wwPDB EM Validation Summary Report (i)

Aug 30, 2026 – 12:21 AM JST

PDB ID	:	9VM6 / pdb_00009vm6
EMDB ID	:	EMD-65178
Title	:	Structure of DOCK6 tetramer
Authors	:	Kukimoto-Niino, M.; Katsura, K.; Ishizuka-Katsura, Y.; Yonemochi, M.; Hanada, K.; Shirouzu, M.
Deposited on	:	2025-06-27
Resolution	:	4.27 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 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:

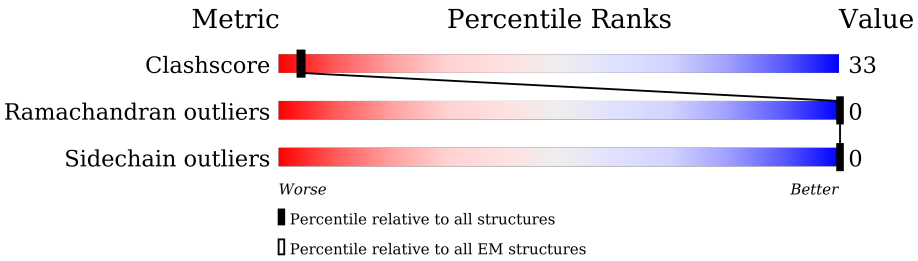
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

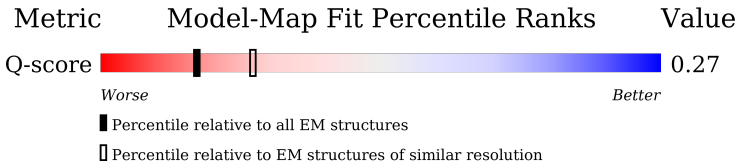
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.27 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	4567 (3.77 - 4.76)

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	2053	38% 44% 18%
1	B	2053	38% 44% 18%
1	C	2053	37% 45% 18%
1	D	2053	38% 44% 18%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 53700 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 Dedicator of cytokinesis protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1683	13425	8576	2321	2469	59	0	0
1	C	1683	13425	8576	2321	2469	59	0	0
1	D	1683	13425	8576	2321	2469	59	0	0
1	B	1683	13425	8576	2321	2469	59	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q96HP0
A	-4	GLY	-	expression tag	UNP Q96HP0
A	-3	SER	-	expression tag	UNP Q96HP0
A	-2	GLY	-	expression tag	UNP Q96HP0
A	-1	GLY	-	expression tag	UNP Q96HP0
A	0	SER	-	expression tag	UNP Q96HP0
C	-5	GLY	-	expression tag	UNP Q96HP0
C	-4	GLY	-	expression tag	UNP Q96HP0
C	-3	SER	-	expression tag	UNP Q96HP0
C	-2	GLY	-	expression tag	UNP Q96HP0
C	-1	GLY	-	expression tag	UNP Q96HP0
C	0	SER	-	expression tag	UNP Q96HP0
D	-5	GLY	-	expression tag	UNP Q96HP0
D	-4	GLY	-	expression tag	UNP Q96HP0
D	-3	SER	-	expression tag	UNP Q96HP0
D	-2	GLY	-	expression tag	UNP Q96HP0
D	-1	GLY	-	expression tag	UNP Q96HP0
D	0	SER	-	expression tag	UNP Q96HP0
B	-5	GLY	-	expression tag	UNP Q96HP0
B	-4	GLY	-	expression tag	UNP Q96HP0
B	-3	SER	-	expression tag	UNP Q96HP0
B	-2	GLY	-	expression tag	UNP Q96HP0

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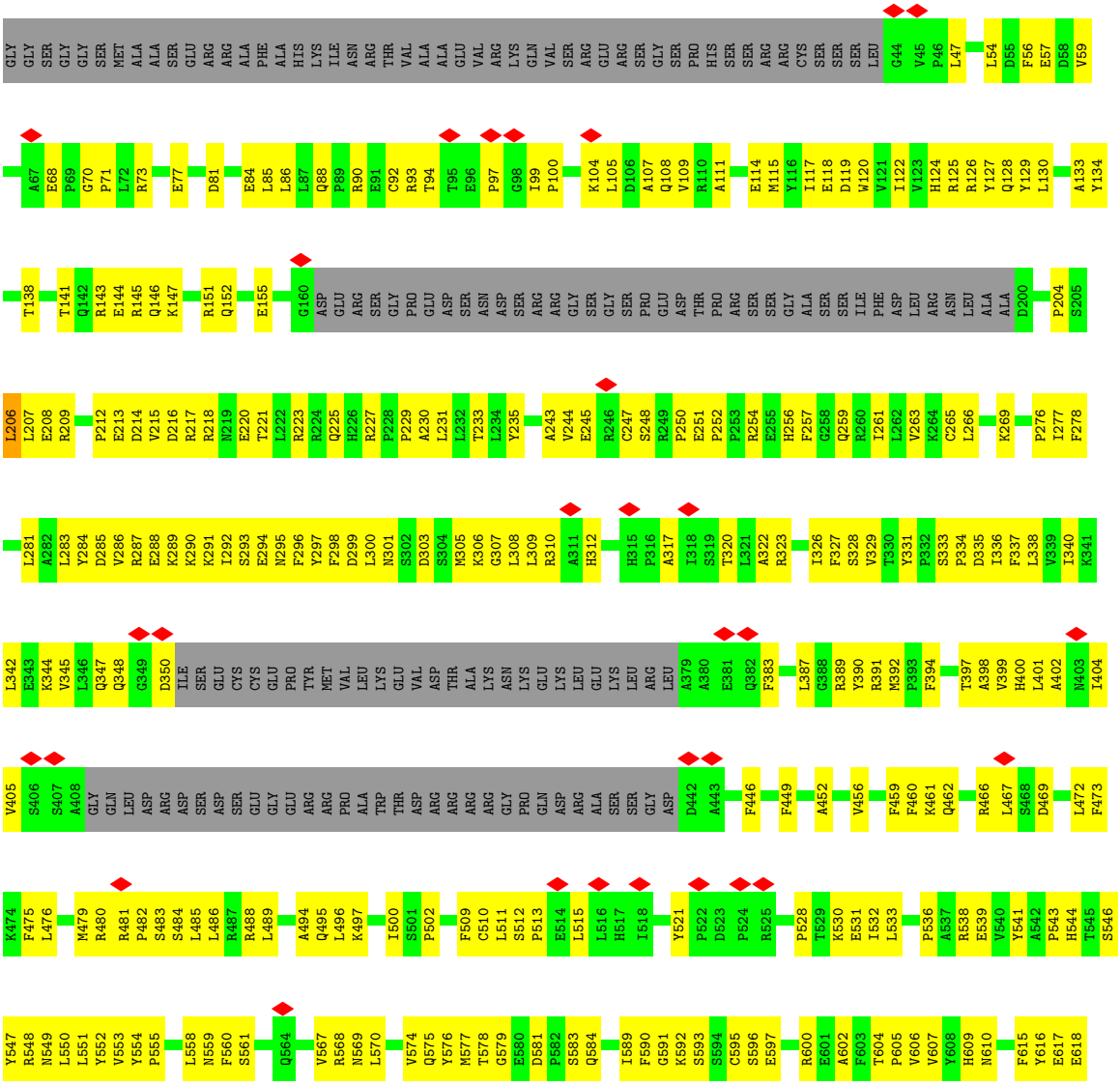
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP Q96HP0
B	0	SER	-	expression tag	UNP Q96HP0

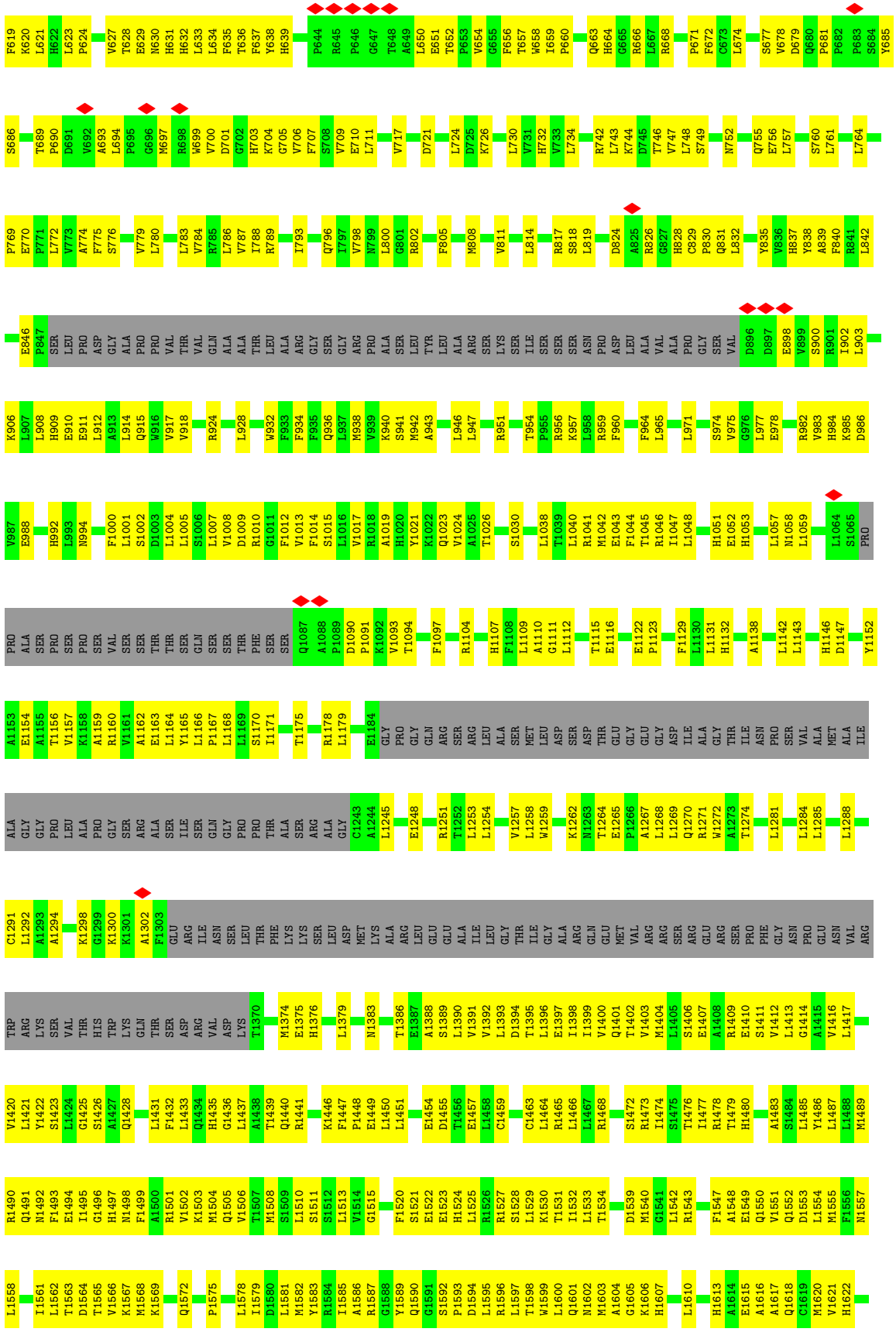
3 Residue-property plots (i)

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 6

Chain A:

