

Summary of integrative structure determination of 52-mer bacterial gasdermin pore model from *Vitiosangium* sp. (PDB ID: 9A84, PDB-Dev ID: PDBDEV_00000369)

1. Model Composition	
Entry composition	Gasdermin bGSDM: chain(s) A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, W, X, Y, Z, AA [a], BA [b], CA [c], DA [d], EA [e], FA [f], GA [g], HA [h], IA [i], JA [j], KA [k], LA [l], MA [m], NA [n], OA [o], PA [p], QA [q], RA [r], SA [s], TA [t], UA [u], VA [v], WA [w], XA [x], YA [y], ZA [z] (234 residues)
Datasets used for modeling	- 2DEM class average, Zenodo: 10.5281/zenodo.10570209 - Experimental model, PDB: 8sl0
2. Representation	
Number of representations	1
Scale	Atomic
Number of <i>rigid</i> and <i>flexible</i> segments	0, 52
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique EM2DRestraint: Number of micrographs: 8930, Image resolution: 1.66
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: 2.61 - Ramachandran outliers: 180 - Sidechain outliers: 511
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
Description	To make the 52-mer pore model, protomer models (PDB 8SL0) were realigned using a custom script and a geometric model based on the number of protomers observed in the major 2D classes (52). Protomers were realigned to preserve the inter-subunit hydrogen bonding pattern observed in the slinky-like oligomer.
Software	<ul style="list-style-type: none">- Python (version v3.9.7)- MDAnalysis (version v2.4.2)