wwPDB EM Validation Summary Report (i)

Feb 24, 2022 – 01:07 am GMT

PDB ID	:	7YXY
EMDB ID	:	EMD-14369
Title	:	Cryo-EM structure of USP9X, local refinement of monomer
Authors	:	Deme, J.C.; Halabelian, L.; Arrowsmith, C.H.; Lea, S.M.; Structural Genomics Consortium (SGC)
Deposited on	:	2022-02-16
Resolution	:	3.10 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

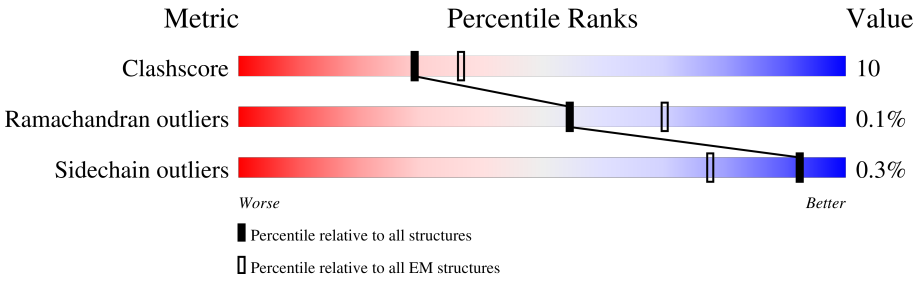
EMDB validation analysis	:	0.0.0.dev97
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	2579	23% 50% 17% 33%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 14031 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 Probable ubiquitin carboxyl-terminal hydrolase FAF-X.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1739	14031	8988	2403	2544	96	1	0

There are 25 discrepancies between the modelled and reference sequences:

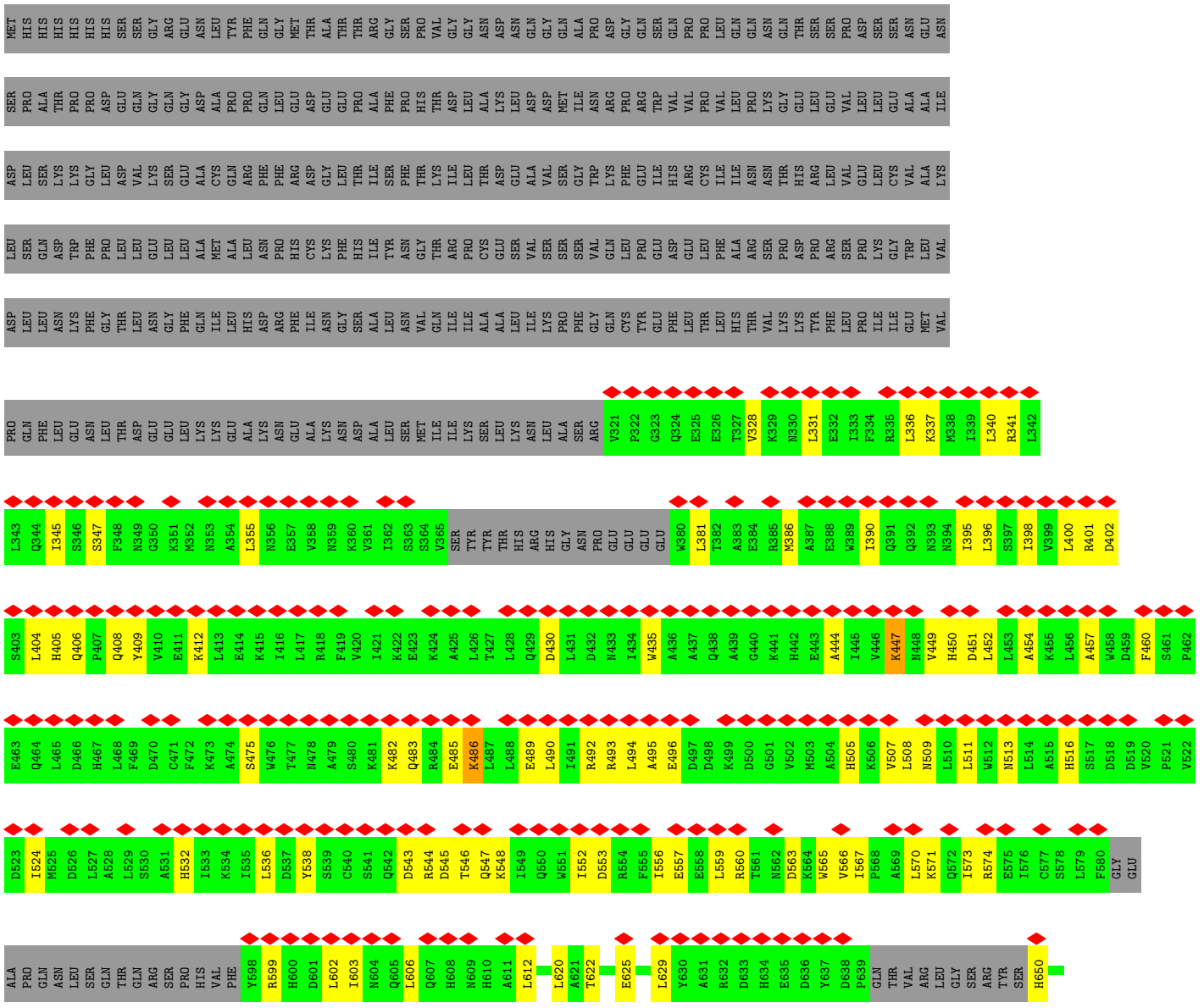
Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP Q93008
A	-16	HIS	-	expression tag	UNP Q93008
A	-15	HIS	-	expression tag	UNP Q93008
A	-14	HIS	-	expression tag	UNP Q93008
A	-13	HIS	-	expression tag	UNP Q93008
A	-12	HIS	-	expression tag	UNP Q93008
A	-11	HIS	-	expression tag	UNP Q93008
A	-10	SER	-	expression tag	UNP Q93008
A	-9	SER	-	expression tag	UNP Q93008
A	-8	GLY	-	expression tag	UNP Q93008
A	-7	ARG	-	expression tag	UNP Q93008
A	-6	GLU	-	expression tag	UNP Q93008
A	-5	ASN	-	expression tag	UNP Q93008
A	-4	LEU	-	expression tag	UNP Q93008
A	-3	TYR	-	expression tag	UNP Q93008
A	-2	PHE	-	expression tag	UNP Q93008
A	-1	GLN	-	expression tag	UNP Q93008
A	0	GLY	-	expression tag	UNP Q93008
A	2555	ASP	-	expression tag	UNP Q93008
A	2556	TYR	-	expression tag	UNP Q93008
A	2557	LYS	-	expression tag	UNP Q93008
A	2558	ASP	-	expression tag	UNP Q93008
A	2559	ASP	-	expression tag	UNP Q93008
A	2560	ASP	-	expression tag	UNP Q93008
A	2561	LYS	-	expression tag	UNP Q93008

