Jianwen Fang, Ph.D.

Biometric Research Branch
Division of Cancer Treatment and Diagnosis
National Cancer Institute
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Research interests

Integrated data analysis, data-mining algorithms, systems biology, structural bioinformatics, software and database development, computational drug discovery.

Education

Dec 2000, Ph. D. in Chemistry, Wayne State University, Detroit, Michigan
May 2002, M. A. in Computer Science Department, Wayne State University, Detroit, Michigan
July 1996, M. Sc. In Chemistry, Shanghai Institute of Organic Chemistry
July 1990, B. Sc. In Applied Chemistry, Dept. of Technical Physics, Peking University

Professional certifications

Sun certified Java professional programmer (Sept 2001)
Oracle certified Oracle professional database application developer (March 2002)

Professional experience

June 2013 – present **National Cancer Institute**

- Computational Biologist

June 2002 – June 2013 **University of Kansas**

- Assistant/Associate scientist and director of Applied Bioinformatics Laboratory (Director: Feb 08 – June 13; Asst: Feb 08 - Jun 11; Assoc: June 11 – June 13)
- Courtesy Assistant/Associate Professor, Department of Electrical Engineering and Computer Science (Asst: Aug 05 - Jun 11; Assoc: June 11 – June 13)
- Affiliated Faculty, Information and Telecommunication Center (Feb 08 – June 13)
- Graduate Program Faculty, Center of Bioinformatics (Jan 09 – June 13)
- Research Assistant Professor, Information and Telecommunication Center (Jan 05 – Feb 08)
- Information Resource Manager/Bioinformatics specialist, Biology Division (Jun 02 – Jan 05)

Referred Publications

85. Fang JP, Gao S, Tai D, Middaugh CR, **Fang JW***. "Identification of properties important to protein aggregation using feature selection." *BMC Bioinformatics* 2013, 14:314.

84. Dasouki MJ, Rafi SK, Olm-Shipman AJO, Wilson NR, Abhyankar S, Ganter B, Furness LM, **Fang JW**, Calado RT, and Saadi I*. "Exome sequencing reveals a thrombopoietin ligand mutation in a Micronesian family with autosomal recessive aplastic anemia." *Blood* 122, no. 20 (2013): 3440-3449.

83. He YQ, Gong L, Fang YP, Zhan Q, Liu HX, Lu YL, Guo GL, Lehman-McKeeman L, **Fang JW**, and Wan YY*. "The role of retinoic acid in hepatic lipid homeostasis defined by genomic binding and transcriptome profiling." *BMC genomics* 14, no. 1 (2013): 575.

82. Hanzlik RP*, Koen YM, and **Fang JW**. "Bioinformatic Analysis of 302 Reactive Metabolite Target Proteins. Which Ones Are Important for Cell Death?." *Toxicological Sciences* 135, no. 2 (2013): 390-401.

81. Fang YP, Wang XK, Michaelis EK, and **Fang JW***. (2013). Classifying aging genes into DNA repair or non-DNA repair-related categories. In *Intelligent Computing Theories and Technology* (pp. 20-29). Springer Berlin Heidelberg.

80. Wang SL, Fang YP and **Fang JW***. (2013). A Simple but Robust Complex Disease Classification Method Using Virtual Sample Template. In *Emerging Intelligent Computing Technology and Applications* (pp. 73-80). Springer Berlin Heidelberg.

79. Wang SL, Fang YP and **Fang JW*.** (2013). Diagnostic prediction of complex diseases using phase-only correlation based on virtual sample template. *BMC Bioinformatics*, *14*(8), 1-11.

78. Thomas AM, Hart SN, Li GD, Lu H, Fang YP, **Fang JW**, Zhong XB, and Guo GL*. "Hepatocyte Nuclear Factor 4 Alpha and Farnesoid X Receptor Co-regulates Gene Transcription in Mouse Livers on a Genome-Wide Scale." *Pharmaceutical research* (2013): 1-11.

77. Hu Y, Liu HX, He YQ, Fang YP, **Fang JW**, and Wan YY*. "Transcriptome profiling and genome-wide DNA binding define the differential role of fenretinide and all-trans RA in regulating the death and survival of human hepatocellular carcinoma Huh7 cells." *Biochemical pharmacology*. 2013 Apr 1;85(7):1007-17.

