



wwPDB NMR Structure Validation Summary Report ⓘ

Apr 15, 2026 – 11:23 AM UTC

PDB ID : 1AH2 / pdb_00001ah2
Title : SERINE PROTEASE PB92 FROM BACILLUS ALCALOPHILUS, NMR, 18
STRUCTURES
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Deposited on : 1997-04-11

This is a wwPDB NMR 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

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

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
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

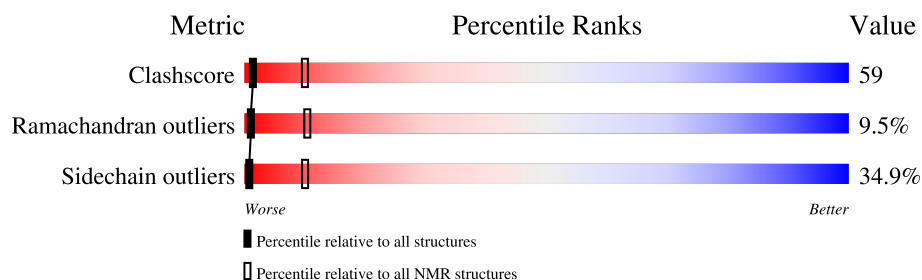
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	269	

2 Ensemble composition and analysis

This entry contains 18 models. Model 9 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:3-A:51, A:55-A:96, A:100-A:251, A:256-A:269 (257)	1.22	9

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 6, 7, 8, 9, 12, 13, 15, 17
2	5, 14
3	3, 18
Single-model clusters	10; 11; 16

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3721 atoms, of which 1839 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SERINE PROTEASE PB92.

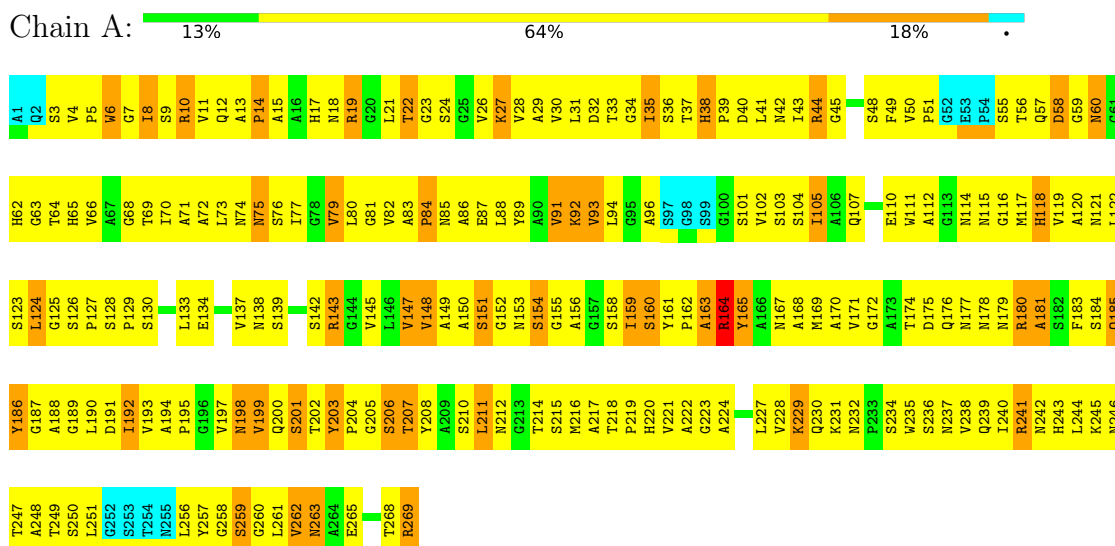
Mol	Chain	Residues	Atoms						Trace
1	A	269	Total	C	H	N	O	S	0
			3721	1151	1839	348	380	3	

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

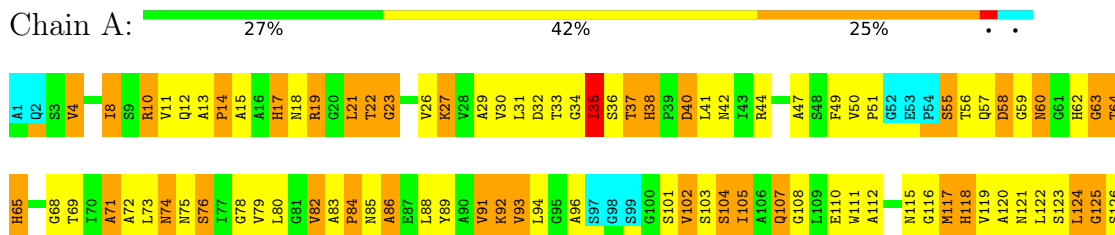
• Molecule 1: SERINE PROTEASE PB92



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 9. Colouring as in section 4.1 above.

