

Referências bibliográficas adicionais

A seguinte lista complementa as referências bibliográficas principais disponíveis no livro *Genômica e evolução*.

- ABAD, P. et al. Genome sequence of the metazoan plant-parasitic nematode *Meloidogyne incognita*. *Nature Biotechnology*, n. 26, p. 909-915, 2008.
- ABRAHAMSEN, M. S. et al. Complete genome sequence of the Apicomplexan, *Cryptosporidium parvum*. *Science*, n. 304, p. 441-445, 2004.
- ACKLAND, G. J.; SIGNITZER, M.; STRATFORD, K.; COHEN, M. H. Cultural hitchhiking on the wave of advance of beneficial technologies. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 8714-8719, 2007.
- ACUÑA-ALONZO, V. et al. A functional *ABCA1* gene variant is associated with low HDL-cholesterol levels and shows evidence of positive selection in Native Americans. *Human Molecular Genetics*, n. 19, p. 2877-2885, 2010.
- ADAMS, M. D.; SUTTON, G. G.; SMITH, H. O.; MYERS, G. W.; VENTER, J. C. The independence of our genome assemblies. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 3025-3026, 2003.
- ADAMS, M. D. et al. The genome sequence of *Drosophila melanogaster*. *Science*, n. 287, p. 2185-2195.
- ADELSON, D. L., RAISON, J. M.; EDGAR, R. C. Characterization and distribution of retrotransposons and simple sequence repeats in the bovine genome. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 12855-12860, 2009.
- AKASHI, H.; EYRE-WALKER, A. Translational selection and molecular evolution. *Current Opinion in Genetics; Development*, n. 8, p. 688-693, 1998.
- AKEY, J. M.; ZHANG, G.; ZHANG, K.; JIN, L.; SHRIVER, M. D. Interrogating a high-density SNP map for signatures of natural selection. *Genome Research*, n. 12, p. 1805-1814, 2002.
- ALCARAZ, L. D. et al. The genome do *Bacillus coahuilensis* reveals adaptations essential for survival in the relic of an ancient marine environment. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 5803-5808, 2008.

- ALLENDORF, F. W.; HARD, J. J. Human-induced evolution caused by unnatural selection through harvest of wild animals. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 9987-9994, 2009.
- ALTER, J. S. The once and future “apeman”. Chimeras, human evolution, and disciplinary coherence. *Current Anthropology*, n. 48, p. 637-652, 2007.
- ALTERMANN, E. et al. Complete genome sequence of the probiotic lactic acid bacterium *Lactobacillus acidophilus* NCFM. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 3906-3912, 2005.
- AMARAL, P. P. R.; NAKAYA, H. I. DNA não-codificador: o lixo que vale ouro? *Ciência Hoje*, n. 38, v. 228, p. 36-42, 2006.
- AMBROSE, S. H. Paleolithic technology and human evolution. *Science*, n. 291, p. 1748-1753, 2001.
- AMEMIYA, C. T.; GOMEZ-CHIARRI, M. Comparative genomics in vertebrate evolution and development. *Journal of Experimental Zoology*, n. 305A, p. 672-682, 2006.
- AMORIM, C. E. G.; WANG, S.; MARRERO, A. R.; SALZANO, F. M.; RUIZ-LINARES, A.; BORTOLINI, M. C. X-chromosomal genetic diversity and linkage disequilibrium patterns in Amerindians and non-Amerindian populations. *American Journal of Human Biology*, 2011 (no prelo).
- ANDRAS, P.; ANDRAS, C. The origins of life – the “protein interaction world” hypothesis: protein interactions were the first form of self-reproducing life and nucleic acids evolved later as memory molecules. *Medical Hypotheses*, n. 64, p. 678-688, 2005.
- ANÔNIMO. A rede nacional de proteoma. *BioPop*, n. 1:18-19, 2005.
- AOKI, K; WAKANO, J. Y.; FELDMAN, M. W. The emergence of social learning in a temporally changing environment: a theoretical model. *Current Anthropology*, n. 46, p. 334-340, 2005.
- APARICIO, S. et al. Whole-genome shotgun assembly and analysis of the genome of *Fugu rubripes*. *Science*, n. 297, p. 1301-1310, 2002.
- ARMBRUST, E. V. et al. The genome of the diatom *Thalassiosira pseudonana*: ecology, evolution, and metabolism. *Science*, n. 306, p. 79-86, 2004.
- ARMELAGOS, G. J., BROWN, P. J.; TURNER, B. Evolutionary, historical and political economic perspectives on health and disease. *Social Science; Medicine*, n. 61, p. 755-765, 2005.

- ARMELAGOS, G. J.; HARPER, K. N. Genomics and the origins of agriculture, Part One. *Evolutionary Anthropology*, n. 14, p. 68-77, 2005a.
- ARMELAGOS, G. J.; HARPER, K. N. Genomics and the origins of agriculture, Part Two. *Evolutionary Anthropology*, n. 14, p. 109-121, 2005b.
- ARNDT, P. F., HWA, T.; PETROV, D. A. Substantial regional variation in substitution rates in the human genome: importance of GC content, gene density, and telomere-specific effects. *Journal of Molecular Evolution*, n. 60, p. 748-763, 2005.
- ARREDI, B., POLONI, E. S.; TYLER-SMITH, C. The peopling of Europe. In: CRAWFORD, M. H. (Ed.). *Anthropological Genetics. Theory, Methods and Applications*. Cambridge: Cambridge University Press, 2007. p. 380-408.
- ASHTON-PROLLA, P.; GIUGLIANI, R. Aconselhamento genético na era genômica. In: MIR, L. (Org.). *Genômica*. São Paulo: Atheneu, 2004. p. 227-234.
- ASSIS, R.; KONDRAHOV, A. S.; KOONIN, E. V.; KONDRAHOV, F. A. Nested genes and increasing organizational complexity of metazoan genomes. *Trends in Genetics*, n. 24, p. 475-478, 2008.
- ASTHANA, S.; NOBLE, W. S.; KRYUKOV, G.; GRANT, C. E.; SUNYAEV, S.; STAMATOYANNOPOULOS, J. A. Widely distributed noncoding purifying selection in the human genome. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 12410-12415, 2007.
- ATWOOD, J. A. III; WEATHERLY, D. B.; MINNING, T. A.; BUNDY, B.; CAVOLA, C.; OPPERDOES, F. R.; ORLANDO, R.; TARLETON, R. L. The *Trypanosoma cruzi* proteome. *Science*, n. 309, p. 473-476, 2005.
- AVERY, O. T.; MACLEOD, C. M.; MCCARTY, M. Studies on the chemical nature of the substance inducing transformation of pneumococcal types. Introduction of transformation by a deoxyribonucleic acid fraction isolated from *Pneumococcus* Type III. *Journal of Experimental Medicine*, n. 79, p. 137-158, 1944.
- AYALA, F. J. 2010. The difference of being human: morality. *Proceedings of the National Academy of Sciences*, USA, n. 107 (Suppl. 2), p. 9015-9022.
- AZOULAY, E. *100,000 Years of Beauty*. 5 v. Paris: Editions Babylone, 2009.
- BAILEY, J. A.; LIU, G.; EICHLER, E. E. An *Alu* transposition model for the origin and expansion of human segmental duplications. *American Journal of Human Genetics*, n. 73, p. 823-834, 2003.

- BAKER, B.; ZAMBRYSKI, P.; STAKAWICZ, B.; DINESH-KUMAR, S. P. Signaling in plant-microbe interactions. *Science*, n. 276, p. 726-733, 1997.
- BARASH, Y.; CALARCO, J. A.; GAO, W.; PAN, Q.; WANG, X.; SHAI, O.; BLENCOWE, J.; FREY, B. J. Deciphering the splicing code. *Nature*, n. 465, p. 53-59, 2010.
- BARBIERI, R. L.; STUMPF, E. R. T. *Origem e Evolução de Plantas Cultivadas*. Brasília: Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA), 2008.
- BARBOSA, J. A. R.; NETTO, L. E. S.; FARAH, C. S.; SCHENKMAN, S.; MENEGUINI, R. The structural molecular biology network of the state of São Paulo, Brazil. *Anais da Academia Brasileira de Ciências*, n. 78, p. 241-253, 2006.
- BARKANA, R. The first stars in the universe and cosmic reionization. *Science*, n. 313, p. 931-934, 2006.
- BARREIRO, L. B.; LAVAL, G.; QUACH, H.; PATIN, E.; QUINTANA-MURCI, L. Natural selection has driven population differentiation in modern humans. *Nature Genetics*, n. 40, p. 340-345, 2008.
- BARROS, H. L. Entropia e vida: a questão do tempo linear. In: EL-HANI, C. B.; VIDEIRA, A. A. P. *O que é Vida? Para Entender a Biologia do Século XXI*. Rio de Janeiro: Relume Dumará, 2000. p. 187-206.
- BASU, M. K.; CARMEL, L.; ROGOZIN, I. B.; KOONIN, E. V. Evolution of protein domain promiscuity in eukaryotes. *Genome Research*, n. 18, p. 449-461, 2008.
- BATTILANA, J.; CARDOSO-SILVA, L.; BARRANTES, R.; HILL, K.; HURTADO, A. M.; SALZANO, F. M.; BONATTO, S. L. Molecular variability of the 16p13.3 region in Amerindians and its anthropological significance. *Annals of Human Genetics*, n. 71, p. 64-76, 2007.
- BATTILANA, J. et al. *Alu* insertion polymorphisms in Native Americans and related Asian populations. *Annals of Human Biology*, n. 33, p. 142-160, 2006.
- BEADLE, G. W.; TATUM, E. L. Genetical control of biochemical reactions in *Neurospora*. *Proceedings of the National Academy of Sciences*, USA, n. 27, p. 499-506, 1941.
- BEHAR, D. M. et al. THE GENOGRAPHIC CONSORTIUM. The dawn of human matrilineal diversity. *American Journal of Human Genetics*, n. 82, p. 1130-1140, 2008.

- BEIKO, R. G.; HARLOW, T. J.; RAGAN, M. A. Highways of gene sharing in prokaryotes. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 14332-14337, 2005.
- BEJERANO, G.; PHEASANT, M.; MAKUNIN, I.; STEPHEN, S.; KENT, W. J.; MATTICK, J. S.; HAUSSLER, D. Ultraconserved elements in the human genome. *Science*, n. 304, p. 1321-1325, 2004.
- BELL, K. S. et al. Genome sequence of the enterobacterial phytopathogen *Erwinia carotovora* subsp. *atroseptica* and characterization of virulence factors. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 11105-11110, 2004.
- BELLE, E. M. S.; BENAZZO, A.; GHIOTTO, S.; COLONNA, V.; BARBUJANI, G. Comparing models on the genealogical relationships among Neandertal, Cro-Magnoid and modern Europeans by serial coalescent simulations. *Heredity*, n. 102, p. 218-225, 2009.
- Belle, E. M. S.; Webster, M. T.; Eyre-Walker, A. Why are young and old repetitive elements distributed differently in the human genome? *Journal of Molecular Evolution*, n. 60, p. 290-296, 2005.
- BENDER, A.; HAJIEWA, P.; MOOSMANN, B. Adaptive antioxidant methionine accumulation in respiratory chain complexes explains the use of a deviant genetic code in mitochondria. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 16496-16501, 2008.
- BERGER, G. Deterministic hypotheses on the origin of life and its reproduction. *Medical Hypotheses*, n. 61, p. 586-592, 2003.
- BERNARDI, G. The neoselectionist theory of genome evolution. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 8385-8390, 2007.
- BERNSTEIN, F. Die geographische Verteilung der Blutgruppen und ihre anthropologische Verteilung. In: *Comitato Italiano per lo Studio dei Problemi della Populazione*. Roma: Istituto Poligrafico dello Stato, 1931.
- BERRIMAN, M.; et al. The genome of the African trypanosome *Trypanosoma brucei*. *Science*, n. 309, p. 416-422, 2005.
- BEVER, T.; MONTALBETTI, M. Noam's ark. *Science*, n. 298, p. 1565-1566, 2002.
- BINGHAM, P. M. Human evolution and human history: a complete theory. *Evolutionary Anthropology*, n. 9, p. 248-257, 2000.

- BISSO-MACHADO, R.; JOTA, M. S.; RAMALLO, V.; PAIXÃO-CÔRTES, V. R.; LACERDA, D. R.; SALZANO, F. M.; BONATTO, S. L.; SANTOS, F. R.; BORTOLINI, M. C. 2011. Distribution of Y-chromosome Q lineages in South Amerindians. 2011 (Submitted).
- BLACK, F. L. Disease susceptibility among New World peoples. In: SALZANO, F.M.; HURTADO, A.M. (Eds.). *Lost Paradises and the Ethics of Research and Publication*. Nova York: Oxford University Press, 2004. p. 146-163.
- BLOOM, J. D., LABTHAVIKUL, S. T., OTEY, C. R.; ARNOLD, F. H. Protein stability promotes evolvability. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 5869-5874, 2006.
- BOGAERT, A. F. Biological versus nonbiological older brothers and men's sexual orientation. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 10771-10774, 2006.
- BON, C. et al. Deciphering the complete mitochondrial genome and phylogeny of the extinct cave bear in the Paleolithic painted cave of Chauvet. *Proceedings of the National Academy*, USA, n. 105, p. 17447-17452, 2008.
- BONNEFONT, J. et al. Evolutionary forces shape the human *RFPL1,2,3* genes toward a role in neocortex development. *American Journal of Human Genetics*, n. 83, p. 208-218, 2008.
- BORGERHOFF MULDER, M.; NUNN, C. L.; TOWNER, M. C. Cultural macroevolution and the transmission of traits. *Evolutionary Anthropology*, n. 15, p. 52-64, 2006.
- BORGES-OSÓRIO, M. R.; ROBINSON, W. M. *Genética Humana*. 2. ed. Porto Alegre: Artmed Editora, Porto Alegre, 2001.
- BORGES-OSÓRIO, M R.; ROBINSON, W. M. *Genética para Odontologia*. Porto Alegre: Artmed Editora, 2006.
- BOROJEVIC, R. Terapias celulares. Promessas e realidades. *Ciência Hoje*, n. 35, v. 206, n. 37-39, 2004.
- BORTOJEVIC, R.; BALDUINO, A. Terapias celulares e bioengenharia tecidual. In: MIR, L. (Org.). *Genômica*. São Paulo: Atheneu, p. 295-306, 2004.
- BORTOLINI, M. C.; THOMAS, M. G.; CHIKHI, L.; AGUILAR, J. A.; CASTRO-DE-GUERRA, D.; SALZANO, F. M.; RUIZ-LINARES, A. Ribeiro's typology, genomes, and Spanish colonialism, as viewed from Gran Canaria and Colombia. *Genetics and Molecular Biology*, n. 27, p. 1-8, 2004.

- BOTTJER, D. J. Os pioneiros. *Scientific American Brasil*, n. 4, v. 46, p. 58-63, 2006.
- BOVINE HAPMAP CONSORTIUM. Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. *Science*, n. 324, p. 528-532, 2009.
- BOWLER, C. et al. The *Phaeodactylum* genome reveals the evolutionary history of diatom genomes. *Nature*, n. 456, p. 239-244, 2008.
- BOWLER, P. J. *The Mendelian Revolution. The Emergence of Hereditarian Concepts in Modern Science and Society*. Baltimore: Johns Hopkins University Press, 1989.
- BOWLES, S. Group competition, reproductive leveling, and the evolution of human altruism. *Science*, n. 314, p. 1569-1572, 2006.
- BOWLES, S. Did warfare among ancestral hunter-gatherers affect the evolution of human social behaviors? *Science*, n. 324, p. 1293-1298, 2009.
- BOWLES, S.; SMITH, E. A.; BORGERHOFF-MULDER, M. The emergence and persistence of inequality in premodern societies. Introduction to the Special Section. *Current Anthropology*, n. 51, p. 7-17, 2010.
- BOWLES, S.; GINTIS, H. *Homo reciprocans*. *Nature*, n. 4151, p. 125-128, 2002.
- BOWRING, S.A.; HOUSH, T. 1995. The earth's early evolution. *Science*, n. 269, p. 1535-1540, 1995.
- BOYD, R.; RICHERSON, P. J. Culture and the evolution of human cooperation. *Philosophical Transactions of the Royal Society B*, n. 364, p. 3281-3288, 2009.
- BRASIER, M. D.; GREEN, O. R.; JEPHCOAT, A. P.; KLEPPE, A. K.; VAN KRANENDONK, M. I.; LINDSAY, J. F.; STEELE, A.; GRASSINEAU, N. V. Questioning the evidence for earth's oldest fossils. *Nature*, n. 416, p. 76-81, 2002.
- BRAYTON, K. A.; KAPPMEYER, L. S.; HERNDON, D. R.; DARK, M. J.; TIBBALS, D. L.; PALMER, G. H.; MCGUIRE, T. C.; KNOWLES JR., D. P. Complete genome sequencing of *Anaplasma marginale* reveals that the surface is skewed to two superfamilies of outer membrane proteins. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 844-849, 2005.
- BREMBS, B. Towards a scientific concept of free will as a biological trait: spontaneous actions and decision-making in invertebrates. *Proceedings of the Royal Society B*, Published ahead of print, doi 10.1098/rspb.2010.2325, 2011.
- BRIDGES, C. B. Nondisjunction as proof of the chromosome theory of heredity. *Genetics*, n. 1, p. 1-52 and p.107-163, 1916.
- BROCK, T. D. *The Emergence of Bacterial Genetics*. Cold Spring Harbor: Cold Spring Harbor Laboratory Press, 1990.

