



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:19 AM UTC

PDB ID : 6JZ4 / pdb\_00006jz4  
Title : b-glucuronidase from Ruminococcus gnavus in complex with D-glucaro-d-lactam  
Authors : Dashnyam, P.; Lin, H.Y.  
Deposited on : 2019-04-30  
Resolution : 1.71 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

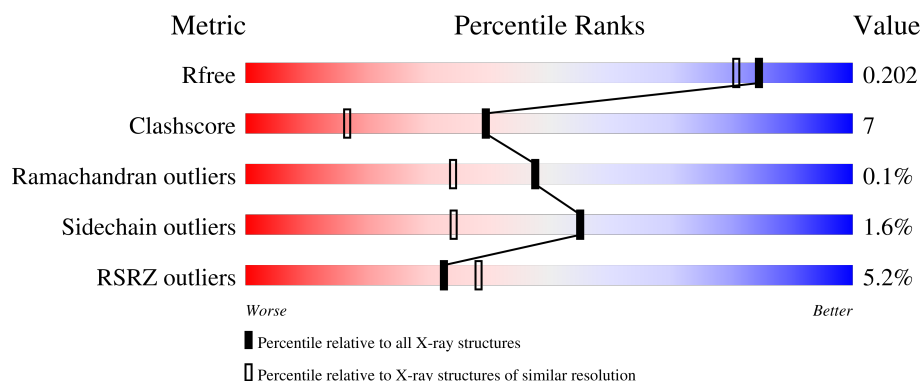
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

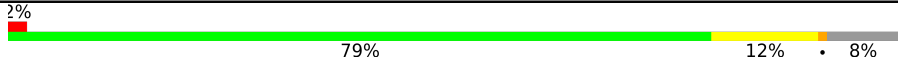
The reported resolution of this entry is 1.71 Å.

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) | Similar resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-------------------------------------------------------|
| $R_{free}$            | 180053                      | 1039 (1.72-1.72)                                      |
| Clashscore            | 190562                      | 1049 (1.72-1.72)                                      |
| Ramachandran outliers | 187476                      | 1041 (1.72-1.72)                                      |
| Sidechain outliers    | 187428                      | 1041 (1.72-1.72)                                      |
| RSRZ outliers         | 180081                      | 1039 (1.72-1.72)                                      |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | A     | 627    |  |
| 1   | B     | 627    |  |

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10256 atoms, of which 30 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Beta-glucuronidase.

| Mol | Chain | Residues | Atoms |      |     |     |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 1   | A     | 576      | Total | C    | N   | O   | S  | 0       | 0       | 0     |
|     |       |          | 4717  | 3042 | 767 | 885 | 23 |         |         |       |
| 1   | B     | 577      | Total | C    | N   | O   | S  | 0       | 0       | 0     |
|     |       |          | 4725  | 3047 | 768 | 886 | 24 |         |         |       |

There are 48 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| A     | -23     | MET      | -      | initiating methionine | UNP Q6W7J7 |
| A     | -22     | HIS      | -      | expression tag        | UNP Q6W7J7 |
| A     | -21     | HIS      | -      | expression tag        | UNP Q6W7J7 |
| A     | -20     | HIS      | -      | expression tag        | UNP Q6W7J7 |
| A     | -19     | HIS      | -      | expression tag        | UNP Q6W7J7 |
| A     | -18     | HIS      | -      | expression tag        | UNP Q6W7J7 |
| A     | -17     | HIS      | -      | expression tag        | UNP Q6W7J7 |
| A     | -16     | SER      | -      | expression tag        | UNP Q6W7J7 |
| A     | -15     | SER      | -      | expression tag        | UNP Q6W7J7 |
| A     | -14     | GLY      | -      | expression tag        | UNP Q6W7J7 |
| A     | -13     | VAL      | -      | expression tag        | UNP Q6W7J7 |
| A     | -12     | ASP      | -      | expression tag        | UNP Q6W7J7 |
| A     | -11     | LEU      | -      | expression tag        | UNP Q6W7J7 |
| A     | -10     | GLY      | -      | expression tag        | UNP Q6W7J7 |
| A     | -9      | THR      | -      | expression tag        | UNP Q6W7J7 |
| A     | -8      | GLU      | -      | expression tag        | UNP Q6W7J7 |
| A     | -7      | ASN      | -      | expression tag        | UNP Q6W7J7 |
| A     | -6      | LEU      | -      | expression tag        | UNP Q6W7J7 |
| A     | -5      | TYR      | -      | expression tag        | UNP Q6W7J7 |
| A     | -4      | PHE      | -      | expression tag        | UNP Q6W7J7 |
| A     | -3      | GLN      | -      | expression tag        | UNP Q6W7J7 |
| A     | -2      | SER      | -      | expression tag        | UNP Q6W7J7 |
| A     | -1      | ASN      | -      | expression tag        | UNP Q6W7J7 |
| A     | 0       | GLY      | -      | expression tag        | UNP Q6W7J7 |
| B     | -23     | MET      | -      | initiating methionine | UNP Q6W7J7 |