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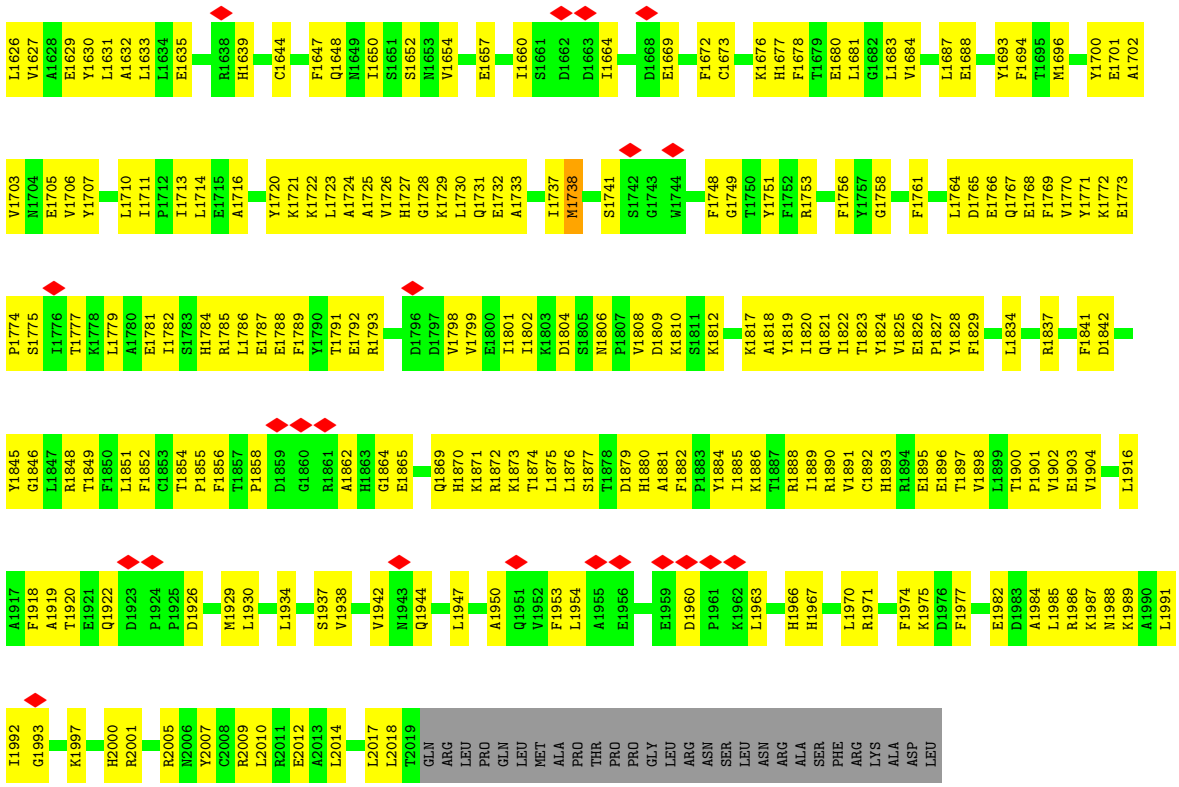
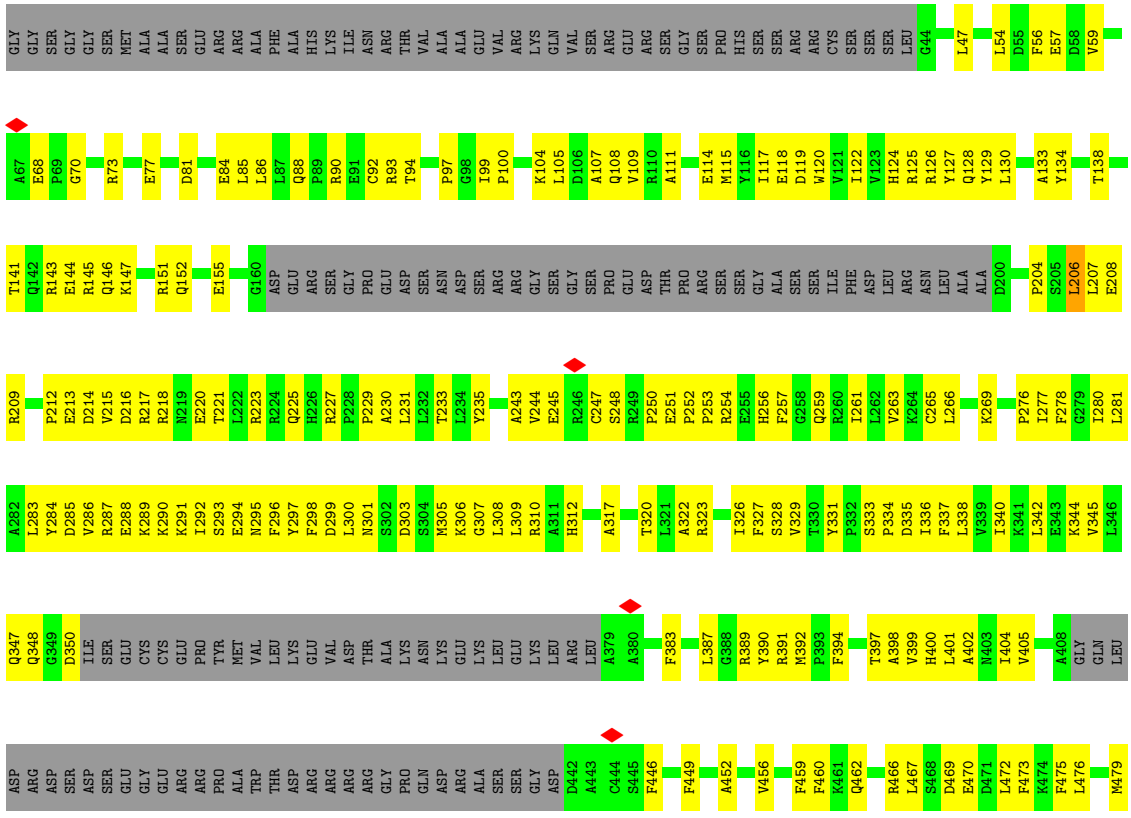
S686 T689 P690 D691 V692 A693 L694 P695 G696 M697 R698 W699 V700 D701 G702 H703 K704 G705 V706 F707 S708 V709 E710 L711 V717 D721 L724 D725 K726 L730 V731 H732 V733 L734 R742 L743 K744 D745 T746 V747 L748 S749 N752 Q755 E756 L757 S760 L761 L764
P769 E770 P771 L772 V773 A774 F775 S776 V779 L780 L783 V784 R785 L786 V787 I788 R789 I793 Q796 I797 V798 N799 L800 G801 R802 F805 M808 V811 L814 R817 S818 L819 D824 A825 R826 G827 H828 C829 P830 Q831 L832 Y835 V836 H837 Y838 A839 F840 R841 L842
E846 P847 SER LEU PRO ASP GLY ALA PRO PRO VAL THR VAL GLN ALA ALA THR LEU ALA ARG GLY SER GLY ARG PRO ALA SER LEU TYR LEU ALA ARG SER LYS SER ILE SER SER SER ASN PRO ASP LEU ALA VAL ALA PRO GLY SER VAL D896 D897 E898 V899 S900 R901 I902 L903
K906 L907 L908 H909 E910 E911 L912 A913 L914 Q915 W916 V917 V918 R924 L928 W932 F933 F934 F935 Q936 L937 M938 V939 K940 S941 M942 A943 L946 L947 R951 T954 P955 R956 K957 L958 R959 F960 F964 L965 L971 S974 V975 G976 L977 E978 R982 V983 H984 K985 D986
V987 E988 H992 L993 N994 F1000 L1001 S1002 D1003 L1004 L1005 S1006 L1007 V1008 D1009 R1010 G1011 F1012 V1013 F1014 S1015 L1016 V1017 R1018 A1019 H1020 Y1021 K1022 Q1023 V1024 A1025 T1026 S1030 L1038 T1039 L1040 R1041 M1042 E1043 F1044 T1045 R1046 I1047 L1048 H1051 E1052 H1053 L1057 N1058 L1059 L1064 S1065 PRO
PRO ALA SER PRO SER PRO SER VAL SER SER THR THR SER GLN SER SER THR PHE SER SER Q1087 A1088 P1089 D1090 P1091 K1092 V1093 T1094 F1097 R1104 H1107 F1108 L1109 A1110 G1111 L1112 T1115 E1116 E1122 P1123 F1129 L1130 L1131 H1132 A1138 L1142 L1143 H1146 D1147 Y1152
A1153 E1154 A1155 T1156 V1157 K1158 A1159 R1160 V1161 A1162 E1163 L1164 Y1165 L1166 P1167 L1168 L1169 S1170 I1171 T1175 R1178 L1179 E1184 GLY PRO GLY GLN ARG SER ARG LEU ALA SER MET LEU ASP SER ASP THR GLU GLY GLU GLY ASP ILE ALA GLY THR ILE ASN PRO SER VAL ALA MET ALA ILE
ALA GLY GLY PRO LEU ALA PRO PRO GLY SER ARG ALA SER ILE SER GLN GLY PRO PRO THR ALA SER ARG ALA GLY C1243 A1244 L1245 E1248 R1251 T1252 L1253 L1254 V1257 L1258 W1259 K1262 N1263 T1264 E1265 P1266 A1267 L1268 L1269 Q1270 R1271 W1272 A1273 T1274 L1281 L1284 L1285 L1288
C1291 L1292 A1293 A1294 K1298 G1299 K1300 K1301 A1302 F1303 GLU ARG ILE ASN SER LEU THR PHE LYS SER LEU ASP MET LYS ALA ARG LEU GLU GLU ALA ILE LEU GLY THR ARG VAL ARG ARG SER ARG GLU ARG PRO PHE GLY ASN PRO GLU ASN VAL ARG
TRP ARG LYS SER VAL THR HIS TRP LYS GLN THR SER ASP ARG VAL ASP LYS T1370 M1374 E1375 H1376 L1379 ASP N1383 T1386 E1387 A1388 S1389 L1390 V1391 V1392 L1393 D1394 T1395 L1396 E1397 I1398 I1399 V1400 Q1401 T1402 V1403 M1404 L1405 S1406 E1407 A1408 R1409 E1410 S1411 V1412 L1413 G1414 A1415 V1416 L1417
V1420 L1421 Y1422 S1423 L1424 G1425 S1426 A1427 Q1428 L1431 F1432 L1433 Q1434 H1435 G1436 L1437 A1438 T1439 Q1440 R1441 K1446 F1447 P1448 E1449 L1450 L1451 E1454 D1455 T1456 E1457 L1458 C1459 C1463 L1464 R1465 L1466 L1467 R1468 S1472 R1473 I1474 S1475 T1476 I1477 R1478 T1479 H1480 A1483 S1484 L1485 Y1486 L1487 L1488 M1489
R1490 Q1491 N1492 F1493 E1494 I1495 G1496 H1497 N1498 F1499 A1500 R1501 V1502 K1503 M1504 Q1505 V1506 T1507 M1508 S1509 L1510 S1511 S1512 L1513 V1514 G1515 F1520 S1521 E1522 E1523 H1524 L1525 R1526 R1527 S1528 L1529 K1530 T1531 I1532 L1533 T1534 D1539 M1540 G1541 L1542 R1543 F1547 A1548 E1549 Q1550 V1551 Q1552 D1553 L1554 M1555 F1556 N1557
L1558 I1561 L1562 T1563 D1564 T1565 V1566 K1567 M1568 K1569 Q1572 P1575 L1578 I1579 D1580 L1581 M1582 Y1583 R1584 I1585 A1586 R1587 G1588 Y1589 Q1590 G1591 S1592 P1593 D1594 L1595 R1596 L1597 T1598 W1599 L1600 Q1601 N1602 M1603 A1604 G1605 K1606 H1607 L1610 H1613 A1614 E1615 A1616 A1617 Q1618 C1619 M1620 V1621 H1622



- Molecule 1: Dedicator of cytokinesis protein 6

Chain C:



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D1539 M1540 G1541 L1542 R1543
F1547 A1548 E1549 Q1550 V1551 Q1552 D1553 L1554 M1555 F1556 N1557 L1558
I1561 L1562 T1563 D1564 T1565 V1566 K1567 M1568 K1569
Q1572
P1575
L1578
T1439 Q1440 R1441
K1446 F1447 P1448 E1449 L1450 L1451
E1454 D1455 T1456 E1457 L1458 C1459
C1463 L1464 R1465 L1466 L1467 R1468
S1472 R1473 I1474 S1475 T1476 I1477 R1478 T1479 H1480 A1481 S1482 A1483 Q1484 L1485 Y1486 L1487 L1488 M1489 R1490 Q1491 N1492 F1493 E1494 I1495 G1496 H1497 N1498 F1499 A1500 R1501 V1502 K1503 M1504 Q1505 V1506
M1374 E1375 H1376
L1379
N1383
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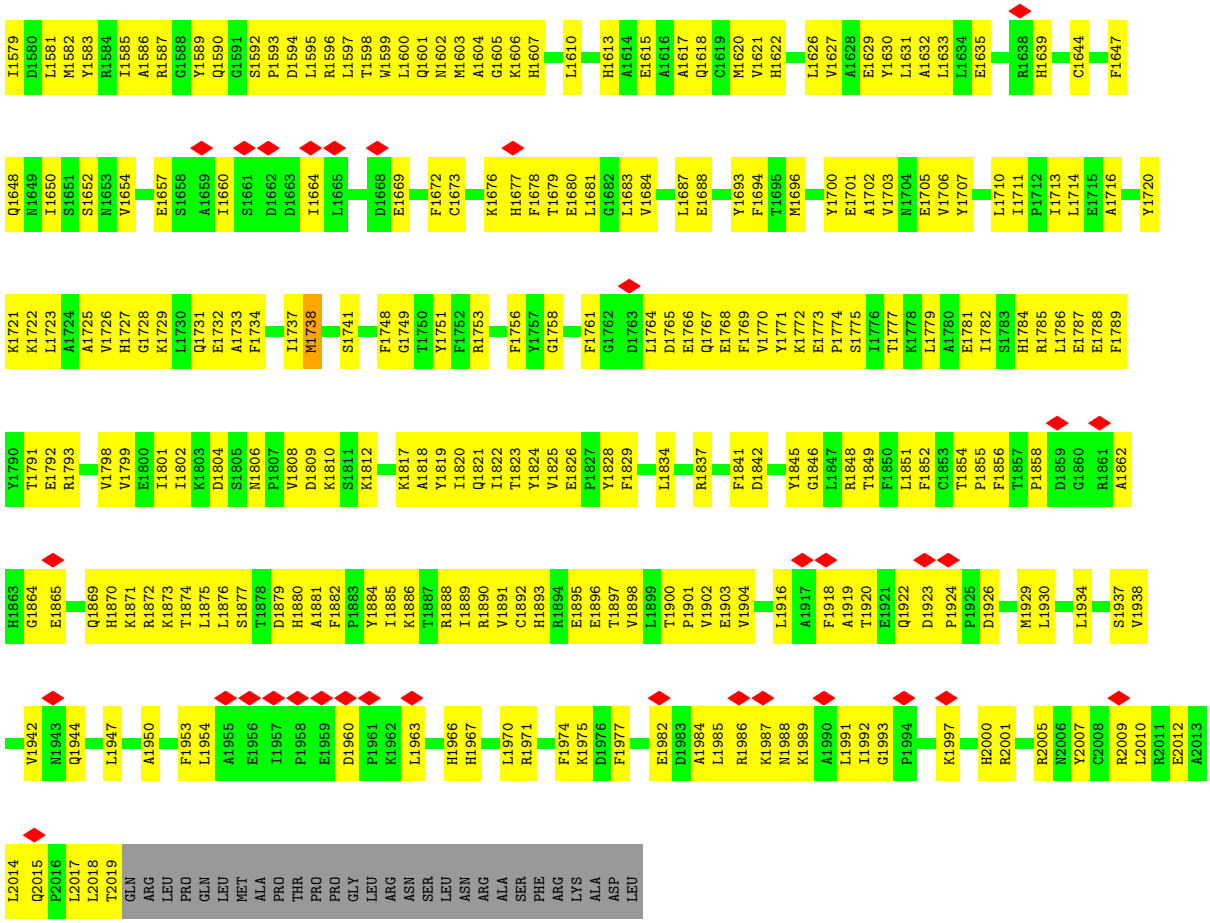
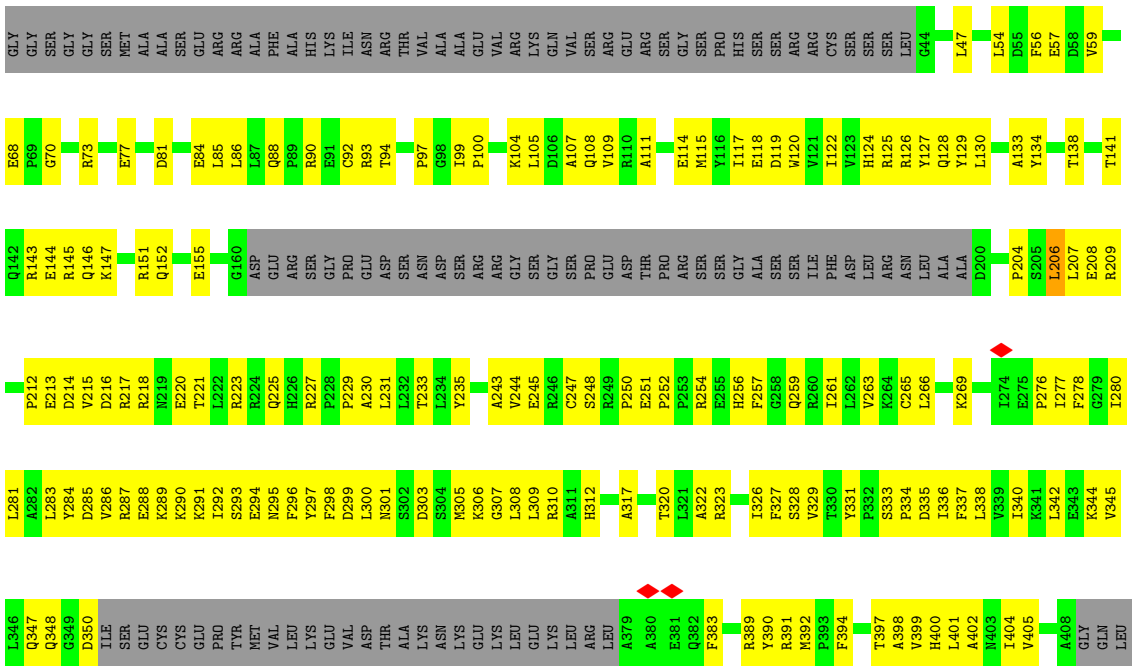
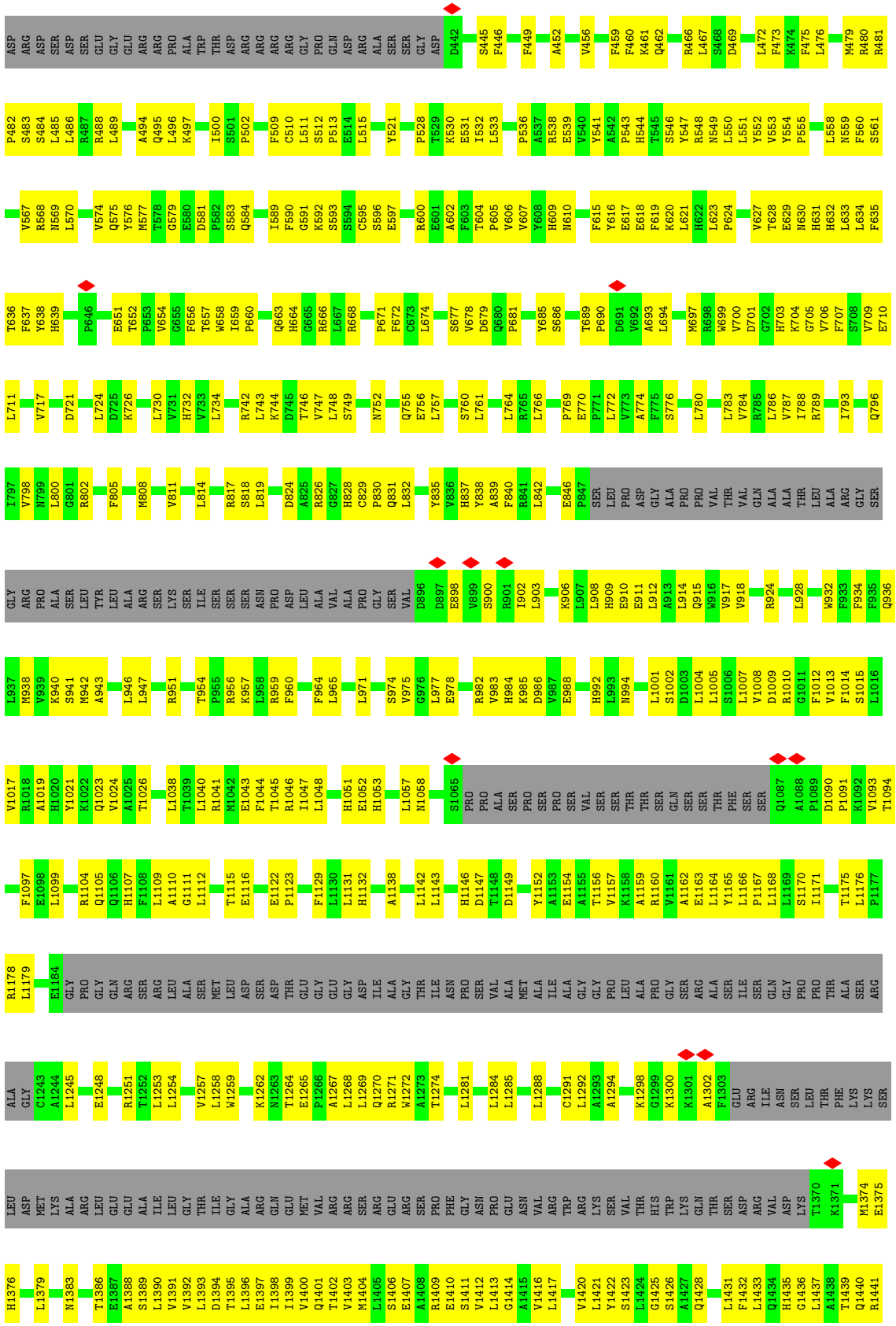
V1420 L1421 Y1422 S1423 L1424 G1425 S1426 A1427 Q1428
L1431 F1432 L1433 Q1434 H1435 G1436 L1437 A1438
PHE LYS LYS SER LEU ASP MET LYS ALA ARG LEU GLU GLU GLU ALA ILE LEU GLY THR ILE LYS SER ARG ARG SER GLU ALA ARG ARG GLU MET VAL ARG ARG SER ARG GLU GLY ASN PRO GLU ASN VAL ARG TRP ARG LYS SER VAL THR HIS TRP LYS GLN THR SER ASP ARG VAL ASP LYS T1370
THR ALA SER ARG ALA GLY C1243 A1244 L1245 E1248 R1251 T1252 L1253 L1254 V1257 L1258 W1259 K1262 N1263 T1264 E1265 P1266 A1267 L1268 L1269 Q1270 R1271 W1272 A1273 T1274 L1281 L1284 L1285 L1288 C1291 L1292 A1293 A1294 K1298 G1299 K1300 K1301 A1302 F1303 GLU ARG ILE ASN SER LEU THR
T1175 L1176 P1177 R1178 L1179 E1184 GLY PRO GLY GLN ARG SER ARG LEU ALA SER MET LEU ASP SER ASP THR GLU GLY GLU GLY ASP ILE ALA GLY THR ILE ASN PRO SER VAL ALA MET ALA ILE ALA GLY GLY PRO LEU ALA PRO SER THR SER GLN GLY PRO PRO
D1090 P1091 K1092 V1093 T1094 F1097 E1098 L1099 R1104 Q1105 Q1106 H1107 F1108 L1109 A1110 G1111 L1112 T1115 E1116 E1122 P1123 F1129 H1132 A1138 L1142 L1143 H1146 D1147 T1148 D1149 Y1152 A1153 E1154 A1155 T1156 V1157 K1158 A1159 R1160 V1161 A1162 E1163 L1164 Y1165 L1166 P1167 L1168 L1169 S1170 I1171
F1012 V1013 F1014 S1015 L1016 V1017 R1018 A1019 H1020 Y1021 K1022 Q1023 V1024 A1025 T1026 L1038 T1039 L1040 R1041 M1042 E1043 F1044 T1045 R1046 I1047 L1048 H1051 E1052 H1053 L1057 N1058 S1065 PRO PRO ALA SER PRO SER PRO SER VAL SER SER THR THR SER GLN SER SER THR PHE SER Q1087 A1088 P1089
F933 F934 F935 Q936 L937 M938 V939 K940 S941 M942 A943 L946 L947 R951 T954 P955 R956 K957 L958 R959 F960 F964 L965 L971 S974 V975 G976 L977 E978 R982 V983 H984 K985 D986 V987 E988 H992 L993 N994 F1000 L1001 S1002 D1003 L1004 L1005 S1006 L1007 V1008 D1009 R1010 G1011
ALA ARG GLY SER GLY ARG PRO ALA SER LEU TYR LEU ALA ARG SER LYS SER ILE SER SER SER ASN PRO ASP LEU ALA VAL ALA PRO GLY SER VAL D896 D897 E898 V899 S900 R901 I902 L903 K906 L907 L908 H909 E910 E911 L912 A913 L914 Q915 W916 V917 V918 R924 L928 W932
I793
Q796 I797 V798 N799 L800 G801 R802 F805 M808 V811 L814 R817 S818 L819 D824 A825 R826 G827 H828 C829 P830 Q831 L832 Y835 V836 H837 Y838 A839 F840 R841 L842 E846 P847 SER LEU PRO ASP GLY ALA PRO PRO VAL THR VAL GLN ALA ALA THR LEU
S708 V709 E710 L711 V717 D721 L724 D725 K726 L730 V731 H732 V733 L734 R742 L743 K744 D745 T746 V747 L748 S749 N752 Q755 E756 L757 S760 L761 L764 R765 L766 P769 E770 P771 L772 V773 A774 F775 S776 V779 L780 L783 V784 R785 L786 V787 I788 R789
L634 F635 T636 F637 Y638 H639 P646 L650 E651 T652 P653 V654 G655 F656 T657 W658 I659 P660 Q663 H664 G665 R666 L667 R668 P671 F672 C673 L674 S677 V678 D679 Q680 P681 Y685 S686 T689 P690 D691 V692 A693 L694 M697 R698 W699 V700 D701 G702 H703 K704 G705 V706 F707
F560 S561 V567 R568 N569 L570 V574 Q575 Y576 M577 T578 G579 E580 D581 P582 S583 Q584 I589 F590 G591 K592 S593 S594 C595 S596 E597 R600 E601 A602 F603 T604 P605 V606 V607 Y608 H609 N610 F615 Y616 E617 E618 F619 K620 L621 H622 L623 P624 V627 T628 E629 N630 H631 H632 L633
R480 R481 P482 S483 S484 L485 L486 R487 R488 L489 A494 Q495 L496 K497 I500 S501 P502 F509 C510 G511 S512 P513 E514 L515 Y521 P528 T529 K530 E531 I532 L533 P536 A537 R538 E539 V540 Y541 A542 P543 H544 T545 S546 Y547 R548 N549 L550 L551 Y552 Y553 Y554 P555 L558 N559



