



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 20, 2020 – 12:20 PM BST

PDB ID : 1GAV
Title : BACTERIOPHAGE GA PROTEIN CAPSID
Authors : Tars, K.; Bundule, M.; Liljas, L.
Deposited on : 1997-01-28
Resolution : 3.40 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

| | | |
|--------------------------------|---|--|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.13 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | 2.13 |

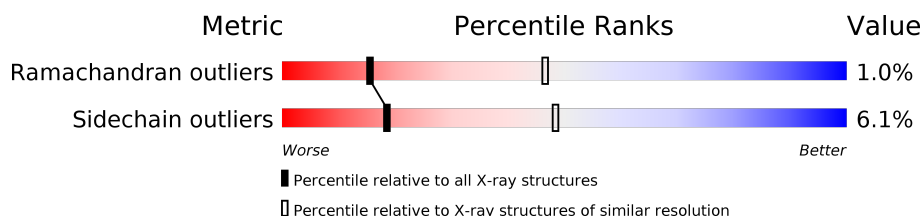
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



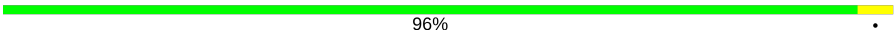

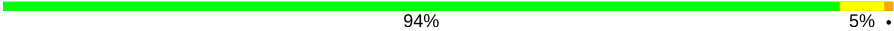
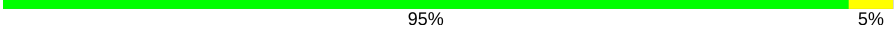

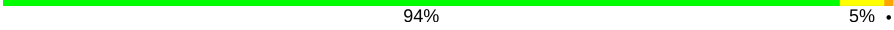
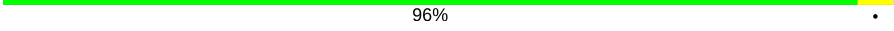

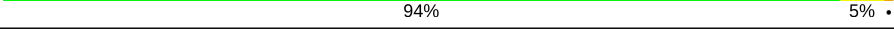
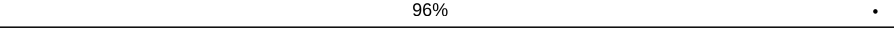

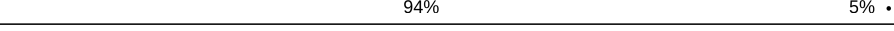
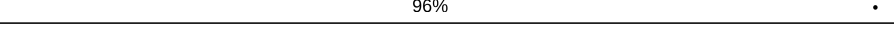

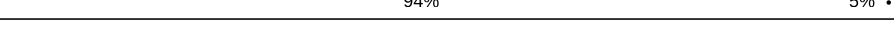
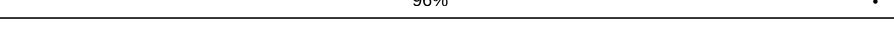
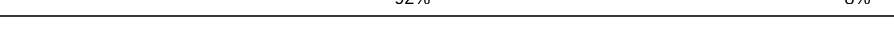
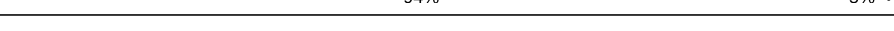
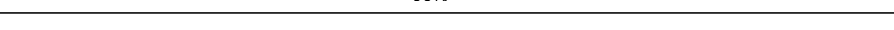
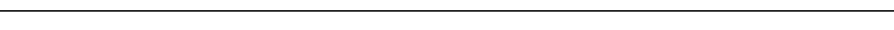
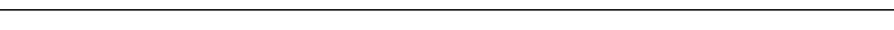
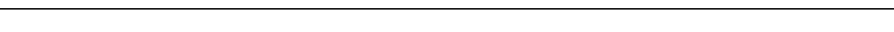
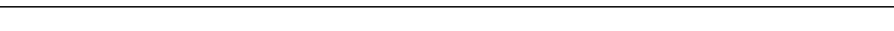
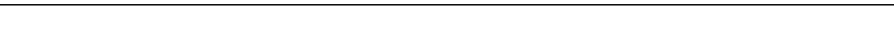

| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|---|
| Ramachandran outliers | 138981 | 1038 (3.48-3.32) |
| Sidechain outliers | 138945 | 1038 (3.48-3.32) |

