



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:35 PM UTC

PDB ID : 6WGE / pdb_00006wge
EMDB ID : EMD-21663
Title : Cryo-EM structure of human Cohesin-NIPBL-DNA complex without STAG1
Authors : Shi, Z.B.; Gao, H.; Bai, X.C.; Yu, H.
Deposited on : 2020-04-05
Resolution : 3.90 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

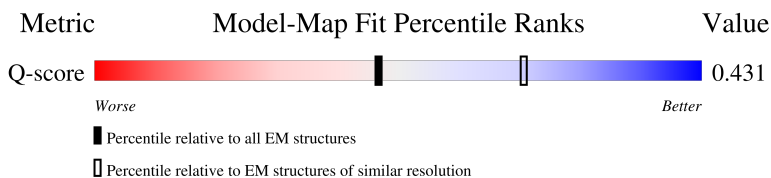
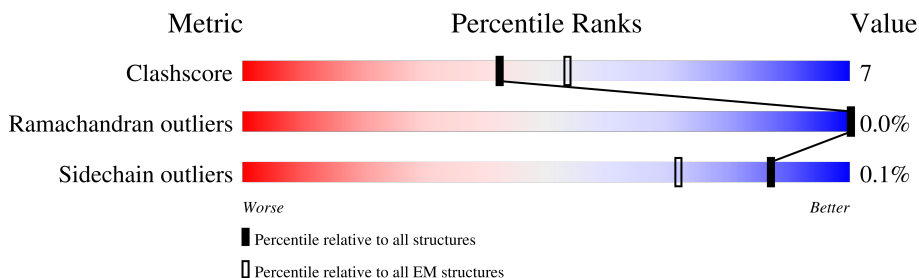
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



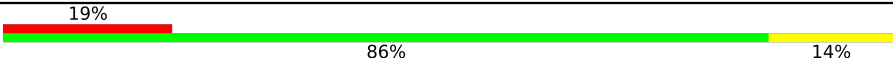
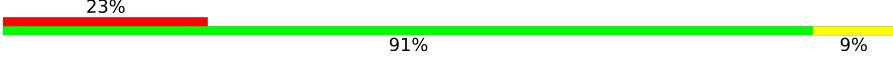
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	1233	
2	B	1217	
3	C	631	
4	E	1642	

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Mol	Chain	Length	Quality of chain
5	F	43	
6	G	43	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 20194 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 Structural maintenance of chromosomes protein 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	390	Total	C	N	O	S	0	0
			3099	1968	534	588	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1157	GLN	GLU	engineered mutation	UNP Q14683

- Molecule 2 is a protein called Structural maintenance of chromosomes protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	490	Total	C	N	O	S	0	0
			4008	2543	697	750	18		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1144	GLN	GLU	engineered mutation	UNP Q9UQE7

- Molecule 3 is a protein called Double-strand-break repair protein rad21 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	174	Total	C	N	O	S	0	0
			1395	893	251	243	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	172	ALA	ARG	engineered mutation	UNP O60216
C	279	ALA	ASP	engineered mutation	UNP O60216
C	450	ALA	ARG	engineered mutation	UNP O60216

- Molecule 4 is a protein called Nipped-B-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	1226	Total	C	N	O	S	0	0
			9865	6290	1675	1829	71		

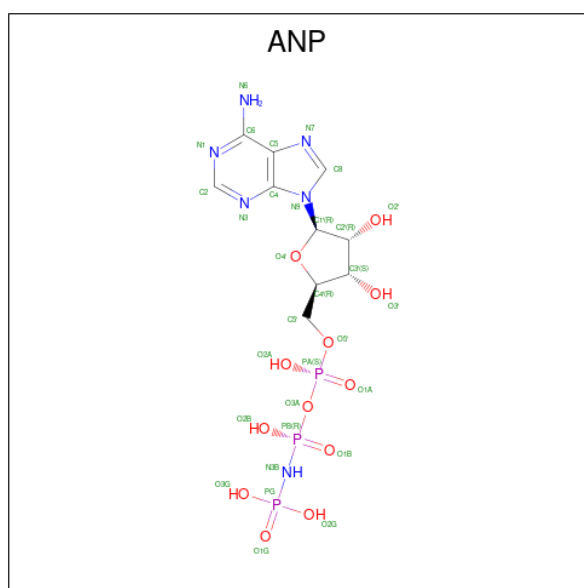
- Molecule 5 is a DNA chain called DNA (43-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	43	Total	C	N	O	P	0	0
			903	430	215	215	43		

- Molecule 6 is a DNA chain called DNA (43-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	43	Total	C	N	O	P	0	0
			860	430	86	301	43		

- Molecule 7 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).



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

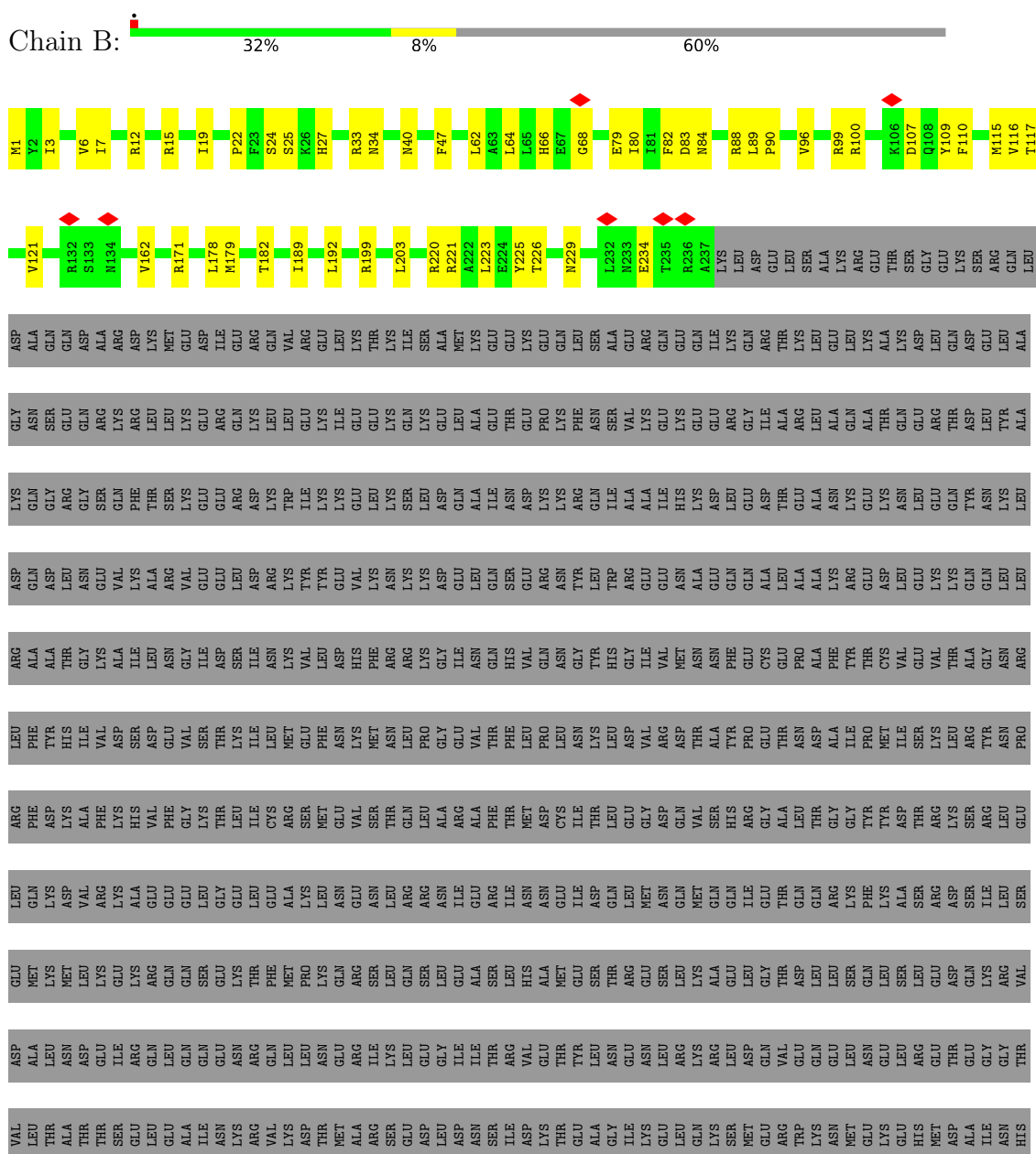
- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
8	A	1	Total 1	Mg 1	0
8	B	1	Total 1	Mg 1	0

