

Updated on March 23, 2017

Daisuke Kihara, Ph.D.
Professor of Biological Sciences and Computer Science
Purdue University

Office

Purdue University
Department of Biological Sciences/Computer Science
Hockmyer 229/ LWSN 1208
West Lafayette, IN 47907
Tel: (765) 496-2284 Fax: (765) 496-1189
E-mail: dkihara@purdue.edu
http://www.bio.purdue.edu/molecular_biosciences/directory.php?refID=166
<http://www.cs.purdue.edu/faculty/dkihara.html>
<http://kiharalab.org> (Lab)

Education

1999 Ph.D. (Science) in Bioinformatics
Kyoto University, Faculty of Science, Japan, Advisor: Minoru Kanehisa
1996 M.S. in Bioinformatics
Kyoto University, Faculty of Science, Japan
1994 B.S. in Biochemistry
The University of Tokyo, College of Arts and Sciences, Japan

Positions held

2014.8-present	Full Professor
2015.1-2015.8	Visiting Scientist , Eli Lilly, Indianapolis
2009.8-2014.8	Associate professor
2003.8-2009.8	tenure-track Assistant professor Purdue University, West Lafayette, Indiana Department of Biological Sciences/Computer Sciences (joint appointment)
2002.9-2003.7	Senior Postdoctoral Research Associate Advisor: Jeffrey Skolnick Buffalo Center of Excellence in Bioinformatics, Buffalo, NY, USA
1999-2002.9	Postdoctoral Research Associate Advisor: Jeffrey Skolnick Donald Danforth Plant Science Center, St. Louis, MO, USA
1998-1999	Research Assistant Bioinformatics Center Institute for Chemical Research, Kyoto University, Japan

Awards

- Showalter University Faculty Scholar, Purdue University, 2013-2018
- The Seed of Success Award (earned a grant over \$1M/year), Purdue University, 2005, 2006, 2007, 2008, 2010, 2012, 2014
- Best Oral Presentation Award “Origin of protein superfamily and superfolds”, 3D-SIG 2015, an ISMB satellite meeting on Structural Bioinformatics and Computational Biophysics, Dublin, Ireland, July 10-11, 2015

- Best paper award, Great Lakes Bioinformatics Conference (GLBIO) 2011 (an official conference of the International Society for Computational Biology, ISCB), May 1-3, 2011
- International Structural Genomics Organization Poster Prize, International Conference on Structural Genomics 2011, Toronto, Canada, May 10-14, 2011
- Best paper award, the 21st International Conference on Genome Informatics (GIW2010), December, 2010

Publications

- [131] MPFit: Computational tool for predicting moonlighting proteins.
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- [130] Using PFP and ESG protein function prediction webservers.
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- [129] NaviGO: Interactive tool for visualization and functional similarity and coherence analysis with gene ontology.
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- [127] Prediction of local quality of protein structure models considering spatial neighbors in graphical models.
W.H. Shin, X. Kang & D. Kihara.
Scientific Reports, 7: 40629 (2017).
- [126] BindML/BindML+: Detecting protein-protein interaction interface propensity from amino acid substitution patterns.
Q. Wei, D. La, & D. Kihara.
Methods in Mol. Biol., 1529: 279-289 (2017)
- [125] Predicting real-valued protein residue fluctuation using FlexPred.
Lenna X. Peterson, Michal Jamroz, Andrzej Kolinski, & Daisuke Kihara
Methods in Mol. Biol., 1484: 175-186 (2017)
- [124] Discovery of nicotinamide adenine dinucleotide binding proteins in the Escherichia coli proteome using a combined energetic- and structural-bioinformatics-based approach.
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- [123] Human and server docking prediction for CAPRI round 30-35 using LZerD with combined scoring functions.
L.X. Peterson, H. Kim, J. Esquivel-Rodriguez, A. Roy, X. Han, W.H. Shin, J. Zhang, G. Terashi, M. Lee, & D. Kihara.
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- [122] PL-PatchSurfer2: Improved local surface matching-based virtual screening methods that is tolerant to target and ligand structure variation.
W.H. Shin, C. Christoffer, J. Wang, & D. Kihara.
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- [121] Missing gene identification using functional coherence scores.
M. Chitale, I. K. Khan, & D. Kihara
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- (original version) The Boltzmann sequence-structure channel.
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- [118] Ranking protein-protein docking models using steered molecular dynamics and potential of mean force calculations.
L. J. Kingsley, J. Esquivel-Rodriguez, D. Kihara, & M A. Lill.
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- [117] Genome-scale prediction of moonlighting proteins using diverse protein association information.
I. K. Khan & D. Kihara.
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M. Jamroz, A. Kolinski, & D. Kihara.
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- [115] Energetic coupling between ligand binding and dimerization in E. coli phosphoglycerate mutase.
N.W. Gardner, L.K. Monroe, D. Kihara, & C. Park
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D. Kihara
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M.F. Lensink, L.X. Peterson, H.R. Kim, A. Roy, J. Esquivel-Rodriguez, D. Kihara, & S. J. Wodak. (98 authors)
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Y. Xiong, J. Esquivel-Rodriguez, L. Sael, & D. Kihara.
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J. Esquivel-Rodríguez & D. Kihara.
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J. Esquivel-Rodriguez, & D. Kihara
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- [7] TOUCHSTONE: An ab initio Protein Structure Prediction Method that Uses Threading-based Tertiary Restraints.
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- [5] Defrosting the Frozen Approximation: PROSPECTOR – A New Approach to Threading.
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Books

- [3] Protein function prediction, *Methods in Molecular Biology*, D. Kihara (ed.) Springer, (2017)
- [2] Protein structure prediction (3rd Edition), *Methods in Molecular Biology*, D. Kihara (ed.) Springer, (2014)
- [1] Protein function prediction for omics era, D. Kihara, (ed.) Springer, (2011)

Miscellaneous Publication:

- [2] The International Society of Computational Biology presents: the Great Lakes Bioinformatics Conference, May 16-18, 2014, Cincinnati, Ohio.
J. Cavalcoli, L. Welch, B. Aronow, S. Draghici, & D. Kihara
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- [1] WWW Homepages for Biophysicists. Part 1-6.
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Invited/Selected Oral Presentations

- [172] In silico screening and modeling of protein-drug and protein-protein interactions, Albert Einstein College of Medicine, New York, NY, Jan. 24, 2017
- [171] 12th Critical Assessment of Techniques for Protein Structure Prediction (CASP12) Evaluation meeting, CAPRI docking & Quality assessment round table Gaeta, Italy, December 10-13, 2016
- [170] In silico screening and modeling of protein-drug and protein-protein interactions, Biomedical Informatics Speaker Series, Cincinnati Children's Hospital & University of Cincinnati, Nov. 18, 2016
- [169] In silico screening and modeling of protein-drug and protein-protein interactions, Purdue University Center for Cancer Research Seminar Series, Purdue Institute for drug discovery, November 17, 2016
- [168] Predicting gene functions: Departing from single gene-single function paradigm, Bioinformatics seminar, Purdue University, Oct. 25, 2016
- [167] Genome-wide discovery of protein-ligand interactions by a combined computational and energy-based approach, International Conference on Computational Genomics and Proteomics, Guanacaste, Costa Rica, Oct. 18-22, 2016
- [166] "The Boltzmann Sequence-Structure Channel" by A. Magner, D. Kihara, & W. Szpankowski, IEEE International Symposium in Information Theory, Barcelona, Spain, July 10-15, 2016

- [165] Considering chain flexibility in protein structure evaluation, 3D-SIG, Orlando Florida, July 8-9, 2016
- [164] Genome-scale prediction of moonlighting proteins using diverse protein association information, I. K. Khan & D. Kihara, Function-SIG at ISMB, Orlando Florida, July 9, 2016
- [163] PL-PatchSurfer: Molecular surface-based virtual screening program", National Institute of Advanced Industrial and Science, Tokyo Japan, June 17, 2016
- [162] Computational modeling of various types of protein complexes, Molecular modeling of energy storage devices & Biomolecular complexes, CERM 2016 47th Central Region Meeting of American Chemical Society, May 19, 2016
- [161] Ensemble-based evaluation for protein structure models, The 3rd International Conference on Mathematical & Computational Medicine May 16-18, 2016
- [159-60] The Hitchhiker's guide to the biomolecular galaxy, Purdue University, May 11-12, 2016:
- "IDR-LZerD: structure prediction of disordered protein interactions", Lenna Peterson
 - "An automated Alpha tracing from cryo-EM map", Genki Terashi
- [158] Human and server prediction using LZerD with combined scoring functions", 6th CPARI protein docking prediction evaluation meeting, April 17-19 2016, Tel Aviv, Israel
- [157] Computational docking of multifarious protein complexes, Dept. of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, Feb. 29, 2016
- [156] PL-PatchSurfer: A fast surface-patch-based virtual screening program using three dimensional Zernike descriptors, 60th Biophysical Society meeting, Los Angeles, Feb. 27- March 2, 2016
- [155] Computational docking of multifarious protein complexes, Dept. of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, Feb. 29, 2016
- [154] Protein structure prediction using residue- and fragment-environment potential in CASP11, 3rd International Conference on Protein and RNA Structure Prediction, Punta Cana, Dominican Republic, Dec. 14-18, 2015
- [153] Unified biomolecular 3D surface matching for big data in structural and chemical biology, Workshop on Big Data and Computational Sciences, University of Kansas, Lawrence, Kansas, Nov. 21, 2015
- [152] Patch-Surfer and PL-PatchSurfer: Predicting binding ligands for target proteins by molecular surface similarity and complementarity, University of Kansas, Lawrence, Kansas, Nov. 20, 2015
- [151] Protein structure prediction using residue- and fragment-environment potential in CASP11, KIAS Workshop, Korea Institute for Advanced Study, Seoul, Korea, September 17-19, 2015
- [150] Origin of protein superfamilies and superfolds" (oral presentation), 3D-SIG 2015, Dublin, Ireland, July 10-11, 2015. Received the Best Oral Presentation Award
- [149] Gene function prediction in biological contexts, Hokkaido University, Sapporo, Japan, July 2, 2015
- [148] On the origin of protein superfamilies and superfolds. 4th SNU Bioinformatics Workshop, Seoul National University, Seoul, Korea, June 29-30, 2015.
- [147] Genome-scale identification and characterization of moonlighting proteins. The 15th Annual Meeting of the Protein Science Society of Japan. Tokushima, Japan, June 24-26, 2015
- [146] Surface structure-based ligand prediction for target proteins and application for drug development", D. Kihara, Workshop on "Drug development based on predicted structure and function of target proteins", Tokyo University of Pharmacy and Life Sciences, Hachioji, Tokyo, Japan, June 23, 2015
- [145] Comparison and fitting of molecular shapes for low-resolution structural data, RIKEN, Yokohama, Japan, June 19, 2015
- [143-4] Great Lakes Bioinformatics Conference (GLBIO 2015), Purdue University, IN, May 18-20, 2015
- (talk) IAS: Interaction specific GO term associations for predicting protein-protein interaction networks. Satwica Yerneni, Ishita K. Khan, Qing Wei & D. Kihara
 - (talk) Residue environment score for selecting protein structure models and protein-protein docking models. Hyung-Rae Kim & D. Kihara

- [142] PL-PatchSurfer: surface-patch-based virtual screening program using three dimensional Zernike descriptors. Purdue Mini-Symposium on Integrated Structure, Function, and Interactions of Protein Universe. Purdue University, May 13-14, 2015.
- [141] EM-Surfer: real-time electron microscopy map database search. Purdue Mini-Symposium on Integrated Structure, Function, and Interactions of Protein Universe. Purdue University, May 13-14, 2015.
- [140] Selecting protein structure models with a residue environment score that recognizes multi-residue interactions. The Chem-Bio Informatics Society, Tokyo Institute of Technology, Tokyo, Japan, June 22, 2015.
- [139] Detecting local residue environment similarity for recognizing near-native protein structure models. From Computational Biophysics to Systems Biology (CBSB2015), The University of Oklahoma, Oklahoma, May 17-19, 2015.
- [138] Fast shape-based global and local electron density map search. J. Esquivel-Rodriguez, X. Han, C. Christoffer, X. Kang, L. Monroe, & D. Kihara, the 59th Biophysical Society Annual Meeting, Baltimore, MA, Feb. 7-11, 2015.
- [137] Phase transition in a sequence-structure channel. A. Magner, D. Kihara & W. Szpankowski. Information Theory and Applications, Scripps Seaside Forum, La Jolla, CA, Feb. 1-3, 2015.
- [136] Local image comparison using Krawtchouk moment invariants. A. Sit & D. Kihara, 2015 Joint Mathematics Meetings, San Antonio, Jan. 12, 2015
- [135] Invited talk at Free Modeling category, 11th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction (CASP11), Riviera Maya, Mexico, Dec. 7-10, 2014
- [134] Exploring Protein-Ligand Interactions Using Molecular Local Surface Comparison Methods. Department of Chemistry, Purdue University, Dec. 5, 2014
- [133] Detecting local residue environment similarity for recognizing near-native structure models. Coarse-Grained Modeling of Structure and Dynamics of Biomacromolecules, Telluride, CO, Aug 4-8, 2014
- [132] A proteomic strategy for global analysis of protein complex composition and localization in Arabidopsis leaves. Aryal Uma, Jun Xie, Daisuke Kihara, Mark Hall, Dan Szymanski, 25th International Conference on Arabidopsis Research (ICAR), University of British Columbia, Vancouver, Canada, July 28-Aug. 1, 2014
- [131] Genome-scale Identification and Characterization of Moonlighting Proteins, The Biological and Biomedical Consequences of Protein Moonlighting , London, UK, 29-30 July 2014
- [130] Comparison and fitting of molecular shapes and low-resolution structural data, EBI, Hinxton, UK, July 28, 2014.
- [129] Why Protein Folds and Superfamilies have Skewed Distributions?, Zing Conference on Protein Folding, Punta Cana, Dominican Republic, July 16-19, 2014
- [128] Small-angle x-ray scattering reveals the structure of the catalytic domain of a plant cellulose synthase and its assembly into dimers. P.S. Rushton, N. Carpita A.T. Olek, C.V. Stauffacher, C. Rayon, L. Makowski, H.R. Kim, P. Ciesielski, J. Badger, L.N. Paul, D. Kihara, M. Crowley, & M. E. Himmel, Plant Biology 2014, Portland, Oregon, Jul 12-16, 2014.
- [127] PFP: Protein function prediction using distantly related sequences and function association, Automatic Function Prediction Meeting (AFP-SIG), Boston, July 11-12, 2014
- [126] Genome-scale identification and characterization of moonlighting proteins, I. Khan & D. Kihara, Automatic Function Prediction Meeting (AFP-SIG), Boston, July 11-12, 2014
- [125] Predicting protein complex assembly pathway using multiple-protein docking algorithm, Yoichiro Togawa, Juan Esquivel-Rodriguez, Amit Roy, & D. Kihara, 3D-SIG, Boston, July 11-12, 2014
- [124] Navigating 3D Electron Microscopy Density Maps and Protein Shapes with EM-SURFER and 3D-SURFER 2.0, Juan Esquivel-Rodriguez, Yi Xiong, Juan Esquivel-Rodriguez, Xusi Han, Shuomeng Guang, and Daisuke Kihara, Great Lakes Bioinformatics Conference (GLBIO 2014), Cincinnati, OH, May 16-18, 2014