- BRÜGGEMANN, H.; BÄUMER, S.; FRICKE, W. F.; WIEZER, A.; LIESEGANG, H.; DECKER, I.; HERZBERG, C., MARTÍNEZ-ARIAS, R.; MERKL, R.; HENNE, A.; GOTTSCHALK, G. The genome sequence of *Clostridium tetani*, the causative agent of tetanus disease. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 1316-1321, 2003.
- BRUNER, E.; MANZI, G.; ARSUAGA, J. L. Encephalization and allometric trajectories in the genus *Homo*: evidence from the Neandertal and modern lineages. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 15335-15340, 2003.
- BRYSON, J. W.; BETZ, S. F.; LU, H. S.; SUICH, D. J.; ZHOU, H. H.; O'NEIL, K. T.; DEGRADO, W. F. Protein design: a hierachic approach. *Science*, n. 270, p. 935-941, 1995.
- BUELL, C. R. et al. 2003. The complete genome sequence of the *Arabidopsis* and tomato pathogen *Pseudomonas syringae* pv. tomato DC3000. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 10181-10186.
- BULACH, D. M. et al. Genome reduction in *Leptospira borgpetersenii* reflects limited transmission potential. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 14560-14565, 2006.
- BURBANO, H. A. et al. Targeted investigation of the Neanderthal genome by array-based sequence capture. *Science*, n. 328, p. 723-725, 2010.
- BURNETT, R. M. More barrels from the viral tree of life. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 3-4, 2006.
- BURR, B. et al. The map-based sequence of the rice genome. *Nature*, n. 436, p. 793-800, 2005.
- BUSS, D. M. *The Dangerous Passion*. Why Jealousy is as Necessary as Love and Sex. Nova York: The Free Press, 2000.
- BUSTAMANTE, C. D. et al. Natural selection on protein-coding genes in the human genome. *Nature*, n. 437, p. 1153-1157, 2005.
- C. elegans* Sequencing Consortium. Genome sequence of the nematode *C. elegans*: a platform for investigating biology. *Science*, n. 282, p. 2012-2018, 1998.

- CALLEGARI-JACQUES, S. M.; CROSSETTI, S. G.; KOHLRAUSCH, F. B.; SALZANO, F. M.; TSUNETO, L. T.; PETZL-ERLER, M. L.; HILL, K.; HURTADO, A. M.; HUTZ, M. H. The β -globin gene cluster distribution revisited – patterns in Native American populations. *American Journal of Physical Anthropology*, n. 134, p. 190-197, 2007.
- CALLEGARI-JACQUES, S. M.; HILL, K.; HURTADO, A. M.; RODRIGUES, L. T.; BAU, C. H. D.; SALZANO, F. M. Genetic clues about the origin of Aché hunter-gatherers of Paraguay. *American Journal of Human Biology*, n. 20, p. 735-737, 2008.
- CALLEGARI-JACQUES, S. M.; TARAZONA-SANTOS, E. M.; GILMAN, R. H.; HERRERA, P.; CABRERA, L.; SANTOS, S. E. B.; MORÉS, L.; HUTZ, M. H.; SALZANO, F. M. *Autosome STRs in Native South America* – testing models of association with geography and language. 2011 (Submitted).
- CARLSON, C. S.; THOMAS, D. J.; EBERLE, M. A.; SWANSON, J. E.; LIVINGSTON, R. J.; RIEDER, M. J.; NICKERSON, D. A. Genomic regions exhibiting positive selection identified from dense genotype data. *Genome Research*, n. 15, p. 1553-1565, 2005.
- CARLTON, J. M. et al. Comparative genomics of the neglected human malaria parasite *Plasmodium vivax*. *Nature*, n. 455, p. 757-763, 2008.
- CARNEIRO, R. L. The transition from quantity to quality: a neglected causal mechanism in accounting for social evolution. *Proceedings of the National Academy of Sciences*, USA, n. 97, p. 12926-12931, 2000.
- CARRITT, B.; KEMP, T. J.; POULTER, M. Evolution of the human RH (Rhesus) blood group genes: a 50 year old prediction (partially) fulfilled. *Human Molecular Genetics*, n. 6, p. 843-850, 1997.
- CASHMORE, A. R. The Lucretian swerve: the biological basis of human behavior and criminal justice system. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 4499-4504, 2010.
- CASPI, A.; MCCLAY, J.; MOFFITT, T. E.; MILL, J.; MARTIN, J.; CRAIG, I. W.; TAYLOR, A.; POULTON, R. Role of genotype in the cycle of violence in maltreated children. *Science*, n. 297, p. 851-854, 2002.
- CASTRO, L.; TORO, M. A. The evolution of culture: from primate social learning to human culture. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 10235-10240, 2004.

- CAVALCANTI, A. R. O.; LEITE, E. S.; NETO, B. B.; FERREIRA, R. 2004. On the classes of aminoacyl-tRNA synthetases, amino acids and the genetic code. *Origins of Life and Evolution of the Biosphere*, n. 34, p. 407-420.
- CAVALIER-SMITH, T. 1998. A revised six-kingdom system of life. *Biological Reviews*, n. 73, p. 203-266, 1998.
- CAVALIER-SMITH, T. The tiny enslaved genome of a rhizarian alga. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 9379-9380, 2006.
- CELA-CONDE, C. J. et al. Sex-related similarities and differences in the neural correlates of beauty. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 3847-3852, 2009.
- CELA-CONDE, C. J.; AYALA, F. J. Genera of the human lineage. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 7684-7689, 2003.
- CELNIKER, S. E. et al. Unlocking the secrets of the genome. *Nature*, n. 459, p. 927-930, 2009.
- CHAIX, R.; AUSTERLITZ, F.; KHEGAY, T.; JACQUESSON, S.; HAMMER, M. F.; HEYER, E.; QUINTANA-MURCI, L. The genetic or mythical ancestry of descent groups: lessons from the Y chromosome. *American Journal of Human Genetics*, n. 75, p. 1113-1116, 2004.
- CHAMPION, O. L.; GAUNT, M. W.; GUNDOGDU, O.; ELMI, A.; WITNEY, A. A.; HINDS, J.; DORRELL, N.; WREN, B. W. Comparative phylogenomics of the food-borne pathogen *Campylobacter jejuni* reveals genetic markers predictive of infection source. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 16043-16048, 2005.
- CHANDONIA, J-M.; BRENNER, S. E. The impact of structural genomics: expectations and outcomes. *Science*, n. 311, p. 347-351, 2006.
- CHECK, E. The trials of gene therapy. *Nature*, n. 420, p. 107-118, 2002.
- CHEN, C. T. L.; WANG, J. C.; COHEN, B. A. The strength of selection on ultraconserved elements in the human genome. *American Journal of Human Genetics*, n. 80, p. 692-704, 2007.
- CHEN, F-C., CHEN, C-J., LI, W-H.; CHUANG, T-J. Human-specific insertions and deletions inferred from mammalian genome sequences. *Genome Research*, n. 17, p. 16-22, 2007.
- CHENOWETH, S. F.; BLOWS, M. W. Dissecting the complex genetic basis of mate choice. *Nature Reviews Genetics*, n. 7, p. 681-692, 2006.

- CHIARONI, J.; UNDERHILL, P. A.; CAVALLI-SFORZA, L. L. Y chromosome diversity, human expansion, drift, and cultural evolution. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 20174-20179, 2009.
- CHICKEN GENOME CONSORTIUM. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, n. 432, p. 695-716, 2004.
- CHICKEN POLYMORPHISM CONSORTIUM. A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. *Nature*, n. 432, p. 717-722, 2004.
- Chies, T. T. S. Genomas vegetais. In: FREITAS, L. B.; BERED, F. (Orgs.). *Genética: Evolução Vegetal*. Porto Alegre: Editora da Universidade Federal do Rio Grande do Sul, 2003. p. 243-261.
- CHIMPANZEE GENOME CONSORTIUM. Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*, n. 437, p. 69-87, 2005.
- CHIUSANO, M. L.; ALVAREZ-VALIN, F.; DI GIULIO, M.; D'ONOFRIO, G.; AMMIRATO, G.; COLONNA, G.; BERNARDI, G. Second codon positions of genes and the secondary structures of proteins. Relationships and implications for the origin of the genetic code. *Gene*, n. 261, p. 63-69, 2000.
- CHIVIAN, D. et al. Environmental genomics reveals a single-species ecosystem deep within earth. *Science*, n. 322, p. 275-278, 2008.
- CHO, N-H. et al. The *Orientia tsutsugamuchi* genome reveals massive proliferation of conjugative type IV secretion system and host-cell interaction genes. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 7981-7986, 2007.
- CHOI, I-G.; KIM, S-H. Global extent of horizontal gene transfer. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 4489-4494, 2007.
- CHOI, J-K.; BOWLES, S. The coevolution of parochial altruism and war. *Science*, n. 318, p. 636-640, 2007.
- CHURCH, D. M. ET AL.; THE MOUSE GENOME SEQUENCING CONSORTIUM. Lineage-specific biology revealed by a finished genome assembly of the mouse. *PloS Biology*, n. 7, p. e1000112, 2009.
- COHAN, F. M.; KOEPPEL, A. F. The origins of ecological diversity in prokaryotes. *Current Biology*, n. 18, p. 1024-1034, 2008.

- COHEN, S. N.; CHANG, A. C. Y.; BOYER, H. W.; HELLING, R. B. Construction of biologically functional bacterial plasmids *in vitro*. *Proceedings of the National Academy of Sciences*, USA, n. 70, p. 3240-3244, 1973.
- COIMBRA JR., C. E. A.; SANTOS, R. V. Emerging health needs and epidemiological research in indigenous peoples in Brazil. In: SALZANO, F. M.; HURTADO, A. M. (Eds.). *Lost Paradises and the Ethics of Research and Publication*. Nova York: Oxford University Press, 2004. p. 89-109.
- COLE, S. T. et al. Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence. *Nature*, n. 393, p. 537-544, 1998.
- COLE, S. W.; AREVALO, J. M. G.; TAKAHASHI, R.; SLOAN, E. K.; LUTGENDORF, S. K.; SOOD, A. K.; SHERIDAN, J. F.; SEEMAN, T. E. Computacional identification of gene-social environment interaction at the human *IL6* locus. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 5681-5686, 2010.
- COLLINS, N. E. et al. The genome of the heartwater agent *Erllichia ruminantium* contains multiple tandem repeats of actively variable copy number. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 838-843, 2005.
- COMAS, J. *Manual de Antropología Física*. Cidade do México: Universidad Nacional Autónoma de México, 1966.
- CONARD, N. J. Cultural modernity: consensus or conundrum? *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 7621-7622, 2010.
- CONROY, M. J.; BULLOUGH, P. A.; MERRICK, M.; AVENT, N. D. Modelling the human rhesus proteins: implications for structure and function. *British Journal of Haematology*, n. 131, p. 543-551, 2005.
- COOK, R. J. The molecular mechanisms responsible for resistance in plant-pathogen interactions of the gene-for-gene type function more broadly than previously imagined. *Proceedings of the National Academy of Sciences*, USA, p. 95, p. 9711-9712, 1998.
- COOP, G.; PICKRELL, J. K.; NOVEMBRE, J.; KUDARAVALLI, S.; LI, J.; ABSHER, D.; MYERS, R. M.; CAVALLI-SFORZA, L. L.; FELDMAN, M. W.; PRITCHARD, J. K. The role of geography in human adaptation. *PLoS Genetics*, n. 5, p. e1000500, 2009.
- CORDERO, O. X.; SNEL, B.; HOGEWEG, P. Coevolution of gene families in prokaryotes. *Genome Research*, n. 18, p. 462-468, 2008.

- CRICK, F. *Life Itself*. Its Origin and Nature. Nova York: Simon and Schuster, 1982.
- CRICK, F. *Que Loco Proposito*. Una Visión Personal del Descubrimiento Científico. Barcelona: Tusquets Editores, 1989.
- CRICK, F. H. C.; BARNETT, L.; BRENNER, S.; WATTS-TOBIN, R. J. General nature of the genetic code for proteins. *Nature*, n. 192, p. 1227-1232, 1961.
- CROSSETTI, S. G.; DEMARCHI, D. A.; RAIMANN, P. E.; SALZANO, F. M.; HUTZ, M. H.; CALLEGARI-JACQUES, S. M. Autosomal STR genetic variability in the Gran Chaco Native population: homogeneity or heterogeneity? *American Journal of Human Biology*, n. 20, p. 704-711, 2008.
- CURCIO, J.; BELFORT, M. The beginning of the end: links between ancient retroelements and modern telomerases. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 9107-9108, 2007.
- CURRIE, T. E.; MACE, R. Political complexity predicts the spread of ethnolinguistic groups. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 7339-7344, 2009.
- D'ERRICO, F.; VANHAEREN, M.; BARTON, N.; BOUZOUGGAR, A.; MIENIS, H.; RICHTER, D.; HUBLIN, J.-J.; MCPHERRON, S. P.; LOZEUET, P. Additional evidence on the use of personal ornaments in the Middle Paleolithic of North Africa. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 15051-15056, 2009.
- DA CUNHA, J. P. C. et al. Bioinformatics construction of the human cell surfaceome. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 16752-16757, 2009.
- DAGAN, T.; MARTIN, W. Ancestral genome sizes specify the minimum rate of lateral gene transfer during prokaryote evolution. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 870-875, 2007.
- DAGAN, T.; ARTZY-RANDRUP, Y.; MARTIN, W. Modular networks and cumulative impact of lateral transfer in prokaryote genome evolution. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 10039-10044, 2008.
- DANNA, K.; NATHANS, D. 1971. Specific cleavage of Simian Virus 40 DNA by restriction endonuclease of *Haemophilus influenzae*. *Proceedings of the National Academy of Sciences*, USA, n. 68, p. 2913-2917, 1971.

- DARWIN, C. *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*. Londres: John Murray, 1859.
- Darwin, C. 1871. *The Descent of Man and Selection in Relation to Sex*. Londres: Murray, 1871 (edição brasileira, São Paulo: Hemus, 1974).
- DAVIDSON, I.; MCGREW, W. C. Stone tools and the uniqueness of human culture. *Journal of the Royal Anthropological Institute*, n. 11, p. 793-817, 2005.
- DAWKINS, R. 1976 (Tradução 1979). *O Gene Egoísta*. Belo Horizonte: Editora Itatiaia, 1976.
- DE DUVE, C. *Singularities*. Landmarks on the Pathways of Life. Cambridge: Cambridge University Press, 2005.
- DE SALLE, R.; SCHIERWATER, B. An even “newer” animal phylogeny. *BioEssays*, n. 30, p. 1043-1047, 2008.
- DE WITT, P. J. G. M. Pathogen avirulence and plant resistance: a key role for recognition. *Trends in Plant Science*, n. 2, p. 452-458, 1997.
- DEDIU, D.; LADD, D. R. Linguistic tone is related to the population frequency of the adaptive haplogroups of two brain size genes, *ASPM* and *microcephalin*. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 10944-10949, 2007.
- DEHAL, P. et al. The draft genome of *Ciona intestinalis*: insights into chordate and vertebrate origins. *Science*, n. 298, p. 2157-2167, 2002.
- DELBRÜCK, M.; BAILEY JR., W. T. Induced mutations in bacterial viruses. *Cold Spring Harbor Symposia on Quantitative Biology*, n. 11, p. 33-37, 1946.
- DELONG, E. F.; KARL, D. M. Genomic perspectives in microbial oceanography. *Nature*, n. 437, p. 336-342, 2005.
- DELSUC, F.; BRINKMANN, H.; PHILIPPE, H. Phylogenomics and the reconstruction of the tree of life. *Nature Reviews Genetics*, n. 6, p. 361-375, 2005.
- DEMARCHI, D. A.; SALZANO, F. M.; ALTUNA, M. E.; FIEGENBAUM, M.; HILL, K.; HURTADO, A. M.; TSUNETO, L. T.; PETZL-ERLER, M. L.; HUTZ, M. H. *APOE* polymorphism distribution among Native Americans and related populations. *Annals of Human Biology*, n. 32, p. 351-365, 2005.
- DEMPSEY, D. A.; SHAH, J.; KLESSIG, D. F. Salicylic acid and disease resistance in plants. *Critical Reviews in Plant Sciences*, n. 18, p. 547-575, 1999.
- DENNETT, D. C. *Kinds of Minds*. Nova York: Basic Books, 1996.