76. Fang YP, and **Fang JW*.** "Discrimination of soluble and aggregation-prone proteins based on sequence information." *Mol. BioSyst*. 9, no. 4 (2013): 806-811.

75. Liu HX, Fang YP, Hu Y, Gonzalez FJ, **Fang JW**, and Wan YY*. "PPARβ Regulates Liver Regeneration by Modulating Akt and E2f Signaling." *PLOS ONE* 8, no. 6 (2013): e65644.

74. Thomas JC, O'Hara JM, Hu L, Gao FP, Joshi SB, Volkin DB, Robert N. Brey RN, **Fang JW**, Karanicolas J, Mantis NJ, and Middaugh CR*. Effect of single-point mutations on the stability and immunogenicity of a recombinant ricin chain subunit vaccine antigen. *Human Vaccines & Immunotherapeutics* 9:4, 1–9; April 2013.

73. Fang YP, Liu HX, Zhang N, Guo G, Wan YY, **Fang JW***. NURBS: A Database of Experimental and Predicted Nuclear Receptor Binding Sites. 2013 Jan 15; 29(2):295-7.

72. Zhan Q, Fang YP, He YQ, Liu HX, **Fang JW**, Wan YY*. Function annotation of hepatic retinoid x receptor α based on genome-wide DNA binding and transcriptome profiling. *PLoSONE*. 2012. 7(9): e50013.

71. Gao S, Xu S, Fang YP, **Fang JW***. Prediction of Core Cancer Genes Using Multitask Classification Framework. *J Theor Biol*. 2012, 317, 62-70.

70. Li Y, **Fang JW***. PROTS-RF: A Robust Model for Predicting Mutation Induced Protein Stability Change. *PLoSONE*, 2012. 7(10): e47247.

69. Fang YP, Middaugh CR, **Fang JW***. In silico classification of proteins from acidic and neutral cytoplasms. *PLoSONE*. 2012. 7(9): e45585.

68. Tai D and **Fang JW***. SymDex: Increasing the Efficiency of Chemical Fingerprint Similarity Searches for Comparing Large Chemical Libraries by Using Query Set Indexing. *J. Chem. Inf. Model*. 2012, 52 (8), 1926–1935.

67. Wang SL, Li XL, **Fang JW***. Finding minimum gene subsets with heuristic breadth-first search algorithm for robust tumor classification**.** *BMC Bioinformatics* 2012, **13**:178

66. Gao S, Xu S, Fang YP, **Fang JW***. Using multitask classification methods to investigate the kinase-specific phosphorylation sites. *Proteome Science* 2012, 10 (Suppl 1):S7.

65. Li Y, Zhang J, Tai D, Middaugh CR, Zhang Y, **Fang JW***. PROTS: a Fragment Based Protein Thermo-Stability Potential. *Proteins: Structure, Function, and Bioinformatics*. 2012, 80, 1, 81-92.

64. Gao S, Xu S, **Fang JW***. Predicting Kinase-specific Phosphorylation Sites Using a Multitask Classification Framework. Proceedings of 2011 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2011), Atlanta GA, 12-15 Nov 2011. 257-260.

63. Gao S, **Fang JW*.** Identification of Properties Important to Signal Peptides and Signal Anchors Using Feature Selection. *2011 International Conference on Computational Biology and Bioinformatics(CBB2011)*, Shanghai China, 28-30 October, 2011.

62. Li Y, Fang YP, **Fang JW***. Predicting Residue-Residue Contacts Using Random Forest Models. *Bioinformatics*. 2011, 27(24), 3379-3384.

61. Tai D, Chaguturu R, **Fang JW***. K-Screen: A Free Application for High Throughput Screening Data Analysis, Visualization, and Laboratory Information Management. *Comb Chem High Throughput Screen*. 2011, 14, 9, 757-765.

60. **Fang JW***, Tai D. Evaluation of Mutual Information, Genetic Algorithm and SVR for Feature Selection in QSAR Regression. *Curr Drug Discov Technol*. 2011 Jun 1;8(2):107-11.

