



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 09:17 AM UTC

PDB ID : 6JXA / pdb_00006jxa
EMDB ID : EMD-9892
Title : Tel1 kinase compact monomer
Authors : Xin, J.
Deposited on : 2019-04-23
Resolution : 4.30 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

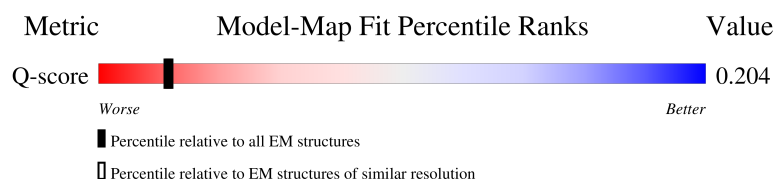
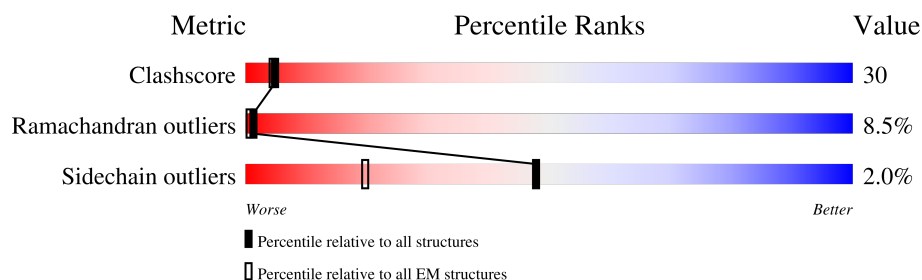
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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	2787	

2 Entry composition

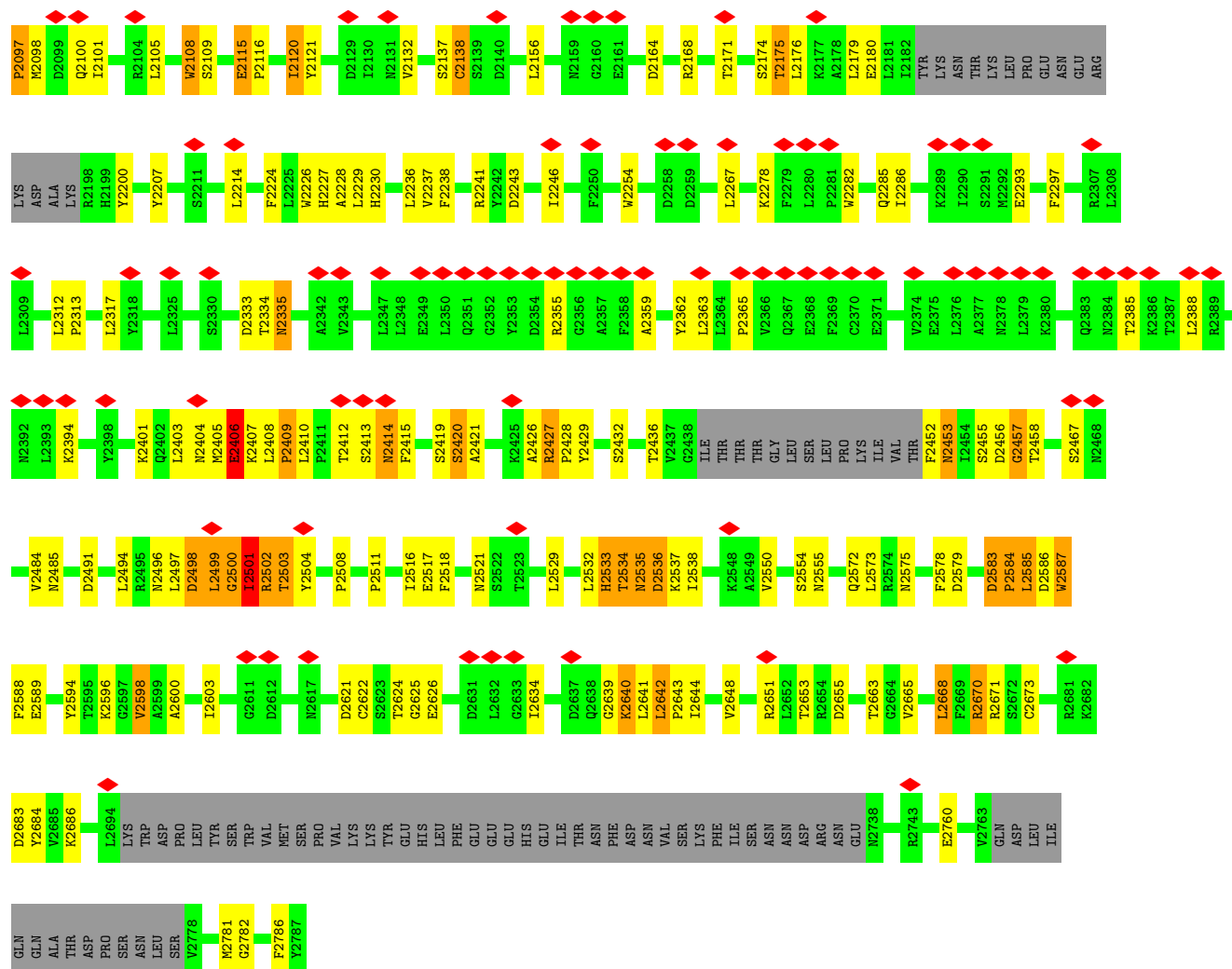
There is only 1 type of molecule in this entry. The entry contains 14100 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase TEL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2244	14100	8748	2594	2720	38	0	0