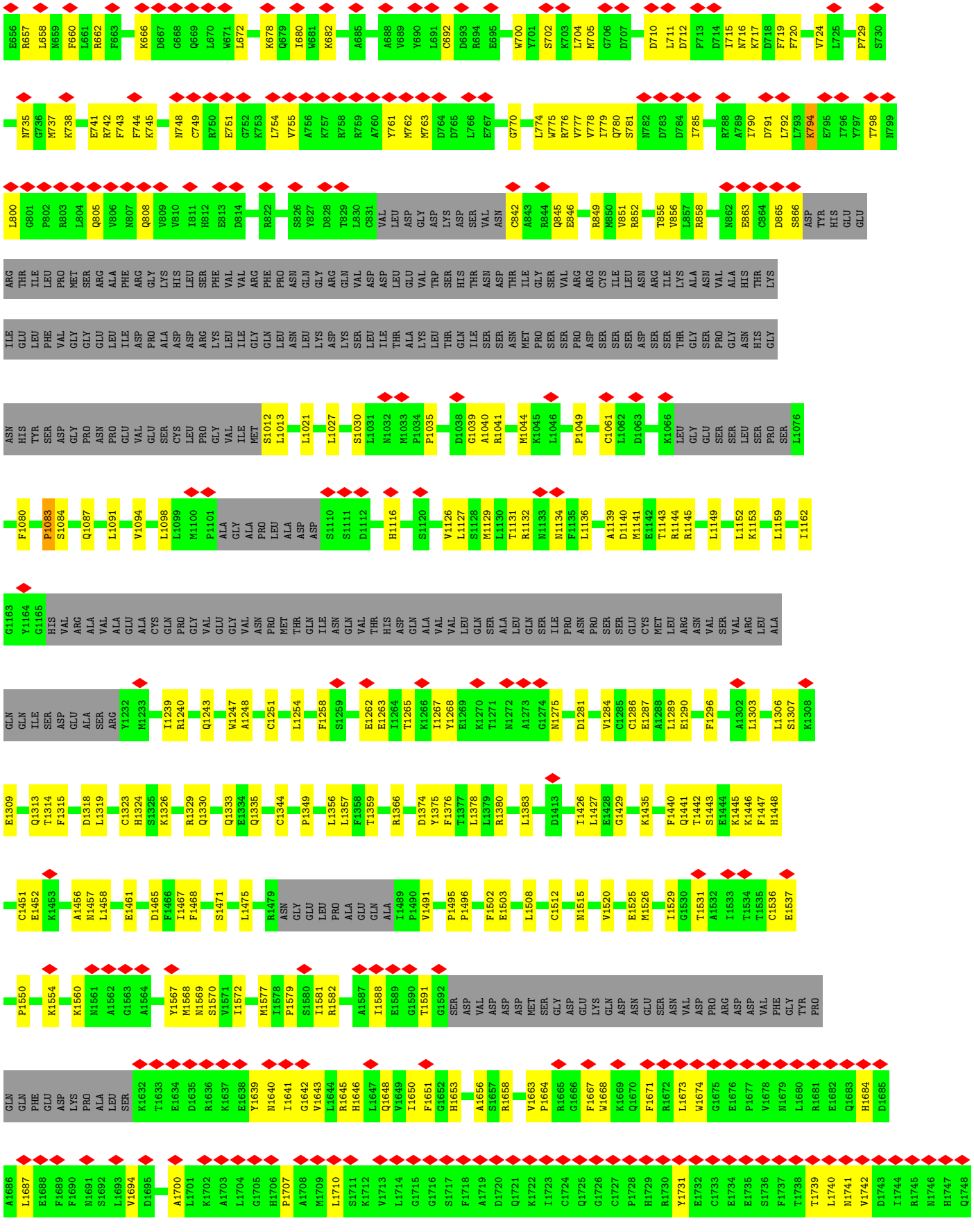
3 Residue-property plots (i)

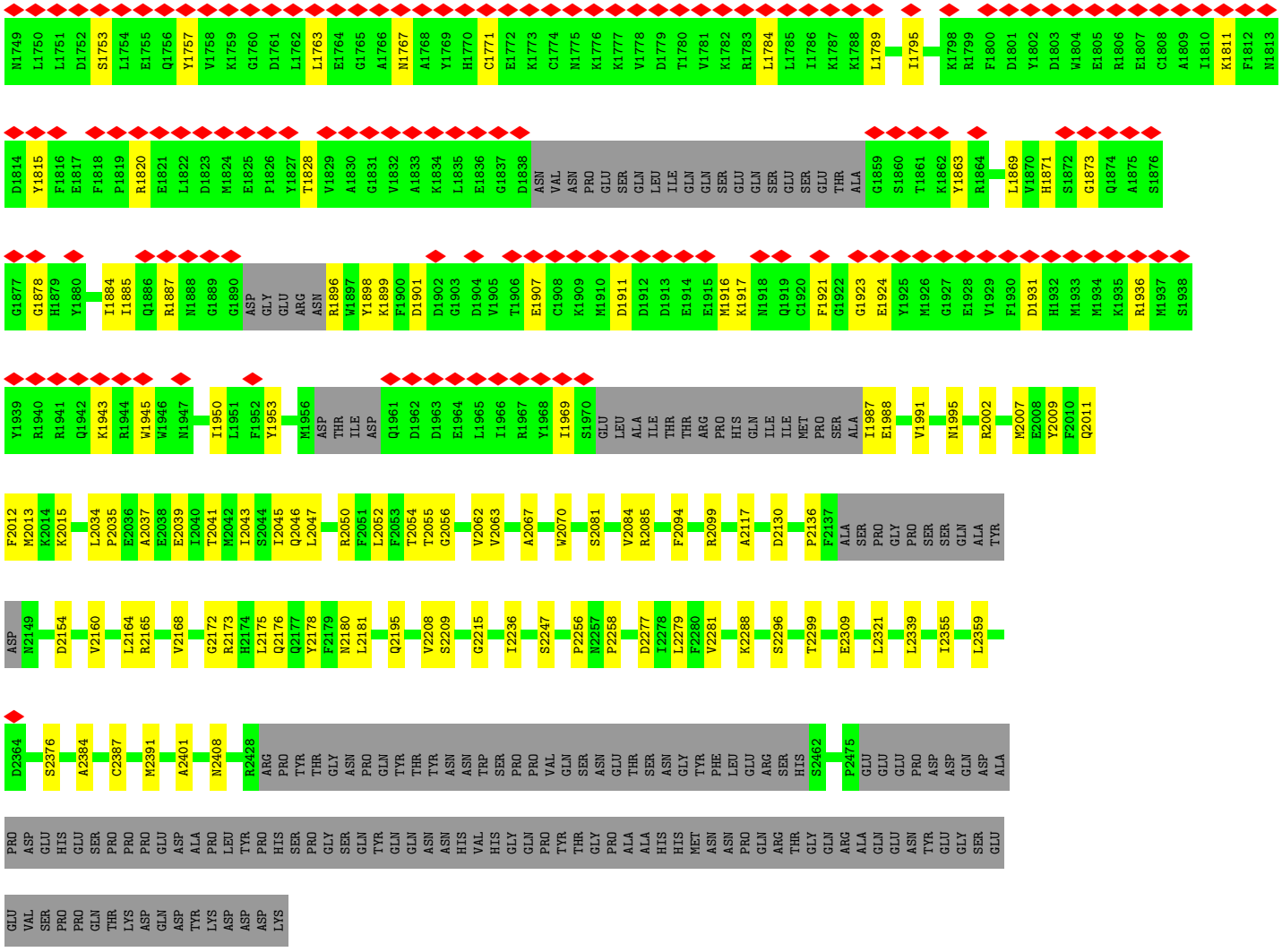
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Probable ubiquitin carboxyl-terminal hydrolase FAF-X

Chain A:




