



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:52 PM UTC

PDB ID : 7QN9 / pdb\_00007qn9  
EMDB ID : EMD-14071  
Title : Cryo-EM structure of human full-length extrasynaptic alpha4beta3delta GABA(A)R in complex with GABA, histamine and nanobody Nb25 in a pre-open/closed state  
Authors : Sente, A.; Desai, R.; Naydenova, K.; Malinauskas, T.; Jounaidi, Y.; Miehl, J.; Zhou, X.; Masiulis, S.; Hardwick, S.W.; Chirgadze, D.Y.; Miller, K.W.; Aricescu, A.R.  
Deposited on : 2021-12-20  
Resolution : 2.90 Å(reported)

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>.

---

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  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

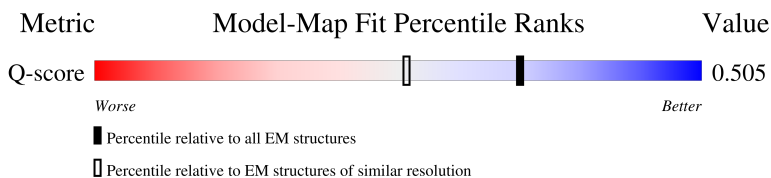
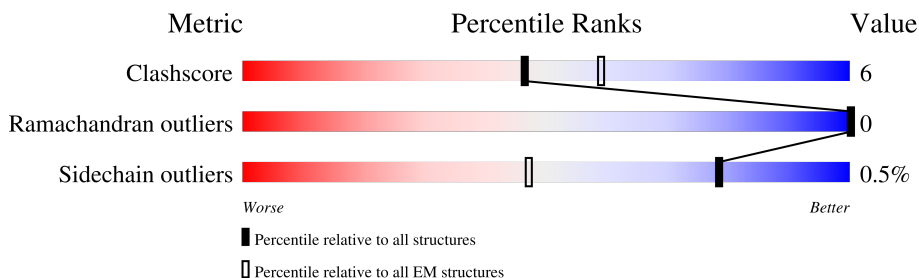
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.90 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                       | 13054 ( 2.40 - 3.40 )                                    |

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     | 554    | <br>49% 11% 40%  |
| 2   | B     | 473    | <br>60% 10% 30%  |
| 2   | C     | 473    | <br>60% 10% 30%  |

*Continued on next page...*

Validation Pipeline (wwPDB-VP) : 2.49

*Continued from previous page...*

| Mol | Chain | Length | Quality of chain                                                                             |
|-----|-------|--------|----------------------------------------------------------------------------------------------|
| 2   | D     | 473    |  60%10%30% |
| 3   | E     | 472    |  56%12%32% |
| 4   | L     | 121    |  85%13%    |
| 4   | M     | 121    |  87%12%    |
| 5   | a     | 3      |  33%67%    |
| 6   | b     | 2      |  100%      |
| 6   | c     | 2      |  100%      |
| 6   | d     | 2      |  100%      |
| 7   | F     | 5      |  80%20%    |
| 7   | G     | 5      |  100%      |
| 7   | H     | 5      |  100%      |

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 15696 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 Gamma-aminobutyric acid receptor subunit alpha-4.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 1   | A     | 333      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2693  | 1758 | 432 | 481 | 22 |         |       |

- Molecule 2 is a protein called Gamma-aminobutyric acid receptor subunit beta-3.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2   | B     | 331      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2720  | 1781 | 444 | 479 | 16 |         |       |
| 2   | C     | 331      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2720  | 1781 | 444 | 479 | 16 |         |       |
| 2   | D     | 331      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2720  | 1781 | 444 | 479 | 16 |         |       |

- Molecule 3 is a protein called Gamma-aminobutyric acid receptor subunit delta.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3   | E     | 321      | Total | C    | N   | O   | S  | 2       | 0     |
|     |       |          | 2579  | 1678 | 422 | 466 | 13 |         |       |

There are 20 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| E     | 453     | GLY      | -      | expression tag | UNP O14764 |
| E     | 454     | GLY      | -      | expression tag | UNP O14764 |
| E     | 455     | SER      | -      | expression tag | UNP O14764 |
| E     | 456     | GLY      | -      | expression tag | UNP O14764 |
| E     | 457     | GLY      | -      | expression tag | UNP O14764 |
| E     | 458     | SER      | -      | expression tag | UNP O14764 |
| E     | 459     | GLY      | -      | expression tag | UNP O14764 |
| E     | 460     | GLY      | -      | expression tag | UNP O14764 |
| E     | 461     | SER      | -      | expression tag | UNP O14764 |
| E     | 462     | GLY      | -      | expression tag | UNP O14764 |
| E     | 463     | LYS      | -      | expression tag | UNP O14764 |

*Continued on next page...*

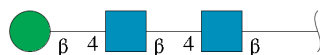
Continued from previous page...

| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| E     | 464     | THR      | -      | expression tag | UNP O14764 |
| E     | 465     | GLU      | -      | expression tag | UNP O14764 |
| E     | 466     | THR      | -      | expression tag | UNP O14764 |
| E     | 467     | SER      | -      | expression tag | UNP O14764 |
| E     | 468     | GLN      | -      | expression tag | UNP O14764 |
| E     | 469     | VAL      | -      | expression tag | UNP O14764 |
| E     | 470     | ALA      | -      | expression tag | UNP O14764 |
| E     | 471     | PRO      | -      | expression tag | UNP O14764 |
| E     | 472     | ALA      | -      | expression tag | UNP O14764 |

- Molecule 4 is a protein called Nanobody Nb25.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 4   | L     | 121      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 940   | 593 | 161 | 182 | 4 |         |       |
| 4   | M     | 121      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 940   | 593 | 161 | 182 | 4 |         |       |

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



| Mol | Chain | Residues | Atoms |    |   |    | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---------|-------|
| 5   | a     | 3        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 39    | 22 | 2 | 15 |         |       |

- Molecule 6 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



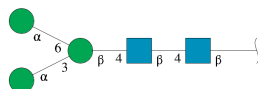
| Mol | Chain | Residues | Atoms |    |   |    | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---------|-------|
| 6   | b     | 2        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 28    | 16 | 2 | 10 |         |       |
| 6   | c     | 2        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 28    | 16 | 2 | 10 |         |       |

Continued on next page...

Continued from previous page...

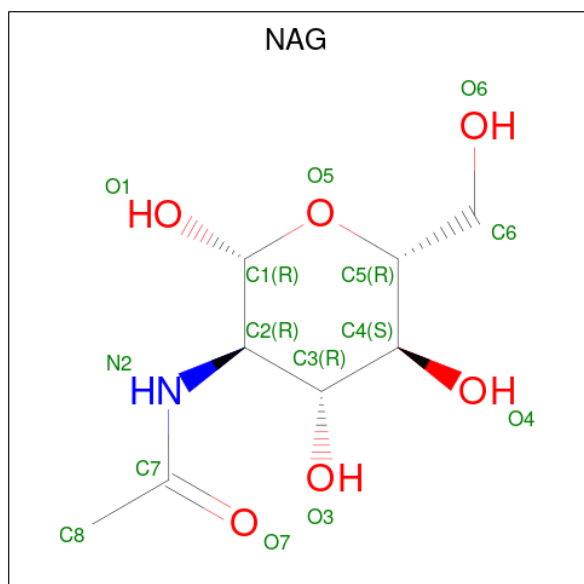
| Mol | Chain | Residues | Atoms |    |   |    | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---------|-------|
| 6   | d     | 2        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 28    | 16 | 2 | 10 |         |       |

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



| Mol | Chain | Residues | Atoms |    |   |    | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---------|-------|
| 7   | F     | 5        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 61    | 34 | 2 | 25 |         |       |
| 7   | G     | 5        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 61    | 34 | 2 | 25 |         |       |
| 7   | H     | 5        | Total | C  | N | O  | 0       | 0     |
|     |       |          | 61    | 34 | 2 | 25 |         |       |

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



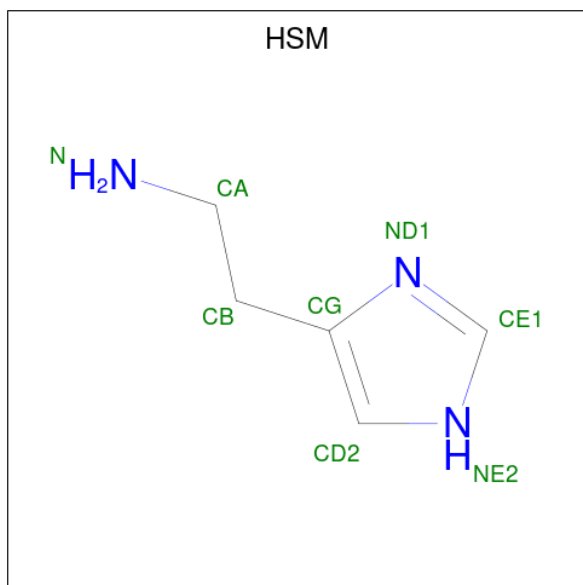
| Mol | Chain | Residues | Atoms |   |   |   | AltConf |
|-----|-------|----------|-------|---|---|---|---------|
| 8   | A     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |

Continued on next page...

*Continued from previous page...*

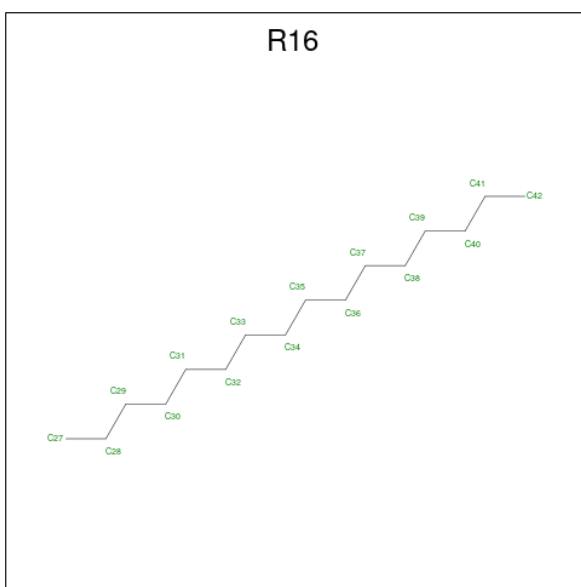
| Mol | Chain | Residues | Atoms |   |   |   | AltConf |
|-----|-------|----------|-------|---|---|---|---------|
| 8   | E     | 1        | Total | C | N | O | 0       |
|     |       |          | 14    | 8 | 1 | 5 |         |

- Molecule 9 is HISTAMINE (CCD ID: HSM) (formula:  $C_5H_9N_3$ ) (labeled as "Ligand of Interest" by depositor).



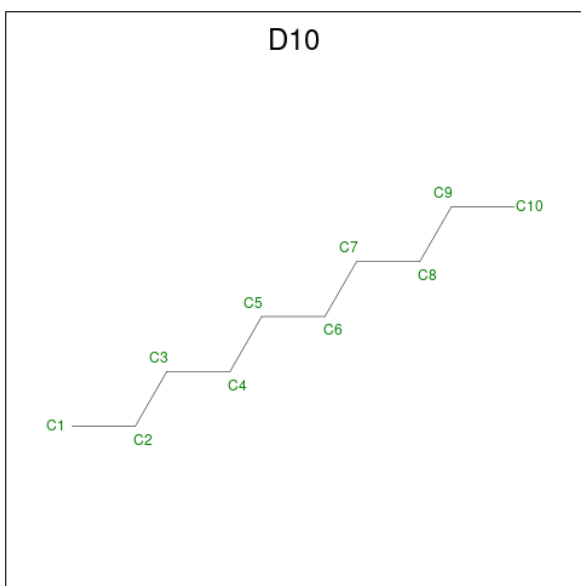
| Mol | Chain | Residues | Atoms |   |   | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 9   | B     | 1        | Total | C | N | 0       |
|     |       |          | 8     | 5 | 3 |         |
| 9   | C     | 1        | Total | C | N | 0       |
|     |       |          | 8     | 5 | 3 |         |
| 9   | D     | 1        | Total | C | N | 0       |
|     |       |          | 8     | 5 | 3 |         |

- Molecule 10 is HEXADECANE (CCD ID: R16) (formula:  $C_{16}H_{34}$ ).



| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 10  | B     | 1        | Total | C  | 0       |
|     |       |          | 16    | 16 |         |

- Molecule 11 is DECANE (CCD ID: D10) (formula:  $C_{10}H_{22}$ ).

