

Sudhir Kumar

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PERSONAL DATA

Business Address: Center for Evolutionary Medicine & Informatics (<http://cemi.asu.edu>)
Biodesign Institute A-240
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EDUCATION

B. E. (Honors) Electrical & Electronics Engineering 1990*

M. Sc. (Honors) Biological Sciences 1990*

Birla Institute of Technology & Science (India) *Concurrent degrees

Ph. D. Genetics (Advisor: Masatoshi Nei) 1996

Pennsylvania State University (USA)

MAJOR RESEARCH THEMES

Molecular Evolution, Evolutionary Medicine, and Bioinformatics

PROFESSIONAL APPOINTMENTS

Director, Center for Evolutionary Medicine & Informatics, Biodesign Institute 2010 – Present

Professor, School of Life Sciences (SoLS), Arizona State University (ASU) 2006 – Present

Director, Center for Evolutionary Functional Genomics, Biodesign Institute 2003 – 2009

Faculty Leader, Genomics, Evolution, and Bioinformatics, SoLS, ASU 2003 – 2004

Associate Professor, SoLS, ASU 2002 – 2006

Assistant Professor, Department of Biology, ASU 1998 – 2002

Postdoctoral Fellow (Nei), Department of Biology, Penn State University 1996 – 1998

Research Assistant (Nei), Department of Biology, Penn State University 1991 – 1996

AWARDS & HONORS

Fellow, American Association for the Advancement of Science (AAAS) 2009

CSE Honorary Professor, School of Computing and Informatics, ASU 2009

Arizona Governor's Celebration of Innovation – Academia (Finalist) 2009

Top-10 Most-Cited author, Computer Science, Web of Science (series discontinued) 2004 – 2009

Visiting Fellowship Award, Japanese Society for Promotion of Science (JSPS) 2007 – 2008

Exemplar Faculty (Promotion to Full Professor), ASU 2006

Secretary (Elected), *Society for Molecular Biology and Evolution* 2004 – 2006

Innovation Award in Functional Genomics, Burroughs-Wellcome Fund 2000

Thomson Reuters ScienceWatch/Web of Science

Current Classic in Multidisciplinary Sciences (*PNAS* 101:11030–11035) 2010

Current Classic in Biology & Biochemistry (*Molec. Biol. Evol.* 24:1596–1599) 2010 – 2011

Current Classic Computer Science (*Briefings in Bioinfo.* 5: 150-163) 2007 – 2010

Hot Paper in Computer Science (*Briefings in Bioinfo.* 9:299-306) 2009

Hot Paper in Computer Science (*Briefings in Bioinfo.* 5:150-163) 2006

<i>Hot Paper</i> in Biology & in Computer Science (<i>Bioinformatics</i> 17:1244-1245),	2004
<i>Hot Paper</i> in Biology (<i>Nature</i> 392: 917-920)	2000
SCIENCE, Editor's Choice, August 25, 2006, <i>Molec. Biol. Evol.</i> 23:1946-1951)	2006
H-index = 48; Total citations to date = 31,000+ (Google Scholar, January edition)	2011

RESEARCH GRANT SUPPORT

Current Grants (PI)

<i>Comparative Molecular Sequence Analysis</i> (R01) Principal Investigator National Institutes of Health (NHGRI)	2007 – 2011
<i>Computational Analysis of Gene Expression Pattern Images</i> (R01) Principal Investigator National Institutes of Health (NHGRI)	2007 – 2011
<i>Re-engineering the MEGA Software Package</i> (R01) Principal Investigator National Institutes of Health (NIGMS/ARRA)	2007 – 2011
<i>Evolutionary Bioinformatics of Human Mutations</i> (R01) Principal Investigator National Institute of Health (NLM)	2010 – 2013

Current Grants (co-PI, Co-Investigator)

<i>Bioinformatics of Molecular Timetrees</i> Co-Principal Investigator [S. B. Hedges, PI] National Science Foundation (DBI)	2009 – 2012
<i>Discovering the Hidden Proteome in the Human Genome</i> (EUREKA, R01) Co-Principal Investigator [J. Chaput, PI] National Institutes of Health	2008 – 2012
<i>Center for Membrane Proteins in Infectious Diseases</i> (MIPD, U54) Co-Principal Investigator [P. Fromme, PI] National Institutes of Health (NIGMS)	2010 – 2015
<i>A Phylogenetic Approach to Metagenomic Analysis</i> (R21) Co-Investigator [A. Filipinski, PI] National Institutes of Health (NHGRI/NIH)	2011 – 2013

Completed Grants/Contracts

<i>Comparative Molecular Sequence Analysis</i> (R01), Principal Investigator, National Institutes of Health	2000 – 2007
<i>Design of a Bioinformatic Database for Functional Evolutionary Footprints in Multigene Families</i> , Principal Investigator, National Science Foundation	2000 – 2004
<i>Emerging Wildlife Diseases: Threats to Amphibian Biodiversity</i> , Co-Investigator, National Science Foundation; PI: J. Collins	2000 – 2008
<i>Development of an Evolutionary Timescale Database</i> , Co-Principal Investigator, National Science Foundation	2001 – 2004
<i>A Computational Biosciences Professional Master's Program</i> , Participating Investigator, Sloan Foundation	2001 – 2003
<i>Computational Genomic Analysis to Identify and Dissect Functionally Important Mutations in Protein Sequences</i> , Principal Investigator, Burroughs-Wellcome Fund, USA	2003 – 2006
<i>Computational Analysis of Gene Expression Pattern Images</i> (R01) Principal Investigator, National Institutes of Health	2003 – 2007
<i>LSAMP Biodesigned Bridges to the Doctorate</i> , Co-Principal Investigator, National Science Foundation	2004 – 2006

<i>Comparative Molecular Sequence Analysis</i> (R01), Principal Investigator, National Institutes of Health	2004 – 2007
<i>Bioinformatics of Assembling the Timescale of Life</i> , Principal Investigator, Science Foundation of Arizona	2007 – 2008
<i>Developing a Bioinformatic Database for Stoichioproteomics</i> National Science Foundation; PI: W. Fagan	2006 – 2010
<i>Machine Learning Approaches for Biological Image Informatics</i> National Science Foundation; PI: J. Ye	2006 – 2010
<i>Team Approach to Translate Novel Biomarkers for Diabetes</i> Co-Investigator; R. Nelson, PI, National Institutes of Health	2009 – 2010

MEMBERSHIPS IN SCIENTIFIC AND PROFESSIONAL ORGANIZATIONS

American Association for the Advancement of Science
 Arizona Arts, Sciences, and Technology Academy (founding fellow)
 American Genetic Association
 The Genetics Society of America
 International Society of Computational Biologists
 Society for Molecular Biology and Evolution
 Society for the Study of Evolution

