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	
Entry composition	- Gabija protein GajA: chain(s) A, B, C, D (626 residues) - Gabija protein GajB: chain(s) E, F, G, H (493 residues) - Gabija anti-defense 1: chain(s) I, J, K, L, M, N, O, P (295 residues)
Datasets used for modeling	- Experimental model, PDB: 8U7I - Experimental model, PDB: 8SM3 - De Novo model, Not available - 3DEM volume, EMDB: EMD-41983
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 16
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	- Clashscore: 45.94 - Ramachandran outliers: 58 - Sidechain outliers: 651
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. Name	None
2. Name	None
Software	- Coot (version 0.8.9.3 EL) - AlphaFold2 (version v2.2.4) - PHENIX (version 1.20.1-4487)