# wwPDB EM Validation Summary Report (i)

Mar 9, 2026 – 03:28 PM UTC

| | | |
|---|---|---|
| PDB ID | : | 9NVP / pdb_00009nvp |
| EMDB ID | : | EMD-49846 |
| Title | : | Structure of Nanchung-Inactive-Calmodulin in complex with Nicotinamide, EDTA |
| Authors | : | Fedor, J.G.; Lee, S.-Y. |
| Deposited on | : | 2025-03-21 |
| Resolution | : | 2.85 Å(reported) |
| Based on initial model | : | 5wo7 |

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.

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

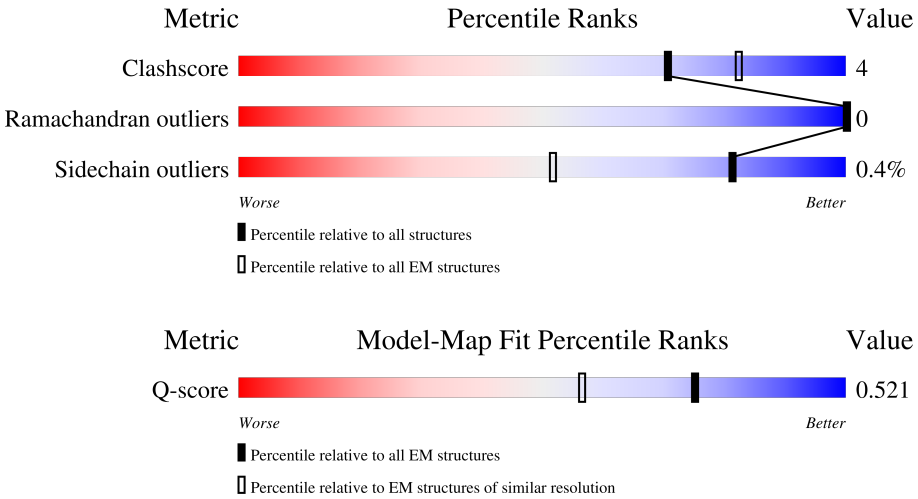
| | | |
|---|---|---|
| EMDB validation analysis | : | 0.0.1.dev132 |
| Mogul | : | 2022.3.0, CSD as543be (2022) |
| MolProbity | : | 4-5-2 with Phenix2.0 |
| Buster-report | : | wwPDB partial adaption of 1.1.7 (2018) |
| Percentile statistics | : | 20250101.v01 (using entries in the PDB archive January 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) | : | 2.49 |

# 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 2.85 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 | 11965 ( 2.35 - 3.35 ) |

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 | B | 984 | 9% 63% 6% 31% |
| 1 | D | 984 | 9% 63% 6% 31% |
| 2 | A | 882 | 9% 74% 7% 19% |
| 2 | C | 882 | 9% 74% 7% 19% |

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| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 3 | E | 149 |   |
| 3 | F | 149 |   |

# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 48920 atoms, of which 24266 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 Inactive.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | B | 679 | Total | C | H | N | O | S | 0 | 0 |
| | | | 10099 | 3336 | 4958 | 867 | 905 | 33 | | |
| 1 | D | 679 | Total | C | H | N | O | S | 0 | 0 |
| | | | 10099 | 3336 | 4958 | 867 | 905 | 33 | | |

There are 14 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| B | 254 | GLN | HIS | conflict | UNP A0A9P0HI19 |
| B | 401 | ILE | LEU | conflict | UNP A0A9P0HI19 |
| B | 427 | ILE | VAL | conflict | UNP A0A9P0HI19 |
| B | 445 | LEU | ILE | conflict | UNP A0A9P0HI19 |
| B | 480 | VAL | ILE | conflict | UNP A0A9P0HI19 |
| B | 487 | ILE | MET | conflict | UNP A0A9P0HI19 |
| B | 607 | VAL | ILE | conflict | UNP A0A9P0HI19 |
| D | 254 | GLN | HIS | conflict | UNP A0A9P0HI19 |
| D | 401 | ILE | LEU | conflict | UNP A0A9P0HI19 |
| D | 427 | ILE | VAL | conflict | UNP A0A9P0HI19 |
| D | 445 | LEU | ILE | conflict | UNP A0A9P0HI19 |
| D | 480 | VAL | ILE | conflict | UNP A0A9P0HI19 |
| D | 487 | ILE | MET | conflict | UNP A0A9P0HI19 |
| D | 607 | VAL | ILE | conflict | UNP A0A9P0HI19 |

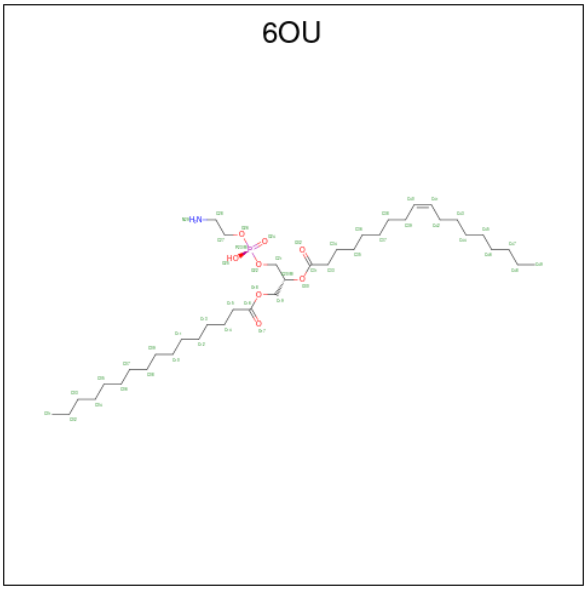
- Molecule 2 is a protein called Nanchung.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | A | 716 | Total | C | H | N | O | S | 0 | 0 |
| | | | 11428 | 3727 | 5680 | 941 | 1024 | 56 | | |
| 2 | C | 716 | Total | C | H | N | O | S | 0 | 0 |
| | | | 11428 | 3727 | 5680 | 941 | 1024 | 56 | | |

- Molecule 3 is a protein called Calmodulin-1.

| Mol | Chain | Residues | Atoms | | | | | | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | E | 131 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1905 | 614 | 905 | 159 | 220 | 7 | | |
| 3 | F | 131 | Total | C | H | N | O | S | 0 | 0 |
| | | | 1905 | 614 | 905 | 159 | 220 | 7 | | |

- Molecule 4 is [(2 {R})-1-[2-azanylethoxy(oxidanyl)phosphoryl]oxy-3-hexadecanoyloxy-propan-2-yl] ( {Z})-octadec-9-enoate (CCD ID: 6OU) (formula: $C_{39}H_{76}NO_8P$).



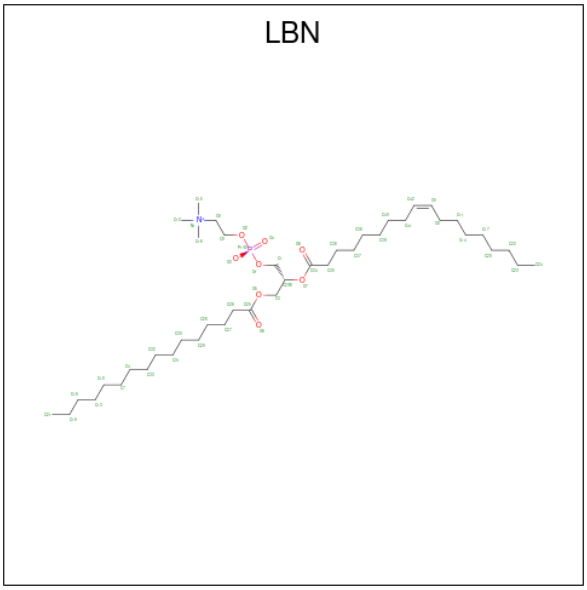

| Mol | Chain | Residues | Atoms | | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| 4 | B | 1 | Total | C | H | N | O | P | 0 |
| | | | 114 | 36 | 68 | 1 | 8 | 1 | |
| 4 | B | 1 | Total | C | H | N | O | P | 0 |
| | | | 66 | 20 | 36 | 1 | 8 | 1 | |
| 4 | B | 1 | Total | C | H | N | O | P | 0 |
| | | | 92 | 29 | 53 | 1 | 8 | 1 | |
| 4 | B | 1 | Total | C | H | N | O | P | 0 |
| | | | 102 | 32 | 60 | 1 | 8 | 1 | |
| 4 | A | 1 | Total | C | H | O | P | | 0 |
| | | | 109 | 36 | 64 | 8 | 1 | | |
| 4 | A | 1 | Total | C | H | N | O | P | 0 |
| | | | 102 | 32 | 60 | 1 | 8 | 1 | |
| 4 | A | 1 | Total | C | H | N | O | P | 0 |
| | | | 102 | 32 | 60 | 1 | 8 | 1 | |
| 4 | A | 1 | Total | C | H | N | O | P | 0 |
| | | | 89 | 27 | 52 | 1 | 8 | 1 | |
| 4 | C | 1 | Total | C | H | N | O | P | 0 |
| | | | 102 | 32 | 60 | 1 | 8 | 1 | |

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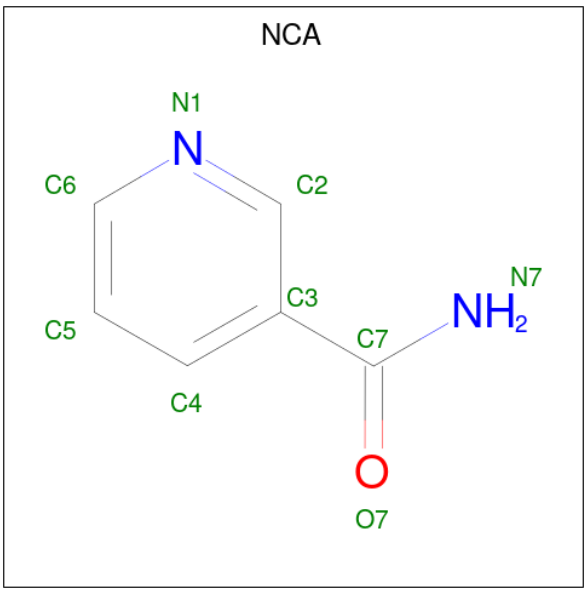
| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 4 | C | 1 | Total C H N O P<br>89 27 52 1 8 1 | 0 |
| 4 | D | 1 | Total C H O P<br>109 36 64 8 1 | 0 |
| 4 | D | 1 | Total C H N O P<br>114 36 68 1 8 1 | 0 |
| 4 | D | 1 | Total C H N O P<br>66 20 36 1 8 1 | 0 |
| 4 | D | 1 | Total C H N O P<br>92 29 53 1 8 1 | 0 |

- Molecule 5 is 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (CCD ID: LBN) (formula: $C_{42}H_{82}NO_8P$).



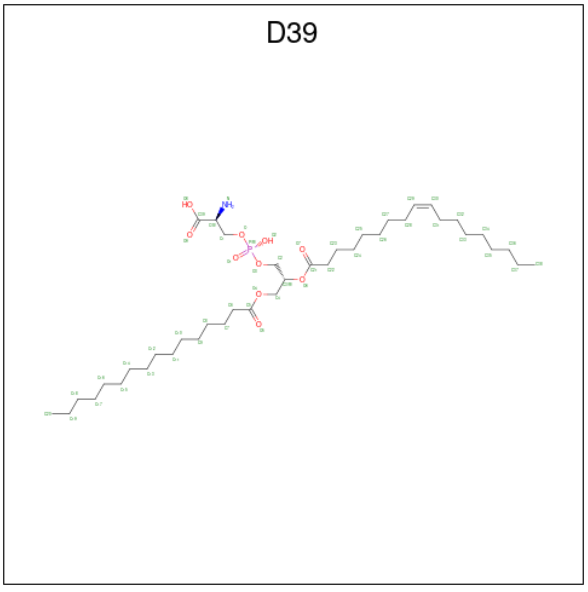

| Mol | Chain | Residues | Atoms | AltConf |
|---|---|---|---|---|
| 5 | B | 1 | Total C H N O P<br>81 25 46 1 8 1 | 0 |
| 5 | B | 1 | Total C H O P<br>83 27 47 8 1 | 0 |
| 5 | A | 1 | Total C H O P<br>98 32 57 8 1 | 0 |
| 5 | C | 1 | Total C H O P<br>98 32 57 8 1 | 0 |
| 5 | D | 1 | Total C H N O P<br>81 25 46 1 8 1 | 0 |
| 5 | D | 1 | Total C H O P<br>83 27 47 8 1 | 0 |

- Molecule 6 is NICOTINAMIDE (CCD ID: NCA) (formula: $C_6H_6N_2O$).




| Mol | Chain | Residues | Atoms | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|
| 6 | A | 1 | Total | C | H | N | O | 0 |
| | | | 15 | 6 | 6 | 2 | 1 | |
| 6 | C | 1 | Total | C | H | N | O | 0 |
| | | | 15 | 6 | 6 | 2 | 1 | |

- Molecule 7 is (2 {S})-2-azanyl-3-[[(2 {R})-3-hexadecanoyloxy-2-[( {Z})-octadec-9-enoyl]oxy-propoxy]-oxidanyl-phosphoryl]oxy-propanoic acid (CCD ID: D39) (formula: $C_{40}H_{76}NO_{10}P$).



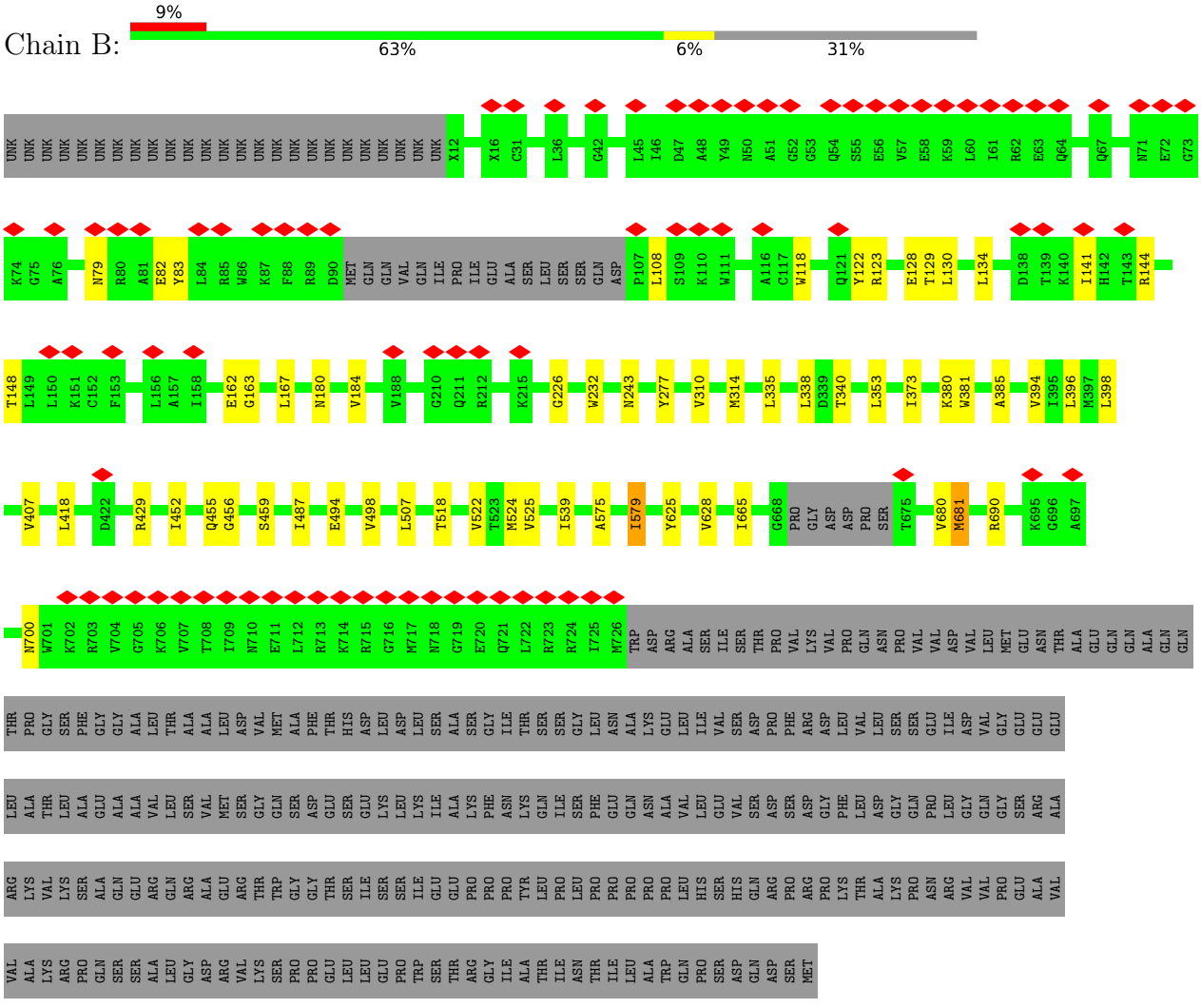
| Mol | Chain | Residues | Atoms | | | | | | AltConf |
|---|---|---|---|---|---|---|---|---|---|
| 7 | A | 1 | Total | C | H | N | O | P | 0 |
| | | | 77 | 24 | 41 | 1 | 10 | 1 | |
| 7 | C | 1 | Total | C | H | N | O | P | 0 |
| | | | 77 | 24 | 41 | 1 | 10 | 1 | |

