Scott D. Briggs, Ph.D.

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Personal

Citizenship: USA

Education and Research Experiences:

Current Appointment:

2008-present	Associate Professor, Purdue University
2003-2008	Assistant Professor, Purdue University Department of Biochemistry

Post-Doctoral Training:

1999-2003	Postdoctoral Fellow, University of Virginia Department of Biochemistry and Molecular Genetics Advisor: C. David Allis, Ph.D.

Graduate Training:

1996-1999	University of Nebraska Medical Center (UNMC) Graduate Ph.D. - Department of Pathology and Microbiology Advisor: Thomas E. Smithgall, Ph.D.

Post-Undergraduate Training:

1992-1996	Research Technologist I & II, Eppley Institute for Research in Cancer, University of Nebraska Medical Center, Omaha Advisor: Thomas E. Smithgall, Ph.D.

Undergraduate Training:

1992-1992	Undergraduate Research, Summer Research Internship Eppley Institute Summer Research Undergraduate Program Advisor: Thomas E. Smithgall, Ph.D.
1990-1992	Undergraduate Research, B.S. Thesis Project University of Northern Iowa, Cedar Falls, Iowa Advisor: Darrell J. Wiens, Ph.D.
1988-1992	University of Northern Iowa, Cedar Falls, Iowa B.S. in Biology; Minor: Chemistry; Minor: Psychology

Fellowships/Awards/Honors/Service:

Associate Professor:

2018 Chair of the organizing committee for the Midwest Chromatin and Epigenetic Meeting
2016 Organizing committee member for the Midwest Chromatin and Epigenetic Meeting
2017 Departmental Nomination for David Pfendler Undergraduate Counselor Award
2012 Departmental Nomination for Richard Kohls Undergraduate Teaching Award
2011 Departmental Nomination for Richard Kohls Undergraduate Teaching Award
2010-2015 Purdue University Faculty Scholar
2009 NIH Molecular Genetics A (MGA) Study Section (ad hoc)

Assistant Professor:

2007-2009 Elected Member of the Epigenetics Society Board of Directors
2007 NIH Molecular Genetics A (MGA) Study Section (ad hoc)
2006 NIH Molecular Genetics A (MGA) Study Section (ad hoc)
2006 Purdue University Seed for Success Award and College of Agriculture Millionaire's Club
2004-2006 Sidney Kimmel Scholar
2003-2006 Walther Assistant Professor of Biochemistry
2003-2004 Leukemia and Lymphoma Society Fellow

Postdoctoral:

2001-2004 Leukemia and Lymphoma Society Fellowship (awarded and transferred)
2001 NIH-NRSA Postdoctoral Fellowship Award (awarded but declined)
1999-2003 University of Virginia, Pratt Supplemental Postdoctoral Fellowship Award

Graduate/Undergraduate:

1999 Norman and Bernice Harris Cancer Research Graduate Student Award
1998-1999 University of Nebraska Medical Center Student Fellowship
1997 Graduate Student Association Career and Industry Forum - Travel Award
1992 Honors Graduate - University of Northern Iowa
1991 Beta Beta Beta - National Biological Honor Society member
1991 Psi Chi - National Honor Society in Psychology member

Membership in Professional and Scientific Societies

- AAAS – Advancing Science Serving Society
- ASBMB – American Society for Biochemistry and Molecular Biology
- Epigenetics Society
- Genetics Society of America

Publications (in reverse-chronological order):

Peer-reviewed Publications: 46 Total Publications (h-index 32, i10index 39)

1. Serratore, N.D., Baker, K.M., Macadlo, L.A., Gress, A.R., Powers, B.L., Atallah, N., Westerhouse K.M., Hall, M.C., Weake, V.M., Briggs, S.D. A Novel Sterol-Signaling Pathway Governs Azole Antifungal Drug Resistance and Hypoxic Gene Repression in *Saccharomyces cerevisiae*. *Genetics*. 2018. doi: 10.1534/genetics.117.300554.