- Molecule 1: Structural maintenance of chromosomes protein 1A



- Molecule 2: Structural maintenance of chromosomes protein 3



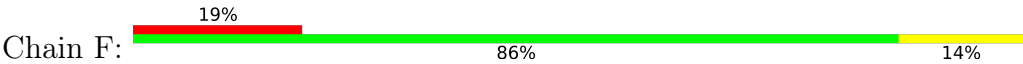


GLU	ILE	PRO	GLN	GLU	L1231	L1232	L1233	Q1237	L1238	N1239	E1240	S1243	E1244	S1245	A1246	K1247	I1248	K1249	A1250	M1251	G1252	D1255	K1256	L1257	D1260	K1261	K1264	I1268	L1269	E1270	K1271	Q1274	S1277	K1278	L1279	S1280	THR	LEU	LEU	ASN	HIS	ASN	ASN	THR	GLU	GLU	E1293	R1294	L1295			
W1296	R1297	D1298	L1299	I1300	M1301	E1302	R1303	K1306	D1309	T1313	T1314	I1315	T1319	M1323	P1324	K1325	A1326	V1327	V1332	R1335	F1342	H1343	L1344	R1357	LEU	ASP	PRO	HIS	GLY	GLY	GLY	LEU	LEU	SER	SER	ALA	LYS	ALA	ARG	LYS	ARG	LEU	ALA	LYS	ILE	VAL	GLN	THR	GLY	Q1380	R1381	V1382
M1385	L1386	K1389	V1390	D1408	V1427	Q1431	S1469	N1472	L1475	ASN	SER	SER	ASP	MET	ASP	GLY	P1484	T1487	Q1488	T1491	Q1499	L1504	P1505	SER	SER	GLU	LYS	ASP	SER	ASN	ALA	GLU	GLU	ASP	ASN	ARG	ILE	LYS	ASN	ILE	ASP	GLN	D1524	V1525	T1528	E1532						
K1552	Q1553	G1554	E1555	R1559	D1568	L1569	L1570	P1579	L1584	L1585	F1596	S1597	M1598	K1599	S1600	T1601	E1602	R1606	V1607	V1616	R1619	L1620	R1621	K1622	D1623	S1627	K1628	M1629	ASP	GLN	GLY	SER	ALA	GLY	ILE	GLU	ARG	ILE	LYS	LEU	GLN	VAL	SER	THR	GLY	GLY	D1646	E1647	I1648	Q1649	Q1650	
L1651	L1656	D1657	Y1658	L1659	T1663	E1664	T1665	D1666	R1673	T1688	E1689	K1690	ALA	MET	LYS	GLN	LYS	ASP	GLU	GLU	SER	SER	GLY	THR	HIS	ALA	K1708	E1709	I1710	E1711	Q1715	E1721	L1727	R1728	S1729	ILE	ILE	LYS	LYS	THR	PRO	SER	GLN	PHE	SER	THR	LEU	LYS	MET			
ASN	SER	D1746	T1747	A1753	I1756	A1761	R1764	Q1768	S1769	F1770	V1780	V1788	R1789	T1790	K1791	L1796	I1806	D1822	N1823	S1826	V1827	R1828	E1829	V1832	E1847	S1863	V1864	E1878	T1886	R1895	D1898	H1914	F1915	T1916	T1917	T1918	M1921	D1922	K1923													
E1924	A1925	M1926	K1929	L1930	T1934	S1958	D1961	S1962	S1963	Y1964	K1965	E1986	E1987	LEU	ALA	ASP	ASP	ASN	LYS	VAL	N1998	R2001	K2034	C2035	S2036	N2039	V2043	V2047	L2050	D2072	L2073	M2074	K2075	Y2080	F2105	E2126	D2127	L2133														
R2142	R2152	D2160	F2161	K2162	Q2163	N2164	S2165	K2166	V2167	N2168	F2198	A2199	F2200	L2201	Q2202	M2207	S2221	D2222	K2223	N2224	S2225	S2226	V2227	T2239	D2252	D2263	L2264	K2265	D2269	Q2273	M2274	L2283	Q2294	Q2311	G2312	L2313	I2314	D2329	R2335	Q2340	Q2341	L2342										
K2347	N2372	THR	CYS	LEU	LYS	ASP	PRO	VAL	ARG	PHE	ARG	GLN	ASP	GLU	SER	S2389	C2392	Y2396	S2397	M2398	L2399	R2400	R2403	R2406	R2407	L2411	L2416	D2419	T2420	A2421	K2422	T2423	D2424	V2425	L2428	L2429	N2434	L2435	T2442	E2445	F2448	L2453										
S2458	V2459	L2465	Q2466	K2469	E2470	S2471	MET	VAL	LYS	ASP	PRO	LYS	ARG	GLU	ARG	LYS	SER	SER	SER	GLU	GLU	VAL	SER	GLU	GLU	VAL	SER	ARG	PRO	LYS	LYS	ARG	ARG	VAL	ASP	SER	ASP	ASP	ASP	ILE	ASN	SER	VAL									
MET	LYS	CYS	LEU	PRO	GLU	ASN	SER	ALA	PRO	L2533	L2534	E2535	L2546	L2547	M2548	L2549	K2550	Q2551	H2552	C2557	Q2565	E2571	S2572	V2575	L2580	N2581	R2582	K2583	V2586	H2587	F2588	H2589	P2590	K2591	Q2592	T2593	L2594	D2595	F2596	R2598	S2599	D2600	M2601	A2602	N2603	S2604	K2605	L2606	T2607	E2608	E2609	
V2610	Y2618	L2619	D2620	L2624	M2625	E2626	H2627	L2628	ASP	ASN	PRO	ASP	ASP	GLU	GLU	THR	GLU	GLU	GLY	ALA	GLN	MET	SER	ALA	GLU	VAL	ASN	ASP	ALA	ASP	ASN	ASN	THR	ILE	ALA	ALA	VAL	VAL	THR	GLN	LYS	ASP	ASP	GLU	SER	SER	GLY	PHE	SER	VAL		

