Sudhir Kumar

Founding Director, Institute for Genomics and Evolutionary Medicine (iGEM)
Laura H. Carnell Professor, Department of Biology
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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

Dean's Distinguished Excellence in Research Award, Temple University	2021

Highly Cited[1] Researcher, Clarivate Web of Science	2022 & 2021
Visiting Fellowship Award, Japanese Society for Promotion of Science	2020 & 2008
Community Service Award, Society for Molecular Evolution and Biology	2017
Fellow of F1000, Faculty of 1000, Ltd.	2017
Outstanding Science Alumni Award, Pennsylvania State University	2015
Top-100 Scientist by Platinum H-Index	2015
Archives of Environmental/Occupational Health (2015) 70:69-67	
Faculty of the Game, Temple vs. Penn State Football, Temple Athletics	2015
Highly Cited Researcher, Thomson-Reuter Web of Science	2014
Most Influential Minds, Thomson Reuters ScienceWatch	2014
Governor's Celebration of Innovation – Academia (Finalist), State of Arizona	2011 & 2009
Fellow (elected), American Association for the Advancement of Science	2009
Citation: 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	
Honorary Professorship, School of Computing and Informatics, ASU	2009
Exemplar Faculty, Arizona State University	2006
Top-10 most-cited scientist in Computer Sciences (Web of Science)	2004
Innovation Award in Functional Genomics, Burroughs Wellcome Fund	2000

CITATIONS/HONORS

257,000+ citations (Google Scholar) 2022

https://tinyurl.com/KumarScholar

H-index	83
i10-index	167

210,000+	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 designations[2] (marked in the list of publications).

Top-100 article of all time 2014

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 (*Nature*, Oct 29/2014).

Top-cited article of the decade 2014

MEGA software article (*Molecular Biology and Evolution* [2007] 24:1596-1599) was the most cited article of the decade in the SCOPUS Agriculture and

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[1] Excerpt 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.

Biological Sciences section.

Faculty of 1000 Prime Highlighted PNAS (2012) 109:19333-1933	2013
SCIENCE editor's choice Molecular Biology and Evolution (2006) 23:1946–1951	2006

PROFESSIONAL AFFILIATIONS

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

PROFESSIONAL SERVICE (major)

Societies

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

Editorial

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

National Institutes of Health (NIH)

Co-Chair	Information Technology in Cancer Research Section	2018
Chair	Genome Variation, and Evolution Study Section	2016 – 2018
Member	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*, Ciscovery 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.

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

Co-Principal Investigator or Major Contributor

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

National Science Foundation

Principal Investigator

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

Reconstructing the contemporary history and progenitor of SARS-CoV-2 strains causing COVID-19 2020 – 2021

Pathogen genomics, COVID-19, phylogenetics

Design of a Bioinformatic Database for Functional Evolutionary Footprints 2000 – 2004

Gene duplications, divergent substitutions, functional genomics

Co-Principal Investigator or Major Contributor

Accelerating the Discovery and Utility of the Timescale of Life 2020 – Present

timetree of life, synthesis, open-source, expansion, TimeTree.org

Identifying Phylogenetically Informative Data from Next-Gen Sequencing 2014 – 2018

Molecular phylogenies, big data, signal, noise

Large-Scale Structured Sparse Learning 2014 – 2017

Machine learning, image analysis, embryogenesis

Enabling Discovery… through a Synthesis of… Evolutionary Histories 2013 – 2016

Timetree of life, synthesis, speciation process, TimeTree.org

Computational Methods for Expression Image Analysis 2011 – 2015

Machine learning, image analysis, Drosophila embryogenesis

Bioinformatics of Molecular TimeTrees 2009 – 2013

Timetree of life, synthesis, speciation process, TimeTree.org

Developing a Bioinformatic Database for Stoichioproteomics 2006 – 2010

The convergence of proteomics and ecological stoichiometry

Machine Learning Approaches for Biological Image Informatics 2006 – 2010

Machine learning, image analysis, gene expression

Development of an Evolutionary Timescale Database 2001 – 2004

The timescale of life, synthesis of evolutionary timetrees, TimeTree.org

Threats to Amphibian Biodiversity (8 years) 2000 – 2008

Emerging wildlife diseases, fungal pathogenesis, databases

NASA Astrobiology

Innovative Molecular Timing… to obtain Accurate Histories of Early Life 2016 – 2020

Deep time, rocks vs. clocks, molecular dating

Science Foundation of Arizona

Bioinformatics of Assembling the Timescale of Life 2007 – 2008

TimeTree database, literature curation, phylogeny

Burroughs-Wellcome Fund

Computationally… Dissect Functionally Important Mutations… 2003 – 2006

Multigene families, Gene duplications, functional divergence

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 review/revision

4. Predicting excess aging of blood and cancer risk by cellular phylogenomics.

5. Bootstrap confidence for tumor evolution estimates from bulk sequencing data.

6. Oxygen triggered the origin of eukaryotes and rise in complexity.

7. Computational reproducibility of molecular phylogenies.

Published in 2023

8. 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* (acceptance pending minor revisions).

