



## Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 12:06 AM UTC

PDB ID : 8WYR / pdb\_00008wyr  
EMDB ID : EMD-37936  
Title : Cryo-EM structure of human CD5L bound to IgM-Fc/J  
Authors : Wang, Y.X.; Su, C.; Xiao, J.Y.  
Deposited on : 2023-10-31  
Resolution : 3.39 Å(reported)

This is a Full wwPDB EM Validation 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  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : **NOT EXECUTED**  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

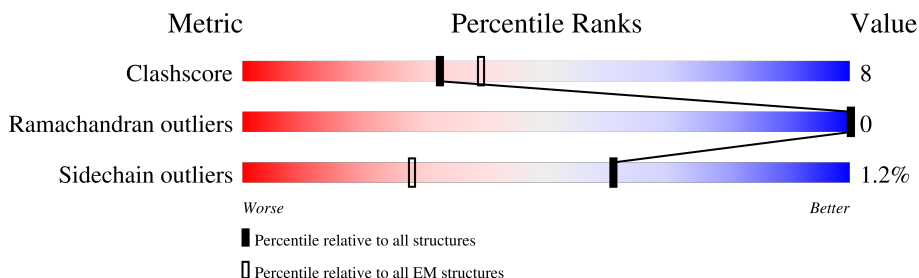
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.39 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) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore            | 229148                      | 23984                       |
| Ramachandran outliers | 224038                      | 23583                       |
| Sidechain outliers    | 223484                      | 23102                       |

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  $\leq 5\%$ .

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | A     | 403    | 44% 13% 42%      |
| 1   | B     | 403    | 43% 14% 43%      |
| 1   | C     | 403    | 42% 14% 44%      |
| 1   | D     | 403    | 43% 12% 44%      |
| 1   | E     | 403    | 44% 12% 44%      |
| 1   | F     | 403    | 43% 12% 44%      |
| 1   | G     | 403    | 39% 16% 44%      |
| 1   | H     | 403    | 46% 11% 42%      |
| 1   | K     | 403    | 46% 11% 42%      |

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| Mol | Chain | Length | Quality of chain                           |
|-----|-------|--------|--------------------------------------------|
| 1   | L     | 403    | <div><div></div><div>46%10%42%</div></div> |
| 2   | J     | 168    | <div><div></div><div>60%14%24%</div></div> |
| 3   | M     | 359    | <div><div></div><div>49%10%41%</div></div> |
| 4   | I     | 2      | <div><div></div><div>50%50%</div></div>    |

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20612 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 Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1   | A     | 232      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1798  | 1132 | 304 | 353 | 9 |         |       |
| 1   | B     | 230      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1780  | 1120 | 302 | 350 | 8 |         |       |
| 1   | C     | 226      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1757  | 1107 | 298 | 344 | 8 |         |       |
| 1   | D     | 227      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1764  | 1111 | 299 | 346 | 8 |         |       |
| 1   | E     | 226      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1757  | 1107 | 298 | 344 | 8 |         |       |
| 1   | F     | 227      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1764  | 1111 | 299 | 346 | 8 |         |       |
| 1   | G     | 225      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1749  | 1103 | 297 | 341 | 8 |         |       |
| 1   | H     | 232      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1798  | 1132 | 304 | 353 | 9 |         |       |
| 1   | K     | 232      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1798  | 1132 | 304 | 353 | 9 |         |       |
| 1   | L     | 232      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1798  | 1132 | 304 | 353 | 9 |         |       |

