



## wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 08:24 PM UTC

PDB ID : 8ZUJ / pdb\_00008zuj  
EMDB ID : EMD-60485  
Title : Pentagonal cluster of BAFF-BAFFR ectodomain complex  
Authors : Lim, C.S.; Lee, J.O.  
Deposited on : 2024-06-09  
Resolution : 2.58 Å(reported)  
Based on initial model : 4V46

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

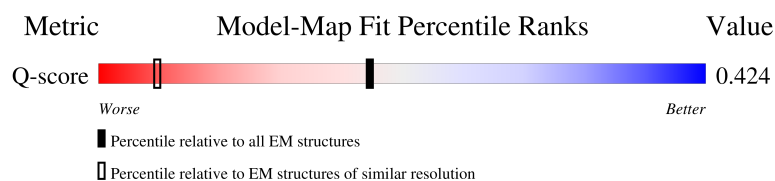
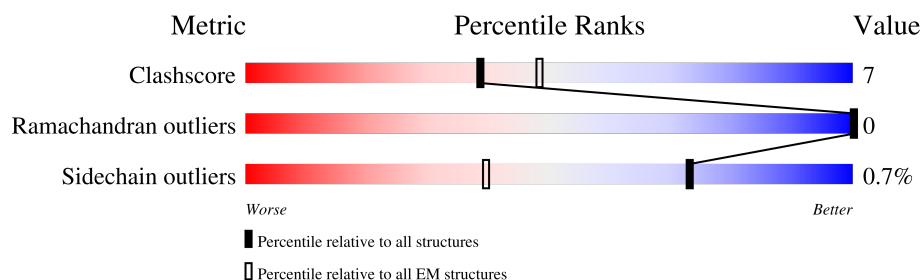
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.58 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<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| Q-score               | -                           | 25397                       | 7675 ( 2.08 - 3.08 )                                     |

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  $\geq 3$ , 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  $\leq 5\%$ . 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     | 101    |                  |
| 1   | B     | 101    |                  |
| 1   | C     | 101    |                  |
| 1   | G     | 101    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | H     | 101    |                  |
| 1   | I     | 101    |                  |
| 1   | M     | 101    |                  |
| 1   | N     | 101    |                  |
| 1   | O     | 101    |                  |
| 1   | S     | 101    |                  |
| 1   | T     | 101    |                  |
| 1   | U     | 101    |                  |
| 1   | Y     | 101    |                  |
| 1   | Z     | 101    |                  |
| 1   | a     | 101    |                  |
| 2   | D     | 157    |                  |
| 2   | E     | 157    |                  |
| 2   | F     | 157    |                  |
| 2   | J     | 157    |                  |
| 2   | K     | 157    |                  |
| 2   | L     | 157    |                  |
| 2   | P     | 157    |                  |
| 2   | Q     | 157    |                  |
| 2   | R     | 157    |                  |
| 2   | V     | 157    |                  |
| 2   | W     | 157    |                  |
| 2   | X     | 157    |                  |
| 2   | b     | 157    |                  |
| 2   | c     | 157    |                  |

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| Mol | Chain | Length | Quality of chain                                                              |
|-----|-------|--------|-------------------------------------------------------------------------------|
| 2   | d     | 157    | <div><div></div><div>11%</div><div>72%</div><div>20%</div><div>8%</div></div> |

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19830 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 Tumor necrosis factor receptor superfamily member 13C.

| Mol | Chain | Residues | Atoms        |          |         |         |        | AltConf | Trace |
|-----|-------|----------|--------------|----------|---------|---------|--------|---------|-------|
| 1   | A     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | B     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | C     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | G     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | H     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | I     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | M     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | N     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | O     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | S     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | T     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | U     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | Y     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | Z     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |
| 1   | a     | 24       | Total<br>179 | C<br>114 | N<br>32 | O<br>29 | S<br>4 | 0       | 0     |

There are 360 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| A     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| A     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| A     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| A     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| A     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| A     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| A     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| A     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| A     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| A     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| A     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| A     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| A     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| A     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| A     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| A     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| A     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| A     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| B     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| B     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| B     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| B     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| B     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| B     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| B     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| B     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| B     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| B     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| B     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| B     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| B     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| B     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| B     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| B     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| B     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| B     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| C     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| C     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| C     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| C     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| C     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| C     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| C     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| C     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| C     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| C     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| C     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| C     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| C     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| C     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| C     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| C     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| C     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| G     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| G     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| G     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| G     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| G     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| G     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| G     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| G     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| G     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| G     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| G     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| G     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| G     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| G     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| G     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| G     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| G     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| H     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| H     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| H     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| H     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| H     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| H     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| H     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| H     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| H     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| H     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| H     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| H     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| H     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| H     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| H     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| H     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| H     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| I     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| I     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| I     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| I     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| I     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| I     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| I     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| I     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| I     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| I     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| I     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| I     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| I     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| I     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| I     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| I     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| I     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| I     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| I     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| I     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
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| I     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| I     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| I     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| M     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| M     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| M     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| M     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| M     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| M     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| M     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| M     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| M     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| M     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| M     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| M     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| M     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| M     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| M     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| M     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| M     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| N     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| N     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| N     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| N     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| N     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| N     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| N     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| N     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| N     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| N     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| N     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| N     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| N     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| N     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| N     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| N     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| N     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| O     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| O     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| O     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| O     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| O     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| O     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| O     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| O     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| O     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| O     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| O     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| O     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| O     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| O     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| O     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| O     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| O     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| O     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| S     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| S     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| S     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| S     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| S     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| S     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| S     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| S     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| S     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| S     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| S     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| S     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| S     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| S     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| S     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| S     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| S     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| T     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| T     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| T     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| T     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| T     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| T     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| T     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| T     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| T     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| T     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| T     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| T     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| T     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| T     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| T     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| T     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| T     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| U     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| U     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| U     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| U     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| U     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| U     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| U     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| U     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| U     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| U     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| U     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| U     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| U     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| U     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| U     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| U     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| U     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| Y     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Y     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| Y     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Y     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| Y     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| Y     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| Y     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Y     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Y     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| Y     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Y     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Y     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Y     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Y     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| Y     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Y     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |
| Z     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Z     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| Z     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Z     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| Z     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| Z     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Z     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Z     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| Z     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| Z     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Z     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Z     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Z     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| Z     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| Z     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| Z     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | -9      | ALA      | -      | expression tag | UNP Q96RJ3 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| a     | -8      | ASP      | -      | expression tag | UNP Q96RJ3 |
| a     | -7      | PRO      | -      | expression tag | UNP Q96RJ3 |
| a     | -6      | ASP      | -      | expression tag | UNP Q96RJ3 |
| a     | -5      | TYR      | -      | expression tag | UNP Q96RJ3 |
| a     | -4      | LYS      | -      | expression tag | UNP Q96RJ3 |
| a     | -3      | ASP      | -      | expression tag | UNP Q96RJ3 |
| a     | -2      | ASP      | -      | expression tag | UNP Q96RJ3 |
| a     | -1      | ASP      | -      | expression tag | UNP Q96RJ3 |
| a     | 0       | ASP      | -      | expression tag | UNP Q96RJ3 |
| a     | 1       | LYS      | -      | expression tag | UNP Q96RJ3 |
| a     | 79      | GLY      | -      | expression tag | UNP Q96RJ3 |
| a     | 80      | GLY      | -      | expression tag | UNP Q96RJ3 |
| a     | 81      | GLY      | -      | expression tag | UNP Q96RJ3 |
| a     | 82      | GLY      | -      | expression tag | UNP Q96RJ3 |
| a     | 83      | SER      | -      | expression tag | UNP Q96RJ3 |
| a     | 84      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 85      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 86      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 87      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 88      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 89      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 90      | HIS      | -      | expression tag | UNP Q96RJ3 |
| a     | 91      | HIS      | -      | expression tag | UNP Q96RJ3 |

- Molecule 2 is a protein called Tumor necrosis factor ligand superfamily member 13b, soluble form.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2   | D     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | E     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | F     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | J     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | K     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | L     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | P     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |

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| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2   | Q     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | R     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | V     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | W     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | X     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | b     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | c     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |
| 2   | d     | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1143  | 736 | 184 | 218 | 5 |         |       |

There are 75 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| D     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| D     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| D     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| D     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| D     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| E     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| E     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| E     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| E     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| E     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| F     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| F     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| F     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| F     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| F     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| J     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| J     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| J     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| J     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| J     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| K     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| K     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| K     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |

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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| K     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| K     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| L     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| L     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| L     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| L     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| L     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| P     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| P     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| P     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| P     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| P     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| Q     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| Q     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| Q     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| Q     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| Q     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| R     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| R     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| R     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| R     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| R     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| V     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| V     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| V     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| V     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| V     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| W     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| W     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| W     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| W     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| W     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| X     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| X     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| X     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| X     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| X     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| b     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| b     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| b     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| b     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| b     | 133     | SER      | -      | expression tag | UNP Q9Y275 |

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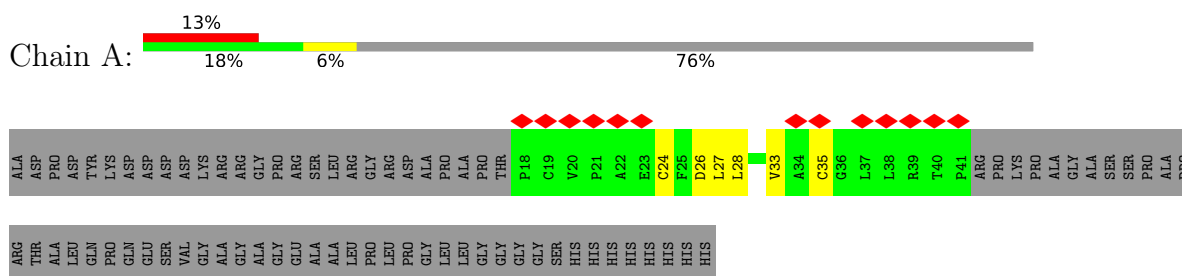
*Continued from previous page...*