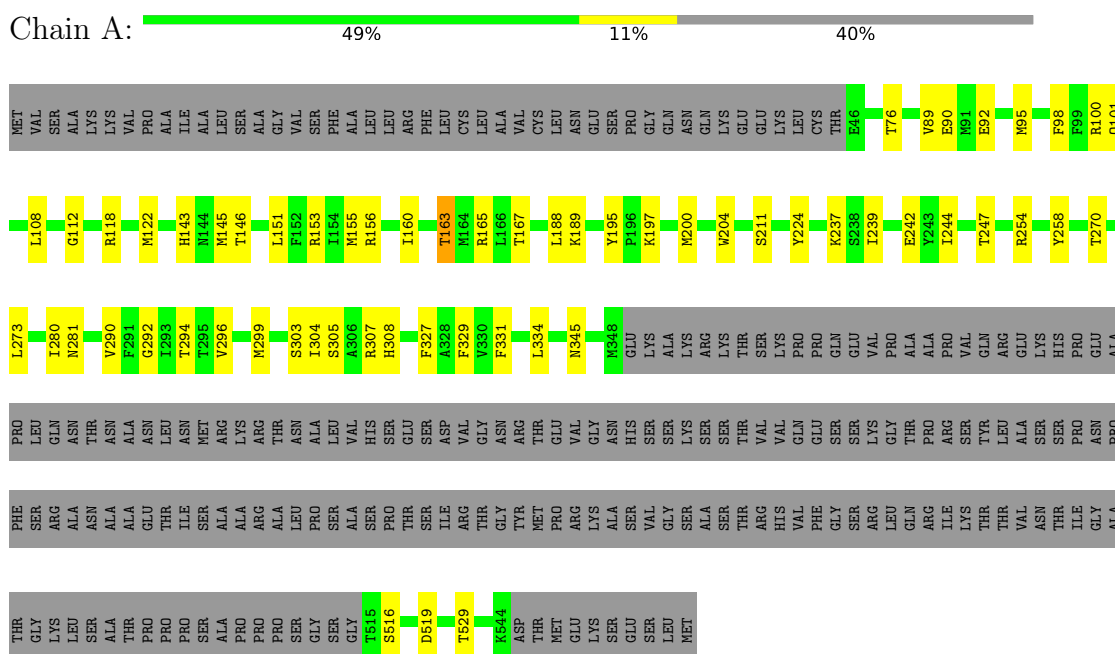


| Mol | Chain | Residues | Atoms |    | AltConf |
|-----|-------|----------|-------|----|---------|
| 11  | D     | 1        | Total | C  | 0       |
|     |       |          | 10    | 10 |         |

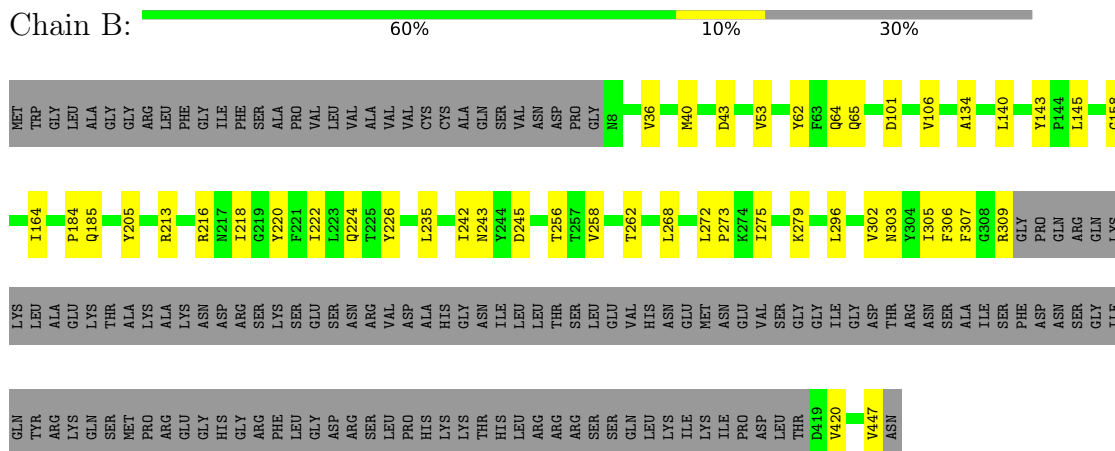
### 3 Residue-property plots

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 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: Gamma-aminobutyric acid receptor subunit alpha-4



#### • Molecule 2: Gamma-aminobutyric acid receptor subunit beta-3



Chain C:

60% 10% 30%

MET TRP GLY LEU ALA GLY GLY ARG ARG LEU PHE PHE ILE PHE ALA PRO VAL LEU VAL ALA VAL VAL CYS CYS ALA ALA GLN SER SER ASN ASP PRO GLY N8 V36 M40 D43 V53 Y62 F63 Q64 Q65 D101 A134 L140 Y143 P144 L145 I164 P190

LYS LEU LEU ARG ALA GLY LYS THR ALA R216 R217 R218 R219 R220 R221 R222 R223 R224 R225 R226 L235 W241 I242 I243 I244 I245 I255 T256 T257 V258 T262 R269 E270 T271 T272 T273 K274 I275 P276 K279 G279 L296 V302 N303 V304 I305 F306 A307 G308 R309 GLY PRO ASN GLN GLN

GLN TYR ARG ARG GLN SER MET PRO PRO ARG GLY HIS HIS ASP ASP ARG ARG LEU LEU LEU HIS HIS ARG ARG ARG SER SER SER GLN LYS ILE ILE ILE ASP THR D419 V420 V447 ASN

Chain D:

60% 10% 30%

MET TRP GLY LEU ALA GLY GLY ARG LEU PHE GLY ILE PHE SER ALA PRO VAL LEU VAL ALA VAL VAL CYS CYS GLN SER ASN ASP PRO GLY H8 M9 V36 M40 D43 V53 Y62 F63 Q64 Q65 D101 R117 A134 L140 Y143 P144 L145

I164 Q185 R216 R217 I218 G219 Y220 F221 I222 L223 T224 T225 Y226 I230 L236 D245 A251 I255 V258 T262 L268 L272 P273 K274 M275 P276 K279 F293 L296 V302 N303 Y304 A305 F306 F307 G308 R309 GLY PRO ASN GLN ARG GLN LYS LYS LYS TYR LEU ARG LYS

Chain E:

56% 12% 32%

Sequence logo showing amino acid conservation across three regions (56%, 12%, 32%). The logo displays amino acid single-letter codes (e.g., MET, ASP, ALA, PRO, ARG, LEU, CYS, GLN, THR, ASN, ASP, ILE, GLY, TYR, VAL, SER, ASN, LEU, ILE, TRP, PRO, ASN, Y85, T86, M87, T88, V89, P90, S94, L100, V127, K142, R145, I152, L153, I156, P172, D181, V193, S197, Q200, I203, F221, A231, S234, S236, L239, Y250, T251, T252, Q253, S254, Y255, L260, L261, V262, A265, M264, S268, S272, R279, T289, M290, T291, T292, L293, M294, R298, L301, L310, D311, W315, V321, F322, A323, A324, L325, V326, D336, T337, ARG, LYS, LYS, GLN, LYS, ALA, LYS, VAL, VAL, SER, ARG, PRO, ARG, GLY, ALA, GLN, GLY, MET, ASP, ARG, ALA, ARG, LEU, ARG, PRO, ILE, LEU, PHE, SER, LEU, SER, ALA, ALA, GLY, VAL) corresponding to positions 1 through 337.

GLY  
GLY  
SER  
GLY  
SER  
GLY  
GLY  
LYS  
THR  
THR  
SER  
GLN  
VAL  
ALA  
PRO  
ALA

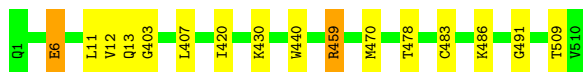
• Molecule 4: Nanobody Nb25

Chain L:  85% 13%



• Molecule 4: Nanobody Nb25

Chain M:  87% 12%

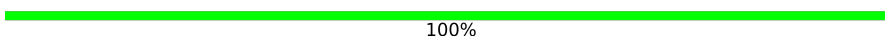


• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:  33% 67% 33%

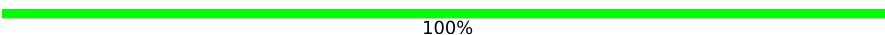


• Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b:  100%

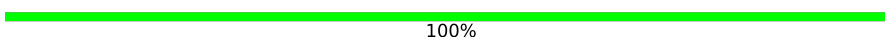


• Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:  100%



• Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:  100%



- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  80% 20%

|      |
|------|
| MAG1 |
| MAG2 |
| BMA3 |
| MAN4 |
| MAN5 |

- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%

|      |
|------|
| MAG1 |
| MAG2 |
| BMA3 |
| MAN4 |
| MAN5 |

- Molecule 7: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%

|      |
|------|
| MAG1 |
| MAG2 |
| BMA3 |
| MAN4 |
| MAN5 |

## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 92694                                   | 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 ( $e^-/\text{\AA}^2$ ) | 40                                      | Depositor |
| Minimum defocus (nm)                 | 700                                     | Depositor |
| Maximum defocus (nm)                 | 2100                                    | Depositor |
| Magnification                        | 130000                                  | Depositor |
| Image detector                       | GATAN K3 (6k x 4k)                      | Depositor |
| Maximum map value                    | 0.086                                   | Depositor |
| Minimum map value                    | -0.031                                  | Depositor |
| Average map value                    | -0.000                                  | Depositor |
| Map value standard deviation         | 0.003                                   | Depositor |
| Recommended contour level            | 0.008                                   | Depositor |
| Map size (Å)                         | 259.84, 259.84, 259.84                  | wwPDB     |
| Map dimensions                       | 290, 290, 290                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 0.89599997, 0.89599997, 0.89599997      | Depositor |

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: R16, HSM, BMA, MAN, D10, 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     | 0.08         | 0/2764  | 0.20        | 0/3749  |
| 2   | B     | 0.12         | 0/2792  | 0.41        | 0/3798  |
| 2   | C     | 0.12         | 0/2792  | 0.41        | 0/3798  |
| 2   | D     | 0.12         | 0/2792  | 0.41        | 0/3798  |
| 3   | E     | 0.08         | 0/2655  | 0.21        | 0/3620  |
| 4   | L     | 0.11         | 0/963   | 0.40        | 0/1304  |
| 4   | M     | 0.11         | 0/963   | 0.40        | 0/1304  |
| All | All   | 0.11         | 0/15721 | 0.35        | 0/21371 |

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 [i](#)

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     | 2693  | 0        | 2703     | 42      | 0            |
| 2   | B     | 2720  | 0        | 2711     | 39      | 0            |
| 2   | C     | 2720  | 0        | 2711     | 47      | 0            |
| 2   | D     | 2720  | 0        | 2711     | 42      | 0            |
| 3   | E     | 2579  | 0        | 2531     | 40      | 0            |
| 4   | L     | 940   | 0        | 887      | 12      | 0            |

*Continued on next page...*

*Continued from previous page...*

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 4   | M     | 940   | 0        | 887      | 11      | 0            |
| 5   | a     | 39    | 0        | 34       | 1       | 0            |
| 6   | b     | 28    | 0        | 25       | 0       | 0            |
| 6   | c     | 28    | 0        | 25       | 0       | 0            |
| 6   | d     | 28    | 0        | 25       | 0       | 0            |
| 7   | F     | 61    | 0        | 52       | 1       | 0            |
| 7   | G     | 61    | 0        | 52       | 0       | 0            |
| 7   | H     | 61    | 0        | 52       | 0       | 0            |
| 8   | A     | 14    | 0        | 13       | 0       | 0            |
| 8   | E     | 14    | 0        | 13       | 1       | 0            |
| 9   | B     | 8     | 0        | 9        | 1       | 0            |
| 9   | C     | 8     | 0        | 9        | 0       | 0            |
| 9   | D     | 8     | 0        | 9        | 0       | 0            |
| 10  | B     | 16    | 0        | 34       | 1       | 0            |
| 11  | D     | 10    | 0        | 22       | 1       | 0            |
| All | All   | 15696 | 0        | 15515    | 191     | 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 6.

