Bibliography

- [1] F. E. Cohen, M. J. E. Sternberg, and W. R. Taylor. Analysis and prediction of the stacking of β -pleated sheets. In R. Jainikie, editor, *Protein Folding*, pages 131–148. Elsivier, Amsterdam, 1980.
- [2] 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.
- [3] F. E. Cohen, M. J. E. Sternberg, and W. R. Taylor. Analysis of the tertiary structure of protein β-sheet sandwiches. J. Molec. Biol., 148:253–272, 1981.
- [4] W. R. Taylor. Analysis and Prediction of Protein Structure. PhD thesis, Department of Zoology (Lab. of Molecular Biophysics), University of Oxford, 1981.
- [5] M. J. E. Sternberg, F. E. Cohen, W. R. Taylor, and R. J. Feldmann. Analysis and prediction of structural motifs in the glycolytic enzymes. *Proc. Roy. Soc. Lond. B*, 293:177–189, 1981.
- [6] 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.
- [7] M. J. E. Sternberg, F. E. Cohen, and W. R. Taylor. A combinatorial approach to the prediction of the tertiary fold of globular proteins. *Biochem. Soc. Trans.*, 10, 1982.
- [8] W. R. Taylor and J. M. Thornton. Prediction of super-secondary structure in proteins. *Nature*, 301:540–542, 1983.
- [9] W. R. Taylor, J. M. Thornton, and W. G. Turnell. A ellipsoidal approximation of protein shape. *J. Molec. Graphics*, 1:30–38, 1983.
- [10] M. J. E. Sternberg and W. R. Taylor. Modelling the ATP-binding site of oncogene products. *FEBS Lett.*, 175:387–392, 1984.

- [11] W. R. Taylor. An algorithm to compare secondary structure predictions. J. Molec. Biol., 173:513–514, 1984. (appendix).
- [12] W. R. Taylor and J. M. Thornton. Recognition of super-secondary structure in proteins. *J. Molec. Biol.*, 173:487–514, 1984.
- [13] J. M. Thornton, B. L. Sibanda, and W. R. Taylor. Variability, modelling and prediction of β-hairpins with reference to the immunoglobulin fold. In E. Reid, G. M. W. Cook, and D. J. Morre, editors, *Investigation and exploitation of antibody combining sites*, pages 23–31. Plenum Pub. Corp., N.Y., 1985.
- [14] R. C. Garratt, W. R. Taylor, and J. M. Thornton. The influence of tertiary structure on secondary structure prediction: accessibility versus predictability for beta-structure. *FEBS Lett.*, 188:59–62, 1985.
- [15] M. J. E. Sternberg and W. R. Taylor. Modelling SRC and the EGF receptors by computer graphics. *Brit. J. Cancer*, 52:411, 1985. (abstract).
- [16] M. J. E. Sternberg, W. R. Taylor, J. Nyakairu, J. Fox, and C. J. Rawlings. Reasoning about protein topology using the logic programming language PROLOG. *J. Molec. Graph.*, 3:108–109, 1985. (abstract).
- [17] C. J. Rawlings, W. R. Taylor, J. Nyakairu, J. Fox, and M. J. E. Sternberg. Reasoning about protein topology using the logic programming language PROLOG. *J. Molec. Graph.*, 3:151–157, 1985.
- [18] J. M. Thornton, M. S. Edwards, W. R. Taylor, and D. J. Barlow. Location of 'continuous' antigenic determinants in the protuding regions of proteins. EMBO J., 5:409–413, 1986.
- [19] N. M. Green, W. R. Taylor, C. J. Brandl, B. Korczak, and D. H. A. MacLennan. Structural and mechanistic implications of the amino acid sequence of calcium transporting ATPases. In C. Evered, editor, *Calcium and the Cell*, volume 122 of *Ciba Found. Symp.*, pages 93–113. J. Wiley and Son, 1986.
- [20] J. B. Rothbard, A. Townsend, M. Edwards, and W. R. Taylor. Pattern recognition among T-cell epitopes. In *Modern trends in human leukemia*, volume VII. Elsevier, Amsterdam, 1986.
- [21] T. J. Knott, R. J. Pease, L. M. Powell, S. C. Wallis, S. C. Rall, T. L. Innerarity, B. Blackhart, W. R. Taylor, A. J. Lusis, B. J. McCarthy, R. W. Mahley, B. Levy-Wilson, and J. Scott. Human apolipoprotein B: complete cDNA sequence and idenification of structural domains in the protein. *Nature*, 323:734–738, 1986. (Taylor, W. R. is misprinted as Taylor, W. H. in the journal).