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| c     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| c     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| c     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| c     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| c     | 133     | SER      | -      | expression tag | UNP Q9Y275 |
| d     | 129     | GLY      | -      | expression tag | UNP Q9Y275 |
| d     | 130     | SER      | -      | expression tag | UNP Q9Y275 |
| d     | 131     | GLY      | -      | expression tag | UNP Q9Y275 |
| d     | 132     | GLY      | -      | expression tag | UNP Q9Y275 |
| d     | 133     | SER      | -      | expression tag | UNP Q9Y275 |

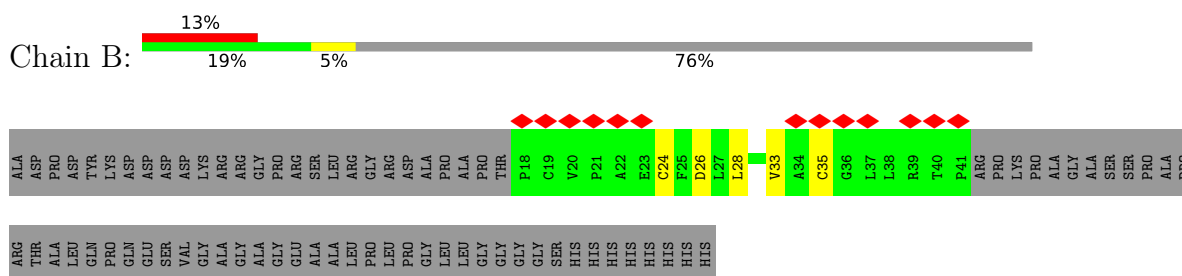
### 3 Residue-property plots [i](#)

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.

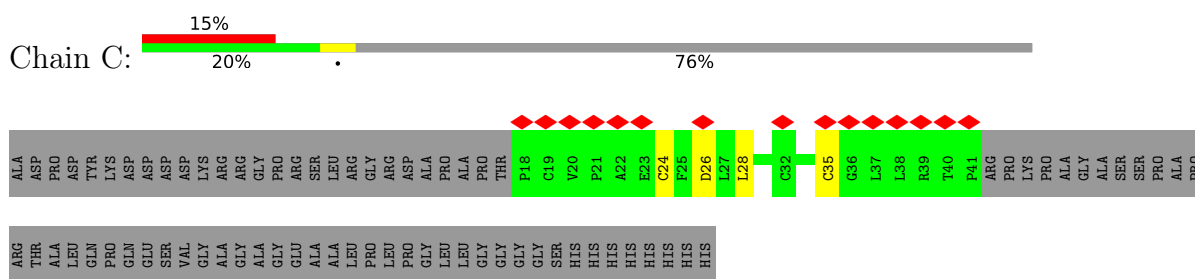
- Molecule 1: Tumor necrosis factor receptor superfamily member 13C



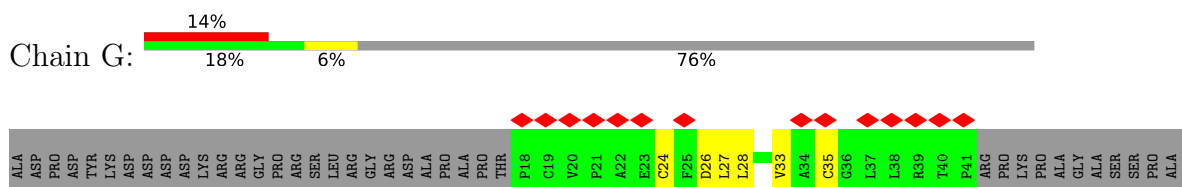
- Molecule 1: Tumor necrosis factor receptor superfamily member 13C



- Molecule 1: Tumor necrosis factor receptor superfamily member 13C



- Molecule 1: Tumor necrosis factor receptor superfamily member 13C





[illegible]

ARG THR  
ASP ALA  
LEU LEU  
GLN GLN  
PRO PRO  
GLU GLU  
SER VAL  
GLY VAL  
ALA ALA  
GLY GLY  
ALA ALA  
GLU GLU  
GLY GLY  
ALA ALA  
LEU LEU  
PRO PRO  
LEU LEU  
PRO PRO  
GLY GLY  
ASP ASP  
PRO PRO  
LEU LEU  
GLY GLY  
HIS HIS  
HIS HIS  
HIS HIS  
HIS HIS  
HIS HIS

- Molecule 1: Tumor necrosis factor receptor superfamily member 13C

Chain a: 

ALA ASP  
PRO PRO  
GLY GLY  
SER SER  
VAL VAL  
GLY GLY  
ALA ALA  
GLY GLY  
ALA ALA  
GLU GLU  
GLY GLY  
ALA ALA  
LEU LEU  
PRO PRO  
THR THR  
P18  
C19  
V20  
P21  
A22  
E23  
C24  
F25  
D26  
L27  
L28  
G32  
V33  
A34  
C35  
G36  
L37  
L38  
R39  
T40  
P41  
ARG  
PRO  
LYS  
PRO  
ALA  
GLY  
ALA  
SER  
SER  
PRO  
ALA

- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

Chain D: 

GLY SER  
GLY GLY  
SER SER  
ALA VAL  
GLN GLN  
GLY GLY  
PRO PRO  
GLU GLU  
THR THR  
V142  
T143  
I150  
A151  
D152  
S153  
E154  
T155  
P156  
T157  
I158  
Y163  
T164  
F165  
S171  
F172  
K173  
R174  
G175  
S176  
K181  
E182  
I185  
L186  
V187  
K188  
E189  
T190  
G191  
Q198  
V199  
L200  
D203  
G209  
R214  
K215  
K216  
V217  
H218  
V219  
F220  
G221  
D222  
E223  
L224  
L229  
F230  
R231  
C232  
I233  
E238  
C245  
Y246  
K252  
L253  
E254  
E255  
G256  
D257  
E258  
L259  
T263  
P264  
D269  
V276  
L285

- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

Chain E: 

GLY SER  
GLY GLY  
SER SER  
ALA VAL  
GLN GLN  
GLY GLY  
PRO PRO  
GLU GLU  
THR THR  
V142  
D145  
I150  
S153  
E154  
I158  
T164  
F165  
S171  
F172  
R174  
G175  
S176  
E179  
E180  
E182  
I185  
L186  
E189  
Q198  
V199  
L200  
G209  
K215  
K216  
E223  
L226  
V227  
C232  
I233  
E238  
C245  
Y246  
E254  
E258  
L259  
I263  
P264  
A268  
D275  
V276  
K283  
L284  
L285

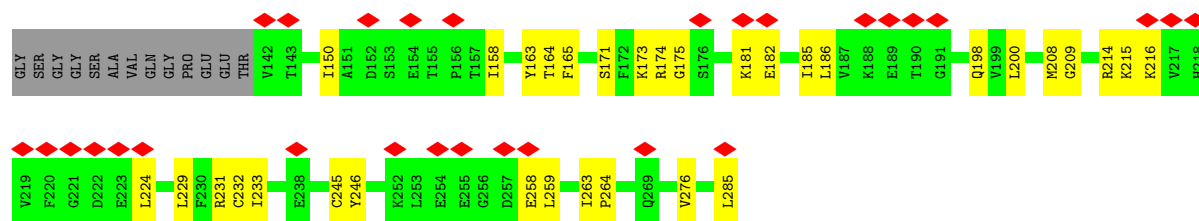
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

Chain F: 

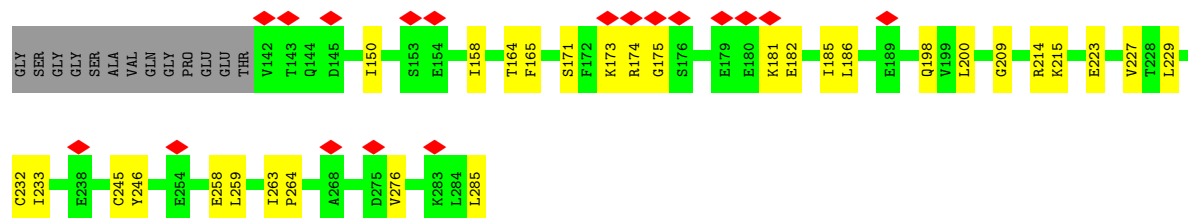
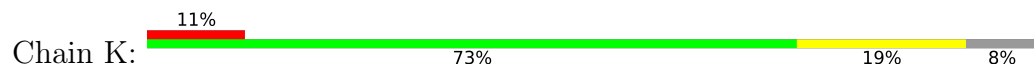
GLY SER  
GLY GLY  
SER SER  
ALA VAL  
GLN GLN  
GLY GLY  
PRO PRO  
GLU GLU  
THR THR  
V142  
I150  
E154  
T157  
I158  
Q159  
K160  
G161  
S162  
Y163  
T164  
F165  
S171  
F172  
K173  
R174  
G175  
S176  
K181  
E182  
I185  
L186  
Q198  
V199  
L200  
K204  
T205  
Y206  
A207  
M208  
G209  
R214  
K215  
E223  
L224  
S225  
L226  
V227  
T228  
L229  
F230  
R231  
C232  
I233  
E238  
T239  
L240  
C245  
Y246  
E258  
L259  
I263  
E266  
N267  
V276  
L285

- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

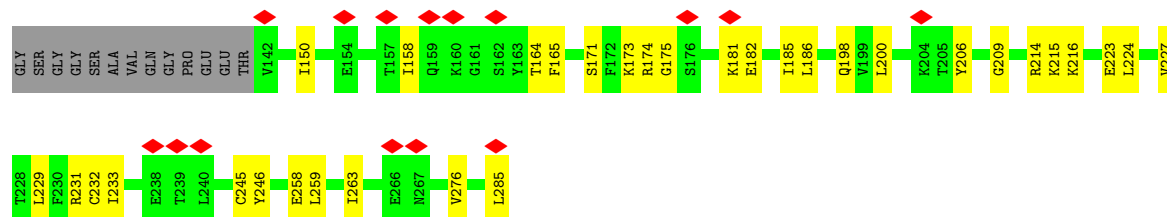
Chain J: 