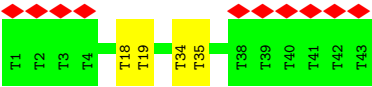
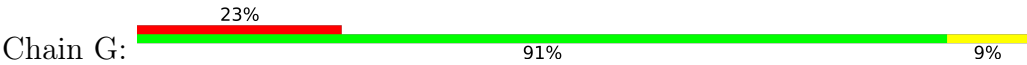
GLN
TRP
MET
ALA
GLY
SER
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ALA
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LEU
TYR
ALA

ALA
LYS
ASP
GLY
THR
SER
SER

● Molecule 5: DNA (43-MER)



● Molecule 6: DNA (43-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	68161	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.159	Depositor
Minimum map value	-0.084	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	321.6, 321.6, 321.6	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	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, MG

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	0.33	0/3154	0.58	0/4237
2	B	0.33	0/4071	0.57	0/5446
3	C	0.27	0/1420	0.62	0/1903
4	E	0.30	0/10021	0.58	0/13509
5	F	0.30	0/1031	0.52	0/1587
6	G	0.34	0/945	0.66	0/1458
All	All	0.31	0/20642	0.58	0/28140

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3099	0	3103	53	0
2	B	4008	0	4072	70	0
3	C	1395	0	1444	25	0
4	E	9865	0	10101	133	0
5	F	903	0	474	4	0
6	G	860	0	517	2	0
7	A	31	0	13	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	31	0	13	4	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
All	All	20194	0	19737	267	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 7.

The worst 5 of 267 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:B:962:LEU:H	2:B:965:LEU:HD23	1.53	0.73
3:C:613:GLN:HE22	3:C:618:SER:HB3	1.56	0.69
4:E:1607:VAL:HG13	4:E:1791:LYS:HG3	1.75	0.68
2:B:40:ASN:HD21	7:B:2000:ANP:H5'2	1.59	0.67
3:C:613:GLN:NE2	3:C:615:GLU:O	2.26	0.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	386/1233 (31%)	353 (92%)	33 (8%)	0	100	100
2	B	484/1217 (40%)	449 (93%)	35 (7%)	0	100	100
3	C	168/631 (27%)	151 (90%)	17 (10%)	0	100	100
4	E	1202/1642 (73%)	1099 (91%)	102 (8%)	1 (0%)	48	80
All	All	2240/4723 (47%)	2052 (92%)	187 (8%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	2606	ILE

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	329/1094 (30%)	328 (100%)	1 (0%)	86	85
2	B	439/1092 (40%)	439 (100%)	0	100	100
3	C	148/563 (26%)	148 (100%)	0	100	100
4	E	1121/1487 (75%)	1119 (100%)	2 (0%)	87	87
All	All	2037/4236 (48%)	2034 (100%)	3 (0%)	87	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	VAL
4	E	1886	THR
4	E	2424	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	2292	HIS
4	E	2434	ASN
4	E	2294	GLN
4	E	2315	HIS
4	E	2551	GLN

5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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$
7	ANP	A	2000	8	33,33,33	1.12	5 (15%)	45,52,52	0.89	4 (8%)
7	ANP	B	2000	8	33,33,33	1.07	5 (15%)	45,52,52	1.16	4 (8%)

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
7	ANP	A	2000	8	-	7/18/38/38	0/3/3/3
7	ANP	B	2000	8	-	10/18/38/38	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	2000	ANP	PG-O1G	3.22	1.51	1.46
7	A	2000	ANP	PB-O1B	2.74	1.50	1.46
7	B	2000	ANP	PG-O2G	-2.68	1.49	1.56
7	B	2000	ANP	PG-O1G	2.63	1.50	1.46
7	A	2000	ANP	PG-O3G	-2.44	1.50	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	2000	ANP	O2B-PB-O1B	4.28	119.05	109.87
7	B	2000	ANP	O1B-PB-N3B	-3.89	106.05	111.77
7	A	2000	ANP	O2B-PB-O1B	3.35	117.06	109.87
7	B	2000	ANP	O3G-PG-O1G	-2.98	105.98	113.45
7	A	2000	ANP	O2G-PG-O1G	-2.12	108.13	113.45

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

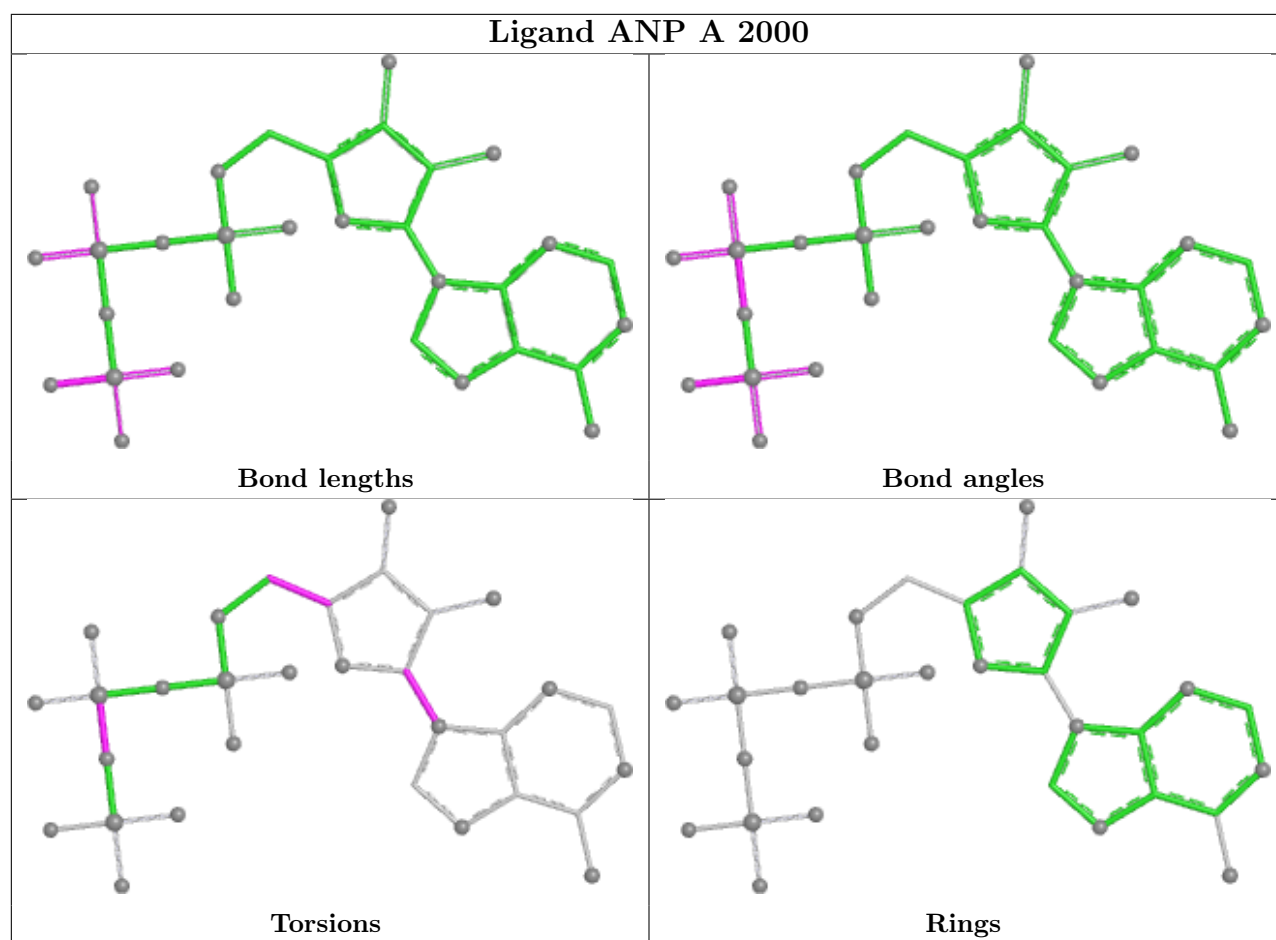
Mol	Chain	Res	Type	Atoms
7	A	2000	ANP	PG-N3B-PB-O1B
7	B	2000	ANP	PB-N3B-PG-O1G
7	B	2000	ANP	PG-N3B-PB-O1B
7	B	2000	ANP	PG-N3B-PB-O3A
7	B	2000	ANP	PA-O3A-PB-O2B

