wwPDB EM Validation Summary Report (i)

Oct 12, 2026 – 12:18 PM JST

PDB ID	:	22VD / pdb_000022vd
EMDB ID	:	EMD-68711
Title	:	Cryo-EM structure of DOCK11
Authors	:	Hisano, T.; Kukimoto-Niino, M.; Shinoda, T.; Katsura, K.; Shirouzu, M.
Deposited on	:	2026-01-25
Resolution	:	3.80 Å(reported)
Based on initial model	:	22VF

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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

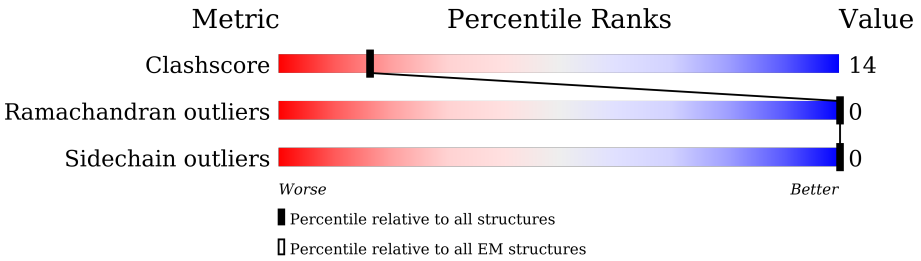
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

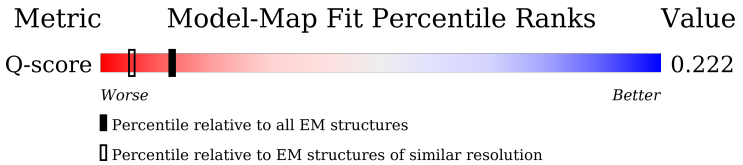
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	2079	33% 58% 26% 16%
1	B	2079	33% 59% 25% 16%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 56736 atoms, of which 28450 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 Dedicator of cytokinesis protein 11.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	1743	28368	9071	14225	2389	2606	77	0	0
1	B	1743	28368	9071	14225	2389	2606	77	0	0

There are 12 discrepancies between the modelled and reference sequences:

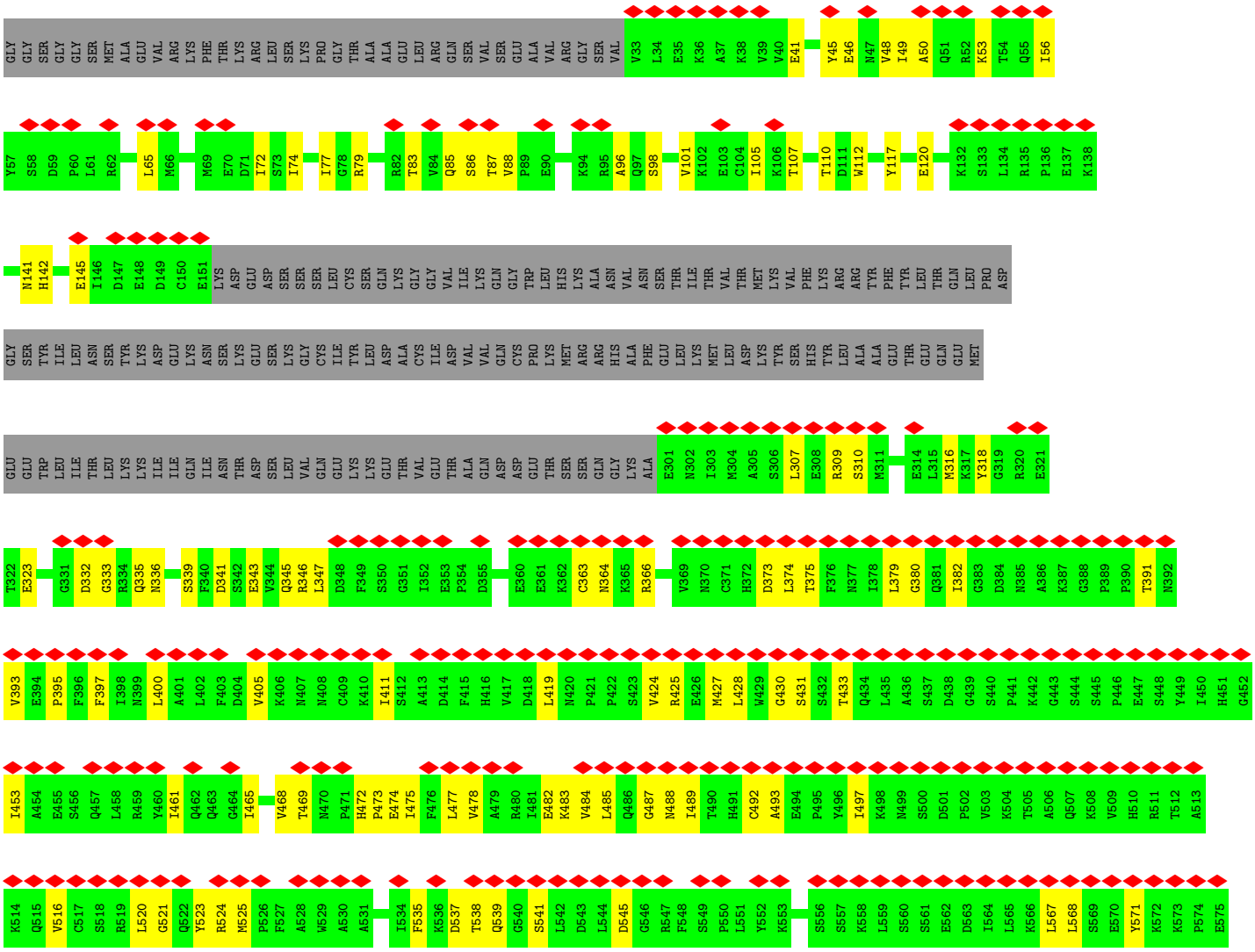
Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q5JSL3
A	-4	GLY	-	expression tag	UNP Q5JSL3
A	-3	SER	-	expression tag	UNP Q5JSL3
A	-2	GLY	-	expression tag	UNP Q5JSL3
A	-1	GLY	-	expression tag	UNP Q5JSL3
A	0	SER	-	expression tag	UNP Q5JSL3
B	-5	GLY	-	expression tag	UNP Q5JSL3
B	-4	GLY	-	expression tag	UNP Q5JSL3
B	-3	SER	-	expression tag	UNP Q5JSL3
B	-2	GLY	-	expression tag	UNP Q5JSL3
B	-1	GLY	-	expression tag	UNP Q5JSL3
B	0	SER	-	expression tag	UNP Q5JSL3

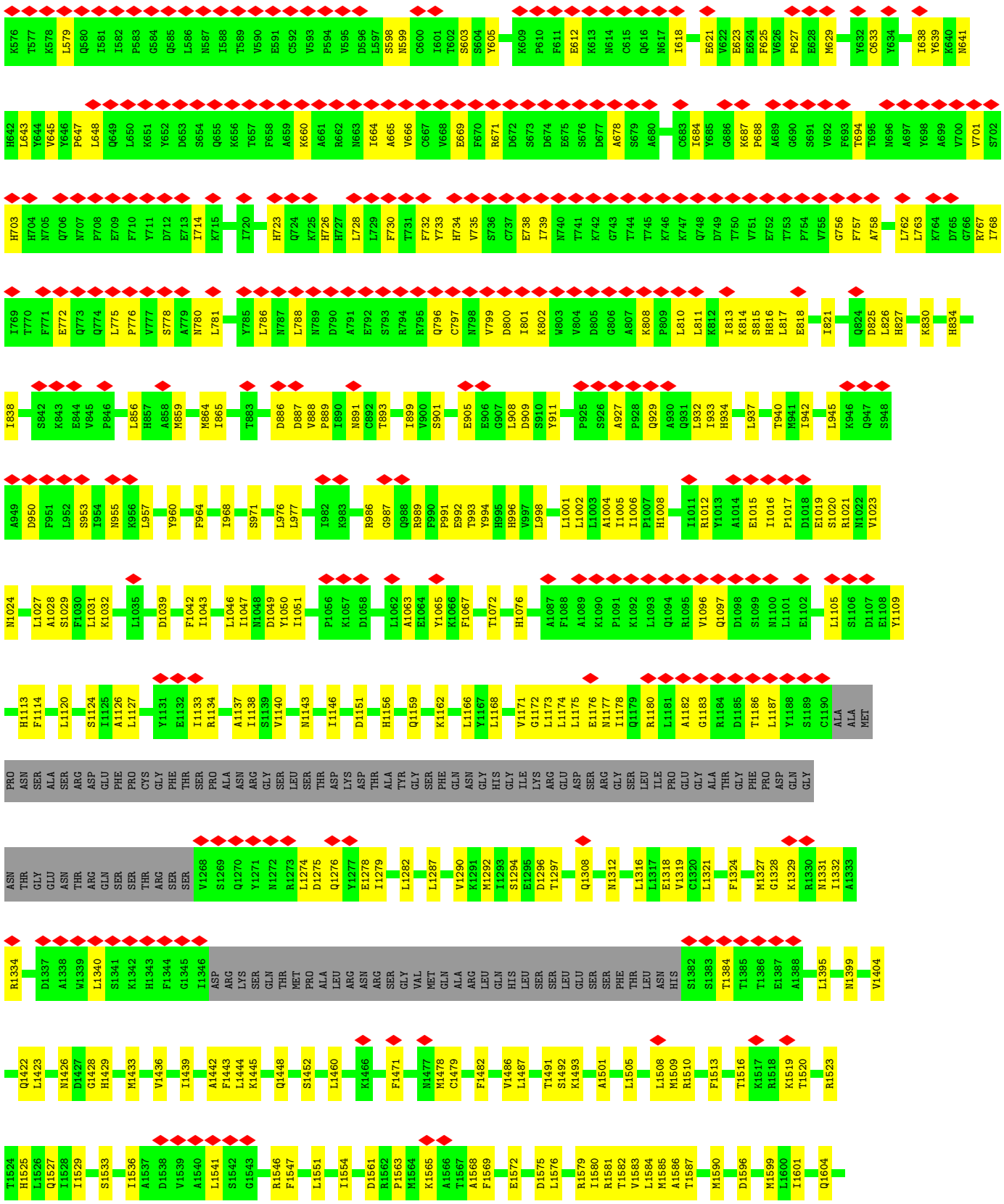
3 Residue-property plots (i)

