

Sudhir Kumar

Founding Director, Institute for Genomics and Evolutionary Medicine (iGEM)
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EDUCATION

- Ph.D. *Genetics*** 1991 – 1996
Pennsylvania State University
University Park, Pennsylvania, USA
Thesis: Molecular Evolutionary Analysis
New Phylogeny Reconstruction Algorithm, Computer Application, and Data Analysis
Mentor: Masatoshi Nei
- M.Sc. *Biological Sciences**** (Hons.) 1985 – 1990
Birla Institute of Technology and Sciences, BITS
Pilani, Rajasthan, India
Thesis: Computer Simulation in Population Genetics
Mentor: Sandhya Mitra
- B.Eng. *Electrical & Electronics engineering**** (Hons.) 1985 – 1990
Birla Institute of Technology and Sciences, BITS
Pilani, Rajasthan, India
**M.Sc. and B.Engg. were completed simultaneously in a visionary dual degree program.*

PROFESSIONAL APPOINTMENTS

Temple University, Philadelphia, Pennsylvania, USA

- Founding Director*, Institute for Genomics and Evolutionary Medicine 2014 – Present
Laura H. Carnell Professor, Department of Biology 2014 – Present
Full Professor, Department of Computer Information & Sciences 2014 – Present

Arizona State University, Tempe, Arizona, USA

- Regents' Professor*, School of Life Sciences 2012 – 2014
Foundation Professor, School of Life Sciences 2011 – 2014
Director, Center for Evolutionary Medicine and Informatics, Biodesign Institute 2010 – 2014
Full Professor, School of Life Sciences 2006 – 2011
Director, Center for Evolutionary Functional Genomics, Biodesign Institute 2003 – 2010
Faculty Leader, Genomics, Evolution & Bioinformatics, School of Life Sciences 2003 – 2004
Associate Professor, School of Life Sciences 2002 – 2006
Assistant Professor, Department of Biology 1998 – 2002

Pennsylvania State University, University Park, USA (Mentor: Masatoshi Nei)

- Postdoctoral Fellow*, Department of Biology 1996 – 1998
Research Assistant, Department of Biology 1991 – 1996

AWARDS AND HONORS

<i>Dean's Distinguished Excellence in Research Award</i> , Temple University	2021
<i>Highly Cited¹ Researcher</i> , Clarivate Web of Science	2022 & 2021
<i>Visiting Fellowship Award</i> , Japanese Society for Promotion of Science	2020 & 2008
<i>Community Service Award</i> , Society for Molecular Evolution and Biology	2017
<i>Fellow of F1000</i> , Faculty of 1000, Ltd.	2017
<i>Outstanding Science Alumni Award</i> , Pennsylvania State University	2015
<i>Top-100 Scientist</i> by Platinum H-Index Archives of Environmental/Occupational Health (2015) 70:69-67	2015
<i>Faculty of the Game</i> , Temple vs. Penn State Football, Temple Athletics	2015
<i>Highly Cited Researcher</i> , Thomson-Reuter Web of Science	2014
<i>Most Influential Minds</i> , Thomson Reuters ScienceWatch	2014
<i>Governor's Celebration of Innovation</i> – Academia (Finalist), State of Arizona	2011 & 2009
<i>Fellow</i> (elected), American Association for the Advancement of Science <i>Citation:</i> Exemplary contributions in evolutionary bioinformatics, particularly in developing high-impact comparative analysis software for biologists and in illuminating the evolutionary dynamics of mutations and species through comparative genomics	2009
<i>Honorary Professorship</i> , School of Computing and Informatics, ASU	2009
<i>Exemplar Faculty</i> , Arizona State University	2006
<i>Top-10</i> most-cited scientist in Computer Sciences (Web of Science)	2004
<i>Innovation Award in Functional Genomics</i> , Burroughs Wellcome Fund	2000

CITATIONS/HONORS

270,000+ citations (Google Scholar) 2023

<https://tinyurl.com/KumarScholar>

H-index 84
i10-index 170

230,000+ citations to software and databases
40,000+ citations to discoveries, methods, books & reviews

HOT Papers / Highly Cited (Web of Science)

Four research articles and 12 software/database articles have received the HOT paper and/or Highly Cited designations² (marked in the list of publications).

Top-100 article of all time

One article describing the MEGA software (Molecular Biology and Evolution, 2007, 24:1596-1599) was among the top-100 most-cited papers of all time (<https://www.nature.com/news/the-top-100-papers-1.16224>).

2014

¹Excerpt from the Web of Science (<https://recognition.webofscience.com/awards/highly-cited/2021/>). Highly Cited Researchers demonstrate significant and broad influence reflected in their publication of multiple highly cited papers over the last decade. These highly cited papers rank in the top 1% by citations for a field or fields and publication year in the Web of Science™. Of the world's population of scientists and social scientists, Highly Cited Researchers are 1 in 1,000.

² Essential Science Indicators (Web of Science) gives this designation when the article is among the top 0.1% of papers from the past two years in its subject category. An article is highly cited when its citation count is in the top 1% of all articles in the last ten years.

<i>Top-cited article of the decade</i>	2014
MEGA software article (<i>Molecular Biology and Evolution</i> [2007] 24:1596-1599) was the most cited article of the decade in the SCOPUS Agriculture and Biological Sciences section.	
<i>Faculty of 1000 Prime Highlighted</i>	2013
PNAS (2012) 109:19333-19333	
<i>SCIENCE editor's choice</i>	2006
Molecular Biology and Evolution (2006) 23:1946–1951	

PROFESSIONAL AFFILIATIONS

<i>Affiliated Faculty</i> , Center for Sustainable Communities, Temple University	2019 – Present
<i>Member</i> , Molecular Therapeutics Program, Fox Chase Cancer Center, USA	2014 – Present
<i>Adjunct Professor</i> , Research Center for Genomics and Bioinformatics Tokyo Metropolitan University, Tokyo, Japan	2013 – Present
<i>Adjunct Professor</i> , Center of Excellence in Genomic Medicine Research King Abdulaziz University, Jeddah, Saudi Arabia	2013 – Present
<i>Guest Professor</i> , Center for Computational and Evolutionary Biology Institute of Zoology at Beijing, China	2007
<i>Affiliate Professor</i> , Department of Biomedical Informatics, Arizona State	2005 – 2007
<i>Adjunct Senior Investigator</i> , Translational Genomics Research Institute, USA	2004 – 2007
<i>Affiliate Professor</i> , School of Computing, Informatics, and Decision Support Engineering, Arizona State University, Tempe, AZ, USA	2002
<i>Associate Member</i> , Astrobiology Research Center, Penn State University	1998

PROFESSIONAL SERVICE (major)

