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## Creating protein folds

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William Wells

Email: wells@biotext.com

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An exon, the basic unit of DNA that gets shuffled around during evolution, has an average coding capacity of 40 amino acids, or roughly half of a small folded protein domain. Exon exchange between homologous proteins can lead to slightly altered proteins, but in the August 29 [Proceedings of the National Academy of Sciences](#) Riechmann and Winter ask whether shuffling between unrelated sequences can generate new folds (*Proc Natl Acad Sci USA* 2000, **97**:10068-10073). Their starting material is DNA encoding half of a beta-barrel domain, plus fragmented genomic DNA from *Escherichia coli*. The fusion products that can fold are selected by their resistance to proteolysis; one of these proteins is significantly more stable than the original intact protein. The genomic segments that survive the selection do not share sequence homology with the starting beta-barrel sequence, although beta structure predominates in the final protein products.

## References

1. DNA shuffling of a family of genes from diverse species accelerates directed evolution.
2. Proceedings of the National Academy of Sciences, [<http://www.pnas.org/>]