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: Dedicator of cytokinesis protein 11

Chain A:

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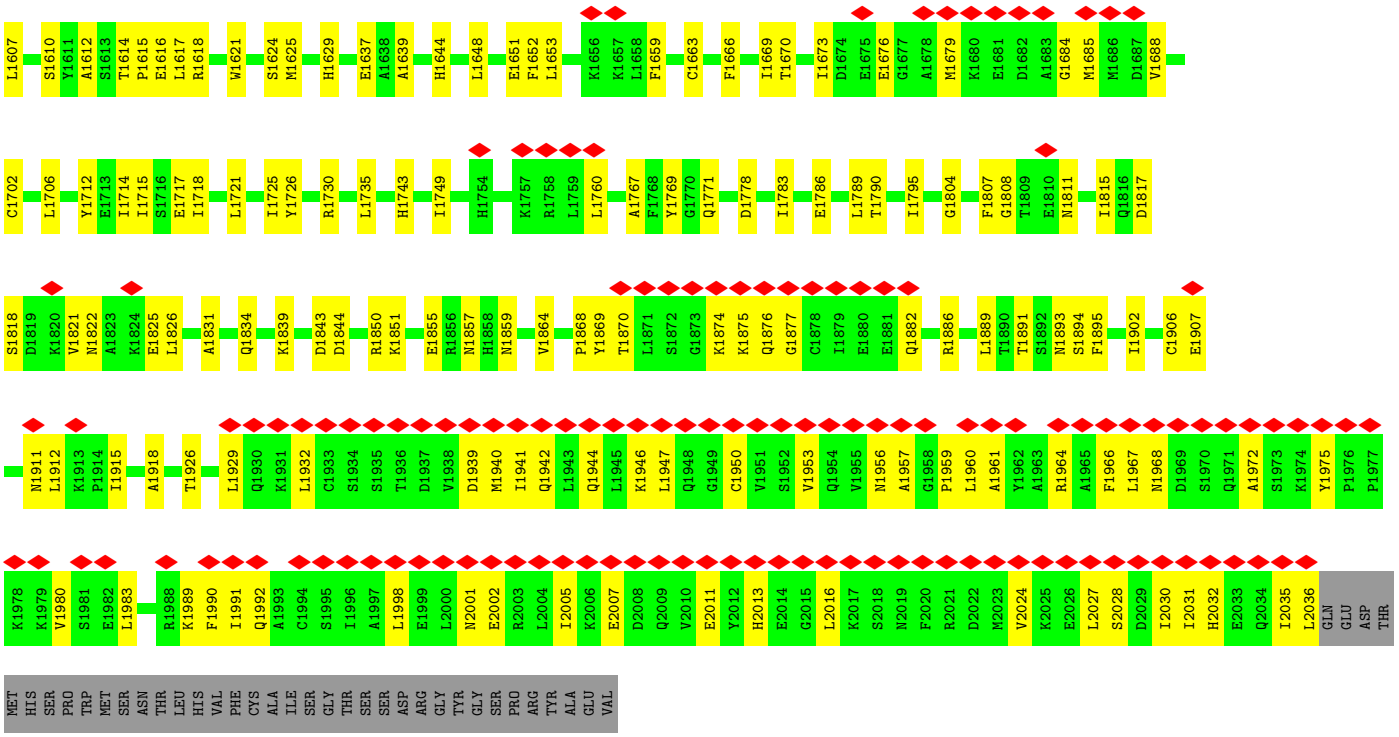
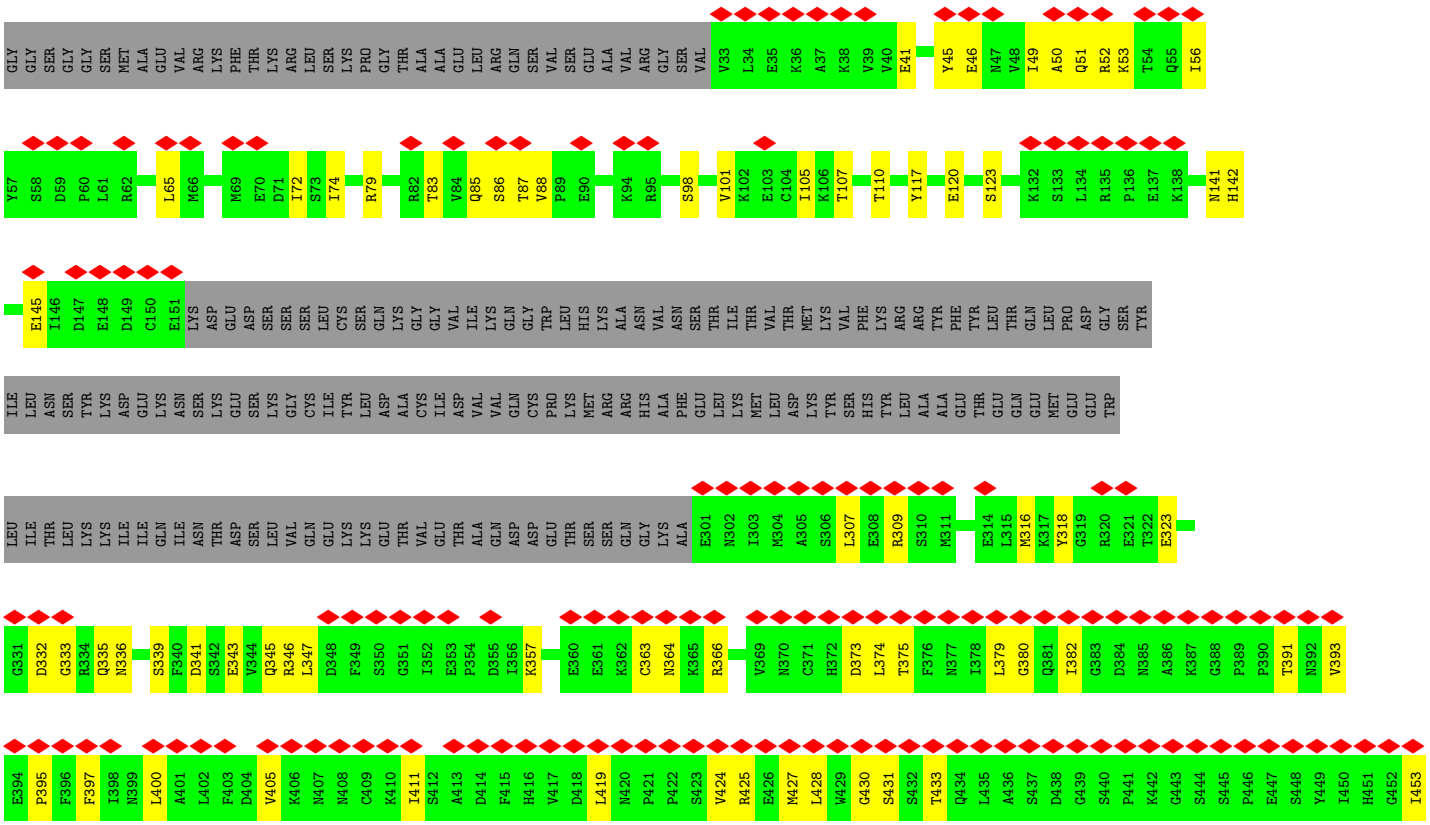
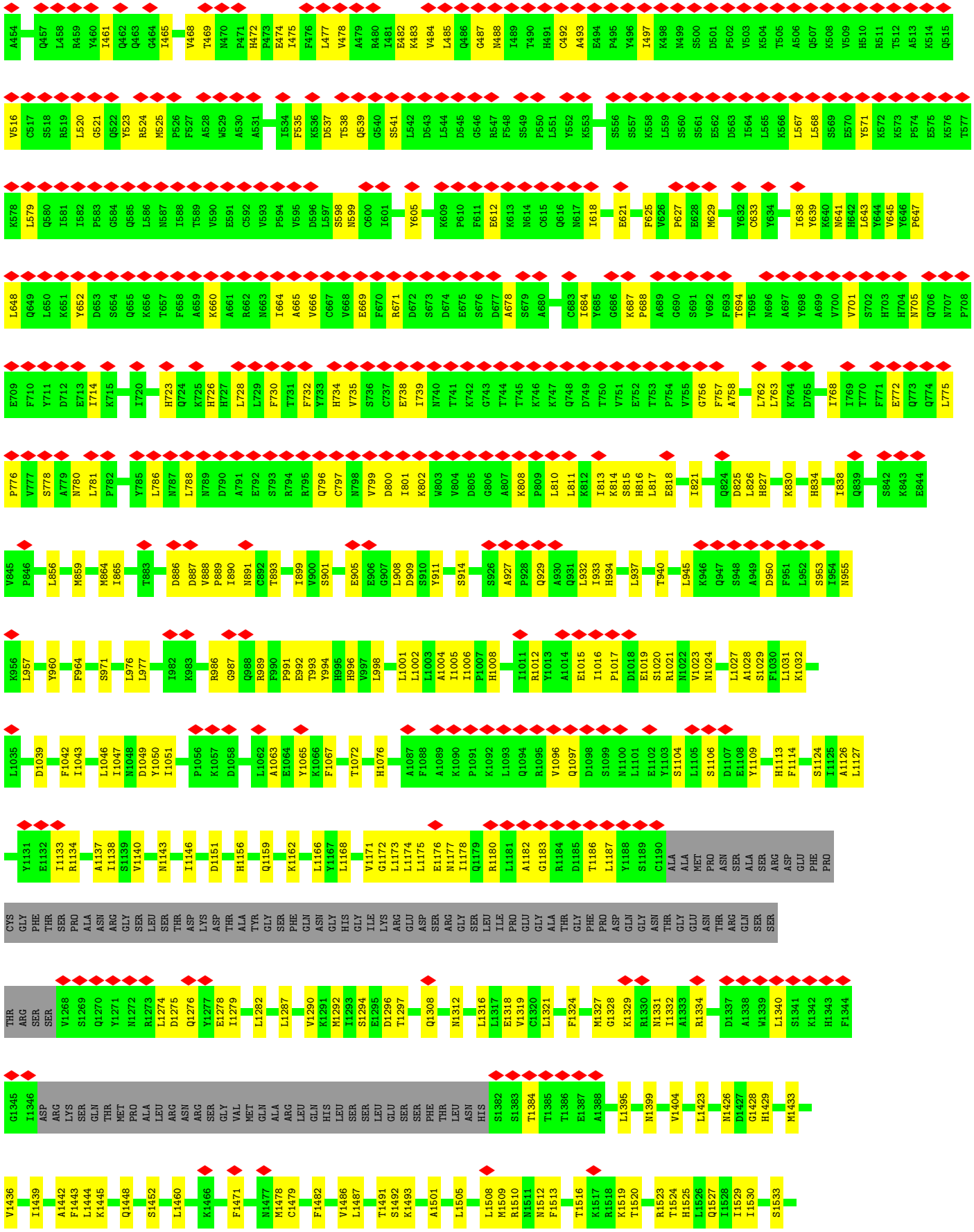
H642 L643 Y644 V645 Y646 P647 L648 Q649 L650 K651 Y652 D653 S654 Q655 K656 T657 F658 A659 K660 A661 R662 N663 I664 A665 V666 C667 V668 E669 F670 R671 D672 S673 D674 E675 S676 D677 A678 S679 A680 C683 I684 Y685 G686 K687 P688 A689 G690 S691 V692 F693 T694 I695 N696 A697 Y698 A699 V700 V701 S702
H703 H704 N705 Q706 N707 P708 E709 F710 Y711 D712 E713 I714 K715 I720 H723 Q724 K725 H726 H727 L728 L729 F730 T731 F732 Y733 H734 V735 S736 C737 E738 I739 N740 T741 K742 G743 T744 T745 K746 K747 Q748 D749 T750 V751 E752 T753 P754 V755 G756 F757 A758 L762 L763 K764 D765 G766 R767 I768
I769 T770 F771 E772 Q773 Q774 L775 P776 V777 S778 A779 N780 L781 Y785 L786 N787 L788 N789 D790 A791 E792 S793 R794 R795 Q796 C797 N798 V799 D800 I801 K802 W803 V804 D805 G806 A807 K808 P809 L810 L811 K812 I813 K814 S815 H816 L817 E818 I821 Q824 D825 L826 H827 K830 H834
I838 S842 K843 E844 V845 P846 L856 H857 A858 M859 M864 I865 T883 D886 D887 V888 P889 I890 N891 C892 T893 I899 V900 S901 E905 E906 G907 L908 D909 S910 Y911 P925 S926 A927 P928 Q929 A930 Q931 L932 I933 H934 L937 T940 M941 I942 L945 K946 Q947 S948
A949 D950 F951 L952 S953 I954 N955 K956 L957 Y960 F964 I968 S971 L976 L977 I982 K983 R986 G987 Q988 R989 F990 P991 E992 T993 Y994 H995 H996 V997 L998 L1001 L1002 L1003 A1004 I1005 I1006 P1007 H1008 I1011 R1012 Y1013 A1014 E1015 I1016 P1017 D1018 E1019 S1020 R1021 N1022 V1023