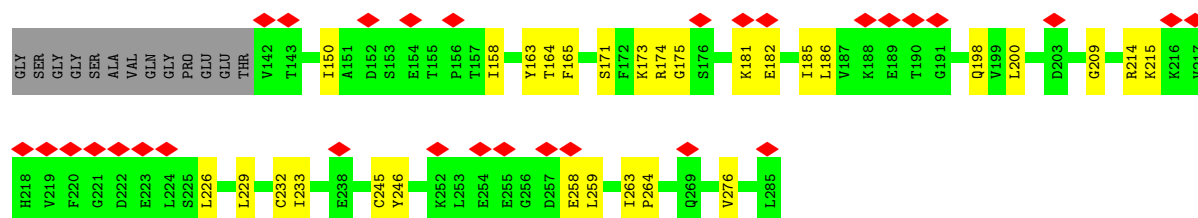
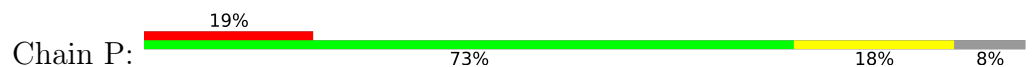
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



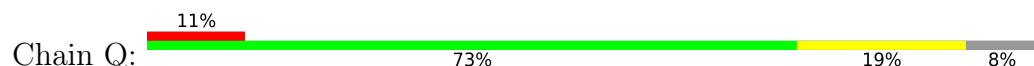
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

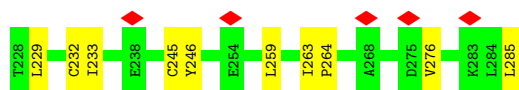


- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

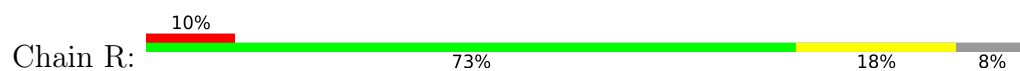


- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form

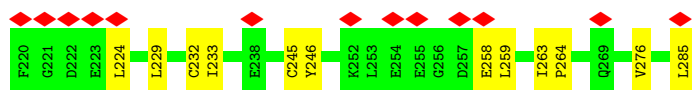
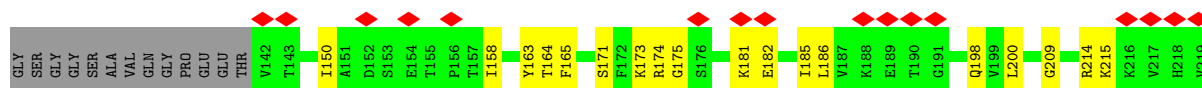
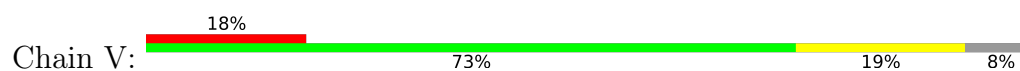




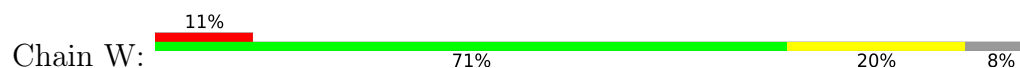
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



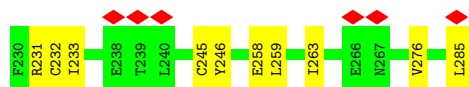
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



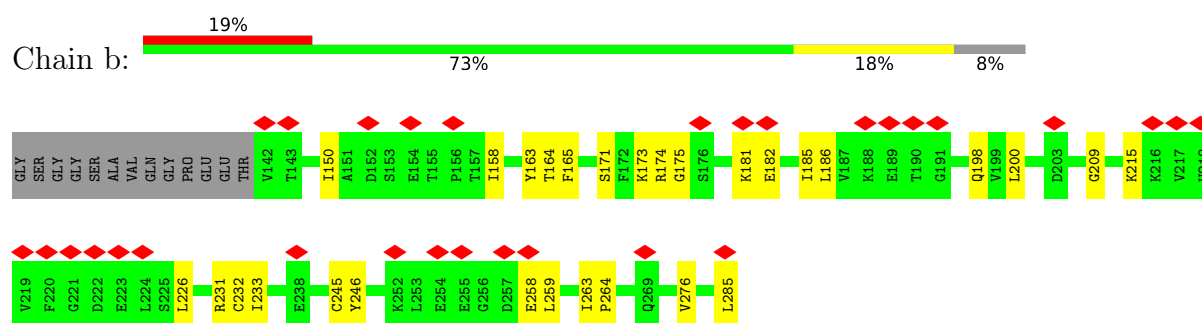
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



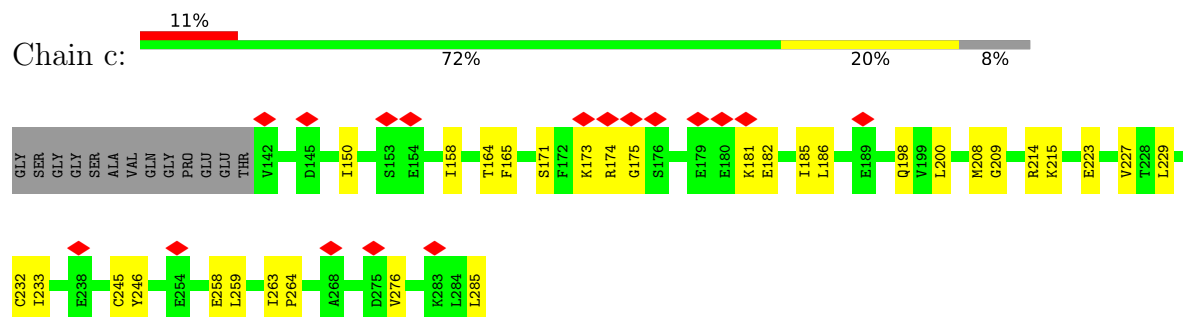
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



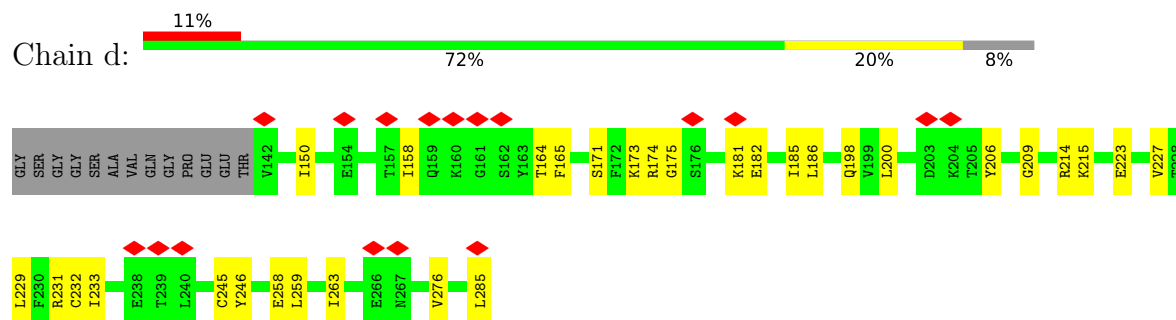
- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



- Molecule 2: Tumor necrosis factor ligand superfamily member 13b, soluble form



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, C5                               | Depositor |
| Number of particles used             | 220800                                  | 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 ( $e^-/\text{\AA}^2$ ) | 50                                      | Depositor |
| Minimum defocus (nm)                 | 800                                     | Depositor |
| Maximum defocus (nm)                 | 2000                                    | Depositor |
| Magnification                        | 100500                                  | Depositor |
| Image detector                       | GATAN K3 BIOQUANTUM (6k x 4k)           | Depositor |
| Maximum map value                    | 3.429                                   | Depositor |
| Minimum map value                    | -2.346                                  | Depositor |
| Average map value                    | -0.000                                  | Depositor |
| Map value standard deviation         | 0.062                                   | Depositor |
| Recommended contour level            | 0.38                                    | Depositor |
| Map size (Å)                         | 328.80002, 328.80002, 328.80002         | wwPDB     |
| Map dimensions                       | 400, 400, 400                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 0.822, 0.822, 0.822                     | 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     | 0.20         | 0/183       | 0.49        | 0/249       |
| 1   | B     | 0.19         | 0/183       | 0.48        | 0/249       |
| 1   | C     | 0.20         | 0/183       | 0.49        | 0/249       |
| 1   | G     | 0.19         | 0/183       | 0.49        | 0/249       |
| 1   | H     | 0.20         | 0/183       | 0.48        | 0/249       |
| 1   | I     | 0.19         | 0/183       | 0.49        | 0/249       |
| 1   | M     | 0.20         | 0/183       | 0.49        | 0/249       |
| 1   | N     | 0.20         | 0/183       | 0.48        | 0/249       |
| 1   | O     | 0.19         | 0/183       | 0.48        | 0/249       |
| 1   | S     | 0.19         | 0/183       | 0.48        | 0/249       |
| 1   | T     | 0.20         | 0/183       | 0.48        | 0/249       |
| 1   | U     | 0.19         | 0/183       | 0.49        | 0/249       |
| 1   | Y     | 0.19         | 0/183       | 0.48        | 0/249       |
| 1   | Z     | 0.20         | 0/183       | 0.48        | 0/249       |
| 1   | a     | 0.19         | 0/183       | 0.49        | 0/249       |
| 2   | D     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | E     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | F     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | J     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | K     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | L     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | P     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | Q     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | R     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | V     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | W     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | X     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | b     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | c     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| 2   | d     | 0.12         | 0/1165      | 0.35        | 0/1574      |
| All | All   | 0.13         | 0/20220     | 0.37        | 0/27345     |