- Molecule 1: Dedicator of cytokinesis protein 6

Chain D:

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P482 S483 S484 L485 L486 R487 R488 L489 A494 Q495 L496 K497 I500 S501 P502 F509 C510 L511 S512 P513 E514 L515 Y521 P528 T529 K530 E531 I532 L533 P536 A537 R538 E539 V540 Y541 A542 P543 H544 T545 S546 Y547 R548 N549 L550 L551 Y552 V553 Y554 P555 L558 N559 F560 S561
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L711 V717 D721 L724 D725 K726 L730 V731 H732 V733 L734 R742 L743 K744 D745 T746 V747 L748 S749 N752 Q755 E756 L757 S760 L761 L764 R765 L766 P769 E770 P771 L772 V773 A774 F775 S776 L780 L783 V784 R785 L786 V787 I788 R789 I793 Q796
I797 V798 N799 L800 G801 R802 F805 M808 V811 L814 R817 S818 L819 D824 A825 R826 G827 H828 C829 P830 Q831 L832 Y835 V836 H837 Y838 A839 F840 R841 L842 E846 P847 SER LEU PRO ASP GLY ALA PRO PRO VAL THR VAL GLN ALA ALA THR LEU ALA ARG GLY SER
GLY ARG PRO ALA SER LEU TYR LEU ALA ARG SER LYS SER ILE SER SER SER ASN PRO ASP LEU ALA VAL ALA PRO GLY SER VAL D896 D897 E898 V899 S900 R901 I902 L903 K906 L907 L908 H909 E910 E911 L912 A913 L914 Q915 N916 V917 V918 R924 L928 W932 F933 F934 F935 Q936
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V1017 R1018 A1019 H1020 Y1021 K1022 Q1023 V1024 A1025 T1026 L1038 T1039 L1040 R1041 M1042 E1043 F1044 T1045 R1046 I1047 L1048 H1051 E1052 H1053 L1057 N1058 S1065 PRO PRO ALA SER PRO SER PRO SER VAL SER SER THR THR SER GLN SER SER THR PHE SER SER Q1087 A1088 P1089 D1090 P1091 K1092 V1093 T1094
F1097 E1098 L1099 R1104 Q1105 Q1106 H1107 F1108 L1109 A1110 G1111 L1112 T1115 E1116 E1122 P1123 F1129 L1130 L1131 H1132 A1138 L1142 L1143 H1146 D1147 T1148 D1149 Y1152 A1153 E1154 A1155 T1156 V1157 K1158 A1159 R1160 V1161 A1162 E1163 L1164 Y1165 L1166 P1167 L1168 L1169 S1170 I1171 T1175 L1176 P1177
R1178 L1179 E1184 GLY PRO GLY GLN ARG SER ARG LEU ALA SER MET LEU ASP SER ASP THR GLU GLY GLU GLY ASP ILE ALA GLY THR ILE ASN PRO SER VAL ALA MET ALA ILE ALA GLY GLY PRO LEU ALA PRO GLY SER ARG ALA SER ILE SER GLN GLY PRO PRO THR ALA SER ARG
ALA GLY C1243 A1244 L1245 E1248 R1251 T1252 L1253 L1254 V1257 L1258 W1259 K1262 N1263 T1264 E1265 P1266 A1267 L1268 L1269 Q1270 R1271 W1272 A1273 T1274 L1281 L1284 L1285 L1288 C1291 L1292 A1293 A1294 K1298 G1299 K1300 K1301 A1302 F1303 GLU ARG ILE ASN SER LEU THR PHE LYS LYS SER
LEU ASP MET LYS ALA ARG LEU GLU GLU ALA ILE LEU GLY THR ILE GLY ALA ARG GLN GLU MET VAL ARG ARG ARG SER ARG GLU ARG SER PRO PHE GLY ASN PRO GLU ASN VAL ARG TRP ARG LYS SER VAL THR HIS TRP LYS GLN THR SER ASP ARG VAL ASP LYS T1370 K1371 M1374 E1375
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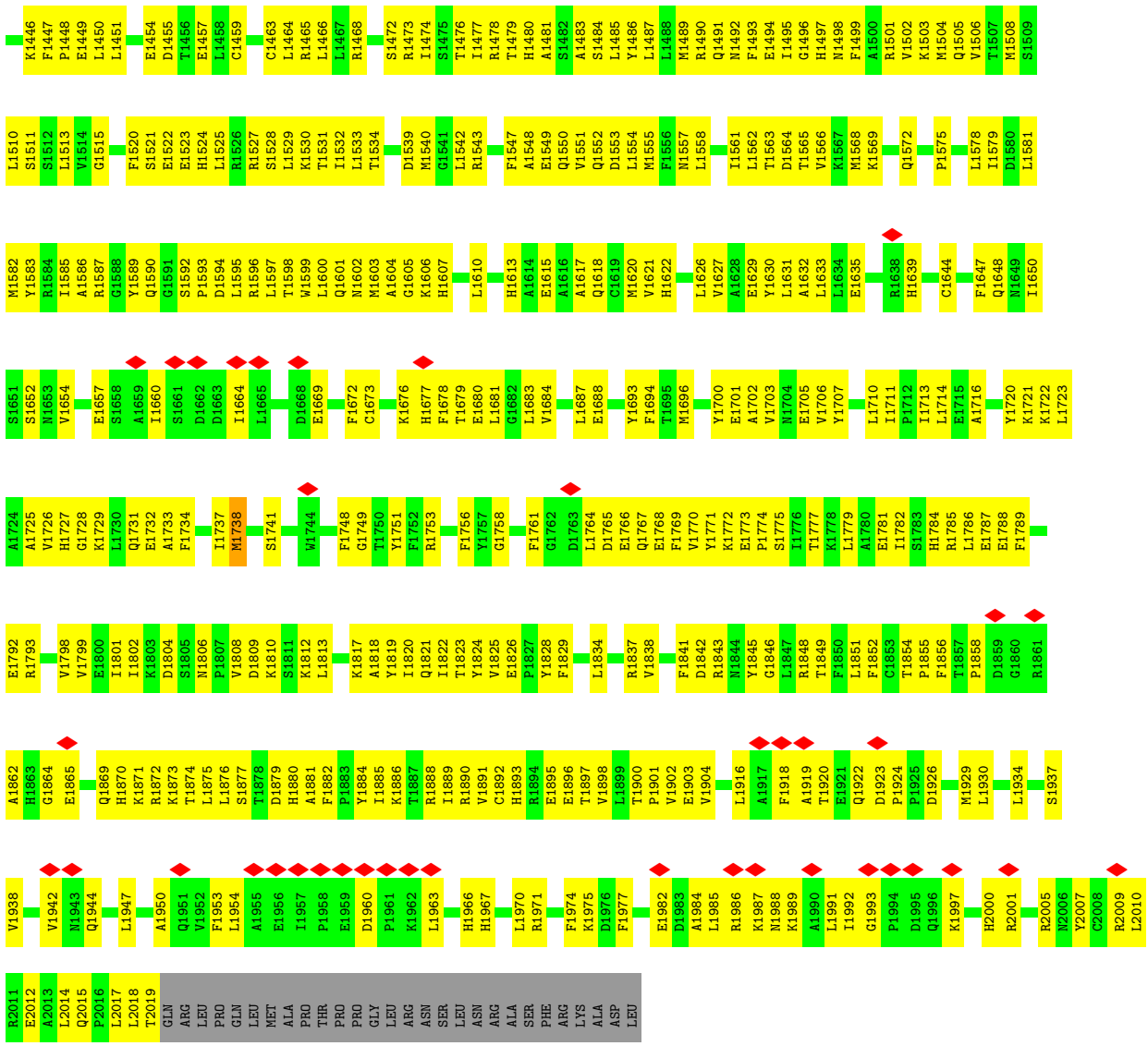
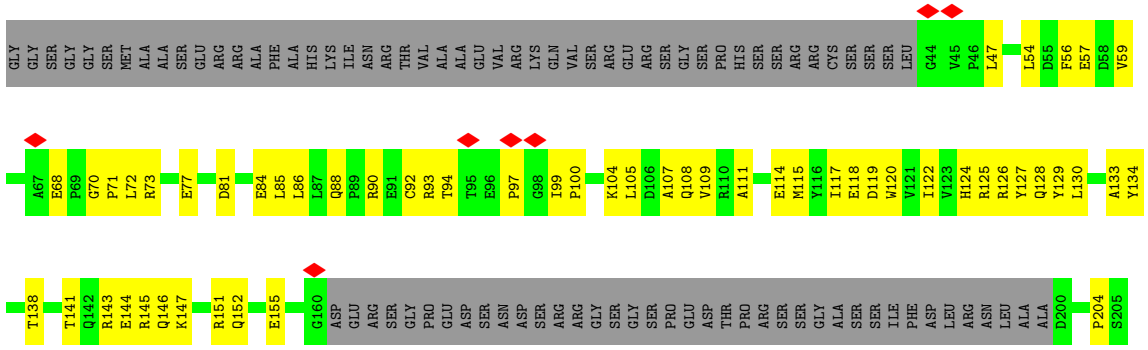
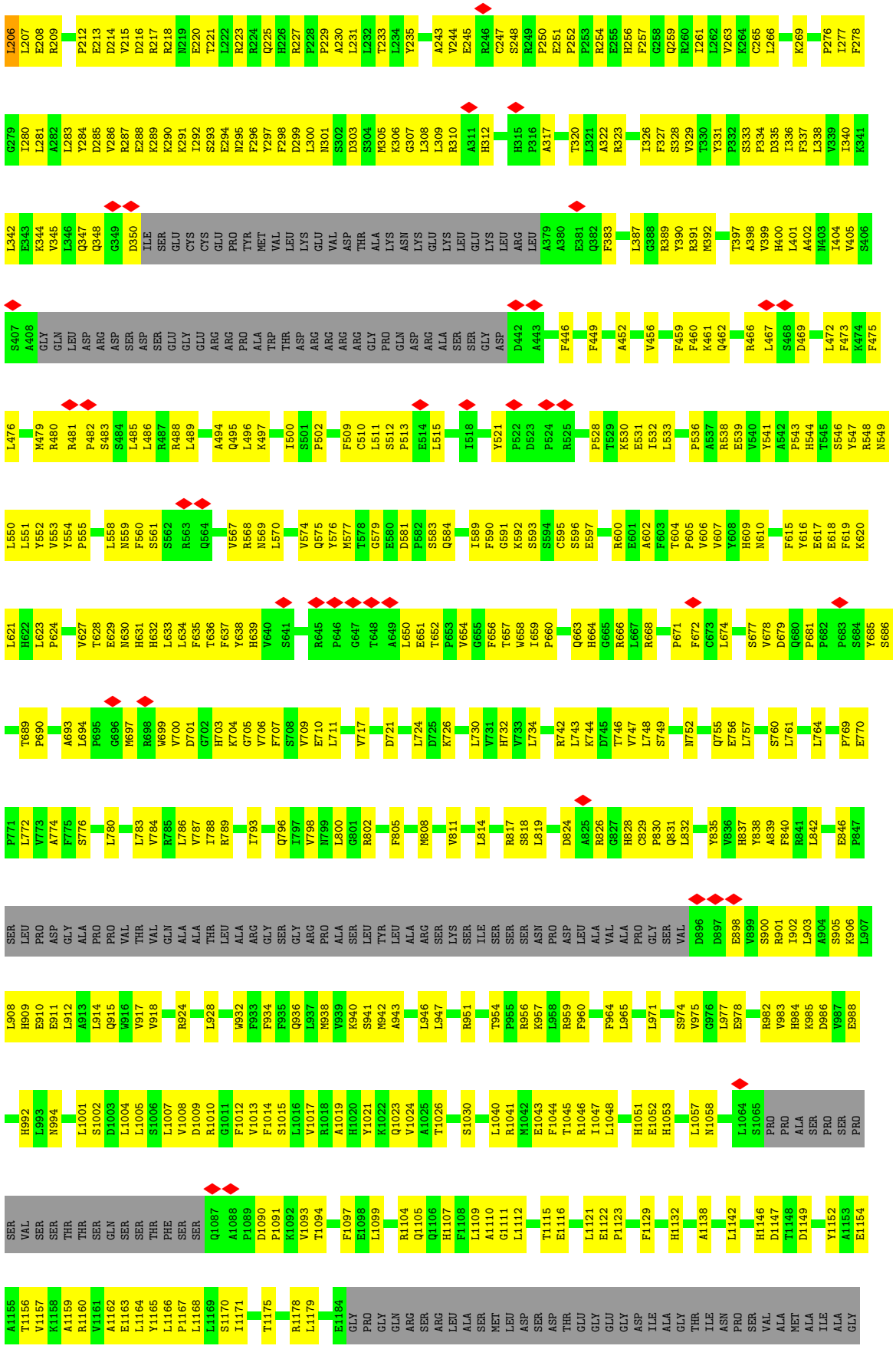


