wwPDB EM Validation Summary Report (i)

Nov 10, 2026 – 06:35 pm GMT

PDB ID	:	9T76 / pdb_00009t76
EMDB ID	:	EMD-55627
Title	:	cryo-EM structure of human LARP1 bound to human mTOR complex 1, focused on mLST8-TOS
Authors	:	Craigie, L.M.; Maier, T.
Deposited on	:	2025-11-10
Resolution	:	3.63 Å(reported)
Based on initial model	:	9F44

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:

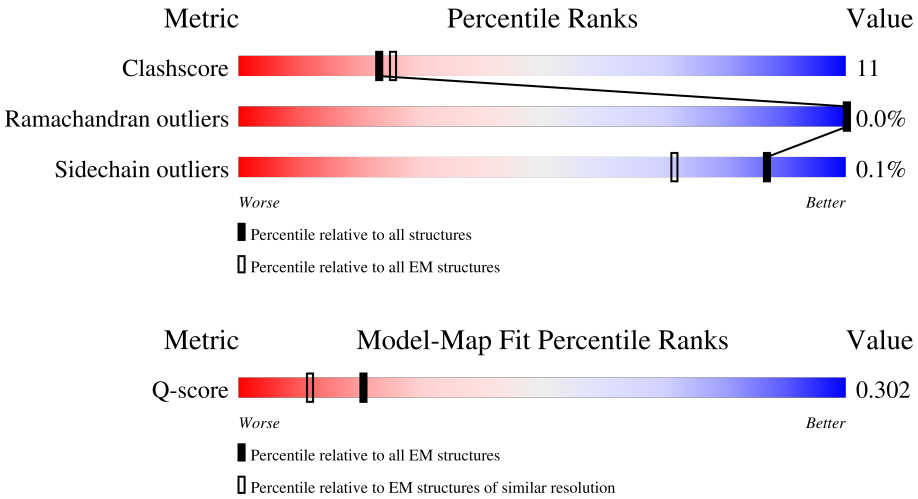
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

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

The reported resolution of this entry is 3.63 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	11696 (3.13 - 4.13)

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	C	326	8% 78% 19%
2	G	1096	99%
3	A	2549	46% 15% 39%
4	E	1363	6% 35% 10% 56%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 20035 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 Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	C	317	2456	1526	436	476	18	0	0

- Molecule 2 is a protein called La-related protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	G	7	64	42	7	15	0	0

- Molecule 3 is a protein called Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	A	1563	12674	8100	2214	2273	87	0	0

- Molecule 4 is a protein called Regulatory-associated protein of mTOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	602	4805	3097	821	854	33	0	0

There are 28 discrepancies between the modelled and reference sequences:

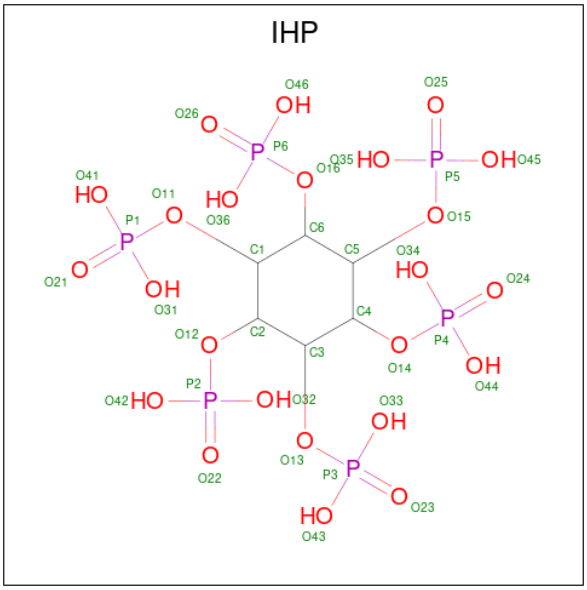
Chain	Residue	Modelled	Actual	Comment	Reference
E	-27	HIS	-	expression tag	UNP Q8N122
E	-26	HIS	-	expression tag	UNP Q8N122
E	-25	HIS	-	expression tag	UNP Q8N122
E	-24	HIS	-	expression tag	UNP Q8N122
E	-23	HIS	-	expression tag	UNP Q8N122
E	-22	HIS	-	expression tag	UNP Q8N122
E	-21	HIS	-	expression tag	UNP Q8N122
E	-20	HIS	-	expression tag	UNP Q8N122
E	-19	HIS	-	expression tag	UNP Q8N122

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-18	HIS	-	expression tag	UNP Q8N122
E	-17	GLU	-	expression tag	UNP Q8N122
E	-16	GLN	-	expression tag	UNP Q8N122
E	-15	LYS	-	expression tag	UNP Q8N122
E	-14	LEU	-	expression tag	UNP Q8N122
E	-13	ILE	-	expression tag	UNP Q8N122
E	-12	SER	-	expression tag	UNP Q8N122
E	-11	GLU	-	expression tag	UNP Q8N122
E	-10	GLU	-	expression tag	UNP Q8N122
E	-9	ASP	-	expression tag	UNP Q8N122
E	-8	LEU	-	expression tag	UNP Q8N122
E	-7	ASP	-	expression tag	UNP Q8N122
E	-6	TYR	-	expression tag	UNP Q8N122
E	-5	LYS	-	expression tag	UNP Q8N122
E	-4	ASP	-	expression tag	UNP Q8N122
E	-3	ASP	-	expression tag	UNP Q8N122
E	-2	ASP	-	expression tag	UNP Q8N122
E	-1	ASP	-	expression tag	UNP Q8N122
E	0	LYS	-	expression tag	UNP Q8N122

- Molecule 5 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



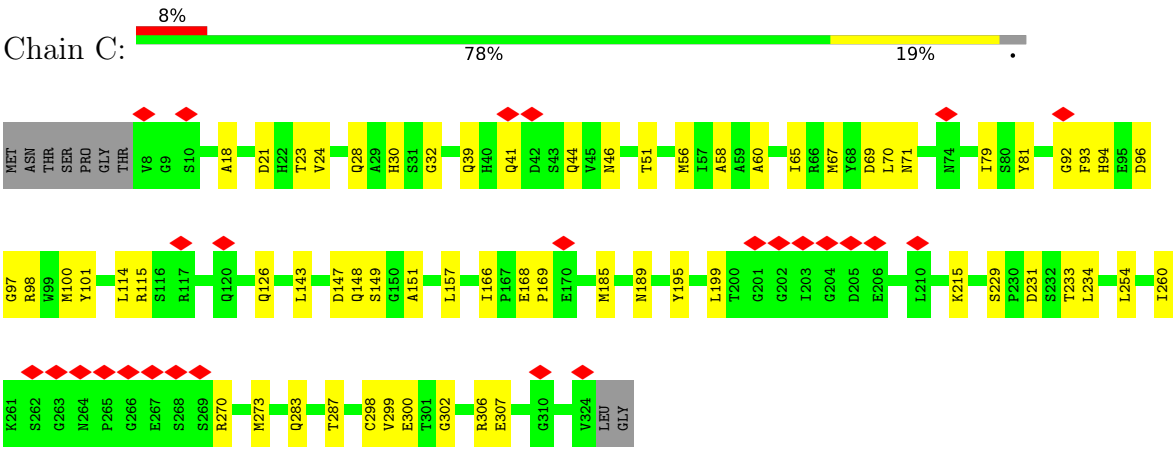
Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	O	P	0
			36	6	24	6	

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.

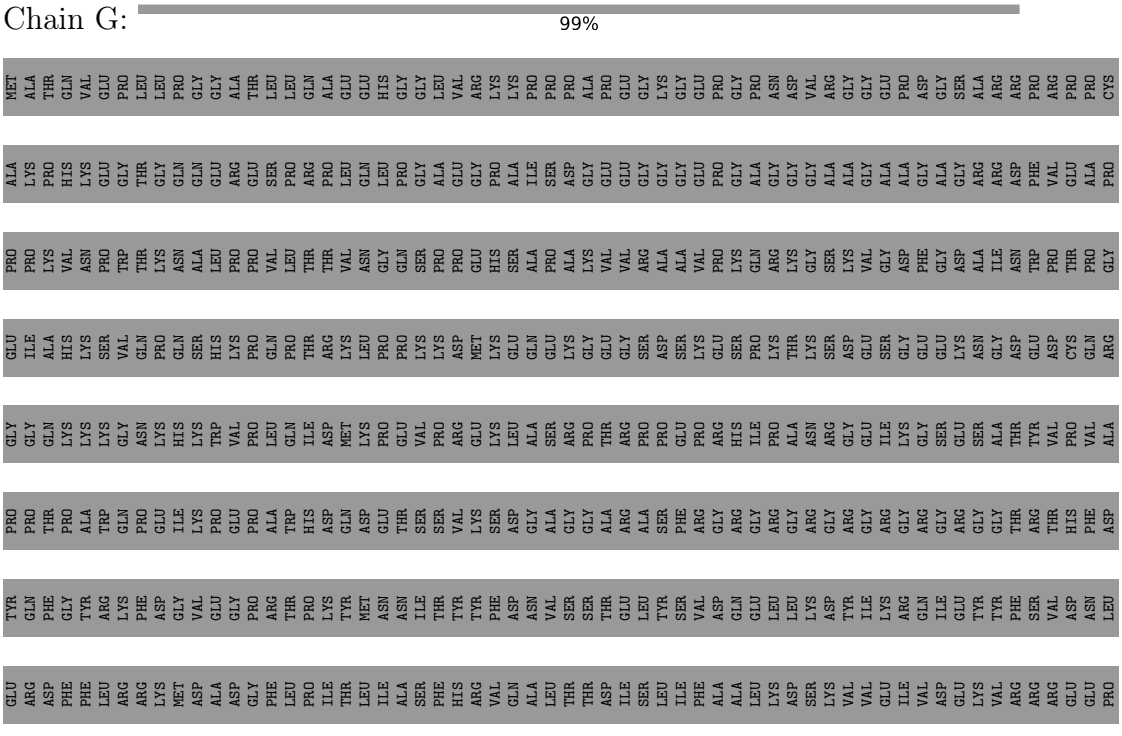
• Molecule 1: Target of rapamycin complex subunit LST8