JOURNAL EDITORIAL AND WEBMASTER SERVICE

<i>Honorary Editor</i> , Biomolecules	2010 – Present
<i>Associate Editor</i> , Quarterly Review of Biology	2010 – Present
<i>Associate Editor</i> , Molecular Biology & Evolution	2005 – Present
<i>Associate Editor</i> , Evolutionary Bioinformatics Online	2005 – Present
<i>Editorial Board</i> , Molecular and Developmental Evolution (J. Exp. Zool.)	2004 – Present
<i>Editorial Board</i> , Genome Research	2005 – 2009
<i>Board of Editors</i> , Gene: Functional Genomics	2005 – 2006
<i>Webmaster</i> , Society for Molecular Biology and Evolution (www.smbe.org)	2004 – 2008
<i>Webmaster</i> , American Genetic Association (www.theaga.org)	1999 – 2007
<i>Associate Editor</i> , Journal of Heredity	1999 – 2005

CONFERENCE/SYMPOSIA/OUTREACH ORGANIZED

Biodesign Data Club (with Joshua LaBaer), Arizona State University (Fall)	2010
Evolutionary Biology in Health and Medicine, Annual meeting of the <i>Society for Molecular Biology and Evolution</i> , Lyon France (July 4 - 8) (co-organized with Joel Dudley and Atul Butte)	2010
Molecular Phylogenetics Symposium, Russia (May 17 – 21)	2010
Hosted FlyBase outreach meeting at ASU (March)	2007
Member, Program Committee, <i>International Conference on Computational Phylogenetics and Molecular Systematics</i> , Moscow State University, Russia (November 16 – 19)	2007
Chair, Annual meeting of the <i>Society for Molecular Biology and Evolution</i> , Arizona State University, Tempe, Arizona (May 24 – 28)	2006
Organizer, Genome Database Workshop @ <i>National Evolutionary Synthesis Center</i> , Wilmington Beach, North Carolina, (May 31 – Jun 3)	2005
Symposium on Evolutionary and Population Genomics in the <i>Future of Statistics Conference at Indian School of Business</i> , Hyderabad, India (Dec. 29 – Jan. 1)	2004

PROFESSIONAL AFFILIATIONS

Guest Professor, Center for Computational and Evolutionary Biology (CCEB),	2007 – Present
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Institute of Zoology at Beijing, China	
Affiliate Professor, School of Computing, Informatics, and Decision Support Engineering, ASU	2002 – Present
Member, NASA Astrobiology/Evolutionary Genomics Focus Group	2000 – Present
Associate Member, Penn State Astrobiology Research Center	1998 – Present
Affiliate Professor, Department of Biomedical Informatics, ASU	2005 – 2007
Adjunct Senior Investigator, Translational Genomics Research Institute (TGen), Phoenix, Arizona	2004 – 2007
Member, Genetics Program, ASU	1998 – 2005

ORGANIZATIONAL REVIEWER & CONSULTANT

Member, 10-year review committee, Institute for Genomics and Bioinformatics (IGB) @ University of California, Irvine	2010
Consultant, Amerigenics, Inc., USA	2006 – 2007
Consultant, Advisory Committee on Evolutionary Bioinformatics, University of South Dakota, USA	2006
Member, five-year review committee, Institute for Genomics and Bioinformatics (IGB) @ University of California, Irvine	2005
Consultant, Pharmacia Corporation, USA	2002 – 2003

PROFESSIONAL ADVISORY BOARDS / WORKING GROUPS

FlyBase Advisory Group	2007 – 2008
Standing Member, BioData Management and Analysis (BDMA) Study Section, National Institutes of Health, USA	2006 – 2010
Member, Informatics Advisory Committee, National Center for Evolutionary Synthesis (NESCent), USA	2006 – 2009
Member, Working Group: Evolutionary Informatics: Supporting Interoperability in Evolutionary Analysis, NESCent, USA	2006 – 2008

EXTRAMURAL TEACHING

Comparative Genomics and Molecular Evolution (June 20–22) 16 th Summer Institute in Statistical Genetics, University of Washington, Seattle, Washington, USA (with S. Muse)	2011 (upcoming)
Molecular Evolution and Phylogenetics (July 13–14) Centers for Disease Control (CDC), Atlanta, Georgia, USA	2009
Distance and Parsimony Methods (June) in <i>Molecular Evolution and Systematics</i> workshop, Chinese Academy of Sciences, Beijing, China	2004

SOFTWARE AND DATABASES

MEGA (1993–):	Molecular Evolutionary Genetics Analysis. Integrated tool for molecular evolutionary and comparative sequence analyses (http://www.megasoftware.net)
PhylTest (1995):	Phylogenetic Hypothesis Testing Software. A simple utility to conduct four cluster analysis (http://www.kumarlab.net/pdf_new/phyltst.zip).
FlyExpress (2003–):	<i>Drosophila melanogaster</i> Expression Pattern Search Engine. A knowledge-base to discover genes with similar patterns of expression (http://www.flyexpress.net)
TimeTree (2006–):	Knowledge-base of species timetrees. A discovery platform to identify all published molecular time estimates for chosen organisms (http://www.timetree.org and iPhone application)
GRASP (2010–):	Genomic Resource Access for Stoichioproteomics. A resource containing stoichiometric information on <i>Drosophila</i> proteins (http://www.graspedb.net)

PUBLICATIONS**1990 – 1999**

1. Hedges SB, Kumar S, Tamura K & Stoneking M (1992) Human origins and analysis of mitochondrial DNA sequences. *Science* 255:737–739.
2. 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; >2500 printed manuals distributed).
3. Kumar S, Tamura K & Nei M (1994) MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. *Computer Applications in Biosciences* 10:189–191.
4. Kumar S (1995) PhylTest: A Program for Testing Phylogenetic Hypotheses. Pennsylvania State University, University Park.
5. Rzhetsky A, Kumar S & Nei M (1995) Four-cluster analysis: a simple method to test phylogenetic hypotheses. *Molecular Biology & Evolution* 12:163–167.
6. Yang Z, Kumar S & Nei M (1995) A new method of inference of ancestral nucleotide and amino acid sequences. *Genetics* 141:1641–1650.
7. Winnepeninckx 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 & Evolution* 12:1132–1137.
8. Hedges SB, Parker PH, Sibley CG & Kumar S (1996) Continental breakup and the ordinal diversification of birds and mammals. *Nature* 381:226–229.
9. Kumar S (1996) A stepwise algorithm for finding minimum evolution trees. *Molecular Biology & Evolution* 13:584–593.
10. Kumar S (1996) Patterns of nucleotide substitution in mitochondrial protein coding genes of vertebrates. *Genetics* 143:537–548.
11. Kumar S, Balczarek KA & Lai Z-C (1996) Evolution of the hedgehog gene family. *Genetics* 142:965–972.
12. Kumar S & Rzhetsky A (1996) Evolutionary relationships of eukaryotic kingdoms. *Journal of Molecular Evolution* 42:183–193.
13. Yang Z & Kumar S (1996) Approximate methods for estimating the pattern of nucleotide substitution and the variation of substitution rates among sites. *Molecular Biology & Evolution* 13:650–659.
14. Balczarek KA, Lai Z-C & Kumar S (1997) Evolution and functional diversification of the Paired box (Pax) DNA-binding domains. *Molecular Biology & Evolution* 14:829–842.
15. Zhang J & Kumar S (1997) Detection of convergent and parallel evolution at the amino acid sequence level. *Molecular Biology & Evolution* 14:527–536.
16. Zhang J, Kumar S & Nei M (1997) Small-sample tests of episodic adaptive evolution: A case study of primate lysozymes. *Molecular Biology & Evolution* 14:1335–1338.
17. Yeager M, Kumar S & Hughes AL (1997) Sequence convergence in the peptide-binding region of primate and rodent MHC class *Ib* molecules. *Molecular Biology & Evolution* 14:1035–1041.
18. 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.
19. Kumar S & Hedges SB (1998) A molecular timescale for vertebrate evolution. *Nature* 392:917–920.
20. 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.
21. Hedges SB & Kumar S (1999) Divergence times of eutherian mammals. *Science* 285:2031a.
22. 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.
23. 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.

