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)
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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
2016	NIH Group Merit Award: NIAMS Lymphocyte Regulomes

Primary publications (peer-reviewed)

* co-first author, + co-corresponding author

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.
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) 165 (5): 1120-1133.

22. Preger Ben-Noon E, **Davis FP**, Stern DL. Evolved repression overcomes enhancer robustness. *Dev Cell*. (2016) 39(5): 572-584.

23. Afzali B*, Gronholm J*, Vandrocova J*, ... **Davis FP** ..., Cooper N+, Laurence ADJ+. BACH2 immunodeficiency illustrates an association between super-enhancers and haploinsufficiency. *Nature Immunology*. (2017) 18: 813-823.

24. Iwata S*, Mikami Y*, ..., O'Shea JJ+, **Davis FP+**, Kanno Y+. The transcription factor T-bet limits amplification of type I IFN transcriptome and circuitry in T helper 1 cells. *Immunity*. (2017) 46(6): 983-991.e4.

Preview by Lazarevic, Szabo, and Glimcher

25. Villarino AV*, Sciume G*, **Davis FP**, Iwata S, Zitti B, Robinson GW, Hennighausen L, Kanno Y, O'Shea JJ. Subset- and tissue-defined STAT5 thresholds control homeostasis and function of innate lymphoid cells. *J Exp Med*. (2017) 214(10): 2999-3014.

26. Xie L, Torigoe SE, Xiao J, Mai DH, Li L, **Davis FP**, Dong P, Marie-Nelly H, Grimm J, Lavis L, Darzacq X, Cattoglio C, Liu Z, Tjian R. A dynamic interplay of enhancer elements regulates Klf4 expression in nave pluripotency. *Genes Dev*. (2017) 31(17):1795-1808.

27. Bentzur A, Shmueli A, Omesi L, Ryvkin J, Knapp JM, Parnas M, **Davis FP**, Shohat-Ophir G. Odorant binding protein 69a connects social interaction to modulation of social responsiveness in Drosophila. *PLoS Genetics*. (2018) 14 (4): e1007328.

28. **Davis FP***, Nern A*, Picard S, Reiser MB, Rubin GM, Eddy SR, Henry GL. A genetic, genomic, and computational resource for exploring neural circuit function. *under review*. bioRxiv preprint 285476.

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 Th17 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)
2017	NIH Immunology Interest Group Workshop, National Conference Center. Leesburg, VA

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*, *Science Immunology*, *Structure*.
2013	Invited participant, NSF BRAIN initiative workshop on comparative brain mapping
2014	Grant reviewer, Thiel Foundation Breakout Labs
2016	Peer reviewer, NIH Fellows Award for Research Excellence
2016	Grant reviewer, National Science Foundation CAREER award

Languages

Fluent: English, Farsi
Intermediate: Spanish