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- EDUCATION
- ◇ **Janelia Farm, Howard Hughes Medical Institute**, Ashburn, VA.  
Postdoctoral training. Adviser: Sean Eddy (Apr 2007 - present)
  - ◇ **University of California, San Francisco**, CA.  
Doctor of Philosophy, Biophysics. Adviser: Andrej Sali (Feb 2003 - Feb 2007)
  - ◇ **Rockefeller University**, New York, NY.  
Graduate coursework in Mathematical and Computational Biology (Aug 2001 - Jan 2003)
  - ◇ **Purdue University**, West Lafayette, IN.  
Doctor of Pharmacy (Aug 1995 - Aug 2001)
- RESEARCH INTERESTS
- ◇ *Neurogenomics* - developing tools to generate neurobiological hypotheses from genomic datasets.
  - ◇ *Transcriptional regulation* - developing quantitative models of gene expression that integrate functional and comparative genomic data.
  - ◇ *Protein structure* - developing computational approaches to analyze and predict protein-protein interactions, in particular for host-pathogen systems.
- AWARDS AND HONORS
- ◇ Howard Hughes Medical Institute Predoctoral Fellowship (Jun 2002 – Mar 2007)
  - ◇ W.M. Keck Training Grant in Mathematical and Computational Biology (Aug 2001 – Jun 2002)
  - ◇ Merck Award for Achievement in Medicinal Chemistry and Molecular Pharmacology, Purdue University School of Pharmacy (2001)
  - ◇ Pfizer Summer Undergraduate Research Fellowship (2000)
  - ◇ Merck Research Scholar Program (1999 – 2000)
  - ◇ Purdue University School of Pharmacy Dean's Undergraduate Research Fellowship (1998)
- RESEARCH EXPERIENCE
- ◇ **Janelia Farm, Howard Hughes Medical Institute**. Ashburn, VA  
(4/2007 – present) Developing and applying computational and experimental genomic approaches to investigate transcriptional regulation in the mammalian nervous system. Developing methods to identify regulatory elements by analyzing and integrating genome-wide data sets of gene expression, chromatin environment, histone modification, transcription factor binding preferences, and comparative genomics. Developed a tool, ALLENMINER, to search for genes expressed in patterns of interest in the mouse brain. Mentored an undergraduate student on analysis of genomic data.
  - ◇ **Dept Biophysics, University of California at San Francisco**. San Francisco, CA  
**Laboratory for Molecular Biophysics, Rockefeller University**. New York, NY  
(8/2001 – 2/2007) Developed and applied computational tools to characterize and predict the structure of protein complexes. Developed a database of structurally defined protein interactions, PIBASE, that enables a wide range of structural analysis, from the atomic detail of individual interactions to a broad view of protein interaction space. Developed a comparative modeling method for predicting the composition of protein complexes. Applied these tools to predict interactions between host and pathogen proteins for ten human pathogens, including several neglected tropical diseases. Mentored three rotation students and a high school student on a range of structural bioinformatics projects.

