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and
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San Diego State University

Grants
(Total funding as PI: $27.1M)

7/13-6/23 **Role:** *Principal Investigator*. **Title:** Functional and Evolutionary Significance of Novel Mutations in MDR-XDR TB. **Source**: NIH R01AI105185. This ten-year project studies the emergence and genetic mechanisms of resistance to two first line anti-TB drugs (isoniazid and rifampicin), and five second line anti-TB drugs (amikacin, kanamycin, capreomycin, moxifloxacin, and ofloxacin). The last four years of the project will study the emergence and genetic and epigenetic mechanisms of resistance to four new anti-TB drugs (bedaquiline, linezolid, clofazimine, and delamanid) and pyrazinamide in tuberculosis (TB).

9/10-8/14 **Role:** SDSU *Site Principal Investigator* (in charge of Bioinformatics for the GCDD consortium: http://gcdd.ucsd.edu/) with Antonino Catanzaro (UCSD, Medicine) as PI. **Title:** Global Consortium for Drug-resistant TB Diagnostics (GCDD) This project aimed to map out the genetic mechanism of resistance to first and second line drugs. **Source**: NIH U01AI082229. **Total SDSU Site Budget:** $826,931

8/10-1/17 **Role:** *Principal Investigator*, Co-Investigators: Richard Levine (SDSU Statistics) and Andrew Su (Novartis Genomic Research Institute) **Title:** Statistical Biomedical Informatics Track. This funding provided support for minority students in the Biomedical Informatics Program. **Source**: NSF 0966391. **Total Budget**: $598,000

7/10-6/14 **Role**: *Senior Investigator and* SDSU *Site Principal Investigator* with Lucila Ohno-Machado (UCSD, Medicine) as the PI. **Title**: iDASH: Integrating Data for Analysis Anonymization, and Sharing. The focus of this project was the secondary use and anonymization of patient medical records. **Source**: NIH U54HL108460. **SDSU Site Budget**: $375,750

1/07-12/11 **Role**: *Principal Investigator*. Co-Investigators: Thomas Scott (VP for Research, SDSU) and Keith Boyum (Associate Vice Chancellor for Academic Affairs, CSU Office of the Chancellor). **Title**: Advancing Professional Science Master's Programs in the California State University (CSU) System. **Source**: Alfred P. Sloan Foundation (#2008-6-6) and CSU system (#97C00-3). **Total Budget**: $18.01M. ($1.37M from Alfred P. Sloan Foundation and $16.64M from CSU Chancellor's Office and 12 CSU campuses)

8/07-7/08 **Role**: *Senior Investigator and* SDSU *Site Principal Investigator*. PI: Dr. Andrew Su (Scripps Research Institute and Genomic Institute of Novartis Research). **Title**: BioGPS Portal. **Source**: NIH R01GM083924. **SDSU Site Budget**: $36,243

5/06-4/08 **Role**: *Co-Principal Investigator*. **Title**: Cardiac Cell Calcium Pathway. Source: California Metabolic Research Foundation. **Total Budget**: $25,817

1/04-12/05 **Role**: *Principal Investigator*. **Source**: Alfred P. Sloan Foundation, CSU, and SDSU. Title: Professional Masters Degrees in Sciences in the State of California—a feasibility study. **Source**: Alfred P. Sloan Foundation (#2003-12-9), CSU Chancellor's Office (#CK 221250), and College of Sciences at SDSU. **Total Budget**: $227,000 (Sloan: $182,000, CSU Chancellor's Office $25,000, and SDSU College of Sciences: $20,000).

1997-2000 **Role**: *Co-Principal Investigator*. PI: Dr. Robert Cherniak. **Title**: *Cryptococcus neoformans*: Epitope Antibodies and Structure. **Source**: NIH RO1AI31769. **Total Budget**: $2.5M

1995-1999 **Role**: *Senior Investigator*. PI: Dr. Peter Albersheim. **Title**: Resource Center for Biomedical Complex Carbohydrates. **Source**: NIH P41-RR-05351. **Total Budget**: $10M

Publications

Selected Books & Journal Editorials

1. **Valafar, F.** 2002. **Editor**, "Techniques in Bioinformatics and Medical Informatics", *New York Academy of Sciences*. Vol. 980, December 2002. 314 pages with 24 sections on clinical applications. (http://onlinelibrary.wiley.com/doi/10.1111/nyas.2002.980.issue-1/issuetoc) (https://www.amazon.com/Techniques-Bioinformatics-Medical-Informatics-Sciences-dp-1573314331/dp/1573314331/ref=mt_paperback)
2. **Valafar F.** 2001. **Author**, Chapter 4: "Application of Neural Networks in Medicine and Biology" of the book titled *Introduction to Intelligent Control Systems Using Artificial Neural Networks and Fuzzy Logic*. CRC Press, ISBM: 0849318750.
3. **Valafar, F.** 2000-2006. **Editor**, *Proceedings of the International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences* (*METMBS*). ISBN numbers: 1-892512-60-2 (Volume I), 1-892512-61-0 (Volume II), and 1-892512-62-9 (complete set). CSREA press, USA, 2000-2006.