There are 340 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| A     | 195     | SER      | -      | linker  | UNP P60568 |
| A     | 196     | ALA      | -      | linker  | UNP P60568 |
| A     | 197     | TRP      | -      | linker  | UNP P60568 |
| A     | 198     | SER      | -      | linker  | UNP P60568 |
| A     | 199     | HIS      | -      | linker  | UNP P60568 |
| A     | 200     | PRO      | -      | linker  | UNP P60568 |
| A     | 201     | GLN      | -      | linker  | UNP P60568 |
| A     | 202     | PHE      | -      | linker  | UNP P60568 |
| A     | 203     | GLU      | -      | linker  | UNP P60568 |
| A     | 204     | LYS      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| A     | 205     | GLY      | -      | linker  | UNP P60568 |
| A     | 206     | GLY      | -      | linker  | UNP P60568 |
| A     | 207     | GLY      | -      | linker  | UNP P60568 |
| A     | 208     | SER      | -      | linker  | UNP P60568 |
| A     | 209     | GLY      | -      | linker  | UNP P60568 |
| A     | 210     | GLY      | -      | linker  | UNP P60568 |
| A     | 211     | GLY      | -      | linker  | UNP P60568 |
| A     | 212     | SER      | -      | linker  | UNP P60568 |
| A     | 213     | GLY      | -      | linker  | UNP P60568 |
| A     | 214     | GLY      | -      | linker  | UNP P60568 |
| A     | 215     | SER      | -      | linker  | UNP P60568 |
| A     | 216     | ALA      | -      | linker  | UNP P60568 |
| A     | 217     | TRP      | -      | linker  | UNP P60568 |
| A     | 218     | SER      | -      | linker  | UNP P60568 |
| A     | 219     | HIS      | -      | linker  | UNP P60568 |
| A     | 220     | PRO      | -      | linker  | UNP P60568 |
| A     | 221     | GLN      | -      | linker  | UNP P60568 |
| A     | 222     | PHE      | -      | linker  | UNP P60568 |
| A     | 223     | GLU      | -      | linker  | UNP P60568 |
| A     | 224     | LYS      | -      | linker  | UNP P60568 |
| A     | 225     | ILE      | -      | linker  | UNP P60568 |
| A     | 226     | ASP      | -      | linker  | UNP P60568 |
| A     | 227     | THR      | -      | linker  | UNP P60568 |
| A     | 228     | THR      | -      | linker  | UNP P60568 |
| B     | 195     | SER      | -      | linker  | UNP P60568 |
| B     | 196     | ALA      | -      | linker  | UNP P60568 |
| B     | 197     | TRP      | -      | linker  | UNP P60568 |
| B     | 198     | SER      | -      | linker  | UNP P60568 |
| B     | 199     | HIS      | -      | linker  | UNP P60568 |
| B     | 200     | PRO      | -      | linker  | UNP P60568 |
| B     | 201     | GLN      | -      | linker  | UNP P60568 |
| B     | 202     | PHE      | -      | linker  | UNP P60568 |
| B     | 203     | GLU      | -      | linker  | UNP P60568 |
| B     | 204     | LYS      | -      | linker  | UNP P60568 |
| B     | 205     | GLY      | -      | linker  | UNP P60568 |
| B     | 206     | GLY      | -      | linker  | UNP P60568 |
| B     | 207     | GLY      | -      | linker  | UNP P60568 |
| B     | 208     | SER      | -      | linker  | UNP P60568 |
| B     | 209     | GLY      | -      | linker  | UNP P60568 |
| B     | 210     | GLY      | -      | linker  | UNP P60568 |
| B     | 211     | GLY      | -      | linker  | UNP P60568 |
| B     | 212     | SER      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| B     | 213     | GLY      | -      | linker  | UNP P60568 |
| B     | 214     | GLY      | -      | linker  | UNP P60568 |
| B     | 215     | SER      | -      | linker  | UNP P60568 |
| B     | 216     | ALA      | -      | linker  | UNP P60568 |
| B     | 217     | TRP      | -      | linker  | UNP P60568 |
| B     | 218     | SER      | -      | linker  | UNP P60568 |
| B     | 219     | HIS      | -      | linker  | UNP P60568 |
| B     | 220     | PRO      | -      | linker  | UNP P60568 |
| B     | 221     | GLN      | -      | linker  | UNP P60568 |
| B     | 222     | PHE      | -      | linker  | UNP P60568 |
| B     | 223     | GLU      | -      | linker  | UNP P60568 |
| B     | 224     | LYS      | -      | linker  | UNP P60568 |
| B     | 225     | ILE      | -      | linker  | UNP P60568 |
| B     | 226     | ASP      | -      | linker  | UNP P60568 |
| B     | 227     | THR      | -      | linker  | UNP P60568 |
| B     | 228     | THR      | -      | linker  | UNP P60568 |
| C     | 195     | SER      | -      | linker  | UNP P60568 |
| C     | 196     | ALA      | -      | linker  | UNP P60568 |
| C     | 197     | TRP      | -      | linker  | UNP P60568 |
| C     | 198     | SER      | -      | linker  | UNP P60568 |
| C     | 199     | HIS      | -      | linker  | UNP P60568 |
| C     | 200     | PRO      | -      | linker  | UNP P60568 |
| C     | 201     | GLN      | -      | linker  | UNP P60568 |
| C     | 202     | PHE      | -      | linker  | UNP P60568 |
| C     | 203     | GLU      | -      | linker  | UNP P60568 |
| C     | 204     | LYS      | -      | linker  | UNP P60568 |
| C     | 205     | GLY      | -      | linker  | UNP P60568 |
| C     | 206     | GLY      | -      | linker  | UNP P60568 |
| C     | 207     | GLY      | -      | linker  | UNP P60568 |
| C     | 208     | SER      | -      | linker  | UNP P60568 |
| C     | 209     | GLY      | -      | linker  | UNP P60568 |
| C     | 210     | GLY      | -      | linker  | UNP P60568 |
| C     | 211     | GLY      | -      | linker  | UNP P60568 |
| C     | 212     | SER      | -      | linker  | UNP P60568 |
| C     | 213     | GLY      | -      | linker  | UNP P60568 |
| C     | 214     | GLY      | -      | linker  | UNP P60568 |
| C     | 215     | SER      | -      | linker  | UNP P60568 |
| C     | 216     | ALA      | -      | linker  | UNP P60568 |
| C     | 217     | TRP      | -      | linker  | UNP P60568 |
| C     | 218     | SER      | -      | linker  | UNP P60568 |
| C     | 219     | HIS      | -      | linker  | UNP P60568 |
| C     | 220     | PRO      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| C     | 221     | GLN      | -      | linker  | UNP P60568 |
| C     | 222     | PHE      | -      | linker  | UNP P60568 |
| C     | 223     | GLU      | -      | linker  | UNP P60568 |
| C     | 224     | LYS      | -      | linker  | UNP P60568 |
| C     | 225     | ILE      | -      | linker  | UNP P60568 |
| C     | 226     | ASP      | -      | linker  | UNP P60568 |
| C     | 227     | THR      | -      | linker  | UNP P60568 |
| C     | 228     | THR      | -      | linker  | UNP P60568 |
| D     | 195     | SER      | -      | linker  | UNP P60568 |
| D     | 196     | ALA      | -      | linker  | UNP P60568 |
| D     | 197     | TRP      | -      | linker  | UNP P60568 |
| D     | 198     | SER      | -      | linker  | UNP P60568 |
| D     | 199     | HIS      | -      | linker  | UNP P60568 |
| D     | 200     | PRO      | -      | linker  | UNP P60568 |
| D     | 201     | GLN      | -      | linker  | UNP P60568 |
| D     | 202     | PHE      | -      | linker  | UNP P60568 |
| D     | 203     | GLU      | -      | linker  | UNP P60568 |
| D     | 204     | LYS      | -      | linker  | UNP P60568 |
| D     | 205     | GLY      | -      | linker  | UNP P60568 |
| D     | 206     | GLY      | -      | linker  | UNP P60568 |
| D     | 207     | GLY      | -      | linker  | UNP P60568 |
| D     | 208     | SER      | -      | linker  | UNP P60568 |
| D     | 209     | GLY      | -      | linker  | UNP P60568 |
| D     | 210     | GLY      | -      | linker  | UNP P60568 |
| D     | 211     | GLY      | -      | linker  | UNP P60568 |
| D     | 212     | SER      | -      | linker  | UNP P60568 |
| D     | 213     | GLY      | -      | linker  | UNP P60568 |
| D     | 214     | GLY      | -      | linker  | UNP P60568 |
| D     | 215     | SER      | -      | linker  | UNP P60568 |
| D     | 216     | ALA      | -      | linker  | UNP P60568 |
| D     | 217     | TRP      | -      | linker  | UNP P60568 |
| D     | 218     | SER      | -      | linker  | UNP P60568 |
| D     | 219     | HIS      | -      | linker  | UNP P60568 |
| D     | 220     | PRO      | -      | linker  | UNP P60568 |
| D     | 221     | GLN      | -      | linker  | UNP P60568 |
| D     | 222     | PHE      | -      | linker  | UNP P60568 |
| D     | 223     | GLU      | -      | linker  | UNP P60568 |
| D     | 224     | LYS      | -      | linker  | UNP P60568 |
| D     | 225     | ILE      | -      | linker  | UNP P60568 |
| D     | 226     | ASP      | -      | linker  | UNP P60568 |
| D     | 227     | THR      | -      | linker  | UNP P60568 |
| D     | 228     | THR      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| E     | 195     | SER      | -      | linker  | UNP P60568 |
| E     | 196     | ALA      | -      | linker  | UNP P60568 |
| E     | 197     | TRP      | -      | linker  | UNP P60568 |
| E     | 198     | SER      | -      | linker  | UNP P60568 |
| E     | 199     | HIS      | -      | linker  | UNP P60568 |
| E     | 200     | PRO      | -      | linker  | UNP P60568 |
| E     | 201     | GLN      | -      | linker  | UNP P60568 |
| E     | 202     | PHE      | -      | linker  | UNP P60568 |
| E     | 203     | GLU      | -      | linker  | UNP P60568 |
| E     | 204     | LYS      | -      | linker  | UNP P60568 |
| E     | 205     | GLY      | -      | linker  | UNP P60568 |
| E     | 206     | GLY      | -      | linker  | UNP P60568 |
| E     | 207     | GLY      | -      | linker  | UNP P60568 |
| E     | 208     | SER      | -      | linker  | UNP P60568 |
| E     | 209     | GLY      | -      | linker  | UNP P60568 |
| E     | 210     | GLY      | -      | linker  | UNP P60568 |
| E     | 211     | GLY      | -      | linker  | UNP P60568 |
| E     | 212     | SER      | -      | linker  | UNP P60568 |
| E     | 213     | GLY      | -      | linker  | UNP P60568 |
| E     | 214     | GLY      | -      | linker  | UNP P60568 |
| E     | 215     | SER      | -      | linker  | UNP P60568 |
| E     | 216     | ALA      | -      | linker  | UNP P60568 |
| E     | 217     | TRP      | -      | linker  | UNP P60568 |
| E     | 218     | SER      | -      | linker  | UNP P60568 |
| E     | 219     | HIS      | -      | linker  | UNP P60568 |
| E     | 220     | PRO      | -      | linker  | UNP P60568 |
| E     | 221     | GLN      | -      | linker  | UNP P60568 |
| E     | 222     | PHE      | -      | linker  | UNP P60568 |
| E     | 223     | GLU      | -      | linker  | UNP P60568 |
| E     | 224     | LYS      | -      | linker  | UNP P60568 |
| E     | 225     | ILE      | -      | linker  | UNP P60568 |
| E     | 226     | ASP      | -      | linker  | UNP P60568 |
| E     | 227     | THR      | -      | linker  | UNP P60568 |
| E     | 228     | THR      | -      | linker  | UNP P60568 |
| F     | 195     | SER      | -      | linker  | UNP P60568 |
| F     | 196     | ALA      | -      | linker  | UNP P60568 |
| F     | 197     | TRP      | -      | linker  | UNP P60568 |
| F     | 198     | SER      | -      | linker  | UNP P60568 |
| F     | 199     | HIS      | -      | linker  | UNP P60568 |
| F     | 200     | PRO      | -      | linker  | UNP P60568 |
| F     | 201     | GLN      | -      | linker  | UNP P60568 |
| F     | 202     | PHE      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| F     | 203     | GLU      | -      | linker  | UNP P60568 |
| F     | 204     | LYS      | -      | linker  | UNP P60568 |
| F     | 205     | GLY      | -      | linker  | UNP P60568 |
| F     | 206     | GLY      | -      | linker  | UNP P60568 |
| F     | 207     | GLY      | -      | linker  | UNP P60568 |
| F     | 208     | SER      | -      | linker  | UNP P60568 |
| F     | 209     | GLY      | -      | linker  | UNP P60568 |
| F     | 210     | GLY      | -      | linker  | UNP P60568 |
| F     | 211     | GLY      | -      | linker  | UNP P60568 |
| F     | 212     | SER      | -      | linker  | UNP P60568 |
| F     | 213     | GLY      | -      | linker  | UNP P60568 |
| F     | 214     | GLY      | -      | linker  | UNP P60568 |
| F     | 215     | SER      | -      | linker  | UNP P60568 |
| F     | 216     | ALA      | -      | linker  | UNP P60568 |
| F     | 217     | TRP      | -      | linker  | UNP P60568 |
| F     | 218     | SER      | -      | linker  | UNP P60568 |
| F     | 219     | HIS      | -      | linker  | UNP P60568 |
| F     | 220     | PRO      | -      | linker  | UNP P60568 |
| F     | 221     | GLN      | -      | linker  | UNP P60568 |
| F     | 222     | PHE      | -      | linker  | UNP P60568 |
| F     | 223     | GLU      | -      | linker  | UNP P60568 |
| F     | 224     | LYS      | -      | linker  | UNP P60568 |
| F     | 225     | ILE      | -      | linker  | UNP P60568 |
| F     | 226     | ASP      | -      | linker  | UNP P60568 |
| F     | 227     | THR      | -      | linker  | UNP P60568 |
| F     | 228     | THR      | -      | linker  | UNP P60568 |
| G     | 195     | SER      | -      | linker  | UNP P60568 |
| G     | 196     | ALA      | -      | linker  | UNP P60568 |
| G     | 197     | TRP      | -      | linker  | UNP P60568 |
| G     | 198     | SER      | -      | linker  | UNP P60568 |
| G     | 199     | HIS      | -      | linker  | UNP P60568 |
| G     | 200     | PRO      | -      | linker  | UNP P60568 |
| G     | 201     | GLN      | -      | linker  | UNP P60568 |
| G     | 202     | PHE      | -      | linker  | UNP P60568 |
| G     | 203     | GLU      | -      | linker  | UNP P60568 |
| G     | 204     | LYS      | -      | linker  | UNP P60568 |
| G     | 205     | GLY      | -      | linker  | UNP P60568 |
| G     | 206     | GLY      | -      | linker  | UNP P60568 |
| G     | 207     | GLY      | -      | linker  | UNP P60568 |
| G     | 208     | SER      | -      | linker  | UNP P60568 |
| G     | 209     | GLY      | -      | linker  | UNP P60568 |
| G     | 210     | GLY      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| G     | 211     | GLY      | -      | linker  | UNP P60568 |
| G     | 212     | SER      | -      | linker  | UNP P60568 |
| G     | 213     | GLY      | -      | linker  | UNP P60568 |
| G     | 214     | GLY      | -      | linker  | UNP P60568 |
| G     | 215     | SER      | -      | linker  | UNP P60568 |
| G     | 216     | ALA      | -      | linker  | UNP P60568 |
| G     | 217     | TRP      | -      | linker  | UNP P60568 |
| G     | 218     | SER      | -      | linker  | UNP P60568 |
| G     | 219     | HIS      | -      | linker  | UNP P60568 |
| G     | 220     | PRO      | -      | linker  | UNP P60568 |
| G     | 221     | GLN      | -      | linker  | UNP P60568 |
| G     | 222     | PHE      | -      | linker  | UNP P60568 |
| G     | 223     | GLU      | -      | linker  | UNP P60568 |
| G     | 224     | LYS      | -      | linker  | UNP P60568 |
| G     | 225     | ILE      | -      | linker  | UNP P60568 |
| G     | 226     | ASP      | -      | linker  | UNP P60568 |
| G     | 227     | THR      | -      | linker  | UNP P60568 |
| G     | 228     | THR      | -      | linker  | UNP P60568 |
| H     | 195     | SER      | -      | linker  | UNP P60568 |
| H     | 196     | ALA      | -      | linker  | UNP P60568 |
| H     | 197     | TRP      | -      | linker  | UNP P60568 |
| H     | 198     | SER      | -      | linker  | UNP P60568 |
| H     | 199     | HIS      | -      | linker  | UNP P60568 |
| H     | 200     | PRO      | -      | linker  | UNP P60568 |
| H     | 201     | GLN      | -      | linker  | UNP P60568 |
| H     | 202     | PHE      | -      | linker  | UNP P60568 |
| H     | 203     | GLU      | -      | linker  | UNP P60568 |
| H     | 204     | LYS      | -      | linker  | UNP P60568 |
| H     | 205     | GLY      | -      | linker  | UNP P60568 |
| H     | 206     | GLY      | -      | linker  | UNP P60568 |
| H     | 207     | GLY      | -      | linker  | UNP P60568 |
| H     | 208     | SER      | -      | linker  | UNP P60568 |
| H     | 209     | GLY      | -      | linker  | UNP P60568 |
| H     | 210     | GLY      | -      | linker  | UNP P60568 |
| H     | 211     | GLY      | -      | linker  | UNP P60568 |
| H     | 212     | SER      | -      | linker  | UNP P60568 |
| H     | 213     | GLY      | -      | linker  | UNP P60568 |
| H     | 214     | GLY      | -      | linker  | UNP P60568 |
| H     | 215     | SER      | -      | linker  | UNP P60568 |
| H     | 216     | ALA      | -      | linker  | UNP P60568 |
| H     | 217     | TRP      | -      | linker  | UNP P60568 |
| H     | 218     | SER      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| H     | 219     | HIS      | -      | linker  | UNP P60568 |
| H     | 220     | PRO      | -      | linker  | UNP P60568 |
| H     | 221     | GLN      | -      | linker  | UNP P60568 |
| H     | 222     | PHE      | -      | linker  | UNP P60568 |
| H     | 223     | GLU      | -      | linker  | UNP P60568 |
| H     | 224     | LYS      | -      | linker  | UNP P60568 |
| H     | 225     | ILE      | -      | linker  | UNP P60568 |
| H     | 226     | ASP      | -      | linker  | UNP P60568 |
| H     | 227     | THR      | -      | linker  | UNP P60568 |
| H     | 228     | THR      | -      | linker  | UNP P60568 |
| K     | 195     | SER      | -      | linker  | UNP P60568 |
| K     | 196     | ALA      | -      | linker  | UNP P60568 |
| K     | 197     | TRP      | -      | linker  | UNP P60568 |
| K     | 198     | SER      | -      | linker  | UNP P60568 |
| K     | 199     | HIS      | -      | linker  | UNP P60568 |
| K     | 200     | PRO      | -      | linker  | UNP P60568 |
| K     | 201     | GLN      | -      | linker  | UNP P60568 |
| K     | 202     | PHE      | -      | linker  | UNP P60568 |
| K     | 203     | GLU      | -      | linker  | UNP P60568 |
| K     | 204     | LYS      | -      | linker  | UNP P60568 |
| K     | 205     | GLY      | -      | linker  | UNP P60568 |
| K     | 206     | GLY      | -      | linker  | UNP P60568 |
| K     | 207     | GLY      | -      | linker  | UNP P60568 |
| K     | 208     | SER      | -      | linker  | UNP P60568 |
| K     | 209     | GLY      | -      | linker  | UNP P60568 |
| K     | 210     | GLY      | -      | linker  | UNP P60568 |
| K     | 211     | GLY      | -      | linker  | UNP P60568 |
| K     | 212     | SER      | -      | linker  | UNP P60568 |
| K     | 213     | GLY      | -      | linker  | UNP P60568 |
| K     | 214     | GLY      | -      | linker  | UNP P60568 |
| K     | 215     | SER      | -      | linker  | UNP P60568 |
| K     | 216     | ALA      | -      | linker  | UNP P60568 |
| K     | 217     | TRP      | -      | linker  | UNP P60568 |
| K     | 218     | SER      | -      | linker  | UNP P60568 |
| K     | 219     | HIS      | -      | linker  | UNP P60568 |
| K     | 220     | PRO      | -      | linker  | UNP P60568 |
| K     | 221     | GLN      | -      | linker  | UNP P60568 |
| K     | 222     | PHE      | -      | linker  | UNP P60568 |
| K     | 223     | GLU      | -      | linker  | UNP P60568 |
| K     | 224     | LYS      | -      | linker  | UNP P60568 |
| K     | 225     | ILE      | -      | linker  | UNP P60568 |
| K     | 226     | ASP      | -      | linker  | UNP P60568 |