- DENNETT, D. C. *Freedom Evolves*. Nova York: Viking, 2003.
- DERELLE, E. et al. 2006. Genome analyses of the smallest free-living eukaryote *Ostreococcus tauri* unveils many unique features. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 11647-11652, 2006.
- DIETERICH, C. et al. The *Pristionchus pacificus* genome provides a unique perspective on nematode lifestyle and parasitism. *Nature Genetics*, n. 40, p. 1193-1198, 2008.
- DOBZHANSKY, T. Human genetics – an outsider's view. *Cold Spring Harbor Symposia on Quantitative Biology*, n. 29, p. 1-7, 1964.
- Dobzhansky, T. *Genetics of the Evolutionary Process*. Nova York: Columbia University Press, 1970.
- DOKHOLYAN, N. V.; BULDYREV, S. V.; HAVLIN, S.; STANLEY, H. E. Distributions of dimeric tandem repeats in non-coding and coding DNA sequences. *Journal of Theoretical Biology*, n. 202, p. 273-282, 2000.
- DOMINGUES, H. M. B.; SÁ, M. R.; GLICK, T. *A Recepção do Darwinismo no Brasil*. Rio de Janeiro: Editora Fiocruz, 2003.
- DOMÍNGUEZ-BELLO, M. G.; PÉREZ, M. E.; BORTOLINI, M. C.; SALZANO, F. M.; PERICCHI, L. R.; ZAMBRANO-GUZMÁN, O.; LINZ, B. Amerindian *Helicobacter pylori* strains go extinct, as European strains expand their host range. *PLoS One*, n. 3, p. e3307, 2008.
- DOOLITTLE, R. F. The origins and evolution of eukaryotic proteins. *Philosophical Transactions of the Royal Society London, Series B*, n. 349, p. 235-240, 1995.
- DOOLITTLE, W. F.; ZHAXYBAYEVA, O. On the origin of prokaryotic species. *Genome Research*, n. 19, p. 744-756, 2009.
- DOOLITTLE, R. F.; FENG, D-F.; TSANG, S.; CHO, G.; LITTLE, E. Determining divergence times of the major kingdoms of living organisms with a protein clock. *Science*, n. 271, p. 470-477, 1996.
- DORNELLES, C. L.; BATTILANA, J.; FAGUNDES, N. J. R.; FREITAS, L. B.; BONATTO, S. L.; SALZANO, F. M. Mitochondrial DNA and *Alu* insertions in a genetically peculiar population: the Ayoreo Indians of Bolivia and Paraguay. *American Journal of Human Biology*, n. 16, p. 479-488, 2004.
- Dornelles, C. L.; Bonatto, S. L.; Freitas, L. B.; Salzano, F. M. Is haplogroup X present in extant South American Indians? *American Journal of Physical Anthropology*, n. 127, p. 439-448, 2005.

- DOUGLAS, S.; ZAUNER, S.; FRAUNHOLZ, M.; BEATON, M.; PENNY, S.; DENG, L-T.; WU, X.; REITH, M.; CAVALIER-SMITH, T.; MAIER, U-G. The highly reduced genome of an enslaved algal nucleus. *Nature*, n. 410, p. 1091-1096, 2001.
- DRISCOLL, C. A.; MACDONALD, D. W.; O'BRIEN, S. J. From wild animals to domestic pets, an evolutionary view of domestication. *Proceedings of the National Academy of Sciences*, USA, n. 106 (suppl. 1), p. 9971-9978, 2009.
- DRUMMOND, D. A.; BLOOM, J. D.; ADAMI, C.; WILKE, C. O.; ARNOLD, F. H. Why highly expressed proteins evolve slowly. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 14338-14343, 2005.
- DUAN, Z.; ANDRONESCU, M.; SCHUTZ, K.; MCILWAIN, S.; KIM, Y. J.; LEE, C.; SHENDURE, J.; FIELDS, S.; BLAU, C. A.; NOBLE, W. S. A three-dimensional model of the yeast genome. *Nature*, n. 465, p. 363-367, 2010.
- DUARTE, N. C.; BECKER, S. A.; JANISHIDI, N.; THIELE, I.; MO, M. L.; VO, T. D.; SRIVAS, R.; PALSSON, B. O. Global reconstruction of the human metabolic network based on genomic and bibliomic data. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 1777-1782, 2007.
- DUFRESNE, A. et al. Genome sequence of the cyanobacterium *Prochlorococcus marinus* SS120, a nearly minimal oxytrophic genome. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 10020-10025, 2003.
- DUPONT, C. L.; BUTCHER, A.; VALAS, R. B.; BOURNE, P. E.; CASTANO-ANOLLÉS, G. History of biological metal utilization inferred through phylogenomic analysis of protein structures. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 10567-10572, 2010.
- DURKHEIM, E. *The Elementary Forms of the Religious Life*. Nova York: The Free Press, 1995.
- DWYER, D. S. Assembly of exons from unitary transposable genetic elements: implications for the evolution of protein-protein interactions. *Journal of Theoretical Biology*, n. 194, p. 11-27, 1998.
- DYSON, F. *Infinito em Todas as Direções*. Do Gene à Conquista do Universo. São Paulo: Editora Best Seller, 1989.
- EARL, D. J.; DEEM, M. W. Evolvability is a selectable trait. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 11531-11536, 2004.

- EBERHARD, W. G. Postcopulatory sexual selection: Darwin's omission and its consequences. *Proceedings of the National Academy of Sciences*, USA, n. 106 (Suppl. 1), p. 10025-10032, 2009.
- EDGAR, H. J. H.; HUNLEY, K. L. Race reconciled? How biological anthropologists view race variation. *American Journal of Physical Anthropology*, n. 139, p. 1-102, 2009.
- EHRLICH, P. R.; WILSON, E. O. Biodiversity studies: science and policy. *Science*, n. 253, p. 758-762, 1991.
- EICHINGER, L. et al. The genome of the social amoeba *Dictyostelium discoideum*. *Nature*, n. 435, p. 43-57, 2005.
- EIZIRIK, E.; HAAG, T.; SANTOS, A. S.; SALZANO, F. M.; SILVEIRA, L.; AZEVEDO, F. C. C.; FURTADO, M. M. Jaguar Conservation Genetics. *Cat News Special Issue*, n. 4, p. 31-34, 2008.
- EKELUND, C. K.; JØRGENSEN, F. S.; PETERSEN, O. B.; SUNDBERG, K.; TABOR, A.; DANISH FETAL MEDICINE RESEARCH GROUP. Impacto de uma nova política nacional para rastreamento da síndrome de Down na Dinamarca: estudo de coorte populacional. *BMJ*, Porto Alegre, n. 2, p. 153-163, 2009.
- ELLEGREN, H. Comparative genomics and the study of evolution by natural selection. *Molecular Ecology*, n. 17, p. 4586-4596, 2008.
- ELLIS, L. *Theories of Rape*. Inquiries into the Causes of Sexual Aggression. Nova York: Hemisphere, 1989.
- EL-SAYED, N. M. et al. Comparative genomics of trypanosomatid parasitic Protozoa. *Science*, n. 309, p. 404-409, 2005a.
- El-Sayed, N. M. et al. The genome sequence of *Trypanosoma cruzi*, etiologic agent of Chagas disease. *Science*, n. 309 p. 409-415, 2005b.
- ELSON, J. L.; TURNBULL, D. M.; HOWELL, N. Comparative genomics and the evolution of human mitochondrial DNA: assessing the effects of selection. *American Journal of Human Genetics*, n. 74, p. 229-238, 2004.
- ENDICOT, P.; HO, S. Y. W.; METSPALU, M.; STRINGER, C. Evaluating the mitochondrial timescale of human evolution. *Trends in Ecology and Evolution*, n. 24, p. 515-521, 2009.
- Ernst, W.; Hohnholz, J. H.; Bittner, A. Tropical forests. *Natural Resources and Development*, n. 45/46, p.1-158, 1997.

- ESPAGNE, E.; DUPUY, C.; HUGHET, E.; CATTOLICO, L.; PROVOST, B.; MARTINS, N.; POIRIÉ, M.; PERIQUET, G.; DREZEN, J. M. Genome sequence of a polydnavirus: insights into symbiotic virus evolution. *Science*, n. 306, p. 286-289, 2004.
- FAGUNDES, N. J. R.; RAY, N.; BEAUMONT, M.; NEUENSCHWANDER, S.; SALZANO, F. M.; BONATTO, S. L.; EXCOFFIER, L. Statistical evaluation of alternative models of human evolution. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 17614-17619, 2007.
- FAGUNDES, N. J. R.; SALZANO, F. M.; BATZER, M. A.; DEININGER, P. L.; BONATTO, S. L. Worldwide genetic variation at the 3'-UTR region of the LDLR gene: possible influence of natural selection. *Annals of Human Genetics*, n. 69, p. 389-400, 2005.
- FAGUNDES, N. J. R. et al. Mitochondrial population genomics supports a single pre-Clovis origin with a coastal route for the peopling of the Americas. *American Journal of Human Genetics*, n. 82, p. 1-10, 2008.
- FAWCETT, J. A.; MAERE, S.; VAN DE PEER, Y. Plants with double genomes might have had a better chance to survive the Cretaceous-Tertiary extinction event. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 5737-5742, 2009.
- FEDOROV, A.; MERICAN, A. F.; GILBERT, W. Large-scale comparison of intron positions among animal, plant, and fungal genes. *Proceedings of the National Academy of Sciences*, USA, n. 99, p. 16128-16133, 2002.
- FEHR, E.; FISCHBACHER, U. The nature of human altruism. *Nature*, n. 425, p. 785-791, 2003.
- FEIL, H. et al. Comparison of the complete genome sequences of *Pseudomonas syringae* pv. *syringae* B728a and pv. *tomato* DC3000. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 11064-11069, 2005.
- FEINBERG, D. R. Are human faces and voices ornaments signaling common underlying cues to mate value? *Evolutionary Anthropology*, n. 17, p. 112-118, 2008.
- FERRY, J. G.; HOUSE, C. H. The stepwise evolution of early life driven by energy conservation. *Molecular Biology and Evolution*, n. 23, p. 1286-1292, 2006-.

- FINKLER, C.; GIACOMET, C.; MUSCHNER, V. C.; SALZANO, F. M.; FREITAS, L. B. Molecular investigations of pathogenesis-related Bet v 1 homologues in *Passiflora* (Passifloraceae). *Genética*, n. 124, p. 117-125, 2005.
- FINLAYSON, C. et al. Late survival of Neanderthals at the southernmost extreme of Europe. *Nature*, n. 443, p. 850-853, 2006.
- FLEISCHMANN, R. et al. Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science*, n. 269, p. 496-512, 1995.
- FLEISCHMANN, R. D.; et al. Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. (first genome of free-living organism ever completely sequenced). *Science*, n. 269, p. 496-513, 1995.
- FRAGASZY, D. Making space for traditions. *Evolutionary Anthropology*, n. 12, p. 61-70, 2003.
- FRANKEN, T. G. Cronologia da ciência brasileira (1500-1945). In: SCHWARTZMAN, S. *Formação da Comunidade Científica Brasileira*. São Paulo/Rio de Janeiro: Companhia Editora Nacional e Financiadora de Estudos e Projetos, 1979. p. 333-446.
- FRANKHAM, R.; BALLOU, J. D.; BRISCOE, D. A. *Fundamentos de Genética da Conservação*. Ribeirão Preto: Sociedade Brasileira de Genética, 2008.
- FRANKLIN, R. E.; GOSLING, R. G. Molecular configuration in sodium thymonucleate. *Nature*, n. 171, p. 740-741, 1953.
- FRASER, C. M. et al. The minimal gene complement of *Mycoplasma genitalium*. *Science*, n. 270, p. 397-403, 1995.
- FREIRE-MAIA, N. *Teoria da Evolução: de Darwin à teoria sintética*. Belo Horizonte/São Paulo: Itatiaia e Edusp, 1988.
- Freitas, L. B.; Koehler-Santos, P.; Salzano, F. M. Pathogenesis-related proteins in Brazilian wheat genotypes: protein induction and partial gene sequencing. *Ciência Rural*, n. 33, p. 497-500, 2003a.
- FREITAS, L. B.; BONATTO, S. L.; SALZANO, F. M. Evolutionary implications of intra- and interspecific molecular variability of pathogenesis-related proteins. *Brazilian Journal of Biology*, n. 63, p. 437-448, 2003b.
- FRY, I. The role of natural selection in the origin of life. *Origins of Life and Evolution of the Biosphere*, n. 41, p. 3-16, 2011.
- FUENTES, A. A new synthesis. Resituating approaches to the evolution of human behavior. *Anthropology Today*, n. 25, v. 3, p. 12-17, 2009.

- FUSELLI, S. et al. Analysis of nucleotide diversity of *NAT2* coding region reveals homogeneity across Native American populations and high intra-population diversity. *The Pharmacogenomics Journal*, n. 7, p. 144-152, 2007.
- GAGE, T. B. Are modern environments really bad for us? Revisiting the demographic and epidemiologic transitions. *Yearbook of Physical Anthropology*, n. 18, p. 96-117, 2005.
- GALAGAN, J. E. et al. The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature*, n. 422, p. 859-868, 2003.
- GALAGAN, J. E. et al. Sequencing of *Aspergillus nidulans* and comparative analysis with *A. fumigatus* and *A. oryzae*. *Nature*, n. 438, p. 1105-1115, 2005.
- GARDNER, M. J. et al. Genome sequence of *Theileria parva*, a bovine pathogen that transforms lymphocytes. *Science*, n. 309, p. 134-137, 2005.
- GARNIER, T. et al. The complete genome sequence of *Mycobacterium bovis*. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 7877-7882, 2003.
- GARRIGAN, D.; HEDRICK, P. W. Detecting adaptive molecular polymorphisms: lessons from the MHC. *Evolution*, n. 57, p. 1707-1722, 2003.
- GEERTZ, C. Religion as a cultural system. In: Banton, M. (Ed.). *Anthropological Approaches to the Study of Religion*. Londres: Tavistock, 1966. p. 1-46.
- GHEDIN, E. et al. Draft genome of the filarial nematode parasite *Brugia malayi*. *Science*, n. 317, p. 1756-1760, 2007.
- GIANOULIS, T. A. et al. Quantifying environmental adaptation of metabolic pathways in metagenomics. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 1374-1379, 2009.
- GIBSON, D. G. et al. Creation of a bacterial cell controlled by a chemically synthesized genome. *Science*, n. 329, p. 52-56, 2010.
- GIFFORD, R. J.; KATZOURAKIS, A.; TRISTEM, M.; PYBUS, O. G.; WINTERS, M.; SHAFER, R. W. A transitional endogenous lentivirus from the genome of a basal primate and implications for lentivirus evolution. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 20362-20367, 2008.
- GIL, R. et al. The genome sequence of *Blochmannia floridianus*: comparative analysis of reduced genomes. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 9388-9393, 2003.

- GILBERT, M. T. P. et al. Intraspecific phylogenetic analysis of Siberian wooly mammoths using complete mitochondrial genomes. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 8327-8332, 2008.
- GILLESPIE, J. H. The Causes of Molecular Evolution. Nova York: Oxford University Press, 1991.
- GILLESPIE, J. H. On Ohta's hypothesis: most amino acid substitutions are deleterious. *Journal of Molecular Evolution*, n. 40, p. 64-69, 1995.
- GILSON, P. R.; SU, V.; SLAMOVITS, C. H.; REITH, M. E.; KEELING, P. J.; MCFADDEN, G. I. Complete nucleotide sequence of the chlorarachniophyte nucleomorph: nature's smallest nucleus. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 9566-9571, 2006.
- GLASS, J. I.; ASSAD-GARCIA, N.; YOOSEPH, S.; LEWIS, M. R.; MARUF, M.; HUTCHISON, C. A. III; SMITH, H. O.; VENTER, J. C. Essential genes of a minimal bacterium. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 425-430, 2006.
- GLICK, T. Introdução. In: DOMINGUES, H. M. B.; SÁ, M. R.; GLICK, T. (Orgs.). *A Recepção do Darwinismo no Brasil*. Rio de Janeiro: Editora Fiocruz, 2003a. p. 19-27.
- GLICK, T. O positivismo brasileiro na sombra do darwinismo: o grupo Ideia Nova em Desterro. In: DOMINGUES, H. M. B.; SÁ, M. R.; GLICK, T. (Org.). *A Recepção do Darwinismo no Brasil*. Rio de Janeiro: Editora Fiocruz, 2003b, p. 181-189.
- GOH, K.; CUSICK, M. E.; VALLE, D.; CHILDS, B.; VIDAL, M.; BARABÁSI, A-L. The human disease network. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 8685-8690, 2007.
- GOFFEAU, A. et al. Life with 6000 genes. *Science*, n. 274, p. 546-567, 1996.
- GOJOBORI, J.; TANG, H.; AKEY, J. M.; WU, C-I. Adaptive evolution in humans revealed by the negative correlation between the polymorphism and fixation phases of evolution. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 3907-3912, 2007.
- GONZÁLEZ, J. M. et al. Genome analysis of the proteorhodopsin-containing marine bacterium *Polaribacter* sp MED152 (Flavobacteria). *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 8724-8729, 2008.
- GONZÀLEZ-DUARTE, R.; ALBALAT, R. Merging protein, gene and genomic data: the evolution of the MDR-ADH family. *Heredity*, n. 95, p. 184-197, 2005.

