wwPDB EM Validation Summary Report ⓘ

Aug 30, 2026 – 12:16 AM JST

PDB ID	:	9VM3 / pdb_00009vm3
EMDB ID	:	EMD-65175
Title	:	Structure of DOCK6-Cdc42 complex
Authors	:	Kukimoto-Niino, M.; Katsura, K.; Ishizuka-Katsura, Y.; Yonemochi, M.; Hanada, K.; Shirouzu, M.
Deposited on	:	2025-06-27
Resolution	:	4.52 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

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

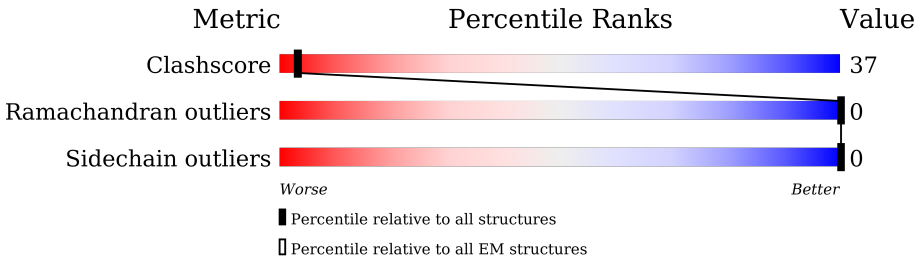
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

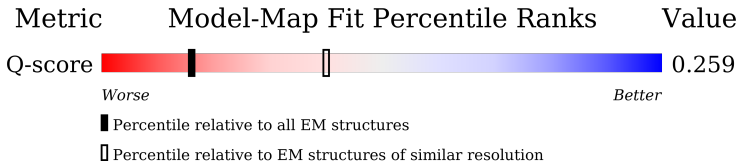
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.52 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	2506 (4.02 - 5.02)

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	32% 50% 18%
1	C	2053	32% 50% 18%
2	B	195	8% 39% 52% 9%
2	D	195	7% 42% 49% 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 29720 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
1	A	1688	Total	C	N	O	S	0	0
			13471	8606	2331	2475	59		
1	C	1688	Total	C	N	O	S	0	0
			13471	8606	2331	2475	59		

There are 12 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

- Molecule 2 is a protein called Cell division control protein 42 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	178	Total	C	N	O	S	0	0
			1389	894	221	267	7		
2	D	178	Total	C	N	O	S	0	0
			1389	894	221	267	7		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	GLY	-	expression tag	UNP P60953

Continued on next page...

Continued from previous page...

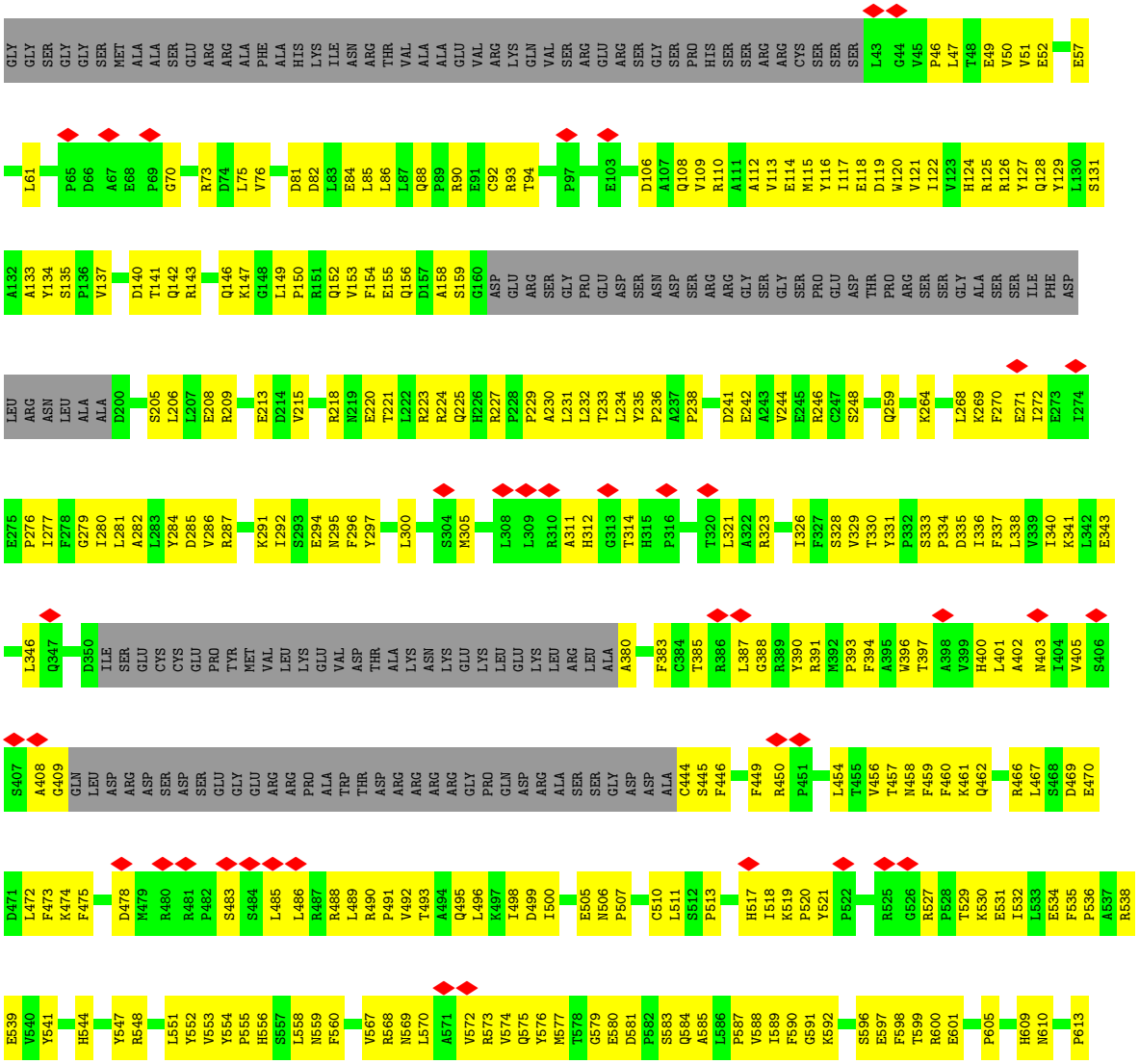
Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	SER	-	expression tag	UNP P60953
B	-4	SER	-	expression tag	UNP P60953
B	-3	GLY	-	expression tag	UNP P60953
B	-2	SER	-	expression tag	UNP P60953
B	-1	SER	-	expression tag	UNP P60953
B	0	GLY	-	expression tag	UNP P60953
B	15	ALA	GLY	engineered mutation	UNP P60953
B	188	SER	-	expression tag	UNP P60953
D	-6	GLY	-	expression tag	UNP P60953
D	-5	SER	-	expression tag	UNP P60953
D	-4	SER	-	expression tag	UNP P60953
D	-3	GLY	-	expression tag	UNP P60953
D	-2	SER	-	expression tag	UNP P60953
D	-1	SER	-	expression tag	UNP P60953
D	0	GLY	-	expression tag	UNP P60953
D	15	ALA	GLY	engineered mutation	UNP P60953
D	188	SER	-	expression tag	UNP P60953

