

# MBE Citation Classics (2013 Edition)

Sudhir Kumar<sup>1,2</sup>

<sup>1</sup>School of Life Sciences, Arizona State University

<sup>2</sup>Center for Evolutionary Medicine and Informatics, Biodesign Institute, Arizona State University

Starting this year, *Molecular Biology and Evolution* (MBE) will release a list of articles designated Citation Classics to celebrate and highlight the diversity and impact of MBE publications in molecular evolutionary research. Early (1983–2007) and Recent (2008–2012) Citation Classics were selected based on the highest number of citations per year in each period. For the Early category, life-time citation impacts of publications from 1983 to 2007 were obtained from Thomson Reuters Web of Knowledge on 15 October 2012. From the resulting set (>3,500), 18 publications reporting biological discoveries and 18 publications reporting methods and resources were designated Early Citation Classics. For the Recent category, seven discovery and seven methods and resources publications were selected based on the highest number of citations per year for publications between 2008 and 2012 (>1,300). Overall, a total of 1% of MBE's publications is given Citation Classic designations, which are presented below in reverse chronological order.

## Discoveries

### MBE Recent Citation Classics (2008–2012)

*A phylogenomic approach to resolve the arthropod tree of life* (2010)

Meusemann and colleagues in Volume 27(11) Pp. 2451–2464.

*Improved phylogenomic taxon sampling noticeably affects nonbilaterian relationships* (2010)

Pick and colleagues in Volume 27(9) Pp. 1983–1987.

*Revisiting the insect mitochondrial molecular clock: the mid-Aegean trench calibration* (2010)

Papadopoulou and colleagues in Volume 27(7) Pp. 1659–1672.

*Timing of genome duplications relative to the origin of the vertebrates: Did cyclostomes diverge before or after?* (2009)

Kuraku and colleagues in Volume 26(1) Pp. 47–59.

*Confirming the phylogeny of mammals by use of large comparative sequence data sets* (2008)

Prasad and colleagues in Volume 25(9) Pp. 1795–1808.

*On the expansion of the pentatricopeptide repeat gene family in plants* (2008)

O'Toole and colleagues in Volume 25(6) Pp. 1120–1128.

*Strong variations of mitochondrial mutation rate across mammals—the longevity hypothesis* (2008)

Nabholz and colleagues in Volume 25(1) Pp. 120–130.

### MBE Early Citation Classics (1983–2007)

*Paleontological evidence to date the tree of life* (2007)  
Benton and colleagues in Volume 24(1) Pp. 26–53.

*A single determinant dominates the rate of yeast protein evolution* (2006)

Drummond and colleagues in Volume 23(2) Pp. 327–337.

*Multigene analyses of bilaterian animals corroborate the monophyly of Ecdysozoa, Lophotrochozoa, and Protostomia* (2005)

Philippe and colleagues in Volume 22(5) Pp. 1246–1253.

*Divergence population genetics of chimpanzees* (2005)

Won and Hey in Volume 22(2) Pp. 297–307.

*Microsatellites within genes: Structure, function, and evolution* (2004)

Li and colleagues in Volume 21(6) Pp. 991–1007.

*A molecular timeline for the origin of photosynthetic eukaryotes* (2004)

Yoon and colleagues in Volume 21(5) Pp. 809–818.

*Fugu genome analysis provides evidence for a whole-genome duplication early during the evolution of ray-finned fishes* (2004)

Christoffels and colleagues in Volume 21(6) Pp. 1146–1151.

*The evolution of transcriptional regulation in eukaryotes* (2003)

Wray and colleagues in Volume 20(9) Pp. 1377–1419.

*Prokaryotic evolution in light of gene transfer* (2002)

Gogarten and colleagues in Volume 19(12) Pp. 2226–2238.

*Nuclear-encoded, plastid-targeted genes suggest a single common origin for Apicomplexan and Dinoflagellate plastids* (2001)

Fast and colleagues in Volume 18(3) Pp. 418–426.

*The yeast protein interaction network evolves rapidly and contains few redundant duplicate genes* (2001)

Wagner in Volume 18(7) Pp. 1283–1292.

*Comparative evolutionary analysis of chalcone synthase and alcohol dehydrogenase loci in Arabidopsis, Arabis, and related genera (Brassicaceae)* (2000)

Koch and colleagues in Volume 17(10) Pp. 1483–1498.

*A comparative summary of genetic distances in the vertebrates from the mitochondrial cytochrome b gene* (1998)

Johns and Avise in Volume 15(11) Pp. 1481–1490.

