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**Ph.D., Johns Hopkins University, 1993**

**Protein engineering; Enzymology; Gene regulation; Bioinformatics; Bioorganic chemistry**

### ***Research Interests***

Our research team has investigated structure-function relationship of human and fungal enzymes employing molecular and cellular biological, biochemical, biophysical, and bioinformatics methodologies.

For human RNase family, a novel endocytosis mechanism through direct protein-protein interaction between human eosinophil cationic protein (ECP) and human carboxypeptidase has been firstly discovered in 2004. In 2007, another endocytosis mechanism, lipid raft-dependent macropinocytosis, mediated through direct protein-polysaccharide interaction between human ECP and cell surface heparan sulfate proteoglycan (HSPG) has also been identified and characterized. The consequent apoptotic effects on tumor cells are under investigation. As for the cytotoxic effects of human RNases, the signal peptide of ECP has been identified to be play a critical role in terms of triggering induction of transforming growth factor  $\alpha$  (TGF $\alpha$ ), leading to proliferation of human cells. Interestingly, the expression of the signal peptide of ECP results in growth inhibition of bacterial and yeast cells. In addition, crucial residues involved in the membrane permeability and antimicrobial activity of human RNase 7 has also been determined. Furthermore, novel transcription factors governing differential transcriptional activation of human ECP and eosinophil-derived neurotoxin (EDN) promoters in tumor cells have been identified and characterized.

For fungal glucoamylase and carbohydrate binding module (CBM) family, the structure-function relationship of *Rhizopus oryzae* glucoamylase and its starch binding domain (SBD) have been determined to reveal a unique starch binding model. The three dimensional structures of unliganded and liganded SBD have been resolved by NMR and X-ray crystallography. In addition, yeast engineering has been established to enhance recombinant protein expression and secretion. Discovery of novel SBD structure and ligand binding mode has led to a series of patent design and industrial application. Moreover, an unusual SBD-derived amyloid-like fibril formation mechanism was discovered.

Aside from molecular and cellular biological approaches, several novel bioinformatics tools have been developed for multiple sequence comparison to identify unique peptide motifs in members of protein families. Such tools are useful in facilitating peptide antigen design, and characterization of specific protein functions.

### **Recent Publications**

1. Wang, H.-Y., Ho, P.-C., Lan, C.-Y., **Chang, M. D.-T.\*** (2008). Transcription regulation of human eosinophil RNases by the liver-enriched hepatocyte nuclear factor 4. *J. Cell. Biochem.* (accepted on Nov. 5, 2008).
2. Liu, W.-T., Lin, S.-C., Chou, W.-I., Liu, T.-H., Pan, R.-L., Tzou, D.-L., Hua, T.-E., **Chang, M. D.-T.\*** (2008). Identification and characterization of a novel fibril forming peptide in fungal starch binding domain. *Biochem. Biophys. Res. Commun.* (in press, accepted on Oct. 20, 2008).
3. Tung, J.-Y., **Chang, M. D.-T.**, Chou, W.-I., Liu, Y.-Y., Yeh, Y.-H., Chang, F.-Y., Lin, S.-C., Qiu, Z.-L., Sun, Y.-J. (2008). Crystal structures of starch binding domain of *Rhizopus oryzae* glucoamylase reveal a polysaccharide binding path. *Biochem. J.* 416(1), 27-36.
4. Huang, R.-Y., Chang, H.-T., Lan, C.-Y., Pai, T.-W., Wu, C.-N., Ling, C.-M., and **Chang, M. D.-T.** (2008). Development and evaluation of a sensitive enzyme-linked oligonucleotide-sorbent assay for detection of polymerase chain reaction-amplified hepatitis C virus of genotypes 1-6. *J. Virol. Method.* 151, 211-216.
5. Fan, T.-C., Fang, S.-L., Hwang, C.-S., Hsu, C.-Y., Lu, X.-A., Hung, S.-C., Lin, S.-C., Liu, W.-T., **Chang, M. D.-T.\*** (2008). Characterization of molecular interactions between eosinophil cationic protein and heparin. *J. Biol. Chem.* 283, 25468-25474..
6. Yen, C.-N., Lin, Y.-R., **Chang, M. D.-T.**, Tien, C.-W., Wu, Y.-C., Liao, C.-J., Hu, Y.-C. (2008). Use of porous alginate sponges for substantial chondrocyte expansion and matrix production: Effects of seeding density. *Biotechnol. Prog.* 24, 452-457.
7. Chao, C.-C., Sun, F.-C., Wang, C.-H., Lo, C.-W., Chang, Y.-S., Chang, K.-C., **Chang, M. D.-T.**, Lai, Y.-K. (2008). Concerted actions of multiple transcription elements confer differential transactivation of HSP90 isoforms in geldanamycin-treated 9L rat gliosarcoma cells. *J. Cell. Biochem.* 104, 1286-1296.
8. Shu, C.-W., Sun, F.-C., Cho, J.-H., Lin, C.-C., Chen, P.-Y., **Chang, M. D.-T.**, Fu, H.-W., Lai, Y.-K. (2008). GRP78 and Raf-1 cooperatively confer resistance to endoplasmic reticulum stress-induced apoptosis. *J. Cell. Physiol.* 215, 627-635.
9. Fan, T.-c., Chang, H.-T., Chen, I.-W., Wang, H.-Y., **Chang, M. D.-T.\*** (2007). A heparan sulfate facilitated pathway for the internalization of eosinophil cationic protein through lipid raft-dependent macropinocytosis. *Traffic*, 8, 1778-1795.
10. Lin, S.-C., Liu, W.-T., Liu, S.-H., Hsiung, B.-K., Chou, W.-I., Lin, I. P., Sheu, C.-C., **Chang, M. D.-T.\*** (2007). Role of linker region in the expression and secretion of *Rhizopus oryzae* glucoamylase. *BMC Biochemistry* 8, 9.
11. Wang, H.-Y., Chang, H.-T., Pai, T.-W., Wu, C.-I., Lee, Y.-H., Tai, S.-L., Tang, C.-Y., Chou, W.-Y., **Chang, M. D.-T. \*** (2007). Transcriptional regulation of eosinophil derived neurotoxin by MAZ and Sp1 is governed by a characteristic DNA sequence motif. *BMC Mol. Biol.* 8, 89.