- [22] I. Nikas, J. McLauchlan, A. J. Davison, W. R. Taylor, and J. B. Clemments. Predicted structural features of ribonucleotide reductase. *Proteins*, 1, 1986.
- [23] T. L. Blundell, D. Barlow, B. L. Sibanda, J. M. Thornton, W. R. Taylor, I. J. Tickle, M. J. E. Sternberg, J. E. Pitts, I. Haneef, and A. M. Hemmings. Three-dimensional structural aspects of the design of new proteins. *Phil. Trans. Roy. Soc. (Lond.)*, A317:333–344, 1986.
- [24] D. J. Barlow, T. L. Blundell, M. S. Edwards, B. L. Sibanda, M. J. E. Sternberg, W. R. Taylor, and J. M. Thornton. The analysis of homologous tertiary structures and the design of novel proteins. In M. Inouye and R. Sarma, editors, *Protein Engineering: Applications in Science, Medicine, and Industry*, chapter 3, pages 29–40. Academic Press (Inc.), Orlando, USA, 1986.
- [25] W. R. Taylor. Identification of protein sequence homology by consensus template alignment. J. Molec. Biol., 188:233–258, 1986.
- [26] C. J. Rawlings, W. R. Taylor, J. Nyakairu, J. Fox, and M. J. E. Sternberg. Using PROLOG to represent and reason about protein structure. *Lecture Notes in Computer Science*, 1986.
- [27] W. R. Taylor. The classification of amino acid conservation. *J. Theor. Biol.*, 119:205–218, 1986.
- [28] W. R. Taylor. Toward a practical grammar of protein structure: protein structure prediction by template fitting. In R. Fletterick and M. Zoller, editors, Computer Graphics and Molecular Modeling, Current Communications in Molecular Biology, chapter 14, pages 77–84. Cold Spring Harbor Laboratory, New-York, 1986.
- [29] W. R. Taylor. A general algorithm for the recognition of sequence patterns in globular proteins. *J. Molec. Biol.*, 188:254–258, 1986. (appendix).
- [30] M. J. Zvelebil, G. J. Barton, W. R. Taylor, and M. J. E. Sternberg. Prediction of protein secondary structure and active sites using the alignment of homologous sequences. J. Molec. Biol., 195:957–961, 1987.
- [31] W. R. Taylor. Multiple sequence alignment by a pairwise algorithm. *Comp. App. Bio. Sci.*, 3:81–87, 1987.
- [32] M. J. Geisow, J. H. Walker, C. Boustead, and W. R. Taylor. Anexins a new family of Ca²⁺-regulated phospholipid-binding proteins. *Bioscience Reports*, 7:289–298, 1987.

- [33] W. R. Taylor and M. J. Geisow. A predicted structure for the calcium dependant membrane binding proteins p32, p35 and p36. *Prot. Eng.*, 1:183–187, 1987.
- [34] M. Bajaj, M. Waterfield, J. Schlessinger, W. R. Taylor, and T. L. Blundell. On the tertiary structures of the extracellular domains of the EGF and insulin receptors. *Biochim. Biophys. Acta*, 916:220–226, 1987.
- [35] L. H. Pearl and W. R. Taylor. Sequence specificity of retroviral proteases. *Nature*, 328:482, 1987. (Communication).
- [36] J. Engel, W. R. Taylor, M. Paulsson, H. Sage, and B. Hogan. Calcium binding domains and calcium induced conformational transition of SPARC/BM-40/osteonectin, an extracellular glycoprotein expressed in mineralized and nonmineralized tissues. *Biochemistry*, 26:6958–6965, 1987.
- [37] L. H. Pearl and W. R. Taylor. A structural model for the retroviral proteases. *Nature*, 329:351–354, 1987.
- [38] N. M. Green, W. R. Taylor, and D. H. A. MacLennan. A consensus structure for cation pumps. In W. D. Stein and S. J. D. Karlish, editors, *Ion Pumps*, Prog. Clin. Biol. Res., pages 15–24. Alan R. Liss, New York, 1988.
- [39] V. Rodrigues, M. Chaudhri, M. Knight, H. Meadows, A. E. Chambers, W. R. Taylor, C. Kelly, and A. J. G. Simpson. Predicted structure of a major *Schistosoma mansoni* eggshell protein. *Molec. Biochem. Parasitology*, 32:7–14, 1988.
- [40] S. A. Taylor, J. Lewis, J. Pacy, W. R. Taylor, and R. G. Price. Glomerular basement membrane thickness in male and female rats fed sucrose-rich diets. In M. C. Gubler and M. Sternberg, editors, *Progress in Basement Membrane Research: Renal and related aspects in health and disease*, pages 205–209. John Libbey, Eurotext Ltd., 1988.
- [41] J. B. Rothbard, R. I. Lechler, K. Howland, V. Bal, D. D. Eckels, R. Sekaly, E. O. Long, W. R. Taylor, and J. R. Lamb. A structural model of HLA-DR1 restricted T-cell antigen recognition. *Cell*, 52:515–523, 1988.
- [42] W. R. Taylor. A flexible method to align large numbers of biological sequences. *J. Molec. Evol.*, 28:161–169, 1988. The correct year is 1989.
- [43] J. B. Rothbard and W. R. Taylor. A sequence pattern common to T-cell epitopes. *EMBO J.*, 7:93–100, 1988.
- [44] W. R. Taylor. Pattern matching methods in protein sequence comparison and structure prediction. *Prot. Engng.*, 2:77–86, 1988.