Select Peer-Reviewed Journal Publications

* Indicates graduate or undergraduate student, project scientist, or postdoc directly supervised by me

1. Alyamani EJ, Marcus SA, Ramirez-Busby SM, Hansen C, Rashid J, El-kholy A, Spalink D, **Valafar F**, Almehdar HA, Fatani AJ, Khiyami MA, and Talaat AM. Genomic analysis of the emergence of drug-resistant strains of Mycobacterium tuberculosis in the Middle East. *Nature Scientific Report*, Sci Rep. 2019 Mar 14;9(1):4474. doi: 10.1038/s41598-019-41162-9.
2. Ramirez-Busby SM, Rodwell TC, Fink L, Catanzaro D, Jackson RL, Pettigrove M, Catanzaro A, and **Valafar F**. A Multinational Analysis of Mutations and Heterogeneity in PZase, RpsA, and PanD Associated with Pyrazinamide Resistance in M/XDR *Mycobacterium tuberculosis*. *Nature Scientific Report*, 2017 Jun 19. doi: 10.1038/s41598-017-03452-y
3. Marney MW, Metzger RP, Hecht D, **Valafar, F**. Modeling the structural origins of drug resistance to isoniazid via key mutations in *Mycobacterium tuberculosis* catalase-peroxidase, KatG. *Tuberculosis*, Elsevier, SN: 1472-9792, DOI: 10.1016/j.tube.2017.11.007, 2017/12/07.
4. Elghraoui A, Modlin S*, **Valafar F**. SMRT Genome Assembly Corrects, Reference Errors, Resolving the Genetic Basis of Virulence in Mycobacterium tuberculosis. *BMC Genomics*, DOI: 10.1186/s12864-017-3687-5
5. Alotaibi M, Reyes BD, Le T, Luong P, **Valafar F**, Metzger RP, Fogel GB, Hecht D. Structure-based analysis of Bacilli and plasmid dihydrofolate reductase evolution. *J Mol Graph Model*, 2017, doi: 10.1016/j.jmgm.2016.10.011
6. Georghiou SB, Seifert M, Catanzaro D, Garfein RS, **Valafar F**, Crudu V, Rodrigues C, Victor TC, Catanzaro A, and Rodwell TC. Frequency and Distribution of Tuberculosis Resistance-Associated Mutations between Mumbai, Moldova, and Eastern Cape. *Antimicrobial Agents and Chemotherapy*, April 2016, doi: 10.1128/AAC.00222-16.
7. Torres J*, Paul L, Rodwell TC, Victor TC, Amallrajaa AM*, Elghraouia A*, Goodmanson A*, Ramirez-Busby SM*, Chawlaa A*, Zadorozhnya V*, Streicherb L, Sirgel FA, Catanzaro D, Rodrigues C, Glere M, Crudu V, Catanzaro A, **Valafar F**. Novel katG Mutations Identified in Isoniazid-Resistant Clinical *Mycobacterium tuberculosis* Isolates. *Nature Journal of Emerging Microbes & Infections* (2015) **4**, e42; doi:10.1038/emi.2015.42. (http://www.nature.com/articles/emi201542)
8. **Valafar F**. Pathogenesis of multi drug-resistant and extensively drug-resistant tuberculosis as a determinant of future treatment success. *International Journal of Mycobacteriology*. DOI: 10.1016/j.ijmyco.2016.11.017

9. Catanzaro A, Rodwell TC, Catanzaro DG, Garfein RS, Jackson RL, Seifert M, Georghiou SB, Trollip A, Groessl E, Hillery N, Crudu V, Victor TC, Rodrigues C, Lin GS, **Valafar F**, Desmond E, Eisenach K. Performance Comparison of Three Rapid Tests for the Diagnosis of Drug-Resistant Tuberculosis. *PLoS One*. 2015 Aug 31;10(8):e0136861. doi: 10.1371/journal.pone.0136861.

10. Ramirez-Busby SM*, **Valafar F**. Systematic Review of Mutations in Pyrazinamidase Associated with Pyrazinamide Resistance in *Mycobacterium tuberculosis* Clinical Isolates. *J Antimicrobial and Chemotherapy* September 2015, doi: 10.1128/AAC.00204-15.

11. Garfein RS, Catanzaro D, Rodwell TC, Avelos E, Jackson L, Kaping J, Evasco H, Rodrigues C, Crudu V, Lin S-YG, Grossel E, Hillery N, Trollip A, Ganiats T, Victor TC, Glere M, Eisenach K, **Valafar F**, Channick J, Qian L, Catanzaro A. Phenotypic and Genotypic Diversity in a Multinational Sample of Drug-resistant Mycobacterium *tuberculosis* Isolates. International Journal of *Tuberculosis and Lung Disease*, Volume 19, Number 4, 1 April 2015, pp. 420-427(8).

12. Hillery N, Groessl EJ, Trollip A, Catanzaro D, Jackson L, Rodwell TC, Garfein RS, Lin S, Eisenach K, Ganiats TG, Park D, **Valafar F**, Rodrigues C, Crudu V, Victor TC, Catanzaro A. The Global Consortium for Drug-resistant Tuberculosis Diagnostics (GCDD): Design of a multi-site, head-to-head study of three rapid tests to detect extensively drug-resistant tuberculosis. *Trials*. 2014 Nov 6;15:434. doi: 10.1186/1745-6215-15-434

13. Colman R, Schupp JM, Hicks ND, Smith DE, Buchhagen DL, **Valafar F**, Crudu V, Romancenco E, Noroc E, Jackson L, Catanzaro D, Rodwell TC, Catanzaro A, Keim P, Engelthaler DM. Detection of low-level mixed-population drug resistance in *Mycobacterium tuberculosis* using high fidelity amplicon sequencing. *PLOS One*, DOI: 10.1371/journal.pone.0126626.