59. Yang JW, Hutchinson IV, Shah T, **Fang JW**, Min DI. Gene polymorphism of vascular endothelial growth factor -1154 G>A is associated with hypertensive nephropathy in a Hispanic population. *Mol Biol Rep*. 2011; 38:2419-2425.

58. Cai S, **Fang JW***, Li QS, Borchardt RT, Kuczera K, Middaugh CR, and Schowen RL. Comparative kinetics of cofactor association and dissociation for the human and trypanosomal S-adenosylhomocysteine hydrolases. 3. The role of lysyl and tyrosyl residues of the C-terminal extension. *Biochemistry*, 2010 Sep 28;49(38):8434-41.

57. Jiang L, **Fang JW,** Moore DS, Gogichaeva NV, Galeva NA, Michaelis ML, Zaidi A. Age-associated changes in synaptic lipid raft proteins revealed by two-dimensional fluorescence difference gel electrophoresis. Neurobiol Aging. 2010 Dec; 31(12):2146-59.

56. Li Y, **Fang JW.*** Distance-dependent statistical potentials for discriminating thermophilic and mesophilic proteins. *Biochem. Biophys. Res. Commun*. 396, 3, 736-741, 2010.

55. Li Y, Middaugh CR, **Fang JW**.* A novel scoring function for discriminating hyperthermophilic and mesophilic proteins with application to predicting relative thermostability of protein mutants. *BMC Bioinformatics*. 2010 Jan 28;11(1):62.

54. Thomas AM, Hart SN, Kong B, **Fang JW**, Zhong XB, Guo GL. Genome-wide tissue-specific farnesoid X receptor binding in mouse liver and intestine. *Hepatology*. 51, 4, 1410-1419, 2009.

53. Cai S, Li QS, **Fang JW**, Borchardt RT, Kuczera K, Middaugh CR, and Schowen RL The Rationale for Targeting the NAD/NADH Cofactor Binding Site of Parasitic S-Adenosyl-L-Homocysteine Hydrolase for the Design of Anti-Parasitic Drugs. *Nucleosides Nucleotides & Nucleic Acids*. 28, 5-7, Special Issue, 485-503, 2009.

52. Li QS, Cai S, **Fang JW**, Borchardt RT, Kuczera K, Middaugh CR, and Schowen RL. Evaluation of NAD(H) Analogues as Selective Inhibitors for Trypanosoma Cruzi S-Adenosylhomocysteine Hydrolase. *Nucleosides Nucleotides & Nucleic Acids*. 28, 5-7, Special Issue, 473-484, 2009.

51. Liu S, Tang W, **Fang JW**, Ren J, Li H, Xiao Z, Quarles LD. Novel Regulators of Fgf23 Expression and Mineralization in Hyp Bone. *Mol Endocrinol*. 2009 Sep; 23(9):1505-18.

50. **Fang JW,** Koen YM, Hanzlik RP. Bioinformatic analysis of xenobiotic reactive metabolite target proteins and their interacting partners. *BMC Chem Biol*. 2009 Jun 12;9(1):5.

49. Hanzlik RP, **Fang JW,** Koen YM. Filling and mining the reactive metabolite target protein database. *Chem Biol Interact*. 2009 Apr 15;179(1):38-44.

48. Chen DC, **Fang JW,** Yu JW. "Predicting Blood-Brain Barrier Penetration by Stochastic Discrimination". *Proceedings of 2008 International Conference on BioMedical Engineering and Informatics* (BMEI 2008), May 28-30, 2008, Sanya, Hainan, China.

47. Li QS, Cai S, **Fang JW,** Borchardt RT, Kuczera K, Middaugh CR, and Schowen RL. "Comparative kinetics of cofactor association and dissociation for the human and trypanosomal S-adenosylhomocysteine hydrolases. 2. The role of helix 18 stability". *Biochemistry*. 47(17), 4983-91, 2008.

47. Tubb MT, Silva AGD, **Fang JW**, Tso P, Davidson WS. A three-dimensional homology model of lipid-free apolipoprotein A-IV using cross-linking and mass spectrometry. *J. Biol. Chem*. 283(25):17314-23, 2008.

