



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 05:30 am GMT

PDB ID : 4IS4
Title : The glutamine synthetase from the dicotyledonous plant *M. truncatula* is a decamer
Authors : Seabra, A.R.; Carvalho, H.; Pereira, P.J.B.
Deposited on : 2013-01-16
Resolution : 2.35 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

<http://wwpdb.org/validation/2016/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) | : | 1.9-1692 |
| EDS | : | trunk28620 |
| Percentile statistics | : | 20161228.v01 (using entries in the PDB archive December 28th 2016) |
| Refmac | : | 5.8.0135 |
| CCP4 | : | 6.5.0 |
| Ideal geometry (proteins) | : | Engh & Huber (2001) |
| Ideal geometry (DNA, RNA) | : | Parkinson et al. (1996) |
| Validation Pipeline (wwPDB-VP) | : | recalc28949 |

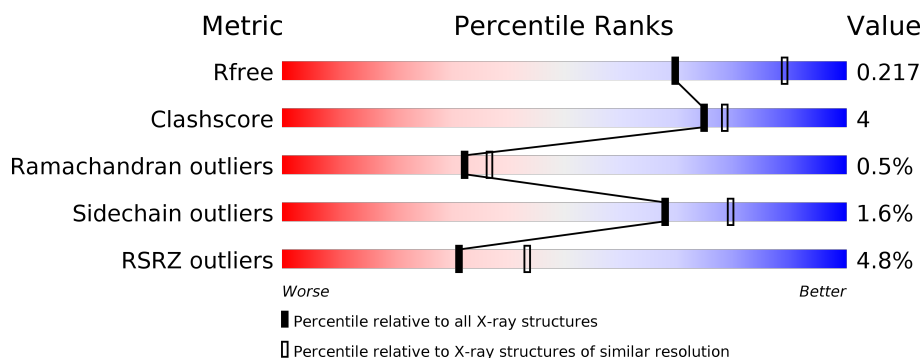
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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)) |
|-----------------------|-----------------------------|---|
| R_{free} | 100719 | 1522 (2.38-2.34) |
| Clashscore | 112137 | 1626 (2.38-2.34) |
| Ramachandran outliers | 110173 | 1605 (2.38-2.34) |
| Sidechain outliers | 110143 | 1606 (2.38-2.34) |
| RSRZ outliers | 101464 | 1528 (2.38-2.34) |

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. 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 | 378 | <div> <div>2%</div> <div> <div></div> <div>82%</div> <div>8%</div> <div>10%</div> </div> </div> |
| 1 | B | 378 | <div> <div>5%</div> <div> <div></div> <div>70%</div> <div>11%</div> <div>19%</div> </div> </div> |
| 1 | C | 378 | <div> <div>4%</div> <div> <div></div> <div>72%</div> <div>9%</div> <div>18%</div> </div> </div> |
| 1 | D | 378 | <div> <div>3%</div> <div> <div></div> <div>72%</div> <div>8%</div> <div>20%</div> </div> </div> |
| 1 | E | 378 | <div> <div>4%</div> <div> <div></div> <div>72%</div> <div>6%</div> <div>22%</div> </div> </div> |
| 1 | F | 378 | <div> <div>6%</div> <div> <div></div> <div>73%</div> <div>8%</div> <div>19%</div> </div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 1 | G | 378 | <div><div><div>4%</div><div>72%</div><div>10%</div><div>18%</div></div></div> |
| 1 | H | 378 | <div><div><div>3%</div><div>72%</div><div>8%</div><div>20%</div></div></div> |
| 1 | I | 378 | <div><div><div>4%</div><div>70%</div><div>9%</div><div>20%</div></div></div> |
| 1 | J | 378 | <div><div><div>3%</div><div>73%</div><div>7%</div><div>20%</div></div></div> |

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 24909 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 Glutamine synthetase.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 1 | A | 339 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2636 | 1680 | 446 | 501 | 9 | | | |
| 1 | B | 306 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2378 | 1520 | 397 | 452 | 9 | | | |
| 1 | C | 311 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2424 | 1551 | 405 | 459 | 9 | | | |
| 1 | D | 304 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2360 | 1514 | 388 | 449 | 9 | | | |
| 1 | E | 293 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2276 | 1462 | 373 | 432 | 9 | | | |
| 1 | F | 307 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2389 | 1530 | 397 | 453 | 9 | | | |
| 1 | G | 311 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2419 | 1547 | 404 | 459 | 9 | | | |
| 1 | H | 302 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2354 | 1509 | 389 | 447 | 9 | | | |
| 1 | I | 303 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2356 | 1512 | 387 | 448 | 9 | | | |
| 1 | J | 302 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2348 | 1505 | 387 | 447 | 9 | | | |