ASP	GLN	SER	TYR	GLN	SER	PHE	GLU	VAL	LEU	SER	I750	I753	V759	L760	E767	I768	V769	I770	D771	F772	I773	T782	GLY	THR	SER	ALA	ILE	ASN	PHE	GLU	ALA	SER	GLU	ASP	THR	GLN	ASN	SER	PRO	TYR	THR	ILE	GLY	GLY	ARG	PHE	GLN							
LYS	PRO	LEU	HIS	S816	T817	Y825	L826	TRP	SER	PRO	GLU	ASN	SER	ILE	S925	D940	N941	S942	F943	S1041	T944	G945	V946	A947	P948	T949	F1053	S1054	E1055	E1056	T1057	M1058	M1059	H1066	F1070	I1071	T980	F981	L982	K983	C984	L985	L864	A867	V884	L885	G886	E887	K888	L889	L890	C891	N892	H893
Y894	A910	P913	Q914	W915	LEU	SER	TYR	PRO	GLU	ASN	ASN	S925	D940	N941	S942	F943	S1041	T944	G945	V946	A947	P948	T949	F1053	S1054	E1055	E1056	T1057	M1058	M1059	H1066	F1070	I1071	T980	F981	L982	K983	C984	L985	S991	N995	L996	M997	N998	I1000	S1001	S1002	S1013	I1014	I1015				
F1016	I1019	K1020	S1021	L1022	P1025	P1026	S1029	S1033	A1034	F1035	S925	D940	N941	S942	F943	S1041	T944	G945	V946	A947	P948	T949	F1053	S1054	E1055	E1056	T1057	M1058	M1059	H1066	F1070	I1071	T980	F981	L982	K983	C984	L985	S991	N995	L996	M997	N998	I1000	S1001	S1002	S1013	I1014	I1015					
GLU	LYS	TRP	ASP	ILE	SER	PHE	PHE	ASP	ILE	HIS	E1129	V1136	K1150	D1154	M1155	P1177	L1178	S1182	I1192	L1193	P1194	I1195	I1196	K1203	Y1204	K1205	K1206	K1207	Y1208	R1209	L1210	L1211	M1212	T1220	ASP	LEU	GLY	SER	L1225	F1236	P1237	P1243	V1251	S1252										
MET	TYR	TRP	TYR	PRO	LEU	ILE	PRO	LEU	ALA	GLY	ALA	V1270	F1284	E1296	S1299	K1304	L1305	A1308	S1325	M1329	F1330	I1331	I1332	I1333	R1334	F1338	L1339	Q1343	I1344	I1366	E1367	P1368	N1372	F1373	C1375	Y1380	L1381	R1382	L1387	S1388														
F1391	Q1392	R1401	T1416	G1418	M1419	I1420	V1421	Q1422	D1423	E1430	L1431	L1432	D1433	D1436	C1437	D1441	V1442	V1443	L1444	R1453	R1454	P1455	S1465	H1476	V1477	E1480	S1483	K1484	R1495	R1496	I1497	E1501	VAL	GLN	ARG	GLU	ARG	THR	ASN	ASN	ASN	GLU	VAL											
H1515	R1524	H1525	Q1528	H1530	M1531	I1532	Y1533	A1543	E1550	V1551	E1556	C1557	Y1561	L1562	Y1565	E1571	F1576	R1577	I1580	P1590	V1595	L1596	N1597	A1598	I1599	Y1600	P1601	N1605	F1606	G1607	M1608	E1609	S1610	F1611	I1612	P1622	L1627	S1628	K1629	F1630	A1631	S1633												
L1634	I1635	H1636	Q1637	H1638	F1640	P1643	P1644	P1650	L1661	D1665	L1666	F1667	L1668	L1669	T1671	Y1672	K1676	M1680	R1684	I1689	A1690	M1691	L1692	L1693	H1694	V1695	E1699	I1700	K1701	L1702	K1703	M1704	L1705	F1706	M1707	V1708	L1724	L1730	D1731	E1734	Q1737	I1738	S1739											
L1740	K1741	I1742	K1743	F1744	F1745	K1746	F1747	G1748	Y1749	L1750	L1751	F1752	E1753	E1754	M1755	D1756	Q1769	K1770	I1771	C1774	I1775	N1776	D1777	G1778	D1779	F1780	L1781	R1785	P1786	F1787	H1788	S1789	N1795	SER	ILE	ASN	ARG	ASP	THR	TRP	LYS	R1807	F1808	L1809	F1810									
M1811	M1812	A1813	D1814	F1815	D1816	A1817	M1818	Y1819	THR	THR	SER	LEU	GLU	GLU	M1827	T1831	S1832	A1833	D1836	S1837	F1838	Y1839	Y1840	S1844	S1853	S1854	D1855	V1856	Y1857	P1871	V1874	D1875	S1876	K1877	A1878	K1879	I1885	L1888	F1894	S1895	E1896	K1897	L1898	L1899	D1908	S1909	H1912							
Q1916	T1917	T1922	A1925	I1930	K1931	I1932	A1933	I1935	P1936	Q1937	D1938	V1939	SER	T1940	S1941	F1942	P1943	Q1944	T1945	L1946	G1948	S1948	D2037	D2038	P2039	S2040	V2041	F2051	A2054	W2058	E2059	S2060	R2061	Y1963	D1964	H1965	K1966	T1967	L1968	L1969	S2082	E2083	S2084	L2085	L1975	S1980	L1984	V1988	C1990					
G2007	I2010	A2011	N2012	G2013	A2014	N2021	ALA	THR	LEU	MET	SER	SER	LYS	THR	VAL	LYS	ASN	ILE	ALA	LYS	LEU	TYR	D2037	D2038	P2039	S2040	V2041	F2051	A2054	W2058	E2059	S2060	R2061	D2072	L2073	L2074	N2080	I2081	E2082	S2084	L2085	L1975	S1980	L1984	V1988	C1990								