46. Silva RA, Huang R, Morris J, **Fang JW,** Gracheva EO, Ren G, Kontush A, Jerome WG, Rye KA, Davidson WS. Structure of apolipoprotein A-I in spherical high density lipoproteins of different sizes. *Proc Natl Acad Sci U S A*. 2008 Aug 26;105(34):12176-81.

44. Hu C, Fang JW, Borchardt RT, Schowen RL, Kuczera K. Molecular dynamics simulations of domain motions of substrate-free S-Adenosyl-L-homocysteine hydrolase in solution. *PROTEINS: Structure, Function, and Bioinformatics*. 71(1), 131-143, 2008.

43. **Fang JW*,** Dong YH, Salamat-miller N, Middaugh CR. DB-PABP: a database of polyanion binding proteins. *Nucleic Acid Research.* 36(Database issue):D303-D306, 2008.

42. **Fang JW***, Dong YH, Williams TD, Lushington GH. "Feature selection in validating mass spectrometry database search results". *Journal of Bioinformatics and Computational Biology.* 6(1):223-40. 2008.

41. Theerthama B, Wang JL, **Fang JW,** and Lushington GH. "Novel algorithms for the identification of biologically informative chemical diversity metrics". *Current Computer-Aided Drug Design. 4(1):* 23-34, 2008.

40. Chen XW, Han B, **Fang JW,** Haasl RJ. A new kernel method for large-scale protein-protein interaction prediction. *Int. J. Data Mining and Bioinformatics.* 2(2):145-56. 2008.

39. **Fang JW,** Grzymala-Busse JW. "Predicting Penetration Across the Blood-Brain Barrier - a Rough Set Approach". *Proceedings of 2007 IEEE International Conference on Granular Computing, IEEE Computer Society Press*, pp. 231-236.

38. Wickstrum JR, Skredenske JM, Kolin A, Jin DJ, **Fang JW**, Egan SM. Transcription Activation by the DNA-Binding Domain of the AraC Family Protein RhaS in the Absence of its Effector-Binding Domain. *Journal of Bacteriology*. 189, 14, 4984-4993, 2007.

37. **Fang JW,** Grzymala-Busse JW. Mining Mass Spectrometry Database Search Results—A Rough Set Approach. *RSEISP 2007, LNAI 4585*, 340–349, 2007.

36. Sang Y, Teresa Ortega M, Rune K, Xiau W, Zhang G, Soulages JL, Lushington GH, **Fang JW**, Williams TD, Blecha F, Melgarejo T. Canine cathelicidin (K9CATH): Gene cloning, expression, and biochemical activity of a novel pro-myeloid antimicrobial peptide. *Dev Comp Immunol*. 31, 1278-1296, 2007.

35. **Fang JW*,** Salamat-miller N, Dong YH, Middaugh CR. "Prediction of Polyanion Binding Potential in Proteins Using Random Forest". *Proceedings of BIOCOMP'07*, 427-431, 2007.

34. Hanzlik RP, Koen TM, Theertham B, Dong YH, and **Fang J.W.** The Reactive Metabolite Target Protein Database - A Web-Accessible Resource. *BMC Bioinformatics*. 2007, 8:95.

33. Li QS, Cai S, Borchardt RT, **Fang JW,** Kuczera K, Middaugh CR, and Schowen RL. Comparative kinetics of cofactor association and dissociation for the human and trypanosomal S-adenosylhomocysteine hydrolases. 1. Basic features of the association and dissociation processes. *Biochemistry*, 46, 19, 5798-5809, 2007.

32. Salamat-Miller N, **Fang JW,** Seidel C, Smalter A, Assenov Y, Albrechat M, Middaugh CR. A Network-Based Analysis of Polyanion Binding Proteins Utilizing Human Protein Arrays. *J. Biol. Chem.* 282, 14, 10153-10163, 2007.

31. Suprenant KA, Bloom N, **Fang JW,** Lushington GH. The Major Vault Protein is Related to the Toxic Anion Resistance Protein (TELA) Family. *J. Exp. Biol*. 210, 946-955, 2007.

30. Salamat-Miller NS, **Fang JW**, Seidel C, Smalter A, Assenov Y, Albrecht M, Middaugh1 CR. A Network-Based Analysis of Polyanion Binding Proteins Utilizing Yeast Protein Arrays. *Molecular and Cellular Proteomics*, 5, 12, 2263-2278, 2006.