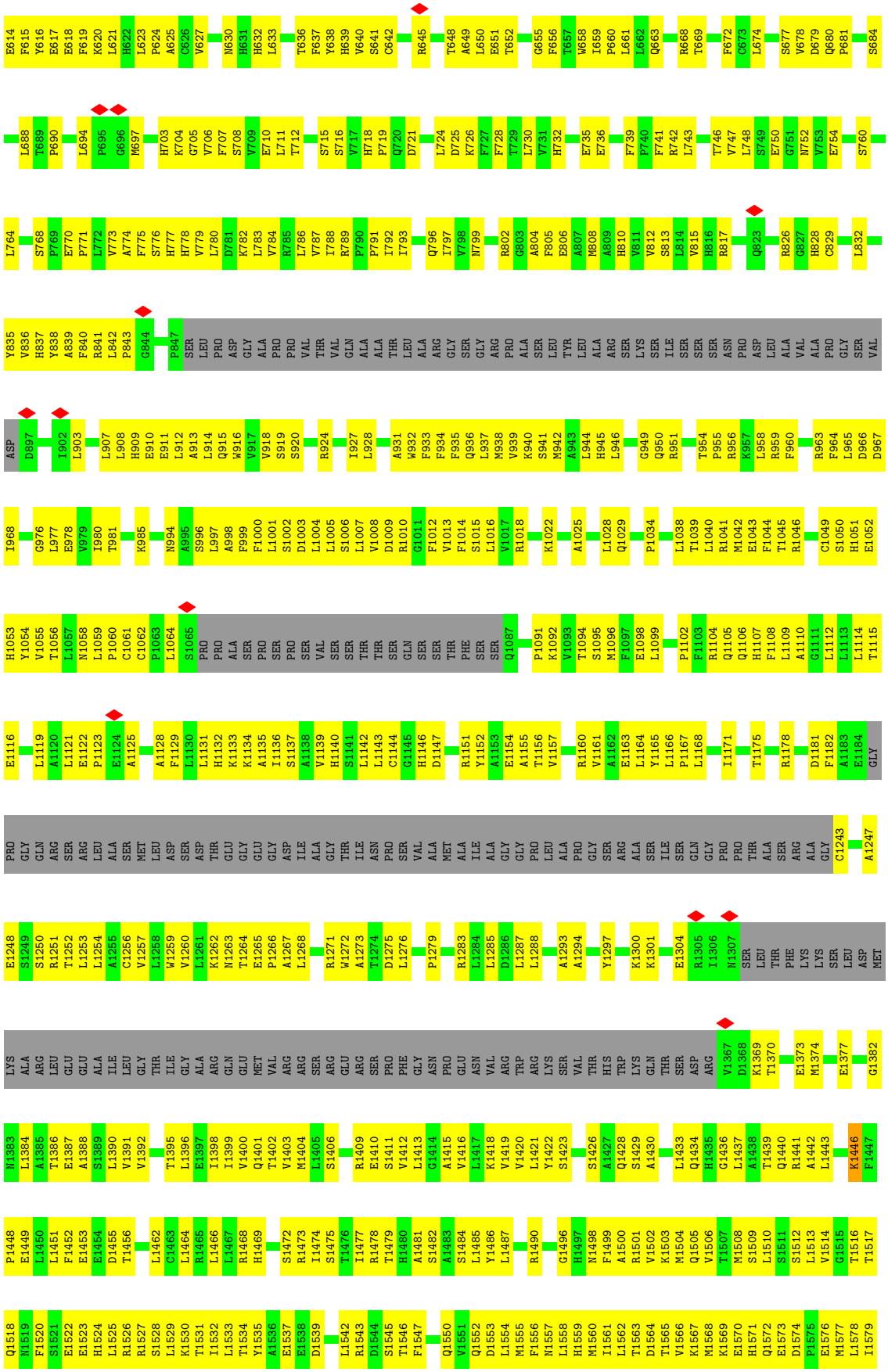
3 Residue-property plots (i)

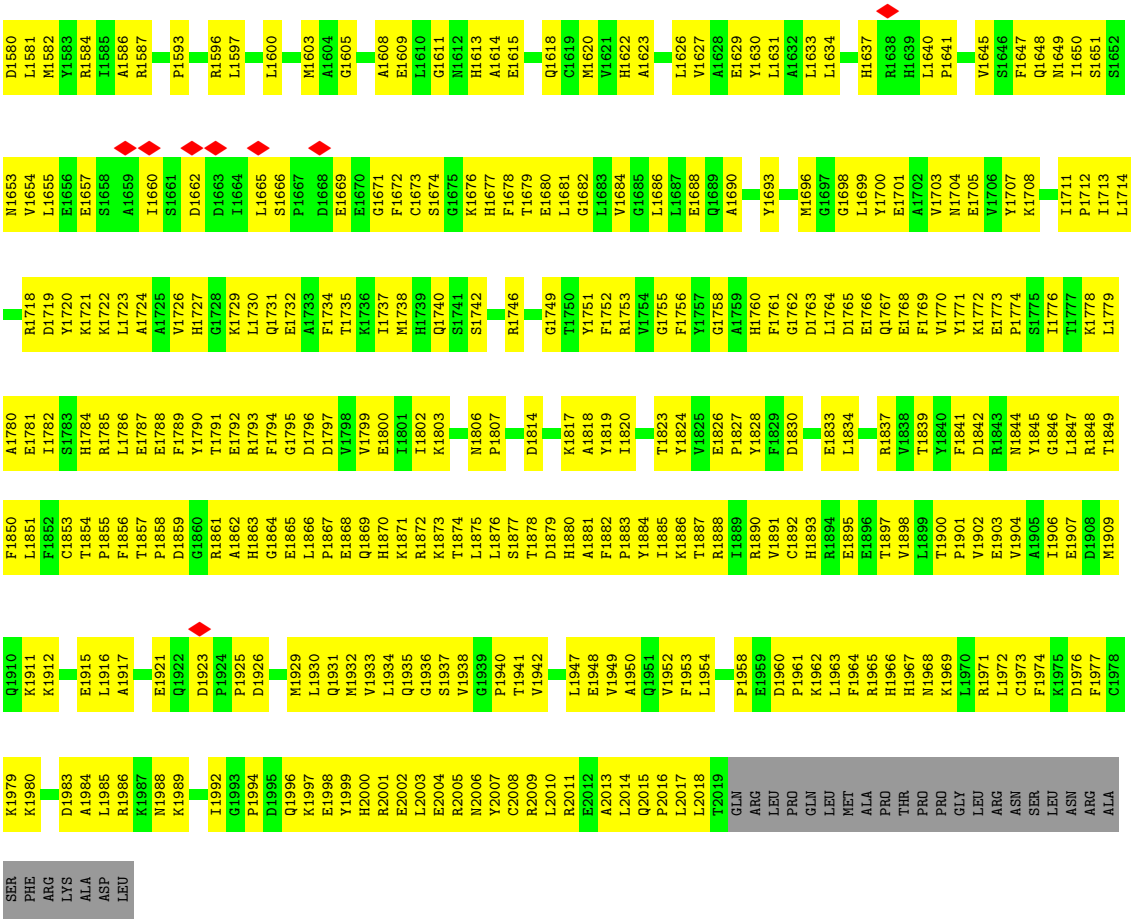
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