# 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: Inactive

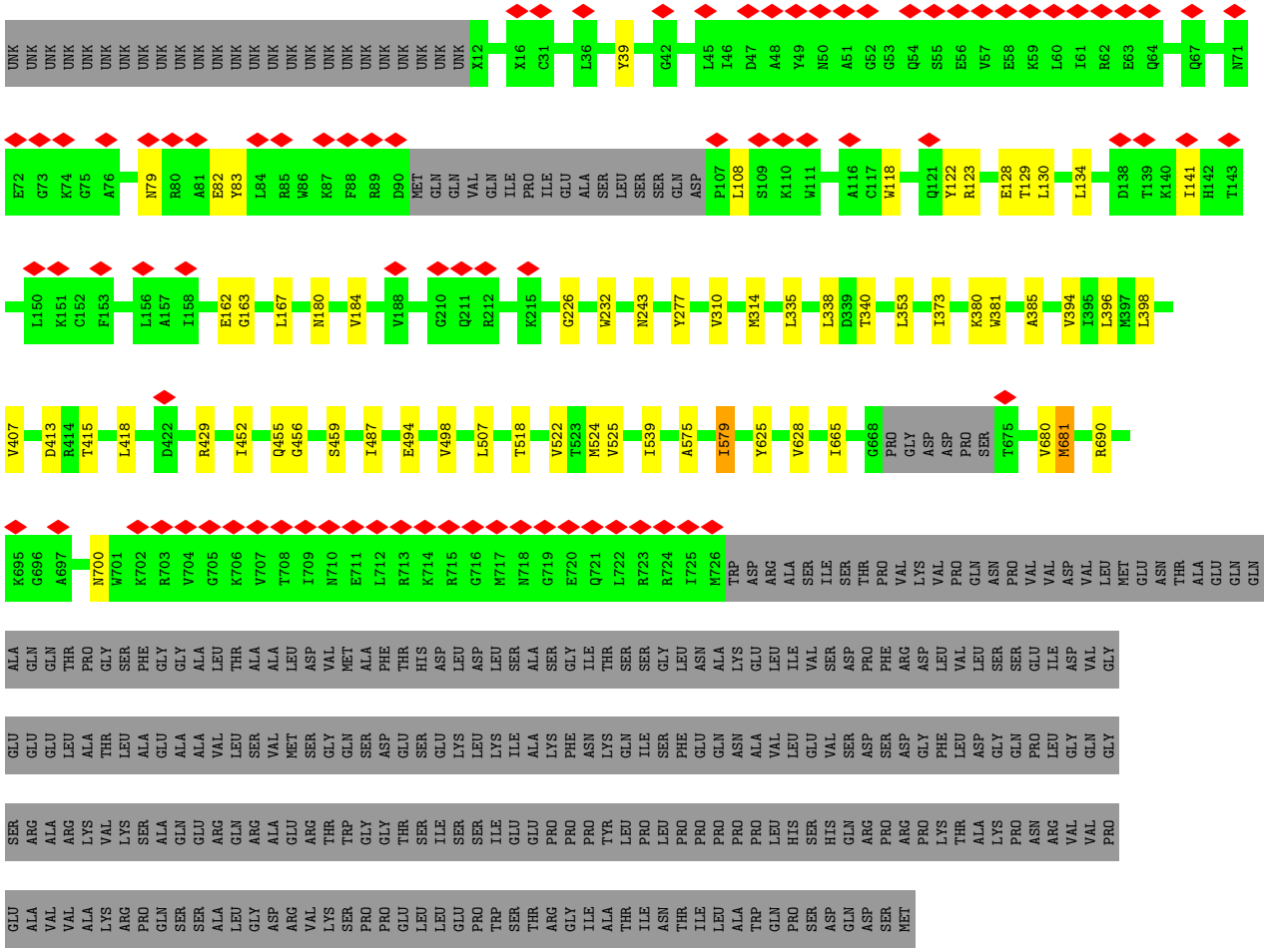
Chain B:




• Molecule 1: Inactive

Chain D:

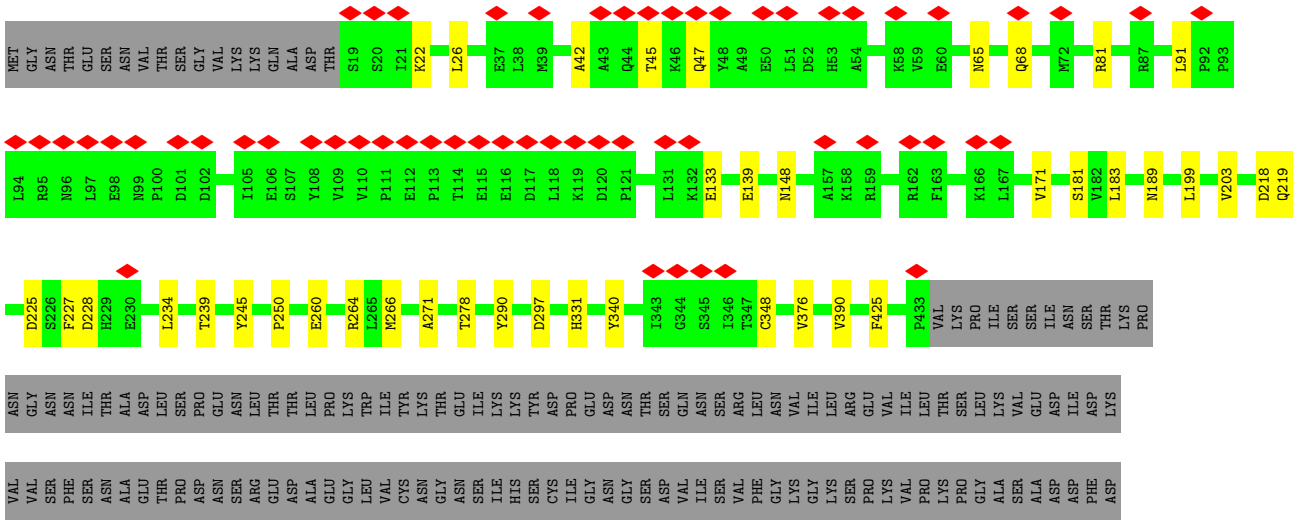


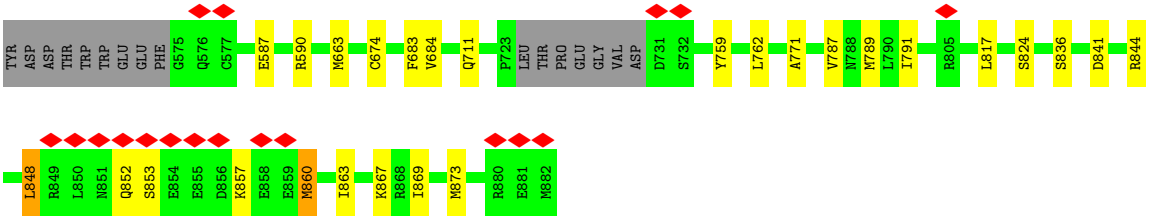


• Molecule 2: Nanchung

Chain A:

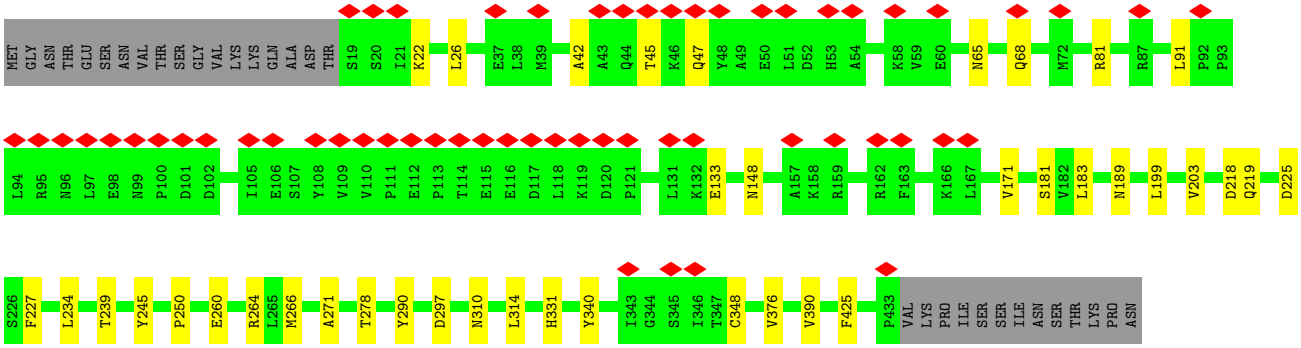


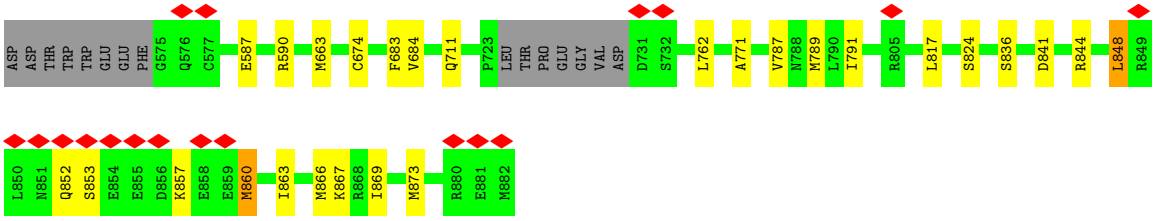





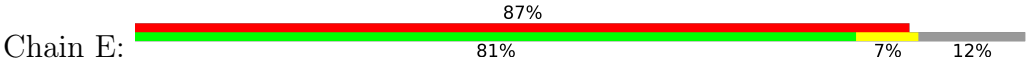

• Molecule 2: Nanchung

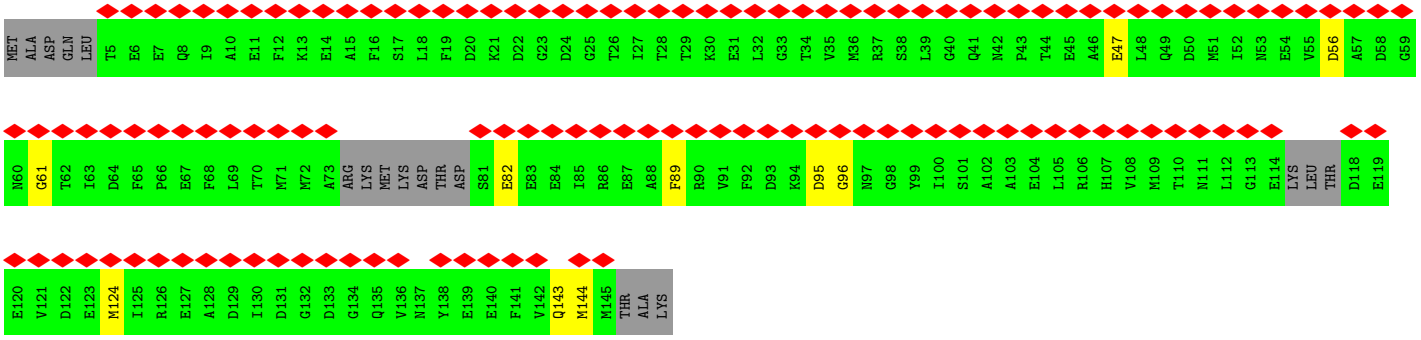


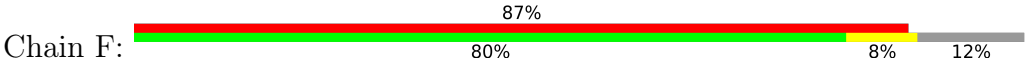

• Molecule 3: Calmodulin-1

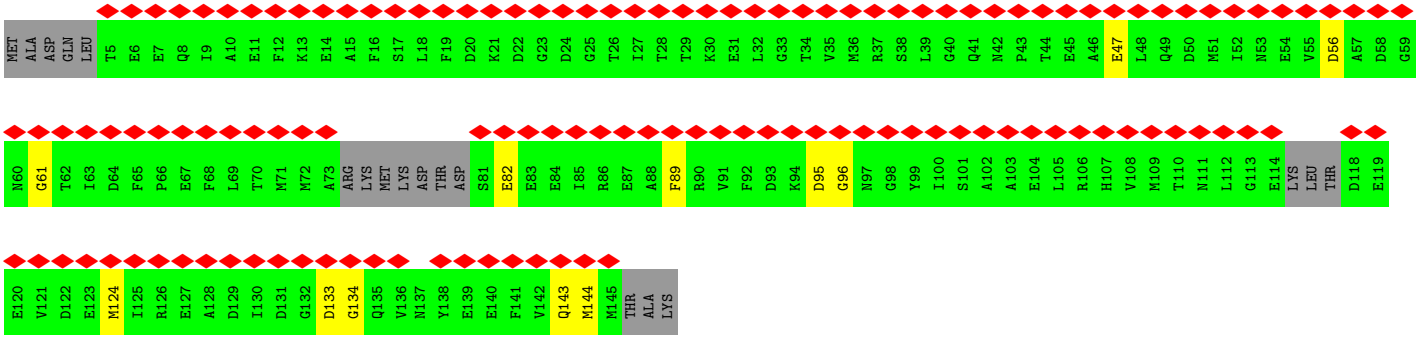



• Molecule 3: Calmodulin-1

Chain F:


87%
80%
8%
12%


MET ALA ASP GLN LEU T5 E6 E7 Q8 I9 A10 E11 F12 K13 E14 A15 F16 S17 L18 F19 D20 K21 D22 G23 D24 G25 T26 I27 T28 T29 K30 E31 L32 G33 T34 V35 M36 R37 S38 L39 G40 Q41 N42 P43 T44 E45 A46 E47 L48 Q49 D50 M51 I52 N53 E54 V55 D56 A57 D58 G59
N60 G61 T62 I63 D64 F65 P66 E67 F68 L69 T70 M71 M72 A73 ARG LYS MET LYS ASP THR ASP S81 E82 E83 E84 I85 R86 E87 A88 F89 R90 V91 F92 D93 K94 D95 G96 N97 G98 Y99 I100 S101 A102 A103 E104 L105 R106 H107 V108 M109 T110 N111 L112 G113 E114 LYS LEU THR D118 E119
E120 V121 D122 E123 M124 I125 R126 E127 A128 D129 I130 D131 G132 D133 G134 Q135 V136 N137 Y138 E139 E140 F141 V142 Q143 M144 M145 THR ALA LYS

# 4 Experimental information (i)

| Property | Value | Source |
|---|---|---|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 271938 | 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 ($e^-/Å^2$) | 60 | Depositor |
| Minimum defocus (nm) | 1000 | Depositor |
| Maximum defocus (nm) | 2200 | Depositor |
| Magnification | 81000 | Depositor |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 7.289 | Depositor |
| Minimum map value | -4.940 | Depositor |
| Average map value | 0.007 | Depositor |
| Map value standard deviation | 0.182 | Depositor |
| Recommended contour level | 0.7 | Depositor |
| Map size (Å) | 302.40002, 302.40002, 302.40002 | wwPDB |
| Map dimensions | 280, 280, 280 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.08, 1.08, 1.08 | Depositor |

# 5 Model quality

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NCA, D39, LBN, 6OU

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 | B | 0.17 | 0/5230 | 0.26 | 0/7105 |
| 1 | D | 0.17 | 0/5230 | 0.26 | 0/7105 |
| 2 | A | 0.19 | 0/5881 | 0.32 | 2/7966 (0.0%) |
| 2 | C | 0.19 | 0/5881 | 0.32 | 2/7966 (0.0%) |
| 3 | E | 0.09 | 0/1009 | 0.22 | 0/1357 |
| 3 | F | 0.09 | 0/1009 | 0.22 | 0/1357 |
| All | All | 0.18 | 0/24240 | 0.29 | 4/32856 (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($^o$) |
|---|---|---|---|---|---|---|---|
| 2 | C | 189 | ASN | CA-C-N | 7.90 | 133.32 | 122.34 |
| 2 | C | 189 | ASN | C-N-CA | 7.90 | 133.32 | 122.34 |
| 2 | A | 189 | ASN | CA-C-N | 7.45 | 133.31 | 122.36 |
| 2 | A | 189 | ASN | C-N-CA | 7.45 | 133.31 | 122.36 |

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 | B | 5141 | 4958 | 4974 | 38 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | D | 5141 | 4958 | 4974 | 39 | 0 |
| 2 | A | 5748 | 5680 | 5702 | 44 | 0 |
| 2 | C | 5748 | 5680 | 5702 | 43 | 0 |
| 3 | E | 1000 | 905 | 903 | 6 | 0 |
| 3 | F | 1000 | 905 | 903 | 8 | 0 |
| 4 | A | 166 | 236 | 0 | 0 | 0 |
| 4 | B | 157 | 217 | 0 | 0 | 0 |
| 4 | C | 79 | 112 | 0 | 0 | 0 |
| 4 | D | 160 | 221 | 0 | 0 | 0 |
| 5 | A | 41 | 57 | 0 | 0 | 0 |
| 5 | B | 71 | 93 | 0 | 1 | 0 |
| 5 | C | 41 | 57 | 0 | 0 | 0 |
| 5 | D | 71 | 93 | 0 | 0 | 0 |
| 6 | A | 9 | 6 | 6 | 0 | 0 |
| 6 | C | 9 | 6 | 6 | 0 | 0 |
| 7 | A | 36 | 41 | 0 | 0 | 0 |
| 7 | C | 36 | 41 | 0 | 0 | 0 |
| All | All | 24654 | 24266 | 23170 | 168 | 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 4.