14. **Valafar F**, Ramirez-Busby SM, Torres J, Paul LV, Rodwell TC, Victor TC, Rodrigues C, Gler MT, Crudu V, Catanzaro A. Prognostic Significance of Novel katG Mutations in Mycobacterium Tuberculosis. *International Journal of Mycobacteriology*. doi:10.1016/j.ijmyco.2014.11.043. 2015; (4)1:51-52.

15. Rodwell TC, **Valafar F**, Douglas J, Qian L, Garfein RS, Chawla A, Torres J*, Zadorozhny V*, Soo Kim M*, Hoshide M, Catanzaro D, Jackson L, Lin G, Desmond E, Rodrigues C, Eisenach K, Victor TC, Ismail N, Crudu V, Gle MT, Catanzaro A. Predicting Extensively Drug-resistant Tuberculosis (XDR-TB) Phenotypes with Genetic Mutations. *J Clin Microbiol*. 2014; 52(3):781-9. PMCID: PMC395777,110.1128/JCM.02701-13.

16. Bowman BN*, McAdam PR, Vivona S, Zhang JX, Luong T, Belew RK, Sahota H, Guiney D, **Valafar F**, Fierer J, Woelk CH. Improving Reverse Vaccinology with a Machine Learning Approach, ***Vaccine*** 2011 Oct 19;29(45):8156-64. doi:10.1016/j.vaccine.2011.07.142. Epub 2011 Aug 22.
Journal Impact factor at time of submission: **3.467**

17. Rudy J* and **Valafar F.**, Empirical comparison of cross-platform normalization methods for gene expression data. ***BMC Bioinformatics*** 2011, **12**:467.doi:10.1186/1471-2105-12-467. Epub 2011 Dec7.
Journal Impact factor at time of submission: **3.03**

18. Huss J III*, Lindenbaum P, Martone M, Roberts D, Pizarro A, **Valafar F**, Hogenesch J, Su A. The Gene Wiki: Community intelligence applied to human gene annotation. ***Nucleic Acid Research***, 38(1), D633-D639. doi:10.1093/nar/gkp760. 2010
Journal Impact factor at time of submission: **7.836**

19. J. L. Turner, S. T. Kelley, J. S. Otto, **F. Valafar** and A. J Bohonak. Parallelization and optimization of genetic analyses in Isolation by Distance Web Service. ***BMC Genetics***, 10:28 doi:10.1186/1471-2156-10-28. Epub 2009 June 19.
Journal Impact factor at time of submission: **2.49**

20. J. W. Huss III*, C. Orozco, J. Goodale, C. Wu, S. Batalov, T. J. Vickers, **F. Valafar**, A. I. Su. A Gene Wiki for Community Annotation of Gene Function. ***PLoS Biology***. 2008 July; 6(7): e175. doi:10.1371/journal.pbio.0060175
Journal Impact factor at time of submission: **14.101** Featured in over 75 articles internationally:
   - USA Today: http://www.usatoday.com/tech/webguide/internetlife/2008-07-10-gene-wiki_N.htm

- Sydney Morning Herald: http://www.smh.com.au/news/web/wikipedia-to-catalogue-human-genes/2008/07/08/1215282797061.html

21. J. Wegrzyn*, T. Drudge*, **F. Valafar**, and V. Hook. Bioinformatic Analyses of Mammalian 5'-UTR Sequence Properties of mRNAs Predicts Alternative Translation Initiation Sites. ***BMC Bioinformatics***, 2008, 9:232. doi:10.1186/1471-2105-9-232
Impact Factor at time of submission: **4.958**

22. G. Hernandez*, **F. Valafar**, W. E. Stumph. Insect Small Nuclear RNA Gene Promoters Evolve Rapidly yet Retain Conserved Features Involved in Determining Promoter Activity and RNA Polymerase Specificity. ***Nucleic Acid Research***. 35(1): 21-34 2007, Oxford University Press. doi:10.1093/nar/gkl98
Impact Factor at time of submission: **6.954**

23. **Valafar, F.** 2002. Invited article: Pattern Recognition Techniques in Microarray Data Analysis: A Survey. Special Issue ***Annals of New York Academy of Sciences***, Techniques in Bioinformatics and Medical Informatics. Volume 980, December 2002, 41-64. Cited by over 150 articles. http://onlinelibrary.wiley.com/doi/10.1111/j.1749-6632.2002.tb04888.x/pdf. Impact Factor: **2.67**

24. Valafar H.*, J. H. Prestegard, and **F. Valafar** 2002. Datamining Protein Structure Databanks for Crystallization patterns of Proteins. Special Issue ***Annals of New York Academy of Sciences***, Techniques in Bioinformatics and Medical Informatics. Volume 980, December 2002, 13-22.
Impact Factor: **2.67**

25. Valafar H.* and **F. Valafar** 2002. Data Mining and Knowledge Discovery in Proton Nuclear Magnetic Resonance (^{1}H-NMR) Spectra using Frequency Information Transformation (FIT). Journal of ***Knowledge Based Systems***. Special issue on Knowledge Discovery and Data Mining. Elsevier publications. **15** (2002) 251-259.
Impact Factor: **1.574**