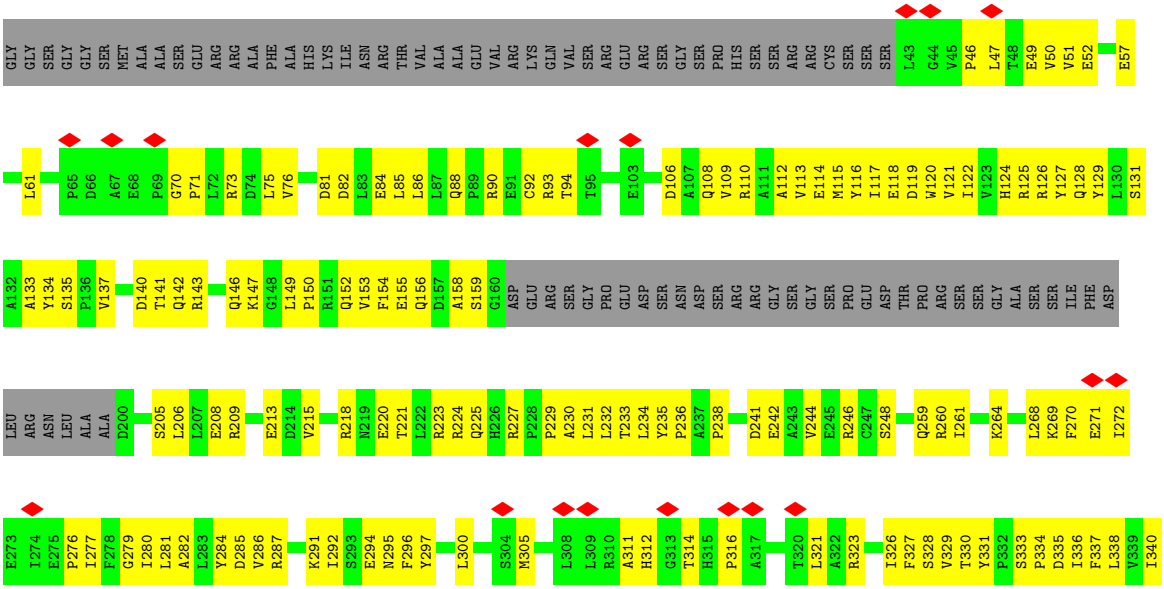


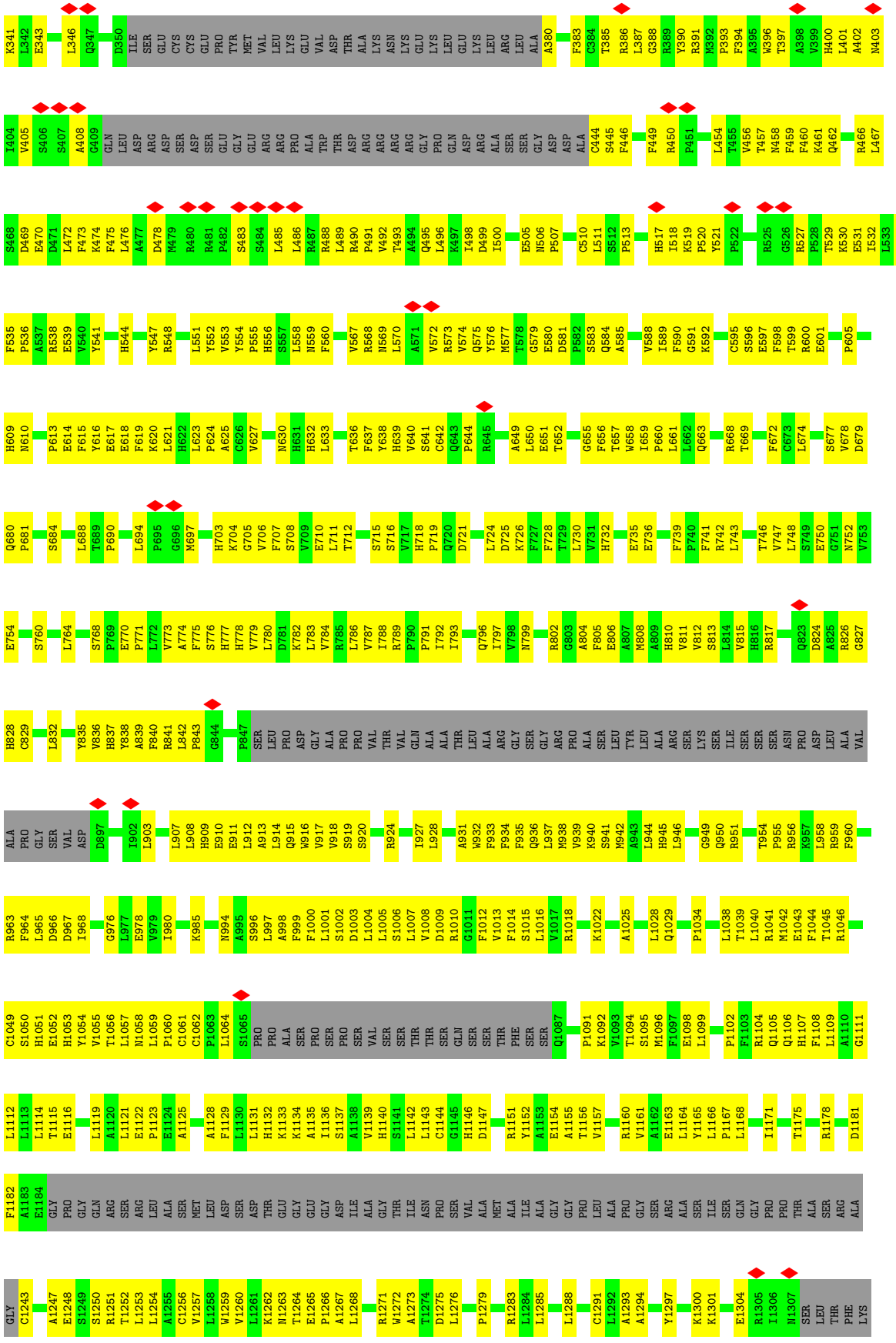


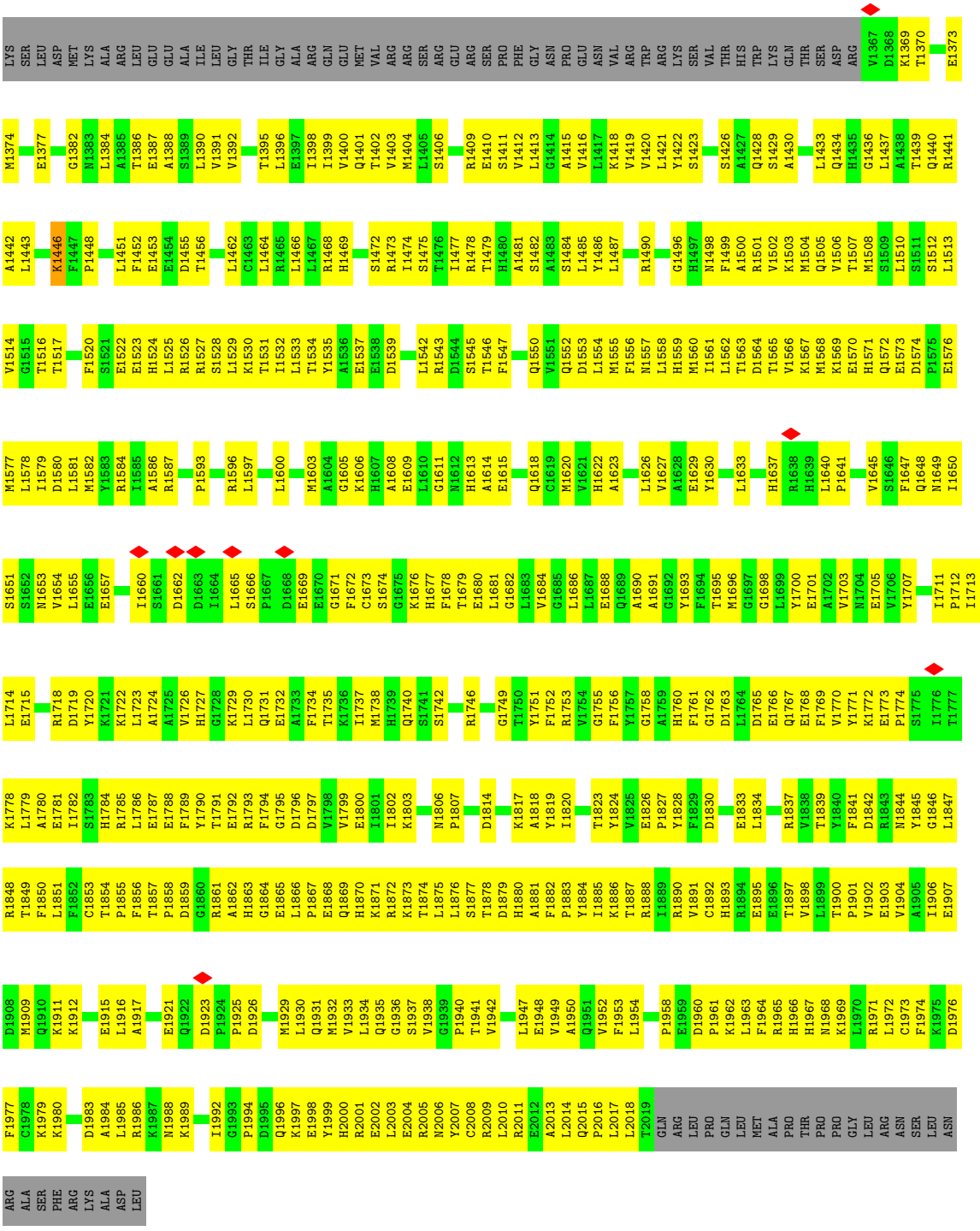


• Molecule 1: Dedicator of cytokinesis protein 6

Chain C:

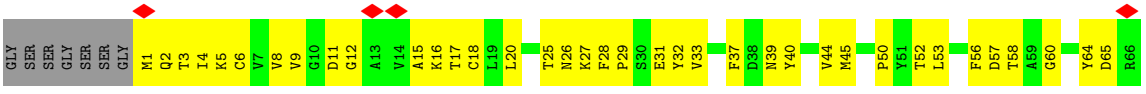


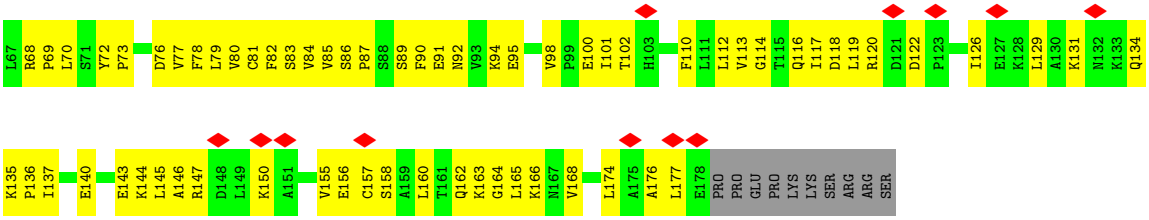

K341 L342 E343 L346 Q347 D350 ILE SER GLU CYS CYS GLU PRO TYR MET VAL LEU LYS GLU VAL ASP THR ALA LYS ASN LYS GLU LYS LEU GLU LYS LEU ARG LEU ALA A380 F383 C384 T385 R386 L387 G388 R389 Y390 R391 M392 P393 F394 A395 W396 T397 A398 V399 H400 L401 A402 N403
I404 V405 S406 S407 A408 G409 GLN LEU ASP ARG 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 ASP ALA C444 S445 F446 F449 R450 P451 L454 T455 V456 T457 N458 F459 F460 K461 Q462 R466 L467
S468 D469 E470 D471 L472 F473 K474 F475 L476 A477 D478 M479 R480 R481 P482 S483 S484 L485 L486 R487 R488 L489 R490 P491 V492 T493 A494 Q495 L496 K497 I498 D499 I500 E505 N506 P507 C510 L511 S512 P513 H517 I518 K519 P520 Y521 P522 R525 G526 R527 P528 T529 K530 E531 I532 L533 E534
F535 P536 A537 R538 E539 V540 Y541 H544 Y547 R548 L551 Y552 V553 Y554 P555 H556 S557 L558 N559 F560 V567 R568 N569 L570 A571 V572 R573 V574 Q575 Y576 M577 T578 G579 E580 D581 P582 S583 Q584 A585 V588 I589 F590 G591 K592 C595 S596 E597 F598 T599 R600 E601 P605
H609 N610 P613 E614 F615 Y616 E617 E618 F619 K620 L621 H622 L623 P624 A625 C626 V627 N630 H631 H632 L633 T636 F637 Y638 H639 V640 S641 C642 Q643 P644 R645 A649 L650 E651 T652 G655 F656 T657 W658 I659 P660 L661 L662 Q663 R668 T669 F672 C673 L674 S677 V678 D679
Q680 P681 S684 L688 T689 P690 L694 P695 G696 M697 H703 K704 G705 V706 F707 S708 V709 E710 L711 T712 S715 S716 V717 H718 P719 Q720 D721 L724 D725 K726 F727 F728 T729 L730 V731 H732 E735 E736 F739 P740 F741 R742 L743 T746 V747 L748 S749 E750 G751 N752 V753
E754 S760 L764 S768 P769 E770 P771 L772 V773 A774 F775 S776 H777 H778 V779 L780 D781 K782 L783 V784 R785 L786 V787 I788 R789 P790 P791 I792 I793 Q796 I797 V798 N799 R802 G803 A804 F805 E806 A807 M808 A809 H810 V811 V812 S813 L814 V815 H816 R817 Q823 D824 A825 R826 G827
H828 C829 L832 Y835 V836 H837 Y838 A839 F840 R841 L842 P843 G844 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 ASP D897 I902 L903 L907 L908 H909 E910 E911 L912 A913 L914 Q915 W916 V917 V918 S919 S920 R924 I927 L928 A931 W932 F933 F934 F935 Q936 L937 M938 V939 K940 S941 M942 A943 L944 H945 L946 G949 Q950 R951 T954 P955 R956 K957 L958 R959 F960
R963 F964 L965 D966 D967 I968 G976 L977 E978 V979 I980 K985 N994 A995 S996 L997 A998 F999 F1000 L1001 S1002 D1003 L1004 L1005 S1006 L1007 V1008 D1009 R1010 G1011 F1012 V1013 F1014 S1015 L1016 V1017 R1018 K1022 A1025 L1028 Q1029 P1034 L1038 T1039 L1040 R1041 M1042 E1043 F1044 T1045 R1046
C1049 S1050 H1051 E1052 H1053 Y1054 V1055 T1056 L1057 N1058 L1059 P1060 C1061 C1062 P1063 L1064 S1065 PRO PRO ALA SER PRO SER PRO SER VAL SER SER THR THR SER GLN SER SER THR PHE SER SER Q1087 P1091 K1092 V1093 T1094 S1095 M1096 F1097 E1098 L1099 P1102 F1103 R1104 Q1105 Q1106 H1107 F1108 L1109 A1110 G1111
L1112 L1113 L1114 T1115 E1116 L1119 A1120 L1121 E1122 P1123 E1124 A1125 A1128 F1129 L1130 L1131 H1132 K1133 K1134 A1135 I1136 S1137 A1138 V1139 H1140 S1141 L1142 L1143 C1144 G1145 H1146 D1147 R1151 Y1152 A1153 E1154 A1155 T1156 V1157 R1160 V1161 A1162 E1163 L1164 Y1165 L1166 P1167 L1168 I1171 T1175 R1178 D1181
F1182 A1183 E1184 GLY PRO GLY GLN ARG SER ARG LEU 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
GLY C1243 A1247 E1248 S1249 S1250 R1251 T1252 L1253 L1254 A1255 C1256 V1257 L1258 W1259 V1260 L1261 K1262 N1263 T1264 E1265 P1266 A1267 L1268 R1271 W1272 A1273 T1274 D1275 L1276 P1279 R1283 L1284 L1285 L1288 C1291 L1292 A1293 A1294 Y1297 K1300 K1301 E1304 R1305 I1306 N1307 SER LEU THR PHE LYS



• Molecule 2: Cell division control protein 42 homolog

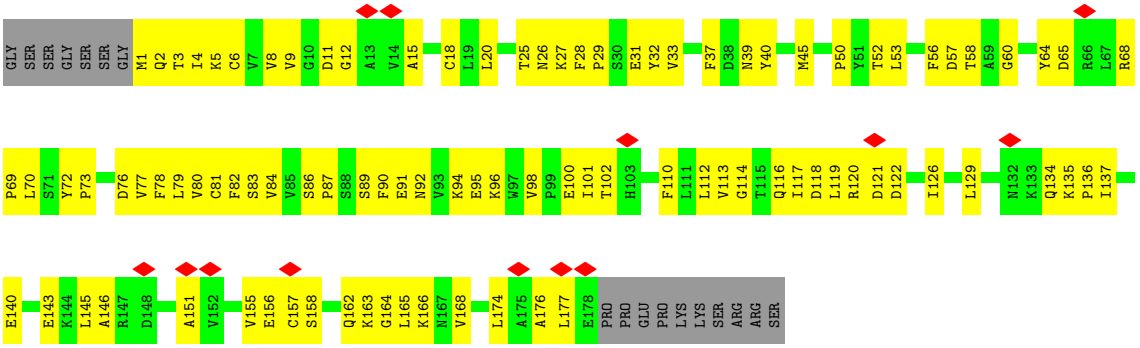
Chain B:





• Molecule 2: Cell division control protein 42 homolog

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	370326	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 ($e^-/Å^2$)	48.5	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	0.077	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	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

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	0.34	0/13787	0.53	2/18706 (0.0%)
1	C	0.34	0/13787	0.53	2/18706 (0.0%)
2	B	0.22	0/1419	0.43	0/1932
2	D	0.22	0/1419	0.43	0/1932
All	All	0.33	0/30412	0.52	4/41276 (0.0%)

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	C	1446	LYS	CA-C-N	-5.11	116.59	122.52
1	C	1446	LYS	C-N-CA	-5.11	116.59	122.52
1	A	1446	LYS	CA-C-N	-5.11	116.60	122.52
1	A	1446	LYS	C-N-CA	-5.11	116.60	122.52

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	13471	0	13448	1040	0
1	C	13471	0	13448	1021	0
2	B	1389	0	1407	105	0
2	D	1389	0	1407	90	0
All	All	29720	0	29710	2202	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 37.

The worst 5 of 2202 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:259:GLN:HB2	1:A:329:VAL:HB	1.45	0.99
1:C:259:GLN:HB2	1:C:329:VAL:HB	1.45	0.96
1:A:1849:THR:HA	1:A:1876:LEU:O	1.67	0.93
1:C:1849:THR:HA	1:C:1876:LEU:O	1.67	0.93
1:A:1749:GLY:HA3	1:A:1773:GLU:O	1.69	0.92

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	1672/2053 (81%)	1492 (89%)	180 (11%)	0	100	100
1	C	1672/2053 (81%)	1493 (89%)	179 (11%)	0	100	100
2	B	176/195 (90%)	162 (92%)	14 (8%)	0	100	100
2	D	176/195 (90%)	162 (92%)	14 (8%)	0	100	100
All	All	3696/4496 (82%)	3309 (90%)	387 (10%)	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	1476/1773 (83%)	1476 (100%)	0	100	100
1	C	1476/1773 (83%)	1476 (100%)	0	100	100
2	B	158/172 (92%)	158 (100%)	0	100	100
2	D	158/172 (92%)	158 (100%)	0	100	100
All	All	3268/3890 (84%)	3268 (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 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	575	GLN
1	C	1968	ASN
1	C	799	ASN
2	D	26	ASN
1	C	1550	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 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.

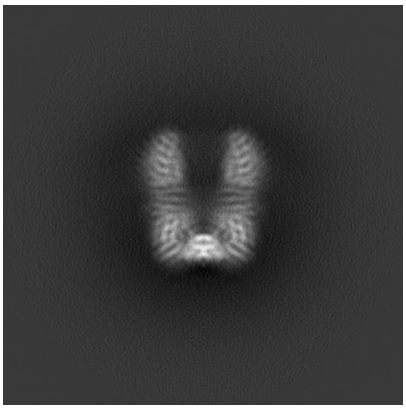
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-65175. These allow visual inspection of the internal detail of the map and identification of artifacts.