The worst 5 of 191 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1           | Atom-2          | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|-----------------|--------------------------|-------------------|
| 2:C:220:TYR:HB2  | 2:D:276:PRO:HA  | 1.56                     | 0.85              |
| 2:D:272:LEU:HD13 | 2:D:279:LYS:HE3 | 1.59                     | 0.85              |
| 2:B:272:LEU:HD13 | 2:B:279:LYS:HE3 | 1.59                     | 0.85              |
| 2:D:305:ILE:HG23 | 2:D:309:ARG:HD2 | 1.59                     | 0.84              |
| 2:C:272:LEU:HD13 | 2:C:279:LYS:HE3 | 1.59                     | 0.84              |

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     | 329/554 (59%)   | 323 (98%)  | 6 (2%)  | 0        | 100         | 100 |
| 2   | B     | 327/473 (69%)   | 322 (98%)  | 5 (2%)  | 0        | 100         | 100 |
| 2   | C     | 327/473 (69%)   | 322 (98%)  | 5 (2%)  | 0        | 100         | 100 |
| 2   | D     | 327/473 (69%)   | 322 (98%)  | 5 (2%)  | 0        | 100         | 100 |
| 3   | E     | 319/472 (68%)   | 313 (98%)  | 6 (2%)  | 0        | 100         | 100 |
| 4   | L     | 117/121 (97%)   | 111 (95%)  | 6 (5%)  | 0        | 100         | 100 |
| 4   | M     | 117/121 (97%)   | 111 (95%)  | 6 (5%)  | 0        | 100         | 100 |
| All | All   | 1863/2687 (69%) | 1824 (98%) | 39 (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     | 302/486 (62%)   | 301 (100%)  | 1 (0%)   | 86          | 96  |
| 2   | B     | 298/417 (72%)   | 297 (100%)  | 1 (0%)   | 86          | 96  |
| 2   | C     | 298/417 (72%)   | 297 (100%)  | 1 (0%)   | 86          | 96  |
| 2   | D     | 298/417 (72%)   | 297 (100%)  | 1 (0%)   | 86          | 96  |
| 3   | E     | 276/389 (71%)   | 276 (100%)  | 0        | 100         | 100 |
| 4   | L     | 97/97 (100%)    | 95 (98%)    | 2 (2%)   | 47          | 77  |
| 4   | M     | 97/97 (100%)    | 95 (98%)    | 2 (2%)   | 47          | 77  |
| All | All   | 1666/2320 (72%) | 1658 (100%) | 8 (0%)   | 78          | 93  |

5 of 8 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 4   | M     | 459 | ARG  |
| 4   | M     | 6   | GLU  |
| 4   | L     | 6   | GLU  |
| 2   | D     | 64  | GLN  |
| 4   | L     | 459 | ARG  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2   | D     | 267 | HIS  |
| 4   | L     | 1   | GLN  |
| 2   | D     | 303 | ASN  |
| 4   | M     | 1   | GLN  |
| 3   | E     | 233 | GLN  |

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

24 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 | $\# Z  > 2$ |
| 7   | NAG  | F     | 1   | 2,7  | 14,14,15     | 0.24 | 0           | 17,19,21    | 0.44 | 0           |
| 7   | NAG  | F     | 2   | 7    | 14,14,15     | 0.24 | 0           | 17,19,21    | 0.49 | 0           |
| 7   | BMA  | F     | 3   | 7    | 11,11,12     | 0.60 | 0           | 15,15,17    | 0.73 | 0           |
| 7   | MAN  | F     | 4   | 7    | 11,11,12     | 0.20 | 0           | 15,15,17    | 0.22 | 0           |
| 7   | MAN  | F     | 5   | 7    | 11,11,12     | 0.18 | 0           | 15,15,17    | 0.23 | 0           |
| 7   | NAG  | G     | 1   | 2,7  | 14,14,15     | 0.23 | 0           | 17,19,21    | 0.41 | 0           |
| 7   | NAG  | G     | 2   | 7    | 14,14,15     | 0.23 | 0           | 17,19,21    | 0.49 | 0           |
| 7   | BMA  | G     | 3   | 7    | 11,11,12     | 0.58 | 0           | 15,15,17    | 0.79 | 0           |
| 7   | MAN  | G     | 4   | 7    | 11,11,12     | 0.21 | 0           | 15,15,17    | 0.23 | 0           |
| 7   | MAN  | G     | 5   | 7    | 11,11,12     | 0.19 | 0           | 15,15,17    | 0.23 | 0           |
| 7   | NAG  | H     | 1   | 2,7  | 14,14,15     | 0.25 | 0           | 17,19,21    | 0.41 | 0           |
| 7   | NAG  | H     | 2   | 7    | 14,14,15     | 0.23 | 0           | 17,19,21    | 0.52 | 0           |

| Mol | Type | Chain | Res | Link | Bond lengths |      |          | Bond angles |      |          |
|-----|------|-------|-----|------|--------------|------|----------|-------------|------|----------|
|     |      |       |     |      | Counts       | RMSZ | # Z  > 2 | Counts      | RMSZ | # Z  > 2 |
| 7   | BMA  | H     | 3   | 7    | 11,11,12     | 0.57 | 0        | 15,15,17    | 0.83 | 0        |
| 7   | MAN  | H     | 4   | 7    | 11,11,12     | 0.20 | 0        | 15,15,17    | 0.23 | 0        |
| 7   | MAN  | H     | 5   | 7    | 11,11,12     | 0.21 | 0        | 15,15,17    | 0.23 | 0        |
| 5   | NAG  | a     | 1   | 1,5  | 14,14,15     | 0.24 | 0        | 17,19,21    | 0.45 | 0        |
| 5   | NAG  | a     | 2   | 5    | 14,14,15     | 0.22 | 0        | 17,19,21    | 0.44 | 0        |
| 5   | BMA  | a     | 3   | 5    | 11,11,12     | 0.54 | 0        | 15,15,17    | 0.72 | 0        |
| 6   | NAG  | b     | 1   | 6,2  | 14,14,15     | 0.24 | 0        | 17,19,21    | 0.43 | 0        |
| 6   | NAG  | b     | 2   | 6    | 14,14,15     | 0.24 | 0        | 17,19,21    | 0.44 | 0        |
| 6   | NAG  | c     | 1   | 6,2  | 14,14,15     | 0.23 | 0        | 17,19,21    | 0.41 | 0        |
| 6   | NAG  | c     | 2   | 6    | 14,14,15     | 0.22 | 0        | 17,19,21    | 0.44 | 0        |
| 6   | NAG  | d     | 1   | 6,2  | 14,14,15     | 0.23 | 0        | 17,19,21    | 0.39 | 0        |
| 6   | NAG  | d     | 2   | 6    | 14,14,15     | 0.22 | 0        | 17,19,21    | 0.44 | 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   |
|-----|------|-------|-----|------|---------|-----------|---------|
| 7   | NAG  | F     | 1   | 2,7  | -       | 0/6/23/26 | 0/1/1/1 |
| 7   | NAG  | F     | 2   | 7    | -       | 0/6/23/26 | 0/1/1/1 |
| 7   | BMA  | F     | 3   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 7   | MAN  | F     | 4   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 7   | MAN  | F     | 5   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 7   | NAG  | G     | 1   | 2,7  | -       | 0/6/23/26 | 0/1/1/1 |
| 7   | NAG  | G     | 2   | 7    | -       | 0/6/23/26 | 0/1/1/1 |
| 7   | BMA  | G     | 3   | 7    | -       | 2/2/19/22 | 0/1/1/1 |
| 7   | MAN  | G     | 4   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 7   | MAN  | G     | 5   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 7   | NAG  | H     | 1   | 2,7  | -       | 0/6/23/26 | 0/1/1/1 |
| 7   | NAG  | H     | 2   | 7    | -       | 0/6/23/26 | 0/1/1/1 |
| 7   | BMA  | H     | 3   | 7    | -       | 2/2/19/22 | 0/1/1/1 |
| 7   | MAN  | H     | 4   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 7   | MAN  | H     | 5   | 7    | -       | 0/2/19/22 | 0/1/1/1 |
| 5   | NAG  | a     | 1   | 1,5  | -       | 0/6/23/26 | 0/1/1/1 |
| 5   | NAG  | a     | 2   | 5    | -       | 0/6/23/26 | 0/1/1/1 |
| 5   | BMA  | a     | 3   | 5    | -       | 0/2/19/22 | 0/1/1/1 |
| 6   | NAG  | b     | 1   | 6,2  | -       | 0/6/23/26 | 0/1/1/1 |
| 6   | NAG  | b     | 2   | 6    | -       | 0/6/23/26 | 0/1/1/1 |
| 6   | NAG  | c     | 1   | 6,2  | -       | 0/6/23/26 | 0/1/1/1 |
| 6   | NAG  | c     | 2   | 6    | -       | 1/6/23/26 | 0/1/1/1 |
| 6   | NAG  | d     | 1   | 6,2  | -       | 0/6/23/26 | 0/1/1/1 |

Continued on next page...

*Continued from previous page...*

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

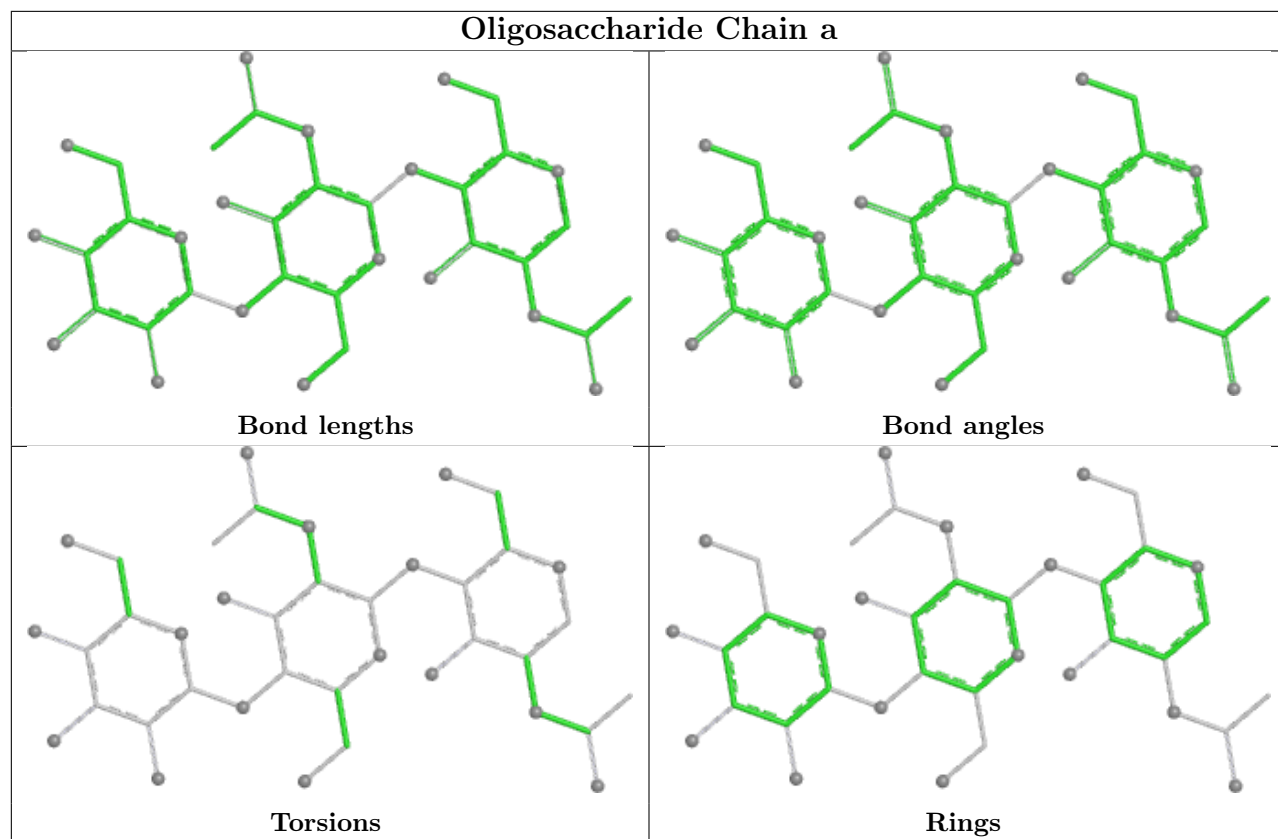
| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 7   | H     | 3   | BMA  | C4-C5-C6-O6 |
| 7   | H     | 3   | BMA  | O5-C5-C6-O6 |
| 7   | G     | 3   | BMA  | C4-C5-C6-O6 |
| 7   | G     | 3   | BMA  | O5-C5-C6-O6 |
| 6   | c     | 2   | NAG  | C1-C2-N2-C7 |