Societies

<i>President</i> (elected)	Society for Molecular Biology and Evolution	2013
<i>Councilor</i>	Society for Molecular Biology and Evolution	2012 – 2022
<i>Secretary</i> (elected)	Society for Molecular Biology and Evolution	2004 – 2006
<i>Webmaster</i>	Society for Molecular Biology and Evolution	2004 – 2008
<i>Webmaster</i>	American Genetic Association	1999 – 2007

Editorial

<i>Specialty Chief Editor</i>	Frontiers in Bioinformatics	2023
<i>Editor-in-Chief</i>	Molecular Biology and Evolution	2012 – 2022
<i>Associate Editor</i>	Journal of Heredity	1999 – 2005
<i>Associate Editor</i>	Molecular Biology and Evolution	2005 – 2012
<i>Associate Editor</i>	Evolutionary Bioinformatics	2005 – 2014
<i>Associate Editor</i>	Gene: Functional Genomics	2005 – 2006
<i>Associate Editor</i>	Quarterly Reviews of Biology	2010 – 2014
<i>Editorial Board</i>	Molecular and Developmental Evolution	2004 – 2010
<i>Editorial Board</i>	Genome Research	2005 – 2009
<i>Editorial Board</i>	Bioinformatics and Biology Insights	2009 – 2014
<i>Editorial Board</i>	Biomolecules	2010 – 2014

National Institutes of Health (NIH)

<i>Co-Chair</i>	Information Technology in Cancer Research Section	2018
<i>Chair</i>	Genome Variation, and Evolution Study Section	2016 – 2018
<i>Member</i>	Genome Variation and Evolution Study Section	2014 – 2016

Member BioData Management and Analysis Study Section 2006 – 2010

National Science Foundation

Member Information Technology Research-Medium Panel 2003

Member Information Technology Research-Small Panel 2002

ADVISOR AND CONSULTANT

Scientific Advisory Board Member, Discovery Bio Inc., USA 2021 – Present

Scientific Advisory Board Member, Eloxx Pharmaceuticals, USA 2018 – 2021

Advisory Board, SICCS, Northern Arizona University, USA 2016 – 2019

Member, Thought Leader Summit, American Heart Association, USA 2015

Member, Review Committee, Genomic Sciences Program, NC State U. 2015

Advisory Board, Münster Graduate School of Evolution, Münster, Germany 2011

Member, Review Committee, Inst. Genomics & Bioinfo. U. California, Irvine 2010 & 2005

Co-founder and Chief Scientific Officer, Espis Vaccines, USA 2008 – 2010

Advisory Board, FlyBase, Harvard University, USA 2007 – 2008

Advisory Member, Committee on Evolutionary Bioinfo. U. South Dakota 2006

Member, NESCent group on Evolutionary Informatics (Interoperability) 2006 – 2008

Consultant, Amerigenics, Inc., USA 2006

Advisory Committee Member, National Center for Evolutionary Synthesis 2006 – 2009

Consultant, Pharmacia Corporation, USA 2002 – 2003

Member, Astrobiology/Evolutionary Genomics Focus Group, NASA 2000

TRAINING AND CURRICULUM DEVELOPMENT

Temple University, Philadelphia, Pennsylvania, USA

Developer and *Coordinator*, Bachelor of Science (BS) in Genomic Medicine 2020 – Present

Developer, Genomics and Bioinformatics concentration in Data Science (BS) 2017

Developer and *Coordinator*, Undergraduate certificate in Genomic Medicine 2016 – Present

Co-Principal Investigator, Innovating Graduate Stem Education through
Bio-Social Partnerships, National Science Foundation 2015 – 2020

Arizona State University, Tempe, Arizona, USA

Co-Director, Biological Design Doctoral Program 2012 – 2013

Coordinator, Academic exchange/Collaboration, Tokyo Metropolitan Univ. 2012

Investigator, Computational Biosciences Professional Master's Sloan Foundation 2001 – 2003

Investigator, Biodesigned Bridges to the Doctorate, National Science Foundation 2004 – 2006

MEMBERSHIPS IN SCIENTIFIC & PROFESSIONAL ORGANIZATIONS

American Association for the Advancement of Science

American Association for Cancer Research

American Genetic Association

Genetics Society of America

Human Genome Variation Society

International Society of Computational Biologists (lifetime)

National Association of Biology Teachers

Society for Molecular Biology and Evolution (lifetime)

Society for the Study of Evolution (lifetime)

LEADERSHIP OF INSTITUTIONAL AND GLOBAL ORGANIZATIONS

Center for Evolutionary Functional Genomics at Arizona State University

2002 – 2010

I was invited to lead a university-wide initiative in Genome Informatics in collaboration with the Computer Science department leaders in 2000. This initiative's success was the precursor to establishing a new Center for Evolutionary Functional Genomics (EFG) in the newly formed Biodesign Institute. EFG became an intellectual hub of well-funded interdisciplinary research and graduate training. I collaborated with Life Sciences, Anthropology, Computer Sciences, and Biomedical Informatics leaders to recruit and mentor many outstanding faculty members in evolutionary biology, functional genomics, infectious diseases, and big data informatics.

Center for Evolutionary Medicine and Informatics at Arizona State University

2010 – 2014

Recognizing the emerging importance of evolution and medicine's interface, I led the evolution of EFG into the Center for Evolutionary Medicine and Informatics (CEMI). CEMI developed world leaders in evolutionary medicine, synthetic genetics, epidemiology, and machine learning. It was featured in *Nature Medicine* (12/2010, 16:1346) as the premier evolutionary medicine center globally, with four major themes: Personal Genomics, Disease Origins, Functional Proteomics, and Discovery Bioinformatics. High scholarly impact, considerable extramural funding, and training of many interdisciplinary graduates were highlights of CEMI.

Molecular Biology and Evolution (MBE)

2012 – 2022

I served the scientific community as the Editor-in-Chief of MBE for ten years. MBE received ~1,500 manuscripts annually, which I handled editorially in close collaboration with 60 eminent scientists and four staff members. We made MBE the top specialist journal in molecular evolution that publishes fundamental discoveries, methods, and tools. During my term, I modernized the MBE website, made the editorial system more efficient and transparent, established a press office for outreach, and developed mechanisms to celebrate authors. Consequently, MBE became a high-impact, fast turn-around journal. I also managed production, the press office, website updates, and budgets (\$1M annually). We proudly generated income for the *Society for Molecular Biology and Evolution*, supporting scientific conferences, initiatives, and young investigators.

Institute for Genomics and Evolutionary Medicine at Temple University

2014 – Present

A Temple-wide institute with a mission to harness molecular evolutionary rules of life to make breakthroughs in genome medicine and biodiversity, develop innovative computational methods for big data, and train young minds to pursue the next generation of challenges. We have developed research and teaching excellence at the convergence of genomics, evolution, and medicine, with a strong focus on machine learning, somatic evolution of tumors, malaria epidemiology, and infectious and complex diseases. The Institute has already made a big impact through outstanding scholarship and software and database product developments and has a solid record of extramural funding and teaching. The Institute has also successfully developed a high-performance computing environment collaboratively through extramural funding from local (PA Commonwealth University Enhancement program) and national agencies (National Science Foundation).

