

GUY OSHIRO, Ph.D.

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SUMMARY

Informatics specialist with broad experience in drug discovery and over 9 years of industry experience. Advanced discovery stage program from initial concept into the clinic. Helped drive biomarker exploration during preclinical stage and validated surrogate biomarkers in the clinic. A dedicated team player with a track record of accomplishments.

- Solid background in informatics, drug discovery, genetics, molecular biology and biochemistry
- Strong mathematical background with a degree in Mathematics-Physics
- Hands-on knowledge of modern biotechnology including microarrays, qPCR, RNAi, uHTS assay development, and robotic automation
- Over 15 years of laboratory bench experience

Computer/Informatic Skills:

- | | | |
|--------------------------|----------------|------------------|
| • R | • Perl | • Ruby on Rails |
| • Matlab | • Turbo Pascal | • C |
| • LabSynch | • Spotfire | • GeneSpring |
| • Seurat | • Condoseo | • Pipeline Pilot |
| • Vector NTI | • GCG | • Prism |
| • MS Sharepoint Services | • Unix | • SQL |

PROFESSIONAL EXPERIENCE

JOHN MCNEIL & CO., San Diego, CA

Scientific Application Developer

2008 - Present

Develop custom software solutions to analyze, present, and record complex scientific data streams.

KALYPSYS, INC., San Diego, CA

Informatics Principal Scientist

2008

Develop solutions to analyze, manage, and disseminate results from uHTS screens, preclinical data, and clinical data.

- Set up a near real time analysis data flow scheme to quickly process uHTS data and provide immediate feedback to the assay development team and screening team to allow the teams to make necessary modifications to improve the quality of the uHTS screening campaigns.
- Developed a robust system to analyze preclinical qPCR data utilizing the R statistical language and Labsynch to electronically capture the associated metadata.
- Co-developed an analysis process to analyze clinical qPCR biomarker data. Set up a system to verify patient samples with associated data points. Collated and submitted the blinded data to the clinical CRO for final analysis.

Biology Principal Scientist**2004 – 2008**

Initiate and lead discovery projects

- Project leader for ophthalmology target with an external corporate research partner. Led the program from initial assay development to the selection of potential early development compounds (EDC). Significant interaction with the corporate partners through regular team teleconferences and quarterly project reviews. Coordinated various activities with other departments and external CROs. Directly supervised one to three team members and guided the efforts of two to three matrixed team members.
- Project leader for PPAR δ agonist program. Led Kalypsys's first drug discovery program from assay development to clinical development. Active participant through clinical development as a member of the clinical development team. The lead compound recently completed a Phase Ib clinical trial. Directly supervised one to four team members as well as coordinated various activities with other departments and external CROs.
- Dedicated a research associate to identify a liquid biomarker that could translate from preclinical studies to human clinical trials.
- Trained the clinical CRO to collect samples for biomarker studies.
- Designed and implemented a web-based Research Portal to effectively manage discovery research projects using Microsoft Sharepoint Services.

Assay Development Senior Scientist**2002 – 2004**

Develop assays for lead discovery projects and lead programs through the drug discovery stages and gates

- Project leader for PPAR δ agonist program.
- Led the genomics project team to build a world-class set of shRNA plasmids. Conducted genome wide RNAi screens.
- Played a major role in designing the new biology lab space
- Directly supervised 2.5 research associates.

Biotechnology Scientist***2001 – 2002***

Enable the target and drug discovery process

- PPAR project leader.
- Developed an automated method to generate a worklist to hit pick potential hits for subsequent confirmation screens.
- Analyzed initial uHTS data sets with co-developed PERL scripts, Spotfire, and Pipeline Pilot.
- Established the Kalypsys uHTS screening paradigm.
- Set up a document hierarchy to efficiently manage discovery projects.
- In charge of the initial set up of the biology lab.
- Directly supervised 1.5 research associates.

