

BIOGRAPHICAL SKETCH

NAME Wu, Cathy H, Ph.D.	POSITION TITLE Edward G. Jefferson Chair and Director, Center for Bioinformatics & Computational Biology, UD Director, Protein Information Resource (PIR), UD&GU Director, Bioinformatics Master's Program, UD Professor, Computer & Information Sciences, UD Professor, Biochemistry & Molecular Biology, GU		
CURRENT AFFILIATION University of Delaware (UD), Newark, DE & Georgetown University (GU), Washington, DC			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
National Taiwan University, Taiwan	B.S.	1978	Plant Pathology
Purdue University, West Lafayette, IN	M.S./Ph.D.	1984	Molecular Plant Pathology
Michigan State University, East Lansing, MI	Postdoc.	1986	Molecular Biology
University of Texas at Tyler, TX	M.S.	1989	Computer Science

List of five recent publications by the candidate:

- McGarvey PB, Huang H, Mazumder R, Zhang J, Chen Y, Zhang C, Cammer S, Will R, Odle M, Sobral B, Moore M, **Wu CH**. (2009) Systems integration of biodefense omics data for analysis of pathogen-host interactions and identification of potential targets. *PLOS One* 4, e7162.
 - Huang H, McGarvey PB, Suzek BE, Mazumder R, Zhang J, Chen Y, **Wu CH**. (2011) A comprehensive protein-centric ID mapping service for molecular data integration. *Bioinformatics* 27, 1190-1191.
 - Natale DA, Arighi CN, Barker WC, Blake JA, Bult CJ, Caudy M, Drabkin HJ, D'Eustachio P, Evsikov AV, Huang H, Nchoutmboube J, Roberts NV, Smith B, **Wu CH**. (2011) The Protein Ontology (PRO): A structured representation of protein forms and complexes. *Nucl. Acids Res.* 39, D539-545.
 - Hu ZZ, Kagan BL, Ariazic EA, Rosenthala DS, Zhanga L, Li JV, Huang H, **Wu CH**, Jordan VC, Riegela AT, Wellsteina A. (2011) Proteomic analysis of pathways involved in estrogen-induced growth and apoptosis in breast cancer cells. *PLOS One* (in press)
 - Legrain P, Aebersold R, Archakov A, Bairoch A, Bala K, Beretta L, Bergeron J, Borchers C, Corthals GL, Costello CE, Deutsch EW, Domon B, Hancock W, He F, Hochstrasser D, Marko-Varga G, Salekdeh GH, Sechi S, Snyder M, Srivastava S, Uhlen M, **Wu CH**, Yamamoto T, Paik YK, Omenn GS. (2011) The Human Proteome Project: Current state and future direction. *Mol Cell Proteomics* 2011 Apr 29. [Epub ahead of print]
- Book: **Wu CH**, Chen C. (Editors) (2011) *Bioinformatics for Comparative Proteomics*. Series *Methods in Molecular Biology*. Vol. 694, Walker, John M (Series Editor), Humana Press. ISBN 978-1-60761-976-5

Please indicate in 200 words or less the reason(s) why you would be a suitable candidate for the HUPO Council elections.

Contributions to Proteomic Science. Dr. Wu has conducted protein bioinformatics research for 20 years and has directed the Protein Information Resource (PIR) since 1999 as a major bioinformatics resource that supports genomic, proteomic and systems biology research. She is the PI/Co-PI on several large consortium projects, including the UniProt, Protein Ontology, and BioCreative. She serves on several advisory boards, including the NIH Protein Structure Initiative Advisory Committee and the PDB Scientific Advisory Board. She has published six books and conference proceedings and more than 160 peer-reviewed papers, and given over 120 invited talks.

Contributions to HUPO. Dr. Wu has served on the Board of Directors of both International HUPO (2005-2008) and USHUPO (2008-present; executive committee since 2010). In 2008, she co-chaired the scientific organizing committee of the USHUPO Conference, a successful meeting that attracted >500 participants, the largest USHUPO meeting to date. She has played a key role in HUPO initiatives, including the Human Proteome Project (HPP), and has chaired the Bioinformatics and Biostatistics subcommittee of the USHUPO Initiative. Her leadership role in protein databases, bioinformatics, and international consortia including the UniProt, has been highly respected and appreciated by both the US proteomic community and the world at large.