

Integrative Structure Validation Report ?

March 27, 2025 - 10:00 AM PDT

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

Integrative Modeling Validation Version 2.0

Python-IHM Version 1.8

MolProbity Version 4.5.2

PDB ID	9A0C
PDB-Dev ID	PDBDEV_00000048
Structure Title	Refined structure of MR78 Antibody in complex with Marburg glycoprotein using Rosetta
Structure Authors	Sangha AK; Dong J; Williamson L; Hashiguchi T; Saphire EO; Crowe JE; Meiler J
Deposited on	2020-04-19

This is a PDB-IHM IM Structure Validation Report for a publicly released PDB-IHM entry.

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

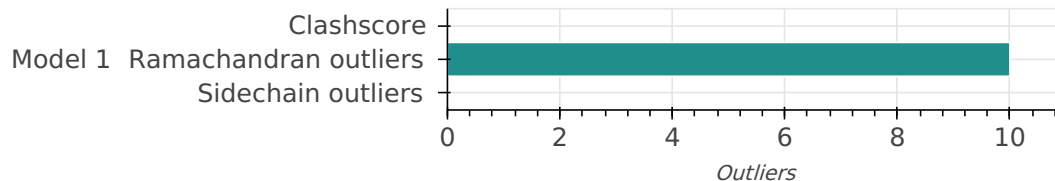
A user guide is available at https://pdb-ihm.org/validation_help.html with specific help available everywhere you see the ? symbol.

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

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



Ensemble information ?

This entry consists of 0 distinct ensemble(s).

Summary ?

This entry consists of 1 model(s). A total of 2 datasets were used to build this entry.

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	1	Marburg Glycoprotein 1	M	152	-	1-152	100.00 / 100.00	Atomic
		2	Marburg Glycoprotein 2	N	83	-	1-83	100.00 / 100.00	Atomic
		3	MR78 antibody heavy chain	O	106	-	1-106	100.00 / 100.00	Atomic
		4	MR78 antibody light chain	P	124	-	1-124	100.00 / 100.00	Atomic

Datasets used for modeling ?

There are 2 unique datasets used to build the models in this entry.

ID	Dataset type	Database name	Data access code
1	Experimental model	PDB	3X2D
2	X-ray diffraction data	PDB	5UQY

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	Rosetta refinement	–	None	–	False	False

There is 1 software package reported in this entry.

ID	Software name	Software version	Software classification	Software location
1	ROSETTA	Not available	model building	https://github.com/RosettaCommons

Data quality ?

X-ray diffraction

Validation for this section is under development.

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.

Standard geometry: bond outliers ?

There are no bond length outliers.

Standard geometry: angle outliers ?

There are 4 bond angle outliers in this entry (0.08% of 5052 assessed bonds). A summary is provided below.

Chain	Res	Type	Atoms	Z	Observed (Å)	Ideal (Å)	Model ID (Worst)	Models (Total)
M	143	ASN	CA-CB-CG	5.46	118.06	112.60	1	1
N	57	LEU	C-N-CA	4.50	129.81	121.70	1	1
M	50	PRO	CA-N-CD	4.40	118.16	112.00	1	1

Chain	Res	Type	Atoms	Z	Observed (Å)	Ideal (Å)	Model ID (Worst)	Models (Total)
O	96	PHE	CA-CB-CG	4.11	117.91	113.80	1	1

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	0.00	0

There are no too-close contacts.

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	457	413	34	10

There are 10 unique backbone outliers. Detailed list of outliers are tabulated below.

Chain	Res	Type	Models (Total)
M	6	ALA	1
M	7	SER	1
M	10	GLN	1
M	119	ASP	1
N	11	SER	1
N	14	LEU	1
N	24	ILE	1
N	58	LEU	1
N	69	LEU	1
O	78	LEU	1

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	400	398	2	0

Fit of model to data used for modeling ?

X-ray diffraction

Validation for this section is under development.

Fit of model to data used for validation ?

Validation for this section is under development.

Acknowledgments

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