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25708	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.135	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.035	Depositor
Map size ($\text{\AA}$)	345.6, 345.6, 345.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.35, 1.35, 1.35	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.02	3/14196 (0.0%)	1.29	113/19391 (0.6%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1899	LEU	CB-CG	-6.91	1.39	1.53
1	A	1975	LEU	CB-CG	-6.75	1.40	1.53
1	A	1972	ARG	NE-CZ	5.34	1.39	1.33

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1691	MET	N-CA-C	-11.99	100.95	114.62
1	A	1382	ARG	N-CA-C	-11.10	98.10	108.75
1	A	1962	PHE	CA-CB-CG	-10.75	103.05	113.80
1	A	1331	ILE	N-CA-C	-10.28	100.69	111.58
1	A	22	ASN	N-CA-C	-9.21	100.84	112.90

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	14100	0	10698	739	0
All	All	14100	0	10698	739	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 30.

The worst 5 of 739 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:1939:VAL:HB	1:A:1990:CYS:CB	1.34	1.51
1:A:1939:VAL:CB	1:A:1990:CYS:HB2	1.41	1.49
1:A:1694:HIS:CE1	1:A:1730:LEU:HD13	1.46	1.49
1:A:215:LEU:CB	1:A:325:THR:HA	1.43	1.46
1:A:2603:ILE:HD11	1:A:2673:CYS:SG	1.57	1.43

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	2174/2787 (78%)	1724 (79%)	266 (12%)	184 (8%)	0 9

5 of 184 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ILE
1	A	19	LYS
1	A	90	VAL
1	A	95	VAL
1	A	196	VAL

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	A	881/2569 (34%)	863 (98%)	18 (2%)	48 66

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2501	ILE
1	A	2670	ARG
1	A	2668	LEU
1	A	1990	CYS
1	A	2499	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2004	ASN
1	A	2227	HIS
1	A	2533	HIS
1	A	2404	ASN
1	A	2414	ASN

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 ⓘ

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

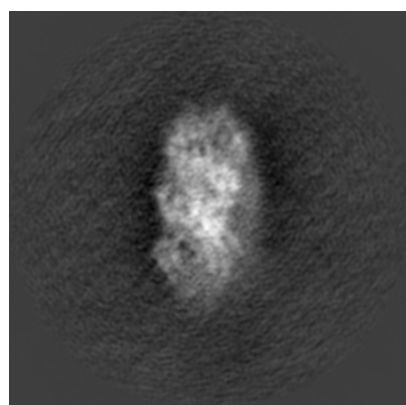
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9892. These allow visual inspection of the internal detail of the map and identification of artifacts.

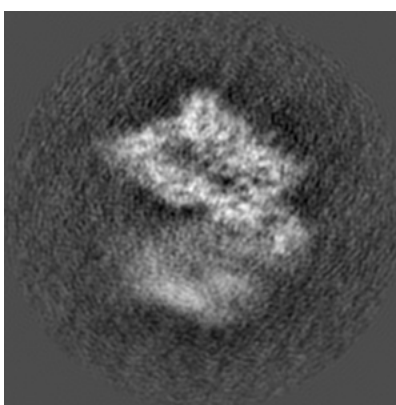
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