- [123] Unified biomolecular 3D surface matching for proteins, ligands, and interactions. Iowa State University, Apr 10, 2014.
- [122] Evaluating protein structure models considering local structure contexts, 2nd Zing Protein and RNA Structure Prediction Conference, Cancun, Mexico, Dec. 1-5, 2013
- [121] Prediction of macromolecular structures of protein interactions, Beckman Institute, Univ. Illinois at Urbana-Champaign, Oct 28, 2013
- [120] Prediction of macromolecular structures of protein interactions. Frontiers in Bioinformatics and Computational Biology, Cold Spring Harbor Conferences Asia, Suzhou, China, Sept. 23-27, 2013.
- [119] Computational prediction of protein function and protein-protein docking. University College London, Sep. 13, 2013
- [118] Predicting gene function in biological contexts , 2nd ACSL International Summer School, Imperial College London, Sep 8-14, 2013
- [117] Unified biomolecular 3D surface matching for proteins, ligands, and interactions, Eli Lilly, Lilly Grand Rounds, Eli Lilly, Indianapolis, Aug 14, 2013
- [116] Machine learning approach for protein structure modeling, Telluride Workshop on Modeling Biomolecular Structures, Interactions, and Functions, Telluride, CO, July 1-5, 2013.
- [115] Structure prediction of protein interactions, Seoul National University, Dept. of Chemistry, Seoul, Korea, June 27, 2013
- [114] Information flow in biological systems, Chung-Ang University, 4th International Conference of Biostatistics and Bioinformatics, Seoul, Korea, June 25, 2013
- [113] Predicting gene function in biological contexts, Seoul National University, Computer Science and Engineering, Seoul, Korea, June 24, 2013.
- [112] Information flow in biological systems, Tokyo Institute of Technology, June 21, 2013
- [111] Predictions of structures of protein interactions. Univ. Chicago Computation Institute, Chicago, IL, May 20, 2013
- [110] Macromolecular structure modeling and EM fitting. D. Kihara & J. Esquivel-Rodriguez, 5th CAPRI (Critical Assessment of Predicted Interactions), Utrecht, the Netherlands, April 17-19, 2013.
- [109] Predictions of Protein Function, Structures, Dynamics, and Interactions. Bioinformatics and Machine Learning Roundtable, Qatar Computing Res. Institute, Doha, Qatar, March 19-20, 2013.
- [108] Macromolecular Structure Modeling and Electron Microscopy Fitting Using 3D Zernike Descriptors. Highlights Track, ISCB-Asia/SCCG 2012, Shenzhen, China, Dec. 17-19, 2012.
- [107] Binding ligand prediction by comparing local surface patches of potential pocket regions. Zing conference, Mathematical and Computational Medicine, Xcaret, Cancun, Mexico, Dec. 1-15, 2012.
- [106] Predictions of structures of protein interactions. International Summer School of Life & Health Science, Education Academy of Computational Life Sciences, Tokyo Institute of Technology, Shonan, Kanagawa, Sept. 3-5, 2012
- [105] Suboptimal alignments & 3D Zernike descriptors for structure prediction and docking. Workshop on Coarse-grained modeling of structure and dynamics of biomacromolecules, Telluride, CO, July 23-27, 2012.
- [104] A "catalytic dimer" hypothesis for the synthesis of cellulose and other (1,4)-beta-glycans Nicholas C. Carpita, Anna T. Olek, Catherine J. Rayon, Lee Makowski, Shi-you Ding , Peter Ciesielski, Lake Paul, Subhangi Ghosh, Daisuke Kihara, Michael Crowley, Michael Himmel, Jeffrey Bolin, The 23rd International Conference on Arabidopsis Research (ICAR), Vienna, Austria, July 3-7, 2012
- [103] Predictions of structures of protein interactions. Telluride Meeting on Protein folding and Dynamics: From experiment to theory, Telluride, Colorado, June 17-21, 2012
- [102] Predicting binding ligand and protein docking using surface shape". D. Kihara, Graduate School of Information Science, Tohoku University, Sendai, Japan. May 30, 2012
- [101] Predictions of structures of protein interactions. Bioinformatics Seminar series at Institute of Chemical Research, Kyoto University, Uji, Kyoto, Japan. May 28, 2012

- [100] Structural features that predict real-value fluctuations of globular proteins, M. Jamroz, A. Kolinski & D. Kihara, at Special Session, " Proteins in motion: Computational studies in protein flexibility and dynamics" co-organized by D. Kihara & L. Kurgan, Great Lakes Bioinformatics Conference (GLBIO) 2012, May 15-17, 2012, Ann Arbor, MI.
- [99] Computational characterization of moonlighting proteins using Gene Ontology annotations (selected talk), by I. Khan, M. Chitale, & D. Kihara, Great Lakes Bioinformatics Conference (GLBIO) 2012, May 15-17, 2012, Ann Arbor, MI.
- [98] Macromolecular structure modeling and electron microscopy fitting using 3D Zernike descriptors (selected talk), J. Esquivel-Rodriguez, & D. Kihara, Great Lakes Bioinformatics Conference (GLBIO) 2012, May 15-17, 2012, Ann Arbor, MI.
- [97] Sequence- and structure-based protein function prediction. The Research Institute at Nationwide Children's hospital, The Ohio State University, March, 22, 2012.
- [96] Functional coherence assessment for protein groups and its application to pathway assignment, Zing conference, IECA (International E. coli Alliance) 2011, Cancun, Mexico, Dec. 5-9, 2011
- [95] Unified Molecular Representation for Protein Shape Comparison and Interaction, Zing conference on Protein and RNA Structure Prediction", Cancun, Mexico, Dec. 3-7, 2011
- [94] Next generation structural bioinformatics and gene function prediction
Biological Sciences Research Retreat, Swan Lake resort, Plymouth IN, Nov. 5, 2011
- [93] Next generation protein 3D structure analysis: Rapid global/local surface comparison, docking, and low-resolution data. D. Kihara, Dept. of Biological Sciences Faculty Research Presentations, Purdue University, Oct. 27, 2011
- [92] Protein surface representation for ligand binding site screening, Eli Lilly, Indianapolis, October 3, 2011
- [91] Next Generation Protein 3D Structure Analysis: Rapid Global/Local Surface Comparison, Docking and Low-Resolution Data, University of Alberta, Edmonton, Canada, September 16, 2011
- [90] Binding ligand prediction by comparing local surface patches of potential pocket regions. Computational Biology Research Center, Tokyo, Japan, September 2, 2011
- [89] Next generation protein structure analysis for structure comparison and interaction prediction. Fukushima Medical University, Fukushima, Japan, September 1, 2011.
- [88] Binding ligand prediction by comparing local surface patches of potential pocket regions. RIKEN, Yokohama, Japan, August 30, 2011
- [87] Unified molecular representation for protein shape comparison and interaction. ICR Symposium to Celebrate the Bioinformatics Center's 10 Year Anniversary and New Restructuring, Institute for Chemical Research, Kyoto University, Uji, Kyoto, Japan, August 29, 2011
- [86] Next generation protein 3D structure analysis: rapid global/local surface comparison and low-resolution data. Seoul National University, Dept. of Computer Science and Engineering, August 22, 2011
- [85] Function Prediction for Systems Level: Functional Coherence of Protein Groups and Identification of Missing Genes. M. Chitale & D. Kihara, Automated Function Prediction SIG, International Conference on Intelligent Systems for Molecular Biology (ISMB), Vienna, July 15-16, 2011
- [84] Protein-protein docking prediction: from pairwise docking, docking interface prediction, and multiple protein docking.
Workshop on "Modeling Biomolecular Structures, Interactions, and Functions, Telluride, Colorado, June 13-17, 2011.
- [79-83] 4 lectures, Faculty of Chemistry, Warsaw University, Poland, May 23-27, 2011
- Template-based structure prediction and quality assessment using suboptimal alignments
 - Sequence-based function prediction: from prediction of single genes to functional coherence for protein groups

- Protein-protein docking prediction: from pairwise docking, docking using docking interface information, and multiple protein docking
 - Binding ligand prediction by Comparing Local Surface Patches of Potential Pocket Regions
- [78] Surface Representation for Molecular Global and Local Shape Comparison and Docking. International Institute of Molecular and Cell Biology, Warsaw, Poland, May 25, 2011
- [71-77] 6 selected oral presentations at Great Lakes Bioinformatics Conference 2011, May 2-4, 2011, Ohio University, Athens, Ohio
- Protein-protein Interaction Sites Prediction using Phylogenetic Substitution Models, D. La, & D.Kihara
 - Protein Docking Prediction Using Predicted Protein-Protein Interface, B. Li, & D. Kihara
 - Multi-LZerD: Multiple Protein Docking for Asymmetric Complexes, J. Esquivel-Rodriguez, & D. Kihara
 - Rapid Comparison and Multimeric Protein Complex Fitting for Low-Resolution Electron Microscopy Data", J. Esquivel-Rodriguez, L. Sael, & D. Kihara
 - Patch-Surfer: Alignment Free Surface Patch-Based Ligand Binding Pocket Comparison, L. Sael, & D. Kihara
 - Functional Coherence Assessment for Protein Groups and its Application to Pathway Assignment, M. Chitale, & D. Kihara
- [70] Prediction of protein-protein interaction sites, pair-wise, and multiple protein docking, Academy of Mathematics and Systems Science, Chinese Academy of Science, Beijing, China, December 20, 2010
- [69] Improved Protein Surface Comparison and Application to Low-Resolution Protein Structure Data. L. Sael, & D. Kihara, The 21st International Conference on Genome Informatics, Hangzhou, China, December 16-18, 2010
- [68] Binding ligand prediction using local surface Zernike descriptors. Shanghai Institute of Materia Medica, Chinese Academy of Science, Shanghai, China, December 15, 2010
- [67] Sequence-based function prediction: from prediction of single genes to functional coherence for protein groups. Institute of Biochemistry and Cell Biology, Chinese Academy of Science, Shanghai, China, December 15, 2010
- [66] Protein-protein docking prediction: from pairwise docking, docking using docking interface information, and multiple docking. Shanghai Jiaotong University, Shanghai, China, December 14, 2010
- [65] Sequence-based function prediction: from prediction of single genes to functional coherence for protein groups. Fudan University, Shanghai, China, December 13, 2010
- [64] Real-Time Ligand Binding Pocket Database Search Using Local Surface Zernike Descriptors. R. Chikhi, L. Sael, D. Kihara, 3D-SIG, ISMB 2010, Boston MA, July 9-10, 2010
- [63] Protein surface representation for structure-based function prediction and docking. Telluride workshop on "Coarse-grained modeling of structure and dynamics of biomacromolecules" Telluride, CO, July 5-9, 2010
- [62] Molecular surface representation for protein shape comparison and docking. Korea Institute for Advanced Study (KIAS), Seoul, Korea, June 30, 2010
- [61] Structure of gene functional space in genomes The First International Conference for Industrial Statistics and Bioinformatics, The Research Center for Data Science, Chung-Ang University, Seoul, Korea, June 29, 2010
- [60] Protein surface representation for fast structure search, docking, and function prediction Nara Institute of Science and Technology (NAIST), Nara, Japan, January 7, 2010
- [59] Protein surface representation for fast structure search, docking, and function prediction Dept. of Computer Science, Tokyo Institute of Technology, Tokyo, Japan, Dec 28, 2009

- [58] Protein structure bioinformatics for predicting structure, docking, and function
Nanomedicine Development Center, University of Cincinnati, Nov 5, 2009
- [57] Global and local protein surface comparison and its applications
Telluride Workshop on “Method development for protein structure prediction and design”,
Telluride Science Research Center, Telluride, Colorado, June 15-19, 2009
- [56] Protein surface comparison for function prediction and docking
Dept. of Statistics, Chung-Ang University, Seoul Korea, May 15, 2009
- [55] Algorithms for biological sequence analysis
Dept. of Statistics, Chung-Ang University, Seoul Korea, May 14, 2009
- [54] Novel bioinformatics approaches for studying protein sequence, structure, and function in omics era.
Division of Bio-Medical Informatics, Center for Genome Science, National Institute of Health, Seoul, Korea, May 13, 2009
- [53] Annotating protein structures by surface shape comparison”, Biochemistry seminar, Dept. of Chemistry, Purdue University, Feb 27, 2009.
- [52] Annotating protein structures by surface shape comparison.
e-Bioinformatics session in 4th IEEE International Conference on e-Science, IUPUI, Indianapolis, Dec. 12, 2008
- [51] Informatics approaches for studying protein sequence, structure, and function in omics era.
Dept. of Biological Sciences, Purdue University, October 15, 2008
- [50] Quality assessment of template-based protein structure prediction.
University of Illinois at Chicago, Department of Bioengineering, Chicago, IL, February 26, 2008
- [49] Computational protein structure and function prediction.
Chung-Ang University, Statistics Department, Seoul, Korea, December 27, 2007
- [48] Template-based protein structure prediction and beyond.
Korea Institute for Advanced Study (KIAS), Daejeon, Korea., December 26, 2007
- [47] Protein function prediction for proteomics era.
7th KIAS-Soongsil Conference, Soongsil Univ., Seoul, Korea., October 4-6, 2007
- [46] A fast method for high throughput comparison of tertiary structure and physicochemical properties. (Session chair)
Biomedical Engineering Society Annual Meeting, Los Angeles, CA, September 26-29, 2007
- [45] Surface shape-based protein structure classification and search.
Interface 2007: the 39th Symposium on the interface of statistics, computing science, and applications, Doubletree Hotel, Philadelphia, May 23-26, 2007
- [44] Protein function and structure prediction for proteomics analyses.
Indiana University, Dept. of Informatics, Bloomington, IN, May 3, 2007.
- [43] Advanced techniques for protein function prediction and protein tertiary structure search for proteomics analyses.
Nara Institute of Science and Technology, Nara, Japan, December 28, 2006
- [42] Bioinformatics: Introduction and advanced topics.
Graduate program, Kansai Medical University, Osaka, Japan, December 25, 2006
- [41] Advanced techniques for protein function prediction and protein tertiary structure search for proteomics analyses.
Ajinomoto Life Science Institute, Kawasaki, Japan, December 22, 2006
- [40] Round table discussion on function prediction at Critical Assessment of Techniques for Protein Structure Prediction (CASP7) Asilomar Conference Center, CA, November 26-30, 2006
- [39] Enhanced protein function prediction for proteomics analysis.
Daisuke Kihara & Troy Hawkins, Biomedical Engineering Society Annual Meeting 2006, Systems Biology and Bioinformatics track, Hyatt Regency Chicago, IL. IUPUI, Indianapolis, IN, October 12, 2006.
- [38] Protein function prediction from sequence and structure.
Center for Computational Biology and Bioinformatics, IUPUI, Indianapolis, IN, October 6, 2006.