29. Rider V, Isuzugawa K, Twarog M, Jones S, Cameron B, Imakawa K, **Fang JW** . Progesterone Initiates Wnt-β-Catenin Signaling But Estradiol Is Required For Nuclear Activation and Synchronous Proliferation of Rat Uterine Stromal Cells. *J. Endocrinol*. 191(3):537-48, 2006.

28. **Fang JW,** Grzymala-Busse JW. "Leukemia Prediction from Gene Expression Data: A Rough Set Approach." *Lecture Notes in Computer Science*: 4029, 899-908, 2006.

27. **Fang JW**, Grzymala-Busse JW. "Mining of MicroRNA Expression Data: A Rough Set Approach." *Lecture Notes in Computer Science*: 4062, 758-765, 2006.

26. **Fang JW***, Dong YH, Lushington GH, Ye QZ, Georg GI. "Support Vector Machines in HTS Data Mining: Type I MetAPs Inhibition Study." *J. Biomolecular Screening* 11 (2): 138-144, 2006.

25. Haasl RJ, **Fang JW.*** "Mining protein-protein interaction data." *Current Bioinformatics* 1, 2: 197-205, 2006. (Invited review)

24. **Fang, J.W.***; Haasl, R.J.; Dong, Y.H.; Lushington, G. H. “Discover protein sequence signatures from protein-protein interaction data” *BMC Bioinformatics* 6: 277, 2005.

23. Gangani DD, Hilliard GH, **Fang JW**, Macha S, and Davidson WS. "A Three Dimensional Molecular Model of Lipid-free Apolipoprotein A-I Determined by Cross-linking/Mass Spectrometry and Sequence Threading." *Biochemistry* 44: 2759-2769, 2005.

22. Marchin M, Kelly PT and **Fang JW*** "Tracker: continuous HMMER and BLAST searching." *Bioinformatics* 21: 388-389, 2005.

21. Chen XW, **Fang JW**, Wang XK. “Discovering Transcription Factor Binding Sites in the Yeast Saccharomyces Cerevisiae. *Currents in Computational Molecular Biology* 2004, 461.

20. Ram JL, Ritchie RP, **Fang JW**, Gonzales FS, Selegean JP. “Sequence-based source tracking of Escherichia coli based on genetic diversity of beta-glucuronidase.” *J. of Environmental Quality* 33: 1024-1032, 2004.

19. Xian M, Fatima Z, Zhang W, **Fang JW**, Li HF, Pei DH, Loo J, Stevenson T, Wang PG. “Identification of alpha-galactosyl epitope mimetics through rapid generation and screening of C-linked glycopeptide library.” *J. Combi. Chem.* 6: 126-134, 2004.

18. Wang JQ, Zhang BY, **Fang JW**, Sujino K, Li H, Otter A, Hindsgaul O, Palcic MM, Wang PG. “Frontal affinity chromatography coupled to mass spectrometry: An effective method for K-d determination and screening of alpha-gal derivatives binding to anti-Gal antibodies (IgG).” *J. Carbohydrate Chemistry* 22: 347-376, 2003.

17. Zhang JB, Kowal P, **Fang JW,** Andreana P, Wang PG. "Efficient chemoenzymatic synthesis of globotriose and its derivatives with a recombinant -(14)-galactosyltransferase." *Carbohydrate Research* 337: 969-976, 2002.

16. Chen X, **Fang JW,** Zhang J, Liu ZY, Andreana P, Kowal P, Wang PG. "Sugar nucleotide regeneration beads (superbeads): a versatile tool for practical synthesis of oligosaccharides." *J. Am. Chem. Soc.* 123: 2081-2082, 2001.

15. **Fang JW,** Wang PG. “Synthesis of alpha Galactosyl Epitope Derivatives Using a Fusion Enzyme.” *Carbohydrate Research* 329: 873-878, 2000.

14. Chen X, Zhang W, Wang JQ, **Fang JW,** Wang PG. "Production of a-Galatosyl epitopes via combined use of two recombinant whole cells harboring UDP-galactose 4-epimerase and a1,3galactosyltransferase." *Biotech. Progress* 16: 595-599, 2000.