26. Valafar H.*, **F. Valafar**, Alan Darvill, Peter Albersheim, Abdullah Kutlar, Christy Woods, and John Hardin, 2000. Predicting the effectiveness of Hydroxyurea in Individual Sickle Cell Anemia Patients. *Journal of* ***Artificial Intelligence in Medicine***. **18 (2):** 133-148 February 2000.
Impact Factor: **1.891**

27. **Valafar F.,** H. Valafar* 1999. CCRC-Net: An Internet-Based Spectral Database for Complex Carbohydrates, Using Artificial Neural Networks Search Engines. ***Trends in Analytical Chemistry* (TRAC)**, **18 (8)** 508-512 August 1999.
Impact Factor: **6.623**

28. Cherniak R., H. Valafar*, L. C. Morris*, and **F. Valafar** 1998. *Cryptococcus neoformans* Chemotyping by Quantitative Analysis of ^{1}H-NMR Spectra of Glucuronoxylomannans Using a Computer Based Artificial Neural Network. ***Clinical and Vaccine Immunology*** March 1998 **5(2):** 146-159. Impact Factor: **3.217** Cited over 170 times.

29. Cherniak R., H. Valafar*, L. C. Morris*, and **F. Valafar** 1997. *Cryptococcus neoformans* Chemotyping by Quantitative Analysis of ^{1}H-NMR Spectra of Glucuronoxylomannans Using a Computer Based Neural Network. ***American Society for Microbiology (ASM)***. 97th General Meeting, Miami, Florida, May 4-8, F39 page 266.

30. **Valafar F.** and O. K. Ersoy. 1996. PNS modules for the synthesis of parallel self-organizing hierarchical neural networks. *Journal of* ***Circuits, Systems, and Signal Processing*** 15(1):23-50.

Select Peer-Reviewed Conference Publications

* Indicates graduate or undergraduate student, project scientist, or postdoc directly supervised by me

1. Invited Talk: Stanford University, School of Medicine, "The Genetic and Epigenetic Basis of Virulence and Antibiotic Resistance in *Mycobacterium tuberculosis* (*Mtb*)," School of Medicine, Stanford University, Stanford, CA, United States. (September 7, 2017).

2. Invited Talk: The Republican Research and practical Centre for Pulmonology and TB, "Pathogenesis of Drug Resistance as a Molecular Basis for tuberculosis Prognostics," The Republican Research and practical Centre for Pulmonology and TB, Minsk, Belarus. (August 11, 2017).

3. Invited Talk: Karolinska Institute, "The Molecular Basis for Phenotypic Diversity of *Mycobacterium tuberculosis*," Public Health Agency of Sweden, Kariloniska Institute, Stockholm, Sweden. (August 9, 2017).
4. Invited Talk: Institute of Tropical Medicine, "The Molecular Epidemeology of *Mycobacterium tuberculosis*," Institute of Tropical Medicine, Antwerp, Belgium. (August 7, 2017).
5. ESM Congress, "Characterization of Variants Observed in pncA, rpsA, and panD and Association to PZA Susceptibility Testing and Pyrazinamidase Activity in MDR/XDR *M. tuberculosis* Clinical Strains," European Society for Mycobacteriology, Sibenik, Croatia. (June 27, 2017).
6. ESM Congress, "Characterizing Heterogeneous DNA Methylation in *Mycobacterium tuberculosis* Clinical Isolates with Single-Molecule Real-Time (SMRT) Sequencing," European Society for Mycobacteriology, Sibenik, Croatia. (June 25, 2017).
7. ASM Conference on Tuberculosis: Past, Present, and Future, "Canonical and Novel Variants in DNA Gyrase of mostly XDR Clinical *Mtb* Isolates from Four High TB Burden Countries," American Society for Microbiology, Brooklin, NY, United States. (April 3, 2017).
8. ASM Conference on Tuberculosis: Past, Present, and Future, "Constructing A Genome-Scale Model of Metabolism and Gene Expression For *Mycobacterium tuberculosis*," American Society for Microbiology, Brooklin, NY, United States. (April 3, 2017).
9. ASM Conference on Tuberculosis: Past, Present, and Future, "“Hole” Genome Sequencing: Illumina Blind Spots in *Mycobacterium tuberculosis* Genome," American Society for Microbiology, Brooklin, NY, United States. (April 3, 2017).
10. ASM Conference on Tuberculosis: Past, Present, and Future, "Annotating the *M. tuberculosis* Hypotheticome: Annotations with Unspecific or Absent Products via Literature Review," American Society for Microbiology, Brooklin, NY, United States. (April 2, 2017).
11. ASM Conference on Tuberculosis: Past, Present, and Future, "Annotating the *M. tuberculosis* Hypotheticome: In Silico Prediction of Gene Product Using Structural Homology," American Society for Microbiology, Brooklin, NY, United States. (April 2, 2017).
12. ASM Conference on Tuberculosis: Past, Present, and Future, "Characterization of Variants Observed In pncA, rpsA, And panD and Association to PZA Susceptibility Testing and Pyrazinamidase Activity In MDR/XDR *M. tuberculosis* Clinical Strains," American Society for Microbiology, Brooklin, NY, United States. (April 2, 2017).
13. ASM Conference on Tuberculosis: Past, Present, and Future, "Characterizing Heterogeneous DNA Methylation in *Mycobacterium tuberculosis* Clinical Isolates with Single-Molecule Real-Time (SMRT) Sequencing," American Society for Microbiology, Brooklin, NY, United States. (April 2, 2017).
14. Tuberculosis 2016, "Prevalence of PZase, PanD, and RpsA Mutations in Multidrug- and Extensively-Drug Resistant *Mycobacterium tuberculosis* Clinical Isolates," EMBO (European Molecular Biology Organization), Institute Pasteur, Paris, France. (September 23, 2016).
15. Tuberculosis 2016, "Lineage-specific Copy Number and Distribution of IS6110 in de novo-assembled *Mtb* Isolates," EMBO (European Molecular Biology Organization), Institute Pasteur, Paris, France. (September 21, 2016).
16. Tuberculosis 2016, "MIRU-Heuristics for Evaluation of Repeats and their Ordinal (MIRU-HERO): MIRU analysis on genomic sequencing data," EMBO (European Molecular Biology Organization), Institute Pasteur, Paris, France. (September 20, 2016).
17. Tuberculosis 2016, "Whole genome phylogenetic analysis of M/XDR-TB clinical isolates from high burden countries," EMBO (European Molecular Biology Organization), Institute Pasteur, Paris, France. (September 20, 2016).
18. Tuberculosis 2016, "Lineage-based analysis of genomic methylation and variations within methyltransferases in *Mycobacterium tuberculosis* using kinetic data from Single- Molecule Real-Time