- [37] Low resolution and uncertainty in protein structure and function prediction. Symposium on Protein functional and folding motion, Institute for Protein Research, Osaka Univ., Osaka, Japan, September 28-29, 2006.
- [36] PFP: sequence-based annotation of sequences and local sequence motifs with contextual GO term associations. Troy Hawkins, Stan Luban, Daisuke Kihara, The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine, May 19-20, 2006.
- [35] Bridging geometric protein surface features and phylogenetic information for rapid identification of protein-protein interaction interfaces. David La, Dennis Liversay, Daisuke Kihara, The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine, May 19-20, 2006.
- [34] Enhanced Automated Function Prediction for Proteomics Analysis. Bioinformatics Seminar Series, Dept. of Statistics, Purdue University, January 24, 2006
- [33] Protein Function Prediction in the Structural Genomics Era. International Symposium, From Genomics to Chemical Genomics: 10th Anniversary of KEGG. PALULU Plaza, Kyoto, Japan, December 15-16, 2005
- [32] Protein Function Prediction in the Proteomics Era. International Symposium on Frontiers of Computational Science 2005 Noyori Conference Hall, Nagoya University, Japan, December 12-13, 2005
- [31] Protein function prediction methods beyond BLAST search. Structural Biology Seminar Series, Dept. of Biological Sciences, Purdue University, November 16, 2005
- [30] Protein function prediction in structural genomics era. Computing Research Institute, CS&E Seminar Series, Purdue University, October 19, 2005
- [29] Protein function prediction from sequence and structure. Mini-Workshop on Computational Studies on Proteins, Children's Hospital Research Foundation, Cincinnati, Ohio, Sep. 8, 2005
- [28] The use of context-based functional association in automated protein function prediction methods. Automated Function Prediction – Special Interest Group, (AFP-SIG), ISMB (International Conference on Intelligent Systems for Molecular Biology), Detroit, Michigan, 24, June, 2005.
- [27] Voxelized Protein Model for Fast Protein Docking and Function Prediction. Midwest Computational Structural Biology Workshop Brook Lodge, Michigan State University, Augusta, Michigan, April 30 – May 1, 2005
- [26] Toward a better template-based protein structure prediction. Dept. of Chemistry, Biochemistry Division seminar, Purdue University, 1 April, 2005
- [25] Conserved Small RNA Families in Gamma-Proteobacteria. Computational Biology Research Center, Tokyo, Japan, 28 December 2004.
- [24] Computational sequence and structure analyses. Biological Sciences Faculty Research Presentations, Dept. of Biological Sciences, Purdue University, 9 December, 2004
- [23] Comparative genomics study of non-coding RNA in Gamma-proteobacteria Ecolunch, Dept. of Biological Sciences, Purdue University, 17 November, 2004
- [22] Genome-scale Protein Structure Assignment to Microbial Genome Sequences. Ninth Annual Purdue University Biophysics Symposium, 25 October 2003
- [21] PDB is a Covering Set of Small Protein Structures. Bioinformatics Center, Kyoto University, Japan, 20 October 2003.
- [20] Genome-scale protein structure assignment to microbial genomes. International Workshop for Escherichia coli towards New Biology in the 21st Century. Awaji-shima, Japan, 15-17 October, 2003

- [19] Revisiting protein Structure Space – PDB is a Covering Set of Small Protein Structures. Computational Biology Research Center, Tokyo, Japan, 14 October 2003.
- [18] Revisiting Protein Structure Space for Prediction – PDB is a Covering Set of Small Protein Structures. Bioinformatics Seminar Series, Purdue University, 9 September 2003.
- [17] Protein Structure/Function Prediction on a Genome Scale. The Whitney Laboratory/Dept. of Computer Science, University of Florida, Gainesville, Florida, 7-8 April, 2003.
- [16] Genome Scale Protein Structure Prediction. Computer Science Dept., Virginia Polytechnic Institute and State University, Blacksburg, Virginia, 3 April, 2003.
- [15] Protein Structure/Function Prediction on a Genome Scale. Dept. of Biology, The University of Nebraska at Omaha, Omaha, Nebraska, 1 April, 2003.
- [14] Protein Structure/Function Prediction on a Genome Scale. Dept. of Biological Sciences, Purdue University, West Lafayette, Indiana, 25 March, 2003.
- [13] Protein Structure/Function Prediction on a Genome Scale. Dept. of Informatics, Indiana University, Bloomington, Indiana, 6 March, 2003.
- [12] Protein Structure/Function Prediction on a Genome Scale. Dept. of Biology, University of Kentucky, Lexington, Kentucky, 4 February, 2003.
- [11] Protein Structure/Function Prediction on a Genome Scale. Donald Danforth Plant Science Center, St. Louis, Missouri, 28 October, 2002.
- [10] Ab initio Protein Structure Prediction Method on a Genome Scale. Computational Biology Research Center, Tokyo, Japan, 12 October, 2001
- [9] An Ab initio Protein Structure Method Using a Lattice Model. Structural Bioinformatics Division Seminar, Yokohama City University, Japan, 11 October, 2001
- [8] A Lattice Model Based Protein Structure Prediction which Does Not Use Template Structures of Homologous Proteins. Biophysics Department Seminar, Nagoya University, Japan, 10 October, 2001
- [7] TOUCHSTONE: Ab initio Structure Prediction Method Using Restraints Derived from Threading. Research Society of Computational Genomics, the Biophysical Society of Japan Institute for Protein Research, Osaka University, Japan, 9 October, 2001
- [6] Ab initio Protein Structure Prediction Using Restraints Derived from Threading. Department of Biochemistry, Cambridge University, UK, 9 September, 2001
- [5] Toward Genome Scale Ab initio Protein Folding Prediction. Conference on “Experimental & Theoretical Approach for Protein Folding”, sponsored by Mirai Kaitaku Kenkyukai (Frontier Research Society) Okazaki Conference Center, Institute for Molecular Science, Okazaki, Japan, 10-12 January, 2001
- [4] Prediction of Protein Structure and Function on a Genome Scale. Jeffrey Skolnick, Andrzej Kolinski, Daisuke Kihara and Piotr Rotkiewicz. 23rd Annual Meeting of Molecular Biology Society of Japan, Kobe, Japan, 15 December, 2000
- [3] Generalized Comparative Modeling of Protein Structures. Electrotechnical Laboratory, National Inst. of Advanced Industrial Science, Tsukuba, Japan, 18 September, 2000
- [2] Analyses of Genome Sequences through Internet. Kansai Medical University, Japan, 24 March, 1998
- [1] Current Status of Prediction of Transmembrane Segments in Proteins and Application to Genome Sequences. Summer School of Biophysical Society of Japan for Young Scientists (Under sponsorship by The Biophysical Society of Japan) P.40, Kobe, Japan, 29-31 July, 1998

Poster and Other Presentations

- [174] Efficient computational framework for biological 3D image data retrieval (poster), M. Zhu, C. Belth, A. Sit, & D. Kihara, NSF SI2 PI Meeting, Arlington, VA, Feb. 21-22, 2017
- [172-3] The Hitchhiker's guide to the biomolecular galaxy, Purdue University, May 11-12, 2016:
- Identification of protein-protein interactions in *Arabidopsis thaliana* using mass spectrometry and computational methods, Ziyun Ding, & D. Kihara
 - Navigating 3D Electron Microscopy Density Maps and Protein Shapes with EM-SURFER and 3D-SURFER 2.0, Xusi Han, & D. Kihara
- [171] Significance of amino acid entropy and mutual information in multiple sequence alignments, Josh McGraw & D. Kihara, Undergraduate Research Poster Symposium, April 12, 2016, Purdue University
- [167-170] Great Lakes Bioinformatics Conference (GLBIO 2015), Purdue University, IN, May 18-20, 2015
- (poster) Protein side-chain conformation prediction methods are accurate in different residue environments. Lenna Peterson, X. Kang, & D. Kihara
 - (poster) PL-PatchSurfer2.0: A fast virtual screening program using surface patch based on 3DZernike Descriptors. Woong-Hee Shin & D. Kihara
 - (poster) Genome-scale identification and characterization of moonlighting proteins. Ishita Khan & D. Kihara
 - (poster) Fitting of multiple protein chains by iterative manipulation of cryo-EM maps. Lyman Monroe & D. Kihara
- [165-6] Undergraduate Research Poster Symposium, Purdue University, April 14, 2015
- Distributed heterogeneous cluster computing with computational proteomics, Aditya Vaidyam, & D.Kihara
 - Analysis of bioinformartics databases, Weichuan Luo, Tiange Dong, Andrew Walden, Tianmu Hu, Ray Ji, Eric Petit, Tomii Lee, & D. Kihara
- [164] Fast large scale comparison and structure fitting for low-resolution electron microscopy maps (poster), Juan Esquivel-Rodriguez & D. Kihara, 3D-SIG, Boston, July 11-12, 2014
- [163] Towards Plant-specific protein gene function prediction (poster), Akshay Kumar, Ishita Khan, D. Kihara, Plant Biology 2014, Portland, Oregon, Jul 12-16, 2014
- [161] Exploring protein interfaces: Steered molecular dynamics and free energy calculations to rank protein-protein docking poses. L.J. Kingsley, J. Esquivel-Rodriguez, D. Kihara, M. Lill, Great Lakes Drug Metabolism & Disposition Group 2014 Meeting, Sheraton Indianapolis City Centre Hotel, Indianapolis, IN, May 15-16, 2014
- [159-160] Undergraduate Research Poster Symposium, Purdue University, April 8, 2014
- Logic patterns for finding functionally related genes in *Escherichia coli*, Ishita Khan, Tiange Dong, Linzi Chen, Weichuan Luo, D. Kihara
 - Interactive visualization of Gene Ontology hierarchy, Qing Wei, I. Khan, D. Kihara
- [156-8] The Office of Interdisciplinary Graduate Programs, Spring Reception Poster Presentation , Purdue University, April 2, 2014
- Assessing Protein Side - Chain Conformation Prediction Methods in Different Residue Environments, Lenna Peterson
 - Genome - scale Identification and Characterization of Moonlighting Proteins, Ishita Khan
 - Enhanced Electron Microscopy Fitting Using Markov Random Fields, Juan Esquivel-Rodriguez
- [155] 3D-SURFER 2.0: web platform for real-time comparison, visualization and characterization of protein surfaces" Y. Xiong, J. Esquivel-Rodriguez, L. Sael & D. Kihara, Annual Symposium of the Protein Society , Boston, MA, July 20-23, 2013
- [154] Biochemical characterization of an *Arabidopsis* pectin methylesterase AtPME3 and a pectin methylesterase inhibitor. F. Senechal, M. L'Enfant, JM Domon, E. Rosiau, P. Marcello, O. Surcouf, J. Esquivel-Rodriguez, A. Mareck, F. Guerineau, H-R. Kim, E. Bonnin, E. Jamet, J.

- Mravec, D. Kihara, M-C. Ralet, P. Lerouge, J. Pelloux, C. Rayon, The XI Cell Wall Meeting, Nantes, July 7-12, 2013
- [153] Characterization of cytosolic protein complexes in plants using multi-step chromatographic separation and quantitative mass spectrometry. U. Aryal, Y. Xiong, E. Mallery, M. Hall, J. Xie, D. Kihara, D. Szymanski. American Soc. for Mass Spectrometry, June 9-13, 2013, Minneapolis, MN.
- [152] Protein docking prediction guided by predicted protein-protein interface. D. Kihara, B. Li, J. Esquivel-Rodriguez, & D. La, 5th CAPRI (Critical Assessment of Predicted Interactions), Utrecht, the Netherlands, April 17-19, 2013.
- [151] Development of computational method for visualizing disordered regions during protein docking. Arthi Anand & D. Kihara, Undergraduate Research Poster Symposium, Purdue University, March 26, 2013.
- [150] EM-LZerD: EM Map Fitting for Multimeric Protein Complexes Using Rotation Invariant Surface Representation. J. E.-Rodriguez & D. Kihara Structural Analysis of Supramolecular Assemblies by Hybrid Methods, Keystone Symposia, Lake Tahoe, Mar 3-7, 2013.
- [149] Computational function prediction for moonlighting proteins. I Khan, M. Chitale, C. Rayon, D. Kihara. Sigma Xi Graduate Student/Post Doc Poster Competition, Purdue Univ, Feb.13, 2013.
- [148] Macromolecular structure modeling and electron microscopy fitting using 3D Zernike descriptors. D. Kihara, J. Esquivel-Rodriguez. Biophysical Society 57th Annual Meeting, February 2-6, 2013, Philadelphia, PA.
- [147] Next generation molecular surface representation for rapid global/local protein shape comparison, docking, and low-resolution data. D. Kihara, National Centers for Biomedical Computing (NCBC) Showcase, Nov. 8-9, Natcher Conference Center, Bethesda, MD
- [146] Local Similarity Search of Physicochemical Properties in Protein-Ligand Binding Sites. Lee Sael & Daisuke Kihara
Translational Bioinformatics Conference (TBC) 2012, Jeju Island, Korea, Oct 13-16, 2012
- [145] Novel quantitative proteomic methods to discover and localize protein complexes. U.K. Aryal, Y. Xiong, E. Mallery, M.C. Hall, J. Xie, D. Kihara, P.N. Baker, D. B. Szymanski 2012 Plant Genome Awardee Meeting, National Science Foundation, Arlington, VA, Sep. 6-7, 2012.
- [144] Biochemical characterization of an Arabidopsis pectin methylesterase AtPME3 and a pectin methylesterase inhibitor. F. Senechal, J-M Domon, M. L'Enfant, D. Tall-Ndoye, J. Esquievel-Rodriguez, F. Guerineau, HR Kim, E. Jamet, E. Bonnin, D. Kihara, M-C Ralet, J. Pelloux, C. Rayon
Gordon Conference on Plant Cell Wall, Colby College, Waterville, ME, August 5-10, 2012
- [143] Computational function prediction for moonlighting proteins. Ishita Khan, Meghana Chitale, Catherine Rayon, Daisuke Kihara
Automatic Function Prediction-Special Interest Group (AFP-SIG), ISMB Satellite meeting, Long Beach, CA, July 13-14, 2012
- [141-2] 3DSIG 2012, Structural Bioinformatics and Computational Biophysics, ISMB Satellite meeting, Long Beach, CA, July 13-14, 2012
- Fitting multimeric protein complexes into electron microscopy maps using 3D Zernike descriptors, Juan Esquivel-Rodriguez, Daisuke Kihara
 - Prediction of real-value fluctuation of globular proteins, Michal Jamroz, Andrzej Kolinski, Daisuke Kihara
- [140] A 'catalytic dimer' hypothesis for the synthesis of cellulose and other (1,4)-beta-glycans Nicholas C. Carpita (oral presentation), Anna T. Olek, Catherine J. Rayon, Lee Makowski, Shiyou Ding, Peter Ciesielski, Lake Paul, Subhangi Ghosh, Daisuke Kihara, Michael Crowley, Michael Himmel, Jeffrey Bolin
The 23rd International Conference on Arabidopsis Research (ICAR), Vienna, Austria, July 3-7, 2012

