著作目錄 Publication List

DR Tzu-Hsien YANG 楊子賢

PUBLICATIONS

[1] **T.-H. Yang***, Y.-C. Yang, and K.-C. Tu, "regCNN: identifying *Drosophila* genome-wide *cis*-regulatory modules via integrating the local patterns in epigenetic marks and transcription factor binding motifs," *Computational and Structural Biotechnology Journal*, vol. (Accepted), 2021. (SCI 2020 impact factor = 7.271 , Ranking 15% (45/298) in Biochemistry & Molecular Biology)

[2] **T.-H. Yang***, "An aggregation method to identify the RNA meta-stable secondary structure and its functionally interpretable structure ensemble," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, vol. (Early Access), 2021. (SCI 2020 impact factor = 3.710 , Ranking 12% (15/125) in Statistics & Probability)

[3] **T.-H. Yang**, Y.-H. Chiang, S.-C. Shiue, Y.-C. Yang, K.-C. Tu, Y.-Y. Tseng, J. T. Tseng*, and W.-S. Wu*, "Cancer DEIso: an integrative analysis platform for investigating differentially expressed gene-level and isoform-level human cancer markers," *Computational and Structural Biotechnology Journal*, vol. 19, pp. 5149–5159, 2021. (SCI 2020 impact factor = 7.271 , Ranking 15% (45/298) in Biochemistry & Molecular Biology)

[4] **T.-H. Yang***, C.-Y. Wang, H.-C. Tsai, and C.-T. Liu, "Human IRES Atlas: an integrative platform for studying IRES-driven translational regulation in humans," *Database*, vol. 2021, 2021. (SCI 2020 impact factor = 3.451 , Ranking 24% (14/58) in Mathematical & Computational Biology)

[5] **T.-H. Yang**, S.-C. Shiue, K.-Y. Chen, Y.-Y. Tseng, and W.-S. Wu, "Identifying piRNA targets on mRNAs in C. elegans using a deep multi-head attention network," *BMC Bioinformatics*, vol. 22, no. 1, pp. 1–23, 2021. (SCI 2020 impact factor = 3.169, Ranking 27% (16/58) in Mathematical & Computational Biology)

[6] **T.-H. Yang***, "Transcription factor regulatory modules provide the molecular mechanisms for functional redundancy observed among transcription factors in yeast," *BMC Bioinformatics*, vol. 20, no. 23, pp. 1–16, 2019. (SCI 2018 impact factor = 2.511, Ranking 15.3% (9/59) in Mathematical & Computational Biology)

[7] **T.-H. Yang**, C.-C. Wang, P.-C. Hung, and W.-S. Wu*, "*cis*MEP: an integrated repository of genomic epigenetic profiles and *cis*-regulatory modules in Drosophila," *BMC Systems Biology*, vol. 8, no. Suppl 4, p. S8, 2014. (SCI 2013 impact factor = 2.85, Ranking 13% (7/52) in Mathematical & Computational Biology)

[8] **T.-H. Yang**, C.-C. Wang, Y.-C. Wang, and W.-S. Wu*, "YTRP: a repository for yeast transcriptional regulatory pathways," *Database*, vol. 2014: article ID bau014; doi:10.1093/database/bau014, 2014. (SCI 2013 impact factor = 4.2 , Ranking 11% (5/47) in Mathematical & Computational Biology)

[9] **T.-H. Yang**, H.-T. Chang, C.-C. Wang, E. S. Hsiao, J.-L. Sun, H.-Y. Wu, P.-C. Liao*, and W.-S. Wu*, "iPhos: toolkit to streamline the alkaline phosphatase assisted comprehensive LC-MS phosphoproteome investigation," *BMC Bioinformatics*, vol. 15, no. Suppl 16, p. S10, 2014. (SCI 2013 impact factor = 2.67, Ranking 15% (8/52) in Mathematical & Computational Biology)

[10] P.-C. Hung, **T.-H. Yang**, H.-J. Liao*, and W.-S. Wu*, "The Yeast Nucleosome Atlas (YNA) database: An integrative gene mining platform for studying chromatin structure and its regulation in yeast," *BMC Genomics*, vol. 15, no. Suppl 9, p. S5, 2014. (SCI 2013 impact factor = 4.041, Ranking 18% (29/165) in Biotechnology & Applied Microbiology)

[11] **T.-H. Yang** and W.-S. Wu*, "Identifying biologically interpretable transcription factor knockout targets by jointly analyzing the transcription factor knockout microarray and the ChIP-chip data," *BMC Systems Biology*, vol. 6, no. 1, p. 102, 2012. (SCI 2011 impact factor = 3.15, Ranking 10.6% (5/47) in Mathematical & Computational Biology)

[12] **T.-H. Yang** and W.-S. Wu*, "Inferring functional transcription factor-gene binding pairs by integrating transcription factor binding data with transcription factor knockout data," *BMC Systems Biology*, vol. 7, no. Suppl 6, p. S13, 2013. (SCI 2012 impact factor = 2.982, Ranking 15% (7/47) in Mathematical & Computational Biology)

[13] F.-J. Lai, C.-C. Chiu, **T.-H. Yang**, Y.-M. Huang*, and W.-S. Wu*, "Identifying functional transcription factor binding sites in yeast by considering their positional preference in the promoters," *PLOS ONE*, vol. 8, no. 12, p. e83791, 2013. (SCI 2012 impact factor = 3.73, Ranking 13% (7/56) in Multidisciplinary Sciences)

CONFERENCE

[1] R.-Q. Hong, T. Gao, Y.-H. Yu, and **T.-H. Yang***, "Annotating the genome-wide *cis*-regulatory modules in *Drosophila* via a deep channel-attention network," in *International Conference on Bioinformatics (InCoB)*, Nov. 2021. (Oral-Poster)

[2] C.-Y. Wang, K.-C. Tu, Y.-C. Yang, H.-C. Tsai, and **T.-H. Yang***, "農作蜜棗損傷原因之高效能分類," in *International Conference on Technologies and Applications of Artificial Intelligence (TAAI)*, Nov. 2021. (Oral)

[3] Y.-H. Yu, J.-X. Xu, C.-F. Liao, and **T.-H. Yang***, "Automatic transcriptional factor-gene interaction literature evidence extraction via temporal convolutional neural networks," in *International Conference on Bioinformatics (INCOB)*, Nov. 2020. (Oral-Poster)

[4] D.-Y. Guo and **T.-H. Yang***, "Melanoma detection via deep transfer learning," in *International Conference on Bioinformatics (InCoB)*, Nov. 2020. (Oral-Poster)

[5] Y.-C. Lin and **T.-H. Yang***, "Novel biological metrics for evaluating the functional significance of RNA secondary structure predictions," in *International Conference on Bioinformatics (InCoB)*, Nov. 2020. (Oral-Poster)