- GONZÁLEZ-JOSÉ, R.; BORTOLINI, M. C.; SANTOS, F. R.; BONATTO, S. L. The peopling of America: craniofacial shape variation on a continental scale and its interpretation from an interdisciplinary view. *American Journal of Physical Anthropology*, n. 137, p. 175-187, 2008.
- GOUYON, P-H., HENRY, J-P.; ARNOULD, J. *Gene Avatars*. The Neo-Darwinian Theory of Evolution. Nova York: Kluwer Academic/Plenum, 2002.
- GRAMMER, K.; FINK, B.; MØLLER, A. P.; THORNHILL, R. Darwinian aesthetics: sexual selection and the biology of beauty. *Biological Reviews of the Cambridge Philosophical Society*, n. 78, p. 385-407, 2003.
- GREEN, R. E. et al. A draft sequence of the Neandertal genome. *Science*, n. 328, p. 710-722, 2010.
- GRIFFITH, R. W. A specific scenario for the origin of life and the genetic code based on peptide/oligonucleotide interdependence. *Origins of Life and Evolution of the Biosphere*, n. 39, p. 517-531, 2009.
- GRIMES, B. F. Ethnologue. *Languages of the World*. 12. ed. Dallas: Summer Institute of Linguistics, 1992.
- GUISINGER, M. M.; KUEHL, J. V.; BOORE, J. L.; JANSEN, R. K. Genome-wide analyses of Geraniaceae plastid DNA reveal unprecedent patterns of increased nucleotide substitutions. *Proceedings of the National Academy of Sciences, USA*, n. 105, p. 18424-18429, 2008.
- GURVEN, M. The evolution of contingent cooperation. *Current Anthropology*, n. 47, p. 185-192, 2006.
- HAAG, T.; SANTOS, A. S.; DE ANGELO, C.; SRBEK-ARAUJO, A. C., SANA, D. A.; MORATO, R. G.; SALZANO, F. M.; EIZIRIK, E. Development and testing of an optimized method for DNA-based identification of jaguar (*Panthera onca*) and puma (*Puma concolor*) faecal samples for use in ecological and genetic studies. *Genetica*, n. 136, p. 505-512, 2009.
- HAAG, T. et al. Molecular tracking of jaguar melanism using faecal DNA. *Conservation Genetics*, n. 11, p. 1239-1242, 2010a.
- HAAG, T.; SANTOS, A. S.; SANA, D. A.; MORATO, R. G.; CULLEN JR., L.; CRAWSHAW JR., P. G.; DE ANGELO, C.; DI BITETTI, M.; SALZANO, F. M.; EIZIRIK, E. The effect of habitat fragmentation on the genetic structure of a top predator: loss of diversity and high differentiation among remnant populations of Atlantic Forest jaguars (*Panthera onca*). (Submitted). 2010b.

- HEBSGAARD, M. B.; WIUF, C.; GILBERT, M. T. P.; GLENNER, H.; WILLERSLEV, E. Evaluating Neanderthal genetics and phylogeny. *Journal of Molecular Evolution*, n. 64, p. 50-60, 2007.
- HACKETT, S. J. et al. A phylogenomic study of birds reveals their evolutionary history. *Science*, n. 320, p. 1763-1768, 2008.
- HALARY, S.; LEIGH, J. W.; CHEAIB, B.; LOPEZ, P.; BAPTESTE, E. Network analyses structure genetic diversity in independent genetic worlds. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 127-132, 2010.
- HALLAM, S. J.; KONSTANTIDINIS, K. T.; PUTNAM, N.; SCHLEPER, C.; WATANABE, Y-I.; SUGAHARA, J.; PRESTON, C.; DE LA TORRE, J.; RICHARDSON, P. M.; DELONG, E. F. Genomic analysis of the uncultivated marine crenarcheote *Cenarchaeum symbiosum*. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 18296-18301, 2006.
- HALLPIKE, C. R. Reply to Dunbar. *Journal of the Royal Anthropological Institute*, n. 8, p. 763-765, 2002.
- HAMBLIN, M. T.; THOMPSON, E. E.; DI RIENZO, A. Complex signatures of natural selection at the Duffy blood group locus. *American Journal of Human Genetics*, n. 70, p. 369-383, 2002.
- HAMES, R.; KUZARA, J. The nexus of Yanomamö growth, health, and demography. In: SALZANO, F. M.; HURTADO, A. M. (Eds.). *Lost Paradises and the Ethics of Research and Publication*. Nova York: Oxford University Press, 2004. p. 110-145.
- HAMPL, V.; HUG, L.; LEIGH, J. W.; DACKS, J. B.; LANG, B. F.; SIMPSON, A. G. B.; ROGER, A. J. Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic “supergroups”. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 3859-3864, 2009.
- HAN, K.; LEE, J.; MEYER, T. J.; REMEDIOS, P.; GOODWIN, L.; BATZER, M. A. L1 recombination-associated deletions generate human genomic variation. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 19366-19371, 2008.
- HANCOCK, A. M.; WITONSKY, D. B.; GORDON, A. S.; ESHEL, G.; PRITCHARD, J. K.; COOP, G.; DI RIENZO, A. Adapations to climate in candidate genes for common metabolic disorders. *PloS Genetics*, n. 4, p. e32, 2008.
- HARRIS, C. R. The evolution of jealousy. *American Scientist*, n. 92, p. 62-71, 2004.

- HARRIS, E. E. Searching the genome for our adaptations. *Evolutionary Anthropology*, n. 17, p. 146-157, 2008.
- HAUSMANN, R. *História da Biologia Molecular*. Ribeirão Preto: Sociedade Brasileira de Genética, 1997.
- HAWKINS, J. S.; GROVER, C. E.; WENDEL, J. F. Repeated big bangs and the expanding universe: directionality in plant genome size evolution. *Plant Science*, n. 174, p. 557-562, 2008.
- HAWKS, J.; WANG, E. T.; COCHRAN, G. M.; HARPENDING, H. C.; MOYZIS, R. K. Recent acceleration of human adaptive evolution. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 20753-20758, 2007.
- HAYGOOD, R.; BABBITT, C. C.; FEDRIGO, O.; WRAY, G. A. Contrasts between adaptative coding and noncoding changes during human evolution. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 7853-7857, 2010.
- HEDGES, S. B.; KUMAR, S. Genomic clocks and evolutionary timescales. *Trends in Genetics*, n. 19, p. 200-206, 2003.
- HEIBERG, A. N. *The Humanitarian Challenge in a World of Conflict*: the Plight of Land-mine Victims. Tóquio: United Nations University, 1999.
- HEIZER JR., E. M.; RAYFORD, D. W.; RAYMER, M. L.; DOOM, T. E.; MILLER, R. V.; KRANE, D. E. Amino acid cost and codon-usage biases in 6 prokaryotic genomes: a whole-genome analysis. *Molecular Biology and Evolution*, n. 23, p. 1670-1680, 2006.
- HELPENBEIN, K. G.; FOURCADE, H. M.; VANJANI, R. G.; BOORE, J. L. The mitochondrial genome of *Paraspadella gotoi* is highly reduced and reveals that chaetognaths are a sister group to protostomes. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 10639-10643, 2004.
- HELLER, A. H. et al. Intra- and intercontinental molecular variability of an *Alu* insertion in the 3' untranslated region of the *LDLR* gene. *Human Biology*, n. 76, p. 591-604, 2004.
- HENN, B. M. et al. Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. *Proceedings of the National Academy of Sciences*, USA, n. 108, p. 5154-5162, 2011.
- HENRY, J. M. *Livro da Tribo*. São Paulo: Editora Livro da Tribo, 2002.
- HENSILWOOD, C. S. et al. Emergence of modern human behavior. Middle Stone Age engravings from South Africa. *Science*, n. 295, p. 1278-1280, 2002.

- HERSHEY, A. D. Spontaneous mutations in bacterial viruses. *Cold Spring Harbor Symposia on Quantitative Biology*, n. 11, p. 67-77, 1946.
- HERSHEY, A. D.; CHASE, M. Independent functions of viral protein and nucleic acid in growth of bacteriophage. *Journal of General Physiology*, n. 36, p. 39-56, 1952.
- HESCHL, A. *The Intelligent Genome*. On the Origin of the Human Mind by Mutation and Selection. Berlim: Springer, 1998.
- HEWLETT, B. S., DE SILVESTRI, A.; GUGLIELMINO, R. Semes and genes in Africa. *Current Anthropology*, n. 43, p. 313-321, 2002.
- HIBBS, D. A.; OLSSON, O. Geography, biogeography, and why some countries are rich and others are poor. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 3715-3720, 2004.
- HIETT, P. J. The place of life in our theories. *BioSystems*, n. 47, p. 157-176, 1998.
- HILLENMEYER, M. E. et al. The chemical genomic portrait of yeast: uncovering a phenotype for all genes. *Science*, n. 320, p. 362-365, 2008.
- HILL, K.; BARTON, M.; HURTADO, A. M. The emergence of human uniqueness: characters underlying behavioral modernity. *Evolutionary Anthropology*, n. 18, p. 187-200, 2009.
- HIRAO, I. et al. An unnatural base pair for incorporating aminoacid analogs into proteins. *Nature Biotechnology*, n. 20, p. 177-182, 2002.
- HOLDEN, M. T. G. et al. Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 14230-14245, 2004a.
- HOLDEN, M. T. G. et al. Complete genomes of two clinical *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 9786-9791, 2004b.
- HOLT, R. A. et al. The genome sequence of the malaria mosquito *Anopheles gambiae*. *Science*, n. 298, p. 129-149, 2002.
- HONGOH, Y.; SHARMA, V. K.; PRAKASH, T.; NODA, S.; TOH, H.; TAYLOR, T. D.; KUDO, T.; SAKAKI, Y.; TOYODA, A.; HATTORI, M.; OHKUMA, M. Genome of an endosymbiont coupling N₂ fixation to cellulose within protist cells in termite gut. *Science*, n. 322, p. 1108-1109, 2008.
- HORSE GENOME CONSORTIUM. Draft genome of *Equus caballus*. 2007. Disponível em: <www.ncbi.nih.gov/Genbank>. Acesso: 25 mai. 2011.

- HOU, J.; JUN, S-R.; ZHANG, C.; KIM, S-H. Global mapping of the protein structure space and application in structure-based inference of protein function. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 3651-3656, 2005.
- HUANG, C-H.; PENG, J. Evolutionary conservation and diversification of Rh family genes and proteins. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 15512-15517, 2005.
- HUGHES, A. L. Gene duplication and the origin of novel proteins. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 8791-8792, 2005.
- HUGHES, A. L.; HUGHES, M. K. Natural selection on the peptide-binding regions of major histocompatibility complex molecules. *Immunogenetics*, n. 42, p. 233-243, 1995.
- HUGHES, J. R.; CHENG, J-F.; VENTRESS, N.; PRABHAKAR, S.; CLARK, K.; ANGUITA, E.; DE GOBBI, M.; DE JONG, P.; RUBIN, E.; HIGGS, D. R. Anotation of cis-regulatory elements by identification, subclassification, and functional assessment of multispecies conserved sequences. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 9830-9835, 2005a.
- HUGHES, A. L.; PACKER, B.; WELCH, R.; CHANOCK, S. J.; YEAGER, M. High level of functional polymorphism indicates a unique role of natural selection at human immune system loci. *Immunogenetics*, n. 57, p. 821-827, 2005b.
- HÜNEMEIER, T.; CARVALHO, C.; MARRERO, A. R.; SALZANO, F. M.; PENA, S. D. J.; BORTOLINI, M. C. Niger-Congo speaking populations and the formation of the Brazilian gene pool: mtDNA and Y-chromosome data. *American Journal of Physical Anthropology*, n. 133, p. 854-867, 2007.
- HÜNEMEIER, T.; NEVES, A. G.; NORNBERG, I.; HILL, K.; HURTADO, A. M.; CARNESE, F. R.; GOICOECHEA, A. S.; HUTZ, M. H.; SALZANO, F. M.; CHIES, J. A. B. T-cell and chemokine receptor variation in South Amerindian populations. *American Journal of Human Biology*, n. 17, p. 515-518, 2005.
- HÜNEMEIER, T.; SALZANO, F. M.; BORTOLINI, M. C. *TCOF1 T/Ser* variant and brachycephaly in dogs. *Animal Genetics*, n. 40, p. 357-358, 2009.
- HÜNEMEIER, T. et al. *Gene-culture dynamics: an example involving Native Americans*, 2011 (Submitted).
- HURAULT, J. La population des Indiens de Guyane française. *Population*, n. 20, p. 603-632; p. 801-828, 1965.

- HURTADO, A. M.; HURTADO, I.; HILL, K. Public health and adaptive immunity among natives of South America. In: SALZANO, F. M.; HURTADO, A. M. (Eds.). *Lost Paradises and the Ethics of Research and Publication*. Nova York: Oxford University Press, 2004. p. 164-190.
- HUTZ, M. H.; MATTEVI, V. S.; ALMEIDA, S.; ZEMBRZUSKI, V. M.; SALZANO, F. M. Association of the dopamine D2 receptor gene with obesity in Native Brazilians. *Progress in Obesity Research*, n. 9, p. 370-372, 2003.
- IAFRATE, A. J.; FEUK, L.; RIVERA, M. N.; LISTEWNICK, M. L.; DONAHOE, P. K.; QI, Y.; SCHERER, S. W.; LEE, C. Detection of large-scale variation in the human genome. *Nature Genetics*, n. 36, p. 949-951, 2004.
- IBBA, M.; LOSEY, H. C.; KAWARABAYASI, Y.; KIKUCHI, H.; BUNJUN, S.; SÖLL, D. Substrate recognition by class I lysyl-tRNA synthetases: a molecular basis for gene displacement. *Proceedings of the National Academy of Sciences*, USA, n. 96, p. 418-423, 1999.
- IKEHARA, K. Origins of gene, genetic code, protein and life: comprehensive view of life systems from a GNC-SNS primitive genetic code hypothesis. *Journal of Biosciences*, n. 27, p. 165-186, 2002.
- IKEHARA, K.; OMORI, Y.; ARAI, R.; HIROSE, A. A novel theory on the origin of the genetic code: a GNC-SNS hypothesis. *Journal of Molecular Evolution*, n. 54, p. 530-538, 2002.
- INGHAM, J. M.; SPAIN, D. H. Sensual attachment and incest avoidance in human evolution and child development. *Journal of the Royal Anthropological Institute*, n. 11, p. 677-701, 2005.
- IRIARTE, J. Narrowing the gap. Exploring the diversity of food-production economies in the Americas. *Current Anthropology*, n. 50, p. 677-680, 2009.
- ITAYA, M.; TSUGE, K.; KOIZUMI, M.; FUJITA, K. Combining two genomes in one cell: stable cloning of the *Synechocystis* PCC6803 genome in the *Bacillus subtilis* 168 genome. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 15971-15976, 2005.
- IVANOVA, N. et al. Genome sequence of *Bacillus cereus* and comparative analysis with *Bacillus anthracis*. *Nature*, n. 423, p. 87-91, 2003.
- IVENS, A. C. et al. The genome of the kinetoplastid parasite *Leishmania major*. *Science*, n. 309, p. 436-442, 2005.