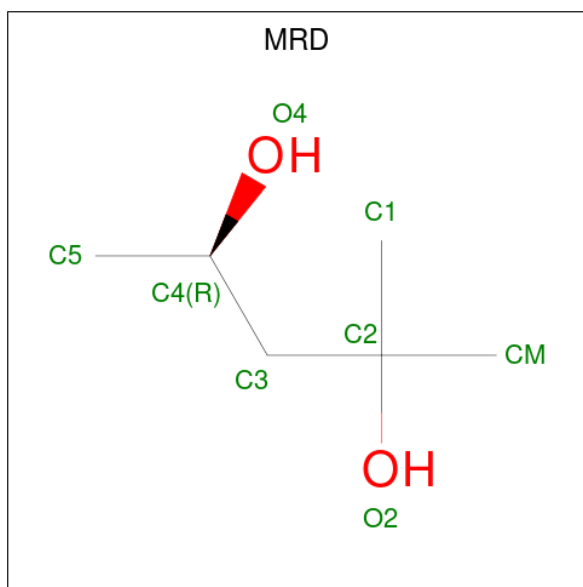
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| Chain | Residue | Modelled | Actual | Comment        | Reference  |
|-------|---------|----------|--------|----------------|------------|
| B     | -22     | HIS      | -      | expression tag | UNP Q6W7J7 |
| B     | -21     | HIS      | -      | expression tag | UNP Q6W7J7 |
| B     | -20     | HIS      | -      | expression tag | UNP Q6W7J7 |
| B     | -19     | HIS      | -      | expression tag | UNP Q6W7J7 |
| B     | -18     | HIS      | -      | expression tag | UNP Q6W7J7 |
| B     | -17     | HIS      | -      | expression tag | UNP Q6W7J7 |
| B     | -16     | SER      | -      | expression tag | UNP Q6W7J7 |
| B     | -15     | SER      | -      | expression tag | UNP Q6W7J7 |
| B     | -14     | GLY      | -      | expression tag | UNP Q6W7J7 |
| B     | -13     | VAL      | -      | expression tag | UNP Q6W7J7 |
| B     | -12     | ASP      | -      | expression tag | UNP Q6W7J7 |
| B     | -11     | LEU      | -      | expression tag | UNP Q6W7J7 |
| B     | -10     | GLY      | -      | expression tag | UNP Q6W7J7 |
| B     | -9      | THR      | -      | expression tag | UNP Q6W7J7 |
| B     | -8      | GLU      | -      | expression tag | UNP Q6W7J7 |
| B     | -7      | ASN      | -      | expression tag | UNP Q6W7J7 |
| B     | -6      | LEU      | -      | expression tag | UNP Q6W7J7 |
| B     | -5      | TYR      | -      | expression tag | UNP Q6W7J7 |
| B     | -4      | PHE      | -      | expression tag | UNP Q6W7J7 |
| B     | -3      | GLN      | -      | expression tag | UNP Q6W7J7 |
| B     | -2      | SER      | -      | expression tag | UNP Q6W7J7 |
| B     | -1      | ASN      | -      | expression tag | UNP Q6W7J7 |
| B     | 0       | GLY      | -      | expression tag | UNP Q6W7J7 |