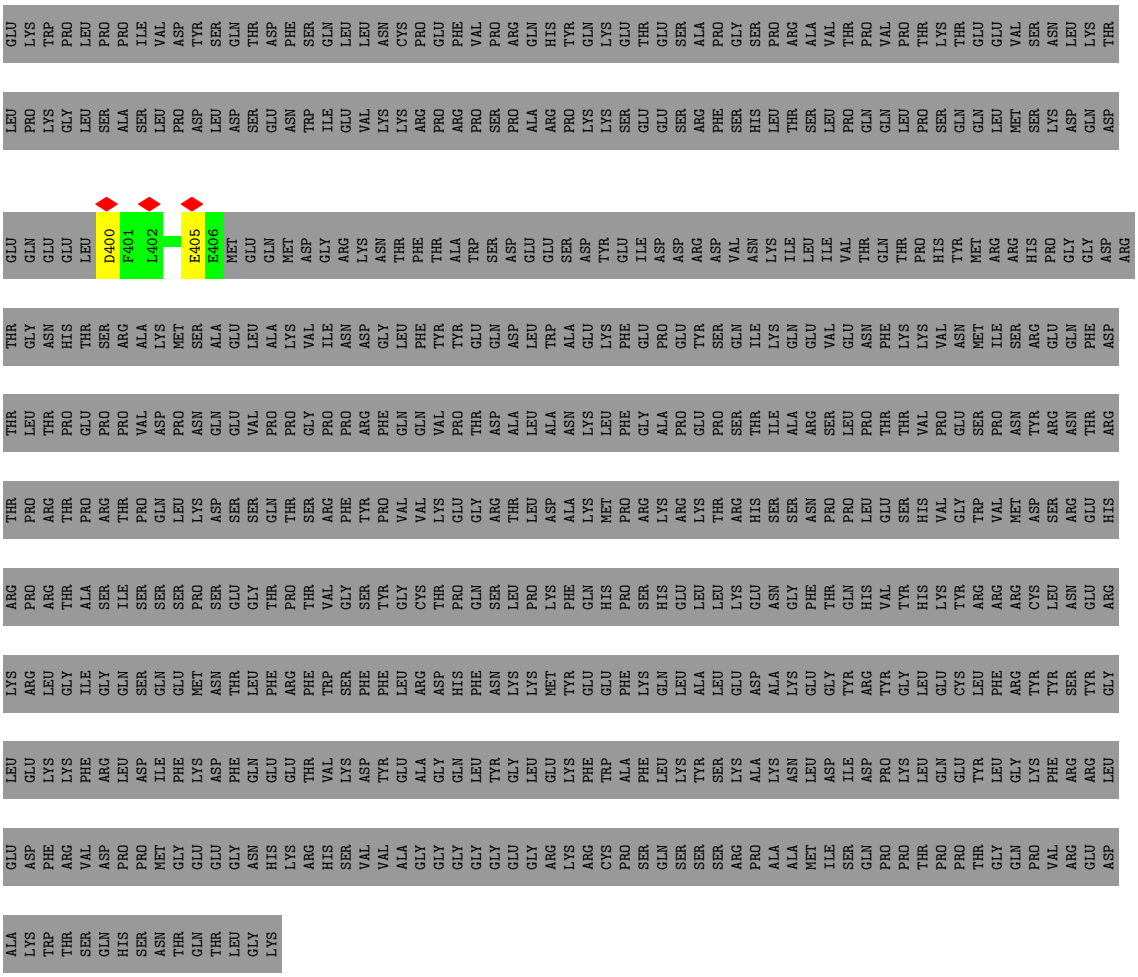
Chain C:



• Molecule 2: La-related protein 1

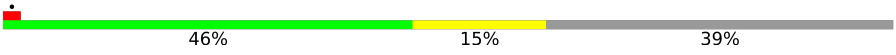
Chain G:

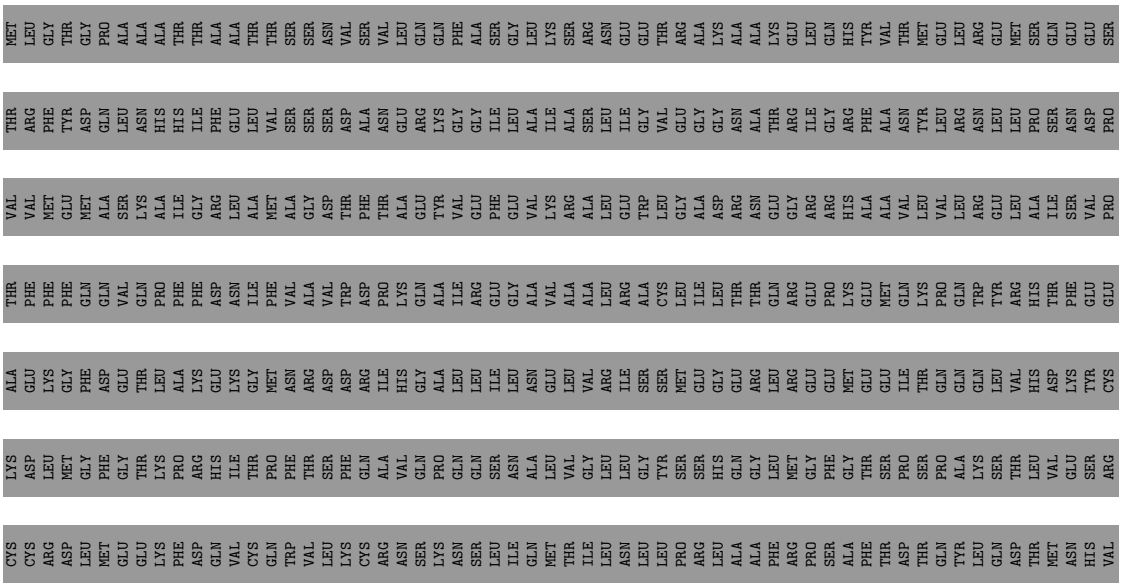


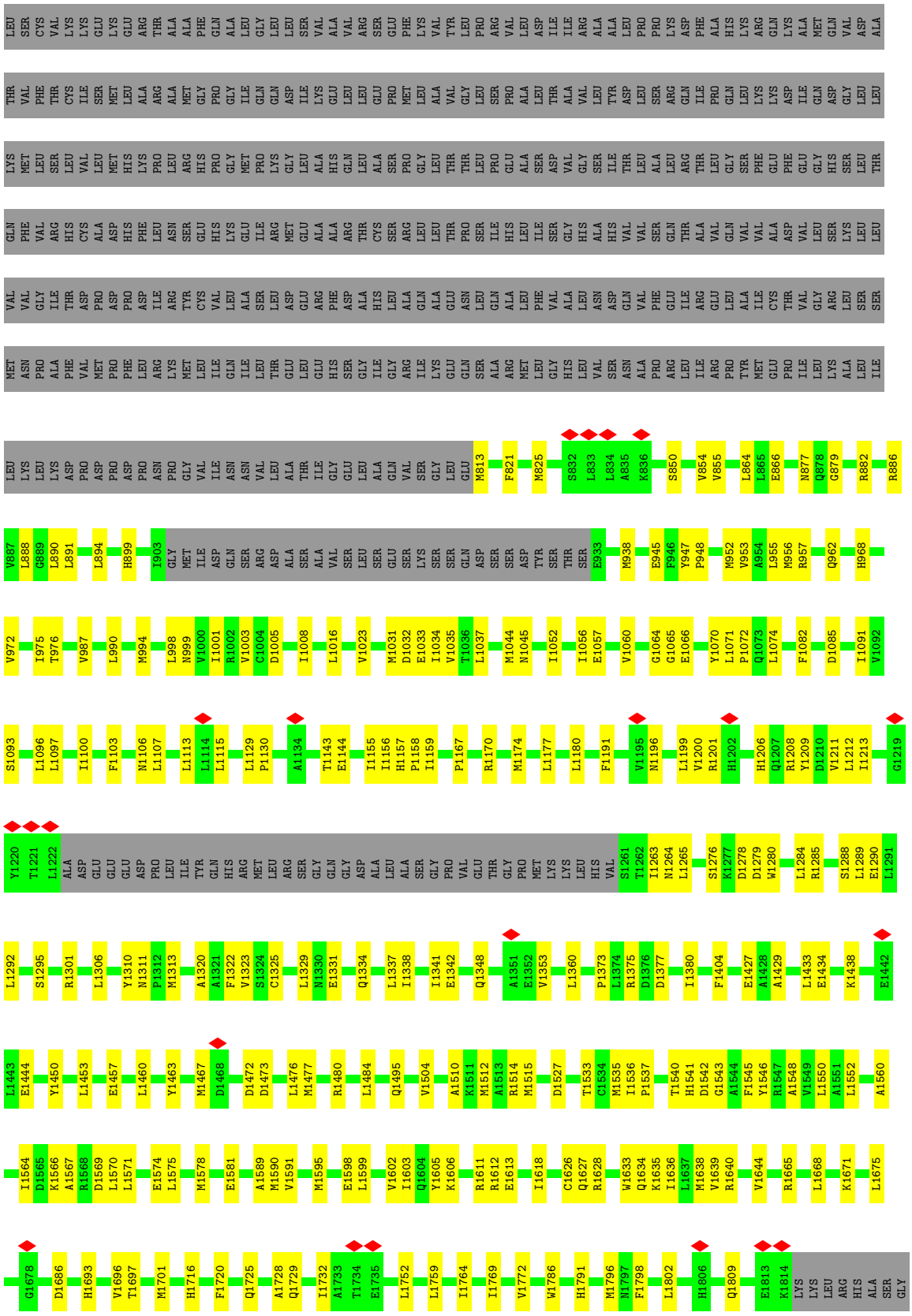


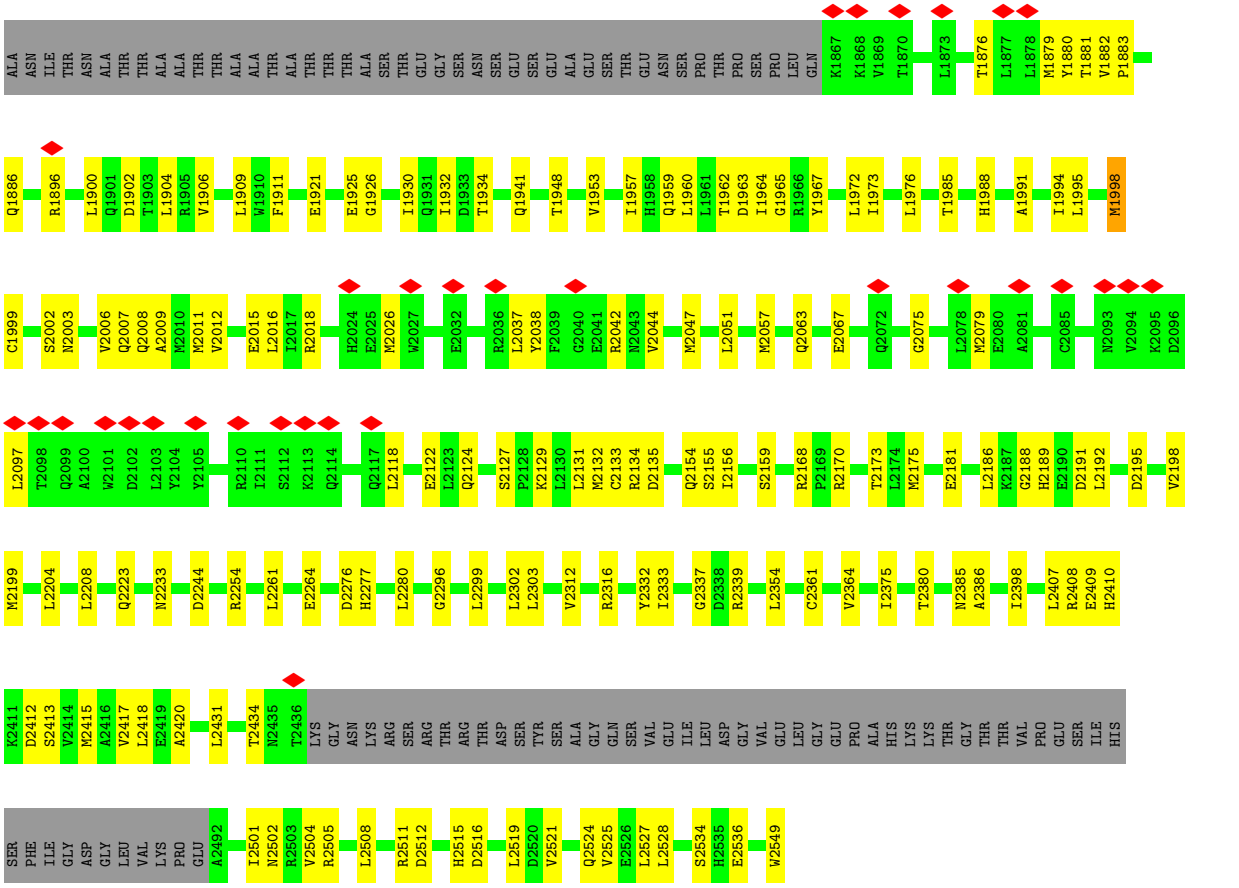
• Molecule 3: Serine/threonine-protein kinase mTOR

Chain A:





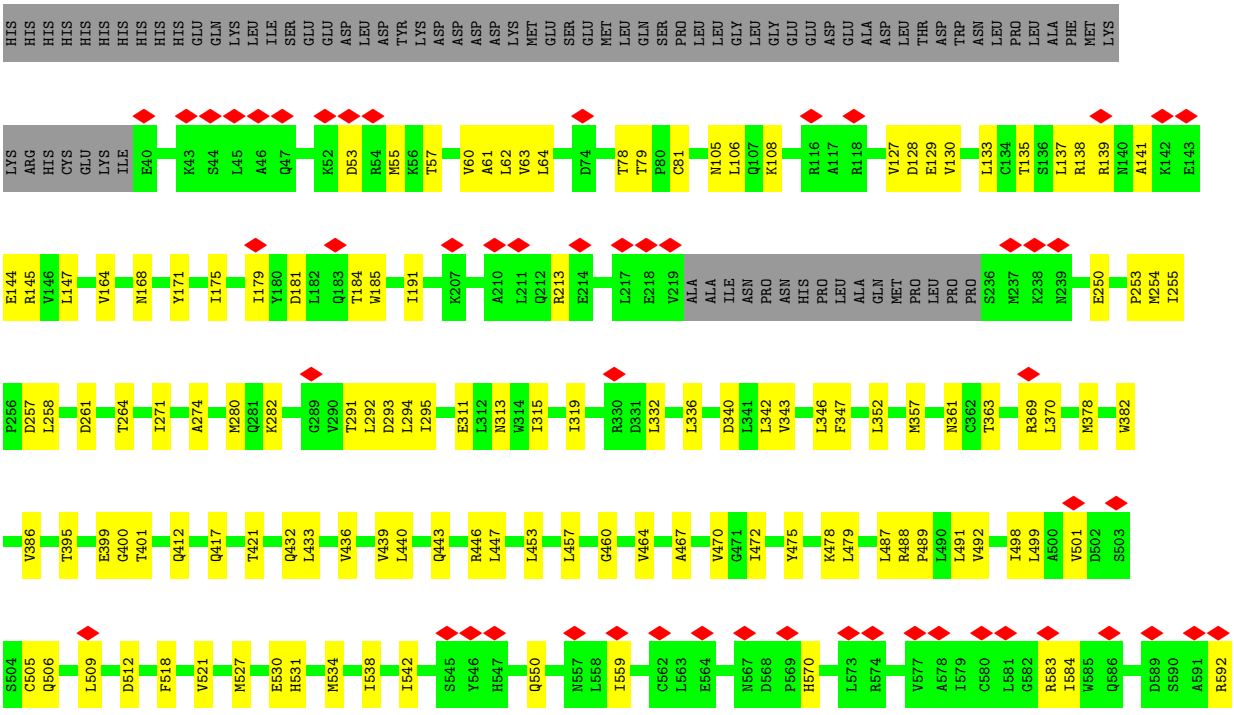

LEU SER CYS VAL LYS LYS GLU LYS GLU ARG THR ALA ALA PHE GLN ALA LEU GLY LEU LEU SER VAL ALA ALA VAL ARG SER GLU PHE LYS VAL TYR LEU PRO ARG VAL LEU ASP ILE ILE ARG ALA ALA ALA VAL ARG SER GLU PRO PRO LYS ASP PHE ALA HIS LYS ARG GLN LYS ALA MET GLN VAL ASP ALA
THR VAL PHE THR CYS ILE SER MET LEU ALA ARG ALA MET GLY PRO GLY ILE GLN GLN ASP ILE LYS GLU LEU LEU GLU PRO MET LEU ALA VAL GLY LEU SER PRO GLU ALA ARG GLN ILE PRO GLN LEU LYS LYS ASP ILE GLN ASP GLY LEU LEU
LYS MET LEU SER LEU VAL LEU MET MET HIS LYS PRO LEU ARG HIS PRO GLY MET PRO LYS GLY LEU ALA ALA HIS GLN LEU GLU ALA SER PRO GLY LEU THR THR LEU PRO GLU ALA LEU SER ASP VAL GLY SER ILE THR LEU ALA LEU ARG THR LEU GLY SER PHE GLU PHE GLU ALA ASP VAL LEU GLY ARG LEU SER LEU THR
GLN PHE VAL ARG HIS CYS ALA ASP HIS PHE LEU ASN SER GLU HIS LYS GLU ILE ARG MET GLU ALA ALA HIS ARG THR CYS SER ARG LEU LEU THR PRO SER ILE HIS LEU ILE SER GLY HIS ALA HIS VAL VAL SER GLN THR ALA VAL GLN VAL VAL ALA ASP VAL LEU SER LYS LEU LEU
VAL VAL GLY ILE THR ASP PRO ASP PRO ASP ILE ARG TYR CYS VAL LEU ALA SER LEU ASP GLU ARG PHE ASP ALA HIS LEU ASN ASP GLN VAL PHE GLU ILE ARG GLU LEU ALA ILE CYS THR VAL GLY ARG LEU SER LEU
MET ASN PRO ALA PHE VAL MET PRO PHE LEU ARG LYS MET LEU ILE GLN ILE LEU THR GLU LEU ASP PRO ASN PRO ASP PRO ASN PRO GLY VAL ILE ASN VAL LEU ALA THR ILE GLY GLU LEU ALA GLN VAL SER GLY LEU GLU M613 F821 M825 S832 L833 L834 A835 K836 S850 V854 V855 L864 L865 E866 N877 Q878 G879 R882 R886
V887 L888 G889 L890 L891 L894 H899 I903 GLY MET ILE ASP GLN SER ARG ASP ALA SER ALA VAL SER LEU SER GLU SER LYS SER SER GLN ASP SER SER ASP TYR SER THR SER E933 M938 E945 P946 Y947 P948 M952 V953 A954 L955 M956 R957 Q962 H968
V972 I975 T976 V987 L990 M994 L998 N999 V1000 I1001 R1002 V1003 C1004 D1005 I1008 L1016 V1023 M1031 D1032 E1033 I1034 V1035 T1036 L1037 M1044 N1045 I1052 I1056 E1057 V1060 G1064 G1065 E1066 Y1070 L1071 P1072 Q1073 L1074 F1082 D1085 I1091 V1092
S1093 L1096 L1097 I1100 F1103 N1106 L1107 L1113 L1114 L1115 L1129 P1130 A1134 T1143 E1144 I1155 I1156 H1157 P1158 I1159 P1167 R1170 M1174 L1177 L1180 F1191 V1195 N1196 L1199 V1200 R1201 H1202 H1206 Q1207 R1208 Y1209 D1210 V1211 L1212 I1213 G1219
Y1220 T1221 L1222 ALA ASP GLU GLU GLU ASP PRO LEU ILE TYR GLN HIS ARG MET LEU ARG SER GLY GLN GLY ASP ALA LEU ALA SER GLY PRO VAL GLU THR GLY PRO MET LYS LYS LEU HIS VAL S1261 T1262 I1263 N1264 L1265 S1276 K1277 D1278 D1279 W1280 L1284 R1285 S1288 L1289 E1290 L1291
L1292 S1295 R1301 L1306 Y1310 N1311 P1312 M1313 A1320 A1321 F1322 V1323 S1324 C1325 L1329 N1330 E1331 Q1334 L1337 I1338 I1341 E1342 Q1348 A1351 E1352 V1353 L1360 P1373 L1374 R1375 D1376 D1377 I1380 F1404 E1427 A1428 A1429 L1433 E1434 K1438 E1442
L1443 E1444 Y1450 L1453 E1457 L1460 Y1463 M1467 D1468 D1472 D1473 L1476 M1477 R1480 L1484 Q1495 V1504 A1510 K1511 M1512 A1513 R1514 M1515 D1527 T1533 C1534 M1535 I1536 P1537 T1540 H1541 D1542 G1543 A1544 F1545 Y1546 R1547 A1548 V1549 L1550 A1551 L1552 A1560
I1564 D1565 K1566 A1567 R1568 D1569 L1570 L1571 E1574 L1575 M1578 E1581 A1589 M1590 V1591 M1595 E1598 L1599 V1602 I1603 Q1604 Y1605 K1606 R1611 R1612 E1613 I1618 C1626 Q1627 R1628 W1633 Q1634 K1635 I1636 L1637 M1638 V1639 R1640 V1644 R1665 L1668 K1671 L1675
G1678 D1686 H1693 V1696 T1697 M1701 H1716 F1720 Q1725 A1728 Q1729 I1732 A1733 T1734 E1735 L1752 L1759 I1764 I1769 V1772 W1786 H1791 M1796 N1797 F1798 L1802 H1806 Q1809 E1813 K1814 LYS LYS LEU ARG HIS ALA SER GLY