N1024 L1027 A1028 S1029 F1030 L1031 K1032 L1035 D1039 F1042 I1043 L1046 I1047 N1048 D1049 Y1050 I1051 P1056 K1057 D1058 L1062 A1063 E1064 Y1065 K1066 F1067 T1072 H1076 A1087 F1088 A1089 K1090 P1091 K1092 L1093 Q1094 R1095 V1096 Q1097 D1098 S1099 N1100 L1101 E1102 L1105 S1106 D1107 E1108 Y1109
H1113 F1114 L1120 S1124 I1125 A1126 L1127 Y1131 E1132 I1133 R1134 A1137 I1138 S1139 V1140 N1143 I1146 D1151 H1156 Q1159 K1162 L1166 Y1167 L1168 V1171 G1172 L1173 L1174 L1175 E1176 N1177 I1178 Q1179 R1180 L1181 A1182 G1183 R1184 D1185 T1186 L1187 Y1188 S1189 C1190 ALA ALA MET
PRO ASN SER ALA SER ARG ASP GLU PHE PRO CYS GLY PHE THR SER PRO ALA ASN ARG GLY SER LEU SER THR ASP LYS ASP THR ALA TYR GLY SER PHE GLN ASN GLY HIS GLY ILE LYS ARG GLU ASP SER ARG GLY SER LEU ILE PRO GLU GLY ALA THR GLY PHE PRO ASP GLN GLY
ASN THR GLY GLU ASN THR ARG GLN SER SER THR ARG SER SER V1268 S1269 Q1270 Y1271 N1272 R1273 L1274 D1275 Q1276 Y1277 E1278 I1279 L1282 L1287 V1290 K1291 M1292 I1293 S1294 E1295 D1296 T1297 Q1308 N1312 L1316 L1317 E1318 V1319 C1320 L1321 F1324 M1327 G1328 K1329 R1330 N1331 I1332 A1333
R1334 D1337 A1338 W1339 L1340 S1341 K1342 H1343 F1344 G1345 I1346 ASP ARG LYS SER GLN THR MET PRO ALA LEU ARG ASN ARG SER GLY VAL MET GLN ALA ARG LEU GLN HIS LEU SER SER LEU GLU SER SER PHE THR LEU ASN HIS S1382 S1383 T1384 T1385 T1386 E1387 A1388 L1395 N1399 V1404
Q1422 L1423 N1426 D1427 G1428 H1429 M1433 V1436 I1439 A1442 F1443 L1444 K1445 Q1448 S1452 L1460 K1466 F1471 N1477 M1478 C1479 F1482 V1486 L1487 T1491 S1492 K1493 A1501 L1505 L1508 M1509 R1510 F1513 T1516 K1517 R1518 K1519 T1520 R1523
T1524 H1525 L1526 Q1527 I1528 I1529 S1533 I1536 A1537 D1538 V1539 A1540 L1541 S1542 G1543 R1546 F1547 L1551 I1554 D1561 R1562 P1563 M1564 K1565 A1566 T1567 A1568 F1569 E1572 D1575 L1576 R1579 I1580 R1581 T1582 V1583 L1584 M1585 A1586 T1587 M1590 D1596 M1599 L1600 I1601 Q1604