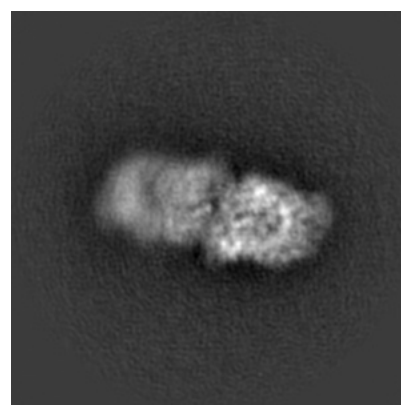
6.1.1 Primary map



X



Y

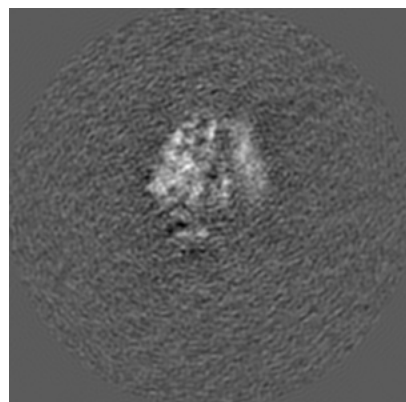


Z

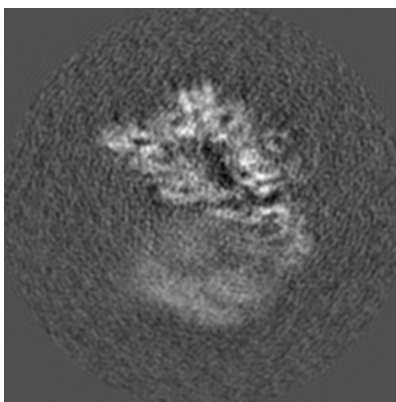
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

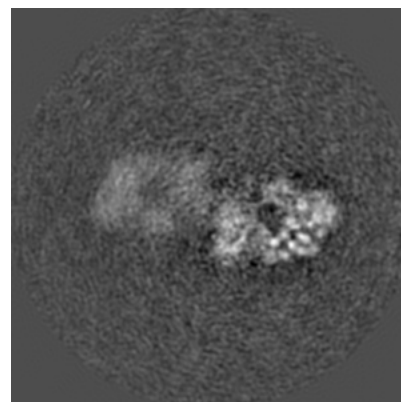
6.2.1 Primary map



X Index: 128



Y Index: 128

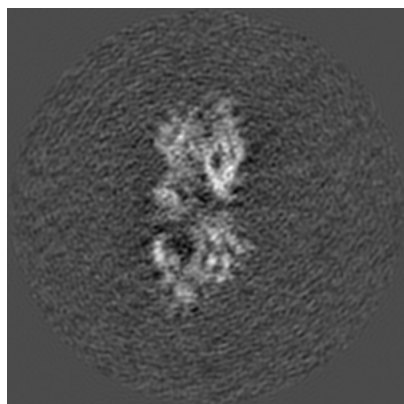


Z Index: 128

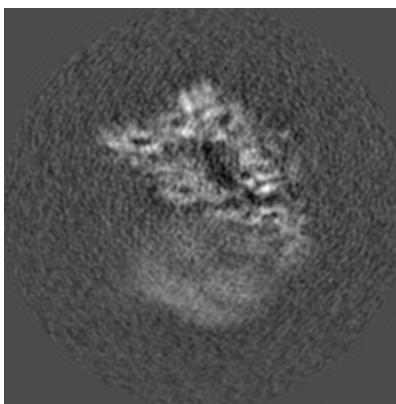
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

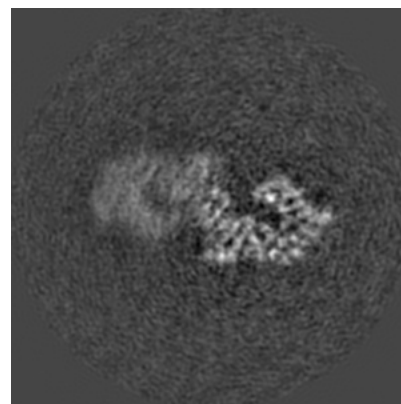
6.3.1 Primary map



X Index: 158



Y Index: 127

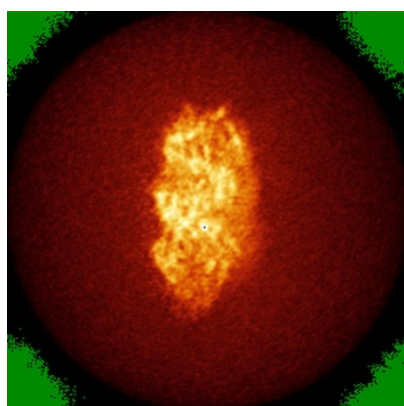


Z Index: 137

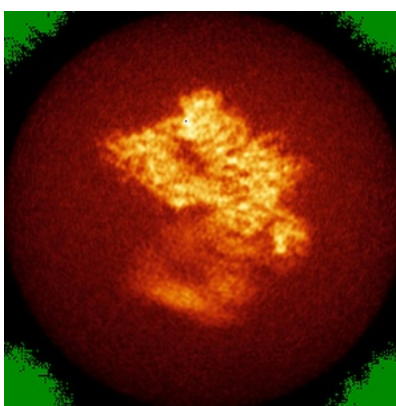
The images above show the largest variance slices of the map in three orthogonal directions.