- JACKSON, M. S.; OLIVER, K.; LOVELAND, J.; HUMPHRAY, S.; DUNHAM, I.; ROCCHI, M.; VIGGIANO, L.; PARK, J. P.; HURLES, M. E.; SANTIBANEZ-KOREF, M. Evidence for widespread reticulate evolution within human duplicons. *American Journal of Human Genetics*, n. 77, p. 824-840, 2005.
- JACOB, F. *O Jogo dos Possíveis*. Ensaio sobre a Diversidade do Mundo Vivo. Lisboa: Gradiva, 1989.
- JACOB, F. *O Rato, a Mosca e o Homem*. São Paulo: Companhia das Letras, 1998.
- JAILON, O. et al. Genome duplication in the teleost fish *Tetraodon nigroviridis* reveals the early vertebrate proto-karyotype. *Nature*, n. 431, p. 946-957, 2004.
- JAKOBSSON, M. et al. Genotype, haplotype and copy-number variation in worldwide human populations. *Nature*, n. 451, p. 998-1003, 2008.
- JANSON, C. H.; SMITH, E. A. The evolution of culture: new perspectives and evidence. *Evolutionary Anthropology*, n. 12, p. 57-60, 2003.
- JOHANSSON, A.; GYLLENSTEN, U. Identification of local selective sweeps in human populations since the exodus from Africa. *Hereditas*, n. 145, p. 126-137, 2008.
- JONES, D. Group nepotism and human kinship. *Current Anthropology*, n. 41, p. 779-809, 2000.
- JONES, P. A. et al. Moving AHEAD with an international human epigenome project. *Nature*, n. 454, p. 711-715, 2008.
- JONES, T. et al. The diploid genome sequence of *Candida albicans*. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 7329-7334, 2004.
- JOYCE, G. F. Booting up life. *Nature*, n. 420, p. 278-279, 2002.
- KAISER, J. Population databases boom, from Iceland to the USA. *Science*, n. 298, p. 1158-1161, 2002.
- KAISER, M.; BRAUER, S.; STONEKING, M. A genome scan to detect candidate regions influenced by local natural selection in human populations. *Molecular Biology and Evolution*, n. 20, p. 893-900, 2003.
- KANAI, R.; FEILDEN, T.; FIRTH, C.; REES, G. Political orientations are correlated with brain structure in young adults. *Current Biology*, n. 21, p. 1-4, 2011.
- KASAHARA, M. et al. The medaka draft genome and insights into vertebrate genome evolution. *Nature*, n. 447, p. 714-719, 2007.
- KATZ, L. A. Changing perspectives on the origin of eukaryotes. *Trends in Ecology and Evolution*, n. 13, p. 493-497, 1998.

- KATZMAN, S.; KERN, A. D.; BEJERANO, G.; FEWELL, G.; FULTON, L.; WILSON, R. K.; SALAMA, S. R.; HAUSSLER, D. Human genome ultraconserved elements are ultraselected. *Science*, n. 317, p. 915, 2007.
- KAWASHIMA, T. et al. Archaeal adaptation to higher temperatures revealed by genomic sequence of *Thermoplasma volcanium*. *Proceedings of the National Academy of Sciences*, USA, n. 97, p. 14257-14262, 2000.
- KEIM, C. N.; ABREU, F.; LINS, U.; BARROS, F. L.; FARINA, M. Cell organization and ultrastructure of a magnetotactic multicellular organism. *Journal of Structural Biology*, n. 145, p. 254-262, 2004a.
- KELLEY, J. L.; MADEOY, J.; CALHOUN, J. C.; SWANSON, W.; AKEY, J. M. 2006. Genomic signatures of positive selection in humans and the limits of outlier approaches. *Genome Research*, n. 16, p. 980-989, 2006.
- KELLEY, J. L.; SWANSON, W. J. Positive selection in the human genome: from genome scans to biological significance. *Annual Reviews of Genomics and Human Genetics*, n. 9, p. 143-160, 2008.
- KELLY, R. C. The evolution of lethal intergroup violence. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 15294-15298, 2005.
- KENDAL, J.; TEHRANI, J. J.; ODLING-SMEE, J. Human niche construction in interdisciplinary focus. *Philosophical Transactions of the Royal Society B*, p. 366, p. 785-792, 2011.
- KERMARREC, N.; ROUBINET, F.; APOIL, P-A.; BLANCHER, A. Comparison of allele *O* sequences of the human and non-human primate ABO system. *Immunogenetics*, n. 49, p. 517-526, 1999.
- KHAYAT, R.; TANG, L.; LARSON, E. T.; LAWRENCE, C. M.; YOUNG, M.; JOHNSON, J. E. Structure of an archaeal virus capsid protein reveals a common ancestry to eukaryotic and bacterial viruses. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 18944-18949, 2005.
- KIDD, J. M. et al. Mapping and sequencing of structural variation from eight human genomes. *Nature*, n. 453, p. 56-64, 2008.
- KIMURA, M. Evolutionary rate at the molecular level. *Nature*, n. 217, p. 624-626, 1968.
- KIMURA, M. *The Neutral Allele Theory of Molecular Evolution*. Cambridge: Cambridge University Press, 1983.

- KIMURA, M.; OHTA, T. Protein polymorphism as a phase of molecular evolution. *Nature*, n. 229, p. 467-469, 1971.
- KIMURA, R.; FUJIMOTO, A.; TOKUNAGA, K.; OHASHI, J. A practical genome scan for population-specific strong selective sweeps that have reached fixation. *PloS One*, n. 2, p. e286, 2007.
- KIMURA, R.; OHASHI, J.; MATSUMURA, Y.; NAKAZAWA, M.; INAOKA, T.; OHTSUKA, R.; OSAWA, M.; TOKUNAGA, K. 2008. Gene flow and natural selection in Oceanic human populations inferred from genome-wide SNP typing. *Molecular Biology and Evolution*, n. 25, p. 1750-1761.
- KING, R. C.; STANSFIELD, W. D. *A Dictionary of Genetics*. 6. Ed. Nova York: Oxford University Press, 2002.
- KIRBY, S.; DOWMAN, M.; GRIFFITHS, T. L. Innateness and culture in the evolution of language. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 5241-5245, 2007.
- KIRKPATRICK, R. C. The evolution of human homosexual behavior. *Current Anthropology*, n. 41, p. 385-413, 2000.
- KITANO, T.; SUMIYAMA, K.; SHIROISHI, T.; SAITOU, N. Conserved evolution of the Rh50 gene compared to its homologous Rh blood group gene. *Biochemical and Biophysical Research Communications*, n. 249, p. 78-85, 1998.
- KITANO, T.; UMETSU, K.; TIAN, W.; YAMAZAKI, K.; SAITOU, N. Tempo and mode of evolution of the Rh blood group genes before and after gene duplication. *Immunogenetics*, n. 59, p. 427-431, 2007.
- KLASSON, L. et al. The mosaic genome structure of the *Wolbachia* wRi strain infecting *Drosophila simulans*. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 5725-5730, 2009.
- KLEEREBEZEM, M. et al. Complete genome sequence of *Lactobacillus plantarum* WCFS1. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 1990-1995, 2003.
- KOBAYASHI, K. et al. Essential *Bacillus subtilis* genes. *Proceedings of the National Academy of Sciences*, USA, p. 100, p. 4678-4683, 2003.
- KOEHLER-SANTOS, P.; LORENZ-LEMKE, A. P.; MUSCHNER, V. C.; BONATTO, S. L.; SALZANO, F. M.; FREITAS, L. B. Molecular genetic variation in *Passiflora alata* (Passifloraceae), an invasive species in southern Brazil. *Biological Journal of the Linnean Society*, n. 88, p. 611-630, 2006a.

- KOEHLER-SANTOS, P.; LORENZ-LEMKE, A. P.; SALZANO, F. M.; FREITAS, L. B. Ecological evolutionary relationships in *Passiflora alata* from Rio Grande do Sul, Brazil. *Brazilian Journal of Biology*, n. 66, p. 809-816, 2006b.
- KOHLRAUSCH, F. B.; CALLEGARI-JACQUES, S. M.; TSUNETO, L. T.; PETZLER, M. L.; HILL, K.; HURTADO, A. M.; SALZANO, F. M.; HUTZ, M. H. Geography influences microsatellite polymorphism diversity in Amerindians. *American Journal of Physical Anthropology*, n. 126, p. 463-470, 2005.
- KOLKER, E. et al. Global profile of *Shewanella oneidensis* MR-1: expression of hypothetical genes and improved functional annotations. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 2099-2104, 2005.
- KOONIN, E. V. Orthologs, paralogs, and evolutionary genomics. *Annual Review of Genetics*, n. 39, p. 309-338, 2005.
- KOONIN, E. V.; WOLF, Y. I.; KAREV, G. P. The structure of the protein universe and genome evolution. *Nature*, n. 420, p. 218-223, 2002.
- KOONIN, E. V.; NOVOZHILOV, A. S. Origin and evolution of the genetic code: the universal enigma. *IUBMB Life*, n. 61, p. 99-111, 2009.
- KORBEL, J. O. et al. 2007. Paired-end mapping reveals extensive structural variation in the human genome. *Science*, n. 318, p. 420-426.
- KOVER, P. X.; CAICEDO, A. L. The genetic architecture of disease resistance in plants and the maintenance of recombination by parasites. *Molecular Ecology*, n. 10, p. 1-16, 2001.
- KRAKAUER, D. C.; SASAKI, A. Noisy clues to the origin of life. *Proceedings of the Royal Society of London, Series B*, n. 269, p. 2423-2428, 2002.
- KRAUSE, J.; ORLANDO, L.; SERRE, D.; VIOLA, B.; PRÜFER, K.; RICHARDS, M. P.; HUBLIN, J-J.; HÄNNI, C.; DEREVIANKO, A. P.; PÄÄBO, S. Neanderthals in Central Asia and Siberia. *Nature*, n. 449, p. 902-904, 2007.
- KREIMER, A.; BORENSTEIN, E.; GOPHNA U.; RUPPIN, E. The evolution of modularity in bacterial metabolic networks. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 6976-6981, 2008.
- KREITMAN, M.; AKASHI, H. Molecular evidence for natural selection. *Annual Review of Ecology and Systematics*, n. 26, p. 403-422, 1995.
- KRINGS, M.; STONE, A.; SCHMITZ, R. W.; KRAINITZKI, H.; STONEKING, M.; PÄÄBO, S. Neanderthal DNA sequences and the origin of modern humans. *Cell*, n. 90, p. 19-30, 1997.

- KUBO, T.; MIKAMI, T. Organization and variation of angiosperm mitochondrial genome. *Physiologia Plantarum*, n. 129, p. 6-13, 2007.
- Kudaravalli, S.; Veyrieras, J-B.; Stranger, B. E.; Dermitzakis, E. T.; Pritchard, J. K. Gene expression levels are a target of recent natural selection in the human genome. *Molecular Biology and Evolution*, n. 26, p. 649-658, 2009.
- KUMAR, S.; FILIPSKI, A.; SWARNA, V.; WALKER, A.; HEDGES, S. B. Placing confidence limits on the molecular age of human-chimpanzee divergence. *Proceedings of the National Academy of Sciences, USA*, n. 102, p. 18842-18847, 2005.
- KUO, C-H.; WARES, J. P.; KISSINGER, J. C. The Apicomplexan whole-genome phylogeny: an analysis of incongruence among gene trees. *Molecular and Biological Evolution*, n. 25, p. 2689-2698, 2008.
- KUPER, A. Changing the subject – about cousin marriage, among other things. *Journal of the Royal Anthropological Institute*, n. 14, p. 717-735, 2008.
- KUPFERMANN, H.; SATTA, Y.; TAKAHATA, N.; TICHY, H.; KLEIN, J. Evolution of *Mhc-DRB* introns: implications for the origin of primates. *Journal of Molecular Evolution*, n. 48, p. 663-674, 1999.
- KURODA, M. et al. Whole genome sequence of *Staphylococcus saprophyticus* reveals the pathogenesis of uncomplicated urinary tract infection. *Proceedings of the National Academy of Sciences, USA*, n. 102, p. 13272-13277, 2005.
- KUROKI, Y. et al. Comparative analysis of chimpanzee and human Y chromosomes unveils complex evolutionary pathway. *Nature Genetics*, n. 38, p. 158-167, 2006.
- LABORIT, H. *Deus Não Joga Dados*. São Paulo: Trajetória Cultural, 1988.
- LALAND, K. N.; ODLING-SMEE, J.; FELDMAN, M. W. Cultural niche construction and human evolution. *Journal of Evolutionary Biology*, n. 14, p. 22-33, 2001.
- LALAND, K. N.; HOPPITT, W. Do animals have culture? *Evolutionary Anthropology*, n. 12, p. 150-159, 2003.
- LANE, C. E.; VAN DEN HEUVEL, K.; KOZERA, C.; CURTIS, B. A.; PARSONS, B. J.; BOWMAN, S.; ARCHIBALD, J. M. Nucleomorph genome of *Hemiselmis andersenii* reveals complete intron loss and compaction as a driver of protein structure and function. *Proceedings of the National Academy of Sciences, USA*, n. 104, p. 19908-19913, 2007.
- LANE, N.; MARTIN, W. The energetics of genome complexity. *Nature*, n. 467, p. 929-934, 2010.

- LARSON, G. et al. Patterns of East Asian pig domestication, migration, and turnover revealed by modern and ancient DNA. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 7686-7691, 2010.
- LARSSON, P. et al. The complete genome sequence of *Francisella tularensis*, the causative agent of tularemia. *Nature Genetics*, n. 37, p. 153-159, 2005.
- LAURANCE, W. F.; COCHRANE, M. A.; BERGEN, S.; FEARNSIDE, P. M.; DELAMÔNICA, P.; BARBER, C.; D'ANGELO, S.; FERNANDES, T. The future of the Brazilian Amazon. *Science*, n. 291, p. 438-439, 2001.
- LAVAL, G.; PATIN, E.; BARREIRO, L. B.; QUINTANA-MURCI, L. Formulating a historical and demographic model of recent human evolution based on resequencing data from noncoding regions. *PLoS One*, n. 5, p. e10284, 2010.
- Lazcano, A. Which way to life? *Origins of Life and Evolution of the Biosphere*, n. 40, p. 161-167, 2010.
- LEDERBERG, J.; TATUM, E. L. Novel genotypes in mixed cultures of biochemical mutants of bacteria. *Cold Spring Harbor Symposia on Quantitative Biology*, n. 11, p. 113-114, 1946.
- LEIRIA, L. B.; ROISENBERG, I.; SALZANO, F. M.; BANDINELLI, E. Introns 1 and 22 inversions and Factor VIII inhibitors in patients with severe haemophilia A in southern Brazil. *Haemophilia*, n. 15, p. 309-313, 2009.
- LEITE, F. P. N.; SANTOS, S. E. B.; RODRÍGUEZ, E. M. R.; CALLEGARI-JACQUES, S. M.; DEMARCHI, D. A.; TSUNETO, L. T.; PETZL-ERLER, M. L.; SALZANO, F. M.; HUTZ, M. H. Linkage disequilibrium patterns and genetic structure of Amerindian and non-Amerindian Brazilian populations revealed by long-range X-STR markers. *American Journal of Physical Anthropology*, n. 139, p. 404-412, 2009.
- LEITE, F. P. N. et al. Y-STR analysis in Brazilian and South Amerindian populations. *American Journal of Human Biology*, n. 20, p. 359-363, 2008.
- LEMONS, J. P. S.; ROCHA, J. F. V. Interconexão entre o homem e a natureza. *Ciência Hoje*, n. 22, v. 129, p. 46-55, 1997.
- LEVY, M. S. F. A escolha do cônjuge. *Revista Brasileira de Estudos Populacionais*, n. 26, p. 117-133, 2009.
- LEWIN, B. *Genes VIII*. Porto Alegre: Artmed Editora, 2000.
- LEWIS, M. P. *Ethnologue*. Languages of the World, 16. ed. Dallas: Summer Institute of Linguistics, 2009.

- Lewontin, R. 2000. The problems of population genetics. In: Singh, R.S.; Krimbas, C.B. (eds.). *Evolutionary Genetics*. From Molecules to Morphology. Cambridge University Press, Cambridge, p. 5-23.
- LI, J. Z. et al. Worldwide human relationships inferred from genome-wide patterns of variation. *Science*, n. 319, p. 1100-1104, 2008.
- LI, L.; BANNANTINE, J. P.; ZHANG, Q.; AMONSIN, A.; MAY, B. J.; ALT, D.; BANERJI, N.; KANJILAL, S.; KAPUR, V. The complete genome sequence of *Mycobacterium avium* subspecies *paratuberculosis*. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 12344-12349, 2005.
- LIEBERMAN, E.; MICHEL, J-B.; JACKSON, J.; TANG, T.; NOWAK, M. A. Quantifying the evolutionary dynamics of language. *Nature*, n. 449, p. 713-716, 2007.
- LIEBERMAN, P. The evolution of human speech. Its anatomical and neural bases. *Current Anthropology*, n. 48, p. 39-66, 2007.
- LIFSON, S. On the crucial stages in the origin of animate matter. *Journal of Molecular Evolution*, n. 44, p. 1-8.
- LIMA-ROSA, C. A. V.; CANAL, C. W.; FALLAVENA, P. R. V.; FREITAS, L. B.; SALZANO, F. M. LEIO258 microsatellite variability and its relationship to *B-F* haplotypes in Brazilian (blue-egg Caipira) chickens. *Genetics and Molecular Biology*, n. 28, p. 386-389, 2005.
- LIMA-ROSA, C. A. V.; CANAL, C. W.; STRECK, A. F.; FREITAS, L. B.; DELGADO-CAÑEDO, A.; BONATTO, S. L.; SALZANO, F. M. *B-F* DNA sequence variability in Brazilian (blue-egg Caipira) chickens. *Animal Genetics*, n. 35, p. 278-284, 2004.
- LIND, P. A.; ANDERSSON, D. I. Whole-genome mutational biases in bacteria. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 17878-17883, 2008.
- LINDBLAD-TOH, K. ET AL.; BROAD INSTITUTE GENOME SEQUENCING PLATFORM. Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature*, n. 438, p. 803-819, 2005.
- LITI, G.; LOUIS, E. J. Yeast evolution and comparative genomics. *Annual Review of Microbiology*, n. 59, p. 135-153, 2005.