13. Chen X, Liu Z, Wang J, **Fang JW,** Fan H, Wang PG. “Changing the donor cofactor bovine alpha 1,3-galactosyltransferase by fusion with UDP-galactose 4-epimerase - More efficient biocatalysis for synthesis of alpha-Gal epitopes.” *J. Biol. Chem.* 275: 31594-31600, 2000.

12. Wang JQ, Zhang BY, **Fang JW**, Zhang W, Sujino K, Janczuk A, Qian XP, Chen X, Hindsgaul O, Palcic M, Wang PG. “Human anti-Gal antibody affinity chromatography with mass spectrometric detection: An efficient method for screening a-Gal derivatives.” *Biochemistry-US* 39: 156, 2000.

11. Xie WH, **Fang JW,** Li J, Wang PG. “Lanthanide Triflates Catalyzed Reactions of Imines with Ethyl Diazoacetate: Formation of Aziridines in Protic Media.” *Tetrahedron* 55: 12929-12938, 1999.

10. Zhang, W.; Xie, W.H.; **Fang, J.W.**; Wang, P.G. "Ytterbium (III) Trifluoromethanesulfonate Catalyzed Solid Phase Aza Diels-Alder Reaction and Subsequent Facile Adduct Release." *Tetrahedron Lett*. 55: 12929-12938, 1999.

9. **Fang JW,** Chen X, Zhang W, Wang PG. "Chemoenzymatic Synthesis of alpha-Gal Epitope Derivatives Containing Free Amino Groups: Efficient Separation and Further Manipulation." *J. Org. Chem*. 64: 4089-4094, 1999.

8. Zhang W, Xie W, **Fang JW,** Wang PG. "Recent Progresses in Glycochemistry and Green Chemistry." *Current Org. Chem.* 3: 241-267, 1999.

7. Janczuk A, Li J, Zhang W, Chen X, Chen Y, **Fang JW**, Wang J, Wang PG. "alpha-Gal Oligosaccharides: Chemistry and Potential Biomedical Application." *Current Medicinal Chem.* 6: 155, 1999.

6. Li J, Ksebati MB, Zhang W, Guo Z, Wang J, Yu L, **Fang JW,** Wang PG. "Conformational Analysis of Alpha Galactosyl Epitopes Involved in the Hyperacute Rejection upon Xenotransplantation." *Carbohydr. Res*. 315: 76-88, 1999.

5. **Fang JW,** Li J, Chen X, Zhang Y, Wang J, Guo Z, Brew K, Wang PG. "A Highly Efficient Chemo-Enzymatic Synthesis of alpha-Galactosyl Epitopes with a Recombinant 1,3-Galactosyltransferase." *J. Am. Chem. Soc.* 120: 6635-6638, 1998.

4. **Fang JW,** Xie W, Li J, Wang PG. "Chemical and Enzymatic Synthesis of Glycoconjugates 3: Synthesis of Lactosamine by Thermophilic Galactosidase Catalyzed Galactosylation on a Multigram Scale." *Tetrahedron Lett*. 39: 919, 1998.

3. **Fang JW,** Li ZY. "Chemo-Enzymatic Synthesis of a Four-Chiral-Center Portion of A-23187 (calsimycin)." *Chinese Chem. Lett*. 8: 111, 1997.

2. Ward OP, **Fang JW,** Li ZY. "Lipase-Catalyzed Synthesis of a Sugar Ester Containing Arechidonic Acid." *Enzyme Microb. Tech*. 20: 52, 1997.

1. **Fang JW**, Li ZY. "Lipase-Catalyzed Double Kinetic Resolution of dl-2,4-Dimethyl-1,5-pentanediol: A Useful Synthon in Natural Product Synthesis." *Chinese Chem. Lett*. 7: 129, 1997.

Posters

1. **Fang JW**, Yoder C, Box K, Castillo D, Brown D, Abdullayev A and Blumenstiel J. The epigenetics of transposon control by small RNA in Drosophila virilis, Allerton, IL, October 29-30, 2010.
2. Galeva N, Tai D, **Fang JW**, Williams TD*. "MassMapper: aid to high resolution peptide interrogation". 58th ASMS Conference on Mass Spectrometry and Allied Topics, May 23 - 27, 2010, Salt Lake City, Utah.
3. **Fang JW***, Grzymala-Busse JW*. "Novel Data Mining Algorithms for Cancer Research---Applications to Genomics, Proteomics, and Drug Discovery". KUCC Research Symposium 2009, Nov 20, 2009, Kansas City.
4. **Fang JW***, Dong YH, Williams TD, Lushington GH. "Using Peptide Properties to Improve the Accuracy of Peptide Identification through MS/MS and Database Search". 2006 Biennial Institutional Development Award (IDeA) Program Symposium, July 20 - 22, Washington, D.C.
5. **Fang JW**, Theertham B, Koen YM, Hanzlik RP*. "The reactive metabolite target protein database: a web-accessible resource". KCALSI 2006, March 30, 2006, Kansas City, Kansas.

6. Dong YH, Yang Y, Barton J, **Fang JW***. "Computational Prediction of Beta-sheet Arrangement". COBRE EAB, March 4, 2006, Lawrence, Kansas
7. **Fang JW***, Haasl RJ, Dong YH, Lushington GH. "Discover protein sequence signatures from protein-protein interaction data", COBRE EAB, March 4, 2006, Lawrence, Kansas.
8. **Fang JW**, Theertham B, Koen YM, Hanzlik RP*. "The reactive metabolite target protein database: a web-accessible resource". COBRE EAB, March 4, 2006.
9. **Fang JW***, Haasl RJ, Dong YH, Lushington GH. "Discover protein sequence signatures from protein-protein interaction data". K-INBRE symposium, Jan 14-15, 2006,
10. Dong YH, Yang Y, Barton J, **Fang JW***. "Computational Prediction of Beta-sheet Arrangement". K-INBRE symposium, Jan 14-15, 2006.
11. **Fang JW**, Theertham B, Koen YM, Hanzlik RP*. "The reactive metabolite target protein database: a web-accessible resource". Biological Reactive Intermediates Conference VII, Jan 4, 2006, Tucson, AR.

Oral presentations

1. "Protein Structure and Sequence Mining for Improving Computational Design of Stable Proteins", Drug Discovery Chemistry, April 17-19, 2012, San Diego, CA. (Invited).
2. "Protein structures and sequence mining for improving computational design of stable proteins." ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB), Oct 7-10, 2012, Orlando, FL.
3. "Introduction to Applied Bioinformatics Laboratory", PSF-COBRE meeting, Oct 15, 2008, Lawrence, KS.
4. "Developing useful databases for life scientists", Functional Genomics Consortium 2008 Spring Symposium, March 5, Kansas State University. Manhattan, KS. (Invited).
5. "Prediction of Polyanion Binding Potential in Proteins Using Random Forest", BIOCOMP'07, June 2007, Las Vegas, NV.
6. "Machine Learning Approaches in QSAR and HTS Data-mining", East China University of Science and Technology, May 10, 2005, Shanghai, China. (Invited).

Professional activities

- **Editorial member:**
  - Current Bioinformatics
  - Drug Designing
- **Conference committee:**
  - Organizing Committee member of 2nd International Conference on Medicinal Chemistry & Computer Aided Drug Designing, October 15-17, 2013, Las Vegas, USA.
  - Program Committee Member of 2013 Ninth International Conference on Intelligent Computing (ICIC 2013), July 28-31, 2013, Nanning, China.
  - Organizing Committee member of the International Conference and Exhibition on Computer Aided Drug Design & QSAR, Oct 29-31, 2012, Chicago, USA.
  - Program Committee Member of 2011 International Conference on Computational Biology and Bioinformatics (CBB2011), Shanghai, China.
  - Program Committee Member of 2nd Machine Learning in Biomedicine and Bioinformatics Workshop (MLBB), December 11-13, 2008, San Diego, CA, USA
  - Technical Committee of IEEE World Congress on Computational Intelligence (WCCI 2008)
  - Referee for the Eighth International Conference on Control, Automation, Robotics and Vision (ICARCV 2004); 2008 International Conference on BioMedical Engineering and Informatics (BMEI2008); Fourth International Symposium on Bioinformatics Research and Applications (ISBRA08).
- **Grant reviewer:**