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| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| K     | 227     | THR      | -      | linker  | UNP P60568 |
| K     | 228     | THR      | -      | linker  | UNP P60568 |
| L     | 195     | SER      | -      | linker  | UNP P60568 |
| L     | 196     | ALA      | -      | linker  | UNP P60568 |
| L     | 197     | TRP      | -      | linker  | UNP P60568 |
| L     | 198     | SER      | -      | linker  | UNP P60568 |
| L     | 199     | HIS      | -      | linker  | UNP P60568 |
| L     | 200     | PRO      | -      | linker  | UNP P60568 |
| L     | 201     | GLN      | -      | linker  | UNP P60568 |
| L     | 202     | PHE      | -      | linker  | UNP P60568 |
| L     | 203     | GLU      | -      | linker  | UNP P60568 |
| L     | 204     | LYS      | -      | linker  | UNP P60568 |
| L     | 205     | GLY      | -      | linker  | UNP P60568 |
| L     | 206     | GLY      | -      | linker  | UNP P60568 |
| L     | 207     | GLY      | -      | linker  | UNP P60568 |
| L     | 208     | SER      | -      | linker  | UNP P60568 |
| L     | 209     | GLY      | -      | linker  | UNP P60568 |
| L     | 210     | GLY      | -      | linker  | UNP P60568 |
| L     | 211     | GLY      | -      | linker  | UNP P60568 |
| L     | 212     | SER      | -      | linker  | UNP P60568 |
| L     | 213     | GLY      | -      | linker  | UNP P60568 |
| L     | 214     | GLY      | -      | linker  | UNP P60568 |
| L     | 215     | SER      | -      | linker  | UNP P60568 |
| L     | 216     | ALA      | -      | linker  | UNP P60568 |
| L     | 217     | TRP      | -      | linker  | UNP P60568 |
| L     | 218     | SER      | -      | linker  | UNP P60568 |
| L     | 219     | HIS      | -      | linker  | UNP P60568 |
| L     | 220     | PRO      | -      | linker  | UNP P60568 |
| L     | 221     | GLN      | -      | linker  | UNP P60568 |
| L     | 222     | PHE      | -      | linker  | UNP P60568 |
| L     | 223     | GLU      | -      | linker  | UNP P60568 |
| L     | 224     | LYS      | -      | linker  | UNP P60568 |
| L     | 225     | ILE      | -      | linker  | UNP P60568 |
| L     | 226     | ASP      | -      | linker  | UNP P60568 |
| L     | 227     | THR      | -      | linker  | UNP P60568 |
| L     | 228     | THR      | -      | linker  | UNP P60568 |

- Molecule 2 is a protein called Immunoglobulin J chain.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 2   | J     | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1010  | 622 | 176 | 203 | 9 |         |       |

There are 9 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| J     | 137     | TYR      | -      | expression tag | UNP P01591 |
| J     | 138     | PRO      | -      | expression tag | UNP P01591 |
| J     | 139     | TYR      | -      | expression tag | UNP P01591 |
| J     | 140     | ASP      | -      | expression tag | UNP P01591 |
| J     | 141     | VAL      | -      | expression tag | UNP P01591 |
| J     | 142     | PRO      | -      | expression tag | UNP P01591 |
| J     | 143     | ASP      | -      | expression tag | UNP P01591 |
| J     | 144     | TYR      | -      | expression tag | UNP P01591 |
| J     | 145     | ALA      | -      | expression tag | UNP P01591 |

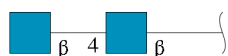
- Molecule 3 is a protein called Interleukin-2,CD5 antigen-like.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3   | M     | 213      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1669  | 1026 | 315 | 309 | 19 |         |       |

There are 10 discrepancies between the modelled and reference sequences:

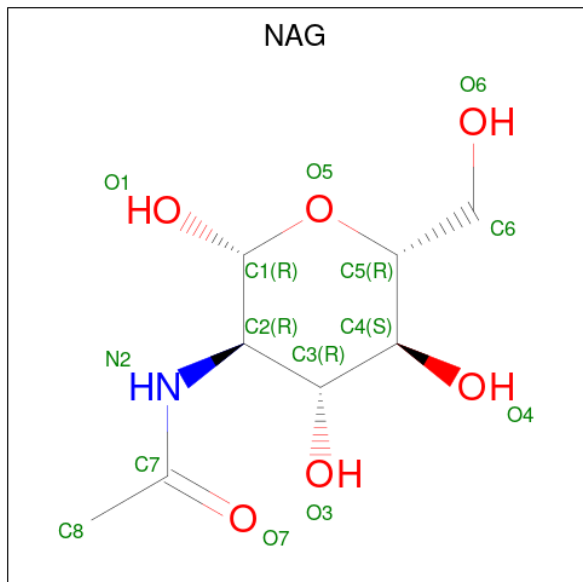
| Chain | Residue | Modelled | Actual | Comment | Reference  |
|-------|---------|----------|--------|---------|------------|
| M     | 10      | ARG      | -      | linker  | UNP P60568 |
| M     | 11      | ILE      | -      | linker  | UNP P60568 |
| M     | 12      | HIS      | -      | linker  | UNP P60568 |
| M     | 13      | HIS      | -      | linker  | UNP P60568 |
| M     | 14      | HIS      | -      | linker  | UNP P60568 |
| M     | 15      | HIS      | -      | linker  | UNP P60568 |
| M     | 16      | HIS      | -      | linker  | UNP P60568 |
| M     | 17      | HIS      | -      | linker  | UNP P60568 |
| M     | 18      | HIS      | -      | linker  | UNP P60568 |
| M     | 19      | HIS      | -      | linker  | UNP P60568 |

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



| Mol | Chain | Residues | Atoms |    |   |    |  | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|--|---------|-------|
| 4   | I     | 2        | Total | C  | N | O  |  | 0       | 0     |
|     |       |          | 28    | 16 | 2 | 10 |  |         |       |

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).



| Mol | Chain | Residues | Atoms |   |   |   | AltConf |
|-----|-------|----------|-------|---|---|---|---------|
| 5   | A     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | B     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | C     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | D     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | E     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | F     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | G     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | H     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | K     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |
| 5   | L     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |

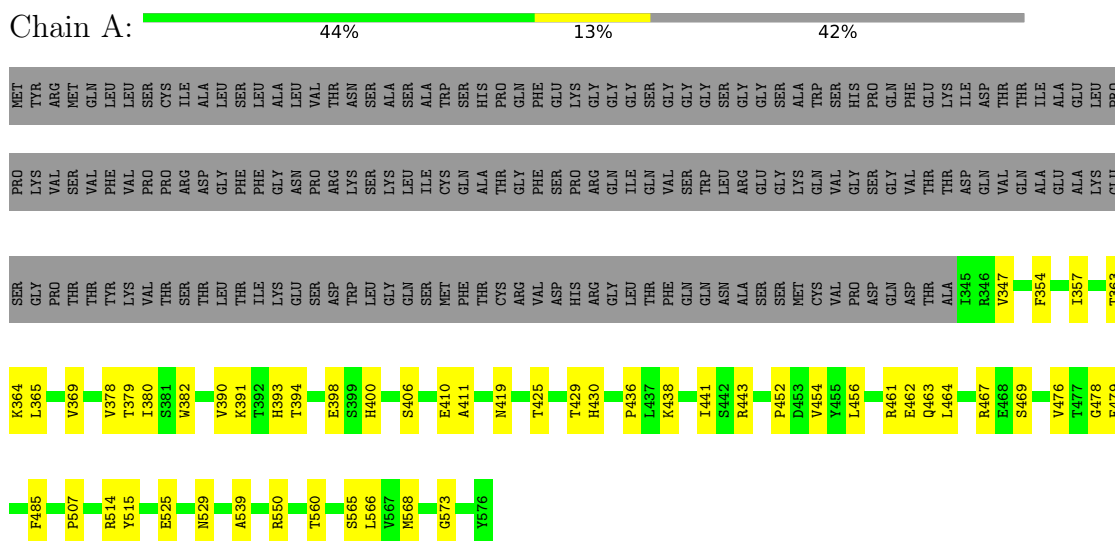
- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 6   | M     | 2        | Total | Ca | 0       |
|     |       |          | 2     | 2  |         |

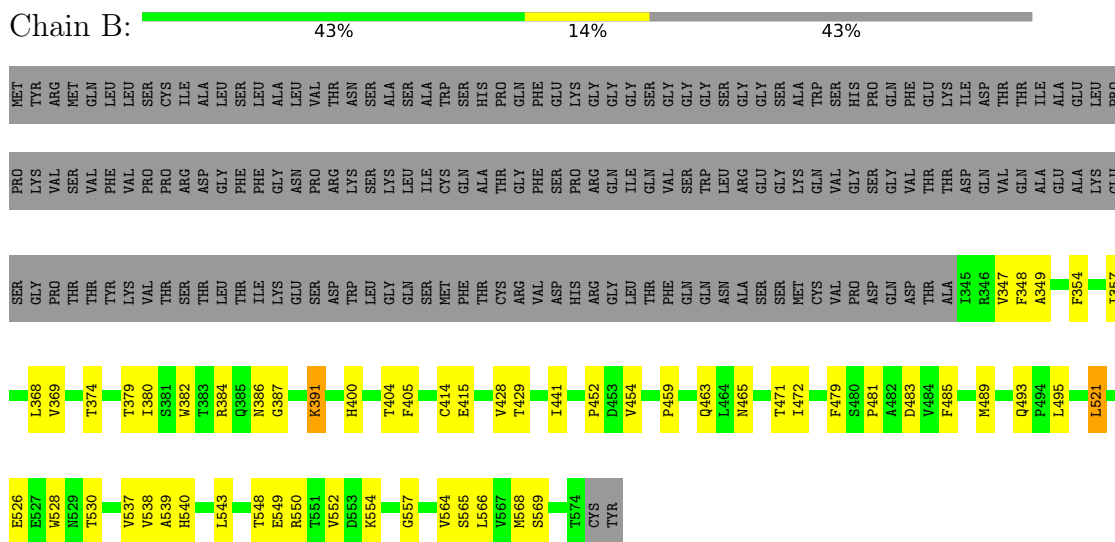
### 3 Residue-property plots

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. 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. 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: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu



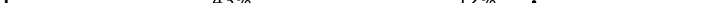
- Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu

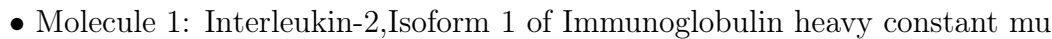
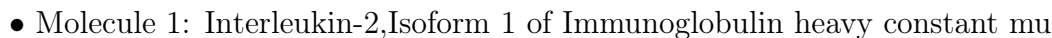


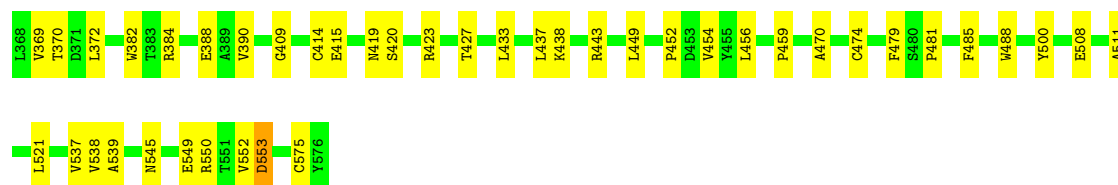
- Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu





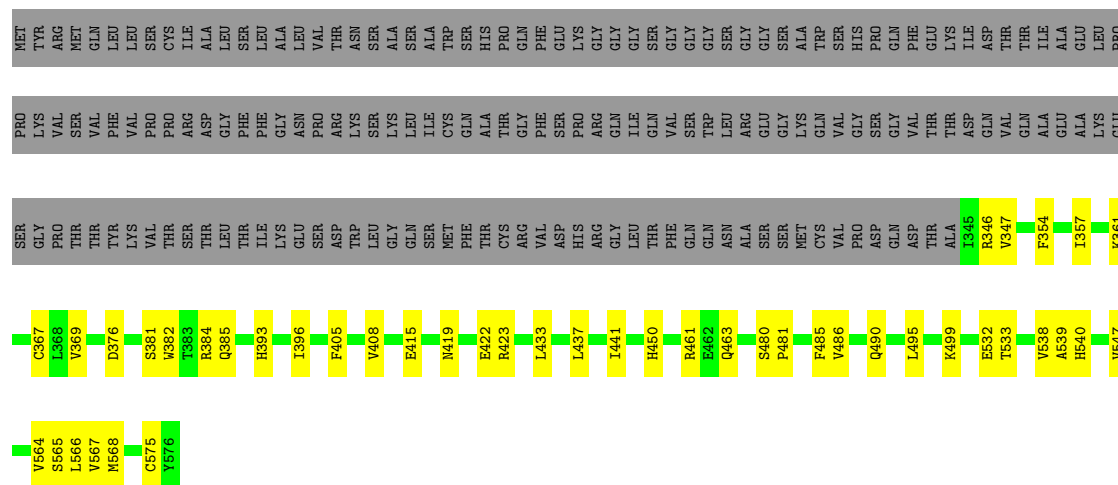
- Chain F:  43% 12% . 44%





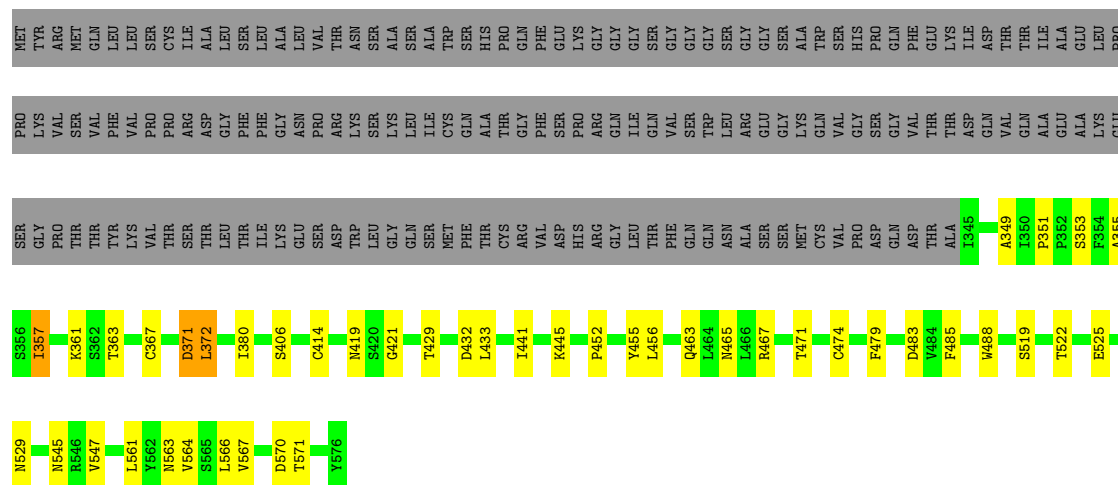
- Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu

Chain K: 46% 11% 42%



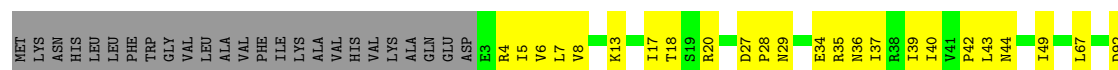
- Molecule 1: Interleukin-2,Isoform 1 of Immunoglobulin heavy constant mu

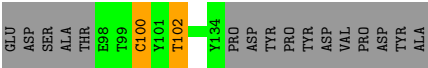
Chain L: 46% 10% 42%



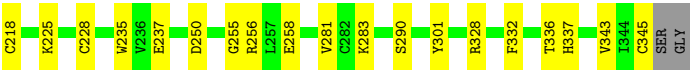
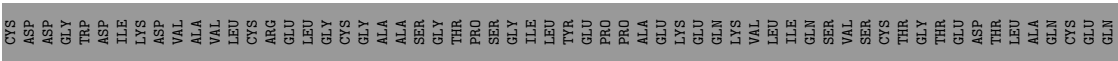
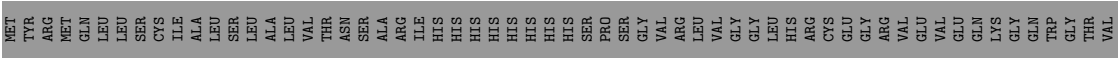
- Molecule 2: Immunoglobulin J chain

Chain J: 60% 14% 24%





● Molecule 3: Interleukin-2,CD5 antigen-like



● Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



## 4 Experimental information

| Property                             | Value               | Source    |
|--------------------------------------|---------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE     | Depositor |
| Imposed symmetry                     | POINT, Not provided |           |
| Number of particles used             | 381470              | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF   | Depositor |
| CTF correction method                | NONE                | Depositor |
| Microscope                           | FEI TITAN KRIOS     | Depositor |
| Voltage (kV)                         | 300                 | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 1.5                 | Depositor |
| Minimum defocus (nm)                 | 1000                | Depositor |
| Maximum defocus (nm)                 | 1500                | Depositor |
| Magnification                        | Not provided        |           |
| Image detector                       | GATAN K3 (6k x 4k)  | Depositor |

## 5 Model quality

### 5.1 Standard geometry

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

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     | 0.32         | 0/1844      | 0.58        | 0/2526          |
| 1   | B     | 0.34         | 0/1825      | 0.58        | 1/2500 (0.0%)   |
| 1   | C     | 0.51         | 0/1802      | 0.64        | 0/2468          |
| 1   | D     | 0.44         | 0/1809      | 0.68        | 3/2478 (0.1%)   |
| 1   | E     | 0.38         | 0/1802      | 0.61        | 1/2468 (0.0%)   |
| 1   | F     | 0.50         | 0/1809      | 0.82        | 7/2478 (0.3%)   |
| 1   | G     | 0.33         | 0/1794      | 0.64        | 1/2457 (0.0%)   |
| 1   | H     | 0.28         | 0/1844      | 0.56        | 0/2526          |
| 1   | K     | 0.26         | 0/1844      | 0.52        | 0/2526          |
| 1   | L     | 0.34         | 0/1844      | 0.64        | 3/2526 (0.1%)   |
| 2   | J     | 0.33         | 0/1023      | 0.60        | 0/1390          |
| 3   | M     | 0.24         | 0/1710      | 0.61        | 0/2311          |
| All | All   | 0.37         | 0/20950     | 0.63        | 16/28654 (0.1%) |

There are no bond length outliers.

All (16) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 1   | F     | 480 | SER  | N-CA-C | -9.69 | 97.52       | 109.83   |
| 1   | E     | 483 | ASP  | N-CA-C | 8.55  | 123.36      | 109.76   |
| 1   | D     | 483 | ASP  | N-CA-C | 8.49  | 121.28      | 110.24   |
| 1   | F     | 479 | PHE  | N-CA-C | 7.57  | 120.58      | 109.07   |
| 1   | F     | 482 | ALA  | N-CA-C | -7.41 | 105.12      | 112.97   |
| 1   | F     | 534 | TYR  | N-CA-C | -6.29 | 98.95       | 109.07   |
| 1   | B     | 391 | LYS  | N-CA-C | -5.76 | 100.60      | 109.76   |
| 1   | D     | 476 | VAL  | N-CA-C | -5.43 | 101.59      | 108.93   |
| 1   | D     | 473 | THR  | N-CA-C | 5.40  | 117.70      | 108.90   |
| 1   | L     | 545 | ASN  | CA-C-N | 5.30  | 131.66      | 121.54   |
| 1   | L     | 545 | ASN  | C-N-CA | 5.30  | 131.66      | 121.54   |
| 1   | F     | 384 | ARG  | CA-C-N | 5.16  | 131.40      | 121.54   |

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| Mol | Chain | Res | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 1   | F     | 384 | ARG  | C-N-CA   | 5.16  | 131.40      | 121.54   |
| 1   | G     | 493 | GLN  | CA-CB-CG | 5.15  | 124.40      | 114.10   |
| 1   | F     | 483 | ASP  | N-CA-C   | -5.08 | 104.67      | 111.02   |
| 1   | L     | 547 | VAL  | N-CA-C   | 5.00  | 115.48      | 108.17   |

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     | 1798  | 0        | 1752     | 34      | 0            |
| 1   | B     | 1780  | 0        | 1738     | 37      | 0            |
| 1   | C     | 1757  | 0        | 1716     | 36      | 0            |
| 1   | D     | 1764  | 0        | 1723     | 33      | 0            |
| 1   | E     | 1757  | 0        | 1716     | 36      | 0            |
| 1   | F     | 1764  | 0        | 1724     | 34      | 0            |
| 1   | G     | 1749  | 0        | 1713     | 41      | 0            |
| 1   | H     | 1798  | 0        | 1751     | 27      | 0            |
| 1   | K     | 1798  | 0        | 1750     | 31      | 0            |
| 1   | L     | 1798  | 0        | 1751     | 33      | 0            |
| 2   | J     | 1010  | 0        | 993      | 21      | 0            |
| 3   | M     | 1669  | 0        | 1570     | 22      | 0            |
| 4   | I     | 28    | 0        | 25       | 0       | 0            |
| 5   | A     | 14    | 0        | 13       | 0       | 0            |
| 5   | B     | 14    | 0        | 13       | 0       | 0            |
| 5   | C     | 14    | 0        | 13       | 0       | 0            |
| 5   | D     | 14    | 0        | 13       | 0       | 0            |
| 5   | E     | 14    | 0        | 13       | 0       | 0            |
| 5   | F     | 14    | 0        | 13       | 0       | 0            |
| 5   | G     | 14    | 0        | 13       | 0       | 0            |
| 5   | H     | 14    | 0        | 13       | 0       | 0            |
| 5   | K     | 14    | 0        | 13       | 1       | 0            |
| 5   | L     | 14    | 0        | 13       | 0       | 0            |
| 6   | M     | 2     | 0        | 0        | 0       | 0            |
| All | All   | 20612 | 0        | 20052    | 343     | 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 8.