- LLOYD, E. A. Units of selection. In: Keller, G.F.; Lloyd, G.A. (Eds.). *Keywords in Evolutionary Biology*. Cambridge (MA): Harvard University Press, 1992. p. 334-340.
- LOCKE, J. L. Rank and relationships in the evolution of spoken language. *Journal of the Royal Anthropological Institute*, n. 7, p. 37-50, 2001.
- LOFTUS, B. et al. The genome of the protist parasite *Entamoeba histolytica*. *Nature*, n. 433, p. 865-868, 2005a.
- LOFTUS, B. J. et al. The genome of the basidiomycetous yeast and human pathogen *Cryptococcus neoformans*. *Science*, n. 307, p. 1321-1324, 2005b.
- LONG, M., ROSENBERG, C.; GILBERT, W. Intron phase correlations and the evolution of the intron-exon structure of genes. *Proceedings of the National Academy of Sciences*, USA, n. 92, p. 12495-12499, 1995.
- LORENZ-LEMKE, A. P.; MUSCHNER, V. C.; BONATTO, S. L.; CERVI, A. C.; SALZANO, F. M.; FREITAS, L. B. Phylogeographic inferences concerning evolution of Brazilian *Passiflora actinia* and *P. elegans* (Passifloraceae) based on ITS (nrDNA) variation. *Annals of Botany*, n. 95, p. 799-806, 2005.
- LOWE, C. B.; BEJERANO, G.; HAUSSLER, D. Thousands of human mobile element fragments undergo strong purifying selection near developmental genes. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 8005-8010, 2007.
- LUFT, L. *Pensar é Transgredir*. Rio de Janeiro: Record, 2004.
- LURIA, S. E.; DELBRÜCK, M. Mutations of bacteria from virus sensitivity to virus resistance. *Genetics*, n. 28, p. 491-511, 1943.
- LWOFF, A.; GUTMANN, A. La libération de bactériophages par la lyse d'une bactérie lysogène. *Comptes Rendus, Academie des Sciences* (Paris), n. 230, p. 154-156, 1950.
- LYNCH, M. *The Origins of Genome Architecture*. Sunderland: Sinauer, 2007.
- MA, J.; RATAN, A.; RANEY, B. J.; SUH, B. B.; MILLER, W.; HAUSSLER, D. The infinite sites model of genome evolution. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 14254-14261, 2008.
- MA, W.; YU, C. Intramolecular RNA replicase: possibly the first self-replicating molecule in the RNA world. *Origins of Life and Evolution of the Biosphere*, n. 36, p. 413-420, 2005.

- MACE, R. Evolutionary ecology of human life history. *Animal Behavior*, n. 59, p. 1-10, 2000.
- MACHIDA, M. et al. Genome sequencing and analysis of *Aspergillus oryzae*. *Nature*, n. 438, p. 1157-1161, 2005.
- MARCUS, G. F. Before the word. *Nature*, n. 431, p. 745, 2004.
- MARGULIS, L.; CHAPMAN, M.; GUERRERO, R.; HALL, J. The last eukaryotic common ancestor (LECA): acquisition of cytoskeletal motility from aerotolerant spirochetes in the Proterozoic Eon. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 13080-13085, 2006.
- MARGULIS, L.; SAGAN, D. *O que é Sexo?* Rio de Janeiro: Jorge Zahar Editor, 2002.
- MARRA, M. A. et al. The genome sequence of the SARS-associated coronavirus. *Science*, n. 300, p. 1399-1404, 2003.
- MARRERO, A. R.; LEITE, F. P. N.; CARVALHO, B. A.; PERES, L. M.; KOMMERS, T. C.; CRUZ, I. M.; SALZANO, F. M.; RUIZ-LINARES, A.; SILVA JUNIOR, W. A.; BORTOLINI, M. C. Heterogeneity of the genome ancestry of individuals classified as white in the state of Rio Grande do Sul, Brazil. *American Journal of Human Biology*, n. 17, p. 496-506, 2005.
- MARRERO, A. R. et al. Pre- and post-Columbian gene and cultural continuity: the case of the *gaucho* from southern Brazil. *Human Heredity*, n. 64, p. 160-171, 2007a.
- MARRERO, A. R.; SILVA-JUNIOR, W. A.; BRAVI, C. M.; HUTZ, M. H.; PETZLER, M. L.; RUIZ-LINARES, A.; SALZANO, F. M.; BORTOLINI, M. C. Demographic and evolutionary trajectories of the Guarani and Kaingang natives of Brazil. *American Journal of Physical Anthropology*, n. 132, p. 301-310, 2007b.
- MARTH, G. et al. Sequence variations in the public human genome data reflect a bottlenecked population history. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 376-381, 2003.
- MARTH, G. T.; CZABARKA, E.; MURVAI, J.; SHERRY, S. T. The allele frequency spectrum in genome-wide human variation data reveals signals of differential demographic history in three large world populations. *Genetics*, n. 166, p. 351-372, 2004.
- MARTIN, W.; MÜLLER, M. The hydrogen hypothesis for the first eukaryote. *Nature*, n. 392, p. 37-41, 1998.
- MARTIN, W.; RUSSELL, M. J. On the origins of cells: a hypothesis for the evolutionary transitions from abiotic geochemistry to chemoautotrophic

- prokaryotes, and from prokaryotes to nucleated cells. *Philosophical Transactions of the Royal Society London*, Series B, n. 358, p. 59-85, 2003.
- MARTINEZ, D. et al. Genome sequence of the lignocellulose degrading fungus *Phanerochaete chrysosporium* strain RP78. *Nature Biotechnology*, n. 22, p. 695-700, 2004.
- MARTINEZ, D. et al. Genome, transcriptome, and secretome analysis of wood decay fungus *Postia placenta* supports unique mechanisms of lignocellulose conversion. *Proceedings of the National Academy of Sciences USA*, p. 1954-1959, 2009.
- MATEUS-PEREIRA, L. H.; SOCORRO, A.; FERNANDEZ, I.; MASLEH, M.; VIDAL, D.; BIANCHI, N. O.; BONATTO, S. L.; SALZANO, F. M.; HERRERA, R. J. Phylogenetic information in polymorphic L1 and *Alu* insertions from East Asians and Native American populations. *American Journal of Physical Anthropology*, n. 128, p. 171-184, 2005.
- MATISOO-SMITH, E. The peopling of Oceania. In: CRAWFORD, M. H. (ed.). *Anthropological Genetics. Theory, Methods and Applications*. Cambridge: Cambridge University Press, 2007. p. 409-432.
- MATSUZAKI, M. et al. Genome sequence of the ultrasmall unicellular red alga *Cyanidioschyzon merolae* 10D. *Nature*, n. 428, p. 653-657, 2004.
- Mattevi, V. S.; Coimbra JR., C. E. A.; Santos, R. V.; Salzano, F. M.; Hutz, M. H. Association of the low-density lipoprotein receptor gene with obesity in Native American populations. *Human Genetics*, n. 106, p. 546-552, 2000.
- MATTIANGELI, V.; RYAN, A. W.; MCMANUS, R.; BRADLEY, D. G. A genome-wide approach to identify genetic loci with a signature of natural selection in the Irish population. *Genome Biology*, n. 7, p. R74, 2006.
- MAYR, E. What Makes Biology Unique? *Considerations on the Autonomy of a Scientific Discipline*. Cambridge: Cambridge University Press, 2004.
- MAYR, E.; PROVINE, W. B. *The Evolutionary Synthesis. Perspectives on the Unification of Biology*. Cambridge: Harvard University Press, 1980.
- MAYR, G. *What Makes Biology Unique?* Considerations on the Autonomy of a Scientific Discipline. Cambridge: Cambridge University Press, 2004.
- MAZIÈRES, S.; CALLEGARI-JACQUES, S. M.; CROSSETTI, S. G.; DUGOUJON, J-M.; LARROUY, G.; BOIS, E.; CRUBÉZY, E.; HUTZ, M. H.; SALZANO, F. M. French Guiana Amerindian demographic history as revealed by autosomal and Y-chromosome STRs. *Annals of Human Biology*, n. 38, p. 76-83, 2011.

- MAZIÈRES, S.; SEVIN, A.; CALLEGARI-JACQUES, S. M.; CRUBÉZY, E.; LARROUY, G.; DUGOUJON, J-M.; SALZANO, F. M. Population genetic dynamics in the French Guiana region. *American Journal of Human Biology*, n. 21, p. 113-117, 2009.
- MAZIÈRES, S.; SEVIN, A.; CRUBÉZY, E.; SALZANO, F. M.; LARROY, G. Genetic studies in French Guiana populations: synthesis. *American Journal of Physical Anthropology*, n. 132, p. 292-300, 2007.
- MAZIÈRES, S. et al. Uniparental (mtDNA, Y-chromosome) polymorphisms in French Guiana and two related populations – implications for the region's colonization. *Annals of Human Genetics*, n. 72, p. 145-156, 2008.
- MCELREATH, R.; BOYD, R.; RICHERSON, P. J. 2003. Shared norms and the evolution of ethnic markers. *Current Anthropology*, n. 44, p. 122-129.
- McInerney, M .J. et al. The genome of *Synthrophus aciditrophicus*: life at the thermodynamic limit of microbial growth. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 7600-7605, 2007.
- MCKAY, D. S.; GIBSON JR., E. K.; THOMAS-KEPRTA, K. L.; VALI, H.; ROMANEK, C. S.; CLEMETT, S. J.; CHELLIER, X. D. F.; MAECHLING, C. R.; ZARE, R. N. Search for past life on Mars: possible relic biogenic activity in Martian meteorite ALH84001. *Science*, n. 273, p. 924-930, 1996.
- MCLEOD, M. P. et al. The complete genome of *Rhodococcus* sp RHA1 provides insights into a catabolic powerhouse. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 15582-15587, 2006.
- MCLYSAGHT, A.; BALDI, P. F.; GAUT, B. S. Extensive gene gain associated with adaptive evolution of poxviruses. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 15655-15660, 2003.
- MCNALLY, K. L. et al. Genomewide SNP variation reveals relationships among landraces of modern varieties of rice. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 12273-12278, 2009.
- MCVEAN, G.; SPENCER, C. C. A. Scanning the human genome for signals of selection. *Current Opinion in Genetics Development*, n. 16, p. 624-629, 2006.
- MCVICKER, G.; GORDON, D.; DAVIS, C.; GREEN, P. Widespread genomic signatures of natural selection in hominid evolution. *PLoS Genetics*, n. 5, p. e1000471, 2009.

- MEDINA, M. Genomes, phylogeny, and evolutionary systems biology. *Proceedings of the National Academy of Sciences, USA*, n. 102 (Supplement 1), p. 6630-6635, 2005.
- MELLARS, P. The impossible coincidence. A single-species model for the origins of modern human behavior in Europe. *Evolutionary Anthropology*, n. 14, p. 12-27, 2005.
- MELLARS, P. Why did modern human populations disperse from Africa *ca* 60,000 years ago? A new model. *Proceedings of the National Academy of Sciences, USA*, n. 103, p. 9381-9386, 2006.
- MENDEL, G. Versuche über Pflanzen-Hybriden. *Verhandlungen des naturforschenden Vereines in Brünn*, n. 4, p. 3-47, 1866.
- MENNA-BARRETO, M.; BENDER, A. L.; BONATTO, S. L.; FREITAS, L. B.; SALZANO, F. M.; TSUNETO, L. T.; PETZL-ERLER, M. L. Human T-cell lymphotropic virus type II in Grarani Indians, southern Brazil. *Cadernos de Saúde Pública*, n. 21, p. 1947-1951, 2005.
- MESOUDI, A.; LALAND, K. N. Culturally transmitted paternity beliefs and the evolution of human mating behavior. *Proceedings of the Royal Society B*, n. 274, p. 1273-1278, 2007.
- MESOUDI, A.; WHITEN, A.; LALAND, K. N. Is human cultural evolution darwinian? Evidence reviewed from the perspective of *The Origin of Species*. *Evolution*, n. 58, p. 1-11, 2004.
- MESSING, J. et al. Sequence composition and genome organization of maize. *Proceedings of the National Academy of Sciences, USA*, n. 101, p. 14349-14354, 2004.
- METHÉ, B. A. et al. The psychrophilic lifestyle as revealed by the genome sequence of *Colwellia psychrerythraea*. *Proceedings of the National Academy of Sciences, USA*, n. 102, p. 10913-10918, 2005.
- MICHELMORE, R. W.; MEYERS, B. C. Clusters of resistance genes in plants evolve by divergent selection and a birth-and-death process. *Genome Research*, n. 8, p. 1113-1130, 1998.
- MICHOD, R. E.; VIOSSAT, Y.; SOLARI, C. A.; HURAND, M.; NEDELCU, A. M. Life-history evolution and the origin of multicellularity. *Journal of Theoretical Biology*, n. 239, p. 257-272, 2006.

MIKKELSEN, T. S. ET AL.; BROAD INSTITUTE GENOME SEQUENCING PLATFORM; BROAD INSTITUTE WHOLE GENOME ASSEMBLY TEAM; GRAVES, J. A. M.; PONTING, C. P.; BREEN, M.; SAMOLLOW, P. B.; LANDER, E. S.; LINDLAD-TOH, K. Genome of the marsupial *Monodelphis domestica* reveals innovation in non-coding sequences. *Nature*, n. 447, p. 167-177, 2007.

MILLER, W. et al. Sequencing the nuclear genome of the extinct woolly mammoth. *Nature*, n. 456, p. 387-390, 2008.

MINETA, K.; NAKAZAWA, M.; CEBRIÀ, F.; IKEO, K.; AGATA, K.; GOJOBORI, T. Origin and evolutionary process of the CNS elucidated by comparative genomics analysis of planarian ESTs. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 7666-7671, 2003.

MING, R. et al. The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus). *Nature*, n. 452, p. 991-996, 2008.

MITHEN, S. *A Pré-História da Mente. Uma Busca das Origens da Arte, da Religião e da Ciência*. São Paulo: Editora UNESP, 2002.

MITHEN, S. *The Singing Neanderthals. The Origins of Music, Language, Mind and Body*. Cambridge: Harvard University Press, 2006.

MITTERMEIER, R. A.; WERNER, T.; AYRES, J. M.; FONSECA, G. A. B. O país da megadiversidade. *Ciência Hoje*, n. 14, v. 81, p. 20-27, 1992.

Mock, T et al. 2008. Whole-genome expression profiling of the marine diatom *Thalassiosira pseudonana* identifies genes involved in silicon bioprocesses. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 1579-1584.

MONGODIN, E. F. et al. The genome of *Salinibacter ruber*: convergence and gene exchange among hyperhalophilic bacteria and archaea. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 18147-18152, 2005.

MORAN, M. A. et al. Genome sequence of *Silicibacter pomeroyi* reveals adaptations to the marine environment. *Nature*, n. 432, p. 910-913, 2004.

MORENO-ESTRADA, A.; TANG, K.; SIKORA, M.; MARQUÈS-BONET, T.; CASALS, F.; NAVARRO, A.; CALAFELL, F.; BERTRANPETIT, J.; STONEKING, M.; BOSCH, E. Interrogating 11 fast-evolving genes for signatures of recent positive selection in worldwide human populations. *Molecular Biology and Evolution*, n. 26, p. 2285-2297, 2009.