9. 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

10. Kumar S (2022) Embracing green computing in molecular phylogenetics. *Molecular Biology and Evolution* 39: msac043 (4 pp).

11. 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).

12. 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).

13. 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.

14. 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).

15. 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).

16. 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).

17. 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).

18. 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).

19. Babaian C & Kumar S (2022) Epistasis storyboarded. *The American Biology Teacher* 84:562-569.

20. Babaian C & Kumar S (2022) Storyboarding for biology: An authentic STEAM experience. *The American Biology Teacher* 84:328-335.

21. 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).

22. 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).

23. 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).

24. 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

25. Kumar S & Sharma S (2021) Evolutionary sparse learning for phylogenomics. *Molecular Biology and Evolution* 38:4674-4682.

26. 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.

27. Sharma S & Kumar S (2021) Fast and accurate bootstrap confidence limits on genome-scale phylogenies using little bootstraps. *Nature Computational Science* 1:573-577.

28. [4]Tamura K, Stecher G & Kumar S (2021) MEGA11: Molecular Evolutionary Genetics Analysis version 11. *Molecular Biology and Evolution* 38:3022-3027.

29. 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.

30. 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.

31. 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.

32. 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).

33. Barba-Montoya J, Tao Q & Kumar S (2021) Assessing rapid relaxed-clock methods for phylogenomic dating. *Genome Biology and Evolution* 13: evab251 (14 pp).

34. 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.

35. 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.

36. 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).

37. Chroni A & Kumar S (2021) Tumors are evolutionary island-like ecosystems. *Genome Biology and Evolution* 13: evab276 (11 pp).

38. Dasari K, Somarelli JA, Kumar S & Townsend JP (2021) The somatic molecular evolution

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[4] WoS Hot paper

of cancer: mutation, selection, and epistasis. *Progress in Biophysics and Molecular Biology* 165:56-65.

39. 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.

40. Scheinfeldt LB, Brangan A, Kusic DM, Kumar S & Gharani N (2021) Common treatment, common variant: Evolutionary prediction of functional pharmacogenomic variants. *Journal of Personalized Medicine* 11:131(13 pp).

41. Babaian C & Kumar S (2021) How to build a super predator: From genotype to phenotype. *American Biology Teacher* 83:138-146.

42. Cai L, Wang Z, Kulathinal R, Kumar S, Ji S (2021) Deep low-shot learning for biological image classification and visualization from limited training samples. *IEEE Transactions on Neural Networks and Learning Systems*. 10.1109/TNNLS.2021.3106831 (11 pp).

Published in 2020

43. Kumar S, Chroni A, Tamura K, Sanderford M, Oladeinde O, Aly V, Vu T & Miura S (2021) PathFinder: Bayesian inference of clone migration histories in cancer. *Bioinformatics* 36 (S2): i675–i683.

44. Barba-Montoya J, Tao Q & Kumar S (2021) Using a GTR+Γ substitution model for dating sequence divergence when stationarity and time-reversibility assumptions are violated. *Bioinformatics* 36 (S2): i884–i894.

45. Tao Q, Barba-Montoya J, Huuki L, Durnan MK & Kumar S (2020) Relative efficiencies of simple and complex substitution models in estimating divergence times in phylogenomics. *Molecular Biology and Evolution* 37:1819–1831.

46. Leitner T & Kumar S (2020) Where did SARS-CoV-2 come from? *Molecular Biology and Evolution 37:*2463:2464.

47. Kulathinal R, Yoo Y & Kumar S (2020) The bits and bytes of biology: Digitalization fuels an emerging generative platform for biological innovation. Pp. 253-265 in *Handbook of Digital Innovation*, edited by Satish Nambisan (Edward Elgar Publishers, UK).