There are 220 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| A | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| A | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| A | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| A | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| A | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |
| A | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| A | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |
| A | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| A | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| A | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| A | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| A | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| A | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| A | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| A | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| A | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| A | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
| A | -4 | GLY | - | EXPRESSION TAG | UNP O04998 |
| A | -3 | SER | - | EXPRESSION TAG | UNP O04998 |
| A | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| A | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| A | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| B | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| B | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| B | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| B | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| B | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| B | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| B | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| B | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| B | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| B | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| B | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
| B | -4 | GLY | - | EXPRESSION TAG | UNP O04998 |
| B | -3 | SER | - | EXPRESSION TAG | UNP O04998 |
| B | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| B | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| B | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| C | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| C | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| C | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| C | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| C | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |
| C | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| C | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| C | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| C | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
| C | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| C | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| C | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| C | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| C | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| C | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| C | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| C | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
| C | -4 | GLY | - | EXPRESSION TAG | UNP O04998 |
| C | -3 | SER | - | EXPRESSION TAG | UNP O04998 |
| C | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| C | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| C | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| D | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| D | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| D | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| D | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| D | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| D | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| D | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| D | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| D | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| D | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| D | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
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| D | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| D | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| D | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| E | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| E | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| E | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| E | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| E | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| E | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| E | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |
| E | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| E | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
| E | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| E | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| E | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| E | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| E | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| E | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| E | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| E | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
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| E | -3 | SER | - | EXPRESSION TAG | UNP O04998 |
| E | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| E | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| E | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| F | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| F | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| F | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| F | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
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| F | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| F | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| F | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| F | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
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| F | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| G | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
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| G | -19 | SER | - | EXPRESSION TAG | UNP O04998 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| G | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| G | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |
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| G | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| G | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| G | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
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| G | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| H | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| H | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
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| H | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
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| H | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| H | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |
| H | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| H | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
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| H | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
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| H | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| H | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| H | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| H | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
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| H | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| H | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| H | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| I | -21 | MET | - | EXPRESSION TAG | UNP O04998 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| I | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| I | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
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| I | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| I | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
| I | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| I | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| I | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| I | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| I | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| I | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| I | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| I | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
| I | -4 | GLY | - | EXPRESSION TAG | UNP O04998 |
| I | -3 | SER | - | EXPRESSION TAG | UNP O04998 |
| I | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| I | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |
| I | 0 | SER | - | EXPRESSION TAG | UNP O04998 |
| J | -21 | MET | - | EXPRESSION TAG | UNP O04998 |
| J | -20 | GLY | - | EXPRESSION TAG | UNP O04998 |
| J | -19 | SER | - | EXPRESSION TAG | UNP O04998 |
| J | -18 | SER | - | EXPRESSION TAG | UNP O04998 |
| J | -17 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -16 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -15 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -14 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -13 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -12 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -11 | SER | - | EXPRESSION TAG | UNP O04998 |
| J | -10 | SER | - | EXPRESSION TAG | UNP O04998 |
| J | -9 | GLY | - | EXPRESSION TAG | UNP O04998 |
| J | -8 | LEU | - | EXPRESSION TAG | UNP O04998 |
| J | -7 | VAL | - | EXPRESSION TAG | UNP O04998 |
| J | -6 | PRO | - | EXPRESSION TAG | UNP O04998 |
| J | -5 | ARG | - | EXPRESSION TAG | UNP O04998 |
| J | -4 | GLY | - | EXPRESSION TAG | UNP O04998 |
| J | -3 | SER | - | EXPRESSION TAG | UNP O04998 |
| J | -2 | HIS | - | EXPRESSION TAG | UNP O04998 |
| J | -1 | ALA | - | EXPRESSION TAG | UNP O04998 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| J | 0 | SER | - | EXPRESSION TAG | UNP O04998 |