The worst 5 of 168 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) |
|---|---|---|---|
| 2:C:863:ILE:HG23 | 2:C:867:LYS:HZ3 | 1.62 | 0.63 |
| 1:B:700:ASN:ND2 | 3:E:47:GLU:OE1 | 2.33 | 0.61 |
| 1:B:108:LEU:HD23 | 1:B:108:LEU:O | 2.02 | 0.59 |
| 3:F:47:GLU:OE1 | 1:D:700:ASN:ND2 | 2.34 | 0.59 |
| 1:D:108:LEU:O | 1:D:108:LEU:HD23 | 2.02 | 0.59 |

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 | B | 666/984 (68%) | 654 (98%) | 12 (2%) | 0 | 100 | 100 |
| 1 | D | 666/984 (68%) | 654 (98%) | 12 (2%) | 0 | 100 | 100 |
| 2 | A | 710/882 (80%) | 688 (97%) | 22 (3%) | 0 | 100 | 100 |
| 2 | C | 710/882 (80%) | 688 (97%) | 22 (3%) | 0 | 100 | 100 |
| 3 | E | 125/149 (84%) | 123 (98%) | 2 (2%) | 0 | 100 | 100 |
| 3 | F | 125/149 (84%) | 123 (98%) | 2 (2%) | 0 | 100 | 100 |
| All | All | 3002/4030 (74%) | 2930 (98%) | 72 (2%) | 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 | B | 504/812 (62%) | 502 (100%) | 2 (0%) | 84 | 92 |
| 1 | D | 504/812 (62%) | 502 (100%) | 2 (0%) | 84 | 92 |
| 2 | A | 619/787 (79%) | 616 (100%) | 3 (0%) | 81 | 90 |
| 2 | C | 619/787 (79%) | 616 (100%) | 3 (0%) | 81 | 90 |
| 3 | E | 104/127 (82%) | 104 (100%) | 0 | 100 | 100 |
| 3 | F | 104/127 (82%) | 104 (100%) | 0 | 100 | 100 |
| All | All | 2454/3452 (71%) | 2444 (100%) | 10 (0%) | 81 | 92 |

5 of 10 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | C | 860 | MET |
| 1 | D | 579 | ILE |
| 1 | D | 681 | MET |
| 2 | A | 848 | LEU |
| 2 | A | 860 | MET |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 2 | C | 122 | ASN |
| 2 | C | 169 | ASN |
| 1 | D | 627 | HIS |
| 1 | D | 336 | ASN |
| 1 | D | 549 | 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)

24 ligands are 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 | $\#\|Z\| > 2$ |
| 4 | 6OU | C | 905 | - | 36,36,48 | 1.02 | 4 (11%) | 39,41,53 | 0.95 | 2 (5%) |
| 4 | 6OU | A | 904 | - | 41,41,48 | 0.97 | 4 (9%) | 44,46,53 | 1.13 | 3 (6%) |
| 5 | LBN | C | 904 | - | 40,40,51 | 1.26 | 3 (7%) | 43,45,59 | 1.15 | 2 (4%) |
| 4 | 6OU | B | 1003 | - | 38,38,48 | 1.01 | 4 (10%) | 41,43,53 | 0.88 | 2 (4%) |
| 4 | 6OU | A | 907 | - | 36,36,48 | 1.01 | 4 (11%) | 39,41,53 | 0.95 | 2 (5%) |
| 5 | LBN | D | 1005 | - | 34,34,51 | 1.28 | 2 (5%) | 40,42,59 | 0.98 | 2 (5%) |

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Counts | RMSZ | $\#\|Z\|>2$ | Counts | RMSZ | $\#\|Z\|>2$ |
| 4 | 6OU | D | 1001 | - | 44,44,48 | 0.93 | 4 (9%) | 47,49,53 | 0.93 | 2 (4%) |
| 5 | LBN | A | 905 | - | 40,40,51 | 1.26 | 3 (7%) | 43,45,59 | 1.15 | 2 (4%) |
| 4 | 6OU | D | 1002 | - | 45,45,48 | 0.93 | 4 (8%) | 48,50,53 | 0.89 | 2 (4%) |
| 5 | LBN | B | 1005 | - | 35,35,51 | 1.49 | 3 (8%) | 38,40,59 | 1.33 | 4 (10%) |
| 4 | 6OU | B | 1006 | - | 41,41,48 | 0.97 | 4 (9%) | 44,46,53 | 1.17 | 4 (9%) |
| 4 | 6OU | B | 1002 | - | 29,29,48 | 1.14 | 4 (13%) | 32,34,53 | 1.11 | 2 (6%) |
| 7 | D39 | A | 903 | - | 34,35,51 | 1.35 | 5 (14%) | 36,42,58 | 1.11 | 2 (5%) |
| 7 | D39 | C | 902 | - | 34,35,51 | 1.36 | 5 (14%) | 36,42,58 | 1.11 | 2 (5%) |
| 4 | 6OU | B | 1001 | - | 45,45,48 | 0.93 | 4 (8%) | 48,50,53 | 0.89 | 2 (4%) |
| 4 | 6OU | A | 901 | - | 44,44,48 | 0.93 | 4 (9%) | 47,49,53 | 0.93 | 2 (4%) |
| 6 | NCA | C | 901 | - | 9,9,9 | 2.01 | 2 (22%) | 11,11,11 | 1.47 | 2 (18%) |
| 6 | NCA | A | 902 | - | 9,9,9 | 2.02 | 2 (22%) | 11,11,11 | 1.48 | 2 (18%) |
| 5 | LBN | D | 1006 | - | 35,35,51 | 1.48 | 3 (8%) | 38,40,59 | 1.33 | 4 (10%) |
| 4 | 6OU | C | 903 | - | 41,41,48 | 0.97 | 4 (9%) | 44,46,53 | 1.13 | 3 (6%) |
| 4 | 6OU | D | 1004 | - | 38,38,48 | 1.00 | 4 (10%) | 41,43,53 | 0.88 | 2 (4%) |
| 4 | 6OU | A | 906 | - | 41,41,48 | 0.97 | 3 (7%) | 44,46,53 | 1.16 | 4 (9%) |
| 5 | LBN | B | 1004 | - | 34,34,51 | 1.28 | 2 (5%) | 40,42,59 | 0.98 | 2 (5%) |
| 4 | 6OU | D | 1003 | - | 29,29,48 | 1.14 | 4 (13%) | 32,34,53 | 1.11 | 2 (6%) |

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 |
|---|---|---|---|---|---|---|---|
| 4 | 6OU | C | 905 | - | - | 18/40/40/52 | - |
| 4 | 6OU | A | 904 | - | - | 24/45/45/52 | - |
| 5 | LBN | C | 904 | - | - | 26/44/44/55 | - |
| 4 | 6OU | B | 1003 | - | - | 24/42/42/52 | - |
| 4 | 6OU | A | 907 | - | - | 18/40/40/52 | - |
| 5 | LBN | D | 1005 | - | - | 16/38/38/55 | - |
| 4 | 6OU | D | 1001 | - | - | 20/48/48/52 | - |
| 5 | LBN | A | 905 | - | - | 26/44/44/55 | - |
| 4 | 6OU | D | 1002 | - | - | 27/49/49/52 | - |
| 5 | LBN | B | 1005 | - | - | 16/37/37/55 | - |
| 4 | 6OU | B | 1006 | - | - | 26/45/45/52 | - |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|---|---|---|---|---|---|---|---|
| 4 | 6OU | B | 1002 | - | - | 13/33/33/52 | - |
| 7 | D39 | A | 903 | - | - | 16/41/41/57 | - |
| 7 | D39 | C | 902 | - | - | 16/41/41/57 | - |
| 4 | 6OU | B | 1001 | - | - | 27/49/49/52 | - |
| 4 | 6OU | A | 901 | - | - | 20/48/48/52 | - |
| 6 | NCA | C | 901 | - | - | 0/4/4/4 | 0/1/1/1 |
| 6 | NCA | A | 902 | - | - | 0/4/4/4 | 0/1/1/1 |
| 5 | LBN | D | 1006 | - | - | 16/37/37/55 | - |
| 4 | 6OU | C | 903 | - | - | 24/45/45/52 | - |
| 4 | 6OU | D | 1004 | - | - | 24/42/42/52 | - |
| 4 | 6OU | A | 906 | - | - | 26/45/45/52 | - |
| 5 | LBN | B | 1004 | - | - | 16/38/38/55 | - |
| 4 | 6OU | D | 1003 | - | - | 13/33/33/52 | - |

The worst 5 of 85 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|---|---|---|---|---|---|---|---|
| 5 | B | 1005 | LBN | P1-O3 | 6.68 | 1.79 | 1.54 |
| 5 | D | 1006 | LBN | P1-O3 | 6.67 | 1.79 | 1.54 |
| 5 | C | 904 | LBN | P1-O2 | 5.06 | 1.79 | 1.59 |
| 5 | A | 905 | LBN | P1-O2 | 5.05 | 1.79 | 1.59 |
| 6 | A | 902 | NCA | C7-N7 | 4.99 | 1.42 | 1.33 |

The worst 5 of 58 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 5 | B | 1005 | LBN | O2-P1-O4 | 4.55 | 128.58 | 110.83 |
| 5 | D | 1006 | LBN | O2-P1-O4 | 4.54 | 128.54 | 110.83 |
| 4 | A | 904 | 6OU | C12-C11-C10 | 4.37 | 136.48 | 114.37 |
| 4 | C | 903 | 6OU | C12-C11-C10 | 4.36 | 136.42 | 114.37 |
| 5 | C | 904 | LBN | C8-C5-C42 | 4.35 | 157.45 | 124.83 |

There are no chirality outliers.

5 of 452 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 4 | B | 1001 | 6OU | O18-C19-C20-O30 |
| 4 | B | 1001 | 6OU | C21-O22-P23-O24 |
| 4 | B | 1001 | 6OU | C21-O22-P23-O25 |

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| Mol | Chain | Res | Type | Atoms |
|---|---|---|---|---|
| 4 | B | 1001 | 6OU | C21-O22-P23-O26 |
| 4 | B | 1001 | 6OU | O26-C27-C28-N29 |

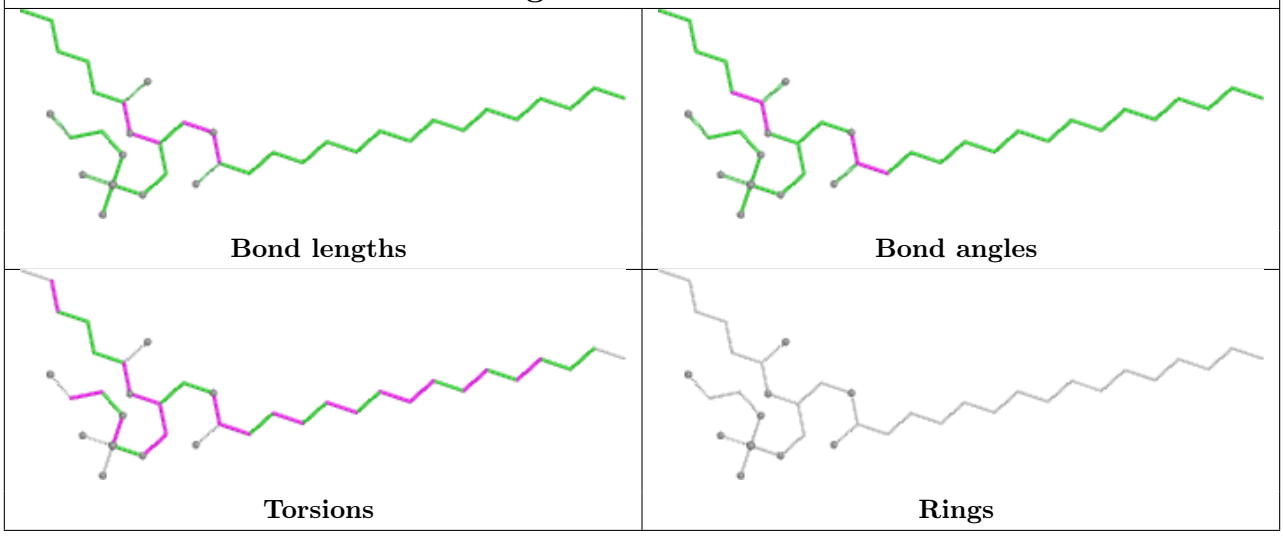
There are no ring outliers.

1 monomer is involved in 1 short contact:

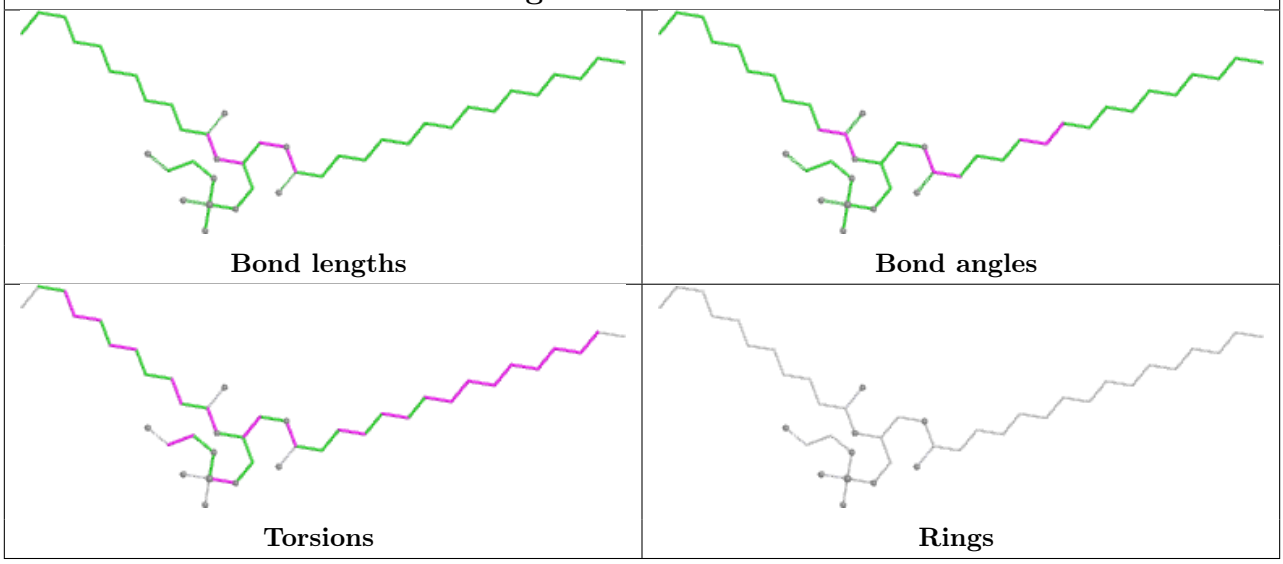
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|---|---|---|---|---|---|
| 5 | B | 1004 | LBN | 1 | 0 |

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.