24. 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.
- 2000 – 2009**
25. Nei M & Kumar S (2000) *Molecular Evolution and Phylogenetics*. Oxford University Press, New York (333 pp). (Translated in Chinese, Japanese, and Russian)
 26. Kumar S, Mitnik C, Valente G & Floyd-Smith G (2000) Expansion and molecular evolution of the interferon-induced 2'-5' oligoadenylate synthetase gene family. *Molecular Biology & Evolution* 17:738–750.
 27. Kumar S, Hedrick P, Dowling T, & Stoneking M (2000) Questioning evidence for recombination in human mitochondrial DNA. *Science* 288:1931a.
 28. 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.
 29. 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.
 30. Kumar S (2000) A review of the book *Genomes* by TA Brown. The Quarterly Review of *Biology* 75:316–317.
 31. Kumar S, Tamura K, Jakobsen IB & Nei M (2001) MEGA2: Molecular Evolutionary Genetics Analysis software. *Bioinformatics* 17:1244–1245.
 32. Gerber AS, Loggins R, Kumar S & Dowling TE (2001) Does non-neutral evolution shape observed patterns of DNA variation in animal mitochondrial genomes? *Annual Review of Genetics* 35:539–566.
 33. Kumar S & Filipski A (2001 and 2008) *Molecular Phylogeny Reconstruction*. *Encyclopedia of Life Sciences* Macmillan Reference Ltd, Oxford, UK. (www.els.net).
 34. Kumar S & Filipski A (2001) *Molecular Clock Testing*. *Encyclopedia of Life Sciences*, Macmillan Reference Ltd, Oxford, UK. (www.els.net).
 35. Kumar S, Gadagkar SR, Filipski A & Gu X (2001) Determination of the number of conserved chromosomal segments between species. *Genetics* 157:1387–1395.
 36. 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.
 37. Kumar S & Panchanathan S (2001) Elucidating gene interaction networks based on gene expression pattern image analysis. *Proceedings of the International Conference on Biomedical Engineering* 5A:232–234.
 38. Rosenberg MS & Kumar S (2001) Traditional phylogenetic reconstruction methods reconstruct shallow and deep evolutionary relationships equally well. *Molecular Biology & Evolution* 18:1823–1827.
 39. Rosenberg MS & Kumar S (2001) Incomplete taxon sampling is not a problem for phylogenetic inference. *Proceedings of the National Academy of Sciences (USA)* 98:10751–10756.
 40. Miller MP & Kumar S (2001) Understanding human disease mutations through the use of interspecific genetic variation. *Human Molecular Genetics* 10: 2319–2328.
 41. Hedrick P & Kumar S (2001) Mutation and linkage disequilibrium in human mtDNA. *European Journal of Human Genetics* 9:969–972.
 42. Hedges SB, Chen H, Kumar S, Wang DY-C, Thompson AS, & Watanabe H (2001) A genomic timescale for the origin of eukaryotes. *BMC Evolutionary Biology* 1:4 (10 pp).
 43. Jayaraman K, Panchanathan S, & Kumar S (2001) Classification and indexing of gene expression images. *Proceedings of Society of Photo-optical Instrumentation Engineers* 4472:471–481.
 44. Hedges SB & Kumar S (2002) Vertebrate genomes compared. *Science* 297:1283–1285.
 45. 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.
 46. 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.