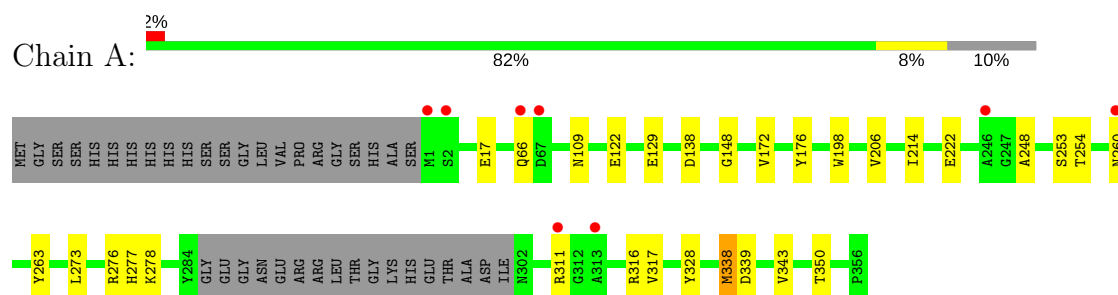
- Molecule 2 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|--------------|----------|---------|---------|
| 2 | A | 122 | Total 122 | O 122 | 0 | 0 |
| 2 | B | 66 | Total 66 | O 66 | 0 | 0 |
| 2 | C | 98 | Total 98 | O 98 | 0 | 0 |
| 2 | D | 83 | Total 83 | O 83 | 0 | 0 |
| 2 | E | 111 | Total 111 | O 111 | 0 | 0 |
| 2 | F | 76 | Total 76 | O 76 | 0 | 0 |
| 2 | G | 103 | Total 103 | O 103 | 0 | 0 |
| 2 | H | 80 | Total 80 | O 80 | 0 | 0 |
| 2 | I | 109 | Total 109 | O 109 | 0 | 0 |
| 2 | J | 121 | Total 121 | O 121 | 0 | 0 |

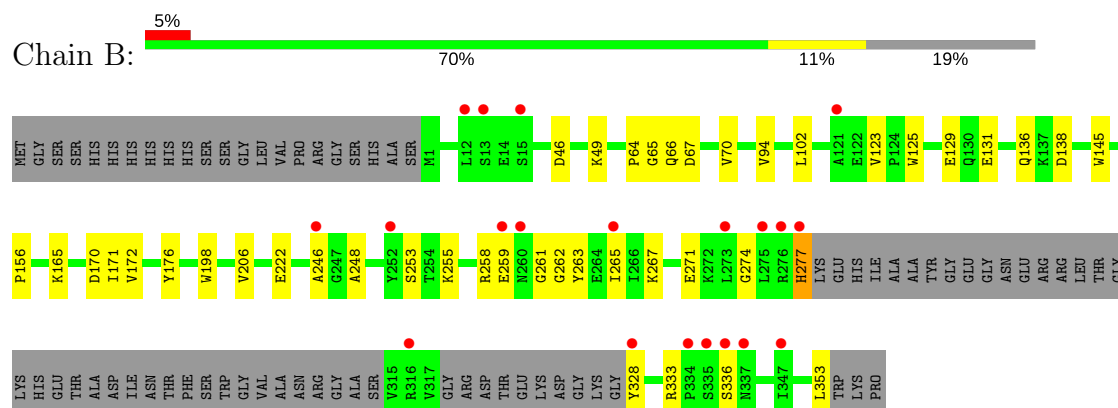
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

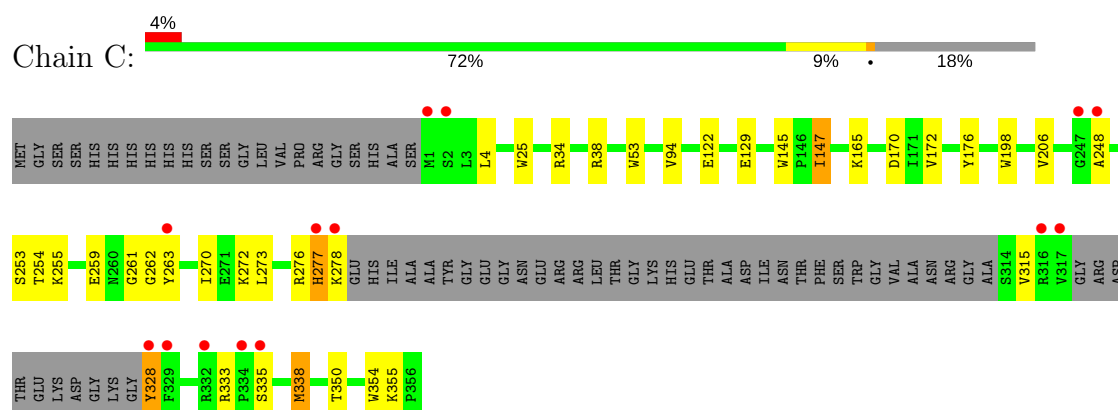
• Molecule 1: Glutamine synthetase



• Molecule 1: Glutamine synthetase



• Molecule 1: Glutamine synthetase



Chain D:

72%

3%

8%

20%

Chain E:

4% 72% 6% 22%

MET GLY SER SER HIS HIS HIS HIS HIS SER SER GLY VAL VAL PRO ARG ARG GLY SER HIS HIS ALA SER M1 S2 L3 K79 A121 E122 G148 P156 K165 V172 Y176 V193 M194 W198 A245 G247 A248 T254 K255 S256 K257 R258 E259 ASN GLY GLY THR

GLU I265 K268 K269 I270 E271 K272 L273 R276 HIS LYS GLU HIS ILE ALA ALA TYR GLY GLU GLY ASN GLU ARG ARG LEU THR LYS HIS GLU THR ALA ASP ILE ASN THR PHE SER TRP GLY VAL ALA ASN ARG GLY ALA SER VAL ARG VAL ARG ASP THR GLU LYS ASP GLY

LYS GLY TYR F329 F330 F331 ARG ARG ARG PRO SER ASN ASN M338 T350 T354 K355 P356

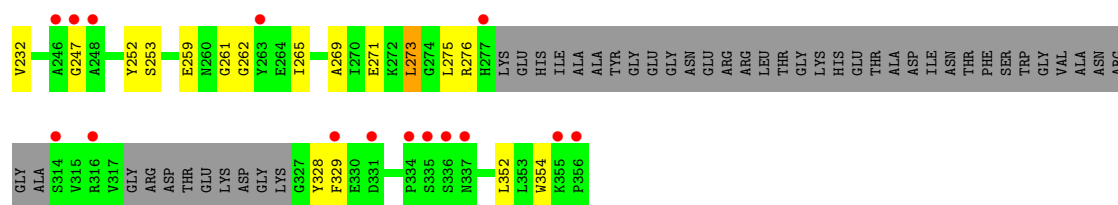
Chain F:

Sequence logo for Chain F. The y-axis represents information content in bits. The x-axis shows positions 1 to 300. A color scale at the top indicates conservation levels: 6% (red), 73% (green), 8% (yellow), and 19% (grey).

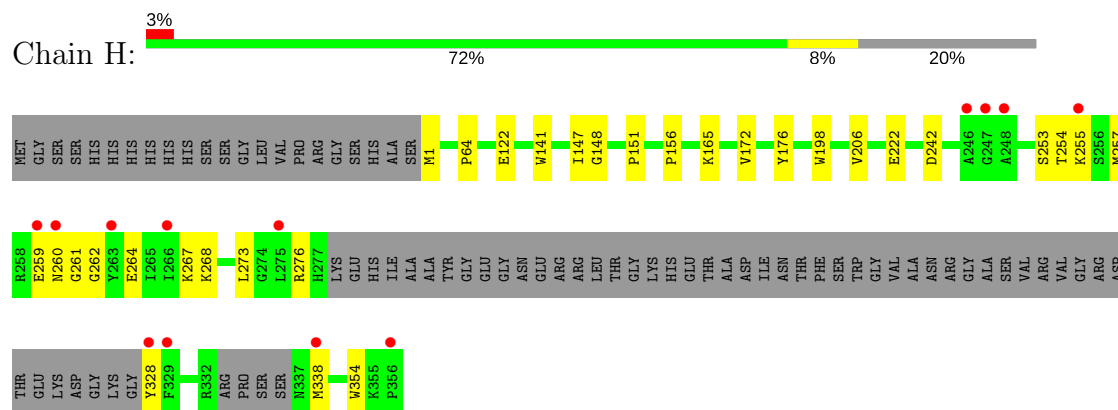
Chain G:

| Category | Percentage |
|----------|------------|
| Green | 72% |
| Yellow | 10% |
| Red | 4% |
| Grey | 18% |

