

教師簡介資料

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研究興趣與成果(中/英文)			
<p>中文：</p> <p>主要利用國家同步輻射研究中心(NSRRC)和日本 SPring-8 同步加速器之 X 光及蛋白質結晶學實驗站，來進行蛋白質與小分子結構與功能研究。實驗室設有生命科學研究之分子生物、生化及蛋白質結晶學設備。研究方向主要針對厭氧菌中多種蛋白質結構與功能關係的探討，以了解厭氧菌在無氧環境中的生命作用機制。由病人檢體中分離出來的厭氧菌，尤其對於某些硫化菌的生長代謝過程，及其間所牽涉到的所有蛋白質/酵素。探討這些蛋白質/酵素的生理功能，分子結構及與疾並間的可能關連。初期的研究以 <i>Desulfovibrio gigas</i> 或 <i>Desulfovibrio vulgaris</i> 的硫化菌做為模式。先分離純化相關蛋白質/酵素，再探討它們的分子結構，最後找出在動物細胞上可能的結合位置。另外也針對稻米發芽時在無氧及有氧環境下的細胞生長與鞘葉伸展相關的蛋白質進行結構功能之研究。稻米是目前已知具無氧發育物種中的高等生物，且其基因已被充分研究並解讀出。目前實驗室已得到超過 150 個基因，具重要蛋白質活性功能，正進行其結構分析。長期計畫將從稻米基因中找出更完整的相關功能蛋白質，進行系統性研究，以進一步了解稻米的無氧及有氧發育過程。另外實驗室亦廣泛研究一些重要蛋白質結構及功能之關係，如細胞膜蛋白質，以解決生物上未知的訊息，進行結構生物、基因體及藥物設計之研究。</p>			
<p>英文：</p> <p>My major research interest is to study crystal structure and functional relationship of various proteins, including protein-DNA/RNA interaction, virus, membrane proteins, enzymes, and other functional important proteins related to drug discovery by protein crystallography using synchrotron X-ray from NSRRC and SPring-8. Our laboratory is equipped with advanced facilities of molecular biology, biophysics, biochemistry and protein crystallography. The primary interest focuses on sulfate-reducing bacteria (SRB), the strict anaerobes, containing an electron transfer chain from pyridine nucleotides to molecular oxygen. We tend to study the structure and function of important proteins and metalloproteins of SRB, <i>Desulfovibrio gigas</i> and <i>vulgaris</i> to understand the life process mechanisms in anaerobic and aerobic environment. The future target will be extended to pathogenic bacteria from patients.</p> <p>Another long term project is to study rice coleoptile elongation during seed germination and the early stages of seeding growth under anaerobic, aerobic and stress environment. Several hundreds of proteins have been identified to involve in those anaerobic processes in our laboratory. We intend to search more complete related genes and proteins to systematically study the crystal structure and functional relationships. The information will provide not only the better understanding for anaerobic processes during seed germination and coleoptile elongation but also the implication for possible mechanisms of other different species.</p>			

Selected Publications

[2006] C.-J. Chen*, Y.-H. Lin, Y.-C. Huang and M.-Y. Liu, *Crystal structure of rubredoxin from *Desulfovibrio gigas* to ultra-high 0.68 Å resolution*, **Biochem. Biophys. Res. Comm.** 349, 79-90 (2006).

[2005] F. Elmi, H.-T. Lee, J.-Y. Huang, Y.-C. Hsieh, Y.-L. Wang, Y.-J. Chen, S.-Y. Shaw and C.-J. Chen*, *Stereoselective esterase from *Pseudomonas putida* reveal an α/β hydrolase fold for *D*- β acetylthioisobutyric acid synthesis*, **J. Bacteriol.** 187, 8470-8476 (2005).

[2005] S.-C. Lee, H.-H. Guan, C.-H. Wang, W.-N. Huang, C.-J. Chen* and W. Wu, *Structural basis of venom citrate-dependent heparan sulfate-mediated cell surface retention of cobra cardiotoxin A3*, **J. Biol. Chem.** 280, 9567-9577 (2005).

[2005] J.-Y. Huang, T. Chang, C.-Y. Chang and C.-J. Chen*, *Crystal structure of a nucleoside diphosphate kinase required for coleoptile elongation in rice (*Oryza sativa* L.)*, **J. Struct. Biol.** 150, 309-318 (2005).

[2005] T.-S. Chen, F.Y. Chung, S.-C. Chang, W.-N. Huang, K.Y. Chien, P.-L. Wu, K.-S. Goh, H.-C. Lin, C.-J. Chen* and W. Wu, *Group I cobra cardiotoxins as conformational analogues of cyclolinopeptide A*, **Biochemistry**, 44, 7414-7426 (2005).

[2005] Y.-C. Hsieh, M.-Y. Liu, J. LeGall and C.-J. Chen*, *Anaerobic purification and crystallization to improve the crystal quality: ferredoxin II from *Desulfovibrio gigas**, **Acta Crystallogr.** D61, 780-783 (2005).

[2003] C.-J. Chen*, M.-Y. Liu, C. Chang, W. J. Payne, B.-C. Wang and J. LeGall, *Crystal structure of nucleoside diphosphate kinase from *Bacillus halodenitrificans* at 2.2 Å resolution, an enzyme co-expressed of its activity with a Mn-superoxide dismutase*, **J. Struct. Biol.** 142, 247-255 (2003).

[2003] C.-J. Chen*, M.-Y. Liu, Y.-T. Chen and J. LeGall, *Preparation and X-ray crystallography analysis of rubredoxin crystals from *Desulfovibrio gigas* to beyond ultra-high 0.68 Å resolution*, **Biochem. Biophys. Res. Comm.** 308, 684-688 (2003).