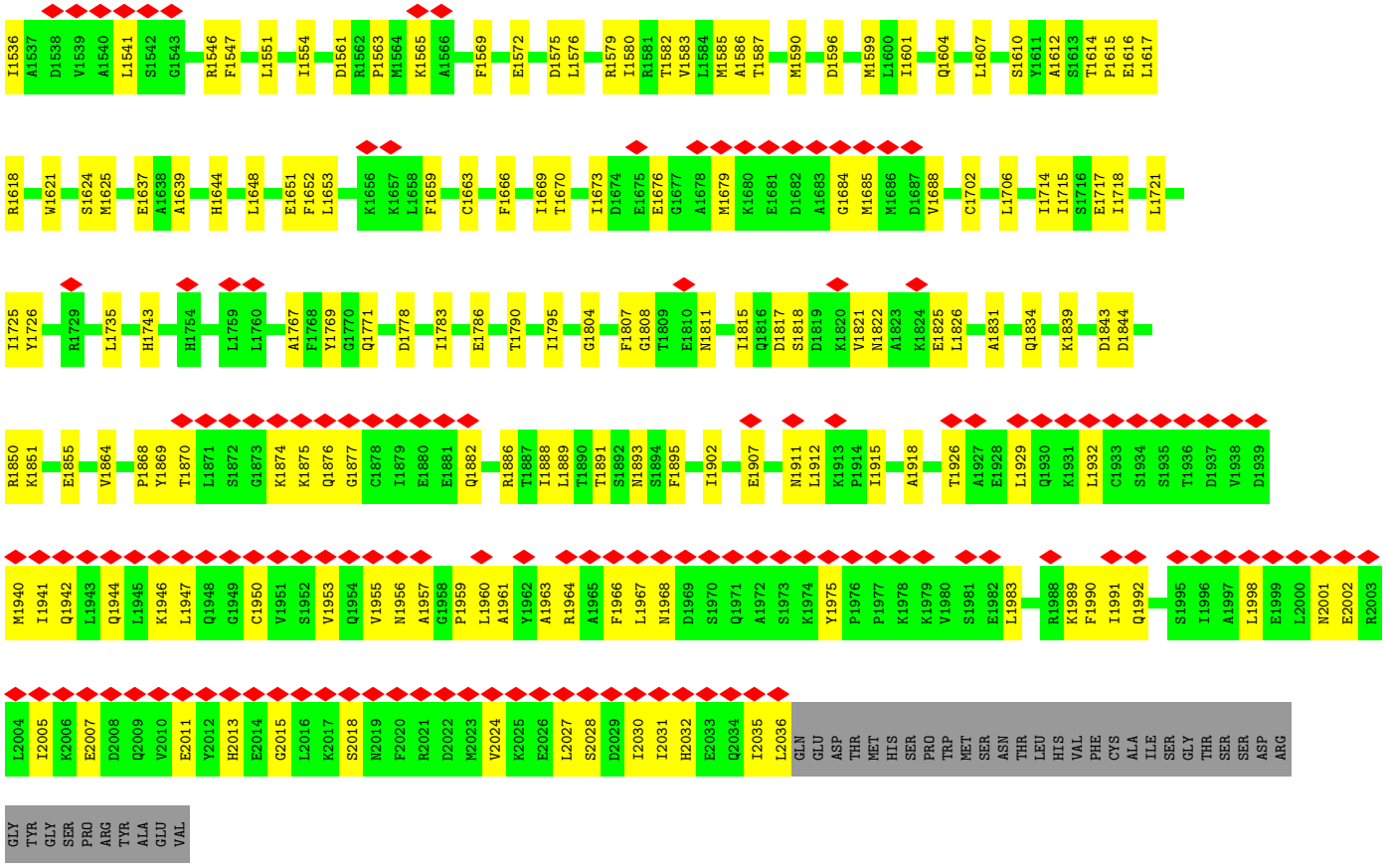


- Molecule 1: Dedicator of cytokinesis protein 11

Chain B:




A454 Q457 L458 R459 Y460 I461 Q462 Q463 G464 I465 V468 T469 N470 P471 H472 P473 E474 I475 F476 L477 V478 A479 R480 I481 E482 K483 V484 L485 Q486 G487 N488 I489 T490 H491 C492 A493 E494 P495 Y496 I497 K498 N499 S500 D501 P502 V503 K504 T505 A506 Q507 K508 V509 H510 R511 T512 A513 K514 Q515
V516 C517 S518 R519 L520 G521 Q522 Y523 R524 M525 P526 F527 A528 W529 A530 A531 I534 F535 K536 D537 T538 Q539 G540 S541 L542 D543 L544 D545 G546 R547 F548 S549 P550 L551 Y552 K553 S556 S557 K558 L559 S560 S561 E562 D563 I564 L565 K566 L567 L568 S569 E570 Y571 K572 K573 P574 E575 K576 T577
K578 L579 Q580 I581 I582 P583 G584 Q585 L586 M587 I588 T589 V590 E591 C592 V593 P594 V595 D596 L597 S598 N599 C600 I601 Y605 K609 P610 F611 E612 K613 N614 C615 Q616 M617 I618 E621 F625 V626 P627 E628 M629 Y632 C633 Y634 I638 Y639 K640 N641 H642 L643 Y644 V645 Y646 P647
L648 Q649 L650 K651 Y652 D653 S654 Q655 K656 T657 F658 A659 K660 A661 R662 N663 I664 A665 V666 C667 V668 E669 F670 R671 D672 S673 D674 E675 S676 D677 A678 S679 A680 C683 I684 Y685 G686 K687 P688 A689 G690 S691 V692 F693 T694 T695 N696 A697 Y698 A699 V700 V701 S702 H703 H704 N705 Q706 N707 P708
E709 F710 Y711 D712 E713 I714 K715 I720 H723 Q724 K725 H726 H727 L728 L729 F730 T731 F732 Y733 H734 V735 S736 C737 E738 I739 N740 T741 K742 G743 T744 T745 K746 K747 Q748 D749 T750 V751 E752 T753 P754 V755 G756 F757 A758 L762 L763 K764 D765 I768 I769 T770 F771 E772 Q773 Q774 L775
P776 V777 S778 A779 N780 L781 P782 Y785 L786 N787 L788 N789 D790 A791 E792 S793 R794 R795 Q796 C797 N798 V799 D800 I801 K802 W803 V804 D805 G806 A807 K808 P809 L810 L811 K812 I813 K814 S815 H816 L817 E818 I821 Q824 D825 L826 H827 K830 H834 I838 Q839 S842 K843 E844
V845 P846 L856 M859 M864 I865 T883 D886 D887 V888 P889 I890 N891 C892 T893 I899 V900 S901 E905 E906 G907 L908 D909 S910 Y911 S914 S926 A927 P928 Q929 A930 Q931 L932 I933 H934 L937 T940 L945 K946 Q947 S948 A949 D950 F951 L952 S953 I954 N955
K956 L957 Y960 F964 S971 L976 L977 T982 K983 R986 G987 Q988 R989 F990 P991 E992 T993 Y994 H995 H996 V997 L998 L1001 L1002 L1003 A1004 I1005 I1006 P1007 H1008 I1011 R1012 Y1013 A1014 E1015 I1016 P1017 D1018 E1019 S1020 R1021 N1022 V1023 N1024 L1027 A1028 S1029 F1030 L1031 K1032
L1035 D1039 F1042 I1043 L1046 I1047 N1048 D1049 Y1050 I1051 P1056 K1057 D1058 L1062 A1063 E1064 Y1065 K1066 F1067 T1072 H1076 A1087 F1088 A1089 K1090 P1091 K1092 L1093 Q1094 R1095 V1096 Q1097 D1098 S1099 N1100 L1101 E1102 Y1103 S1104 L1105 S1106 D1107 E1108 Y1109 H1113 F1114 S1124 I1125 A1126 L1127
Y1131 E1132 I1133 R1134 A1137 I1138 S1139 V1140 N1143 I1146 D1151 H1156 Q1159 K1162 L1166 Y1167 L1168 V1171 G1172 L1173 L1174 L1175 E1176 N1177 I1178 Q1179 R1180 L1181 A1182 G1183 R1184 D1185 T1186 L1187 Y1188 S1189 C1190 ALA ALA MET PRO ASN SER ALA SER ARG ASP GLU PHE PRO
CYS GLY PHE THR SER PRO ALA ASN ARG GLY SER LEU SER THR ASP LYS ASP THR ALA TYR GLY SER PHE GLN ASN GLY HIS GLY ILE LYS ARG GLU ASP SER ARG GLY SER LEU ILE PRO GLU GLY ALA THR GLY PHE PRO ASP GLN GLY ASN THR GLY GLU ASN THR ARG GLN SER SER
THR ARG SER SER V1268 S1269 Q1270 Y1271 N1272 R1273 L1274 D1275 Q1276 Y1277 E1278 I1279 L1282 L1287 V1290 K1291 M1292 I1293 S1294 E1295 D1296 T1297 Q1308 N1312 L1316 L1317 E1318 V1319 C1320 L1321 F1324 M1327 G1328 K1329 R1330 N1331 I1332 R1334 D1337 A1338 W1339 L1340 S1341 K1342 H1343 F1344
G1345 I1346 ASP ARG LYS SER GLN THR MET PRO ALA LEU ARG ASN ARG SER GLY VAL MET GLN ALA ARG LEU GLN HIS LEU SER SER LEU GLU SER SER PHE THR LEU ASN HIS S1382 S1383 T1384 T1385 T1386 E1387 A1388 L1395 N1399 V1404 L1423 N1426 D1427 G1428 H1429 M1433
V1436 I1439 A1442 F1443 L1444 K1445 Q1448 S1452 L1460 K1466 F1471 N1477 M1478 C1479 F1482 V1486 L1487 T1491 S1492 K1493 A1501 L1505 L1508 M1509 R1510 N1511 N1512 F1513 T1516 K1517 R1518 K1519 T1520 R1523 T1524 H1525 L1526 Q1527 I1528 I1529 I1530 S1533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R1618 W1621 S1624 M1625 E1637 A1638 A1639 H1644 L1648 E1651 F1652 L1653 K1656 K1657 L1658 F1659 C1663 F1666 I1669 T1670 I1673 D1674 E1675 E1676 G1677 A1678 M1679 K1680 E1681 D1682 A1683 G1684 M1685 M1686 D1687 V1688 C1702 L1706 I1714 I1715 S1716 E1717 I1718 L1721
I1725 Y1726 R1729 L1735 H1743 H1754 L1759 L1760 A1767 F1768 Y1769 G1770 Q1771 D1778 I1783 E1786 T1790 T1795 G1804 F1807 G1808 T1809 E1810 N1811 I1815 Q1816 D1817 S1818 D1819 K1820 V1821 N1822 A1823 K1824 E1825 L1826 A1831 Q1834 K1839 D1843 D1844
R1850 K1851 E1855 V1864 P1868 Y1869 T1870 L1871 S1872 G1873 K1874 K1875 Q1876 G1877 C1878 I1879 E1880 E1881 Q1882 R1886 T1887 I1888 L1889 T1890 T1891 S1892 N1893 S1894 F1895 I1902 E1907 N1911 L1912 K1913 P1914 I1915 A1918 T1926 A1927 E1928 L1929 Q1930 K1931 L1932 C1933 S1934 S1935 T1936 D1937 V1938 D1939
M1940 I1941 Q1942 L1943 Q1944 L1945 K1946 L1947 Q1948 G1949 C1950 V1951 S1952 V1953 Q1954 V1955 N1956 A1957 G1958 P1959 L1960 A1961 Y1962 A1963 R1964 A1965 F1966 L1967 N1968 D1969 S1970 Q1971 A1972 S1973 K1974 Y1975 P1976 P1977 K1978 K1979 V1980 S1981 E1982 L1983 R1988 K1989 F1990 I1991 Q1992 S1995 I1996 A1997 L1998 E1999 L2000 N2001 E2002 R2003
L2004 I2005 K2006 E2007 D2008 Q2009 V2010 E2011 Y2012 H2013 E2014 G2015 L2016 K2017 S2018 N2019 F2020 R2021 D2022 M2023 V2024 K2025 E2026 L2027 S2028 D2029 I2030 I2031 H2032 E2033 Q2034 I2035 L2036 GLN GLU ASP THR MET HIS SER PRO TRP MET SER ASN THR LEU HIS VAL PHE CYS ALA ILE SER GLY THR SER SER ASP ARG
GLY TYR GLY SER PRO ARG TYR ALA GLU VAL

