

Twenty Selected Papers

- [1] F. E. Cohen, M. J. E. Sternberg, and W. R. Taylor. Analysis and prediction of protein β -sheet structures by a combinatorial approach. *Nature*, 285:378–382, 1980.
- [2] F. E. Cohen, M. J. E. Sternberg, and W. R. Taylor. Analysis and prediction of the packing of α -helices against a β -sheet in the tertiary structure of globular proteins. *J. Molec. Biol.*, 156:821–862, 1982.
- [3] W. R. Taylor and J. M. Thornton. Prediction of super-secondary structure in proteins. *Nature*, 301:540–542, 1983.
- [4] W. R. Taylor. Identification of protein sequence homology by consensus template alignment. *J. Molec. Biol.*, 188:233–258, 1986.
- [5] L. H. Pearl and W. R. Taylor. A structural model for the retroviral proteases. *Nature*, 329:351–354, 1987.
- [6] W. R. Taylor. A flexible method to align large numbers of biological sequences. *J. Molec. Evol.*, 28:161–169, 1988.
- [7] W. R. Taylor and C. A. Orengo. Protein structure alignment. *J. Molec. Biol.*, 208:1–22, 1989.
- [8] W. R. Taylor. Towards protein tertiary fold prediction using distance and motif constraints. *Prot. Engng.*, 4:853–870, 1991.
- [9] D. T. Jones, W. R. Taylor, and J. M. Thornton. A new approach to protein fold recognition. *Nature*, 358:86–89, 1992.
- [10] W. R. Taylor. Protein fold refinement: building models from idealised folds using motif constraints and multiple sequence data. *Prot. Engng.*, 6:593–604, 1993.
- [11] A. Aszódi and W. R. Taylor. Folding polypeptide α -carbon backbones by distance geometry methods. *Biopolymers*, 34:489–506, 1994.

- [12] W. R. Taylor, D. T. Jones, and N. M. Green. A method for α -helical integral membrane protein fold prediction. *Prot. Struct. Funct. Genet.*, 18:281–294, 1994.
- [13] W. R. Taylor, T. P. Flores, and C. A. Orengo. Multiple protein structure alignment. *Prot. Sci.*, 3:1858–1870, 1994.
- [14] A. Aszódi, M. J. Gradwell, and W. R. Taylor. Global fold determination from a small number of distance restraints. *J. Molec. Biol.*, 251:308–326, 1995.
- [15] W. R. Taylor. Multiple sequence threading: an analysis of alignment quality and stability. *J. Molec. Biol.*, 269:902–943, 1997.
- [16] W. R. Taylor. Dynamic databank searching with templates and multiple alignment. *J. Molec. Biol.*, 280:375–406, 1998.
- [17] W. R. Taylor. Protein structure domain identification. *Prot. Engng.*, 12:203–216, 1999.
- [18] W. R. Taylor. A deeply knotted protein and how it might fold. *Nature*, 406:916–919, 2000.
- [19] W. R. Taylor. A periodic table for protein structure. *Nature*, 416:657–660, 2002.
- [20] W. R. Taylor, G. J. Bartlett, V. Chelliah, D. Klose, K. Lin, T. Sheldon, and I. Jonassen. Prediction of protein structure from ideal forms. *Proteins: struct., funct., bioinfo.*, 70:1610–1619, 2008.