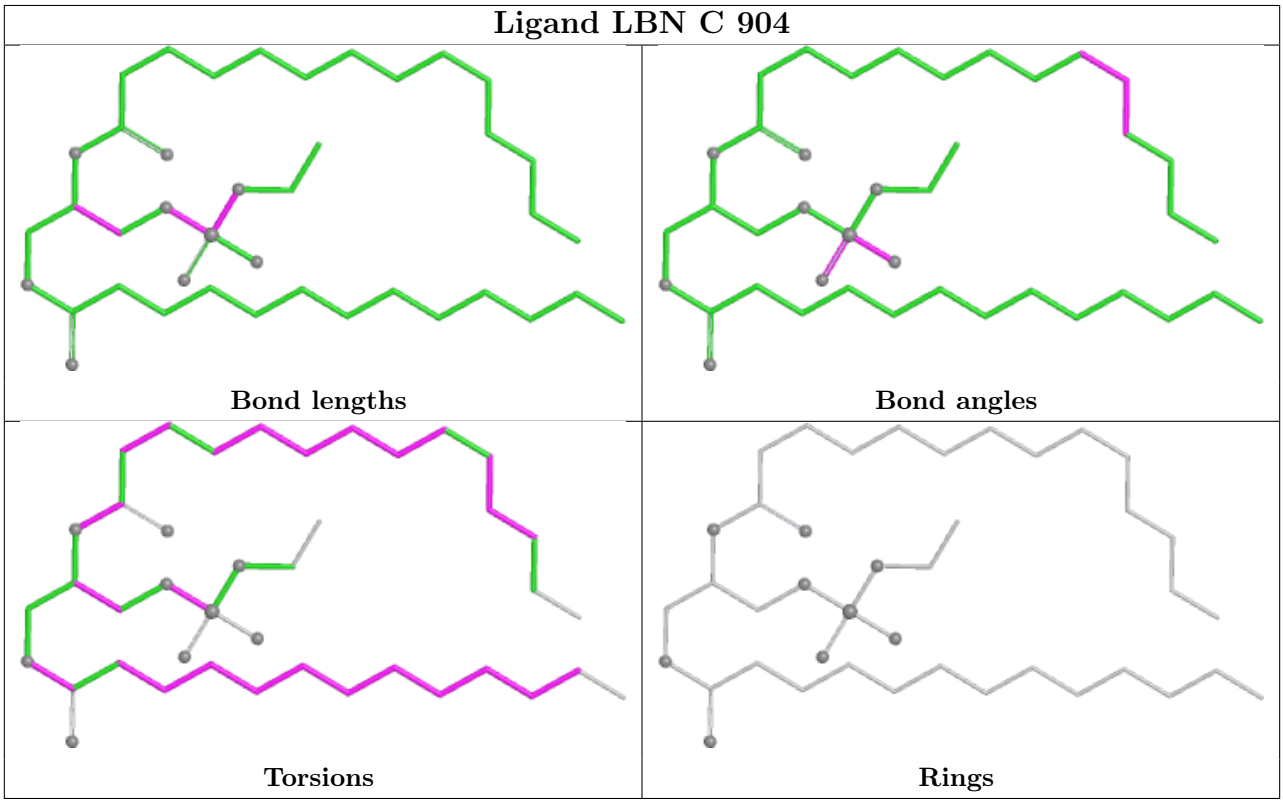
**Ligand 6OU C 905**



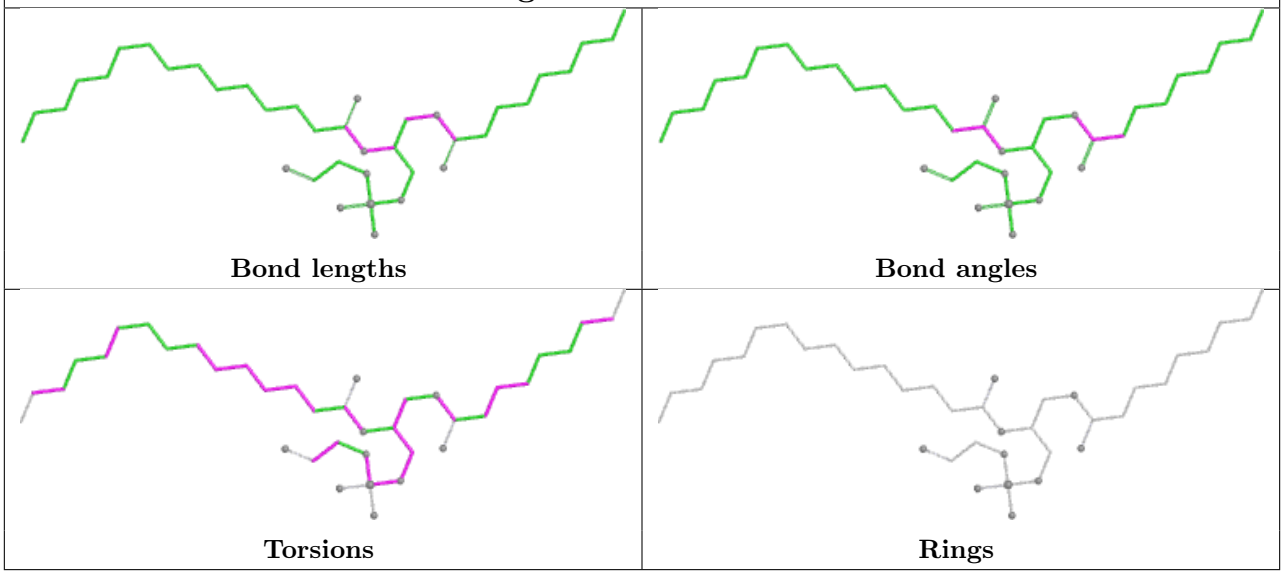
## Ligand 6OU A 904



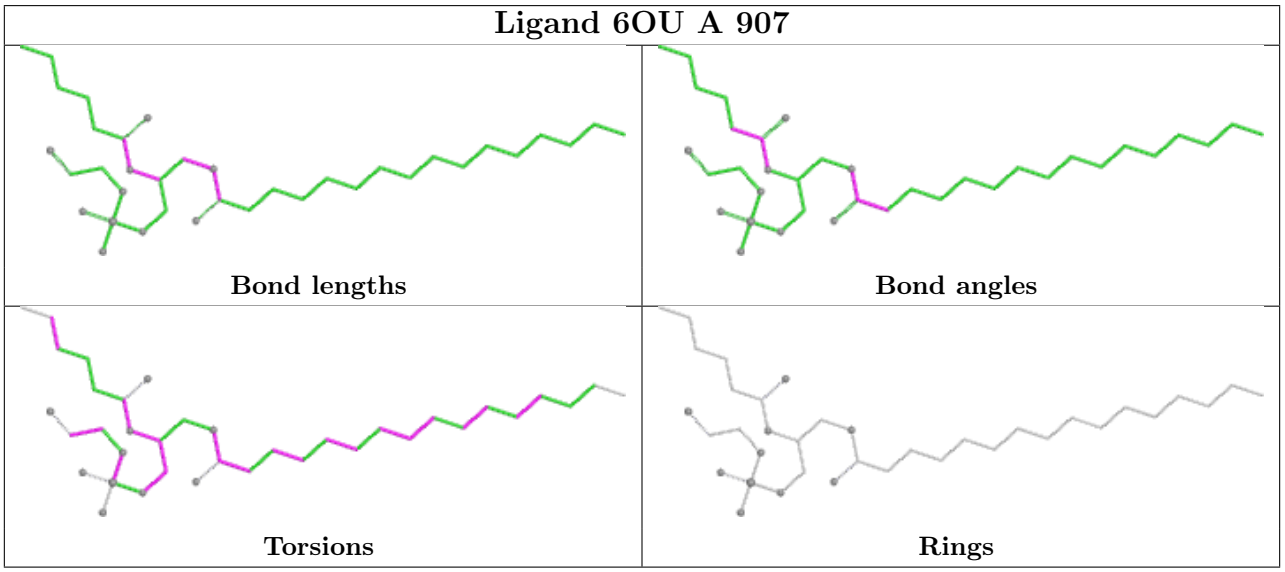

## Ligand LBN C 904



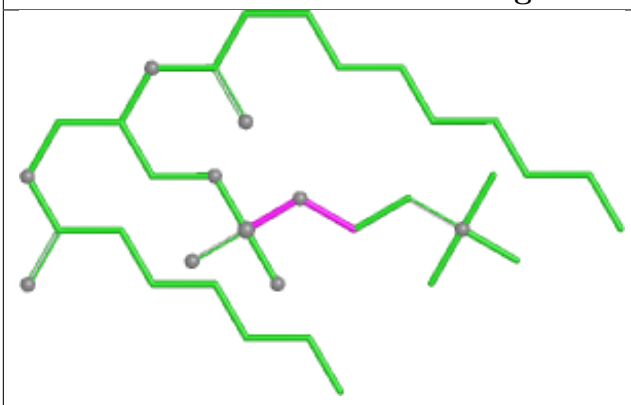
**Ligand 6OU B 1003**



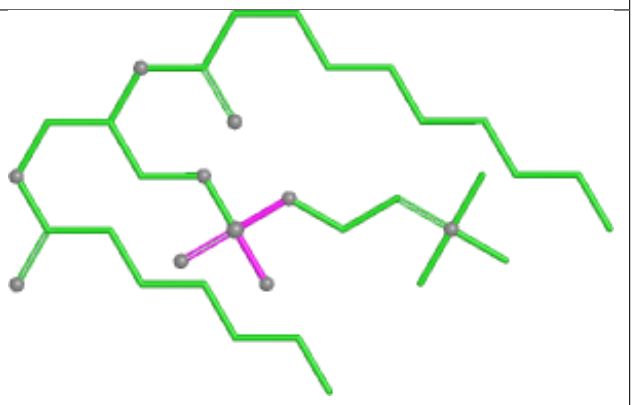

**Ligand 6OU A 907**



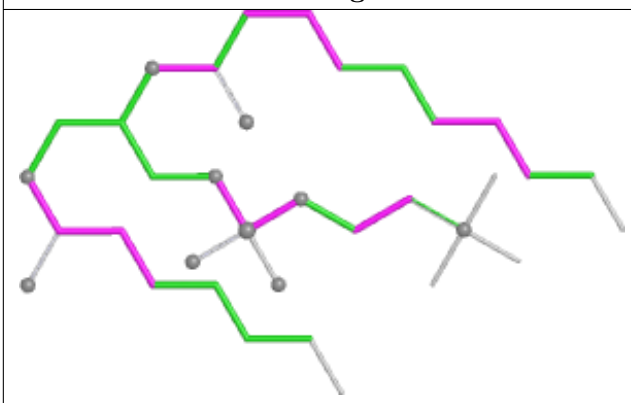
## Ligand LBN D 1005



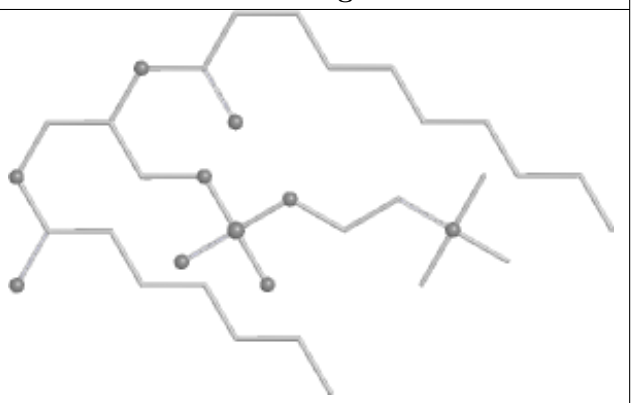
Bond lengths



Bond angles

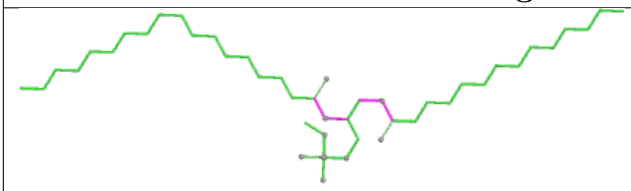


Torsions

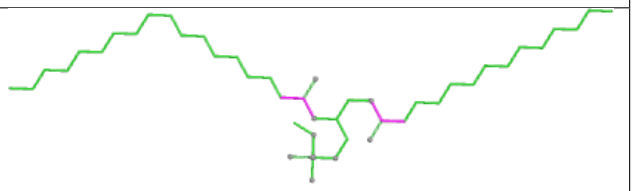


Rings

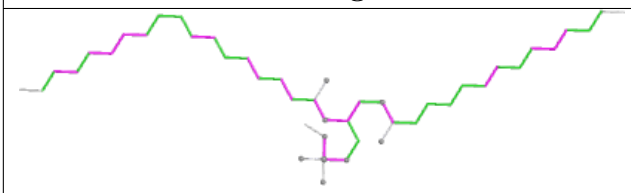
## Ligand 6OU D 1001



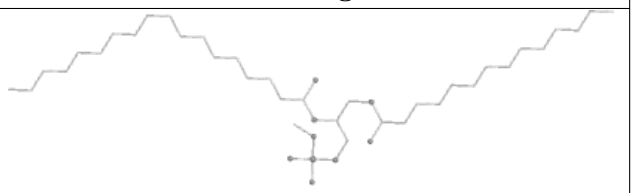
Bond lengths



Bond angles

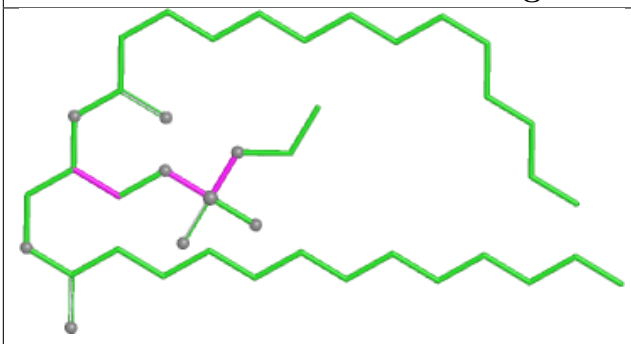


Torsions

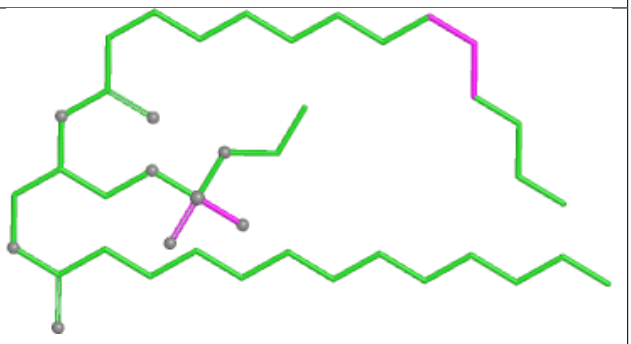


Rings

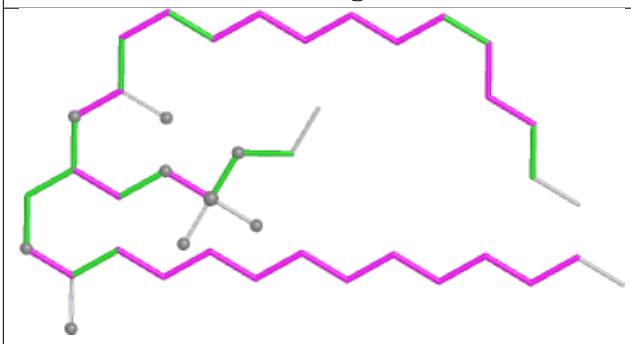
**Ligand LBN A 905**



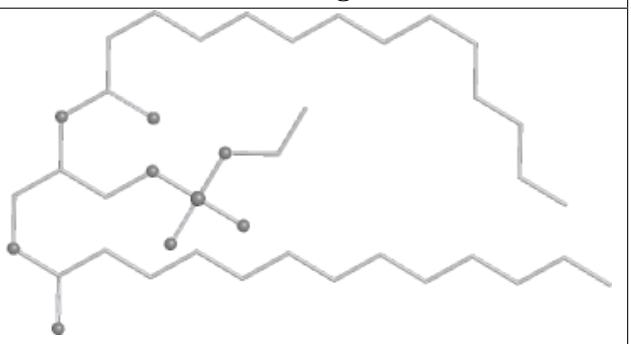
Bond lengths



Bond angles

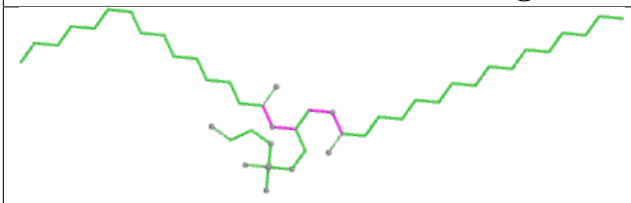


Torsions