• Molecule 1: SERINE PROTEASE PB92



Q200	S130
S201	
T202	L133
Y203	E134
P204	Q135
G205	A136
S206	V137
T207	N138
Y208	
A209	R143
S210	
L211	V147
	V148
S215	A149
M216	A150
A217	S151
T218	G152
P219	N153
H220	S154
V221	G155
A222	
	S158
V228	I159
K229	S160
Q230	Y161
K231	P162
N232	A163
	R164
W235	Y165
S236	A166
N237	N167
V238	A168
Q239	M169
T240	A170
R241	V171
N242	G172
H243	
L244	D175
K245	Q176
N246	N177
T247	N178
A248	N179
T249	R180
S250	A181
L251	
G252	Q185
S253	Y186
T254	G187
M255	A188
L256	
Y257	D191
G258	I192
S259	V193
G260	A194
L261	P195
V262	G196
N263	V197
A264	N198
	Y199
T268	

R269

5 Refinement protocol and experimental data overview

The models were refined using the following method: *DGSA*.

Of the 20 calculated structures, 18 were deposited, based on the following criterion: *NO NOE AND H-BOND VIOLATIONS > 0.5 Å*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR	structure solution	3.1

No chemical shift data was provided.

6 Model quality i

6.1 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 (average) 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	1.49±0.01	0±0/1840 (0.0± 0.0%)	1.27±0.01	1±1/2514 (0.1± 0.0%)
All	All	1.49	4/33120 (0.0%)	1.27	26/45252 (0.1%)

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	Planarity
1	A	0.0±0.0	7.4±0.9
All	All	0	133

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	100	GLY	N-CA	5.73	1.49	1.44	13	3
1	A	95	GLY	N-CA	5.20	1.49	1.44	3	1

5 of 7 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	138	ASN	N-CA-C	-6.35	104.36	111.28	16	13
1	A	23	GLY	N-CA-C	-5.67	108.11	115.59	11	8
1	A	96	ALA	N-CA-C	-5.45	107.01	113.38	18	1
1	A	157	GLY	N-CA-C	-5.40	107.53	115.30	14	1
1	A	161	TYR	N-CA-C	-5.25	103.46	110.07	6	1

There are no chirality outliers.

5 of 8 unique planar outliers are listed below. They are sorted by the frequency of occurrence in

the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	10	ARG	Sidechain	17
1	A	19	ARG	Sidechain	17
1	A	143	ARG	Sidechain	17
1	A	164	ARG	Sidechain	17
1	A	269	ARG	Sidechain	17

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1807	1774	1774	211±21
All	All	32526	31932	31932	3795

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 59.

5 of 1876 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:LEU:HD23	1:A:93:VAL:HG21	1.01	1.28	3	10
1:A:72:ALA:HB3	1:A:81:GLY:N	0.99	1.70	7	12
1:A:20:GLY:C	1:A:21:LEU:HD13	0.99	1.83	7	1
1:A:121:ASN:C	1:A:122:LEU:HD13	0.98	1.82	7	4
1:A:186:TYR:CD2	1:A:190:LEU:HD22	0.97	1.94	5	1

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	256/269 (95%)	180±6 (71±2%)	51±4 (20±2%)	24±4 (9±2%)	1	10
All	All	4608/4842 (95%)	3249 (71%)	923 (20%)	436 (9%)	1	10

5 of 98 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	84	PRO	18
1	A	163	ALA	18
1	A	198	ASN	17
1	A	14	PRO	15
1	A	79	VAL	15

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. 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	186/194 (96%)	121±5 (65±3%)	65±5 (35±3%)	1	10
All	All	3348/3492 (96%)	2180 (65%)	1168 (35%)	1	10

5 of 157 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	91	VAL	18
1	A	263	ASN	18
1	A	38	HIS	17
1	A	143	ARG	16
1	A	147	VAL	16

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided