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On the cover, several representatives of the human cell pocketome, a collection of thousands of small-molecule binding envelopes in a cell proteome. The binding envelopes, shown in *yellow*, were predicted from three-dimensional models of proteins without using any knowledge of the bound ligands (shown in *stick models*). The envelopes can be clustered into categories according to their size, shape, and physicochemical properties. For details, see the article by An *et al.*, pages 752–761.

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