2. Li, F., Zheng, L.D., Chen, X., Zhao, X., **Briggs, S.D.,** and Du, H.N. Gcn5-mediated Rph1 acetylation regulates its autophagic degradation under DNA Damage Stress. *Nucleic Acids Res.* 45:5183-5197, 2017 doi: 10.1093/nar/gkx129.

3. Zhang, Y., Serratore, N.D., and **Briggs, S.D**. *N-ICE* plasmids for generating N-terminal 3 × FLAG tagged genes that allow inducible, constitutive or endogenous expression in Saccharomyces cerevisiae. *Yeast*. 34: 223-235, 2017 doi: 10.1002/yea.3226.

4. Harmeyer, K.M., South, P.F., Bishop, B., Ogas, J., and **Briggs, S.D.** Immediate chromatin immunoprecipitation and on-bead quantitative PCR analysis: a versatile and rapid ChIP procedure. *Nucleic Acids Res.* 43(6):e38, 2015 doi: 10.1093/nar/gku1347*. Highlighted in Biotechniques; https://www.biotechniques.com/news/ZipChIP-Speeds-Up-Chromatin-Research/biotechniques-357956.html*

5. South, P.F., Harmeyer, K.M., Serratore, N.D. and **Briggs, S.D.** H3K4 methyltransferase Set1 is involved in maintenance of ergosterol homeostasis and resistance to Brefeldin A. *PNAS, USA*, 110:E1016-25. doi: 10.1073/pnas.1215768110, 2013. *http://www.purdue.edu/uns/PurdueToday/archive/2013/02-February/130226PurdueToday.htm* http://www.purdue.edu/newsroom/releases/2013/Q1/yeast-study-yields-potential-for-new-cholesterol,-anti-fungal-drugs.html

6. Mersman DP, Du HN, Fingerman IM, South PF, and **Briggs, SD.** A charge-based interaction conserved within the H3K4 methyltransferase complexes is needed for protein stability, histone methylation, and gene expression. *J. Biol. Chem.*, 287:2652-2665, 2012.

7. South, P.F. and ***Briggs, S.D.** ASH2L (ash2 (absent, small, or homeotic)-like (Drosophila)). Atlas Genet Cytogenet Oncol Haematol. August 2011. (Review) URL : *http://AtlasGeneticsOncology.org/Genes/ASH2LID44404ch8p11.html*

8. South, P.F. and ***Briggs, S.D.** Understanding the structure and function of ASH2L. Atlas Genet Cytogenet Oncol Haematol. June 2011. (Review) URL : *http://AtlasGeneticsOncology.org/Deep/ASH2LFunctionID20097.html*

9. Du, H.N. & **Briggs, S.D.** A nucleosome surface formed by Histone H4, H2A, and H3 residues is needed for proper histone H3 K36 methylation, histone acetylation and repression of cryptic Transcription. *J. Biol. Chem.*, 285: 11704-11713, 2010.

10. South, P.F., Fingerman, I.M., Mersman, D.P., Du, H.N., **Briggs, S.D.** A conserved interaction between the SDI domain of Bre2 and the Dpy-30 Domain of Sdc1 is required for histone methylation and gene expression. *J. Biol. Chem*. 285: 595-607, 2010.

11. Plazas-Mayorca, M.D., Zee, B.M., Young, N.M., Fingerman, I.M., LeRoy, G., **Briggs, S.D.** and Garcia, B.A. One-pot shotgun quantitative mass spectrometry characterization of histones. *Journal of Proteome Research* 8: 5367-5374, 2009.

12. Mersman, D.P., Harmeyer, K.M., and **Briggs, S.D.** To be or NOT to be Demethylated. *Cell Cycle* 8:2135-2137, 2009. (Review).

