



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2018 – 08:46 am GMT

PDB ID : 2SFA  
Title : SERINE PROTEINASE FROM STREPTOMYCES FRADIAE ATCC 14544  
Authors : Kitadokoro, K.; Tsuzuki, H.  
Deposited on : 1994-04-25  
Resolution : 1.60 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  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

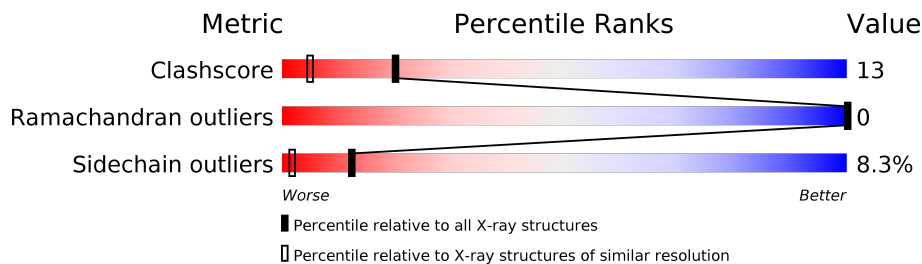
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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	122078	3200 (1.60-1.60)
Ramachandran outliers	120005	3115 (1.60-1.60)
Sidechain outliers	119972	3114 (1.60-1.60)

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  $\geq 3$ , 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	191	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1423 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 SERINE PROTEINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	191	Total	C	N	O	S	0	0	0
			1337	816	240	277	4			

- Molecule 2 is water.

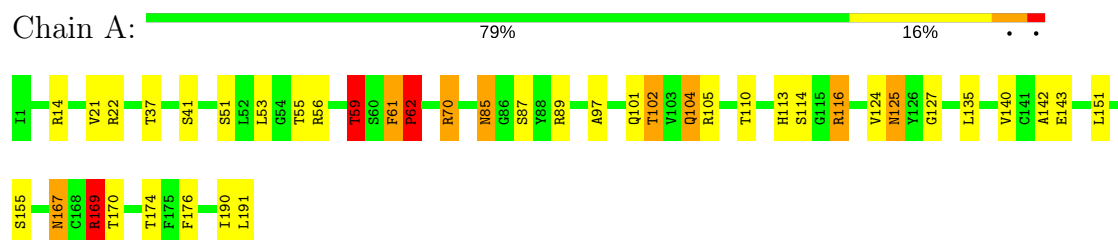
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	86	Total	O	0	0
			86	86		

### 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 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.

Note EDS was not executed.

#### • Molecule 1: SERINE PROTEINASE



## 4 Data and refinement statistics

Xtriage (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, $\alpha$ , $\beta$ , $\gamma$	69.05 Å 72.76 Å 29.84 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.60	Depositor
% Data completeness (in resolution range)	85.2 (8.00-1.60)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.182 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1423	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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	1.48	3/1359 (0.2%)	1.91	25/1844 (1.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	62	PRO	N-CD	34.42	1.96	1.47
1	A	62	PRO	N-CA	-18.21	1.16	1.47
1	A	62	PRO	CA-C	5.56	1.64	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	PRO	N-CA-CB	30.76	140.21	103.30
1	A	62	PRO	CA-N-CD	-20.31	83.07	111.50
1	A	61	PHE	C-N-CA	13.73	179.66	122.00
1	A	56	ARG	NE-CZ-NH1	12.45	126.53	120.30
1	A	116	ARG	NE-CZ-NH1	11.93	126.26	120.30
1	A	22	ARG	NE-CZ-NH1	11.16	125.88	120.30
1	A	62	PRO	CA-CB-CG	-11.04	83.03	104.00
1	A	61	PHE	C-N-CD	-10.61	97.26	120.60
1	A	169	ARG	NE-CZ-NH1	10.55	125.58	120.30
1	A	105	ARG	NE-CZ-NH1	10.35	125.48	120.30
1	A	70	ARG	NE-CZ-NH1	-8.37	116.11	120.30
1	A	62	PRO	N-CA-C	-8.19	90.80	112.10
1	A	22	ARG	NE-CZ-NH2	-7.37	116.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	70	ARG	CD-NE-CZ	-6.87	113.99	123.60
1	A	59	THR	CA-CB-CG2	6.74	121.84	112.40
1	A	116	ARG	NE-CZ-NH2	-6.67	116.97	120.30
1	A	62	PRO	CB-CA-C	6.63	128.58	112.00
1	A	14	ARG	NE-CZ-NH1	-6.22	117.19	120.30
1	A	22	ARG	CD-NE-CZ	6.08	132.11	123.60
1	A	169	ARG	CD-NE-CZ	5.89	131.85	123.60
1	A	70	ARG	NH1-CZ-NH2	5.71	125.68	119.40
1	A	56	ARG	NH1-CZ-NH2	-5.33	113.54	119.40
1	A	104	GLN	O-C-N	5.29	131.16	122.70
1	A	89	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	A	102	THR	N-CA-CB	5.09	119.98	110.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	62	PRO	CA

There are no planarity outliers.