(SMRT) sequencing technology in clinical isolates," EMBO (European Molecular Biology Organization), Institute Pasteur, Paris, France. (September 19, 2016).

19. Tuberculosis 2016, "SMRT genome assembly corrects reference errors, resolving the genetic basis of virulence in *Mycobacterium tuberculosis*," EMBO (European Molecular Biology Organization), Institute Pasteur, Paris, France. (September 19, 2016).A Amallraja*, A Goodmanson*, S Ramirez-Busby, R Shanmugam*, TC Rodwell, D Catanzaro, C Rodrigues, MT Gler, TC Victor, V Crudu, T Catanzaro, F Valafar. Variants in DNA gyrase and efflux pumps in Fluoroquinolone Resistant Clinical Mtb Isolates. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA
20. CK Chan*, R Shanmugam*, TC Rodwell, C Rodrigues, MT Gler, TC Victor, V Crudu, T Catanzaro, S Hoffner, F Valafar, Phylogenetic analysis of clinical *Mycobacterium tuberculosis* isolates from high-burden countries. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
21. A Elghraoui, LD Fink, AP Goodmanson*, F Valafar. de novo Assembly and Genome Closure of 51 MDR/XDR *Mtb* clinical isolates. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
22. L Fink*, A Elghraoui, S Ramirez-Busby, S Hoffner, T Rodwell, R Garfein, C Rodrigues, T Catanzaro, F Valafar. Structural Variation in PZA-monoresistant *Mtb*. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
23. S Modlin*, S Patel*, L Fink*, A Elghraoui, S Hoffner, F Valafar. Lineage-specific Copy Number and Distribution of IS6110 in de novo-assembled *Mtb* Isolates. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
24. Y Kim*, D Oh*, A Elghraoui, F Valafar. HADTB: Hub for Aggregated Data in Tuberculosis, an aggregated database for sharing, annotating, and analyzing tuberculosis genomic data. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
25. S Ramirez-Busby, L Fink*, T Rodwell, M Pettigrove, L Jackson, D Catanzaro, A Goodmanson*, A Amallraja*, R Shanmugam*, C Rodrigues, M Gler, T Victor, V Crudu, A Catanzaro, F Valafar. Prevalence of PZase, PanD, and RpsA Mutations in MDR/XDR-TB Clinical Isolates. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
26. R Shanmugam*, C Chan*, S Ramirez-Busby, T Rodwell, C Rodrigues, M Gler, T Victor, V Crudu, S Hoffner, A Catanzaro, F Valafar. Whole Genome Analysis of M. tuberculosis clinical isolates reveals distinct evolutionary pattern in PE/PPE genes. Keystone Symposium on Tuberculosis Comorbidity and Immunopathogenesis. Feb. 28 – March 3, 2016, Keystone, Colorado, USA.
27. Ramirez-Busby SM*, Rodwell TC, Garfein RS, Rodrigues RS, Gler RS, Victor TC, Crudu TC, Catanzaro A, **Valafar F**, Phylogenetic Trends of pncA Mutations in *Mycobacterium tuberculosis* Clinical Strains. 9th *International Conference on the Pathogenesis of Mycobacterial Infections*, 26-29 June 2014, Stockholm, Sweden.
28. **Valafar F**, Torres J*, Victor TC, Rodwell TC, Garfein RS, Rodrigues C, Gler MT, Crudu V, Catanzaro T. Novel *katG* Mutations Identified in *Mycobacterium tuberculosis* Provide a More Comprehensive Diagnostics for Isoniazid Resistance and Better Clinical Management of Drug Resistant TB. 9th *International Conference on the Pathogenesis of Mycobacterial Infections*, 26-29 June 2014, Stockholm, Sweden.
29. **Valafar F**, Rodwell TC, Garfein RS, Rodrigues C, Gler MT, Victor TC, Crudu V, Catanzaro A. Beyond Diagnosis and Towards Prognosis of Tuberculosis with Whole-Genome Sequencing. 9th *International Conference on the Pathogenesis of Mycobacterial Infections*, 26-29 June 2014, Stockholm, Sweden.
30. Rodwell TC, **Valafar F**, Garfein RS, Rodrigues C, Victor TC, Crudu V, Catanzaro A. Interpreting the mutations that predict phenotypic drug resistance in *M. tuberculosis*. *US-Japan Cooperative Medical*

Science Program's 16th International Conference on Emerging Infectious Diseases in the Pacific Rim: Antimicrobial Drug Resistance in Bacterial and Parasitic Diseases; February 9-13, 2014; Dhaka, Bangladesh. 2014.