Genomics Institute of the Novartis Research Foundation (GNF), La Jolla, CA *1999-2001****Postdoctoral Research Fellow***

Functional genomics studies in yeast

- Identified novel genes in yeast by using a combination of gene expression analysis and proteomics. Analyzed datasets with custom Perl scripts, Matlab scripts and GeneSpring.
- Characterized novel genes in yeast by studying the phenotypic growth of a collection of tagged yeast deletion strains and analyzing the gene expression patterns grown under a variety of growth conditions.
- High throughput compound screens to identify novel anti-fungal agents. Analyzed uHTS data sets with a combination of custom Perl scripts and Spotfire.
- Supervised 3 research associates

TRAINING AND PROFESSIONAL DEVELOPMENT**SPOTFIRE, San Diego, CA*****2008*****Spotfire Developer Training Course**

Learned how to customize and extend the standard functionality of Spotfire, a powerful application to visualize and analyze large datasets, by creating tools and guides that improve the capability and productivity of the end user. The mathematical and statistical prowess of Spotfire can be further extended by running external algorithms on a R server. Fully automatic data processing is possible by scripting the entire Spotfire analysis suite programmatically.

BIG NERD RANCH, Atlanta, GA**2008****Ruby on Rails Boot Camp**

Learned agile programming in a highly flexible framework for rapid prototyping and deployment of web-based, database-backed applications. Ruby on Rails is a full-stack framework for developing database-backed web applications according to the Model-View-Control pattern.

LEADERSHIP EDGE, San Diego, CA**2007****From the Laboratory to Leadership Management Training Course**

Learned effective management strategies including conflict resolution, the art of delegation, and directing productive teams in a dynamic environment.

EDUCATION**UNIVERSITY OF COLORADO HEALTH SCIENCES CENTER, Denver, CO****Ph.D., Molecular Biology**

Thesis Advisor: Dr. Robert Sclafani, studied regulation of the cell cycle in *Saccharomyces cerevisiae*.

WHITMAN COLLEGE, Walla Walla, WA**Bachelor of Arts**

Major: Mathematics-Physics, Minors: Biology, Chemistry

TEACHING EXPERIENCE**AMERICAN ASSOC. OF CANCER RESEARCH (AACR), Aspen, CO****1997 – 1998****AACR Molecular Biology Workshop Facilitator**

Instructed medical fellows in modern molecular biology techniques including yeast two-hybrid assays.

UNIVERSITY OF COLORADO MEDICAL SCHOOL, Denver, CO**1994****Physiology Supplemental Instructor**

Lead medical students on discussions in physiology to improve their understanding of the course material.

KAUI HIGH and INTERMEDIATE SCHOOL, Lihue, HI**1992 – 1993****Math and Science Teacher**

Taught eight-grade mathematics and ninth-grade physical science course.

PATENTS

Govek, S.P., Oshiro, G., Noble, S.A., Malecha, J.W., Shiau, A.K., **Aryl-substituted heterocyclic inhibitors of phosphodiesterase 4**. PCT Int. Appl. (2008), 84pp. CODEN: PIXXD2 WO 2008045663 A2 20080417

Govek, S.P., Oshiro, G., Noble, S.A., Malecha, J.W., Shiau, A.K., **Heterocyclic inhibitors of phosphodiesterase 4**. PCT Int. Appl. (2008), 44pp. CODEN: PIXXD2 WO 2008045664 A2 20080417

Shiau, A.K., Massari, M.E., Oshiro, G., Kabakibi, A., Malecha, J.W., Noble, S.A., **Methods for the selective modulation of PPAR**. U.S. Pat. Appl. Publ. (2007), 25pp., Cont.-in-part of U.S. Ser. No. 258,463. CODEN: USXXCO US 2007190079 A1 20070816

Noble, S.A., Oshiro, G., Malecha, J.W., Zhao, C., Duron, S.G., Lindstrom, A.K., Shiau, A. K., Lou, B., Govek, S.P., Thomas, D.J., **Sulfonyl-substituted bicyclic compounds as modulators of PPAR, and their preparation, pharmaceutical compositions and use for treatment of various diseases**. U.S. Pat. Appl. Publ. (2006), 72pp., Cont.-in-part of U.S. Ser. No. 258,463. CODEN: USXXCO US 2006205736 A1 20060914

PUBLICATIONS/PRESENTATIONS

Malecha, J.W., Oshiro, G., Kabakibi, A., Zhao, C., Duron, S.G., Lindstrom, A.K., Shiau, A. K., Lou, B., Govek, S.P., Thomas, D.J., Chen, J., Magnuson, G., Staszewski, L., Dozier, S., Noble, S.A., (2008) Design, synthesis, and structure-activity relationships of Sulfonyl-substituted bicyclic compounds as novel, potent PPAR delta agonists. Manuscript in preparation.