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   | A     | 179   | 0        | 180      | 5       | 0            |
| 1   | B     | 179   | 0        | 180      | 3       | 0            |
| 1   | C     | 179   | 0        | 180      | 3       | 0            |
| 1   | G     | 179   | 0        | 180      | 5       | 0            |
| 1   | H     | 179   | 0        | 180      | 3       | 0            |
| 1   | I     | 179   | 0        | 180      | 4       | 0            |
| 1   | M     | 179   | 0        | 180      | 3       | 0            |
| 1   | N     | 179   | 0        | 180      | 4       | 0            |
| 1   | O     | 179   | 0        | 180      | 4       | 0            |
| 1   | S     | 179   | 0        | 180      | 4       | 0            |
| 1   | T     | 179   | 0        | 180      | 3       | 0            |
| 1   | U     | 179   | 0        | 180      | 4       | 0            |
| 1   | Y     | 179   | 0        | 180      | 4       | 0            |
| 1   | Z     | 179   | 0        | 180      | 3       | 0            |
| 1   | a     | 179   | 0        | 180      | 4       | 0            |
| 2   | D     | 1143  | 0        | 1145     | 19      | 0            |
| 2   | E     | 1143  | 0        | 1145     | 19      | 0            |
| 2   | F     | 1143  | 0        | 1145     | 20      | 0            |
| 2   | J     | 1143  | 0        | 1145     | 21      | 0            |
| 2   | K     | 1143  | 0        | 1145     | 18      | 0            |
| 2   | L     | 1143  | 0        | 1145     | 21      | 0            |
| 2   | P     | 1143  | 0        | 1145     | 18      | 0            |
| 2   | Q     | 1143  | 0        | 1145     | 20      | 0            |
| 2   | R     | 1143  | 0        | 1145     | 18      | 0            |
| 2   | V     | 1143  | 0        | 1145     | 18      | 0            |
| 2   | W     | 1143  | 0        | 1145     | 20      | 0            |
| 2   | X     | 1143  | 0        | 1145     | 20      | 0            |
| 2   | b     | 1143  | 0        | 1145     | 18      | 0            |
| 2   | c     | 1143  | 0        | 1145     | 19      | 0            |
| 2   | d     | 1143  | 0        | 1145     | 19      | 0            |
| All | All   | 19830 | 0        | 19875    | 291     | 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 7.

The worst 5 of 291 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:O:28:LEU:O | 2:R:231:ARG:NH1 | 2.31                     | 0.64              |
| 1:I:28:LEU:O | 2:L:231:ARG:NH1 | 2.31                     | 0.64              |
| 1:U:28:LEU:O | 2:X:231:ARG:NH1 | 2.31                     | 0.64              |
| 1:C:28:LEU:O | 2:F:231:ARG:NH1 | 2.31                     | 0.63              |
| 1:a:28:LEU:O | 2:d:231:ARG:NH1 | 2.31                     | 0.63              |

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     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | B     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | C     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | G     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | H     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | I     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | M     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | N     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | O     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | S     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | T     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |
| 1   | U     | 22/101 (22%) | 21 (96%) | 1 (4%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Favoured   | Allowed | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|---------|----------|-------------|-----|
| 1   | Y     | 22/101 (22%)    | 21 (96%)   | 1 (4%)  | 0        | 100         | 100 |
| 1   | Z     | 22/101 (22%)    | 21 (96%)   | 1 (4%)  | 0        | 100         | 100 |
| 1   | a     | 22/101 (22%)    | 21 (96%)   | 1 (4%)  | 0        | 100         | 100 |
| 2   | D     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | E     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | F     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | J     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | K     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | L     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | P     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | Q     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | R     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | V     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | W     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | X     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | b     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | c     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| 2   | d     | 142/157 (90%)   | 139 (98%)  | 3 (2%)  | 0        | 100         | 100 |
| All | All   | 2460/3870 (64%) | 2400 (98%) | 60 (2%) | 0        | 100         | 100 |

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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     | 21/76 (28%) | 21 (100%) | 0        | 100         | 100 |
| 1   | B     | 21/76 (28%) | 21 (100%) | 0        | 100         | 100 |
| 1   | C     | 21/76 (28%) | 21 (100%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Rotameric  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|-------------|-----|
| 1   | G     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | H     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | I     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | M     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | N     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | O     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | S     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | T     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | U     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | Y     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | Z     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 1   | a     | 21/76 (28%)     | 21 (100%)  | 0        | 100         | 100 |
| 2   | D     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | E     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | F     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | J     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | K     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | L     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | P     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | Q     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | R     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | V     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | W     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | X     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | b     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | c     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| 2   | d     | 126/134 (94%)   | 125 (99%)  | 1 (1%)   | 73          | 87  |
| All | All   | 2205/3150 (70%) | 2190 (99%) | 15 (1%)  | 73          | 88  |

5 of 15 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | Q     | 233 | ILE  |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | c     | 233 | ILE  |
| 2   | R     | 233 | ILE  |
| 2   | d     | 233 | ILE  |
| 2   | X     | 233 | ILE  |

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   | R     | 242 | ASN  |
| 2   | V     | 242 | ASN  |
| 2   | d     | 242 | ASN  |
| 2   | b     | 242 | ASN  |
| 2   | d     | 218 | HIS  |

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

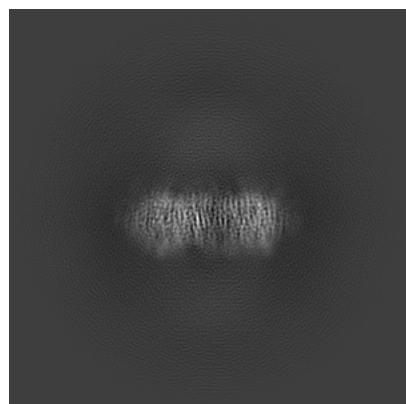
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60485. These allow visual inspection of the internal detail of the map and identification of artifacts.

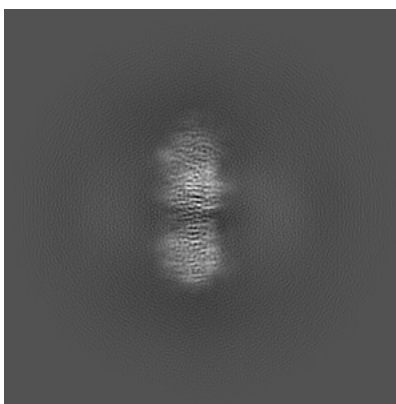
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

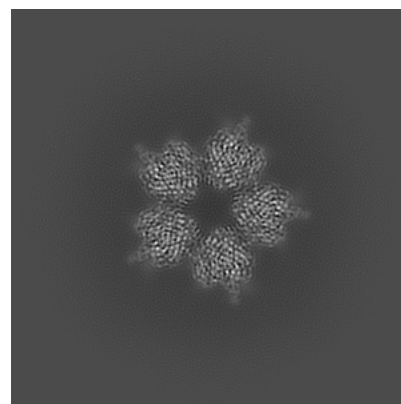
#### 6.1.1 Primary map



X

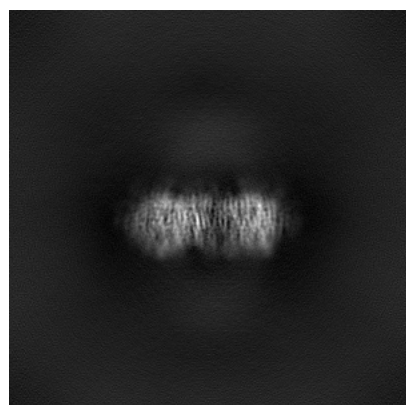


Y

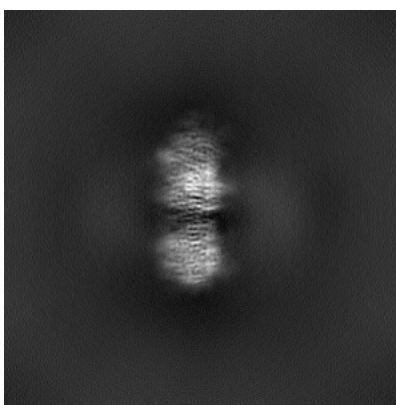


Z

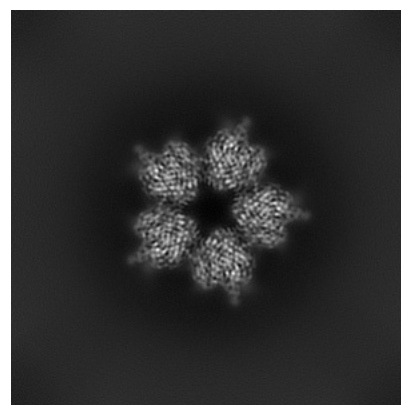
#### 6.1.2 Raw map



X



Y

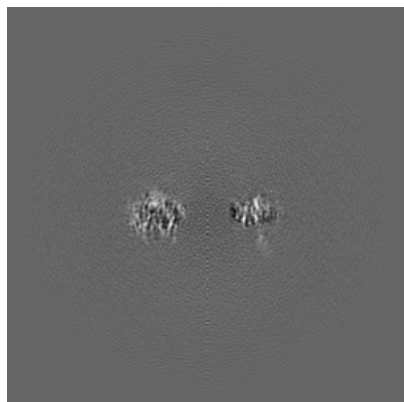


Z

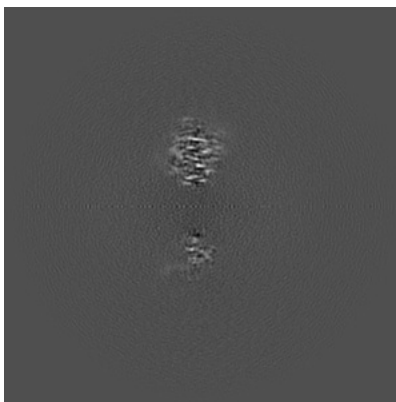
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

