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## BIOGRAPHICAL SKETCH

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NAME Kosaku Shinoda	POSITION TITLE Postdoctoral Scholar		
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
Keio University, Japan	B.S.	2006	Bioinformatics
Keio University, Japan	Ph.D.	2012	Systems Biology
University of California, San Francisco	Postdoctoral	2012	Developmental biology

### A. Positions and Honors

#### Positions and Employment

2006-2011 Research Scientist, Human Metabolome Technologies, Inc.  
2009-2010 Research Fellow, Institute for Advanced Biosciences, Keio University, Japan.  
2010-2011 Research Associate, Institute for Advanced Biosciences, Keio University, Japan.  
2011-2012 Junior Specialist, University of California, San Francisco, USA.  
2013-present Postdoctoral Scholar, University of California, San Francisco, USA.

#### Other Experience and Professional Memberships

Member, American Heart Association.  
Member, The Metabolomics Society.  
Member, Human Proteome Organisation (HUPO).

#### Honors and Awards

2004 Best poster presentation award, Chem-Bioinformatics Society Annual Meeting.  
2010 The Tokyo Biochemical Research Foundation fellowship  
2011-2012 Grant-in-Aid for Young Scientists (B)  
The Japanese Society for the Promotion of Science  
2013 Young Investigator Grant, The Nakatomi Foundation  
2013-present JSPS Fellowship (Research Abroad)  
The Japanese Society for the Promotion of Science

### B. Peer Reviewed Publications

#### Most relevant to the current application (in chronological order)

1. **Shinoda, K.**, Sugimoto, M., Yachie, N., Sugiyama, N., Masuda, T., Robert, M., Soga, T. and Tomita, M. (2006) Prediction of liquid chromatographic retention times of peptides generated by protease digestion of the Escherichia coli proteome using artificial neural networks. *J Proteome Res*, **5**, 3312-3317.
2. Sugiyama, N., Masuda, T., **Shinoda, K.**, Nakamura, A., Tomita, M. and Ishihama, Y. (2007) Phosphopeptide enrichment by aliphatic hydroxy acid-modified metal oxide chromatography for nano-LC-MS/MS in proteomics applications. *Mol Cell Proteomics*, **6**, 1103-1109.
3. **Shinoda, K.**, Tomita, M. and Ishihama, Y. (2008) Aligning LC peaks by converting gradient retention times to retention index of peptides in proteomic experiments. *Bioinformatics*, **24**, 1590-1595.

4. Ohno, H., **Shinoda, K.**, Spiegelman, BM. and Kajimura, S. (2012) PPAR  $\gamma$  agonists induce a white-to-brown fat conversion through stabilization of PRDM16 protein. *Cell Metabolism*, **15**, 395-404. PMID: PMC3410936.
5. Sharp, LZ., **Shinoda, K.**, Ohno, H., Scheel, DW., Tomoda, E., Ruiz, L., Hu, H., Wang, L., Pavlova, Z., Gilsanz, V. and Kajimura S. (2012) Human BAT possesses molecular signatures that resemble beige/brite cells. *PLoS One*, **7**, e49452. PMID: PMC35000293.
6. Ohno, H.(\*), **Shinoda, K.(\*)**, Ohyama, K.(\*), Sharp LZ. and Kajimura, S. (2013) EHMT1 controls brown adipose cell fate and thermogenesis through the PRDM16 complex. *Nature*, **504**, 163-167. (\* co-first author). PMID: PMC3855638.

#### **Additional recent publications of importance to the field (in chronological order)**

1. **Shinoda, K.**, Yachie, N., Masuda, T., Sugiyama, N., Sugimoto, M., Soga, T. and Tomita, M. (2006) HybGFS: A hybrid method for genome-fingerprint scanning. *BMC Bioinformatics*, **7**, 479. PMID: PMC1643838.
2. Arakawa, K., Yamada, Y., **Shinoda, K.**, Nakayama, Y. and Tomita, M. (2006) GEM System: Automatic prototyping of cell-wide metabolic pathway models from genomes. *BMC Bioinformatics*, **7**, 168. PMID: PMC1435936.
3. **Shinoda, K.**, Sugimoto, M., Tomita, M. and Ishihama, Y. (2008) Informatics for peptide retention properties in proteomic LC-MS. *Proteomics*, **8**, 787-798.
4. **Shinoda, K.**, Tomita, M. and Ishihama, Y. (2010) emPAI Calc--for the estimation of protein abundance from large-scale identification data by liquid chromatography-tandem mass spectrometry. *Bioinformatics*, **26**, 576-577.

### **C. Current Active and Pending Research Support**

#### **Active**

The Japanese Society for the Promotion of Science  
JSPS Fellowship (Research Abroad)

04/01/2013-03/31/2015

#### **Phosphoproteomic profiling toward the development of pharmacological method for brown adipocyte induction *in vivo***

To identify novel protein kinases regulating white-to-brown fat conversion by using improved phospho-peptide enrichment technology

Role: PI/Fellow