12. Wan, C.-F., Chen, W.-H., Chen, Cheng-Ta, **Chang, M. D.-T.**, Lo, L.-C., Li, Y.-K. (2007). Mutagenesis and mechanistic study of a family 54  $\alpha$ -L-arabinofuranosidase from *Trichoderma koningii*. *Biochem. J.* 401, 551-558.
13. Chang, H.T., Kao, Y.L., Wu, C.M., Fan, T.C., Lai, Y.K., Huang, K.L., Chang, Y.S., Tsai, J.J., and **Chang, M.D.-T.** (2007). Signal peptide of eosinophil cationic protein upregulates transforming growth factor- $\alpha$  expression in human cells. *Journal of Cellular Biochemistry* 100, 1266-1275.
14. Huang, Y.C., Lin, Y.M., Chang, T.W., Wu, S.J., Lee, Y.S., **Chang, M.D.-T.**, Chen, C., Wu, S.H., and Liao, Y.D. (2007). The flexible and clustered lysine residues of human ribonuclease 7 are critical for membrane permeability and antimicrobial activity. *Journal of Biological Chemistry* 282, 4626-4633.
15. Liu, Y.N., Lai, Y.T., Chou, W.I., **Chang, M.D.-T.**, and Lyu, P.C. (2007). Solution structure of family 21 carbohydrate-binding module from *Rhizopus oryzae* glucoamylase. *Biochemical Journal* 403, 21-30.
16. Chang, H.-T., Pai, T.-W., Fan, T.-c., Su, B.-H., Wu, P.-C., Tang, C.-Y., Liu, S.-H., and **Chang, M. D.-T.\*** (2006). A reinforced merging methodology for identification of unique peptide motifs in members of protein families. *BMC Bioinformatics* 7, 38.
17. Pai, T.-W.\*, Su, B.-H, Wu, P.-C., **Chang, M. D.-T.\***, Chang, H.-T., Fan, T.-C., and Liu, S.-H. (2006). Unique peptide identification of RNase family sequences based on reinforced merging algorithms. *Journal of Bioinformatics and Computational Biology* 4, 75-92.
18. Chou, W.-I., Pai, T.-W., Liu, S.-H., Hsiung, B.-K., and **Chang, M. D. T.\*** (2006). The Family 21 Carbohydrate Binding Module of Glucoamylase from *Rhizopus oryzae* Consists of Two Sites with Distinct Binding Specificities. *Biochem. J.* 396, 469-477.
19. Pai, T.-W.\*, **Chang, M. D.-T.\***, Tzou, W.-S., Su, B.-H., Wu, P.-C., Chang, H.-T., and Chou, W.-I. (2006). A R<sub>E</sub>MUS: a tool for identification of unique peptide segments as epitopes. *Nucleic Acid Res.* 34, W198-201.
20. Chang, Y.-S., Lo, C.-W., Sun, F.-C., **Chang, M. D.-T.**, and Lai, Y.-K. (2006). Differential expression of Hsp90 isoforms in geldanamycin-treated 9L cells. *Biochem. Biophys. Res. Commun.* 344, 37-44.
21. Lai, C.-W., Chan, Z.-R., Yang, D.-G., Lo, W.-H., Lai, Y.-K., **Chang, M. D.-T.**, and Hu, Y.-C. (2006). Accelerated induction of apoptosis in insect cells by baculovirus-expressed SARS-CoV membrane protein. *FEBS Lett.* 580, 3829-3834.
22. Chiou, S.-H., Yang, Y.-P., Lin, J.-C., Hsu, C.-H., Yang, Y.-T., Lee, C.-H., Ho, L.-T., Hsu, W.-M., Ku, H.-H., Chen, S.-J., Chen, S. S.-L., **Chang, M. D.-T.**, Wu, C.-W., and Juan, L.-R. (2006). The immediate early 2 protein of human cytomegalovirus mediates the apoptotic control in HCMV retinitis through activation of cellular FLICE-inhibitory protein. *J. Immunol.* 177, 6199-206.
23. Liu, S.-H., Chou, W.-I., Sheu, C.-C., and **Chang, M. D.-T.\*** (2005) Improved secretory