47. Kumar S & Subramanian S (2002) Mutation rates in mammalian genomes. *Proceedings of the National Academy of Sciences (USA)* 99:803–808.
48. Kumar S, Jayaraman K, Panchanathan S, Gurunathan R, Marti-Subirana A & Newfeld SJ (2002) BEST: A novel computational approach for comparing gene expression patterns from early stages of *Drosophila melanogaster* development. *Genetics* 162:2037–2047.
49. Tamura K & Kumar S (2002) Evolutionary distance estimation under heterogeneous substitution pattern among lineages. *Molecular Biology & Evolution* 19:1727–1736.
50. Jiang Z, Melville JS, Cao H, Kumar S, Filipski A & Verrinder Gibbins AM (2002) Measuring conservation of contiguous sets of autosomal markers on bovine and porcine genomes in relation to the map of the human genome. *Genome* 45:769–776.
51. Hedges SB & Kumar S (2003) Genomic clocks and evolutionary timescales. *Trends in Genetics* 19:200–206.
52. Lorson C & Kumar S (2003) A review of the book *Genomes (second edition)* by T.A. Brown. *The Quarterly Review of Biology* 78:225.
53. 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 & Phylogenetics* 27:165–167.
54. Subramanian S & Kumar S (2003) Neutral substitutions occur as a faster rate in exons than in noncoding DNA in primate genomes. *Genome Research* 13:838–844.
55. Rosenberg MS & Kumar S (2003) Taxon sampling, bioinformatics, and phylogenomics. *Systematic Biology* 52:119–124.
56. Rosenberg MS, Subramanian S & Kumar S (2003) Patterns of transitional mutation biases within and among mammalian genomes. *Molecular Biology & Evolution* 20:988–993.
57. Rosenberg MS & Kumar S (2003) Heterogeneity of nucleotide frequencies among evolutionary lineages and phylogenetic inference. *Molecular Biology & Evolution* 20:610–621.
58. Miller MP, Parker JD, Rissing SW, & Kumar S (2003) Quantifying the intragenic distribution of human disease mutations. *Annals of Human Genetics* 67:567–579.
59. Jancovich J, Mao J, Chinchar VG, Wyatt C, Case S, Kumar S, Valente G, Subramanian S, Davidson EW, Collins JP & Jacobs BL (2003) Genomic sequence of a ranavirus (family Iridoviridae) associated with salamander mortalities in North America. *Virology* 316:90–103.
60. Kumar S, Tamura K & Nei M (2004) MEGA3: Integrated software for Molecular Evolutionary Genetics Analysis and sequence alignment. *Briefings in Bioinformatics* 5:150–163.
61. Hedges SB & Kumar S (2004) Precision of molecular time estimates. *Trends in Genetics* 20:242–247.
62. Kumar S & Filipski A (2004) Phylogenetic Analysis. *Dictionary of Bioinformatics and Computational Biology* edited by Hancock J & Zvelebil M, Wiley-Liss, New York.
63. Tamura K, Subramanian S & Kumar S (2004) Temporal patterns of fruit fly evolution revealed by mutation clocks. *Molecular Biology and Evolution* 21:36–44.
64. Briscoe A, Gaur C & Kumar S (2004) The spectrum of human rhodopsin disease mutations through the lens of interspecific variation. *Gene* 332:107–118.
65. Tamura K, Masatoshi Nei, & Kumar S (2004) Prospects for inferring very large phylogenies using the neighbor-joining method. *Proceedings of the National Academy of Sciences (USA)* 101:11030–11035.
66. Subramanian S & Kumar S (2004) Gene expression intensity shapes evolutionary rates of the proteins encoded by the vertebrate genome. *Genetics* 168:373–381.
67. Gurunathan R, Van Emden B, Panchanathan S & Kumar S (2004) Identifying spatially similar gene expression patterns in early stage fruit fly embryo images: binary feature versus invariant moment digital representations. *BMC Bioinformatics* 5:202 (13 pp).
68. Garghesha M, Antin P, Van Emden B, Panchanathan S & Kumar S (2004) Image registration and similarity computation for chicken gene expression patterns. *Genomic Signal Processing and Statistics (GENSIPS)*, IEEE Signal Processing Society (4 pp).
69. Kumar S (2005) Molecular clocks: four decades of evolution. *Nature Reviews Genetics* 6:654–662.
70. Kumar S & Hedges SB (2005) Pushing back the expansion of introns in animal genomes. *Cell* 123:1182–1184.

71. Filipski A & Kumar S (2005) Comparative Genomics in Eukaryotes. In *The Evolution of the Genome* edited by Ryan TG. Elsevier, San Diego, pp 521–583.
72. Kumar S & Filipski A (2005) Reconstructing Vertebrate Phylogeny. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics* edited by Subramaniam S. John Wiley & Sons, New York.
73. Kumar S, Filipski A, Swarna V, Walker A & Hedges SB (2005) Placing confidence limits on the molecular age of the human-chimpanzee divergence. *Proceedings of the National Academy of Sciences (USA)* 102:18842–18847.
74. Gadagkar SR, Rosenberg MS & Kumar S (2005) Inferring species phylogenies from multiple genes: concatenated sequence tree versus consensus gene tree. *Journal of Experimental Zoology (Molecular & Developmental Evolution)* 304B:64–74.
75. Gadagkar SR & Kumar S (2005) Maximum likelihood outperforms maximum parsimony even when evolutionary rates are heterotachous. *Molecular Biology and Evolution* 22:2139–2141.
76. Gargasha M, Yang J, Van Emden B, Panchanathan S & Kumar S (2005) Automatic annotation techniques for gene expression images of the fruit fly embryo. *Proceedings of Society of Photo-optical Instrumentation Engineers* 5960:576–583.
77. Hedges SB, Dudley J & Kumar S (2006) TimeTree: a public knowledge-base of divergence times among organisms. *Bioinformatics* 22: 2971–2972.
78. Kumar S and the FlyExpress Consortium (2006/2009) FlyExpress: A knowledge-base of spatiotemporal expression patterns at a genomic-scale in the fruit-fly embryogenesis. Arizona State University, Tempe, Arizona. (www.flyexpress.net)
79. Hedges SB, Kumar S & van Tuinen M (2006) Constraining fossil calibrations for molecular clocks. *BioEssays* 28:770–771.
80. Elser JJ, Fagan WF, Subramanian S & Kumar S (2006) Signatures of ecological resource availability in the animal and plant proteomes. *Molecular Biology & Evolution* 23:1946–1951.
81. Subramanian S & Kumar S (2006) Higher intensity of natural selection on >90% of the human genes revealed by the intrinsic replacement mutation rates. *Molecular Biology & Evolution* 23:2283–2287.
82. Subramanian S & Kumar S (2006) Evolutionary anatomies of positions and types of disease-associated and neutral amino acid mutations in the human genome. *BMC Genomics* 7:306 (9 pp).
83. Ye J, Chen J, Li Q & Kumar S (2006) Classification of Drosophila embryonic developmental stage range based on gene expression pattern images. *Computational Systems Bioinformatics Conference* 4:293–298.
84. Xia X & Kumar S (2006) Codon-based detection of positive selection can be biased by heterogeneous distribution of polar amino acids along protein sequences. *Computational Systems Bioinformatics Conference* 4:335–340.
85. Tamura K, Dudley J, Nei M & Kumar S (2007) MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology & Evolution* 24:1596–1599.
86. Kumar S & Filipski A (2007) Multiple sequence alignment: in pursuit of homologous DNA positions. *Genome Research* 17:127–135.
87. Kumar S & Dudley J (2007) Bioinformatics software for biologists in the genomics era. *Bioinformatics* 23:1713–1717.
88. Filipski A, Prohaska S & Kumar S (2007) Detecting molecular signatures of adaptive evolution. In *Evolutionary Genomics and Proteomics* edited by Pagel M & Pomiankowski A. Sinauer Associates, Massachusetts, pp 241–254.
89. Kumar S with many authors (2007) Sequence Assembly and Alignment Tech Guide. *Genome Technology* (10 pp).
90. Colbourn CJ & Kumar S (2007) Lower bounds on multiple sequence alignment using exact 3-way alignment. *BMC Bioinformatics* 8:140 (8 pp).
91. Zhang Y, Sturgill D, Parisi M, Kumar S & Oliver B (2007) Constraint and turnover in sex-biased gene expression in the genus *Drosophila*. *Nature* 450:233–237.
92. Clark AG, ..., Kumar S, ..., Drosophila 12 Genomes Consortium (2007) Evolution of genes and genomes on the *Drosophila* phylogeny. *Nature* 450:203–218.