- MORGAN, T. H.; STURTVANT, A. H.; MULLER, H. J.; BRIDGES, C. B. *The Mechanism of Mendelian Heredity*. Nova York: Henry Holt, 1915.
- MORRISS-KAY, G. M. The evolution of human artistic creativity. *Journal of Anatomy*, n. 216, p. 158-176, 2010.
- MOUSE GENOME CONSORTIUM. Initial sequencing and comparative analysis of the mouse genome. *Nature*, n. 420, p. 520-562, 2002.
- MULKIDJANIAN, A. Y. et al. The cyanobacterial genome core and the origin of photosynthesis. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 13126-13131, 2006.
- MULLER, M. N.; WRANGHAM, R. W. *Sexual Coercion in Primates and Humans: an Evolutionary Perspective on Male Aggression against Females*. Cambridge (MA): Harvard University Press, 2009.
- MUSCHNER, V. C.; LORENZ-LEMKE, A. P.; VECCHIA, M.; BONATTO, S. L.; SALZANO, F. M.; FREITAS, L. B. Differential organellar inheritance in *Passiflora's* (Passifloraceae) subgenera. *Genetica*, n. 128, p. 449-453, 2006.
- NARDI, N. B.; VENTURA, A. M. Terapia gênica. In: MIR, L. (Org.). *Genômica*. São Paulo: Atheneu, 2004 p. 625-640.
- NEALSON, K. A Korarchaeote yields to genome sequencing. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 8805-8806, 2008.
- Neel, J. V.; Salzano, F. M. Further studies on the Xavante Indians. X. Some hypotheses-generalizations resulting from these studies. *American Journal of Human Genetics*, n. 19, p. 554-574, 1967.
- NEI, M. The new mutation theory of phenotypic evolution. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 12235-12242, 2007.
- NETTLE, D. Beyond nature versus culture: cultural variation as an evolved characteristic. *Journal of the Royal Anthropological Institute*, n. 15, p. 223-253, 2009.
- NIELSEN, R. et al. Darwinian and demographic forces affecting human protein coding genes. *Genome Research*, n. 19, p. 838-849, 2009.
- NIERMANN, W. C. et al. Structural flexibility in the *Burkholderia mallei* genome. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 14246-14251, 2004.
- NIERMANN, W. C. et al. Genomic sequence of the pathogenic and allergenic filamentous fungus *Aspergillus fumigatus*. *Nature*, n. 438, p. 1151-1156, 2005.

- NISHIHARA, H.; MARUYAMA, S.; OKADA, N. Retroposon analysis and recent geological data suggest near-simultaneous divergence of the three superorders of mammals. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 5235-5240, 2009.
- NISHIYAMA, T. et al. Comparative genomics of *Physcomitrella pattene* gametophytic transcriptome and *Arabidopsis thaliana*: implication for land plant evolution. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 8007-8012, 2003.
- Nowak, M. A. Five rules for the evolution of cooperation. *Science*, n. 314, p. 1560-1563, 2006.
- NOWAK, M. A., TARNITA, C. E.; WILSON, E. O. The evolution of eusociality. *Nature*, n. 466, p. 1057-1062, 2010.
- NOZAWA, M.; KAWAHARA, Y.; NEI, M. Genomic drift and copy number variation of sensory receptor genes in humans. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 20421-20426, 2007.
- NÜRNBERGER, T. Signal perception in plant pathogen defense. *Cellular and Molecular Life Sciences*, n. 55, p. 167-182, 1999.
- O'REILLY, P. F.; BIRNEY, E.; BALDING, D. J. Confounding between recombination and selection, and the Ped/Pop method for detecting selection. *Genome Research*, n. 18, p. 1304-1313.
- OH, J. D. et al. The complete genome sequence of a chronic atrophic gastritis. *Helicobacter pylori* strain: evolution during disease progression. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 9999-10004, 2006.
- OHTA, T. The nearly neutral theory of molecular evolution. *Annual Review of Ecology and Systematics*, n. 23, p. 263-286, 1992.
- OLEKSYK, T. K.; ZHAO, K.; DE LA VEGA, F. M.; GILBERT, D. A.; O'BRIEN, S. J.; SMITH, M. W. Identifying selected regions from heterozygosity and divergence using a light-coverage genomic data set from two human populations. *PloS One*, p. e1712, 2008.
- OLIVA, A. Quanto mais teorias, melhor para a ciência? *Ciência Hoje*, n. 17, v. 99, p. 14-17, 1994.
- OLSON, M. V. When less is more: gene loss as an engine of evolutionary change. *American Journal of Human Genetics*, n. 64, p. 18-23, 1999.

- OPPERMAN, C. H. et al. Sequence and genetic map of *Meloidogyne hapla*: a compact nematode genome for plant parasitism. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 14802-14807, 2008.
- ORGAN, C. L.; SCHWEITZER, M. H.; ZHENG, W.; FREIMARK, L. M.; CANTLEY, L. C.; ASARA, J. M. Molecular phylogenetics of mastodon and *Tyrannosaurus rex*. *Science*, n. 320, p. 499, 2008.
- ORGEL, L. E. *As Origens da Vida*. Moléculas e Seleção Natural. Brasília: Editora da Universidade de Brasília, 1985.
- OTA, T.; SITNIKOVA, T.; NEI, M. Evolution of vertebrate immunoglobulin variable gene segments. *Current Topics in Microbiology and Immunology*, n. 248, p. 221-245, 2000.
- OTTENSOOSER, F. Cálculo do grau de mistura racial através dos grupos sanguíneos. *Revista Brasileira de Biologia*, n. 4, p. 531-537, 1944.
- PACHECO, J. A. F. Estamos sozinhos no universo? *Ciência Hoje*, n. 22 v. 130, p. 38-45, 1997.
- PAIN, A. et al. Genome of the host-cell transforming parasite *Theileria annulata* compared with *T. parva*. *Science*, n. 309, p. 131-133, 2005.
- PAIN, A. et al. The genome of the simian and human malaria parasite *Plasmodium knowlesi*. *Nature*, n. 455, p. 799-803, 2008.
- PAIXÃO-CÔRTES, V. R.; MEYER, D.; PEREIRA, T. V.; MAZIÈRES, S.; ELION, J.; KRISHNAMOORTHY, R.; ZAGO, M. A.; SILVA JR., W. A.; SALZANO, F. M.; BORTOLINI, M. C. Genetic variation among major human geographic groups supports a peculiar evolutionary trend in PAX9. *PLoS One*, n. 6, p. e15656, 2011.
- PÁL, C.; PAPP, B.; LERCHER, M. J. An integrated view of protein evolution. *Nature Reviews Genetics*, n. 7, p. 337-348, 2006.
- PALENIK, B. et al. Genome sequence of *Synechococcus* CC 9311: insights into adaptation to a coastal environment. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 13555-13559, 2006.
- PALENIK, B. et al. The tiny eukaryote *Ostreococcus* provides genomic insights into the paradox of plankton speciation. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 7705-7710, 2007.

- PALMENBERG, A. C.; SPIRO, D.; KUZMICKAS, R.; WANG, S.; DJIKENG, A.; RATHE, J. A.; FRASER-LIGGETT, C. M.; LIGGETT, S. B. Sequencing and analyses of all known human rhinovirus genomes reveal structure and evolution. *Science*, n. 324, p. 55-59, 2009.
- PAPAVERO, N. Fritz Muller e a comprovação da teoria de Darwin. In: DOMINGUES, H. M. B.; SÁ, M. R.; GLICK, T. (Org.). *A Recepção do Darwinismo no Brasil*. Rio de Janeiro: Editora Fiocruz, 2003. p. 29-44.
- PATERSON, A. H. et al. The *Sorghum bicolor* genome and the diversification of grasses. *Nature*, n. 457, p. 551-556, 2009.
- PATTERSON, N.; RICHTER, D. J.; GNERRE, S.; LANDER, E. S.; REICH, D. Genetic evidence for complex speciation of humans and chimpanzees. *Nature*, n. 441, p. 1103-1108, 2006.
- PAYNE, J. L. et al. Two-phase increase in the maximum size of life over 35 billion years reflects biological innovation and environmental opportunity. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 24-27, 2009.
- PAYSEUR, B. A.; CUTTER, A. D.; NACHMAN, M. W. Searching for evidence of positive selection in the human genome using patterns of microsatellite variability. *Molecular Biology and Evolution*, n. 19, p. 1143-1153, 2002.
- PENNISI, E. Speaking in tongues. *Science*, n. 303, p. 1321-1323, 2004.
- PEREIRA, T. V. et al. 2006. Natural selection and molecular evolution in Primate PAX9 gene, a major determinant of tooth development. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 5676-5681, 2006.
- PERTILLE, F.; PALUDO, E.; HERKENHOFF, M. E.; FONTEQUE, G. V.; FREITAS, L. B., SALZANO, F. M.; LIMA-ROSA, C. A. V. 2009. Variabilidade genética da região controladora do mtDNA (alça-D) de galinhas caipiras brasileiras. *Resumos, 55., Congresso Brasileiro de Genética*, 2009. Disponível em?: <www.sbg.org.br>. Acesso: 15 fev. 2011.
- PETTAY, J. C.; KRUNK, L. E. B.; JOKELA, J.; LUMMAA, V. Heritability and genetic constraints of life-history trait evolution in preindustrial humans. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 2838-2843, 2005.
- PHILLIPPE, H. et al. Phylogenomics revives traditional views on deep animal relationships. *Current Biology*, n. 19, p. 706-712, 2009.

- PICKRELL, J. K. et al. Signals of recent positive selection in a worldwide sample of human populations. *Genome Research*, n. 19, p. 826-837, 2009.
- PINTO JR., W. Diagnóstico pré-natal. In: MIR, L. (Org.). *Genômica*. São Paulo: Atheneu, 2004. p. 549-569.
- POPA, R. A sequential scenario for the origin of biological chirality. *Journal of Molecular Evolution*, n. 44, p. 121-127, 1997.
- POULTON, J.; KENNEDY, S.; OAKESHOTT, P.; WELLS, D. Prevenindo a transmissão de doenças do DNA mitochondrial herdadas da mãe. *BMJ*, Porto Alegre, n. 2, p. 165-179, 2009.
- POWELL, A.; SHENNAN, S.; THOMAS, M. G. Late Pleistocene demography and the appearance of modern human behavior. *Science*, n. 324, p. 1298-1301, 2009.
- PRABAKHAR, S.; NOONAN, J. P.; PÄÄBO, S.; RUBIN, E. M. Accelerated evolution of conserved noncoding sequences in humans. *Science*, n. 314, p. 786, 2006.
- PRABHAKAR, S.; NOONAN, J. P.; PÄÄBO, S.; RUBIN, E. M. Accelerated evolution of conserved noncoding sequences in humans. *Science*, n. 314, p. 786, 2006.
- PRENTISS, W. C.; CHATTERS, J. C. Cultural diversification and decimation in the prehistoric record. *Current Anthropology*, n. 44, p. 33-58, 2003.
- PRICE, A. L. et al. A genomewide admixture map for Latino populations. *American Journal of Human Genetics*, n. 80, p. 1024-1036, 2007.
- PRICE, D. H. *Atlas of World Cultures*. London: Sage, 1990.
- PRICE, D. H. Buying a piece of anthropology. Part 1: Human ecology and unwitting anthropological research for the CIA. *Anthropology Today*, n. 23, v.3, p. 8-13, 2007a.
- PRICE, D. H. Buying a piece of anthropology. Part 2: The CIA and our tortured past. *Anthropology Today*, n. 23, v. 5, p. 17-22, 2007b.
- PROVINE, W. B. *The Origins of Theoretical Population Genetics*. Chicago: University of Chicago Press, 1971.
- PROVINE, W. B. *Sewall Wright and Evolutionary Biology*. Chicago: University of Chicago Press, 1986.
- PUTNAM, N. H. et al. The amphioxus genome and the evolution of the chordate karyotype. *Nature*, n. 453, p. 1064-1071, 2008.
- PUTS, D. A.; JORDAN, C. L.; BREEDLOVE, S. M. O brother, where art thou? The fraternal birth-order effect on male sexual orientation. *Proceedings of the National Academy of Sciences USA*, n. 103, p. 10531-10532, 2006.

- QIRKO, H. The institutional maintenance of celibacy. *Current Anthropology*, n. 43, p. 321-329, 2002.
- QUACH, H. et al. Signatures of purifying and local positive selection in human miRNAs. *American Journal of Human Genetics*, n. 84, p. 316-327, 2009.
- RAMENSKY, V. E.; NURTDINOV; NEVEROV, A. D.; MIRONOV, A. A.; GELFAND, M. S. Positive selection in alternatively spliced exons of human genes. *American Journal of Human Genetics*, n. 83, p. 94-98, 2008.
- RANEA, J. A. G.; SILLERO, A.; THORNTON, J. M.; ORENGO, C. A. Protein superfamily evolution and the Last Universal Common Ancestor (LUCA). *Journal of Molecular Evolution*, n. 63, p. 513-525, 2006.
- RANNALA, B.; YANG, Z. Phylogenetic inference using whole genomes. *Annual Review of Genomics and Human Genetics*, n. 9, p. 17-31, 2008.
- RAOULT, D.; AUDIC, S.; ROBERT, C.; ABERGEL, C.; RENESTO, P.; OGATA, H.; SCOLA, B. L.; SUZAN, M.; CLAVERIE, J-M. The 1.2 megabase genome sequence of mimivirus. *Science*, n. 306, p. 1344-1350, 2004.
- RASKIN, S.; PETZL-ERLER, M. L.; PHILLIPS, J. A. III; PEREIRA-FERRARI, L.; PROBST, C. M.; FAUCZ, F. R.; SOTOMAYOR, V.; SALZANO, F. M.; CULPI, L. Cystic fibrosis gene variability in two southern Brazilian Amerindian populations: analysis of the ΔF508 mutation and the KM19 and XV2C haplotypes. *Human Biology*, n. 79, p. 79-91, 2007.
- RASMUSSEN, S.; CHEN, L.; DEAMER, D.; KRAKAUER, D. C.; PACKARD, N. H.; STADLER, P. F.; BEDAU, M. A. Transitions from nonliving to living matter. *Science*, n. 303, p. 963-965, 2004.
- RAT GENOME CONSORTIUM. Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, n. 428, p. 493-521, 2004.
- READ, T. D. et al. The genome sequence of *Bacillus anthracis* Ames and comparison to closely related bacteria. *Nature*, n. 423, p. 81-86, 2003.
- REDON, R. et al. Global variation in copy number in the human genome. *Nature*, n. 444, p. 444-454, 2006.
- REID, M.; MOHANDAS, N. Red blood cell group antigens: structure and function. *Seminars in Hematology*, n. 41, p. 93-117, 2004.
- RENO, M. L.; HELD, N. L.; FIELDS, C. J.; BURKE, P. V.; WHITAKER, R. J. Biogeography of the *Sulfolobus islandicus* pan-genome. *Proceedings of the National Academy of Sciences USA*, n. 106, p. 8605-8610, 2009.

- RHESUS GENOME CONSORTIUM. Evolutionary and biomedical insights from the Rhesus macaque genome. *Science*, n. 316, p. 222-234, 2007.
- RIBEIRO, B. G. *Suma Etnológica Brasileira*. v. 1. Petrópolis: Vozes e Financiadora de Estudos e Projetos, 1986.
- RIBEIRO, D. The culture-historical configurations of the American peoples. *Current Anthropology*, n. 11, p. 403-434, 1970.
- RICE, G.; TANG, L.; STEDMAN, K.; ROBERTO, F.; SPUHLER, J.; GILLITZER, E.; JOHNSON, J. E.; DOUGLAS, T.; YOUNG, M. The structure of a thermophilic archaeal virus shows a double-stranded DNA viral capsid type that spans all domains of life. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 7716-7720, 2004.
- RICHARDSON, A. O.; PALMER, J. D. Horizontal gene transfer in plants. *Journal of Experimental Botany*, n. 58, p. 1-9, 2007.
- RIDLEY, M. *Evolução*. 3. ed. Porto Alegre: Artmed, Porto Alegre, 2006.
- ROACH, J. C.; GLUSMAN, G.; ROWEN, L.; KAUR, A.; PURCELL, M. K.; SMITH, K. D.; HOOD, L. E.; ADEREM, A. The evolution of vertebrate Toll-like receptors. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 9577-9582, 2005.
- ROBINSON, R. Jump-starting a cellular world: investigating the origin of life, from soup to networks. *Plos Biology*, n. 3, p. 1860-1863, 2005.
- RODRIGUES, A. D. Sobre as línguas indígenas e sua pesquisa no Brasil. *Ciência e Cultura*, n. 57, p. 35-38, 2005.
- RODRÍGUEZ-TRELLES, F.; TARRÍO, R.; AYALA, F. J. Convergent neofunctionalization by positive Darwinian selection after ancient recurrent duplication of the *xanthine dehydrogenase* gene. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 13413-13417, 2003.
- ROGERS, D. S.; EHRLICH, P. R. Natural selection and cultural rates of change. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 3416-3420, 2008.
- ROGERS, J. The finished genome sequence of *Homo sapiens*. *Cold Spring Harbor Symposia on Quantitative Biology*, n. 68, p. 1-11, 2003.
- ROSE, M. R. *Darwin's Spectre*. Evolutionary Biology in the Modern World. Princeton: Princeton University Press, 1998.