- [45] W. R. Taylor. Macromolecular structure and specificity. Speculations in Science and Technology, 11:79–80, 1988. (book review).
- [46] W. R. Taylor. A template based method of pattern matching in protein sequences. *Prog. Biophys. Molec. Biol.*, 54:159–252, 1989.
- [47] W. R. Taylor and C. A. Orengo. Protein structure alignment. *J. Molec. Biol.*, 208:1–22, 1989.
- [48] J. B. Rothbard, R. Busch, K. Howland, V. Bal, C. Fenton, W. R. Taylor, and J. R. Lamb. Structural analysis of a peptide HLA class II complex: identification of critical interaactions for its formation and recognition by T-cell receptor. *Int. Immunology*, 1:479–486, 1989.
- [49] J. M. Thornton and W. R. Taylor. Protein structure prediction. In J. B. C. Findlay and M. J. Geisow, editors, *Protein Sequencing: A Practical Approach*, chapter 7, pages 147–190. IRL Press, Oxford, 1989.
- [50] J. B. Rothbard, H. C. Bodmer, K. Howland, R. M. Pemberton, B. E. Askonas, and W. R. Taylor. T-cell recognition of a peptide/H2-Kd complex. EMBO J., 8:2321–2328, 1989.
- [51] W. R. Taylor and C. A. Orengo. A holistic approach to protein structure comparison. *Prot. Eng.*, 2:505–519, 1989.
- [52] W. R. Taylor and N. M. Green. The predicted secondary structures of the nucleotide-binding sites of six cation-transporting ATPases lead to a probable tertiary fold. *Eur. J. Biochem.*, 179:241–248, 1989.
- [53] W. R. Taylor, C. A. Orengo, and L. H. Pearl. Comparison of predicted and X-ray crystal structures of retroviral proteases. In M. Ikehara, editor, *Protein engineering: protein design in basic research, medicine, and industry*, pages 21–27. Japan Scientific Press, Tokyo; Springer-Verlag, Berlin, 1990.
- [54] C. Kelly, P. Evans, J. K. C. Ma, L. A. Bergmeier, W. R. Taylor, L. J. Brady, S. F. Lee, A. S. Bleiweis, and T. Lehner. Sequencing and characterization of the 185 KDa cell-surface antigen of *Streptococcus mutans*. Archives of Oral Biology, 35 S, 1990.
- [55] W. R. Taylor. Hierarchical method to align large numbers of biological sequences. In R. F. Doolittle, editor, *Molecular Evolution: computer analysis of protein and nucleic acid sequences*, volume 183 of *Meth. Enzymol.*, chapter 29, pages 456–474. Academic Press, San Diego, CA, USA., 1990.
- [56] C. A. Orengo and W. R. Taylor. A rapid method for protein structure alignment. J. Theor. Biol., 147:517–551, 1990.

- [57] W. R. Taylor. Comparison of predicted and X-ray crystal structures of retroviral proteases. *Prot. Engng.*, 3:282, 1990. (abstract).
- [58] R. Garratt, J. M. Thornton, and W. R. Taylor. An extension of secondary structure prediction towards the prediction of tertiary structure. *FEBS Lett.*, 208:141–146, 1991.
- [59] W. R. Taylor and D. T. Jones. Templates, consensus patterns and motifs. *Current Opinion in Struct. Biol.*, 1:327–333, 1991.
- [60] F. Rippmann and W. R. Taylor. Visualization of structural similarity in proteins. J. Molec. Graph., 9:3–16, 1991.
- [61] W. R. Taylor. Sequence analysis: spinning in hyperspace. *Nature*, 353:388–389, 1991. (News and Views).
- [62] W. R. Taylor. Towards protein tertiary fold prediction using distance and motif constraints. *Prot. Engng.*, 4:853–870, 1991.
- [63] R. J. La Polla, J. A. Haron, C. G. Kelly, W. R. Taylor, Bohart C., M. Hendricks, J. Pyati, R. T. Graff, J. K. C. Ma, and T. Lehner. Sequence and structural analysis of surface protein antigen-I/II (SPAA) of Streptococcus sobrinus. Infection and Immunity;, 59:2677–2685, 1991.
- [64] F. Rippmann, W. R. Taylor, J. B. Rothbard, and N. M. Green. A hypothetical model for the peptide binding domain of hsp70 based on the peptide binding domain of HLA. *EMBO Journal*, 10:5–10, 1991.
- [65] C. A. Orengo, N. P. Brown, and W. R. Taylor. Fast protein structure comparison for databank searching. Prot. Struct. Funct. Genet., 14:139– 167, 1992.
- [66] W. R. Taylor, editor. Patterns in Protein sequence and Structure, volume 7 of Springer series in Biophysics (ed. Bayley, P. M.). Springer-Verlag, Heidelberg, 1992.
- [67] D. T. Jones, W. R. Taylor, and J. M. Thornton. The rapid generation of mutation data matrices from protein sequences. *Comp. App. Bio. Sci.*, 8:275–282, 1992.
- [68] D. T. Jones, W. R. Taylor, and J. M. Thornton. A new approach to protein fold recognition. *Nature*, 358:86–89, 1992.
- [69] W. R. Taylor. Patterns, predictions and problems (introduction). In W. R. Taylor, editor, Patterns in Protein sequence and Structure, volume 7 of Springer series in Biophysics (ed. Bayley, P. M.), pages 1–9. Springer-Verlag, Heidelberg, 1992.

