



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 04:12 am GMT

PDB ID : 1EI3
Title : CRYSTAL STRUCTURE OF NATIVE CHICKEN FIBRINOGEN
Authors : Yang, Z.; Mochalkin, I.; Veerapandian, L.; Riley, M.; Doolittle, R.F.
Deposited on : 2000-02-23
Resolution : 5.50 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

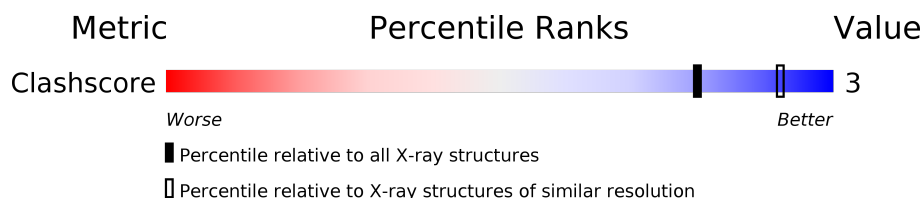
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.50 Å.


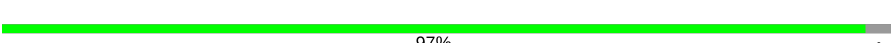
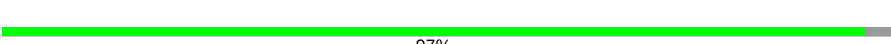
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1021 (7.20-3.76)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	491	
1	D	491	
2	B	464	
2	E	464	
3	C	409	
3	F	409	

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			

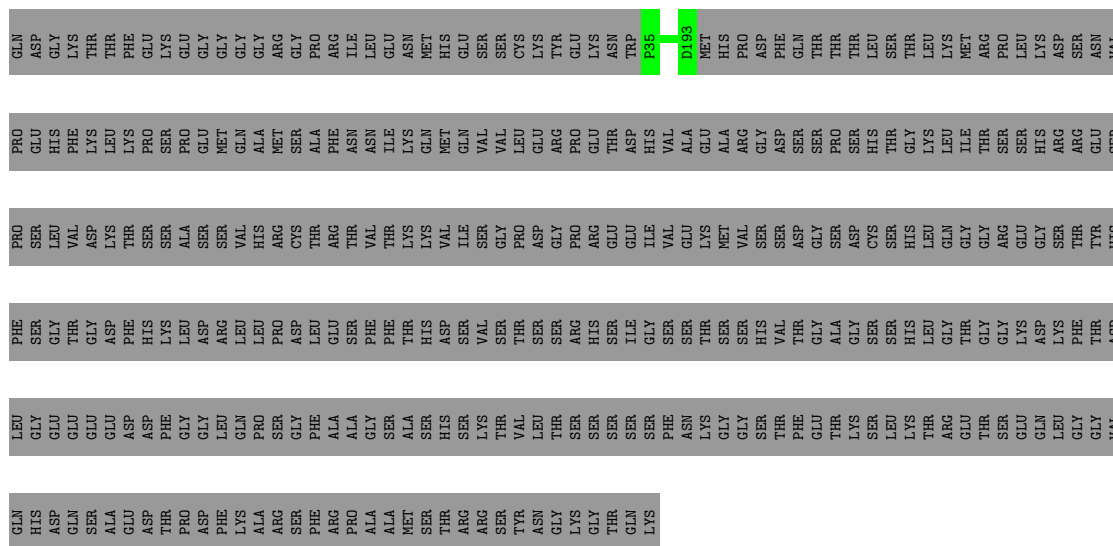
- Molecule 3 is a protein called FIBRINOGEN.

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.