LEADERSHIP OF MAJOR EDUCATIONAL INITIATIVES

B.S. Genomic Medicine 2021

Led the development and implementation of a new undergraduate degree (BS) in *Genomic Medicine* to prepare the next generation of researchers and professionals interested in careers in human health with a strong foundation in the life sciences that emphasizes the medical relevance of genomics and evolutionary biology. On average, 25 new undergraduates enroll in this major every year.

B.S. Data Science (Genomics/Bioinformatics concentration) 2017

Developed the curriculum of the *Genomics and Bioinformatics* concentration of a new undergraduate degree (BS) in *Data Science Medicine* to matriculate graduates with a strong background in mathematics, computational thinking, and biological data analysis, making them well-equipped to analyze large quantities of data for biological discoveries. Currently, 10+ undergraduates enroll annually in this major, with the numbers growing every year.

Certificate in Genomic Medicine 2016

Led the development of a certificate program available to all undergraduate students to supplement their degree programs, regardless of their major, to become conversant in topics relevant to the interplay of genomics and evolution in medicine. More than 100 students have already completed this certificate.

LEADERSHIP OF MAJOR RESEARCH RESOURCES

MEGA: Molecular Evolutionary Genetics Analysis software 1993 – Present

megasoftware.net

This is user-friendly software to analyze molecular sequences. First published in 1993, it is currently in its 11th major release and is fully cross-platform. It is downloaded over 350,000 times each year (2.5 million downloads to date) and cited in over 20,000 publications annually (> 200,000-lifetime citations). It continues to be developed actively.³

TimeTree: The Timescale of Life knowledge-base 2004 – Present

timetree.org

TimeTree is a knowledge base for scientists and the general public to access divergence times estimated from molecular dates and published in peer-reviewed scientific journals. It currently contains a global evolutionary synthesis of the evolutionary tree of >140,000 species based on published dates from >4,000 articles. Over 250,000 queries are launched annually on this web resource and an associated iPhone app. It continues to be expanded actively.

FlyExpress: Co-expressed Developmental Genes by Image Analysis 2003 – 2016

flyexpress.net

FlyExpress database contains 100,000+ images of expression from ~5,000 genes derived from high-throughput in situ hybridization studies and more than 30,000 images extracted and curated from peer-reviewed articles. It provides unique tools to search the library of in situ embryonic images through image matching. This database was last updated in 2016.

³ MEGA's 25-year history is chronicled in a news story in *Molecular Biology and Evolution* (2018) 35:1558–1560.

RESEARCH GRANTS

National Institutes of Health (NIH)

Principal Investigator

Methods for Evolutionary Genomics Analysis <i>Comparative genomics, sparse learning, molecular evolution</i>	2021 – Present
Bioinformatics of Metastatic Migration Histories <i>Bayesian methods, tumor phylogenetics, somatic variation</i>	2020 – Present
Inferring Molecular Evolutionary Rates and Divergence Dates <i>Relative rates, divergence times, software development</i>	2017 – 2021
Evolutionary Bioinformatics of Tumor profiles <i>Bulk-sequencing, clone deconvolution, multi-tumor analytics</i>	2016 – 2020
Evolutionary Bioinformatics of Human Mutations <i>Mendelian mutation diagnosis, machine learning, mypeg.info</i>	2010 – 2014
Re-Engineering the MEGA Software Package <i>Refactoring and hardening MEGA, including testing and debugging</i>	2007 – 2011
Computational Analysis of Gene Expression Pattern Images (12 years) <i>Drosophila, embryogenesis, image analysis, flyexpress.net</i>	2003 – 2015
Comparative Molecular Sequence Analysis (15 years) <i>Statistical Methods, MEGA, molecular phylogenetics</i>	2000 – 2015

Co-Principal Investigator or Major Contributor

Cellular Phylogenetics and Evolution <i>Big data, phylogenetics, somatic evolution</i>	2022 – Present
Bayesian Evolution-Aware Methods for Tumor Single Cell Sequences <i>Single-cell sequencing, imputation, statistical methods, phylogeny</i>	2017 – 2021
eQTL Mega-analysis for... Multi-enhancer Gene Regulation <i>GWAS, evolutionary probabilities, CRISPR, polymorphisms</i>	2016 – 2020
Computational Diagnosis of Non-syn Variations using Structural Dynamics <i>Disease mutation diagnosis, protein structures, phylomedicine</i>	2014 – 2017
Methods for Evol. Informed Network Analysis to Discover Disease Variation <i>GWAS, evolutionary probabilities, diabetes, polymorphisms</i>	2013 – 2017
Rational Design... of Effective DNA-Scaffolded Nicotine Vaccines <i>Evolutionary vaccinology, smoking, drug discovery, polymorphisms</i>	2013 – 2016
A Phylogenetic Approach to Metagenomic Analysis <i>Minimum evolution, phylogenetic placement, rRNA sequencing</i>	2011 – 2014
Center for Membrane Proteins in Infectious Diseases <i>Protein structure, evolutionary optimization, crystallization</i>	2010 – 2015
Team Approach to Translate Novel Biomarkers for Diabetes <i>Proteomics, polymorphisms, disease markers</i>	2009 – 2010
Discovering The Hidden Proteome in The Human Genome <i>mRNA display, cap-independent translation-enhancing elements</i>	2008 – 2012

National Science Foundation

Principal Investigator

Understanding Epistasis: The Key for Genotype to Phenotype Mapping <i>The convergence of many disciplines to discover epistasis</i>	2019 – Present
Open-source, Extensible, and Cross-platform MEGA <i>MEGA software, multi-platform, plug-in architecture</i>	2017 – 2021

