

Integrative Structure Validation Report ?

August 27, 2026 - 08:59 AM PDT

The following software was used in the production of this report:

IHMValidation Version 3.2

Python-IHM Version 2.9

MolProbity Version 4.5.2

PDB ID	9A9I pdb_00009a9i
Structure Title	CS-Rosetta model of the cysteine-rich domain of the 15-kDa selenoprotein (SEP15) using backbone chemical shifts and residual dipolar couplings
Structure Authors	Williams, R.V.; Gierasch, L.M.
Deposited on	2025-02-28

This is a PDB-IHM Structure Validation Report.

We welcome your comments at helpdesk@pdb-ihm.org

A user guide is available at https://pdb-ihm.org/validation_help.html with specific help available everywhere you see the ? symbol.

List of references used to build this report is available [here](#).

1. Overview ?

1.1. Summary ?

This entry consists of 10 model(s). A total of 1 dataset(s) were used to build this entry.

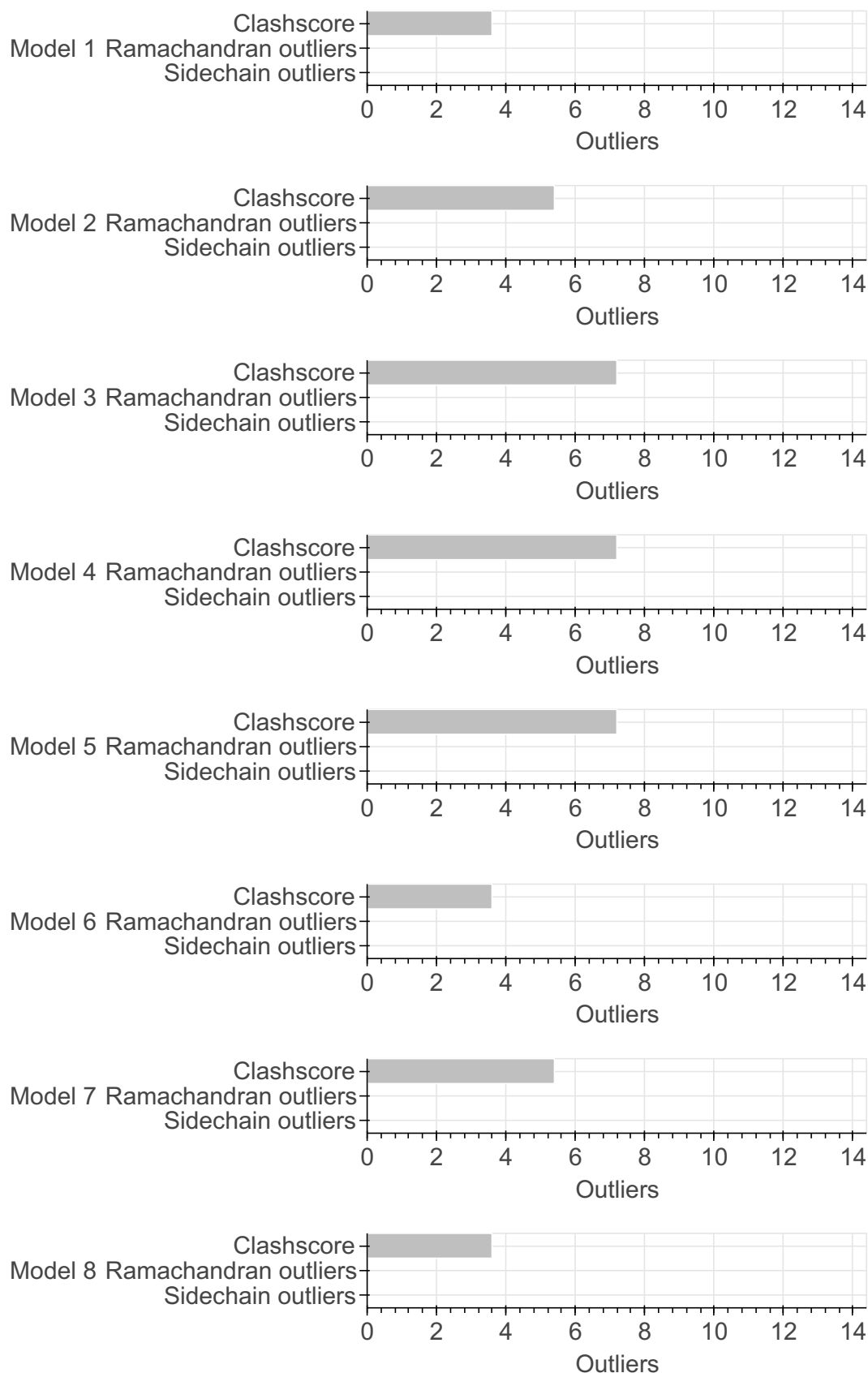
Name	Type	Count
NMR data	Experimental data	1