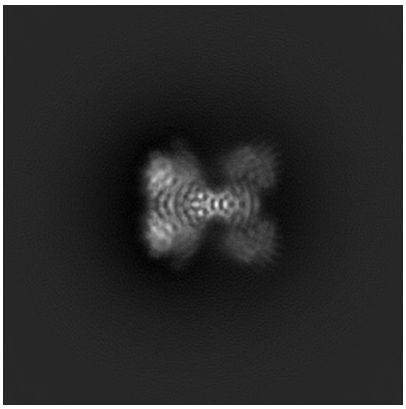
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

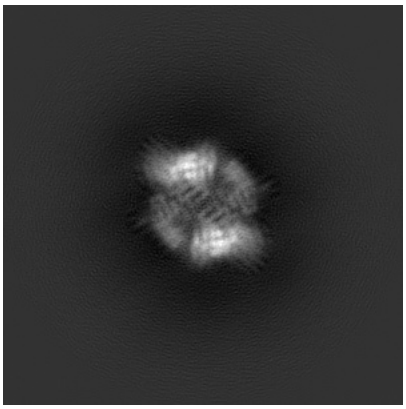
6.1.1 Primary map



X

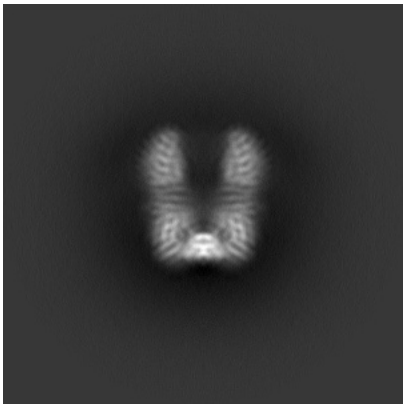


Y

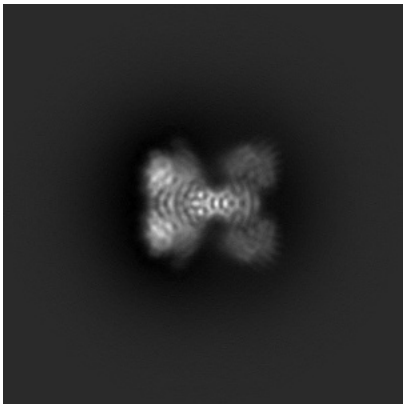


Z

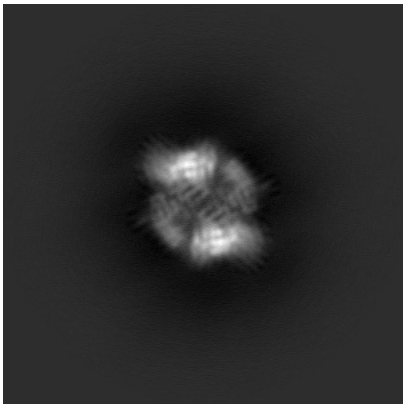
6.1.2 Raw map



X



Y

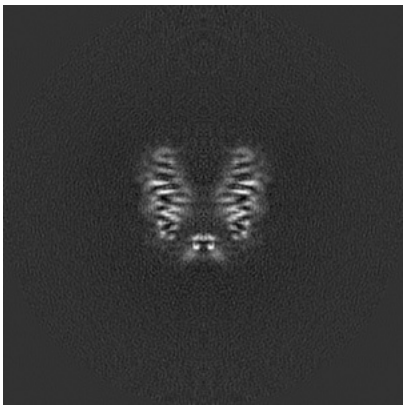


Z

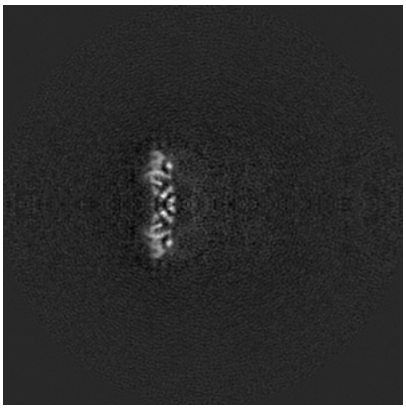
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

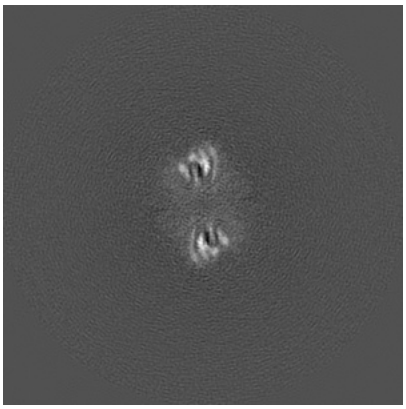
6.2.1 Primary map



X Index: 170

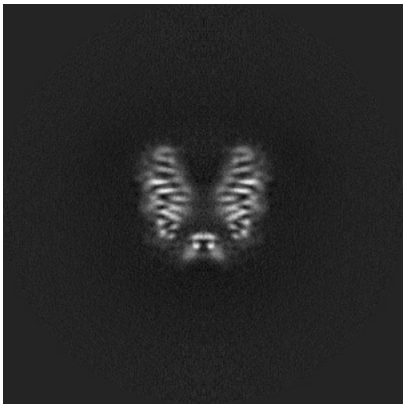


Y Index: 170

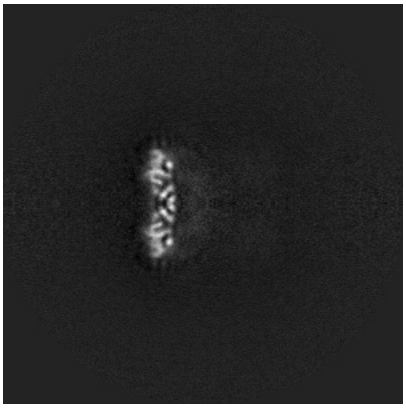


Z Index: 170

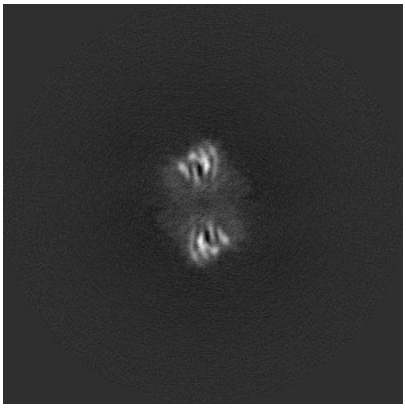
6.2.2 Raw map



X Index: 170



Y Index: 170

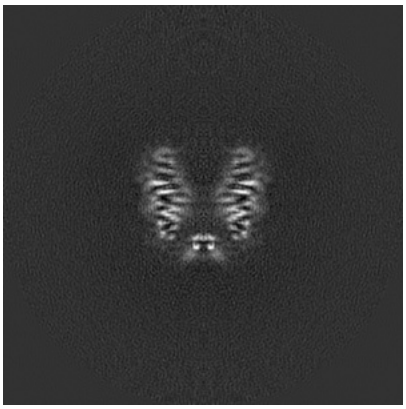


Z Index: 170

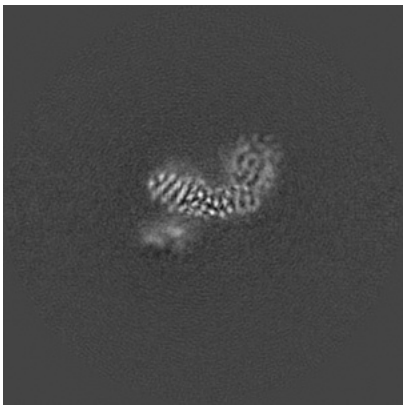
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

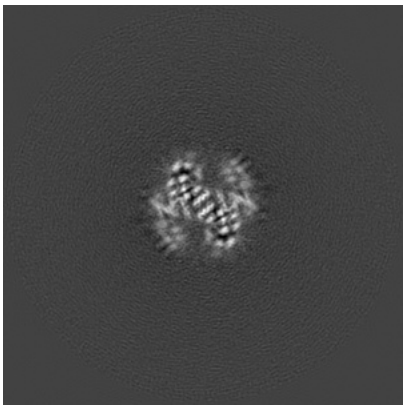
6.3.1 Primary map



X Index: 170

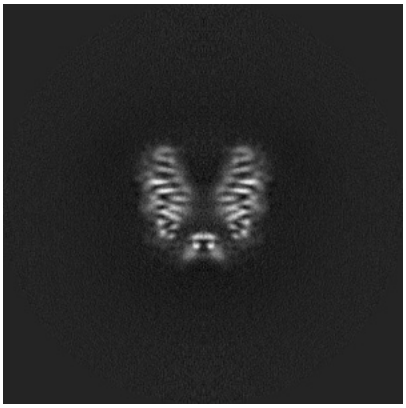


Y Index: 138

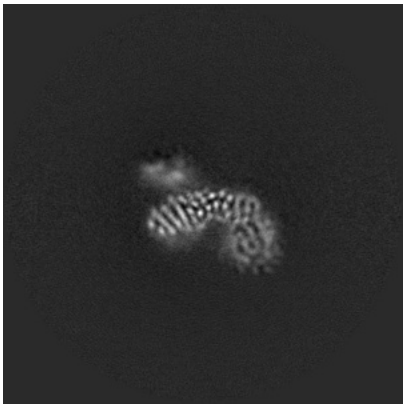


Z Index: 134

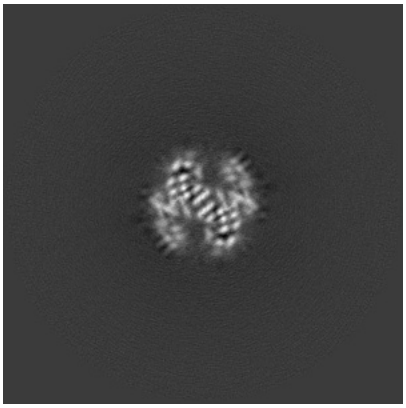
6.3.2 Raw map



X Index: 170



Y Index: 202

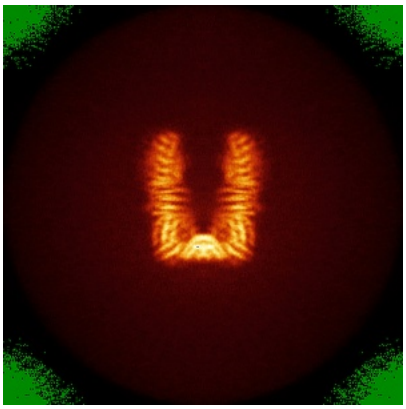


Z Index: 134

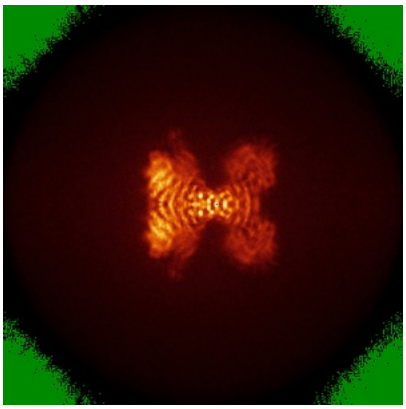
The images above show the largest variance slices of the map in three orthogonal directions.

