# wwPDB EM Validation Summary Report

Nov 14, 2022 – 10:37 PM EST

| | | |
|---|---|---|
| PDB ID | : | 7JPU |
| EMDB ID | : | EMD-22423 |
| Title | : | Structure of an endocytic receptor |
| Authors | : | Gully, B.S.; Rossjohn, J.; Berry, R. |
| Deposited on | : | 2020-08-09 |
| Resolution | : | 5.00 Å(reported) |
| Based on initial models | : | 1DQO, 1QDD, 2V5P |

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.

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

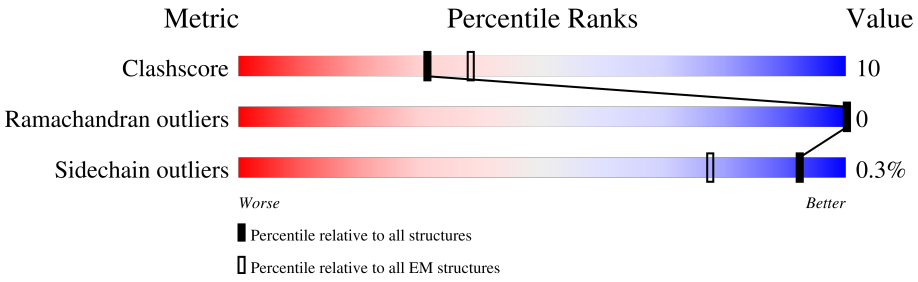
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev43 |
| MolProbity | : | 4.02b-467 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| MapQ | : | 1.9.9 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.31.2 |

# 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 5.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|---|---|---|
| Clashscore | 158937 | 4297 |
| Ramachandran outliers | 154571 | 4023 |
| Sidechain outliers | 154315 | 3826 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 1722 | 7% 51% 16% 33% |
| 1 | B | 1722 | 8% 52% 15% 33% |
| 1 | C | 1722 | 8% 51% 16% 33% |
| 1 | D | 1722 | 8% 53% 14% 33% |

## 2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 35936 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 Lymphocyte antigen 75.

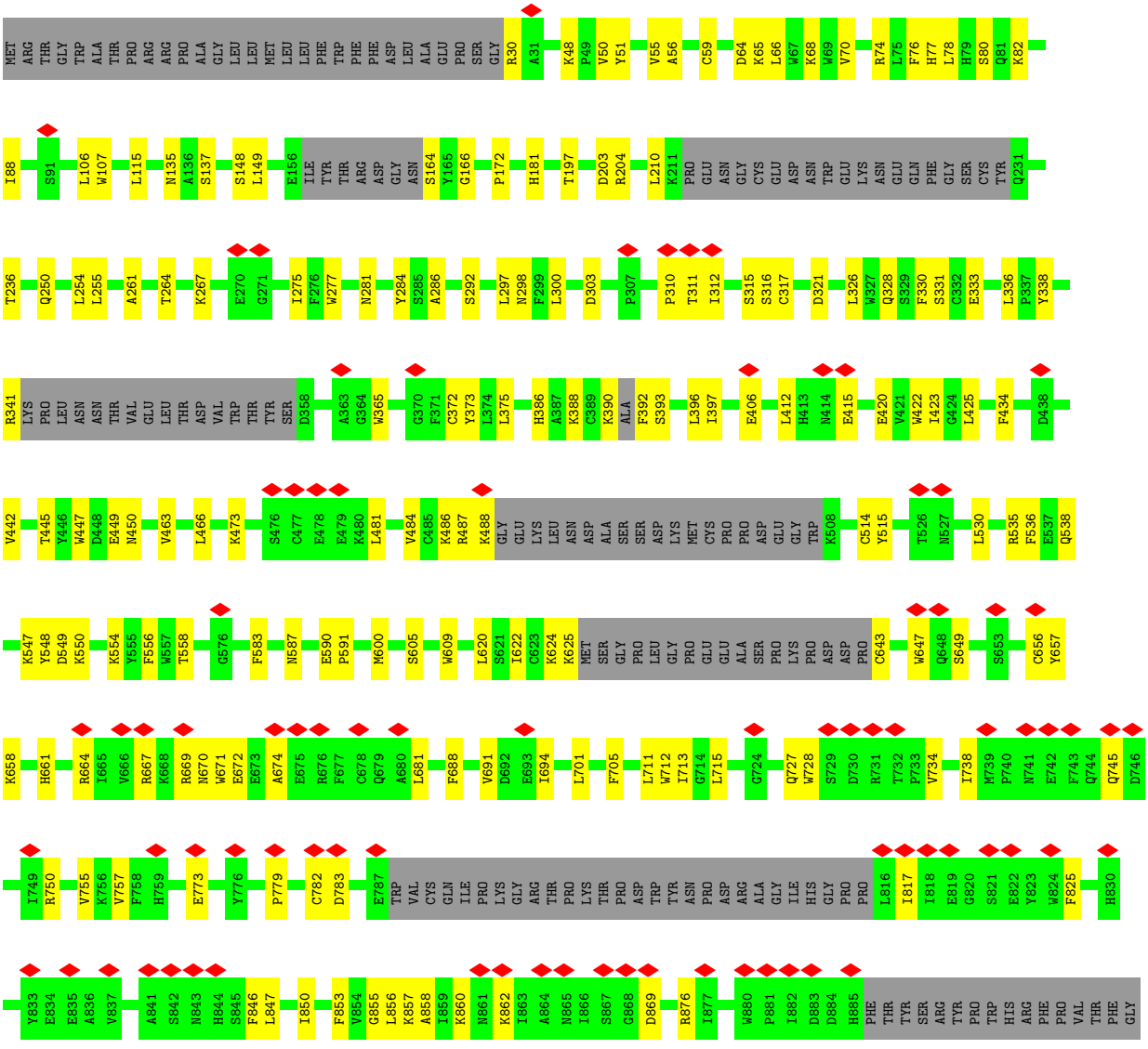
| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 1156 | Total | C | N | O | S | 0 | 0 |
| | | | 8986 | 5794 | 1522 | 1611 | 59 | | |
| 1 | B | 1156 | Total | C | N | O | S | 0 | 0 |
| | | | 8986 | 5794 | 1522 | 1611 | 59 | | |
| 1 | C | 1156 | Total | C | N | O | S | 0 | 0 |
| | | | 8986 | 5794 | 1522 | 1611 | 59 | | |
| 1 | D | 1155 | Total | C | N | O | S | 0 | 0 |
| | | | 8978 | 5788 | 1521 | 1610 | 59 | | |

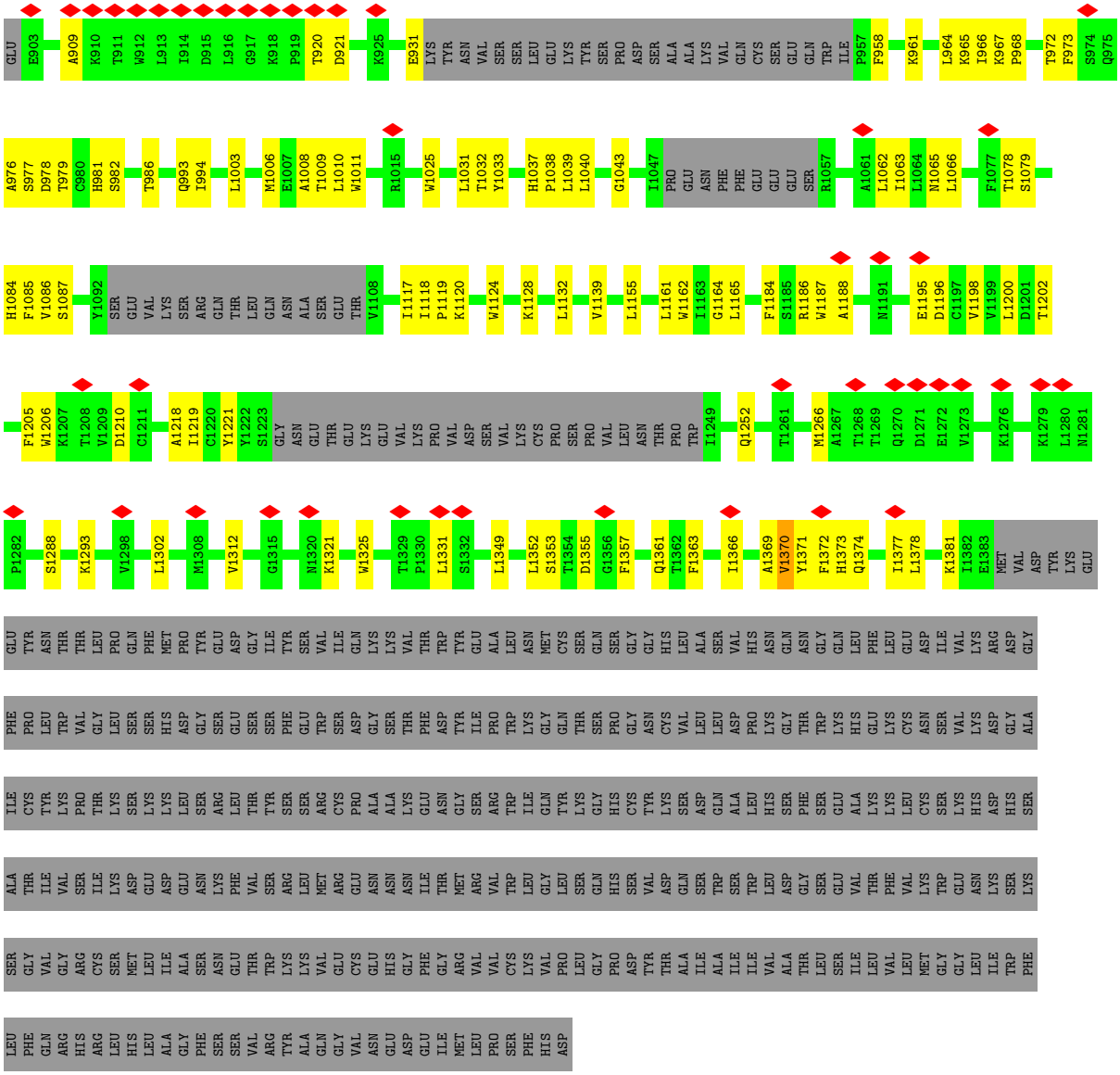
# 3 Residue-property plots (i)