31. **Valafar F**, Torres J, Victor TC, Rodwell TC, Garfein RS, Rodrigues C, Gler MT, Crudu V, Catanzaro T. **Abstract selected for oral presentation:** Novel *katG* Mutations Identified in *Mycobacterium tuberculosis* Provide a More Comprehensive Diagnostics for Isoniazid Resistance and Better Clinical Management of Drug Resistant TB. *International Union Against Tuberculosis and Lung Disease: 18th Conference of The Union North American Region; February 27-March 1, 2014*
32. **F Valafar**, Rodwell TC, Garfein RS, Rodrigues C, Gler MT, Victor TC, Crudu V, Catanzaro A. PacDAP: A Whole Genome Sequencing Platform for Identifying Mutations Associated with Drug Resistance in *Mycobacterium tuberculosis. International Union Against Tuberculosis and Lung Disease: 18th Conference of The Union North American Region; February 27-March 1, 2014*
33. Rodwell TC, **Valafar F,** Garfein RS, Douglas J, Rodrigues C, Crudu V, Victor TC, Catanzaro A. Sensitivity and specificity of mutations for predicting global XDR-TB phenotypes. *International Union Against Tuberculosis and Lung Disease: 44th Union World Conference on Lung Health*; October 30th - November 2nd, 2013; Paris, France.
34. **Valafar F**, Rodwell TC, Garfein RS, Rodrigues C, Gler MT, Victor TC, Crudu V, Catanzaro A. Clincal molecular diversity of tuberculosis on a genome-wide scale: lessons learnt for molecular diagnostics. *International Union Against Tuberculosis and Lung Disease: 44th Union World Conference on Lung Health*; October 30th -November 2nd, 2013; Paris, France.
35. Colman RE, Schupp JA, Smith D, Keim PS, **Valafar F**, Rodwell TC, Catanzaro A, Engelthaler DE. Advancing heteroresistance detection in tuberculosis using single molecule-overlapping read (smor) analysis. IDWeek 2013 Conference; October 2-6, 2013; San Francisco, CA. 2013.
36. Rodwell TC, **Valafar F**, Garfein RS, Douglas J, Rodrigues C, Crudu V, Victor TC, Gler M, Catanzaro A. Predicting XDR-TB Phenotypes Accurately with Single Nucleotide Polymorphisms. *17th Annual Conference: International Union Against Tuberculosis and Lung Disease – North America Region*; February 28 - March 2, 2013; Vancouver, BC, Canada. 2013.
37. **Valafar F**, Catanzaro A. **Abstract selected for Oral Presentation:** Application of Whole Genome Sequencing (WGS) to Diagnosis of Drug Resistance in Tuberculosis. *APHL 8th National Conference on Laboratory Aspects of Tuberculosis*. August 19-21, 2013. San Diego, California
38. Rodwell TC, **Valafar F**, Garfein R, Douglas J, Rodrigues C, Crudu V, Victor T, Catanzaro A. Detecting XDR-TB phenotypes with single nucleotide polymorphisms. *International Union Against Tuberculosis and Lung Disease: 43rd Union World Conference on Lung Health*; November 13, 2012; Kuala Lumpur, Malaysia. 2012
39. Ballas SK, McCarthy WF, Bauserman RL, **Valafar F**, Waclawiw M, Barton BA & Kutlar A. (2009) Definition of the Responder to Hydroxyurea Therapy: Revisited. 51st Annual Meeting of the ***American Society of Hematology (ASH)***. December 5-8, 2009, New Orleans, LA
40. A. Salim*, **F. Valafar**. Reconstruction of Gene Regulatory Networks from Temporal Microarray Data Using Order Estimation Criteria and Artificial Neural Networks, *IEEE World Congress on Computational Intelligence*, and *International Joint Conference on Neural Networks* (IJCNN'06), Vancouver, Canada, July 16-21 2006, 4588-4593.

Select Invited Lectures

2005-Present Seventy Eight Invited Lectures and Talks, in 15 countries (Austria, Belarus, Belgium, China, Croatia, France, India, Italy, Mexico, Moldova, South Africa, Sweden, Switzerland, Uganda, and USA), including 36 webinars with participants from around the globe in the last seven years as part of the International Union Against Tuberculosis and Lung Disease (IUTLD). In the US, I have delivered lectures at CDC, NIH, and a number of academic institutions. Diseases discussed: Drug-resistant tuberculosis, MRSA, cryptococcus neoformans, and tracking the spread of H1N1. A short selection of the more significant talks given in the last three years is listed below:

May 22, 2018 **"On the Emergence of Enhanced Phenotypes (Multi-Drug Resistance, Hyper Virulence) in TB-HIV Coinfected Hosts: Host Immunity Revisited"**, Institute of Tropical Medicine, Antwerp, Belgium

May 25, 2018 **"Effects of Molecular Diagnostics on Epidemiology and Detectability of Drug Resistance in Tuberculosis"**, Karolinska Institute, Stockholm, Sweden

May 28, 2018 **"Molecular Diagnostics for Infectious Diseases: Significance of Background Mutations as a Determinant of Treatment Outcome"**, The Republican Research and Practical Centre for Pulmonology and Tuberculosis, Minsk, Belarus

Jan. 05, 2018 **"The Genome-Wide Hunt for Elusive Keystone Mutations in Drug Resistant *Mtb*"**, Division of Pulmonary and Critical Care Medicine, Johns Hopkins University.