- ◇ **Dept Medicinal Chemistry, Purdue University.** West Lafayette, IN  
(6/1999 – 8/2001) Modeled the three dimensional structures of the Epidermal Growth Factor family of signaling ligands to characterize the structural and physicochemical basis of binding specificities for the EGFR receptor family. *Adviser: Prof. Carol B. Post.*
- ◇ **Dept Industrial and Physical Pharmacy, Purdue University.** West Lafayette, IN  
(5/1998 – 8/1998) Characterized nanometer-scale properties of pharmaceutically relevant polymer surfaces and protein-adsorbed polymer surfaces, using atomic force microscopy (AFM). Used AFM surface analysis to determine the cause of a formulation problem that arose during the manufacturing of a pharmaceutical product. *Adviser: Prof. Kinam Park.*
- ◇ **Dept Medicinal Chemistry, Purdue University.** West Lafayette, IN  
(5/1997 – 8/1997) Proposed and synthesized several analogues of the cosalane/alkenyldiarylmethane series of non-nucleoside HIV reverse transcriptase (RT) inhibitors. Analogues were proposed based on computational docking into the HIV RT structure. The routes of synthesis of two of these structures were proposed and then synthesized. *Adviser: Prof. Mark Cushman.*

- PUBLICATIONS
15. Proteome-wide prediction of protein and ligand binding sites using structure. **Davis FP.** *submitted 2009.*
  14. The overlap of small molecule and protein binding sites within families of protein structures. **Davis FP,** Sali A. *PLoS Computational Biology.* *in press.*
  13. A tool for the identification of genes expressed in patterns of interest using the Allen Brain Atlas. **Davis FP,** Eddy SR. *Bioinformatics* (2009) 25(13):1647-54 [link](#)
  12. MODBASE, a database of annotated comparative protein structure models and associated resources. Pieper U, Eswar N, Webb BM, Eramian D, Kelly L, Barkan DT, Carter H, Mankoo P, Karchin R, Marti-Renom MA, **Davis FP,** Sali A. *Nucleic Acids Res* (2009) 37:D347-54. [link](#)
  11. Host-pathogen protein interactions predicted by comparative modeling. **Davis FP,** Barkan DT, Narayanan E, McKerrow JH, Sali A. *Protein Science* (2007) 16: 2585-2596 [link](#)
  10. DBAli tools: mining the protein structure space. Marti-Renom MA, Pieper U, Madhusudhan MS, Rossi A, Eswar N, **Davis FP,** Al-Shahrour F, Dopazo J, Sali A. *Nucleic Acids Research* (2007) 35: W393-7 [link](#)
  9. The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. Marti-Renom MA, Rossi A, Al-Shahrour F, **Davis FP,** Pieper U, Dopazo J, Sali A. *BMC Bioinformatics* (2007) 8: S4. [link](#)
  8. Structural modeling of protein interactions by analogy: application to PSD-95. Korkin D, **Davis FP,** Alber F, Luong T, Shen MY, Lucic V, Kennedy MB, Sali A. *PLoS Computational Biology* (2006) 2(11):e153. [link](#)
  7. Protein complex compositions predicted by structural similarity. **Davis FP,** Braberg H, Shen MY, Pieper U, Madhusudhan MS, Sali A. *Nucleic Acids Research* (2006) 34: 2943-2952. [link](#)
  6. MODBASE: a database of annotated comparative protein structure models and associated resources. Pieper U, Eswar N, **Davis FP,** Braberg H, Madhusudhan MS, Rossi A, Marti-Renom M, Karchin R, Webb BM, Eramian D, Shen MY, Kelly L, Melo F, Sali A. *Nucleic Acids Research* (2006) 34: D291-D295. [link](#)
  5. Localization of protein-binding sites within families of proteins. Korkin D, **Davis FP,** Sali A. *Protein Science* (2005) 14: 2350-2360. [link](#)
  4. The optimal size of a globular protein domain: a simple sphere-packing model. Shen MY, **Davis FP,** Sali A. *Chemical Physics Letters* (2005) 405: 224-228. [link](#)
  3. PIBASE: a comprehensive database of structurally defined protein interactions. **Davis FP,** Sali A. *Bioinformatics* (2005) 21(9): 1901-1907. [link](#)
  2. A structural perspective on protein-protein interactions. Russell RB, Alber F, **Davis FP,** Aloy P, Korkin D, Pichaud M, Topf M, Sali A. *Curr Opin Struct Biol* (2004) 14(3): 313-324. [link](#)
  1. MODBASE, a database of annotated comparative protein structure models, and associated resources. Pieper U, Eswar N, Braberg H, Madhusudhan MS, **Davis FP,** Stuart AC, Mirkovic N, Rossi A, Marti-Renom MA, Fiser A, Webb B, Greenblatt D, Huang CC, Ferrin TE, Sali A. *Nucleic Acids Res* (2004) 32 Database issue: D217-22. [link](#)

- RESOURCES DEVELOPED
- ◇ **ALLENMINER** a tool for identification of genes expressed in patterns of interest using the Allen Brain Atlas. <http://research.janelia.org/davis/allenminer>
  - ◇ **PIBASE ligands** Structural analysis of overlapping small molecule and protein binding sites within families of protein structures. <http://pibase.janelia.org/ligands>
  - ◇ **Predicted host-pathogen interactions** Structure-based prediction of host-pathogen protein-protein interactions for ten human pathogens. <http://salilab.org/hostpathogen>
  - ◇ **MODBASE complexes** Structure-based prediction of protein-protein interactions in *S. cerevisiae*. <http://salilab.org/modbase>
  - ◇ **PIBASE** Analysis of structurally characterized protein interfaces. <http://pibase.janelia.org>
- ORAL PRESENTATIONS
- ◇ ALLENMINER - a tool to identify genes expressed in patterns of interested using the Allen Brain Atlas. CSHL / WT Genome Informatics Meeting. Wellcome Trust Conference Center, Hinxton, UK. Septemer 12, 2008.
