

**BIOGRAPHICAL SKETCH**

Provide the following information for the key personnel and other significant contributors in the order listed on Form Page 2.  
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NAME A. Pia Abola		POSITION TITLE Research Fellow	
eRA COMMONS USER NAME			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	YEAR(s)	FIELD OF STUDY
Princeton University; Princeton, NJ	BA	1990	Chemistry
University of California, Berkeley; Berkeley, CA	PhD	1995	Molecular and Cell Biology
Stanford University; Palo Alto, CA	Postdoctoral	2000	Biological Sciences

**A. Positions**

- 1990 Summer Research Scholar - Brookhaven National Laboratory, Upton, NY - Walter Mangel, Advisor
- 1990-1995 Graduate Student Researcher/Graduate Student Instructor - Molecular and Cell Biology, UC Berkeley; Nicholas Cozzarelli, Advisor
- 1995-2000 Postdoctoral Researcher - Biological Sciences, Stanford University; Sharon Long, Advisor
- 2000-2001 Staff Scientist - Stanford Genome Technology Center
- 2001-2005 (Hiatus to care for family)
- 2005-Present Research Fellow - The Molecular Sciences Research Institute, Berkeley, CA

**B. Selected peer-reviewed publications (in chronological order).**

- McGrath WJ, Abola AP, Toledo DL, Brown MT, and Mangel WF. (1996). Characterization of human adenovirus proteinase activity in disrupted virus particles. *Virology* 217:131-138.
- Benjamin KR, Abola AP, Kanaar R, and Cozzarelli NR (1996). Contributions of supercoiling to Tn3 resolvase and phage Mu *gin* site-specific recombination. *Journal of Molecular Biology* 256(1):50-65.
- Abola AP, Willits MG, Wang RC, and Long SR (1999). Reduction of APS instead of PAPS in cysteine biosynthesis by *Rhizobium meliloti* and other Rhizobiaceae. *Journal of Bacteriology*, 181(17):5280-5287.
- Lander ES, et al. (2001) Initial sequencing and analysis of the human genome. *Nature* 409(6822):860-921.
- Galibert F, et al. (2001) The composite genome of the legume symbiont *Sinorhizobium meliloti*. *Science*. 293(5530):668-72.
- Barnett MJ, et al. (2001) Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* pSymA megaplasmid. *Proc Natl Acad Sci U S A*. 98(17):9883-8.
- O'Hara EF, Williams MB, Rott L, Abola P, Hansen N, Jones T, Gurjal MR, Federspiel N, Butcher EC. (2005). Modified representational difference analysis: isolation of differentially expressed mRNAs from rare cell populations. *Anal Biochem*. 2005 Jan 15;336(2):221-30.

**C. Research Support.**

3 P50 HG002370-04S1

09/23/05 – 06/30/07

NIH/NHGRI

Title: Supplement to Promote Reentry into Biomedical or Behavioral Research Careers, Center for Genomic Experimentation and Computation

Role: Research Fellow

The goal of this project is to purify the components of the yeast pheromone responsive MAP kinase cascade and obtain kinetic measurements to constrain the computational models of the signaling pathway.