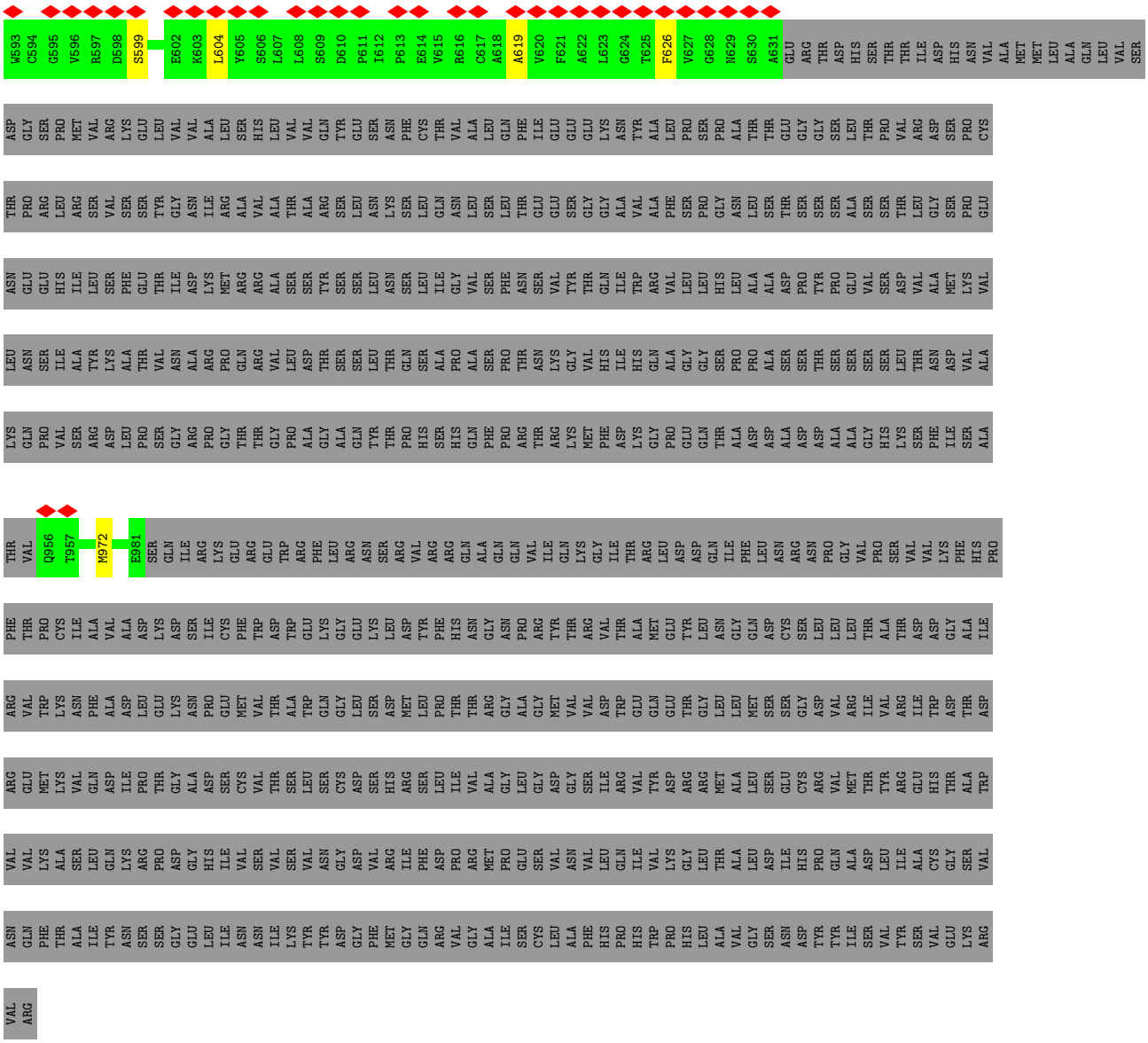


• Molecule 4: Regulatory-associated protein of mTOR

Chain E:






W593 C594 G595 V596 R597 D598 S599 E602 K603 L604 Y605 S606 L607 L608 S609 D610 P611 I612 P613 E614 V615 R616 C617 A618 A619 V620 F621 A622 L623 G624 T625 F626 V627 G628 N629 S630 A631 Q956 T957 M972 E981

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	269597	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 ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.499	Depositor
Minimum map value	-0.270	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	467.2, 467.2, 467.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.97333336, 0.97333336, 0.97333336	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IHP

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	C	0.09	0/2514	0.25	0/3426
2	G	0.06	0/65	0.19	0/86
3	A	0.11	0/12955	0.29	0/17549
4	E	0.11	0/4927	0.27	0/6712
All	All	0.11	0/20461	0.28	0/27773

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

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	C	2456	0	2341	42	0
2	G	64	0	48	2	0
3	A	12674	0	12783	310	0
4	E	4805	0	4837	93	0
5	A	36	0	6	0	0
All	All	20035	0	20015	443	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 11.

The worst 5 of 443 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)
3:A:1284:LEU:HD11	3:A:1353:VAL:HG22	1.56	0.88
3:A:1772:VAL:HG11	3:A:1796:MET:HE3	1.59	0.83
1:C:229:SER:OG	1:C:231:ASP:OD1	1.98	0.81
3:A:2534:SER:OG	3:A:2536:GLU:OE1	1.98	0.80
3:A:1964:ILE:HG22	3:A:1972:LEU:HD11	1.62	0.79

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	C	315/326 (97%)	303 (96%)	12 (4%)	0	100	100
2	G	5/1096 (0%)	5 (100%)	0	0	100	100
3	A	1553/2549 (61%)	1507 (97%)	46 (3%)	0	100	100
4	E	596/1363 (44%)	580 (97%)	15 (2%)	1 (0%)	43	71
All	All	2469/5334 (46%)	2395 (97%)	73 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	E	81	CYS

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	C	269/276 (98%)	269 (100%)	0	100 100
2	G	7/948 (1%)	7 (100%)	0	100 100
3	A	1386/2220 (62%)	1384 (100%)	2 (0%)	88 87
4	E	531/1191 (45%)	531 (100%)	0	100 100
All	All	2193/4635 (47%)	2191 (100%)	2 (0%)	87 87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	1495	GLN
3	A	1998	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
4	E	67	ASN
4	E	531	HIS
4	E	405	HIS
3	A	1446	GLN
3	A	2293	ASN

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)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	IHP	A	2601	-	36,36,36	0.74	1 (2%)	54,60,60	0.36	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	IHP	A	2601	-	-	2/30/54/54	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2601	IHP	P3-O13	2.83	1.64	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2601	IHP	C2-O12-P2-O42
5	A	2601	IHP	C3-O13-P3-O43

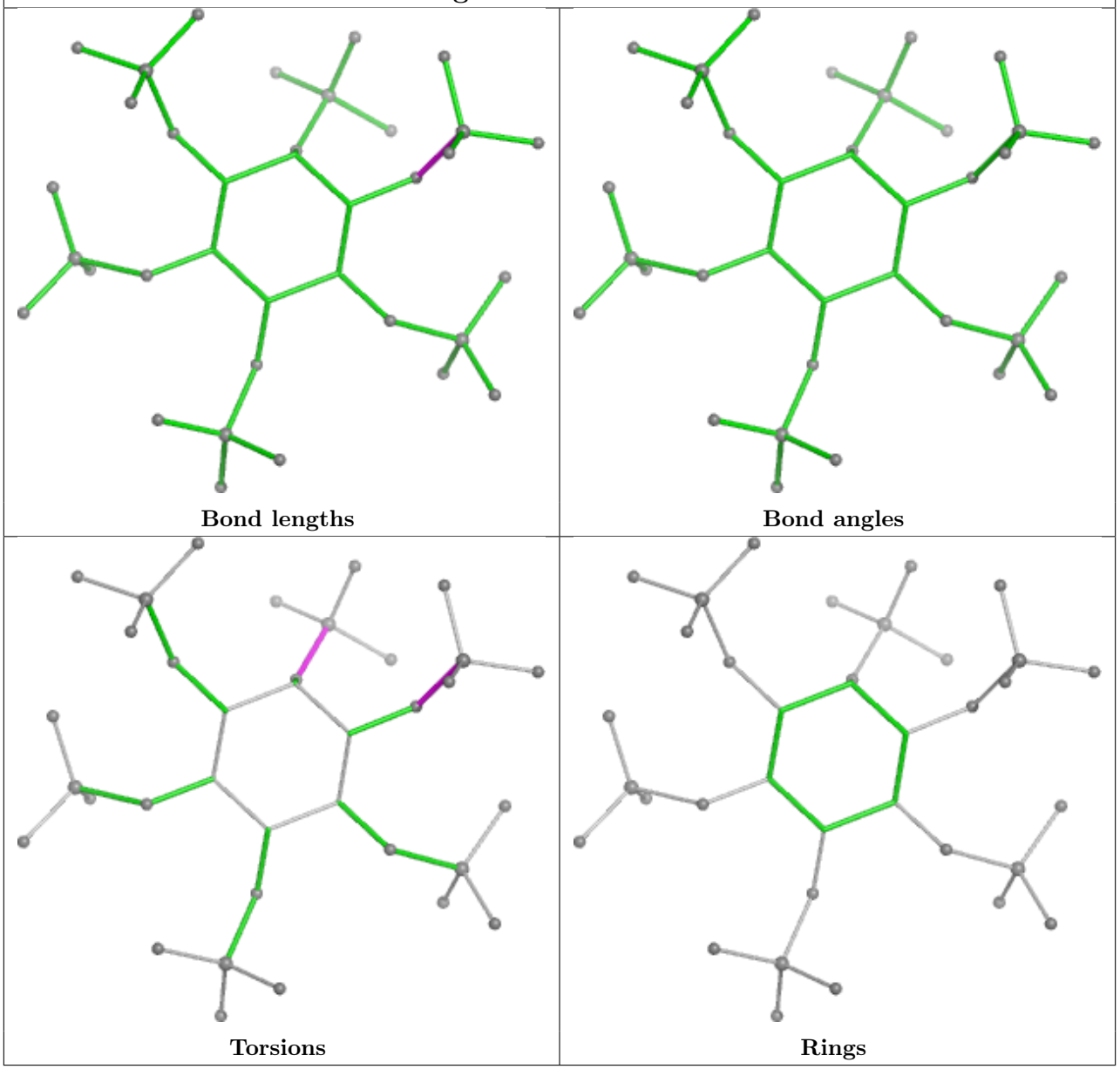
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand IHP A 2601



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.