All (343) 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:F:547:VAL:HG11 | 1:G:545:ASN:HD21 | 1.53                     | 0.72              |
| 1:B:472:ILE:HG21 | 1:B:552:VAL:HG11 | 1.72                     | 0.72              |
| 1:A:454:VAL:HG12 | 1:A:476:VAL:HG22 | 1.71                     | 0.71              |
| 1:B:537:VAL:HG12 | 1:B:549:GLU:HG2  | 1.72                     | 0.71              |
| 1:B:454:VAL:HG21 | 1:B:538:VAL:HG11 | 1.73                     | 0.71              |
| 2:J:43:LEU:HB2   | 1:L:570:ASP:HA   | 1.75                     | 0.68              |
| 1:G:348:PHE:HB2  | 1:G:368:LEU:HB3  | 1.74                     | 0.67              |
| 1:C:457:LEU:HD22 | 1:C:475:LEU:HD21 | 1.75                     | 0.67              |
| 1:C:454:VAL:HG21 | 1:C:538:VAL:HG11 | 1.79                     | 0.64              |
| 3:M:214:THR:HG23 | 3:M:216:GLN:H    | 1.61                     | 0.64              |
| 1:H:384:ARG:HD2  | 1:H:388:GLU:HB3  | 1.80                     | 0.64              |
| 1:H:456:LEU:HD23 | 1:H:552:VAL:HG12 | 1.80                     | 0.64              |
| 1:G:490:GLN:HE21 | 1:G:495:LEU:HD11 | 1.63                     | 0.63              |
| 1:G:383:THR:HB   | 1:G:387:GLY:HA2  | 1.80                     | 0.63              |
| 1:H:414:CYS:SG   | 1:H:415:GLU:N    | 2.71                     | 0.62              |
| 1:G:374:THR:HA   | 1:G:405:PHE:HB2  | 1.82                     | 0.62              |
| 1:B:400:HIS:HB2  | 1:B:404:THR:HB   | 1.82                     | 0.61              |
| 1:L:372:LEU:HD12 | 1:L:433:LEU:HD23 | 1.81                     | 0.61              |
| 1:L:414:CYS:SG   | 3:M:191:CYS:N    | 2.72                     | 0.61              |
| 1:F:367:CYS:SG   | 1:F:368:LEU:N    | 2.74                     | 0.61              |
| 1:F:350:ILE:HB   | 1:F:366:THR:HB   | 1.83                     | 0.61              |
| 1:C:395:ASN:HB2  | 1:C:408:VAL:HB   | 1.83                     | 0.60              |
| 1:G:485:PHE:HB3  | 1:G:539:ALA:HB3  | 1.84                     | 0.60              |
| 1:H:357:ILE:HG13 | 1:H:363:THR:HG22 | 1.84                     | 0.59              |
| 1:C:459:PRO:HD3  | 1:C:472:ILE:HG23 | 1.84                     | 0.59              |
| 1:G:365:LEU:HD21 | 1:G:413:ILE:HD11 | 1.84                     | 0.59              |
| 1:K:415:GLU:O    | 1:K:419:ASN:ND2  | 2.36                     | 0.59              |
| 1:L:452:PRO:HG3  | 1:L:479:PHE:HB3  | 1.85                     | 0.59              |
| 1:H:545:ASN:OD1  | 1:H:545:ASN:N    | 2.36                     | 0.59              |
| 1:E:345:ILE:N    | 1:E:371:ASP:O    | 2.36                     | 0.58              |
| 1:A:365:LEU:HB2  | 1:A:411:ALA:HB3  | 1.85                     | 0.58              |
| 1:K:385:GLN:HG3  | 1:K:423:ARG:HB2  | 1.85                     | 0.58              |
| 3:M:235:TRP:HE1  | 3:M:237:GLU:HG3  | 1.69                     | 0.58              |
| 1:E:485:PHE:HB3  | 1:E:539:ALA:HB3  | 1.85                     | 0.58              |
| 1:C:347:VAL:HG13 | 1:C:369:VAL:HG22 | 1.87                     | 0.57              |
| 1:E:416:ASP:HA   | 1:E:419:ASN:HB2  | 1.87                     | 0.57              |
| 1:A:382:TRP:HB3  | 1:A:390:VAL:HG23 | 1.86                     | 0.57              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:L:488:TRP:NE1  | 1:L:519:SER:OG   | 2.32                     | 0.57              |
| 1:H:347:VAL:HG12 | 1:H:369:VAL:HG12 | 1.85                     | 0.57              |
| 1:A:347:VAL:HA   | 1:A:369:VAL:HA   | 1.87                     | 0.56              |
| 1:A:461:ARG:HH12 | 1:B:557:GLY:HA2  | 1.71                     | 0.56              |
| 1:E:457:LEU:HB3  | 1:F:457:LEU:HD23 | 1.88                     | 0.56              |
| 1:F:545:ASN:OD1  | 1:G:487:GLN:NE2  | 2.39                     | 0.56              |
| 1:C:501:VAL:HG12 | 1:D:509:PRO:HG3  | 1.86                     | 0.56              |
| 1:L:471:THR:HG22 | 1:L:522:THR:HG22 | 1.87                     | 0.56              |
| 1:B:459:PRO:HD3  | 1:B:472:ILE:HG12 | 1.88                     | 0.55              |
| 1:A:566:LEU:HD13 | 1:L:566:LEU:HD22 | 1.88                     | 0.55              |
| 3:M:328:ARG:HH21 | 3:M:332:PHE:HB3  | 1.71                     | 0.55              |
| 1:B:414:CYS:SG   | 1:B:415:GLU:N    | 2.78                     | 0.55              |
| 1:C:456:LEU:HD21 | 1:C:472:ILE:HG22 | 1.89                     | 0.55              |
| 1:F:414:CYS:HB3  | 1:G:414:CYS:HB3  | 1.88                     | 0.55              |
| 1:D:490:GLN:NE2  | 1:D:532:GLU:OE1  | 2.40                     | 0.55              |
| 1:H:553:ASP:OD2  | 1:H:553:ASP:N    | 2.38                     | 0.55              |
| 1:K:485:PHE:HB3  | 1:K:539:ALA:HB3  | 1.88                     | 0.54              |
| 1:B:485:PHE:HB3  | 1:B:539:ALA:HB3  | 1.88                     | 0.54              |
| 1:C:525:GLU:OE2  | 1:C:529:ASN:ND2  | 2.40                     | 0.54              |
| 1:D:484:VAL:HG23 | 1:D:540:HIS:HB2  | 1.90                     | 0.54              |
| 1:E:365:LEU:HD13 | 1:E:413:ILE:HD13 | 1.88                     | 0.54              |
| 1:L:525:GLU:OE1  | 1:L:529:ASN:ND2  | 2.40                     | 0.54              |
| 1:E:484:VAL:HG12 | 1:E:540:HIS:HB2  | 1.87                     | 0.54              |
| 1:F:369:VAL:HG23 | 1:F:403:ALA:HB1  | 1.89                     | 0.54              |
| 2:J:36:ASN:ND2   | 1:L:563:ASN:OD1  | 2.35                     | 0.54              |
| 2:J:44:ASN:ND2   | 1:L:570:ASP:OD2  | 2.39                     | 0.54              |
| 1:C:568:MET:HE1  | 1:K:564:VAL:HG11 | 1.89                     | 0.54              |
| 1:A:485:PHE:HB3  | 1:A:539:ALA:HB3  | 1.89                     | 0.53              |
| 1:C:348:PHE:HB2  | 1:C:368:LEU:HB2  | 1.89                     | 0.53              |
| 1:C:570:ASP:OD1  | 1:C:570:ASP:N    | 2.41                     | 0.53              |
| 3:M:164:GLN:NE2  | 3:M:205:GLN:OE1  | 2.41                     | 0.53              |
| 1:F:363:THR:OG1  | 1:F:413:ILE:O    | 2.27                     | 0.53              |
| 1:A:461:ARG:HH21 | 1:A:560:THR:HG22 | 1.74                     | 0.53              |
| 1:F:381:SER:HB2  | 1:F:427:THR:HB   | 1.90                     | 0.53              |
| 1:D:535:THR:HG22 | 1:D:551:THR:HG22 | 1.91                     | 0.53              |
| 2:J:6:VAL:HA     | 2:J:18:THR:HG22  | 1.90                     | 0.53              |
| 2:J:42:PRO:HG3   | 2:J:102:THR:HG22 | 1.90                     | 0.53              |
| 1:K:381:SER:HA   | 1:K:393:HIS:HE1  | 1.74                     | 0.53              |
| 1:B:374:THR:HA   | 1:B:405:PHE:HB2  | 1.89                     | 0.53              |
| 1:C:375:TYR:HB2  | 1:C:431:THR:HB   | 1.91                     | 0.52              |
| 1:G:454:VAL:HG11 | 1:G:538:VAL:HG11 | 1.90                     | 0.52              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:F:347:VAL:HG11 | 1:F:426:CYS:HB3  | 1.92                     | 0.52              |
| 1:G:400:HIS:ND1  | 1:G:402:ASN:OD1  | 2.43                     | 0.52              |
| 1:G:425:THR:HG22 | 1:G:440:THR:H    | 1.75                     | 0.52              |
| 3:M:164:GLN:HB3  | 3:M:167:TRP:HB2  | 1.90                     | 0.52              |
| 1:B:463:GLN:HE22 | 1:B:471:THR:HG22 | 1.75                     | 0.52              |
| 1:C:380:ILE:O    | 1:C:393:HIS:ND1  | 2.33                     | 0.52              |
| 1:E:423:ARG:NH1  | 1:E:425:THR:OG1  | 2.43                     | 0.52              |
| 1:K:486:VAL:HG22 | 1:K:538:VAL:HG22 | 1.92                     | 0.52              |
| 1:F:354:PHE:HA   | 1:F:357:ILE:HG12 | 1.92                     | 0.52              |
| 1:E:486:VAL:HG22 | 1:E:538:VAL:HG22 | 1.92                     | 0.51              |
| 1:K:369:VAL:HB   | 1:K:405:PHE:HB3  | 1.93                     | 0.51              |
| 3:M:153:VAL:N    | 3:M:160:TYR:O    | 2.38                     | 0.51              |
| 1:H:485:PHE:HB3  | 1:H:539:ALA:HB3  | 1.93                     | 0.51              |
| 1:A:379:THR:HB   | 1:A:429:THR:HB   | 1.92                     | 0.51              |
| 1:B:349:ALA:HB1  | 1:B:441:ILE:HD11 | 1.92                     | 0.51              |
| 1:A:464:LEU:O    | 1:A:467:ARG:NH1  | 2.44                     | 0.51              |
| 1:F:471:THR:HG22 | 1:F:522:THR:HG22 | 1.93                     | 0.51              |
| 1:L:371:ASP:HB3  | 1:L:406:SER:HB3  | 1.92                     | 0.51              |
| 1:D:555:SER:HA   | 1:D:558:LYS:HE2  | 1.93                     | 0.51              |
| 1:B:566:LEU:HD13 | 1:K:566:LEU:HD11 | 1.94                     | 0.50              |
| 1:C:417:ASP:HB3  | 1:C:424:PHE:HE1  | 1.74                     | 0.50              |
| 1:D:481:PRO:HD2  | 1:D:540:HIS:CE1  | 2.47                     | 0.50              |
| 1:G:454:VAL:HG12 | 1:G:476:VAL:HG13 | 1.93                     | 0.50              |
| 1:B:348:PHE:N    | 1:B:368:LEU:O    | 2.44                     | 0.50              |
| 1:H:345:ILE:HA   | 1:H:372:LEU:HD13 | 1.92                     | 0.50              |
| 2:J:29:ASN:ND2   | 1:L:465:ASN:OD1  | 2.42                     | 0.50              |
| 1:L:421:GLY:HA3  | 1:L:445:LYS:HE2  | 1.94                     | 0.50              |
| 1:B:347:VAL:HG22 | 1:B:369:VAL:HG13 | 1.94                     | 0.50              |
| 1:C:535:THR:HG22 | 1:C:551:THR:HG22 | 1.93                     | 0.50              |
| 1:H:452:PRO:HG3  | 1:H:479:PHE:HB3  | 1.94                     | 0.50              |
| 3:M:256:ARG:NH2  | 3:M:258:GLU:OE2  | 2.44                     | 0.50              |
| 1:E:454:VAL:HG11 | 1:E:538:VAL:HG21 | 1.93                     | 0.50              |
| 1:F:414:CYS:HB3  | 1:G:414:CYS:CB   | 2.42                     | 0.50              |
| 1:H:419:ASN:HA   | 1:H:443:ARG:HE   | 1.76                     | 0.50              |
| 1:F:433:LEU:HB2  | 1:F:436:PRO:HD2  | 1.93                     | 0.50              |
| 1:E:564:VAL:HG21 | 1:F:564:VAL:HG21 | 1.94                     | 0.49              |
| 1:A:354:PHE:HA   | 1:A:357:ILE:HG12 | 1.93                     | 0.49              |
| 1:G:384:ARG:HH11 | 1:G:388:GLU:HG3  | 1.77                     | 0.49              |
| 1:G:481:PRO:HB2  | 1:G:540:HIS:HE2  | 1.77                     | 0.49              |
| 1:L:432:ASP:OD2  | 1:L:432:ASP:N    | 2.46                     | 0.49              |
| 1:G:473:THR:HG22 | 1:G:520:ILE:HG22 | 1.95                     | 0.49              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:A:391:LYS:NZ   | 1:A:394:THR:OG1  | 2.44                     | 0.49              |
| 1:E:478:GLY:HA2  | 1:E:514:ARG:HB3  | 1.94                     | 0.49              |
| 1:H:420:SER:O    | 1:H:423:ARG:NH2  | 2.44                     | 0.49              |
| 1:E:386:ASN:ND2  | 1:E:388:GLU:OE1  | 2.45                     | 0.49              |
| 1:H:537:VAL:HG12 | 1:H:549:GLU:HB2  | 1.94                     | 0.49              |
| 3:M:201:ILE:HD13 | 3:M:228:CYS:HB3  | 1.94                     | 0.49              |
| 2:J:13:LYS:HD2   | 2:J:67:LEU:HD21  | 1.95                     | 0.49              |
| 1:A:463:GLN:NE2  | 1:A:469:SER:O    | 2.41                     | 0.49              |
| 1:D:537:VAL:HG21 | 1:E:545:ASN:HD22 | 1.78                     | 0.48              |
| 1:K:565:SER:OG   | 5:K:601:NAG:O7   | 2.25                     | 0.48              |
| 1:A:573:GLY:O    | 1:K:461:ARG:NH2  | 2.46                     | 0.48              |
| 1:K:490:GLN:O    | 1:K:533:THR:OG1  | 2.30                     | 0.48              |
| 1:H:345:ILE:N    | 1:H:370:THR:O    | 2.46                     | 0.48              |
| 1:L:353:SER:HB2  | 1:L:483:ASP:HB3  | 1.94                     | 0.48              |
| 1:B:354:PHE:HA   | 1:B:357:ILE:HD12 | 1.94                     | 0.48              |
| 1:D:365:LEU:HD13 | 1:D:413:ILE:HB   | 1.95                     | 0.48              |
| 3:M:255:GLY:HA2  | 3:M:301:TYR:HD2  | 1.78                     | 0.48              |
| 1:F:364:LYS:NZ   | 1:F:412:SER:OG   | 2.41                     | 0.48              |
| 3:M:178:GLN:HB3  | 3:M:214:THR:HA   | 1.96                     | 0.48              |
| 1:A:478:GLY:HA2  | 1:A:514:ARG:HB3  | 1.96                     | 0.48              |
| 1:C:385:GLN:HE21 | 1:C:423:ARG:HH21 | 1.60                     | 0.48              |
| 1:D:345:ILE:HB   | 1:D:372:LEU:HD22 | 1.95                     | 0.48              |
| 1:C:511:ALA:HB1  | 1:C:514:ARG:HE   | 1.79                     | 0.48              |
| 1:C:348:PHE:N    | 1:C:368:LEU:O    | 2.43                     | 0.48              |
| 1:C:567:VAL:HA   | 1:D:567:VAL:HB   | 1.95                     | 0.47              |
| 1:A:436:PRO:HB2  | 1:A:438:LYS:HG3  | 1.94                     | 0.47              |
| 1:E:457:LEU:HD23 | 1:F:457:LEU:HB3  | 1.96                     | 0.47              |
| 1:F:382:TRP:HD1  | 1:F:390:VAL:HG23 | 1.79                     | 0.47              |
| 1:C:442:SER:OG   | 1:C:443:ARG:N    | 2.45                     | 0.47              |
| 3:M:170:ARG:HB3  | 3:M:210:GLY:HA3  | 1.96                     | 0.47              |
| 1:B:379:THR:O    | 1:B:429:THR:OG1  | 2.31                     | 0.47              |
| 1:B:528:TRP:CZ2  | 1:B:554:LYS:HA   | 2.49                     | 0.47              |
| 2:J:44:ASN:ND2   | 1:L:570:ASP:O    | 2.48                     | 0.47              |
| 1:A:425:THR:HB   | 1:A:438:LYS:HB3  | 1.97                     | 0.47              |
| 1:H:454:VAL:HG21 | 1:H:538:VAL:HG11 | 1.95                     | 0.47              |
| 3:M:186:LEU:HB3  | 3:M:237:GLU:HB2  | 1.96                     | 0.47              |
| 1:F:483:ASP:O    | 1:F:484:VAL:C    | 2.57                     | 0.47              |
| 1:E:518:HIS:CD2  | 1:F:520:ILE:HD11 | 2.50                     | 0.47              |
| 1:F:396:ILE:HG23 | 1:F:407:ALA:HA   | 1.97                     | 0.47              |
| 2:J:37:ILE:HD12  | 1:L:564:VAL:HG22 | 1.96                     | 0.47              |
| 1:K:354:PHE:HA   | 1:K:357:ILE:HG12 | 1.97                     | 0.47              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:K:376:ASP:OD1  | 1:K:376:ASP:N    | 2.47                     | 0.47              |
| 1:A:380:ILE:O    | 1:A:393:HIS:ND1  | 2.48                     | 0.47              |
| 1:F:438:LYS:HA   | 1:F:438:LYS:HD3  | 1.76                     | 0.47              |
| 1:A:467:ARG:HA   | 1:A:525:GLU:HG3  | 1.96                     | 0.47              |
| 1:E:483:ASP:O    | 1:E:540:HIS:HD2  | 1.97                     | 0.47              |
| 1:D:475:LEU:O    | 1:D:476:VAL:C    | 2.57                     | 0.47              |
| 1:D:502:THR:HA   | 1:D:519:SER:HA   | 1.97                     | 0.47              |
| 1:F:508:GLU:HG3  | 1:F:509:PRO:HD2  | 1.97                     | 0.47              |
| 2:J:20:ARG:NH1   | 2:J:34:GLU:OE1   | 2.47                     | 0.47              |
| 1:K:495:LEU:HD23 | 1:K:499:LYS:HD2  | 1.97                     | 0.47              |
| 1:D:467:ARG:HH11 | 1:D:525:GLU:HB3  | 1.80                     | 0.46              |
| 1:C:349:ALA:HA   | 1:C:367:CYS:HA   | 1.98                     | 0.46              |
| 1:G:380:ILE:HD11 | 1:G:428:VAL:HG12 | 1.97                     | 0.46              |
| 1:D:479:PHE:HB2  | 1:D:540:HIS:CE1  | 2.51                     | 0.46              |
| 1:G:479:PHE:HB2  | 1:G:540:HIS:CE1  | 2.51                     | 0.46              |
| 2:J:49:ILE:HD13  | 2:J:100:CYS:O    | 2.14                     | 0.46              |
| 1:C:430:HIS:HB3  | 1:C:433:LEU:H    | 1.80                     | 0.46              |
| 1:E:463:GLN:OE1  | 1:E:471:THR:OG1  | 2.32                     | 0.46              |
| 1:B:382:TRP:HB3  | 1:B:384:ARG:HH22 | 1.79                     | 0.46              |
| 1:B:526:GLU:O    | 1:B:530:THR:OG1  | 2.32                     | 0.46              |
| 1:L:349:ALA:HA   | 1:L:367:CYS:HA   | 1.98                     | 0.46              |
| 1:E:454:VAL:HG23 | 1:E:550:ARG:HG3  | 1.97                     | 0.46              |
| 1:B:489:MET:HB3  | 1:B:489:MET:HE2  | 1.67                     | 0.46              |
| 1:D:383:THR:OG1  | 1:D:425:THR:O    | 2.32                     | 0.46              |
| 1:D:420:SER:OG   | 1:D:422:GLU:OE1  | 2.33                     | 0.46              |
| 1:K:396:ILE:HG22 | 1:K:408:VAL:H    | 1.81                     | 0.46              |
| 1:K:567:VAL:HB   | 1:L:567:VAL:HA   | 1.98                     | 0.46              |
| 1:C:463:GLN:HG2  | 1:C:469:SER:O    | 2.16                     | 0.46              |
| 1:D:413:ILE:HD13 | 1:D:424:PHE:HE2  | 1.81                     | 0.46              |
| 1:F:349:ALA:HA   | 1:F:367:CYS:HA   | 1.98                     | 0.46              |
| 2:J:4:ARG:HD2    | 2:J:20:ARG:HD2   | 1.97                     | 0.46              |
| 2:J:92:ASP:N     | 2:J:92:ASP:OD1   | 2.48                     | 0.45              |
| 1:A:419:ASN:HB3  | 1:A:443:ARG:HH21 | 1.81                     | 0.45              |
| 1:B:354:PHE:N    | 1:B:483:ASP:OD1  | 2.44                     | 0.45              |
| 1:F:452:PRO:HD2  | 1:F:543:LEU:HG   | 1.97                     | 0.45              |
| 1:K:361:LYS:HD3  | 1:K:361:LYS:HA   | 1.86                     | 0.45              |
| 1:C:351:PRO:HB3  | 1:C:418:TRP:CZ2  | 2.51                     | 0.45              |
| 1:C:475:LEU:O    | 1:C:476:VAL:C    | 2.57                     | 0.45              |
| 1:D:360:THR:O    | 1:D:361:LYS:HB3  | 2.16                     | 0.45              |
| 1:G:396:ILE:HG23 | 1:G:407:ALA:HA   | 1.96                     | 0.45              |
| 1:H:433:LEU:HD13 | 1:H:437:LEU:HD21 | 1.98                     | 0.45              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:L:351:PRO:HB3  | 1:L:441:ILE:HG12 | 1.98                     | 0.45              |
| 1:G:400:HIS:CD2  | 1:G:401:PRO:HD2  | 2.51                     | 0.45              |
| 1:E:385:GLN:HE22 | 1:E:423:ARG:H    | 1.63                     | 0.45              |
| 1:E:417:ASP:OD1  | 1:E:418:TRP:N    | 2.50                     | 0.45              |
| 3:M:163:CYS:HB3  | 3:M:228:CYS:HB2  | 1.51                     | 0.45              |
| 1:B:566:LEU:HD21 | 1:B:568:MET:HE3  | 1.98                     | 0.45              |
| 3:M:208:CYS:HB3  | 3:M:218:CYS:HB2  | 1.87                     | 0.45              |
| 1:F:420:SER:OG   | 1:F:422:GLU:OE2  | 2.34                     | 0.45              |
| 1:G:535:THR:HB   | 1:G:549:GLU:HG3  | 1.99                     | 0.45              |
| 1:A:456:LEU:HD12 | 1:A:456:LEU:HA   | 1.74                     | 0.45              |
| 1:L:474:CYS:HB3  | 1:L:519:SER:HB3  | 1.98                     | 0.45              |
| 1:C:455:TYR:HD2  | 1:C:475:LEU:HD12 | 1.81                     | 0.45              |
| 1:C:467:ARG:HA   | 1:C:525:GLU:HG3  | 1.98                     | 0.45              |
| 1:D:347:VAL:HA   | 1:D:369:VAL:HA   | 1.99                     | 0.45              |
| 1:K:367:CYS:SG   | 1:K:382:TRP:NE1  | 2.90                     | 0.45              |
| 1:E:384:ARG:NH2  | 1:E:389:ALA:O    | 2.42                     | 0.45              |
| 1:F:382:TRP:H    | 1:F:390:VAL:HB   | 1.82                     | 0.45              |
| 2:J:37:ILE:HB    | 1:L:564:VAL:HG13 | 1.98                     | 0.45              |
| 1:D:568:MET:HE3  | 1:G:562:TYR:HE1  | 1.80                     | 0.44              |
| 1:A:568:MET:HB2  | 1:A:568:MET:HE3  | 1.74                     | 0.44              |
| 1:F:481:PRO:C    | 1:F:483:ASP:H    | 2.25                     | 0.44              |
| 1:G:347:VAL:HG21 | 1:G:439:GLN:HE21 | 1.81                     | 0.44              |
| 1:G:422:GLU:O    | 1:G:442:SER:OG   | 2.35                     | 0.44              |
| 1:G:449:LEU:HD23 | 1:G:542:ALA:HA   | 2.00                     | 0.44              |
| 2:J:49:ILE:CD1   | 2:J:100:CYS:HB3  | 2.47                     | 0.44              |
| 1:L:357:ILE:HD13 | 1:L:357:ILE:HA   | 1.85                     | 0.44              |
| 1:E:491:ARG:HE   | 1:E:491:ARG:HB3  | 1.64                     | 0.44              |
| 1:H:508:GLU:HG2  | 1:H:511:ALA:HB3  | 1.98                     | 0.44              |
| 1:B:493:GLN:OE1  | 1:B:493:GLN:N    | 2.47                     | 0.44              |
| 1:B:569:SER:HA   | 1:C:569:SER:HB2  | 1.98                     | 0.44              |
| 1:D:471:THR:HG22 | 1:D:522:THR:HG22 | 1.98                     | 0.44              |
| 1:A:398:GLU:O    | 1:A:406:SER:OG   | 2.35                     | 0.44              |
| 1:D:363:THR:HB   | 1:D:413:ILE:O    | 2.16                     | 0.44              |
| 1:G:472:ILE:HG21 | 1:G:552:VAL:HG11 | 2.00                     | 0.44              |
| 1:E:450:HIS:N    | 1:E:480:SER:OG   | 2.49                     | 0.44              |
| 1:K:481:PRO:HD2  | 1:K:540:HIS:CE1  | 2.53                     | 0.44              |
| 1:G:489:MET:HB3  | 1:G:489:MET:HE2  | 1.70                     | 0.44              |
| 1:H:454:VAL:O    | 1:H:550:ARG:NH1  | 2.50                     | 0.44              |
| 1:G:345:ILE:N    | 1:G:371:ASP:O    | 2.51                     | 0.44              |
| 1:A:525:GLU:OE2  | 1:A:529:ASN:ND2  | 2.50                     | 0.43              |
| 1:C:457:LEU:HD12 | 1:D:460:ALA:HB2  | 1.99                     | 0.43              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 2:J:40:ILE:HD13  | 1:L:567:VAL:HB   | 2.00                     | 0.43              |
| 3:M:203:LEU:O    | 3:M:225:LYS:N    | 2.50                     | 0.43              |
| 1:A:565:SER:HA   | 1:B:565:SER:HB3  | 2.00                     | 0.43              |
| 1:B:380:ILE:HG23 | 1:B:428:VAL:HG12 | 1.99                     | 0.43              |
| 1:B:386:ASN:OD1  | 1:B:386:ASN:N    | 2.47                     | 0.43              |
| 1:B:495:LEU:HD13 | 1:B:521:LEU:HD11 | 2.00                     | 0.43              |
| 1:D:452:PRO:HB3  | 1:D:476:VAL:HG12 | 2.00                     | 0.43              |
| 1:A:363:THR:O    | 1:A:363:THR:OG1  | 2.34                     | 0.43              |
| 1:K:490:GLN:NE2  | 1:K:532:GLU:OE1  | 2.50                     | 0.43              |
| 1:G:457:LEU:HD11 | 1:G:475:LEU:HD22 | 2.00                     | 0.43              |
| 1:H:449:LEU:HD13 | 1:H:481:PRO:HG2  | 1.99                     | 0.43              |
| 1:K:450:HIS:N    | 1:K:480:SER:OG   | 2.47                     | 0.43              |
| 1:B:391:LYS:HD2  | 1:B:391:LYS:HA   | 1.80                     | 0.43              |
| 1:D:481:PRO:HD2  | 1:D:540:HIS:HE1  | 1.81                     | 0.43              |
| 1:G:416:ASP:O    | 1:G:420:SER:OG   | 2.28                     | 0.43              |
| 1:G:493:GLN:HA   | 1:G:494:PRO:HD3  | 1.91                     | 0.43              |
| 1:H:545:ASN:HD22 | 1:K:547:VAL:HG11 | 1.84                     | 0.43              |
| 1:G:451:ARG:HE   | 1:G:544:PRO:HD3  | 1.84                     | 0.43              |
| 1:L:363:THR:HB   | 1:L:414:CYS:HA   | 2.01                     | 0.43              |
| 1:A:378:VAL:HG13 | 1:A:430:HIS:HE1  | 1.84                     | 0.42              |
| 1:D:489:MET:HA   | 1:D:494:PRO:HA   | 2.00                     | 0.42              |
| 1:D:558:LYS:HA   | 1:D:559:PRO:HD3  | 1.83                     | 0.42              |
| 1:E:416:ASP:OD1  | 1:E:416:ASP:N    | 2.45                     | 0.42              |
| 1:G:527:GLU:O    | 1:G:530:THR:OG1  | 2.37                     | 0.42              |
| 1:G:553:ASP:H    | 1:G:556:THR:HG22 | 1.84                     | 0.42              |
| 1:L:355:ALA:HA   | 1:L:485:PHE:HB2  | 2.00                     | 0.42              |
| 1:L:456:LEU:HA   | 1:L:456:LEU:HD12 | 1.72                     | 0.42              |
| 1:B:452:PRO:HG3  | 1:B:479:PHE:HB3  | 2.01                     | 0.42              |
| 1:G:481:PRO:HD2  | 1:G:540:HIS:CE1  | 2.53                     | 0.42              |
| 1:B:465:ASN:HD22 | 1:L:571:THR:HB   | 1.85                     | 0.42              |
| 1:G:568:MET:HE3  | 1:G:568:MET:HB2  | 1.83                     | 0.42              |
| 3:M:173:LYS:HB2  | 3:M:173:LYS:HE2  | 1.81                     | 0.42              |
| 1:F:564:VAL:HG22 | 1:G:564:VAL:HB   | 2.02                     | 0.42              |
| 2:J:35:ARG:HH22  | 1:K:461:ARG:HH22 | 1.68                     | 0.42              |
| 1:A:393:HIS:HA   | 1:A:410:GLU:HG3  | 2.00                     | 0.42              |
| 1:A:452:PRO:HB3  | 1:A:479:PHE:HB3  | 2.02                     | 0.42              |
| 1:D:351:PRO:HB3  | 1:D:441:ILE:HG12 | 2.01                     | 0.42              |
| 1:E:489:MET:HA   | 1:E:494:PRO:HA   | 2.01                     | 0.42              |
| 1:F:372:LEU:HD23 | 1:F:372:LEU:HA   | 1.90                     | 0.42              |
| 3:M:283:LYS:HE3  | 3:M:283:LYS:HB2  | 1.83                     | 0.42              |
| 1:C:470:ALA:O    | 1:C:522:THR:HA   | 2.19                     | 0.42              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:H:382:TRP:HB3  | 1:H:390:VAL:HG22 | 2.01                     | 0.42              |
| 1:H:500:TYR:HB3  | 1:H:521:LEU:HD13 | 2.00                     | 0.42              |
| 1:K:382:TRP:HH2  | 1:K:441:ILE:HD13 | 1.84                     | 0.42              |
| 1:A:364:LYS:HE2  | 1:A:364:LYS:HB2  | 1.91                     | 0.42              |
| 1:C:456:LEU:HD12 | 1:C:536:CYS:HB2  | 2.01                     | 0.42              |
| 1:D:452:PRO:HD2  | 1:D:543:LEU:HG   | 2.01                     | 0.42              |
| 1:G:445:LYS:HB2  | 1:G:445:LYS:HE2  | 1.69                     | 0.42              |
| 1:B:543:LEU:HD13 | 1:B:548:THR:HG23 | 2.01                     | 0.42              |
| 1:E:526:GLU:O    | 1:E:530:THR:OG1  | 2.34                     | 0.42              |
| 1:F:370:THR:HA   | 1:F:403:ALA:HB2  | 2.02                     | 0.42              |
| 2:J:8:VAL:HG22   | 2:J:17:ILE:HB    | 2.01                     | 0.42              |
| 1:D:382:TRP:NE1  | 1:D:409:GLY:O    | 2.43                     | 0.42              |
| 1:B:481:PRO:HD2  | 1:B:540:HIS:CE1  | 2.55                     | 0.42              |
| 1:C:457:LEU:HA   | 1:C:458:PRO:HD3  | 1.83                     | 0.42              |
| 1:E:349:ALA:HA   | 1:E:367:CYS:HA   | 2.01                     | 0.42              |
| 1:F:396:ILE:HD13 | 1:F:408:VAL:HG22 | 2.02                     | 0.42              |
| 1:H:575:CYS:SG   | 1:K:575:CYS:N    | 2.93                     | 0.42              |
| 1:K:384:ARG:NH2  | 1:K:422:GLU:OE1  | 2.53                     | 0.42              |
| 1:E:438:LYS:HE2  | 1:E:438:LYS:HB3  | 1.85                     | 0.41              |
| 1:C:485:PHE:HB3  | 1:C:539:ALA:HB3  | 2.02                     | 0.41              |
| 3:M:250:ASP:OD1  | 3:M:301:TYR:OH   | 2.29                     | 0.41              |
| 3:M:290:SER:HA   | 3:M:345:CYS:HB3  | 2.02                     | 0.41              |
| 1:H:474:CYS:HB2  | 1:H:488:TRP:CZ2  | 2.56                     | 0.41              |
| 1:E:353:SER:O    | 1:E:356:SER:OG   | 2.31                     | 0.41              |
| 1:K:347:VAL:HG23 | 1:K:437:LEU:HD12 | 2.03                     | 0.41              |
| 1:K:433:LEU:HD23 | 1:K:433:LEU:HA   | 1.95                     | 0.41              |
| 1:D:549:GLU:OE2  | 1:E:545:ASN:ND2  | 2.43                     | 0.41              |
| 1:E:562:TYR:HB2  | 1:E:564:VAL:HG23 | 2.03                     | 0.41              |
| 1:B:384:ARG:HG3  | 1:B:387:GLY:H    | 1.85                     | 0.41              |
| 1:C:423:ARG:HB3  | 1:C:440:THR:HB   | 2.02                     | 0.41              |
| 1:H:459:PRO:HG3  | 1:H:470:ALA:HB1  | 2.02                     | 0.41              |
| 2:J:27:ASP:HA    | 2:J:28:PRO:HD3   | 1.89                     | 0.41              |
| 1:B:379:THR:OG1  | 1:B:429:THR:O    | 2.36                     | 0.41              |
| 1:E:545:ASN:OD1  | 1:E:545:ASN:N    | 2.39                     | 0.41              |
| 1:H:367:CYS:H    | 1:H:409:GLY:HA3  | 1.86                     | 0.41              |
| 1:A:454:VAL:O    | 1:A:550:ARG:HG3  | 2.21                     | 0.41              |
| 1:D:408:VAL:HG13 | 1:D:410:GLU:H    | 1.86                     | 0.41              |
| 1:C:429:THR:HG22 | 1:C:436:PRO:HB3  | 2.03                     | 0.41              |
| 1:D:462:GLU:H    | 1:D:462:GLU:HG3  | 1.70                     | 0.41              |
| 1:E:372:LEU:HA   | 1:E:372:LEU:HD23 | 1.85                     | 0.41              |
| 1:L:463:GLN:NE2  | 1:L:471:THR:OG1  | 2.46                     | 0.41              |

