



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:09 pm BST

PDB ID : 1EI3  
Title : CRYSTAL STRUCTURE OF NATIVE CHICKEN FIBRINOGEN  
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Deposited on : 2000-02-23  
Resolution : 5.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11



## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1896 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 FIBRINOGEN.

| Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 1   | A     | 159      | Total C<br>159 159 | 0       | 0       | 159   |
| 1   | D     | 153      | Total C<br>153 153 | 0       | 0       | 153   |

- Molecule 2 is a protein called FIBRINOGEN.

| Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 2   | B     | 395      | Total C<br>395 395 | 0       | 0       | 395   |
| 2   | E     | 395      | Total C<br>395 395 | 0       | 0       | 395   |

- Molecule 3 is a protein called FIBRINOGEN.

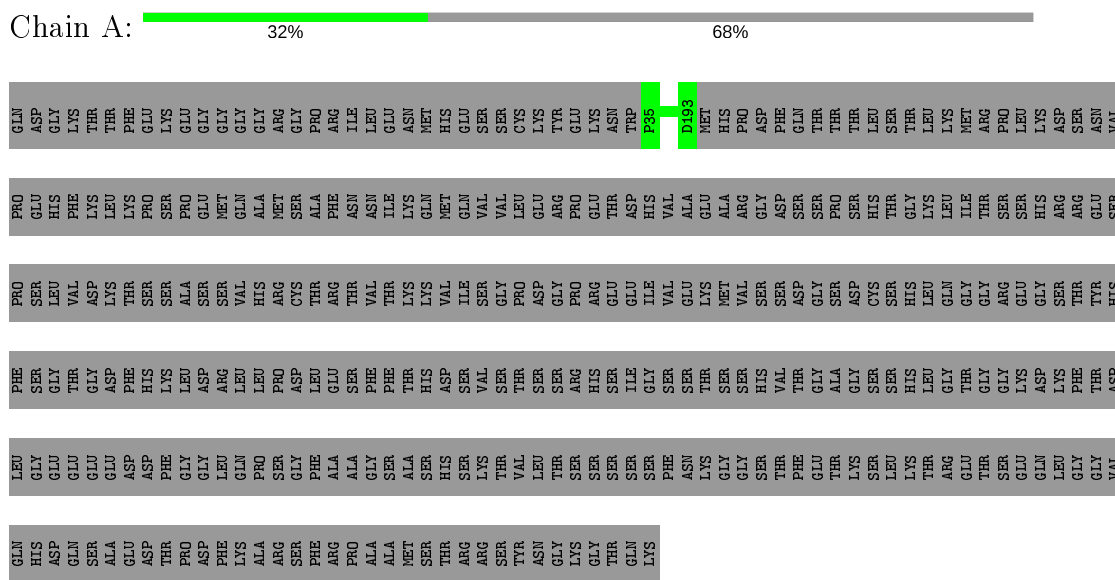
| Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf | Trace |
|-----|-------|----------|--------------------|---------|---------|-------|
| 3   | C     | 397      | Total C<br>397 397 | 0       | 0       | 397   |
| 3   | F     | 397      | Total C<br>397 397 | 0       | 0       | 397   |

### 3 Residue-property plots [i](#)

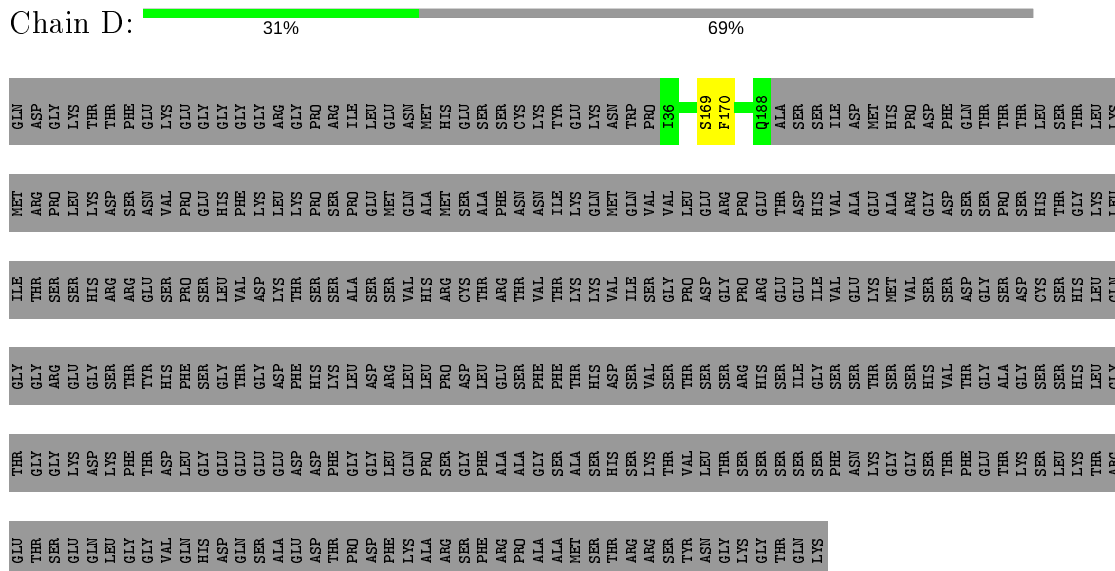
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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.