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

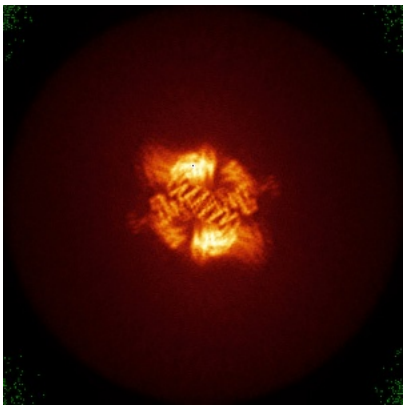
6.4.1 Primary map



X



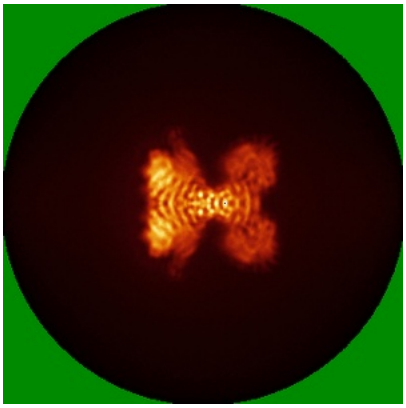
Y



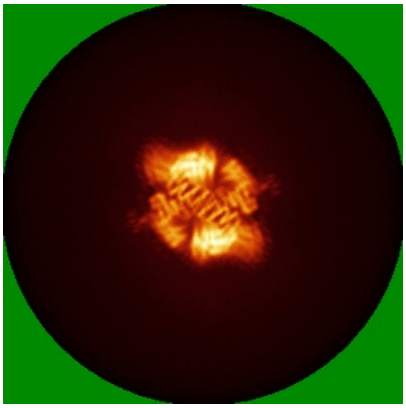
Z

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.

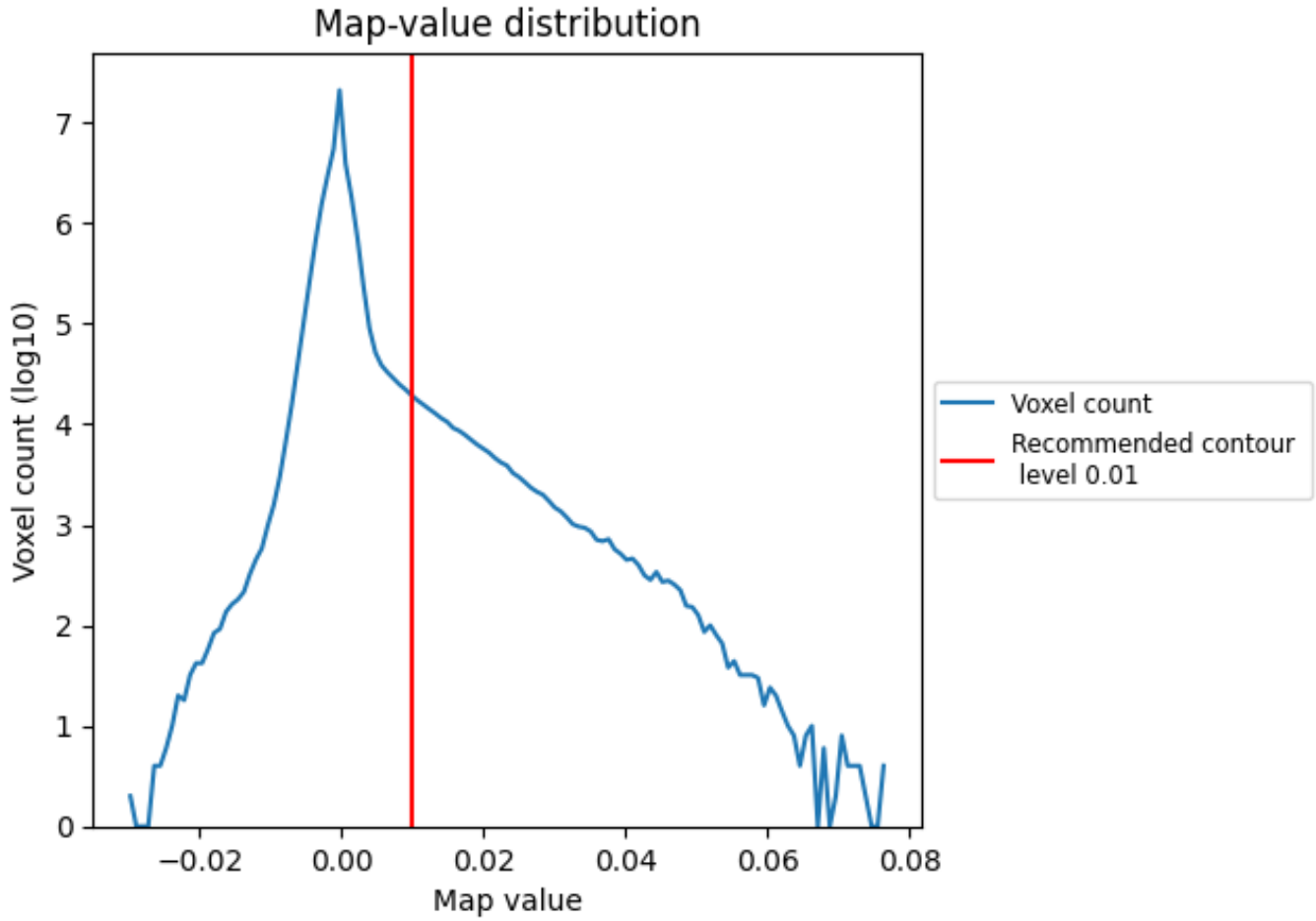
6.6 Mask visualisation (i)

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

7 Map analysis

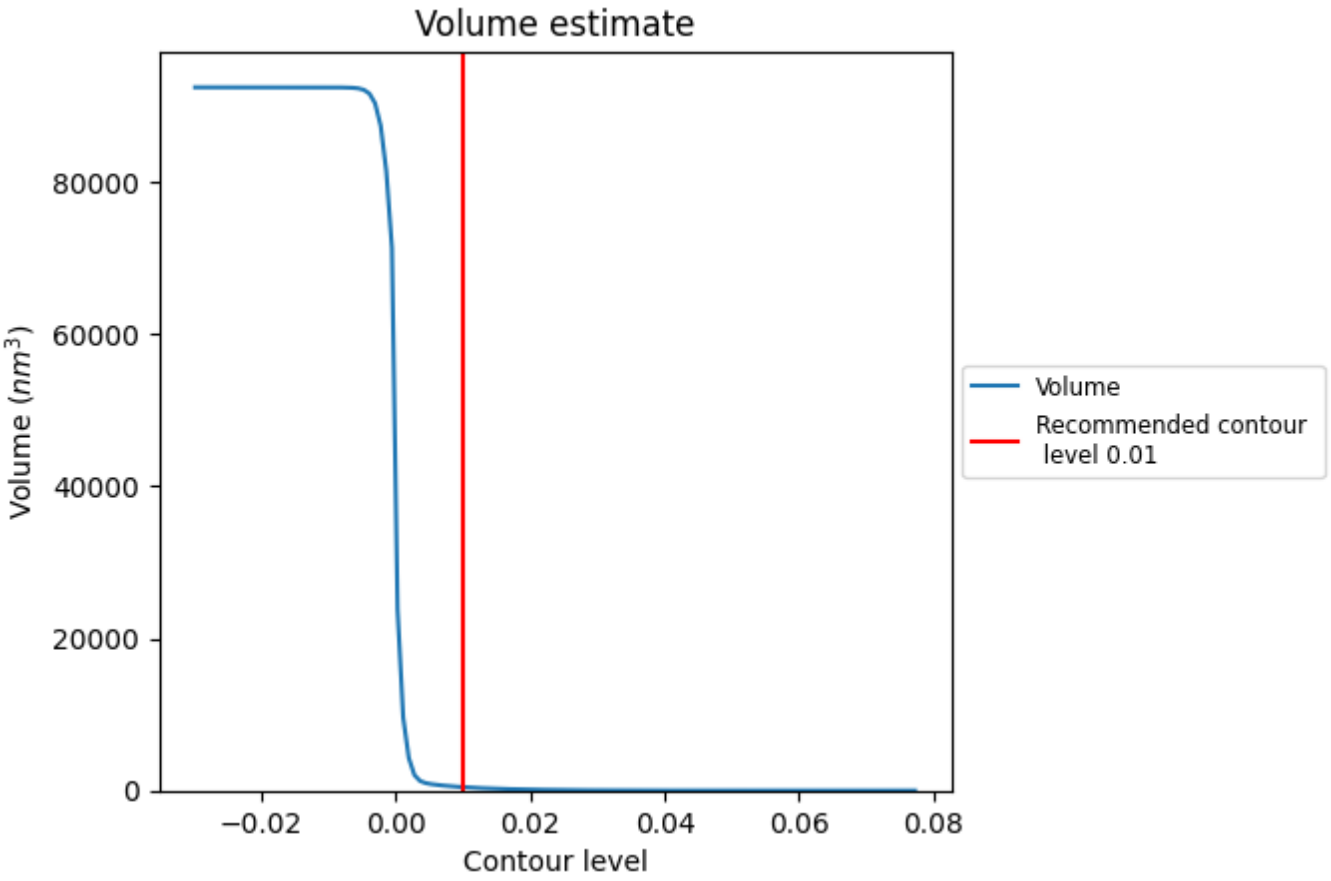
This section contains the results of statistical analysis of the map.