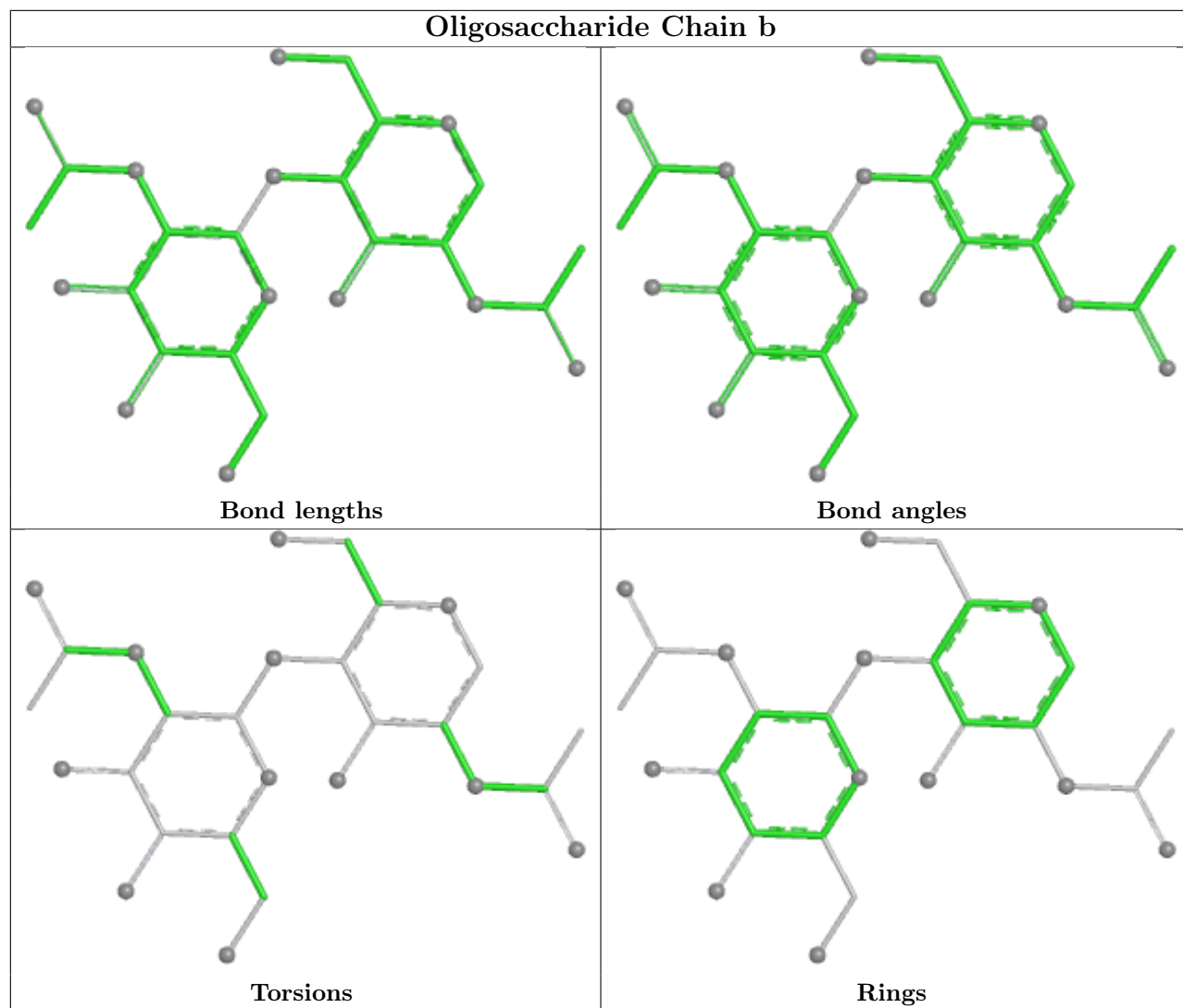
There are no ring outliers.

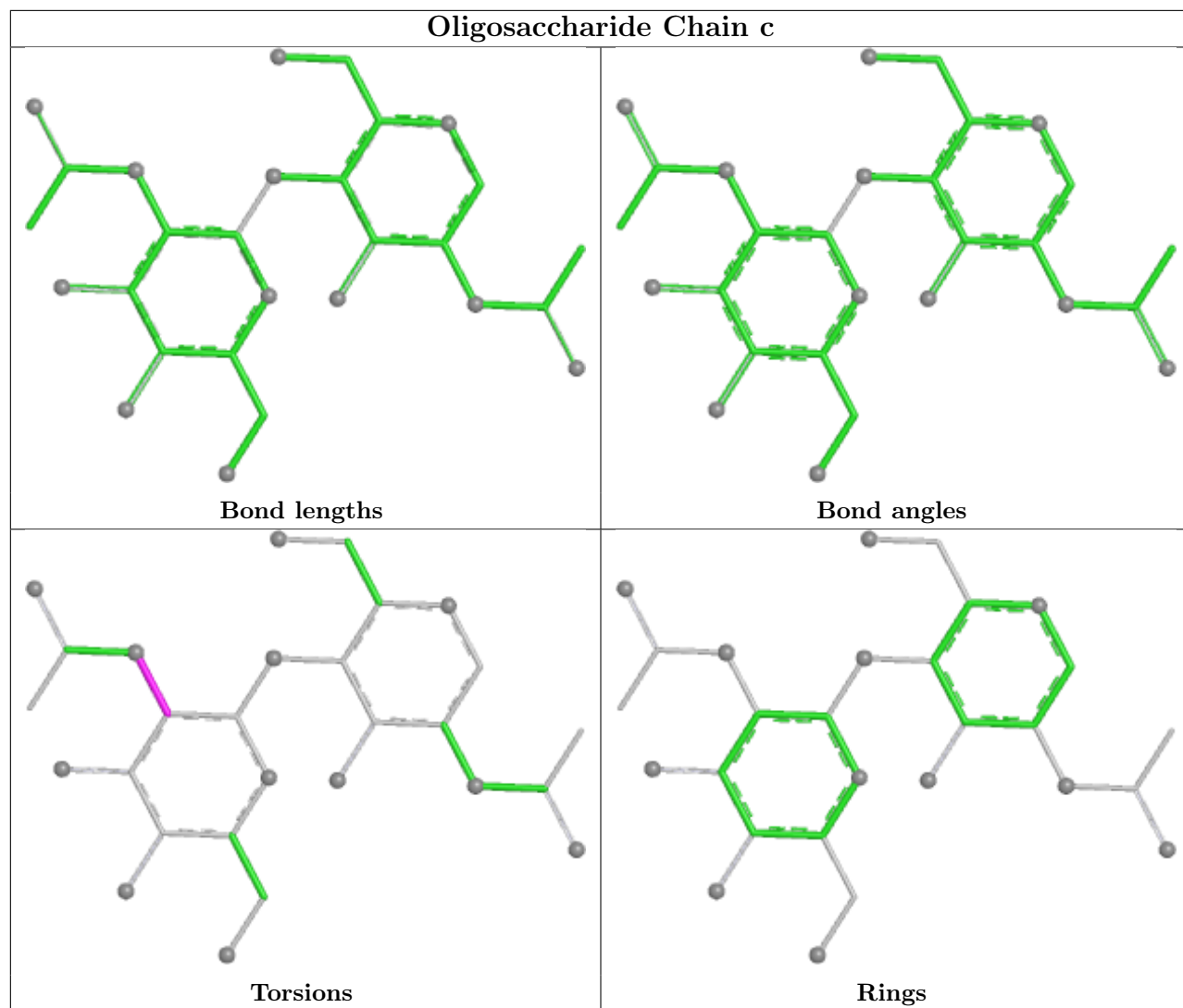
2 monomers are involved in 2 short contacts:

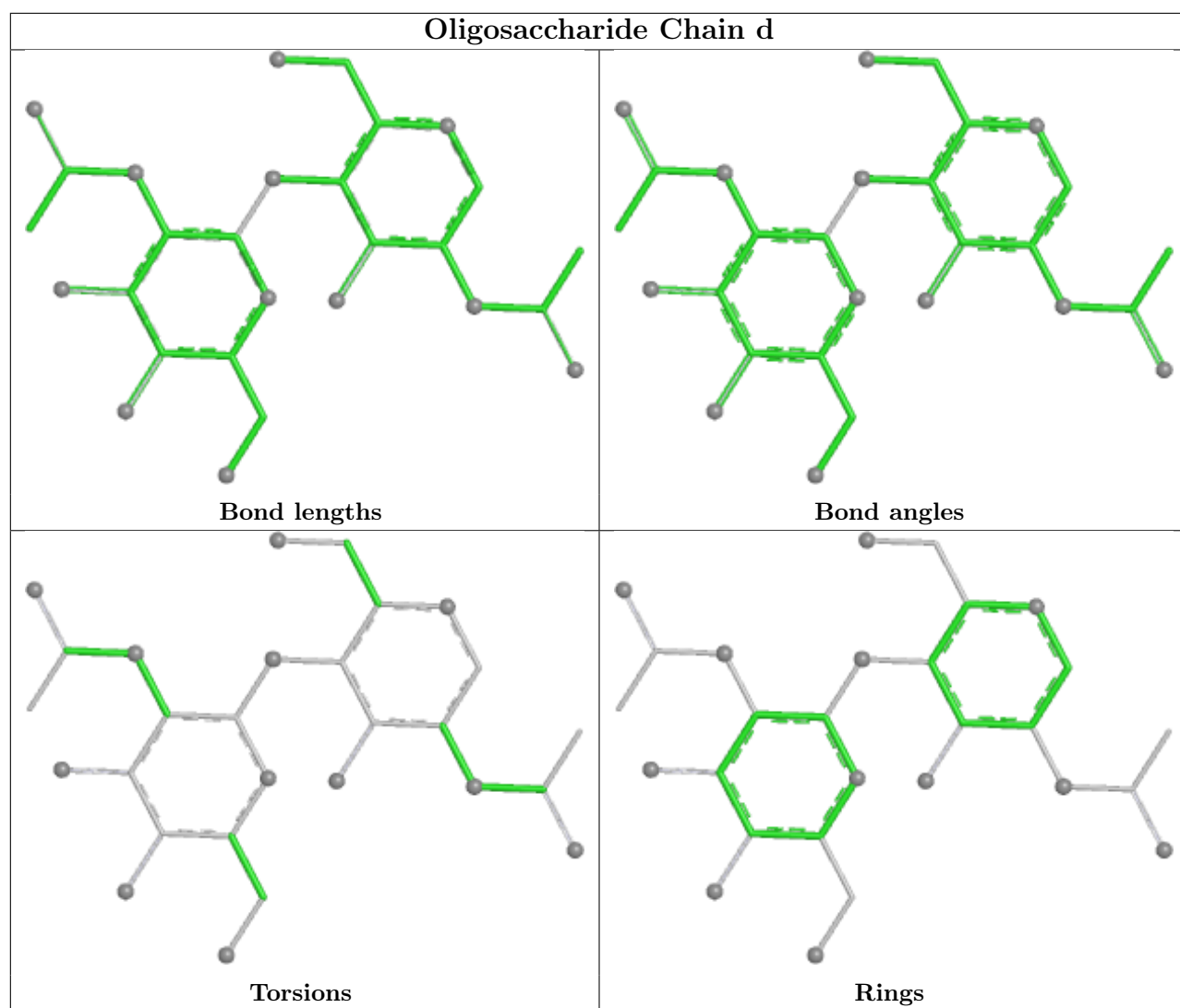
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 7   | F     | 1   | NAG  | 1       | 0            |
| 5   | a     | 2   | NAG  | 1       | 0            |

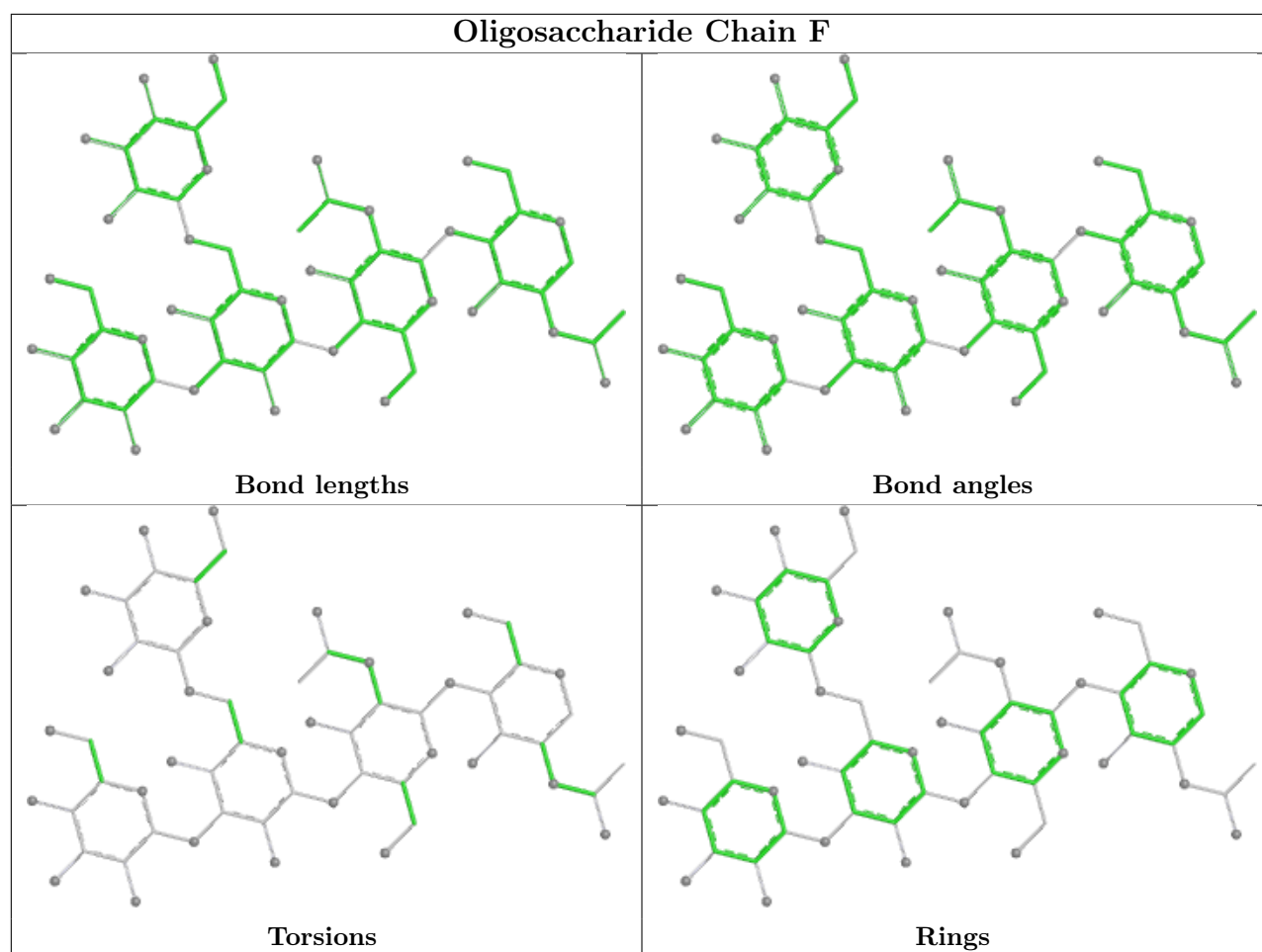
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