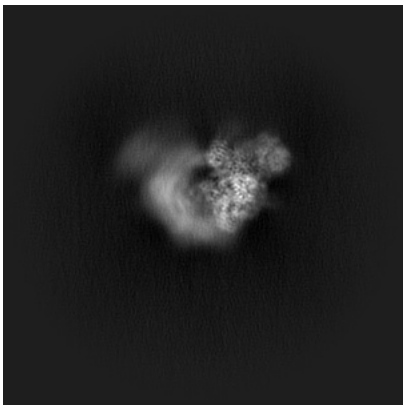
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55627. These allow visual inspection of the internal detail of the map and identification of artifacts.

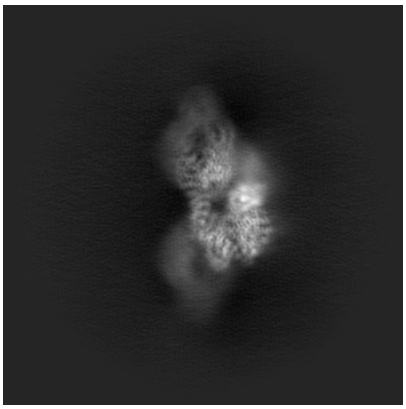
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

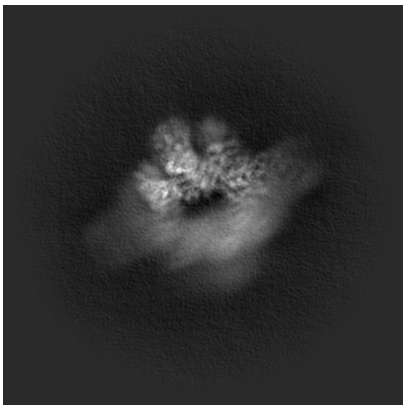
6.1.1 Primary map



X

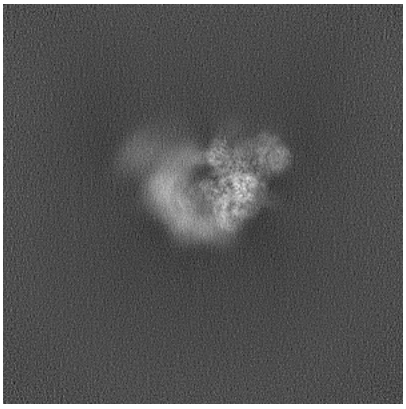


Y

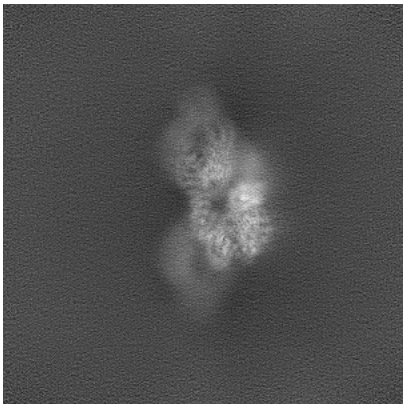


Z

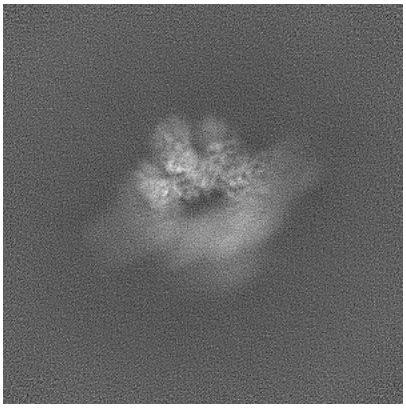
6.1.2 Raw map



X



Y

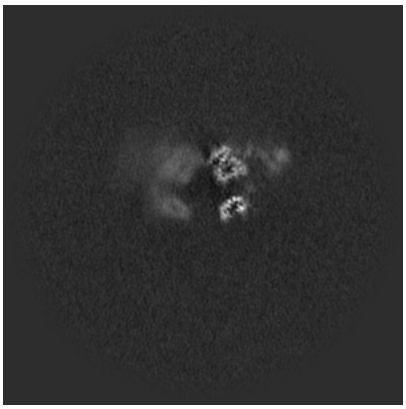


Z

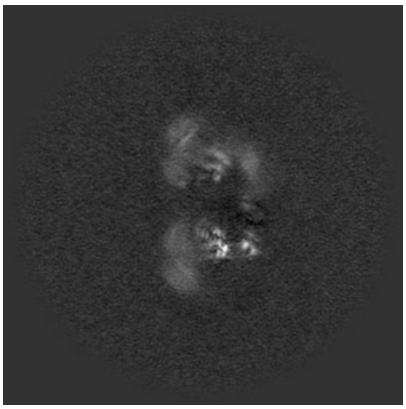
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

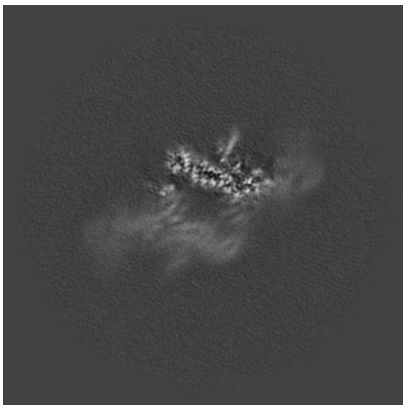
6.2.1 Primary map



X Index: 240

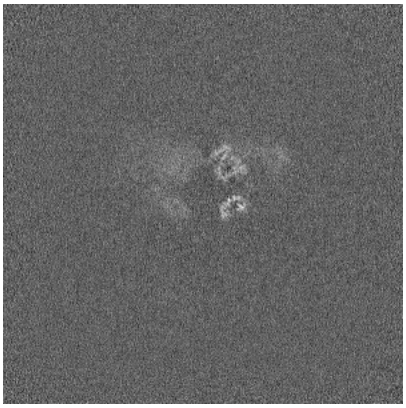


Y Index: 240

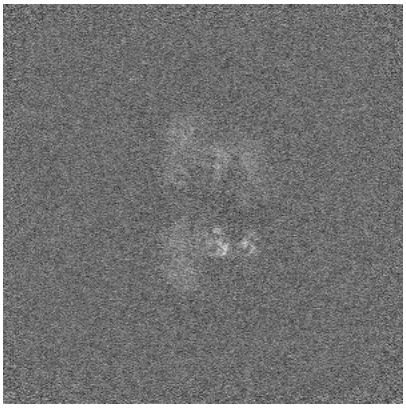


Z Index: 240

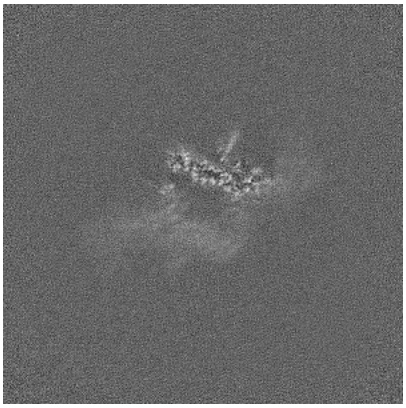
6.2.2 Raw map



X Index: 240



Y Index: 240

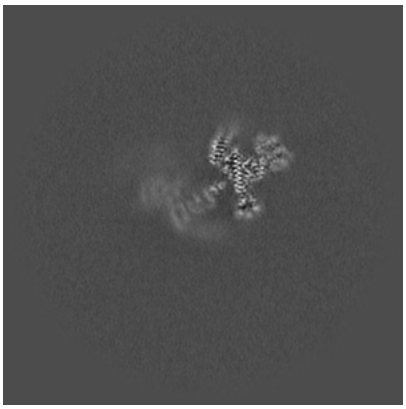


Z Index: 240

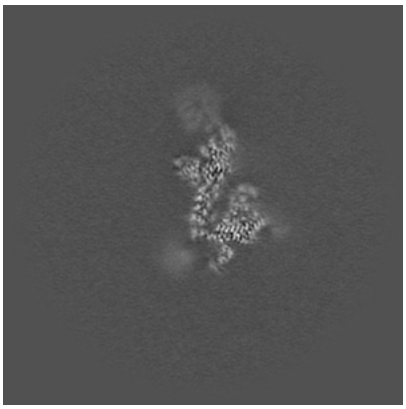
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 211