E656 R657 L658 N659 F660 L661 R662 F663 K666 D667 G668 Q669 L670 W671 L672 K678 Q679 I680 W681 K682 A685 A688 V689 Y690 L691 C692 D693 R694 E695 W700 Y701 S702 K703 L704 M705 G706 D707 D710 L711 D712 P713 D714 I715 N716 K717 D718 F719 F720 V724 L725 P729 S730
N735 G736 M737 K738 E741 R742 F743 F744 K745 N748 C749 R750 E751 G752 K753 L754 V755 A756 K757 R758 R759 A760 Y761 M762 W763 D764 D765 L766 E767 G770 L774 W775 R776 V777 V778 I779 Q780 S781 N782 D783 D784 I785 R788 A789 I790 D791 L792 L793 K794 E795 I796 Y797 T798 N799
L800 G801 P802 R803 L804 Q805 V806 N807 Q808 V809 V810 I811 H812 E813 D814 R822 S826 Y827 D828 T829 L830 C831 VAL LEU ASP GLY ASP LYS ASP SER VAL ASN C842 A843 R844 Q845 E846 R849 M850 V851 R852 T855 V856 L857 R858 N862 E863 C864 D865 S866 ASP TYR HIS GLU GLU
ARG THR ILE LEU PRO MET SER ARG ALA PHE ARG GLY LYS HIS LEU SER PHE VAL VAL ARG PHE PRO ASN GLN GLY ARG GLN VAL ASP ASP LEU GLU VAL TRP SER HIS THR ASN ASP THR ILE GLY SER VAL ARG ARG CYS ILE LEU ASN ARG ILE LYS ALA ASN VAL ALA HIS THR LYS
ILE GLU LEU PHE VAL GLY GLY GLU LEU ILE ASP PRO ALA ASP ASP ARG LYS LEU ILE GLY GLN LEU ASN LEU LYS ASP LYS SER LEU ILE THR ALA LYS LEU THR GLN ILE SER SER ASN MET PRO SER SER PRO ASP SER SER SER ASP SER SER THR GLY SER PRO GLY ASN HIS GLY
ASN HIS TYR SER ASP GLY PRO ASN PRO GLU VAL GLU SER CYS LEU PRO GLY VAL ILE MET S1012 L1013 L1021 L1027 S1030 L1031 N1032 M1033 P1034 P1035 D1038 G1039 A1040 R1041 M1044 K1045 L1046 P1049 C1061 L1062 D1063 K1066 LEU GLY GLU SER SER LEU SER PRO SER L1076
F1080 P1083 S1084 Q1087 L1091 V1094 L1098 L1099 M1100 P1101 ALA GLY ALA PRO LEU ALA ASP ASP S1110 S1111 D1112 H1116 S1120 V1126 L1127 S1128 M1129 L1130 T1131 R1132 N1133 N1134 F1135 L1136 A1139 D1140 M1141 E1142 T1143 R1144 R1145 L1149 L1152 K1153 L1159 I1162
G1163 Y1164 G1165 HIS VAL ARG ALA VAL ALA GLU ALA ALA CYS GLN PRO GLY VAL GLU GLY VAL ASN PRO MET THR GLN ILE ASN GLN VAL THR HIS ASP GLN ALA ALA VAL VAL LEU GLN SER ALA LEU GLN SER ILE PRO ASN PRO SER SER GLU CYS MET LEU ARG ASN VAL SER VAL ARG LEU ALA
GLN GLN ILE SER ASP GLU ALA SER ARG Y1232 M1233 I1239 R1240 Q1243 W1247 A1248 C1251 L1254 F1258 S1259 E1262 E1263 T1264 T1265 K1266 I1267 Y1268 E1269 K1270 T1271 N1272 A1273 G1274 N1275 D1281 V1284 C1285 C1286 E1287 A1288 L1289 E1290 F1296 A1302 L1303 L1306 S1307 K1308
E1309 Q1313 T1314 F1315 D1318 L1319 C1323 H1324 S1325 K1326 R1329 Q1330 Q1333 E1334 Q1335 C1344 P1349 L1356 L1357 F1358 T1359 R1366 D1374 Y1375 F1376 T1377 L1378 L1379 R1380 L1383 D1413 I1426 L1427 E1428 G1429 K1435 F1440 Q1441 T1442 S1443 E1444 K1445 K1446 F1447 H1448
C1451 E1452 K1453 A1456 N1457 L1458 E1461 D1465 F1466 I1467 F1468 S1471 L1475 R1479 ASN GLY GLU LEU PRO ALA GLU GLN ALA I1489 P1490 V1491 P1495 P1496 F1502 E1503 L1508 C1512 N1515 V1520 E1525 M1526 I1529 G1530 T1531 A1532 I1533 T1534 T1535 C1536 E1537
P1550 K1554 K1560 N1561 A1562 G1563 A1564 Y1567 M1568 N1569 S1570 V1571 I1572 M1577 I1578 P1579 S1580 I1581 R1582 A1587 I1588 E1589 G1590 T1591 G1592 SER ASP VAL ASP ASP ASP MET SER GLY ASP GLU LYS GLN ASP ASN GLU SER ASN VAL ASP PRO ARG ASP ASP VAL PHE GLY TYR PRO
GLN GLN PHE GLU ASP LYS PRO ALA LEU SER K1632 T1633 E1634 D1635 R1636 K1637 E1638 Y1639 N1640 I1641 G1642 V1643 L1644 R1645 H1646 L1647 Q1648 V1649 I1650 F1651 G1652 H1653 A1656 S1657 R1658 V1663 P1664 R1665 G1666 F1667 W1668 K1669 Q1670 F1671 R1672 L1673 W1674 G1675 E1676 P1677 V1678 N1679 L1680 R1681 E1682 Q1683 H1684 D1685
A1686 L1687 E1688 F1689 F1690 N1691 S1692 L1693 V1694 D1695 A1700 L1701 K1702 A1703 L1704 G1705 H1706 P1707 A1708 M1709 L1710 S1711 K1712 V1713 L1714 G1715 G1716 S1717 F1718 A1719 D1720 Q1721 K1722 I1723 C1724 Q1725 G1726 C1727 P1728 H1729 R1730 Y1731 E1732 C1733 E1734 E1735 S1736 F1737 T1738 T1739 L1740 N1741 V1742 D1743 I1744 R1745 N1746 H1747 Q1748