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	511163	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 ($e^-/Å^2$)	50.3	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.794	Depositor
Minimum map value	-0.334	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.251	Depositor
Map size (Å)	532.0, 532.0, 532.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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	0.17	0/14457	0.44	0/19534
1	B	0.17	0/14457	0.44	0/19534
All	All	0.17	0/28914	0.44	0/39068

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	14143	14225	14221	415	0
1	B	14143	14225	14221	394	0
All	All	28286	28450	28442	807	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 807 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:B:1783:ILE:HD11	1:B:1889:LEU:HD11	1.52	0.91
1:A:1783:ILE:HD11	1:A:1889:LEU:HD11	1.52	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:768:ILE:HG21	1:B:817:LEU:HD13	1.54	0.87
1:A:768:ILE:HG21	1:A:817:LEU:HD13	1.54	0.85
1:B:816:HIS:ND1	1:B:818:GLU:OE1	2.13	0.81

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	1735/2079 (84%)	1650 (95%)	85 (5%)	0	100	100
1	B	1735/2079 (84%)	1651 (95%)	84 (5%)	0	100	100
All	All	3470/4158 (84%)	3301 (95%)	169 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	1586/1875 (85%)	1586 (100%)	0	100	100
1	B	1586/1875 (85%)	1586 (100%)	0	100	100
All	All	3172/3750 (85%)	3172 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	420	ASN
1	B	704	HIS
1	B	703	HIS
1	B	721	HIS
1	A	721	HIS

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)

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.

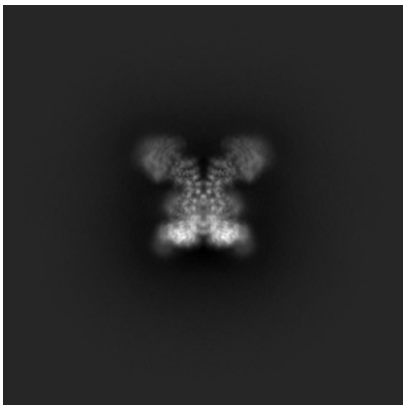
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-68711. These allow visual inspection of the internal detail of the map and identification of artifacts.

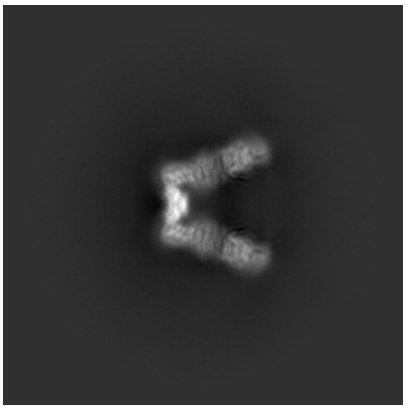
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

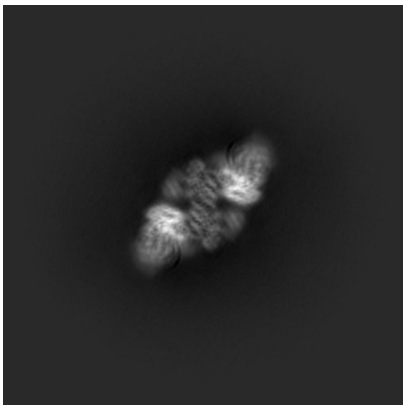
6.1.1 Primary map



X

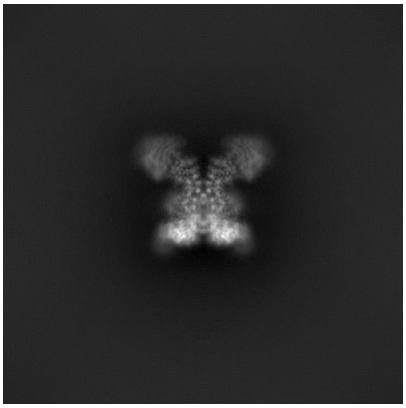


Y

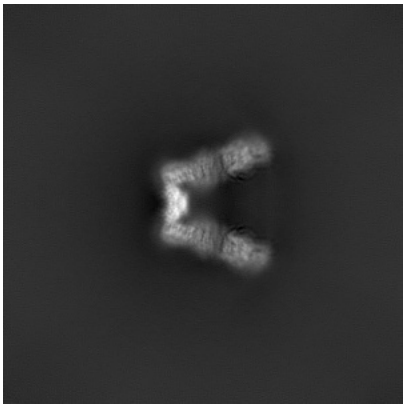


Z

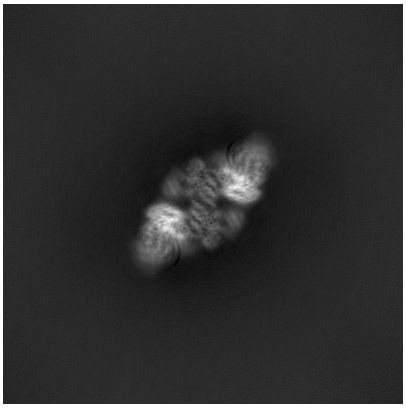
6.1.2 Raw map



X



Y

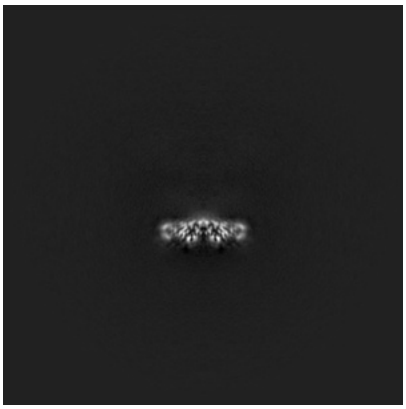


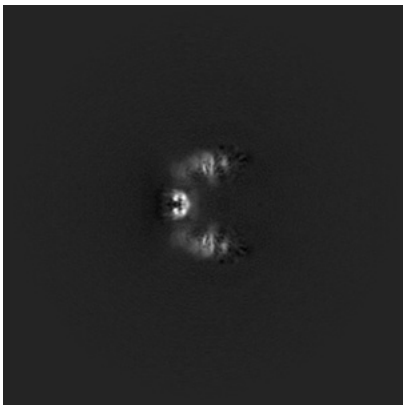
Z

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

6.2 Central slices (i)

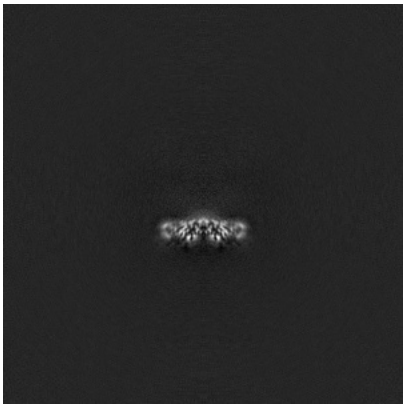
6.2.1 Primary map

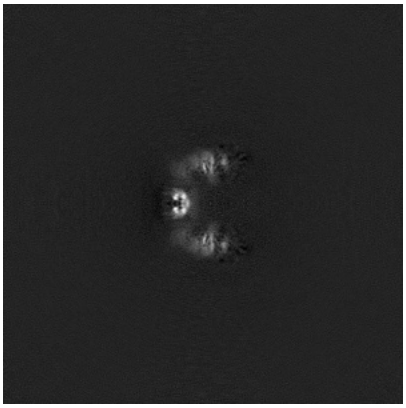

X Index: 200


Y Index: 200

Z Index: 200

6.2.2 Raw map


X Index: 200

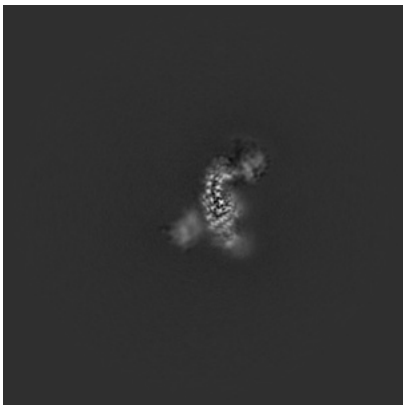

Y Index: 200

Z Index: 200

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: 234

Y Index: 185

Z Index: 173

6.3.2 Raw map

X Index: 233

Y Index: 185

Z Index: 172

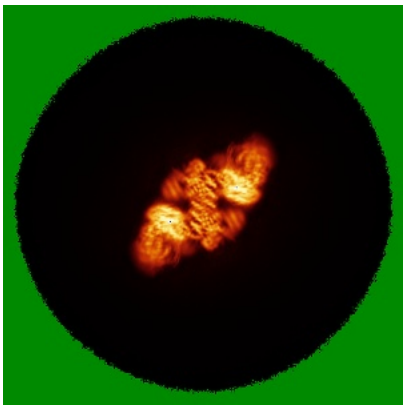
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map

