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Spot the protein

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Finding a particular protein in a 2 gigabyte electron tomographic reconstruction of an organelle is not easy. Brute-force matching of molecular shapes is, in theory, possible, but in practice too computationally intensive because all rotations of an object must be tested. To reduce the computational load, Böhm *et al*. report in the December 19 Proceedings of the National Academy of Sciences that they have devised a two-step strategy (*Proc Natl Acad Sci USA* 2000, **97**:14245-14250). First they scan for objects of the correct size, as determined by curvature of the objects' surfaces. Only then are these particles compared with known structures to see if they match. Böhm *et al*. test the system using three protein complexes that are somewhat related in shape and size (the 20S proteasome, the GroEL chaperonin, and the thermosome), and find that they can find and differentiate between the three in solution. The next test will be to tackle a real cell in all its complexity.

References

1. Electron tomography of ice-embedded prokaryotic cells.

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