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.

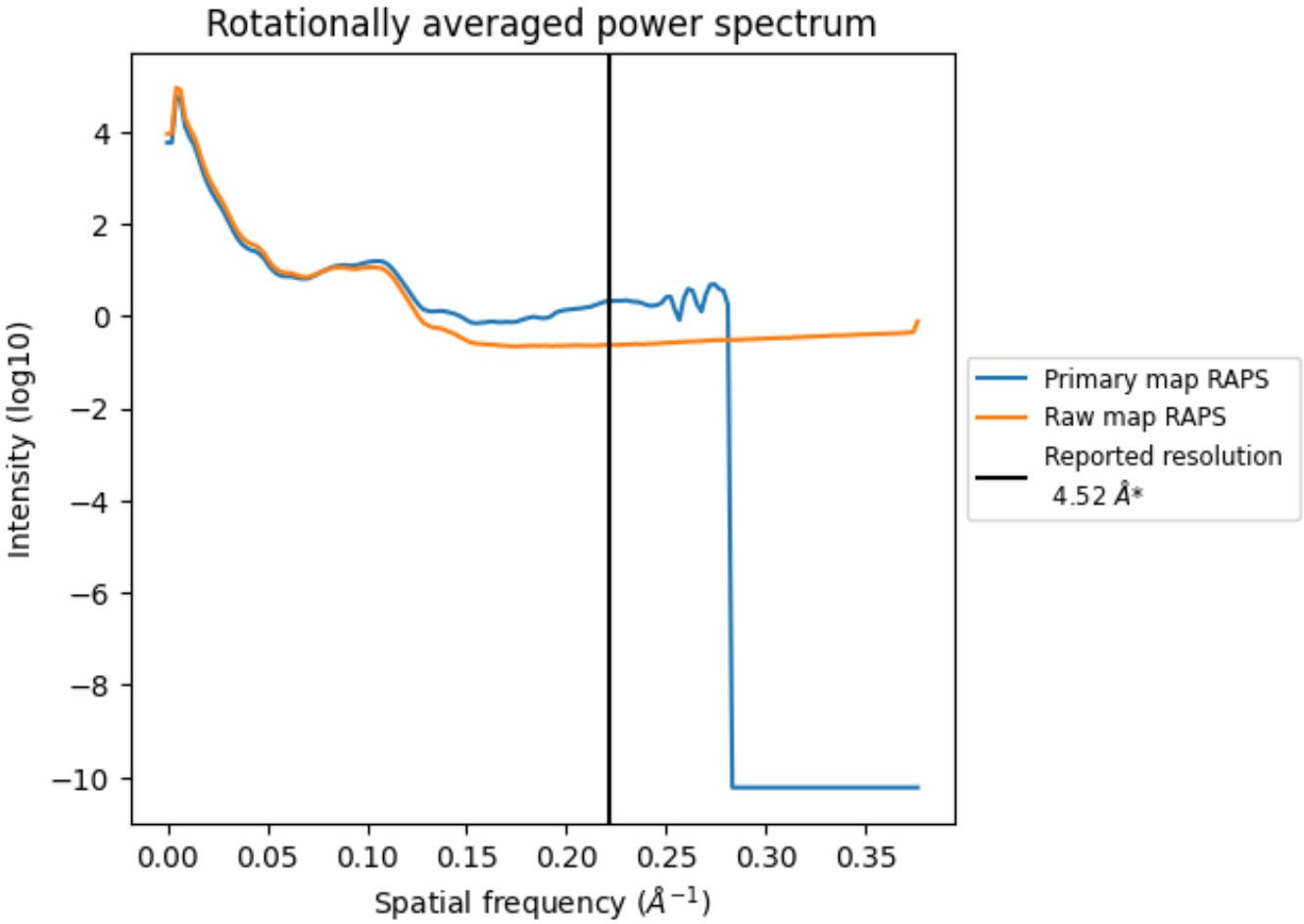
7.2 Volume estimate (i)



The volume at the recommended contour level is 453 nm^3; this corresponds to an approximate mass of 409 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)

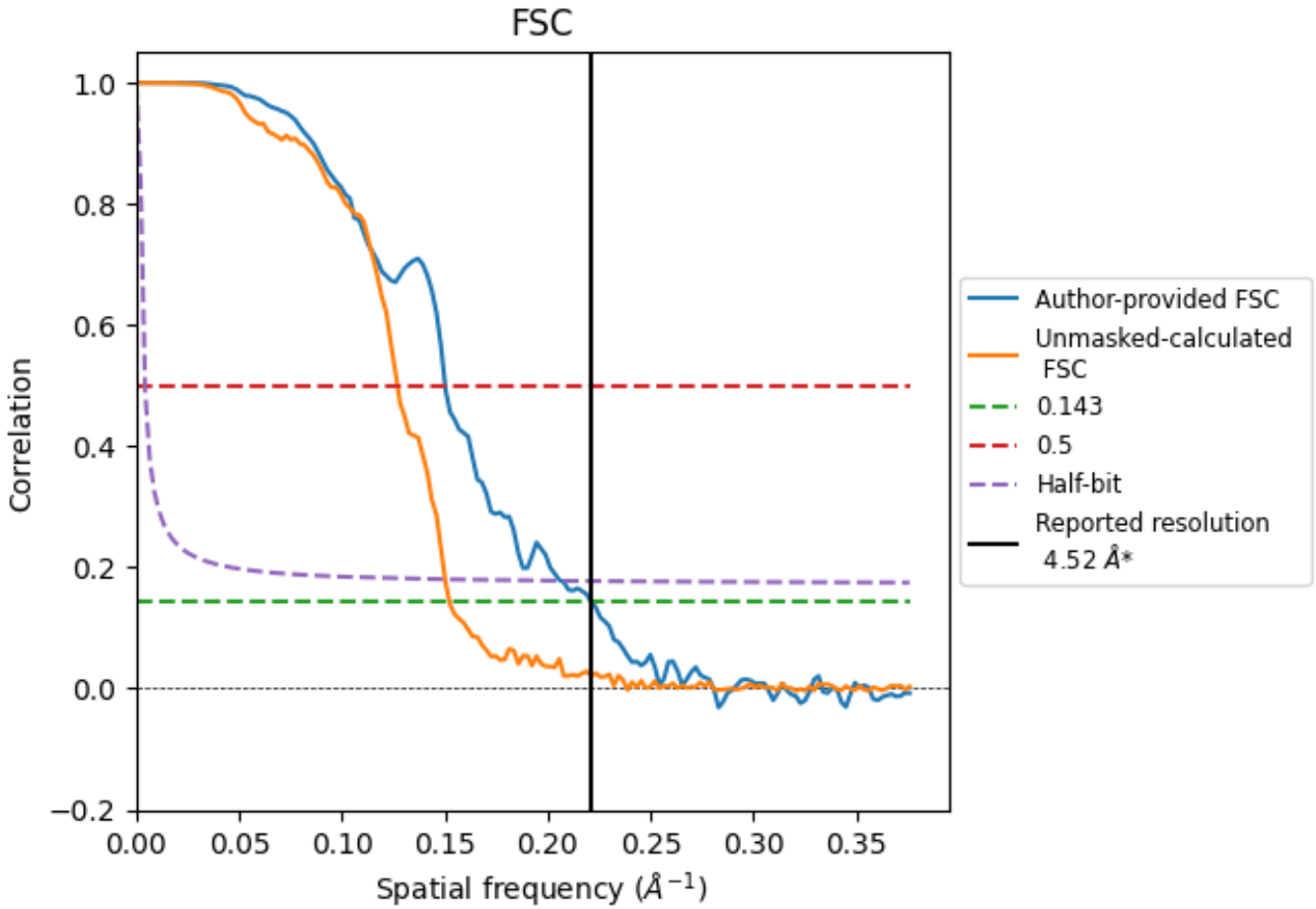


*Reported resolution corresponds to spatial frequency of 0.221 Å^{-1}

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 0.221 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.52	-	-
Author-provided FSC curve	4.52	6.66	4.84
Unmasked-calculated*	6.57	7.87	6.66