48. Miura S, Tamura K, Pond S, Huuki LA, Priest J, Deng J & Kumar S (2020) A new method for inferring timetrees from temporally sampled molecular sequences. *PLoS Computational Biology* 16 (24 pp).

49. Miura S, Vu T, Deng J, Buturla T, Oladeinde O, Choi J & Kumar S (2020) Power and pitfalls of computational methods for inferring clone phylogenies and mutation orders from bulk sequencing data. *Scientific Reports* 10:3498 (21 pp).

50. Tao Q, Tamura K, Mello B & Kumar S (2020) Reliable confidence intervals for RelTime estimates of evolutionary divergence times. *Molecular Biology and Evolution* 37:280-290.

51. [5]Stecher G, Tamura K & Kumar S (2020) Molecular Evolutionary Genetics Analysis (MEGA) for macOS. *Molecular Biology and Evolution* 37:1237-1239.

52. Babaian C & Kumar S (2020) Molecular memories of a Cambrian fossil. *American Biology Teacher* 83:586–595.

53. Campitelli P, Modi T, Kumar S, Ozkan SB (2020) The Role of conformational dynamics and allostery in modulating protein evolution. *Annual Review of Biophysics* 49:269-290.

54. Somarelli J, …,Kumar S, … (2020) Molecular biology and evolution of cancer: from discovery to action. *Molecular Biology and Evolution* 37:320-326.

55. Chandrashekar P, …, Kumar S, … (2020) Somatic selection distinguishes oncogenes and tumor suppressor genes. *Bioinformatics* 36:1712-1717.

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[5] WoS Highly Cited; MBE Emerging Classic

56. Zhou X, …, Sanderford M, …, S. Kumar, … (2020) Beaver and naked mole rat genomes reveal common paths to longevity. *Cells Reports* 32:(13 pp).

57. Pyott SJ, …, Sanderford M, Kumar S, … (2020) Human hearing loss mutations are adaptive for subterranean hearing in African mole-rats. *Current Biology* 30:1-13.

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202. Kumar S & Gadagkar SR (2000) Efficiency of the neighbor-joining method in reconstructing deep and shallow evolutionary relationships in large phylogenies. *Journal of Molecular Evolution* 51:544–553.

203. Purdom PW, Bradford PG, Tamura K & Kumar S (2000) Single column discrepancy and dynamic max-mini optimizations for quickly finding the most parsimonious evolutionary trees. *Bioinformatics* 16:140–151.

Published in 1999

204. Hedges SB & Kumar S (1999) Divergence times of eutherian mammals. *Science* 285:2031a.

205. Newfeld SJ, Wisotzkey RG & Kumar S (1999) Molecular evolution of a development pathway: Phylogenetic analyses of transforming growth factor-β family ligands, receptors, and Smad signal transducers. *Genetics* 152:783–795.

206. Wang Y-C, Kumar S & Hedges SB (1999) Divergence time estimates for the early history of animal phyla and the origin of plants, animals, and fungi. *Proceedings of the Royal Society, London. B* 266:163–171.

207. O'Brien S, Eisenberg JF, Miyamoto M, Hedges SB, Kumar S & Wilson DE (1999) Genome Maps 10. Comparative Genomics. Mammalian radiations (wall chart). Science 286:463–478.

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208. [22]Kumar S & Hedges SB (1998) A molecular timescale for vertebrate evolution. *Nature* 392:917–920.

209. Nei M, Kumar S & Takahashi K (1998) The optimization principle in phylogenetic analysis tends to give incorrect topologies when the number of nucleotides or amino acids used is small. *Proceedings of the National Academy of Sciences (USA)* 95:12390–12397.

Published in 1997

210. Balczarek KA, Lai Z-C & Kumar S (1997) Evolution and functional diversification of the Paired box (Pax) DNA-binding domains. *Molecular Biology and Evolution* 14:829–842.

211. Zhang J & Kumar S (1997) Detection of convergent and parallel evolution at the amino acid sequence level. *Molecular Biology and Evolution* 14:527–536.

212. Zhang J, Kumar S & Nei M (1997) Small-sample tests of episodic adaptive evolution: A case study of primate lysozymes. *Molecular Biology and Evolution* 14:1335–1338.

213. Yeager M, Kumar S & Hughes AL (1997) Sequence convergence in the peptide-binding region of primate and rodent MHC class Ib molecules. *Molecular Biology and Evolution* 14:1035–1041.