- 
- Chemical structure of EVA (Ethylvinylacetate) showing stereochemistry and labels:
- CA(S)**: Chiral center at C1 (top-left) with a wedged bond to the vinyl group.
  - CB(R)**: Chiral center at C2 (bottom-left) with a dashed bond to the hydroxyl group.
  - CD1(R)**: Chiral center at C3 (bottom-right) with a wedged bond to the hydroxyl group.
  - CG(S)**: Chiral center at C4 (top-right) with a dashed bond to the hydroxyl group.
  - CAE**: Chiral center at C5 (top-right) with a wedged bond to the vinyl group.
  - OG**: Hydroxyl group at C2 (bottom-left).
  - OH**: Hydroxyl group at C3 (bottom-right).
  - OH**: Hydroxyl group at C4 (top-right).
  - OH**: Hydroxyl group at C5 (top-right).
  - OH**: Hydroxyl group at C6 (bottom-left).
  - OH**: Hydroxyl group at C7 (top-left).
  - OH**: Hydroxyl group at C8 (top-right).
  - OH**: Hydroxyl group at C9 (bottom-right).
  - OH**: Hydroxyl group at C10 (bottom-left).
  - OH**: Hydroxyl group at C11 (top-right).
  - OH**: Hydroxyl group at C12 (top-left).
  - OH**: Hydroxyl group at C13 (bottom-right).
  - OH**: Hydroxyl group at C14 (bottom-left).
  - OH**: Hydroxyl group at C15 (top-right).
  - OH**: Hydroxyl group at C16 (top-left).
  - OH**: Hydroxyl group at C17 (bottom-right).
  - OH**: Hydroxyl group at C18 (bottom-left).
  - OH**: Hydroxyl group at C19 (top-right).
  - OH**: Hydroxyl group at C20 (top-left).
  - OH**: Hydroxyl group at C21 (bottom-right).
  - OH**: Hydroxyl group at C22 (bottom-left).
  - OH**: Hydroxyl group at C23 (top-right).
  - OH**: Hydroxyl group at C24 (top-left).
  - OH**: Hydroxyl group at C25 (bottom-right).
  - OH**: Hydroxyl group at C26 (bottom-left).
  - OH**: Hydroxyl group at C27 (top-right).
  - OH**: Hydroxyl group at C28 (top-left).
  - OH**: Hydroxyl group at C29 (bottom-right).
  - OH**: Hydroxyl group at C30 (bottom-left).
  - OH**: Hydroxyl group at C31 (top-right).
  - OH**: Hydroxyl group at C32 (top-left).
  - OH**: Hydroxyl group at C33 (bottom-right).
  - OH**: Hydroxyl group at C34 (bottom-left).
  - OH**: Hydroxyl group at C35 (top-right).
  - OH**: Hydroxyl group at C36 (top-left).
  - OH**: Hydroxyl group at C37 (bottom-right).
  - OH**: Hydroxyl group at C38 (bottom-left).
  - OH**: Hydroxyl group at C39 (top-right).
  - OH**: Hydroxyl group at C40 (top-left).
  - OH**: Hydroxyl group at C41 (bottom-right).
  - OH**: Hydroxyl group at C42 (bottom-left).
  - OH**: Hydroxyl group at C43 (top-right).
  - OH**: Hydroxyl group at C44 (top-left).
  - OH**: Hydroxyl group at C45 (bottom-right).
  - OH**: Hydroxyl group at C46 (bottom-left).
  - OH**: Hydroxyl group at C47 (top-right).
  - OH**: Hydroxyl group at C48 (top-left).
  - OH**: Hydroxyl group at C49 (bottom-right).
  - OH**: Hydroxyl group at C50 (bottom-left).
  - OH**: Hydroxyl group at C51 (top-right).
  - OH**: Hydroxyl group at C52 (top-left).
  - OH**: Hydroxyl group at C53 (bottom-right).
  - OH**: Hydroxyl group at C54 (bottom-left).
  - OH**: Hydroxyl group at C55 (top-right).
  - OH**: Hydroxyl group at C56 (top-left).
  - OH**: Hydroxyl group at C57 (bottom-right).
  - OH**: Hydroxyl group at C58 (bottom-left).
  - OH**: Hydroxyl group at C59 (top-right).
  - OH**: Hydroxyl group at C60 (top-left).
  - OH**: Hydroxyl group at C61 (bottom-right).
  - OH**: Hydroxyl group at C62 (bottom-left).
  - OH**: Hydroxyl group at C63 (top-right).
  - OH**: Hydroxyl group at C64 (top-left).
  - OH**: Hydroxyl group at C65 (bottom-right).
  - OH**: Hydroxyl group at C66 (bottom-left).
  - OH**: Hydroxyl group at C67 (top-right).
  - OH**: Hydroxyl group at C68 (top-left).
  - OH**: Hydroxyl group at C69 (bottom-right).
  - OH**: Hydroxyl group at C70 (bottom-left).
  - OH**: Hydroxyl group at C71 (top-right).
  - OH**: Hydroxyl group at C72 (top-left).
  - OH**: Hydroxyl group at C73 (bottom-right).
  - OH**: Hydroxyl group at C74 (bottom-left).
  - OH**: Hydroxyl group at C75 (top-right).
  - OH**: Hydroxyl group at C76 (top-left).
  - OH**: Hydroxyl group at C77 (bottom-right).
  - OH**: Hydroxyl group at C78 (bottom-left).
  - OH**: Hydroxyl group at C79 (top-right).
  - OH**: Hydroxyl group at C80 (top-left).
  - OH**: Hydroxyl group at C81 (bottom-right).
  - OH**: Hydroxyl group at C82 (bottom-left).
  - OH**: Hydroxyl group at C83 (top-right).
  - OH**: Hydroxyl group at C84 (top-left).
  - OH**: Hydroxyl group at C85 (bottom-right).
  - OH**: Hydroxyl group at C86 (bottom-left).
  - OH**: Hydroxyl group at C87 (top-right).
  - OH**: Hydroxyl group at C88 (top-left).
  - OH**: Hydroxyl group at C89 (bottom-right).
  - OH**: Hydroxyl group at C90 (bottom-left).
  - OH**: Hydroxyl group at C91 (top-right).
  - OH**: Hydroxyl group at C92 (top-left).
  - OH**: Hydroxyl group at C93 (bottom-right).
  - OH**: Hydroxyl group at C94 (bottom-left).
  - OH**: Hydroxyl group at C95 (top-right).
  - OH**: Hydroxyl group at C96 (top-left).
  - OH**: Hydroxyl group at C97 (bottom-right).
  - OH**: Hydroxyl group at C98 (bottom-left).
  - OH**: Hydroxyl group at C99 (top-right).
  - OH**: Hydroxyl group at C100 (top-left).

| Mol | Chain | Residues | Atoms |   |   |   |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---|---|---|---------|---------|
| 2   | A     | 1        | Total | C | H | N | O | 0       | 0       |
|     |       |          | 21    | 6 | 8 | 1 | 6 |         |         |
| 2   | B     | 1        | Total | C | H | N | O | 0       | 0       |
|     |       |          | 21    | 6 | 8 | 1 | 6 |         |         |

- Molecule 3 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



| Mol | Chain | Residues | Atoms |   |    |   | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|----|---|---------|---------|
| 3   | A     | 1        | Total | C | H  | O | 0       | 0       |
|     |       |          | 22    | 6 | 14 | 2 |         |         |

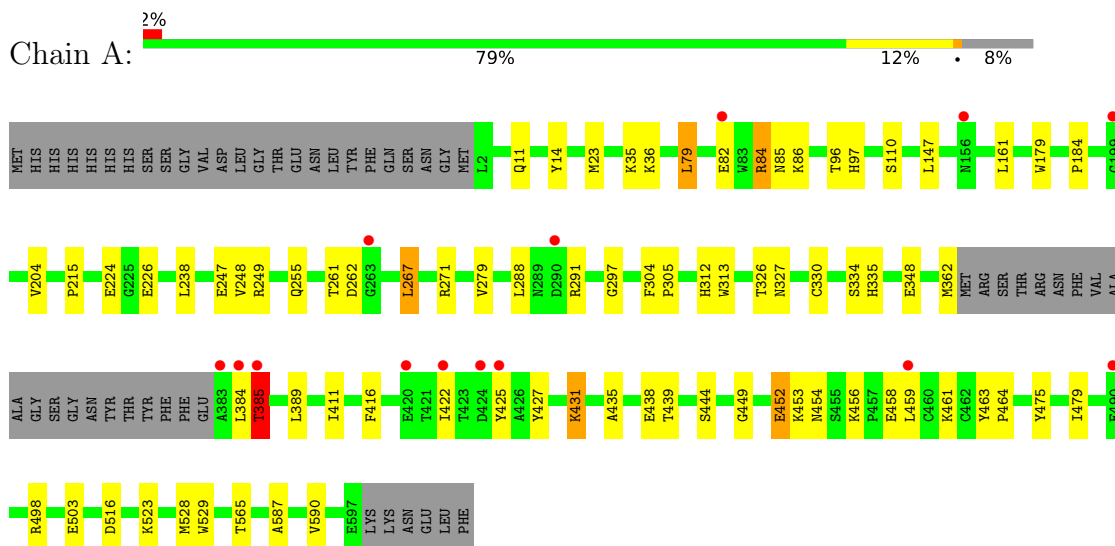
- Molecule 4 is water.