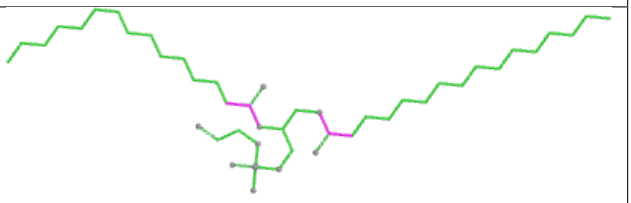


Rings

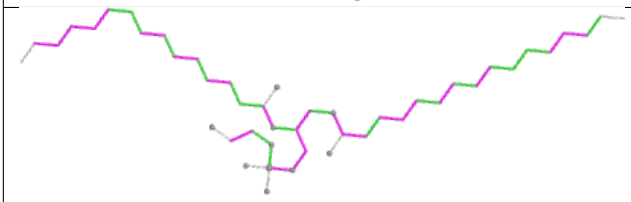
**Ligand 6OU D 1002**



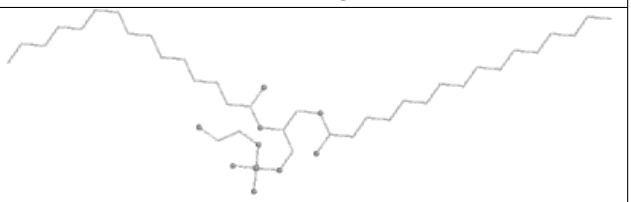
Bond lengths



Bond angles

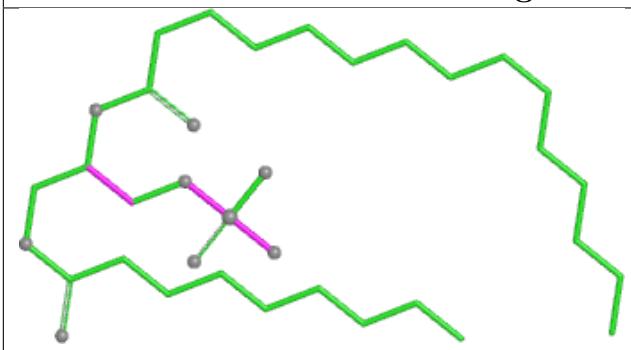


Torsions

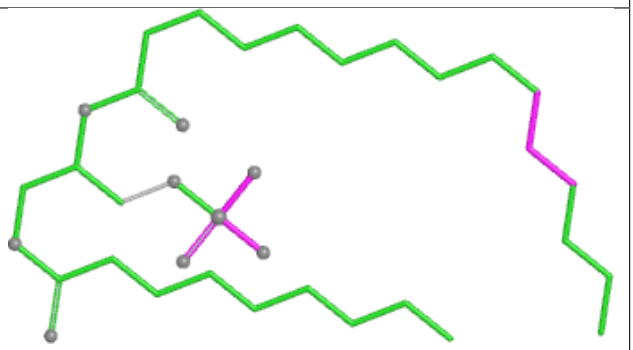


Rings

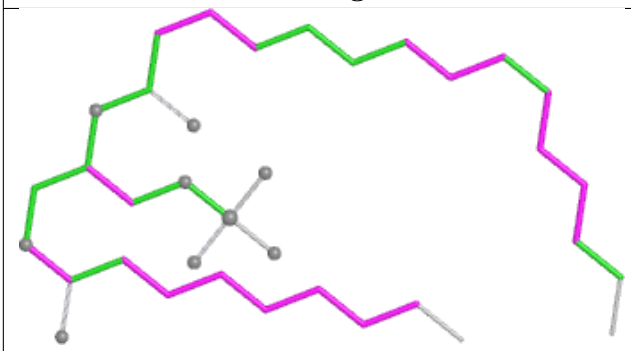
## Ligand LBN B 1005



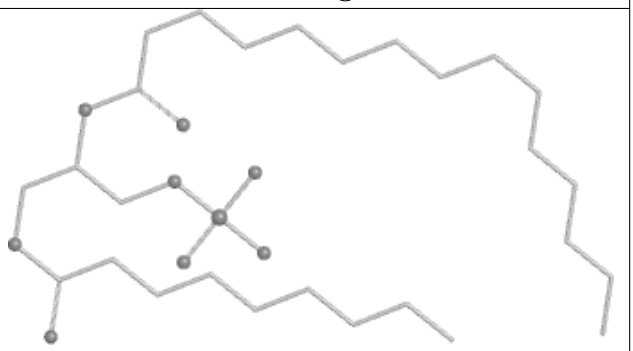
Bond lengths



Bond angles

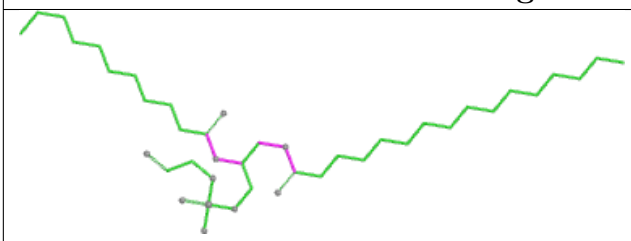


Torsions

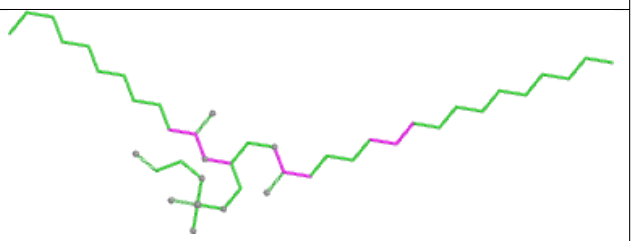


Rings

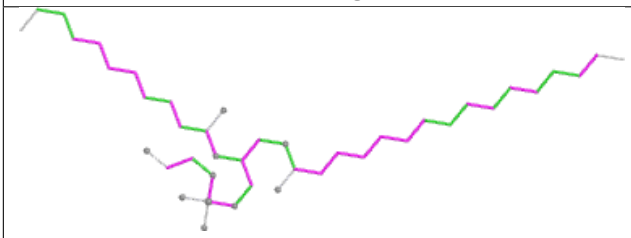
## Ligand 6OU B 1006



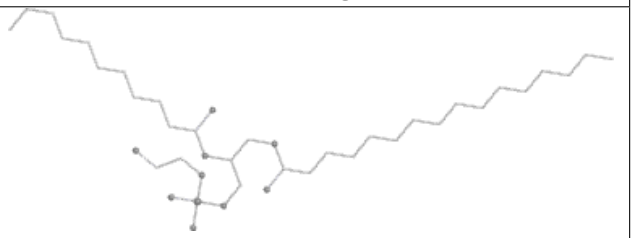
Bond lengths



Bond angles

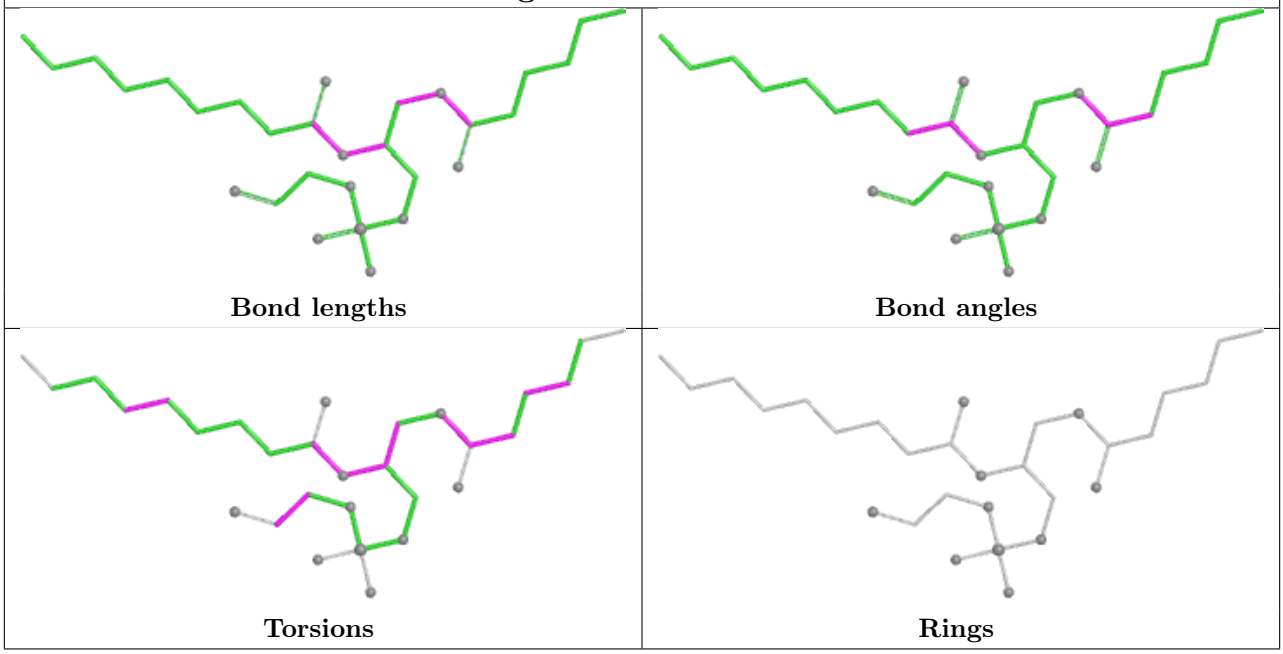


Torsions

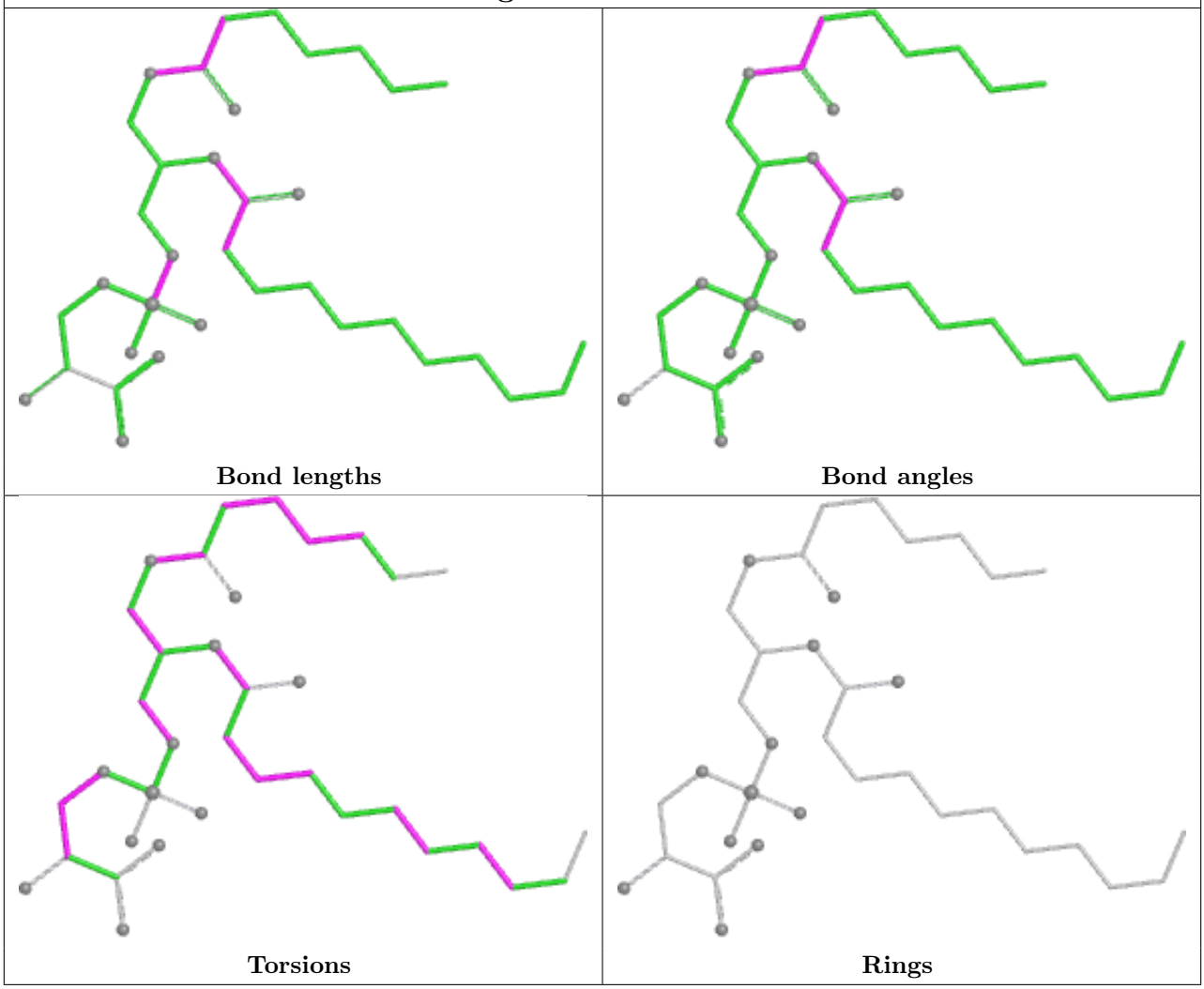


Rings

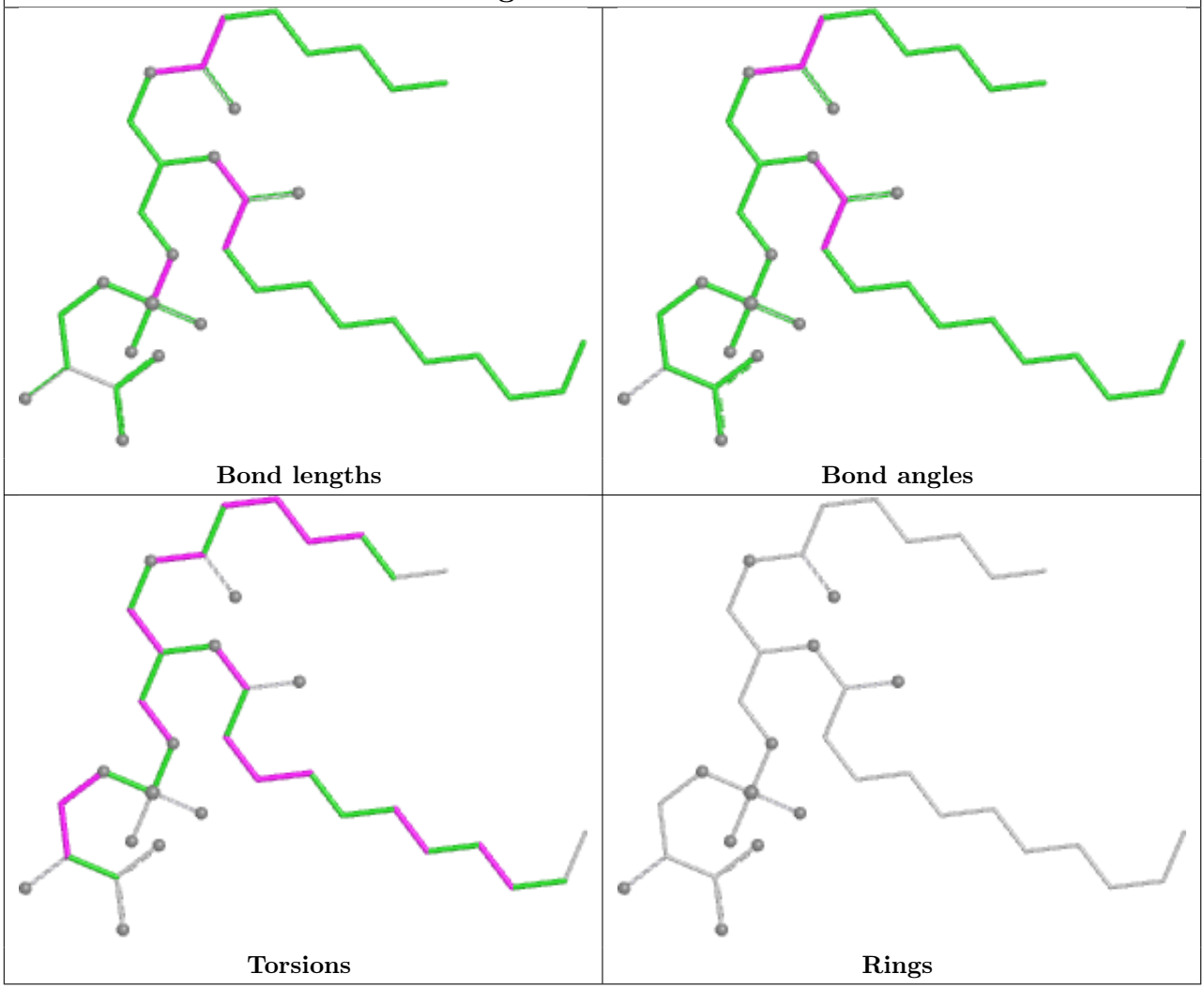
**Ligand 6OU B 1002**



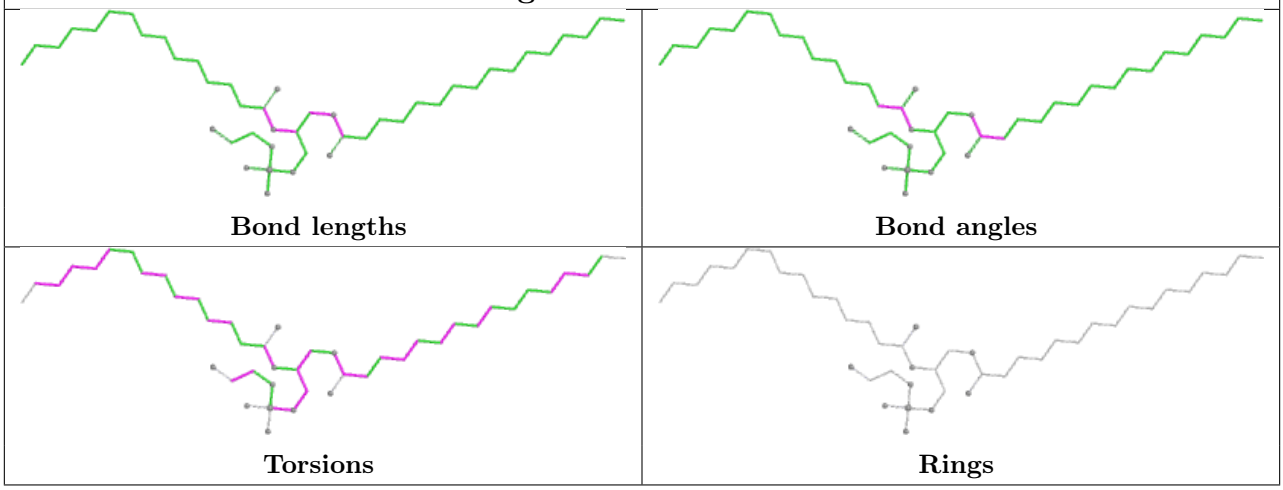

**Ligand D39 A 903**



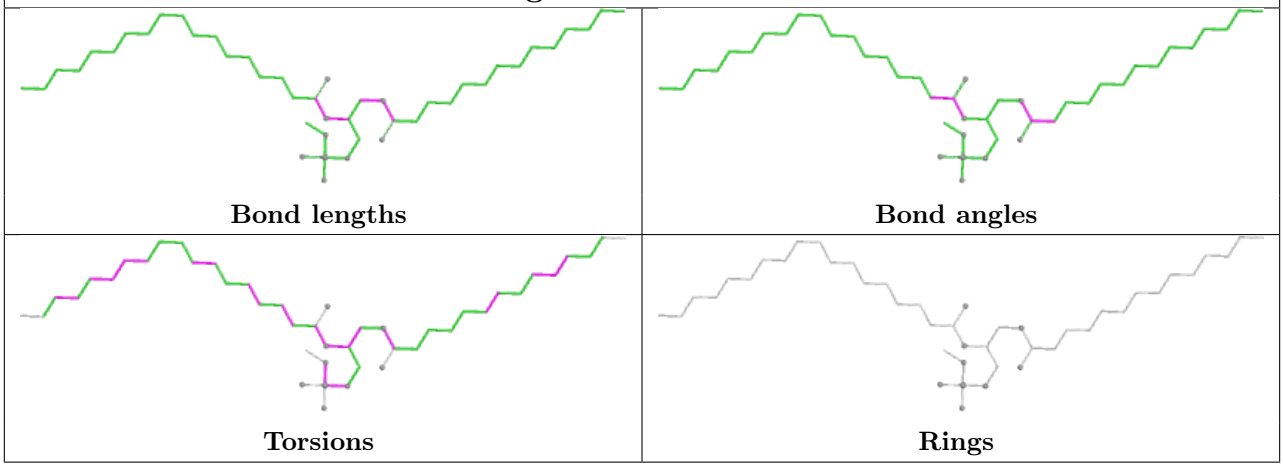
**Ligand D39 C 902**



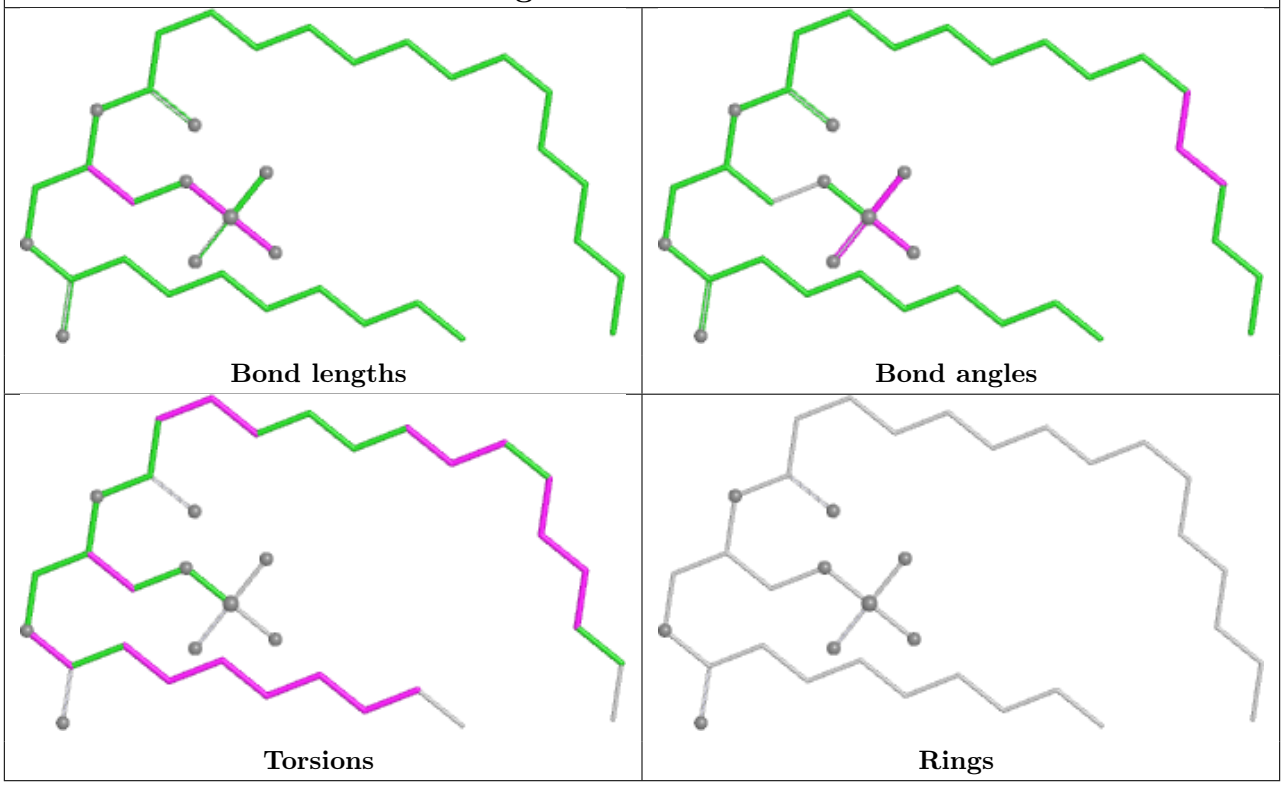