Reconstructing the contemporary history and progenitor of SARS-CoV-2 strains causing COVID-19 <i>Pathogen genomics, COVID-19, phylogenetics</i>	2020 – 2021
Design of a Bioinformatic Database for Functional Evolutionary Footprints <i>Gene duplications, divergent substitutions, functional genomics</i>	2000 – 2004
<i>Co-Principal Investigator or Major Contributor</i>	
Accelerating the Discovery and Utility of the Timescale of Life <i>timetree of life, synthesis, open-source, expansion, TimeTree.org</i>	2020 – Present
Identifying Phylogenetically Informative Data from Next-Gen Sequencing <i>Molecular phylogenies, big data, signal, noise</i>	2014 – 2018
Large-Scale Structured Sparse Learning <i>Machine learning, image analysis, embryogenesis</i>	2014 – 2017
Enabling Discovery... through a Synthesis of... Evolutionary Histories <i>Timetree of life, synthesis, speciation process, TimeTree.org</i>	2013 – 2016
Computational Methods for Expression Image Analysis <i>Machine learning, image analysis, Drosophila embryogenesis</i>	2011 – 2015
Bioinformatics of Molecular TimeTrees <i>Timetree of life, synthesis, speciation process, TimeTree.org</i>	2009 – 2013
Developing a Bioinformatic Database for Stoichioproteomics <i>The convergence of proteomics and ecological stoichiometry</i>	2006 – 2010
Machine Learning Approaches for Biological Image Informatics <i>Machine learning, image analysis, gene expression</i>	2006 – 2010
Development of an Evolutionary Timescale Database <i>The timescale of life, synthesis of evolutionary timetrees, TimeTree.org</i>	2001 – 2004
Threats to Amphibian Biodiversity (8 years) <i>Emerging wildlife diseases, fungal pathogenesis, databases</i>	2000 – 2008
<u>NASA Astrobiology</u>	
Innovative Molecular Timing... to obtain Accurate Histories of Early Life <i>Deep time, rocks vs. clocks, molecular dating</i>	2016 – 2020
<u>Science Foundation of Arizona</u>	
Bioinformatics of Assembling the Timescale of Life <i>TimeTree database, literature curation, phylogeny</i>	2007 – 2008
<u>Burroughs-Wellcome Fund</u>	
Computationally... Dissect Functionally Important Mutations... <i>Multigene families, Gene duplications, functional divergence</i>	2003 – 2006

PUBLICATIONS

Books and guides

1. Kumar S, Tamura K & Nei M (1993) A Guide to Molecular Evolutionary Genetics Analysis Program for Microcomputers, Institute of Molecular Evolutionary Genetics, Pennsylvania State University, University Park, PA (140 pp; >2,500 printed manuals distributed).
2. Nei M & Kumar S (2000) Molecular Evolution and Phylogenetics. Oxford University Press, New York (333 pp). (*Translated in Chinese, Japanese, and Russian.*)
3. Hedges SB & Kumar S (2009) The Timetree of Life. Oxford University Press, New York (550 pp; edited volume with 81 contributions).

In preparation

4. Oxygen triggered the origin of eukaryotes and rise in complexity.
5. Predicting excess aging of blood and cancer risk by cellular phylogenomics.

Submitted

6. Split-transformer impute (ST): Genotype imputation using a transformer-based model.

In review/revision

7. Evolutionary sparse learning reveals the shared genetic basis of convergent traits.
8. Understanding the evolutionary landscape of the SARS-COV2 spike protein by integrating candidate adaptive polymorphisms with protein dynamics.
9. Balancing selection is common for beneficial alleles in a human population.

Accepted/in press

10. Craig JM, Kumar S & Hedges SB (2023) The origin of eukaryotes and rise in complexity were synchronous with the rise in oxygen. *Frontiers in Bioinformatics* (in press).

Published in 2023

11. Miura S, Dolker T, Sanderford M & Kumar S* (2023) Improving cellular phylogenies through the integrated use of mutation order and optimality principles. *Computational and Structural Biotechnology Journal* 21:3894-3903.
12. Barba-Montoya J, Sharma S & Kumar S* (2023) Molecular timetrees using relaxed clocks and uncertain phylogenies. *Frontiers in Bioinformatics* 3:1225807 (13 pp).
13. Kumar S*, Tao Q, Lamarca AP & Tamura K (2023) Computational reproducibility of molecular phylogenies. *Molecular Biology and Evolution* 40:msad165 (23 pp).
14. Kumar S* & Gojobori T (2023) Obituary: Masatoshi Nei (1931-2023). *Molecular Biology and Evolution* 40:msad149 (5 pp).
15. Zhang J & Kumar S* (2023) Masatoshi Nei (1931-2023). *Nature Ecology and Evolution* 7 (2 pp).
16. Huzar J, Shenoy M, Sanderford M, Kumar S & Miura S (2023) Bootstrap confidence for molecular evolutionary estimates from tumor bulk sequencing data. *Frontiers in Bioinformatics* 3:1090730 (11 pp).
17. Ose NJ, Campitelli P, Patel R, Kumar S* & Ozkan SB (2023) Protein dynamics provide mechanistic insights about epistasis among common missense polymorphisms. *Biophysical Journal* 122:2938-2947.
18. Stanojevic M, Andjelkovic J, Kasprowicz A, Huuki LA, Chao J, Hedges SB, Kumar S* & Obradovic Z (2023) Discovering research articles containing evolutionary timetrees by machine learning. *Bioinformatics* 39:btad035 (7 pp).
19. Karim S, Iqbal MS, Ahmad N, Ansari MS, Mirza Z, Merdad A, Jastaniah S & Kumar S (2023) Gene expression study of breast cancer using Welch Satterthwaite t-test, Kaplan-Meier estimator plot and Huber loss robust regression model. *Journal of King Saud University – Science* 35:102447 (9 pp).

Published in 2022

20. Kumar S (2022) Embracing green computing in molecular phylogenetics. *Molecular Biology and Evolution* 39:msac043 (4 pp).
21. Kumar S*, Suleski M, Craig JM, Kasprowicz AE, Sanderford M, Li M, Stecher G & Hedges SB (2022) TimeTree 5: An expanded resource for species divergence times. *Molecular Biology and Evolution* 39:msac174 (6 pp).
22. Sharma S & Kumar S* (2022) Taming the selection of optimal substitution models in