• Molecule 1: Dedicator of cytokinesis protein 6

Chain B:

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G279 I280 L281 A282 L283 Y284 D285 V286 R287 E288 K289 K290 K291 I292 S293 E294 N295 F296 Y297 F298 D299 L300 N301 S302 D303 S304 M305 K306 G307 L308 L309 R310 A311 H312 H315 P316 A317 T320 L321 A322 R323 I326 F327 S328 V329 T330 Y331 P332 S333 P334 D335 I336 F337 L338 W339 I340 K341
L342 E343 K344 V345 L346 Q347 Q348 G349 D350 ILE SER GLU CYS CYS GLU PRO TYR MET VAL LEU LYS GLU VAL ASP THR ALA LYS ASN LYS GLU LYS GLU LYS LEU ARG LEU A379 A380 E381 Q382 F383 L387 G388 R389 Y390 R391 M392 T397 A398 V399 H400 L401 A402 N403 I404 V405 S406
S407 A408 GLY GLN LEU ASP ARG ASP SER ASP SER GLU GLY GLU ARG ARG PRO ALA TRP THR ASP ARG ARG ARG ARG GLY PRO GLN ASP ARG ALA SER SER GLY ASP D442 A443 F446 F449 A452 V456 F459 F460 K461 Q462 R466 L467 S468 D469 L472 F473 K474 F475
L476 M479 R480 R481 P482 S483 S484 L485 L486 R487 R488 L489 A494 Q495 L496 K497 I500 S501 P502 F509 C510 L511 S512 P513 E514 L515 I518 Y521 P522 D523 P524 R525 P528 T529 K530 E531 I532 L533 P536 A537 R538 E539 V540 Y541 A542 P543 H544 T545 S546 Y547 R548 N549
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T689 P690 A693 L694 P695 G696 M697 R698 W699 V700 D701 G702 H703 K704 G705 V706 F707 S708 V709 E710 L711 V717 D721 L724 D725 K726 L730 V731 H732 V733 L734 R742 L743 K744 D745 T746 V747 L748 S749 N752 Q755 E756 L757 S760 L761 L764 P769 E770
P771 L772 V773 A774 F775 S776 L780 L783 V784 R785 L786 V787 I788 R789 I793 Q796 I797 V798 N799 L800 G801 R802 F805 M808 V811 L814 R817 S818 L819 D824 A825 R826 G827 H828 C829 P830 Q831 L832 Y835 V836 H837 Y838 A839 F840 R841 L842 E846 P847
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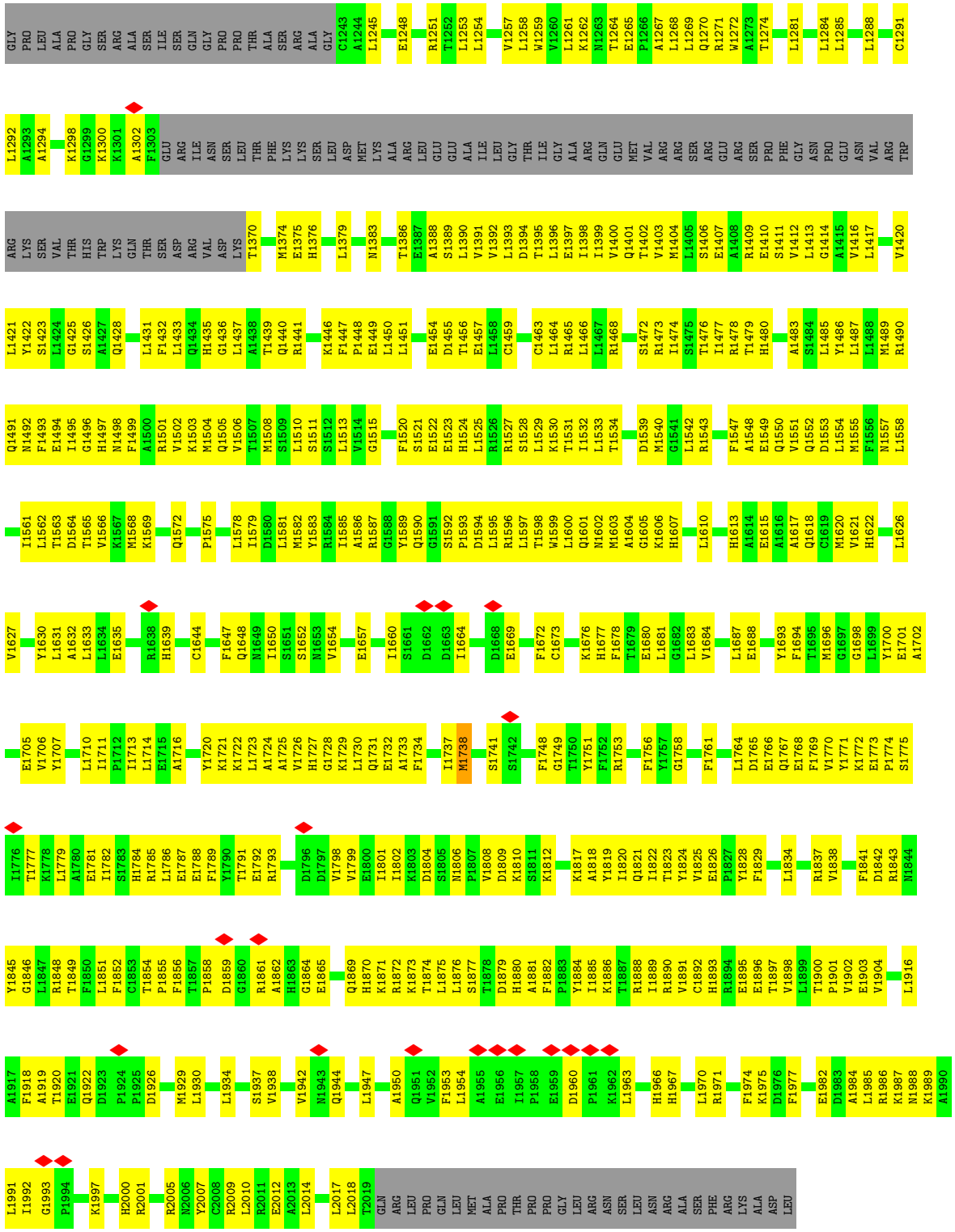
L908 H909 E910 E911 L912 A913 L914 Q915 W916 V917 V918 R924 L928 W932 F933 F934 F935 Q936 L937 M938 V939 K940 S941 M942 A943 L946 L947 R951 T954 P955 R956 K957 L958 R959 F960 F964 L965 L971 S974 V975 G976 L977 E978 R982 V983 H984 K985 D986 V987 E988
H992 L993 N994 L1001 S1002 D1003 L1004 L1005 S1006 L1007 V1008 D1009 R1010 G1011 F1012 V1013 F1014 S1015 L1016 V1017 R1018 A1019 H1020 Y1021 K1022 Q1023 V1024 A1025 T1026 S1030 L1040 R1041 M1042 E1043 F1044 T1045 R1046 I1047 L1048 H1051 E1052 H1053 L1057 N1058 L1064 S1065 PRO PRO ALA SER PRO PRO SER PRO
SER VAL SER SER THR THR SER SER THR PHE SER SER Q1087 A1088 P1089 D1090 P1091 K1092 V1093 T1094 F1097 E1098 L1099 R1104 Q1105 Q1106 H1107 F1108 L1109 A1110 G1111 L1112 T1115 E1116 L1121 E1122 P1123 F1129 H1132 A1138 L1142 H1146 D1147 T1148 D1149 Y1152 A1153 E1154
A1155 T1156 V1157 K1158 A1159 R1160 V1161 A1162 E1163 L1164 Y1165 L1166 P1167 L1168 L1169 S1170 I1171 T1175 R1178 L1179 E1184 GLY PRO GLY GLN ARG SER ARG LEU ALA SER MET LEU ASP SER ASP THR GLU GLY GLU GLY ASP ILE ALA GLY THR ILE ASN PRO SER VAL ALA MET ALA ILE ALA GLY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L1292 A1293 A1294 K1298 G1299 K1300 K1301 A1302 F1303 GLU ARG ILE ASN SER LEU THR PHE LYS LYS SER LEU ASP MET LYS ALA ARG LEU GLU GLU ALA ILE LEU GLY THR ILE GLY ALA ARG GLN GLU MET VAL ARG ARG SER PRO PHE GLY ASN PRO GLU ASN VAL ARG TRP
ARG LYS SER VAL THR HIS TRP LYS GLN THR SER ASP ARG VAL ASP LYS T1370 M1374 E1375 H1376 L1379 N1383 T1386 E1387 A1388 S1389 L1390 V1391 V1392 L1393 D1394 T1395 L1396 E1397 I1398 I1399 V1400 Q1401 T1402 V1403 M1404 L1405 S1406 E1407 A1408 R1409 E1410 S1411 V1412 L1413 G1414 A1415 V1416 L1417 V1420
L1421 Y1422 S1423 L1424 G1425 S1426 A1427 Q1428 L1431 F1432 L1433 Q1434 H1435 G1436 L1437 A1438 T1439 Q1440 R1441 K1446 F1447 P1448 E1449 L1450 L1451 E1454 D1455 T1456 E1457 L1458 C1459 C1463 L1464 R1465 L1466 L1467 R1468 S1472 R1473 I1474 S1475 T1476 I1477 R1478 T1479 H1480 A1483 S1484 L1485 Y1486 L1487 L1488 M1489 R1490
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V1627 Y1630 L1631 A1632 L1633 L1634 E1635 R1638 H1639 C1644 F1647 Q1648 N1649 I1650 S1651 S1652 N1653 V1654 E1657 I1660 S1661 D1662 D1663 I1664 D1668 E1669 F1672 C1673 K1676 H1677 F1678 T1679 E1680 L1681 G1682 L1683 V1684 L1687 E1688 Y1693 F1694 T1695 M1696 G1697 G1698 L1699 Y1700 E1701 A1702
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L1991 I1992 G1993 P1994 K1997 H2000 R2001 R2005 N2006 Y2007 C2008 R2009 L2010 R2011 E2012 A2013 L2014 L2017 L2018 T2019 GLN ARG LEU PRO GLN LEU MET ALA PRO THR PRO PRO GLY LEU ARG ASN SER LEU ASN ARG ALA SER PHE ARG LYS ALA ASP LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	163250	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 ($e^-/Å^2$)	49.5	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.080	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	452.2, 452.2, 452.2	wwPDB
Map dimensions	340, 340, 340	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	0.40	0/13741	0.55	1/18646 (0.0%)
1	B	0.40	0/13741	0.55	1/18646 (0.0%)
1	C	0.40	0/13741	0.55	1/18646 (0.0%)
1	D	0.40	0/13741	0.55	1/18646 (0.0%)
All	All	0.40	0/54964	0.55	4/74584 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1738	MET	CB-CG-SD	-6.24	93.97	112.70
1	A	1738	MET	CB-CG-SD	-6.24	93.98	112.70
1	D	1738	MET	CB-CG-SD	-6.23	94.00	112.70
1	C	1738	MET	CB-CG-SD	-6.22	94.02	112.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	LEU	Peptide

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Mol	Chain	Res	Type	Group
1	B	206	LEU	Peptide
1	C	206	LEU	Peptide
1	D	206	LEU	Peptide

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	13425	0	13390	885	0
1	B	13425	0	13390	879	0
1	C	13425	0	13390	891	0
1	D	13425	0	13390	893	0
All	All	53700	0	53560	3506	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 33.

