

Faculty Profile

 

- [Faculty Directory](#)
- [Research Group Homepage](#)

Elizabeth Vierling

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Education and Appointments

- Ph.D. 1982, University of Chicago

Research Interests

- Biochemistry
- "Metabolism, Signaling, and Regulation"
- Nucleic Acids and Genomes
- Protein and Membrane Biochemistry
- Structural Biology

Research Summary

Plant molecular biology; biochemistry and function of molecular chaperones

Research in our laboratory is aimed at understanding the mechanism of action and biological roles of molecular chaperones/heat shock proteins, both during stress (primarily heat stress) and during normal growth and development. In addition, we have an expanding program to define factors other than chaperones that are essential for heat stress tolerance. Our research extends from protein structural studies to molecular and quantitative genetic analysis, and utilizes *Arabidopsis thaliana*, the cyanobacterium *Synechocystis* PCC6803, and the yeast *Saccharomyces cerevisiae* as model organisms. On the structural side our work is contributing to basic knowledge of chaperone structure and function, while at the level of the whole organism, we are unraveling stress responses and mechanisms of stress tolerance. These studies involve basic biochemistry as well as molecular and transmission genetics. We are also employing microarray genomic techniques and have active collaborations in mass spectrometry and crystallography.

One class of chaperones that are the subject of major research effort is the alpha-crystallin related small (s) HSPs. *In vitro*, sHSPs act as molecular chaperones to prevent the irreversible heat-denaturation of other proteins. *In vivo*, mutations in these proteins in mammals are responsible for certain types of myopathies as well as cataract formation. sHSPs also accumulate in specific cancers and in neurodegenerative disease. We are pursuing both biochemical and genetic approaches to investigate further the function and mechanism of chaperone activity of the sHSPs through protein purification and *in vitro* assays of chaperone activity, as well as genetic analysis to identify and characterize sHSP mutants.

To define other genes involved in stress tolerance, we have a program of both forward and reverse genetics and gene microarray experiments. Using a forward genetic screen for loss-of-thermotolerance we have identified mutants in another class of chaperones important to plants, Hsp101, a member of the AAA+ family of ATPases, which appears to be involved in disassociating protein aggregates accumulated during stress. Other mutants uncovered in this screen are being investigated. By probing Arabidopsis whole genome microarrays we have identified genes associated with acclimation to high temperature, and are now testing their importance using loss-of-function mutants.

Selected Publications

Basha, E., C. Jones, V. Wysocki, [E. Vierling](#). Mechanistic differences between two conserved classes of small heat shock proteins found in the plant cytosol. *J. Biol. Chem.* 285:11489-11497 (2010).

Stengel, F., A. J. Baldwin, A. J. Painter, N. Jaya, E. Basha, L. E. Kay, [E. Vierling](#), C. V. Robinson, J. L.P. Benesch. Quaternary dynamics and plasticity underlie small heat shock protein chaperone function. *Proc. Natl. Acad. Sci.* 107:2007-2012 (2010).

Jaya, N., V. Garcia*, [E. Vierling](#). Substrate binding site flexibility of the small heat shock protein molecular chaperones. *Proc. Natl. Acad. Sci.* 106:15604-15609 (2009).

Cheng, G., E. Basha, V.H. Wysocki, [E. Vierling](#). Insights into small heat shock protein and substrate structure during chaperone action derived from hydrogen/deuterium exchange and mass spectrometry. *J. Biol. Chem.*, 283:26634-42 (2008) Featured as "Paper of the Week". PMID: 18621732.

Lee, U., C. Wie*, B. O. Fernandez, M. Feelisch, [E. Vierling](#). Modulation of nitrosative stress by S-nitrosoglutathione reductase is critical for thermotolerance and plant growth. *Plant Cell* 20: 786-802, (2008).

Offerdahl, E., T. Baldwin, L. Elfring, [E. Vierling](#), M. Ziegler. Reading questions in large lecture courses. *J. College Teaching*, March/April: 34-38 (2008).

Tonsor, S.J., C. Scott, I. Boumanza, T.R. Liss, J.L. Brodsky, . Heat shock protein 101 effects in *Arabidopsis thaliana*: Genetic variation, fitness and pleiotropy in controlled environments. *Mol. Ecol.*, 17: 1614-1626 (2008).

Larkindale, J., [E. Vierling](#). Core genome responses involved in acclimation to high temperature. *Plant Physiol.* 146: 748-761 (2008).

Siddique, M., S. Gernhard, P. von Koskull-Döring, [E. Vierling](#), K-D. Scharf. The plant sHSP superfamily: Five new members in *Arabidopsis thaliana* with unexpected properties. *Cell Stress & Chaperones*, in press (2008).

Schramm, F., J. Larkindale, K. Kiehlmann, G. Arnab, G. Englich, G., [E. Vierling](#), P. von Koskull-Döring. A cascade of transcription factor DREB2A and heat stress transcription factor HsfA3 regulates the heat stress response of *Arabidopsis*. *Plant J.* 53: 264-274 (2008).

McClellan, C.A., T.J. Turbeyville, E.M. K. Wijeratne, A. Kerschen, [E. Vierling](#), C. Queitsch, L. Whitesell, A.A. Gunatilaka. A rhizosphere fungus enhances *Arabidopsis* thermotolerance through production of an Hsp90 inhibitor. *Plant Physiol* 145: 174-182 (2007). Highlighted in Science *Stke* <http://stke.sciencemag.org/cgi/content/abstract/sigtrans;2007/403/tw333>

Kotak, S., [E. Vierling](#), H. Bäumllein, P. von Koskull-Döring. A novel transcriptional cascade regulating heat stress proteins during seed development in *Arabidopsis*. *Plant Cell* 19:182-195 (2007).

Kwon, Y., S-H. Kim, M-S. Jung, M-S. Kim, J-E. Oh, H-W. Ju, K-I. Kim, [E. Vierling](#), H. Lee, S-W. Hong. *Arabidopsis hot2* encodes an endochitinase-like protein that is essential for tolerance to heat, salt and drought stresses. *Plant J.* 49:184-193 (2007).

Lee, U., I. Rioflorida, S-W. Hong, J. Larkindale, E. R.Waters, [E. Vierling](#). The *Arabidopsis*

ClpB/Hsp100 family of proteins: Chaperones for stress and chloroplast development. *Plant Journal* 49: 115-127 (2007).

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Lee,U., C. Wie, M. Escobar, B. Williams, S.-W. Hong, [E. Vierling](#). Genetic analysis reveals domain interactions of *Arabidopsis* Hsp100/ClpB and cooperation with the sHsp chaperone system. *Plant Cell*, 17:559-571 (2005).

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Lum, R., J. M. Tkach, [E. Vierling](#), and J. R. Glover. Evidence for an unfolding/threading mechanism for protein disaggregation by *Saccharomyces cerevisiae* Hsp104. *J. Biol. Chem.* 279: 29139 - 29146 (2004).

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