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

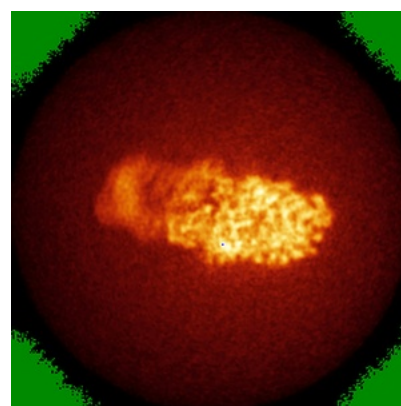
6.4.1 Primary map



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 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

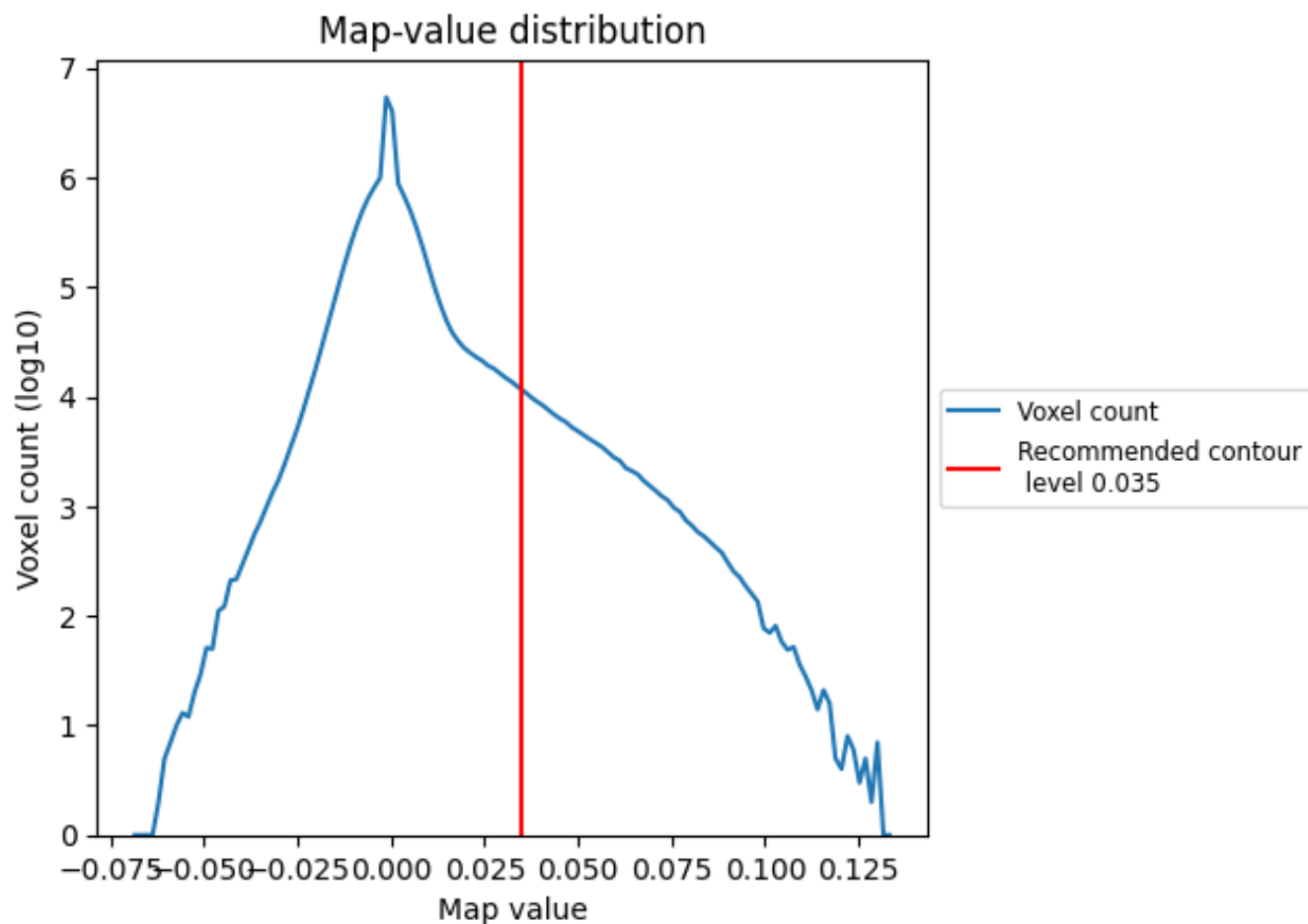
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