214. Leitner TL, Kumar S & Albert J (1997) Tempo and mode of nucleotide substitutions in gag and env gene fragments in Human Immunodeficiency Virus Type 1 populations with a known transmission history. *Journal of Virology* 71:4761–4770.

Published in 1996

215. Kumar S (1996) A stepwise algorithm for finding minimum evolution trees. *Molecular Biology and Evolution* 13:584–593.

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

217. Kumar S, Balczarek KA & Lai Z-C (1996) Evolution of the hedgehog gene family. *Genetics*

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142:965–972.

218. Kumar S & Rzhetsky A (1996) Evolutionary relationships of eukaryotic kingdoms. *Journal of Molecular Evolution* 42:183–193.

219. Hedges SB, Parker PH, Sibley CG & Kumar S (1996) Continental breakup and the ordinal diversification of birds and mammals. *Nature* 381:226–229.

220. Yang Z & Kumar S (1996) Approximate methods for estimating the pattern of nucleotide substitution and the variation of substitution rates among sites. *Molecular Biology and Evolution* 13:650–659.

Published in 1995

221. Kumar S (1995) PhylTest: A Program for Testing Phylogenetic Hypotheses. Pennsylvania State University, University Park.

222. Rzhetsky A, Kumar S & Nei M (1995) Four-cluster analysis: A simple method to test phylogenetic hypotheses. *Molecular Biology & Evolution* 12:163–167.

223. Yang Z, Kumar S & Nei M (1995) A new method of inference of ancestral nucleotide and amino acid sequences. *Genetics* 141:1641–1650.

224. Winnepenninckx W, Backeljau T, Mackey LY, Brooks JM, De-Wachter R, Kumar S & Garey JR (1995) 18S rRNA data indicate that Aschelminthes are polyphyletic in origin and consist of at least three distinct clades. *Molecular Biology and Evolution* 12:1132–1137.

Published in 1994

225. 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

226. Hedges SB, Kumar S, Tamura K & Stoneking M (1992) Human origins and analysis of mitochondrial DNA sequences. *Science* 255:737–739.

Book reviews and other publications

227. Kumar S (2000) A review of the book Genomes by TA Brown. *The Quarterly Review of Biology* 75:316–317.

228. Kumar S & Filipski A (2001 and 2008) Molecular Phylogeny Reconstruction. *Encyclopedia of Life Sciences Macmillan Reference Ltd*, Oxford, UK. (www.els.net).

229. Kumar S & Filipski A (2001) Molecular Clock Testing. *Encyclopedia of Life Sciences, Macmillan Reference Ltd*, Oxford, UK. (www.els.net).

230. 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.

231. Rawls A & Kumar S (2002) A review of the book *Genomic Regulatory Systems: Development and Evolution* by E. H. Davidson. The Quarterly Review of Biology 77:456.

232. Lorson C & Kumar S (2003) A review of the book *Genomes* (second edition) by T.A. Brown. The Quarterly Review of Biology 78:225.

233. Kumar S (2003) MacTrees made easy, a review of the book *Phylogenetic trees made easy: a how-to-manual for molecular biologists* by Hall BG. Molecular Evolution and Phylogenetics 27:165–167.

234. Kumar S & Filipski A (2004) Bayesian Phylogenetic Analysis. *Dictionary of Bioinformatics and Computational Biology* edited by Hancock J & Zvelebil M, Wiley-Liss, New York.

235. Kumar S & Filipski A (2005) Reconstructing Vertebrate Phylogeny. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics* edited by Subramaniam S. John Wiley

& Sons, New York.

236. Kumar S and other authors (2007) Sequence Assembly and Alignment Tech Guide. In *Genome Technology* (10 pp).

237. Battistuzzi FU, Filipski A & Kumar S (2011) Molecular clock: testing (version 2.0). *Encyclopedia of Life Sciences*. John Wiley & Sons, Ltd, Chichester, UK (7pp) (www.els.net).

238. Kumar S (2013) Foreword for the book *Molecular Genetics: Concepts and Development* by S Mitra. MacMillan India Limited.

239. Kumar S (2017) F1000Prime Recommendation of *Shen et al., Nat Ecol Evol 2017, 1(5):126* in F1000Prime (DOI: 10.3410/f.727814781.793536165).

240. Kumar S (2017) F1000Prime Recommendation of Warnock RCM et al., Proc Biol Sci 2017, 284(1857) (DOI: 10.3410/f.727752709.793536398).