- [70] W. R. Taylor. New paths from dead ends. *Nature*, 356:478–479, 1992. (News and Views).
- [71] W. R. Taylor. Sequencing and computer time. *Science*, 258:1421, 1992. (Letter).
- [72] N. B. LaThangue and W. R. Taylor. A structural similarity between mamalian and yeast transcription factors for cell-cycle-regulated genes. *Trends* in Cell Biol., 3:75–76, 1993.
- [73] C. A. Orengo, T. P. Flores, D. T. Jones, W. R. Taylor, and J. M. Thornton. Recurring structural motifs in proteins with different functions. *Current Biology*, 3:131–139, 1993.
- [74] W. R. Taylor and D. T. Jones. Deriving an amino acid distance matrix. *J. Theor. Biol.*, 164:65–83, 1993.
- [75] A. Aszódi and W. R. Taylor. Connection topology of proteins. *Comp. App. Bio. Sci.*, 9:523–529, 1993.
- [76] D. T. Jones, C. A. Orengo, W. R. Taylor, and J. M. Thornton. Progress towards recognising protein folds from amino acid sequence. *Prot. Engng.*, 6 (supplement):124, 1993. (abstract).
- [77] W. R. Taylor. Protein fold refinement: building models from idealised folds using motif constraints and multiple sequence data. *Prot. Engng.*, 6:593–604, 1993.
- [78] W. R. Taylor, D. T. Jones, and A. W. Segal. A structural model for the nucleotide binding domain of the cytochrome b_{-245} β -chain. *Protein Science*, 2:1675–1685, 1993.
- [79] W. R. Taylor. Modelling protein structure from remote sequence similarity: an approach to tertiary structure prediction. In S. Suhai, editor, *Computational methods in genome research*, pages 317–328. Plenum Pub. Corp., 1993.
- [80] C. A. Orengo and W. R. Taylor. A local alignment method for protein structure motifs. *J. Molec. Biol.*, 233:488–497, 1993.
- [81] C. A. Orengo, T. P. Flores, W. R. Taylor, and J. M. Thornton. Identification and classification of protein fold families. *Prot. Engng.*, 6:485–500, 1993.
- [82] W. R. Taylor. Modelling protein structure from remote sequence similarity. In R. Lavery and E. Westhof, editors, *Molecular modelling and graphics applied to structure-function relationships*. INSERM, Paris, 1993.

- [83] W. R. Taylor. Protein structure prediction from sequence. Computers and Chem., 17:117–122, 1993.
- [84] D. L. Stokes, W. R. Taylor, and N. M. Green. Structure, transmembrane topology and helix packing of P-type ion pumps. *FEBS Lett.*, 346:32–38, 1994.
- [85] S. Bhattacharya, N. Navaratnam, J. R. Morrison, J. Scott, and W. R. Taylor. Cytosine nucleoside/nucleotide deaminases and apolipoprotein B mRNA editing. *TIBS*, pages 105–106, 1994.
- [86] J. M. Thornton, C. M. Orengo, D. T. Jones, and W. R. Taylor. Protein motifs and folding recognition. *Biophys. J.*, page 241, 1994. (abstract).
- [87] C. Chothia and W. R. Taylor. Sequences and topology. Curr. Op. Struct. Biol., 4:381–382, 1994. (editorial overview).
- [88] K. Hatrick and W. R. Taylor. Sequence conservation and correlation measures in protein structure prediction. *Computers Chem.*, 18:245–250, 1994.
- [89] W. R. Taylor. Protein structure modelling from remote sequence similarity. J. Biotechnology, 12:281–291, 1994. Special issue: Genome Research/Molecular Biotechnology, Part 1. ed., Helmut Blöcker.
- [90] 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.
- [91] D. T. Jones, W. R. Taylor, and J. M. Thornton. A mutation data matrix for transmembrane proteins. *FEBS Lett.*, pages 269–275, 1994.
- [92] C. A. Orengo, T. P. Flores, W. R. Taylor, and J. M. Thornton. Protein fold families and structural motifs. In *Proceedings of the NATO ARW workshop on statistical mechanics, protein structure and protein substrate interactions*, 1994.
- [93] A. Aszódi and W. R. Taylor. Folding polypeptide α -carbon backbones by distance geometry methods. *Biopolymers*, 34:489–506, 1994.
- [94] A. Aszódi and W. R. Taylor. Secondary structure formation in model polypeptide chains. *Prot. Engng.*, 7:633–644, 1994.
- [95] D. T. Jones, W. R. Taylor, and J. M. Thornton. A model recognition approach to the prediction of all-helical membrane protein structure and topology. *Biochemistry*, 33:3038–3049, 1994.