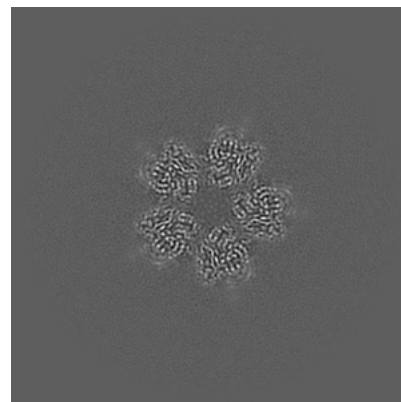
### 6.2.1 Primary map



X Index: 200

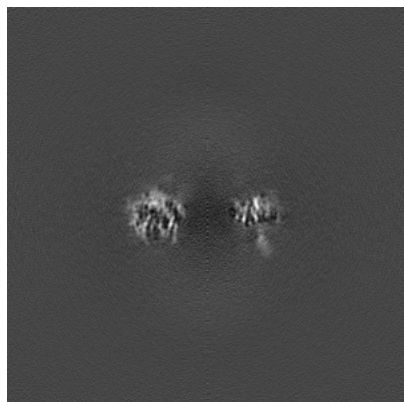


Y Index: 200

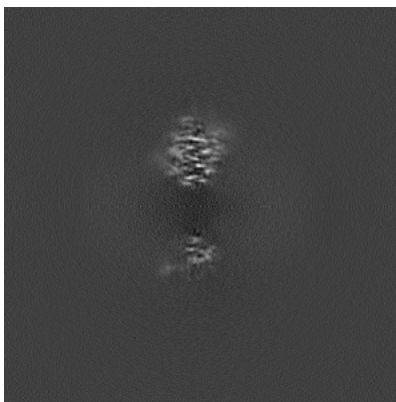


Z Index: 200

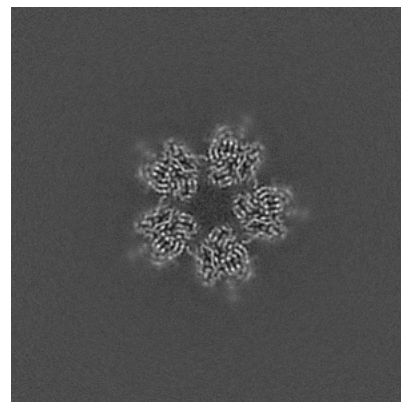
### 6.2.2 Raw map



X Index: 200



Y Index: 200

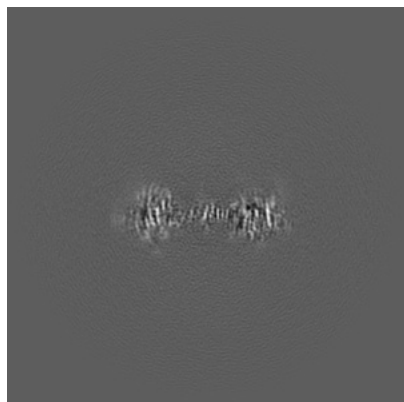


Z Index: 200

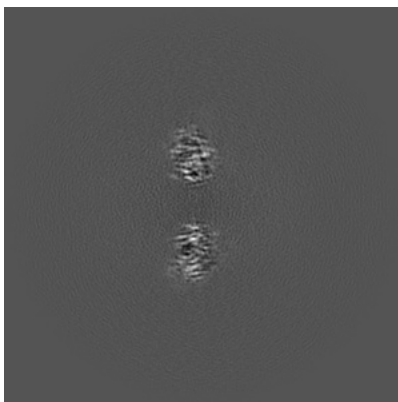
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

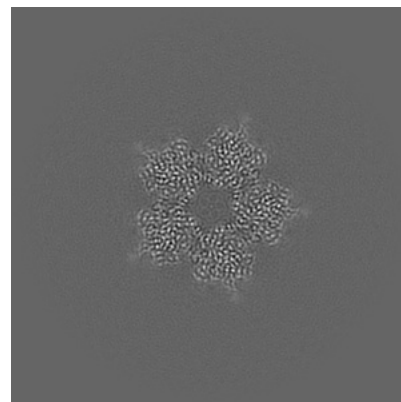
### 6.3.1 Primary map



X Index: 225

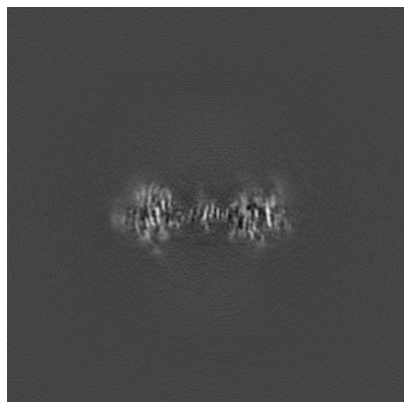


Y Index: 188

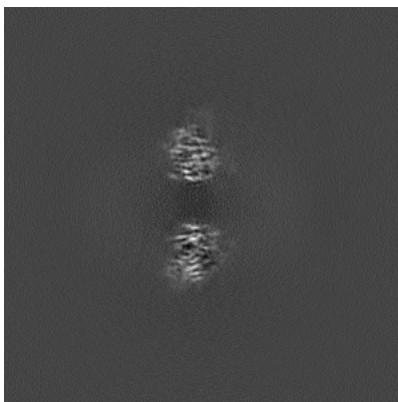


Z Index: 191

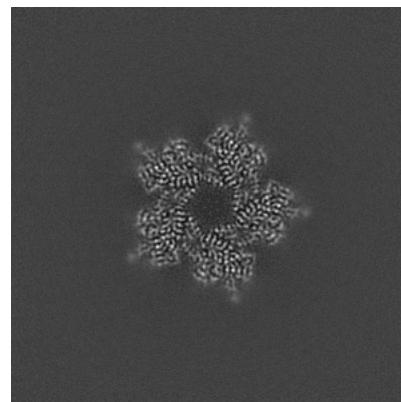
### 6.3.2 Raw map



X Index: 225



Y Index: 188

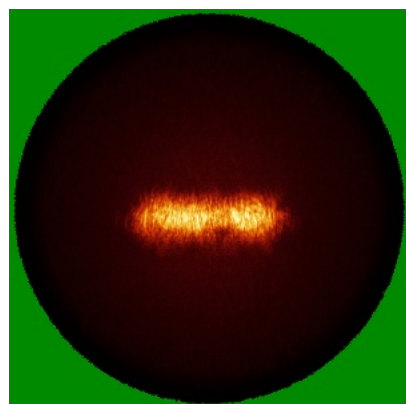


Z Index: 192

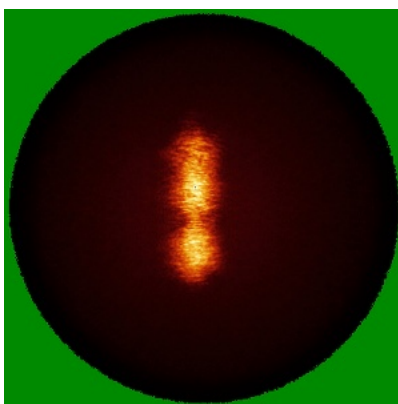
The images above show the largest variance slices of the map in three orthogonal directions.

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

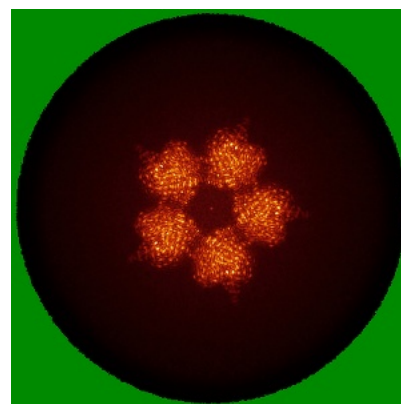
### 6.4.1 Primary map



X

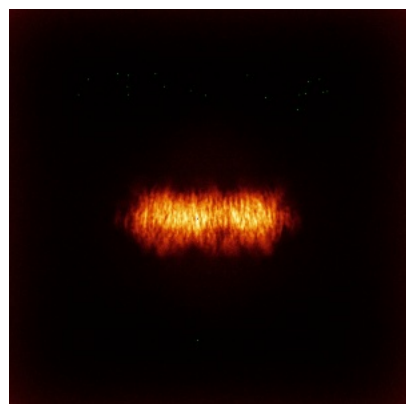


Y

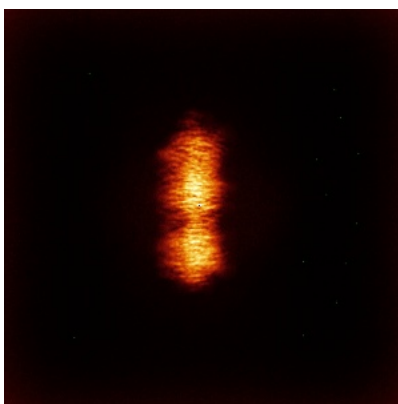


Z

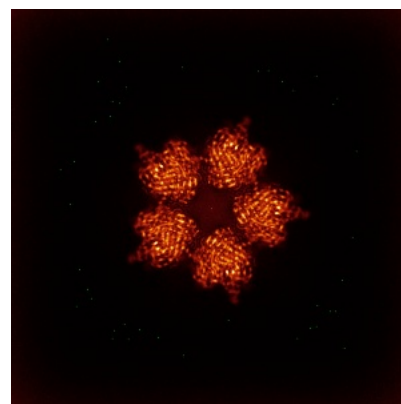
### 6.4.2 Raw map



X



Y

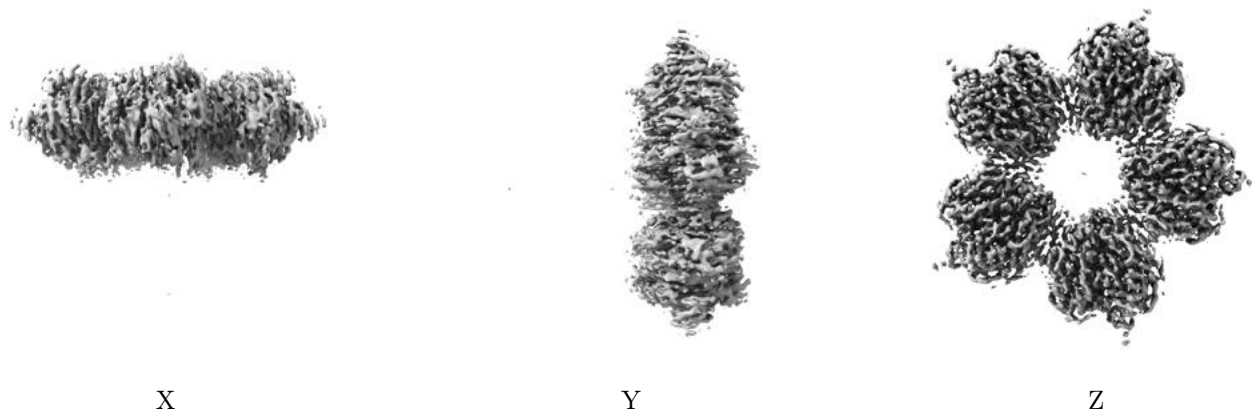


Z

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.