The worst 5 of 3506 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:633:LEU:HB2	1:A:659:ILE:HB	1.46	0.98
1:D:633:LEU:HB2	1:D:659:ILE:HB	1.46	0.98
1:B:633:LEU:HB2	1:B:659:ILE:HB	1.46	0.97
1:C:633:LEU:HB2	1:C:659:ILE:HB	1.46	0.96
1:C:476:LEU:HA	1:C:479:MET:HG2	1.47	0.95

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	1667/2053 (81%)	1533 (92%)	134 (8%)	0	100	100
1	B	1667/2053 (81%)	1534 (92%)	133 (8%)	0	100	100
1	C	1667/2053 (81%)	1533 (92%)	134 (8%)	0	100	100
1	D	1667/2053 (81%)	1533 (92%)	134 (8%)	0	100	100
All	All	6668/8212 (81%)	6133 (92%)	535 (8%)	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	1470/1773 (83%)	1470 (100%)	0	100	100
1	B	1470/1773 (83%)	1470 (100%)	0	100	100
1	C	1470/1773 (83%)	1470 (100%)	0	100	100
1	D	1470/1773 (83%)	1470 (100%)	0	100	100
All	All	5880/7092 (83%)	5880 (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 83 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	1689	GLN
1	B	1053	HIS
1	D	1844	ASN
1	B	544	HIS
1	B	1497	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.

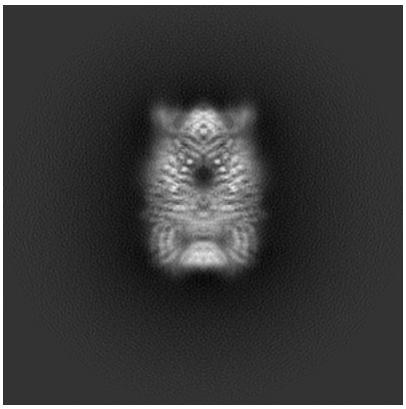
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-65178. 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



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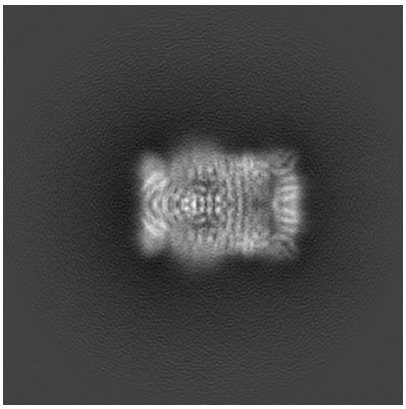

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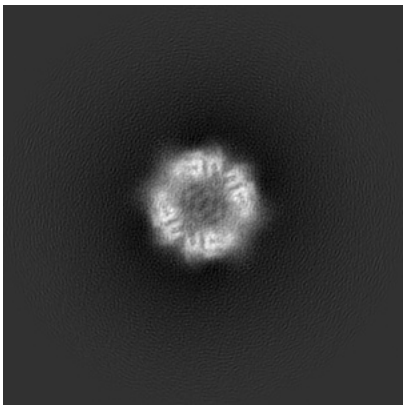
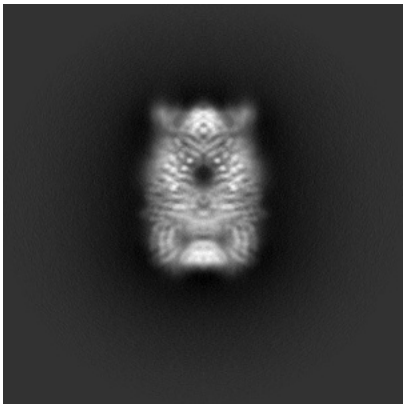


Z

6.1.2 Raw map



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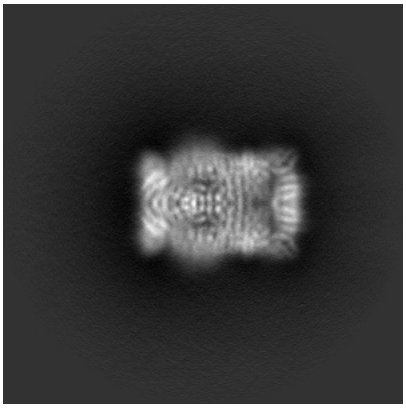

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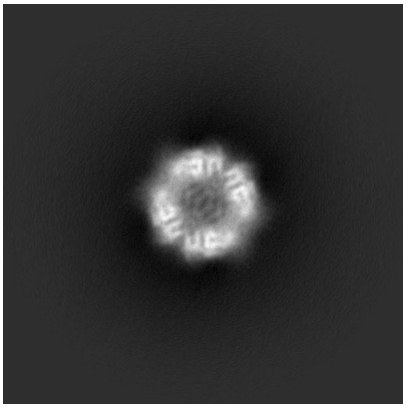
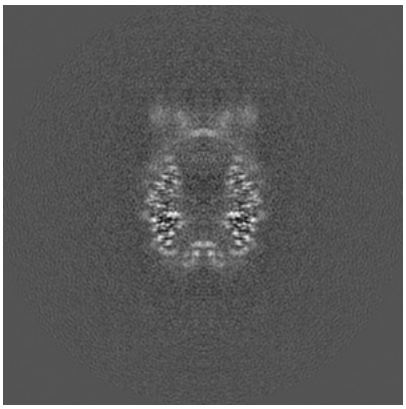


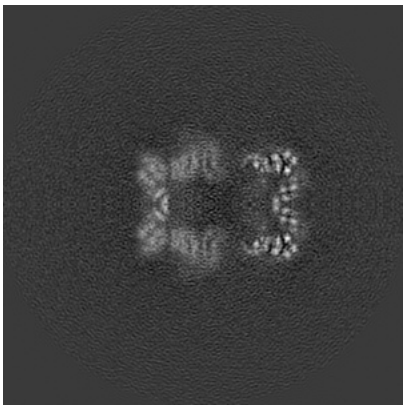
Z

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

6.2 Central slices (i)

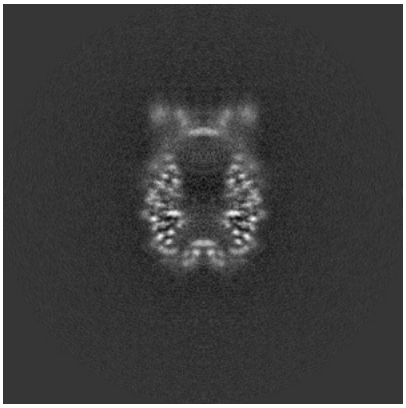
6.2.1 Primary map

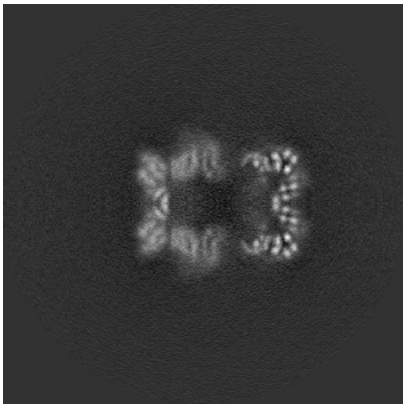

X Index: 170

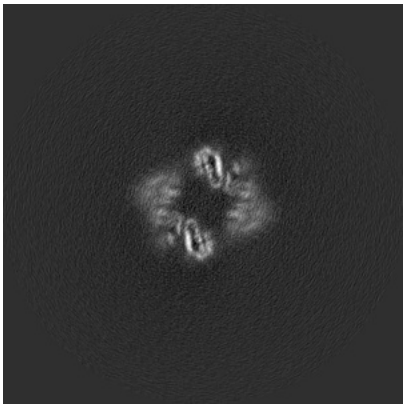

Y Index: 170

Z Index: 170

6.2.2 Raw map


X Index: 170

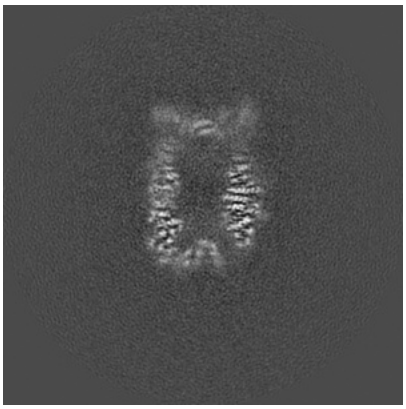

Y Index: 170


Z Index: 170

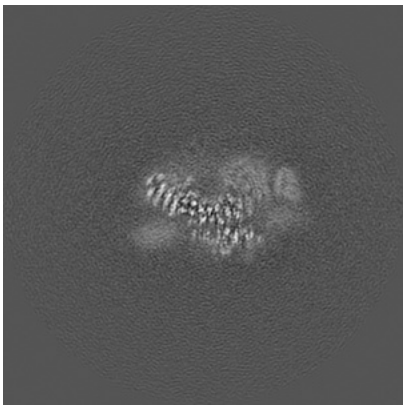
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



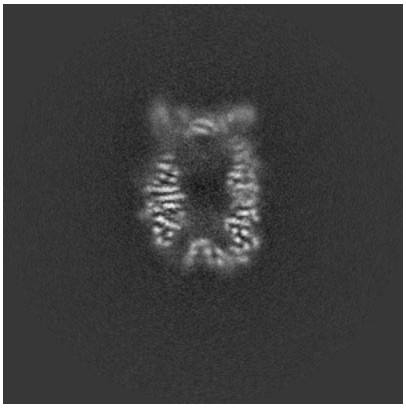
X Index: 174



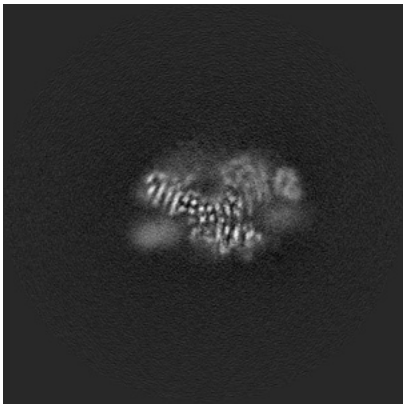
Y Index: 142

Z Index: 168

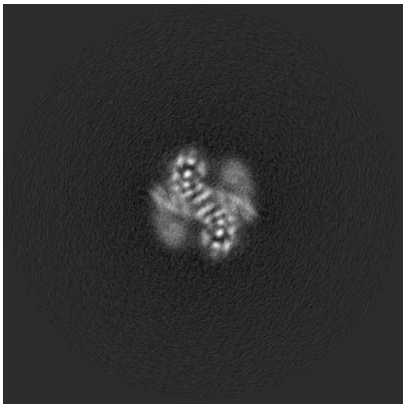
6.3.2 Raw map



X Index: 166



Y Index: 143

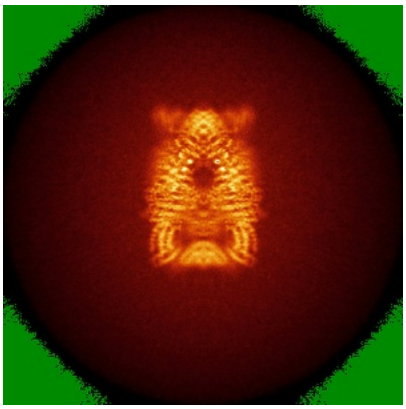


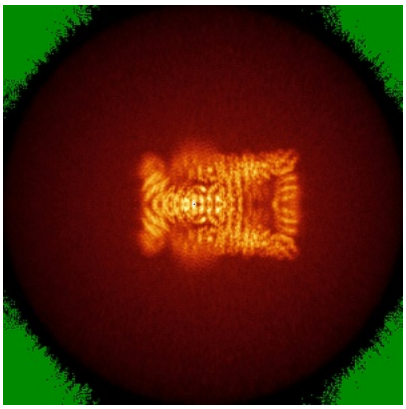
Z Index: 128

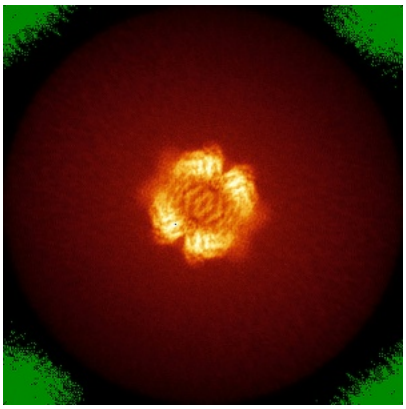
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map

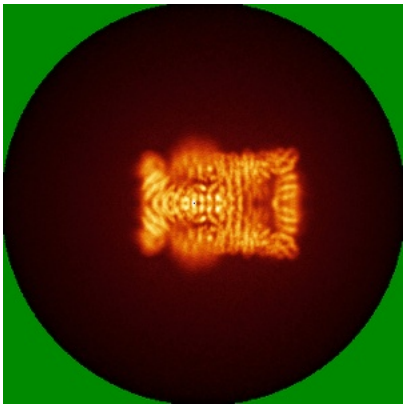

X

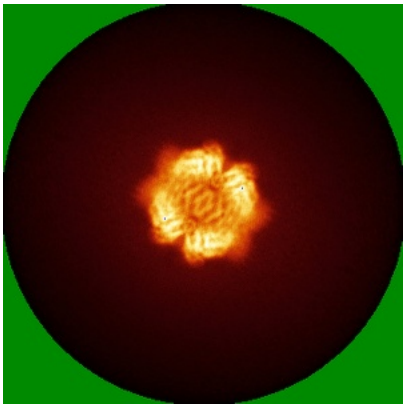

Y


Z

6.4.2 Raw map

X

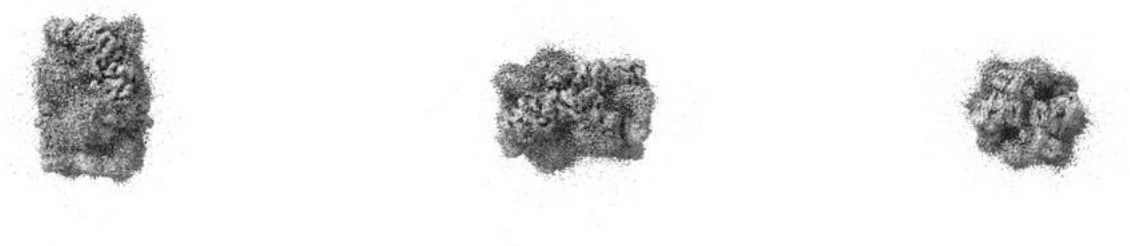

Y


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 0.01. 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.