- [96] W. R. Taylor and A. Aszódi. Building protein folds using distance geometry: towards a general modeling and prediction method. In K. M. Merz and S. M. LeGrand, editors, *The protein folding problem and tertiary structure prediction*, chapter 6, pages 165–192. Birkhäuser (Springer-Verlag), Boston, MA., USA, 1994.
- [97] W. R. Taylor. Remotely related sequences and structures: analysis and predictive modelling. *Trends Biotech.*, 12:154–157, 1994.
- [98] W. R. Taylor and K. Hatrick. Compensating changes in protein multiple sequence alignments. *Prot. Engng.*, 7:341–348, 1994.
- [99] W. R. Taylor. Motif-biased protein sequence alignment. *J. Comp. Biol.*, 1:297–311, 1994.
- [100] A. Aszódi and W. R. Taylor. Modelling secondary structure formation by distance geometry techniques. In H. Bohr and S. Brunak, editors, *Distance based approaches to protein structure determination*, pages 222–236. IOS press, Elsevier (Amsterdam), 1994.
- [101] W. R. Taylor, T. P. Flores, and C. A. Orengo. Multiple protein structure alignment. *Prot. Sci.*, 3:1858–1870, 1994.
- [102] W. R. Taylor and A. Aszódi. Modelling and predicting protein structure using distance geometry. In H. Bohr and S. Brunak, editors, *Distance based approaches to protein structure determination*, pages 213–221. IOS press, Elsevier (Amsterdam), 1994.
- [103] W. R. Taylor. An investigation of conservation-biased gap-penalties for multiple protein sequence alignment. *Gene*, 165:GC27-35, 1995. Internet journal Gene Combis: http://www.elsevier.nl/locate/genecombis.
- [104] W. R. Taylor and D. T. Jones. Modelling and predicting α -helical transmembrane structures. In H. Bohr and S. Brunak, editors, *Protein Folds:* A Distance Based Approach, pages 283–293. CRC Press Inc., Boca Raton, Florida, U.S.A., 1995.
- [105] A. Aszódi and W. R. Taylor. Estimating polypeptide α -carbon distances from multiple sequence alignments. J. Math. Chem., 17:167–184, 1995.
- [106] W. R. Taylor. Sequence alignment of proteins and nucleic acids. In R. A. Meyers, editor, Molecular Biology and Biotechnology: comprehensive desk reference, pages 856–859. VCH, New York, USA, 1995.
- [107] A. Aszódi, M. J. Gradwell, and W. R. Taylor. Protein fold determination using a small number of distance restraints. In H. Bohr and S. Brunak,

- editors, *Protein Folds: A Distance Based Approach*, pages 85–97. CRC Press Inc., Boca Raton, Florida, U.S.A., 1995.
- [108] W. R. Taylor and N. M. Green. Structure in Protein Chemistry (by J. Kyte). Nature, 375:372, 1995. (book review).
- [109] 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.
- [110] N. P. Brown, C. A. Orengo, and W. R. Taylor. A protein structure comparison methodology. *Computers Chem.*, 20:359–380, 1996.
- [111] C. A. Orengo and W. R. Taylor. SSAP: sequential structure alignment program for protein structure comparison. In R. F. Doolittle, editor, *Computer methods for macromolecular sequence analysis*, volume 266 of *Meth. Enzymol.*, pages 617–635. Academic Press, Orlando, FA, USA., 1996.
- [112] A. Aszódi and W. R. Taylor. Homology modelling by distance geometry. Folding & Design, 1:325–334, 1996.
- [113] W. R. Taylor. A non-local gap-penaly for profile alignment. *Bull. Math. Biol.*, 58:1–18, 1996.
- [114] E. Werner, A. A. Holder, A. Aszódi, and W. R. Taylor. A novel 11-residue coilled-coil motif predicts a histidine zipper. *Prot. Pept. Lett.*, 3:139–146, 1996.
- [115] W. R. Taylor. Multiple protein sequence alignment: algorithms for gap insertion. In R. F. Doolittle, editor, *Computer methods for macromolecular sequence analysis*, volume 266 of *Meth. Enzymol.*, pages 343–367. Academic Press, Orlando, FA, USA., 1996.
- [116] W. R. Taylor. Sequence alignment of proteins and nucleic acids. In R. A. Meyers, editor, Encyclopedia of Molecular Biology and Molecular Medicine, volume 5, pages 419–428. VCH, New York, USA, 1997.
- [117] J. Heringa and W. R. Taylor. Three-dimensional domain duplication, swapping and stealing. *Curr. Op. Struct. Biol.*, 7:416–421, 1997.
- [118] D. D. Pollock and W. R. Taylor. Effectiveness of correlation analysis in identifying protein residues undergoing correlated evolution. *Prot. Engng.*, 10:647–657, 1997.
- [119] W. R. Taylor and C. A. Orengo. Protein fold topology and structural families. In G. Allen, editor, *Protein: a comprehensive treatise*, pages 143–169. JAI Press Inc., U.S.A., 1997.