## 5.2 Too-close contacts

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	1337	0	1266	35	0
2	A	86	0	0	2	5
All	All	1423	0	1266	35	5

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 13.

All (35) 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:62:PRO:CD	1:A:62:PRO:N	1.96	1.21
1:A:167:ASN:HD22	1:A:169:ARG:H	1.01	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ASN:HD21	1:A:87:SER:HB2	1.35	0.89
1:A:167:ASN:ND2	1:A:169:ARG:H	1.73	0.86
1:A:61:PHE:C	1:A:62:PRO:CD	2.49	0.81
1:A:85:ASN:H	1:A:85:ASN:HD22	1.34	0.74
1:A:167:ASN:HD22	1:A:169:ARG:N	1.83	0.72
1:A:104:GLN:HG2	1:A:114:SER:HB3	1.73	0.71
1:A:70:ARG:HH11	1:A:70:ARG:HG2	1.57	0.68
1:A:70:ARG:HG2	1:A:70:ARG:NH1	2.07	0.67
1:A:125:ASN:HD22	1:A:127:GLY:H	1.46	0.62
1:A:61:PHE:O	1:A:62:PRO:CD	2.49	0.60
1:A:167:ASN:HD21	1:A:169:ARG:HB2	1.70	0.57
1:A:125:ASN:ND2	1:A:127:GLY:H	2.03	0.56
1:A:167:ASN:ND2	1:A:170:THR:H	2.03	0.55
1:A:37:THR:OG1	1:A:59:THR:HB	2.07	0.54
1:A:70:ARG:HH11	1:A:70:ARG:CG	2.15	0.52
1:A:167:ASN:HD21	1:A:170:THR:H	1.58	0.51
1:A:85:ASN:N	1:A:85:ASN:HD22	2.01	0.50
1:A:167:ASN:ND2	1:A:169:ARG:N	2.52	0.49
1:A:124:VAL:HG12	1:A:135:LEU:CD1	2.44	0.48
1:A:167:ASN:ND2	1:A:169:ARG:HB2	2.27	0.48
1:A:116:ARG:NE	2:A:273:HOH:O	2.19	0.48
1:A:97:ALA:HA	1:A:101:GLN:OE1	2.15	0.47
1:A:116:ARG:CD	2:A:273:HOH:O	2.61	0.47
1:A:85:ASN:ND2	1:A:87:SER:H	2.14	0.46
1:A:70:ARG:NH1	1:A:70:ARG:CG	2.68	0.45
1:A:110:THR:O	1:A:113:HIS:HE1	2.00	0.45
1:A:41:SER:O	1:A:55:THR:HA	2.17	0.45
1:A:142:ALA:CB	1:A:174:THR:HG21	2.48	0.43
1:A:21:VAL:HG12	1:A:190:ILE:HD13	2.00	0.43
1:A:110:THR:O	1:A:113:HIS:CE1	2.72	0.42
1:A:143:GLU:OE2	1:A:167:ASN:HB2	2.20	0.42
1:A:151:LEU:HB2	1:A:176:PHE:CD2	2.56	0.41
1:A:140:VAL:O	1:A:174:THR:HG23	2.22	0.40

All (5) 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)
2:A:225:HOH:O	2:A:228:HOH:O[1_554]	0.30	1.90
2:A:248:HOH:O	2:A:276:HOH:O[1_554]	0.31	1.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:259:HOH:O	2:A:277:HOH:O[1_554]	0.34	1.86
2:A:211:HOH:O	2:A:263:HOH:O[1_554]	0.88	1.32
2:A:245:HOH:O	2:A:254:HOH:O[2_555]	1.78	0.42

## 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	189/191 (99%)	185 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	133/133 (100%)	122 (92%)	11 (8%)	12	2

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	SER
1	A	53	LEU
1	A	59	THR
1	A	62	PRO
1	A	85	ASN

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Mol	Chain	Res	Type
1	A	102	THR
1	A	125	ASN
1	A	155	SER
1	A	167	ASN
1	A	169	ARG
1	A	191	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	113	HIS
1	A	125	ASN
1	A	167	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 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 [i](#)

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.