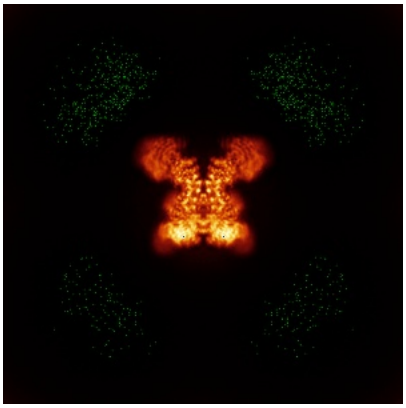
X

Y

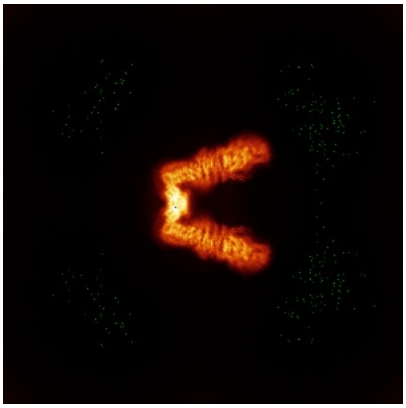


Z

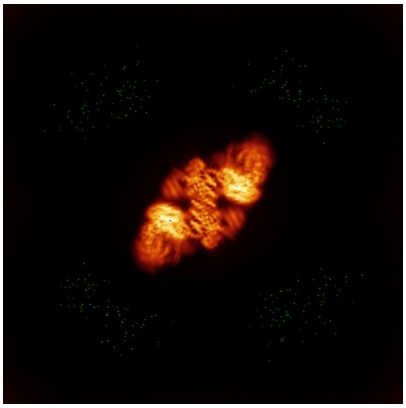
6.4.2 Raw map



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.

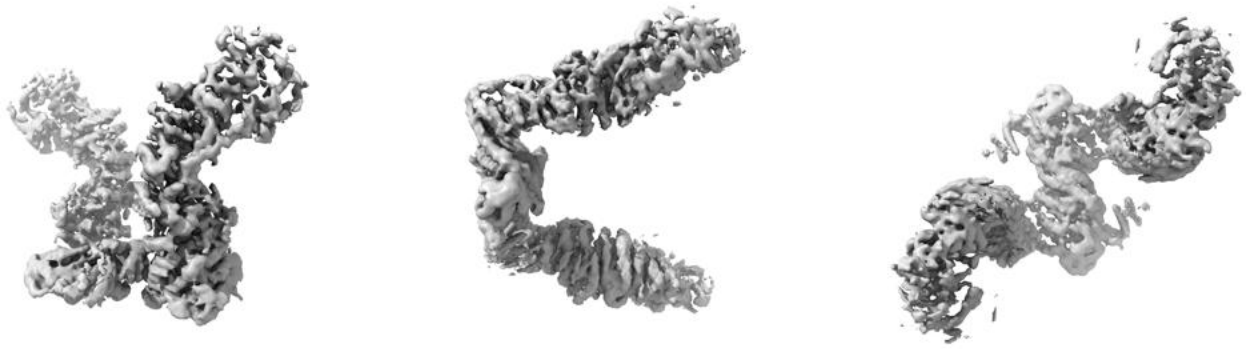
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.251. 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



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.

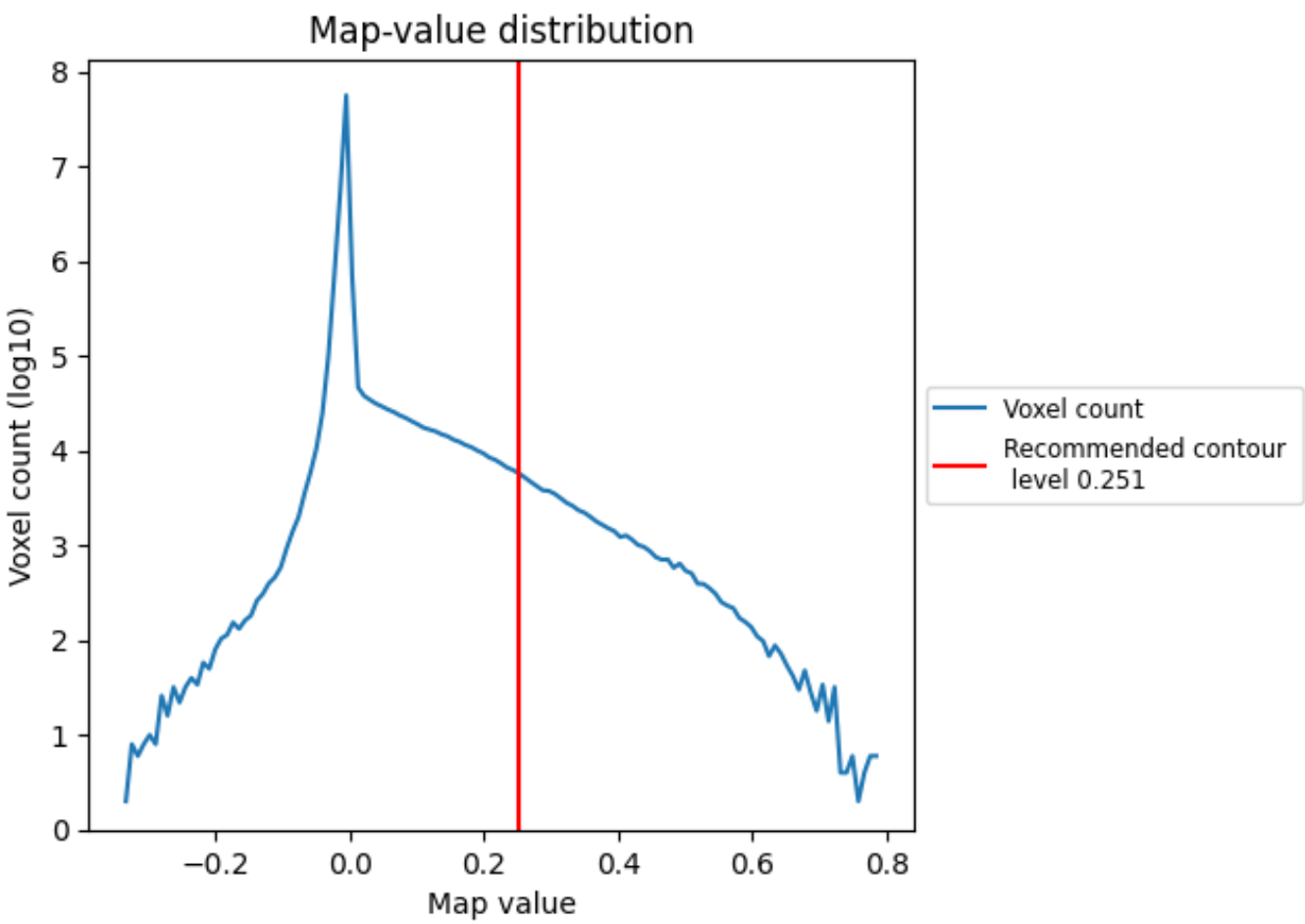
6.6 Mask visualisation (i)

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

7 Map analysis (i)

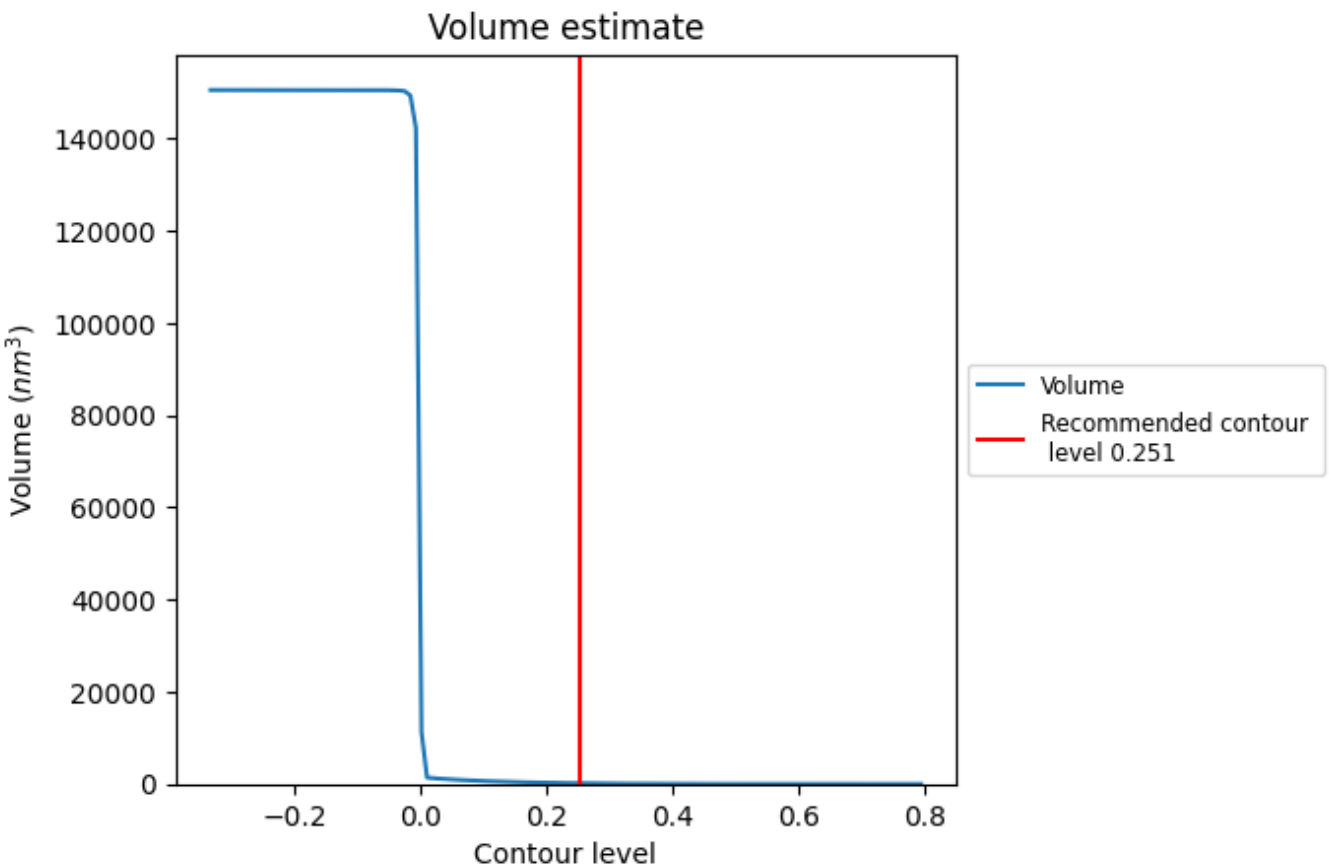
This section contains the results of statistical analysis of the map.