- [120] A. Aszódi and W. R. Taylor. Hierarchical inertial projection: a fast distance matrix embedding algorithm. *Computers Chem.*, 21:13–23, 1997.
- [121] A. Aszódi, R. E. J. Munro, and W. R. Taylor. Distance based comparative modelling. *Folding & Design*, 2, suppl.:S3–S6, 1997.
- [122] W. R. Taylor. Random models for double dynamic score normalisation. *J. Molec. Evol.*, 44:S174–S180, 1997. Special issue in memory of Kimura.
- [123] W. R. Taylor. Evolution and relationships of protein families. In M. J. Bishop and C. J. Rawlings, editors, *Nucleic acid and protein sequence analysis: a practical approach (second edition)*, Practical approach (eds. Rickwood, D. and Hames, B. D.), pages 313–340. IRL Press, Oxford, 1997.
- [124] W. R. Taylor and R. E. J. Munro. Multiple sequence threading: Conditional gap placement. *Folding & Design*, 2, suppl.:S33–S39, 1997.
- [125] A. Aszódi, R. E. J. Munro, and W. R. Taylor. Protein modelling by multiple sequence threading and distance geometry. *Proteins*, pages 38–42, 1997.
- [126] W. R. Taylor. Multiple sequence threading: an analysis of alignment quality and stability. J. Molec. Biol., 269:902–943, 1997.
- [127] W. R. Taylor. Residual colours: a proposal for aminochromography. *Prot. Engng.*, 10:743–746, 1997. (Forum section).
- [128] D. G. Higgins and W. R. Taylor. Multiple sequence alignment. In M. Crochemore and D. Gusfield, editors, Protein Sequence and Structure, volume 807 of Lecture Notes in Computer Science, pages 237–244. Springer-Verlag, Berlin, 1998.
- [129] E. Werner, W. R. Taylor, and Holder. A plasmodium chabaudi protein contains a repetitive region with a predicted spectrin-like structure. *Molec. Biochem. Parisitology.*, 94:185–196, 1998.
- [130] D. T. Jones and W. R. Taylor. Towards structural genomics for transmembrane proteins. *Biochem. Soc. Trans.*, 26:429–438, 1999.
- [131] K. Rittinger, W. R. Taylor, S. J. Smerdon, and S. J. Gamblin. Support for shared ancestry of gaps. *Nature*, 392:448, 1998.
- [132] W. R. Taylor. Dynamic databank searching with templates and multiple alignment. *J. Molec. Biol.*, 280:375–406, 1998.
- [133] R. E. J. Munro and W. R. Taylor. Structure prediction and molecular modelling. In R. E. Reid, editor, *Peptide and Protein drug analysis*, pages 115–132. Marcel Dekker, Inc., 1999.

- [134] I. Jonassen, I. Eidhammer, and W. R. Taylor. Discovery of local packing motifs in protein structures. *Proteins: struc. funct. gene.*, 34:206–219, 1999.
- [135] D. D. Pollock, W. R. Taylor, and N. Goldman. Coevolving protein residues: maximum likelihood identification and relationship to structure. *J. Molec. Biol.*, 287:187–198, 1999.
- [136] W. R. Taylor and N. P. Brown. Iterated sequence databank search methods. *Comp. Chem.*, 23:365–385, 1999.
- [137] W. R. Taylor. Protein structure alignment using iterated double dynamic programming. *Prot. Sci*, 8:654–665, 1999.
- [138] W. R. Taylor. Protein structure domain identification. *Prot. Engng.*, 12:203–216, 1999.
- [139] W. R. Taylor and N. P. Brown. QUEST: an iterated sequence databank search method. In S. Suhai, editor, *Genomics and Proteonomics: functional and computational aspects*, pages 67–82. Kluwer Acad./Plenum Pub. Corp., 2000.
- [140] W. R. Taylor. The properties of amino acids in sequences. In M. J. Bishop, editor, *Nucleic acid and protein databases: a practical approach (second edition)*, pages 81–103. Academic Press, 1999. Chapter 5.
- [141] W. R. Taylor, G. Sælensminde, and I. Eidhammer. Multiple protein structure alignment using double-dynamic programming. *Comp. Chem.*, 24:3–12, 2000.
- [142] I. Eidhammer, I. Jonassen, and W. R. Taylor. Structure comparison and structure patterns. *J. Compu. Biol.*, 7:658–716, 2000.
- [143] I. Jonassen, I. Eidhammer, S. H. Grindhaug, and W. R. Taylor. Searching the protein structure databank with weak sequence patterns and structural constraints. *J. Molec. Biol.*, 304:599–619, 2000.
- [144] W. R. Taylor. Searching for the ideal forms of proteins. *Biochem. Soc. Trans.*, 28:264–269, 2000.
- [145] D. G. Higgins and W. R. Taylor. Preface. In D. Higgins and W. Taylor, editors, *Bioinformatics: Sequence structure and databases*, pages v-ix. Oxford University Press, 2000.
- [146] W. R. Taylor. A deeply knotted protein and how it might fold. *Nature*, 406:916–919, 2000.