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 4   | A     | 403      | Total | O   | 0       | 0       |
|     |       |          | 403   | 403 |         |         |
| 4   | B     | 347      | Total | O   | 0       | 0       |
|     |       |          | 347   | 347 |         |         |

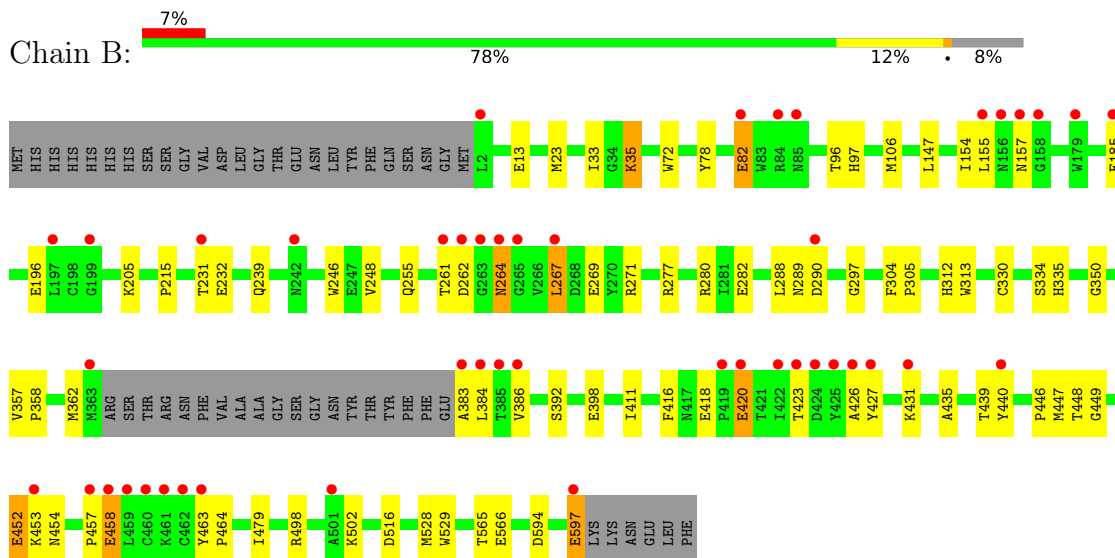
### 3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: Beta-glucuronidase



#### • Molecule 1: Beta-glucuronidase



## 4 Data and refinement statistics

| Property                                                                | Value                                                       | Source           |
|-------------------------------------------------------------------------|-------------------------------------------------------------|------------------|
| Space group                                                             | C 1 2 1                                                     | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 161.21Å 101.90Å 111.30Å<br>90.00° 130.90° 90.00°            | Depositor        |
| Resolution (Å)                                                          | 28.50 – 1.71<br>28.50 – 1.71                                | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | 62.0 (28.50-1.71)<br>88.8 (28.50-1.71)                      | Depositor<br>EDS |
| $R_{merge}$                                                             | 0.06                                                        | Depositor        |
| $R_{sym}$                                                               | (Not available)                                             | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 3.49 (at 1.72Å)                                             | Xtriage          |
| Refinement program                                                      | PHENIX 1.9_1692                                             | Depositor        |
| R, $R_{free}$                                                           | 0.168 , 0.203<br>0.180 , 0.202                              | Depositor<br>DCC |
| $R_{free}$ test set                                                     | 2019 reflections (1.38%)                                    | wwPDB-VP         |
| Wilson B-factor (Å <sup>2</sup> )                                       | 12.2                                                        | Xtriage          |
| Anisotropy                                                              | 0.004                                                       | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.38 , 42.1                                                 | EDS              |
| L-test for twinning <sup>2</sup>                                        | $\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$ | Xtriage          |
| Estimated twinning fraction                                             | 0.019 for -h-2*k,-k,l                                       | Xtriage          |
| $F_o, F_c$ correlation                                                  | 0.95                                                        | EDS              |
| Total number of atoms                                                   | 10256                                                       | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 18.0                                                        | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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: EVA, MRD

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     | 0.63         | 9/4851 (0.2%)  | 0.76        | 1/6579 (0.0%)  |
| 1   | B     | 0.54         | 3/4859 (0.1%)  | 0.76        | 5/6589 (0.1%)  |
| All | All   | 0.59         | 12/9710 (0.1%) | 0.76        | 6/13168 (0.0%) |

The worst 5 of 12 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 1   | B     | 448 | THR  | C-O   | -8.22 | 1.15        | 1.23     |
| 1   | A     | 161 | LEU  | C-O   | -7.68 | 1.15        | 1.24     |
| 1   | B     | 566 | GLU  | C-O   | -6.83 | 1.15        | 1.23     |
| 1   | A     | 79  | LEU  | C-O   | -6.17 | 1.15        | 1.24     |
| 1   | A     | 84  | ARG  | C-O   | -6.15 | 1.16        | 1.23     |