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: Lymphocyte antigen 75

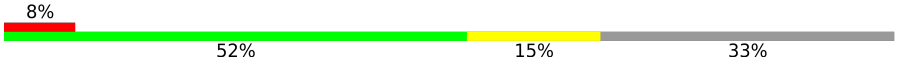
Chain A:

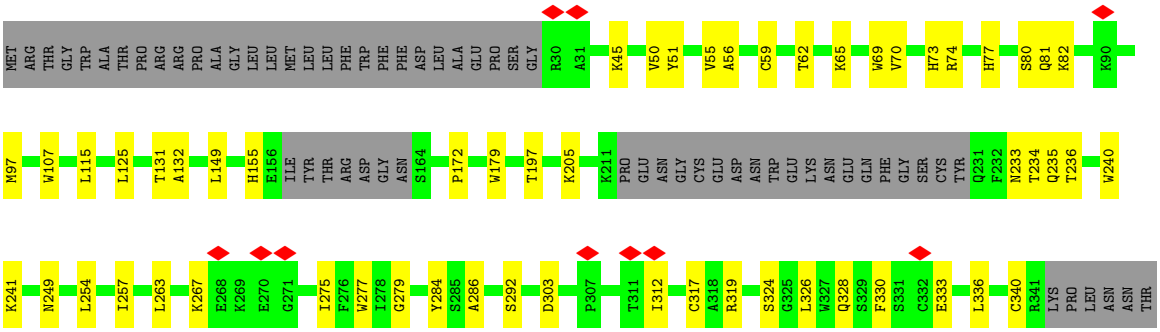



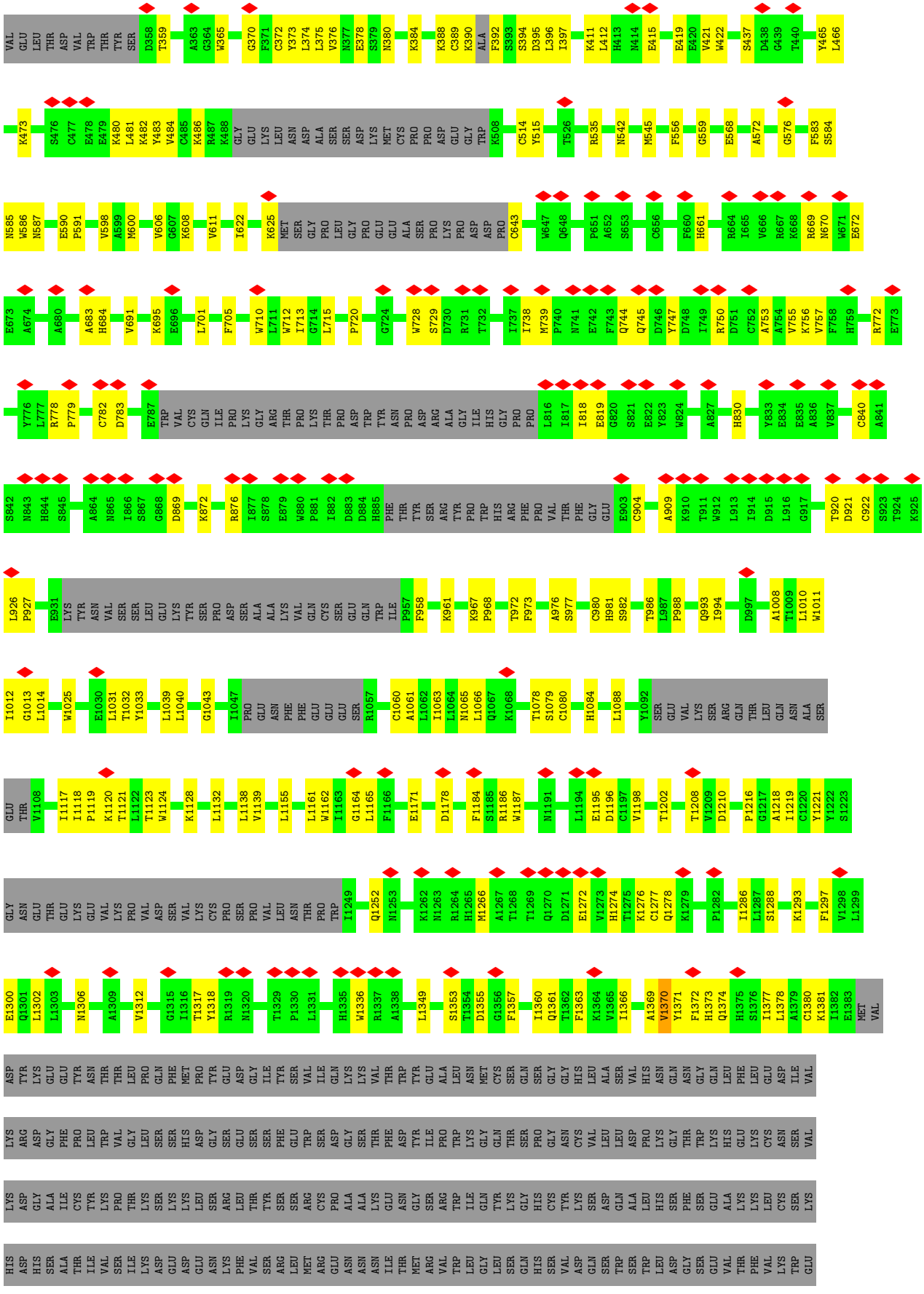


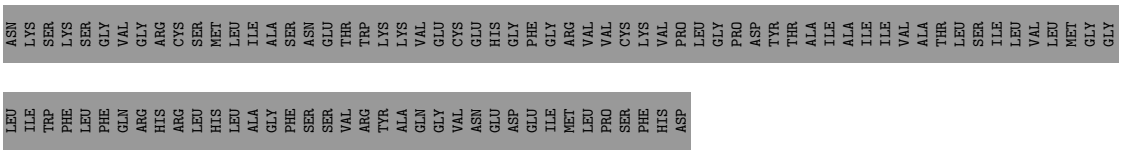
• Molecule 1: Lymphocyte antigen 75

Chain B:



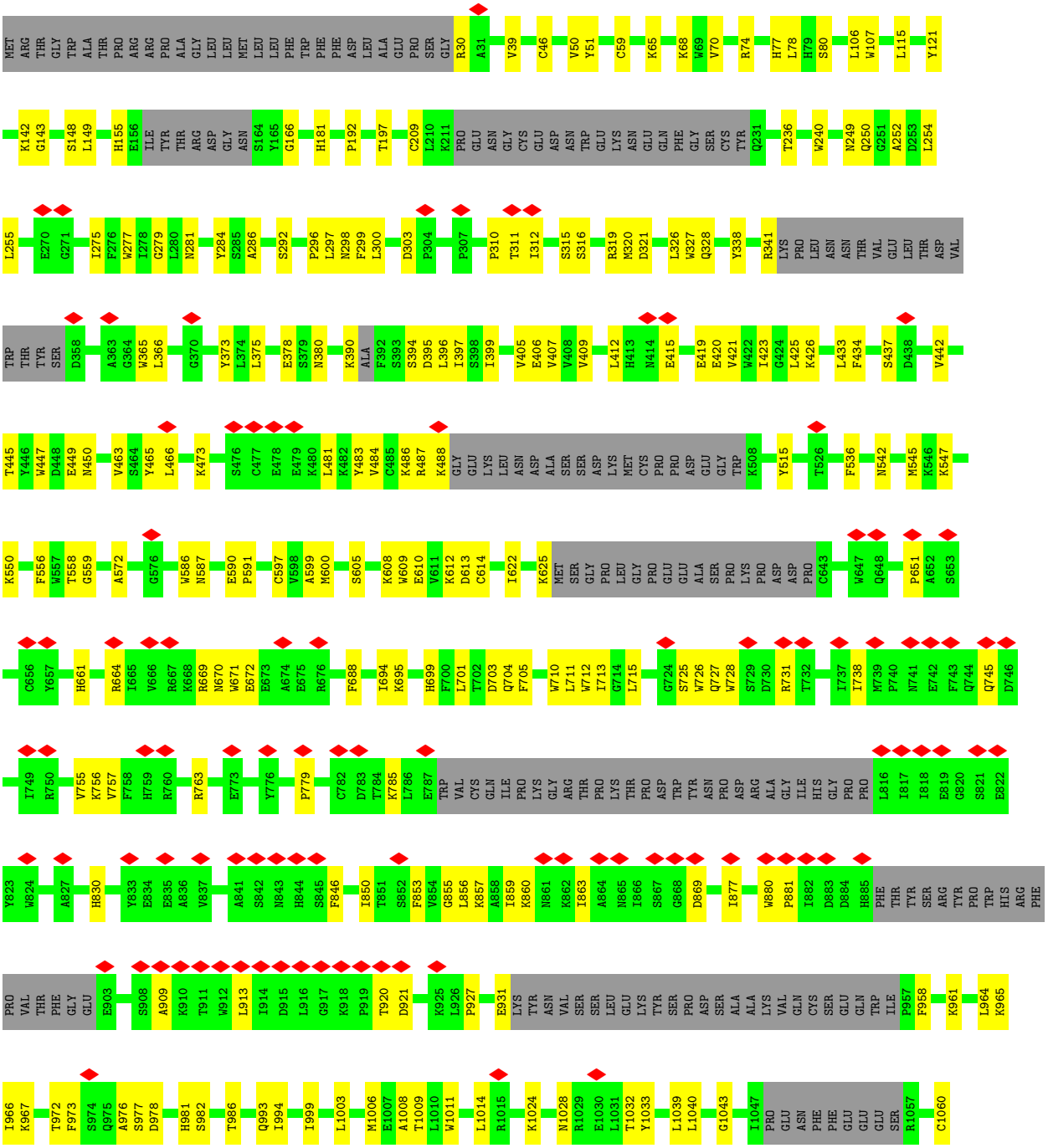



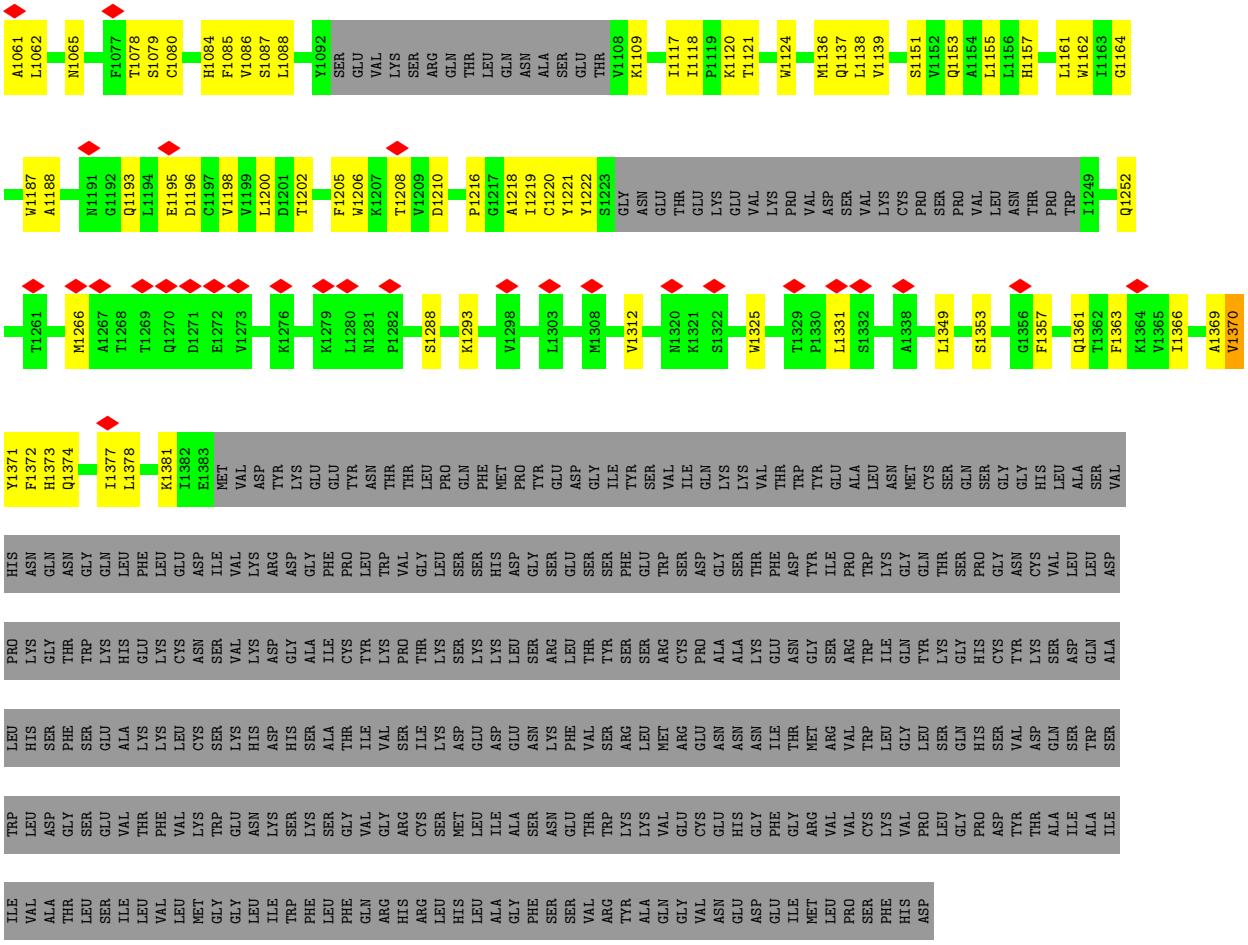




• Molecule 1: Lymphocyte antigen 75

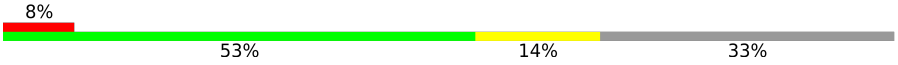
Chain C:

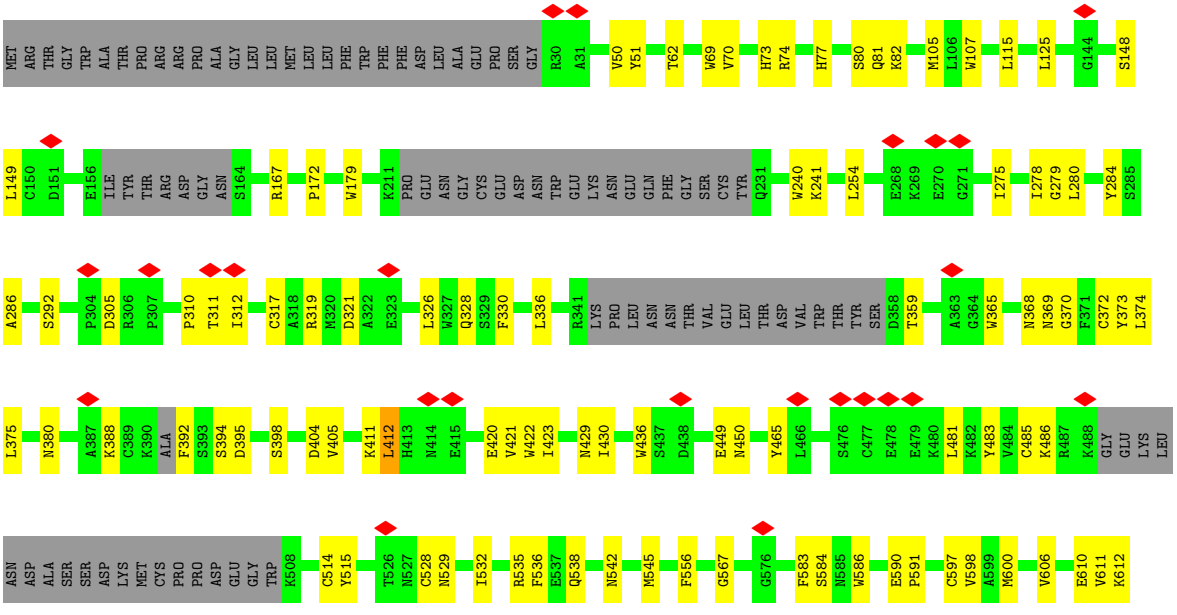



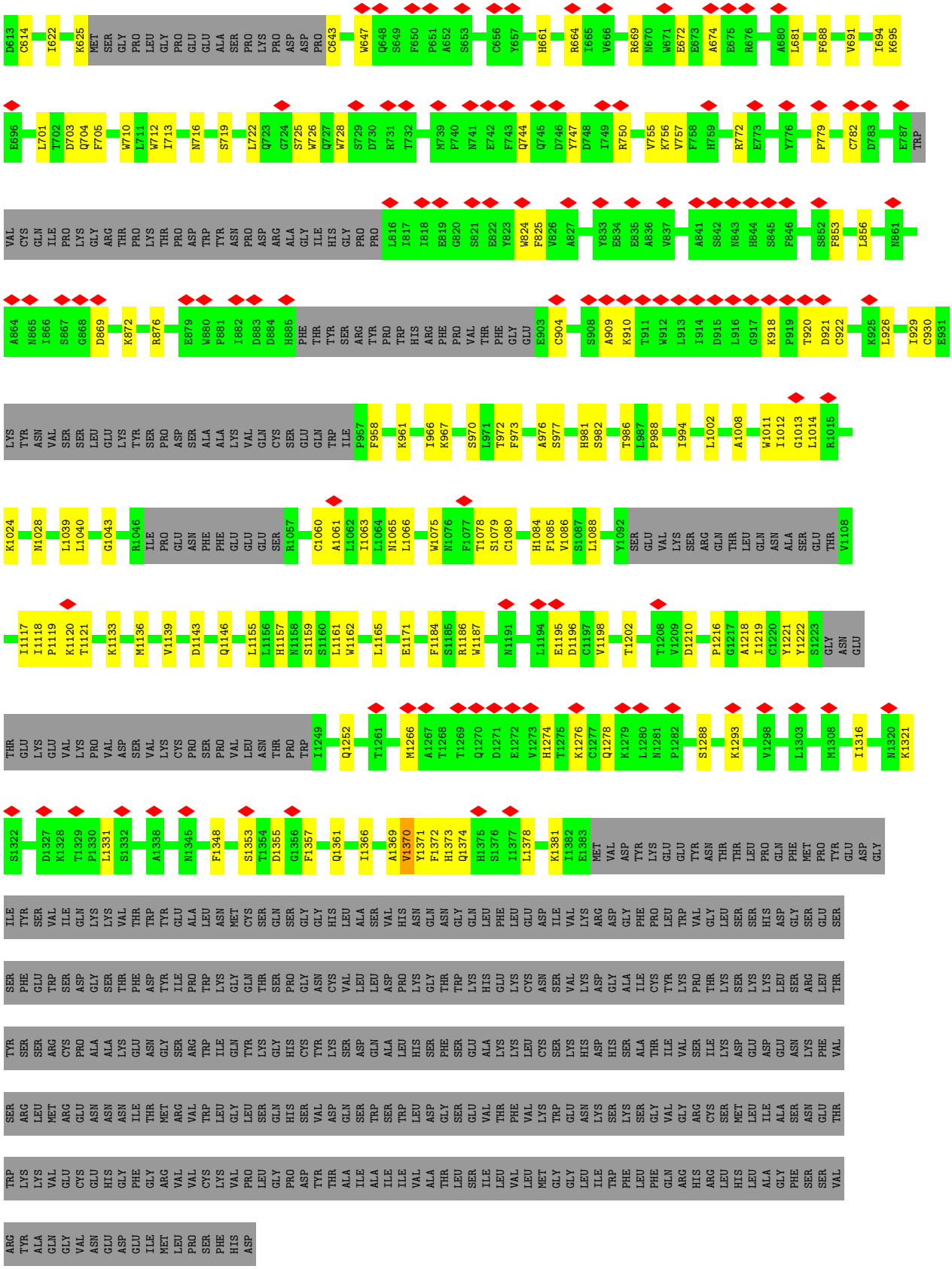


• Molecule 1: Lymphocyte antigen 75

Chain D:




D613 C614 I622 K625 MET SER GLY PRO LEU GLY PRO GLU GLU ALA SER PRO LYS PRO ASP ASP PRO C643 W647 Q648 S649 F650 P651 A652 S653 C656 Y657 H661 R664 I665 V666 R669 N670 W671 E672 E673 A674 E675 R676 A680 L681 F688 V691 I694 K695
E696 L701 T702 D703 Q704 F705 W710 L711 W712 I713 N716 S719 L722 Q723 G724 S725 W726 Q727 W728 S729 D730 R731 T732 W739 P740 N741 E742 F743 Q744 Q745 D746 Y747 D748 I749 R750 V755 K756 V757 F758 H759 R772 E773 Y776 P779 C782 D783 E787 TRP
VAL CYS GLN ILE PRO LYS GLY ARG THR PRO LYS THR PRO ASP TRP TYR ASN PRO ASP ARG ALA GLY ILE HIS GLY PRO PRO L816 I817 I818 E819 G820 S821 E822 Y823 W824 F825 V826 A827 Y833 E834 E835 A836 V837 A841 S842 N843 H844 S845 F846 S852 F853 L856 N861
A864 N865 I866 S867 G868 D869 K872 R876 E879 W880 P881 I882 D883 D884 H885 PHE THR TYR SER ARG TYR PRO TRP HIS ARG PHE PRO VAL THR PHE GLY GLU E903 C904 S908 A909 K910 T911 W912 L913 I914 D915 L916 G917 K918 P919 T920 D921 C922 K925 L926 I929 C930 E931
LYS TYR ASN VAL SER SER LEU GLU LYS TYR SER PRO ASP SER ALA ALA LYS VAL GLN CYS SER GLU GLN TRP ILE P957 F958 K961 I966 K967 S970 L971 T972 F973 A976 S977 H981 S982 T986 L987 P988 I994 L1002 A1008 W1011 I1012 G1013 L1014 R1015
K1024 N1028 L1039 L1040 G1043 R1046 ILE PRO GLU ASN PHE PHE GLU GLU GLU SER R1057 C1060 A1061 L1062 I1063 L1064 N1065 L1066 W1075 N1076 F1077 T1078 S1079 C1080 H1084 F1085 V1086 S1087 L1088 Y1092 SER GLU VAL LYS SER ARG GLN THR LEU GLN ASN ALA SER GLU THR V1108
I1117 I1118 P1119 K1120 T1121 K1133 M1136 V1139 D1143 Q1146 L1155 L1156 H1157 N1158 S1159 S1160 L1161 W1162 L1165 E1171 F1184 S1185 R1186 W1187 N1191 L1194 E1195 D1196 C1197 V1198 T1202 T1208 V1209 D1210 P1216 G1217 A1218 I1219 C1220 Y1221 Y1222 S1223 GLY ASN GLU
THR GLU LYS GLU VAL LYS PRO VAL ASP SER VAL LYS CYS PRO SER PRO VAL LEU ASN THR PRO TRP I1249 Q1252 T1261 M1266 A1267 T1268 T1269 Q1270 D1271 E1272 V1273 H1274 T1275 K1276 C1277 Q1278 K1279 L1280 N1281 P1282 S1288 K1293 V1298 L1303 M1308 I1316 N1320 K1321
S1322 D1327 K1328 T1329 P1330 L1331 S1332 A1338 N1345 F1348 S1353 T1354 D1355 G1356 F1357 Q1361 I1366 A1369 V1370 Y1371 F1372 H1373 Q1374 H1375 S1376 I1377 L1378 K1381 I1382 E1383 MET VAL ASP TYR LYS GLU GLU TYR ASN THR THR LEU PRO GLN PHE MET PRO TYR GLU ASP GLY
ILE TYR SER VAL ILE GLN LYS LYS VAL THR TRP TYR GLU ALA LEU ASN MET CYS SER GLN SER GLY GLY HIS LEU ALA SER VAL HIS ASN GLN ASN GLY HIS LEU PHE LEU GLU ASP ILE VAL LYS ARG ASP GLY PHE PRO LEU TRP VAL GLY LEU SER SER HIS ASP GLY SER GLU SER
SER PHE GLU TRP SER ASP GLY SER THR PHE ASP TYR ILE PRO TRP LYS GLY GLN THR SER PRO GLY ASN CYS VAL LEU LEU ASP PRO LYS GLY THR TRP LYS HIS GLU LYS CYS ASN SER VAL LYS ASP GLY ALA ILE CYS TYR LYS PRO THR LYS SER SER LYS LYS LEU SER ARG LEU THR
TYR SER SER ARG CYS PRO ALA ALA LYS GLU ASN GLY SER ARG TRP ILE GLN TYR LYS GLY HIS CYS TYR LYS SER ASP GLN ALA LEU HIS SER PHE SER GLU ALA LYS LYS LEU CYS SER LYS HIS ASP HIS SER ALA THR ILE VAL SER LYS ASP GLU GLU ASN LYS PHE VAL
SER ARG LEU MET ARG GLU ASN ASN ILE THR MET ARG VAL TRP LEU GLY LEU SER GLN HIS SER VAL ASP GLN SER TRP SER TRP LEU ASP GLY SER GLU VAL THR PHE VAL LYS TRP GLU ASN LYS SER LYS SER GLY VAL GLY ARG CYS SER MET LEU ILE ALA SER ASN GLU THR
TRP LYS LYS VAL GLU CYS GLU HIS GLY ARG VAL VAL CYS LYS VAL PRO LEU GLY PRO ASP TYR THR ALA ILE ALA ILE LEU VAL ALA THR LEU SER ILE LEU VAL LEU LEU MET GLY GLY LEU ILE TRP PHE LEU PHE GLN ARG HIS ARG LEU HIS LEU ALA GLY PHE SER SER VAL
ARG TYR ALA GLN GLY VAL ASN GLU ASP GLU ILE MET LEU PRO SER PHE HIS ASP

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, D2 | Depositor |
| Number of particles used | 102569 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/Å^2$) | 63 | Depositor |
| Minimum defocus (nm) | Not provided | |
| Maximum defocus (nm) | Not provided | |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |
| Maximum map value | 0.071 | Depositor |
| Minimum map value | -0.033 | Depositor |
| Average map value | 0.001 | Depositor |
| Map value standard deviation | 0.004 | Depositor |
| Recommended contour level | 0.009 | Depositor |
| Map size (Å) | 248.04, 248.04, 248.04 | wwPDB |
| Map dimensions | 234, 234, 234 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.06, 1.06, 1.06 | 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 | 0.24 | 0/9247 | 0.45 | 1/12580 (0.0%) |
| 1 | B | 0.24 | 0/9247 | 0.44 | 1/12580 (0.0%) |
| 1 | C | 0.24 | 0/9247 | 0.45 | 1/12580 (0.0%) |
| 1 | D | 0.24 | 0/9239 | 0.44 | 2/12569 (0.0%) |
| All | All | 0.24 | 0/36980 | 0.45 | 5/50309 (0.0%) |

There are no bond length outliers.