production of glucoamylase in *Pichia pastoris* by combination of genetic manipulations. *Biochem. Biophys. Res. Commun.* 326, 817-824.

24. Liu, S.-H., Chou, W.-I., Lin, S.-C., Sheu, C.-C., and **Chang, M. D.-T.\*** (2005). Molecular genetic manipulation of *Pichia pastoris* SEC4 governs cell growth and glucoamylase secretion. *Biochem. Biophys. Res. Commun.* 336, 1172-1180.
25. Lai, C.-W., Chung, Y.-C., Lai, Y.-K., **Chang, M. D.-T.**, and Hu, Y.-C. (2005). Expression and purification of N and E proteins from Severe Acute Respiratory Syndrome (SARS)-associated coronavirus: A comparative study. *Biotechnol. Lett.* 27, 883-891.
26. Wang, K.-C., Wu, J.-C., Chung, Y.-C., Ho, Y.-C., **Chang, M. D.-T.**, and Hu, Y.-C. (2005). Baculovirus as a highly efficient gene delivery vector for the expression of hepatitis delta virus antigens in mammalian cells. *Biotechnol. Bioeng.* 89, 464-473.
27. Hsu, C.-H., **Chang, M. D.-T.**, Tai, K.-Y., Wang, P.-S., Yang, Y.-T., Chen, C.-J., Wang, Y.-H., Lee, S.-C., Wu, C.-W., and Juan, L.-J. (2004). HCMV IE2-mediated inhibition of HAT activity downregulates p53 function. *EMBO J.* 23, 2269-2280.
28. Wu, C.-M., Chang, H. -T., and **Chang, M. D.-T.\*** (2004). Membrane-bound carboxypeptidase facilitates endocytosis of eosinophil cationic protein. *Biochem. J.* 382, 841-848.
29. Wu, C.-M., and **Chang, M. D.-T.\*** (2004). Signal peptide of eosinophil cationic protein is toxic to cells lacking signal peptide peptidase. *Biochem. Biophys. Res. Commun.* 322, 585-592.
30. Pai, T.-W., Chu, J.-H., and **Chang, M. D.-T.\*** (2004). Internal jumping searching algorithms for bio-sequence pattern matching. *J. Computers* 16, 20-28.
31. Tang, C.-Y., Lu, C.-L., and Chang, M. D.-T., Tsai, Y.-T., Sun, Y.-J., Chao, K.-M., Chang, J.-M., Chiou, Y.-H., Wu, C.-M., Chang, H.-T., Chou, W.-I. (2003). Constrained multiple sequence alignment tool development and its application to RNase family alignment. *Journal of Bioinformatics and Computational Biology* 1, 267-287.
32. Cheng, T.-J., Tseng, Y.-F., Chang, W.-M., and **Chang, M. D.-T.**, Lai, Y.-K. (2003). Retaining of the assembly capability of vimentin phosphorylated by mitogen-activated protein kinase-activated protein kinase-2. *J. Cell. Biochem.* 89, 589-602.