The worst 5 of 6 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms    | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|-------|-------------|----------|
| 1   | B     | 264 | ASN  | CA-C-N   | 7.34  | 130.31      | 122.38   |
| 1   | B     | 264 | ASN  | C-N-CA   | 7.34  | 130.31      | 122.38   |
| 1   | B     | 264 | ASN  | N-CA-C   | -6.18 | 105.39      | 113.12   |
| 1   | A     | 385 | THR  | N-CA-CB  | 5.52  | 119.81      | 110.49   |
| 1   | B     | 82  | GLU  | CB-CG-CD | 5.50  | 121.95      | 112.60   |

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     | 4717  | 0        | 4506     | 57      | 0            |
| 1   | B     | 4725  | 0        | 4515     | 74      | 0            |
| 2   | A     | 13    | 8        | 8        | 0       | 0            |
| 2   | B     | 13    | 8        | 8        | 0       | 0            |
| 3   | A     | 8     | 14       | 14       | 1       | 0            |
| 4   | A     | 403   | 0        | 0        | 2       | 0            |
| 4   | B     | 347   | 0        | 0        | 3       | 0            |
| All | All   | 10226 | 30       | 9051     | 124     | 0            |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 124 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:B:35:LYS:HE3   | 1:B:35:LYS:H    | 1.37                     | 0.89              |
| 1:A:255:GLN:NE2  | 1:A:271:ARG:HD3 | 1.88                     | 0.88              |
| 1:A:427:TYR:CE2  | 1:A:431:LYS:HE2 | 2.19                     | 0.78              |
| 1:B:35:LYS:H     | 1:B:35:LYS:CE   | 1.96                     | 0.78              |
| 1:A:255:GLN:HE21 | 1:A:271:ARG:HD3 | 1.47                     | 0.78              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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     | 572/627 (91%)   | 555 (97%)  | 16 (3%) | 1 (0%)   | 43          | 31  |
| 1   | B     | 573/627 (91%)   | 556 (97%)  | 17 (3%) | 0        | 100         | 100 |
| All | All   | 1145/1254 (91%) | 1111 (97%) | 33 (3%) | 1 (0%)   | 48          | 34  |

All (1) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 385 | THR  |

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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     | 502/546 (92%)   | 497 (99%) | 5 (1%)   | 68          | 53 |
| 1   | B     | 503/546 (92%)   | 492 (98%) | 11 (2%)  | 45          | 23 |
| All | All   | 1005/1092 (92%) | 989 (98%) | 16 (2%)  | 55          | 34 |

5 of 16 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | B     | 458 | GLU  |
| 1   | B     | 452 | GLU  |
| 1   | B     | 264 | ASN  |
| 1   | B     | 420 | GLU  |
| 1   | B     | 239 | GLN  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | B     | 41  | ASN  |
| 1   | B     | 505 | ASN  |
| 1   | B     | 575 | HIS  |
| 1   | A     | 454 | ASN  |
| 1   | A     | 255 | GLN  |

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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 | $\# Z  > 2$ |
| 2   | EVA  | A     | 701 | -    | 13,13,13     | 1.57 | 2 (15%)     | 13,19,19    | 1.70 | 1 (7%)      |
| 3   | MRD  | A     | 702 | -    | 7,7,7        | 1.33 | 1 (14%)     | 9,10,10     | 1.17 | 1 (11%)     |
| 2   | EVA  | B     | 701 | -    | 13,13,13     | 1.61 | 2 (15%)     | 13,19,19    | 1.65 | 1 (7%)      |

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   |
|-----|------|-------|-----|------|---------|-----------|---------|
| 2   | EVA  | A     | 701 | -    | -       | 1/3/24/24 | 0/1/1/1 |
| 3   | MRD  | A     | 702 | -    | -       | 3/5/5/5   | -       |
| 2   | EVA  | B     | 701 | -    | -       | 0/3/24/24 | 0/1/1/1 |

All (5) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms  | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 2   | A     | 701 | EVA  | CG-CD1 | -4.08 | 1.47        | 1.53     |
| 2   | B     | 701 | EVA  | CG-CD1 | -3.88 | 1.47        | 1.53     |
| 3   | A     | 702 | MRD  | O2-C2  | -2.99 | 1.37        | 1.44     |
| 2   | B     | 701 | EVA  | CG-CB  | 2.47  | 1.58        | 1.52     |

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| Mol | Chain | Res | Type | Atoms | Z    | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|------|-------------|----------|
| 2   | A     | 701 | EVA  | CG-CB | 2.17 | 1.58        | 1.52     |

All (3) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms     | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 2   | A     | 701 | EVA  | OAK-CAE-N | -4.93 | 116.15      | 122.67   |
| 2   | B     | 701 | EVA  | OAK-CAE-N | -4.61 | 116.57      | 122.67   |
| 3   | A     | 702 | MRD  | CM-C2-C1  | -2.89 | 104.16      | 110.63   |

There are no chirality outliers.