Numerous transposed sequences of mitochondrial cytochrome oxidase I-II in aphids of the genus *Sitobion* (Hemiptera: Aphididae) (1996)

Sunnucks and Hales in Volume 13(3) Pp. 510–524.

Population-growth makes waves in the distribution of pairwise genetic-differences (1992)

Rogers and Harpending in Volume 9(3) Pp. 552–569.

Relationships between gene trees and species trees (1988)

Pamilo and Nei in Volume 5(5) Pp. 568–583.

Slipped-strand mispairing—a major mechanism for DNA-sequence evolution (1987)

Levinson and Gutman in Volume 4(3) Pp. 203–221.

Codon usage and transfer-RNA content in unicellular and multicellular organisms (1985)

Ikemura in Volume 2(1) Pp. 13–34.

## Methods and Resources

### MBE Recent Citation Classics (2008–2012)

MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods (2011)

Tamura and colleagues in Volume 28(10) Pp. 2731–2739.

Isolation with migration models for more than two populations (2010)

Hey in Volume 27(4) Pp. 905–920.

Bayesian inference of species trees from multilocus data (2010)

Heled and Drummond in Volume 27(3) Pp. 570–580.

SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building (2010)

Gouy and colleagues in Volume 27(2) Pp. 221–224.

FastTree: Computing large minimum evolution trees with profiles instead of a distance matrix (2009)

Price and colleagues in Volume 26(7) Pp. 1641–1650.

An improved general amino acid replacement matrix (2008)

Le and Gascuel in Volume 25(7) Pp. 1307–1320.

jModelTest: Phylogenetic model averaging (2008)

Posada in Volume 25(7) Pp. 1253–1256.

### MBE Early Citation Classics (1983–2007)

MEGA4: Molecular evolutionary genetics analysis (MEGA) software version 4.0 (2007)

Tamura and colleagues in Volume 24(8) Pp. 1596–1599.

PAML 4: Phylogenetic analysis by maximum likelihood (2007)

Yang in Volume 24(8) Pp. 1586–1591.

Microsatellite null alleles and estimation of population differentiation (2007)

Chapuis and Estoup in Volume 24(3) Pp. 621–631.

Application of phylogenetic networks in evolutionary studies (2006)

Huson and Bryant in Volume 23(2) Pp. 254–267.

Bayes empirical Bayes inference of amino acid sites under positive selection (2005)

Yang and colleagues in Volume 22(4) Pp. 1107–1118.

Bayesian coalescent inference of past population dynamics from molecular sequences (2005)

Drummond and colleagues in Volume 22(5) Pp. 1185–1192.

Evaluation of an improved branch-site likelihood method for detecting positive selection at the molecular level (2005)

Zhang and colleagues in Volume 22(12) Pp. 2472–2479.

Estimating absolute rates of molecular evolution and divergence times: a penalized likelihood approach (2002)

Sanderson in Volume 19(1) Pp. 101–109.

Statistical properties of new neutrality tests against population growth (2002)

Ramos-Onsins and Rozas in Volume 19(12) Pp. 2092–2100.

A general empirical model of protein evolution derived from multiple protein families using a maximum-likelihood approach (2001)

Whelan and Goldman in Volume 18(5) Pp. 691–699.

Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis (2000)

Castresana in Volume 17(4) Pp. 540–552.

Multiple comparisons of log-likelihoods with applications to phylogenetic inference (1999)

Shimodaira and Hasegawa in Volume 16(8) Pp. 1114–1116.

Median-joining networks for inferring intraspecific phylogenies (1999)

Bandelt and colleagues in Volume 16(1) Pp. 37–48.

Quartet puzzling: a quartet maximum-likelihood method for reconstructing tree topologies (1996)

Strimmer and vonHaeseler in Volume 13(7) Pp. 964–969.

Maximum-likelihood-estimation of molecular haplotype frequencies in a diploid population (1995)

Excoffier and Slatkin in Volume 12(5) Pp. 921–927.

Estimation of the number of nucleotide substitutions in the control region of mitochondrial-DNA in humans and chimpanzees (1993)

Tamura and Nei in Volume 10(3) Pp. 512–526.

The neighbor-joining method—a new method for reconstructing phylogenetic trees (1987)

Saitou and Nei in Volume 4(4) Pp. 406–425.

Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions (1986)

Nei and Gojobori in Volume 3(5) Pp. 418–426.