N1749 L1750 L1751 D1752 S1753 L1754 E1755 Q1756 Y1757 V1758 K1759 G1760 D1761 L1762 L1763 E1764 G1765 A1766 N1767 A1768 Y1769 H1770 C1771 E1772 K1773 C1774 N1775 K1776 K1777 V1778 D1779 T1780 V1781 K1782 R1783 L1784 L1785 I1786 K1787 K1788 L1789 I1795 K1798 R1799 F1800 D1801 Y1802 D1803 W1804 E1805 R1806 E1807 C1808 A1809 I1810 K1811 F1812 N1813
D1814 Y1815 F1816 E1817 F1818 P1819 R1820 E1821 L1822 D1823 M1824 E1825 P1826 Y1827 T1828 V1829 A1830 G1831 V1832 A1833 K1834 L1835 E1836 G1837 D1838 ASN VAL ASN PRO GLU SER GLN LEU ILE GLN GLN SER GLU GLN SER GLU SER GLU THR ALA G1859 S1860 T1861 K1862 Y1863 R1864 L1869 V1870 H1871 S1872 G1873 Q1874 A1875 S1876
G1877 G1878 H1879 Y1880 I1884 I1885 Q1886 R1887 N1888 G1889 G1890 ASP GLY GLU ARG ASN R1896 W1897 Y1898 K1899 F1900 D1901 D1902 G1903 D1904 V1905 T1906 E1907 C1908 K1909 M1910 D1911 D1912 D1913 E1914 E1915 M1916 K1917 N1918 Q1919 C1920 F1921 G1922 G1923 E1924 Y1925 M1926 G1927 E1928 V1929 F1930 D1931 H1932 M1933 M1934 K1935 R1936 M1937 S1938
Y1939 R1940 R1941 Q1942 K1943 R1944 W1945 W1946 N1947 I1950 L1951 F1952 Y1953 M1956 ASP THR ILE ASP Q1961 D1962 D1963 E1964 L1965 I1966 R1967 Y1968 I1969 S1970 GLU LEU ALA ILE THR THR ARG PRO HIS GLN ILE ILE MET PRO SER ALA I1987 E1988 V1991 N1995 R2002 M2007 E2008 Y2009 F2010 Q2011
F2012 M2013 K2014 K2015 L2034 P2035 E2036 A2037 E2038 E2039 I2040 T2041 M2042 I2043 S2044 I2045 Q2046 L2047 R2050 F2051 L2052 F2053 T2054 T2055 G2056 V2062 V2063 A2067 W2070 S2081 V2084 R2085 F2094 R2099 A2117 D2130 P2136 F2137 ALA SER PRO GLY PRO SER SER GLN ALA TYR
ASP N2149 D2154 V2160 L2164 R2165 V2168 G2172 R2173 H2174 L2175 Q2176 Q2177 Y2178 F2179 N2180 L2181 Q2195 V2208 S2209 G2215 I2236 S2247 P2256 N2257 P2258 D2277 I2278 L2279 F2280 V2281 K2288 S2296 T2299 E2309 L2321 L2339 I2355 L2359
D2364 S2376 A2384 C2387 M2391 A2401 N2408 R2428 ARG PRO TYR THR GLY ASN PRO GLN TYR THR TYR ASN ASN ASN TRP SER PRO PRO VAL GLN SER ASN GLU THR SER ASN GLY TYR PHE LEU GLU ARG SER HIS S2462 P2475 GLU GLU GLU PRO ASP ASP GLN ASP ALA
PRO ASP GLU HIS GLU SER PRO PRO PRO GLU ASP ALA PRO LEU TYR PRO HIS SER PRO GLY SER GLN TYR GLN GLN ASN ASN ASN HIS VAL HIS GLY GLN PRO TYR THR GLY PRO ALA ALA HIS HIS MET ASN ASN PRO GLN ARG THR GLY GLN ARG ALA ALA GLN GLU GLU ASN TYR GLU GLY SER GLU
GLU VAL SER PRO PRO GLN THR LYS ASP GLN ASP TYR LYS ASP ASP ASP LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	330000	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 ($e^-/Å^2$)	56.7	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.402	Depositor
Minimum map value	-1.221	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.323	Depositor
Map size (Å)	372.73602, 372.73602, 372.73602	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8320001, 0.8320001, 0.8320001	Depositor

5 Model quality

5.1 Standard geometry

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	0.25	0/14334	0.48	1/19388 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1083	PRO	CA-N-CD	-5.58	103.69	111.50

There are no chirality outliers.

There are no planarity outliers.

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	14031	0	13943	288	0
All	All	14031	0	13943	288	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 10.

The worst 5 of 288 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:2007:MET:HG2	1:A:2011:GLN:HE22	1.44	0.82
1:A:2054:THR:HG22	1:A:2055:THR:HG23	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:842:CYS:SG	1:A:845:GLN:NE2	2.61	0.74
1:A:658:LEU:HD11	1:A:700:TRP:HB2	1.69	0.73
1:A:543:ASP:O	1:A:547:GLN:NE2	2.22	0.72

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	1706/2579 (66%)	1621 (95%)	84 (5%)	1 (0%)	51 83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	712	ASP

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	1530/2286 (67%)	1526 (100%)	4 (0%)	92 96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	447	LYS
1	A	486	LYS
1	A	794	LYS
1	A	2408	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1653	HIS
1	A	1994	GLN
1	A	2408	ASN
1	A	2011	GLN
1	A	845	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

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.

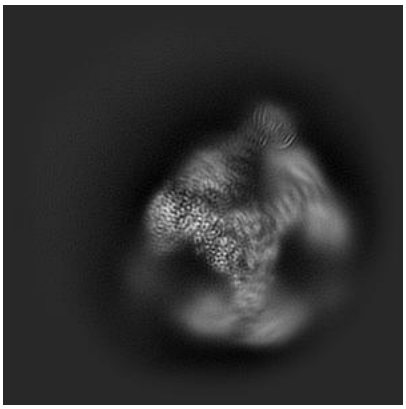
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-14369. These allow visual inspection of the internal detail of the map and identification of artifacts.

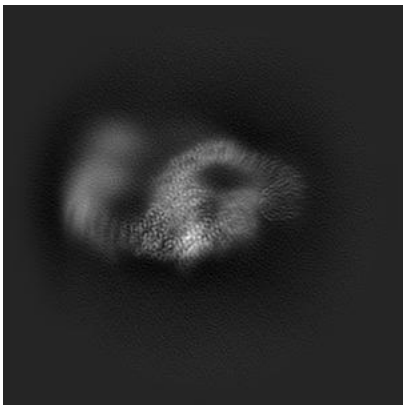
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

6.1.1 Primary map



X



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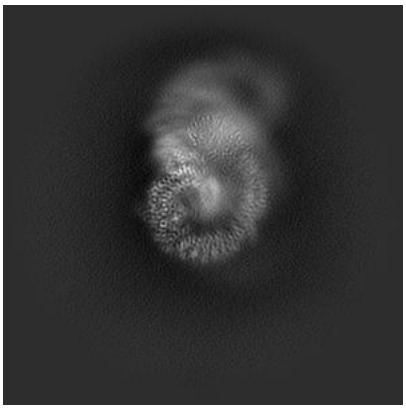
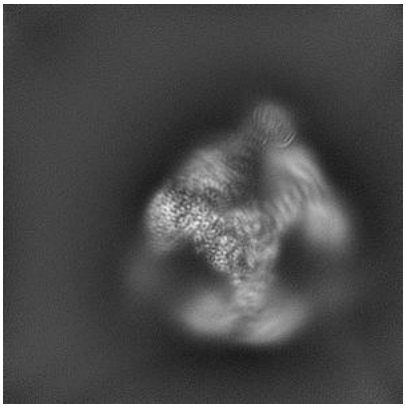


Z

6.1.2 Raw map



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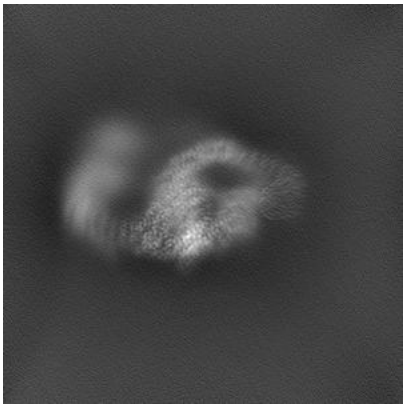
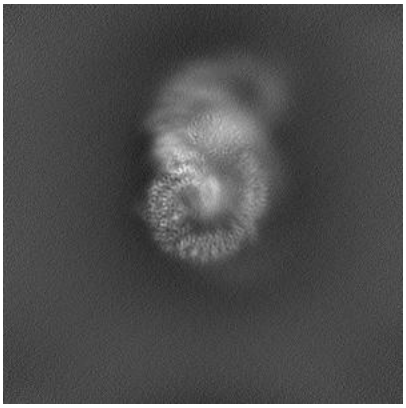


