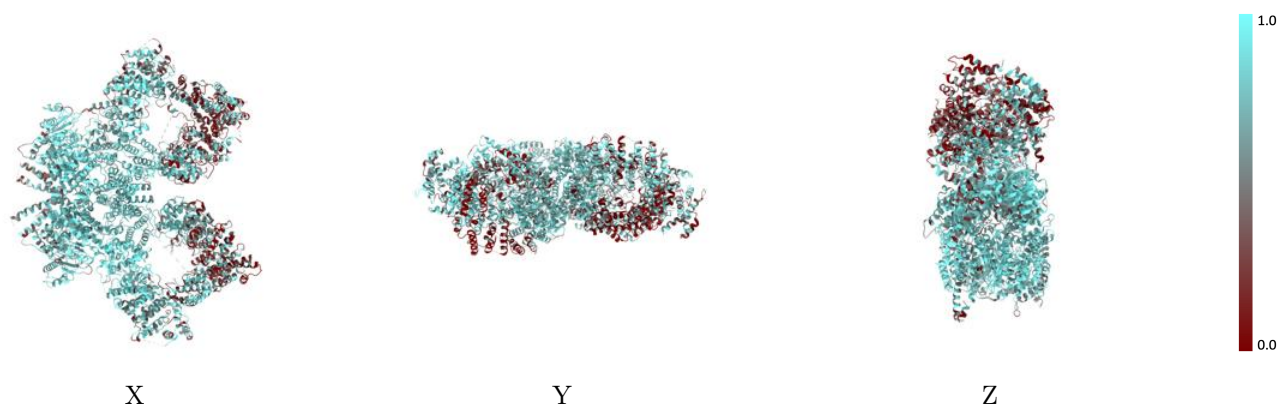
The images above show the 3D surface view of the map at the recommended contour level 0.27 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



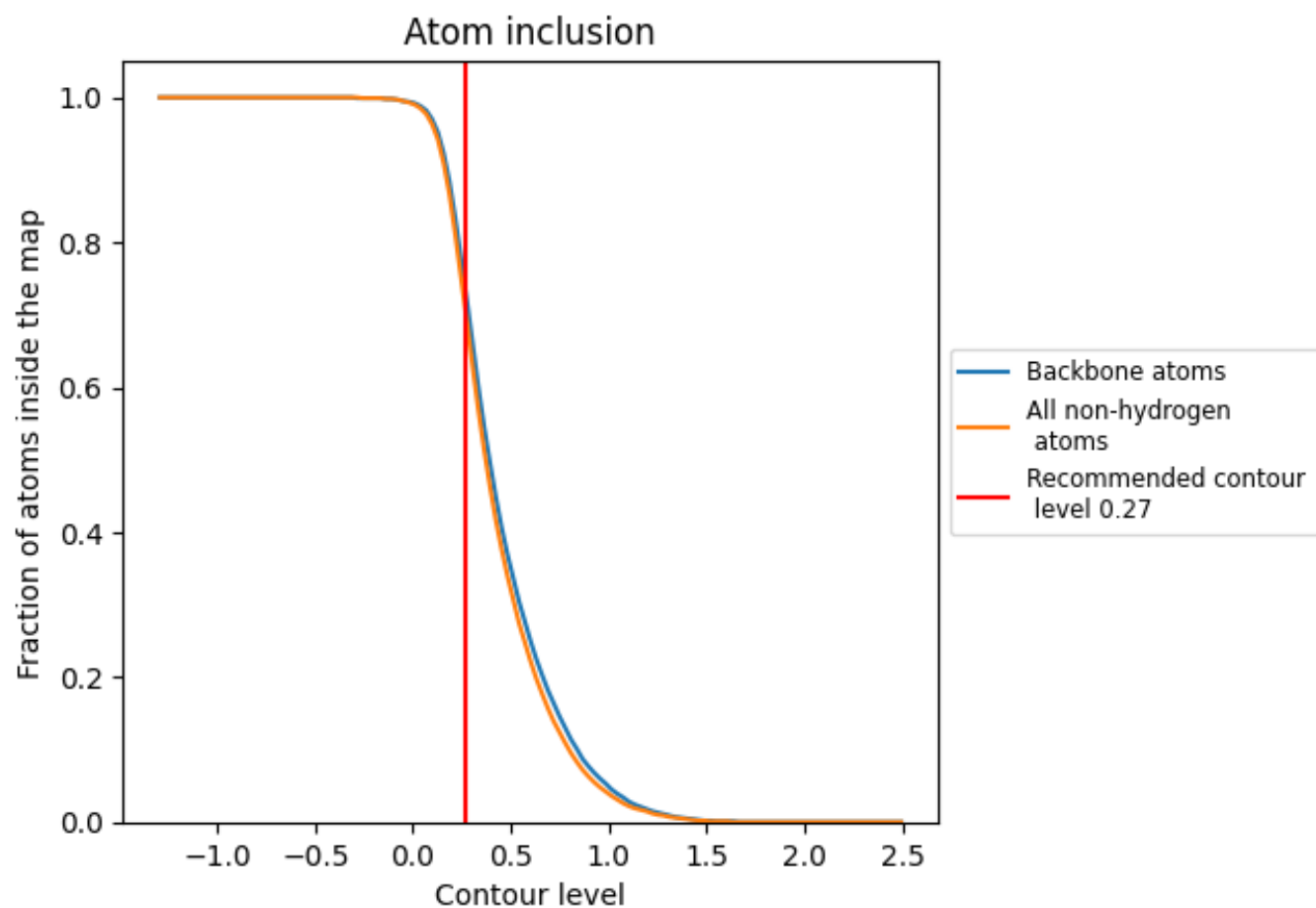
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.27).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 70% 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 (0.27) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7020	0.3170
A	0.6830	0.3180
B	0.7190	0.3170
F	0.8410	0.3680