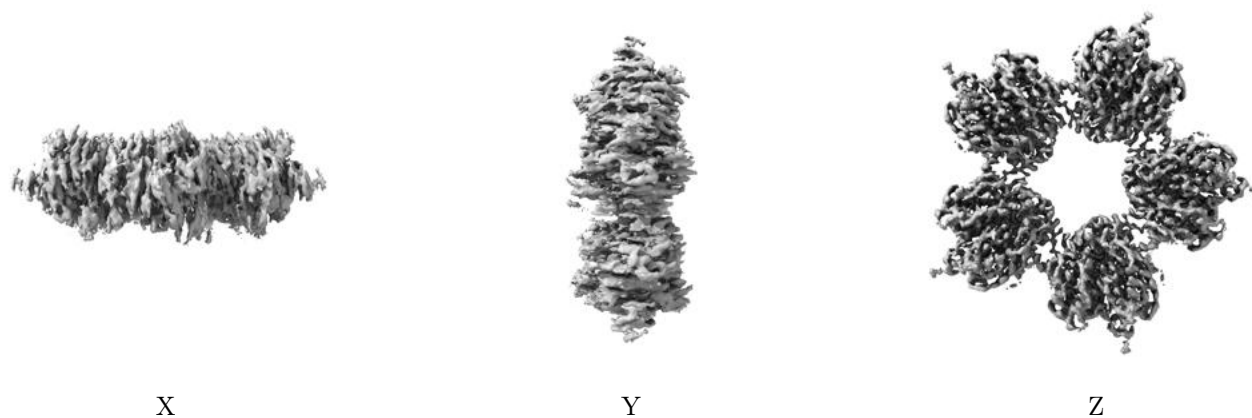
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.38. 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



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

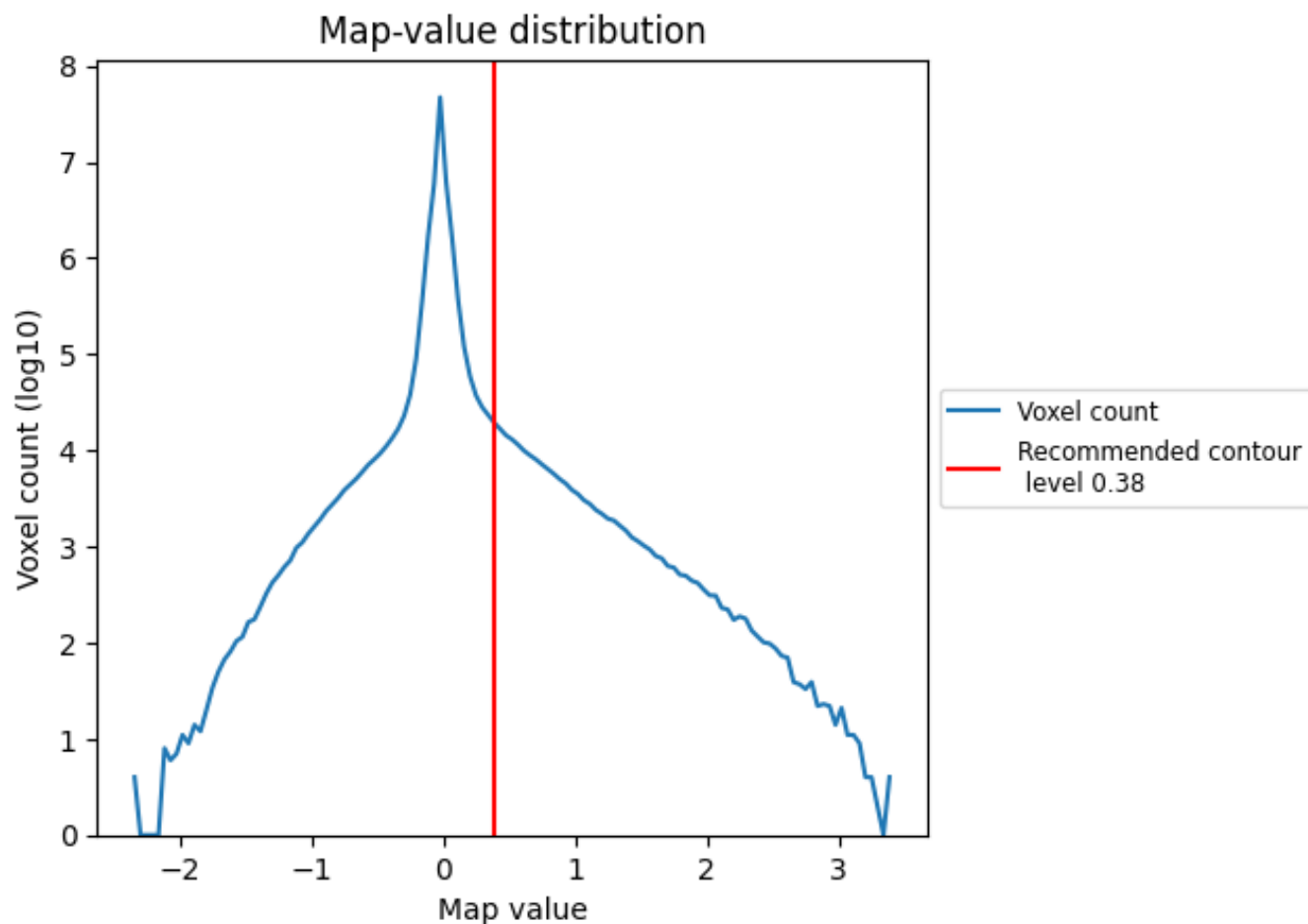
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

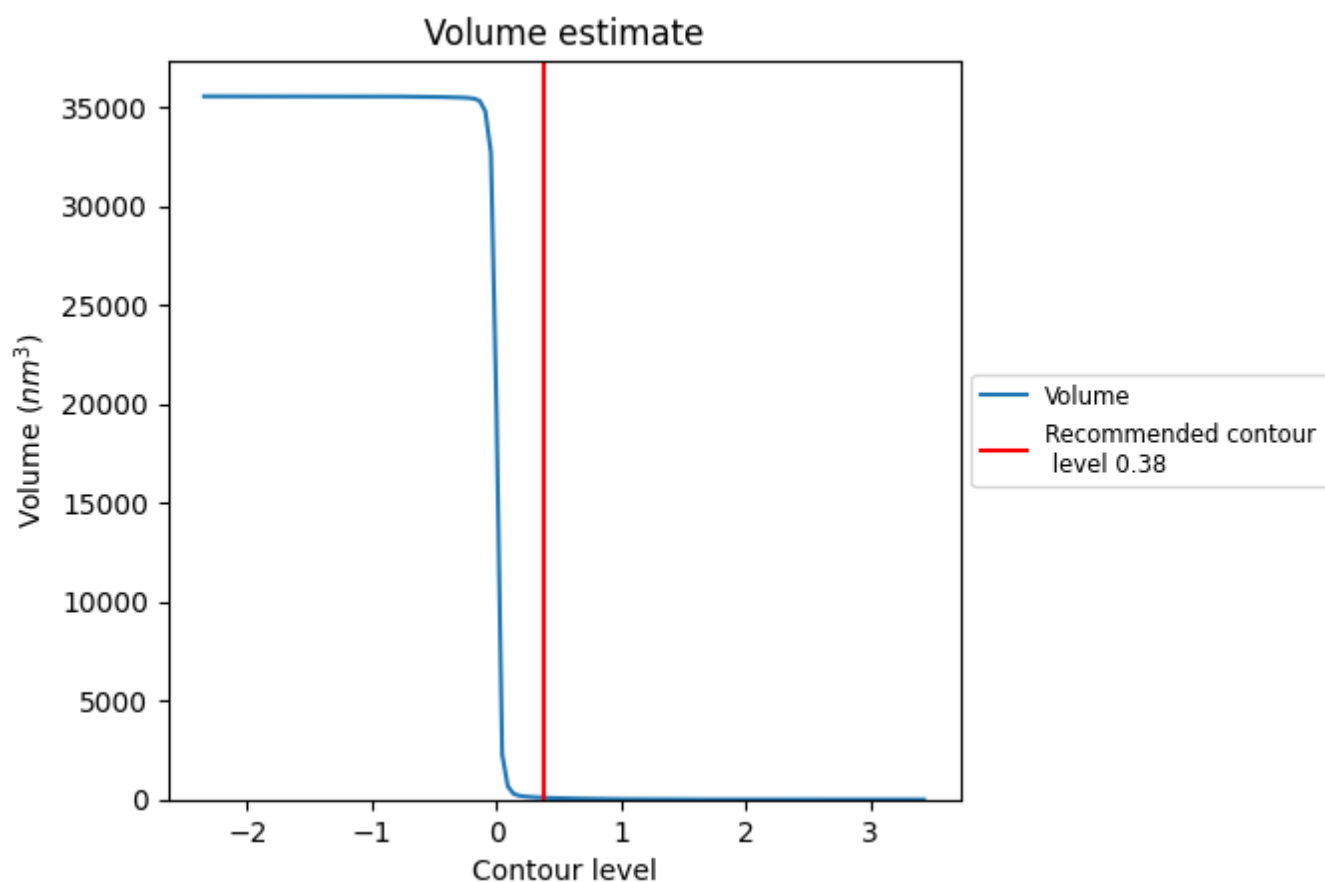
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