#### Book Sections

1. Chen, C.-M., Hsiao, M.-C., Pai, T.-W., Cheng, R., Tzou, W.-S., **Chang, M. D.-T.** (2008) Identify SSR regulators for functional gene sets through cross-species comparison. *Optimization and Systems Biology, Lecture Notes in Operations Research (LNOR)*, vol. 9, Ed. Du, D.-Z. and Zhang, X.-S., ISSN978-5062-9298-4.
2. **Chang, M. D.-T.**, Chang, H.-T., Tzou, W.-S., Liu, C.-H., Zhung, W.-J., Wang, H.-W., Chang, C.-T., Huang, R.-Y., Pai, T.-W. (2007) A database for prediction of unique peptide motifs as linear epitopes. *Bioinformatics Research and Applications, LNBI 4463 (LNCS Subseries)*, Ed Mandoiu, I. and Zelikovsky, A., ISSN 0302-9743, Springer, Germany,

430-440.

3. Chang, H.-T., Fan, T.-c., **Chang, M. D.-T.**, Pai, T.-W., Su, B.-H., Wu, P.-C. (2005) Unique peptide prediction of RNase family sequences based on reinforced merging algorithms. Proceedings of the 3<sup>rd</sup> Asia-Pacific Conference. Ed. Chen, Y.-P. P. & Wong, L., Imperial College Press, London, 289-298.
4. Tang, C.-Y., Lu, C.-L., **Chang, M. D.-T.**, Tsai, Y.-T., Sun, Y.-J., Chao, K.-M., Chang, J.-M., Chiou, Y.-H., Wu, C.-M., Chang, H.-T., Chou, W.-I. (2003) Constrained multiple sequence alignment tool development and its application to RNase family alignment. Proc IEEE Comput Soc Bioinform Conf. 1, 127-123.

#### Patents

1. **張大慈**、范丹琪、林淑娟 嗜酸性球陽離子蛋白之肝素結合位及其用途。中華民國專利，申請中。
2. **Chang, M. D.-T.**, Fan, T.-c., Lin, S.-C. Heparin Binding Motif and Use Thereof., US12/125,008 filing date 5/21/2008.
3. **Chang, M. D.-T.**, Sun, Y.-J., Lyu, P.-C. Amyloid-like Fibril Formation of a Starch Binding Domain. PCT/CN2008/ 61022960, filing date 1/23/2008. Pending.
4. **Chang, M. D.-T.**, Sheu, C.-C. Recombinant protein comprising starch binding domain and use thereof. Japan 2007-557310. Pending.
5. **張大慈**，許嘉欽 包含澱粉結合部位的重組蛋白質及其用途/Recombinant protein comprising starch binding domain and use thereof。中國專利 200680006927.x，申請日期：9/3/2007。Pending。
6. **Chang, M. D.-T.**, Sheu, C.-C. Recombinant protein comprising starch binding domain and use thereof. Europe, DE 238000264, filing date 8/31/2007. Pending.
7. **Chang, M. D.-T.**, Sheu, C.-C. Recombinant protein comprising starch binding domain and use thereof. US11/657,005, filing date 01/24/2007. Divisional application. Pending.
8. **張大慈**、呂平江、孫玉珠、許嘉欽 澱粉吸附區域及其用途 Starch binding domain and use thereof。中華民國專利 096111894，申請日期：96年4月3日。Pending。
9. **Chang, M. D.-T.**, Lyu, P.-C., Sun, Y.-J., Sheu, C.-C. Starch binding domain and use thereof. PCT/CN2006/002915, filing date 10/31/2006. Pending.
10. **張大慈**，許嘉欽 重組蛋白包含澱粉鍵結區域及其應用 Recombinant protein comprising starch binding domain and use thereof。中華民國專利 095106950，申請日期：95年3月2日。Pending。
11. **Chang, M. D.-T.**, Sheu, C.-C. Recombinant protein and method of screening for agents that mediate polypeptide aggregation. PCT/CN2006/000305, Priority date: March 3, 2005, Designated filing date: 3/2/2006. Pending.
12. **張大慈**，許嘉欽 可提升基因表現之核酸及其用途。中華民國專利 094142959，申請