  - ◇ Host-pathogen protein interactions predicted by structure. HHMI Predoctoral Fellows Meeting. Howard Hughes Medical Institute, Chevy Chase, MD. Septemer 25, 2007.
  - ◇ Host-pathogen protein interactions predicted by structure. Biotechnology High Performance Computing Software Applications Institute, U.S. Army Medical Research and Materiel Command, Fort Detrick, Maryland. September 5, 2007.
  - ◇ ErbB binding determinants: a comparative modeling study. Merck Pharmacy Student Research Conference. West Virginia University. Morgantown, WV. October 14, 2000.
- POSTER PRESENTATIONS
- ◇ Davis FP, Eddy SR. A genomic search for molecular evolutionary correlates of regional neuronal connectivity in the mouse brain. Intelligent Systems for Molecular Biology. Stockholm Conference Center. Stockholm, Sweden. June 28, 2009.
  - ◇ Davis FP, Sali A. The overlap of small molecule and protein binding sites within families of protein structures. 3DSIG, Intelligent Systems for Molecular Biology. Stockholm Conference Center. Stockholm, Sweden. June 26, 2009.
  - ◇ Davis FP, Barkan DT, Eswar N, McKerrow JH, Sali A. Host-pathogen protein interactions predicted by structure. Intelligent Systems for Molecular Biology. Vienna Conference Center. Vienna, Austria. July 28, 2007.
  - ◇ Davis FP, Braberg H, Sali A, Madhushudhan MS. Protein Interactions Predicted by Structural Similarity. Modeling of Protein Interactions in Genomes. June 26, 2005. Lawrence, KS.
  - ◇ Davis FP, Sali A. IIBase: A Database of Protein Interfaces. Intelligent Systems for Molecular Biology. Glasgow City Center. Glasgow, UK. July 28, 2004.
  - ◇ Davis FP, Sali A. IIBase: A Database of Protein Interfaces. International Workshop on Structural Analysis of Supramolecular Assemblies by Hybrid Methods. Granlibakken Conference Center. Lake Tahoe, CA. March 18, 2004.
  - ◇ Davis FP, Post CB. ErbB Binding Determinants: A Comparative Modeling Study. Pfizer Summer Undergraduate Research Conference. Pfizer Central Research. Groton, CT. October 13, 2000.
  - ◇ Davis FP, Post CB. Comparative Protein Modeling of the Epidermal Growth Factor-like Domain of Neuregulin Isoforms. American Association of Colleges of Pharmacy Annual Meeting. San Diego, CA. June 6, 2000.
- SERVICE
- ◇ 2003 - present. Peer reviewer for Bioinformatics, BMC Bioinformatics, BMC Genomics, BMC Medical Genomics, Nucleic Acids Research, PLoS Computational Biology, PNAS, Protein Science, Structure.
- LANGUAGES
- ◇ Fluent: English, Farsi
  - ◇ Intermediate: Spanish