Note EDS was not executed.


- Molecule 1: FIBRINOGEN



- Molecule 1: FIBRINOGEN




- Molecule 2: FIBRINOGEN

Chain B:  84% 15%

GLN ALA SER VAL GLU TYR ASP ASN GLU GLU ASP SER PRO GLN ILE ASP ARG ALA HIS ARG PRO LEU ASP LYS ARG GLN GLU ALA ALA PRO THR LEU ARG VAL VAL PRO PRO ILE ILE SER THR GLY TYR GLN ARG ARG PRO PRO LYS GLN ASP LYS GLN ALA MET LYS LYS GLY

PRO ILE ILE TYR PRO ASP ALA G68 E86 L87 R108 Y109 F462 PRO ASP

- Molecule 2: FIBRINOGEN

Chain E:  85% 15%

GLN ALA SER VAL GLU TYR ASP ASN GLU GLU ASP SER PRO GLN ILE ASP ARG ALA HIS ARG PRO LEU ASP LYS ARG GLN GLU ALA ALA PRO THR LEU ARG VAL VAL PRO PRO ILE ILE SER THR GLY TYR GLN ARG ARG PRO PRO LYS GLN ASP LYS GLN ALA MET LYS LYS GLY

PRO ILE ILE TYR PRO ASP ALA G68 E86 L87 F462 PRO ASP

- Molecule 3: FIBRINOGEN

Chain C:  97%

Y1 R338 C339 Q397 GLN HIS SER GLY LEU LYS GLN VAL ASP SER

- Molecule 3: FIBRINOGEN

Chain F:  97%

Y1 R338 C339 Q397 GLN HIS SER GLY LEU LYS GLN VAL ASP SER

## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

| Property   | Value  | Source    |
|--|--|-----------|
| Space group  | P 1 21 1   | Depositor |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$ | 114.73Å 101.85Å 210.23Å<br>90.00° 106.71° 90.00° | Depositor |
| Resolution (Å)   | (Not available) – 5.50                           | Depositor |
| % Data completeness<br>(in resolution range)             | (Not available) ((Not available)-5.50)           | Depositor |
| $R_{merge}$  | 0.09   | Depositor |
| $R_{sym}$  | (Not available)                                  | Depositor |
| Refinement program                                       |  | Depositor |
| R, $R_{free}$  | (Not available) , (Not available)                | Depositor |
| Estimated twinning fraction                              | No twinning to report.                           | Xtrriage  |
| Total number of atoms                                    | 1896   | wwPDB-VP  |
| Average B, all atoms (Å <sup>2</sup> )                   | 20.0   | wwPDB-VP  |

## 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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | A     | 159   | 0        | 0        | 0       | 0            |
| 1   | D     | 153   | 0        | 0        | 1       | 0            |
| 2   | B     | 395   | 0        | 0        | 2       | 0            |
| 2   | E     | 395   | 0        | 0        | 1       | 0            |
| 3   | C     | 397   | 0        | 0        | 1       | 0            |
| 3   | F     | 397   | 0        | 0        | 1       | 0            |
| All | All   | 1896  | 0        | 0        | 6       | 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 3.

All (6) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1         | Atom-2         | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|----------------|--------------------------|-------------------|
| 2:B:108:ARG:CA | 2:B:109:VAL:CA | 2.79                     | 0.61              |
| 2:E:86:GLU:CA  | 2:E:87:LEU:CA  | 2.85                     | 0.54              |
| 3:F:338:ARG:CA | 3:F:339:CYS:CA | 2.93                     | 0.46              |

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| Atom-1         | Atom-2         | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|----------------|--------------------------|-------------------|
| 3:C:338:ARG:CA | 3:C:339:CYS:CA | 2.95                     | 0.43              |
| 1:D:169:SER:CA | 1:D:170:PHE:CA | 2.97                     | 0.43              |
| 2:B:86:GLU:CA  | 2:B:87:LEU:CA  | 2.97                     | 0.42              |

There are no symmetry-related clashes.

### 5.3 Torsion angles [\(i\)](#)

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

There are no protein backbone outliers to report in this entry.

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

There are no protein residues with a non-rotameric sidechain to report in this entry.

#### 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 carbohydrates 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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.