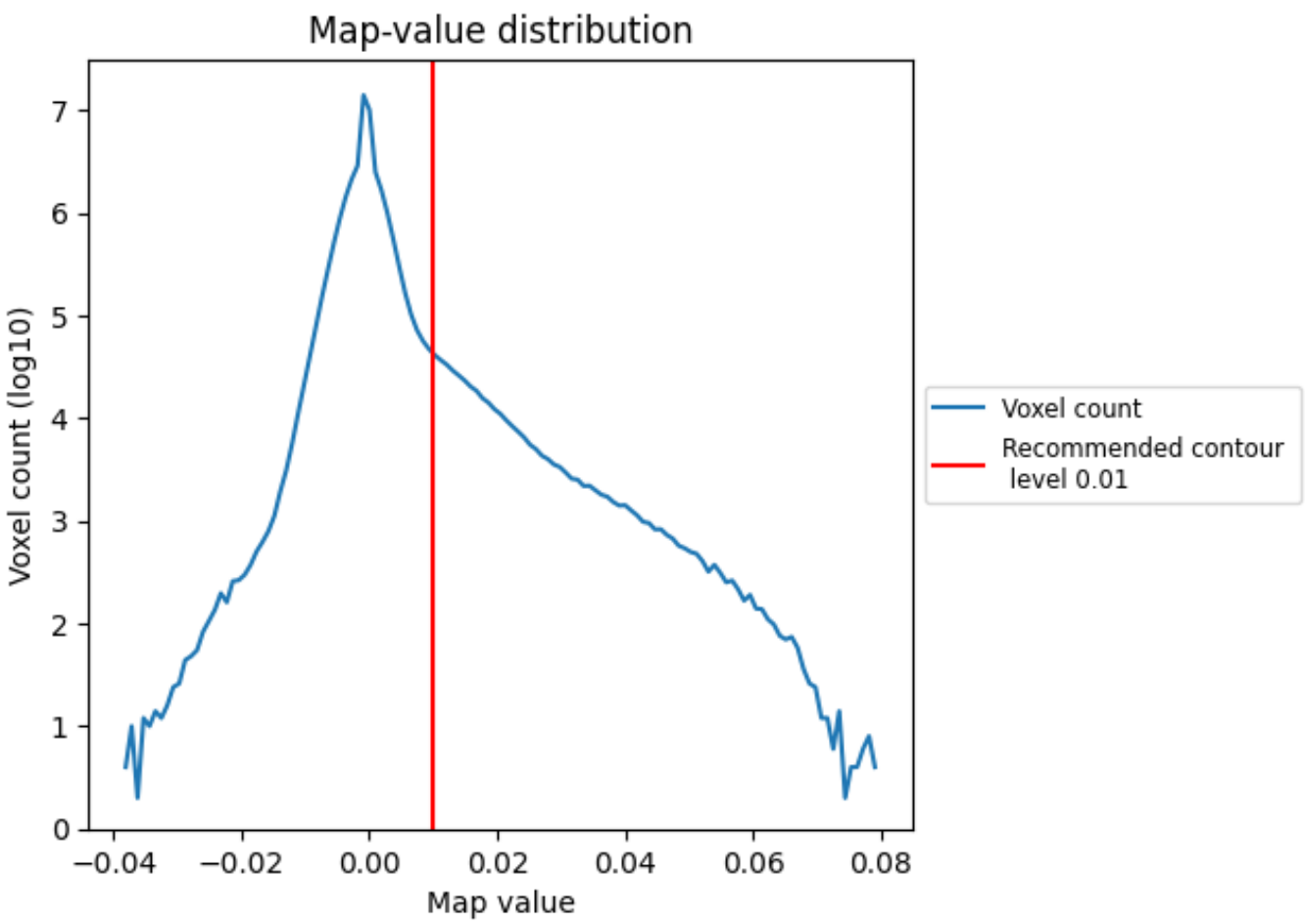
6.6 Mask visualisation (i)

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

7 Map analysis (i)

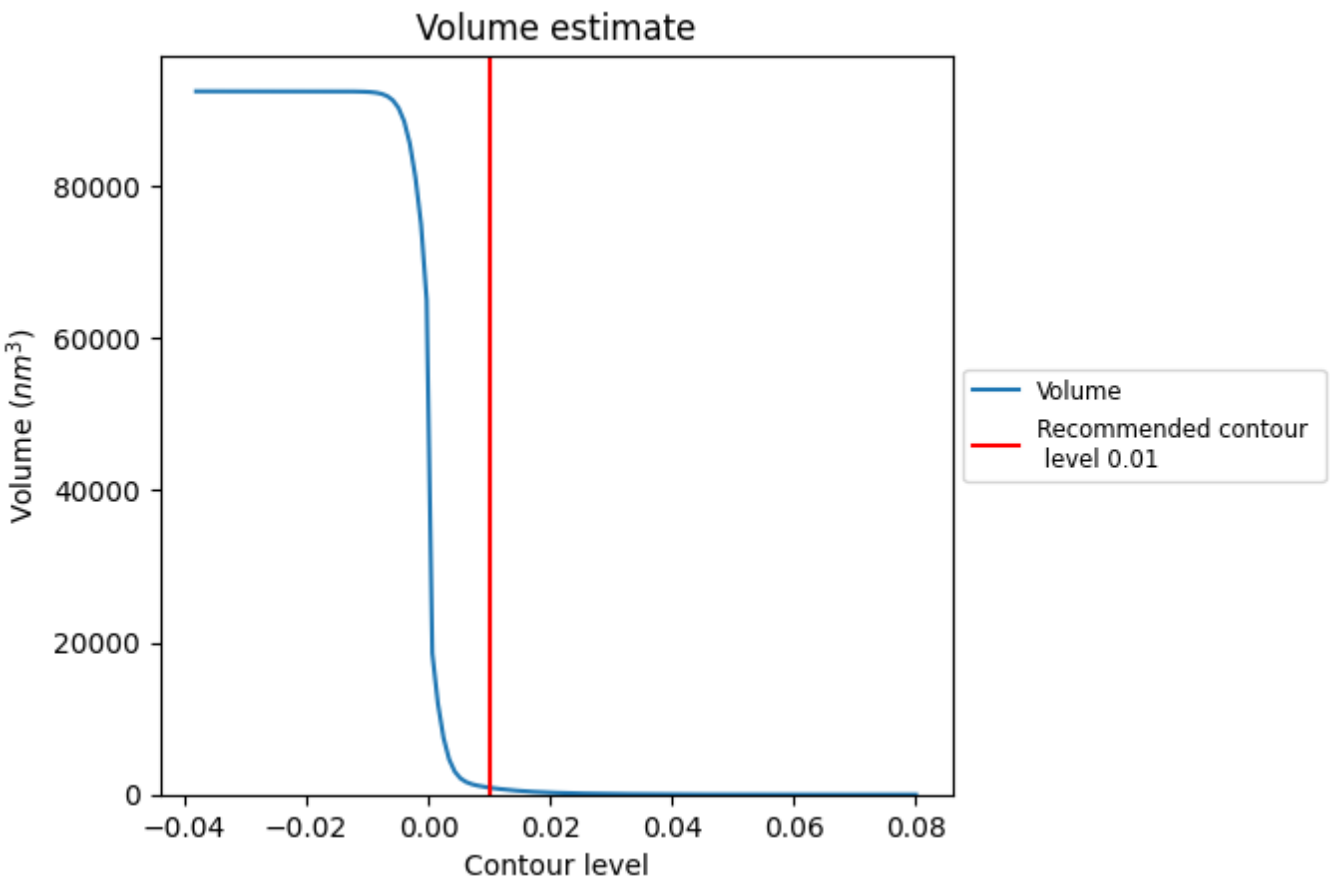
This section contains the results of statistical analysis of the map.

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.

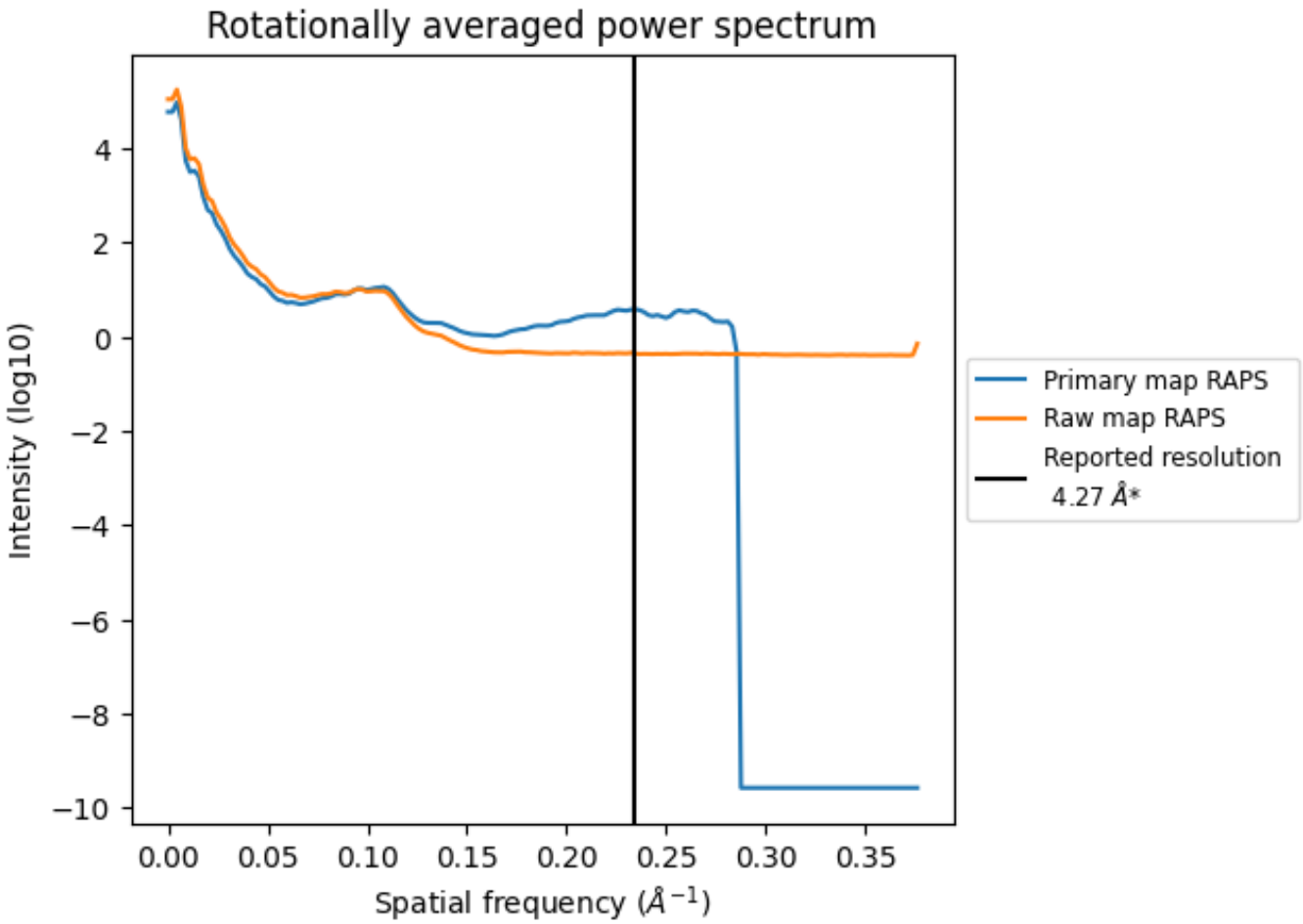
7.2 Volume estimate (i)



The volume at the recommended contour level is 910 nm^3; this corresponds to an approximate mass of 822 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)