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | 0 | 129 | 94% 5% . |
| 1 | 1 | 129 | 94% 5% . |
| 1 | 2 | 129 | 96% . |
| 1 | 3 | 129 | 92% 8% |
| 1 | 4 | 129 | 94% 5% . |
| 1 | 5 | 129 | 96% . |
| 1 | 6 | 129 | 92% 8% |
| 1 | 7 | 129 | 94% 5% . |
| 1 | 8 | 129 | 96% . |
| 1 | 9 | 129 | 92% 8% |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 1 | A | 129 |  96% . |
| 1 | B | 129 |  92% 8% |
| 1 | C | 129 |  94% 5% . |
| 1 | D | 129 |  95% 5% |
| 1 | E | 129 |  92% 8% |
| 1 | F | 129 |  94% 5% . |
| 1 | G | 129 |  96% . |
| 1 | H | 129 |  92% 8% |
| 1 | I | 129 |  94% 5% . |
| 1 | J | 129 |  96% . |
| 1 | K | 129 |  92% 8% |
| 1 | L | 129 |  94% 5% . |
| 1 | M | 129 |  96% . |
| 1 | N | 129 |  92% 8% |
| 1 | O | 129 |  94% 5% . |
| 1 | P | 129 |  96% . |
| 1 | Q | 129 |  92% 8% |
| 1 | R | 129 |  94% 5% . |
| 1 | S | 129 |  96% . |
| 1 | T | 129 |  92% 8% |
| 1 | U | 129 |  94% 5% . |
| 1 | V | 129 |  95% 5% |
| 1 | W | 129 |  92% 8% |
| 1 | X | 129 |  94% 5% . |
| 1 | Y | 129 |  96% . |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 1 | Z | 129 | <div><div></div><div>92%</div><div>8%</div></div> |
| 1 | a | 129 | <div><div></div><div>96%</div><div></div></div> |
| 1 | b | 129 | <div><div></div><div>92%</div><div>8%</div></div> |
| 1 | c | 129 | <div><div></div><div>94%</div><div>5%</div></div> |
| 1 | d | 129 | <div><div></div><div>96%</div><div></div></div> |
| 1 | e | 129 | <div><div></div><div>92%</div><div>8%</div></div> |
| 1 | f | 129 | <div><div></div><div>94%</div><div>5%</div></div> |
| 1 | g | 129 | <div><div></div><div>96%</div><div></div></div> |
| 1 | h | 129 | <div><div></div><div>92%</div><div>8%</div></div> |
| 1 | i | 129 | <div><div></div><div>94%</div><div>5%</div></div> |

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 43335 atoms, of which 0 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 BACTERIOPHAGE GA PROTEIN CAPSID.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 1 | A | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | B | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | C | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | D | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | E | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | F | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | G | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | H | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | I | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | J | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | K | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | L | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | M | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | N | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | O | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |
| 1 | P | 129 | Total | C | N | O | 0 | 0 | 0 |
| | | | 963 | 612 | 164 | 187 | | | |

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| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|---------|---------|-------|
| 1 | Q | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | R | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | S | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | T | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | U | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | V | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | W | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | X | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | Y | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | Z | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 1 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 2 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 3 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 4 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 5 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 6 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 7 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 8 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 9 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | 0 | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | a | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------|----------|----------|----------|---------|---------|-------|
| 1 | b | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | c | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | d | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | e | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | f | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | g | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | h | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |
| 1 | i | 129 | Total 963 | C 612 | N 164 | O 187 | 0 | 0 | 0 |