Y

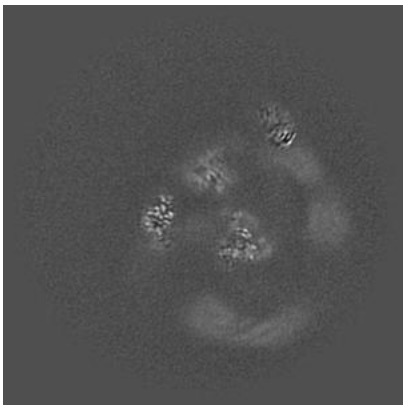


Z

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

6.2 Central slices (i)

6.2.1 Primary map



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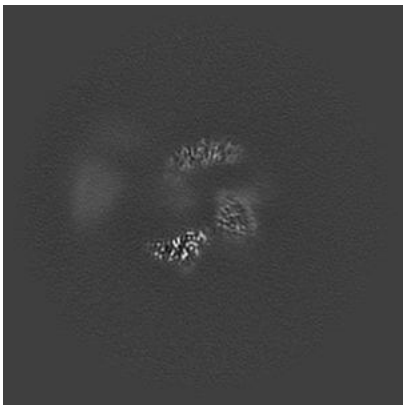
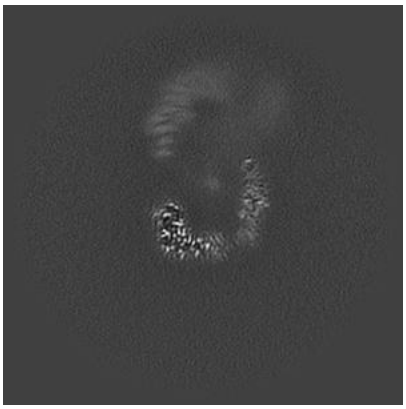
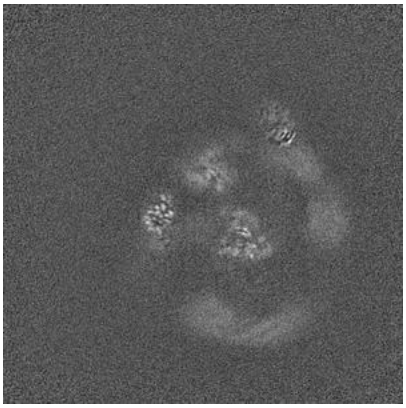


Y Index: 224

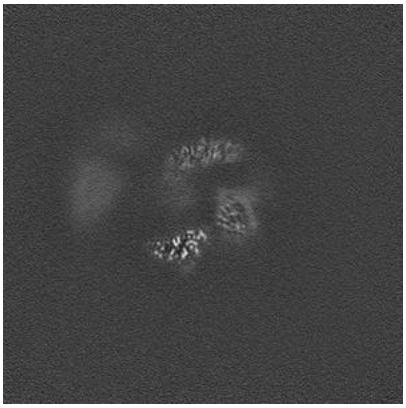


Z Index: 224

6.2.2 Raw map



X Index: 224



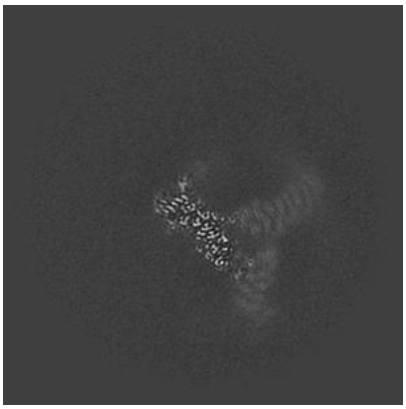
Y Index: 224

Z Index: 224

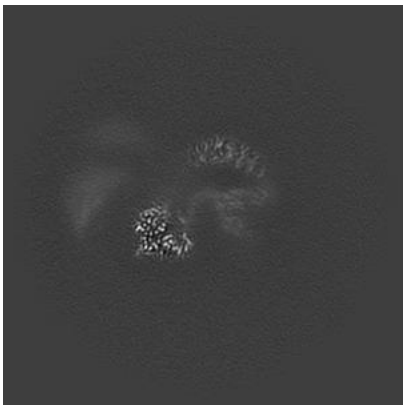
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



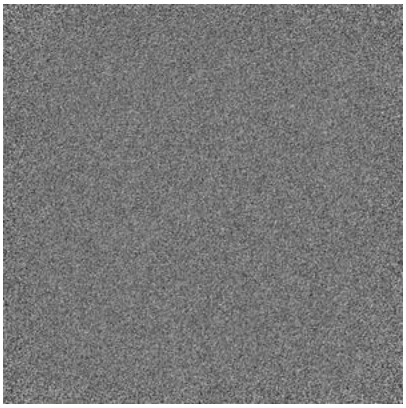
X Index: 182



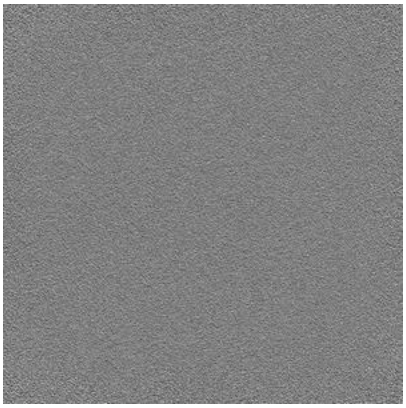
Y Index: 246

Z Index: 202

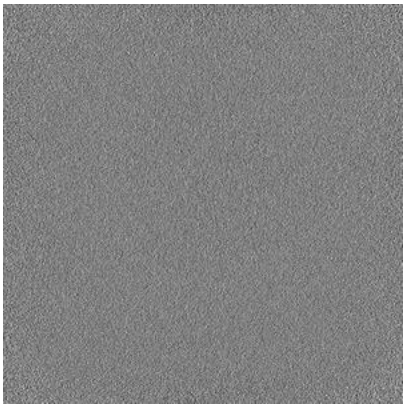
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.323. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

X Y Z

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.