- [139] Logic Patterns of Homologous Genes Across Species. Lillian Liu, Huairuo Ren, Yu Leng, Meghana Chitale, Daisuke Kihara, 2012 Undergraduate Research and Poster Symposium, Purdue University, April 10 2012
- [138] Fitting multimeric protein complexes into electron microscopy maps using 3D Zernike descriptors.
Juan Esquivel-Rodriguez, Daisuke Kihara
6th International Conference on Structural Analysis of Supramolecular Assemblies by Hybrid Methods. Lake Tahoe, CA, March 14-18, 2012
- [137] Computational methods for multiple protein docking for asymmetric complexes.
J. Esquivel-Rodriguez, Daisuke Kihara
Biophysical Society 56th Annual Meeting, San Diego, California, Feb. 25-29, 2012
- [135-6] Sigma Xi Graduate Student Research Award Competition, Purdue University, Feb. 15, 2012
- Macromolecular structure modeling and electron microscopy fitting using 3D Zernike descriptors, J. Esquivel-Rodriguez & D. Kihara
 - In-depth performance evaluation of PFP and ESG sequence-based function prediction methods in CAFA 2011 experiment, I. Khan, M. Chitale, & D. Kihara
- [133-4] Purdue University Nano-Bio Student Symposium, Purdue University, Sept. 1, 2011
- Protein Docking Prediction Using Predicted Protein-Protein Interface, B. Li & D. Kihara
 - Multi-LZERD: Multiple Protein Docking for Asymmetric Complexes, J. E. Rodriguez & Kihara
- [130-2] International Conference on Intelligent Systems for Molecular Biology (ISMB), Vienna, July 17-19, 2011
- Binding ligand prediction by comparing local surface patches of potential pocket regions, L. Sael & D. Kihara
 - MULTI-LZERD: Multiple protein docking for asymmetric complexes, J. Esquivel-Rodriguez & D. Kihara
 - Functional coherence assessment for protein groups and its application to pathway assignment, M. Chitale, S. Palakodety & D. Kihara
- [127-9] 3D-SIG, International Conference on Intelligent Systems for Molecular Biology (ISMB), Vienna, July 15-16, 2011
- Binding ligand prediction by comparing local surface patches of potential pocket regions, L. Sael & D. Kihara
 - Rapid comparison and multimeric protein complex fitting for low-resolution electron microscopy data, D. Kihara, L. Sael & J. Esquivel-Rodriguez
 - MULTI-LZERD: Multiple protein docking for asymmetric complexes, J. Esquivel-Rodriguez & D. Kihara
- [126] Binding ligand prediction by comparing local surface patches of potential pocket regions.
L. Sael & D. Kihara
Automated Function Prediction (AFP) SIG, International Conference on Intelligent Systems for Molecular Biology (ISMB), Vienna, July 15-16, 2011
- [124-5] International Conference on Structural Genomics, May 10-14, 2011, Toronto, Canada.
- Rapid comparison and multimeric protein complex fitting for low-resolution electron microscopy data, J. Esquivel-Rodriguez, L. Sael & D. Kihara
 - Binding ligand prediction by comparing local surface patches of potential pocket regions, L. Sael & D. Kihara
- [121-3] 2011 Undergraduate Research and Poster Symposium, April 12 2011, North Ball Room, Purdue Memorial Union, Purdue University
- Fast identification of interacting proteins by considering shape and sequence features. Roshna Agarwal, Lee Sael, & D. Kihara.
 - SiteHunter: Interactive web application for determining protein ligand binding site location Yinlong Jin, R. Ren, K. Modi, S. Jain, D. La, & D. Kihara.

- Mining association between gene ontology terms by using protein-protein interaction networks. Satwica Yersini, Meghana Chitale & D. Kihara.
- [120] General framework for multiple protein docking. Juan Esquivel-Rodriguez, D. Kihara
Interdisciplinary Graduate Program Spring Reception, PMU, Purdue Univ., April 20, 2011
- [117-9] 3 poster presentations at Discovery Park Student Poster Session, April 6, 2011, Hall for Discovery and Learning Research (DLR), Purdue University
- Information theoretical approaches for protein sequences and structure. Yingfei Ma, & D. Kihara
 - SiteHunter: Interactive web application for determining protein ligand binding site location. Yinlong Jin, R. Ren, K. Modi, S. Jain, D. La, D. Kihara.
 - Docking low-resolution cryo-EM density maps aided by structural homology searching Wansuk Lim, L. Sael, D. Kihara.
- [115-6] Biophysical Society 55th Annual Meeting, Baltimore, Maryland, March 5-9, 2011.
- Novel methods for rapid comparison and multimeric protein complex fitting for low resolution electron microscopy data, Lee Sael, J. Esquivel-Rodriguez, D. Kihara
 - Local protein surface patch method for protein-ligand binding prediction, Lee Sael, J. Esquivel-Rodriguez, D. Kihara
- [111-4] The 21st International Conf. on Genome Informatics, Hangzhou, China, Dec. 16-18, 2010.
- Performance of SUPRB Threading Method in CASP9, M. Kurcinski, D. Kihara
 - Multiple Protein Docking for Asymmetric Hetero Oligomeric Complexes, J. Esquivel-Rodriguez, Y. Yang, D. Kihara
 - Functional coherence for protein groups by considering associations between gene ontology terms. Meghana Chitale, Shriphani Palakodety, D. Kihara
 - Protein Docking Prediction Using Predicted Protein-Protein Interface, B. Li, D. Kihara
- [110] A novel method for protein-protein interaction site prediction with phylogenetic substitution models.
David La, D. Kihara
The 24th Annual Symposium of the Protein Society, San Diego, CA, USA. August 1-5, 2010
- [109] Multiple protein docking prediction based on genetic algorithms and physics based scoring.
Juan Esquivel-Rodriguez, D. Kihara
18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Boston, MA, July 11-13, 2010
- [108] Multiple Protein Docking Prediction Method Which Can Handle Asymmetric Hetero Oligomeric Complexes.
J. Esquivel-Rodriguez, Y. Yang, D. Kihara
3D-SIG, ISMB 2010, Boston, MA, July 9-10, 2010
- [107] Fitting Multimeric Complexes into Cryo-EM Maps Using Protein Docking Procedure and 3D Zernike Descriptors
D. Kihara, J. Esquivel-Rodriguez, L. Sael
3D-SIG, ISMB 2010, Boston, MA, July 9-10, 2010
- [102-6] 2010 Undergraduate Research Poster Symposium, Purdue University, Apr 7, 2010
- Why is there a limited number of protein fold in nature?, A. Magner, Y. D. Yang, & D. Kihara
 - Classification of local surface shape of ligand binding pockets, G. Martinez, Sael L. & Kihara
 - Structure-basis for protein-DNA interaction, William Hoffmann, & D. Kihara
 - Detecting surface shape complementarity for quick identification of interacting proteins, Paul Justin Tack, Roshna Agarwal, Sael Lee, D. Kihara
 - Conservation of sequence and atomic interactions in ligand binding sites of proteins, Sang Wook Lee, Sael Lee, D. Kihara
- [101] Comparative study of protein structure prediction methods
Priyanka Surana, D. Kihara
18th Undergraduate Research Day, Dept. of Biological Sciences, Purdue Univ. Apr. 3, 2010

- [100] A unified protein docking procedure with a shape complementarity screening using 3D Zernike descriptors
D. Kihara, V. Venkatraman, YD Yang, L. Sael
Biophysical Society meeting, San Francisco, CA, Feb 20-24, 2010
- [99] A unified protein docking procedure with a shape complementarity screening using 3D Zernike descriptors and ranking by physics-based scoring.
D. Kihara, J. Esquivel-Rodriguez, V. Venkatraman, D. La, Y.D. Yang, L. Sael, B. Li, S. Ueng, S. Ahrendt.
CAPRI Critical Assessment of Predicted Interactions 4th Evaluation Meeting, Barcelona, Spain, Dec 9-11, 2009
- [98] www.EcoliHub.org: An information resource for experimentation and modeling of E. coli K-12
BL Wanner, WG Aref, T. Conway, KA Datsenko, SC Ess, MR Gribskov, JC Hu, D Kihara, H Mori, D Siegele, DR Whitaker
American Society for Microbiology, May 17-21, 2009, Philadelphia, PA
- [97] N terminal Gly224-Gly411 domain in Listeria adhesion protein (LAP) interacts with receptor Hsp60
B. Jagadessan, D La, D Kihara, AK. Bhunia
American Society for Microbiology, May 17-21, 2009, Philadelphia, PA
- [96-99] The 21st Undergraduate Research Conference at Butler University, Butler University, Indianapolis, IN, April 17, 2009
- Computational protein function prediction, Gregg Thomas & D. Kihara
 - Protein Tertiary Structure Universe Viewed from the Perspective of Surface Shape, Matt Herron & D. Kihara
 - Comparative study of tertiary structure prediction methods, Priyanka Surana & D. Kihara
- [94-95] Biophysical Society Meeting, March 4, 2009, Boston MA.
- Local surface-based protein function prediction using Zernike descriptors. D. Kihara, Sael Lee, Rayan Chikhi
 - Threading without optimizing weighting factors for scoring function. Yifeng D Yang, C. Park, D. Kihara.
- [90-93] Sigma-Xi Graduate Student poster presentation, Stewart Center, Purdue Univ., Feb 18, 2009.
- Threading without optimizing weighting factors for scoring function. Yifeng D Yang, C. Park, D. Kihara.
 - Improvement of template-based protein structure prediction by suboptimal alignments. Hao Chen, D. Kihara.
 - ESG: Extended similarity group method for automated protein function prediction. Meghana Chitale, C. Park, D. Kihara.
 - Protein Representation for Efficient Comparison of Surface Properties. Sael Lee, Bin Li, David La, Raif Rustamov, D. Kihara.
- [89] EcoliHub: An information resource for experimentalists and modelers.
D.R. Whitaker, W. G. Aref, K.A. Datsenko, S. Ess, M.R. Gribskov, D. Kihara, S. Kim, H. Mori, A. Roumani, B.L. Wanner
Intelligent Systems for Molecular Biology (ISMB) 2008, July 19-23, 2008, Toronto, Canada
- [88] ESG: Extended Similarity Group Method for improved automated protein function prediction.
M. Chitale, T. Hawkins, C. Park, D. Kihara
Invited oral presentation at Automated function prediction special Interest Group at ISMB 2008 (AFP/Biosapiens 2008), July 18-19, Toronto, Canada
- [87] Automated protein function prediction using Extended Similarity Group (ESG) of sequences.
M. Chitale, T, Hawkins, C. Park & D. Kihara
Intelligent Systems for Molecular Biology (ISMB) 2008, July 19-23, 2008, Toronto, Canada
- [86] Ecolihub: Development of the www.ecolicommunity.org Information resource. B.L. Wanner, W.G. Aref, K. Datsenko, S. Ess, M.R. Gribskov, D. Kihara, S. Kim, H. Mori, D. R. Whitaker

- American Society for Microbiology, 108th General Meeting, Boston
June 1-5, 2008
- [85] A fast methodology for high throughput comparison of tertiary structure and physicochemical properties
Sael Lee, Bin Li, David La, Raif Rustamov, Daisuke Kihara
The Computer Research Institute Poster Session, Purdue-Industry High Performance Computing Workshop, Purdue Memorial Union, Purdue Univ., April 6, 2008.
- [84] Disorder region prediction of E. coli proteins.
Rupal Trivedi, Yifeng Yang, D. Kihara.
Undergraduate Research and Poster Symposium, College of Science, Purdue University, Purdue Memorial Union, March 31, 2008.
- [83] Computational modeling of ABC transporters.
Priyanka Surana, Yifeng Yang, D. Kihara.
Undergraduate Research and Poster Symposium, College of Science, Purdue University, Purdue Memorial Union, March 31, 2008.
- [82] A fast methodology for high throughput comparison of tertiary structure and physicochemical properties.
D. Kihara, Sael Lee, Bin Li, David La & Raif Rustamov
Meeting of the Biophysical Society 52nd Annual Meeting and 16th International Biophysics Congress, Long Beach, CA
February 2-6, 2008.
- [81] Predicting the error of template-based protein structure modeling by suboptimal alignment stability.
Hao Chen & D. Kihara
Meeting of the Biophysical Society 52nd Annual Meeting and 16th International Biophysics Congress, Long Beach, CA
February 2-6, 2008.
- [80] High-throughput function assignment for proteomics datasets with PFP.
T. Hawkins, M. Chitale & D. Kihara.
The 21st Symposium of the Protein Society, Boston, MA
July 21-25, 2007
- [79] Protein surface representation for fast comparison of tertiary structure and physicochemical properties.
S. Lee, B. Li, D. La, R. Rustamov & D. Kihara.
The 21st Symposium of the Protein Society, Boston, MA
July 21-25, 2007
- [78] Functional enrichment of proteomics datasets with PFP.
T. Hawkins, M. Chitale, S. Luban & D. Kihara.
ISMB 2007, Vienna, Austria.
July 21-25, 2007
- [77] Using sequence similarity scores for automatic gene function annotation in the biomedical literature.
L. Si, D. Yu, D. Kihara & Y. Fang
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [76] Estimating quality of template-based protein models by alignment stability (selected for oral presentation).
H. Chen & D. Kihara
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.