93. Acquisti C, Poste G, Curtiss D & Kumar S (2007) Nullomers: really a matter of natural selection? *PLoS ONE* 2 (3 pp).
 94. Kumar S, Van Emden B, Acquisti C, Fagan WF, Elser JJ (2008) GRASP: Genomic Resource Access for Stoichioproteomics. Arizona State University, Tempe, Arizona. (www.graspedb.net)
 95. Ye J, Janardan R & Kumar S (2008) Biological Image Analysis via Matrix Approximation, *Encyclopedia of Data Warehousing and Mining* (2nd Ed.) edited by John Wang, Idea Group, Inc., Pennsylvania (Pp. 166-170).
 96. Ye J, Chen J, Janardan R & Kumar S (2008) Developmental stage annotation of *Drosophila* gene expression pattern images via an entire solution path for LDA. *ACM Transactions on Knowledge Discovery from Data* 2:1–21.
 97. Ji S, Sun L, Jin R, Kumar S, & Ye J (2008) Automated annotation of *Drosophila* gene expression patterns using a controlled vocabulary. *Bioinformatics* 24:1881–1888.
 98. Kumar S, Dudley J, Nei M & Tamura K (2008) MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. *Briefings in Bioinformatics* 9:299–306.
 99. Hedges SB and Kumar S (2009) TimeTree 2: An expanded public knowledge-base of divergence times among organisms. Pennsylvania and Arizona State Universities, USA. (www.timetree.org)
 100. Hedges SB & Kumar S (2009) *The Timetree of Life*. Oxford University Press, New York (550 pp; edited volume with 81 contributions).
 101. Hedges SB & Kumar S (2009) Discovering the Timetree of Life. In *The Timetree of Life* edited by Hedges SB & Kumar S. Oxford University Press, New York, pp 3–18.
 102. Kumar S, Suleski M, Markov GJ, Lawrence S, Marco A & Filipinski AJ (2009) Positional conservation and amino acids shape the correct diagnosis and population frequencies of benign and damaging personal amino acid mutations. *Genome Research* 19:1562-1569.
 103. Suzuki Y, Gojobori T & Kumar S (2009) Methods for incorporating the hypermutability of CpG dinucleotides in detecting natural selection operating at the amino acid sequence level. *Molecular Biology & Evolution* 26: 2275-2284.
 104. Acquisti C, Elser JJ & Kumar S (2009) Nitrogen-limitation shapes the DNA composition of plant genomes. *Molecular Biology & Evolution* 26:953–956.
 105. Horiike T, Miyata D, Hamada K, Saruhashi S, Shinozawa T, Kumar S, Chakraborty R, Komiyama T & Tateno Y (2009) Phylogenetic construction of 17 bacterial phyla by new method and carefully selected orthologs. *Gene* 429:59–64.
 106. Acquisti C, Kumar S & Elser JJ (2009) Signatures of nitrogen limitation in the elemental composition of the proteins involved in the metabolic apparatus. *Proceedings of the Royal Society, London, B* 276:2605-2610.
 107. Mikhailov KV, Konstantinova AV, Nikitin MA, Troshin PV, Rusin LY, Lyubetsky VA, Panchin YV, Mylnikov AP, Moroz LL, Kumar S & Aleoshin VV (2009) The origin of Metazoa: a transition from temporal to spatial cell differentiation. *BioEssays* 31:758-768.
 108. Ji S, Li Y-X, Zhou Z-H, Kumar S & Ye J (2009) A bag-of-words approach for *Drosophila* gene expression pattern annotation. *BMC Bioinformatics* 10:119 (16 pp).
 109. Marco A, Konikoff C, Karr TL & Kumar S (2009) Relationship between gene co-expression and sharing of transcription factor binding sites in *Drosophila melanogaster*. *Bioinformatics* 25:2473-2477.
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- 2010 – Present**
112. Battistuzzi FU, Filipinski A, Hedges SB & Kumar S (2010) Performance of relaxed clock methods in estimating evolutionary divergence times and their credibility intervals. *Molecular Biology & Evolution* 27: 1289-1300.

113. Stone AC, Battistuzzi FU, Kubatko LS, Perry GH, Trudeau E, Lin H & Kumar S (2010) More reliable estimates of divergence times in Pan using complete mtDNA sequences in and accounting for population structure. *Philosophical Transactions of Royal Society B* 365: 3277-3288.
114. Kazemian M, Blatti C, Richards A, McCutchan M, Wakabayashi-Ito N, Hammonds AS, Celniker SE, Kumar S, Wolfe SA, Brodsky MH & Sinha S (2010) Quantitative analysis of the *Drosophila* segmentation regulatory network using pattern generating potentials. *PLoS Biology* 17: 8 (8 pp).
115. Li YX, Ji S, Kumar S, Ye J, Zhou Z (2010) *Drosophila* gene expression pattern annotation through multi-instance multi-label learning. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. IJCAI2009:1445-1450.
116. Kumar S. (2010) Foreword for the book *GENES: Conceptual, Molecular, and Developmental* by S Mitra. *MacMillan Press, India*.
117. Elser JJ, Acquisti C, and Kumar S (2011) Stoichiogenomics: the evolutionary ecology of macromolecular elemental composition. *Trends in Ecology & Evolution* 26:38-44.
118. Gray VE & Kumar S (2011) Rampant purifying selection conserves positions with post-translational modifications in human proteins. *Molecular Biology & Evolution* (doi: 10.1093/molbev/msr013).
119. Pacheco MA, Battistuzzi FU, Lentino M, Aguilar R, Kumar S & Escalante AA (2011) Evolution of modern birds revealed by Mitogenomics: timing the radiation and origin of major orders. *Molecular Biology & Evolution* (10.1093/molbev/msr014).
120. Kumar S, Filipski AJ, Battistuzzi FU & Tamura K (2011) Statistics and Truth in Phylogenomics. *Molecular Biology & Evolution* (submitted)
121. Battistuzzi FU, Billing-Ross P, Paliwal A & Kumar S (2011) Fast and slow programs implementing relaxed clock methods show similar accuracies in estimating divergence times. (submitted)
122. Konikoff C, McCutchan M, Van Emden B, Busick C, Davis KT, Ji S, Wu L, Ramos H, Brody T, Panchanathan S, Ye J, Karr TL, Newfeld SJ & Kumar S (2011) FlyExpress: Discovering co-expressed genes by comparative analysis of spatial patterns in images of *Drosophila* embryogenesis. (submitted)
123. Tamura K, Peterson D, Peterson N, Stecher G, Nei M & Kumar S (2011) MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, evolutionary distance, and Maximum Parsimony methods. (submitted).
124. Dudley JT, Chen R, Sanderford M, Butte AJ & Kumar S (2011) Evolutionary meta-analysis of risk variants reveals missing heritability in disease association studies. (in preparation).

