



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:15 AM UTC

PDB ID : 2FOK / pdb\_00002fok  
Title : STRUCTURE OF RESTRICTION ENDONUCLEASE FOKI  
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Deposited on : 1998-03-30  
Resolution : 2.30 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

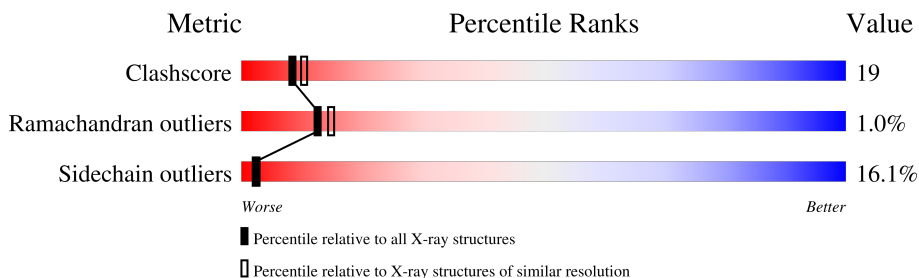
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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  $\geq 3$ , 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	579	 52% 35% 8% . .
1	B	579	 54% 35% 8% . .

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 9427 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 FOKI RESTRICTION ENDONUCLEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	558	4458	2859	764	824	11	0	0	0
1	B	560	4453	2860	759	823	11	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	380	LEU	GLY	conflict	UNP P14870
A	381	GLY	VAL	conflict	UNP P14870
A	382	LYS	THR	conflict	UNP P14870
A	383	PRO	LYS	conflict	UNP P14870
A	384	ASP	GLN	conflict	UNP P14870
B	380	LEU	GLY	conflict	UNP P14870
B	381	GLY	VAL	conflict	UNP P14870
B	382	LYS	THR	conflict	UNP P14870
B	383	PRO	LYS	conflict	UNP P14870
B	384	ASP	GLN	conflict	UNP P14870

- Molecule 2 is water.

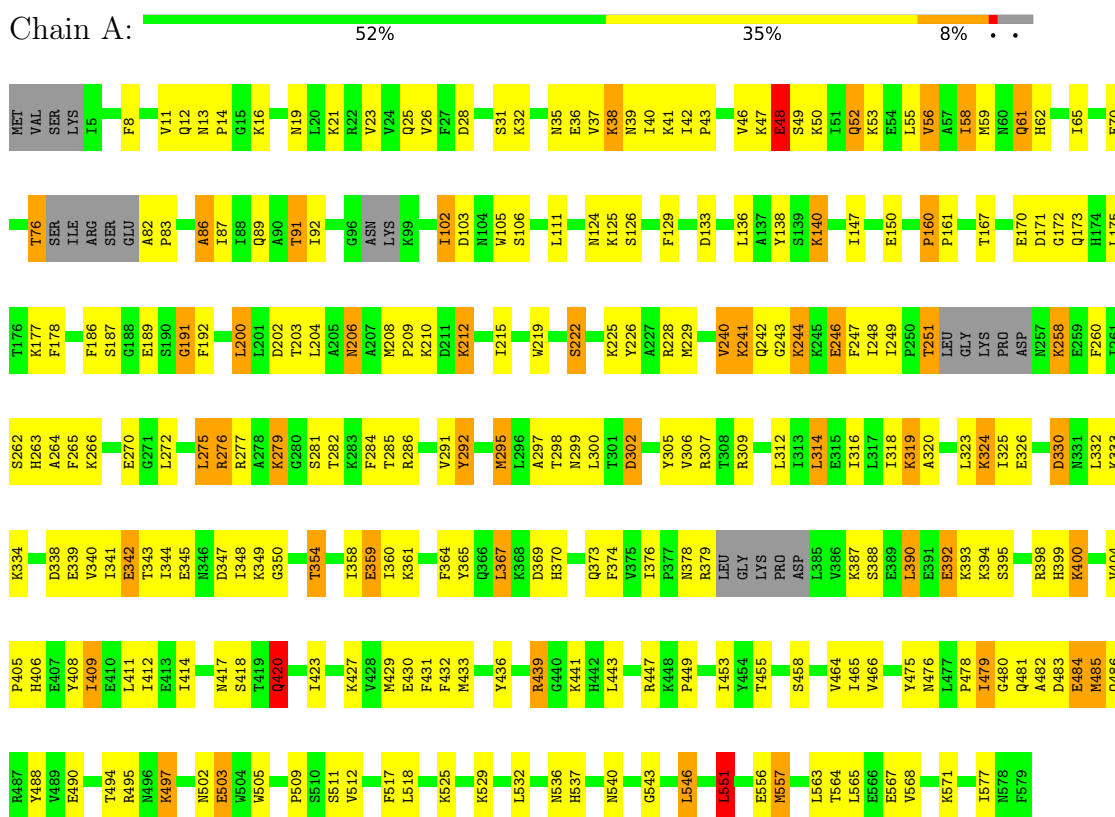
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	282	Total	O	0	0
			282	282		
2	B	234	Total	O	0	0
			234	234		

### 3 Residue-property plots

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.