- [147] D. G. Higgins and W. R. Taylor. Multiple sequence alignment. In D. M. Webster, editor, *Protein structure prediction*, volume 143 of *Methods in Molecular Biology (ed. J. M. Walker)*, pages 1–18. Humana Press, Totowa, New Jersey, USA, 2000.
- [148] W. R. Taylor. Protein structure. In D. J. Balding et al., editor, *Handbook of Statistical genetics*, pages 209–235. John Wiley and Sons Ltd., 2000.
- [149] W. R. Taylor. Protein structure comparison using SAP. In D. M. Webster, editor, *Protein structure prediction*, volume 143 of *Methods in Molecular Biology (ed. J. M. Walker)*, pages 19–32. Humana Press, Totowa, New Jersey, USA, 2000.
- [150] M. Ogun, M. Grainger, W. R. Taylor, and A. A. Holder. The merozoite surface protein-6 gene codes for a 36 kDa-protein associated with the plasmodium falciparum merozoite surface protein-1 complex. Mol. Biochem. Parasitology, 112:91–101, 2001.
- [151] W. R. Taylor. Defining linear segments in protein structure. *J. Molec. Biol.*, 310:1135–1150, 2001.
- [152] W. R. Taylor, A. C. W. May, N. P. Brown, and A. Aszódi. Protein structure: Geometry, topology and classification. *Rep. Prog. Phys.*, 64:517–590, 2001.
- [153] I. Jonassen, I. Eidhammer, D. Conklin, and W. R. Taylor. Structure motif discovery and mining the PDB. *Bioinformatics*, 18:362–367, 2002.
- [154] D. Conklin, I. Jonassen, R. Aasland, and W. R. Taylor. Association of nucleotide patterns with gene function classes: application to human 3' untranslated sequences. *Bioinformatics*, 18:182–189, 2002.
- [155] W. R. Taylor. A periodic table for protein structure. *Nature*, 416:657–660, 2002.
- [156] K. Lin, A. C. May, and W. R. Taylor. Amino acid substitution matrices from an artificial neural network model. *J. Comput Biol.*, 8:471–481, 2002.
- [157] W. R. Taylor, J. Heringa, F. Baud, and T. P. Flores. A Fourier analysis of symmetry in protein structure. *Protein Eng.*, 15:79–89, 2002.
- [158] J. W. Saldanha, P. E. Czabotar, A. J. Hay, and W. R. Taylor. A model for the cytoplasmic domain of the influenza A virus M2 channel by analogy to the HIV-1 Vpu protein. *Protein Peptide Letts.*, 9:495–502, 2002.
- [159] W. R. Taylor. Protein structure comparison using bipartite graph matching. *Mol. Cell. Proteomics*, 1:334–339, 2002.

- [160] K. Lin, A. C. May, and W. R. Taylor. Threading using neural networks (TUNE): the measure of protein sequence-structure compatibility. *Bioinformatics*, 18:1350–1357, 2002.
- [161] W. R. Taylor. Comparing secondary structure 'stick' models of proteins using graph matching with double dynamic programming. In H. Seidel H.-W. Mewes, B. Weiss, editor, *Bioinformatics and Genome Analysis*, chapter 7, pages 133–148. Springer-Verlag, Berlin/Heidelberg, 2002. Ernst Schering Research Foundation Workshop Volume 38.
- [162] K. Lin, A. C. May, and W. R. Taylor. Amino acid encoding schemes from protein structural alignments: multidimensional vectors to describe residue types. *J. Theor. Biol.*, 221:361–365, 2002.
- [163] K. Petersen and W. R. Taylor. Modelling zinc-binding proteins with GAD-GET: Genetic algorithm and distance geometry for exploring topology. J. Molec. Biol., 325:1039–1059, 2003.
- [164] E. Mombelli, R. Morris, W. R. Taylor, and F. Fraternali. Hydrogen-bonding propensities of sphingomyelin in solution and in a bilayer assembly: a molecular dynamics study. *Biophys. J.*, 84:1507–1517, 2003.
- [165] W. R. Taylor, B. Xiao, S. J. Gamblin, and K. Lin. A knot or not a knot? SETting the record 'straight' on proteins. *Comp. Biol. Chem.*, 27:11–15, 2003.
- [166] K. Lin, W. R. Taylor, J. Klienjung, and J. Heringa. CAO matrices from an artificial neural network model. *J. Compu. Biol. Chem.*, 27:93–102, 2003.
- [167] W. R. Taylor and K. Lin. A tangled problem. *Nature*, 421:25, 2003. (concept).
- [168] W. R. Taylor, R. E. J. Munro, K. Petersen, and R. P. Bywater. Ab initio modelling of the N-terminal domain of the secretin receptors. Comp. Biol. Chem., 27:103–114, 2003.
- [169] L. O. Johannissen and W. R. Taylor. Protein fold comparison by the alignment of topological strings. *Prot. Engng.*, 16:949–955, 2004.
- [170] I. Eidhammer, I. Jonassen, and W. R. Taylor. *Protein Bioinformatics: an algorithmic approach to sequence and structure analysis.* J. Wiley, London, 2004. ISBN: 0-470-84839-1.
- [171] K. B. Murray, W. R. Taylor, and J. M. Thornton. Towards the detection and validation of repeats in protein structure. *Proteins: struct. funct. bioinfo.*, 57:365–380, 2004.