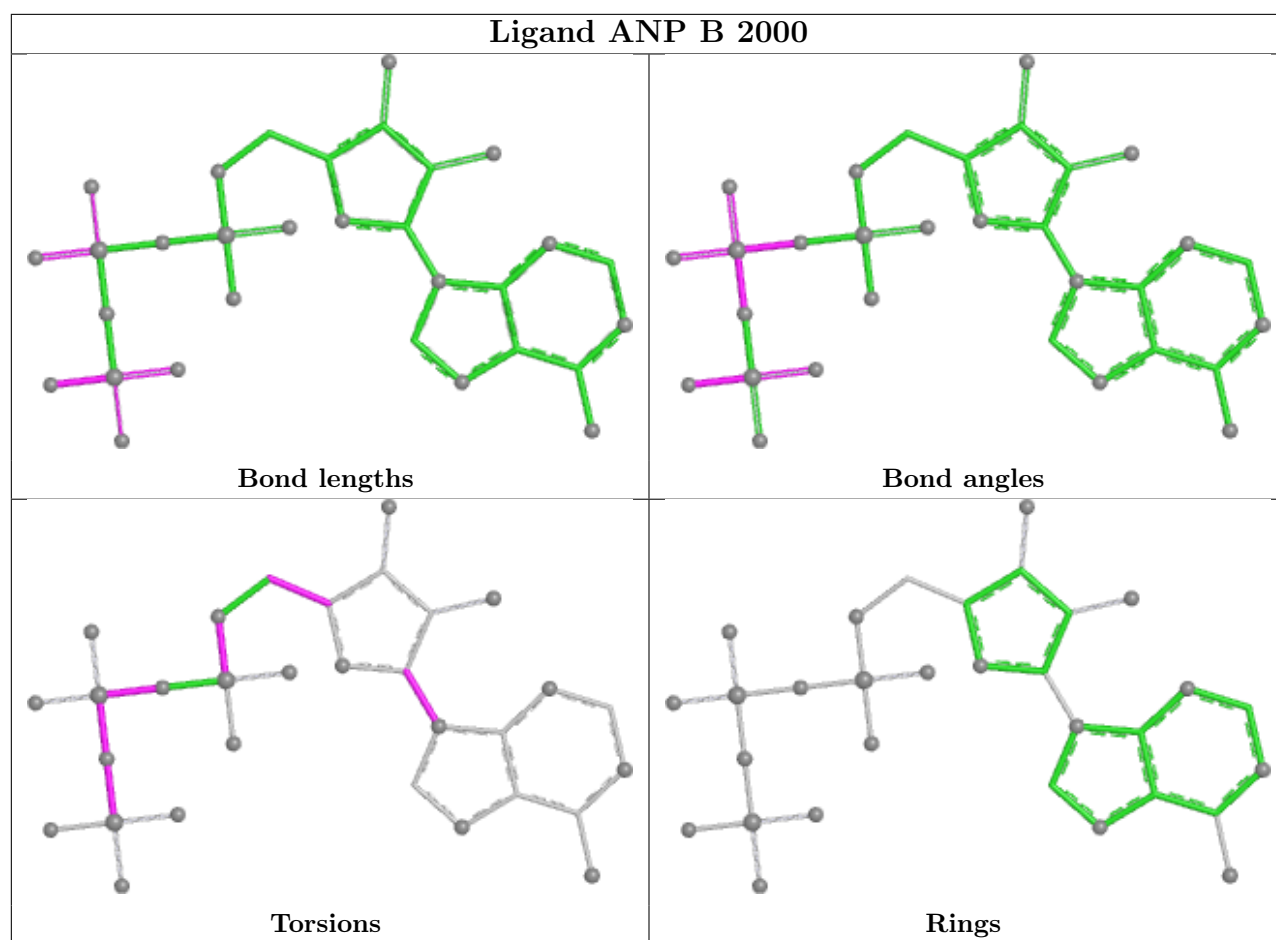
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	2000	ANP	5	0
7	B	2000	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.

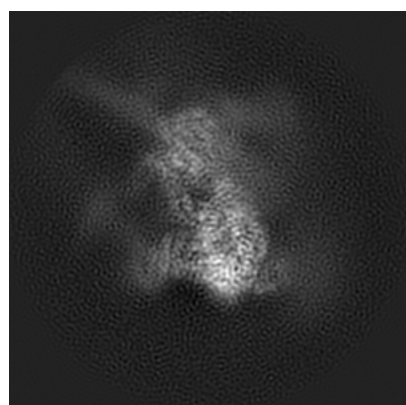
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21663. These allow visual inspection of the internal detail of the map and identification of artifacts.

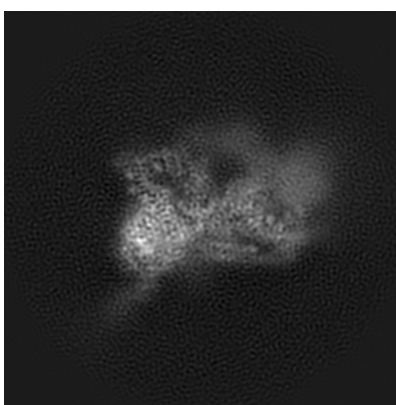
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

