

## **Curriculum Vitae: Fred P. Davis, Pharm.D. Ph.D.**

### **Current position**

Staff Scientist

National Institute of Arthritis and Musculoskeletal and Skin Diseases (NIAMS)  
National Institutes of Health (NIH)  
Bethesda, MD 20892, USA

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### **Education**

1995 - 2001 Doctor of Pharmacy. Purdue University  
2001 - 2003 Graduate courses, Mathematical & Computational Biology. Rockefeller University  
2003 - 2007 Ph.D., Biophysics. University of California, San Francisco. Advisor: Andrej Sali  
2007 - 2013 Postdoctoral training. HHMI Janelia Research Campus. Advisor: Sean Eddy

### **Research positions**

1997 Undergraduate research assistant. Dept. Medicinal Chemistry, Purdue University  
1998 Undergrad. research asst. Dept. Industrial & Physical Pharmacy, Purdue  
1999 - 2001 Undergrad. research asst. Dept. Medicinal Chem. & Molec. Pharmacology, Purdue  
2001 - 2003 Graduate student. Rockefeller University, Laboratory for Molecular Biophysics  
2003 - 2007 Graduate student. University of California, San Francisco; Dept. Biophysics  
2007 - 2013 Postdoctoral Associate. HHMI Janelia Research Campus  
2014 - 2015 Research Specialist. HHMI Janelia Research Campus  
2015 - now Staff Scientist. NIH NIAMS

### **Honors and awards**

1998 Purdue Univ. School of Pharmacy Dean's Undergraduate Research Fellowship  
1999 - 2000 Merck Research Scholar Program  
2000 Pfizer Summer Undergraduate Research Fellowship  
2001 Merck Award for Achievement in Medicinal Chemistry and Molecular Pharmacology,  
Purdue University School of Pharmacy  
2001 - 2002 W.M. Keck Training Grant in Mathematical and Computational Biology  
2002 - 2007 Howard Hughes Medical Institute Predoctoral Fellowship  
2010 InnoCentive challenge award: Probabilistic modeling of spending habits

### Primary publications (peer-reviewed)

1. Pieper U, Eswar N, Braberg H, Madhushudhan MS, **Davis FP**, Stuart AC, Mirkovic N, Rossi A, Marti-Renom MA, Fiser A, *et al.* MODBASE, a database of annotated comparative protein structure models, and associated resources. *Nucleic Acids Res* (2004) 32: D217-22.
2. **Davis FP**, Sali A. PIBASE: a comprehensive database of structurally defined protein interactions. *Bioinformatics* (2005) 21(9): 1901-1907.
3. Shen MY, **Davis FP**, Sali A. The optimal size of a globular protein domain: a simple sphere-packing model. *Chemical Physics Letters* (2005) 405: 224-228.
4. Korkin D, **Davis FP**, Sali A. Localization of protein-binding sites within families of proteins. *Protein Science* (2005) 14: 2350-2360.
5. Pieper U, Eswar N, **Davis FP**, Braberg H, Madhusudhan MS, Rossi A, Marti-Renom M, Karchin R, Webb BM, Eramian D, *et al.* MODBASE: a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research* (2006) 34: D291-D295.
6. **Davis FP**, Braberg H, Shen MY, Pieper U, Madhusudhan MS, Sali A. Protein complex compositions predicted by structural similarity. *Nucleic Acids Research* (2006) 34: 2943-2952.
7. Korkin D, **Davis FP**, Alber F, Luong T, Shen MY, Lucic V, Kennedy MB, Sali A. Structural modeling of protein interactions by analogy: application to PSD-95. *PLoS Computational Biology* (2006) 2(11):e153.
8. Marti-Renom MA, Rossi A, Al-Shahrour F, **Davis FP**, Pieper U, Dopazo J, Sali A. The AnnoLite and AnnoLyze programs for comparative annotation of protein structures. *BMC Bioinformatics* (2007) 8: S4.
9. Marti-Renom MA, Pieper U, Madhusudhan MS, Rossi A, Eswar N, **Davis FP**, Al-Shahrour F, Dopazo J, Sali A. DBAli tools: mining the protein structure space. *Nucleic Acids Research* (2007) 35: W393-7.
10. **Davis FP**, Barkan DT, Narayanan E, McKerrow JH, Sali A. Host-pathogen protein interactions predicted by comparative modeling. *Protein Science* (2007) 16: 2585-2596.
11. 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. MODBASE, a database of annotated comparative protein structure models and associated resources. *Nucleic Acids Research* (2009) 37:D347-54.
12. **Davis FP**, Eddy SR. A tool for the identification of genes expressed in patterns of interest using the Allen Brain Atlas. *Bioinformatics* (2009) 25(13):1647-54.
13. **Davis FP**, Sali A. The overlap of small molecule and protein binding sites within families of protein structures. *PLoS Computational Biology* (2010) 6(2): e1000668. Designated "Featured research".