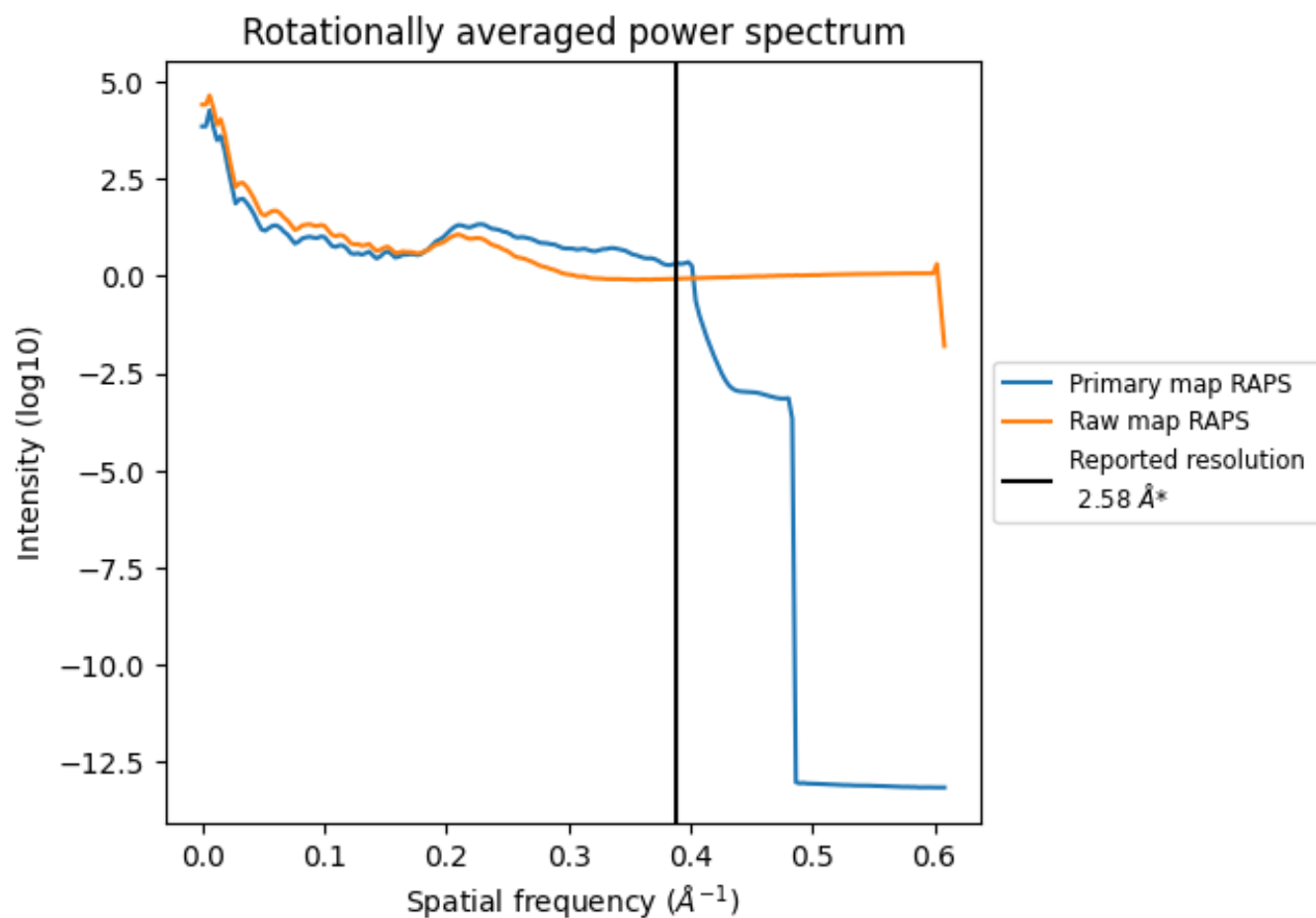
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 94 nm<sup>3</sup>; this corresponds to an approximate mass of 85 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 ⓘ

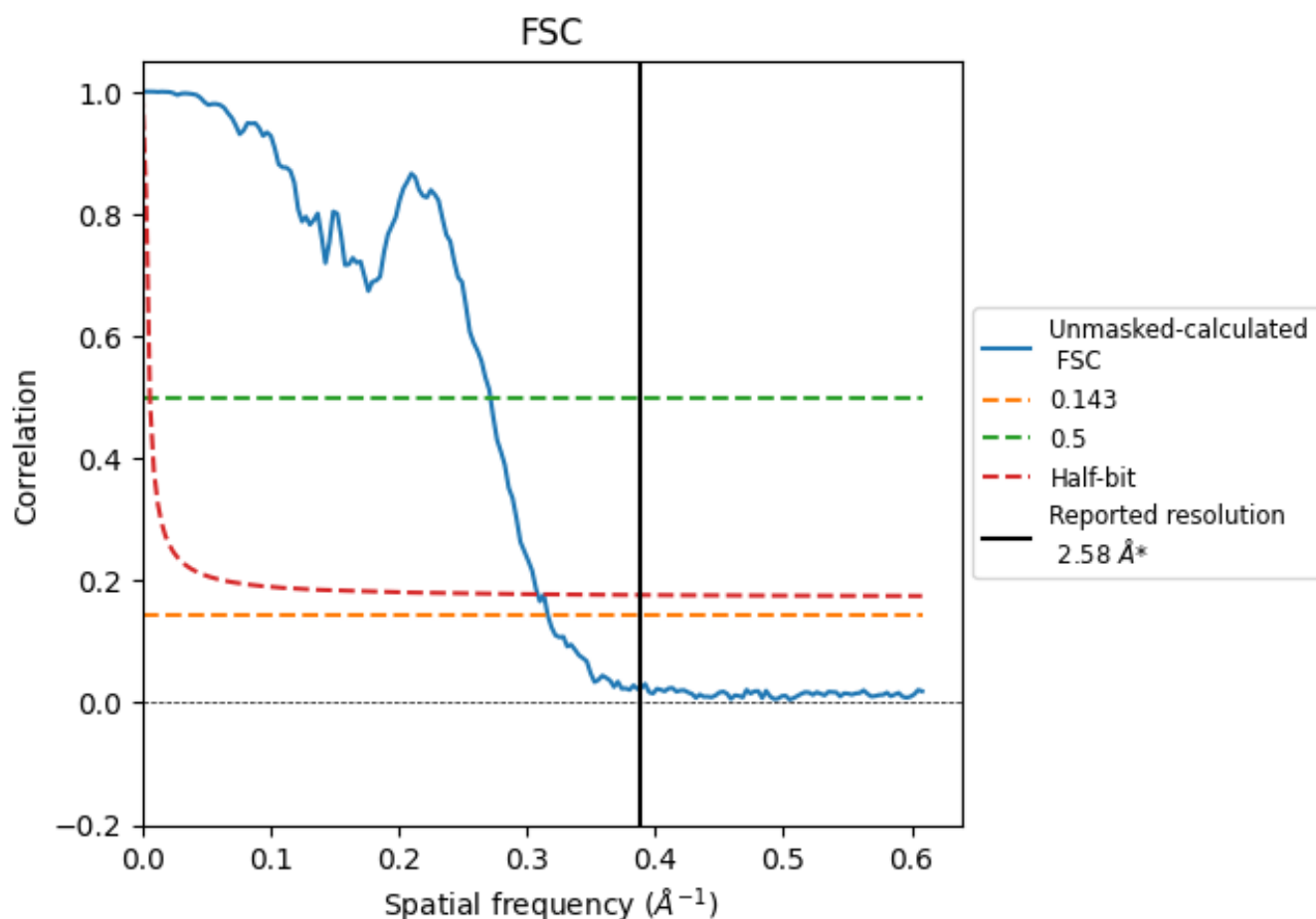


\*Reported resolution corresponds to spatial frequency of 0.388 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.388 \text{ \AA}^{-1}$

## 8.2 Resolution estimates [i](#)

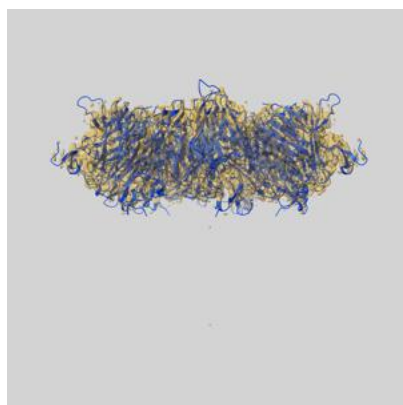
| Resolution estimate (Å)   | Estimation criterion (FSC cut-off) |      |          |
|---------------------------|------------------------------------|------|----------|
|                           | 0.143                              | 0.5  | Half-bit |
| Reported by author        | 2.58                               | -    | -        |
| Author-provided FSC curve | -                                  | -    | -        |
| Unmasked-calculated*      | 3.16                               | 3.68 | 3.24     |

\*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 3.16 differs from the reported value 2.58 by more than 10 %

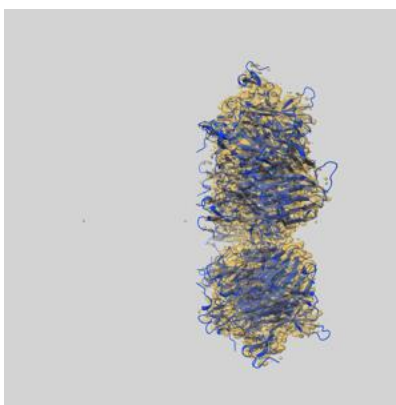
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60485 and PDB model 8ZUJ. Per-residue inclusion information can be found in section [3](#) on page [18](#).