All (5) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 1 | A | 1370 | VAL | C-N-CA | 6.15 | 137.07 | 121.70 |
| 1 | C | 1370 | VAL | C-N-CA | 6.12 | 137.00 | 121.70 |
| 1 | D | 1370 | VAL | C-N-CA | 6.11 | 136.97 | 121.70 |
| 1 | B | 1370 | VAL | C-N-CA | 6.00 | 136.69 | 121.70 |
| 1 | D | 412 | LEU | CA-CB-CG | 5.61 | 128.20 | 115.30 |

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 | 8986 | 0 | 8303 | 186 | 0 |
| 1 | B | 8986 | 0 | 8303 | 161 | 0 |
| 1 | C | 8986 | 0 | 8303 | 185 | 0 |
| 1 | D | 8978 | 0 | 8292 | 155 | 0 |

*Continued on next page...*

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| All | All | 35936 | 0 | 33201 | 672 | 0 |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 672 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:423:ILE:HG23 | 1:A:463:VAL:HG13 | 1.54 | 0.89 |
| 1:C:423:ILE:HG23 | 1:C:463:VAL:HG13 | 1.60 | 0.84 |
| 1:B:421:VAL:HB | 1:B:465:TYR:HB2 | 1.63 | 0.80 |
| 1:B:69:TRP:HE1 | 1:B:73:HIS:HA | 1.45 | 0.79 |
| 1:B:713:ILE:HG13 | 1:B:755:VAL:H | 1.48 | 0.78 |

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 | 1130/1722 (66%) | 1046 (93%) | 84 (7%) | 0 | 100 | 100 |
| 1 | B | 1130/1722 (66%) | 1052 (93%) | 78 (7%) | 0 | 100 | 100 |
| 1 | C | 1130/1722 (66%) | 1051 (93%) | 79 (7%) | 0 | 100 | 100 |
| 1 | D | 1129/1722 (66%) | 1050 (93%) | 79 (7%) | 0 | 100 | 100 |
| All | All | 4519/6888 (66%) | 4199 (93%) | 320 (7%) | 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 | 913/1536 (59%) | 912 (100%) | 1 (0%) | 93 | 96 |
| 1 | B | 913/1536 (59%) | 909 (100%) | 4 (0%) | 91 | 94 |
| 1 | C | 913/1536 (59%) | 911 (100%) | 2 (0%) | 93 | 96 |
| 1 | D | 912/1536 (59%) | 908 (100%) | 4 (0%) | 91 | 94 |
| All | All | 3651/6144 (59%) | 3640 (100%) | 11 (0%) | 92 | 95 |

5 of 11 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | D | 241 | LYS |
| 1 | D | 664 | ARG |
| 1 | D | 1133 | LYS |
| 1 | D | 910 | LYS |
| 1 | B | 1277 | CYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 1 | B | 1252 | GLN |
| 1 | D | 1157 | HIS |
| 1 | C | 249 | ASN |
| 1 | D | 1037 | HIS |
| 1 | D | 585 | 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 monosaccharides in this entry.

## 5.6 Ligand geometry (i)

There are no ligands in this entry.

## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

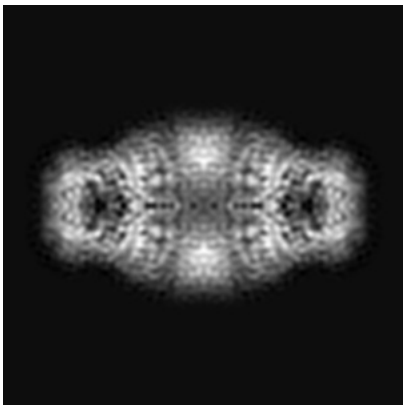
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-22423. These allow visual inspection of the internal detail of the map and identification of artifacts.

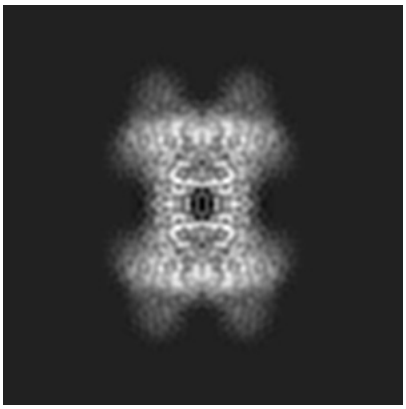
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

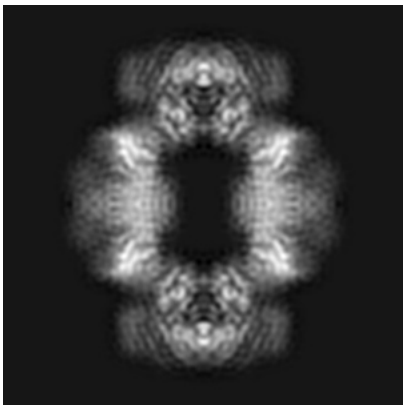
### 6.1.1 Primary map



X

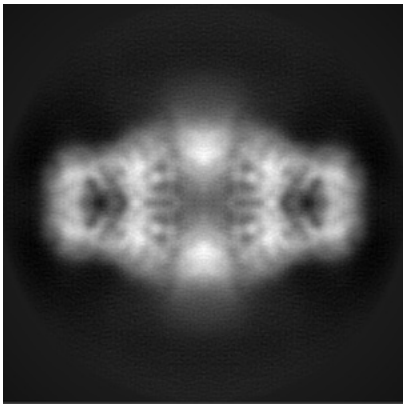


Y

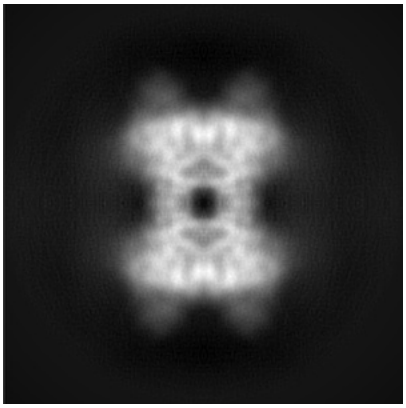


Z

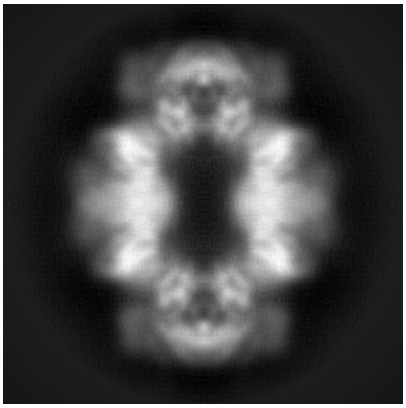
### 6.1.2 Raw map



X



Y



Z

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

## 6.2 Central slices (i)

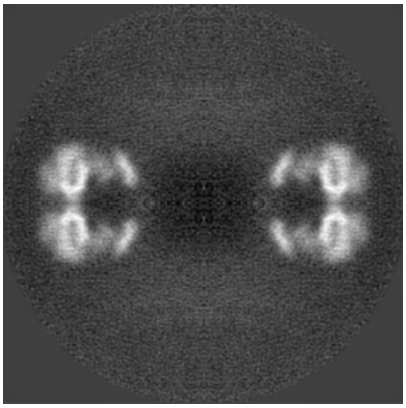
### 6.2.1 Primary map

X Index: 117

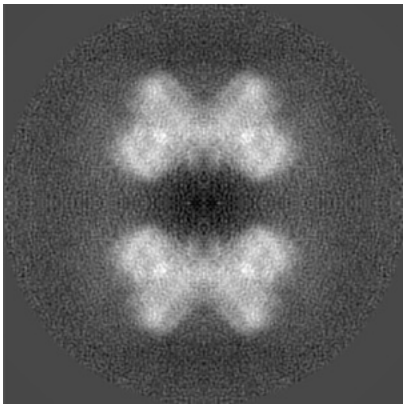
Y Index: 117

Z Index: 117

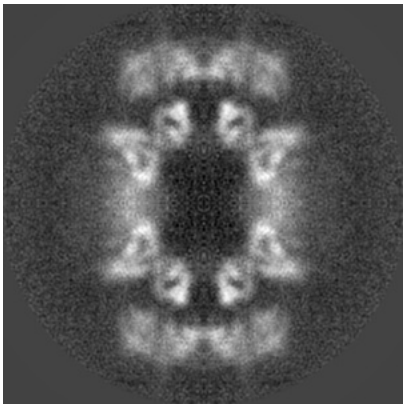
### 6.2.2 Raw map



X Index: 117



Y Index: 117

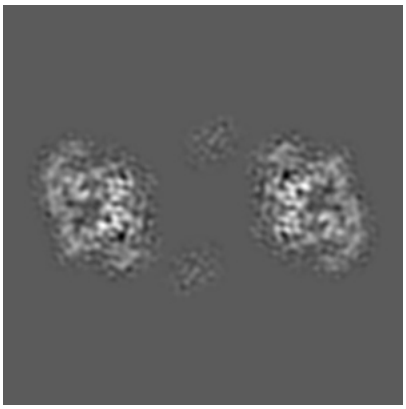


Z Index: 117

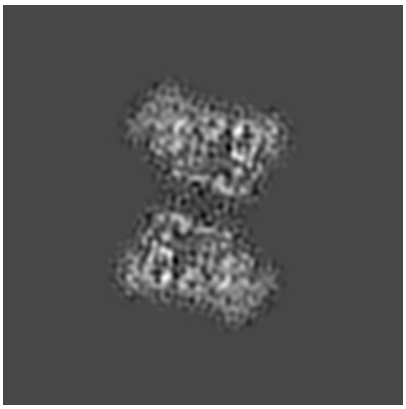
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