- [75] Threading without training weighting factors for scoring functions.
Y.D. Yang & Daisuke Kihara.
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [74] EcoliPredict: structure modeling of E. coli proteome.
P. Spratt, S. Krawczyk, Y.D. Yang & Daisuke Kihara.
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [73] Local geometry characterization of protein surfaces with the visibility criteria.
B. Li, S. Turuvekere, M. Agrawal, K. Ramani & Daisuke Kihara.
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [72] A fast methodology for high throughput comparison of tertiary structure and physicochemical properties.
Sael Lee, David La, Bin Li, Raif Rustamov & Daisuke Kihara.
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [71] Development of methods for missing enzyme/gene prediction with PFP.
Meghana Chitale, Troy Hawkins, & Daisuke Kihara.
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [70] Function prediction for proteomics datasets using PFP.
Troy Hawkins, Meghana Chitale, & Daisuke Kihara.
Indy'07: Indy Regional Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 31-June 2, 2007.
- [69] Structure modeling of E. coli proteome: Quality evaluation.
Preston Spratt, Steve Krawczyk, Yifeng Yang & Daisuke Kihara.
The Computer Research Institute Poster Presentation, Atrium of MSEE building, Purdue University.
April 5, 2007
- [68] Benchmark of new amino acid similarity matrices on recognition of distant protein structures.
Yu-Hsuan Rex Cheng, Hao Chen & Daisuke Kihara.
2007 Undergraduate Research and Poster Symposium, College of Science, Agriculture, Engineering, and Technology, Purdue University.
April 4, 2007.
- [67] Structure modeling of E. coli proteome: Quality evaluation.
Preston Spratt, Steve Krawczyk, Yifeng Yang & Daisuke Kihara.
2007 Undergraduate Research and Poster Symposium, College of Science, Agriculture, Engineering, and Technology, Purdue University.
April 4, 2007.
- [66] Structure modeling of E. coli proteome: Homology models.
Steve Krawczyk, Preston Spratt, Yifeng Yang & D. Kihara
2007 Undergraduate Research and Poster Symposium, College of Science, Agriculture, Engineering, and Technology, Purdue University.
April 4, 2007.
- [65] Structure modeling of E. coli proteome: Quality Evaluation

- Preston Spratt, Steve Krawczyk, Yifeng Yang & Daisuke Kihara.
Dept. of Biological Science Undergraduate Research Presentation, Purdue University,
March 31, 2007.
- [64] PFP: Sequence-based annotation of sequences and local sequence motifs with contextual GO term association
Troy Hawkins, Stan Luban, David La & Daisuke Kihara
Automated Function Prediction meeting, 2006, UC San Diego, San Diego, CA.
Aug 30 – Sep 1, 2006.
- [63] EMD: an ensemble DNA regulatory motif discovery algorithm for Grid computing.
Yifeng D. Yang, Jianjun Hu & Daisuke Kihara.
TeraGrid '06, Indianapolis University Purdue University Indianapolis, Indianapolis, IN,
June 12-15, 2006.
- [62] Template-based protein structure prediction with a reliability measure for structural genomics era.
Hao Chen, Yen Hock Tan, & Daisuke Kihara.
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006.
- [61] Ligand binding site prediction with the visibility criteria.
Bin Li, S. Thruvekere, M. Agrawal, K. Ramani & Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006.
- [60] Multi-resolution protein representation for fast protein structure searching.
Sael Lee, Bin Li, David La, Raif Rustamov, & Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006.
- [59] On the effect of long-range interactions on the secondary structure formation of proteins.
Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006
- [58] Coiled-coil structures in E. coli interactome.
Stan Luban, Akiyasu Yoshizawa & Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006
- [57] Neural network based protein domain prediction.
Yen Hock Tan, Otoniel Venezuela, Evans A. Tapia & Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006.
- [56] Statistical potential-based amino acid similarity matrices for aligning distantly related protein sequences.
Yen Hock Tan, He Huang & Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006
- [55] Accounting for natural flexibility in protein structure prediction comparisons.
Jairav Desai & Daisuke Kihara
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.

- May 19-20, 2006
- [54] EcoliPredict: bioinformatics prediction resource for EcoliHub.
Barry Wanner, Daisuke Kihara, Troy Hawkins & Yifeng D. Yang
The Third Annual Indiana Bioinformatics Conference, Center for Computational Biology and Bioinformatics, Indiana Univ. School of Medicine.
May 19-20, 2006
- [53] EcoliPredict: bioinformatics prediction resource for EcoliHub
Barry Wanner, Daisuke Kihara, Troy Hawkins and Yifeng D. Yang
American Society for Microbiology ASM-FEMS Conference on Protein Traffic in Prokaryotes, Crete, Greece
May 6-10, 2006
- [52] Using Neural Network in Protein Domain Prediction.
Yen Hock Tan and Daisuke Kihara
Undergraduate Research & Poster Symposium, College of Science, Purdue University
April 11, 2006
- [51] Using Neural Network in Protein Domain Prediction.
Yen Hock Tan and Daisuke Kihara
14th Annual Undergraduate Research Day, Dept. of Biological Sciences, College of Science, Purdue University
April 1, 2006
- [50] Including natural protein flexibility in predicted protein structure comparisons.
Jairav Desai and Daisuke Kihara
14th Annual Undergraduate Research Day, Dept. of Biological Sciences, College of Science, Purdue University
April 1, 2006
- [49] Protein structure-sequence alignment with a reliability measure.
Hao Chen and Daisuke Kihara
Sigma Xi Graduate Student Research Poster Presentation, Purdue University
February 14, 2006
- [48] A New Perspective on an Old Tool: Extending the Coverage of Sequence Similarity-Based Function Prediction with PFP.
Troy Hawkins, Stan Luban and Daisuke Kihara
Sigma Xi Graduate Student Research Poster Presentation, Purdue University
February 14, 2006
- [47] Bridging geometric protein surface features and phylogenetic information for rapid identification of protein-protein interaction interfaces.
David La, Denis Liversay and Daisuke Kihara
Sigma Xi Graduate Student Research Poster Presentation, Purdue University
February 14, 2006
- [46] Multi-resolution protein representation.
Sael Lee, Bin Li, David La, Raif Rustamov and Daisuke Kihara
Sigma Xi Graduate Student Research Poster Presentation, Purdue University
February 14, 2006.
- [45] Ligand Binding Sites Prediction with the Visibility Criteria.
Bin Li, Srinivasan Turuvekere, Manish Agrawal, Karthik Ramani and Daisuke Kihara.
Sigma Xi Graduate Student Research Poster Presentation, Purdue University
February 14, 2006
- [44] EMD: An ensemble algorithm for discovering regulatory motifs in DNA sequences.
Yifeng D. Yang, Jianjun Hu, and Daisuke Kihara.
Sigma Xi Graduate Student Research Poster Presentation, Purdue University
February 14, 2006

- [43] A New Perspective on an Old Tool: Extending the Coverage of Sequence Similarity-Based Function Prediction with PFP.
Troy Hawkins, Stan Luban and Daisuke Kihara
16th International Conference on Genome Informatics, Yokohama, Japan
December 19-21, 2005
- [42] Ligand Binding Sites Prediction with the Visibility Criteria.
Bin Li, Srinivasan Turuvekere, Manish Agrawal, Karthik Ramani and Daisuke Kihara
16th International Conference on Genome Informatics, Yokohama, Japan
December 19-21, 2005
- [41] Protein-Protein Docking Algorithm Using Preidentified Binding Site Patches.
Daisuke Kihara, Sael Lee, Karthik Ramani, Srinivasan Turuvekere, Manish Agrawal, And Bin Li
16th International Conference on Genome Informatics, Yokohama, Japan
December 19-21, 2005
- [40] Dependence of the Accuracy of Protein Secondary Structure Prediction on Long-Range Interactions.
Daisuke Kihara
16th International Conference on Genome Informatics, Yokohama, Japan
December 19-21, 2005
- [39] Evaluation and development of protein function prediction.
Stan Luban, Troy Hawkins and Daisuke Kihara (Oral presentation)
16th Annual Argonne Symposium for Undergraduates in Science, Engineering and Mathematics, Argonne National Laboratory, Argonne, Illinois
November 4th, 2005
- [38] Using neural network in protein domain prediction.
Yen Hock Tan, Adolfo Tapia, Otoniel Venezuela, and Daisuke Kihara (Oral presentation)
16th Annual Argonne Symposium for Undergraduates in Science, Engineering and Mathematics, Argonne National Laboratory, Argonne, Illinois
November 4th, 2005
- [37] BioQ: A 3D Querying Engine for Proteins.
Athurva Gore, Bin Li, Karthik Ramani & Daisuke Kihara
Summer Undergraduate Research Fellowship (SURF) Poster Presentation, College of Engineering, College of Science, Purdue University.
August 2, 2005
- [36] Protein-protein Interaction Data Assessment.
Ei Ei Phyu & Daisuke Kihara
Summer Undergraduate Research Fellowship (SURF) Poster Presentation, College of Engineering, College of Science, Purdue University.
August 2, 2005
- [35] Comparison of distantly related protein sequence alignments with multiple amino acid similarity matrices.
Yen Hock Tan & Daisuke Kihara
Summer Undergraduate Research Fellowship (SURF) Poster Presentation, College of Engineering, College of Science, Purdue University.
August 2, 2005
- [34] Comparative study of small RNAs and small peptides in complete genome sequences.
Stan Luban & Daisuke Kihara
Summer Undergraduate Research Fellowship (SURF) Poster Presentation, College of Engineering, College of Science, Purdue University.
August 2, 2005.
- [33] Protein Structure Prediction with ZDock 2.3.

- Luis Avila, Bin Li & Daisuke Kihara
 Marc/Aim Research Presentation, Burton Morgan Center for Entrepreneurship, Purdue University.
 July 28 ,2005
- [32] PFP: Automatic annotation of protein function by relative GO association in multiple function prediction methods.
 Troy Hawkins & Daisuke Kihara
 ISMB, Detroit, Michigan, June 25 – 29, 2005.
- [31] Protein Structure-Sequence Alignment with a Reliability Measure.
 Hao Chen, Yen Hock Tan & Daisuke Kihara.
 Midwest Computational Structural Biology Workshop, Brook Lodge,
 Michigan State University, Augusta, Michigan
 April 30 – May 1, 2005
- [30] Comparing Tertiary Structures of Protein Active Sites.
 Yuhao Lin and Daisuke Kihara.
 Undergraduate Research Day, College of Science & College of Agriculture ,Purdue University.
 April 11, 2005
- [29] Comparative Study of Small RNA and Small Peptides in Complete Genome Sequences.
 Stan Luban and Daisuke Kihara.
 Undergraduate Research Day, College of Science & College of Agriculture, Purdue University.
 April 11, 2005.
- [28] Computer Graphics Program in Foreign Language Instruction.
 Ei Ei Phyu, Kazumi Hatasa and Daisuke Kihara.
 Undergraduate Research Day, College of Science & College of Agriculture ,Purdue University.
 April 11, 2005.
- [27] Comparison of Distantly Related Protein Sequence Alignments with Multiple Amino Acid Similarity Matrices.
 Yen Hock Tan and Daisuke Kihara.
 Undergraduate Research Day, College of Science & College of Agriculture ,Purdue University.
 April 11, 2005.
- [26] Structure-basis of protein-protein interaction.
 Brian Trisler and Daisuke Kihara.
 Undergraduate Research Day, College of Science & College of Agriculture ,Purdue University.
 April 11, 2005.
- [25] Comparative Study of Small RNA and Small Peptides in Complete Genome Sequences.
 Stan Luban and Daisuke Kihara
 The 13th Annual Undergraduate Research Day at Dept. of Biological Sciences,
 Purdue University.
 April 2, 2005
- [24] A structured approach to computational protein function prediction.
 Troy Hawkins and Daisuke Kihara
 Sigma Xi Graduate Student Research Poster Presentation, Purdue University
 February 17, 2005
- [23] Protein Structure-Sequence Alignment with a Reliability Measure.
 Hao Chen and Daisuke Kihara
 Sigma Xi Graduate Student Research Poster Presentation, Purdue University
 February 17, 2005
- [22] A novel method to construct phylogenetic tree based on complete genome sequences.
 Bin Li and Daisuke Kihara
 Sigma Xi Graduate Student Research Poster Presentation, Purdue University
 February 17, 2005
- [21] Conserved structural non-coding RNA families in Gamma-proteobacteria

- Stan Luban and Daisuke Kihara (Oral presentation)
15th Annual Argonne Symposium for Undergraduates in Science, Engineering and Mathematics,
Argonne National Laboratory, Argonne, Illinois
November 5th, 2004
- [20] Improvement of protein sequence alignments for better protein structure prediction.
Yen Hock Tan and Daisuke Kihara (Oral presentation)
15th Annual Argonne Symposium for Undergraduates in Science, Engineering and Mathematics,
Argonne National Laboratory, Argonne, Illinois
November 5th, 2004
- [19] Computational Prediction of Protein Structures and Functions.
Otoniel Venezuela, Troy Hawkins, Evans Tapia, Yen Hock Tan and Daisuke Kihara
Faculty Poster Session, Dept. of Computer Sciences, Purdue University
Stewart Center, Purdue University, 20 September, 2004.
- [18] Computational Prediction of Protein Structures and Functions.
Otoniel Venezuela, Troy Hawkins, Evans Tapia, Yen Hock Tan and Daisuke Kihara
PULSe Program retreat, Purdue University
28 August 2004.
- [17] Feature recognition based identification of potential binding sites on the molecular surfaces.
Srinivasan Turuvekere, Manish Agrawal, Daisuke Kihara, and Karthik Ramani.
The Protein Society 18th Symposium. San Diego, August 14-18, 2004.
- [16] Comparative Study of Structural Non-coding RNAs in Microbial Genomes.
Stanislav Luban and Daisuke Kihara
First Annual Indiana Bioinformatics Conference.
IUPUI, Indianapolis, 27 May, 2004.
- [15] Real-Time Manipulation of Keyframe Animation.
Brian Seckinger, Rodney Weaver and Daisuke Kihara
School of Science Undergraduate Research Day, Purdue University
Purdue University, 17 April, 2004.
- [14] A Web-Interface for a Database of Microbial Intergenic Sequences.
Jason Pardieck and Daisuke Kihara
School of Science Undergraduate Research Day, Purdue University
Purdue University, 17 April, 2004.
- [13] Comparative Study of Structural Non-Coding RNAs
Stanislav Luban and Daisuke Kihara
School of Science Undergraduate Research Day, Purdue University
Purdue University, 17 April, 2004.
- [12] Computational prediction and experimental validation of iron and phosphate gene regulatory sites
in the *Escherichia coli* K-12 and *Pseudomonas aeruginosa* PA01 genomes.
Sam-Il Jung, Kaushik M. Setty, Khurram Siddiqi, Lu Zhou, Barry L. Wanner and Daisuke Kihara
International Workshop for *Escherichia coli* Towards New Biology in the 21st Century.
Awaji-shima, Japan, 15-17 October, 2003.
- [11] All-against-all protein structure comparison reveals the current database (PDB) is a covering set
of small protein structures.
Daisuke Kihara and Jeffrey Skolnick
Corporate Partner Faculty Poster Session, Department of Computer Sciences, Purdue University.
the Buchanan Club at Ross-Ade Stadium, Purdue University, 15 September, 2003.
- [10] PDB is a covering set of a single-domain protein structures.
Daisuke Kihara and Jeffrey Skolnick
Frontiers in Bioinformatics Symposium, Buffalo NY
5-8 June, 2003
- [9] Classification and Analysis of Eukaryotic ABC Transporters in Complete
Eukarya Genomes.