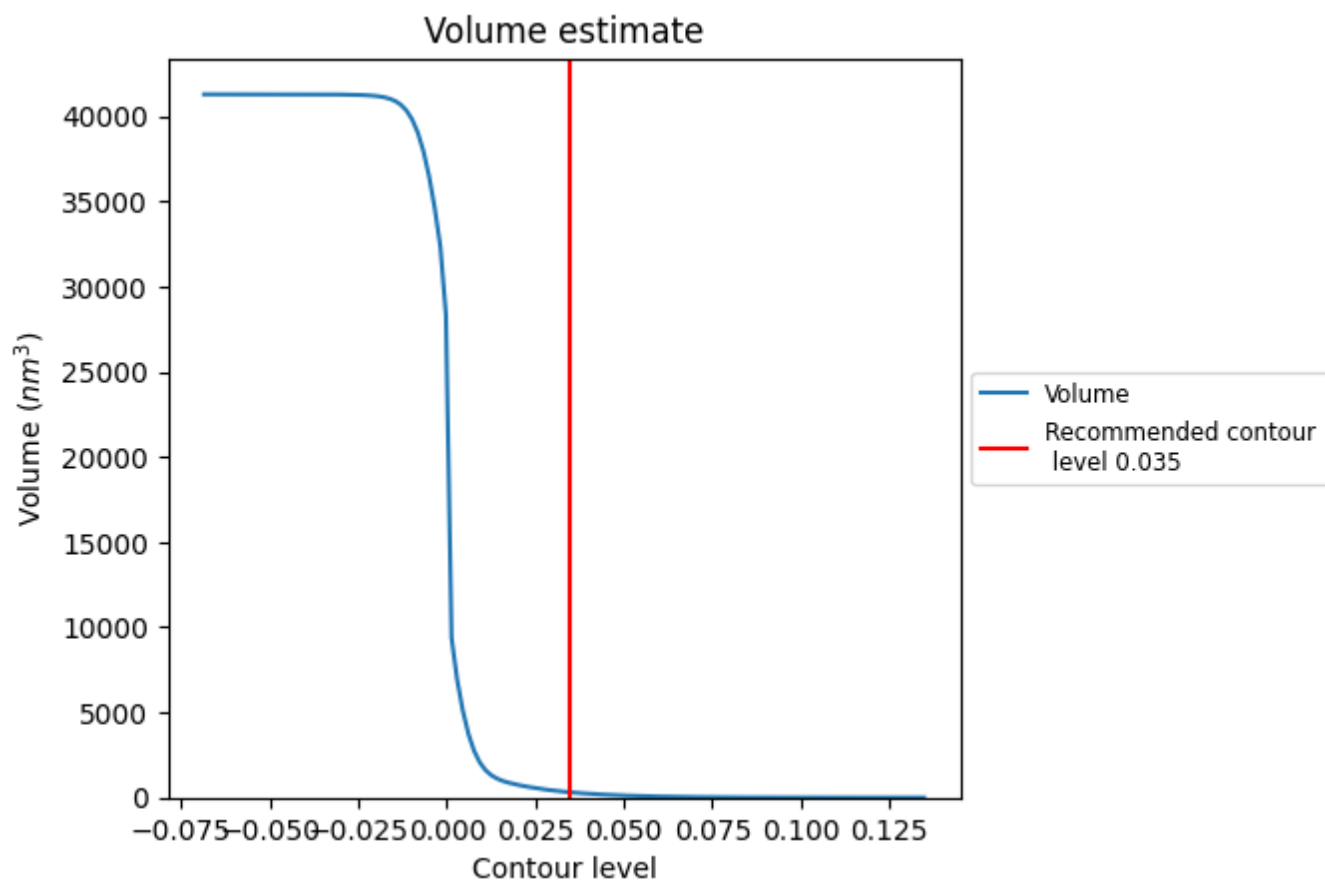
This section contains the results of statistical analysis of the map.

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.

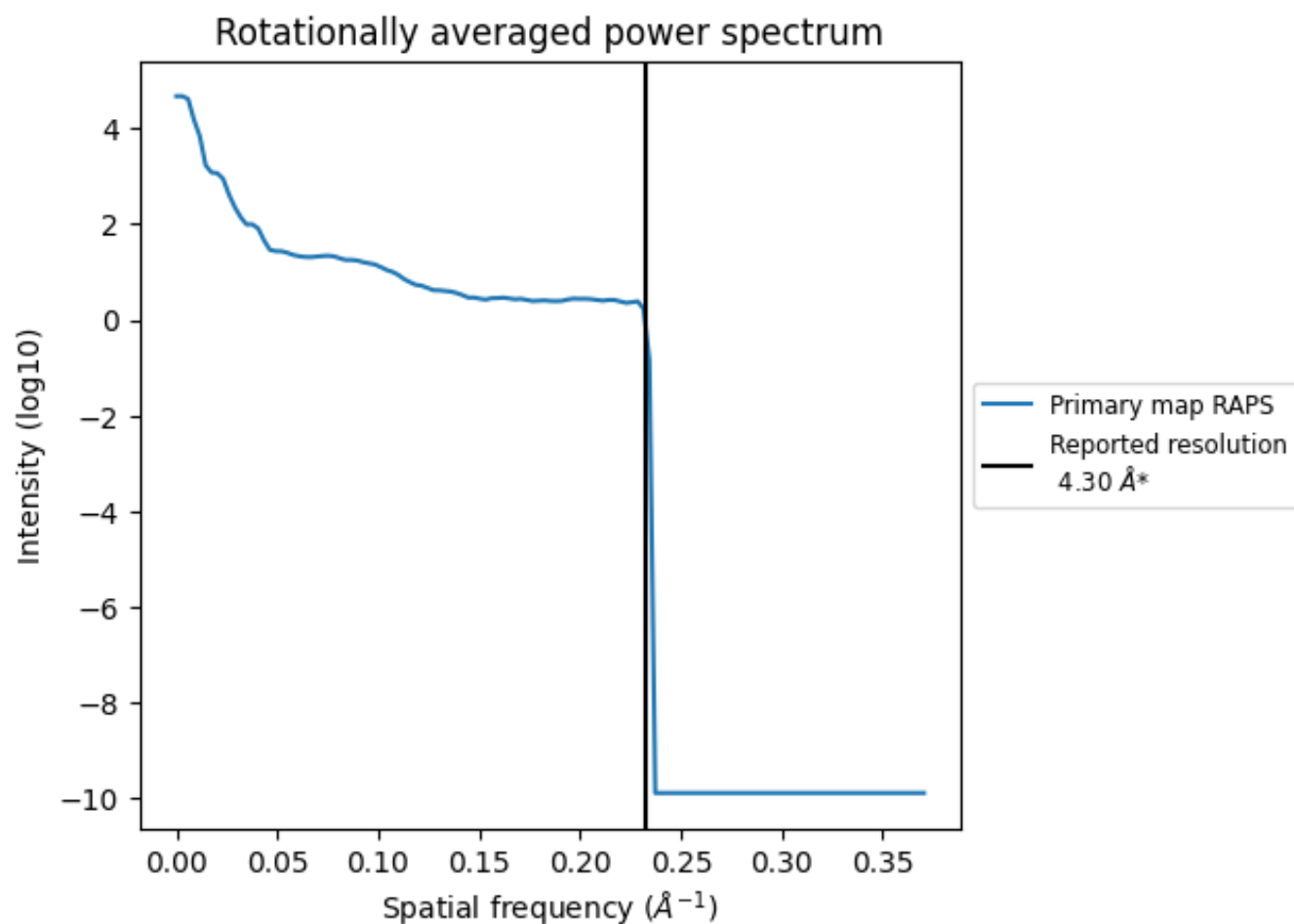
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 307 nm³; this corresponds to an approximate mass of 277 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 0.233 Å⁻¹