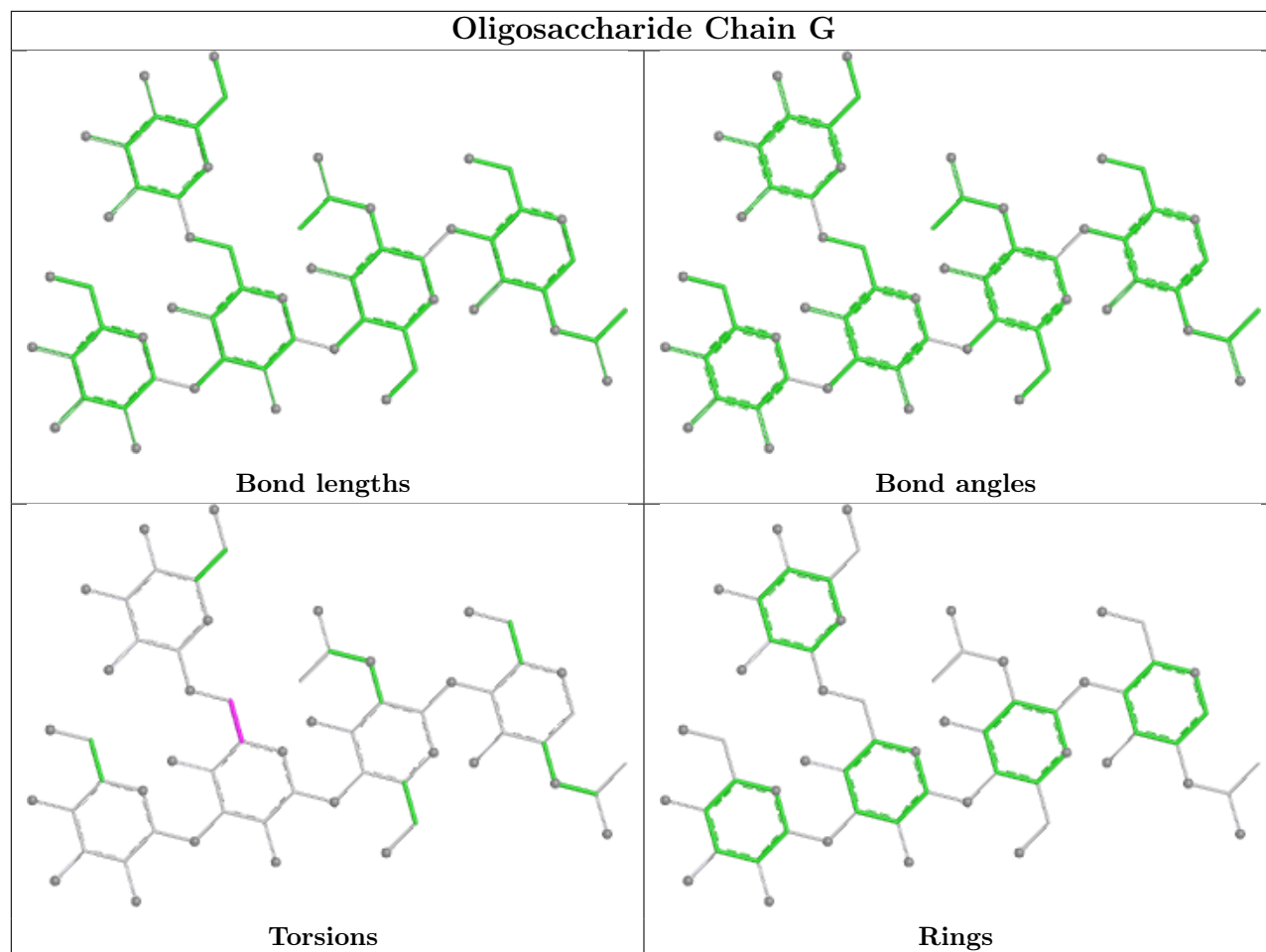


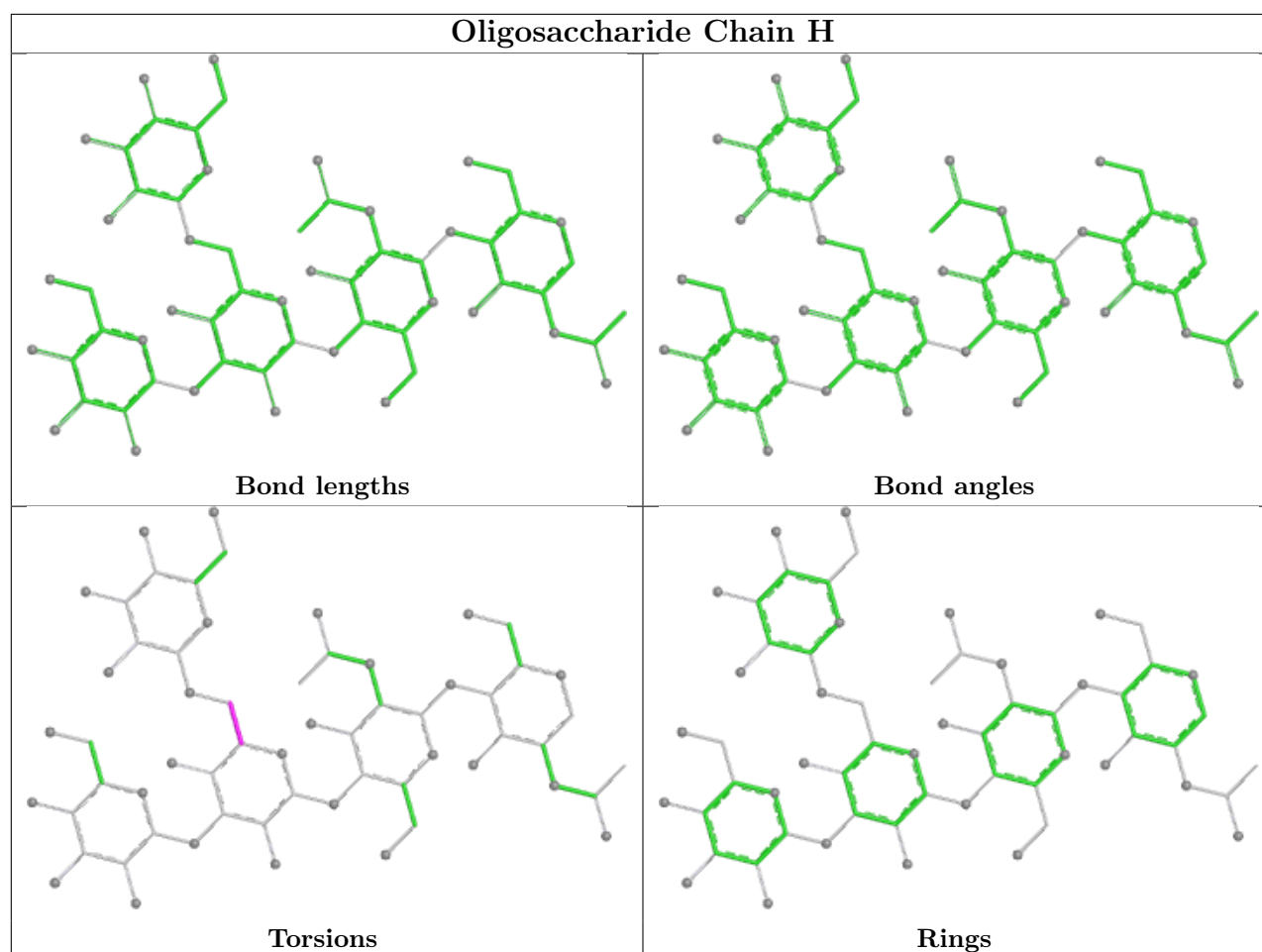












## 5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

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

| Mol | Type | Chain | Res | Link | Bond lengths |      |             | Bond angles |      |             |
|-----|------|-------|-----|------|--------------|------|-------------|-------------|------|-------------|
|     |      |       |     |      | Counts       | RMSZ | $\# Z  > 2$ | Counts      | RMSZ | $\# Z  > 2$ |
| 9   | HSM  | B     | 501 | -    | 8,8,8        | 0.23 | 0           | 9,9,9       | 0.34 | 0           |
| 10  | R16  | B     | 502 | -    | 15,15,15     | 0.12 | 0           | 14,14,14    | 0.11 | 0           |
| 9   | HSM  | C     | 501 | -    | 8,8,8        | 0.24 | 0           | 9,9,9       | 0.33 | 0           |
| 11  | D10  | D     | 501 | -    | 9,9,9        | 0.12 | 0           | 8,8,8       | 0.09 | 0           |
| 8   | NAG  | A     | 601 | 1    | 14,14,15     | 0.23 | 0           | 17,19,21    | 0.45 | 0           |
| 9   | HSM  | D     | 502 | -    | 8,8,8        | 0.24 | 0           | 9,9,9       | 0.33 | 0           |
| 8   | NAG  | E     | 501 | 3    | 14,14,15     | 0.23 | 0           | 17,19,21    | 0.45 | 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   |
|-----|------|-------|-----|------|---------|------------|---------|
| 9   | HSM  | B     | 501 | -    | -       | 0/3/3/3    | 0/1/1/1 |
| 10  | R16  | B     | 502 | -    | -       | 0/13/13/13 | -       |
| 9   | HSM  | C     | 501 | -    | -       | 2/3/3/3    | 0/1/1/1 |
| 11  | D10  | D     | 501 | -    | -       | 0/7/7/7    | -       |
| 8   | NAG  | A     | 601 | 1    | -       | 1/6/23/26  | 0/1/1/1 |
| 9   | HSM  | D     | 502 | -    | -       | 2/3/3/3    | 0/1/1/1 |
| 8   | NAG  | E     | 501 | 3    | -       | 0/6/23/26  | 0/1/1/1 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms        |
|-----|-------|-----|------|--------------|
| 9   | C     | 501 | HSM  | CA-CB-CG-ND1 |
| 9   | C     | 501 | HSM  | CA-CB-CG-CD2 |
| 9   | D     | 502 | HSM  | CA-CB-CG-ND1 |
| 9   | D     | 502 | HSM  | CA-CB-CG-CD2 |
| 8   | A     | 601 | NAG  | O5-C5-C6-O6  |