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.

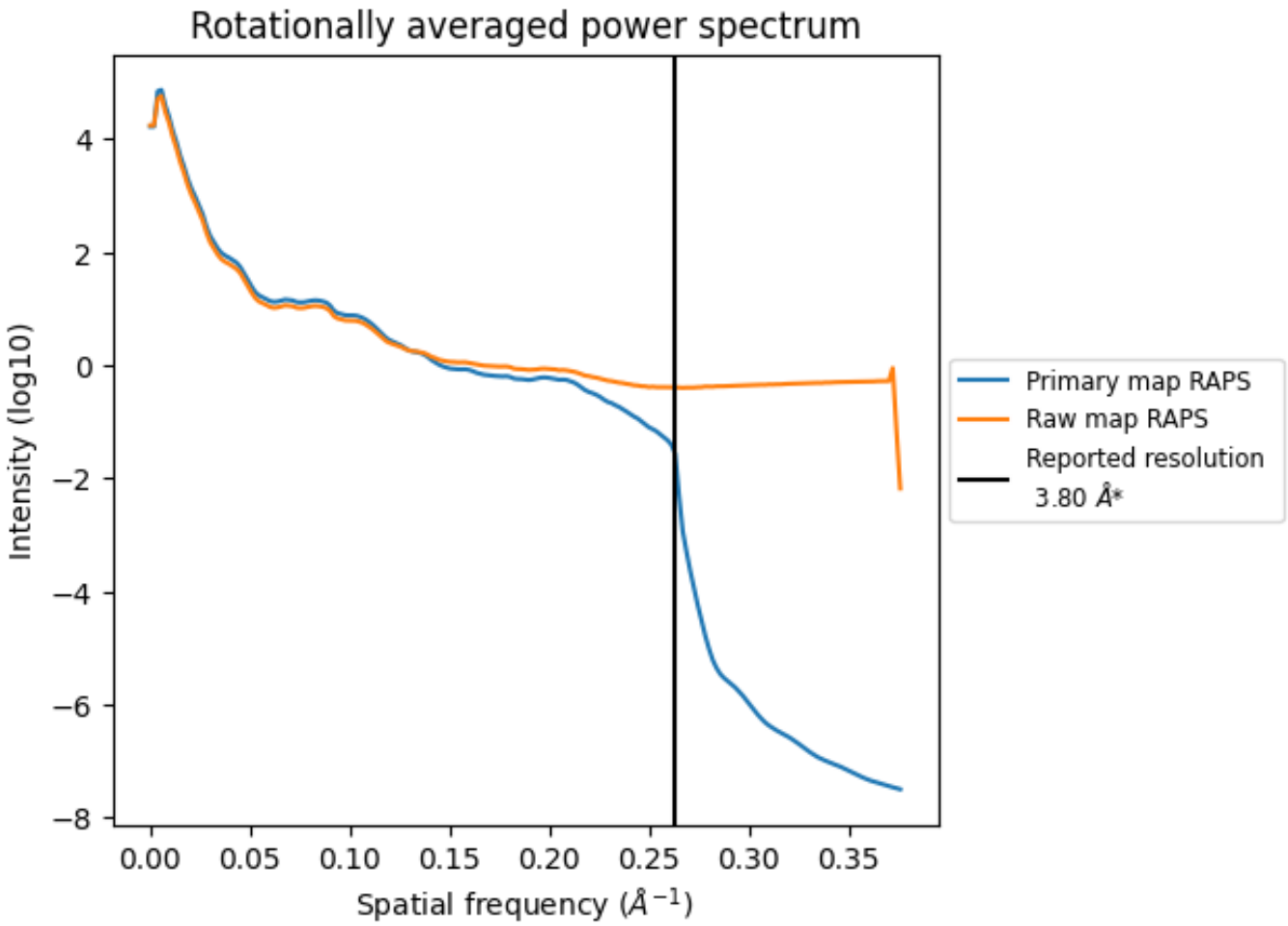
7.2 Volume estimate (i)



The volume at the recommended contour level is 160 nm^3; this corresponds to an approximate mass of 144 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)

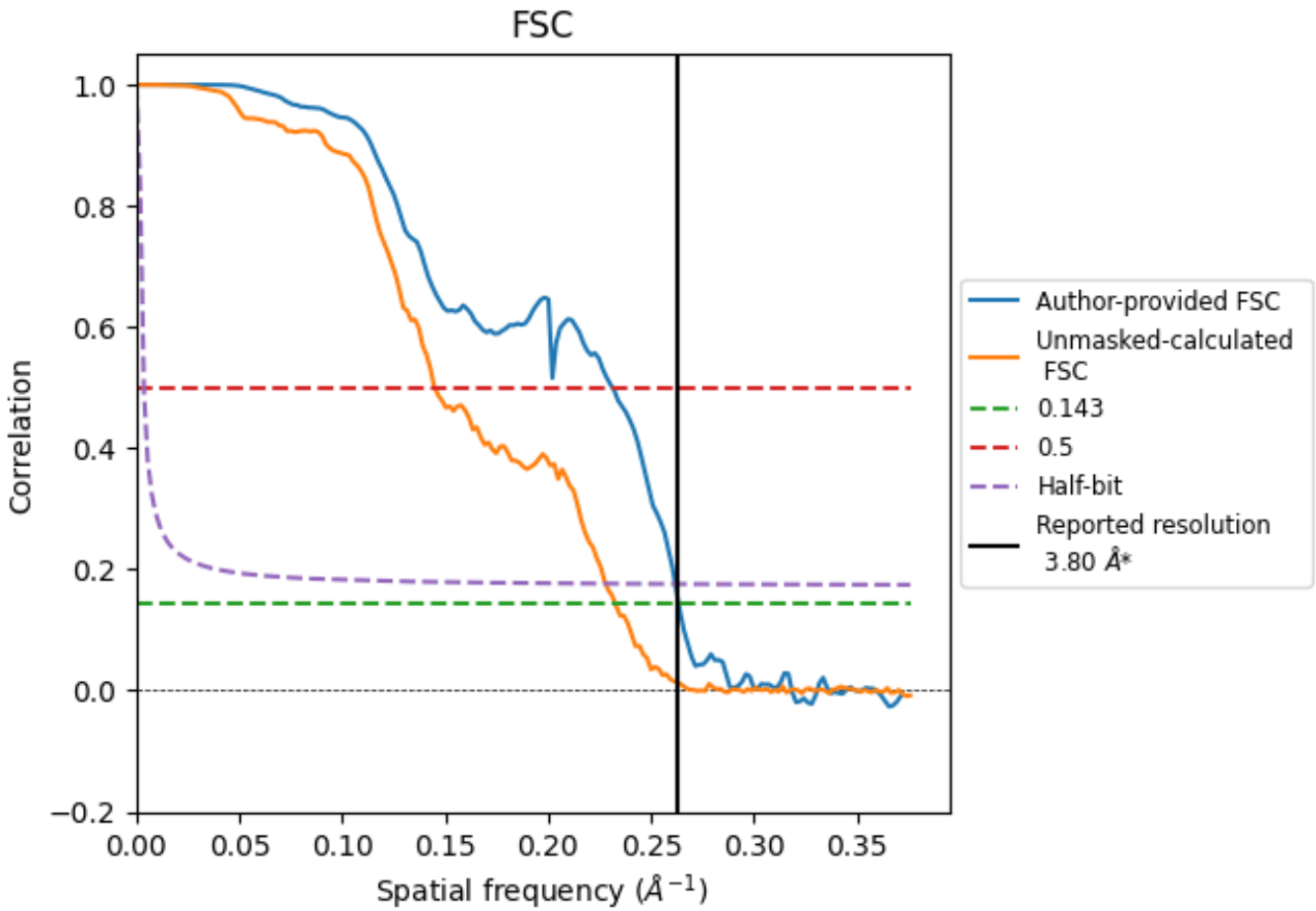


*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

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 0.263 Å^{-1}

8.2 Resolution estimates (i)

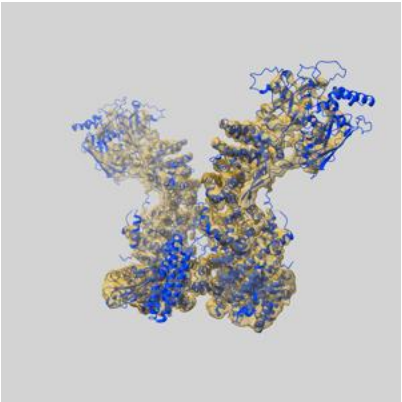
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.80	4.32	3.82
Unmasked-calculated*	4.30	6.90	4.39

*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 4.30 differs from the reported value 3.8 by more than 10 %

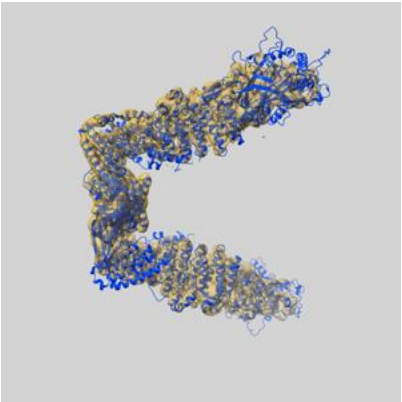
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-68711 and PDB model 22VD. Per-residue inclusion information can be found in section 3 on page 4.

