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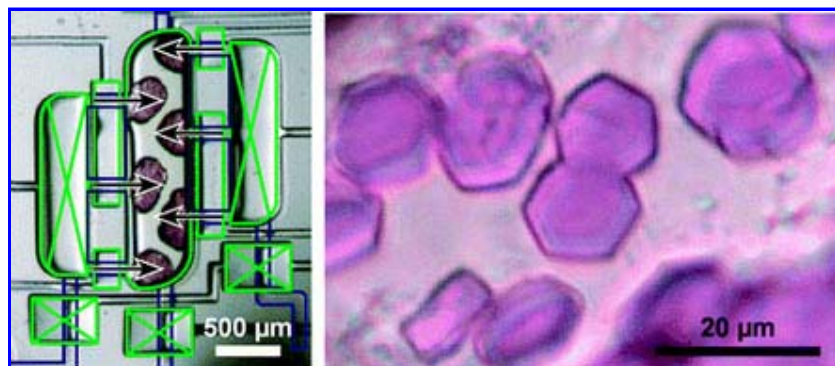
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Finding Crystallization Sweet Spots

Automated device mixes nanoliter quantities of membrane-protein components

[Mitch Jacoby](#)

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Paul Kenis

Mini Mixer Bacteriorhodopsin crystals (right) are grown by this device, which injects a total of 20 nanoliters of aqueous protein solution (brown droplets injected from right and left) into a lipid reservoir. [This video](#) shows the device in action.

Membrane proteins play critical roles in cell signaling and energy transduction, so knowing their crystal structures could help scientists better understand how cells work while also pointing toward new treatments for diseases that involve these proteins. Relatively few membrane-protein structures have been determined, however, because they are notoriously difficult to crystallize and the pure proteins tend to be available only in minute quantities. What's more, today's crystallization methods do not allow experimental conditions to be easily varied, a feature that would hasten the identification of practical crystallization conditions for a particular protein. Now, Sarah L. Perry, [Paul J. A. Kenis](#), and coworkers at the University of Illinois, Urbana-Champaign, have developed a device that enables them to screen crystallization conditions by mixing various compositions and concentrations of aqueous protein solutions and viscous lipids in 20-nanoliter batches (*Cryst. Growth Des.*, DOI: [10.1021/cg900289d](#)). The pneumatically actuated mixer uses just one-thousandth of the material consumed by today's microscale screening tools. In a proof-of-concept experiment, the team used the device to grow crystals of bacteriorhodopsin, a membrane protein commonly used for benchmarking.

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