- Phylogenomics by site subsampling and upsampling. *Molecular Biology and Evolution* 39:msac236 (8 pp).
23. Caraballo-Ortiz M, Miura S, Sanderford M, Dolker T, Tao Q, Weaver S, Pond SLK & Kumar S* (2022) TopHap: Rapid inference of key phylogenetic structures from common haplotypes in large genome collections with limited diversity. *Bioinformatics* 38:2719-2726.
 24. Craig JM, Kumar S* & Hedges SB (2022) Limitations of phylogenomic data can drive inferred speciation rate shifts. *Molecular Biology and Evolution* 39:msac038 (11 pp).
 25. Chroni A, Miura S, Hamilton L, Vu T, Gaffney S, Aly V, Karim S, Sanderford M, Townsend J & Kumar S* (2022) Clone phylogenetics reveals metastatic tumor migrations, maps, and models. *Cancers* 14:4326 (13 pp).
 26. Miura S, Vu T, Choi J, Townsend JP, Karim S & Kumar S* (2022) A phylogenetic approach to study the evolution of somatic mutational processes in cancer. *Communications Biology* 5:617 (11 pp).
 27. Huzar J, Kim H, Kumar S & Miura S (2022) MOCA for integrated analysis of gene expression and genetic variation in single cells. *Frontiers in Genetics* 13:831040 (8 pp).
 28. Patel R, Carnevale V & Kumar S* (2022) Epistasis creates invariant sites and modulates the rate of molecular evolution. *Molecular Biology and Evolution* 39:msac106 (11 pp).
 29. Babaian C & Kumar S (2022) Epistasis storyboarded. *The American Biology Teacher* 84:562-569.
 30. Babaian C & Kumar S (2022) Storyboarding for biology: An authentic STEAM experience. *The American Biology Teacher* 84:328-335.
 31. Ose NJ, Butler BM, Kumar A, Sanderford M, Kumar S* & Ozkan SB (2022) Dynamic coupling of residues within proteins as a mechanistic foundation of many enigmatic pathogenic missense variants. *PLoS Computational Biology* 18:e1010006 (22 pp).
 32. Canuti M, Bianchi S, Kolbl O, Pond SLK, Kumar S, Gori M, Fappani C, Colzani D, Borghi E, Zuccotti GV, Raviglione MC, Tanzi E & Amendola A (2022) Waiting for the truth: Is reluctance in accepting an early origin hypothesis for SARS-CoV-2 delaying our understanding of viral emergence? *BMJ Global Health* 7:e008386 (8 pp).
 33. Amendola A, Canuti M, Bianchi S, Kumar S, Fappani C, Gori M, Colzani D, Pond SLK, Miura S, Baggeri M, Marchi A, Borghi E, Zuccotti GV, Raviglione MC, Magurano F & Tanzi E (2022) Molecular evidence for SARS-CoV-2 in samples collected from patients with morbilliform eruptions since late summer 2019 in Lombardy, Northern Italy. *Environmental Research* 215:113979 (9 pp).
 34. Karim S, Al-Kharraz M, Mirza Z, Noureldin H, Abusamara H, Alganmi N, Merdad A, Jastanlah S, Kumar S, Rasool M, Abuzenadah A & Al-Qahtani M (2022) Development of "Biosearch System" for biobank management and storage of disease associated genetic Information. *Journal of King Saud University – Science* 34:101760 (10 pp).

Published in 2021

35. Kumar S* & Sharma S (2021) Evolutionary sparse learning for phylogenomics. *Molecular Biology and Evolution* 38:4674-4682.
36. Kumar S*, Tao Q, Weaver S, Sanderford M, Caraballo-Ortiz MA, Sharma S, Pond SLK & Miura S (2021) An evolutionary portrait of the progenitor SARS-CoV-2 and its dominant offshoots in COVID-19 pandemic. *Molecular Biology and Evolution* 38:3046-3059.
37. Sharma S & Kumar S* (2021) Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. *Nature Computational Science* 1:573-577.

38. ⁴Tamura K, Stecher G & Kumar S* (2021) MEGA11: Molecular Evolutionary Genetics Analysis version 11. *Molecular Biology and Evolution* 38:3022-3027.
39. Townsend JP, Hassler HB, Wang Z, Miura S, Singh J, Kumar S, Ruddle N, Galvani AP & Dornburg A (2021) The durability of immunity against reinfection by SARS-CoV-2: A comparative evolutionary study. *The Lancet Microbe* 12:e666-e675.
40. Patel R & Kumar S* (2021) Epistasis produces an excess of invariant sites in neutral molecular evolution. *Proceedings of the National Academy of Sciences (USA)* 118:e2018767118.
41. Tao Q, Barba-Montoya J & Kumar S* (2021) Data-driven speciation tree prior for better species divergence times in calibration-poor molecular phylogenies. *Bioinformatics* 37:i102-i110.
42. Barba-Montoya J, Tao Q & Kumar S* (2021) Molecular and morphological clocks for estimating evolutionary divergence times. *BMC Ecology and Evolution* 21:83 (15 pp).
43. Barba-Montoya J, Tao Q & Kumar S* (2021) Assessing rapid relaxed-clock methods for phylogenomic dating. *Genome Biology and Evolution* 13: evab251 (14 pp).
44. Tao Q, Tamura K & Kumar S* (2021) Rapid and reliable methods for molecular dating in *The Molecular Evolutionary Clock: Theory and Practice*, edited by Simon YW Ho (Springer, NY), pp 197-219.
45. Mello B, Tao Q, Barba-Montoya J & Kumar S* (2021) Molecular dating for phylogenies containing a mix of populations and species by using Bayesian and RelTime approaches. *Molecular Ecology Resources* 21:122-136.
46. Chroni A, Miura S, Oladeinde O, Aly V & Kumar S* (2021) Migrations of cancer cells through the lens of phylogenetic biogeography. *Scientific Reports* 11:17184(13 pp).
47. Chroni A & Kumar S* (2021) Tumors are evolutionary island-like ecosystems. *Genome Biology and Evolution* 13: evab276 (11 pp).
48. Dasari K, Somarelli JA, Kumar S & Townsend JP (2021) The somatic molecular evolution of cancer: mutation, selection, and epistasis. *Progress in Biophysics and Molecular Biology* 165:56-65.
49. Liu L, Chandrashekar P, Zeng B, Sanderford MD, Kumar S* & Gibson G (2021) TreeMap: A structured approach to fine mapping of eQTL variants. *Bioinformatics* 37:1125-1134.
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Published in 2002

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Published in 2001

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²¹ WoS Hot paper

201. Kumar S* & Gadagkar SR (2001) Disparity Index: A simple statistic to measure and test the homogeneity of substitution patterns between molecular sequences. *Genetics* 158:1321–1327.
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Published in 2000

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Published in 1999

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Published in 1998

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Published in 1997

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Published in 1996

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226. Kumar S (1996) Patterns of nucleotide substitution in mitochondrial protein-coding genes of vertebrates. *Genetics* 143:537–548.
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Published in 1995

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232. Rzhetsky A, Kumar S & Nei M (1995) Four-cluster analysis: A simple method to test phylogenetic hypotheses. *Molecular Biology & Evolution* 12:163–167.
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235. Kumar S, Tamura K & Nei M (1994) MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. *Computer Applications in Biosciences* 10:189–191.