**Ligand 6OU B 1001**



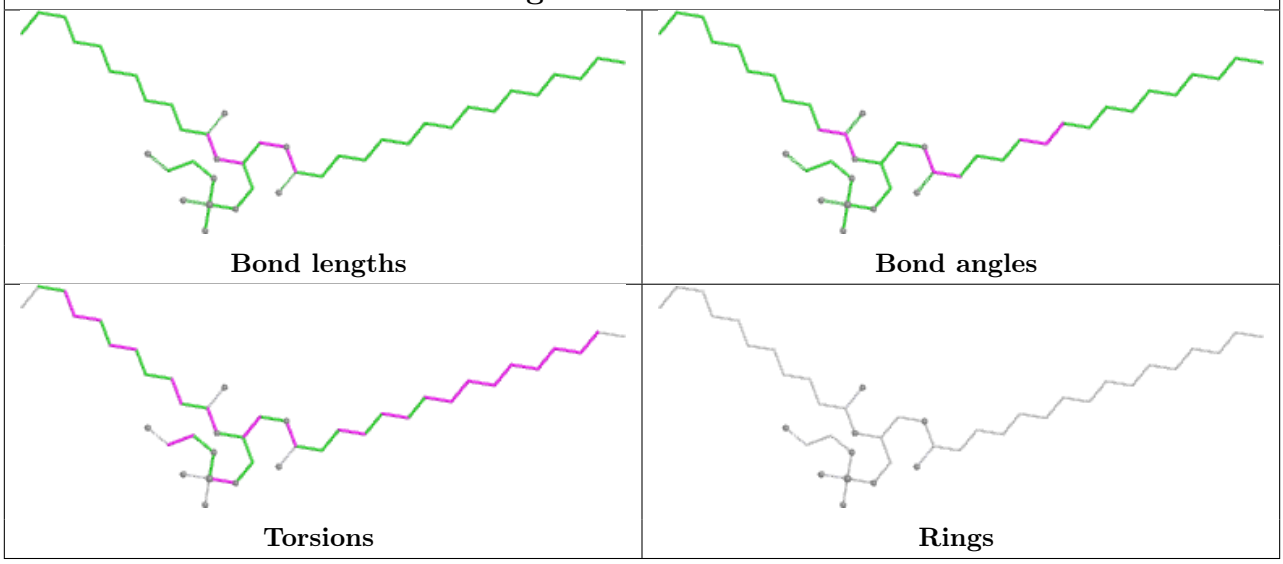
**Ligand 6OU A 901**



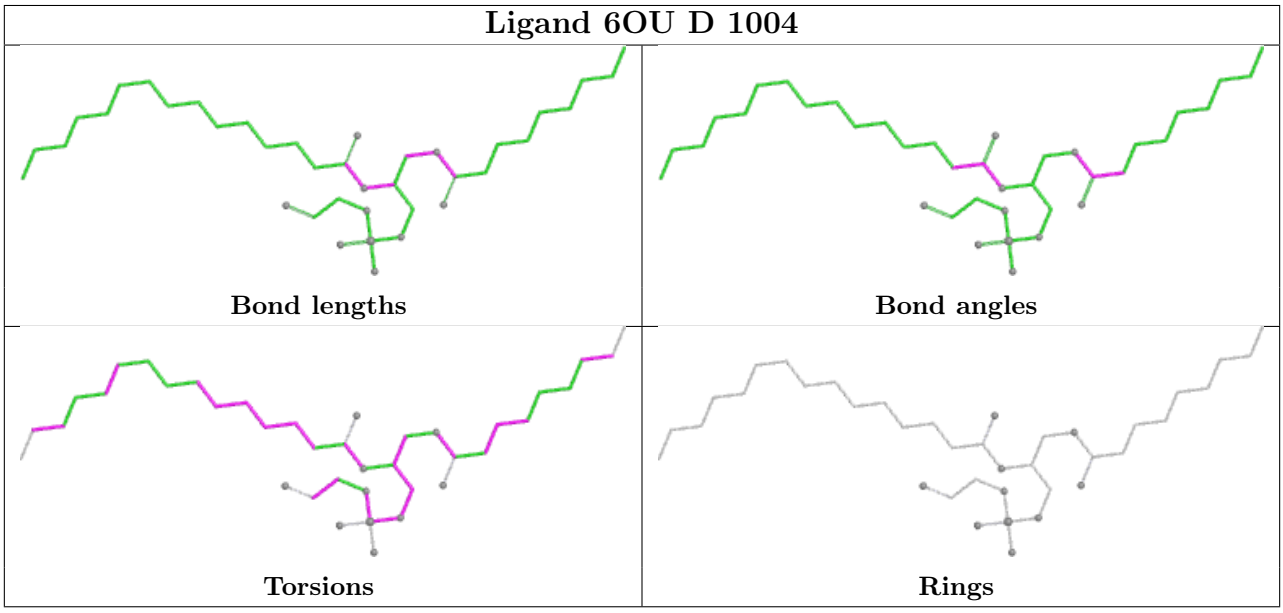

**Ligand LBN D 1006**



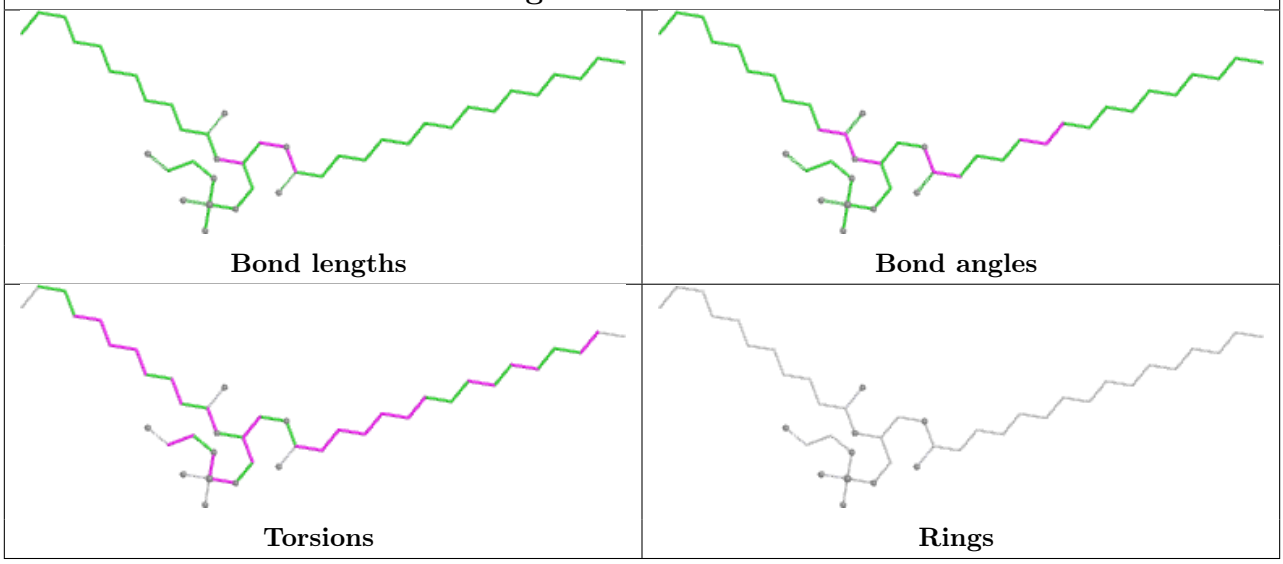
**Ligand 6OU C 903**



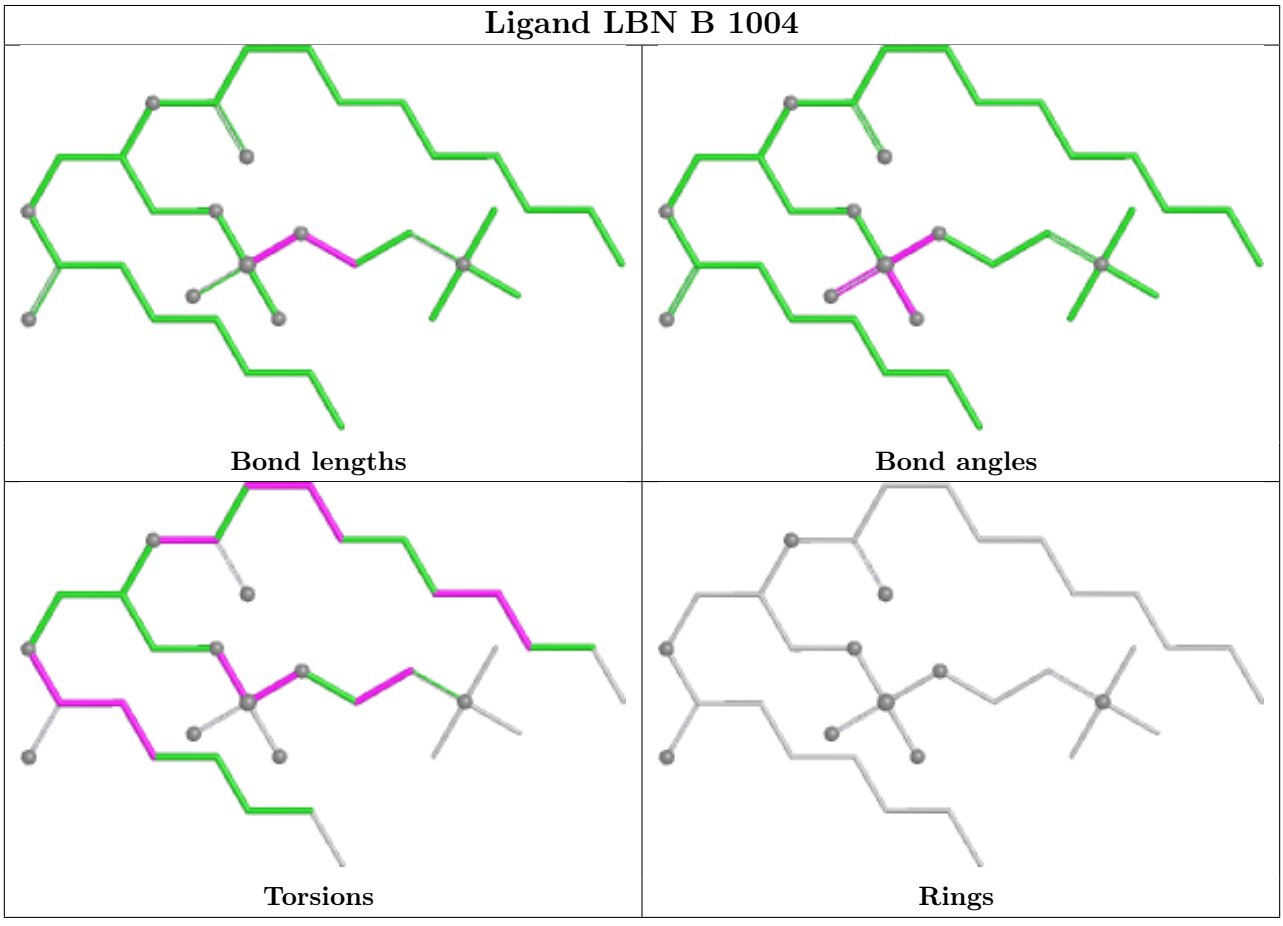

**Ligand 6OU D 1004**



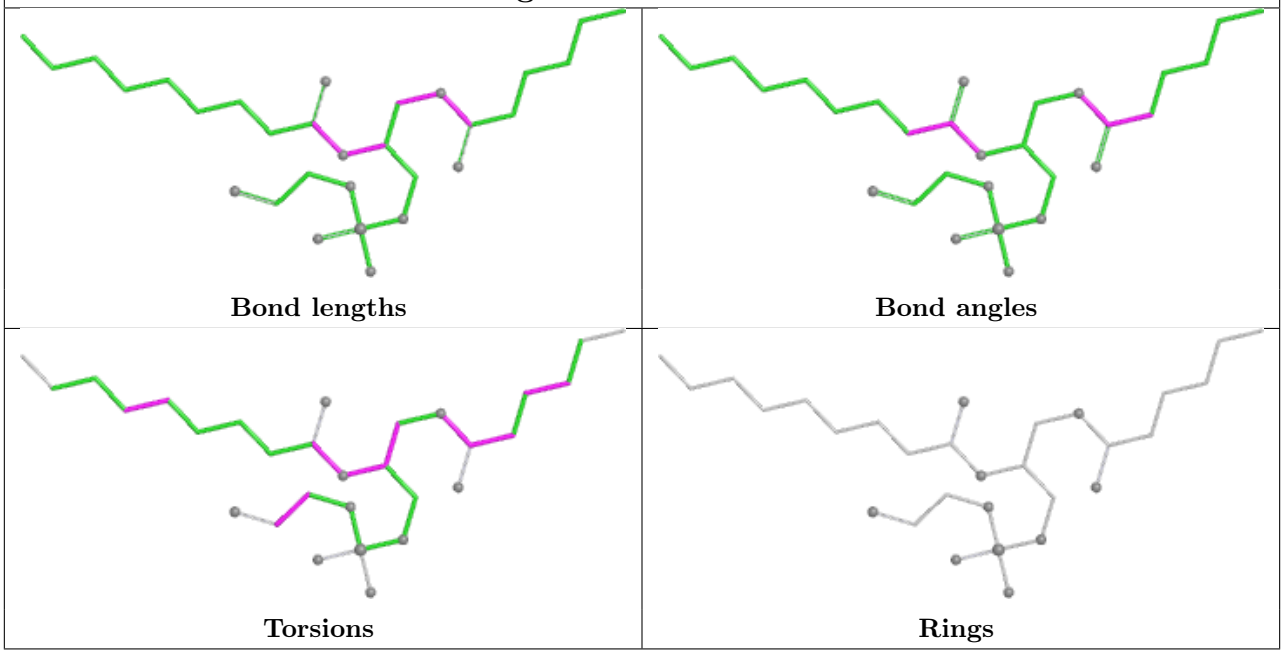
**Ligand 6OU A 906**




**Ligand LBN B 1004**



**Ligand 6OU D 1003**




## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|---|---|---|
| 1 | B | 2 |
| 1 | D | 2 |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|---|---|---|---|---|---|---|
| 1 | B | 16:UNK | C | 31:CYS | N | 12.23 |
| 1 | D | 16:UNK | C | 31:CYS | N | 12.23 |
| 1 | B | 715:ARG | C | 716:GLY | N | 3.11 |
| 1 | D | 715:ARG | C | 716:GLY | N | 3.11 |

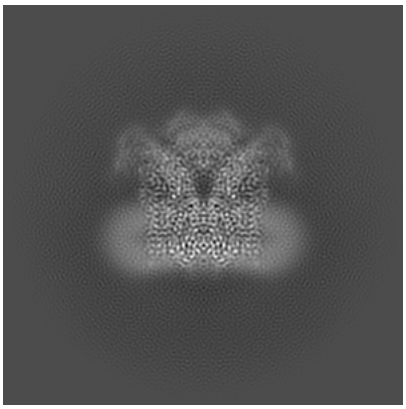
# 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-49846. These allow visual inspection of the internal detail of the map and identification of artifacts.

