Thomas Raymond Holton

The DOE-MBI Institute of Proteomics and Genomics
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Skills

Applications developer for structural genomics, DBA and website administration

Platforms: Linux, Mac, iOS, Android

Languages: PHP, HTML, CSS, MySQL, python, C/C++, Swift, Java, Jquery, Javascript, FORTRAN, LISP, PROLOG,

Domains:

- http://www.doe-mbi.ucla.edu
- http://services.mbi.ucla.edu
- http://neuropsychnorms.com

Experience

August 2000 - PRESENT

University of California, Los Angeles, DOE-MBI Institute, Dr. David Eisenberg, Dr. Duilio Cascio – *Website/Database Administrator and Applications Developer*

- Manager of 3 database servers and 6 webservers, including all back up servers.
- PHP, Javascript, JQuery, Angular, MySQL, python, git, django, Apache, openVZ, C++, Objective C, Java, bash shell, ubuntu, rhel, centos
- Support for Faculty/PostDocs/Graduate Students in developing online services. This includes:
    - Database integration and analysis, such as ProLinks
    - Proteomics and Genomics Informatics investigations
    - Creating new servers for personal and PI projects
    - Providing assistance in development of online services, from core programming to website
    - Database structure analysis to provide proficient, productive querying while minimizing hardware constraints
    - Troubleshooting problems with in house software
    - Maintenance of legacy servers
- Assistant Manager of computer cluster, 140 Linux compute servers using the ROCKS system and 45 Linux workstations

August 1997 - August 2000

Texas A&M University, College Station, TX, Dr. James Sacchettini – *Graduate Student, Scientific Programmer*

- Designing, programming, testing and maintaining software used in the automatic determination of protein structures from X-ray diffraction data of protein crystals. Reference: Acta Cryst.. (2000) D56, 722-734. Programs written in C on SGI (IRIX).
- C++/C, LISP, PROLOG, , TCL/TK, csh/bash shell, FORTRAN
- Experience using graphics software programs, O and SPOCK
- X-ray data analysis and refinement programs, DENZO, CNS, CCP4, and XPLOR.
- Machine Learning, Decision tree applications written in LISP designed for predicting the location of alpha carbons
- Design and maintain various web pages for the project and laboratory.
- Crystallize proteins using various reagents

June 1995 - July 1996

University of Tennessee, Knoxville, TN, Dept. of Chemistry, Dr. Robert J. Hinde – *Research Assistant*

- Design software for predicting polyalanine secondary structure and its folding pathway. Monte Carlo simulations, simulated annealing, and statistical mechanics. Solaris, Sun workstations, C++

Education

August 1997 - August 2000

Texas A&M University, College Stations, TX – *Master of Science*

Structural Biology, X-ray Crystallography, Bioinformatics, Machine Learning

August 1996 - August 1997

Temple University, Philadelphia, PA – *N/A*

1st year graduate student in biochemistry. Protein purification, K-activated CA ion channels, X-ray Crystallography

August 1994 - August 1996

University of Tennessee, Knoxville, TN – *Bachelors of Science*

Chemistry Major

August 1986 - August 1995

University of Tennessee, Knoxville, TN – *Bachelors of Arts*

Music Major

Publications

- Diffusion accessibility as a method for visualizing macromolecular surface geometry. Tsai Y, Holton T, Yeates TO. Protein Sci. 2015 Jul 16. doi: 10.1002/pro.2752. PMID: 26189444
- Heterologous expression of mycobacterial Esx complexes in Escherichia coli for structural studies is facilitated by the use of maltose binding protein fusions. Arbing MA, Chan S, Harris L, Kuo E, Zhou TT, Ahn CJ, Nguyen L, He Q, Lu J, Menchavez PT, Shin A, Holton T, Sawaya MR, Cascio D, Eisenberg D. PLoS One. 2013 Nov 29;8(11):e81753. Doi: 10.1371/journal.pone.0081753. eCollection 2013. PMID: 24312350
- Determining protein structure from electron-density maps using pattern matching. Holton T, Ioerger TR, Christopher JA, Sacchettini JC. Acta Crystallogr D Biol Crystallogr. 2000 Jun;56(Pt 6):722-34. PMID: 10818349
- Active site modifications of organophosphorous hydrolase for improved detoxification of organophosphorus neurotoxins
- Grimsley JK, Disioudi BD, Holton T, Sacchettini JC, Wild, JR in Enzymes in Action, ed. Binne Zwanenberg, Nato Advanced Study Institute, 2000.
- TEXTAL: a pattern recognition system for interpreting electron density maps. Ioerger TR, Holton T, Christopher JA, Sacchettini JC. Proc Int Conf Intell Syst Mol Biol. 1999:130-7. PMID: 10786295