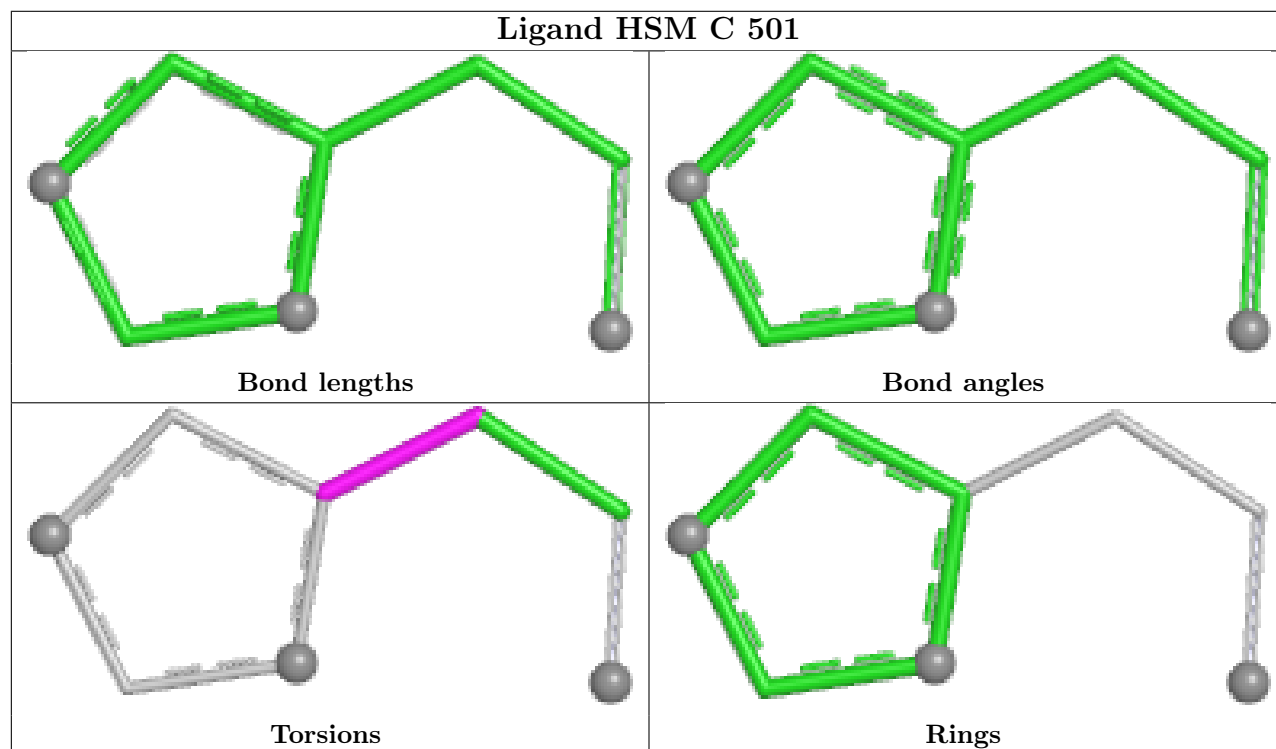
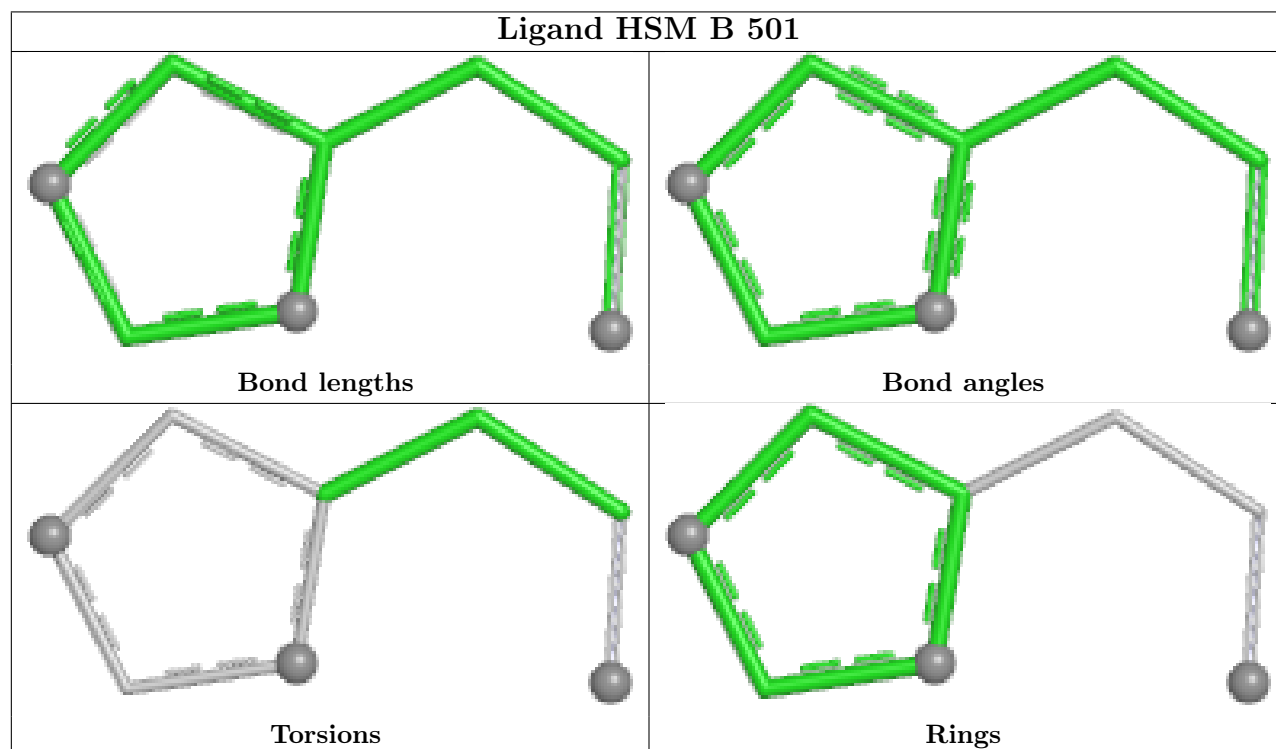
There are no ring outliers.

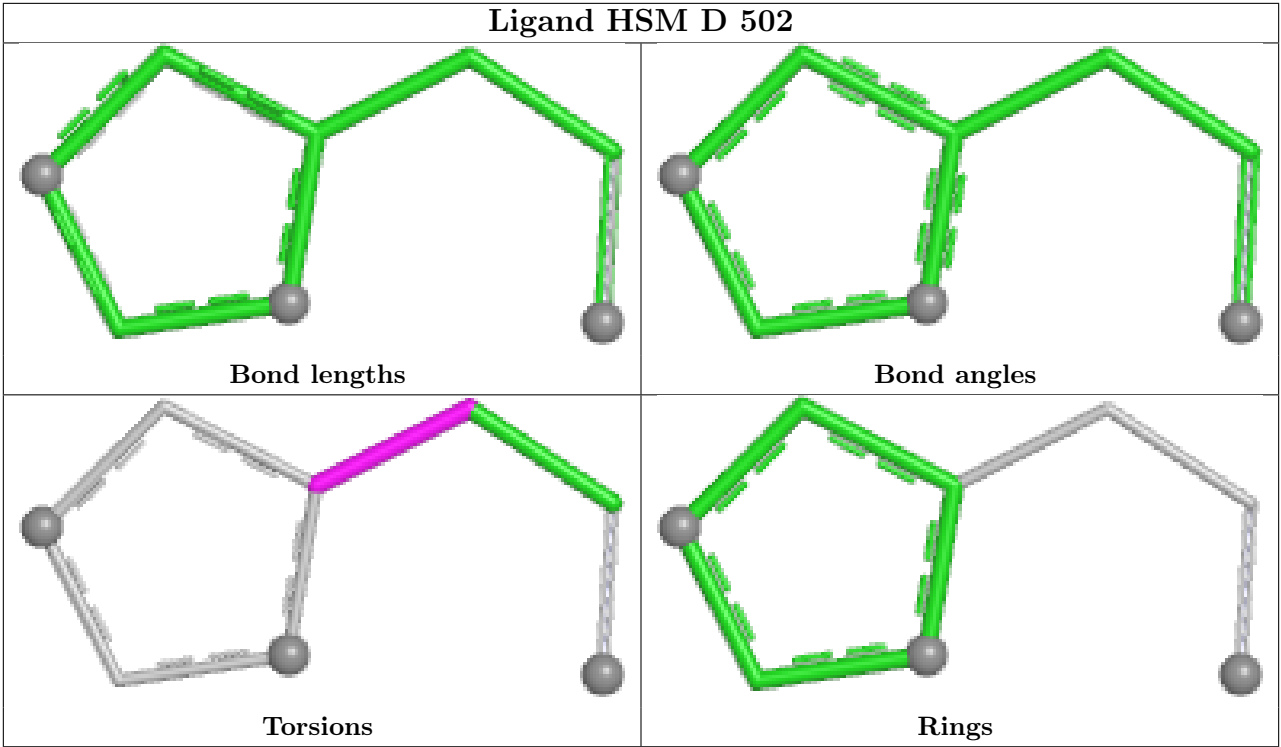
4 monomers are involved in 4 short contacts:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 9   | B     | 501 | HSM  | 1       | 0            |
| 10  | B     | 502 | R16  | 1       | 0            |
| 11  | D     | 501 | D10  | 1       | 0            |
| 8   | E     | 501 | NAG  | 1       | 0            |

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

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





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 4   | L     | 1                |
| 4   | M     | 1                |

All chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | L     | 13:GLN    | C      | 403:GLY   | N      | 7.34         |
| 1     | M     | 13:GLN    | C      | 403:GLY   | N      | 7.34         |

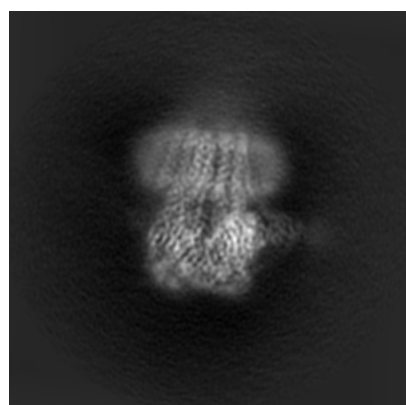
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14071. These allow visual inspection of the internal detail of the map and identification of artifacts.

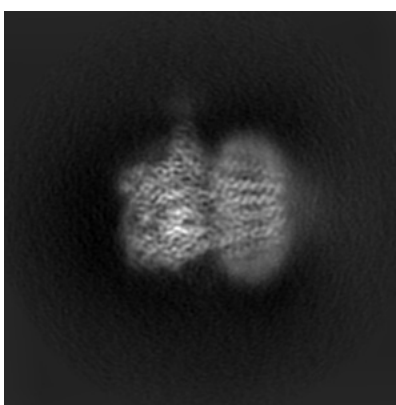
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

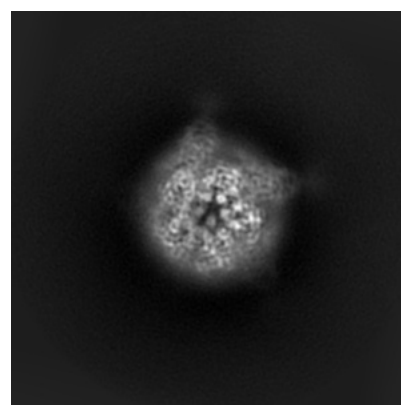
#### 6.1.1 Primary map



X



Y

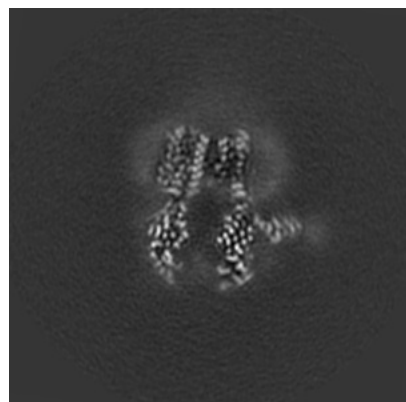


Z

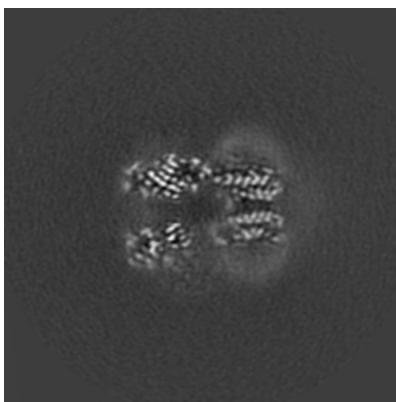
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

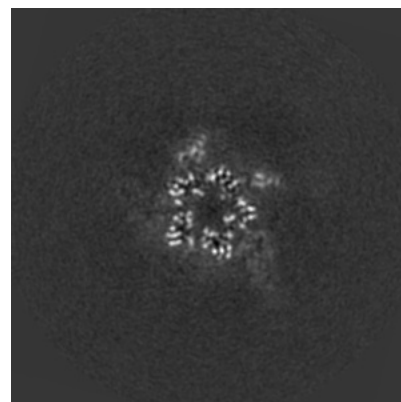
#### 6.2.1 Primary map



X Index: 145



Y Index: 145

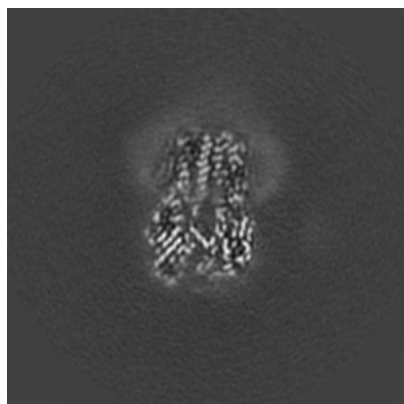


Z Index: 145

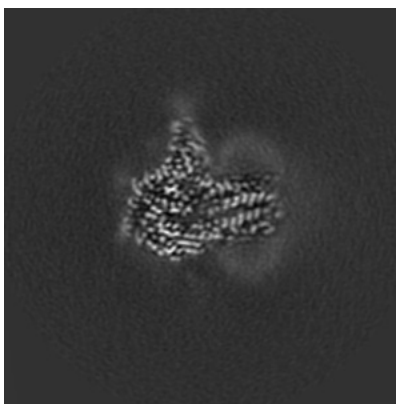
The images above show central slices of the map in three orthogonal directions.