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| Atom-1           | Atom-2           | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:A:507:PRO:HA   | 1:A:515:TYR:HD2  | 1.84                     | 0.41              |
| 1:A:568:MET:HE2  | 2:J:39:ILE:HD12  | 2.03                     | 0.41              |
| 1:B:564:VAL:HG21 | 1:K:568:MET:HE3  | 2.02                     | 0.41              |
| 1:E:452:PRO:HG3  | 1:E:540:HIS:HB3  | 2.03                     | 0.41              |
| 1:K:346:ARG:HA   | 1:K:437:LEU:HD13 | 2.03                     | 0.41              |
| 1:A:462:GLU:OE1  | 1:B:550:ARG:NH1  | 2.52                     | 0.40              |
| 1:E:470:ALA:N    | 1:E:523:VAL:O    | 2.53                     | 0.40              |
| 1:H:427:THR:HG22 | 1:H:438:LYS:HG2  | 2.04                     | 0.40              |
| 1:K:463:GLN:HG2  | 1:L:455:TYR:CZ   | 2.57                     | 0.40              |
| 1:L:361:LYS:HA   | 1:L:361:LYS:HD2  | 1.87                     | 0.40              |
| 1:G:386:ASN:OD1  | 1:G:386:ASN:N    | 2.54                     | 0.40              |
| 1:L:419:ASN:OD1  | 1:L:419:ASN:N    | 2.54                     | 0.40              |
| 3:M:336:THR:OG1  | 3:M:337:HIS:N    | 2.54                     | 0.40              |
| 1:E:518:HIS:NE2  | 1:F:520:ILE:HD11 | 2.36                     | 0.40              |
| 1:G:470:ALA:N    | 1:G:523:VAL:O    | 2.47                     | 0.40              |
| 3:M:281:VAL:HG11 | 3:M:343:VAL:HG21 | 2.04                     | 0.40              |
| 1:C:459:PRO:HD2  | 1:C:528:TRP:CZ2  | 2.56                     | 0.40              |
| 1:F:543:LEU:HD23 | 1:F:543:LEU:HA   | 1.98                     | 0.40              |
| 2:J:27:ASP:OD2   | 1:L:467:ARG:NH2  | 2.54                     | 0.40              |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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     | 230/403 (57%) | 217 (94%) | 13 (6%) | 0        | 100         | 100 |
| 1   | B     | 228/403 (57%) | 216 (95%) | 12 (5%) | 0        | 100         | 100 |
| 1   | C     | 224/403 (56%) | 209 (93%) | 15 (7%) | 0        | 100         | 100 |
| 1   | D     | 225/403 (56%) | 210 (93%) | 15 (7%) | 0        | 100         | 100 |
| 1   | E     | 224/403 (56%) | 211 (94%) | 13 (6%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed        | Favoured   | Allowed  | Outliers | Percentiles |     |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 1   | F     | 225/403 (56%)   | 203 (90%)  | 22 (10%) | 0        | 100         | 100 |
| 1   | G     | 223/403 (55%)   | 214 (96%)  | 9 (4%)   | 0        | 100         | 100 |
| 1   | H     | 230/403 (57%)   | 208 (90%)  | 22 (10%) | 0        | 100         | 100 |
| 1   | K     | 230/403 (57%)   | 216 (94%)  | 14 (6%)  | 0        | 100         | 100 |
| 1   | L     | 230/403 (57%)   | 212 (92%)  | 18 (8%)  | 0        | 100         | 100 |
| 2   | J     | 123/168 (73%)   | 119 (97%)  | 4 (3%)   | 0        | 100         | 100 |
| 3   | M     | 211/359 (59%)   | 191 (90%)  | 20 (10%) | 0        | 100         | 100 |
| All | All   | 2603/4557 (57%) | 2426 (93%) | 177 (7%) | 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     | 206/349 (59%)   | 204 (99%)  | 2 (1%)   | 68          | 75  |
| 1   | B     | 204/349 (58%)   | 203 (100%) | 1 (0%)   | 81          | 81  |
| 1   | C     | 202/349 (58%)   | 198 (98%)  | 4 (2%)   | 48          | 65  |
| 1   | D     | 203/349 (58%)   | 202 (100%) | 1 (0%)   | 81          | 81  |
| 1   | E     | 202/349 (58%)   | 201 (100%) | 1 (0%)   | 81          | 81  |
| 1   | F     | 203/349 (58%)   | 198 (98%)  | 5 (2%)   | 42          | 62  |
| 1   | G     | 201/349 (58%)   | 198 (98%)  | 3 (2%)   | 57          | 69  |
| 1   | H     | 206/349 (59%)   | 205 (100%) | 1 (0%)   | 81          | 81  |
| 1   | K     | 206/349 (59%)   | 206 (100%) | 0        | 100         | 100 |
| 1   | L     | 206/349 (59%)   | 200 (97%)  | 6 (3%)   | 37          | 60  |
| 2   | J     | 120/155 (77%)   | 116 (97%)  | 4 (3%)   | 33          | 57  |
| 3   | M     | 182/304 (60%)   | 181 (100%) | 1 (0%)   | 81          | 81  |
| All | All   | 2341/3949 (59%) | 2312 (99%) | 29 (1%)  | 61          | 72  |