Guha, M., Okamoto, K., Anderson, J., Duron, S., Lindstrom, A., Malecha, J., Oshiro, G., Kabakibi, A., Banerjee, U., Rao, T. (2008) Selective Activation of Peroxisome Proliferator-Activated Receptor (PPAR) reverses key features of metabolic NASH in a rodent model. Manuscript in preparation.

Multani, P., Gillespie, J., Walsh, J., Oshiro, G., Jenkins, D., Willy, P., Gallagher, J., Malecha, J., Cousins, R., Rourick, R., Noble, S., Shiau, A., Rao, T., Fikes, J., Grint, P. (2008) KD3010, a novel selective peroxisome proliferator-activated receptor delta (PPAR δ) agonist, demonstrates safety and improves insulin sensitivity in normal and obese healthy human volunteers. American Diabetes Association Meeting Abstract.

Guha,M., Chuang,J.C., Repa,J., Gardiner,E., Anderson,J., Banerjee, U., Malecha,J., Kabakibi,A., Oshiro,G., Heyman, R., Noble, S., Shiau, A., Rao, T. (2008). Selective and potent PPAR δ agonist KD3010 improves glucose homeostasis in diabetic db/db mice and potentiates glucose-stimulated insulin secretion (GSIS) in mouse islets. American Diabetes Association Meeting Abstract.

Guha,M., Deng,M., Duron,S., Lindstrom,A., Malecha,J., Oshiro,G., Kabakibi,A., Staszewski,L., Rao, T. (2006). Selective Activation of Peroxisome Proliferator-Activated Receptor β/δ holds promise for the treatment of obesity, metabolic syndrome and diabetes. American Diabetes Association Meeting Abstract.

Washburn,M.P., Koller,A., Oshiro,G., Ulaszek,R.R., Plouffe,D., Deciu,C., Winzeler,E., and Yates,J.R., III (2003). Protein pathway and complex clustering of correlated mRNA and protein expression analyses in *Saccharomyces cerevisiae*. Proc. Natl. Acad. Sci. U. S. A *100*, 3107-3112.

Winzeler,E.A., Castillo-Davis,C.I., Oshiro,G., Liang,D., Richards,D.R., Zhou,Y., and Hartl,D.L. (2003). Genetic diversity in yeast assessed with whole-genome oligonucleotide arrays. Genetics *163*, 79-89.

Oshiro,G., Wodicka,L.M., Washburn,M.P., Yates,J.R., III, Lockhart,D.J., and Winzeler,E.A. (2002). Parallel identification of new genes in *Saccharomyces cerevisiae*. Genome Res. *12*, 1210-1220.

Hanway,D., Chin,J.K., Xia,G., Oshiro,G., Winzeler,E.A., and Romesberg,F.E. (2002). Previously uncharacterized genes in the UV- and MMS-induced DNA damage response in yeast. Proc. Natl. Acad. Sci. U. S. A *99*, 10605-10610.

Oshiro,G. and Winzeler,E.A. (2000). Aneuploidy--it's more common than you think. Nat. Biotechnol. *18*, 715-716.

Oshiro,G., Owens,J.C., Shellman,Y., Sclafani,R.A., and Li,J.J. (1999). Cell cycle control of Cdc7p kinase activity through regulation of Dbf4p stability. Mol. Cell Biol. *19*, 4888-4896.

Dohrmann,P.R., Oshiro,G., Tecklenburg,M., and Sclafani,R.A. (1999). RAD53 regulates DBF4 independently of checkpoint function in *Saccharomyces cerevisiae*. Genetics *151*, 965-977.

Shellman,Y.G., Schauer,I.E., Oshiro,G., Dohrmann,P., and Sclafani,R.A. (1998). Oligomers of the Cdc7/Dbf4 protein kinase exist in the yeast cell. Mol. Gen. Genet. *259*, 429-436.