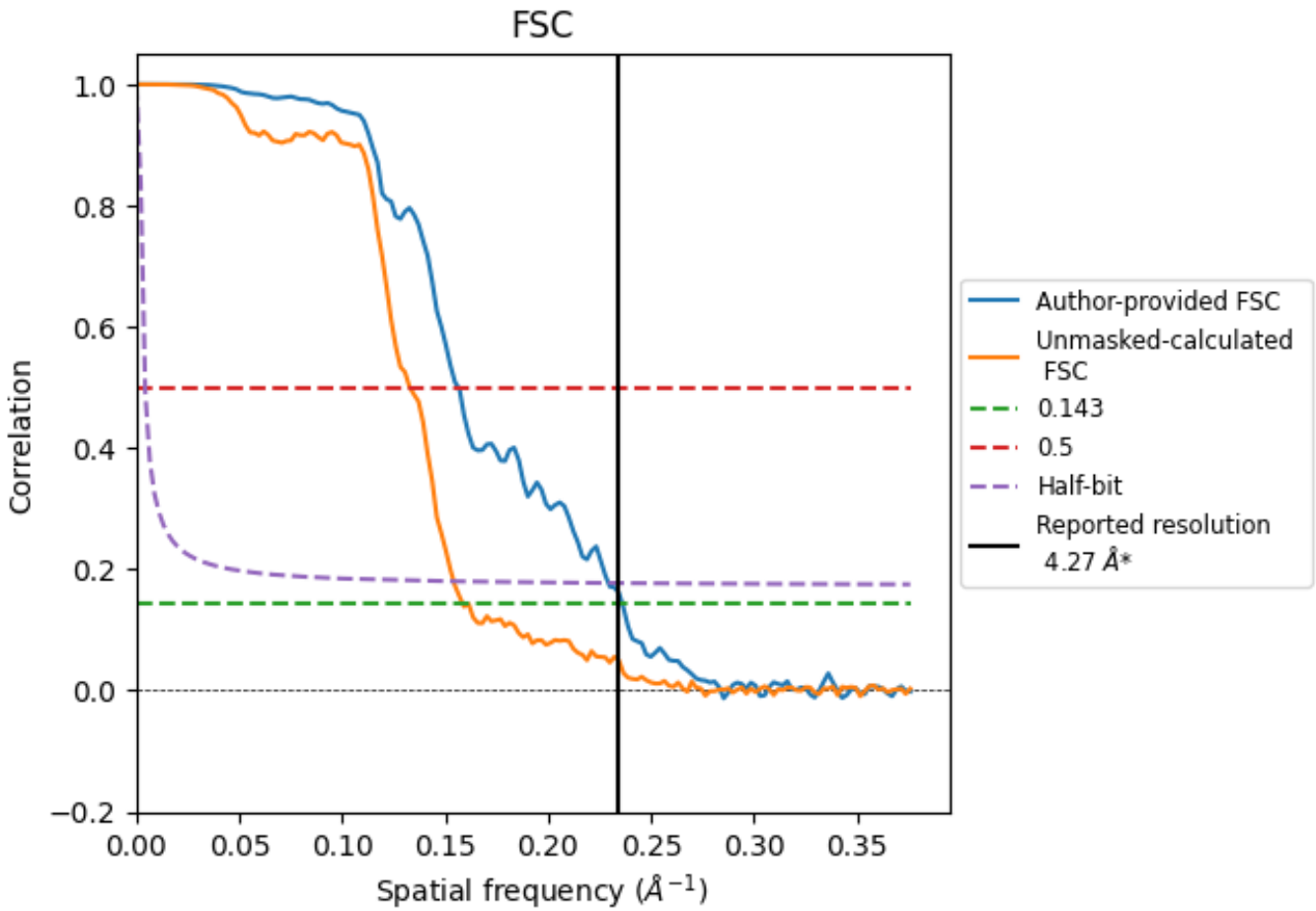


*Reported resolution corresponds to spatial frequency of 0.234 Å^{-1}

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 0.234 Å^{-1}

8.2 Resolution estimates (i)

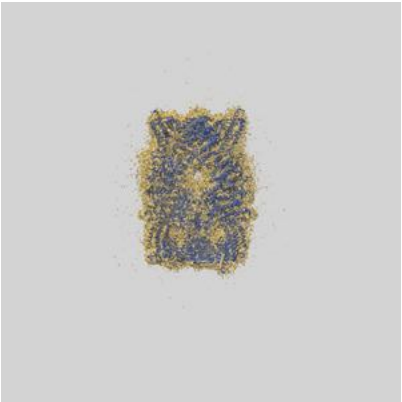
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.27	-	-
Author-provided FSC curve	4.24	6.39	4.36
Unmasked-calculated*	6.31	7.52	6.49

*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 6.31 differs from the reported value 4.27 by more than 10 %

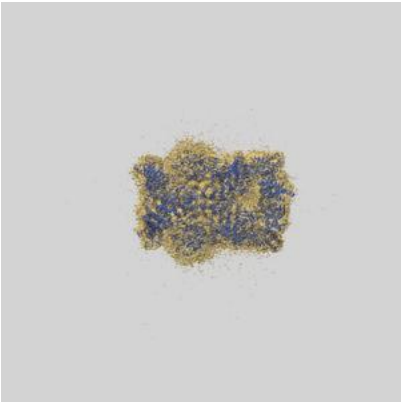
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-65178 and PDB model 9VM6. Per-residue inclusion information can be found in section 3 on page 5.

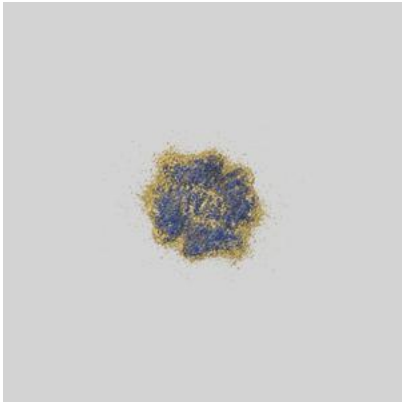
9.1 Map-model overlay (i)



X



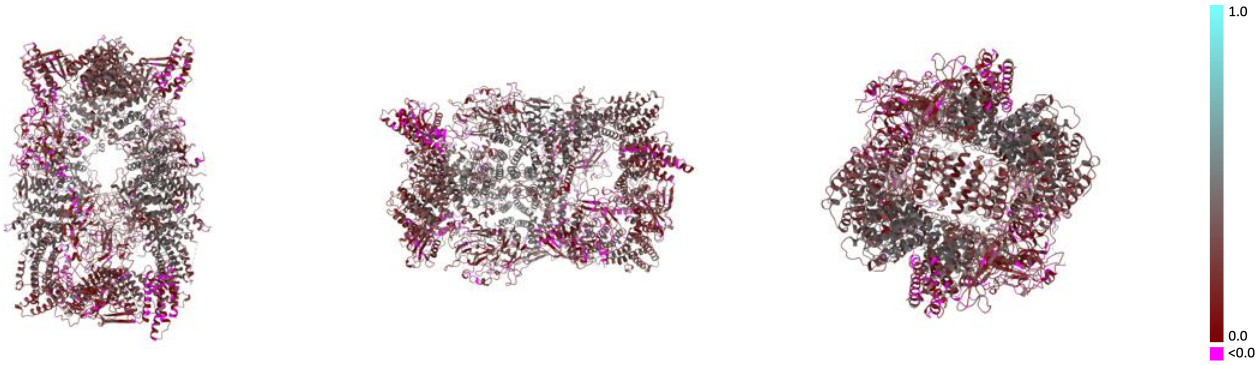
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

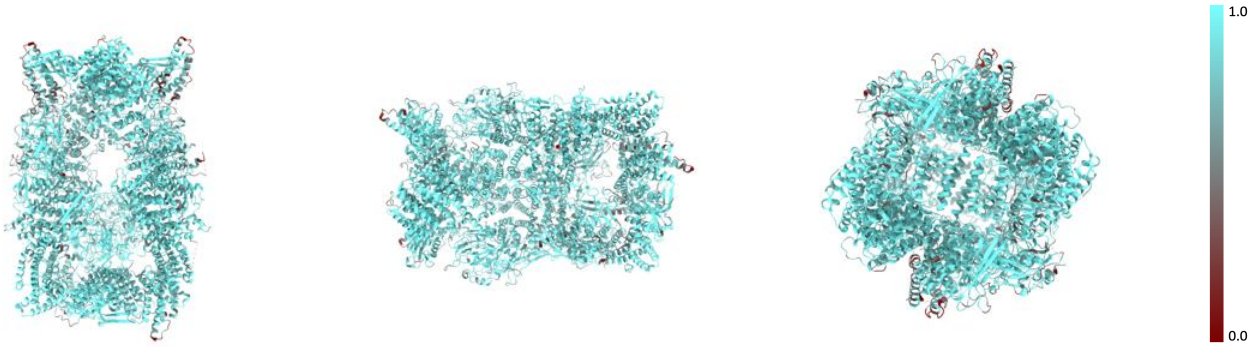
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

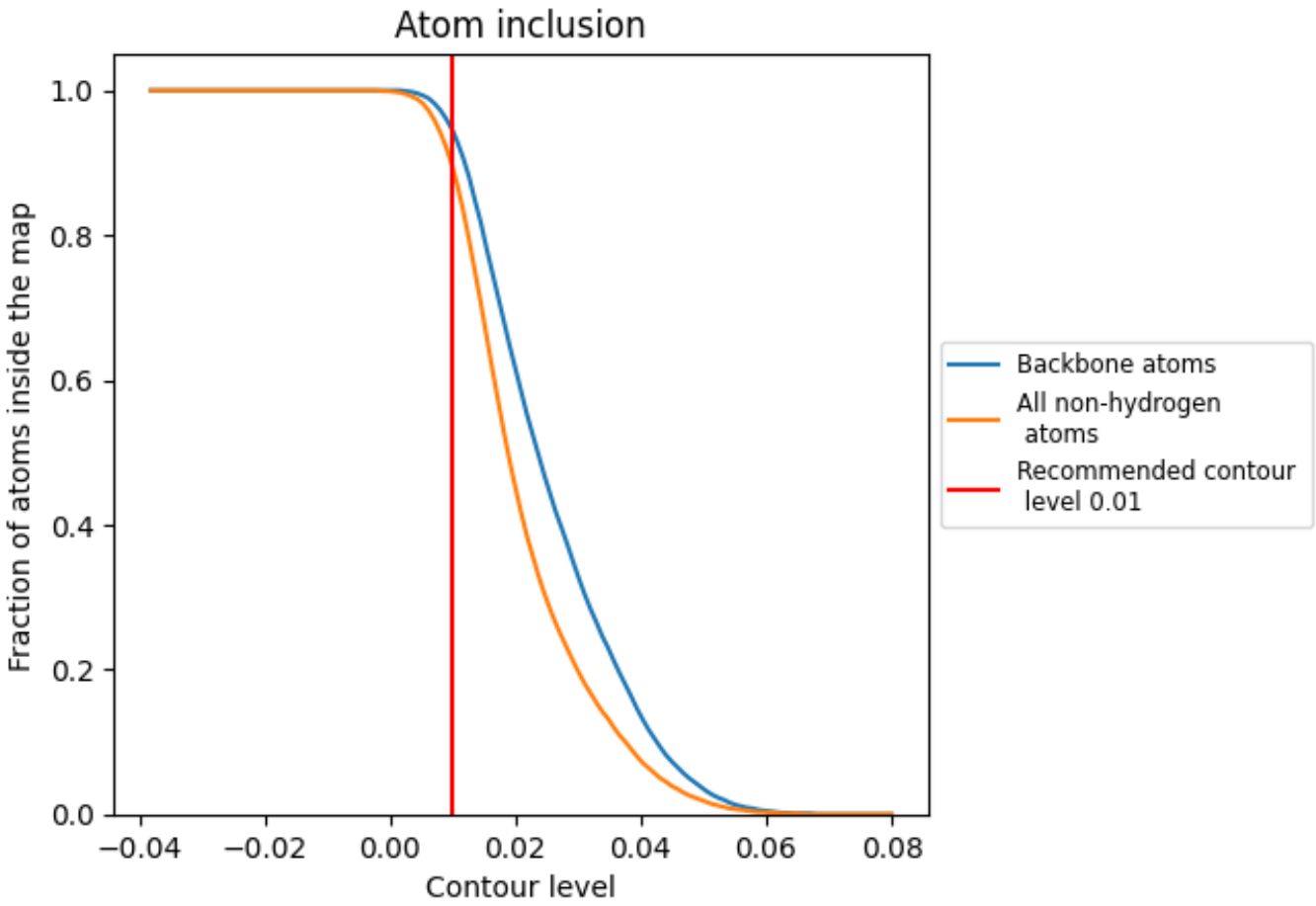
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 89% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8940	0.2700
A	0.8840	0.2410
B	0.8850	0.2430
C	0.9040	0.2990
D	0.9020	0.2980