日期：94 年 12 月 6 日。Pending。

13. **Chang, M. D.-T.**, Sheu, C.-C. Recombinant protein comprising starch binding domain and use thereof. US11/070,271, filing date 03/03/2005. Pending.
14. **Chang, M. D.-T.**, Sheu, C.-C. Nucleic acids for enhancing gene expression and use thereof. US11/006,817, filing date 12/08/2004. Pending.

#### International Conference Presentation

1. Chou, W.-I., Chou, W.-Y., Lin, S.-C., Jiang, T.-Y., C.-Y. Tang, **Chang, M. D.-T.\*** (2008) Functional Residue Prediction by Multiple Sequence Alignment for Carbohydrate Binding Modules. Full paper, 8<sup>th</sup> Atlantic Symposium on Computational Biology and Genome Informatics (CBGI2008, Dec. 15-20), Shenzhen, PRC.
2. Chou, W.-Y., Chou, W.-I., Pai, T.-W., Lin, S.-C., Jiang, T.-Y., Tang, C.-Y., **Chang, M. D.-T.\*** (2008) Weighted multiple sequence alignment among starch-binding carbohydrate binding modules for functional binding site analysis. Poster, The 2<sup>nd</sup> Japan-Taiwan Young Researchers Conference on Computational and Systems Biology (TJYoung2, Nov. 4-6, 2008), Odaiba, Japan. **(Best poster award)**
3. Chen, C.-M., Hsiao, M.-C., Pai, T.-W., Cheng, R., Tzou, W.-S., **Chang, M. D.-T.** (2008) Identification of SSR Regulators for Functional Gene Sets through Cross-Species Comparison. Full paper, The 2<sup>nd</sup> International Symposium on Optimization and Systems Biology (OSB2008, Oct. 31-Nov. 3, 2008), Lijiang, China.
4. Fang, S.-I., Fan, T.-c., Lin, S.-C., **Chang, M. D.-T.\*** (2008) Characterization of molecular interactions between eosinophil cationic protein and heparin sulfate. Poster, The 20<sup>th</sup> FAOBMB Conference (Oct. 23-25, 2008), Taipei, Taiwan, R. O. C.
5. Chou, W.-Y., Chou, W.-I., Pai, T.-W., Lin, S.-C., Chang, F.-Y., Sun, Y.-J., Tang, C.-Y., **Chang, M. D.-T.\*** (2008) Multiple sequence alignment for functional correlation among low similarity sequences. Full paper, Third IAPR International Conference on Pattern Recognition in Bioinformatics (PRIB 2008, Oct. 15-17, 2008), Novotel Sr. Kilda, Melbourne, Australia.
6. **Chang, M. D.-T.\***, Chou, W.-I., Lin, S.-C. (2008) Mapping key ligand binding sites on carbohydrate binding modules with low sequence homology. Poster, the 33<sup>rd</sup> FEBS Congress & 11<sup>th</sup> IUBMB Conference (June 28 – July 3, 2008), Athens, Greece.
7. Lin, S.-C., Liu, W.-T., Chou, W.-I., **Chang, M. D.-T.\*** (2008) The carbohydrate binding module family 21 contains a unique segment directing nano fibril formation. Poster, the 33<sup>rd</sup> FEBS Congress & 11<sup>th</sup> IUBMB Conference (June 28 – July 3, 2008), Athens, Greece.
8. **Chang, M. D.-T.\***, Liu, S.-H., Chou, W.-I., Lin, S.-C., Sheu, C.-C. (2008) Using starch as a super affinity resin to purify recombinant protein - The ultimate low-cost process. Poster, BIO2008 International Convention (June 17-20, 2008), San Diego, CA, U. S. A.
9. Lin, S.-C., Chiang, T.-Y., Hsieh, C.-A., Liu, S.-H., Chou, W.-I., Lyu, P.-C., Sun, Y.-J., **Chang, M. D.-T.\*** (2008) Characterization and engineering of CBM21 starch-binding