14. **Davis FP**. Proteome-wide prediction of overlapping small molecule and protein binding sites using structure. *Molecular Biosystems* (2011) 7(2): 545-547.  
Selected for *Virtual Journal of Biological Physics Research* (2011) 21(3).
15. Girard F, Meszar Z, Marti C, **Davis FP**, Celio M. Gene expression analysis in the parvalbumin-immunoreactive PV1 nucleus of the mouse lateral hypothalamus. *Eur. J. Neurosci.* (2011) 34(12): 1934-1943.
16. Henry GL, **Davis FP**, Picard S, Eddy SR. Cell-type specific genomics of Drosophila neurons. *Nucleic Acids Research.* (2012) 40 (19): 9691-9704.  
Designated "Featured article".
17. **Davis FP**, Eddy SR. Transcription factors that convert adult cell identity are differentially Polycomb repressed. *PLoS One.* (2013) 8 (5): e63407.
18. Striedter GF, Belgard TG, Chen C, **Davis FP**, Finlay BL, Gunturkun O, Hale ME, Harris J, Hecht EE, Hof PR, *et al.* NSF Workshop Report: Discovering General Principles of Nervous System Organization by Comparing Brain Maps Across Species. *Journal of Comparative Neurology.* (2014) 522 (7): 1445-1453. Note: also published in *Brain, Behavior and Evolution*.
19. Mo A\*, Mukamel EA\*, **Davis FP\***, Luo C\*, Henry GL, Picard S, Urich MA, Nery JR, Sejnowski TJ, Lister R, Eddy SR, Ecker JR, Nathans J. Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. *Neuron.* (2015) 86(6): 1369-1384. (\* co-first authors)  
Designated "Issue Highlight", Preview by Steve Henikoff.
20. Mo A, Luo C, **Davis FP**, Mukamel EA, Henry GL, Nery JR, Urich MA, Picard S, Lister R, Eddy SR, Beer MA, Ecker JR, Nathans J. Epigenomic landscapes of retinal rods and cones. *eLife.* (2016) 5:e11613.
21. Shih HY\*, Sciume G\*, Mikami Y\*, Guo L, Sun HW, Brooks SR, Urban Jr JF, **Davis FP**, Kanno Y, O'Shea JJ. Developmental acquisition of regulomes underlies innate lymphoid cell functionality. *Cell.* (2016) in press (\* co-first authors)

### Other publications

1. Russell RB, Alber F, **Davis FP**, Aloy P, Korkin D, Pichaud M, Topf M, Sali A. A structural perspective on protein-protein interactions. *Curr Opin Struct Biol* (2004) 14(3): 313-324. (review).
2. **Davis FP**. Phosphorylation at the interface. *Structure.* (2011) 19: 1726-1727. (commentary).
3. **Davis FP**, Kanno Y, O'Shea JJ. A metabolic switch for Th1 pathogenicity. *Cell.* (2015) 163:1308-1310. (commentary).

## Presentations

- 2007 Biotechnology High Performance Computing Software Applications Institute, U.S. Army Medical Research and Materiel Command, Fort Detrick, Maryland. (invited)
- 2007 HHMI Predoctoral Fellows Meeting. HHMI. Chevy Chase, MD. (conference)
- 2008 Wellcome Trust Genome Informatics. Sanger Centre. Hinxton, UK. (conference)
- 2010 Allen Brain Atlas Data Mining Workshop. Allen Institute for Brain Science, Seattle, WA (invited)
- 2010 Dept. of Ecology and Evolutionary Biology, Princeton University. (seminar)
- 2011 Dept. of Medicinal Chemistry and Molecular Pharmacology, Purdue University. West Lafayette, IN (invited)
- 2012 National Center for Bioinformation Technology, National Institutes of Health. Bethesda, MD (invited)
- 2013 Annual Symposium, HHMI Janelia. Ashburn, VA (seminar)
- 2014 High-throughput sequencing for neuroscience. HHMI Janelia. Ashburn, VA (invited)
- 2014 Center for Cancer Research, National Institutes of Health. Bethesda, MD (invited)

## Software packages and databases.

Available at <http://github.com/fredpdavis>

1. mdlabbook: a markdown-format lab notebook
2. PIBASE: Database of protein-protein interaction structures.
3. Host-pathogen protein interactions predicted by structure.
4. MODTIE: structure-based prediction of binary and higher-order protein complexes.
5. PIBASE ligands: overlapping small molecule and protein binding sites within families of protein structures.
6. HOMOLOBIND: Proteome-wide prediction of protein and ligand binding sites using structure.
7. ALLENMINER: finding genes expressed in patterns of interest using the Allen Brain Atlas.

## Service

- 2003 - now Peer reviewer for *Bioinformatics*, *BMC Bioinformatics*, *BMC Genomics*, *BMC Medical Genomics*, *BMC Systems Biology*, *eLife*, *Genome Research*, *J. Chemical Information and Modeling*, *Nature*, *Neuron*, *Nucleic Acids Res*, *PLoS Comp Biol*, *PLoS One*, *Proc Natl Acad Sci*, *Protein Science*, *Structure*.
- 2013 Invited participant, NSF BRAIN initiative workshop on comparative brain mapping.
- 2014 Grant reviewer, Thiel Foundation Breakout Labs

## Languages

Fluent: English, Farsi  
Intermediate: Spanish