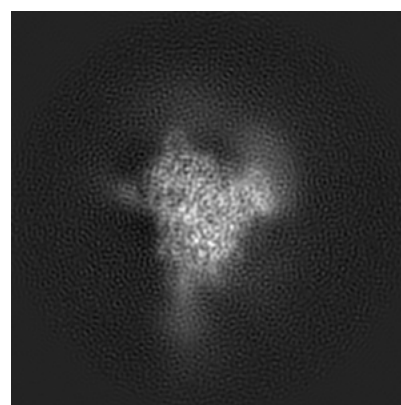
6.1.1 Primary map



X



Y

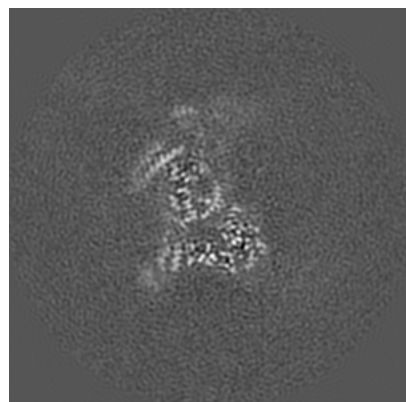


Z

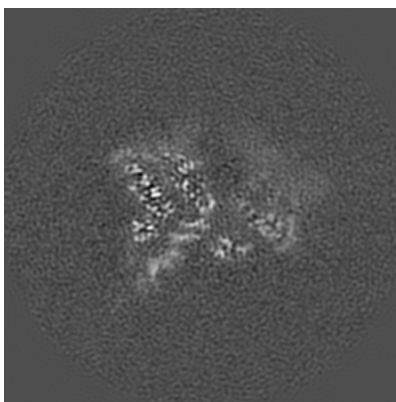
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

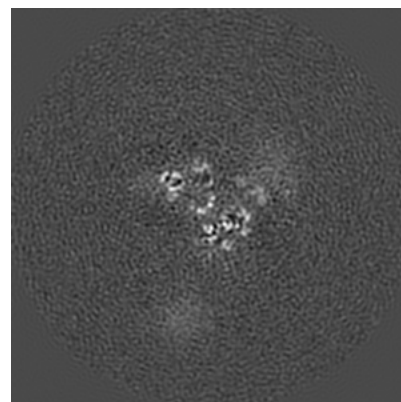
6.2.1 Primary map



X Index: 120



Y Index: 120

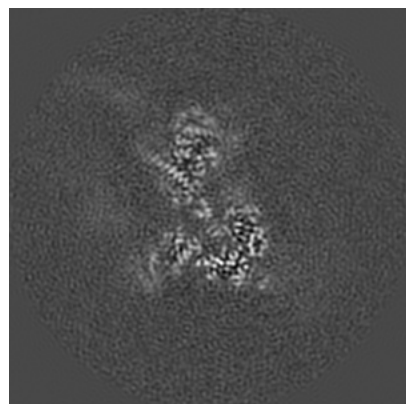


Z Index: 120

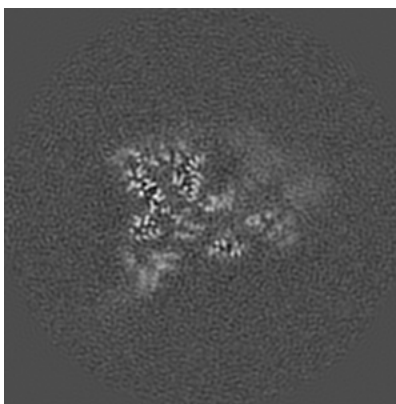
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

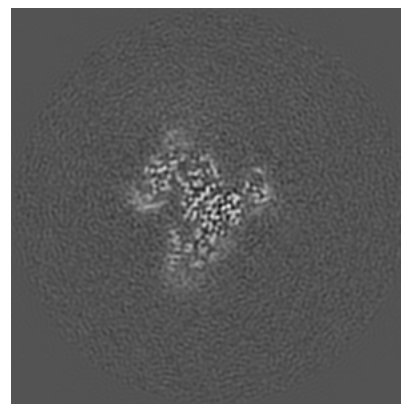
6.3.1 Primary map



X Index: 111



Y Index: 123

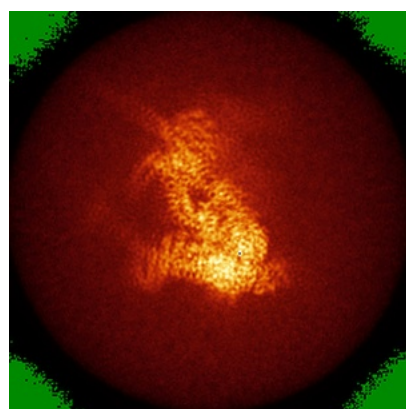


Z Index: 89

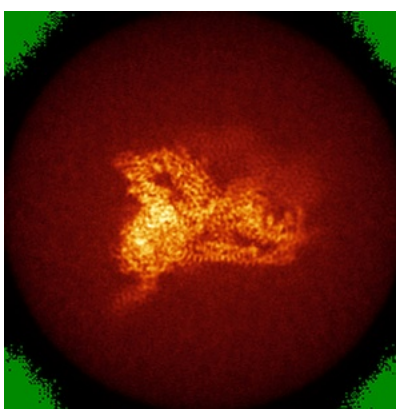
The images above show the largest variance slices of the map in three orthogonal directions.

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

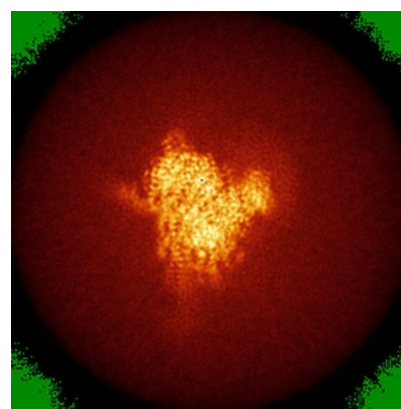
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.032. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