Aug. 25, 2017 **"The Molecular Basis for Phenotypic Diversity in *Mycobacterium tuberculosis*"**, Stanley Ho Center for Emerging Infectious Diseases, Hong Kong, China.

Jun. 06, 2017 **"The Genetic and Epigenetic Basis of Virulence and Antibiotic Resistance in *Mycobacterium tuberculosis* (*Mtb*)"**, School of Medicine, Stanford University, Stanford, California.

Jan. 17, 2017 **"Transmission of Hypervirulence and Antibiotic Resistance in *Mycobacterium tuberculosis* (*Mtb*) among Patients in Hospital Settings"**, Department of Infectious Diseases and Hospital Epidemiology, University Hospital, Zurich, Switzerland.

Jan. 16, 2017 **"The Genetic and Epigenetic Basis of Virulence and Antibiotic Resistance in *Mycobacterium tuberculosis* (*Mtb*)"**, Institute for Medical Microbiology, University of Zurich, Switzerland.

Sep. 23, 2016 **"On the Role of Population Dynamics and Host Immunity in Emergence of Drug Resistance in *Mycobacterium tuberculosis* – A Spatiotemporal Systems Perspective"**, Pasteur Institute, Paris, France.

Feb. 24, 2016 **"Molecular Basis for Drug Resistance in *Mtb*".** Institute for Global Health, Vanderbilt University, Vanderbilt University, Nashville, Tenessee

Jan. 19, 2016 **"Genotyping Fluoroquinolone Resistance in *Mycobacterium tuberculosis*—the Emergence of Mono-Fluoroquinolone Resistance in the United States"**, Webinar organized by Karolinska Institute and the Public Health Agency of Sweden, Stockholm, Sweden. Participants from India, Moldova, Netherlands, the Philippines, South Africa, Sweden, and several institutions from the US (Duke University, Georgia State University, University of Michigan, and University of Pennsylvania).

May 18, 2015 **"On the Causality of Drug Resistance in *Mycobacterium tuberculosis* – A Systems Perspective"**, Pulmonary Grand Rounds, Division of Pulmonary Medicine, School of Medicine, UCSD.

Professional Experience

Research and Development Experience: 14 years

07/2013-Present **Founding Director and Principal Investigator**, *Laboratory for Pathogenesis of Clinical Drug Resistance and Persistence (LPCDRP)* (http://tuberculosis.sdsu.edu/), Alvarado Medical Center, San Diego, California. Created through an R01 funding from NIH, LPCDRP has received a total of over $8M since its inception. This includes $3.5M of competitive renewal funding for its core mission. LPCDRP studies clinically-relevant enhanced phenotypes (e.g. multi/extensive drug resistance, hypervirulence, and persistence) in infectious diseases. Primarily, we study mechanisms and pathogenesis of such phenotypes in *Mycobacterium tuberculosis*. This project involves 10 (seven international and three US) sites. This project involves, GWAS studies using NGS, genomics, functional genomics, epigenomics, metabolic and regulatory network reconstruction, metagenomics, transcriptomics, phylogenomics, and mutagenesis for functional confirmation of the role of the identified molecular markers in emergence of enhanced phenotypes. As the PI, I supervise all aspects of the project including clinical trials, wet lab mutagenesis and phenotypic determinations in BSL3 environment, as well as all software engineering projects for the development of high throughput pipeline for all in silico analyses and the development of a molecular diagnostic pipeline using NGS and TGS. As part of this project we also collaborate with the World Health Organization (WHO) to provide consultation to various international health organizations for procedural implementation of the developed diagnostics platforms. A renewal application (for additional $3.5M) for this project has just been funded. Total current funding: $8M.

8/02-10/2017 **Founding Director**, *Bioinformatics and Medical Informatics Research Center (BMIRC)* (http://informatics.sdsu.edu/), San Diego State University, San Diego, California. Responsibilities include direction of large center-wide research projects, fund raising, writing center grants and industry contracts (center runs entirely on these funds), budgeting and financial planning for the center, management of all aspects of the center (currently includes 35 faculty from SDSU, UCSD, and Scripps and 4 staff members), management of outreach to industry and community, consulting projects with industry, creation and maintenance of informatics laboratories for research and development, industry training in a number of areas within the fields of Biomedical Informatics, Infectious Disease Genomics, Datamining, Systems Engineering, and Computer Science (including Software Engineering for clinical applications). Annual budget: $1M.

8/03-8/12 **Founding Director**, *CSU Professional Science Master's Initiative (CSU-PSM)* (http://www.calstate.edu/psm/), CSU Office of the Chancellor, Long Beach, California. Responsibilities include development, creation, and managing 17 PSM programs on 14 CSU campuses. This included a state-wide assessment of state-wide industry needs (hired California Council on Science and Technology [http://ccst.us/] for this task), state-wide assessment of student interest in new interdisciplinary technology and science domains (hired the Social Science Research Center at CSU Fullerton [http://www.fullerton.edu/ssrc/] to conduct this survey), using the results of the surveys to write proposals to Alfred P. Sloan Foundation and the CSU Chancellor's Office, successfully raising a total of $18.01M in funding for the project, creation of the financial infrastructure of 17 self-supporting programs, continued market and demand analysis, annual fundraising and sustainability, curricular design and the approval process of all 17 programs. Total budget: $18.01M.