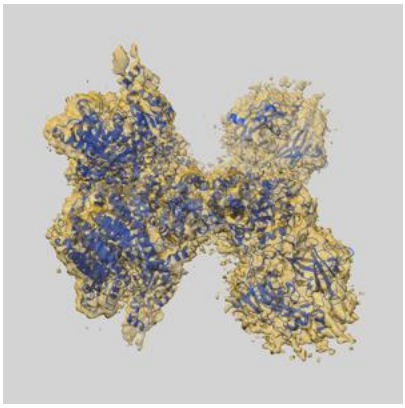
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.57 differs from the reported value 4.52 by more than 10 %

9 Map-model fit

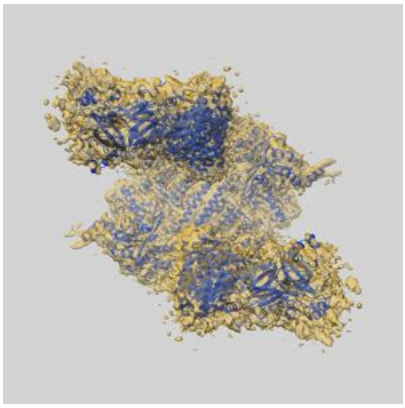
This section contains information regarding the fit between EMDB map EMD-65175 and PDB model 9VM3. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay

X



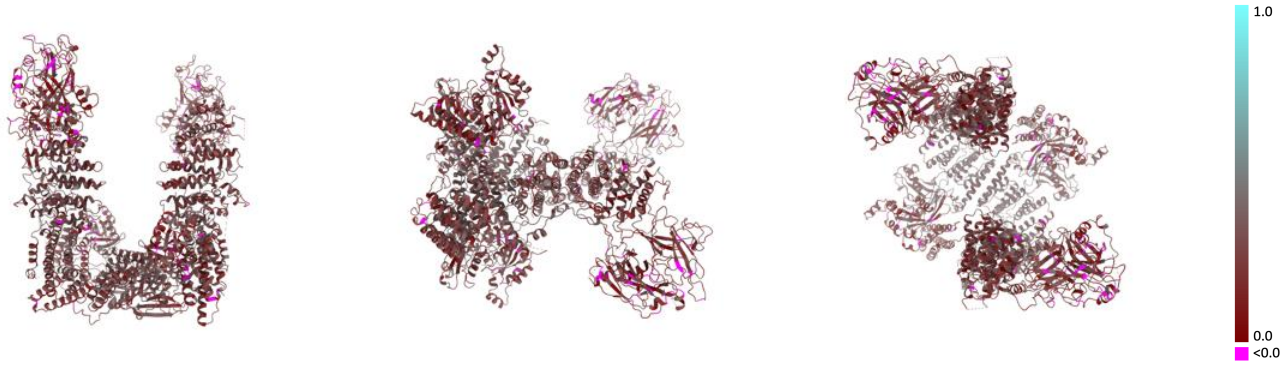
Y



Z

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

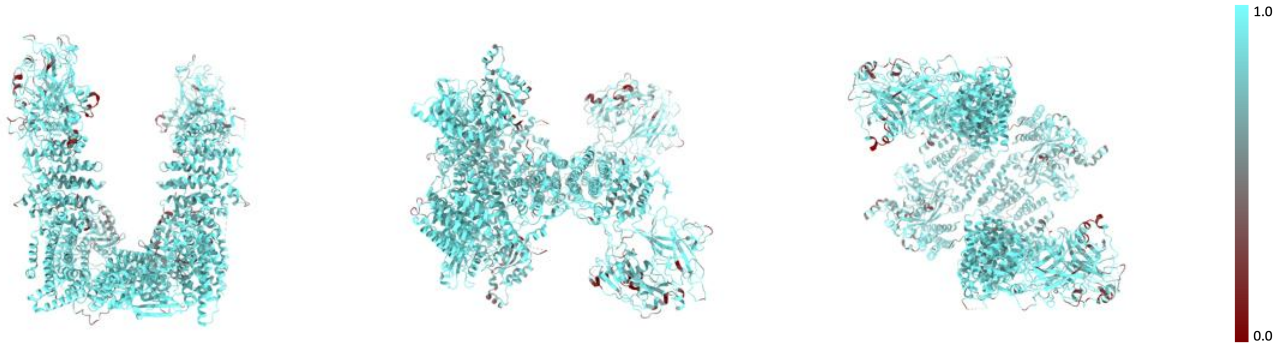
9.2 Q-score mapped to coordinate model (i)



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.

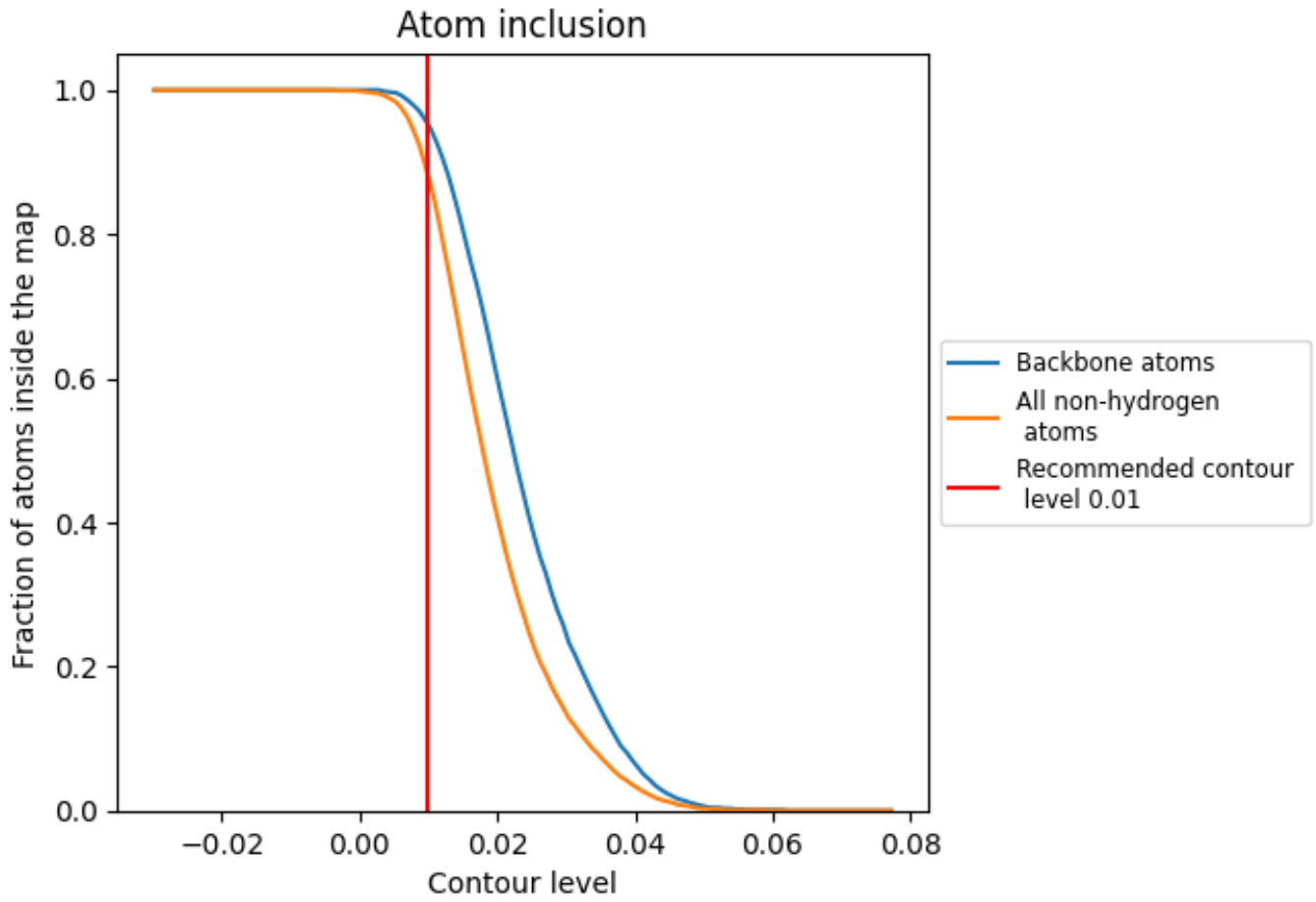
9.3 Atom inclusion mapped to coordinate model (i)



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, 95% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.2590
A	0.8900	0.2630
B	0.7890	0.2200
C	0.8910	0.2630
D	0.7980	0.2270