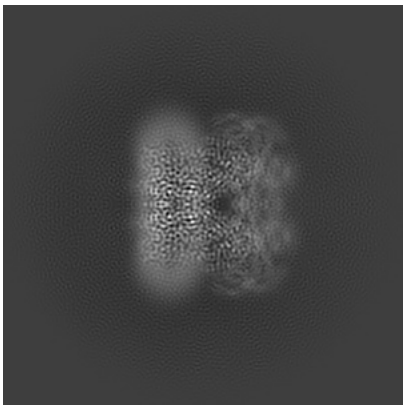
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

## 6.1 Orthogonal projections

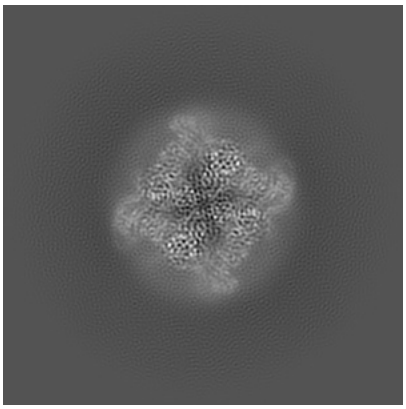
### 6.1.1 Primary map



X

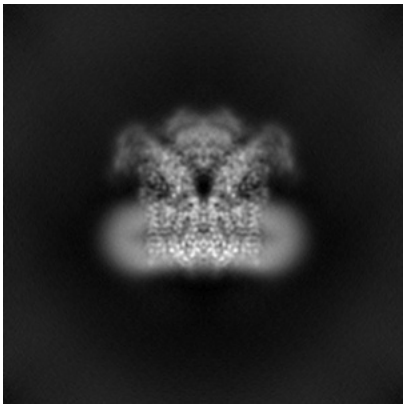


Y

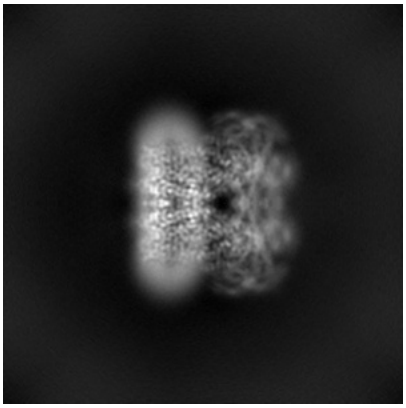


Z

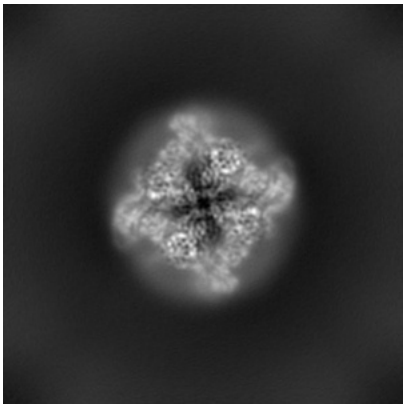
### 6.1.2 Raw map



X



Y

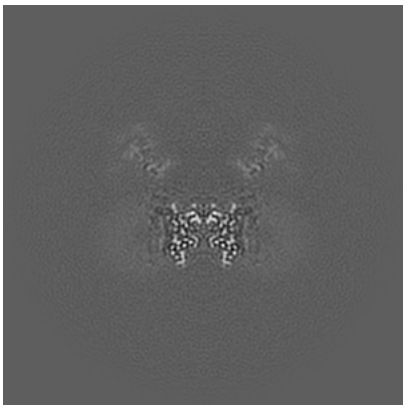


Z

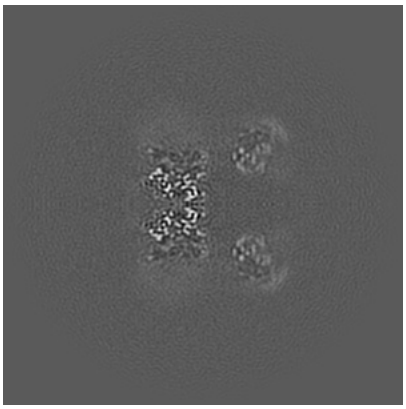
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices (i)

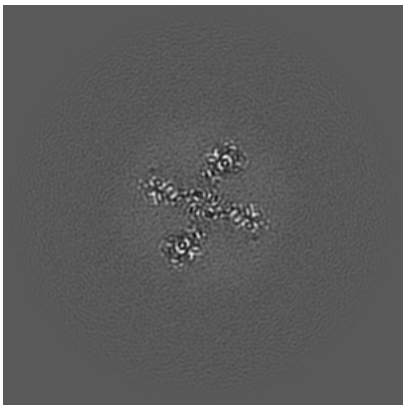
### 6.2.1 Primary map



X Index: 140

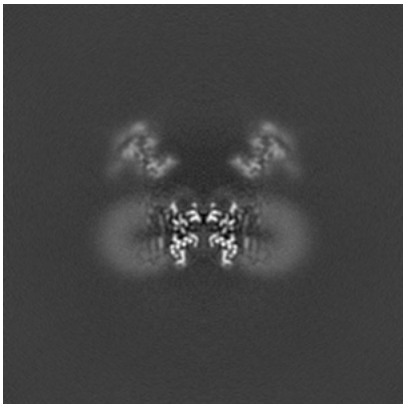


Y Index: 140

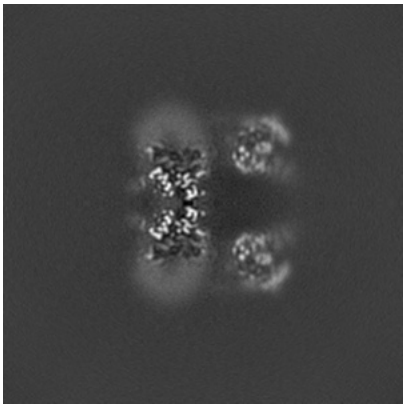


Z Index: 140

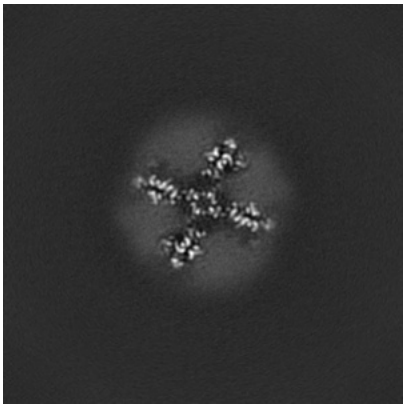
### 6.2.2 Raw map



X Index: 140



Y Index: 140

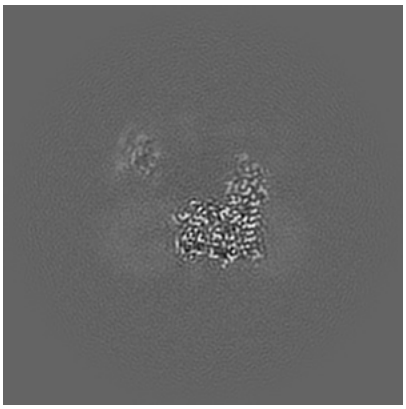


Z Index: 140

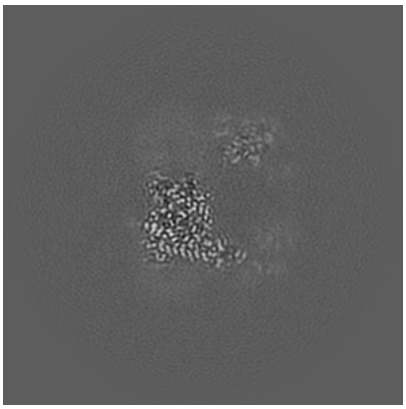
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices (i)

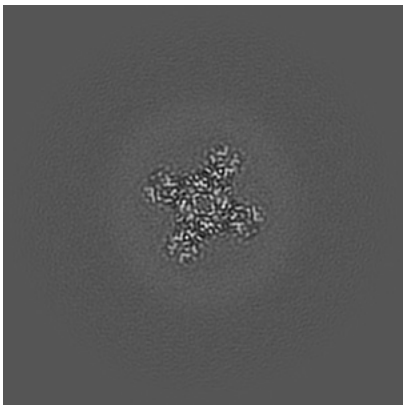
### 6.3.1 Primary map



X Index: 149

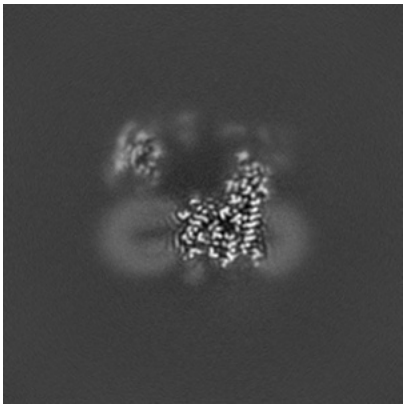


Y Index: 147

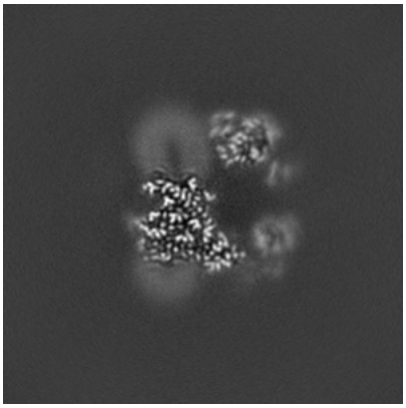


Z Index: 112

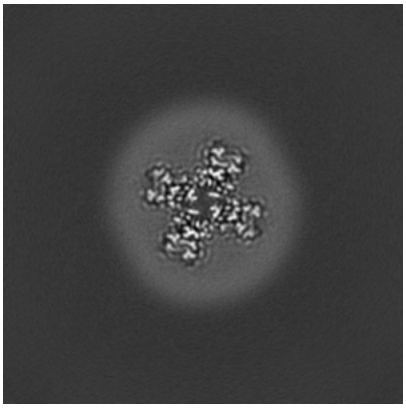
### 6.3.2 Raw map



X Index: 149



Y Index: 149

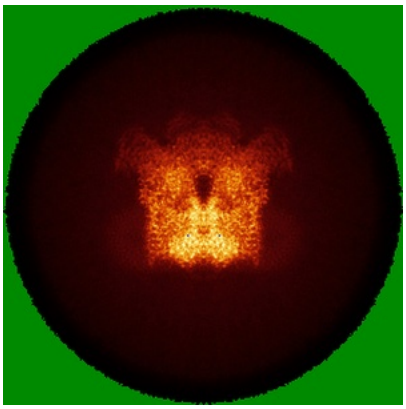


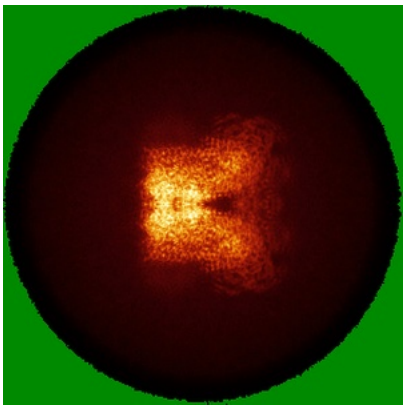
Z Index: 107

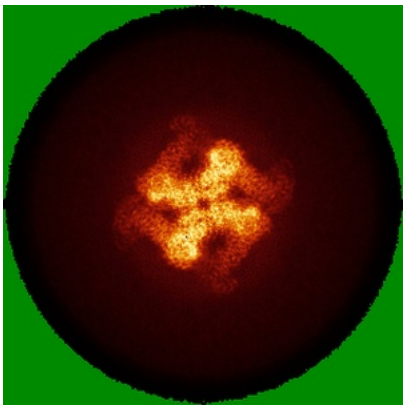
The images above show the largest variance slices of the map in three orthogonal directions.

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

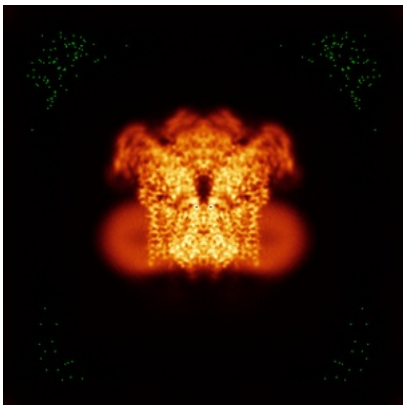
### 6.4.1 Primary map

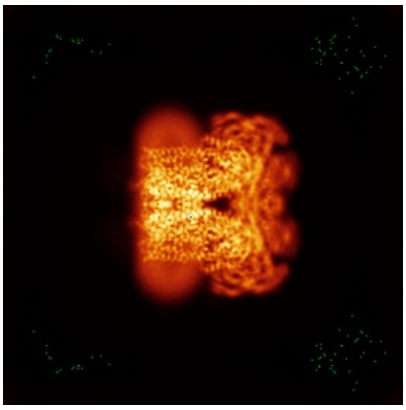

X

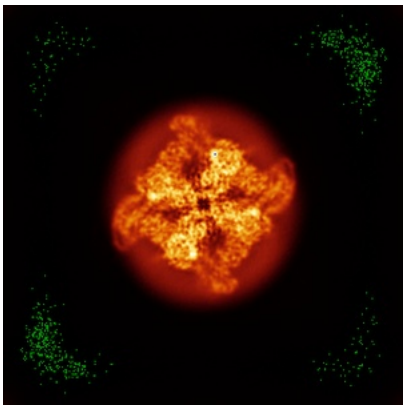

Y


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)

This section was not generated.

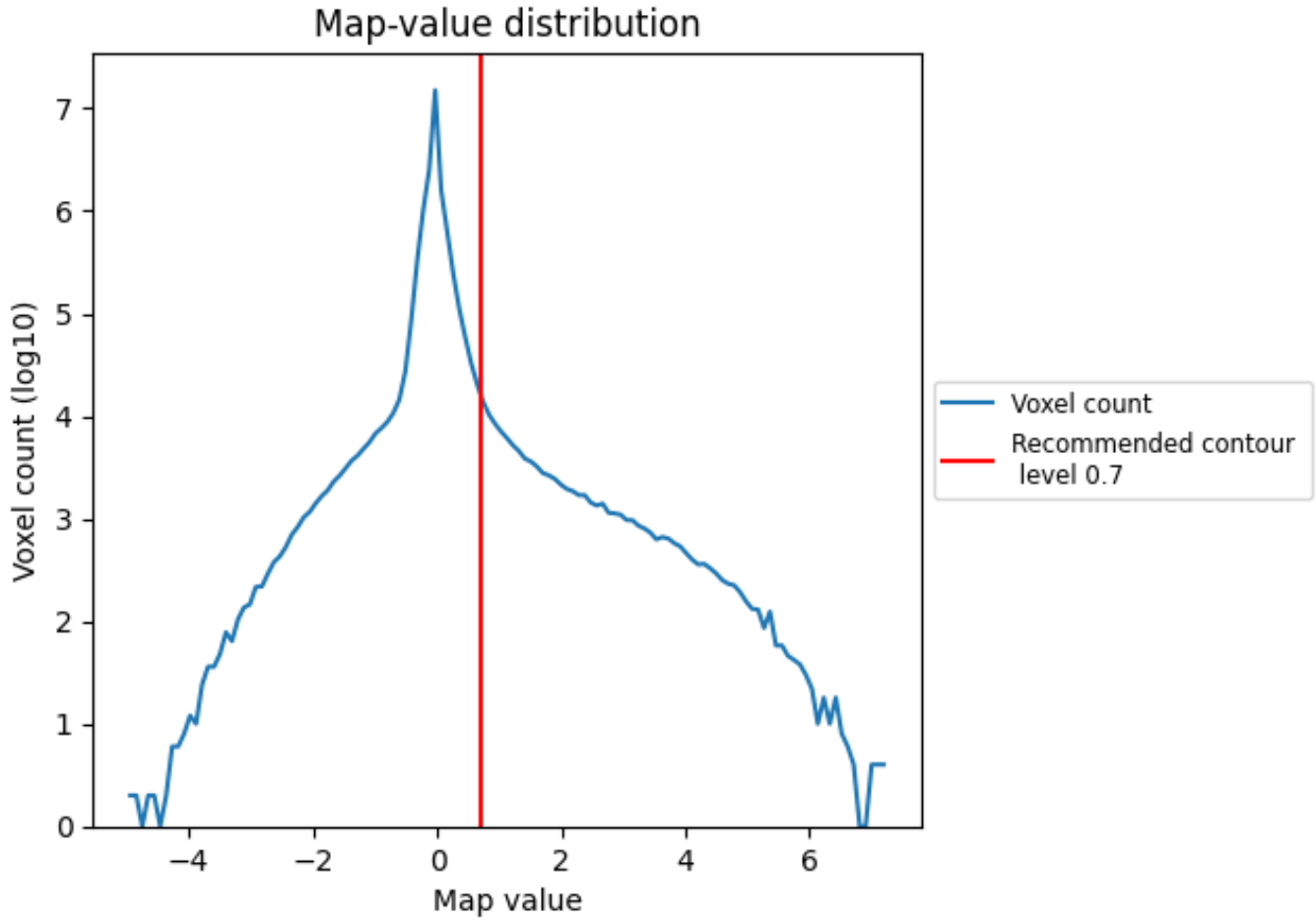
## 6.6 Mask visualisation (i)

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

# 7 Map analysis

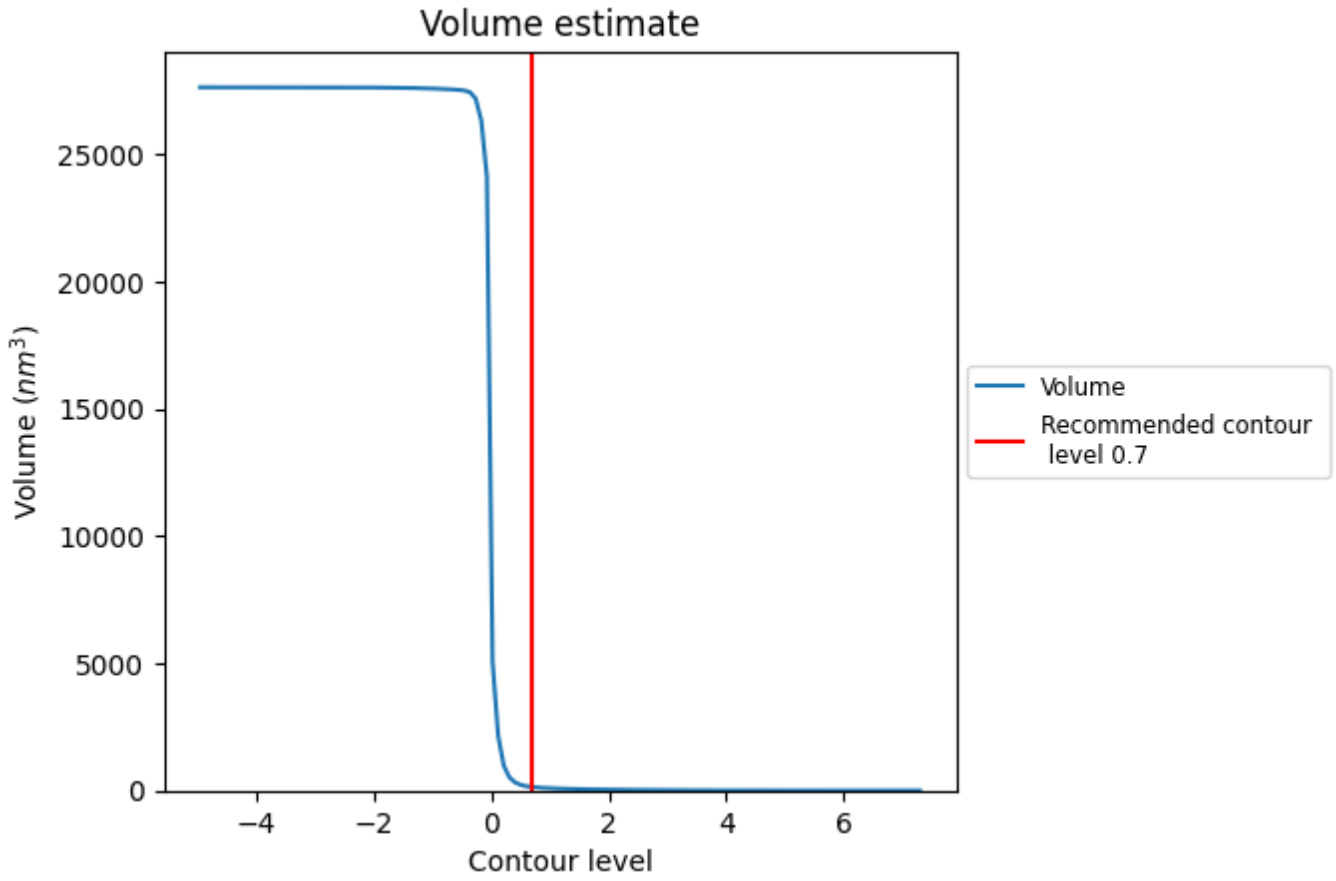
This section contains the results of statistical analysis of the map.