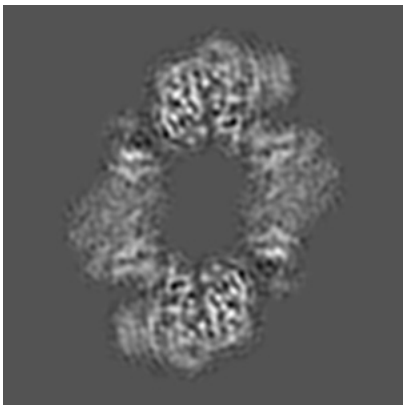
### 6.3.1 Primary map



X Index: 130

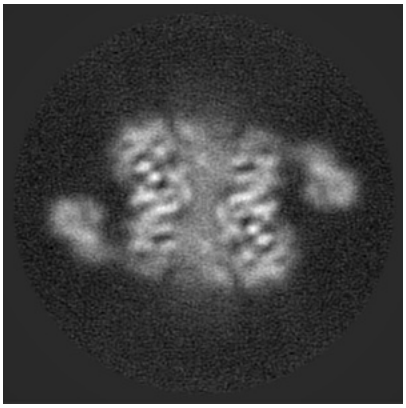


Y Index: 154

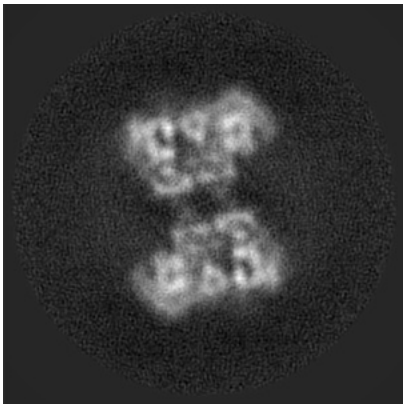


Z Index: 100

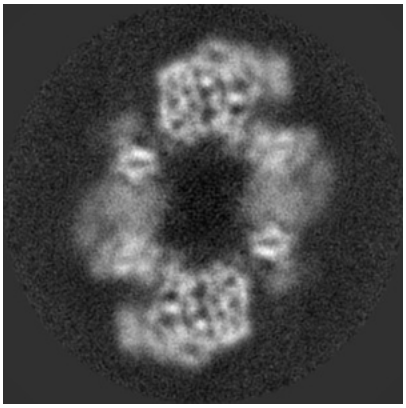
### 6.3.2 Raw map



X Index: 77



Y Index: 79

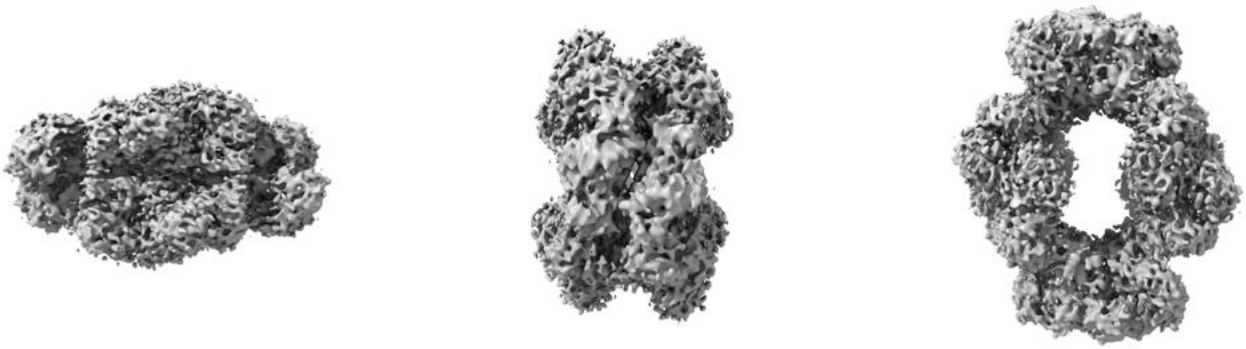


Z Index: 102

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

## 6.4 Orthogonal surface views (i)

### 6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

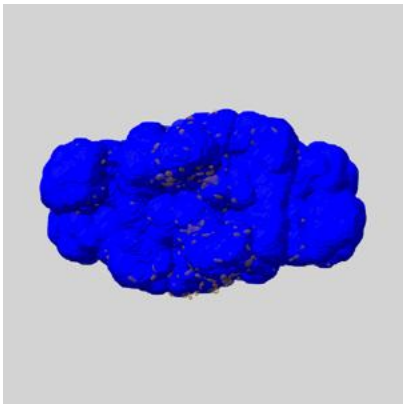
## 6.5 Mask visualisation (i)

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

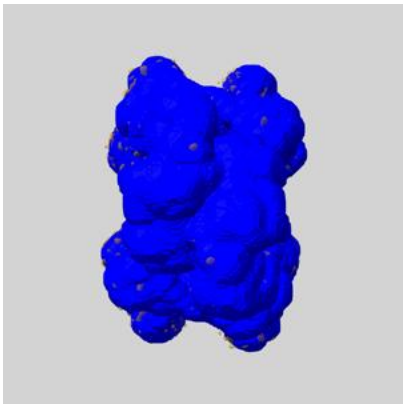
A mask typically either:

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

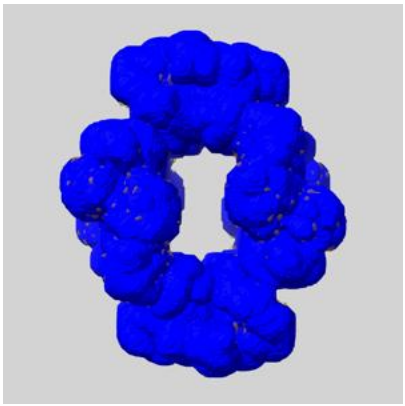
### 6.5.1 emd_22423_msk_1.map (i)



