

轉錄因子找出基因序列 蔡旻燁論文登上JACS期刊

學校要聞

【記者麥嘉儀淡水校園報導】化學系助理教授蔡旻燁與美國萊斯大學化學系博士班研究生Xun Chen及教授Peter G. Wolynes（另擔任Bullard-Welch基金會教授、美國科學院院士），3人共同在美國化學學會出版的《Journal of the American Chemical Society》（JACS）期刊發表論文，以轉錄因子PU.1（一種多功能蛋白質分子，例如骨髓細胞分化、免疫細胞發育等），成功在基因中尋找出正確序列。

該論文於今年2月發表，名稱為：「The Role of Charge Density Coupled DNA Bending in Transcription Factor Sequence Binding Specificity: A Generic Mechanism for Indirect Readout」（DNA彎曲對其轉錄因子序列結合特異性之作用：一種經由電荷密度耦合而能「間接」讀取序列資訊的通用機制）。該期刊為化學領域中的頂尖期刊，涉及化學領域的所有內容。根據ISI的統計數據，JACS也是化學領域內被引最多的期刊，其影響因子為15.419（2021-2022）。

蔡旻燁指出，此篇論文使用本校最先進的電腦模擬技術，研究細胞內生命運作的機制，也就是轉錄因子（一種蛋白質分子）如何於茫茫基因海中，尋找正確的基因序列，以調控基因的表達。他說：「此項研究可以作為生物基礎設計及其相關研究，甚至幫助了解免疫細胞分化、發育的機理，未來可促進新型的抗癌藥物設計策略，與引導新的實驗技術發展。」

蔡旻燁更以「按摩」來比喻這次的研究中，轉錄因子彷彿在DNA細胞上按摩一般，滑動到其較軟的位置，便可以停下來工作，找尋正確的基因序列。他也說明，此次與美國萊斯大學的研究生及教授合作，是因為之前曾在該校的研究中心完成博士後研究，因此共同合作促成了這次的研究成果。

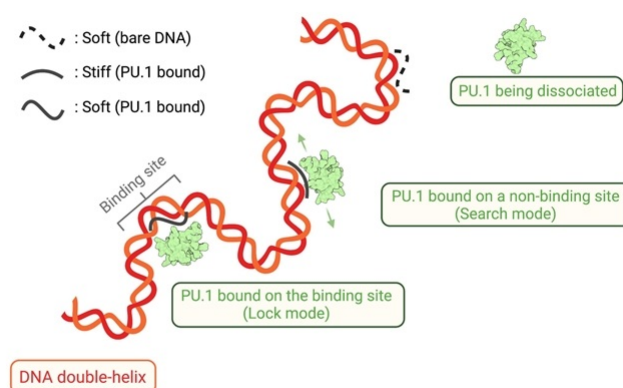
Min-Yeh Tsai, an Assistant Professor of the Department of Chemistry, Xun Chen, a Ph.D. student of the Department of Chemistry at Rice University, and Peter G. Wolynes, Professor of Chemistry at Rice University (Bullard-Welch Foundation Professor, Senior Scientist at the Center for Theoretical Biophysics, and Member of the National Academy of Sciences), jointly published a paper in the Journal of the American Chemical Society (JACS) – founded by the American Chemical Society – and successfully used computers

to simulate the process of the transcription factor PU.1 (a multifunctional protein molecule, such as bone marrow cell differentiation, immune cell development, etc.) finding the correct binding sequence in the gene.

The paper published in February this year is titled: "The Role of Charge Density Coupled DNA Bending in Transcription Factor Sequence Binding Specificity: A Generic Mechanism for Indirect Readout". The binding specificity of PU.1 is achieved primarily via a nonspecific electrostatically-driven DNA mechanism involving the change in the elastic properties of the DNA. We first hypothesize a novel generic mechanism for indirect "shape" readout, where DNA plastically bends in response to the electrostatic coupling driven by PU.1. The journal is the top journal in the field of chemistry, covering everything in the field. According to the ISI statistics, JACS is also the most cited journal in the field of chemistry, with an impact factor of 15.419 (2021-2022).

Min-Yeh Tsai pointed out that this work uses the university's most advanced computer simulation technology to study the working mechanism of life in the cell, that is, how transcription factors (a protein molecule) find the correct binding sequence among vast number of different genes to regulate their expression. This research can be used as a biological basis for gene circuit design and related research, and even help understand the mechanism of immune cell differentiation/development. In the future, it can promote new anti-cancer drug design strategies and guide the development of new experimental techniques.

In addition, Min-Yeh Tsai used "massage" as a metaphor for this study. Transcription factors massages on DNA. When they slide to a softer position, they can stop and locate the correct gene sequence. In the meanwhile, he explained that the collaboration with professor Peter Wolynes at Rice University was funded by Ministry of Science and Technology, Taiwan (R.O.C). He had completed his postdoctoral research at the school's research center before. He is so glad to see this joint collaboration ending up to be quite successful. (英文新聞稿／蔡旻燁提供)



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化學系助理教授蔡旻燁與美國萊斯大學化學系博士班研究生Xun Chen及萊斯大學教授Peter G. Wolynes共同於JACS期刊發表論文，以模型成功在基因中尋找出正確序列。（圖／蔡旻燁提供）