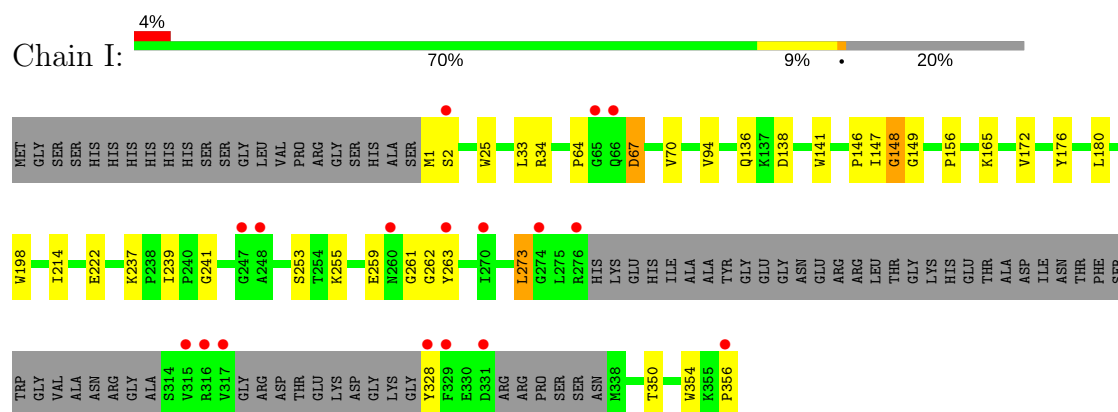
Sequence: MET, GLY, SER, SER, SER, HIS, HIS, HIS, HIS, HIS, HIS, SER, SER, GLY, LEU, VAL, PRO, ARG, ARG, GLY, SER, HIS, HIS, ALA, SER, M1, S2, L3, L4, N54, E69, K79, V94, L102, V119, I147, G148, G149, I161, D170, I171, V172, Y176, V193, M194, W198, V206, T225