13. Mersman, D. P., Du, H.N., Fingerman, I.M., South, P.F. and **Briggs, S.D.** Polyubiquitination of the demethylase Jhd2 controls histone methylation and gene expression. *Genes & Development* 23: 951-962, 2009. *Highlighted in Cell Cycle see publication 12.*

14. Dhawan, R., Luo, H., Foerster, A.M., AbuQamar, S., Du, H.N., **Briggs, S.D.**, Scheid, O.M., and Mengiste, T. HISTONE MONOUBIQUITINATION 1 interacts with a subunit of the mediator complex and regulates defense responses against necrotrophic fungal pathogens. *Plant Cell* 21:1000-1019, 2009.

15. Du, H.N., Fingerman, I.M. and **Briggs, S.D**. Histone H3 K36 methylation is mediated by a *trans*-histone methylation pathway involving an interaction between Set2 and histone H4. *Genes & Development* 22: 2786-2798, 2008.

16. Fingerman, I.M., Du, H.N., and **Briggs, S.D**. Controlling histone methylation via trans-histone pathways. *Epigenetics* 3: 1-6. 2008. (Review).

17. Fingerman, I.M., Du, H.N. and **Briggs, S.D**. Histone methyltransferase assays. *Cold Spring Harbor (CSH) Protocols*. doi:10.1101/pdb.prot4939, 2008.

18. Altaf, M., Utley, R.T., Lacoste, N., Tan, S., **Briggs, S.D.**, and Côté, J. Interplay of chromatin modifiers on a short basic patch of histone H4 tail defines the boundary of telomeric heterochromatin. *Molecular Cell*. 28: 1002-1014, 2007.

19. Fingerman I.M., Li, H.C., and **Briggs, S.D.** A charge-based interaction between histone H4 and Dot1 is required for H3K79 methylation and telomere silencing: Identification of a new trans-histone pathway. *Genes & Development*. 21: 2018-2029, 2007.

20. Laribee R.N., Shibata Y., Mersman D.P., Collins S.R., Kemmeren P., Roguev A., Weissman J.S., **Briggs S.D.**, Krogan N.J. and Strahl B.D. CCR4/NOT complex associates with the proteasome and regulates histone methylation. *PNAS.* 104: 5836-5841, 2007.

21. Shi, X., Kachirskaia, I., Walter, K.L., Kuo, J.H., Lake A., Davrazou, F., Chan, S.M., Martin, D.G., Fingerman, I.M., **Briggs, S.D.**, Howe, L., Utz, P.J., Kutateladze, T.G., Lugovskoy, A.A., Bedford, M.T., and Gozani, O. Proteome-wide analysis in *S. cerevisiae* identifies several PHD fingers as novel direct and selective binding modules of histone H3 methylated at either lysine 4 or lysine 36. *J. Biol. Chem.* 282: 2450-2455, 2007.

22. Bender, L.B., Suh, J., Carroll, C.R., Fong, Y, Fingerman, I.M., **Briggs, S.D.**, Cao, R., Zhang, Y., Reinke, V. and Strome, S. MES-4, an autosome-associated histone methyltransferase that participates in silencing the X chromosomes in the *C. elegans* germ line. *Development*. 133: 3907-3917, 2006.

23. Fingerman, I.M., Wu, C-L., Wilson, B.D. and **Briggs, S.D.** Global loss of Set1-mediated H3 Lys4 trimethylation is associated with silencing defects in *Saccharomyces cerevisiae. J. Biol. Chem*. 280: 28761-28765, 2005.

24. Fingerman I.M. and **Briggs S.D.** p53-mediated transcriptional activation: from test tube to cell. *Cell*. 117: 690-691. 2004. (Preview).

25. Doun S.S., Burgner J.W., **Briggs S.D.** and Rodwell V.W. *Enterococcus faecalis* Phosphomevalonate Kinase. *Protein Science* 14: 1134-9, 2005.

26. Rice J.C., **Briggs S.D.**, Ueberheide B., Barber C.M., Shabanowitz J., Hunt D.F., Shinkai Y. and Allis C.D. Mammalian histone methyltransferases direct different degrees of histone H3 lysine 9 methylation to define distinct domains of silent chromatin. *Mol. Cell.* 12: 1591-1598, 2003.