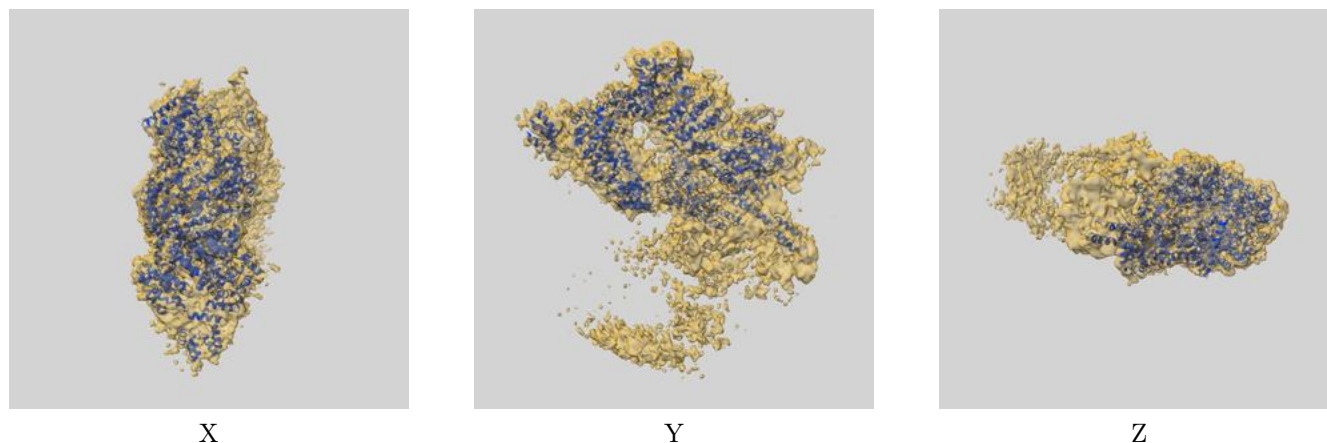
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

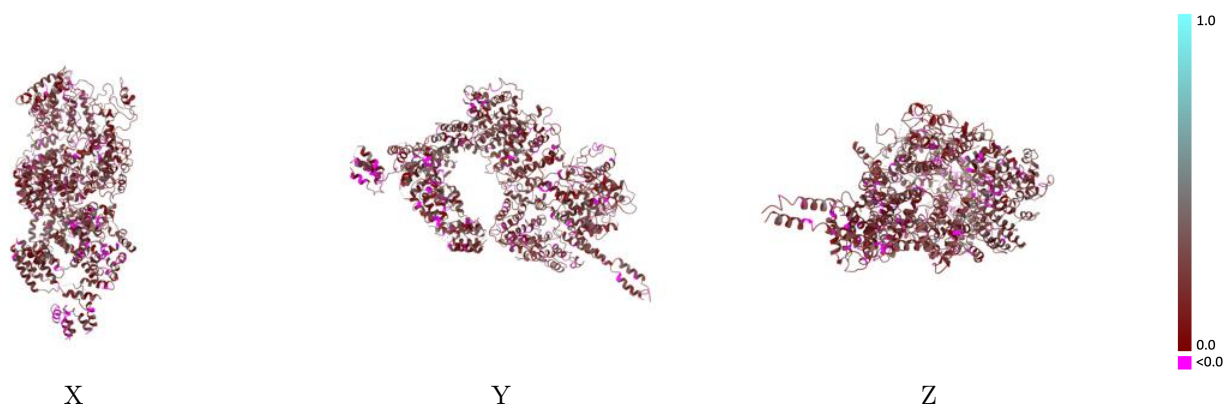
This section contains information regarding the fit between EMDB map EMD-9892 and PDB model 6JXA. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