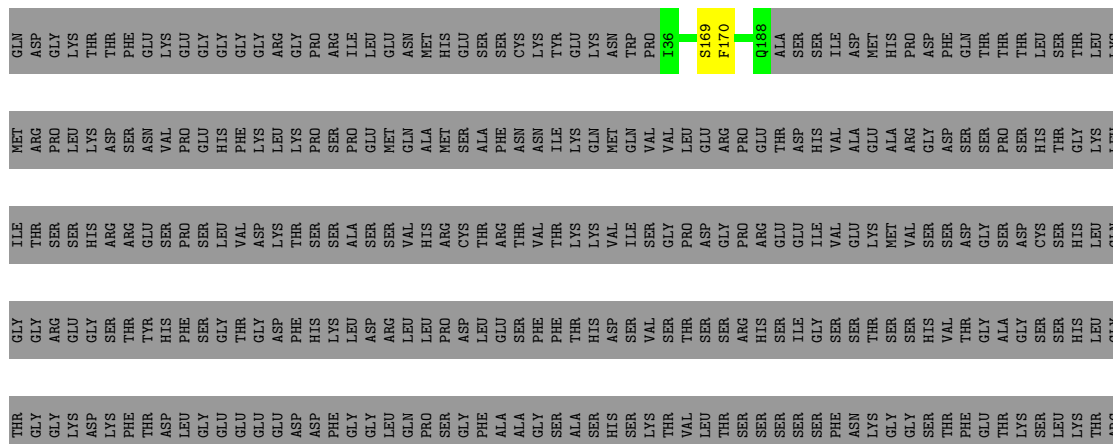
- Molecule 1: FIBRINOGEN

68%



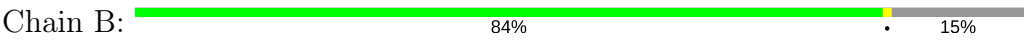
- Molecule 1: FIBRINOGEN

69%



GLU	THR	SER	GLU	GLN	LEU	GLY	VAL	GLN	HIS	ASP	GLN	SER	ALA	GLU	ASP	THR	PRO	ASP	PHE	LYS	ALA	ARG	SER	PHE	ARG	PRO	ALA	ALA	MET	SER	THR	ARG	SER	TYR	ASN	GLY	LYS	GLY	THR	GLN	LYS
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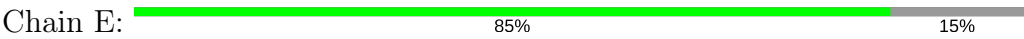
● Molecule 2: FIBRINOGEN



GLN	ALA	SER	VAL	GLU	TYR	PRO	ASP	ASP	ASN	GLU	GLU	ASP	SER	PRO	GLN	ILE	ASP	ALA	ALA	ARG	ALA	HIS	ARG	PRO	LEU	LEU	LYS	ARG	GLN	GLU	ALA	ALA	PRO	THR	LEU	ARG	PRO	VAL	ALA	PRO	PRO	ILE	ILE	SER	GLY	THR	GLY	TYR	GLN	PRO	PRO	ARG	PRO	PRO	LYS	GLN	ASP	LYS	GLN	ALA	MET	LYS	LYS	GLY
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PRO	ILE	ILE	TYR	PRO	ASP	ALA	G68	E86	L87	R108	V109	F462	PRO	ASP
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● Molecule 2: FIBRINOGEN



GLN	ALA	SER	VAL	GLU	TYR	ASP	ASN	GLU	GLU	ASP	SER	PRO	GLN	ILE	ASP	ALA	ALA	ARG	ALA	HIS	ARG	PRO	LEU	LEU	LYS	ARG	GLN	GLU	ALA	ALA	PRO	THR	LEU	ARG	PRO	VAL	ALA	PRO	PRO	ILE	ILE	SER	GLY	THR	GLY	TYR	GLN	PRO	PRO	ARG	PRO	PRO	LYS	GLN	ASP	LYS	GLN	ALA	MET	LYS	LYS	GLY
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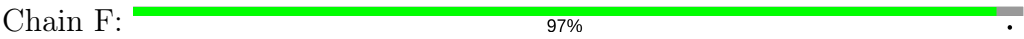
PRO	ILE	ILE	TYR	PRO	ASP	ALA	G68	E86	L87	F462	PRO	ASP
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● Molecule 3: FIBRINOGEN



Y1	R338	C339	Q397	GLN	HIS	SER	GLY	GLY	LEU	LYS	GLN	VAL	GLY	ASP	SER
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● Molecule 3: FIBRINOGEN



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

The worst 5 of 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

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.