INVITED PRESENTATIONS

Upcoming

- Workshop on *Bioinformatic Software for Comparative Genomics and Metagenomics*.
The Smithsonian Institution (SI), American Museum of Natural History (AMNH) 2011
and the Food and Drug Administration (FDA)
Title: MEGA software: Philosophy and Future
- Department of Biomedical Informatics, ASU 2011
- SMBE Symposium on Molecular and Genomic Evolution @ Penn State University 2011
- Invited Keynote speaker, Mini-symposium on *Data Mining for Biomedical Informatics* 2011
@ SIAM International Conference on Data Mining, Mesa, Arizona
- Keynote Speaker, Interdisciplinary Graduate Student's Symposium on 2011
Evolution Across Fields @ Institute for Evolution and Biodiversity,
Muenster, Germany (February 18)
Title: Molecular Evolution in Personal Medicine

Past

- Plenary Speaker, Molecular Phylogenetics Symposium, Russia (May 17-21) 2010
- Stanford University, California, USA 2009
- Symphogen Corporation (Copenhagen) 2009
- Chalk Talk, Physics Department, ASU 2009

- Spirit of Senses Group, Phoenix, Arizona 2009
- University of Cologne, Germany 2009
- Quantitative Expression Analysis workshop @ Drosophila Research Conference, Chicago, Illinois 2009
Title: Challenges in Integrative Analysis of High-Throughput Datasets
- University of North Carolina, Charlotte, NC 2008
- Washington University, St. Louis, MO 2008
- Symposium on *Evolutionary Bioinformatics*, Keynote address, Lava Springs, Idaho State University (Oct 3-5) 2008
Title: Software tools and Knowledge-bases for discoveries from genomes to phenotypes
- Japan Biological Information Research Center (JBIRC), Tokyo, Japan 2008
- 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 2008
- Global Center for Excellence, Hokkaido University, Sapporo, Japan 2008
- Discussion leader, *Computational and Statistical Advances*, Gordon Conference in Molecular Evolution @ Ventura, California (Feb 3-8, 2008) 2008
- SOLUR Program, Arizona State University 2007
- Department of Biomedical Informatics, Arizona State University 2007
- FlyExpress: The Next Steps. FlyBase Advisory Group @ Harvard University, Boston, MA (Sept 15-18) 2007
- Keynote Speaker, Ohio Collaborative Conference on Bioinformatics (OCCBIO) @ Miami University, Oxford, Ohio 2007
Title: Evolutionary anatomies of disease mutations in proteins
- EMBO workshop on “Human Evolution and Disease” @ Center for Cellular and Molecular Biology, Hyderabad, India 2006
Title: Evolutionary anatomies of the locations and types of disease-associated nonsynonymous mutations in the human genome
- Department of Biological Sciences, University of Idaho, Moscow, ID 2006
- Microbiology Department, Montana State University, Bozeman, MT 2006
- ASU *Emeritus Faculty Association Luncheon*, Tempe, AZ 2005
Title: Evolutionary Functional Genomics in the Biodesign Institute: Taking a Computational Approach to Understanding and Harnessing the Biological Design
- Symposium on *Molecular Evolution @ Moscow Conference on Computational Molecular Biology*, Moscow State University, Russia 2005
Title: Placing Confidence Limits on the Molecular Age of the Human-Chimpanzee Divergence
- Symposium on Systems Biology @ Moscow Conference on Computational Molecular Biology, Moscow State University, Russia 2005
Title: Automating Discovery of Gene Interactions by in silico Analysis of in situ Gene Expression Patterns in Fruit Fly Embryos
- Special presentation to the *Panel on Chemical Imaging*, National Academies (USA), Washington DC 2005
Title: In silico Analysis and Management of Fruit Fly Gene Expression Pattern Images
- Symposium on *Evolutionary and Population Genomics @ Future of Statistics Conference*, Hyderabad, India 2004

- Title: Genomic Bounds on the Timing of the Evolutionary Divergence of Humans and Chimpanzees*
- Symposium on *Advances in Methods for Estimating Species Divergence Dates Using Molecular Data @ International Congress of Zoology, Beijing, China* 2004
Title: Genomic Timescales: Precision & Robustness
 - Symposium on *Molecular Phylogeny and Molecular Clocks @ Annual Meeting of the Society for Molecular Biology & Evolution, Penn State University, University Park, PA* 2004
Title: Genomic Timescales: Precision & Robustness
 - Hexapodium, Center for Insect Research, University of Arizona 2004
 - Techniques Workshop @ 44th Annual *Drosophila Research Conference*, Chicago, IL 2003
Title: Basic Expression Search Tool (BEST): Computational Framework for in silico Analysis of in situ Hybridization Data
 - *Comparative and Functional Genomics* Workshop, Sponsored by the *Wellcome Trust and Department of Energy*, Hinxton, Cambridgeshire, UK 2003
Title: Patterns of Point Mutation and Protein Substitution Rates Revealed by Comparative Mammalian Genomics
 - Annual Meeting of the *Society for Molecular Biology & Evolution*, Newport Beach, CA 2003
 - Department of Biology, Duke University, Durham, NC 2003
 - Bioinformatics Research Center, North Carolina State University, Raleigh, NC 2003
 - Symposium on *Evolutionary Genetics @ Annual meeting of the American Genetic Association*, Arizona State University, Tempe, Arizona 2002
Title: Rates of Point Mutation in Mammals
 - The 12th International Workshop on *Beyond the Identification of Transcribed Sequences: Functional, Evolutionary, and Expression Analysis* sponsored by *Department of Energy*, Washington, DC 2002
Title: Building Fruit Fly Developmental Networks: in silico Approaches for analyzing in situ Gene Expression Patterns
 - The 18th International Symposium in Conjunction with Award of the *International Prize for Biology*, Tokyo, Japan 2002
Title: Building Fruit Fly Developmental Networks: in silico approaches for Analyzing in situ Gene Expression Patterns
 - Department of Biology, Indiana University, Bloomington, Indiana 2002
 - Department of Computer Science, Arizona State University, Tempe, AZ 2002
 - Department of Biology, University of Michigan, Ann Arbor, MI 2002
 - International Workshop on *Population Genetics @ University of Montreal*, Montreal, Canada 2001
Title: Estimating Neutral Evolutionary Rates in Mammals
 - ASU President's Community Enrichment Program, Phoenix, Arizona 2001
 - Department of Biology, Ohio State University, Columbus, Ohio 2001
 - Department of Biology, Hong Kong University, Hong Kong, China (2 lectures) 2001
 - Department of Biology, Syracuse University, Syracuse, New York 2001
 - Program in Ecology and Evolutionary Biology, University of Illinois, Urbana Champaign, Illinois 2001
 - Department of Biology, Grand Canyon University, Phoenix, Arizona 2001
 - Ecology & Evolutionary Biology Program/IGERT, Indiana University, Bloomington, Indiana 2001