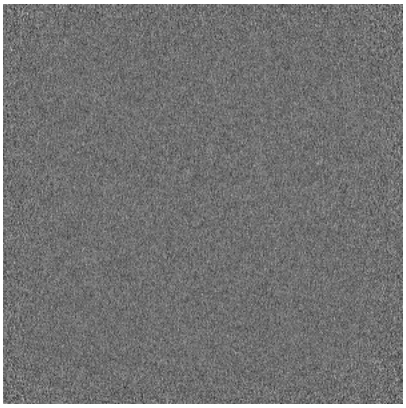


Y Index: 280

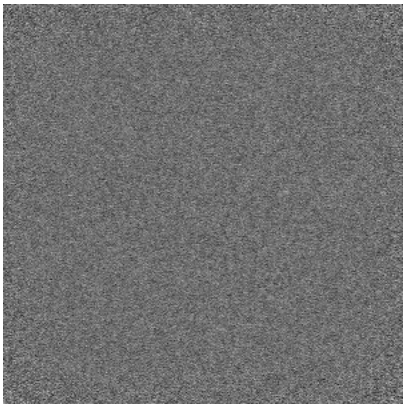


Z Index: 262

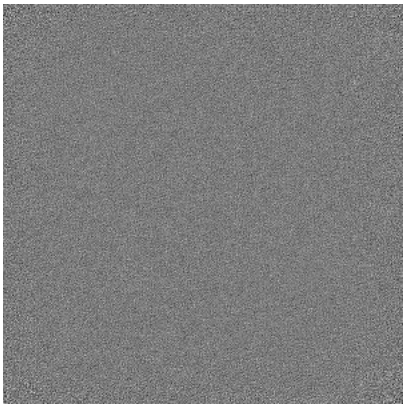
6.3.2 Raw map



X Index: 0



Y Index: 0

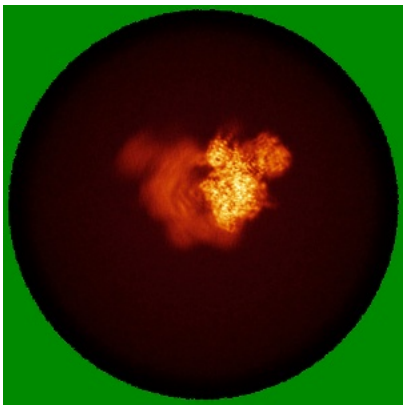


Z Index: 0

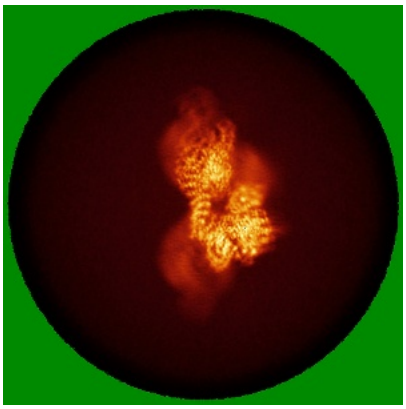
The images above show the largest variance slices of the map in three orthogonal directions.

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

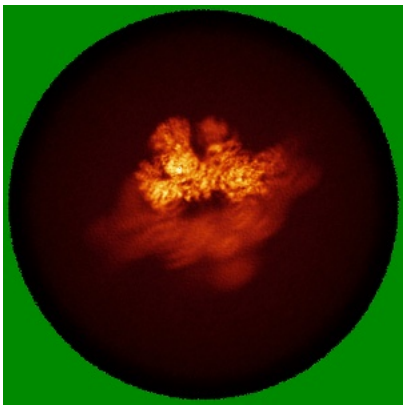
6.4.1 Primary map



X

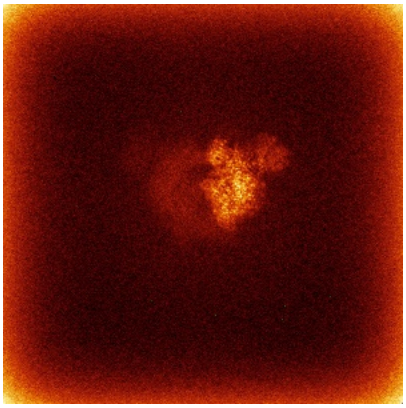


Y

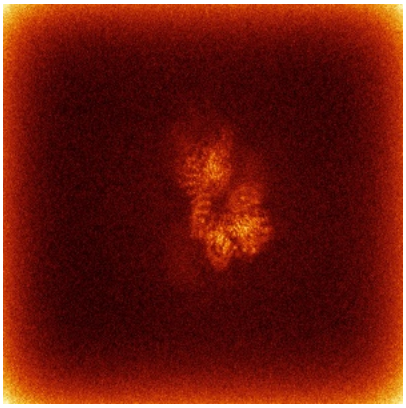


Z

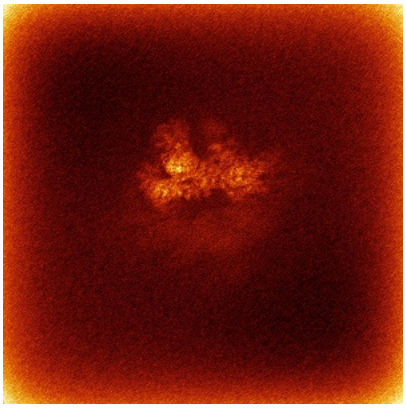
6.4.2 Raw map



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)

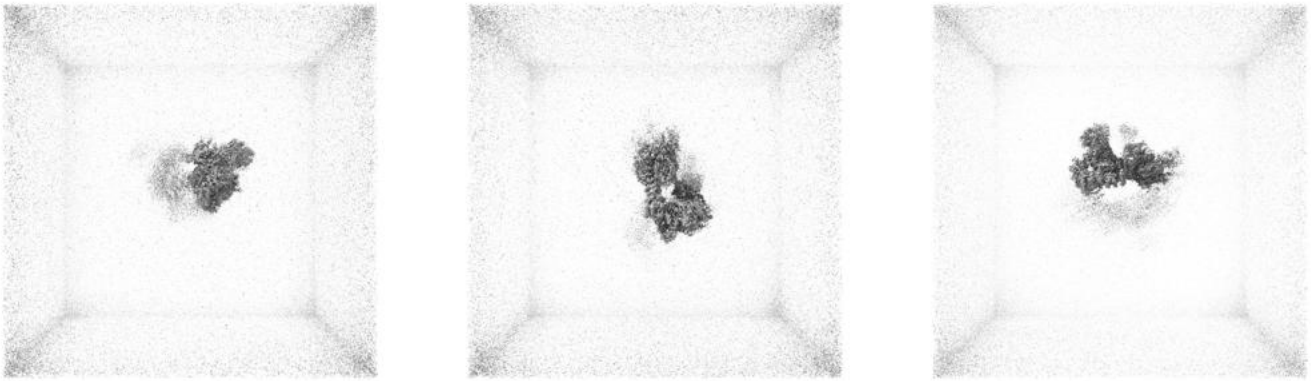
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

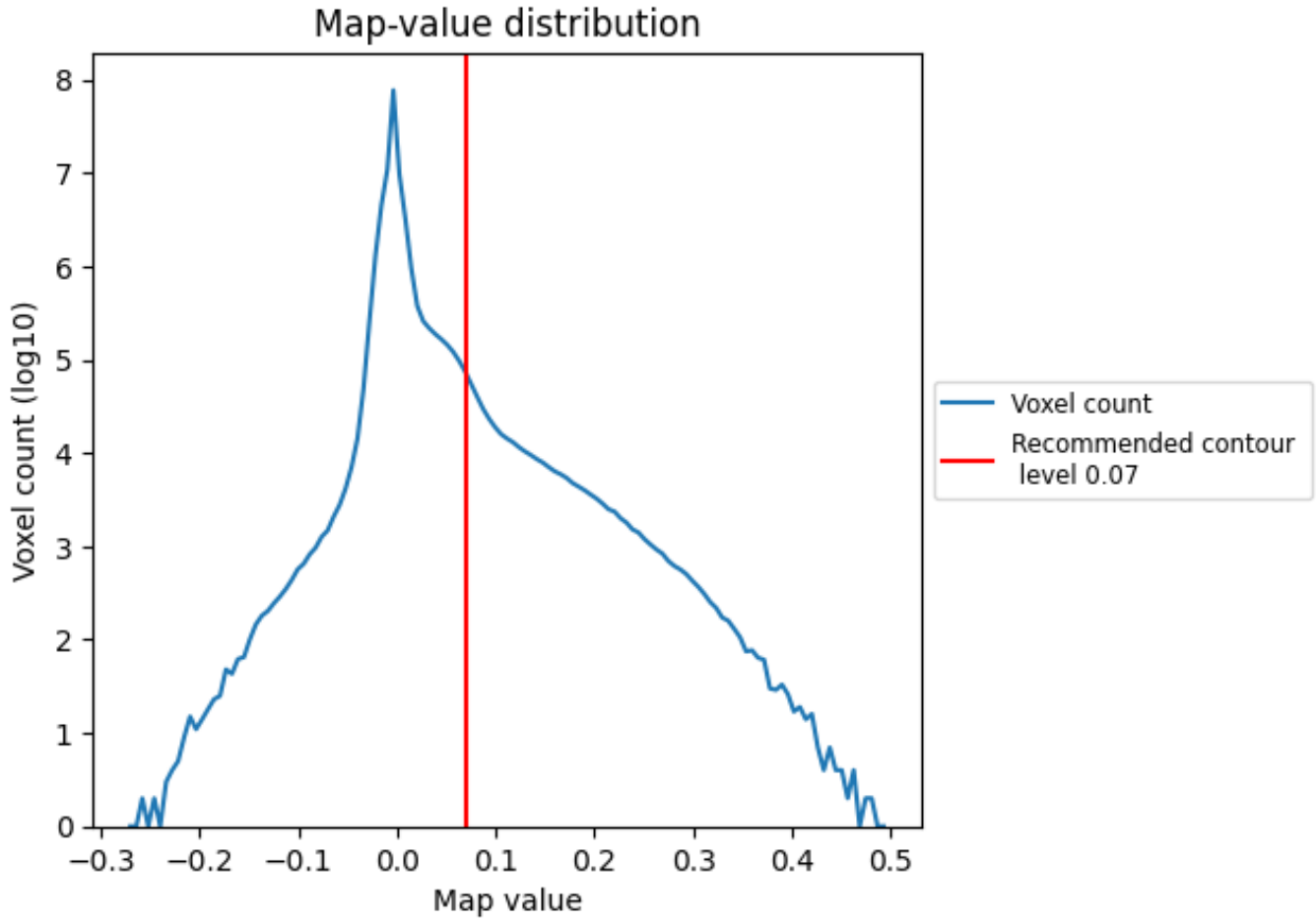
6.6 Mask visualisation (i)