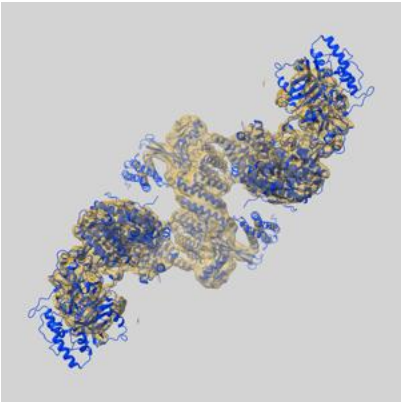
9.1 Map-model overlay (i)



X



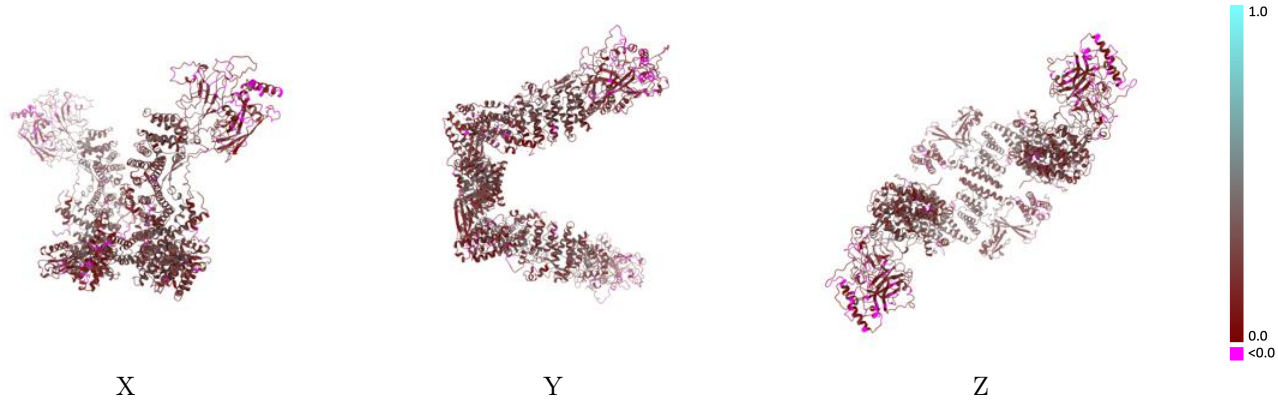
Y



Z

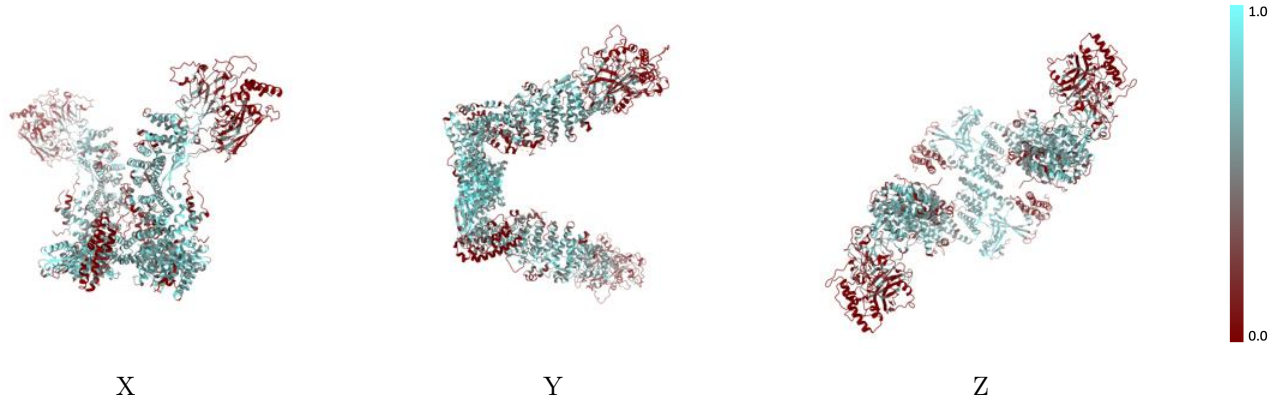
The images above show the 3D surface view of the map at the recommended contour level 0.251 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



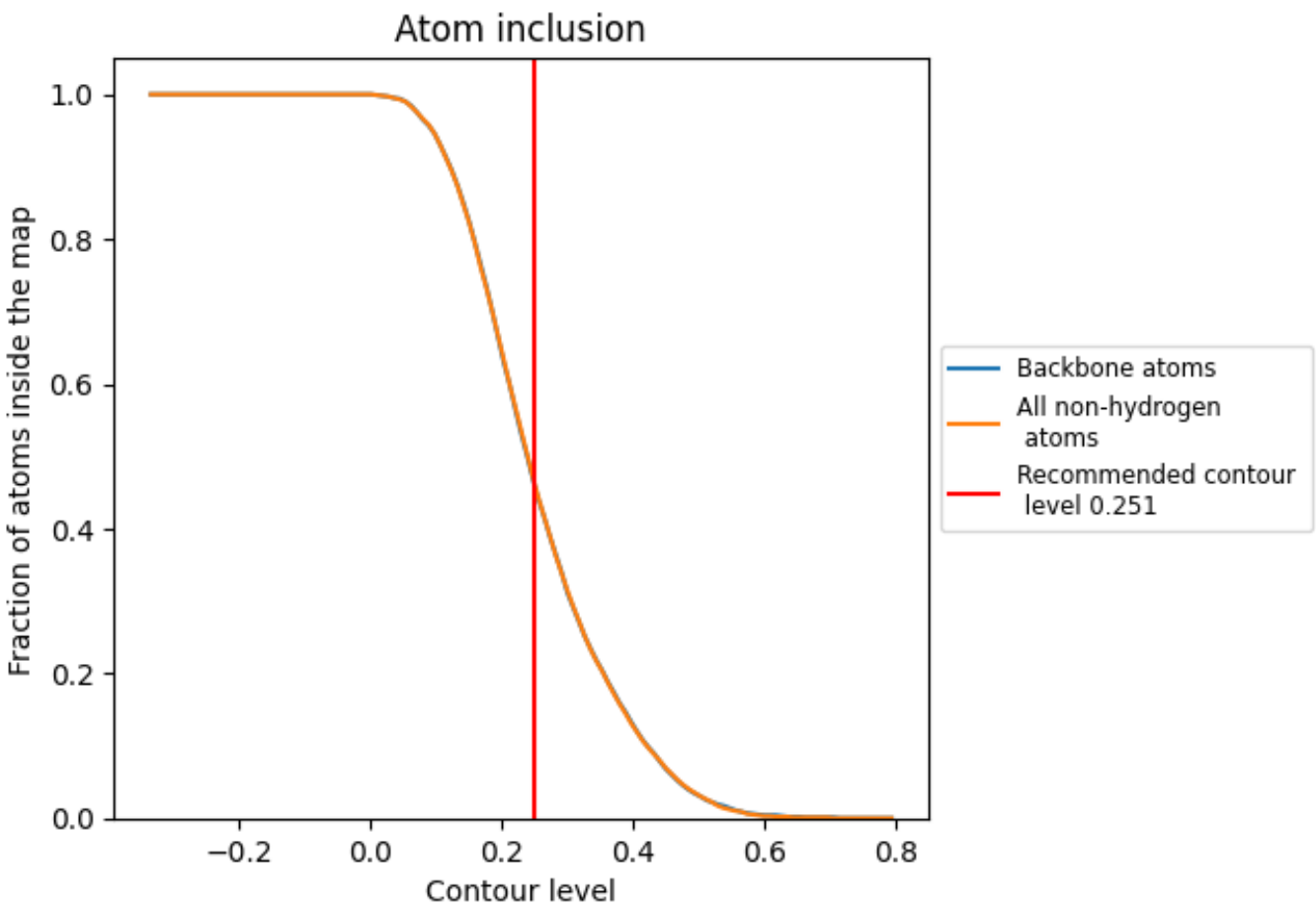
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.251).

9.4 Atom inclusion (i)



At the recommended contour level, 46% of all backbone atoms, 46% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.251) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4600	0.2220
A	0.4650	0.2220
B	0.4670	0.2220