All (4) torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms       |
|-----|-------|-----|------|-------------|
| 2   | A     | 701 | EVA  | O-C-CA-N    |
| 3   | A     | 702 | MRD  | C1-C2-C3-C4 |
| 3   | A     | 702 | MRD  | C2-C3-C4-O4 |
| 3   | A     | 702 | MRD  | CM-C2-C3-C4 |

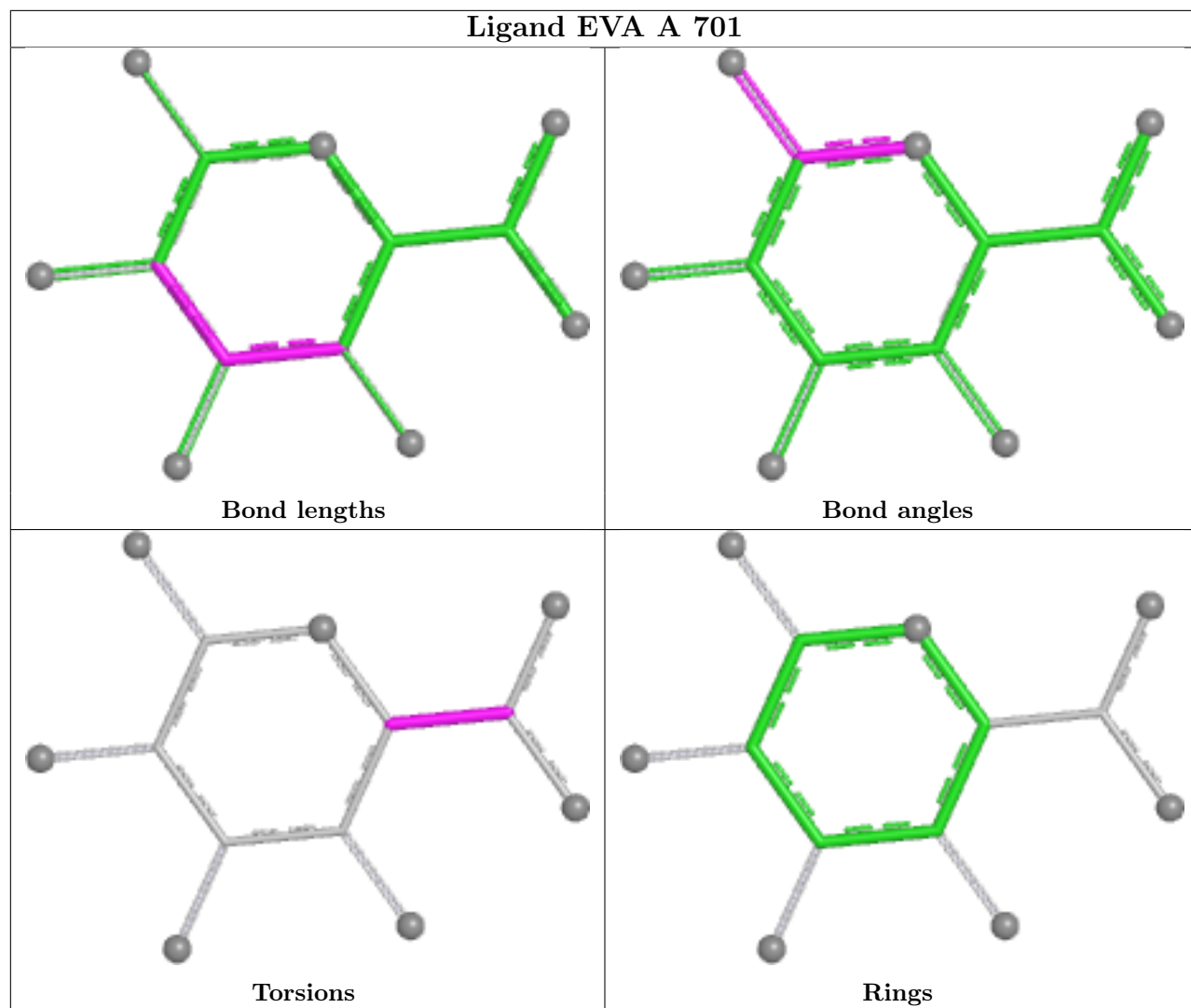
There are no ring outliers.

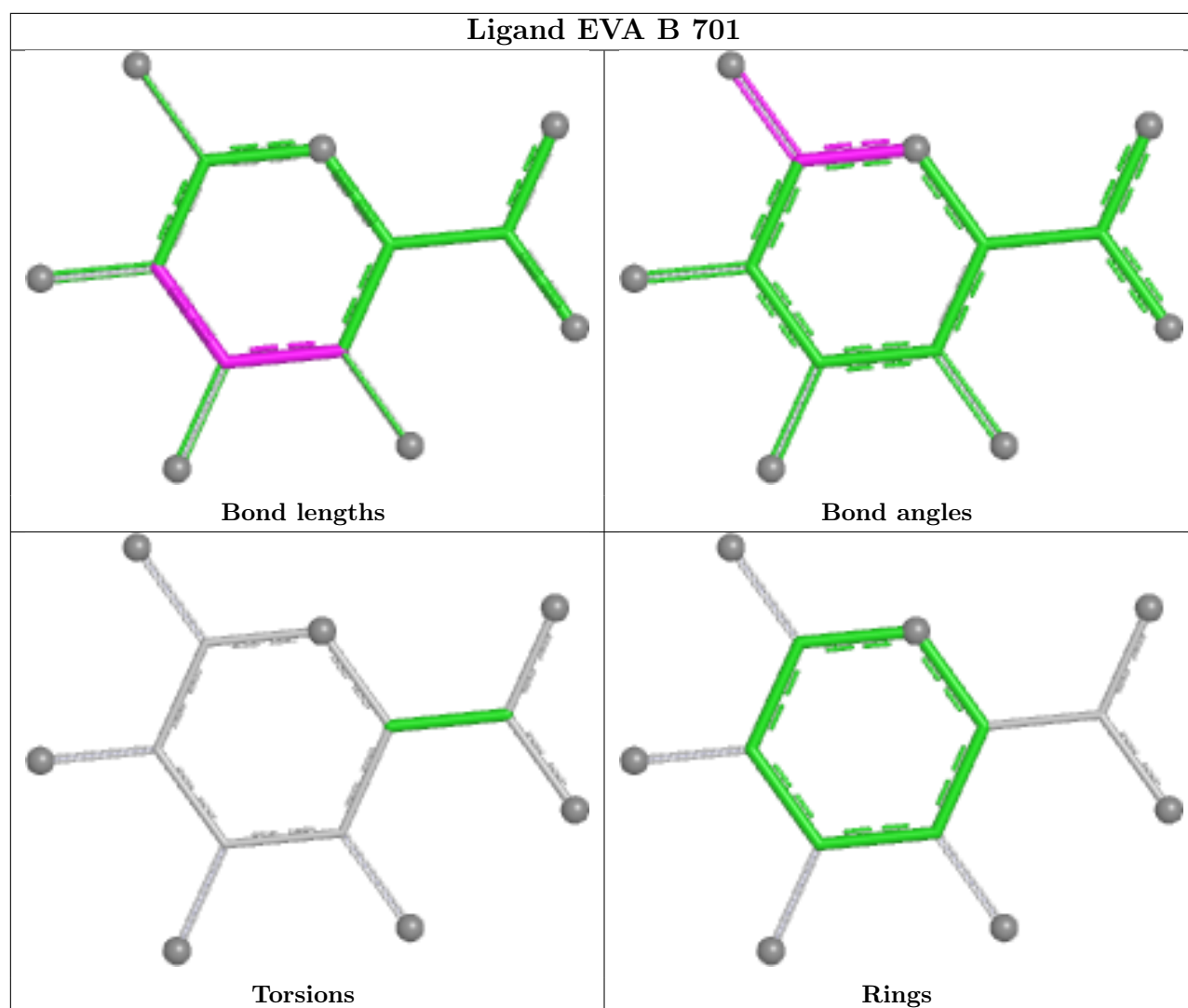
1 monomer is involved in 1 short contact:

| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|-----|------|---------|--------------|
| 3   | A     | 702 | MRD  | 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.

## Ligand EVA A 701





## 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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed        | <RSRZ> | #RSRZ>2       | OWAB(Å <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|---------------|-----------------------|-------|
| 1   | A     | 576/627 (91%)   | -0.08  | 14 (2%) 59 67 | 7, 15, 32, 50         | 0     |
| 1   | B     | 577/627 (92%)   | 0.21   | 46 (7%) 18 24 | 7, 17, 38, 61         | 0     |
| All | All   | 1153/1254 (91%) | 0.07   | 60 (5%) 33 38 | 7, 15, 35, 61         | 0     |

The worst 5 of 60 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1   | B     | 384 | LEU  | 7.2  |
| 1   | A     | 384 | LEU  | 6.6  |
| 1   | B     | 425 | TYR  | 5.9  |
| 1   | A     | 383 | ALA  | 5.7  |
| 1   | B     | 363 | MET  | 5.2  |

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

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

### 6.3 Carbohydrates [i](#)

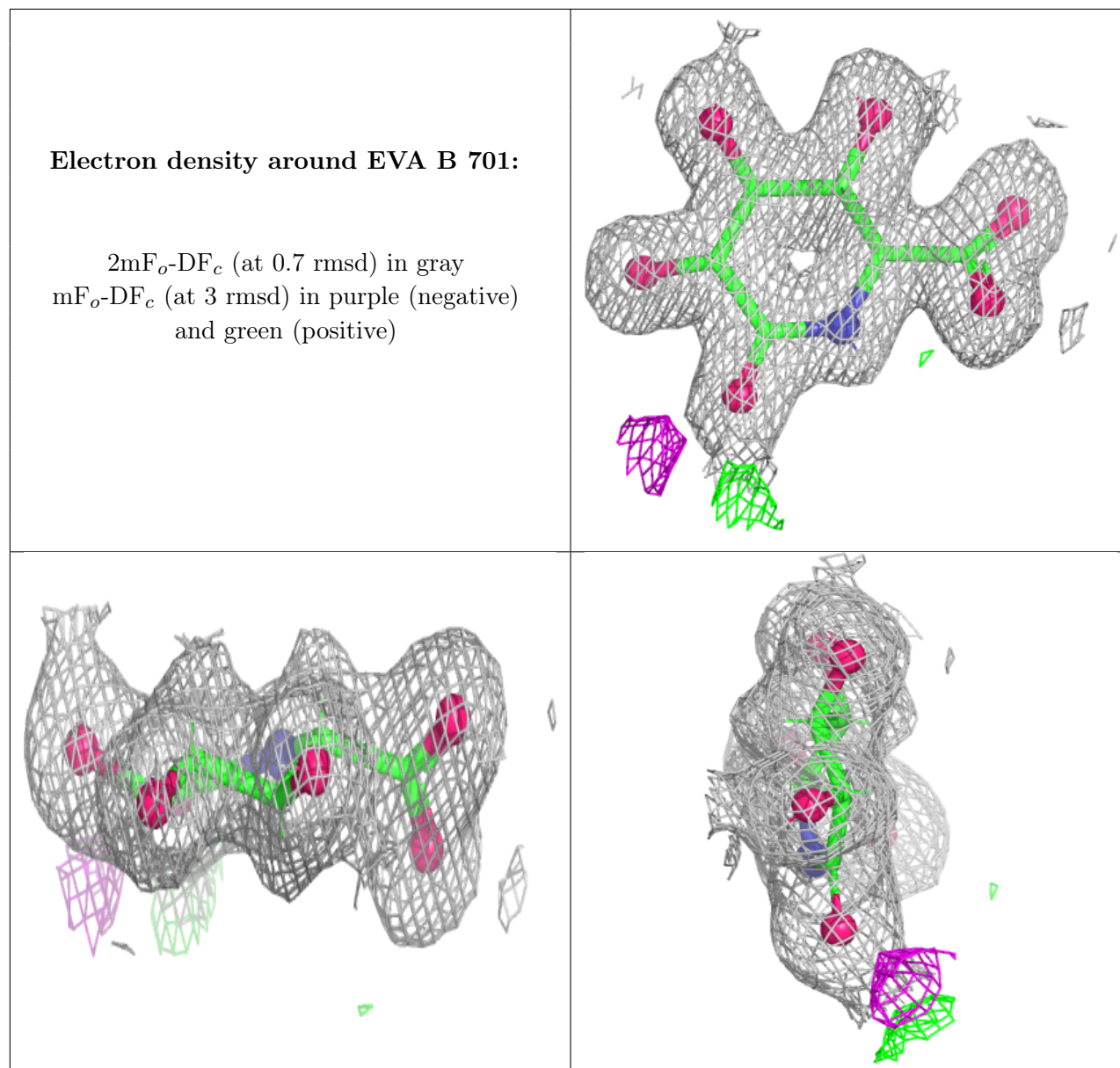
There are no oligosaccharides in this entry.