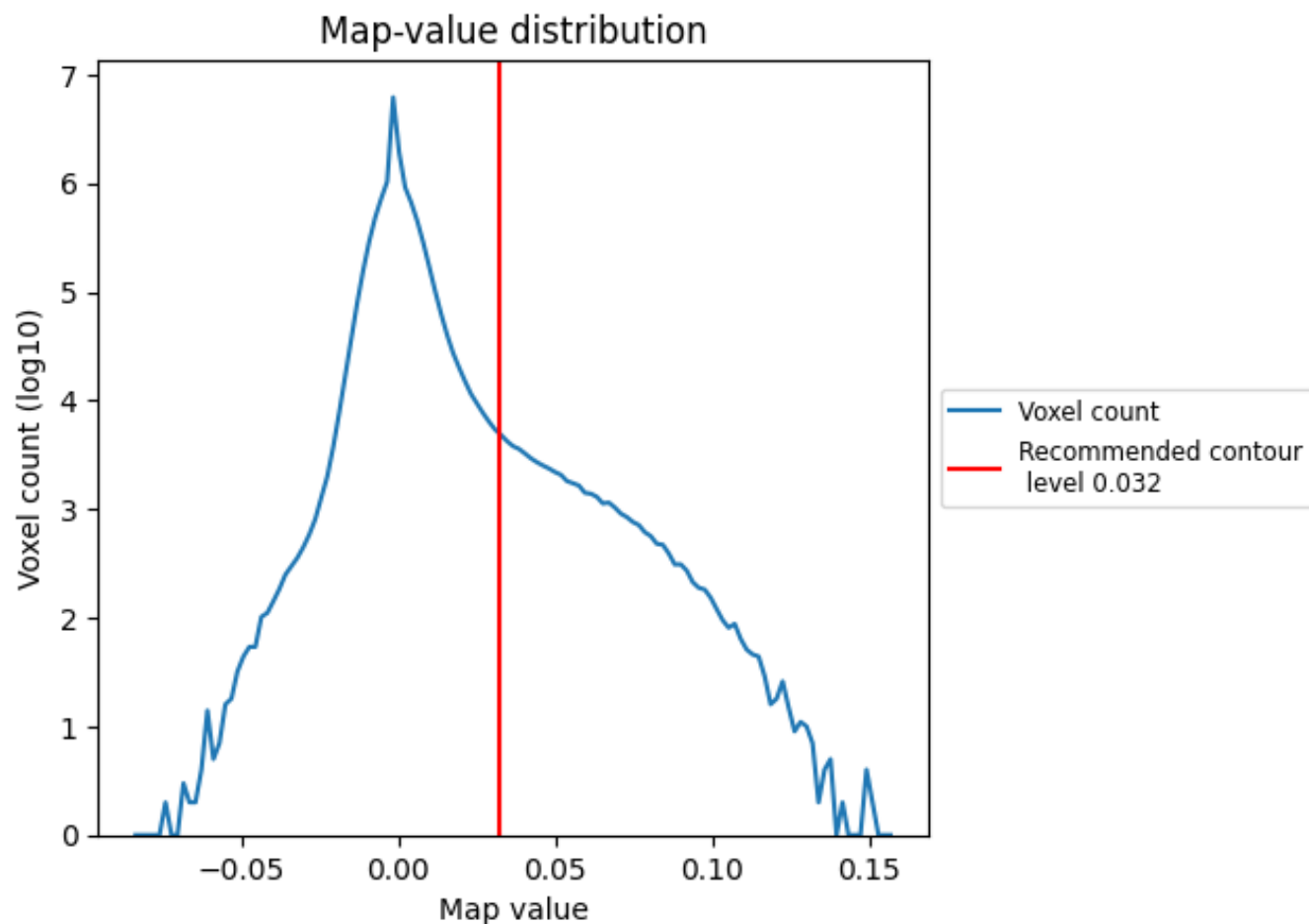
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

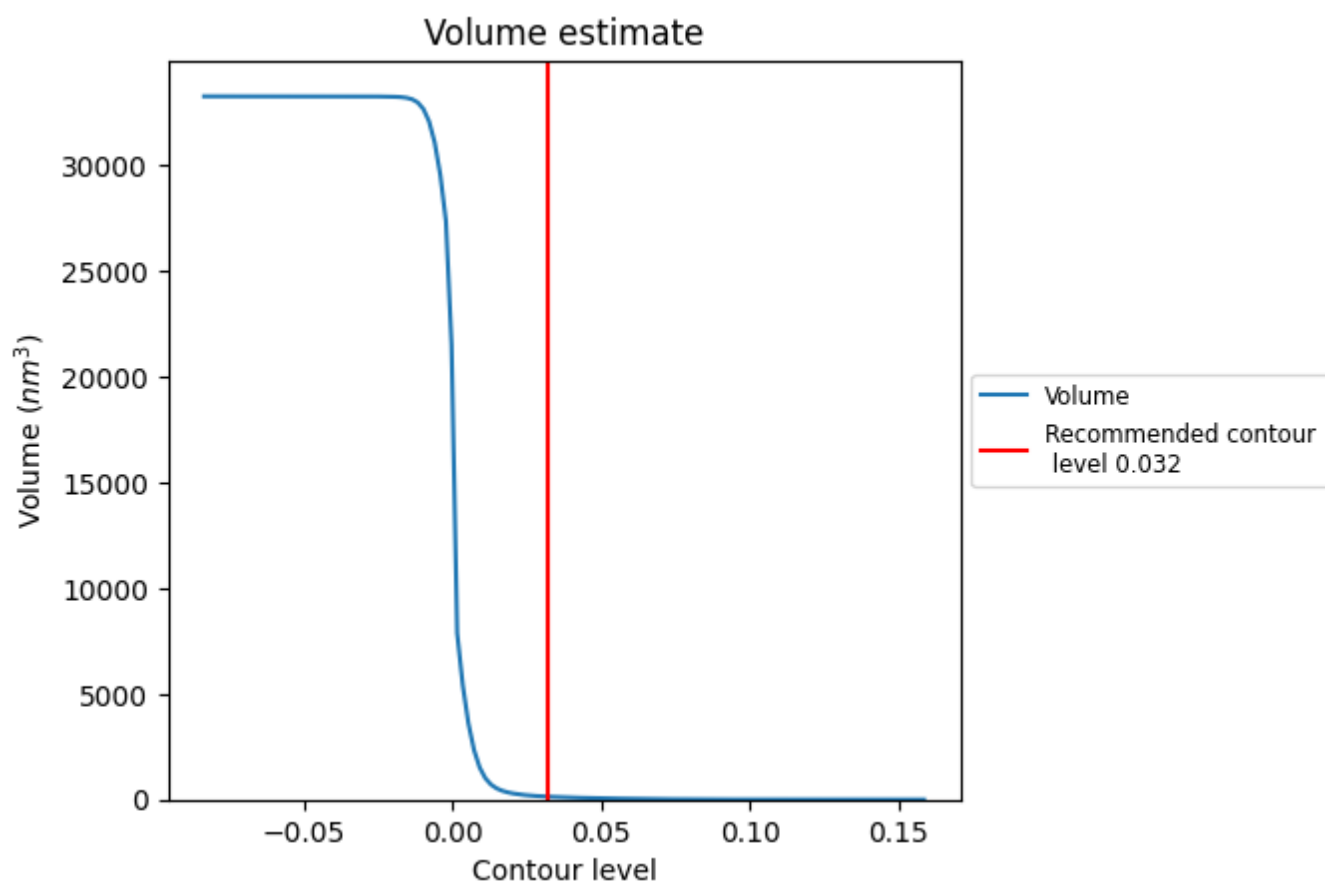
This section contains the results of statistical analysis of the map.

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.

