

Biomedical Engineering

[Home](#)
[About Us](#)
[Research](#)
[Prospective Students](#)
[Current Students](#)
[Faculty & Staff](#)
[Calendar](#)
[Employment](#)
[McCormick Home](#)
[Study Abroad](#)
[MS in Biomedical & Environmental Engineering](#)
[Home](#) > [Faculty & Staff](#) > [Core Faculty](#) > Core Faculty Profile

Core Faculty Profile

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Tai T. Wu

Research Interests

Structural and functional relations of proteins and DNA, especially those pertaining to immunoglobulins and related proteins.

Our theoretical analyses of biological macromolecules may provide a unique insight into some of the fundamental problems in life sciences. On analyzing the length distributions of the third complementarity determining regions of human and mouse T-cell receptors for antigen gamma and delta chains, we have noticed a bi-model form for delta chains. This finding suggests that TCR gamma/delta complexes may or may not be MHC-restricted, i.e. these molecules can serve two different functions. A novel supercoiled DNA molecule can be constructed by connecting the ends of two mutually intercalating, double-stranded, antiparallel DNA ladders. Unlike conventional supercoils, these two complementary single-stranded DNA circles can separate without any breakage of the sugar-phosphate backbone. The long-range order imposed by this structure may be the reason why many biologically active DNA molecules are intact double-stranded circles.

Selected Publications

Journal articles

1. Wu, T. T. (1969) Secondary structures of DNA. *Proceed. Natl. Acad. Sci. USA*, 63: 400-405.
2. Wu, T. T. and Kabat, E. A. (1970): An analysis of the sequences of the variable regions of Bence Jones proteins and myeloma light chains and their implications for antibody complementarity. *J. Exp. Med.*, 132: 211-250.
3. Wu, R. and Wu, T. T. (1996) A novel intact circular dsDNA supercoil. *Bull. Math. Biol.*, 58, 1171-1186.
4. Johnson, G. and Wu, T.T. (2000) Kabat database and its applications: 30 years after the first variability plot. *Nucl. Acids Res.*, 28, 214-218.
5. Wu, T. T. (2006) Flu vaccines for next season. *Curr. Trends Immunol.*, 7, 55-59.

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1. Johnson, G., Kabat, E. A. and Wu, T. T. (1996) Kabat database of sequences of proteins of immunological interest. In *Weir's Handbook of Experimental Immunology*, I. Immunochemistry, D. M. Weir, Ed., Blackwell Science, Chap. 6, 6.1-6.21.
2. Johnson, G. and Wu, T. T. (2004) The Kabat database and a bioinformatics example. In *Antibody Engineering: Methods and Protocols*, B. K. C. Lo, Ed., Human Press Inc.,

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1. Kabat EA, Wu TT, Bilofsky H (1976) VARIABLE REGIONS OF IMMUNOGLOBULIN CHAINS. Bolt Beranek and Newman Inc., Cambridge, MA.
2. Kabat EA, Wu TT, Bilofsky H (1979) SEQUENCES OF IMMUNOGLOBULIN CHAINS. NIH Publication No. 80-2008, Bethesda, MD.
3. Kabat EA, Wu TT, Bilofsky H, Reid-Miller M, Perry H (1983) SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST. NIH Publication No. 369-847, Bethesda, MD.
4. Wu TT (1985) NEW METHODOLOGIES IN STUDIES OF PROTEIN CONFORMATION. Van Nostrand Reinhold Co., New York, NY.
5. Kabat EA, Wu TT, Reid-Miller M, Perry H, Gottesman K (1987) SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST, 4th Ed., U. S. Government Printing Office No. 165-492, Washington, DC.
6. Kabat EA, Wu TT, Perry H, Gottesman K, Foeller C (1991) SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST, 5th Ed. NIH Publication No. 91-3242, Bethesda, MD.
7. Wu TT (2001) ANALYTICAL MOLECULAR BIOLOGY, Kluwer Academic Publishers, Boston, MA.
8. Wu TT (2006) BEST SCIENTIFIC DISCOVERY OR WORST SCIENTIFIC FRAUD OF THE 20TH CENTURY. Research Signpost, Kerala, India.

Conference proceedings

1. Wu, T.T. (1996) Novel activity of topoisomerase I, Mol. Biol. Cell, 7, 101a.
2. Wu, T.T. (1998) Effect of glutathione on nearsightedness due to nuclear cataract, Biophys. J., 74, a370.
3. Wu, T. T. and Johnson, G. (2003) Search for nearly invariant segments in HIV-1 gp120. Biophys. J. Abst., 82, 282a.



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