X



Y

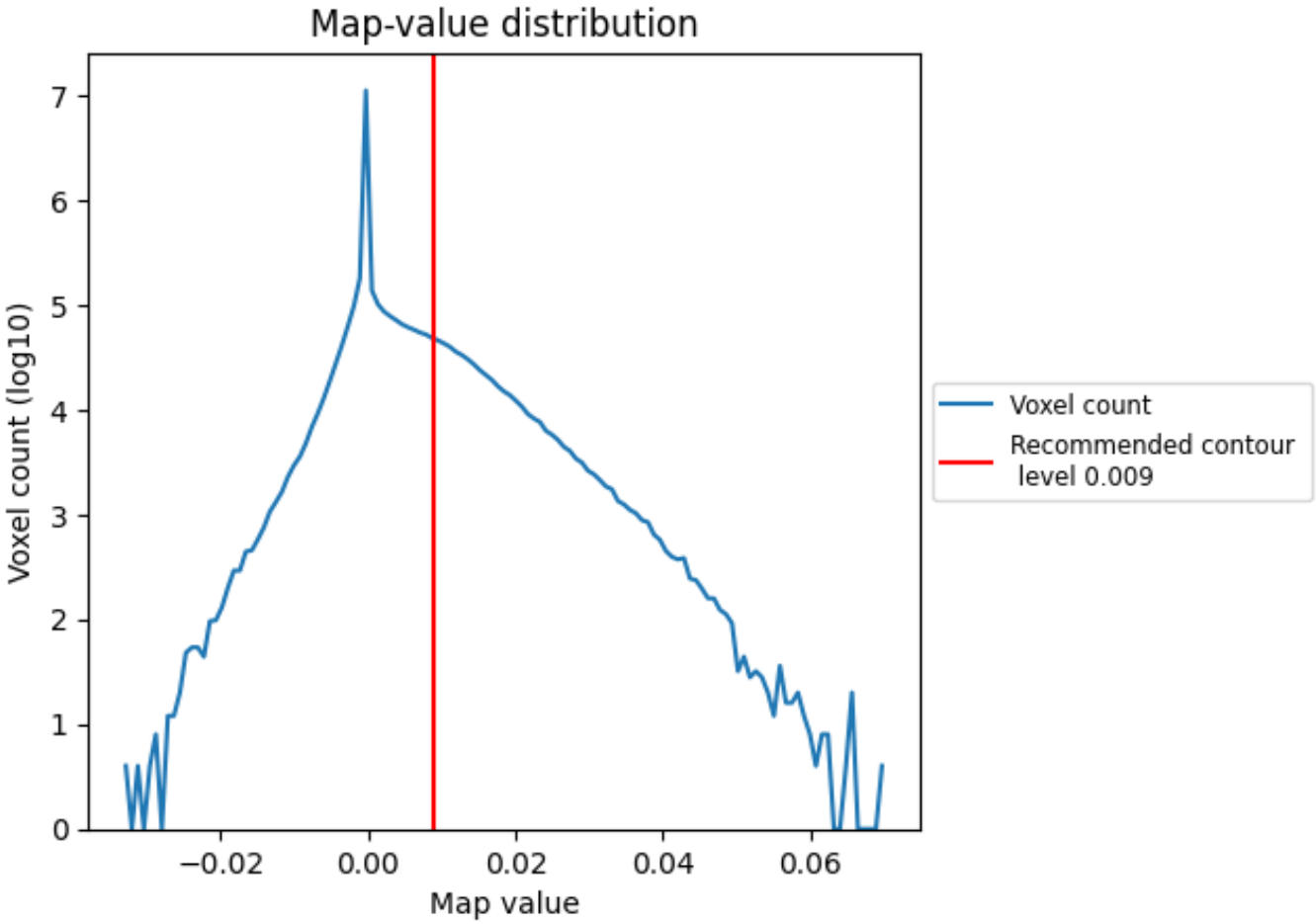


Z

# 7 Map analysis

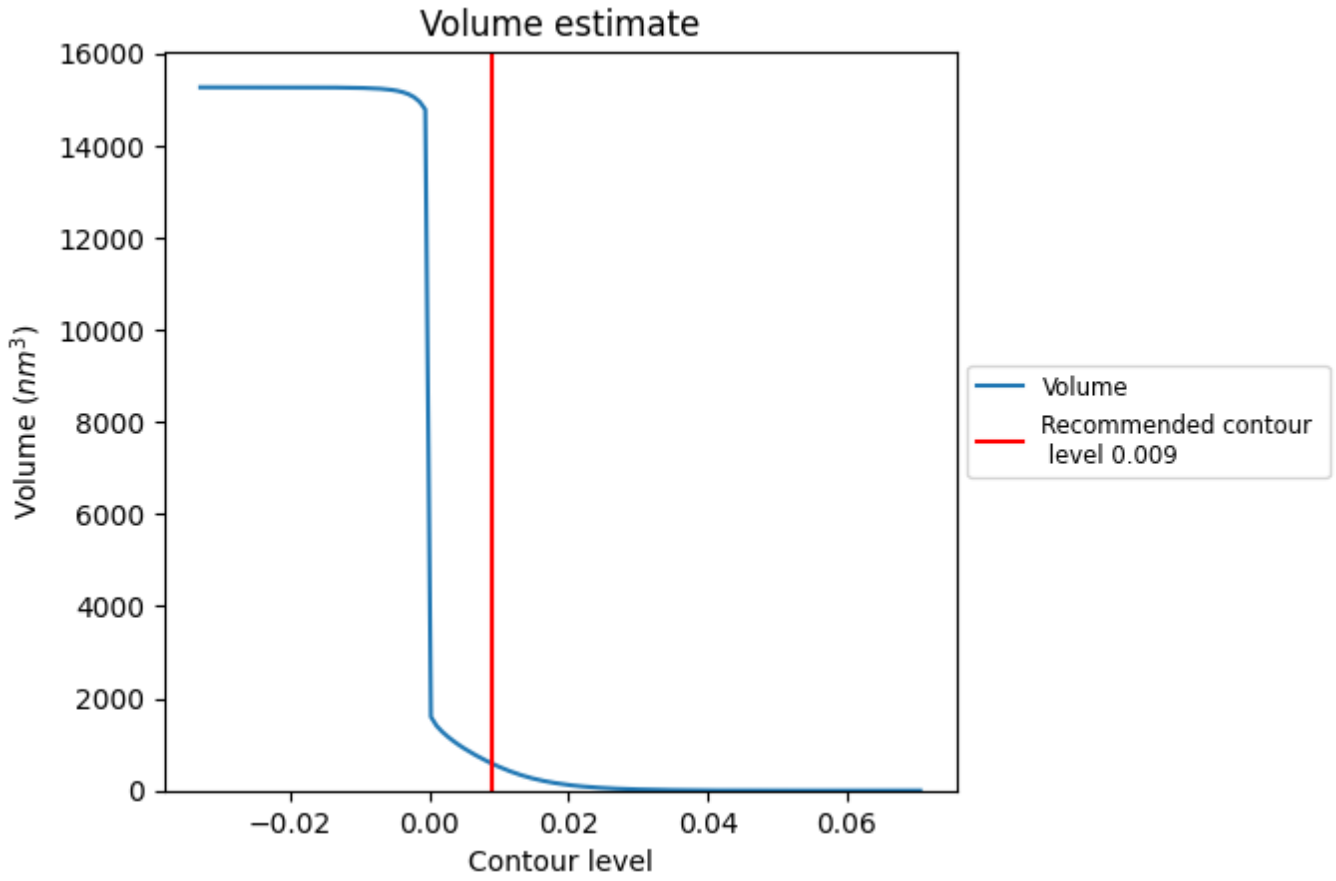
This section contains the results of statistical analysis of the map.

## 7.1 Map-value distribution




The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

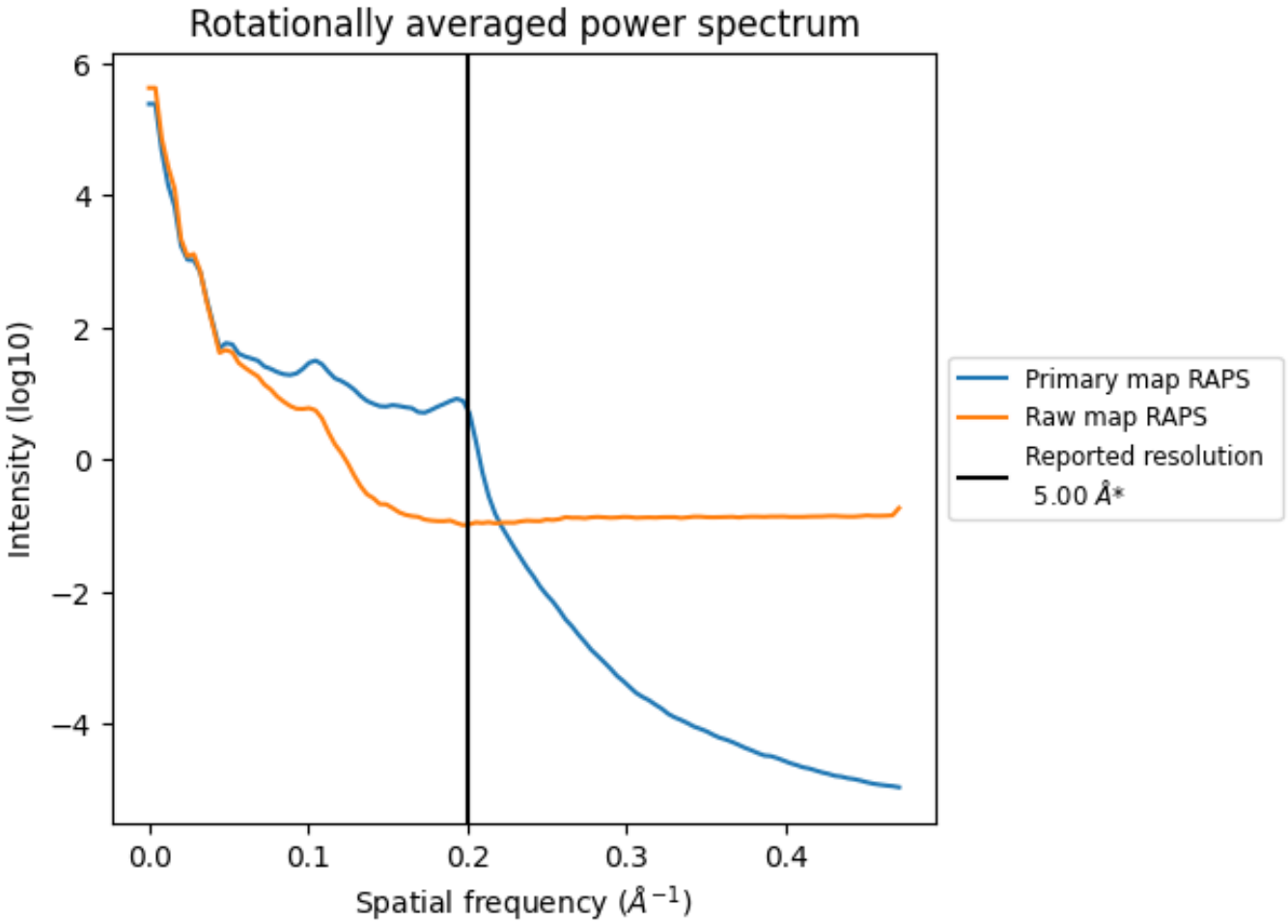
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 588 $nm^3$; this corresponds to an approximate mass of 531 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)

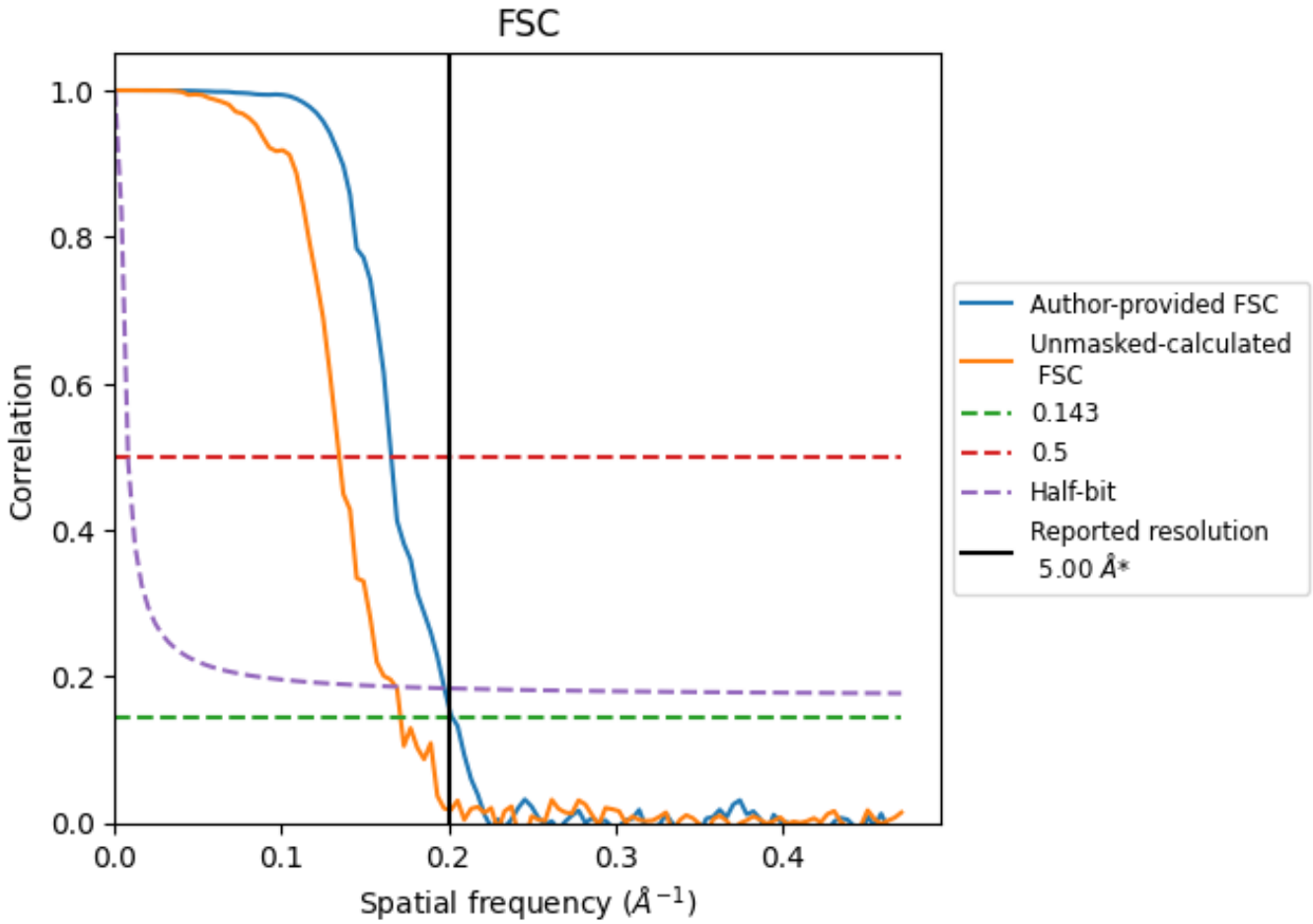



*Reported resolution corresponds to spatial frequency of 0.200 Å$^{-1}$

# 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 0.200 Å$^{-1}$

## 8.2 Resolution estimates (i)

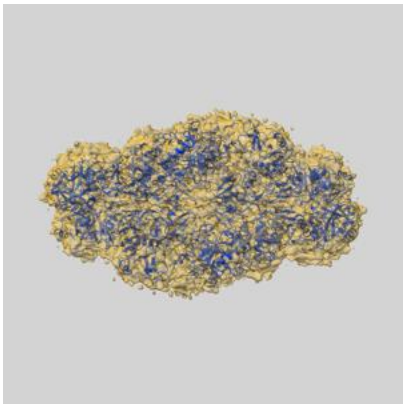
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 5.00 | - | - |
| Author-provided FSC curve | 4.94 | 6.03 | 5.06 |
| Unmasked-calculated* | 5.83 | 7.43 | 5.93 |