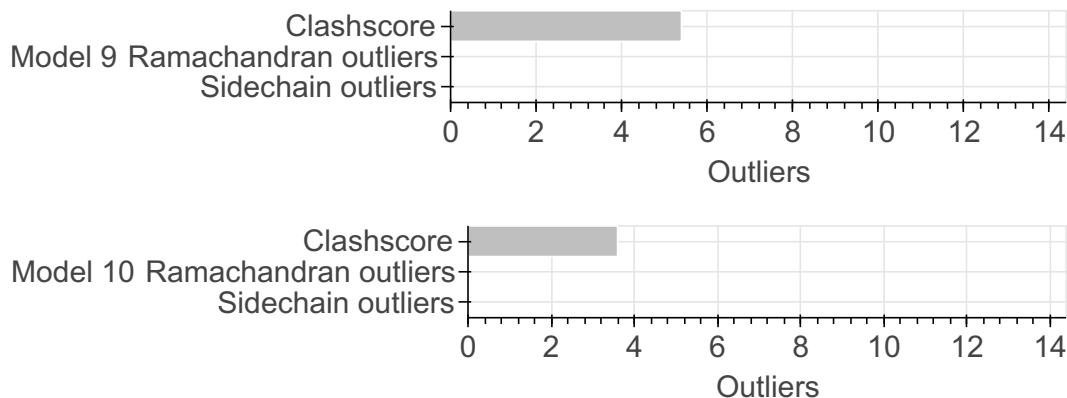
1.2. Overall quality ?

This validation report contains model quality assessments for all structures, data quality and fit to model assessments for SAS and

crosslinking-MS datasets. Data quality and fit to model assessments for other datasets and model uncertainty are under development.
Number of plots is limited to 256.

Model Quality: MolProbity Analysis ?





2. Model Details ?

2.1. Ensemble information ?

This entry consists of 0 distinct ensemble(s).

2.2. Representation ?

This entry has 1 representation(s).

ID	Model(s)	Entity ID	Molecule name	Chain(s) [auth]	Total residues	Rigid segments	Flexible segments	Model coverage/ Starting model coverage (%)	Scale
1	1-10	1	Selenoprotein F cysteine-rich domain	A	52	-	1-52	100.00 / 0.00	Atomic

2.3. Datasets used for modeling ?

There is 1 unique dataset used to build the models in this entry.

ID	Dataset type	Database name	Data access code
1	NMR data	BMRB	52892

2.4. Methodology and software ?

This entry is a result of 1 distinct protocol(s).

Step number	Protocol ID	Method name	Method type	Method description	Number of computed models	Multi state modeling	Multi scale modeling
1	1	1	CS-Rosetta	Not available	3000	False	False

There is 1 software package reported in this entry.

ID	Software name	Software version	Software classification	Software location
1	CS-Rosetta	Not available	model building	https://www.rosettacommons.org/docs/latest/CS-Rosetta

3. Data quality ?

3.4. NMR ?

Validation for this section is under development.