All (29) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 400 | HIS  |
| 1   | A     | 441 | ILE  |
| 1   | B     | 521 | LEU  |
| 1   | C     | 472 | ILE  |
| 1   | C     | 473 | THR  |
| 1   | C     | 474 | CYS  |
| 1   | C     | 475 | LEU  |
| 1   | D     | 475 | LEU  |
| 1   | E     | 480 | SER  |
| 1   | F     | 433 | LEU  |
| 1   | F     | 466 | LEU  |
| 1   | F     | 484 | VAL  |
| 1   | F     | 538 | VAL  |
| 1   | F     | 553 | ASP  |
| 1   | G     | 378 | VAL  |
| 1   | G     | 413 | ILE  |
| 1   | G     | 429 | THR  |
| 1   | H     | 553 | ASP  |
| 2   | J     | 5   | ILE  |
| 2   | J     | 7   | LEU  |
| 2   | J     | 100 | CYS  |
| 2   | J     | 102 | THR  |
| 1   | L     | 357 | ILE  |
| 1   | L     | 371 | ASP  |
| 1   | L     | 372 | LEU  |
| 1   | L     | 380 | ILE  |
| 1   | L     | 429 | THR  |
| 1   | L     | 561 | LEU  |
| 3   | M     | 134 | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 430 | HIS  |
| 1   | A     | 545 | ASN  |
| 1   | C     | 385 | GLN  |
| 1   | C     | 439 | GLN  |
| 1   | C     | 463 | GLN  |
| 1   | C     | 487 | GLN  |
| 1   | D     | 439 | GLN  |
| 1   | F     | 540 | HIS  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | G     | 490 | GLN  |
| 1   | G     | 529 | ASN  |
| 1   | G     | 545 | ASN  |
| 2   | J     | 29  | ASN  |
| 1   | K     | 419 | ASN  |
| 1   | K     | 529 | ASN  |
| 1   | L     | 465 | ASN  |
| 1   | L     | 529 | ASN  |