There are 90 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|------------|
| A | 59 | THR | ALA | VARIANT | UNP P07234 |
| A | 79 | VAL | GLY | VARIANT | UNP P07234 |
| B | 59 | THR | ALA | VARIANT | UNP P07234 |
| B | 79 | VAL | GLY | VARIANT | UNP P07234 |
| C | 59 | THR | ALA | VARIANT | UNP P07234 |
| C | 79 | VAL | GLY | VARIANT | UNP P07234 |
| D | 59 | THR | ALA | VARIANT | UNP P07234 |
| D | 79 | VAL | GLY | VARIANT | UNP P07234 |
| E | 59 | THR | ALA | VARIANT | UNP P07234 |
| E | 79 | VAL | GLY | VARIANT | UNP P07234 |
| F | 59 | THR | ALA | VARIANT | UNP P07234 |
| F | 79 | VAL | GLY | VARIANT | UNP P07234 |
| G | 59 | THR | ALA | VARIANT | UNP P07234 |
| G | 79 | VAL | GLY | VARIANT | UNP P07234 |
| H | 59 | THR | ALA | VARIANT | UNP P07234 |
| H | 79 | VAL | GLY | VARIANT | UNP P07234 |
| I | 59 | THR | ALA | VARIANT | UNP P07234 |
| I | 79 | VAL | GLY | VARIANT | UNP P07234 |
| J | 59 | THR | ALA | VARIANT | UNP P07234 |
| J | 79 | VAL | GLY | VARIANT | UNP P07234 |
| K | 59 | THR | ALA | VARIANT | UNP P07234 |
| K | 79 | VAL | GLY | VARIANT | UNP P07234 |
| L | 59 | THR | ALA | VARIANT | UNP P07234 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|------------|
| L | 79 | VAL | GLY | VARIANT | UNP P07234 |
| M | 59 | THR | ALA | VARIANT | UNP P07234 |
| M | 79 | VAL | GLY | VARIANT | UNP P07234 |
| N | 59 | THR | ALA | VARIANT | UNP P07234 |
| N | 79 | VAL | GLY | VARIANT | UNP P07234 |
| O | 59 | THR | ALA | VARIANT | UNP P07234 |
| O | 79 | VAL | GLY | VARIANT | UNP P07234 |
| P | 59 | THR | ALA | VARIANT | UNP P07234 |
| P | 79 | VAL | GLY | VARIANT | UNP P07234 |
| Q | 59 | THR | ALA | VARIANT | UNP P07234 |
| Q | 79 | VAL | GLY | VARIANT | UNP P07234 |
| R | 59 | THR | ALA | VARIANT | UNP P07234 |
| R | 79 | VAL | GLY | VARIANT | UNP P07234 |
| S | 59 | THR | ALA | VARIANT | UNP P07234 |
| S | 79 | VAL | GLY | VARIANT | UNP P07234 |
| T | 59 | THR | ALA | VARIANT | UNP P07234 |
| T | 79 | VAL | GLY | VARIANT | UNP P07234 |
| U | 59 | THR | ALA | VARIANT | UNP P07234 |
| U | 79 | VAL | GLY | VARIANT | UNP P07234 |
| V | 59 | THR | ALA | VARIANT | UNP P07234 |
| V | 79 | VAL | GLY | VARIANT | UNP P07234 |
| W | 59 | THR | ALA | VARIANT | UNP P07234 |
| W | 79 | VAL | GLY | VARIANT | UNP P07234 |
| X | 59 | THR | ALA | VARIANT | UNP P07234 |
| X | 79 | VAL | GLY | VARIANT | UNP P07234 |
| Y | 59 | THR | ALA | VARIANT | UNP P07234 |
| Y | 79 | VAL | GLY | VARIANT | UNP P07234 |
| Z | 59 | THR | ALA | VARIANT | UNP P07234 |
| Z | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 1 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 1 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 2 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 2 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 3 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 3 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 4 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 4 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 5 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 5 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 6 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 6 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 7 | 59 | THR | ALA | VARIANT | UNP P07234 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|---------|------------|
| 7 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 8 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 8 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 9 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 9 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| 0 | 59 | THR | ALA | VARIANT | UNP P07234 |
| 0 | 79 | VAL | GLY | VARIANT | UNP P07234 |
| a | 59 | THR | ALA | VARIANT | UNP P07234 |
| a | 79 | VAL | GLY | VARIANT | UNP P07234 |
| b | 59 | THR | ALA | VARIANT | UNP P07234 |
| b | 79 | VAL | GLY | VARIANT | UNP P07234 |
| c | 59 | THR | ALA | VARIANT | UNP P07234 |
| c | 79 | VAL | GLY | VARIANT | UNP P07234 |
| d | 59 | THR | ALA | VARIANT | UNP P07234 |
| d | 79 | VAL | GLY | VARIANT | UNP P07234 |
| e | 59 | THR | ALA | VARIANT | UNP P07234 |
| e | 79 | VAL | GLY | VARIANT | UNP P07234 |
| f | 59 | THR | ALA | VARIANT | UNP P07234 |
| f | 79 | VAL | GLY | VARIANT | UNP P07234 |
| g | 59 | THR | ALA | VARIANT | UNP P07234 |
| g | 79 | VAL | GLY | VARIANT | UNP P07234 |
| h | 59 | THR | ALA | VARIANT | UNP P07234 |
| h | 79 | VAL | GLY | VARIANT | UNP P07234 |
| i | 59 | THR | ALA | VARIANT | UNP P07234 |
| i | 79 | VAL | GLY | VARIANT | UNP P07234 |