Academic and Research Appointments: 17 years

8/14-Present **Professor**, Biomedical Informatics Research Center, School of Public Health, and Department of Computer Science, **San Diego State University**, San Diego, CA. Research focus on infectious disease diagnostics and prognostics. Special focus on emergence of enhanced phenotypes in tuberculosis and MRSA infections.

8/01-7/14 **Associate Professor**, Department of Computer Science, **San Diego State University**, San Diego, CA. Research and student supervision have included projects in automated medical decision-making, medical and biochemical pattern recognition, bioinformatics, and high-performance computing.

8/99-7/01 **Research Assistant Professor**, Department of Cognitive and Neural Systems, **Boston University**, Boston, MA. Research and student supervision have included projects in automated medical decision-making, medical and biochemical pattern recognition, Bioinformatics, and computational science.

8/99-7/01 **Director Computational Laboratory,** Department of Cognitive and Neural Systems, **Boston University**, Boston, MA. Projects have included the development (design and implementation) of a distributed computational environment for the department. My research was also involved in taking advantage of the distributed environment (a number of Linux workstations) in speeding up large simulations.

1/97-8/99 **Assistant Research Biochemist**, Department of Biochemistry and Molecular Biology, and the Complex Carbohydrate Research Center of **University of Georgia**, Athens, GA. Duties included the supervision of two NIH funded projects in biomedical applications of artificial neural networks (ANNs) in addition to the responsibilities of my position as project director.

5/96-8/99 **Project Director, Senior Investigator and Chief Information Officer**, Complex Carbohydrate Research Center (CCRC), The **University of Georgia**, Athens, GA. Lead the technological research and development project entitled, "Development of Computer-Assisted Methods for the Structural Characterization of Oligosaccharides", one of four R&D projects of the National Institutes of Health (NIH)-funded Resource Center for Biomedical Complex Carbohydrates. Duties also included the supervision of two junior level postdoctoral research associates.

11/94-4/96 **Postdoctoral Research Associate**, Complex Carbohydrate Research Center (CCRC), University of Georgia, Athens, GA. Research on classifying gas chromatography-electron impact mass spectra (GC-EIMS) of complex carbohydrates using artificial neural networks. This project included developing an artificial neural network system that could learn to identify complex carbohydrates using their mass spectral information.

Awards, and Honors

2000-2006 *Founding Chair*, METMBS. Annual *International Conference on Mathematics and Engineering Techniques in Medicine and Biological Sciences* (METMBS).

June, 2006 *Co-Chair*, the 2006 International Conference on Bioinformatics and Computational Biology (BIOCOMP'06). Las Vegas, Nevada, June 26-29, 2006.

June, 2006 *Achievement award.* In recognition and appreciation of research contributions to the field and to the 2006 World Congress on Computer Science, Computer Engineering, and Applied Computing (*WORLDCOMP'06*).

2001-2005 *Achievement award.* World Academy of Sciences. In recognition and appreciation of research contributions to the field and to the 2005 World Congress in Applied Computing.

2001-2007 *Vice-Chair* Multi-conference in Computer Sciences. Currently includes 14 conferences in various disciplines of Computer Science.

1994-1996 *Postdoctoral Research Fellowship* in Biochemistry and Cell Molecular Biology, Complex Carbohydrate Research Center, University of Georgia, Athens, Georgia.

Fall 90-Win. 92 *David Ross Research Fellowship*, Departments of Speech and Audiology and Electrical Engineering, Purdue University, West Lafayette, Indiana.

Fall 87-Win. 88 *Young Investigator Award.* AT&T Bell Labs, in speech recognition. Department of Electrical Engineering, Michigan Technological University, Houghton, Michigan.

Professional Memberships

- American Society for Microbiology (ASM). 2014 – Present
- European Society for Mycobacteriology (ESM). 2014 – Present
- International Union Against Tuberculosis and Lung Disease (IUATLD) 2012 – Present
- AMIA, American Medical Informatics Association, Jan. 2005-present
- IEEE Signal Processing Society, 1995-present
- IEEE Man, System, and Cybernetics Society, 1995-present
- IEEE Engineering in Medicine and Biology (EMB) Society, 1995-present
- Eta Kappa Nu honor society, 1990-present
- Phi Kappa Phi honor society, 1987-present
- Sigma Xi (scientific research honor society), 1987-present

Education

Jun. 1996 Postdoctoral Research Fellowship. Project: *The role of biomedical complex carbohydrates in development of disease*. Complex Carbohydrate Research Center, University of Georgia, Athens, GA

Dec. 1994 Ph.D. in Electrical and Computer Engineering. Purdue University, W. Lafayette, IN. (GPA: 3.7 on a 4.0 scale) Dissertation on *Parallel, Probabilistic, Self-organizing Neural Networks: Pattern Discovery and Analysis in Complex Systems*

May 1988 M.Sc. in Electrical and Computer Engineering. Michigan Technological University, Houghton, MI. (GPA: 4.0 on a 4.0 scale) Thesis on Pattern Discovery and Analysis for Speech Recognition. Used the system for identification of EEG brain patterns in Audiology

May 1985 Vordiplom in Electrical Engineering. Kaiserslautern University, Kaiserslautern, Germany. (GPA: 3.8 on a 4.0 scale)