Published in 1992

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Book reviews and other publications

237. Kumar S (2000) A review of the book *Genomes* by TA Brown. *The Quarterly Review of Biology* 75:316–317.
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240. Kumar S & Newfeld SJ (2002) A review of the book *Modern Genetic Analysis: Integrating Genes and Genomes* (second edition) by Griffiths AJF, Gelbart WM, Lewontin RC & Miller JH. *The Quarterly Review of Biology* 77:456–457.
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RESEARCH MENTORING

Postdoctoral scholars

Current Jack Craig (2020–) • Jose Barba-Montoya (2018–) • Alessandra Lamarca (2022–)

Past Alan Filipinski (1998–2014) • Antonia Chroni (2018–2022) • Antonio Marco-Castillo (2008–2009) • Anup Som (2005–2007) • Araxi Urrutia (2003–2004) • Bao Hong Shen (2005–2007) • Beatriz Mello (2015–2016) • Caryn Babaian (2021–2022) • Christine Kuslich (2003–2005) • Claudia Acquisti (2006–2010) • Fabia Battistuzzi (2008–2012) • Li Liu (2012–2015) • Lifang Liu (2012–2013) • Marcos Caraballo-Ortiz (2020–2022) • Mark P. Miller (2000–2002) • Michael S. Rosenberg (2000–2003) • Nevin Gerek (2010–2013) • Qiying Tao (2020–2022) • Ravi Patel

(2021) • Sankar Subramanian (2000–2006) • Sayaka Miura (2012–2016) • Sudhindra R. Gadagkar (1998–2003)

Doctoral and graduate students

Current John Allard (2021–) • Lisa Schmelkin (2019–) • Sudip Sharma (2018–)

Past Bindu Koshy • Caryn Babaian • Charlotte Konikoff • Hector Ramos • HoJoon Lee • Jian Yang • Karthik Jayaraman • Louise Huuki • Madhusudhana Gargasha • Michael Suleski • Patrick Kolb • Qiqing Tao • Rajalakshmi Gurunathan • Ravi Patel • Rekha Iyer • Sandhya Durvasala • Shubhra Gupta • Siddarth Selvaraj • Stephanie Rogers • Vinod Swarna • Xiaofen Liu

Undergraduate and graduate research interns

Current Adam Tseng • Anastasia Yankovskiy • Anthony Roman • Benjamin Nguyen • Deyana Tabatabaei • Glenda Armas • Grace Bamba • Louise Dupont • Ryan Tobin • Sarah Chung

Past Adam Orr • Adithya Rajan • Aditya Paliwal • Alexander Woodard • Alicia Varma • Alyza Villa • Amber Ahmed • Anant Bhargava • Anna Freydenzen • Antoine Al-Foune • April Merdon • Ariana Rodriguez • Asaria Jimenez • Brandon Butler • Brandy Buck • Brianna Spell • Bryan Sexton • Candice White • Carol Diaz • Chikku Baiju • Christopher Busick • Cristina Rivera • Diana Alarcon • Diana Tloutan • Elizabeth Santana • Elizabeth Villalba • Emily Davenport • Eric Thomas • Erika Garcia • German Velez • Glenn Markov • Greg McInnes • Hanna Pronina • Hariharan Mohanraj • Harry Ho • Hasnat Hasib • Heather R. DeWall • Heather Wiemann • Ivan Montiel • Jacob Reidhead • Jared Huza • Jenna Makis • Jessica Priest • Jiamen Deng • Jiyeong Choi • Jonathan Falciani • Jose Maldonado • Joy Wenslas Julia Davis • Kailah Davis • Karen Canales • Karen Gomez • Kari Strauss • Kimberly Kukurba • Kristyn Gerold • Krizia Cabrera • Kruti Patel • Lauren Hamilton • Liris Gonzalez • Liz Garcia • Louise Huuki • Maansi Suvarna • Madelyn Shenoy • Mary Kate Durnan • Michael Suleski • Morgan Day • Nandita Nagendra • Natalia Santiago • Nate Sutton • Nicholas Peterson • Nicolas Feddern • Nisarg Patel • Olumide Oladeinde • Oscar Murillo • Paul Billing-Ross • Pegah Biparvah • Rachel Sipes • Raneem Durra • Raul Navedo • Robert Adrian • Roman Johnson • Ronika Nirankari • Sara Vahdatshoar • Simon Lawrence • Stephanie Negron • Stephanie Tate • Stephen McAleer • Stephen Watson • Sujay Rajkumar • Tamera Lanham • Tenzin Dolker • Thania Martinez • Tiffany Buturla • Timothy Sweeney • Tina To • Tracy Vu • Tyler Ebinger • Vanessa Gray • Veena Ganeshan • Veronica Shi • Victor Correa • Viriya Keo • Vivian Aly • Wilda Rivera • Yea Jin Ko

Visiting Scholars/Tech Staff

Ade Banjoko • Aditya Rajan • Annirudha Kadne • Ashini Bolia • Ashly Ruttman • Ben Timmerick • Bernard Van Emden • Bremen Braun • Dana Desonie • Daniel Peterson • David Fisher • David Schwartz • Dishant Patel • Eric Thomas • Glen Stecher • Graziela Valente • Huyentrang Nguyen • Jana McAlpin • Jason Wulf • Jared Knobloch • Joel Dudley • Joseph Svitak • Keith Davis • Kelly Boccia • Lakshmi Viswanathan • Lin-Wei Wu • Mahesh Sundara Raman • Marcos Caraballo-Ortiz • Maxwell Sanderford • Melinda Caballero • Mia Champion • Michael Li • Michael *McCutchan* • Michael Suleski • Natalia Briones • Nicholas Harras • Nicholas Peterson • Nimit Johri • Quan Nguyen • Raj Bayapu • Renee Grothe • Revak Raj Tyagi • Roman Fuentes Ruttman • Sean Dudley • Siddarth Selvaraj • Suganthi Cidambaram Vesna Djinovic • Wayne Parkhurst • Zach Hanson-Hart

CLASSROOM TEACHING

Temple University

Genomic Evolutionary Medicine

2016 –

*Introduces evolutionary principles and perspectives in Genomic Medicine
Designed for junior and senior undergraduate students (BIOL 3112/5112)
Interactive and discovery-based classroom
Enrollment has increased steadily from 49 to 150+
Class satisfaction rating: Exceptional 4.5 (range 1 – 5)*

Seminar in Molecular Phylogenetics

2017 – 2019

Discusses early research articles in molecular phylogenetics (BIOL 8201)
Intended for graduate students; taught two times
Attended by many students and senior scientists
Class satisfaction rating: Maximum 5.0 (range 1 – 5)

Arizona State University

Evolutionary Medicine	2010 – 2013
<i>Introduces molecular evolution through examples from medicine</i>	
<i>Special topics designed for undergraduate to graduate students</i>	
<i>Attended by 12 – 41 students; taught four times (BIO 189/494)</i>	
<i>Class satisfaction rating: Exceptional 1.4 (range 1 - 4)</i>	
Introduction to Comparative Genomics	2001 – 2011
<i>Introduces fundamentals of evolutionary genomics</i>	
<i>Designed for senior undergrads and grad students</i>	
<i>Increasing enrollment from 10 to 41; taught seven times (BIO 494)</i>	
<i>Class satisfaction rating: Exceptional 1.2 (1 – 5)</i>	
Organic Evolution	2000 – 2006
<i>Basic course in evolutionary biology</i>	
<i>Designed for junior undergraduate</i>	
<i>Attended by 106 – 185 students; taught five times</i>	
<i>Class satisfaction rating: Exceptional 1.5 (range 1 – 4)</i>	
Molecular Evolutionary Genetics	1999 – 2000
<i>An advanced course on molecular evolution and phylogenetics</i>	
<i>Designed for graduate students (BIO 594/494)</i>	
<i>Attended by 7 – 14 students; taught three times</i>	
<i>Class satisfaction rating: Exceptional 1.3 (range 1 – 4)</i>	