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

7 Map analysis

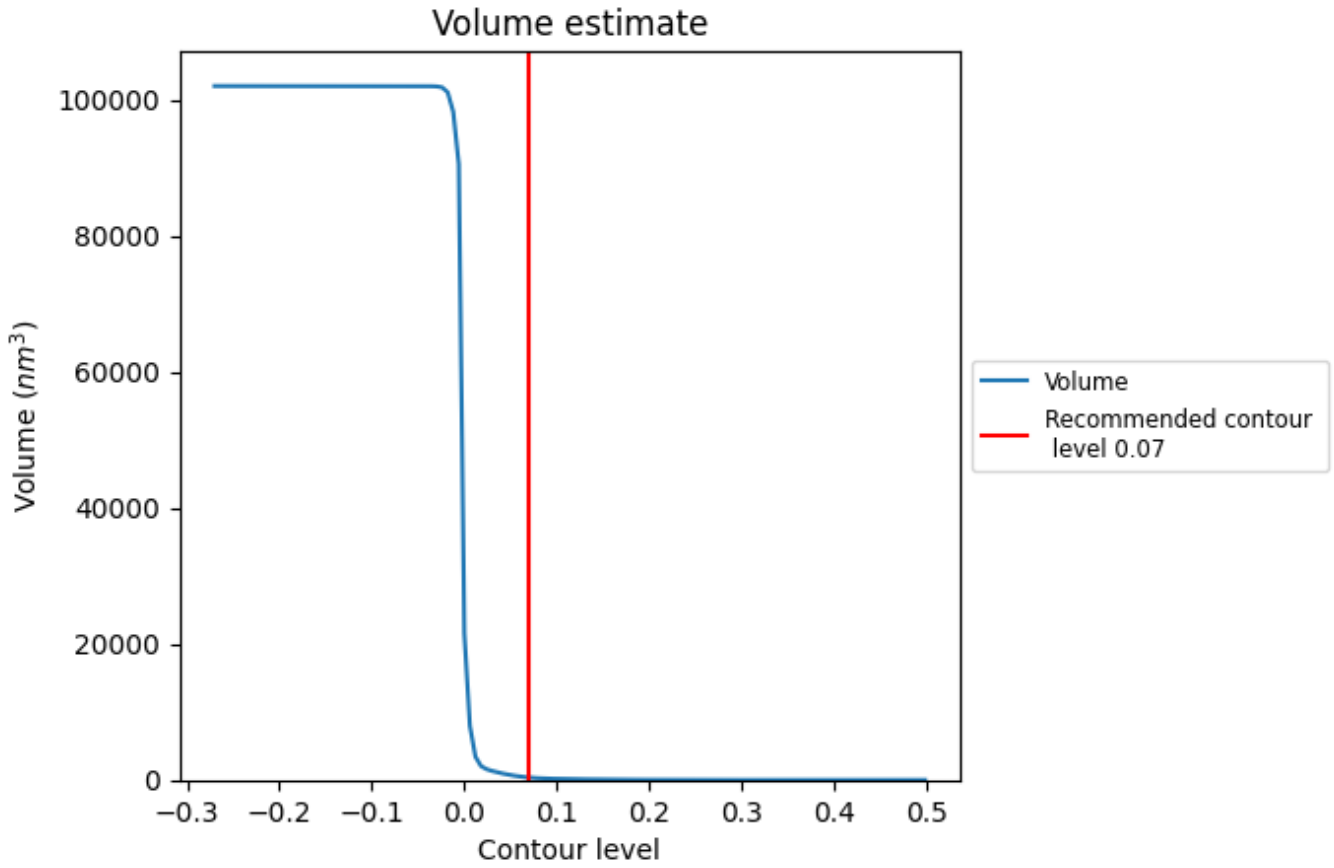
This section contains the results of statistical analysis of the map.

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.

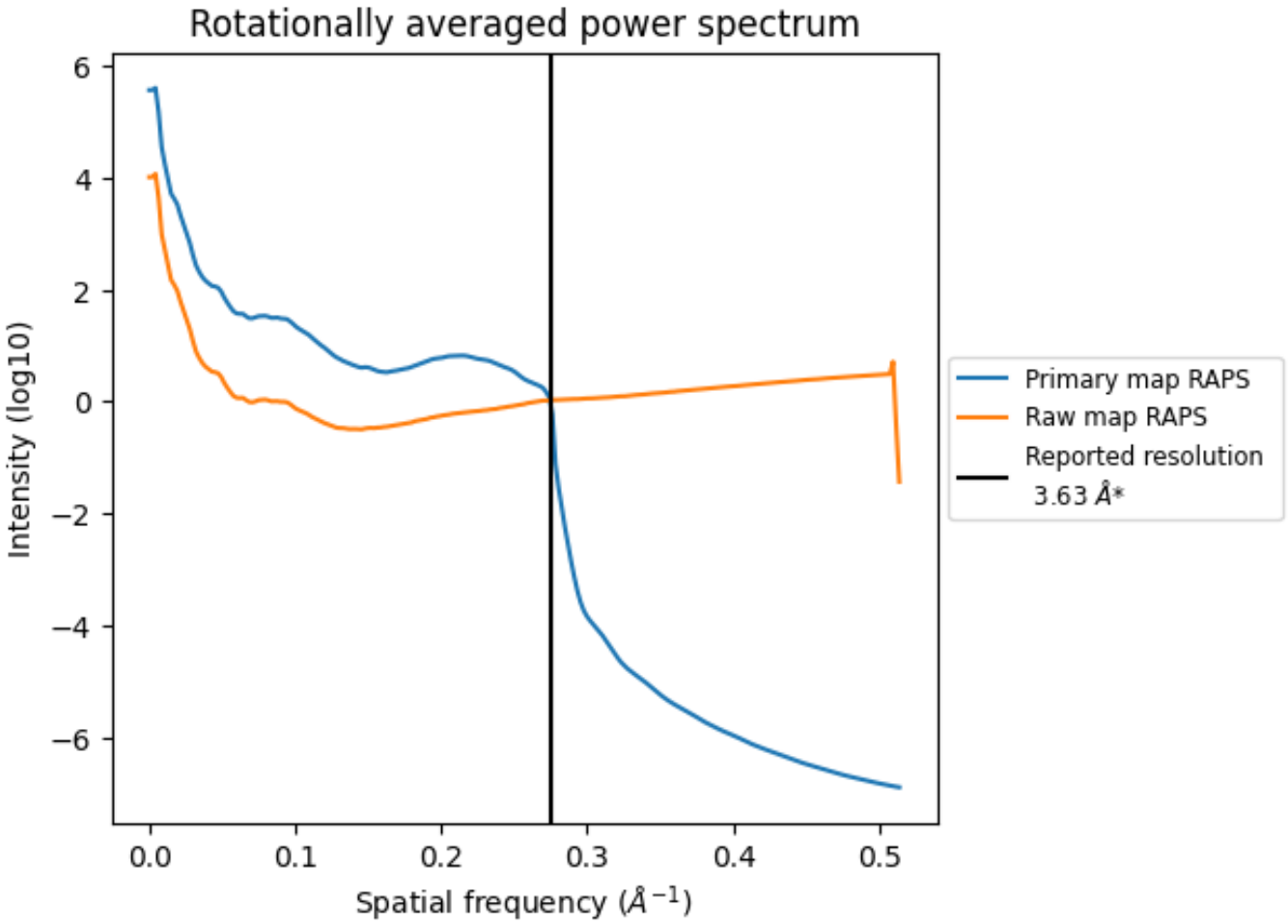
7.2 Volume estimate (i)



The volume at the recommended contour level is 363 nm^3; this corresponds to an approximate mass of 328 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)

