



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:32 PM UTC

PDB ID : 1EI3 / pdb_00001ei3
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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

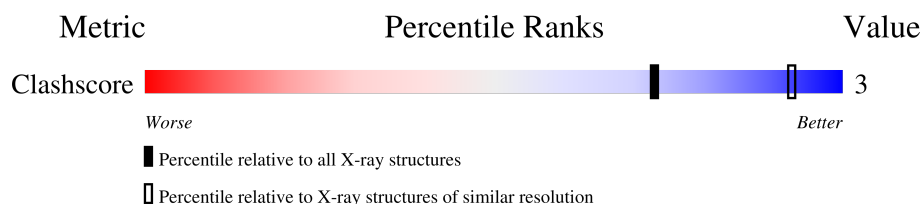
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 Å.

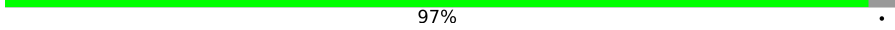
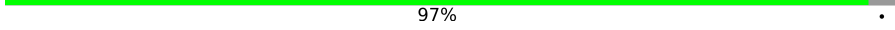
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1147 (7.00-4.00)

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 ≥ 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	491	 32% 68%
1	D	491	 31% 69%
2	B	464	 84% 15%
2	E	464	 85% 15%
3	C	409	 97% .
3	F	409	 97% .

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	0	0	159
			159	159			
1	D	153	Total	C	0	0	153
			153	153			

- Molecule 2 is a protein called FIBRINOGEN.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
2	B	395	Total	C	0	0	395
			395	395			
2	E	395	Total	C	0	0	395
			395	395			

- Molecule 3 is a protein called FIBRINOGEN.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
3	C	397	Total	C	0	0	397
			397	397			
3	F	397	Total	C	0	0	397
			397	397			

Note EDS was not executed.

Chain A:

32%

68%

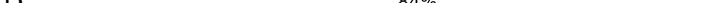
P35

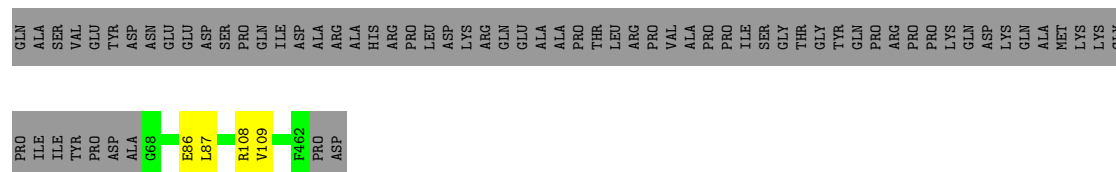
D193

Chain D: 31% 69%

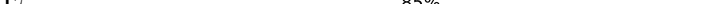
Position	Most Conserved AA
1	GLN
2	ASP
3	GLY
4	GLY
5	LYS
6	LEU
7	LYS
8	THR
9	THR
10	PHE
11	GLU
12	ASN
13	LYS
14	VAL
15	PRO
16	GLU
17	GLY
18	GLY
19	GLY
20	GLY
21	GLY
22	ARG
23	GLY
24	LYS
25	LYS
26	PRO
27	PRO
28	GLY
29	THR
30	THR
31	ILE
32	LEU
33	LEU
34	GLU
35	GLY
36	GLY
37	GLY
38	GLY
39	GLY
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90	GLY
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95	GLY
96	GLY
97	GLY
98	GLY
99	GLY
100	GLY

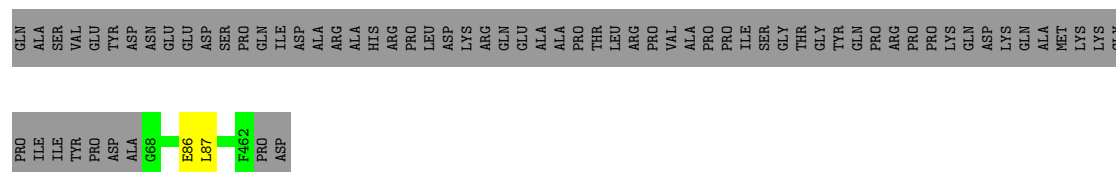
- Molecule 2: FIBRINOGEN

Chain B:  84% 15%



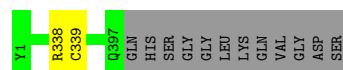
- Molecule 2: FIBRINOGEN

Chain E:  85% 15%



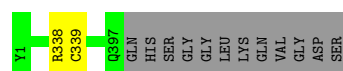
- Molecule 3: FIBRINOGEN

Chain C:  97%



- Molecule 3: FIBRINOGEN

Chain F: 97%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	114.73Å 101.85Å 210.23Å 90.00° 106.71° 90.00°	Depositor
Resolution (Å)	(Not available) – 5.50	Depositor
% Data completeness (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.	Xtriage
Total number of atoms	1896	wwPDB-VP
Average B, all atoms (Å ²)	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 oligosaccharides 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.