27. Milne T., **Briggs S.D.**, Brock H.W., Martin M.E., Gibbs D., Allis C.D. and Hess J.L. MLL targets SET domain methyltransferase activity to *Hox* gene promoters. *Mol. Cell*. 10: 1107-1117, 2002.

28. **Briggs S.D.**, Xiao T., Sun S.W., Caldwell J.A., Shabanowitz J., Hunt D.F., Allis C.D. and Strahl, B.D. *Trans*-histone regulatory pathway in chromatin. *Nature* 418: 498, 2002.

29. Strahl B.D., Grant P.A., **Briggs S.D.**, Sun Z.W., Bone J.R., Caldwell J.A., Mollah S., Cook R.G, Shabanowitz J., Hunt D.F., and Allis C.D. Set2 is a nucleosomal histone H3-selective methyltransferase that mediates transcriptional repression. *Mol. Cell. Biol.* 22: 1298-1306, 2002.

30. Bryk M., **Briggs S.D.**, Strahl B.D., Curcio M.J., Allis C.D., and Winston F. Evidence that Set1, a Factor Required for Methylation of Histone H3, Regulates rDNA Silencing in *S. cerevisiae* by a Sir2-Independent Mechanism. *Current Biology* 12: 165-170, 2002.

31. **Briggs, S.D.** and Strahl, B.D. Unraveling heterochromatin. *Nature Genetics* 30: 239-240, 2002.

32. **Briggs S.D.**, Bryk M., Strahl B.D., Cheung W.L., Davie J.K., Dent S.Y., Winston F., and Allis C.D. Histone H3 lysine 4 methylation is mediated by Set1 and required for cell growth and rDNA silencing in *Saccharomyces cerevisiae*. *Genes & Development* 15: 3286-3295, 2001.

33. Jacobs S.A., Taverna S.D., Zhang Y., **Briggs S.D.**, Li J., Eissenberg J.C., Allis C.D., and Khorasanizadeh S. Specificity of the HP1 chromo domain for the methylated N-terminus of histone H3. *EMBO J.* 20: 5232-5241, 2001.

34. Strahl B.D., **Briggs S.D.**, Brame C.J., Caldwell J.A., Koh S.S., Ma H., Cook R.G., Shabanowitz J., Hunt D.F., Stallcup M.R., and Allis C.D. Methylation of histone H4 at arginine 3 occurs in vivo and is mediated by the nuclear receptor coactivator PRMT1. *Curr. Biol.* 11: 996-1000, 2001. (co-first author manuscript).

35. Wang H., Huang Z.Q., Xia L., Feng Q., Erdjument-Bromage H., Strahl B.D., **Briggs S.D.**, Allis C.D., Wong J., Tempst P., and Zhang Y. Methylation of histone H4 at arginine 3 facilitating transcriptional activation by nuclear hormone receptor. *Science* 293: 853-857, 2001.

36. **Briggs S.D.**, Scholtz B., Jacque J.M., Swingler S., Stevenson M., and Smithgall T.E. HIV-1 Nef promotes survival of myeloid cells by a Stat3-dependent pathway. *J. Biol. Chem*. 276: 25605-25611, 2001.

37. Cheung W.L., **Briggs S.D.**, and Allis C.D. Acetylation and chromosomal functions. *Curr. Opin. Cell Biol*. 12: 326-333, 2000.

38. Smithgall T.E., **Briggs S.D.**, Schreiner S., Lerner E.C., Cheng H., and Wilson M.B. Control of myeloid differentiation and survival by Stats. *Oncogene*. 19: 2612-2618, 2000.

39. **Briggs S.D.**, Lerner E.C., and Smithgall T.E. Affinity of Src family kinase SH3 domains for HIV Nef in vitro does not predict kinase activation by Nef in vivo. *Biochemistry* 39: 489-495, 2000.