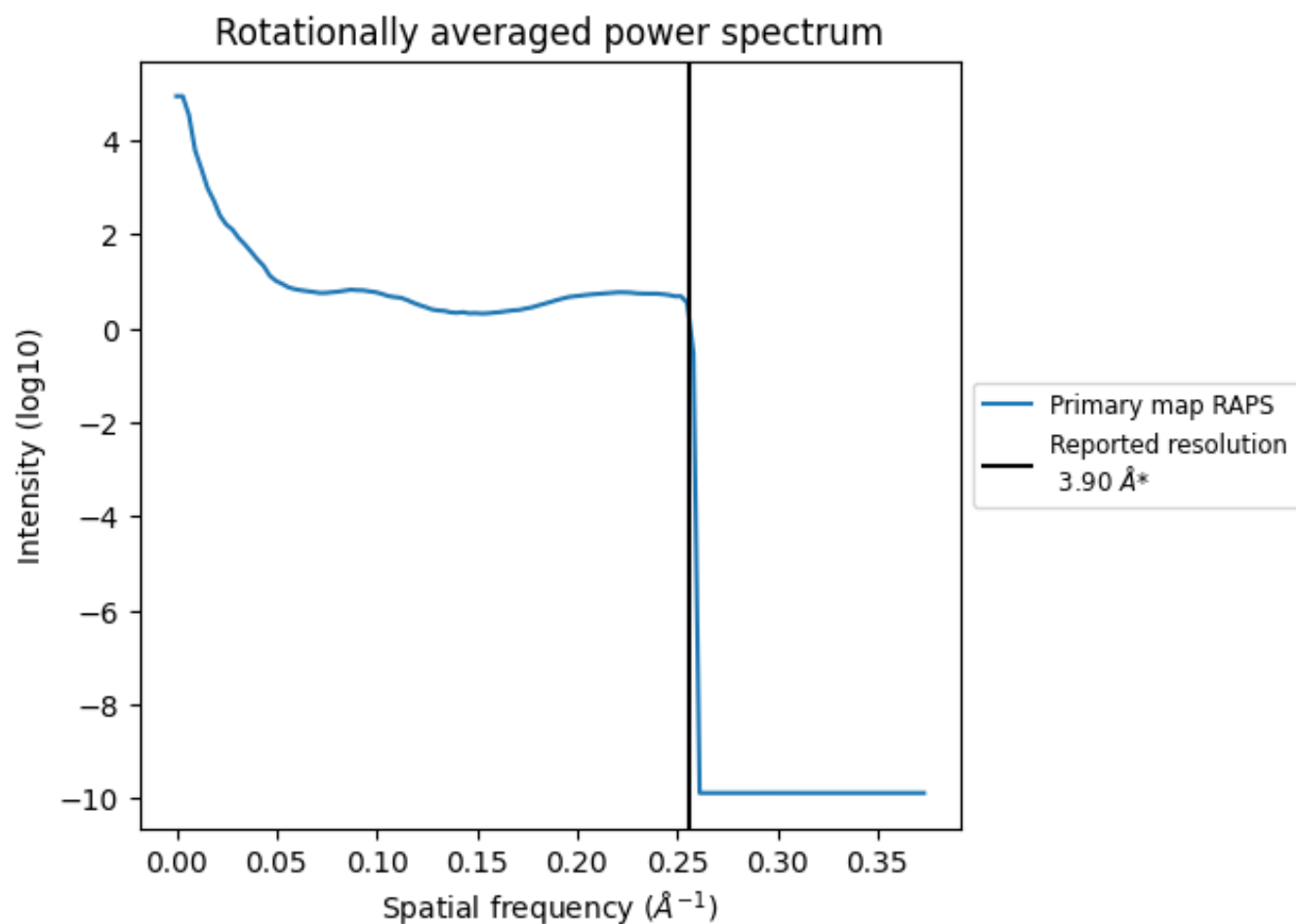
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 138 nm³; this corresponds to an approximate mass of 124 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 ⓘ

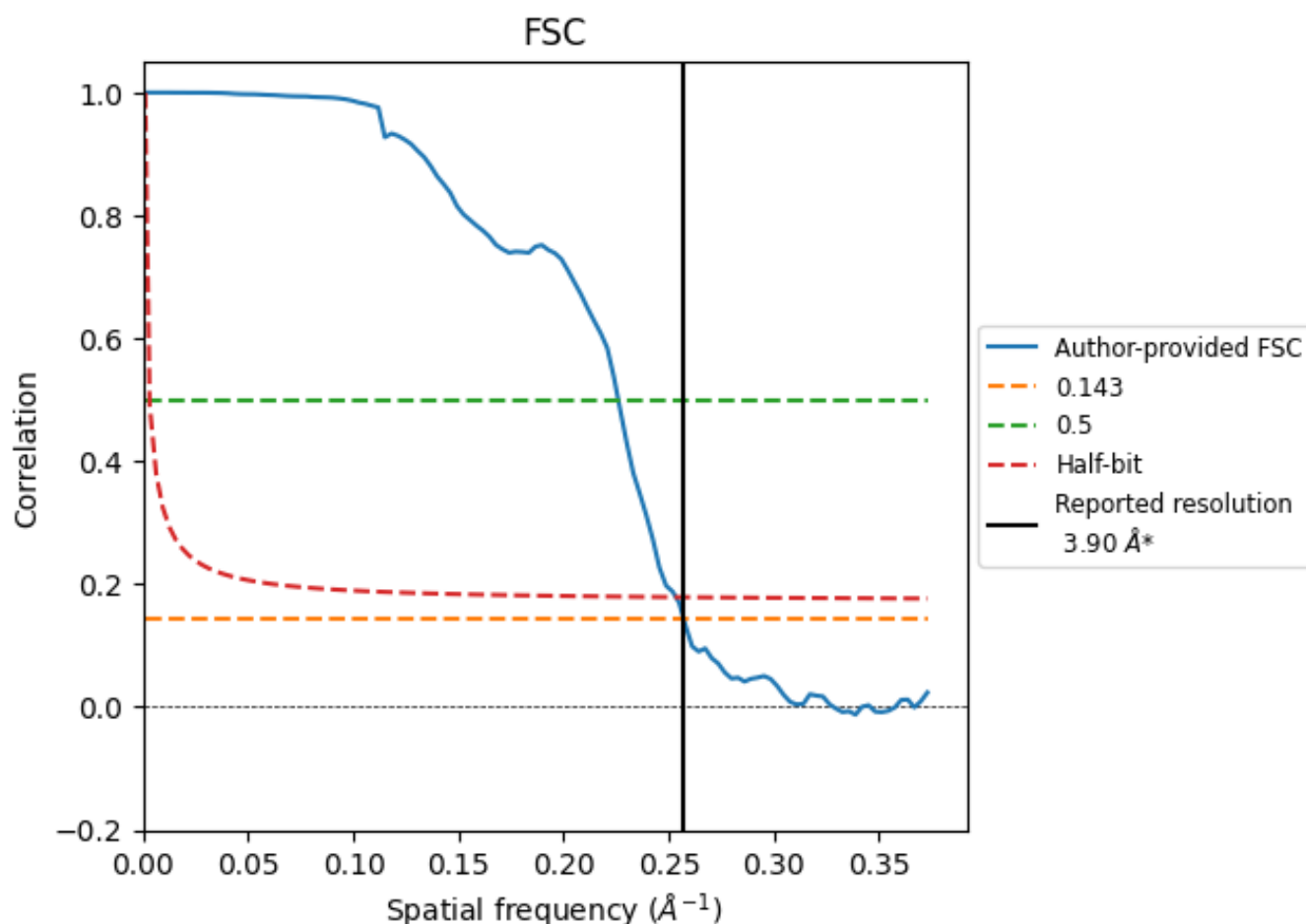


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

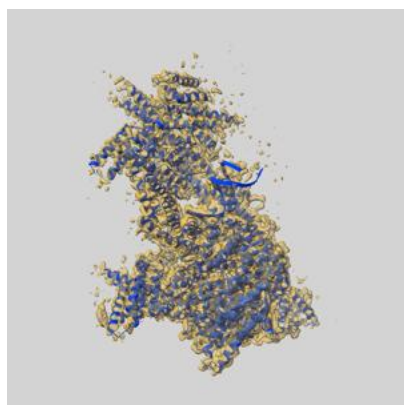
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.89	4.42	3.95
Unmasked-calculated*	-	-	-