- Yoshinobu Igarashi, Daisuke Kihara and Minoru Kanehisa
Genome Informatics 11: pp .274-275, Universal Academy Press, Tokyo (2000)
- [8] Classification and Analysis of Eukaryotic ABC Transporters in Complete Eukarya Genomes.
Yoshinobu Igarashi, Daisuke Kihara and Minoru Kanehisa
The Cold Spring Harbor Laboratory Meeting (New York, May 2000)
- [7] Detection of Membrane Proteins in the Whole Genome Sequences.
Daisuke Kihara and Minoru Kanehisa
Genome Informatics 1997, pp.300-301, Universal Academy Press, Tokyo (1997)
- [6] Systematic Analysis of Enzyme Structures and Metabolic Pathways.
Daisuke Kihara and Minoru Kanehisa
18th Annual Meeting of Molecular Biology Society of Japan (1997)
- [5] Prediction Method of Transmembrane Segments in Proteins Using Multiple Discrimination Functions.
Daisuke Kihara and Minoru Kanehisa
35th Annual Meeting of the Biophysical Society of Japan. P.172 (1997)
- [4] A Prediction Method for Transmembrane Segments in Proteins Utilizing Multiple Discrimination Functions.
Daisuke Kihara, Toshio Shimizu and Minoru Kanehisa
Genome Informatics 1996, pp.244-245, Universal Academy Press, Tokyo (1996)
- [3] Prediction of Transmembrane Segments in Proteins Using Characteristics by their Numbers and Positions.
Daisuke Kihara and Minoru Kanehisa
17th Annual Meeting of Molecular Biology Society of Japan, p.140 (1996)
- [2] Analysis of Transmembrane Helices by the Number, Hydrophobicity and Amphipathy.
Daisuke Kihara and Minoru Kanehisa
33rd Annual Meeting of the Biophysical Society of Japan p.175 (1995)
- [1] Preparation and Characterization of Monoclonal Antibodies Specific for N-terminal Fatty Acids of Transducin Alpha-Subunits.
Koichi Kokame, Osamu Shono, Daisuke Kihara, Yoshitaka Fukada, Masasuke Araki, Toshifumi Takao, Yasutsugu Shimonishi, and Toru Yoshizawa
17th Annual Meeting of the Japanese Biochemical Society, p.1067 (1994)

Research Support

Current:

Collaborative Research: Efficient mathematical and computational framework for biological 3D image data retrieval

(NSF, Mathematical Biology, \$542,383 total, 6/1/2016-5/31/2019) Role: PI

ABI Innovation: Protein functional site identification using sequence variation.

(NSF, ABI, 06/01/2013-05/31/2016, \$480,195) Role: PI

III: Small: Rapid screening of interacting ligands and proteins.

(NSF, \$492,509 total, 8/1/2013-7/31/2016) Role: PI

Novel quantitative proteomic methods to discover and localize endogenous protein complexes.

(NSF, IOS, 10/01/2011-09/30/2015, \$1,709,230 total) Role: co-PI (PI: D. Szymanski)

Deep learning for 3D protein target – drug interaction

(NVIDIA Academic Hardware Grant, one Tesla K40 GPU (~\$3200 value)) Role: PI

Completed Grants

Identification of protein-metabolite interactome.

(NIH, R01, 9/1/2011-05/31/2016, \$1,118,554, total), PI

Designing new ligands for new targets through novel computational methods for binding site characterization.

(Eli Lilly, \$244,969 total, 3/1/2013-4/12/2016) Role: PI

Research Support.

(Eli Lilly, \$42,643 total, 1/1/2015-5/31/2015) Role: PI

Information Transfer in Biological Systems.

(NSF, DMS, 06/01/2008-05/31/2014, \$480,000) Role: co-PI, (PI: Wojciech Szpankowski)

Development of RAVAT: the tool that uncovers the roles of rare variants and their functions on common diseases with next generation sequencing data.

(Global Research Network Program, 2012-2015, 300 million KRW total) Role: co-PI (PI: C. Park)

Template-based protein structure prediction beyond sequence homology.

(NSF, ABI, \$716,001, 06/01/2009-05/31/2013) Role: PI

Surface shape based screening of large protein databases.

(Agency: NIH, R01, Total: \$1,408,659 direct cost, 09/01/2005-08/31/2012, no-cost extension to 2012)

Role: PI

III: Small: Quality assessment of computational protein models.

(NSF, IIS, \$327,606, 09/01/2009 – 08/31/2012) Role: PI

Elucidating genetic pathways for curing retinal degeneration

(Showalter Trust, \$75,000, 6/1/2010-5/31/2012) Role: co-PI, (PI: Yuk Fai Leung)

Comprehensive mapping and annotation of the E. coli Transcriptome.

(NIH, Challenge Grant RC1, \$100,000 total 10/01/2009 – 09/30/2011). Role: co-PI (PI: B. Wanner)

Protein 3D Structure-based rational drug discovery.

(Purdue Res. Foundation, \$1,675,000, 09/01/09 – 08/31/10), Role: PI

Recovery Act administrative Supplement. Parent grant: U24 GM077905-03 Development of the www.EcoliCommunity.org Information Resource.

(NIH, 4/1/09 – 6/30/09, \$410,000 direct) Role: co-PI, (PI: Barry Wanner)

Computational proteomics approaches for rational drug design.

(Computing Research Institute, Purdue University, CRI PRF-SIRG, \$16,375, (7/1/2008- 6/30/2009)

Bayesian models and Monte Carlo strategies in identifying protein or DNA sequence motifs.

(Agency, NSF, Dev. of Math. Sci, \$ 160,246, 7/1/2006-6/30/2009, PI: Jun Xie) Role: co-PI

Development of the www.ecolicommunity.org Information Resource (Agency: NIH, Direct cost:

\$1,499,521, 4/01/2006-3/30/2009, PI: Barry Wanner) Role: co-PI

Protein Structure Prediction (Agdia Inc., direct cost: \$993.0, 3/1/2006-4/30/2006) Role: PI

Development of a Protein sequence-structure alignment method for distantly related proteins. (PRF Summer Faculty Grant, Total \$7,000 direct cost, 06/01/2005-08/31/2005) Role: PI

Structure Basis of Protein-Protein Interactions. (Purdue Alumni Association, Incentive Grants Program, Total \$500 direct cost, 6/01/2005-12/31/2005) Role: PI

Supervised Postdocs

Current

Woong-Hee Shin (PhD in Chemistry), August 2014 – current

Genki Terashi (PhD in Pharmaceutical Sciences) April 2017 - current

Former postdocs

Hyungrae Kim (PhD in physics), September 2011 – August 2016

Jian James Zhang (PhD in Chem. Engineering), August 2014 – May 2015, Zymoworks Inc.

Amit Roy (PhD in physics), December 2013 – December 2015, computational structure biologist, NIH Rocky Mountain Laboratories

Atila Sit (PhD in Appl. Math) Sept. 2012 – July 2014, assistant professor, Eastern Kentucky University, Department of Mathematics

Xiaolei Zhu (PhD in Chem. Engineering), July 2012 – June 2014, assistant professor, Anhui University, China

Bingjie Hu (PhD in Pharmacy), Sept. 2013- May 2014, research scientist at Merck

Yi Xiong (PhD in CS), January 2012 – December 2013, assistant professor, Shanghai Jiaotong University, Shanghai, China

Choi Youn Im (PhD in Statistics), March 2012 – March 2013, research scientist at the Department of Statistics, Chung-Ang University, Seoul, Korea

Sael Lee (PhD in CS, Purdue) August 2010 – July 2011, moved on to researcher at Samsung, Korea, currently assistant professor at CS, SUNY Korea

Mateusz Kurcinski (PhD in Chemistry) March 2010 – March 2011, postdoc at Warsaw University, Chemistry

Vishwesh Venkatraman (PhD in Comp. Chemistry) September 2007 – July 2009, moved onto research scientist at LORIA, France, currently postdoctoral fellow at Dept. of Chemistry, Norwegian Univ. of Sci & Tech, Norway

Jianjun Hu (PhD in CS) Sept. 2004 – August 2005 Currently associate professor in Dept. of Computer Science and Engineering, University of South Carolina

Past Visiting Scholar

Genki Terashi, Junior Associate Professor, School of Pharmacy, Kitasato University, Tokyo, Japan, April 2015 – March 2017 (continuing as a postdoc)

Xinyuan Zhou, Assistant Professor, Dept. of Comp. Science & Technology, Changsha University, China March-December 2015

Catherine Rayon, Professor, Dept. of Biology, Universite de Picardie Jules Verne, France January – May 2012

Uttamkumar Samanta, October 2012 – May 2013

Hangchang Lee, Associate Professor, Dept. of Multi-media Engineering, Hangeung University, Seoul, Korea, Jan. 1. 2009 – May 2009

Changsoon Park, Full Professor at Statistics Dept., Chung-Ang University, Seoul, Korea, Jan 3, 2008 – Feb 28 2008

Supervised programmer

Michael Gillogly: August 2009 – April 2010
Stan Luban: January 2006 – June 2006
Yen Hock Tan: June - August 2004

Supervised Students

Graduated with Ph.D.

Ishita K. Khan (CS, Summer 2016) currently at Ebay
Juan Esquivel (CS, Summer 2014), currently at Google
Meghana Chitale (CS, Spring 2013), currently software engineer at Epic
David La (Biol, Fall 2011) currently postdoc at David Baker lab, Univ. Washington, Seattle
Bin Li (CS, Fall 2011), currently postdoc at La Jolla Institute for Allergy & Immunology
Sael Lee (CS, July 2010) continued as postdoc, currently assistant professor at SUNY Korea, Dept. of CS
Hao Chen (Biol, May, 2010) currently bioinformatics programmer at Langone Medical Center, New York Univ.
Yifeng Yang (Biol, May 2010) currently senior quantitative analyst, Fifth Third Bank
Troy Hawkins, (Biol, October, 2008), currently research scientist at Eli Lilly, Indianapolis
Mingwu Zhang (CS, Fall 2006, co-supervised with Sunil Prabhakar), currently Microsoft

Graduated with MS

Yoichiro Togawa (Biology, Spring 2014), currently at Self Defense Force, Japan
Chao Yuan (PULSe, Spring 2012), MS student in Rice University, Computer Science, currently at Amazon

Current Graduate Students:

Aashish Jain (Biol)
Lenna Peterson (PULSe)
Xusi Han (PULSe)
Ziyun Ding (PULSe)
Lyman Monroe (Biol)
Mengmeng Zhu (PULSe)
Qing Wei (CS)
Charles Christoffer (CS)
Eman Alnabati (CS)
Israa Al-Qassem (CS)

Other Former Graduate Students in the Lab

Xuejiao Kang (CS), (8/12-5/15)
Kristen Johnson (CS) (8/13 – 5/14)
Hongyun Gao, 8/12, (Math, Sci, Dalian U. Tech, China, visiting PhD Student)
Muyi Liu (PULSe) (4-8/2012)
Kyle Krull (PULSe) (Spring 2004)
Mingwu Zhang (CS), (co-supervised with S. Prabhakar; 2004-2006)
Srinivasan S. Turuvekere (ME) (co-supervised with K. Ramani; 2004)

Shiqi Yang (Animal Science) Fall 2016
Xin Cheng (CS) (8/13-5/14)
Farrukh Arslan (ECE) (8/2009-5/2010)

Padmasini Chakravarthy (ECE) (2008-2009)
Mingjie Tang (CS) (8/10-8/11)
Manish Agrawal (ME) (co-supervised with K. Ramani; 2004)
Khurram Siddiqi (EE), (co-supervised with B.L. Wanner; Fall 2003)

Current Undergraduate Students

Hayley Chan (MCMP) Fall 2015-
Andrew Walden (Bio) Summer 2016-
Brian Lembong (Bio) Summer 2016-
Siddharth Prabhu (BME), Fall 2016-
Chelsea Kozel (Bio) Spring 2017-

Sarah Rodenbeck (Biol) Spring 2016-
Aditya Vaidyam (CS) Spring 2015-
Caleb Belth (CS) Fall 2015-
Natalie Oda (Bio) Spring 2017-
Matthew Muhoberac (CS) Spring 2017-

Former Undergraduate Students

Long-Term Research Project (2+ Semesters)

Stan Luban (Bio/CS) (Spring2004-Spring2006)

Ei Ei Phyu (CS), Spring/Fall 2005

Yen Hock Tan (CS) 2004-2006

Jennifer S Reeve (CS) (Summer 2004, 2011)

