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)**

- **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)**

- **A single determinant dominates the rate of yeast protein evolution (2006)** Drummond and colleagues in Volume 23(2) Pp. 327–337.
Numerous transposed sequences of mitochondrial cytochrome oxidase I-II in aphids of the genus Sitobion (Hemiptera: Aphididae) (1996)
Relationships between gene trees and species trees (1988)
Slipped-strand mispairing—a major mechanism for DNA-sequence evolution (1987)
Codon usage and transfer-RNA content in unicellular and multicellular organisms (1985)

Methods and Resources

MBE Recent Citation Classics (2008–2012)
MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods (2011)
Isolation with migration models for more than two populations (2010)
Bayesian inference of species trees from multilocus data (2010)
SeaView version 4: A multiplatform graphical user interface for sequence alignment and phylogenetic tree building (2010)
FastTree: Computing large minimum evolution trees with profiles instead of a distance matrix (2009)
An improved general amino acid replacement matrix (2008)
jModelTest: Phylogenetic model averaging (2008)

MBE Early Citation Classics (1983–2007)
MEGA4: Molecular evolutionary genetics analysis (MEGA) software version 4.0 (2007)
PAML 4: Phylogenetic analysis by maximum likelihood (2007)
Microsatellite null alleles and estimation of population differentiation (2007)

Application of phylogenetic networks in evolutionary studies (2006)
Bayes empirical Bayes inference of amino acid sites under positive selection (2005)
Bayesian coalescent inference of past population dynamics from molecular sequences (2005)
Evaluation of an improved branch-site likelihood method for detecting positive selection at the molecular level (2005)
Statistical properties of new neutrality tests against population growth (2002)
A general empirical model of protein evolution derived from multiple protein families using a maximum-likelihood approach (2001)
Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis (2000)
Castreresana in Volume 17(4) Pp. 540–552.
Multiple comparisons of log-likelihoods with applications to phylogenetic inference (1999)
Median-joining networks for inferring intraspecific phylogenies (1999)
Quartet puzzling: a quartet maximum-likelihood method for reconstructing tree topologies (1996)
Estimation of the number of nucleotide substitutions in the control region of mitochondrial-DNA in humans and chimpanzees (1993)
The neighbor-joining method—a new method for reconstructing phylogenetic trees (1987)
Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions (1986)