- domain. Poster, An International Symposium: Biotechnology for Better Crops, Energy and Health - ABRC 10<sup>th</sup> Anniversary (Apr. 29-May 1, 2008), Taipei, Taiwan, R. O. C.
10. Liu, S.-H., Chou, W.-I., Lin, S.-C., Sheu, C.-C., **Chang, M. D.-T.\*** (2008) Using starch as a super affinity resin to purify recombinant protein-The ultimate low-cost process. Poster, An International Symposium: Biotechnology for Better Crops, Energy and Health - ABRC 10<sup>th</sup> Anniversary (Apr. 29-May 1, 2008), Taipei, Taiwan, R. O. C.
  11. Wang, H.-Y., Pai, T.-W., Chou, W.-Y., **Chang, M. D.-T.\*** (2008) *In silico* and *in vitro* analyses of evolutionary- conserved sequence motif in primate genomes of eosinophil ribonucleases. Poster, The 1<sup>st</sup> Japan-Taiwan Young Researchers Conference on Computational and Systems Biology (Mar 9-11, 2008) Hsinchu, Taiwan, R. O. C. (**Best poster award**)
  12. Chou, W.-Y., **Chang, M. D.-T.\***, Chang, H.-T., Chou, W.-I., Fan, T.-c. Tzou, W.-S., Pai, T.-W.\* (2008) Multiple anchored block sequence alignment based on short consensus motifs. Poster, The 1<sup>st</sup> Japan-Taiwan Young Researchers Conference on Computational and Systems Biology (Mar 9-11, 2008) Hsinchu, Taiwan, R. O. C.
  13. Chou, W.-I., Fan, T.-c., Pai, T.-W., Sun, Y.-J., Chang, F.-Y., Chang, H.-T., Lin, S.-C., Lin, Y.-C. **Chang, M. D.-T.\*** (2008) Mapping key ligand binding sites on carbohydrate binding modules with low sequence homology. Poster, The Sixth Asia- Pacific Bioinformatics Conference (APBC2008, 15-18 January), Kyoto, Japan.
  14. Chang, H.-T., Liu, C.-H., **Chang, M. D.-T.**, Pai, T.-W. (2008) Estimation and extraction of predictive linear epitopes by mathematical morphology approaches. Poster, The Sixth Asia- Pacific Bioinformatics Conference (APBC2008, 15-18 January), Kyoto, Japan.
  15. Liu, S.-H., Chou, W.-I., Lin, S.-C., Sheu, C.-C., **Chang, M. D.-T.\*** (2007) Economic process model for high performance purification of recombinant protein comprising starch binding domain. Poster, the Third Symposium on the Alpha-Amylase Family (September 23-27, 2007), Smolenice Castle, Slovakia. (**Third prize poster award**)
  16. Lin, S.-C., Chou, W.-I., Sheu, C.-C., **Chang, M. D.-T.\*** (2007) Stable linker peptides for recombinant fusion protein expression in *E. coli*. Poster, the Third Symposium on the Alpha-Amylase Family (September 23-27, 2007), Smolenice Castle, Slovakia.
  17. **Chang, M. D.-T.\***, Chou, W.-I., Pai, T.-W., Lyu, P.-C., Sun, Y.-J., Liu, S.-H., Sheu, C.-C., Lin, Y.-C. (2007) Correlation and characterization of functions and secondary/tertiary structures of carbohydrate binding modules. Oral presentation, the Third Symposium on the Alpha-Amylase Family (September 23-27, 2007), Smolenice Castle, Slovakia.
  18. **Chang, M. D.-T.** Lin, S.-C. (2007) Novel endocytosis pathway of human toxins and the application in development of imaging peptide nanoparticle complex. 2007 年兩岸清華大學奈米科技學術研討會，新竹市，中華民國。
  19. Lin, S.-C., Fan, T.-c., **Chang, M. D.-T.\*** (2007) Characterization of heparan sulfate as a cell surface attachment molecule for human eosinophil ribonucleases. Poster, FEBS2007, the 32<sup>nd</sup> FEBS Congress in Vienna (July 7-12, 2007), Vienna, Austria.