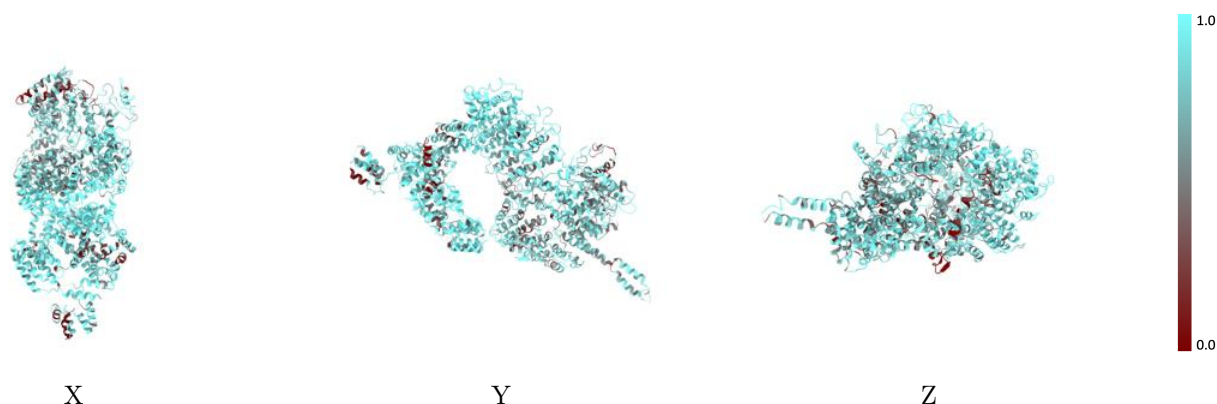
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



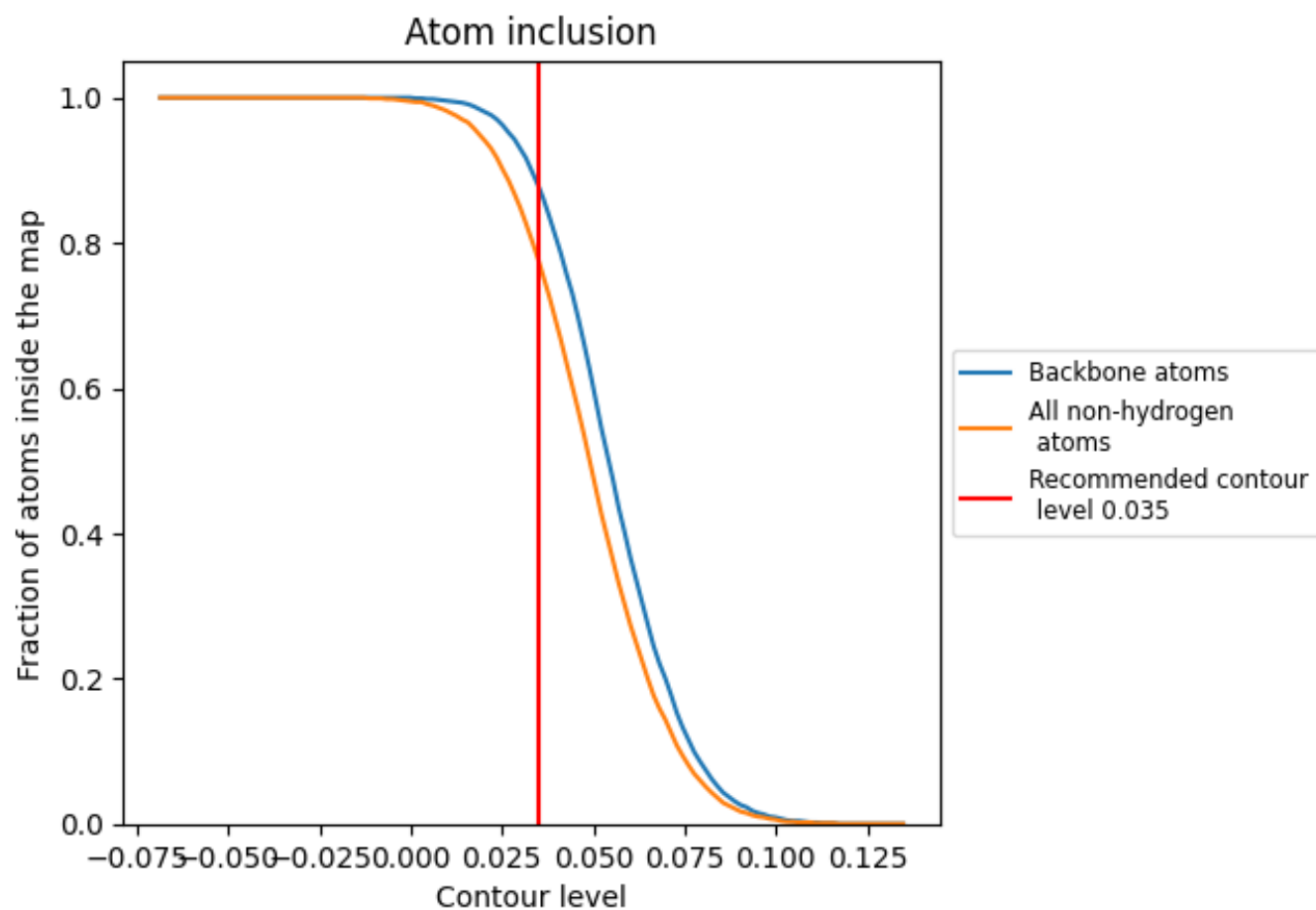
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 78% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7760	0.2040
A	0.7760	0.2040

