

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"> - Marburg Glycoprotein 1: chain(s) M (152 residues) - Marburg Glycoprotein 2: chain(s) N (83 residues) - MR78 antibody heavy chain: chain(s) O (106 residues) - MR78 antibody light chain: chain(s) P (124 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB: 3X2D - X-ray diffraction data, PDB: 5UQY
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 4
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 (uncertainty of models)	Not available
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	<ul style="list-style-type: none"> - Clashscore: 0.00 - Ramachandran outliers: 10 - Sidechain outliers: 0
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined

5. Methodology and Software	
1. <i>Name</i>	Rosetta refinement
<i>Method</i>	?
<i>Number of computed models</i>	?
<i>Software</i>	ROSETTA (version Not available)