CONFERENCE AND SYMPOSIA ORGANIZED

Co-Organizer, Green Computing in Molecular Phylogenetics (7/13)	2022
<i>SMBE Everywhere; Kick-off annual meeting of the Society for Molecular Biology and Evolution (SMBE)</i>	
Organizer, Growing Convergence Research Workshop on Epistasis (4/7)	2021
<i>Temple University, Philadelphia, Pennsylvania, virtual workshop</i>	
Organizer, MEGA 25th Anniversary Workshop (7/8-7/12)	2018
<i>The annual meeting of the Society for Molecular Biology and Evolution (SMBE), Yokohama, Japan</i>	
Coordinator, Workshop in Biogenomics & Nanobiology (4/23-4/24)	2018
<i>International Collaboration Conference, Riyadh, Saudi Arabia</i>	
Organizer, Molecular Evolution and Medicine (9/16-9/17)	2017
<i>Temple University, Philadelphia, USA (100 attendees)</i>	
Organizer, Symposium on Next-Generation Tools	2016
<i>The annual meeting of SMBE, Gold Coast, Australia</i>	
Member, External Advisory Board	2014
<i>The annual meeting of SMBE, Puerto Rico, USA</i>	
Organizer, SMBE Symposium on Phylomedicine	2012
<i>Arizona State University, SU, Tempe, AZ, USA (75 attendees) (03/23-24)</i>	
Member, Global Organizing Committee	2011
<i>The annual meeting of SMBE, Kyoto Japan (7/26–7/30)</i>	
Organizer, Symposium on Evolutionary Biology in Health and Medicine	2010
<i>The annual meeting of SMBE, Lyon France (7/4–7/8)</i>	
<i>co-organizers: J Dudley and A Butte</i>	
Co-organizer, Molecular Phylogenetics Symposium	2010
<i>Moscow State University, Russia (5/17–5/21)</i>	
Member, Committee, International Conference on... Molecular Systematics	2007
<i>Moscow State University, Russia (12/16–12/19)</i>	

<i>Organizer</i> , Annual Meeting of Society for Molecular Biology and Evolution <i>Arizona State University, Tempe, Arizona (5/24–5/28) 750 participants</i>	2006
<i>Organizer</i> , Genome Database Workshop <i>National Evolutionary Synthesis Center, North Carolina (5/31– 6/3)</i>	2005
<i>Organizer</i> , Symposium on Evolutionary and Population Genomics <i>Future of Statistics, Indian School of Business, Hyderabad (12/29–1/1)</i>	2004

INVITED PRESENTATIONS

2023 – 2019

Invited Speaker, McMaster University, Ontario, Canada • *Invited Speaker*, Bioinformatics Session 3, Annual meeting of the Society for the Study of Evolution • *Invited Speaker* (2 talks), Workshop on Malaria molecular epidemiology, population genetics, and evolution, New Delhi, INDIA • *Invited Speaker*, University of Southern California • *Invited Speaker*, 94th Annual Meeting of the Genetics Society of Japan, Sapporo • *Lead speaker*, Global Symposium 2, Annual meetings of Society for Molecular Biology and Evolution • *Invited speaker*, Annual meetings of the Society for Evolutionary Studies, Japan, Numazu • *Keynote*, Center for Computational and Integrative Biology (CCIB), Rutgers University, Camden Campus • *Keynote*, Second International Symposium on Genetics, Federal University of Rio de Janeiro • *Keynote* Presentation, Zakir Husain Delhi College, New Delhi • Symposium on the Origin of the COVID-19 Pandemic, Universite de Paris, France • *Distinguished Speaker Invitation*, Yale University • *Invited Talk*, Duke University • *Plenary*, 4th Chinese Systematics Conference, Beijing • *Nanqiang Lecture*, Xiamen University, China • *Plenary*, NSF China, Xiamen • *Invited Talk*, Peking University • *Invited Talk*, Chinese Academy of Sciences, Beijing • *Headliner*, Symposium on Molecular Biology and Evolution of Cancer, Yale University • *Invited Talk*, University of North Texas, Denton.

2018 – 2015

Invited Presenter, Digital Innovation Workshop, Case Western Reserve University, Cleveland • *Invited Presenter*, Silver Jubilee Workshop for MEGA, Yokohama, Japan • *Invited Talk*, Annual meetings of Society for Molecular Biology and Evolution, Manchester, UK • *Keynote*, Symposium, Tokyo Metropolitan University, Japan • *Invited Talk*, King Abdullah University of Science and Technology (KAUST) • *Invited Talk*, Annual meetings of Society for Molecular Biology and Evolution • *Invited Talk*, University of California (Los Angeles) • *Keynote*, King Abdullah University of Science and Technology (KAUST), Saudi Arabia • *Invited Talk*, University of Pittsburgh • *Invited Presenter*, Symposium in the Annual meetings of Society for Molecular Biology and Evolution • *Invited Talk*, Arizona State University • *Invited Talk*, Northern Arizona University • *Keynote*, International Symposium ISEGB, Kaohsiung, Taiwan • *Invited Presenter*, Biodiversity Workshop, Temple University, Philadelphia • *Invited Talk*, Fox Chase Cancer Center, Philadelphia, PA • *Invited Talk*, University of Maryland, College Park, MD • *Plenary*, Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA.