- [172] A. Stevens, M. Bock, S. Ellis, P. Le Tissier, K. N. Bishop, W. R. Taylor, and J. P. Stoye. Retroviral capsid determinants of the Fv1 NB- and NR-tropism. J. Virology, 78:9592–9598, 2004.
- [173] W. R. Taylor and I. Jonassen. A structural pattern-based method for protein fold recognition. *Proteins: struc. funct. bioinf.*, 56:222–234, 2004.
- [174] W. R. Taylor. A molecular model for transcription in the RNA world based on the ribosome large subunit. *Comp. Biol. Chem.*, 28:313–319, 2004.
- [175] W. R. Taylor and J. P. Stoye. Consensus molecular models for the amino terminal domain of the retrovirus restriction gene *fv1* and the murine leukaemia virus capsid proteins. *JMC Struc. Biology*, 4:1–15, 2004.
- [176] K. Lin, V. A. Simossis, W. R. Taylor, and J. Heringa. A simple and fast secondary structure prediction method using hidden neural networks. *Bioinformatics*, 21:152–159, 2005.
- [177] W. R. Taylor and A. Aszódi. *Protein Geometry, Classification, Topology and Symmetry*. Institute of Physics, 2005. Currently published by CRC Press.
- [178] D. Baker and W. R. Taylor. *Ab initio* structure prediction. In S. Subramanian, editor, *Encyclopedia of genetics, genomics, proteonomics and bioin-formatics*, volume 7–bioinformatics, pages 3245–3251. John Wiley and Sons Ltd., Chichester, U.K., 2005.
- [179] W. R. Taylor. Stirring the primordial soup. Nature, 434:705, 2005.
- [180] W. R. Taylor. Modelling molecular stability in the RNA world. Computational Biology and Chemistry, 29:259–272, 2005.
- [181] W. R. Taylor. Protein folds, knots and tangles. In J. Calvo, K. Millett, E. Rawdon, and A. Stasiak, editors, *Physical and Numerical Models in Knot Theory*, Series on Knots and Everything — Vol. 36, chapter 10, pages 171–202. World Scientific, Singapore, 2005. ISBN: 981-256-187-0.
- [182] W. R. Taylor. Protein structure analysis and prediction. In S. Subramanian, editor, *Encyclopedia of genetics, genomics, proteonomics and bioinformatics*, volume 7–bioinformatics, pages 3245–3251. John Wiley and Sons Ltd., Chichester, U.K., 2005. Introductory review to section 6 (ed.: W.R.Taylor).
- [183] E. A. Snell, N. M. Brooke, W. R. Taylor, D. Casane, H. Philippe, and P. W. H. Holland. An unusual choanoflagellate protein released by hedgehog autocatalytic processing. 273:401–407, 2006.

- [184] J. Vesterstrom and W. R. Taylor. Flexible secondary structure based protein structure comparison applied to the detection of circular permutation. J. Compu. Biol., 13:43–62, 2006.
- [185] I. Jonassen, D. Klose, and W. R. Taylor. Protein model refinement using structural fragment tessellation. *Comp. Chem. Bioinformatics*, 30:360–366, 2006.
- [186] W. R. Taylor, K. Lin, D. Klose, F. Fraternali, and I. Jonassen. Dynamic domain threading. *Proteins, Struct. Funct. Bioinfo.*, 64:601–614, 2006.
- [187] W. R. Taylor. Decoy models for protein structure score normalisation. *J. Molec. Biol.*, 357:676–699, 2006.
- [188] W. R. Taylor. Transcription and translation in an RNA world. *Phil. Trans.* R. Soc. B, 361:1751–1760, 2006.
- [189] W. R. Taylor. A molecular model for the origin of protein translation in an RNA world. *J. Theor. Biol.*, 243:393–406, 2006.
- [190] W. R. Taylor. Topological accessibility shows a distinct asymmetry in the folds of $\beta\alpha$ proteins. *FEBS Lett.*, 580:5263–5267, 2006.
- [191] G. J. Bartlett and W. R. Taylor. Using scores derived from statistical coupling analysis to distinguish correct and incorrect folds in *de-novo* protein structure prediction. *Proteins: struct. funct. bioinfo.*, 71:950–959, 2007.
- [192] D. Klose and W. R. Taylor. Protein structure prediction. In D. J. Balding et al., editor, *Handbook of Statistical genetics*, chapter 10, pages 327–344. John Wiley and Sons Ltd., 2007. Second edition.
- [193] W. R. Taylor. Protein knots and fold complexity: some new twists. Comp. Biol. Chem., 31:151–162, 2007. doi:10.1016/j.compbiolchem.2007.03.002.
- [194] W. R. Taylor. Evolutionary transitions in protein fold space. Curr. Opin. Str. Biol., 17:354–361, 2007.
- [195] S. M. Hollup, W. R. Taylor, and I. Jonassen. Structural fragments in protein model refinement. *Prot. Peptide Lett.*, 15:964–71, 2008.
- [196] V. Chelliah and W. R. Taylor. Functional site prediction selects correct protein models. *BMC Bioinformatics funct. bioinfo.*, 9(Suppl.1):S13, 2008.
- [197] 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.