- Department of Biology, Tokyo Metropolitan University, Tokyo, Japan 2001
- Biomedical Engineering, Indian Institute of Science, Bangalore, India 2001
- Department of Biology, Tokyo Metropolitan University, Tokyo, Japan 2000
- Graduate University for Advanced Studies, Hayama, Japan 2000
- Genetics Program, University of Arizona, Tucson, Arizona 2000
- Birla Institute of Technology & Sciences, Pilani, India 2000
- University of South Carolina, Columbia, South Carolina 2000
- Symposium on *Genomic Diversity* @ Annual meeting of the *American Genetic Association*, Pennsylvania State University, University Park, PA 1999
Title: Genomic Divergence between Species in terms of the Number of Chromosomal Rearrangements
- Department of Biology, Arizona State University-West, Phoenix, Arizona 1999
- Department of Zoology and Genetics, Iowa State University, Ames, Iowa 1998
- Symposium on *Large Phylogenies* @ Annual meeting of the *Society for the Study of Systematic Biology*, University of Colorado, Boulder, Colorado 1997
Title: Inferring Large Phylogenies
- National Cancer Institute, Frederick, Maryland 1997
- Department of Biology, Arizona State University, Tempe, Arizona 1997

TEACHING, MENTORING, UNIVERSITY SERVICE

Classroom Instruction

(Average rating in parentheses; SCALE: 1 = BEST; 4 = WORST)

BIO 455	(Fall)	Introduction to Comparative Genomics		2011
BIO 494	(1.1)	Evolutionary Medicine	(30 students)	2010
BIO 455	(1.2)	Introduction to Comparative Genomics	(25 students)	2009
BIO 455	(1.2)	Introduction to Comparative Genomics	(10 students)	2008
BIO 494	(1.2)	Introduction to Comparative Genomics	(12 students)	2007
BIO 345	(1.4)	Organic Evolution	(180 students)	2006
BIO 345	(1.6)	Organic Evolution	(150 students)	2005
BIO 494	(1.3)	Introduction to Comparative Genomics	(11 students)	2004
BIO 345	(1.4)	Organic Evolution	(185 students)	2003
BIO 494	(1.2)	Introduction to Comparative Genomics	(12 students)	2003
BIO 445	(1.4)	Organic Evolution	(180 students)	2001
BIO 494	(1.3)	Computational Genomics	(7 students)	2001
BIO 445	(1.7)	Organic Evolution	(106 students)	2000
BIO 594	(1.3)	Molecular Evolutionary Genetics	(7 students)	2000
BIO 594	(1.5)	Molecular Evolutionary Genetics	(10 students)	1999
BIO 494	(1.2)	Advanced Evolution	(14 students)	1999

Current Postdoctoral Fellows / Research Scientists

Nevin Gerek, Ph.D., Chemical Engineering, University of Akron, OH	2010 – Present
Project: Quantification of structural dynamics. Developing new methods to quantify the structural dynamics of individual amino acid residues in a protein structure and investigating their evolutionary importance.	
Yingqin Luo, Ph.D., Bioinformatics	2008 – Present
Project: Microbial Genome Evolution. Estimating evolutionary relationships and divergence times of microbial strains (<i>Salmonella</i> genomes).	
Fabia Battistuzzi, Ph.D., Biology/Astrobiology	2008 – Present
Project: Computation of the Timetree of Life. The project focuses on reconstructing the evolutionary history of organisms and their genes, with a focus on timeline of the origin of lineages and traits using the	

vast amount of genomic sequences now available encompassing ancient and recent divergences.

Alan Filipiski, Ph.D., Computer Science, Michigan State 2001 – Present
 Project: Molecular Phylogenetics and Metagenomics. Developing methods and conducting simulation studies for phylogenetic analysis, including its applications to metagenomics.

Past Postdoctoral Fellows Mentored

Claudia, Acquisti, Ph.D., Molecular Evolution, Italy 2006 – 2010
Current Position. Assistant Professor, Institute for Evolution and Biodiversity, University of Muenster, Germany

Antonio Marco-Castillo, Ph.D., Genetics, Spain 2008 – 2009
Current Position. Faculty of Life Sciences, The University of Manchester, England

Bao Hong Shen, Ph.D., Computer Science, Ariz. State Univ. 2005 – 2007
Current Position. Senior R&D Scientist, Communication and Computer Networks UtopiaCompression Corporation, Los Angeles, CA

Anup Som, Ph.D., Bioinformatics, Jadavpur Univ., India 2005 – 2007
Current Position. Medical Faculty in Computational Biology and Bioinformatics at the Institute for Biostatistics and Informatics in Medicine and Ageing Research Univ. of Rostock, Germany

Christine Kuslich, Ph.D., Biomedical Sciences, Univ. of Hawaii 2003 – 2005
Current Position. Senior Vice President, Research & Molecular Diagnostics, Caris Life Sciences, Inc., Phoenix, AZ

Sankar Subramanian, Ph.D., Microbiology, IARI, India 2000 – 2006
Current Position. Postdoctoral Research Fellow, Australian Rivers Institute, Griffith University, Queensland, Australia

Araxi Urrutia, Ph.D., Evolutionary Genomics, Univ. of Bath, UK 2003 – 2004
Current Position. Royal Society Dorothy Hodgkin Research Fellow, Dept. of Biology and Biochemistry, University of Bath, UK

Michael S. Rosenberg, Ph.D., Ecology & Evolution, SUNY-Stony Brook 2000 – 2003
Current Position. Assoc. Professor, School of Life Sciences, Arizona State University (ASU)

Mark P. Miller, Ph.D., Evol & Conservation Genetics—Comp. Biol., NAU 2000 – 2002
Current Position. Research Assistant Professor, Department of Biology, Utah State University, Logan Utah

Sudhindra R. Gadagkar, Ph.D., Biology (Aquaculture Genetics), Canada 1998 – 2003
Current Position. Assistant Professor, Biomedical Sciences, Midwestern University, Glendale, Arizona

Chair/Co-Chair of Graduate Student Committees

Charlotte Konikoff, Ph.D., Molecular and Cellular Biology (Co-Chair) 2007 – 2010

Siddarth Selvaraj, Professional MS in Computational Biosciences (Chair) 2007 – 2008

Bindu Koshy, MS, Electrical Engineering (Chair) 2004 – 2006

Vinod Swarna, MS, Biology (Chair) 2005 – 2007

Hector Ramos, Professional MS in Computational Biosciences (Chair) 2005 – 2006

Rajalakshmi Gurunathan, Ph.D., Computer Science (Chair) 2002 – 2006

Madhusudana Gargasha, Ph.D., Electrical Engg (Co-Chair) 2002 – 2006

Stephanie Rogers, Professional MS in Computational Biosciences (Chair) 2003 – 2005

