

**Summary of integrative structure determination of Refined structure of MR78 Antibody
in complex with Marburg glycoprotein using Rosetta (PDB ID: 9A0C, PDB-Dev ID:
PDBDEV_00000048)**

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - MR78 antibody light chain: Chain P (124 residues) - Marburg Glycoprotein 2: Chain N (83 residues) - MR78 antibody heavy chain: Chain O (106 residues) - Marburg Glycoprotein 1: Chain M (152 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB ID: 3X2D - Other, PDB: 5UQY
2. Representation	
Resolution	Atomic
Number of <i>rigid bodies</i>, <i>flexible units</i>	0, 4
Flexible units	<ul style="list-style-type: none"> - M: 1-152 - N: 1-83 - O: 1-106 - P: 1-124
Structural coverage (<i>rigid bodies</i>)	100%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	1
Model precision (<i>uncertainty of models</i>)	Model precision can not be calculated with one structure
Data quality	Data quality has not been assessed
Model quality: <i>assessment of atomic segments</i>	Model-1: Clashescore = 0.0, Number of Ramachandran outliers = 10, Number of sidechain outliers = 0
Model quality: <i>assessment of excluded volume</i>	Not applicable

<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Method</i>	Rosetta refinement
<i>Name</i>	?
<i>Number of computed models</i>	?
<i>Software</i>	ROSETTA (version Not available)