Rupal Trivedi (Bio) Fall 2007-Spring2008,
Spring 2010

Devin Luckett (Bio) Fall 2008 – Spring 2010

Paul Tuck (CS) Summer 2009 – Spring 2010

Nicket Gupta (CS) Fall 2009-Spring 2010

Malvika Mathur (Bio) Fall 2008 – Spring 2010

Abram Magner (CS/Math)Spring 09 – Spring 10

Matt Herron (Bio/CS) Summer 2008 – Spring 2010

Mi-Sun Kong (Bio) Fall 2010 - Fall 2011

William Hoffman (Biol) Spring 2010 –Spring 2011

Roshna Agrawal (CS) Spring 2010-Summer 2011

Su Lin Ooi (CS) Fall 2011- Summer 2012

Sam Yap (Biol) Spring 2012- Spring 2013

Chang Liu (Math, DURi) Fall 12-Spring 13

Guanqun Mao (CS, DURi) Fall 12-Spring 13

Xiaowei Hong (Biol) Summer 2012 – Spring 2013

Lillian Liu (CS) Spring 2012-Spring 14

Linzi Chen (Biol/Stat, HHMI) Spring'13-Spring 2014

Andrew Walden (Biol/CS) Fall 2014-Fall 2015

Weichuan Luo (Biol), Fall 2013-Spring 2015

Tiange Dong (Biol) Spring 2013-Fall 2015

Charles Christoffer (math/CS) Sprg14-Smr 15

Eric Petit (Biol) Fall 2014-Fall 2015

Josh McGraw (Biol) Summer 2015-Smr 2016

Rodney Weaver (CS) (Spring /Fall 2004)

Jairav Desai (CS, DURi*), 2005-2006

Steve Krawczyk (Bio), Fall 2006, Spring 2007

Preston Spratt (Bio), Fall 2006 – Spring 2008

Steven Ahrendt (Bio/CS) Fall 2008-
Spring 2009

Gregg Thomas (Bio) Summer 2008 – Fall 2009

Priyanka Surana (Bio) Fall 2007 – Spring 2010

Sangwook Lee (Bio) Fall 2009 – Spring 2010

Kunal Modi (CS) Fall 2009 – Fall 2010

Sajat Jain (CS) Fall 2009 – Fall 2010

Shriphani Palakodety (CS) Fall 2009 - Spring 2010

Sanmeet Kanhere (CS) Summer 2010 - Spring 2011

Xin Lu Tan (Stat) Fall 2010-Spring 2011

Benjamin Bastnagel (Bio) Spring 2011- Spring 2012

Yingfei Ma (Stat) Spring 2011-Spring 2012

Vianney Gonzalez (Math, DURi) Fall2012-Sprng 2013

Linsheng Shen (Bio, DURi) Fall 12-Spring 13

Yanan Tao (Biol) Fall 2012- Spring 2013

Minxian Li (CS, Beijing U of Chem Tech,
China) Fall 2012 – Spring 2013

Arthi Anand (Biol) Spring-Fall 2013

Fangyuan Hou (CS) Summer-Fall 2013

Qing Xu (Stat) Summer-Fall 2014

Qing Wei (CS), Spring 2014-Fall 2014

Ray Ji (Biol) Fall 2014-Fall 2015

Yue Wang (Stat) Spring 2014-Summer 2015

Tianzhao Wu (Biol) Fall 2014-Fall 2015

1 (One) Semester Research Project

Jason Pardieck (CS), Spring 2004

Danny Varghese (CS), Spring 2004

Jasmine Williams (MARC/AIM*), Sum.2004

Antonius Sardjito (CS) Summer 2004

Jonathan Williford (CS), Fall 2004

Yuhao Lin (Comp. Engng), Spring 2005

Jiyoung Lee (Bio) Fall 2005

Robert Helms (Bio), Fall 2006

De'Rael Darling (Marc/Aim) Summer 2007

Sparsh Shekhar (CS) Summer 2008

Emily Flynn (Bio) Fall 2008

Shen Liang (CS) Summer 2009

Roy Ren (CS) Fall 2009

Gabriel Martinez (CS) Spring 2010

Shuai Liu (CS) Fall 2010

Satwica Yerneni (Vellore I. Tech, India)SpG11

Liyun Fan (Biol) Spring 2011

Brian Seckinger (CS), Spring 2004

C. Sujjapong (Comp. Eng) (Summer 2004)

Irvan Sutiono (CS), Summer, 2004

Joel Hayburst (CS), Fall 2004

Brian Trisler (CS), Spring 2005

Luis Avila (MARC/AIM), Summer 2005

Howard Chang (CS), Summer 2006

Rex Chang (CS), Spring 2007

Stephen Ueng (CS) Fall 2007

Jared Bannister (CS/Math) Fall 2008

Subhash Atluri (CS) Summer 2009

En-hsun Liu (CS) Summer 2009

Gunjan Raghav (CS) Spring 2010

Yidi Wang (Bio) Fall 2010

Wei-Chia Sun (CS) Fall 10

Yilong Jin (CS) Spring 2011

Hayun Lee (Biol) Spring 2011

Qiting Wu (Bio) Spring 2011
Daniel Lee (BME) Fall 2011
Shing Jay Ong (CS) Fall 2011
Yang Shen (Bio) Spring 2012
Kara Kahue (CS, SROP), Summer 2012
Alex Gao (Stat) Fall 2012
Shawn Deboth (Biol) Spring 2013
Yuqian Chen (Biochem, DURl) Spring 2013
Grant Gumina (CS, DURl) Spring 2013
Tommy Lee (Spring 2015)
Hanfu Zhang (Tsinghua U, Summer 2015)
Alexander Engstrom (Biol) Spring 2016
Alexandre Dias (Fed U Lavras, Brazil) Smr2016

Gaonan Zhang (Bio) Spring 2011
Shucong Zhang (CS) Fall 2011
Zilong Zhou (Math) Fall 2011
Danny Antakli (Bio, HHMI) Summer 2012
Liuning Wang (Stat, DURl) Fall 2012
Wuwei Zhang (CS, DURl), Spring 2013
Aanchal Kanodia (VNIT-Nagpur, India) Sum13
Joel Crist (Biol) Summer 2013
Wen Sun (Biol) Fall 2013
Karan Dua (IIT Roorkee), Summer 2014
Ryan Hancock (Industr. Engng), Summer 2015
Morgan Farrell (Biol) Summer 2016
Shan Lu (BME) Fall 2016

Former Undergraduate Students who entered bioinformatics graduate program

Stan Luban (Biol/CS, graduated 2006) UC San Diego
Steven Ahrendt (CS, graduated 2009) UC Riverside
Priyanka Surana (Biol, graduated 2010) Iowa State University
Sangwook Lee (Biol, graduated 2010) Georgetown University
Devin Luckett (Biol, graduated 2010) New York University
Satwica Yersini (intern, Vellore Inst Tech, India, 2011) Indiana University
Devin Luckett (Biol, graduated 2010) New York University
Gregg Thomas (Biol, graduated 2011) Indiana University
Minxian Li (intern, 9/2012-5/2013, Beijing U of Chem. Tech), Iowa State University

K-12 Students

Aditi Acharya (West Lafayette High), Summer 2014-current
Katie Kranjak, Summer 2005 (high school student, Indiana Academy of Science)

Student Awards

- Ishita Khan, Best presentation/poster award, Function-SIG, ISMB, Orlando, Florida, July 9, 2016
- Lenna Peterson, Bilsland Dissertation Fellowship from the Purdue Graduate School, April, 2016.
- Lenna Peterson, PULSe Outstanding Student Publication of the Year Award, Purdue University, April 2015
- Juan Esquivel-Rodriguez, Best Flash Talk, Great Lakes Bioinformatics (GLBIO), Cincinnati, May 16-18, 2014
- Juan Esquivel-Rodriguez, Excellence in Research Award in Poster presentation by Office of Interdisciplinary Grad Programs, Purdue University, April 9, 2014
- Hyung-Rae Kim, travel award for the 10th meeting of Critical Assessment of Techniques for Protein Structure Prediction (CASP10), Gaeta, Italy, December 9-12, 2012
- Lillian Liu (CS), Best Abstract Award, Undergraduate Research Poster Symposium, Purdue University, April 10, 2012
- Juan Esquivel-Rodriguez (CS), 1st Place Award, Sigma Xi graduate student research poster competition, Purdue University, February 15, 2012
- Meghana Chitale (CS) AFP/CAFA 2011 travel fellowship, for attending Automatic Function Prediction Special Interest Group (SIG), Vienna, Austria, May, 2011
- Meghana Chitale (CS), ISMB 2011 travel fellowship for attending ISMB/ECCB, Vienna, Austria, May 2011.

- Juan Esquivel-Rodriguez (CS), ISMB 2011 travel fellowship for attending ISMB/ECCB, Vienna, Austria, May 2011.
- Meghana Chitale (CS), Bilsland Dissertation Fellowship from the Purdue Graduate School, April, 2011.
- Meghana Chitale (CS), travel grant from the Women in Science Programs, Purdue University, for attending the Critical Assessment of Function Annotations (CAFA) at ISMB, Vienna, Austria, July 2011.
- Gregg Thomas (Biol), Sandy Ostroy Summer Internship Award, Purdue University, Summer 2009
- Yifeng Yang (Biol), Student Travel Grant to attend the 53rd Annual Meeting of the Biophysical Society from Biophysical Society, November 2008.
- Yifeng Yang (Biol), PULSe Travel Award, Purdue University, October 2008
- Priyanka Surana (Biol), 2008 Summer Howard Hughes Undergraduate Research Internship.
- Hao Chen, (Biol), YeungKyung Woo Achieve Excellence travel award from Dept. Biological Sciences, Purdue University, November 2007.
- Hao Chen, (Biol), Student Travel Grant to the 52nd Annual Meeting of the Biophysical Society from Biophysical Society, November 2007.
- Preston Spratt (Biol), High Performance Computing Community Poster Session, Honorable mention, Purdue University, April 2007.
- Troy Hawkins (Biol), Umbarger Outstanding Graduate Student in Research, Dept. of Biological Sciences, Purdue University, Spring, 2007
- Preston Spratt (Biol), 2007 Summer Howard Hughes Undergraduate Research Internship.
- David La (Biol), 1st Place, Sigma Xi Graduate Poster Competition, February 14, 2006
- Yen Hock Tan (CS). Nominated for the Computing Research Association's (CRA) Outstanding Undergraduate Award for 2006 from Dept. of Computer Science
- Athurva Gore (ME) Top Poster Award at the Summer Undergraduate Research Fellowship (SURF) Poster Presentation, College of Engineering, College of Science, Purdue University, August 2, 2005
- Stan Luban (CS/Biol). Outstanding Research Award at the Undergraduate Research Day of College of Science & College of Agriculture, Purdue University. April 11, 2005.
- Otoniel Venezuela (CS). Graduate School Incentive Grant. School of Science, Purdue University. April 8, 2005.
- Yen Hock Tan (CS). Hewlett-Packard Fellowship. April, 2005.
- Ei Ei Phyu (CS). 2005 Howard Hughes Fellowship for Undergraduate Research in Bioinformatics.
- Stan Luban (CS/Biol). 2005 Summer Howard Hughes Undergraduate Research Internship.
- Yen Hock Tan (CS). 2005 Summer Howard Hughes Undergraduate Research Internship.
- Stan Luban (CS/Biol). Honorable Mention in the Computing Research Association's (CRA) Outstanding Undergraduate Award for 2005
- Stan Luban (CS/Biol). 2004 Summer Howard Hughes Undergraduate Research Internship.
- Manish Agrawal and Srinivasan S. Turuvekere (Mechanical Engineering). 2nd place in 2004 Purdue University's Burton D. Morgan Entrepreneurship Competition

Courses Taught

CS590 Computing for Life Sciences, core course in the Computing in Life Science CLS Specialization for graduate program (Fall 2011-2016)

CS590-006 Computing for Life Sciences II (Fall 2009, Fall 2010)

CS497 honors research, coordinator (Fall 2010)

CS490B/Biol495S Introduction to Bioinformatics (Spring 2004, Spring & Fall 2005, Fall 2006-2008)

- Elected for a permanent course in Biology and renumbered to BIOL478 from Fall 2006)
- Also used as BIOL 595 Special Assignment in Computational Life Science (CLS) Master Program

BIOL563/(CS590B) Protein Bioinformatics (Spring 2006-2010, 2012-4, 2016)

BIOL696E Seminar Crystallography (Spring 2006)

Other Teaching Activities

- Short talk at Purdue Science Student Council meeting (Spring 2017)
- Guest lecture at BIOL197, Biology freshman honors seminar (Fall 2016)
- Guest lecture at CHEM599, Visualizing cells & molecules (Spring 2013)
- Guest lecture at CS397, honor research course (Fall 2012, Fall 2015)
- Guest lecture at CS591, honor research course (Fall 2011)
- Guest lecture at CS197, honor research course, (Spring 2009)
- Selected as a participating lab for the International PhD Study in Chemistry Program of Dept. of Chemistry, Warsaw University, Poland (2010).
- Guest lecture at Japanese graduate student association, Purdue University, March 15, 2011
- Guest lecture in SCI190 (Instructor: Bos David, Biology), (11/14/2008)
- Panel discussion, SECANT (Science Education in Computational Thinking)workshop, Purdue University, LWSN building (11/15/2008)
- Preparation discussion lecture to structural biology group in Biology Department for a seminar given by Janet Thornton, a renowned bioinformatics scientist (3/18/2008).
- Faculty panel of the graduate student board of the Department of Computer Science. Discussion about “how to be successful in their job-hunt “, Nov. 22, 2004

Services

Editorial Board

- BMC Bioinformatics (March 2016 – present)
- Scientific Reports (Nature journal) (May 2015 – present)
- Methods, guest editor (2015)
- Associate Editor, International Journal of Knowledge Discovery in Bioinformatics (IJKDB) (January 2009- present)

Review of Grants

Study Section/Panel

- National Institutes of Health (NIH), Biological Data Management and Analysis (BDMA) (Feb. 2015, Feb. 2017)
- NIH, STTR/SBIR (ZRG1) (March 2015, November 2015, March 2016, March 2017)

Ad hoc reviewer

Domestic:

- NIH, ZRG1, STTR/SBIR (June 2012, October 2012, March 2014)
- NIH, Challenge Grant, RC1 (June 2009)
- National Science Foundation (NSF), Division of Biological Infrastructure (DBI) (September 2006, October 2009, January 2015)
- NSF, Molecular Cellular Biosciences (MCB) (February 2009, September 2009, March 2011, April 2011, November 2011, February 2017)
- NSF, Division of Chemistry (March 2007, September 2007, February, 2008)

- Louisiana Board of Regents' Research Competitiveness Subprogram, EPSCoR-style grants program (November, 2009, 2011, 2012, 2013)