Vinod Swarna, Professional MS in Computational Biosciences (Chair) 2003 – 2005

Hoon Lee, Professional MS in Computational Biosciences (Chair) 2003 – 2005

Xiaofen Liu, Professional MS in Computational Biosciences (Chair) 2003 – 2005

Shubhra Gupta, Professional MS in Computational Biosciences (Chair) 2003 – 2004

Jian Yang, MS, Bioinformatics/Computational Biology (Chair)	2002 – 2005
Sandhya Durvasala, MS, Computer Science & Engg (Co-Chair)	2002 – 2004
Patrick Kolb, MNS, Biology (Chair)	2001 – 2003
Rekha Iyer, MS, Molecular & Cell Biology (Chair)	2000 – 2002
Karthik Jayaraman, MS, Electrical Engineering (Co-Chair)	1999 – 2001
Charu Gaur	2003 – 2004

Member of Graduate Student Committees

Joel Dudley, Stanford Biomedical informatics	2011 – Present
Takahiro Muraki, Ph.D., Biology	2006 – Present
Jianhui Chen, Ph.D., Computer Science	2007 – Present
Hugo F. Gante, Ph.D., Biology	2003 – 2010
Shuiwang Ji, Ph.D., Computer Science	2007 – 2010
Michael Schwemm, M.S., Biology	2001 – 2007
Peter Unmack, Ph.D., Biology	1998 – 2005
Evan Carson, Ph.D., Biology	1998 – 2005
Carla Hurt, Ph.D., Biology	1999 – 2005
Daniel Garrigan, Ph.D., Biology	1999 – 2003

Undergraduate/High School Research Assistants

Kristyn Gerold, Greg McInnes, Maxwell Sanderford, Alicia Varma	2010 – Present
Paul Billing-Ross, Vanessa Gray, Glenn Markov, Alexander Woodard, Aditya Paliwal	2009 – Present
Chikku Baiju	2008 – Present
Daniel Peterson	2007 – Present
Jenna Makis, Hariharan Mohanraj, Nate Sutton	2010 – 2010
Michael Suleski, Nicholas Peterson	2007 – 2010
Kimberly Kukurba, Simon Lawrence, Adithya Rajan	2008 – 2010
Stephen Watson, Robert Adrian,	2009 – 2010
Elizabeth Villalba (High school)	2009 – 2009
Nicolas Feddern	2008 – 2009
Kailah Davis	2007 – 2009
Christopher Busick, Bryan Sexton	2006 – 2008
Veronica Shi (High School), Biodesign Summer Intern; Asaria Jimenez, Melizabeth Santana, Yea Jin Ko, Ariana Rodriguez, Stephanie Negron, Thania Martinez, Wilda Rivera, Victor Correa, Liris Gonzalez, Jose Maldonado, German Velez, Cristina Rivera, Krizia Cabrera, Karen Canales, Carol Diaz, Raul Navedo (All from Puerto Rico)	2007
Rachel Sipes	2008 – 2009
Antoine Al-Foune	2007 – 2007
Jacob Reidhead	2001 – 2003
Veena Ganeshan	2000 – 2001
Emily Davenport. Diana Tloutan	2000 – 2000
Heather Wiemann, Evolutionary of multigene family	1998 – 2000
Candice White, DNA sequence analysis	1998 – 1998
Roman Johnson, Evolutionary of multigene family	1999 – 1999

Other Research/Development Lab Personnel

David Fisher, Computer Programming Assistant	2011 – Present
Li Liu, PhD, MD, Research Scientist	2010 – Present
Glen Stecher, Academic Associate	2009 – Present
Michael McCutchan, Database Administrator	2008 – Present
Jason Wulf, Information Technology Officer	2008 – Present

Daniel Peterson, Academic Associate	2007 – Present
Lin-Wei Wu, Scientific Programmer	2005 – Present
Wayne Parkhurst, Multimedia Specialist	2003 – Present
Revak Raj Tyagi, Graduate Associate	2007 – 2010
Nicholas Peterson, Academic Associate	2006 – 2010
Jana McAlpin, Scientific Programmer	2008 – 2009
Siddarth Selvaraj, Graduate Associate	2007 – 2009
Aditya Rajan	2009 – 2009
Mahesh Sundara Raman	2009 – 2009
Suganthi Cidambaram, Lakshmie Viswanathan	2009 – 2010
Annirudha Kadne	2008 – 2009
Melinda Caballero	2008 – 2008
Ashini Bolia	2008 – 2008
Ashly Ruttman, Graduate associate	2005 – 2008
Bernard Van Emden, Faculty Research Associate	2004 – 2008
Joel Dudley, Faculty Research Associate	2001 – 2007
Graziela Valente, Lab Manager & Research Technician	1999 – 2007
Sean Dudley, Systems Administrator	2005 – 2006
Dana Desonie, Scientific Writer	2004 – 2006
Vesna Djinovic, Programming Assistant	2005 – 2005
Joseph Svitak, Programmer	2004 – 2005
Quan Nguyen, Computer Data Base Specialist	2003 – 2005
Renee Grothe, Graphic Artist	2002 – 2004
David Schwartz, Programmer	2000 – 2004
Ben Timmerick, Graphics & Multimedia	2001 – 2002

Major University Committees

<i>Member</i> , University-wide meta planning in Engineering & Informatics	2010 – Present
<i>Member</i> , Executive Committee, Biodesign Institute	2004 – Present
<i>Member</i> , Executive Committee, Computational Biosciences Program	2000 – Present
<i>Chair</i> , Biodesign Personnel Committee	2008 – 2010
<i>Member</i> , Strategic Planning Committee, SoLS	2008 – 2009
<i>Member</i> , Graduate Initiatives in Informatics Committee	2007 – 2008
<i>Member</i> , Web Committee, SoLS	2007 – 2009
<i>Member</i> , Promotion Committee in the Biodesign Institute	2005 – 2008
<i>Member</i> , Steering Committee, Post-Baccalaureate Research Education Program in Biomedical Sciences (PREP) program (NIH-funded)	2005 – 2008
<i>Member</i> , Personnel Committee, Dept. of Biomedical Informatics	2005 – 2007
<i>Member</i> , Insect Neurogenomics Search (open rank)	2004 – 2005
<i>Member</i> , Taskforce on Biomedical Informatics	2004 – 2006
Taskforce was charged with the planning, design, and development of a new Department of Biomedical Informatics	
<i>Member</i> , Executive Committee, School of Life Sciences	2003 – 2004
<i>Member</i> , SoLS Founding Director	2003 – 2004
<i>Representative from ASU</i> in 3 formation meetings of the International Genomics Consortium: Johns Hopkins Univ, Baltimore, MD; M. D. Anderson Cancer Center, Houston, TX; Sun HealthCare, Scottsdale, AZ	2001
<i>Member</i> , Information Technology Hot Team, Prop 301	2000 – 2001
<i>Member</i> , Joint Bioengineering & Computer Science (open rank)	2000 – 2001
<i>Member</i> , Planning Committee, Academic degree program in Comp. Biosci.	2000
<i>Member</i> , Molecular Genetics (Asst. Prof.)	1999