2014 - 2013

Chancellor's Distinguished Speaker, University of Missouri, Columbia, MO • *Keynote Address*, Temple University, Philadelphia, PA • *Invited Speaker* at two symposia, Society for Molecular Biology and Evolution Annual Conference, Puerto Rico • *Invited Presenter*, Research Center for Genomics and Bioinformatics International symposium, Tokyo Metropolitan University, Japan • *Invited Speaker*, Population Genetics Group, University of Bath, England • *Plenary*, Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA • *VWR Distinguished Speaker*, Georgia Tech School of Biology • *Keynote Address*, Molecular Medicine: Next-Gen Sequencing for the Clinic, Frankfurt • *Nei Lecture*, SMBE Annual Meeting at Chicago, Illinois • *Invited Speaker*, Chinese Academy of Sciences (CAS), Beijing, China • *Invited Speaker*, Nanjing Normal University, China • *Invited Speaker*, Center of Excellence in Genomic Medicine Research at King Abdulaziz University, KSA • *Invited Presenter*, Quantitative Biology Colloquium,

University of Arizona, Tucson, AZ • *Invited Speaker*, Mount Sinai School of Medicine CME Seminar Series, New York, NY • *Invited Speaker*, National Cancer Institute Conference of Physical Sciences-Oncology, Scottsdale, Arizona • *Invited Speaker*, Temple University, Department of Biology, Philadelphia, Pennsylvania • *Keynote Speaker*, Sigma Xi, Oakland University, Rochester, Michigan

2012 – 2011

Plenary Speaker, Society for Evolutionary Studies Annual Meetings at Tokyo Metropolitan University • SMBE Annual Meeting (The animal tree of life and its application) at Dublin, Ireland • Biomedicine: Big Data and New Paths to Personalized Medicine, ASU • International Conference on Bioinformatics & Computational Biology at BKK, Thailand • SMBE Satellite Meeting on Phylomedicine at Arizona State University • ORSP Research Seminar Series at Midwestern University, Phoenix, Arizona • Molecular Biosciences Seminar Presentation on Phylomedicine at Montana State • *Keynote Speaker*, Young Scientists' Workshop on Evolutionary Genomics at Tokyo, Japan • SMBE Annual Meeting (Methods for multiple alignment and phylogenetic tree) at Kyoto, Japan • International Society for Molecular Biology/ECCB (SNPSigs Selection) at Vienna, Austria • Workshop on Bioinformatics Software for Comparative Genomics and Metagenomics. The Smithsonian Institution (SI), American Museum of Natural History (AMNH) and the Food and Drug Administration (FDA) • Department of Biomedical Informatics, ASU • Barrett Honors College, ASU • SMBE Symposium on Molecular and Genomic Evolution at Penn State University • Keynote, Mini-symposium on Data Mining for Biomedical Informatics at SIAM International Conference on Data Mining, Mesa, Arizona • *Keynote*, Interdisciplinary Graduate Student's Symposium on Evolution Across Fields at Institute for Evolution and Biodiversity, Muenster, Germany

2010 – 2008

Plenary Speaker, Molecular Phylogenetics Symposium, Russia • Stanford University, California, USA • Symphogen Corporation (Copenhagen) • Chalk Talk, Physics Department, ASU • Spirit of Senses Group, Phoenix, Arizona • University of Cologne, Germany • Quantitative Expression Analysis workshop at Drosophila Research Conference, Chicago, Illinois • University of North Carolina, Charlotte, NC • Washington University, St. Louis, MO • Keynote, Symposium on Evolutionary Bioinformatics, Lava Springs, Idaho State University • Japan Biological Information Research Center (JBIRC), Tokyo, Japan • Symposium on New Insight of Genome Evolution into Fundamental Activities of Life, National Institute of Genetics (NIG) and the Tokyo Institute of Technology (TIT), Japan • Global Center for Excellence, Hokkaido University, Sapporo, Japan • Discussion leader, Computational and Statistical Advances, Gordon Conference in Molecular Evolution at Ventura, California

2007 – 2005

SOLUR Program, Arizona State University • Department of Biomedical Informatics, Arizona State University • FlyBase Advisory Group at Harvard University, Boston, MA • Keynote Speaker, Ohio Collaborative Conference on Bioinformatics (OCCBIO) at Miami University, Oxford, Ohio, • EMBO workshop on "Human Evolution and Disease" at Center for Cellular and Molecular Biology, Hyderabad, India • Department of Biological Sciences, University of Idaho, Moscow, ID • Microbiology Department, Montana State University, Bozeman, MT • ASU Emeritus Faculty Association, Tempe, Arizona • Symposium on Molecular Evolution at Moscow Conference on Computational Molecular Biology, Moscow State University, Russia • Symposium on Systems Biology at Moscow Conference on Computational Molecular Biology, Moscow State University, Russia • Special presentation to the Panel on Chemical Imaging, National Academies (USA), Washington DC

2004 – 2002

Symposium on Evolutionary and Population Genomics at Future of Statistics Conference,

Hyderabad, India • Symposium on Advances in Methods for Estimating Species Divergence Dates using Molecular Data at International Congress of Zoology, Beijing, China • Symposium on Molecular Phylogeny and Molecular Clocks at Annual Meeting of SMBE, Penn State University, University Park, PA • Hexapodium, Center for Insect Research, University of Arizona • Techniques Workshop at 44th Annual Drosophila Research Conference, Chicago, IL • Comparative and Functional Genomics Workshop, Wellcome Trust and Dept. of Energy, Hinxton, Cambridgeshire, UK • Annual Meeting of SMBE, Newport Beach, CA • Department of Biology, Duke University, Durham, NC • Bioinformatics Research Center, North Carolina State University, Raleigh, NC • Symposium on Evolutionary Genetics at Annual meeting of the American Genetic Association, Arizona State University, Tempe, Arizona • The 12th International Workshop on Beyond the Identification of Transcribed Sequences: Functional, Evolutionary, and Expression Analysis sponsored by Department of Energy, Washington, DC • The 18th International Symposium in Conjunction with Award of the International Prize for Biology, Tokyo, Japan • Department of Biology, Indiana University, Bloomington, Indiana • Department of Computer Science, Arizona State University, Tempe, AZ • Department of Biology, University of Michigan, Ann Arbor, Michigan

2001 – 1995

International Workshop on Population Genetics at University of Montreal, Montreal, Canada • ASU President's Community Enrichment Program, Phoenix, Arizona • Department of Biology, Ohio State University, Columbus, Ohio • Department of Biology, Hong Kong University, Hong Kong, China (2 lectures) • Department of Biology, Syracuse University, Syracuse, New York • Program in Ecology and Evolutionary Biology, University of Illinois, Urbana Champaign, Illinois • Department of Biology, Grand Canyon University, Phoenix, Arizona • Ecology & Evolutionary Biology Program/IGERT, Indiana University, Bloomington, Indiana • Department of Biology, Tokyo Metropolitan University, Tokyo, Japan • Biomedical Engineering, Indian Institute of Science, Bangalore, India • Department of Biology, Tokyo Metropolitan University, Tokyo, Japan • Graduate University for Advanced Studies, Hayama, Japan • Genetics Program, University of Arizona, Tucson, Arizona • Birla Institute of Technology & Sciences, Pilani, India • University of South Carolina, Columbia, South Carolina • Symposium on Genomic Diversity at Annual meeting of the American Genetic Association, Pennsylvania State University, University Park, PA • Department of Biology, Arizona State University-West, Phoenix, Arizona • Department of Zoology and Genetics, Iowa State University, Ames, Iowa • Symposium on Large Phylogenies at Annual meeting of the Society for the Study of Systematic Biology, University of Colorado, Boulder, Colorado • National Cancer Institute, Frederick, Maryland • Department of Biology, Arizona State.