International

- AFM-TELETHON Scientific Council, France (January 2017)
- Medical Research Council (MRC), UK (November 2016)
- European Research Council Executive Agency (September 2016)
- Qatar National Research Fund (2012, 2014, 2015)
- Biotechnology and Biological Science Research Council, (BBSRC), UK (July 2012)
- 2012 Edition of the Blue Sky program, French National Research Agency (March 2012)
- The Wellcome Trust, UK/Dept. of Biotechnology India Alliance, Intermediate fellowship (September 2011)
- National Science Centre, Polish Narodowe Centrum Nauki, Poland (August 2011)
- Agency of Science, Research & Technology (A*STAR), Singapore (2010, 2011)
- Luxembourg National Research Fund (FNR), CORE programme (August 2010)
- External reviewer of the Council for the Earth and Life sciences, Netherlands Organization for Scientific Research, Netherlands. (March, 2006)

PhD thesis external examiner:

- University of Zürich, Institute of Biochemistry, Switzerland (June 2013)
- Toyota Technological Institute at Chicago (May 2013)
- Department of Computer Science, National University of Singapore, Singapore (March 2012)
- Department of Electrical and Computer Engineering, University of Alberta, Canada (September, 2011)

Review of Journal Papers

Amino Acids
 Annals of Biomedical Engineering
 Bioinformatics
 Biophysical Journal
 Biophysics (Japan)
 Biopolymers
 BMC Bioinformatics
 BMC Structural Biology
 BMC Systems Biology
 Briefings in Bioinformatics
 Briefings in Functional Genomics and Proteomics
 Cancer Informatics
 Cell Research
 Computational Biology and Chemistry
 Current Protein and Peptide Science
 DNA Research
 FEBS Letters
 Frontiers in Bioengineering
 Future Medicinal Chemistry
 IEEE Transactions on Information Technology in Biomedicine
 IEEE Transactions on Nanobioscience
 IEEE/ACM Transactions on Computational Biology and Bioinformatics
 International Journal of Data Mining and Bioinformatics (IJDMB)
 ISMB (International Conference on Intelligent Systems for Molecular Biology)

Journal of Bioinformatics and Computational Biology (JBCB)
Journal of Computer-Aided Molecular Design
Journal of Computational Chemistry
Journal of Structural Biology
Journal of Theoretical Biology
Nature Communications
Neural Computing & Applications
Nucleic Acid Research
Parallel Computing
PLoS Computational Biology
PLoS ONE
Protein Science
Proteins: Structure, Function, Bioinformatics
Proteome Science
Statistical applications in Genetics and Mol Biol.
Structure
The Pacific Symposium on Biocomputing (PSB)

Review of Books

- Editorial Advisory Review Board, “Biological Data Mining in Protein Interaction Networks” Edited by See-Kiong Ng & Xiao-Li Li, IGI Global Press (March 2008)

Textbook reviews

- Draft chapters of a new protein structure & dynamics textbook from Garland Science (March 2013)
- Proposal of a new bioinformatics textbook from Garland Science (July 2012)
- a draft manuscript of 3 chapters in Practical Bioinformatics to be published from Garland Science publishers (November 2011)
- Proposal for a third edition of a bioinformatics textbook to be published from Wiley (Nov. 2010)
- Proposal for a second edition of a bioinformatics textbook to be published from Garland Science (Sep. 2009)
- a draft manuscript of a textbook on bioinformatics planned to be published from Elsevier Inc. (March 2009)
- a draft manuscript of a book on Computational Approaches for Protein Function Prediction planned to be published from Cambridge University Press (July 2006)
- a draft manuscript for a bioinformatics textbook planned to be published from Brooks/Cole. (December 2005)

Program Committee

- International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics, HI-BI-BI 2017, Sydney, Australia, July 31-Aug 3, 2017
- Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2017), Prague, Czech Republic, July 21-25, 2017
- 8th International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD'17), Lyon, France , August 28-31, 2017
- HiCOMB 2017 16th IEEE International Workshop on High Performance Computational Biology, Buena Vista Palace Hotel, Orlando, FL, California, May 29, 2017
- Steering committee, Great Lakes Bioinformatics Conference (GLBIO) 2017, Chicago, Illinois, May 15-17, 2017
- Symposium on Bioinformatics and Bioforensics (SBB'16), Jaipur, India, September 21-24, 2016.

- International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics, HI-BI-BI 2016, UC Davis, CA, Aug 19-20, 2016
- 7th International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD'16), Porto, Portugal , September 5-8, 2016
- Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2016), Orlando, Florida, July 8-12, 2016
- Steering Committee, Great Lakes Bioinformatics (GLBIO)/Canadian Computational Biology Conference (CCBC), Toronto, Canada, May 16-19,2016
- X-meeting + BSB 2015 11th International Conference of the AB3C + Brazilian Symposium of Bioinformatics, Sao Paulo, Brazil, November 3-6, 2015
- Computational Systems-Biology and Bioinformatics 2015, Bangkok, Thailand, Nov. 22-25, 2015
- ICDM workshop on Biological Data Mining and its Applications in Healthcare, Atlantic City, New Jersey, Nov 13, 2015
- IEEE International Conference on Information Reuse and Integration) IRI 2015, San Francisco, CA, USA August 13-15, 2015
- International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics, HI-BI-BI 2015, Paris, France, Aug 26-27, 2015
- International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD-DEXA'15), Valencia, Spain , September 1-5, 2015
- Program Chair, Great Lakes Bioinformatics (GLBIO) Conference, Purdue University, May, 2015
- The 5th International Conference on Computational Systems-Biology and Bioinformatics (CSBio 2014), Singapore, November 10-12, 2014
- Program Chair, ACLS Tokyo Institute of Technology – Purdue Summer School on Interdisciplinary Science, August 14-16, 2014, Purdue University
- Automatic Function Prediction/Critical Assessment of Automatic Function Assignment (AFP/CAFA) 2014, April 2014
- IEEE International Conference on Data Mining (ICDM 2014) BioDM workshop on "Biological Data Mining and its Applications in Healthcare", Shenzhen, China, Dec 14, 2014.
- The 13th Pacific Rim International Conference on Artificial Intelligence, Gold Coast, Australia, Dec. 1-5, 2014
- International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics, HI-BI-BI 2014, Beijing, China, Aug 18-19, 2014
- 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014), Boston, July 11-15, 2014
- International Workshop on Algorithms for Computational Biology (ACB-2014), September 24-27, 2014, Delhi, India
- 5th International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD-DEXA'14), Munich, Germany, September 1-5, 2014
- Program Chair, Great Lakes Bioinformatics (GLBIO) Conference, Cincinnati Children's Hospital Medical Center, May 16-18, 2014
- International Symposium on Network Analysis and Mining for Health Informatics, Biomedicine and Bioinformatics, Net-HI-BI-BI 2013, Shanghai, China Dec 18-21, 2013
- IEEE International Conference on Data Mining (ICDM 2013) BioDM workshop on "Biological Data Mining and its Applications in Healthcare", Dallas, Texas, Dec 8, 2013.
- Automatic Function Prediction/Critical Assessment of Automatic Function Assignment (AFP/CAFA) 2013, April 2013
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2013, Washington DC, September 22-25, 2013

- 2013 ASE/IEEE International Conference on BioMedical Computing (BiomedCom2013), Washington DC, September 8-14, 2013
- International Symposium on Network Enabled Health Informatics, Bio-Medicine and Bioinformatics (HI-BI-BI 2013), Niagara Falls, Canada, August 26-27, 2013
- BIOTECHNO2013: The Fifth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies, Lisbon, Portugal, March 24-29, 2013.
- 21st Annual International Conference on Intelligent Systems for Molecular Biology (2013 ISMB /ECCB), Berlin, July 19-23, 2013
- 4th International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD'13) Prague, Czech Republic, August 26-30, 2013
- International Conference on Data Mining, (ICDM) 2012 workshop on “Biological Data Mining and its Applications in Healthcare”, Brussels, Belgium, December 10, 2012
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2012, Orlando, Florida, October 7-10, 2012
- 2012 ASE/IEEE International Conference on BioMedical Computing, Washington DC, December 14-16, 2012
- International Symposium on Network Enabled Health Informatics, Bio-Medicine and Bioinformatics (HI-BI-BI 2012), Istanbul, Turkey, August 27-28, 2012
- International Conference and Exhibition on Computer Aided Drug Design & QSAR, Double Tree by Hilton, Chicago, October 29-31, 2012
- "OMICS International Integrative Biology Summit" during 1-3 October 2012 at Chicago, USA.
- 3rd International Workshop on Biological Knowledge Discovery and Data Mining (BIOKDD'12) Vienna, Austria, Sept. 3-7, 2012
- Advisory Committee, Great Lakes Bioinformatics (GLBIO) Conference 2012, Univ. of Michigan, Ann Arbor, Michigan, May 15-17, 2012
- BIOTECHNO2012: The Fourth International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies, St. Maarten, Netherlands Antilles, March 25-29, 2012.
- Automatic Function Prediction/Critical Assessment of Automatic Function Assignment (AFP/CAFA) 2011, February 2012
- ICDM 2011 the IEEE International Conference on Data mining, Workshop on “Biological Data mining and its applications in healthcare”, Vancouver, Canada, Dec 11-14, 2011
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Chicago, IL, August 1-3, 2011
- 11th IEEE International Symposium on Bioinformatics and Bio Engineering (BIBE 2011), Taichung, Taiwan, October 24-26, 2011
- Session chair, 3D-SIG, ISMB, Vienna, Austria, July 15-16, 2011
- Steering committee member, Great Lakes Bioinformatics Conference (GLBIO) 2011, Athens, Ohio, May 2-4, 2011
- BIOTECHNO2011: The Third International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies, Venice, Italy, May 22-27, 2011.
- ICDM 2010 the IEEE International Conference on Data mining, Workshop on “Biological Data mining and its applications in healthcare”, Sydney, Australia, Dec 13, 2010
- The European Conference on Computational Biology 2010, Ghent, Belgium, Sep. 26-29, 2010
- 2010 ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB), Niagara Falls, NY, August 4, 2010
- BIOTECHNO 2010: The second International Conference on Advances in Biotechnologies, Cancun, Mexico, March 7-13, 2010
- Organizer (with Barry Wanner, Michael Gribskov, Dawn Whitaker), IECA Functional Genomics Mini-symposium, Purdue University, April 17, 2010

- GIW 2009: 20th International Conference on Genome Informatics, Yokohama, Japan, December 14-16, 2009
- 24th International Symposium on Computer and Information Sciences (ISCIS2009), Bioinformatics and Bioengineering track, September 14-16, 2009
- ISIBM International Joint Conference on Bioinformatics, Systems Biology and Computational intelligence, Shanghai, China, August 3-6, 2009
- IEEE 9th International Symposium on Bioinformatics & BioEngineering (BIBE09), Taichung, Taiwan, June 22-24, 2009
- Workshop organizer, 4th IEEE International Conference on e-Science, eBioinformatics, Indianapolis, Dec. 12, 2008
- GIW 2008: 19th International Conference on Genome Informatics, Brisbane, Australia, December 1-3, 2008
- Area chair, 2008 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Philadelphia, PA, November 7-9, 2008
- BIBM Workshop on Data Mining in Functional Genomics (DMFG), 2008 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Philadelphia, PA, November 5-7, 2008
- Program Committee and session co-chair, Biomedical Engineering Society Annual Meeting 2007, “Systems Biology and Bioinformatics” track, Los Angeles, CA, September 26-29, 2007.
- IEEE 7th International Symposium on Bioinformatics & BioEngineering (BIBE07), Boston, MA, October 14-17, 2007
- 7th International Workshop on Data Mining in Bioinformatics (BIOKDD '07), August 12th 2007, San Jose, CA, USA
- 2nd VLDB (Very Large DataBases) Workshop on Data Mining in Bioinformatics, September 23-28 2007, University of Vienna, Austria
- 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 6th European Conference on Computational Biology (ECCB) (ISMB/ECCB) 2007, area “Bioinformatics of Disease” , July 21-25, 2007
- HiCOMB 2007: Sixth IEEE International Workshop on High Performance Computational Biology, Renaissance Long Beach Hotel, Long Beach, California, March 26, 2007
- Interface 2007: the 39th Symposium on the interface of statistics, computing science and applications. Doubletree Hotel, Philadelphia on May 23- 26, 2007.
- Program Committee and session co-chair, Biomedical Engineering Society Annual Meeting 2006, “Systems Biology and Bioinformatics” track, Chicago, IL, October 12-14, 2006.
- Scientific Committee, Special Session on Computer Infrastructure for Systems Biology, part of the 18th International Conference on Systems Engineering 2005 (ICSEng'05). August 16-18 2005, Las Vegas, NV.

Internal Services

Department

Biological Sciences:

- Executive Committee, 2015-current
- Convener of Structural Biology and Computational Biology 2016-current
- Convener of Molecular Science Cluster, 2015-2016
- Future of Department Discussion Committee 2014-2015
- International Program & Study Abroad Committee 2014-2015, 2016-2017
- Departmental representative for Computational Life Sciences (CLS) program (2010- on)
- Graduate and advanced studies committee, 2011-2014
- International Programs & Study Abroad, 2013-2014
- PRF/Bililand fellowship review committee 2013, 2017

- Graduate School Admission Committee 2005-6, 2009-2010, 2011-2012
- Review committee of Biophysics Training Grant, June, 2011
- Bioinformatics and Biotechnology Advisory 2005-6, 2006-7
- Umbarger Outstanding Graduate Student Award Review Committee 2005

Computer Science:

- Award Committee 2011-2012
- Undergraduate Committee 2009-2010
- Graduate Study Committee 2007-9, 2012-2016
- Bioinformatics search committee 2004-5, 2005-6, 2006-7

Interdisciplinary

- Representative from Dept. of Biological Sciences for Computational Life Science (CLS) program at Purdue (2010- on)
- Review committee of RNA-Seq Illumina proposals (Bioinformatics Core, Discovery Park, Purdue)

College of Science

- College Grade Appeals Committee 2013-2015
- Member of Bioinformatics Steering Committee (Chair: Rebecca Doerge) 2005-6
- Member of COALESCE bioinformatics & systems biology search committee 2003-4/2004-5/2005-6/2006-7(both Informatics and CS Subcommittee)
- Member of COALESCE systems biology search committee (Chair: Michael Gribskov), 2005-6

University

- Search committee of Computational/Systems Biology Cluster (Chair: Rebecca Doerge) 2013-2014

Others

- Review committee of RNA-Seq Illumina proposals (Bioinformatics Core, Discovery Park, Purdue)

Professional Societies

The Biophysical Society

The Protein Society

The International Society of Computational Biology

Biomedical Engineering Society

The Biophysical Society of Japan

The Molecular Biology Society of Japan

Japanese Society of Bioinformatics