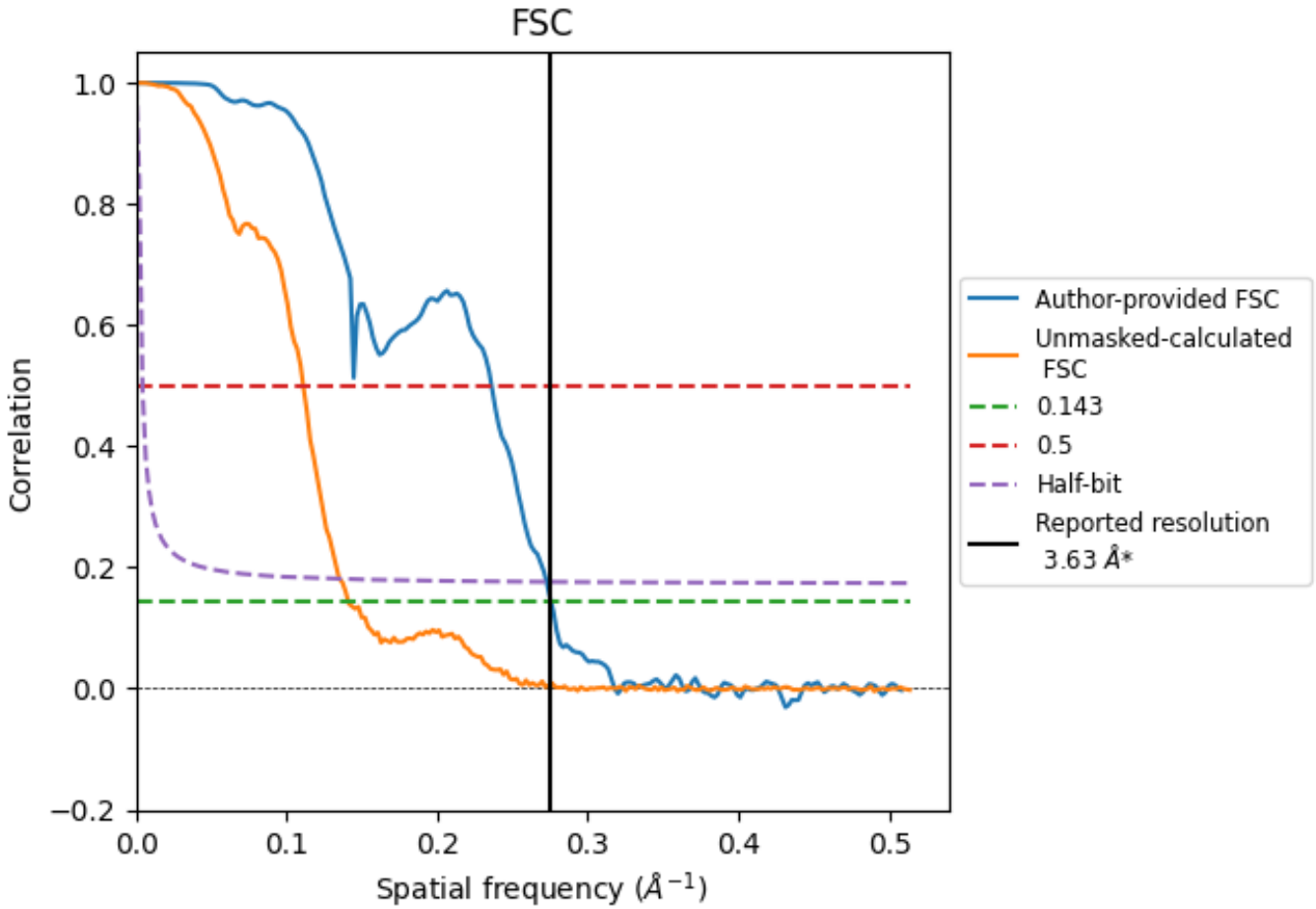


*Reported resolution corresponds to spatial frequency of 0.275 Å^{-1}

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 0.275 Å^{-1}

8.2 Resolution estimates (i)

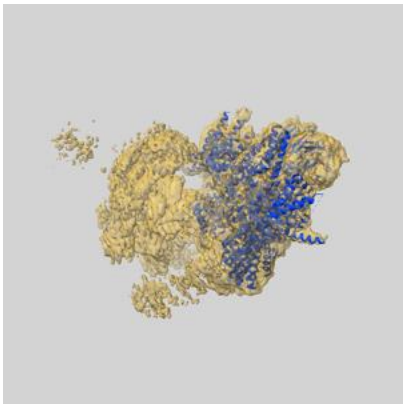
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.63	-	-
Author-provided FSC curve	3.63	4.24	3.67
Unmasked-calculated*	7.09	9.01	7.40

*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 7.09 differs from the reported value 3.63 by more than 10 %

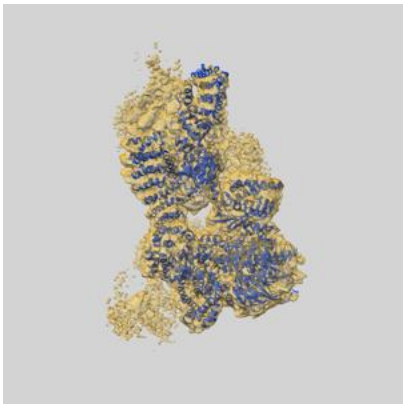
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55627 and PDB model 9T76. Per-residue inclusion information can be found in section 3 on page 5.

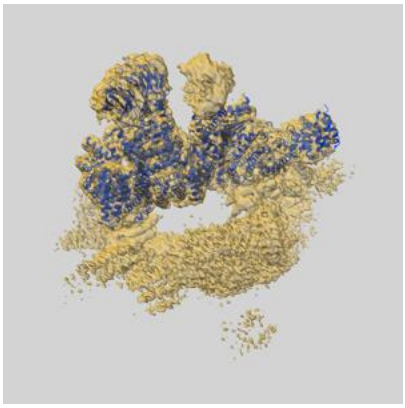
9.1 Map-model overlay



X



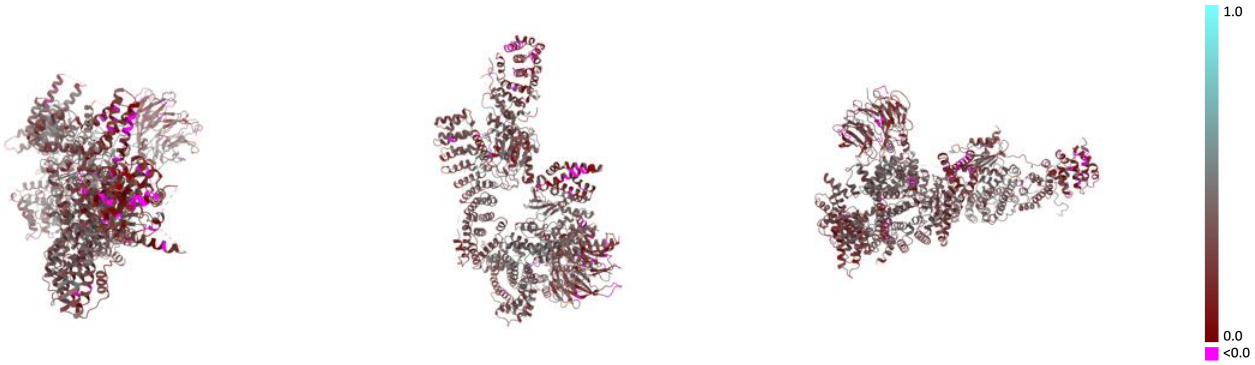
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.07 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.

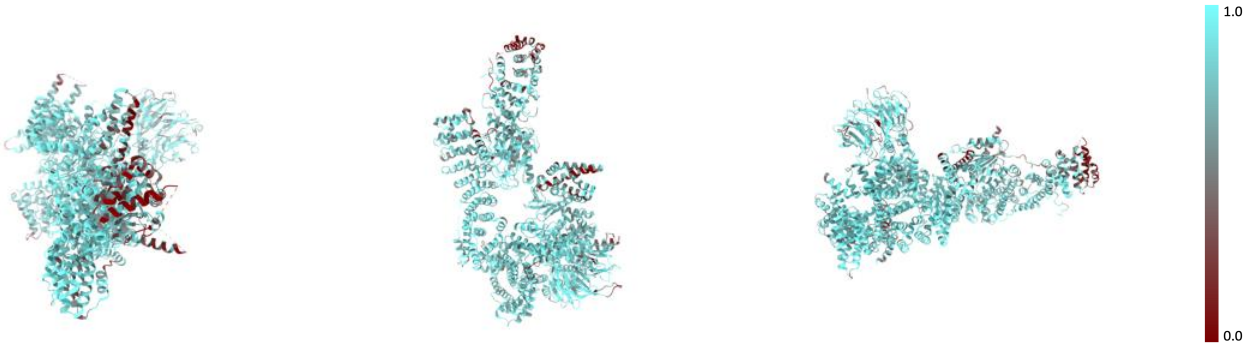
9.2 Q-score mapped to coordinate model (i)



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.

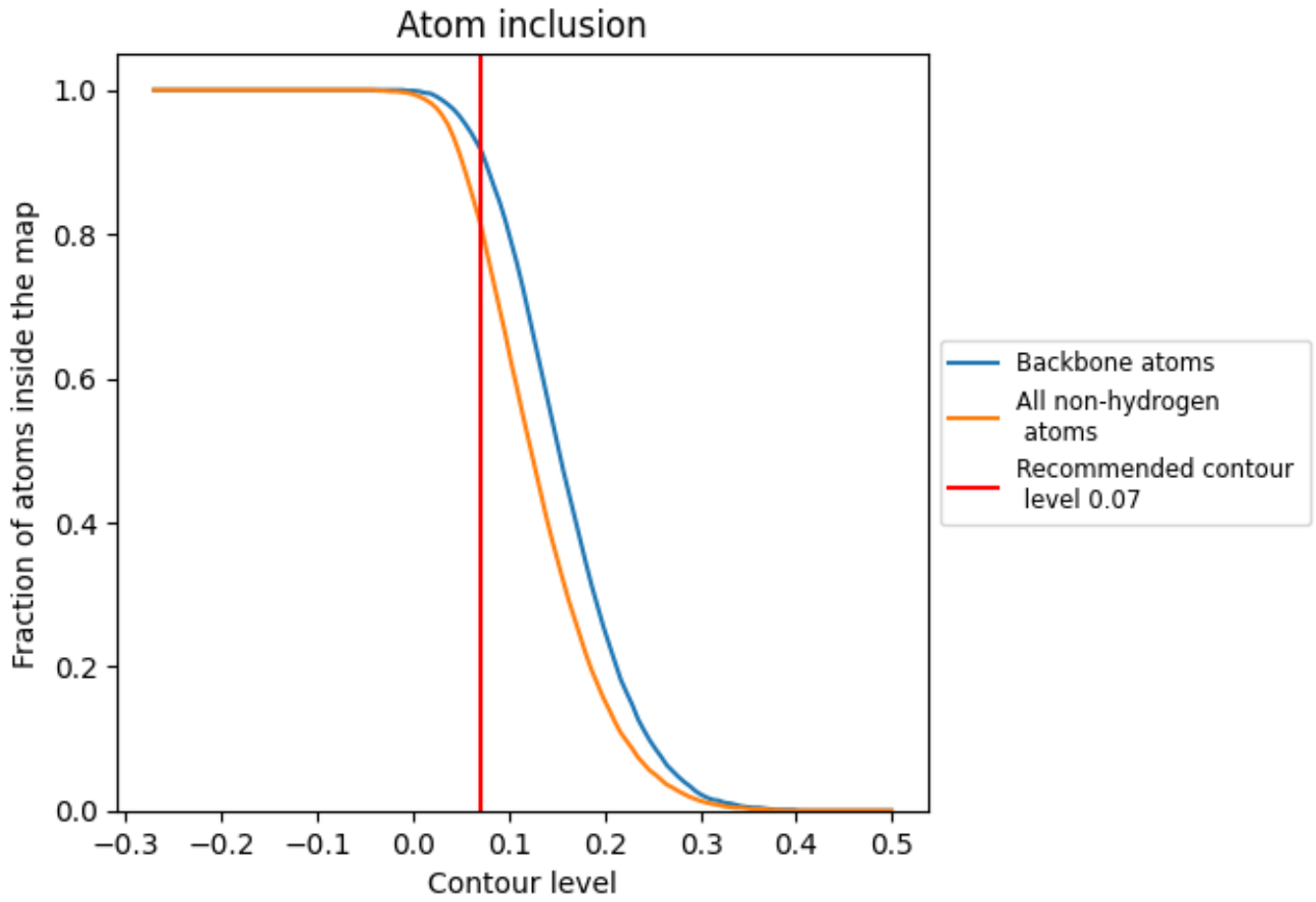
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.07).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 82% 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 (0.07) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.8160	0.3020
A	0.8520	0.3200
C	0.7960	0.2420
E	0.7340	0.2870
G	0.5310	0.2020