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

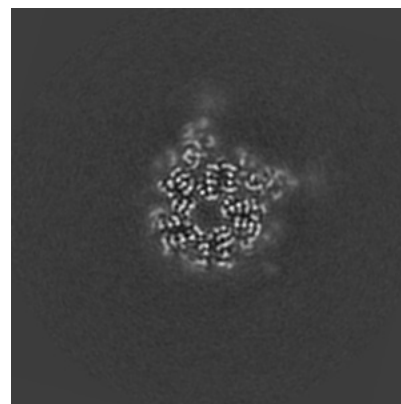
### 6.3.1 Primary map



X Index: 155



Y Index: 163

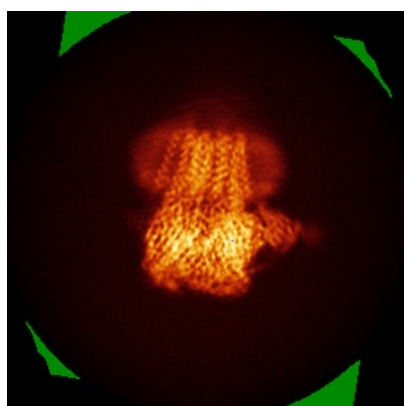


Z Index: 122

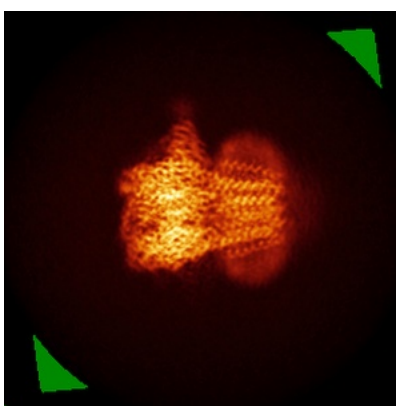
The images above show the largest variance slices of the map in three orthogonal directions.

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

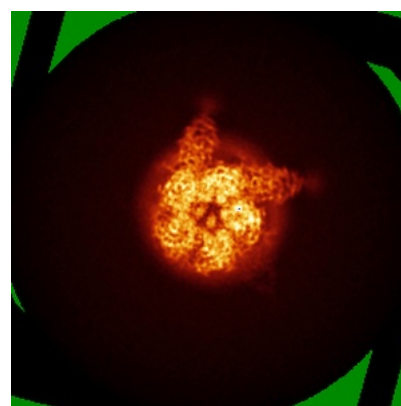
### 6.4.1 Primary map



X



Y



Z

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 0.008. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

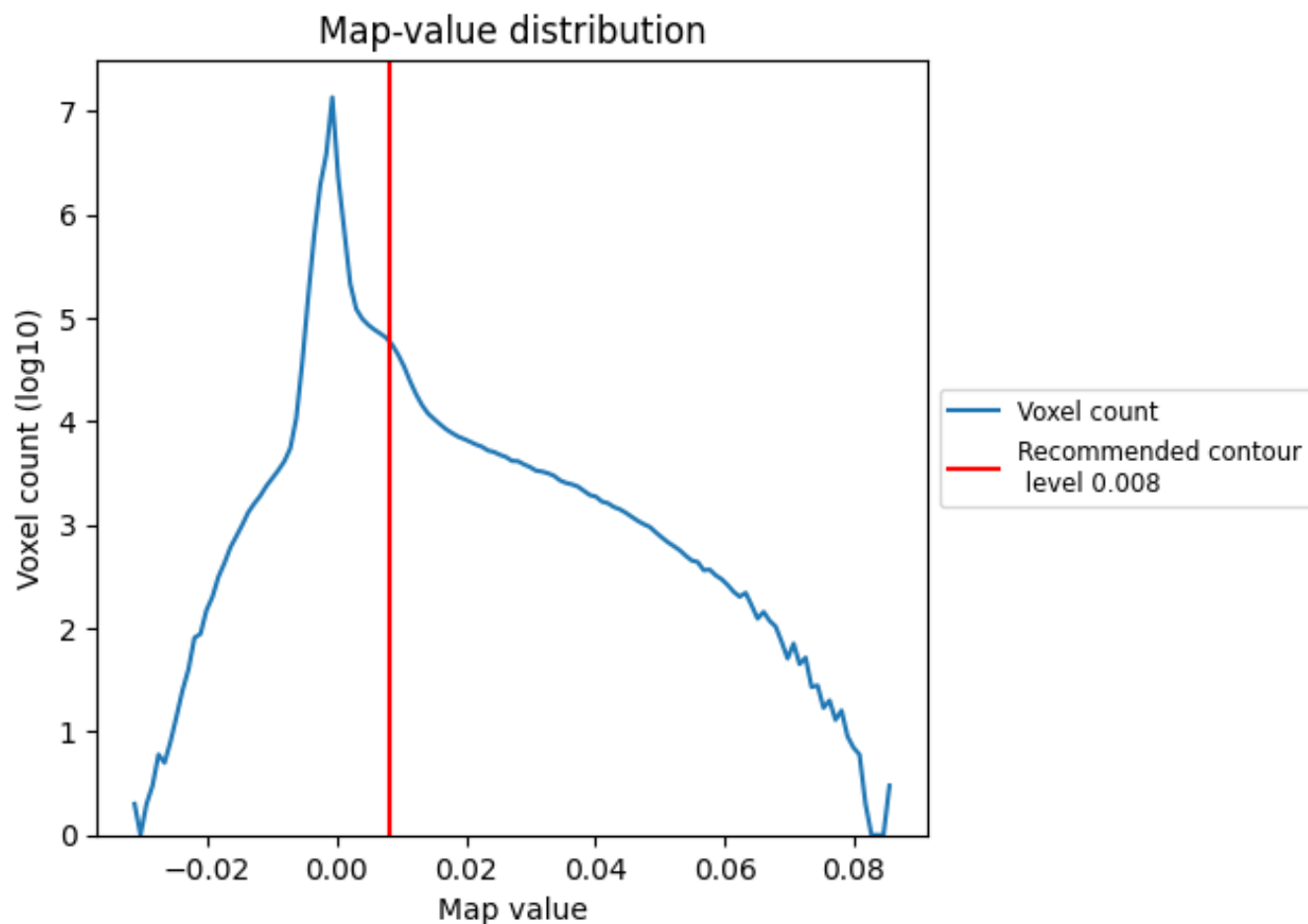
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

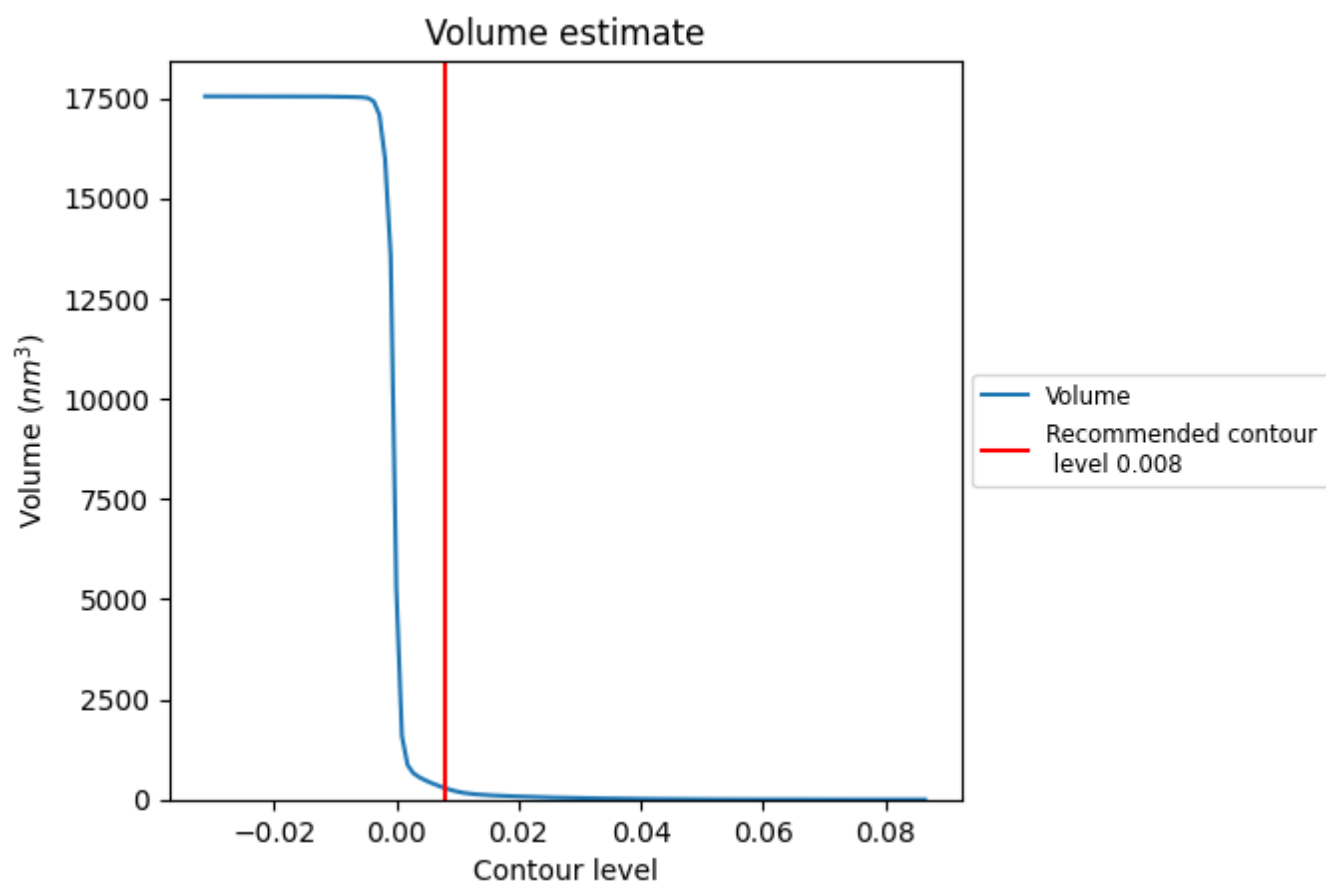
This section contains the results of statistical analysis of the map.