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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: BACTERIOPHAGE GA PROTEIN CAPSID

Chain A:  96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain B:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain C:  94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain D:  95% 5%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain E:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain F:  94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain G:  96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain H:  92% 8% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain I:  94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain J:  96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain K:  92% 8% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain L:  94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain M:  96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain N:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain O:  94% 5%



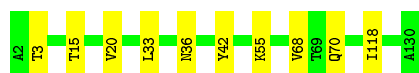
- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain P:  96%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain Q:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain R:  94% 5%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain S:  96%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain T:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain U: 94% 5% •



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain V: 95% 5%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain W: 92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain X: 94% 5% •



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain Y: 96% •



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain Z: 92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 1: 94% 5% •



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 2: 96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 3: 92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 4: 94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 5: 96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 6: 92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 7: 94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 8: 96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 9:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain 0:  94% 5%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain a:  96%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain b:  92% 8%



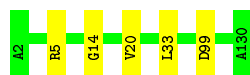
- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain c:  94% 5%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain d:  96%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain e:  92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain f: 94% 5% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain g: 96% .



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain h: 92% 8%



- Molecule 1: BACTERIOPHAGE GA PROTEIN CAPSID

Chain i: 94% 5% .



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | I 2 2 2 | Depositor |
| Cell constants a, b, c, α , β , γ | 272.70 Å 293.50 Å 339.30 Å 90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 30.00 – 3.40 49.31 – 3.39 | Depositor EDS |
| % Data completeness (in resolution range) | 66.0 (30.00-3.40) 65.4 (49.31-3.39) | Depositor EDS |
| R_{merge} | 0.14 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 6.02 (at 3.40 Å) | Xtriage |
| Refinement program | X-PLOR 3.1 | Depositor |
| R, R_{free} | 0.279 , (Not available) 0.220 , (Not available) | Depositor DCC |
| R_{free} test set | No test flags present. | wwPDB-VP |
| Wilson B-factor (Å ²) | 46.8 | Xtriage |
| Anisotropy | 0.124 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.28 , 58.7 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| F_o, F_c correlation | 0.89 | EDS |
| Total number of atoms | 43335 | wwPDB-VP |
| Average B, all atoms (Å ²) | 21.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

