

Summary of integrative structure determination of Structure of the phage immune evasion protein Gad1 bound to the Gabija GajAB complex (PDB ID: 9A3W, PDB-Dev ID: PDBDEV_00000217)

1. Model Composition	
<p>Entry composition</p>	<ul style="list-style-type: none"> - Gabija anti-defense 1: Chain I (131 residues) - Gabija anti-defense 1: Chain M (295 residues) - Gabija anti-defense 1: Chain J (295 residues) - Gabija protein GajB: Chain F (493 residues) - Gabija anti-defense 1: Chain M (159 residues) - Gabija anti-defense 1: Chain O (159 residues) - Gabija anti-defense 1: Chain N (159 residues) - Gabija anti-defense 1: Chain J (131 residues) - Gabija anti-defense 1: Chain P (159 residues) - Gabija anti-defense 1: Chain K (295 residues) - Gabija protein GajA: Chain D (626 residues) - Gabija protein GajB: Chain H (493 residues) - Gabija anti-defense 1: Chain K (131 residues) - Gabija anti-defense 1: Chain N (295 residues) - Gabija anti-defense 1: Chain L (131 residues) - Gabija anti-defense 1: Chain I (295 residues) - Gabija protein GajB: Chain E (493 residues) - Gabija protein GajA: Chain A (626 residues) - Gabija anti-defense 1: Chain L (295 residues) - Gabija protein GajA: Chain B (626 residues) - Gabija anti-defense 1: Chain O (295 residues) - Gabija protein GajB: Chain G (493 residues) - Gabija anti-defense 1: Chain P (295 residues) - Gabija protein GajA: Chain C (626 residues)
<p>Datasets used for modeling</p>	<ul style="list-style-type: none"> - Experimental model, PDB ID: 8U7I - Experimental model, PDB ID: 8SM3 - De Novo model, Not available - 3DEM volume, EMDB: EMD-41983
2. Representation	
<p>Resolution</p>	<p>Atomic</p>
<p>Number of rigid bodies, flexible units</p>	<p>0, 16</p>
<p>Flexible units</p>	<ul style="list-style-type: none"> - A: 1-626 - B: 1-626 - C: 1-626 - D: 1-626 - E: 1-493 - F: 1-493 - G: 1-493 - H: 1-493 - I: 1-295 - J: 1-295 - K: 1-295 - L: 1-295 - M: 1-295 - N: 1-295 - O: 1-295 - P: 1-295

Structural coverage (rigid bodies)	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 (uncertainty of models)	Model precision can not be calculated with one structure
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	Model-1: Clashescore = 45.94, Number of Ramachandran outliers = 58, Number of sidechain outliers = 651
Model quality: assessment of excluded volume	Not applicable
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. Method	None
Name	None
2. Method	None
Name	None
Software	<ul style="list-style-type: none"> - Coot (version 0.8.9.3 EL) - AlphaFold2 (version v2.2.4) - PHENIX (version 1.20.1-4487)