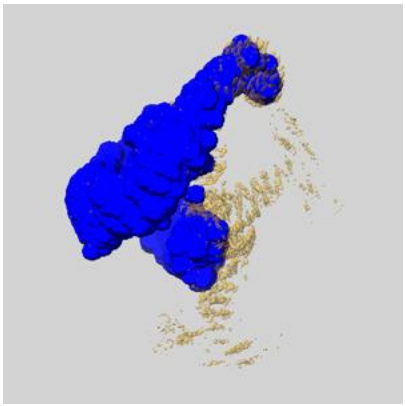
6.5 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

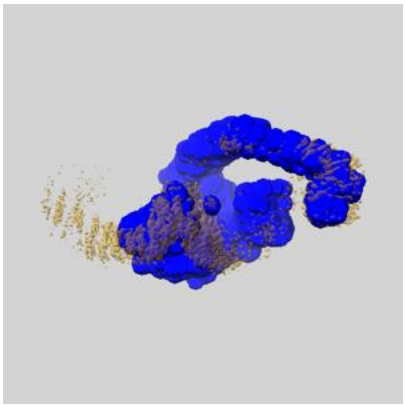
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

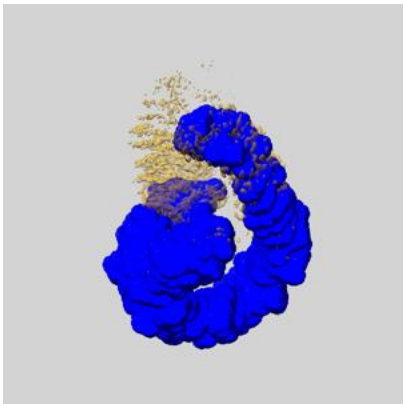
6.5.1 emd_14369_msk_1.map (i)



X



Y

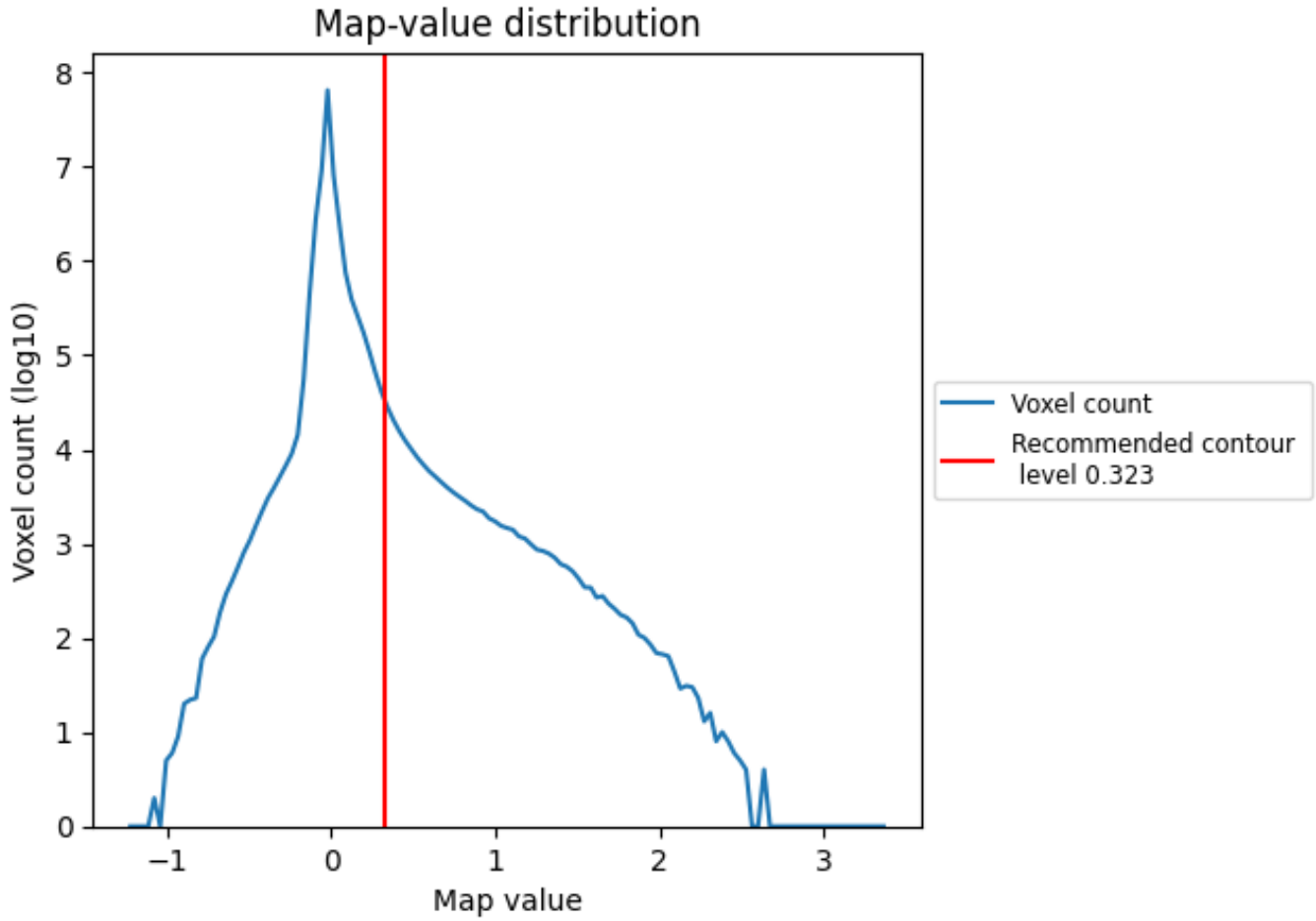


Z

7 Map analysis

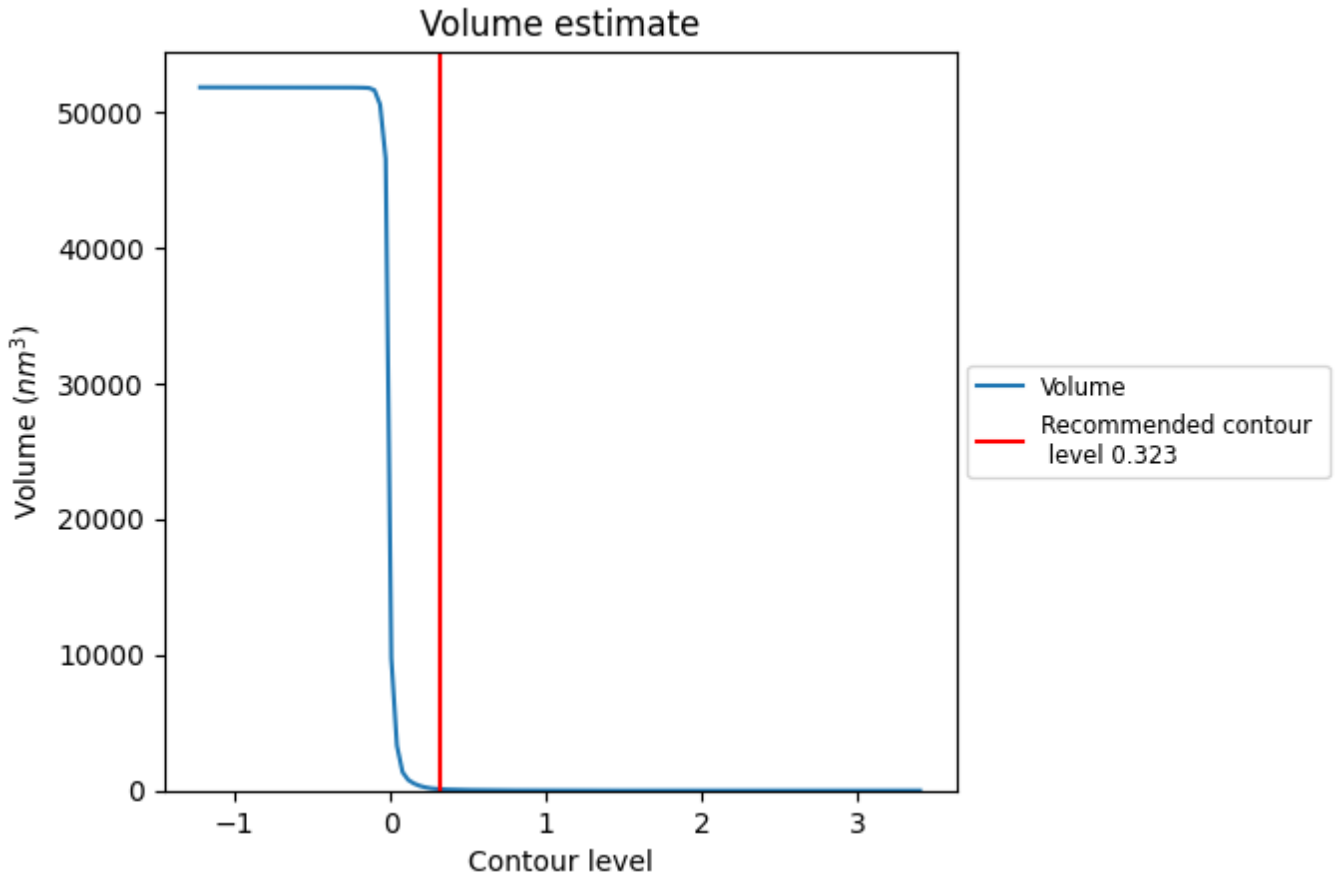
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

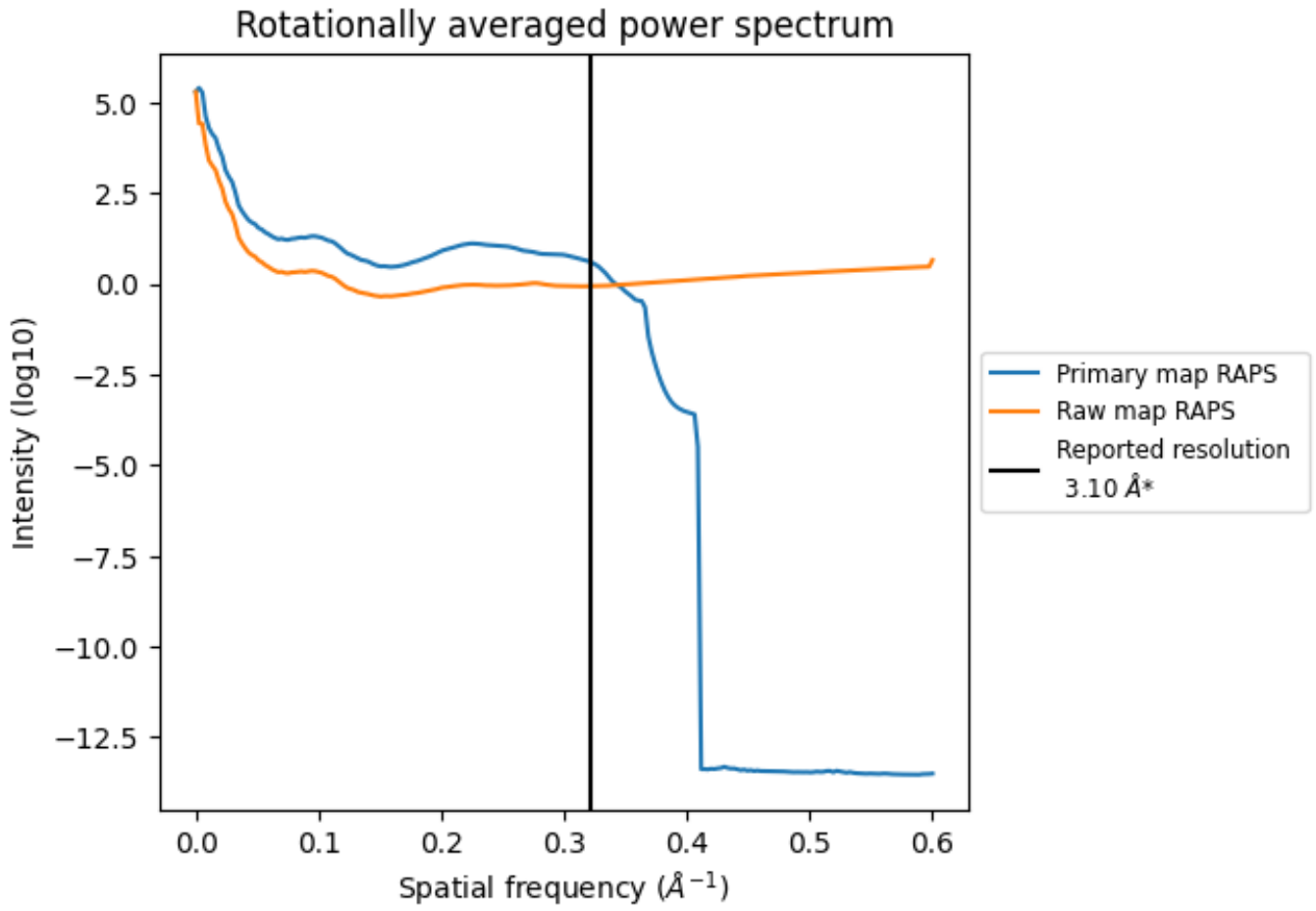
7.2 Volume estimate (i)



The volume at the recommended contour level is 104 nm^3; this corresponds to an approximate mass of 94 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 (i)