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 | 0 | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | 1 | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | 2 | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | 3 | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | 4 | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | 5 | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | 6 | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | 7 | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | 8 | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | 9 | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | A | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | B | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | C | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | D | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | E | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | F | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | G | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | H | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | I | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | J | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | K | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | L | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | M | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | N | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | O | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | P | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | Q | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | R | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | S | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | T | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | U | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | V | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | W | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | X | 0.82 | 0/980 | 0.84 | 0/1336 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|-----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | Y | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | Z | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | a | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | b | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | c | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | d | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | e | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | f | 0.82 | 0/980 | 0.84 | 0/1336 |
| 1 | g | 0.82 | 0/980 | 0.87 | 0/1336 |
| 1 | h | 0.88 | 0/980 | 0.90 | 1/1336 (0.1%) |
| 1 | i | 0.82 | 0/980 | 0.84 | 0/1336 |
| All | All | 0.84 | 0/44100 | 0.87 | 15/60120 (0.0%) |

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|--------|-------|-------------|----------|
| 1 | Q | 42 | TYR | N-CA-C | -5.65 | 95.74 | 111.00 |
| 1 | T | 42 | TYR | N-CA-C | -5.65 | 95.74 | 111.00 |
| 1 | Z | 42 | TYR | N-CA-C | -5.65 | 95.74 | 111.00 |
| 1 | E | 42 | TYR | N-CA-C | -5.65 | 95.75 | 111.00 |
| 1 | K | 42 | TYR | N-CA-C | -5.65 | 95.75 | 111.00 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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 | 0 | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | 1 | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | 2 | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | 3 | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | 4 | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | 5 | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | 6 | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | 7 | 127/129 (98%) | 116 (91%) | 9 (7%) | 2 (2%) | 9 | 34 |
| 1 | 8 | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | 9 | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | A | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | B | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | C | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | D | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | E | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | F | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | G | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | H | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | I | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | J | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | K | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | L | 127/129 (98%) | 116 (91%) | 9 (7%) | 2 (2%) | 9 | 34 |
| 1 | M | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | N | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | O | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | P | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | Q | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | R | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | S | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | T | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | U | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | V | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|----|
| 1 | W | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | X | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | Y | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | Z | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | a | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | b | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | c | 127/129 (98%) | 116 (91%) | 9 (7%) | 2 (2%) | 9 | 34 |
| 1 | d | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | e | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | f | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| 1 | g | 127/129 (98%) | 111 (87%) | 15 (12%) | 1 (1%) | 19 | 51 |
| 1 | h | 127/129 (98%) | 117 (92%) | 9 (7%) | 1 (1%) | 19 | 51 |
| 1 | i | 127/129 (98%) | 117 (92%) | 8 (6%) | 2 (2%) | 9 | 34 |
| All | All | 5715/5805 (98%) | 5172 (90%) | 483 (8%) | 60 (1%) | 15 | 46 |

5 of 60 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 15 | THR |
| 1 | C | 14 | GLY |
| 1 | C | 15 | THR |
| 1 | E | 15 | THR |
| 1 | F | 14 | GLY |

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 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 | 0 | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | 1 | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | 2 | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 1 | 3 | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | 4 | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | 5 | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | 6 | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | 7 | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | 8 | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | 9 | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | A | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | B | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | C | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | D | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | E | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | F | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | G | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | H | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | I | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | J | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | K | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | L | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | M | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | N | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | O | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | P | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | Q | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | R | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | S | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | T | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | U | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | V | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | W | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | X | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|------------------|------------|----------|-------------|----|
| 1 | Y | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | Z | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | a | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | b | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | c | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | d | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | e | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | f | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| 1 | g | 104/104 (100%) | 100 (96%) | 4 (4%) | 33 | 61 |
| 1 | h | 104/104 (100%) | 96 (92%) | 8 (8%) | 13 | 40 |
| 1 | i | 104/104 (100%) | 97 (93%) | 7 (7%) | 16 | 46 |
| All | All | 4680/4680 (100%) | 4395 (94%) | 285 (6%) | 18 | 48 |

5 of 285 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | U | 38 | ARG |
| 1 | Z | 36 | ASN |
| 1 | f | 54 | ASP |
| 1 | U | 90 | LEU |
| 1 | W | 118 | ILE |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | T | 70 | GLN |
| 1 | Y | 36 | ASN |
| 1 | f | 36 | ASN |
| 1 | U | 73 | ASN |
| 1 | W | 36 | ASN |

5.3.3 RNA ⓘ

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.