Thomas Holton

Applications developer for structural genomics, DBA and website adminstration

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DOMAINS:

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

- SAVES v4: Structure Analysis and Verification server

This metaserver runs 6 programs for checking and validating protein structures during and after model refinement.

  - ERRAT standalone server
  - MTZdump - display the information from your MTZ file
  - PDB ADIT compliance check
  - Interactive Ramachandran plot
  - Universal PDB Query Machine
  - PROCHECK standalone server
  - Verify 3D standalone server
  - X-dval: X-ray Data Validation

EDUCATION:

University of Tennessee, Knoxville
Bachelor's in Liberal Arts, Music, 1994

University of Tennessee, Knoxville
Bachelor's in Science, Chemistry, 1995

Temple University, Philadelphia, PA
Department of Biochemistry, 1996-1997

Texas A & M University, College Station, TX
Master of Science, Biochemistry, 2000

OPERATING SYSTEMS:

UNIX, Linux, Apple, Windows, ZFS

LANGUAGES:

PHP, HTML, Javascript, MySQL, python, C, C++, c/bash/sh shell, (Lisp, PROLOG, TCL/TK), WordPress

EXPERIENCE:

University of California, Los Angeles, Molecular Biology Institute, Dr. David Eisenberg, Dr. Duilio Cascio

August 2000 to present: Website/Database Administrator and Applications Developer

Responsibilities include:

- Manager of 3 database servers and 6 webservers, including all back up servers.
- 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
    - Discussing politics
- Assistant Manager of computer cluster, 140 Linux compute servers using the ROCKS system and 45 Linux workstations
- Assistant Manager of the LAN

Texas A & M Biochemistry Department, Dr. James Sacchettini

August 1997 to August 2000:Graduate Student, Scientific Programmer

Responsibilities included 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). Experience using graphics software programs, O and SPOCK, as well as X-ray data analysis and refinement programs, DENZO, CNS, CCP4, and XPLOR. Development of this software involved decision tree applications written in LISP which were designed for predicting the location of alpha carbons of proteins. Also helped design and maintain various web pages for the project and laboratory.

University of Tennessee, Knoxville, Dept. of Chemistry, Dr. Robert J. Hinde

June 1995 to July 1996 :Research Assistant

Working in C++ on Solaris (Sun Workstation), wrote programs for predicting polyalanine secondary structure and its folding pathways. Methods used included monte carlo, simulated annealing, and statistical mechanics

calculations. Possible folding pathways were determined for chains of alanine amino acids however, the methods were never extended to other types of amino acids.

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

REFERENCES PROVIDED UPON REQUEST.