

Publications of the Gross Lab

1. Gross, D.S. and Simpkins, H. 1981. Evidence for two-site binding in the terbium(III)-nucleic acid interaction. *J. Biol. Chem.* **256**: 9593-9598.
2. Gross, D.S., Rice, S.W. and Simpkins, H. 1981. Influence of inorganic cations and histone proteins on the terbium(III)-nucleic acid interaction. *Biochim. Biophys. Acta* **656**: 167-176.
3. Simpkins, H., Thompson, L.M., Waldeck, N., Gross, D.S. and Mooney, D. 1981. Conformational changes in rat liver chromatin after liver regeneration. *Biochem. J.* **193**: 671-678.
4. Gross, D.S., Simpkins, H., Bubencko, E. and Borer, P.N. 1982. Proton magnetic resonance analysis of terbium ion-nucleic acid complexes: Further evidence for two-site binding to polynucleotides. *Arch. Biochem. Biophys.* **219**: 401-410.
5. Ball, D.J., Gross, D.S. and Garrard, W.T. 1983. 5-methylcytosine is localized in nucleosomes that contain histone H1. *Proc. Natl. Acad. Sci. USA* **80**: 5490-5494.
6. Gross, D.S., Huang, S.-Y. and Garrard, W.T. 1985. Chromatin structure of the potential Z-forming sequence (dT-dG)_n•(dC-dA)_n: Evidence for an "alternating-B" conformation. *J. Mol. Biol.* **183**: 251-265.
7. Gross, D.S. and Garrard, W.T. 1986. The ubiquitous potential Z-forming sequence of eukaryotes, (dT-dG)_n•(dC-dA)_n, is not detectable in the genomes of eubacteria, archaebacteria, or mitochondria. *Mol. Cell Biol.* **6**: 3010-3013.
8. Gross, D.S., Szent-Gyorgyi, C. and Garrard, W.T. 1986. Yeast as a model system to dissect the relationship between chromatin structure and gene expression. *In Yeast Cell Biology*, ed. J.B. Hicks (Alan R. Liss, Inc., New York), pp. 345-366.
9. Gross, D.S. and Garrard, W.T. 1987. Poising chromatin for transcription. *Trends Biochem. Sci.* **12**: 293-297.
10. Garrard, W.T., Cockerill, P.N., Hunting, D.W., McDaniel-Gerwig, D., Szent-Gyorgyi, C., Xu, M., and Gross, D.S. 1988. Active and inactive chromatin. *In Chromosome and Chromatin Structure*, ed. K.W. Adolph (Boca Raton, Florida: CRC Press, Inc.), Volume I, pp. 133-178.
11. Gross, D.S. and Garrard, W.T. 1988. Nuclease hypersensitive sites in chromatin. *Ann. Rev. Biochem.* **57**: 159-197.

12. Gross, D.S., Hernandez, E.M., Collins, K.W., and Garrard, W.T. 1988. Vacuum blotting: A simple method for transferring DNA from sequencing gels to nylon membranes. *Gene* **74**: 347-356.
13. McDaniel, D., Caplan, A.J., Lee, M.-S., Adams, C.C., Fishel, B.R., Gross, D.S., and Garrard, W.T. 1989. Basal level expression of the yeast *HSP82* gene requires a heat shock regulatory element. *Mol. Cell. Biol.* **9**: 4789-4798.
14. Gross, D.S., English, K.E., Collins, K.W., and Lee, S. 1990. Genomic footprinting of the yeast *HSP82* promoter reveals marked distortion of the DNA helix and constitutive occupancy of heat shock and TATA elements. *J. Mol. Biol.* **216**: 611-631.
15. Gross, D.S., Adams, C.C., English, K.E., Collins, K.W., and Lee, S. 1990. Promoter function and *in situ* protein/DNA interactions upstream of the yeast *HSP90* heat shock genes. *Antonie van Leeuwenhoek J. Microbiol.* **58**: 175-186.
16. Adams, C.C. and Gross, D.S. 1991. The yeast heat shock response is induced by conversion of cells to spheroplasts and by potent transcriptional inhibitors. *J. Bacteriology* **173**: 7429-7435.
17. Lee, S. and Gross, D.S. 1993. Conditional silencing: The *HMRE* mating-type silencer exerts a rapidly reversible position effect on the yeast *HSP82* heat shock gene. *Mol. Cell. Biol.* **13**: 727-738.
18. Gross, D.S., Adams, C.C., Lee, S., and Stentz, B. 1993. A critical role for heat shock transcription factor in establishing a nucleosome-free region over the TATA-initiation site of the yeast *HSP82* heat shock gene. *EMBO J.* **13**: 3931-3945.
19. Erkine, A.M., Adams, C.C., Gao, M., and Gross, D.S. 1995. Multiple protein-DNA interactions over the yeast *HSC82* heat shock promoter. *Nucleic Acids Res.* **23**: 1822-1829.
20. Erkine, A.M., Szent-Gyorgyi, C., Simmons, S.F., and Gross, D.S. 1995. The upstream sequences of the *HSP82* and *HSC82* genes of *S. cerevisiae*: Regulatory elements and nucleosome positioning motifs. *Yeast* **11**: 573-580.
21. Gross, D.S. 1995. Heat shock factor potentiates the promoter chromatin structure of the yeast *HSP90* genes. *In Advances in Molecular and Cellular Biology: The Nucleosome*, ed. A.P. Wolffe (Greenwich CT: Jai Press Inc.), pp. 151-182.
22. Erkine, A.M., Adams, C.C., Diken, T., and Gross, D.S. 1996. Heat shock factor gains access to the yeast *HSC82* promoter independently of other sequence-

- specific factors and antagonizes nucleosomal repression of basal and induced transcription. *Mol. Cell. Biol.* **16**: 7004-7017.
23. Lee, S. and Gross, D.S. 1996. Role of chromatin structure in *HMRE*-mediated transcriptional repression of the *HSP82* heat shock gene. *J. Microbiol.* **34**: 40-48.
 24. Duttweiler, H.M. and Gross, D.S. 1997. A single tube RNA prep for northern analysis from yeast and other cell types. *Trends Genetics* **13**: 82.
 25. Duttweiler, H.M. and Gross, D.S. 1998. Bacterial growth medium that significantly increases the yield of recombinant plasmid. *BioTechniques* **24**: 438-444.
 26. Erkine, A.M., Magrogan, S.F., Sekinger, E. A. and Gross, D.S. 1999. Cooperative binding of heat shock factor to the yeast *HSP82* promoter *in vivo* and *in vitro*. *Mol. Cell. Biol.* **19**: 1627-1639.
 27. Sekinger, E. A. and Gross, D.S. 1999. *SIR* repression of a yeast heat shock gene: UAS and TATA footprints persist within heterochromatin. *EMBO J.* **18**: 7041-7055.
 28. Raitt, D.C., Erkine, A.M., Johnson, A.L, Makino, K., Morgan, B., Gross, D.S., and Johnston, L.H. 2000. The *Skn7p* response regulator of *Saccharomyces cerevisiae* interacts with *Hsf1p* *in vivo* and is required for the induction of heat shock genes in response to oxidative stress. *Mol. Biol. Cell* **11**: 2335-2347.
 29. Venturi, C. B., Erkine, A.M., and Gross, D.S. 2000. Cell cycle-dependent binding of yeast heat shock factor to nucleosomes. *Mol. Cell. Biol.* **20**: 6435-6448.
 30. Singh, H., Sekinger, E.A., and Gross, D.S. 2000. Chromatin and Cancer: Causes and Consequences. *J. Cell. Biochem. Suppl.* **35**: 61-68.
 31. Sekinger, E. A. and Gross, D. S. 2001. Silenced chromatin is permissive to activator binding and PIC recruitment. *Cell* **105**: 403-414.
 - Featured in News & Comment, *Trends in Genetics* **17**: 381 (2001).
 - Selected as an F1000 Prime article by Faculty of 1000.
 32. Gross, D.S. 2001. Sir proteins as transcriptional silencers. *Trends Biochem. Sci.* **26**: 685-686.
 33. Erkine, A.M. and Gross, D.S. 2003. Dynamic chromatin alterations triggered by natural and synthetic activation domains. *J. Biol. Chem.* **278**: 7755-7764.

34. Dixon, C., Mathias, N., Zweig, R.M., Davis, D.A., and Gross, D.S. 2005. Alpha-synuclein targets the plasma membrane via the secretory pathway and induces toxicity in yeast. *Genetics* **170**: 47-59.
35. Zhao, J., Herrera-Diaz, J. and Gross, D.S. 2005. Domain-wide displacement of histones by activated heat shock factor occurs independently of Swi/Snf and is not correlated with RNA polymerase II density. *Mol. Cell. Biol.* **25**: 8985-8999.
36. Pirrotta, V. and Gross, D. S. 2005. Epigenetic silencing mechanisms in budding yeast and fruitfly: Different paths, same destinations. *Mol. Cell* **18**: 395-398.
37. Singh, H., Erkin, A.M., Kremer, S.B., Duttweiler, H.M., Davis, D.A., Iqbal, J., Gross, R.R. and Gross, D.S. 2006. A functional module of yeast Mediator that governs the dynamic range of heat shock gene expression. *Genetics* **172**: 2169-2184.
38. Gao, L. and Gross, D.S. 2006. Using genomics and proteomics to investigate mechanisms of transcriptional silencing in *Saccharomyces cerevisiae*. *Briefings Functional Genomics Proteomics* **5**: 280-288.
39. Balakrishnan, S.K. and Gross, D.S. 2008. The tumor suppressor p53 associates with gene coding regions and co-traverses with elongating RNA polymerase II in an *in vivo* model. *Oncogene* **27**: 2661-2672.
40. Gao, L. and Gross, D.S. 2008. Sir2 silences gene transcription by targeting the transition between RNA polymerase II initiation and elongation. *Mol. Cell. Biol.* **28**: 3979-3994.
 - Selected as an F1000 Prime article by Faculty of 1000.
41. Kremer, S.B. and Gross, D.S. 2009. The SAGA and Rpd3 chromatin modification complexes dynamically regulate heat shock gene structure and expression. *J. Biol. Chem.* **284**: 32914-32931.
42. Gross, D.S., Klein, R.L. and Witt, S.N. 2011. Therapeutics: Harnessing the power of molecular and pharmacological chaperones. *In Protein Chaperones and Protection from Neurodegenerative Diseases*, ed. S.N. Witt (John Wiley & Sons), pp. 385-421.
43. Kim, S., Balakrishnan, S.K. and Gross, D.S. 2011. p53 interacts with RNA polymerase II through its core domain and impairs Pol II processivity *in vivo*. *PLoS One* **6**: e22183.
44. Chávez, S., Gross, D.S., Hermand, D. and Suñé, C. 2012. Gene control during transcription elongation. *Genetics Research International* **2012**: Article ID 758384.

45. Kremer, S.B., Kim, S., Jeon, J.O., Moustafa, Y.W., Chen, A., Zhao, J. and Gross, D.S. 2012. Role of Mediator in regulating Pol II elongation and nucleosome displacement in *Saccharomyces cerevisiae*. *Genetics* **191**: 95-106.
 - Selected as an F1000 Prime article by Faculty of 1000.
46. Kim, S. and Gross, D.S. 2013. Mediator recruitment to heat shock genes requires dual Hsf1 activation domains and Mediator Tail subunits Med15 and Med16. *J. Biol. Chem.* **288**: 12197-12213.
47. Zhang, H., Gao, L., Anandhakumar, J. and Gross, D.S. 2014. Uncoupling transcription from covalent histone modification. *PLoS Genetics* **10**: e1004202.
 - A comment on this paper (“New & Noteworthy”) appeared on the homepage of the Saccharomyces Genome Database (www.yeastgenome.org) on 1 May 2014.
 - Selected by Abcam as one of the top epigenetics articles May 2014.
 - Featured on the Epigenetics Blog, EpiBeat July 2014.
48. Gross, D.S. 2015. Heterochromatin: Dark matter or variation on a theme? (invited review) *Current Biol.* **25**: R462-R465.
49. Gross D.S., Chowdhary S., Anandhakumar J. and Kainth A.S. 2015. Primer: Chromatin (invited review). *Current Biol.* **25**: R1158-R1163.
50. Anandhakumar J., Moustafa Y.W., Chowdhary S., Kainth A.S. and Gross D.S. 2016. Evidence for multiple Mediator complexes in yeast independently recruited by activated Heat Shock Factor. *Mol. Cell. Biol.* **36**: 1943-1960.
51. Chowdhary, S., Kainth, A.S. and Gross, D.S. 2017. *Heat Shock Protein* genes undergo dynamic alteration in their three-dimensional structure and genome organization in response to thermal stress. *Mol. Cell. Biol.* **37**: e00292-17, pp. 1-22.
52. Krakowiak J., Zheng, X., Patel, N., Anandhakumar, J., Valerius, K., Gross, D.S., Khalil, A.S. and Pincus, D. 2018. Hsf1 and Hsp70 constitute a two-component feedback loop that regulates the yeast heat shock response. *eLife* **7**:e31668, pp. 1-17.
53. Pincus, D., Anandhakumar, J., Thiru, P., Guertin, M.J., Erkin, A.M. and Gross, D.S. 2018. Genetic and epigenetic determinants establish a continuum of Hsf1 occupancy and activity across the yeast genome. *Mol. Biol. Cell* **29**: 3168-3182.
54. Chowdhary, S., Kainth, A.S., Pincus, D. and Gross, D.S. 2019. Heat Shock Factor 1 drives intergenic association of its target gene loci upon heat shock. *Cell Reports* **26**: 18-28.
55. Chowdhary, S., Kainth, A.S. and Gross, D.S. 2020. Chromosome conformation capture that detects novel *cis*- and *trans*-interactions in budding yeast. *Methods* **170**: 4-16.

56. Chowdhary, S., Kainth, A.S. and Gross, D.S. 2020. Methods for mapping three-dimensional genome architecture. *Methods* **170**: 1-3, *Invited Editorial*.
57. Kainth A.S., Meduri, R., Pandit, V., Rubio, L.S. and Gross, D.S. 2020. Shugoshin 2 - a new guardian for heat shock transcription. *EMBO J.* **39**: e104077.
58. Kainth A.S., Chowdhary S., Pincus, D. and Gross D.S. 2021. Primordial Super-Enhancers: Heat Shock-Induced Chromatin Organization. *Trends Cell Biol.* 31: 801-813.
59. Meduri, R., Rubio, L.S., Mohajan, S. and Gross, D.S. 2022. Phase-separation antagonists potently inhibit transcription and broadly increase nucleosome density. *J. Biol. Chem.* **298**: 102365
60. Chowdhary, S., Kainth, A.S., Paracha, S., Gross, D.S. and Pincus, D. 2022. Inducible transcriptional condensates drive 3D genome reorganization in the heat shock response. *Mol. Cell* **82**: 4189-4400.