20. Fan, T.-c., Lin, S.-c., **Chang, M. D.-T.\*** (2007) A Heparan Sulfate-Facilitated and Raft-Dependent Macropinocytosis of Eosinophil Cationic Protein. Poster, FEBS2007, the 32<sup>nd</sup> FEBS Congress in Vienna (July 7-12, 2007) , Vienna, Austria.
21. Wang, H.-W., Chen, J.-M., Chou, W.-Y., **Chang, M. D.-T.**, Pai, T.-W. (2007) Ordered combinatorial feature selection: An information portal for multiple indexing sequence alignment. Poster, International Symposium on Bioinformatics Research and Applications (ISBRA, May 6-10, 2007), Atalanta, Georgia, U. S. A.
22. **Chang, M. D.-T.**, Chang, H.-T., Tzou, W.-S., Liu, C.-H., Zhung, W.-J., Wang, H.-W., Chang, C.-T., Huang, R.-Y., Pai, T.-W. (2007) Oral presentation, A database for prediction of unique peptide motifs as linear epitopes. Oral presentation, International Symposium on Bioinformatics Research and Applications (ISBRA, May 6-10, 2007), Atalanta, Georgia, U. S. A.
23. Pai, T.-W., Chen, J.-M., Su, B.-H., **Chang, M. D.-T.**, Chang, H.-T., Chou, W.-I (2007) Protein Hierarchical Selection: An Information Portal for Multiple Protein Structural Alignment. Poster, The Fifth Asia- Pacific Bioinformatics Conference (APBC2007, January 15-17, 2007), Hong Kong, PRC.
24. Wang, H.-Y., Pai, T.-W., Chang, H.-T., Lee, Y.-H., Chang, Y.-S., Fan, T.-c., Lin, S.-C., **Chang, M. D.-T.\*** (2007) Identification and characterization of novel transcription factor binding motif in the promoter of human ribonuclease. Poster, The Fifth Asia-Pacific Bioinformatics Conference (APBC2007, January 15-17, 2007), Hong Kong, PRC.
25. Chou, W.-Y., Pai, T.-W., Lai, J. Z.-C., Tzou, W.-S., **Chang, M. D.-T.**, Chang, H.-T., Chou, W.-I., Fan, T.-c. (2006) Multiple Indexing Sequence Alignment for Group Feature Identification. Full paper, The Third Annual RECOMB Satellite Workshop on Regulatory Genomics. Singapore, Singapore.
26. Fan, T.-c., **Chang, M. D.-T.\***. (2006) A role for lipid rafts in the uptake and trafficking of eosinophil cationic protein. Poster, The 20<sup>th</sup> IUBMB International Congress of Biochemistry and Molecular Biology and 11th FAOBMB Congress, Kyoto, Japan.
27. Lin, S.-C., Sheu, C.-C., **Chang, M. D.-T.\***. (2006) The linker region of *Rhizopus oryzae* glucoamylase plays an important role in protein secretion. The 20<sup>th</sup> IUBMB International Congress of Biochemistry and Molecular Biology and 11th FAOBMB Congress, Kyoto, Japan.
28. Chou, W.-I, Pai, T.-W., Liu, S.-H., Lin, S.-C., **Chang, M. D.-T.\***. (2006) The Family 21 Carbohydrate Binding Module of Glucoamylase from *Rhizopus oryzae* Consists of Two Sites Playing Distinct Roles in Ligand Binding. Poster, The 20<sup>th</sup> IUBMB International Congress of Biochemistry and Molecular Biology and 11th FAOBMB Congress, Kyoto, Japan.
29. Chang, H.-T., Pai, T.-W., Fan, T.-c., Su, B.-H., Wu, P.-C., Tang, C.-Y., Chang, C.-Tien, **Chang, M. D.-T.\***. (2006) A reinforced merging methodology for mapping unique peptide motifs in members of protein families. Poster, The 20<sup>th</sup> IUBMB International



Congress of Biochemistry and Molecular Biology and 11th FAOBMB Congress, Kyoto, Japan.

30. Su, B.-H., Pai, T.-W., Tzou, W.-S., **Chang, M. D.-T.**, Chang, H.-T., Chou, W.-I. (2006) Constrained multiple structure feature alignment (CMSFA) for unique peptide identification. Poster, The Forth Asia- Pacific Bioinformatics Conference (APBC2006), Taipei, Taiwan, R. O. C.
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