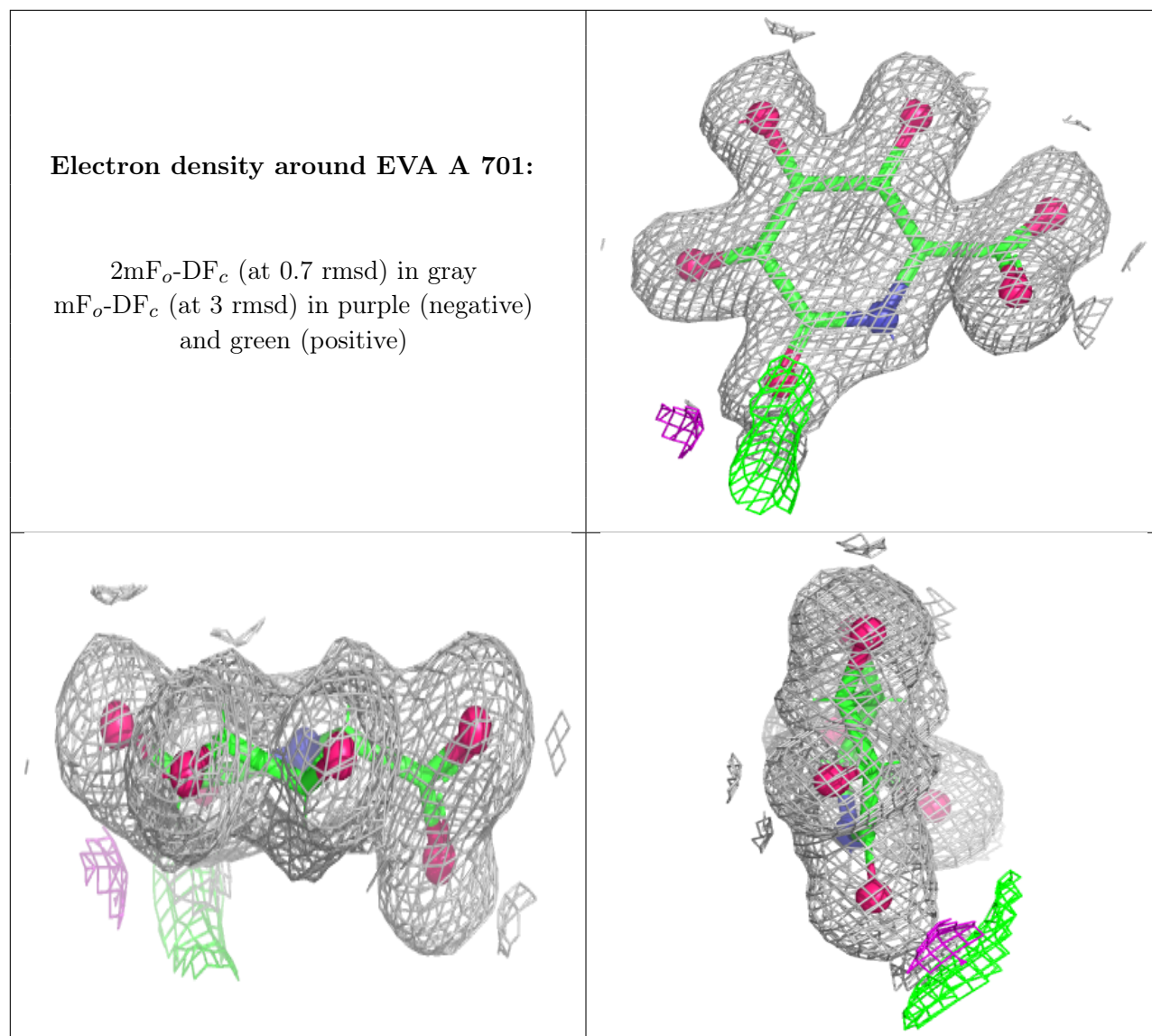
### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

| Mol | Type | Chain | Res | Atoms | RSCC | RSR  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|-----|-------|------|------|-----------------------------|-------|
| 3   | MRD  | A     | 702 | 8/8   | 0.88 | 0.16 | 20,20,20,20                 | 0     |
| 2   | EVA  | B     | 701 | 13/13 | 0.98 | 0.04 | 9,12,14,15                  | 0     |
| 2   | EVA  | A     | 701 | 13/13 | 0.98 | 0.04 | 8,10,12,13                  | 0     |

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.