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

2 monosaccharides 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   | NAG  | I     | 1   | 2,4  | 14,14,15     | 0.20 | 0           | 17,19,21    | 0.65 | 1 (5%)      |
| 4   | NAG  | I     | 2   | 4    | 14,14,15     | 0.35 | 0           | 17,19,21    | 0.50 | 0           |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions  | Rings   |
|-----|------|-------|-----|------|---------|-----------|---------|
| 4   | NAG  | I     | 1   | 2,4  | -       | 0/6/23/26 | 0/1/1/1 |

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| Mol | Type | Chain | Res | Link | Chirals | Torsions  | Rings   |
|-----|------|-------|-----|------|---------|-----------|---------|
| 4   | NAG  | I     | 2   | 4    | -       | 3/6/23/26 | 0/1/1/1 |

There are no bond length outliers.

All (1) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|------|-------------|----------|
| 4   | I     | 1   | NAG  | C1-O5-C5 | 2.21 | 115.15      | 112.19   |

There are no chirality outliers.

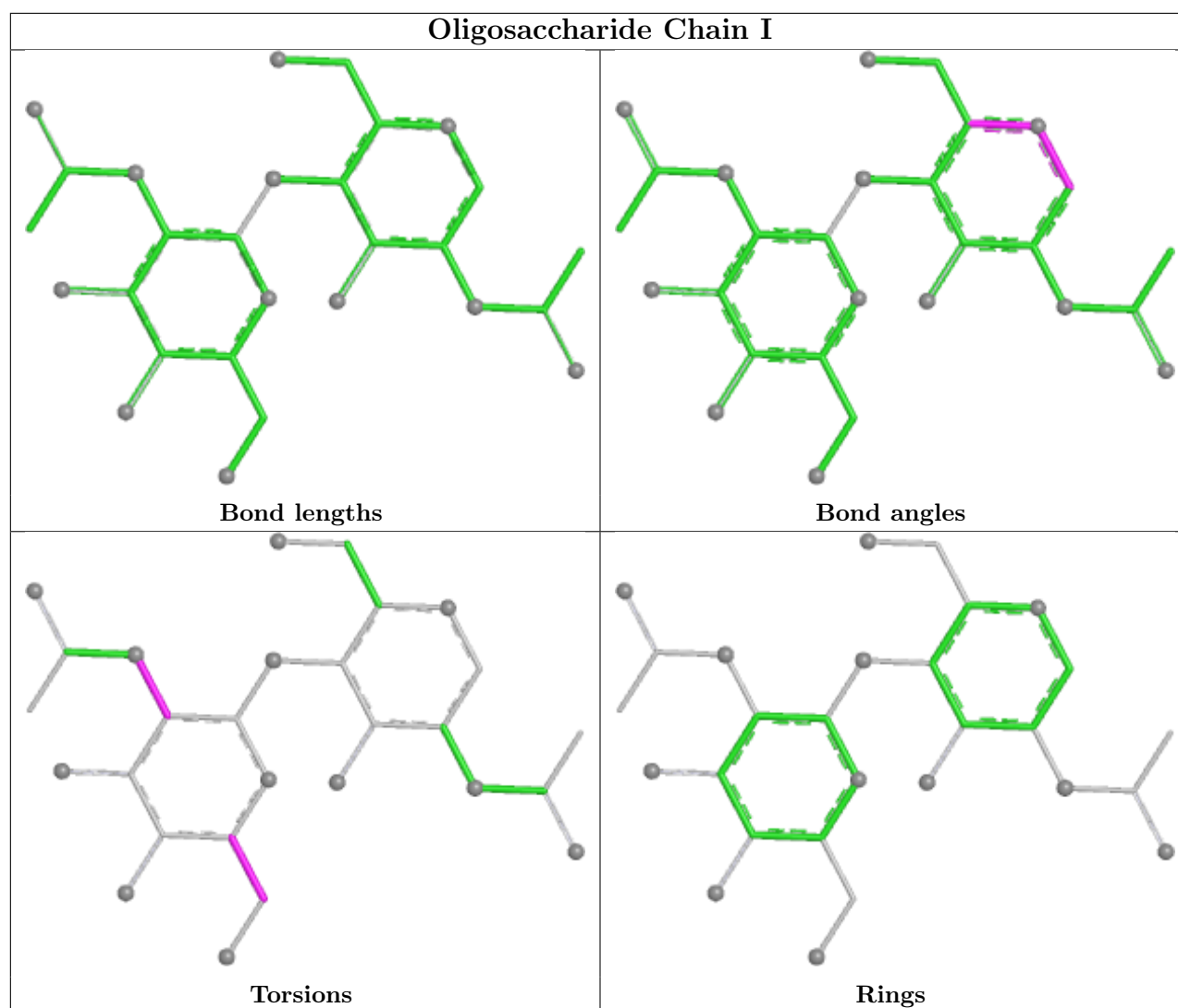
All (3) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 4   | I     | 2   | NAG  | C4-C5-C6-O6 |
| 4   | I     | 2   | NAG  | O5-C5-C6-O6 |
| 4   | I     | 2   | NAG  | C1-C2-N2-C7 |

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

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

| Mol | Type | Chain | Res | Link | Bond lengths |      |             | Bond angles |      |             |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
|     |      |       |     |      | Counts       | RMSZ | $\# Z  > 2$ | Counts      | RMSZ | $\# Z  > 2$ |
| 5   | NAG  | G     | 601 | 1    | 14,14,15     | 0.43 | 0           | 17,19,21    | 0.50 | 0           |
| 5   | NAG  | H     | 601 | 1    | 14,14,15     | 0.45 | 0           | 17,19,21    | 0.78 | 1 (5%)      |
| 5   | NAG  | A     | 601 | 1    | 14,14,15     | 0.42 | 0           | 17,19,21    | 0.59 | 1 (5%)      |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 5   | NAG  | K     | 601 | 1    | 14,14,15     | 0.48 | 0        | 17,19,21    | 0.51 | 0        |
| 5   | NAG  | C     | 601 | 1    | 14,14,15     | 0.47 | 0        | 17,19,21    | 0.47 | 0        |
| 5   | NAG  | D     | 601 | 1    | 14,14,15     | 0.29 | 0        | 17,19,21    | 0.45 | 0        |
| 5   | NAG  | F     | 601 | 1    | 14,14,15     | 0.39 | 0        | 17,19,21    | 0.51 | 0        |
| 5   | NAG  | B     | 601 | 1    | 14,14,15     | 0.44 | 0        | 17,19,21    | 0.57 | 0        |
| 5   | NAG  | E     | 601 | 1    | 14,14,15     | 0.29 | 0        | 17,19,21    | 0.48 | 0        |
| 5   | NAG  | L     | 601 | 1    | 14,14,15     | 0.48 | 0        | 17,19,21    | 0.62 | 0        |

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

| Mol | Type | Chain | Res | Link | Chirals | Torsions  | Rings   |
|-----|------|-------|-----|------|---------|-----------|---------|
| 5   | NAG  | G     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | H     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | A     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | K     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | C     | 601 | 1    | -       | 4/6/23/26 | 0/1/1/1 |
| 5   | NAG  | D     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | F     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | B     | 601 | 1    | -       | 0/6/23/26 | 0/1/1/1 |
| 5   | NAG  | E     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |
| 5   | NAG  | L     | 601 | 1    | -       | 2/6/23/26 | 0/1/1/1 |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z    | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|------|-------------|----------|
| 5   | H     | 601 | NAG  | C1-O5-C5 | 2.73 | 115.84      | 112.19   |
| 5   | A     | 601 | NAG  | C1-O5-C5 | 2.03 | 114.90      | 112.19   |

There are no chirality outliers.

All (20) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 5   | C     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | H     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | C     | 601 | NAG  | O5-C5-C6-O6 |

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| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 5   | F     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | H     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | E     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | F     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | D     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | A     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | C     | 601 | NAG  | C8-C7-N2-C2 |
| 5   | C     | 601 | NAG  | O7-C7-N2-C2 |
| 5   | K     | 601 | NAG  | C8-C7-N2-C2 |
| 5   | K     | 601 | NAG  | O7-C7-N2-C2 |
| 5   | G     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | L     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | L     | 601 | NAG  | O5-C5-C6-O6 |
| 5   | D     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | E     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | G     | 601 | NAG  | C4-C5-C6-O6 |
| 5   | A     | 601 | NAG  | C4-C5-C6-O6 |

There are no ring outliers.

1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 5   | K     | 601 | NAG  | 1       | 0            |

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-37936. 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

This section was not generated.

### 6.2 Central slices

This section was not generated.

### 6.3 Largest variance slices

This section was not generated.

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

This section was not generated.

### 6.5 Orthogonal surface views

This section was not generated.

### 6.6 Mask visualisation

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 ⓘ

This section was not generated.

### 7.2 Volume estimate versus contour level ⓘ

This section was not generated.

### 7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit

This section was not generated.