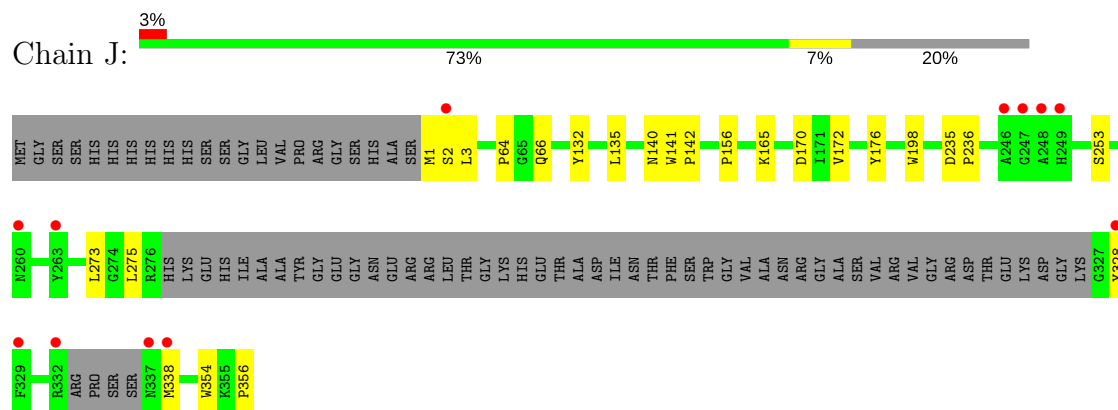
• Molecule 1: Glutamine synthetase



• Molecule 1: Glutamine synthetase



• Molecule 1: Glutamine synthetase



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 1 21 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 99.33Å 101.67Å 188.08Å 90.00° 103.69° 90.00° | Depositor |
| Resolution (Å) | 96.51 – 2.35 96.51 – 2.35 | Depositor EDS |
| % Data completeness (in resolution range) | 98.7 (96.51-2.35) 98.7 (96.51-2.35) | Depositor EDS |
| R_{merge} | 0.08 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 3.14 (at 2.34Å) | Xtriage |
| Refinement program | PHENIX (phenix.refine: 1.8.1_1168) | Depositor |
| R, R_{free} | 0.175 , 0.217 0.174 , 0.217 | Depositor DCC |
| R_{free} test set | 7517 reflections (5.03%) | DCC |
| Wilson B-factor (Å ²) | 37.4 | Xtriage |
| Anisotropy | 0.513 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.34 , 48.9 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$ | Xtriage |
| Estimated twinning fraction | 0.009 for h,-k,-h-l | Xtriage |
| F_o, F_c correlation | 0.95 | EDS |
| Total number of atoms | 24909 | wwPDB-VP |
| Average B, all atoms (Å ²) | 45.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% 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 | A | 0.44 | 0/2710 | 0.60 | 0/3687 |
| 1 | B | 0.39 | 0/2443 | 0.58 | 0/3327 |
| 1 | C | 0.43 | 0/2492 | 0.58 | 0/3392 |
| 1 | D | 0.43 | 0/2425 | 0.57 | 0/3301 |
| 1 | E | 0.45 | 0/2339 | 0.58 | 0/3185 |
| 1 | F | 0.41 | 0/2455 | 0.56 | 1/3341 (0.0%) |
| 1 | G | 0.41 | 0/2487 | 0.59 | 1/3386 (0.0%) |
| 1 | H | 0.40 | 0/2421 | 0.57 | 0/3297 |
| 1 | I | 0.43 | 0/2421 | 0.58 | 0/3296 |
| 1 | J | 0.44 | 0/2414 | 0.57 | 0/3287 |
| All | All | 0.42 | 0/24607 | 0.58 | 2/33499 (0.0%) |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|----------|------|-------------|----------|
| 1 | G | 149 | GLY | N-CA-C | 5.55 | 126.99 | 113.10 |
| 1 | F | 273 | LEU | CA-CB-CG | 5.07 | 126.95 | 115.30 |

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 | 2636 | 0 | 2557 | 20 | 0 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | B | 2378 | 0 | 2315 | 25 | 0 |
| 1 | C | 2424 | 0 | 2363 | 20 | 1 |
| 1 | D | 2360 | 0 | 2296 | 19 | 0 |
| 1 | E | 2276 | 0 | 2221 | 11 | 0 |
| 1 | F | 2389 | 0 | 2322 | 17 | 0 |
| 1 | G | 2419 | 0 | 2353 | 22 | 0 |
| 1 | H | 2354 | 0 | 2284 | 16 | 1 |
| 1 | I | 2356 | 0 | 2293 | 21 | 0 |
| 1 | J | 2348 | 0 | 2280 | 12 | 0 |
| 2 | A | 122 | 0 | 0 | 3 | 0 |
| 2 | B | 66 | 0 | 0 | 0 | 0 |
| 2 | C | 98 | 0 | 0 | 0 | 0 |
| 2 | D | 83 | 0 | 0 | 2 | 0 |
| 2 | E | 111 | 0 | 0 | 0 | 0 |
| 2 | F | 76 | 0 | 0 | 1 | 0 |
| 2 | G | 103 | 0 | 0 | 2 | 0 |
| 2 | H | 80 | 0 | 0 | 1 | 0 |
| 2 | I | 109 | 0 | 0 | 1 | 0 |
| 2 | J | 121 | 0 | 0 | 0 | 0 |
| All | All | 24909 | 0 | 23284 | 173 | 1 |

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 4.

The worst 5 of 173 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:C:122:GLU:HG3 | 1:C:254:THR:HB | 1.61 | 0.82 |
| 1:B:65:GLY:O | 1:B:67:ASP:N | 2.13 | 0.82 |
| 1:A:122:GLU:HG3 | 1:A:254:THR:HB | 1.64 | 0.80 |
| 1:A:338:MET:HG3 | 1:A:343:VAL:HG21 | 1.68 | 0.75 |
| 1:A:311:ARG:HG3 | 1:A:316:ARG:HH22 | 1.52 | 0.74 |

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|-----------------------|--------------------------|-------------------|
| 1:C:355:LYS:O | 1:H:268:LYS:NZ[2_555] | 2.09 | 0.11 |