4. Model quality ?

For models with atomic structures, MolProbity analysis is performed. For models with coarse-grained or multi-scale structures, excluded volume analysis is performed.

4.1b. MolProbity Analysis ?

Excluded volume satisfaction for the models in the entry are listed below. The Analysed column shows the number of particle-particle or particle-atom pairs for which excluded volume was analysed.

Standard geometry: bond outliers ?

There are no bond length outliers.

Standard geometry: angle outliers ?

There are no bond angle outliers.

Too-close contacts ?

The following all-atom clashscore is based on a MolProbity analysis. All-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The table below contains clashscores for all atomic models in this entry.

Model ID	Clash score	Number of clashes
1	3.60	2
2	5.40	3
3	7.19	4
4	7.19	4
5	7.19	4
6	3.60	2
7	5.40	3
8	3.60	2
9	5.40	3
10	3.60	2

There are 29 clashes. The table below contains the detailed list of all clashes based on a MolProbity analysis. Bad clashes are >= 0.4 Angstrom.

Atom 1	Atom 2	Clash(Å)	Model ID (Worst)	Models (Total)
A:36:ASP:N	A:37:PRO:CD	0.57	9	10
A:21:CYS:SG	A:44:GLN:O	0.49	5	6
A:36:ASP:HB3	A:37:PRO:HD3	0.46	6	9
A:36:ASP:N	A:37:PRO:HD2	0.42	3	3

Atom 1	Atom 2	Clash(Å)	Model ID (Worst)	Models (Total)
A:36:ASP:HB2	A:37:PRO:HD3	0.42	3	1

Torsion angles: Protein backbone ?

In the following table, Ramachandran outliers are listed. The Analysed column shows the number of residues for which the backbone conformation was analysed.

Model ID	Analysed	Favored	Allowed	Outliers
1	37	37	0	0
2	37	37	0	0
3	37	37	0	0
4	37	34	3	0
5	37	37	0	0
6	37	37	0	0
7	37	37	0	0
8	37	37	0	0
9	37	37	0	0
10	37	36	1	0

Torsion angles : Protein sidechains ?

In the following table, sidechain rotameric outliers are listed. The Analysed column shows the number of residues for which the sidechain conformation was analysed.

Model ID	Analysed	Favored	Allowed	Outliers
1	35	35	0	0
2	35	35	0	0
3	35	35	0	0
4	35	35	0	0
5	35	35	0	0
6	35	35	0	0
7	35	35	0	0
8	35	35	0	0
9	35	35	0	0
10	35	35	0	0

5. Fit to Data Used for Modeling Assessment ?

5.4. NMR ?

Validation for this section is under development.

6. Fit to Data Used for Validation Assessment ?

Validation for this section is under development.

Acknowledgments

The development of integrative model validation metrics, implementation of a model validation pipeline, and creation of a validation report for integrative structures are funded by NSF awards to the [PDB-IHM team](#) (DBI-1756248, DBI-2112966, DBI-2112967, DBI-2112968, and DBI-1756250) and awards from NSF, NIH, and DOE to the [RCSB PDB](#) (DBI-2321666, R01GM157729, and DE-SC0019749). The PDB-IHM team and members of the [Sali lab](#) contributed model validation metrics and software packages.

Dr. Jill Trewhella, Dr. Dina Schneidman, and members of the [SASBDB](#) repository are acknowledged for their advice and support in implementing SAS validation methods. Team members from the labs of Dr. Juri Rappsilber, Dr. Alexander Leitner, Dr. Andrea Graziadei, and members of [PRIDE](#) database are acknowledged for their advice and support in implementing crosslinking-MS validation methods. We are grateful to Dr. Shruthi Viswanath for discussions about uncertainty assessment of integrative structural models.

Members of the [wwPDB Integrative/Hybrid Methods Task Force](#) provided recommendations and community support for the project.