RESEARCH MENTORING

Postdoctoral scholars

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

Past *Alan Filipski (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) • Qiqing 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 Gargesha • 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 • Benjamin Nguyen • Deyana Tabatabaei • Glenda Armas • Hasnat Hasib • Louise Dupont • Madelyn Shenoy • Nandita Nagendra • Raneem Durra • Ryan Tobin

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 Tlougan • Elizabeth Santana • Elizabeth Villalba • Emily Davenport • Eric Thomas • Erika Garcia • German Velez • Glenn Markov • Greg McInnes • Hanna Pronina • Hariharan Mohanraj • Harry Ho • 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 • Mary Kate Durnan • Michael Suleski • Morgan Day • Natalia Santiago • Nate Sutton • Nicholas Peterson • Nicolas Feddern • Nisarg Patel • Olumide Oladeinde • Oscar Murillo • Paul Billing-Ross • Pegah Biparvah • Rachel Sipes • 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 • Lakshmie 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

Introduces molecular evolution through examples from medicine
Special topics designed for undergraduate to graduate students
Attended by 12 – 41 students; taught four times (BIO 189/494)
Class satisfaction rating: Exceptional 1.4 (range 1 - 4)

Introduction to Comparative Genomics 2001 – 2011

Introduces fundamentals of evolutionary genomics
Designed for senior undergrads and grad students
Increasing enrollment from 10 to 41; taught seven times (BIO 494)
Class satisfaction rating: Exceptional 1.2 (1 – 5)

Organic Evolution 2000 – 2006

Basic course in evolutionary biology
Designed for junior undergraduate
Attended by 106 – 185 students; taught five times
Class satisfaction rating: Exceptional 1.5 (range 1 – 4)

Molecular Evolutionary Genetics 1999 – 2000

An advanced course on molecular evolution and phylogenetics
Designed for graduate students (BIO 594/494)
Attended by 7 – 14 students; taught three times
Class satisfaction rating: Exceptional 1.3 (range 1 – 4)

CONFERENCE AND SYMPOSIA ORGANIZED

Co-Organizer, Green Computing in Molecular Phylogenetics (7/13) 2022

SMBE Everywhere; Kick-off annual meeting of the
Society for Molecular Biology and Evolution (SMBE)

Organizer, Growing Convergence Research Workshop on Epistasis (4/7) 2021
Temple University, Philadelphia, Pennsylvania, virtual workshop

Organizer, MEGA 25th Anniversary Workshop (7/8-7/12) 2018
The annual meeting of the Society for Molecular Biology and Evolution (SMBE), Yokohama, Japan

Coordinator, Workshop in Biogenomics & Nanobiology (4/23-4/24) 2018
International Collaboration Conference, Riyadh, Saudi Arabia

Organizer, Molecular Evolution and Medicine (9/16-9/17) 2017
Temple University, Philadelphia, USA (100 attendees)

Organizer, Symposium on Next-Generation Tools 2016
The annual meeting of SMBE, Gold Coast, Australia

Member, External Advisory Board 2014
The annual meeting of SMBE, Puerto Rico, USA

Organizer, SMBE Symposium on Phylomedicine 2012
Arizona State University, SU, Tempe, AZ, USA (75 attendees) (03/23-24)

Member, Global Organizing Committee 2011
The annual meeting of SMBE, Kyoto Japan (7/26–7/30)

Organizer, Symposium on Evolutionary Biology in Health and Medicine 2010
The annual meeting of SMBE, Lyon France (7/4–7/8)
co-organizers: J Dudley and A Butte

Co-organizer, Molecular Phylogenetics Symposium 2010
Moscow State University, Russia (5/17–5/21)

Member, Committee, International Conference on… Molecular Systematics 2007
Moscow State University, Russia (12/16–12/19)

Organizer, Annual Meeting of Society for Molecular Biology and Evolution 2006
Arizona State University, Tempe, Arizona (5/24–5/28) 750 participants

Organizer, Genome Database Workshop 2005
National Evolutionary Synthesis Center, North Carolina (5/31– 6/3)

Organizer, Symposium on Evolutionary and Population Genomics 2004
Future of Statistics, Indian School of Business, Hyderabad (12/29–1/1)

INVITED PRESENTATIONS

<u>2022 – 2019</u>

Invited Speaker (2 talks), *Workshop on Malaria molecular epidemiology, population genetics, and evolution*, New Delhi, INDIA • *Invited Speaker*, University of Southern California • *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.

<u>2018 – 2015</u>

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, Camridgeshire, 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.