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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 | 335/378 (89%) | 323 (96%) | 11 (3%) | 1 (0%) | 44 | 53 |
| 1 | B | 300/378 (79%) | 289 (96%) | 8 (3%) | 3 (1%) | 18 | 18 |
| 1 | C | 305/378 (81%) | 294 (96%) | 9 (3%) | 2 (1%) | 25 | 27 |
| 1 | D | 296/378 (78%) | 288 (97%) | 8 (3%) | 0 | 100 | 100 |
| 1 | E | 285/378 (75%) | 276 (97%) | 9 (3%) | 0 | 100 | 100 |
| 1 | F | 299/378 (79%) | 288 (96%) | 9 (3%) | 2 (1%) | 25 | 27 |
| 1 | G | 305/378 (81%) | 296 (97%) | 8 (3%) | 1 (0%) | 44 | 53 |
| 1 | H | 296/378 (78%) | 287 (97%) | 7 (2%) | 2 (1%) | 25 | 27 |
| 1 | I | 295/378 (78%) | 284 (96%) | 7 (2%) | 4 (1%) | 13 | 11 |
| 1 | J | 296/378 (78%) | 287 (97%) | 8 (3%) | 1 (0%) | 44 | 53 |
| All | All | 3012/3780 (80%) | 2912 (97%) | 84 (3%) | 16 (0%) | 32 | 37 |

5 of 16 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 277 | HIS |
| 1 | B | 66 | GLN |
| 1 | B | 262 | GLY |
| 1 | C | 262 | GLY |
| 1 | F | 66 | GLN |

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 | A | 277/308 (90%) | 273 (99%) | 4 (1%) | 71 | 82 |
| 1 | B | 253/308 (82%) | 250 (99%) | 3 (1%) | 75 | 86 |
| 1 | C | 258/308 (84%) | 251 (97%) | 7 (3%) | 50 | 63 |
| 1 | D | 250/308 (81%) | 246 (98%) | 4 (2%) | 68 | 79 |
| 1 | E | 242/308 (79%) | 240 (99%) | 2 (1%) | 85 | 91 |
| 1 | F | 253/308 (82%) | 249 (98%) | 4 (2%) | 68 | 79 |
| 1 | G | 257/308 (83%) | 254 (99%) | 3 (1%) | 75 | 86 |
| 1 | H | 249/308 (81%) | 243 (98%) | 6 (2%) | 54 | 67 |
| 1 | I | 250/308 (81%) | 247 (99%) | 3 (1%) | 75 | 86 |
| 1 | J | 248/308 (80%) | 243 (98%) | 5 (2%) | 60 | 73 |
| All | All | 2537/3080 (82%) | 2496 (98%) | 41 (2%) | 68 | 79 |

5 of 41 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | E | 176 | TYR |
| 1 | F | 276 | ARG |
| 1 | J | 140 | ASN |
| 1 | E | 331 | ASP |
| 1 | F | 176 | TYR |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | G | 251 | ASN |

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95th 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 ²) | Q<0.9 |
|-----|-------|-----------------|--------|----------------|-----------------------|-------|
| 1 | A | 339/378 (89%) | 0.06 | 8 (2%) 59 69 | 17, 35, 76, 139 | 0 |
| 1 | B | 306/378 (80%) | 0.38 | 20 (6%) 20 27 | 17, 46, 111, 166 | 0 |
| 1 | C | 311/378 (82%) | 0.12 | 14 (4%) 34 46 | 19, 36, 92, 176 | 0 |
| 1 | D | 304/378 (80%) | 0.25 | 11 (3%) 43 55 | 20, 43, 87, 135 | 0 |
| 1 | E | 293/378 (77%) | 0.16 | 17 (5%) 24 34 | 17, 32, 101, 182 | 0 |
| 1 | F | 307/378 (81%) | 0.20 | 21 (6%) 18 26 | 18, 42, 106, 219 | 0 |
| 1 | G | 311/378 (82%) | 0.24 | 15 (4%) 31 43 | 17, 38, 111, 166 | 0 |
| 1 | H | 302/378 (79%) | 0.27 | 13 (4%) 36 48 | 20, 43, 105, 212 | 0 |
| 1 | I | 303/378 (80%) | 0.20 | 17 (5%) 25 36 | 18, 36, 104, 190 | 0 |
| 1 | J | 302/378 (79%) | 0.22 | 12 (3%) 39 51 | 19, 34, 93, 224 | 0 |
| All | All | 3078/3780 (81%) | 0.21 | 148 (4%) 31 43 | 17, 38, 100, 224 | 0 |

The worst 5 of 148 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | J | 247 | GLY | 15.1 |
| 1 | D | 248 | ALA | 11.9 |
| 1 | H | 248 | ALA | 11.7 |
| 1 | J | 248 | ALA | 10.5 |
| 1 | G | 335 | SER | 8.5 |

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

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.