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

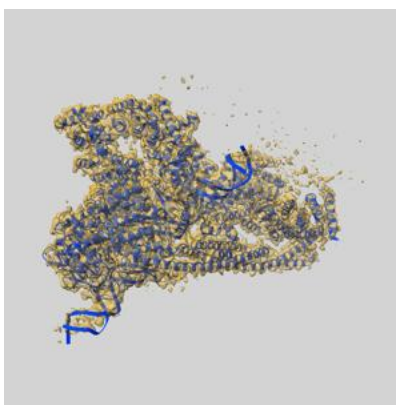
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21663 and PDB model 6WGE. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

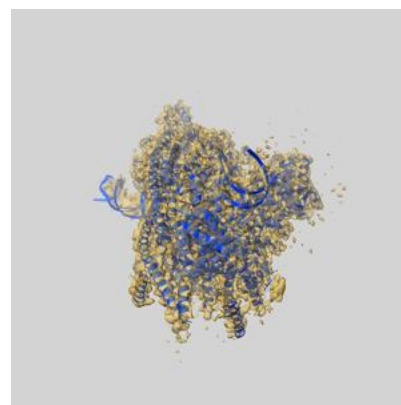
9.1 Map-model overlay [i](#)



X



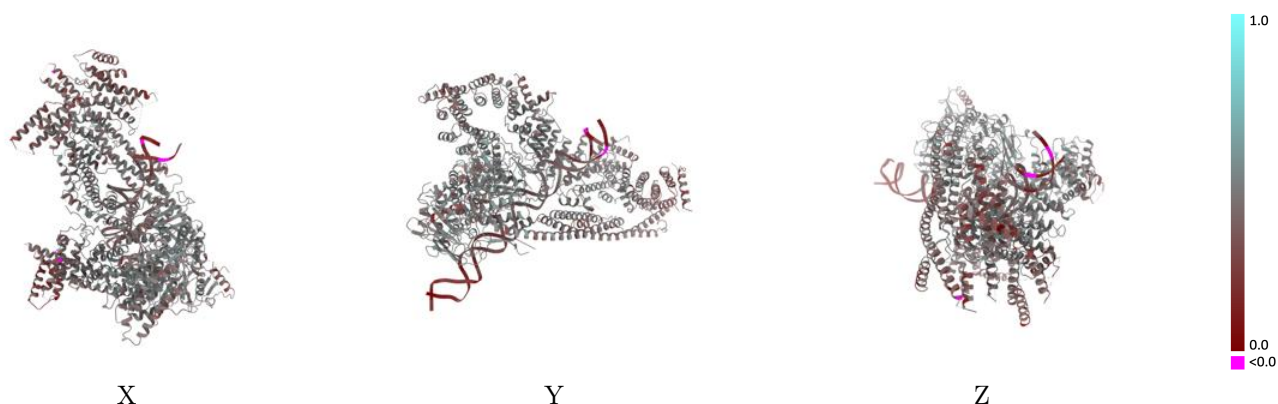
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.032 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](#)

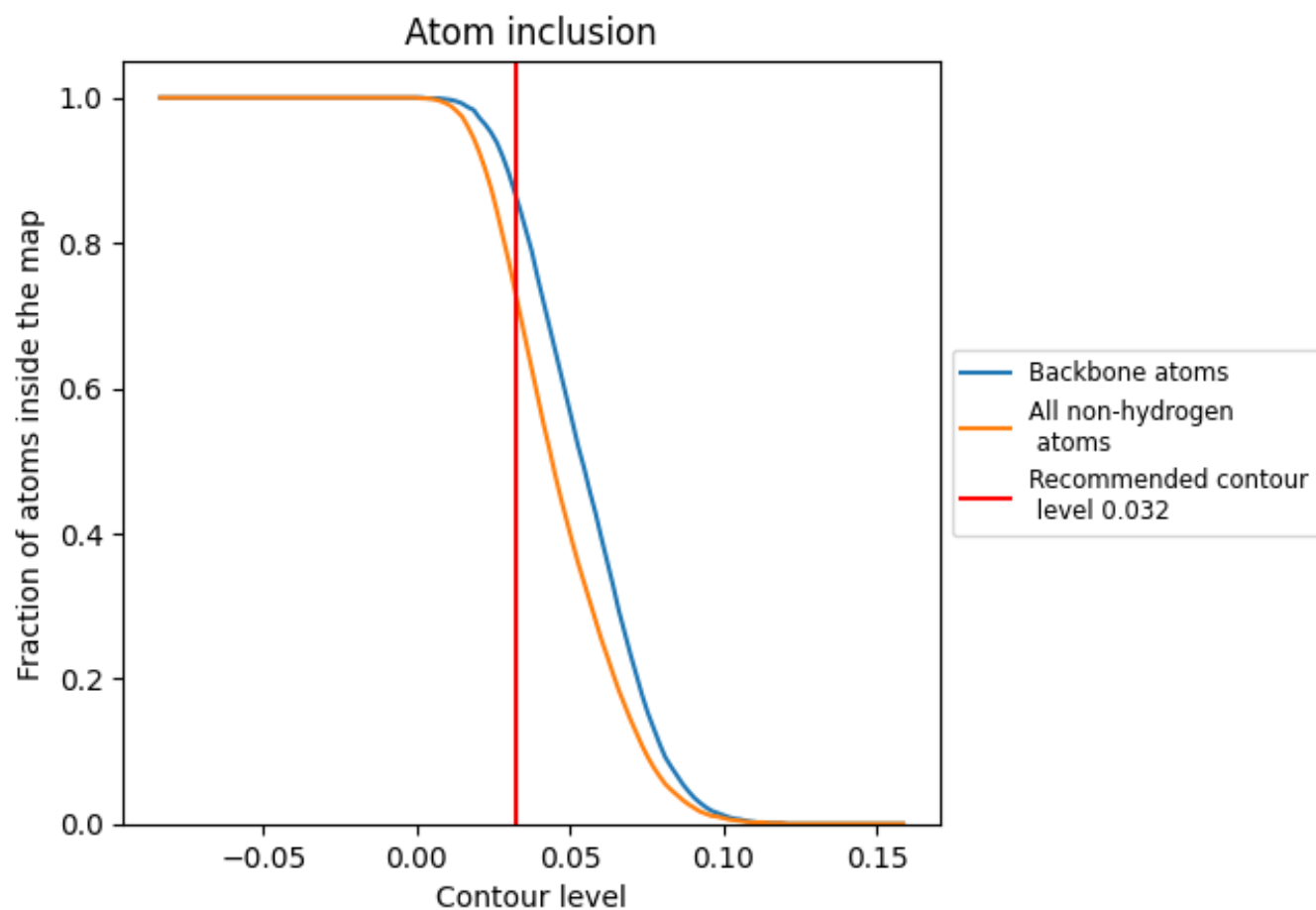


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7350	0.4310
A	0.7840	0.4710
B	0.7570	0.4540
C	0.6980	0.4370
E	0.7300	0.4360
F	0.6580	0.2650
G	0.6500	0.2870