## 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.

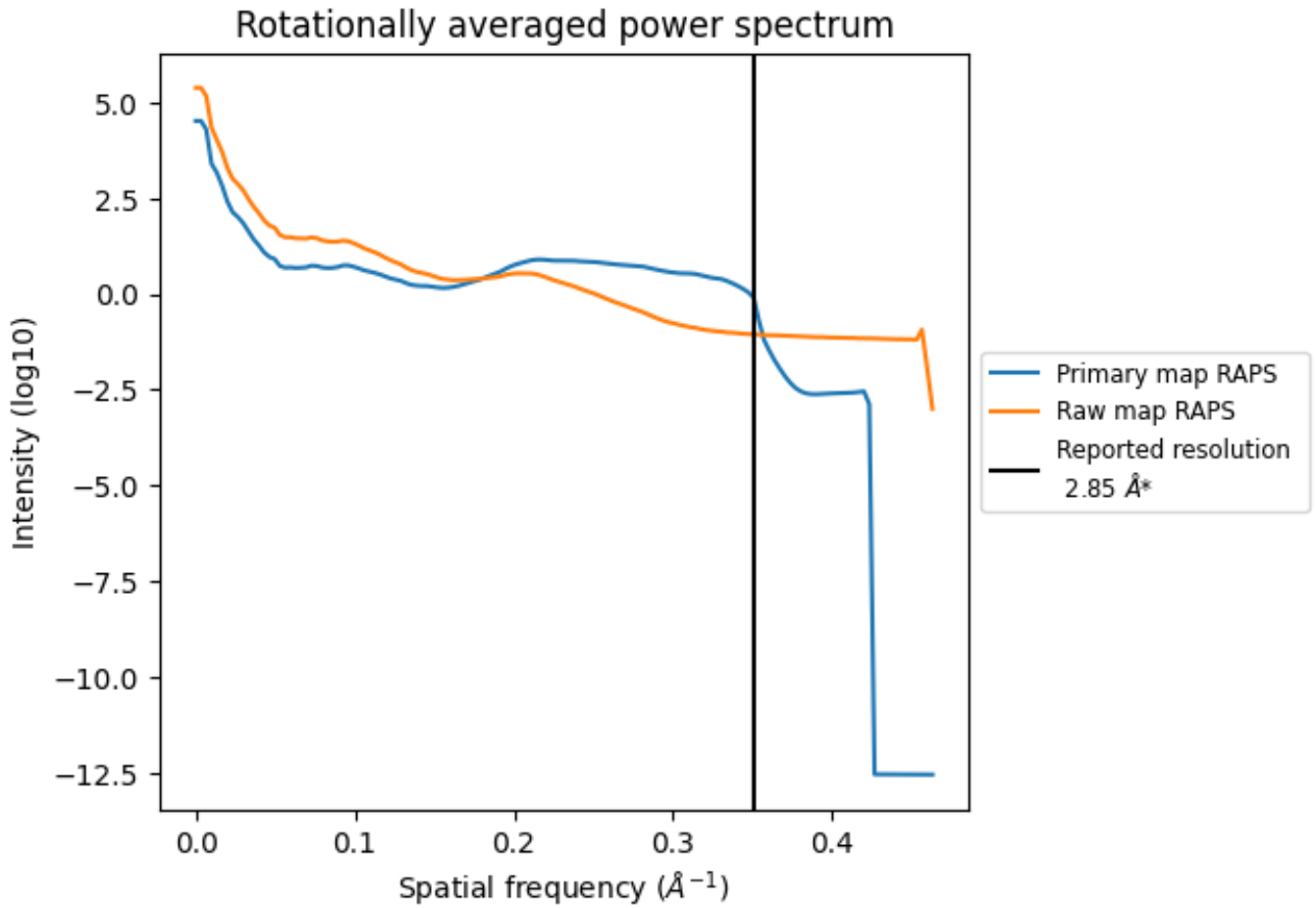
## 7.2 Volume estimate (i)




The volume at the recommended contour level is 139 $nm^3$; this corresponds to an approximate mass of 126 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)

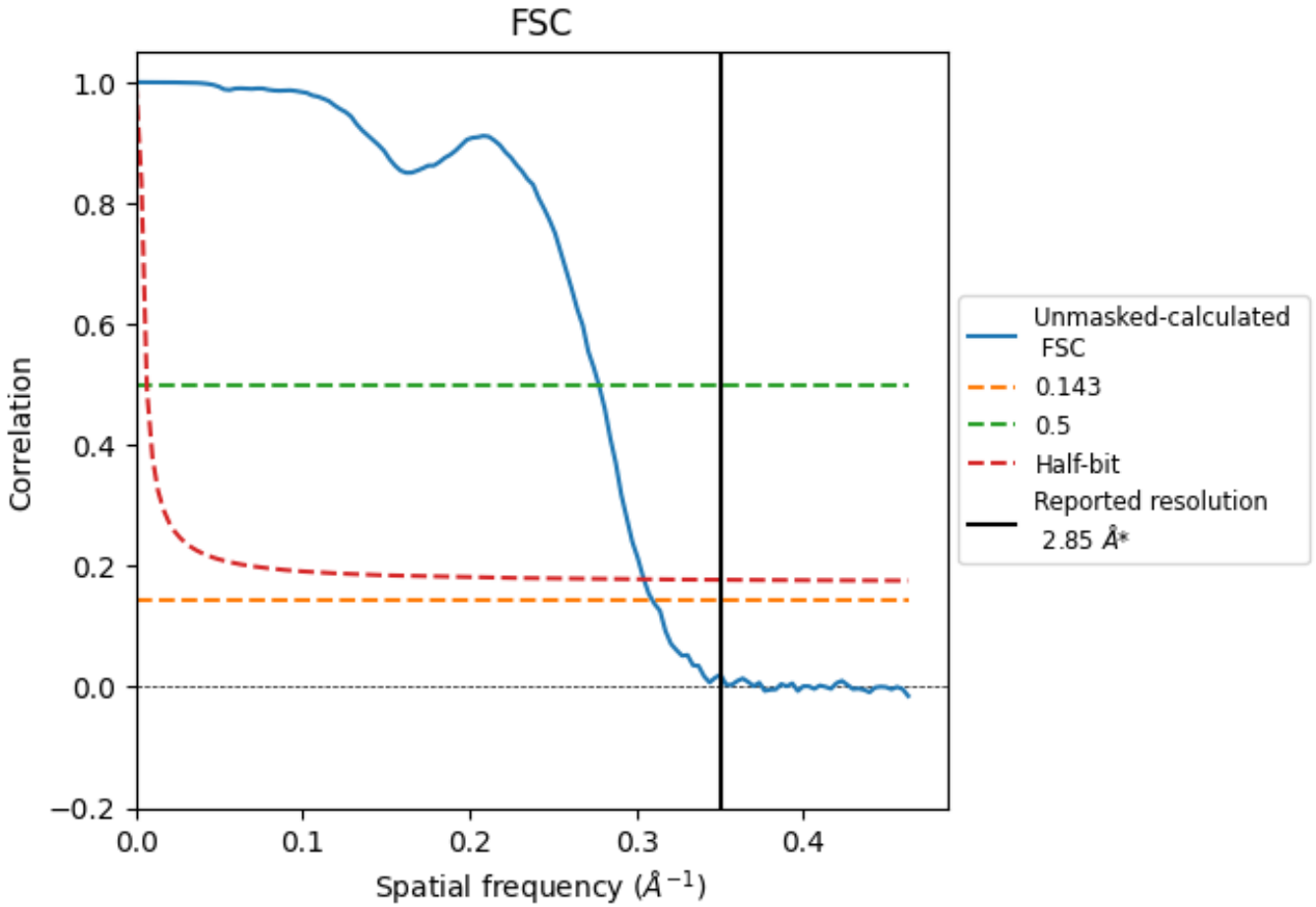



*Reported resolution corresponds to spatial frequency of 0.351 Å$^{-1}$

# 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 0.351 Å$^{-1}$

## 8.2 Resolution estimates (i)

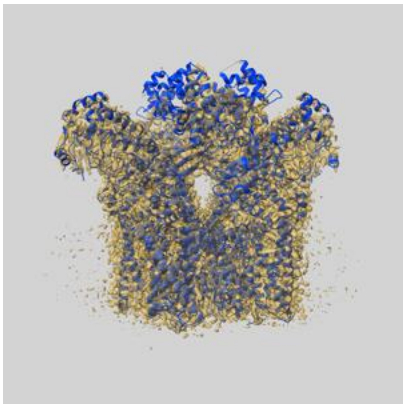
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---|---|---|---|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 2.85 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 3.23 | 3.60 | 3.28 |

*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 3.23 differs from the reported value 2.85 by more than 10 %

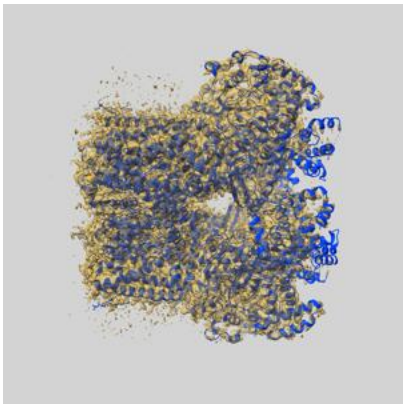
# 9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-49846 and PDB model 9NVP. Per-residue inclusion information can be found in section 3 on page 9.

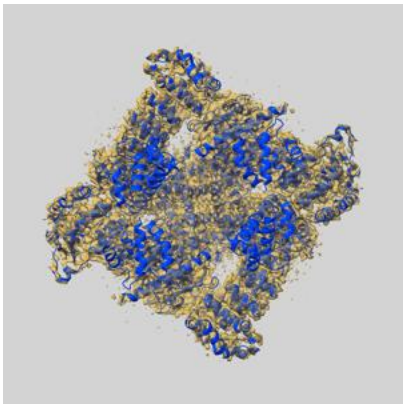
## 9.1 Map-model overlay



X



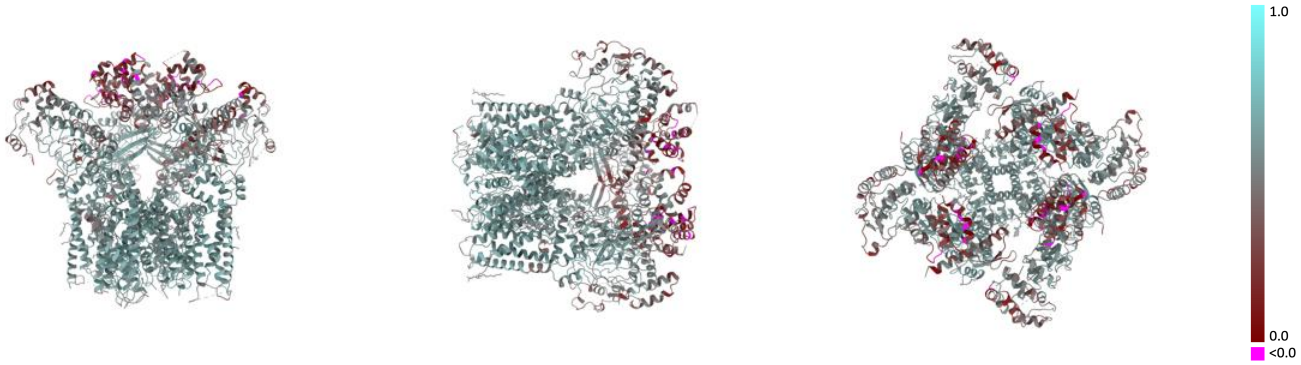
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.7 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.

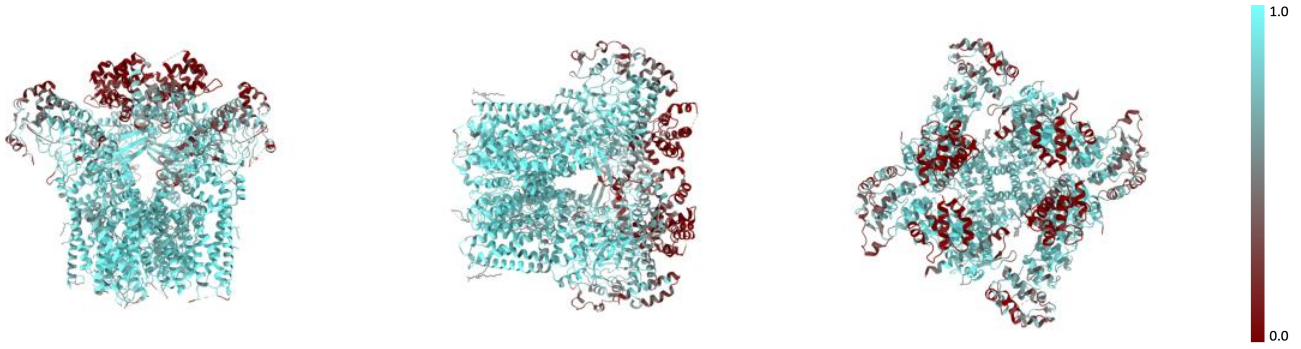
## 9.2 Q-score mapped to coordinate model




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.

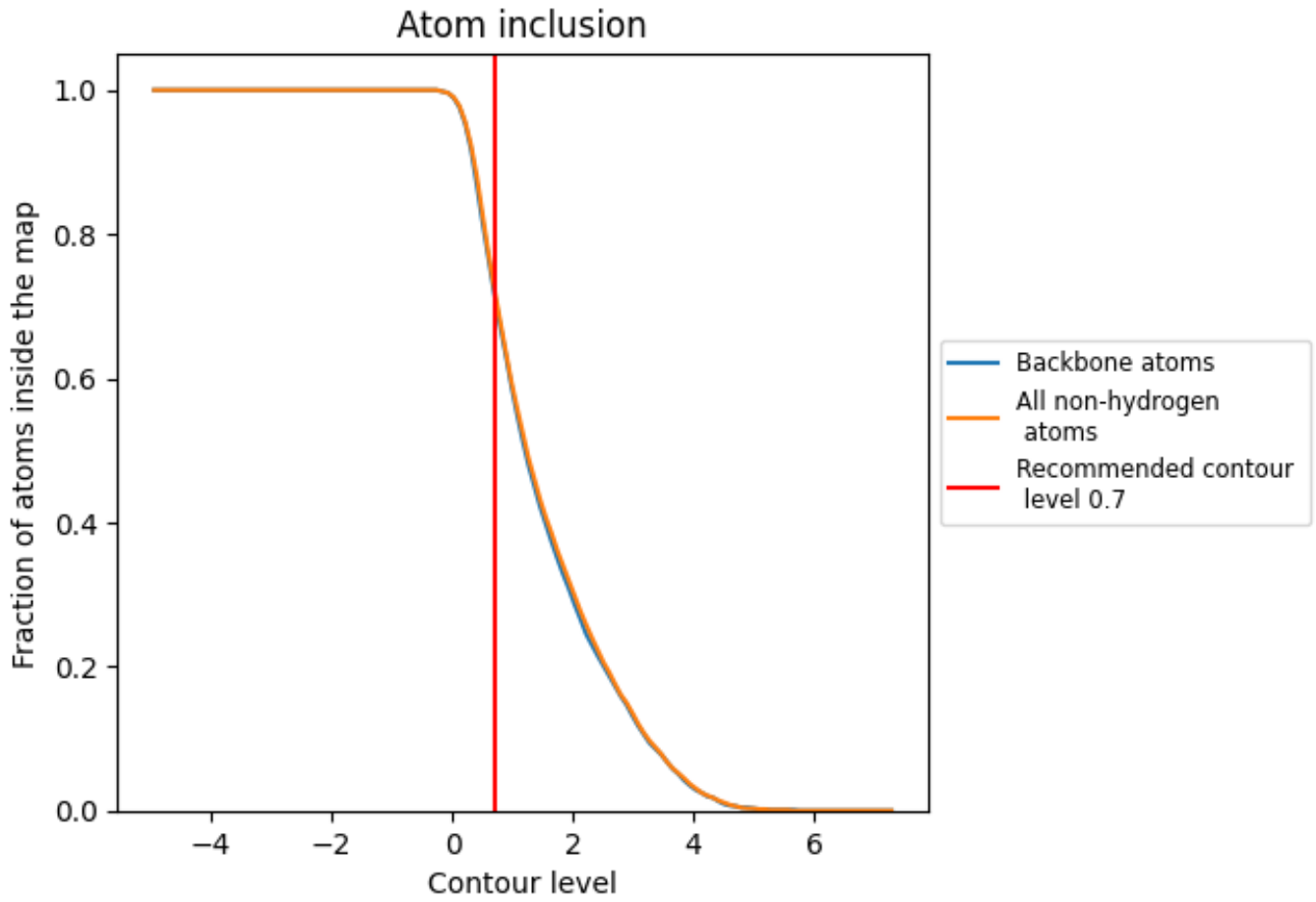
## 9.3 Atom inclusion mapped to coordinate model




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 (0.7).

## 9.4 Atom inclusion (i)




At the recommended contour level, 72% of all backbone atoms, 72% 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 (0.7) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|---|---|---|
| All | 0.7250 | 0.5210 |
| A | 0.7950 | 0.5490 |
| B | 0.7810 | 0.5470 |
| C | 0.7940 | 0.5480 |
| D | 0.7800 | 0.5460 |
| E | 0.0630 | 0.2240 |
| F | 0.0590 | 0.2270 |