*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 5.83 differs from the reported value 5.0 by more than 10 %

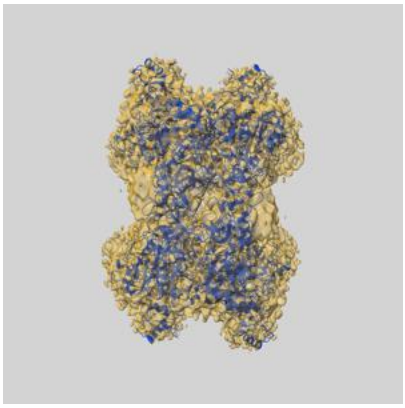
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-22423 and PDB model 7JPU. Per-residue inclusion information can be found in section 3 on page 4.

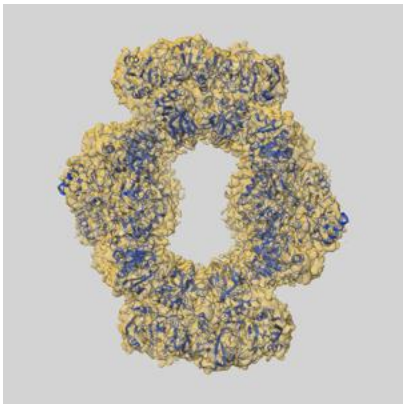
## 9.1 Map-model overlay



X



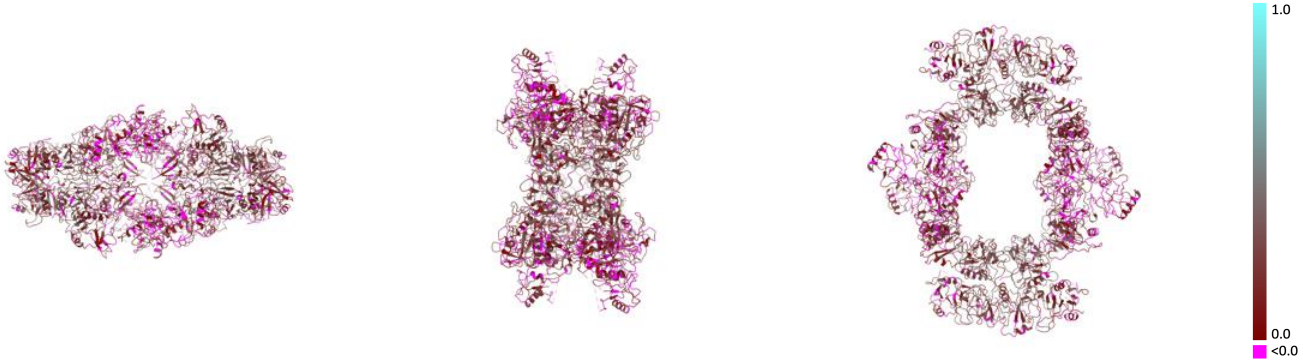
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.009 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.

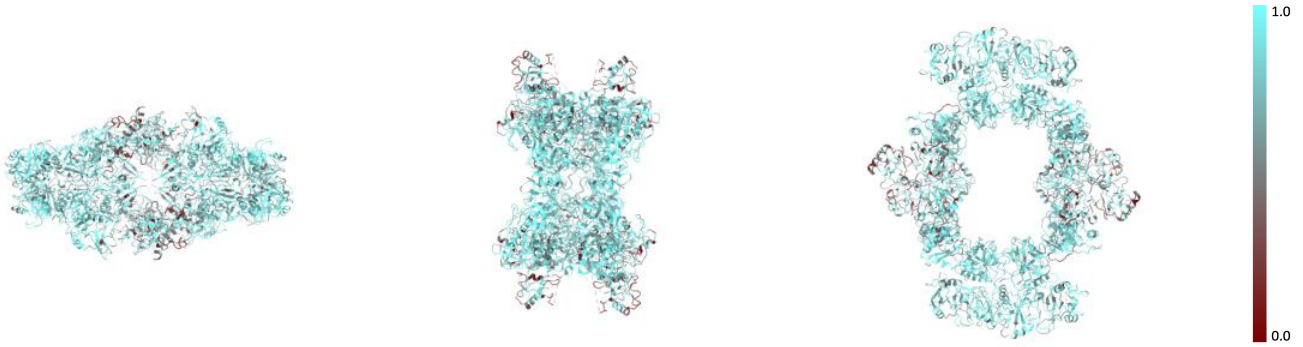
## 9.2 Q-score mapped to coordinate model (i)




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.

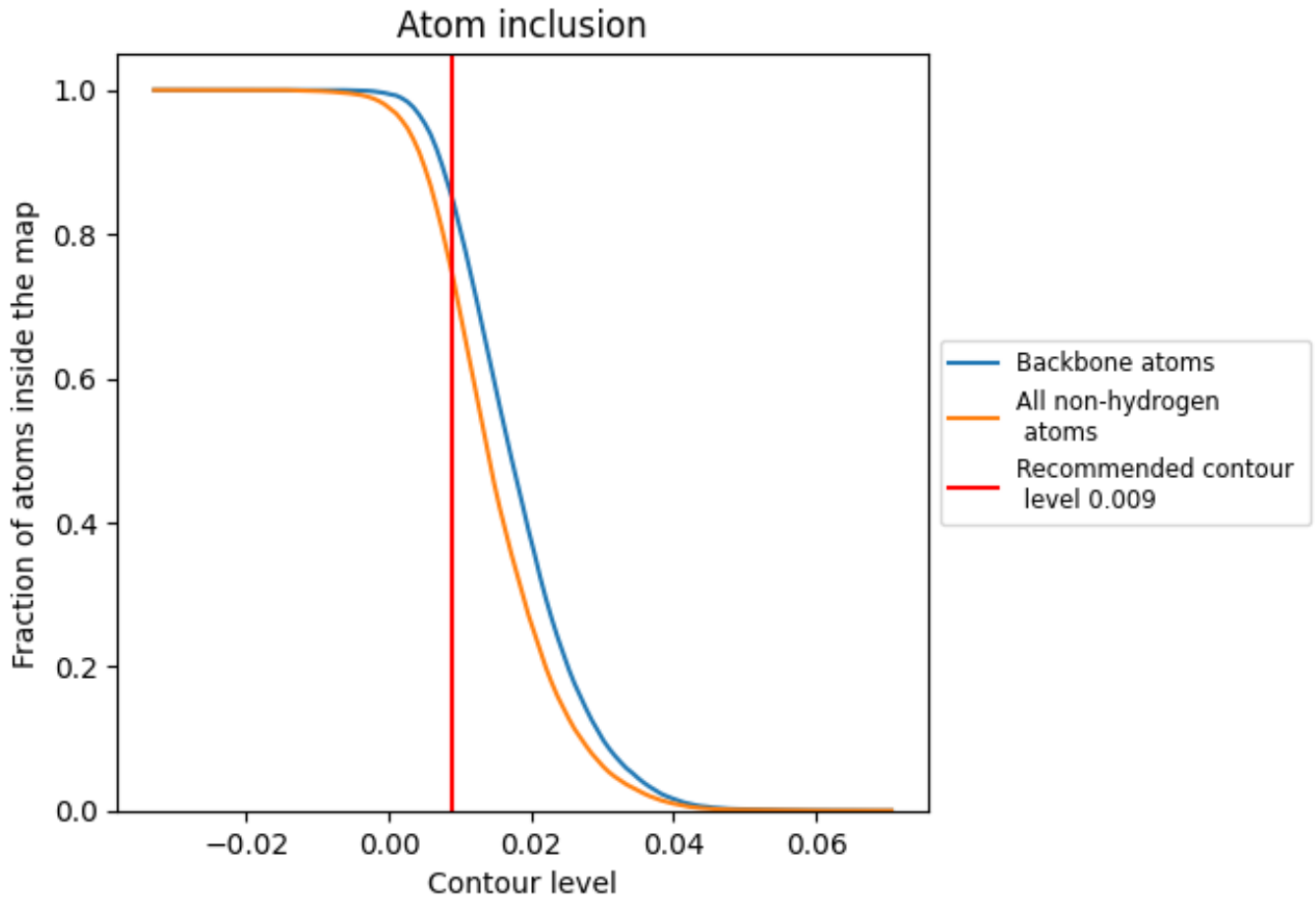
## 9.3 Atom inclusion mapped to coordinate model (i)




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 (0.009).

## 9.4 Atom inclusion (i)




At the recommended contour level, 85% of all backbone atoms, 74% 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 (0.009) and Q-score for the entire model and for each chain.


| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.7424 | 0.1610 |
| A | 0.7454 | 0.1620 |
| B | 0.7408 | 0.1590 |
| C | 0.7430 | 0.1640 |
| D | 0.7406 | 0.1600 |