40. **Briggs S.D.** and Smithgall T.E. SH2-kinase linker mutations release Hck tyrosine kinase and transforming activities in Rat-2 fibroblasts. *J. Biol. Chem.* 274: 26579-26583, 1999.

41. Smithgall T.E., Rogers J.A., Peters K.L., Li J., **Briggs S.D.**, Lionberger J.M., Cheng H., Shibata A., Scholtz B., Schreiner S., and Dunham N. The c-Fes family of protein-tyrosine kinases. Crit. *Rev. Oncog.* 9: 43-62, 1998.

42. **Briggs, S.D.**, Sharkey, M., Stevenson, M., and Smithgall, T.E. SH3-mediated Hck tyrosine kinase activation and fibroblast transformation by the Nef protein of HIV-1. *J. Biol. Chem*. 272: 17899-17902, 1997.

43. Bryant, S.S., **Briggs, S.D.**, Smithgall, T.E., Martin, G.A., McCormick, F., Chang, J.-H., Parsons, S.J., and Jove, R. Two SH2 domains of p120 Ras-GAP bind cooperatively to tyrosine phosphorylated p190 Rho-GAP. *J. Biol. Chem.* 270: 17947-17952, 1995.

44. **Briggs, S.D.**, Bryant, S.S., Jove, R., Sanderson, S.D., and Smithgall, T.E. The Ras GTPase-activating protein (GAP) is an SH3 domain-binding protein and substrate for the Src-related tyrosine kinase, Hck. *J. Biol. Chem.* 270: 14718-14724, 1995.

45. Hjermstad, S., **Briggs, S.D.**, and Smithgall, T.E. Phosphorylation of the *ras* GTPase-activating protein by the p93$^{c\text{-}fes}$ protein-tyrosine kinase *in vitro* and formation of GAP-*fes* complexes via an SH2 domain-dependent mechanism. *Biochemistry* 32: 10519-10525, 1993.

46. Hjermstad, S., Peters, K.L., **Briggs, S.D.**, Glazer, R.I., and Smithgall, T.E. Regulation of the human c-*fes* protein-tyrosine kinase (p93$^{c\text{-}fes}$) by its *src* homology 2 domain and major autophosphorylation site (tyr 713). *Oncogene* 8: 2283-2292, 1993.

List of Published Work in MyBibliography (42 out of 46 total publications):
http://www.ncbi.nlm.nih.gov/sites/myncbi/1TKpVcmHlu6At/bibliography/48047302/public/?sort=date&direction=descending

Google Scholar Page: http://scholar.google.com/citations?user=yo6YObkAAAAJ&hl=en&oi=ao

RESEARCH SUPPORT

Current Research Support

Investigator: Scott D. Briggs
Project/Proposal Title: SET domain epigenetic factors govern antifungal drug efficacy and fungal pathogenesis
Source of Support: NIH R01 – National Institute of Allergy and Infectious Diseases (NIAID)
Total Award Period Covered: 09/24/2018 – 08/21/2023

Investigator: Scott D. Briggs
Project/Proposal Title: Identification of pathways involved in antifungal drug resistance
Source of Support: Purdue College of Agriculture (AgSEED)
Total Award Period Covered: 03/01/2018 – 2/28/2020

Completed Research Support (select)

Investigator: Scott D. Briggs
Project/Proposal Title: The role of Set1-mediated methylation in chromatin function
Source of Support: NIH R01-National Institute of General Medical Sciences (NIGMS)

Investigator: Scott D. Briggs
Project/Proposal Title: The role of Set1-mediated methylation in chromatin function
Source of Support: NIGMS administrative supplement - American Recovery and Reinvestment Act

Investigator: Scott D. Briggs
Support: Past
Project/Proposal Title: Functional Characterization of the Multiple Myeloma Set Domain Protein (MMSET)
Source of Support: Sidney Kimmel Foundation for Cancer Research