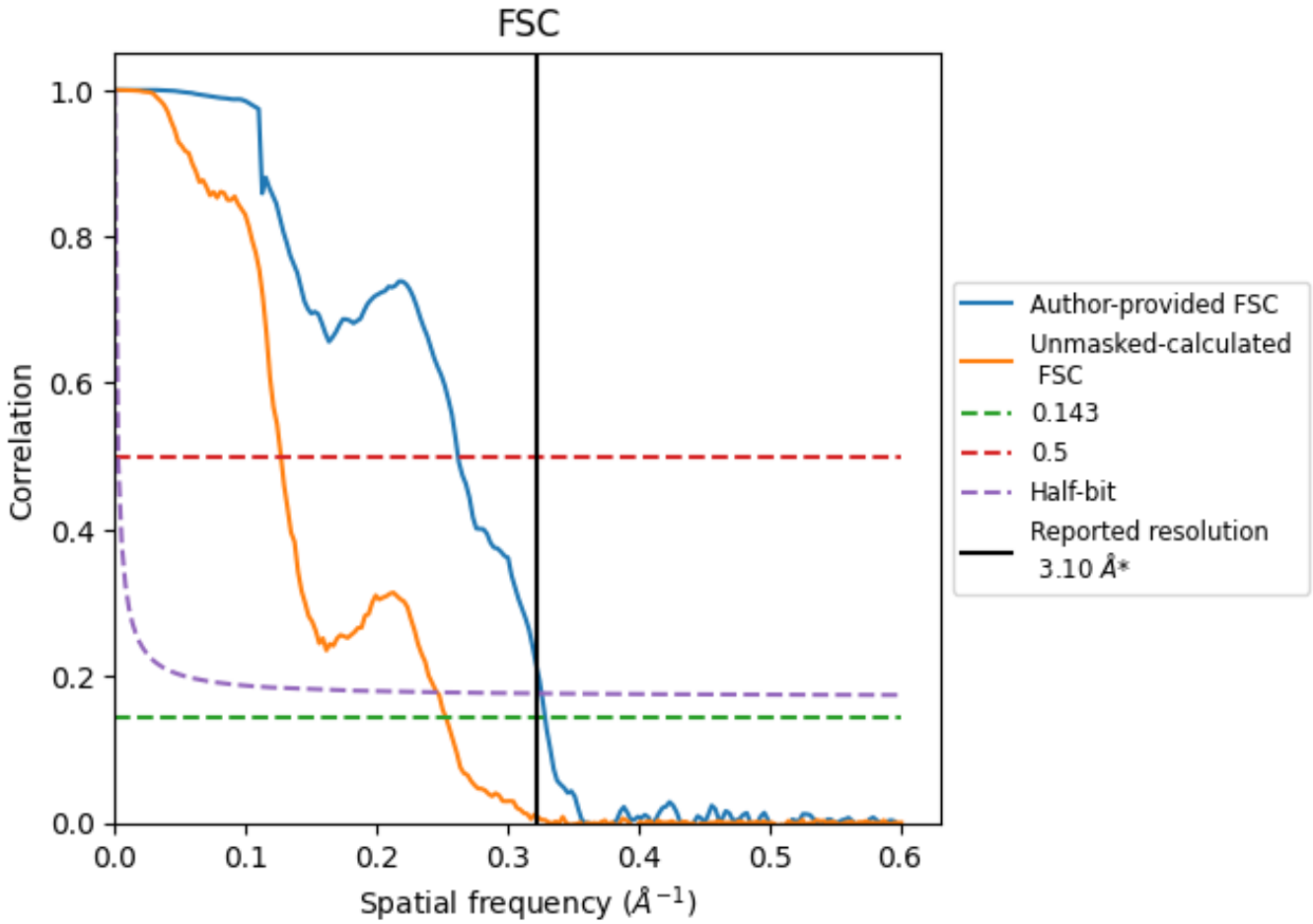


*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

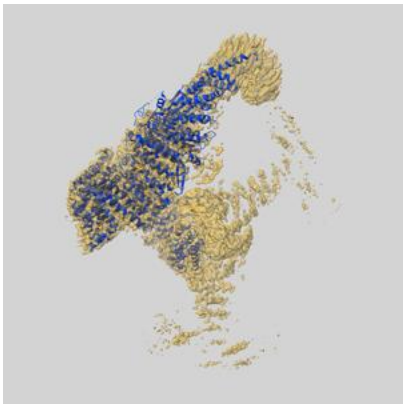
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.04	3.81	3.07
Unmasked-calculated*	3.95	7.88	4.06

*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 3.95 differs from the reported value 3.1 by more than 10 %

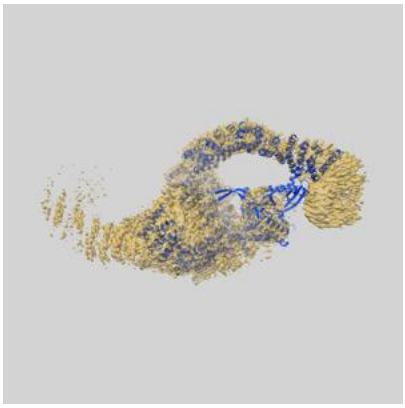
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-14369 and PDB model 7YXY. Per-residue inclusion information can be found in section 3 on page 4.

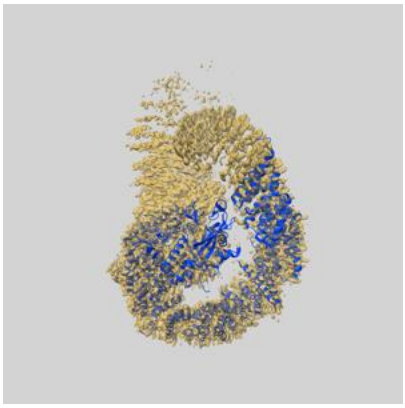
9.1 Map-model overlay



X



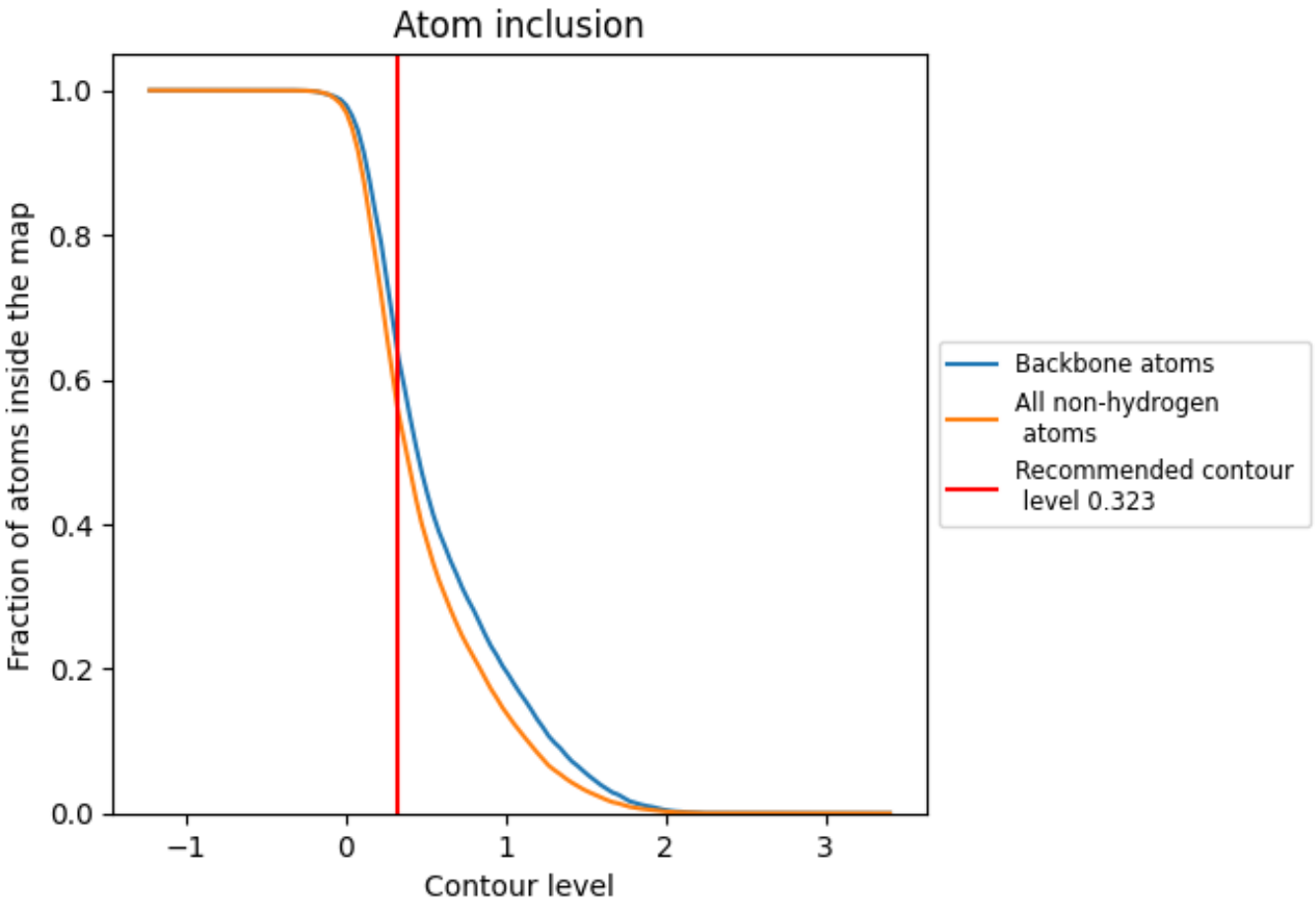
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.323 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 Atom inclusion (i)



At the recommended contour level, 64% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.