### 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.

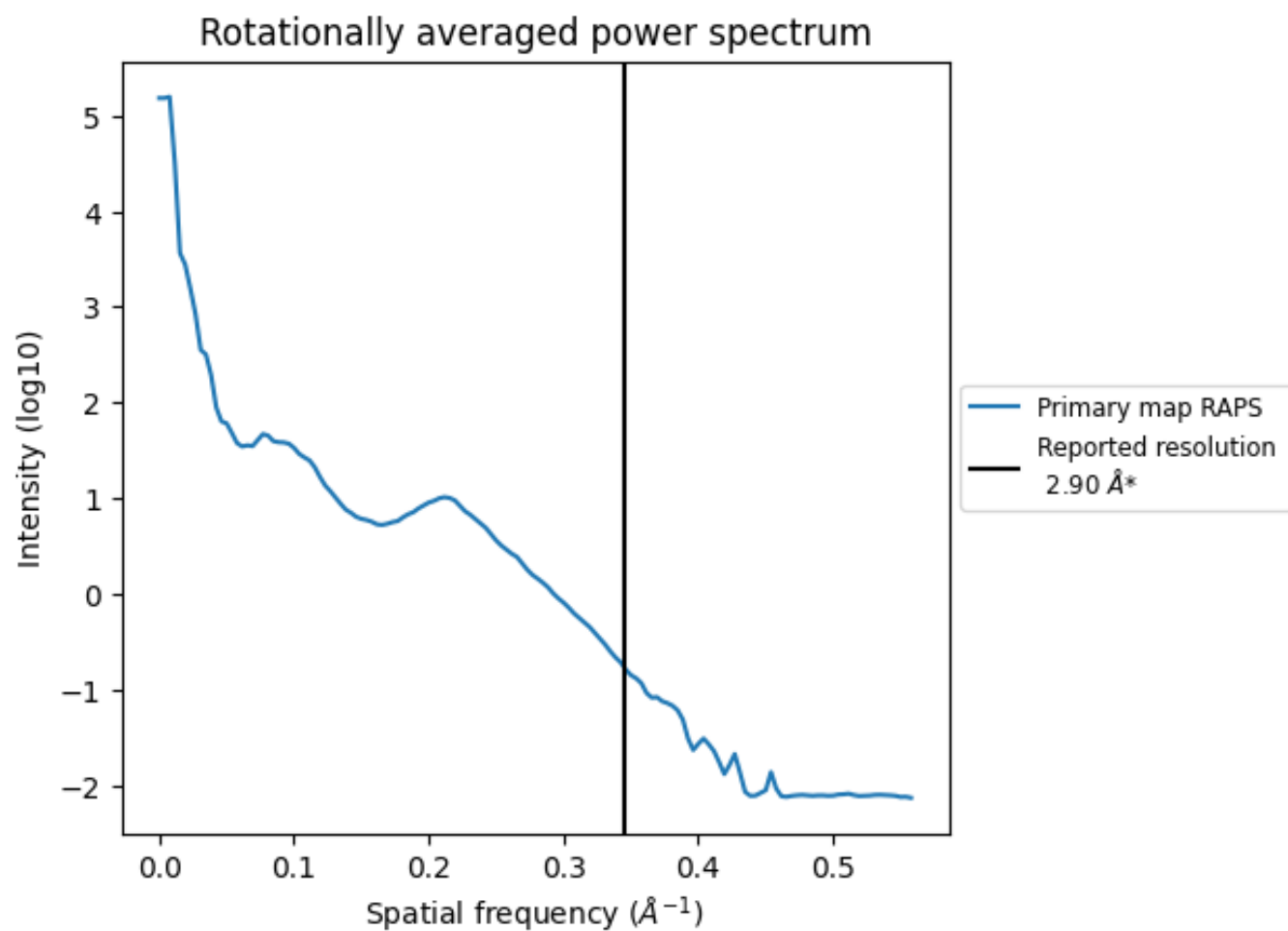
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 283 nm<sup>3</sup>; this corresponds to an approximate mass of 256 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 0.345  $\text{\AA}^{-1}$

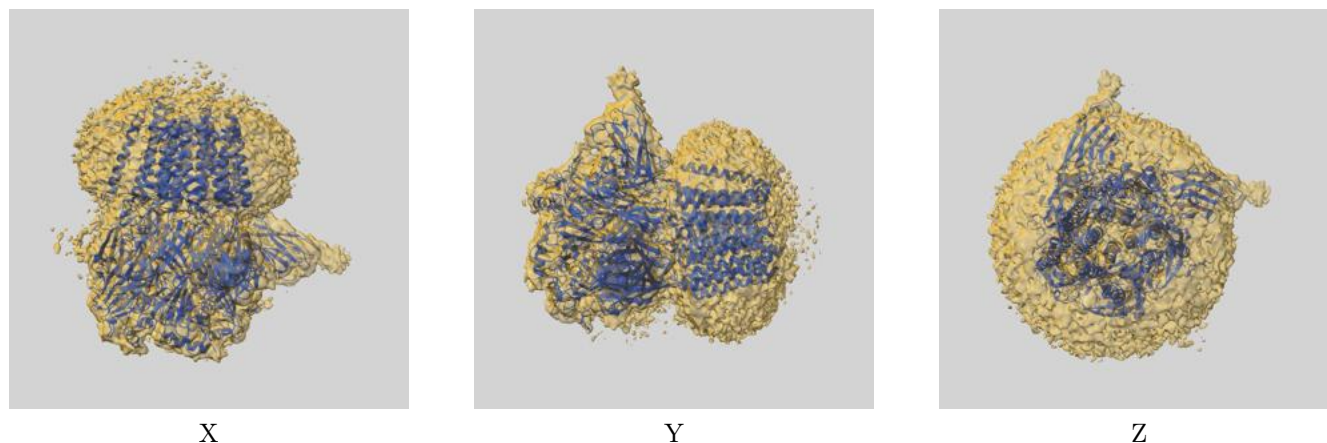
## 8 Fourier-Shell correlation

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

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

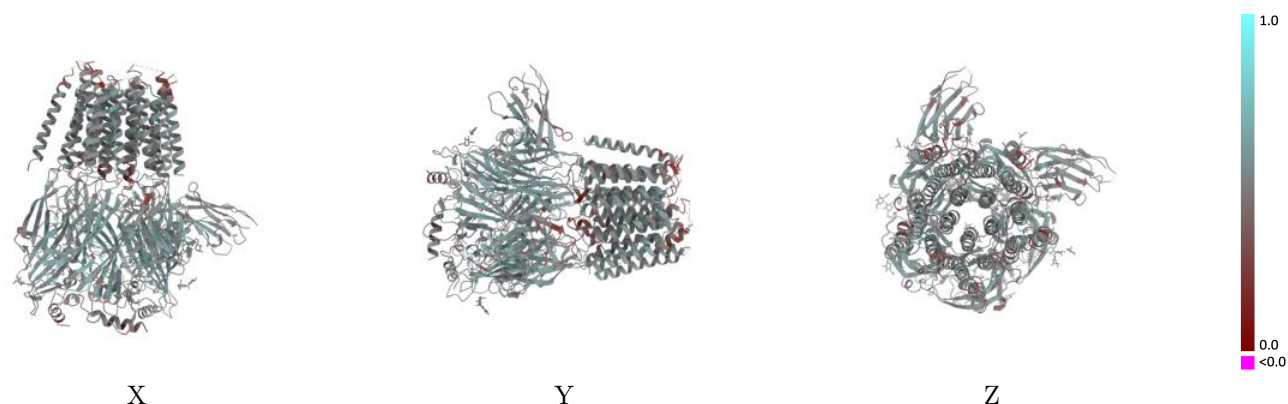
This section contains information regarding the fit between EMDB map EMD-14071 and PDB model 7QN9. Per-residue inclusion information can be found in section [3](#) on page [9](#).

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



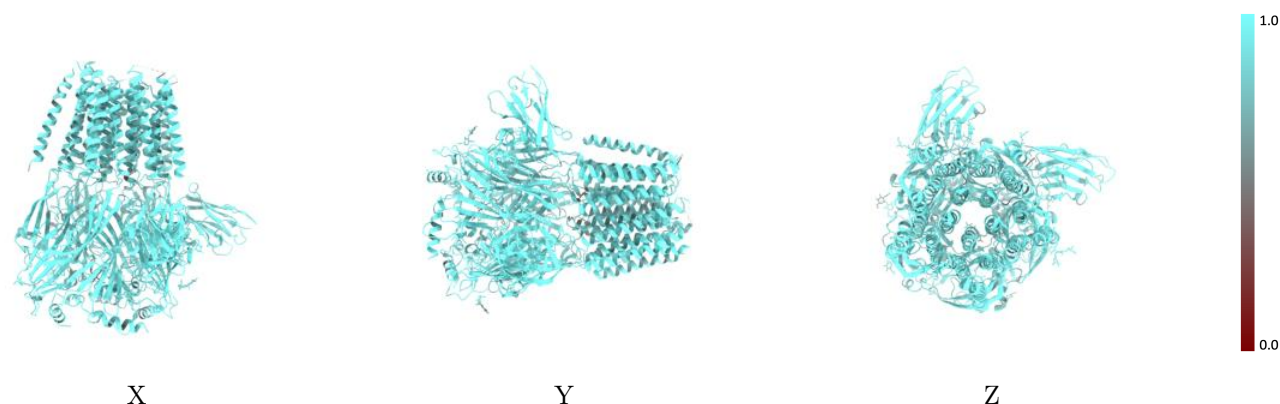
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



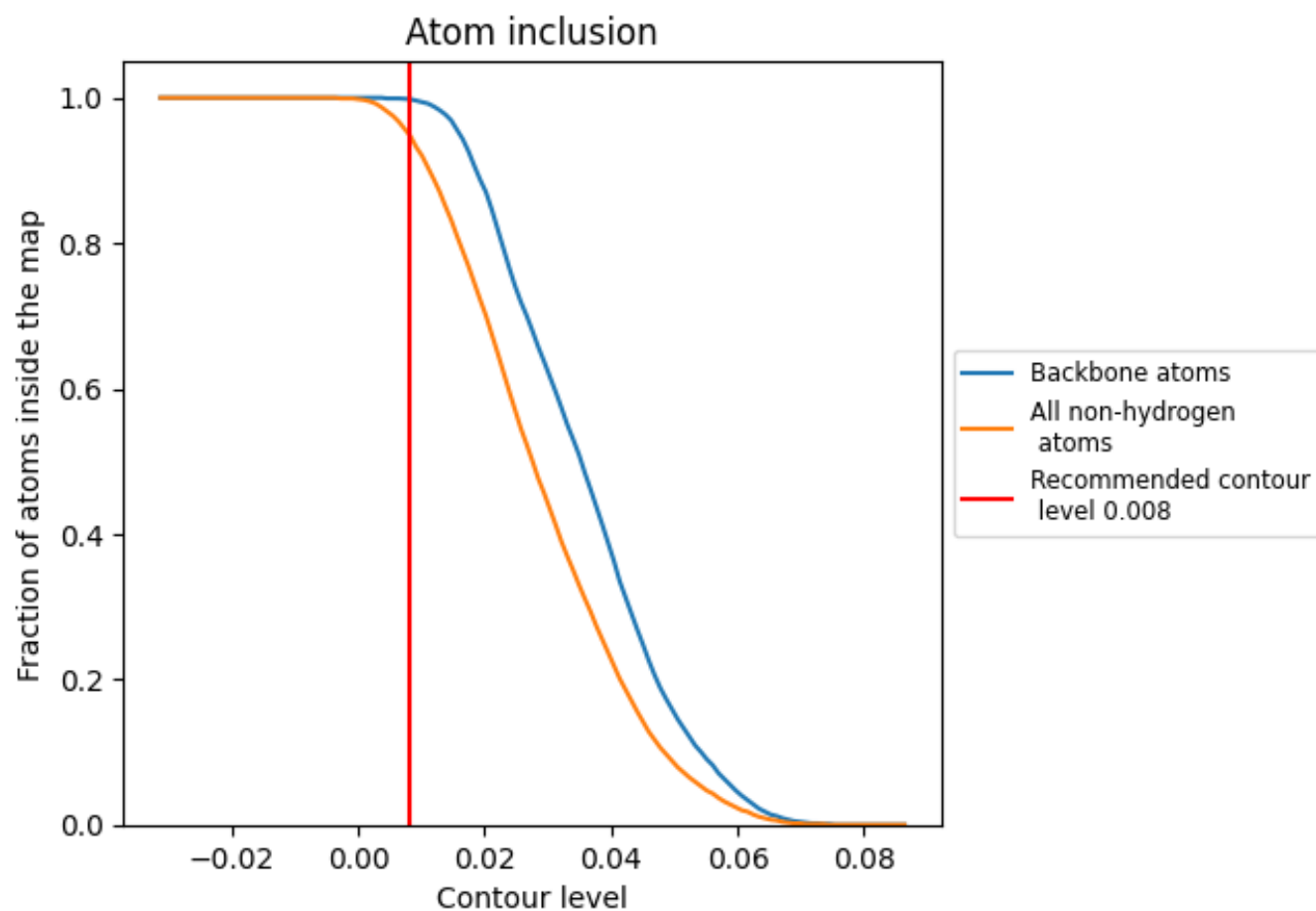
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).

## 9.4 Atom inclusion ⓘ



At the recommended contour level, 100% of all backbone atoms, 95% 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 (0.008) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion     | Q-score            |
|-------|--------------------|--------------------|
| All   | <div></div> 0.9500 | <div></div> 0.5050 |
| A     | <div></div> 0.9440 | <div></div> 0.5010 |
| B     | <div></div> 0.9540 | <div></div> 0.5130 |
| C     | <div></div> 0.9550 | <div></div> 0.5200 |
| D     | <div></div> 0.9460 | <div></div> 0.5060 |
| E     | <div></div> 0.9450 | <div></div> 0.5030 |
| F     | <div></div> 1.0000 | <div></div> 0.4980 |
| G     | <div></div> 0.9840 | <div></div> 0.5020 |
| H     | <div></div> 0.9670 | <div></div> 0.4870 |
| L     | <div></div> 0.9630 | <div></div> 0.4900 |
| M     | <div></div> 0.9660 | <div></div> 0.4810 |
| a     | <div></div> 0.5640 | <div></div> 0.3150 |
| b     | <div></div> 0.8210 | <div></div> 0.4180 |
| c     | <div></div> 0.8930 | <div></div> 0.4590 |
| d     | <div></div> 0.7860 | <div></div> 0.3930 |