- NIH Special Emphasis Panel/Scientific Review Group 2013/01 ZRG1 IMST-G (10) B (Nov 2012)
- Stage-one (mail) reviewer for NIH IMST-10 small business panel (Jan 2012)
- M.J. Murdock Charitable Trust (Jan 2011)

- **Journal Referee**:
  PLOS One, Amino Acids, Journal of Pharmacy and Pharmacology, BBA-Proteins and Proteomics, Bioorganic & Medicinal Chemistry Letters, Drug Discovery Today, the journal of Engineering Letters, BMC Bioinformatics, BMC Genomics, BMC Research Notes, Journal of Biomedicine and Biotechnology, PMC Biophysics, Rapid Communication in Mass Spectrometry, International Journal of Automation and Computing, International Journal of Computational Biology and Drug Design, Computer Methods in Biomechanics and Biomedical Engineering, TALANTA, Bioinformatics, Journal of Computer Science and System Biology, Computational and Structural Biotechnology Journal.

Honors

1997, recipient of Robert Maytag Fellowship at University of Miami.
2013, Leading Light Award, University of Kansas

Research Grants

07/01/12 – 06/30/13 J.R. & Inez Jay Fund (PI: X. Wang) MicroRNA-regulated gene network in selective neuronal vulnerability. Role: Collaborator.

07/01/12 – 06/30/17 NIH 1P20GM103638 (PI: S. Lunte) Molecular analysis of disease pathways. Role: Sequencing core advisor.

07/06/11 – 04/30/15 NIH 5R01DK092100 (PI: Y. Wan) Retinic acid, its receptors, and the liver. Role: Co-I.

04/01/08 – 02/28/13 NIH P01AG12993 (PI: E. Michaelis) Reactive oxygen species and aging.
Role: Informatics leader.

04/01/09 – 03/31/13 NIH 2R01GM021784-31A1 (PI: R. Hanzlik) Reactive metabolites in drug toxicity.
Role: Co-I.

26/09/11 – 08/31/12 NIH 1R56DK090036 (PI: G. Guo) FXR, nuclear receptors, and transcriptional regulation of liver homeostasis. Role: Co-I.

05/01/11 – 04/30/12 NIH P20 RR016475 University of Kansas Medical Center (NIH/NCRR flow through) (PI: T. Williams) Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)
Role: Co-I.

07/01/06–06/30/10 NIH 1R01HL082734-01A1 (PI: W. Davidson) Roles of apolipoprotein A-IV structure/lipid affinity. Role: Co-I.

1/1/09 - 6/30/10 NIH RO1 DK067355 (PI: H. Zhou) Role of Ncb5or in Insulin Production
Role: Bioinformatics Support.

09/01/09 – 08/31/10 Institute for Advancing Medical Innovation PROOF-OF-CONCEPT grant (PI: Karanicolas) Design of a stabilized ricin vaccine. Role: Co-PI.

05/01/09–04/30/10 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: Data storage, analysis, and mining capability for next-gen sequencing. Role: PI.

05/01/10–04/30/11 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: KSCREEN, a HTS data management and analysis system. Role: PI.

02/07-02/09 KU Center for Chemical Methodology and Library Development (PI: G. Lushington), Strategic chemical synthesis guidance via data mining and analysis. Role: Co-I.

05/01/07–04/30/08 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: A web server for Tracker, an automated literature, protein/DNA sequence and domain tracking system. Role: PI.

05/01/07–04/30/08 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: A web server for Tracker, an automated literature, protein/DNA sequence and domain tracking system. Role: PI.

05/01/07–04/30/08 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: Bioinformatics Core Facility. Role: Co-PI.

09/01/04–06/30/07 NIH P01 RR017708 (PI: R. Hanzlik, Project PI: X. Chen) Project: *Computational Proteomics: Protein Interaction Prediction.* Role: Co-PI.

07/01/05–04/30/06 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: Bioinformatics Core Facility. Role: Co-PI.

09/01/06–08/31/07 NIH/NCRR P20 RR016475 *Kansas IDeA Network of Biomedical Research Excellence (K-INBRE)* Project: An Online Clearinghouse for Bioinformatics Software. Role: Co-PI.