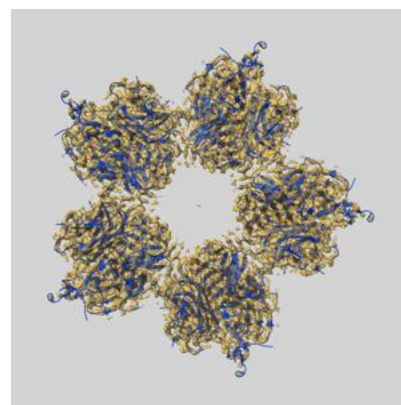
### 9.1 Map-model overlay [i](#)



X



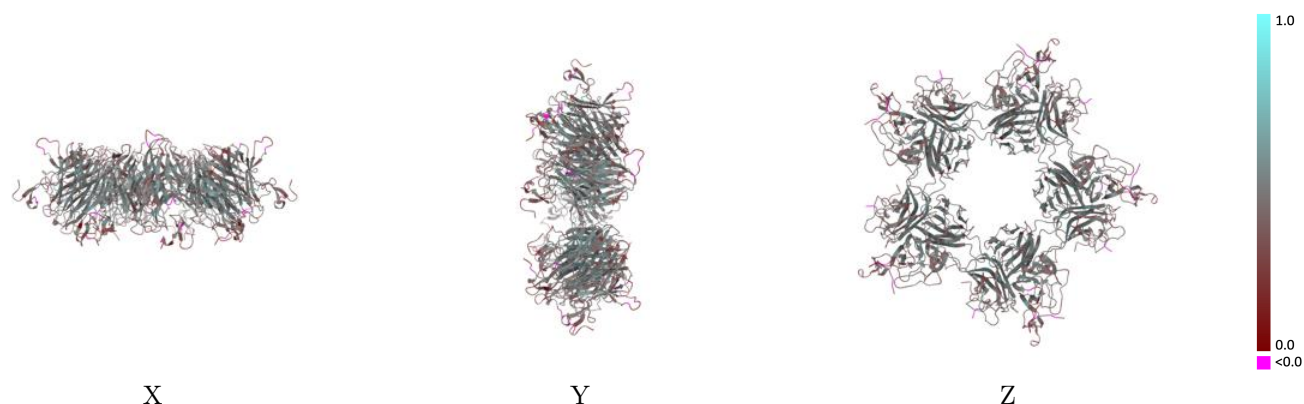
Y



Z

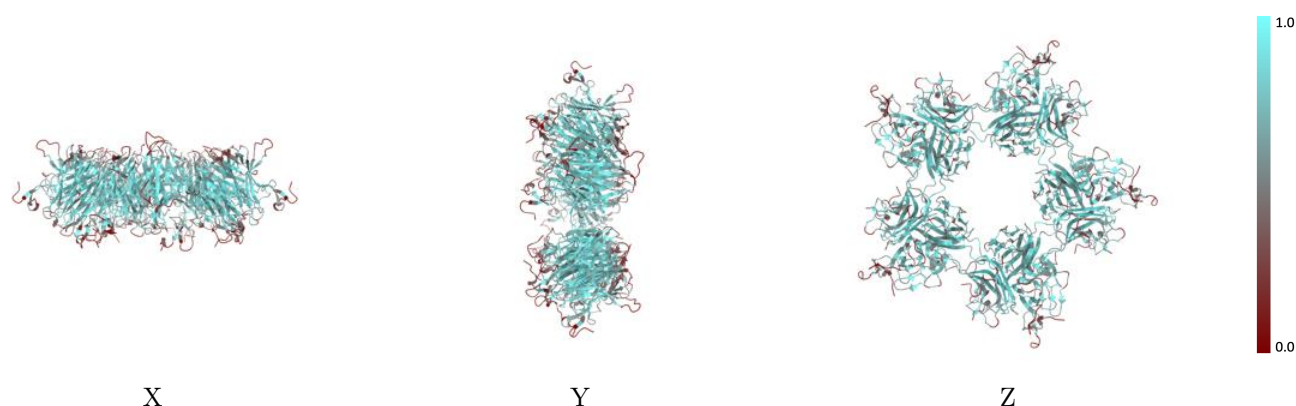
The images above show the 3D surface view of the map at the recommended contour level 0.38 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



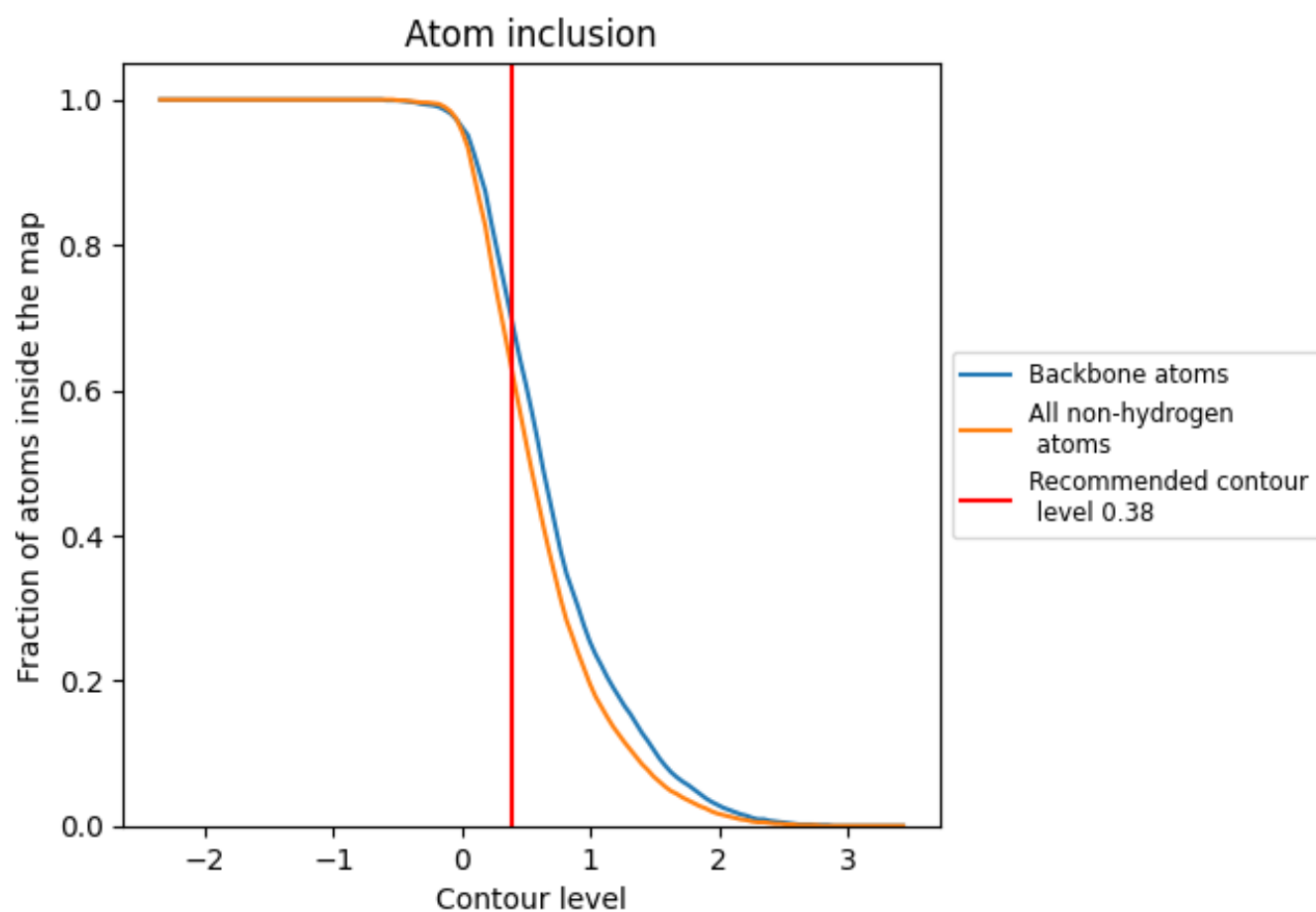
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)



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 (0.38).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 63% 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 (0.38) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| All   |  0.6340   |  0.4240   |
| A     |  0.3490   |  0.3160   |
| B     |  0.3770   |  0.3310   |
| C     |  0.3660   |  0.2880   |
| D     |  0.6270   |  0.4180   |
| E     |  0.6890   |  0.4390   |
| F     |  0.7080   |  0.4630   |
| G     |  0.3540   |  0.3200   |
| H     |  0.3710   |  0.3370   |
| I     |  0.3770   |  0.2840   |
| J     |  0.6270   |  0.4170   |
| K     |  0.6890   |  0.4410   |
| L     |  0.7080   |  0.4650   |
| M     |  0.3540   |  0.3160   |
| N     |  0.3710  |  0.3430  |
| O     |  0.3830 |  0.2900 |
| P     |  0.6290 |  0.4200 |
| Q     |  0.6880 |  0.4400 |
| R     |  0.7090 |  0.4660 |
| S     |  0.3370 |  0.3140 |
| T     |  0.3710 |  0.3380 |
| U     |  0.3770 |  0.2990 |
| V     |  0.6340 |  0.4190 |
| W     |  0.6900 |  0.4410 |
| X     |  0.7060 |  0.4640 |
| Y     |  0.3370 |  0.3170 |
| Z     |  0.3660 |  0.3340 |
| a     |  0.3660 |  0.2920 |
| b     |  0.6310 |  0.4200 |
| c     |  0.6890 |  0.4400 |
| d     |  0.7140 |  0.4620 |