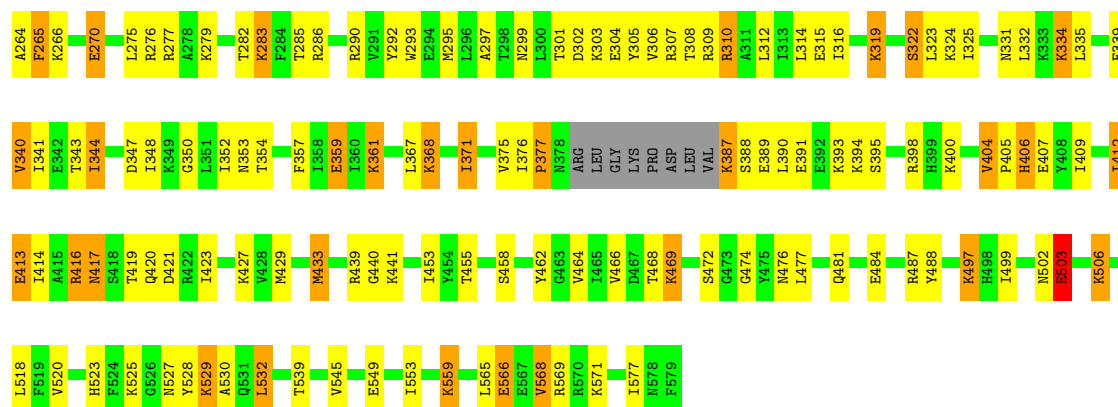
Note EDS was not executed.

- Molecule 1: FOKI RESTRICTION ENDONUCLEASE



- Molecule 1: FOKI RESTRICTION ENDONUCLEASE





## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.01Å 137.17Å 188.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.30	Depositor
% Data completeness (in resolution range)	96.5 (6.00-2.30)	Depositor
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.211 , 0.306	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	9427	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.46	0/4543	0.95	16/6118 (0.3%)
1	B	0.45	0/4539	0.94	20/6115 (0.3%)
All	All	0.45	0/9082	0.94	36/12233 (0.3%)

There are no bond length outliers.

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	376	ILE	N-CA-C	-8.39	99.93	107.56
1	B	127	ASP	N-CA-C	-7.49	101.63	111.74
1	A	86	ALA	N-CA-C	7.33	118.21	107.88
1	B	404	VAL	N-CA-C	7.12	114.04	107.56
1	B	17	PHE	N-CA-C	-6.90	103.76	111.28

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	4458	0	4494	163	0
1	B	4453	0	4486	180	0
2	A	282	0	0	14	0
2	B	234	0	0	8	0
All	All	9427	0	8980	342	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 19.

The worst 5 of 342 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:A:497:LYS:H	1:A:497:LYS:HD2	1.35	0.91
1:B:417:ASN:HB2	1:B:420:GLN:HG2	1.54	0.89
1:B:390:LEU:HD21	1:B:413:GLU:HG2	1.53	0.88
1:B:37:VAL:HA	1:B:41:LYS:HB2	1.55	0.88
1:B:131:ILE:HD13	1:B:136:LEU:HD13	1.53	0.88

There are no symmetry-related clashes.

## 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	A	548/579 (95%)	514 (94%)	31 (6%)	3 (0%)	24 31
1	B	552/579 (95%)	512 (93%)	32 (6%)	8 (1%)	9 9
All	All	1100/1158 (95%)	1026 (93%)	63 (6%)	11 (1%)	12 15

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	48	GLU
1	A	400	LYS
1	A	48	GLU
1	B	503	GLU
1	B	14	PRO

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

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	478/503 (95%)	396 (83%)	82 (17%)	2	2
1	B	475/503 (94%)	404 (85%)	71 (15%)	3	3
All	All	953/1006 (95%)	800 (84%)	153 (16%)	2	2

5 of 153 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	314	LEU
1	B	503	GLU
1	B	332	LEU
1	B	407	GLU
1	B	553	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	60	ASN
1	B	299	ASN
1	B	527	ASN
1	B	331	ASN
1	B	217	ASN

### 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 [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.