Elsewhere in biology

A selection of interesting papers published last month in *Chemistry & Biology*'s sister journals, *Current Biology*, *Folding & Design* and *Structure*, chosen and summarized by the staff of *Chemistry & Biology*.

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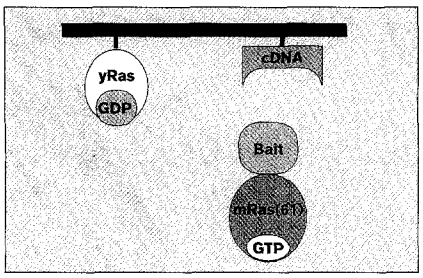
☐ **The Ras recruitment system, a novel approach to the study of protein–protein interactions.**
Yehoshua C Broder, Sigal Katz and Ami Aronheim (1998). *Curr. Biol.* **8**, 1121–1124.

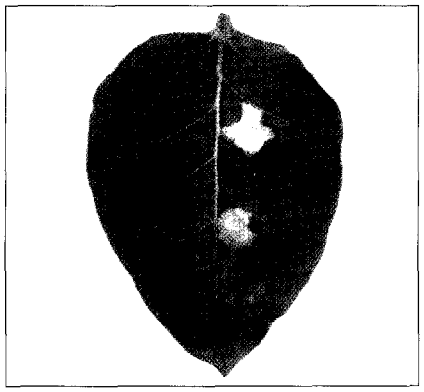
The yeast two-hybrid system represents one of the most efficient approaches currently available for identifying and characterizing protein–protein interactions. Although very powerful, this procedure has several problems and inherent limitations. A new system, the Sos recruitment system (SRS), was developed recently based on a different readout from that of the two-hybrid system. SRS overcomes several of the limitations of the two-hybrid system and thus serves as an attractive alternative for studying protein–protein interactions between known and novel proteins. Because the authors encountered a number of problems using SRS, they developed an improved protein recruitment system, designated the Ras recruitment system (RRS), based on the absolute requirement that Ras be localized to the plasma membrane for its function. Ras membrane localization and activation can be achieved through interaction between two hybrid proteins.



The the effectiveness of the novel RRS system has been demonstrated using five different known protein–protein interactions; two previously unknown protein–protein interactions were identified through a library screening protocol. The RRS system significantly extends the usefulness of the previously described SRS system and overcomes several of its limitations.
28 September 1998, Brief Communication, *Current Biology*.

☐ **Caspases and programmed cell death in the hypersensitive response of plants to pathogens.**
Olga del Pozo and Eric Lam (1998). *Curr. Biol.* **8**, 1129–1132.

The hypersensitive response (HR) is induced by certain plant pathogens and involves programmed cell death (PCD) to restrict the spread of pathogens from the infection site. Concurrent with the induction of cell death, the host activates a defense response. The cell death associated with the HR in several plant–pathogen systems has



morphological similarities to animal apoptosis, which suggests that cell death mechanisms in plants and animals might share common components that lead to similar cellular events. Caspases are conserved cysteine proteases that regulate animal PCD; caspase activity or an involvement of caspases in cell death has yet to be reported in plants. Here, the participation of caspases in HR cell death is investigated. Caspase-specific peptide inhibitors, Ac-YVAD-CMK and Ac-DEVD-CHO, abolished bacteria-induced plant PCD but did not significantly affect the induction of other aspects of HR, such as the expression of defense genes. This result confirmed the previous model that cell death can be uncoupled from defense gene activation during HR. Caspase-like proteolytic activity was detected in tobacco tissues that were developing HR following infection with tobacco mosaic virus. The results provide evidence for the presence of caspase-like plant protease(s) that participate in HR cell death.
28 September 1998, Brief Communication, *Current Biology*.

☐ **Prion protein fragments spanning helix 1 and both strands of β sheet (residues 125–170) show evidence for predominantly helical propensity by CD and NMR.**
Gary J Sharman, Nigel Kenward, Huw E Williams, Michael Landon, R John Mayer and Mark S Searle (1998). *Fold. Des.* **3**, 313–320.

Transmissible spongiform encephalopathies are a group of neurodegenerative disorders of man and animals that are believed to be caused by an α-helical to β-sheet conformational change in the prion protein, PrP. Recently determined NMR structures of recombinant PrP (residues 121–231 and 90–231) have identified a short two-stranded anti-parallel β sheet in the normal cellular form of the protein (PrP^C). This β sheet has been suggested to be involved in seeding the conformational transition to the disease-associated form (PrP^{Sc}) via a partially unfolded intermediate state.The authors describe CD and NMR studies of three peptides (125–170, 142–170 and 156–170) that span the β-sheet and helix 1 region of PrP, forming a large part of the putative PrP^{Sc}–PrP^C binding site that has been proposed to be important for self-seeding replication of PrP^{Sc}. The data suggest that all three peptides in water have predominantly helical propensities, which are enhanced in aqueous methanol (as judged by deviations from random-coil Hα chemical shifts and $^3J_{H\alpha-NH}$ values). Although the helical propensity is most marked in the region corresponding to helix 1 (144–154), it is