- ROY, S. W.; FEDOROV, A.; GILBERT, W. The signal of ancient introns is obscured by intron density and homolog number. *Proceedings of the National Academy of Sciences*, USA, n. 99, p. 15513-15517, 2002.
- RUMPHO, M. E.; WORFUL, J. M.; LEE, J.; KANNAN, K.; TYLER, M. S.; BHATTACHARYA, D.; MOUSTAFA, A.; MANHART, J. R. Horizontal gene transfer of the algal nuclear gene *psbO* to the photosynthetic sea slug *Elysia chlorotica*. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 17867-17871, 2008.
- RUSE, M. *Levando Darwin a Sério*. Uma Abordagem Naturalística da Filosofia. Belo Horizonte: Itatiaia, 1995.
- SABBAGH, A.; DARLU, P.; CRONAU-ROY, B.; POLONI, E. S. Arylamine N-Acetyltransferase 2 (*NAT2*) genetic diversity and traditional subsistence: a worldwide population survey. *PLoS One*, n. 6, p. e18507, 2011.
- SABETI, P. C. ET AL; THE INTERNATIONAL HAPMAP CONSORTIUM. Genome-wide detection and characterization of positive selection in human populations. *Nature*, n. 449, p. 913-918, 2007.
- SABETI, P. C. et al. Detecting recent positive selection in the human genome from haplotype structure. *Nature*, n. 419, p. 832-837, 2002.
- SABETI, P. C.; SCHAFFNER, S. F.; FRY, B.; LOHMUELLER, J.; VARILLY, P.; SHAMOVSKY, O.; PALMA, A.; MIKKELSEN, T. S.; ALTSHULER, D.; LANDER, E. S. Positive natural selection in the human lineage. *Science*, n. 312, p. 1614-1620, 2006.
- SACCONI, C.; PESOLE, G. *Handbook of Comparative Genomics*. Principles and Methodology. Hoboken: Wiley-Liss, 2003.
- SAITOU, N.; YAMAMOTO, F-I. Evolution of primate ABO blood group genes and their homologous genes. *Molecular Biology and Evolution*, n. 14, p. 399-411, 1997.
- SAKAGUCHI, Y.; HAYASHI, T.; KUROKAWA, K.; NAKAYAMA, K.; OSHIMA, K.; FUJINAGA, Y.; OHMSHI, M.; OHTSUBO, E.; HATTORI, M.; OGUMA, K. The genome sequence of *Clostridium botulinum* type C neurotoxin-converting phage and the molecular mechanisms of unstable lysogeny. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 17472-17477, 2005.

- SALMINEN, M. Detecting recombination in viral sequences. In: SALEMI, M.; VANDAMME, A-M. (Eds.). *The Phylogenetic Handbook. A Practical Approach to DNA and Protein Phylogeny*. Cambridge: Cambridge University Press, 2003. p. 348-377.
- SALTHE, S. N. *Evolving Hierarchical Systems. Their Structure and Representation*. Nova York: Columbia University Press, 1985.
- SALZANO, F. M. Genetic aspects of the demography of American Indians and Eskimos. In: HARRISON, G. A.; BOYCE, A. J. (Eds.). *The Structure of Human Populations*. Oxford: Clarendon Press, 1972. p. 234-251.
- SALZANO, F. M. *History of Human Biology in Brazil*. Newcastle Upon Tyne: International Association of Human Biologists, 1990.
- SALZANO, F. M. History and development of human genetics in Brazil. In: Dronamraju, K.R. (Ed.). *The History and Development of Human Genetics. Progress in Different Countries*. Singapore: World Scientific, 1992. p. 228-255.
- SALZANO, F. M. *Biologia, Cultura e Evolução*. 2. ed. Porto Alegre: Editora da Universidade Federal do Rio Grande do Sul, 1993.
- SALZANO, F. M. Brazil. In: SPENCER, F. (Ed.) *History of Physical Anthropology*. v. 1. Nova York: Garland, 1997. p. 207-213.
- SALZANO, F. M. Interethnic variability and admixture in Latin America – social implications. *Revista de Biologia Tropical*, n. 52, p. 405-415, 2004.
- SALZANO, F. M. Evolutionary change – patterns and processes. *Anais da Academia Brasileira de Ciências*, n. 77, p. 627-650, 2005.
- SALZANO, F. M. The prehistoric colonization of the Americas. In: CRAWFORD, M. H. (Ed.). *Anthropological Genetics. Theory, Methods and Applications*. Cambridge: Cambridge University Press, 2007. p. 433-455.
- SALZANO, F. M. Genomics and evolution – a personal appraisal. *Cytogenetic and Genome Research*, n. 128, p. 99-104, 2010.
- SALZANO, F. M. The prehistoric colonization of the Americas: evidences and models. Evolution: *Education and Outreach*, 2011 (Submetido).
- SALZANO, F. M.; CALLEGARI-JACQUES, S. M. *South American Indians. A Case Study in Evolution*. Oxford: Clarendon Press, 1988.
- SALZANO, F. M.; CALLEGARI-JACQUES, S. M. Amerindian and non-Amerindian autosome molecular variability – a test analysis. *Genetica*, n. 126, p. 237-242, 2006.

- SALZANO, F. M.; HUTZ, M. H.; SALAMONI, S. P.; ROHR, P.; CALLEGARI-JACQUES, S. M. Genetic support for proposed patterns of relationship among Lowland South American languages. *Current Anthropology*, n. 46 (Suppl.), p. S121-S129, 2005.
- SANDERSON, M. J. Phylogenetic signal in the eukaryotic tree of life. *Science*, n. 321, p. 121-123, 2008.
- SANGER, F.; NICKLEN, S.; COULSON, A. R. DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences*, USA, n. 74, p. 5463-5467, 1977.
- SANJUÁN, R.; ELENA, S. F. Epistasis correlates to genomic complexity. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 14402-14405, 2006.
- SANJUR, O. I.; PIPERNO, D. R.; ANDRES, T. C.; WESSEL-BEAVER, L. Phylogenetic relationships among domesticated and wild species of *Cucurbita* (Cucurbitaceae) inferred from a mitochondrial gene: implications for crop plant evolution and areas of origin. *Proceedings of the National Academy of Sciences*, USA, n. 99, p. 535-540, 2002.
- SANS, M.; MERRIWETHER, D. A.; HIDALGO, P.C.; BENTANCOUR, N.; WEIMER, T. A.; FRANCO, M. H. L. P.; ALVAREZ, I.; KEMP, B. M.; SALZANO, F. M. Population structure and admixture in Cerro Largo, Uruguay, based on blood markers and mitochondrial DNA polymorphisms. *American Journal of Human Biology*, n. 18, p. 513-524, 2006.
- SANTOS, R. V.; FRY, P. H.; MONTEIRO, S.; MAIO, M. C.; RODRIGUES, J. C.; BASTOS-RODRIGUES, L.; PENA, S. D. J. Color, race, and genomic ancestry in Brazil. Dialogues between anthropology and genetics. *Current Anthropology*, n. 50, p. 787-819, 2009a.
- SANTOS, S. E. B.; RIBEIRO-RODRIGUES, E. M.; RIBEIRO-DOS-SANTOS, A. K. C.; HUTZ, M. H.; TOVO-RODRIGUES, L.; SALZANO, F. M.; CALLEGARI-JACQUES, S. M. Autosomal STR analyses in Native Amazonian tribes suggest a population structure driven by isolation by distance. *Human Biology*, n. 81, p. 71-88, 2009b.

- SCHERER, N. M.; THOMPSON, C. E.; FREITAS, L. B.; BONATTO, S. L.; SALZANO, F. M. Patterns of molecular evolution in pathogenesis-related proteins. *Genetics and Molecular Biology*, n. 28, p. 645-653, 2005.
- SCHIMMEL, P.; POUPLANA, L. R. Genetic code origins: experiments confirm phylogenetic predictions and may explain a puzzle. *Proceedings of the National Academy of Sciences*, USA, n. 96, p. 327-328, 1999.
- SCHISTOSOMA JAPONICUM GENOME SEQUENCING AND FUNCTIONAL ANALYSIS CONSORTIUM.** The *Schistosoma japonicum* genome reveals features of host-parasite interplay. *Nature*, n. 460, p. 345-351, 2009.
- SCHMITT, R.; BONATTO, S. L.; FREITAS, L. B.; MUSCHNER, V. C.; HILL, K.; HURTADO, A. M.; SALZANO, F. M. Extremely limited mitochondrial DNA variability among the Aché natives of Paraguay. *Annals of Human Biology*, n. 31, p. 87-94, 2004.
- SCHOPF, J. W.; KUDRYAVTSEV, A. B.; AGRESTI, D. G.; WDOWLAK, T. J.; CZAJA, A. D. Laser-Raman imagery of earth's earliest fossils. *Nature*, n. 416, p. 73-76, 2002.
- SCHUELER, M. G.; DUNN, J. M.; BIRD, C. P.; ROSS, M. T.; VIGGIANO, L.; NISC COMPARATIVE SEQUENCING PROGRAM; ROCCHI, M.; WILLARD, H. F.; GREEN, E. D. Progressive proximal expansion of the primate X chromosome centromere. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 10563-10568, 2005.
- SCOTT, K. M. et al. The genome of deep-sea vent chemolithoautotroph *Thiomicrospira crunogena* XCL-2. *PLoS Biology*, n. 4, p. 2196-2212, 2006.
- SEAR, R.; MACE, R.; MCGREGOR, T. A. Maternal grandmothers improve nutritional status and survival of children in rural Gambia. *Proceedings of the Royal Society of London*, n. B267, p. 1641-1647, 2000.
- SEIXAS, S.; FERRAND, N.; ROCHA, J. Microsatellite variation and evolution of the human Duffy blood group polymorphism. *Molecular Biology and Evolution*, n. 19, p. 1802-1806, 2002.
- SELL, A.; TOOBY, J.; COSMIDES, L. Formidability and the logic of human anger. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 15073-15078, 2009.

- SELLA, G.; ARDELL, D. H. The coevolution of genes and genetic codes: Crick's frozen accident revisited. *Journal of Molecular Evolution*, n. 63, p. 297-313, 2006.
- SELTSAM, A.; HALLENSLEBEN, M.; KOLLMANN, A.; BLASCZYK, R. The nature of diversity and diversification at the ABO locus. *Blood*, n. 102, p. 3035-3042, 2003.
- SÉMON, M.; DURET, L. Evidence that functional transcription units cover at least half of the human genome. *Trends in Genetics*, n. 20, p. 229-232, 2004.
- SESHADRI, R. et al. 2004. Comparison of the genome of the oral pathogen *Treponema denticola* with other spirochete genomes. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 5646-5651.
- SHANAHAN, T. *The Evolution of Darwinism. Selection, Adaptation, and Progress in Evolutionary Biology*. Cambridge: Cambridge University Press, 2004.
- SHARAN, R.; SUTHRAM, S.; KELLEY, R. M.; KUHN, T.; MCCUINE, S.; UETZ, P.; SITTLER, T.; KARP, R. M.; IDEKER, T. Conserved patterns of protein interaction in multiple species. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 1974-1979, 2005.
- SHARP, A. J. et al. 2005. Segmental duplications and copy-number variation in the human genome. *American Journal of Human Genetics*, n. 77, p. 78-88.
- SHEN, J.; KELLEHER, R. J. III. The presenilin hypothesis of Alzheimer's disease: evidence for a loss-of-function pathogenic mechanism. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 403-409, 2007.
- SHENNAN, S. Population, culture history, and the dynamics of culture change. *Current Anthropology*, n. 41, p. 811-835, 2000.
- SHERMER, M. The demon of determinism. *Science*, n. 300, p. 56-57, 2003.
- SHI, P.; BAKEWELL, M. A.; ZHANG, J. Did brain-specific genes evolve faster in humans than in chimpanzees? *Trends in Genetics*, n. 22, p. 608-613, 2006.
- SHI, T.; FALKOWSKI, P. G. Genome evolution in cyanobacteria: the stable core and the variable shell. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 2510-2515, 2008.
- SHOLTIS, S. J.; NOONAN, J. P. Gene regulation and the origins of human biological uniqueness. *Trends in Genetics*, n. 26, p. 110-118, 2010.
- SHRADER-FRECHETTE, K. Etica y medio ambiente. *Foro Mundial de la Salud*, n. 12, p. 329-339, 1991.

- SHRIVER, M. D.; KENNEDY, G. C.; PARRA, E. J.; LAWSON, H. A.; SONPAR, V.; HUANG, J.; AKEY, J. M.; JONES, K. W. The genomic distribution of population substructure in four populations using 8525 autosomal SNPs. *Human Genomics*, n. 1, p. 274-286, 2004.
- SICKMANN, A. et al. The proteome of *Saccharomyces cerevisiae* mitocondria. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 13207-13212, 2003.
- SIEPEL, A. Phylogenomics of primates and their ancestral populations. *Genome Research*, n. 19, p. 1929-1941, 2009.
- SIGMUND, K. Sympathy and similarity: the evolutionary dynamics of cooperation. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 8405-8406, 2009.
- SILVA, N. V. Uma nota sobre “raça social” no Brasil. *Estudos Afro-Asiáticos*, n. 26, p. 67-80, 1994.
- SIMPSON, G. G. *O Significado da Evolução*. São Paulo: Pioneira, 1962.
- SMALL, K. S.; BRUDNO, M.; HILL, M. M.; SIDOW, A. Extreme genomic variation in a natural population. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 5698-5703, 2007.
- SMITH, B. D.; YARNELL, R. A. Initial formation of an indigenous crop complex in eastern North America at 3800 B.P. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 6561-6566, 2009.
- SNEL, B.; HUYNEN, M. A.; DUTILH, B. E. Genome trees and the nature of genome evolution. *Annual Review of Microbiology*, n. 59, p. 191-209, 2005.
- SOLTIS, D. E.; MOORE, M. J.; BURLEIGH, G.; SOLTIS, P. S. Molecular markers and concepts of plant evolutionary relationships: progress, promise, and future prospects. *Critical Reviews in Plant Science*, n. 28, p. 1-15, 2009.
- SOMEL, M. et al. Transcriptional neoteny in the human brain. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 5743-5748, 2009.
- SOSIS, R.; ALCORTA, C. Signaling, solidarity, and the sacred: the evolution of religious behavior. *Evolutionary Anthropology*, n. 12, p. 264-274, 2003.
- SOUZA, V. A. U. F.; SALZANO, F. M.; PETZL-ERLER, M. L.; NASCIMENTO, M. C.; MAYAUD, P.; BORGES, J. D.; PANNUTI, C. S. Variations in human Herpesvirus Type 8 seroprevalence in Native Americans, South America. *Emerging Infectious Diseases*, n. 16, p. 1003-1006, 2010.

- SPENCER, C. S. Territorial expansion and primary state formation. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 7119-7126, 2010.
- SRIVASTAVA, M. et al. The *Amphimedon queenslandica* genome and the evolution of animal complexity. *Nature*, n. 466, p. 720-726, 2010.
- STAJICH, J. E.; HAHN, M. W. 2005. Disentangling the effects of demography and selection in human history. *Molecular Biology and Evolution*, n. 22, p. 63-73.
- STEARNS, S. C.; KOELLA, J. C. Evolution in Health and Disease. Oxford: Oxford University Press, 2008.
- STEDMAN, H. H.; KOZYAK, B. W.; NELSON, A.; THESLER, D. M.; SU, L. T.; LOW, D. W.; BRIDGES, C. R.; SHRAGER, J. B.; MINUGH-PURVIS, N.; MITCHELL, M. A. Myosin gene mutation correlates with anatomical changes in the human lineage. *Nature*, n. 428, p. 415-418, 2004.
- STEENKAMP, E. T.; WRIGHT, J.; BALDAUF, S. L. The protistan origins of animals and fungi. *Molecular Biology and Evolution*, n. 23, p. 93-106, 2006.
- STEIL, C. A. Cotas Raciais na Universidade. Um Debate. Porto Alegre: Editora da Universidade Federal do Rio Grande do Sul, 2006.
- STEIN, L. D. et al. The genome sequence of *Caenorhabditis briggsae*: a platform for comparative genomics. *PloS Biology*, n. 1, p. 166-192, 2003.
- STEPHENS, J. C. et al. Dating the origin of the CCR5-Δ32 AIDS-resistance allele by the coalescence of haplotypes. *American Journal of Human Genetics*, n. 62, p. 1507-1515, 1998.
- STINEAR, T. P. et al. Insights from the complete genome sequence of *Mycobacterium marinum* on the evolution of *Mycobacterium tuberculosis*. *Genome Research*, n. 18, p. 729-741, 2008.
- STORZ, J. F.; PAYSEUR, B. A.; NACHMAN, M. W. Genome scans of DNA variability in humans reveal evidence for selective sweeps outside of Africa. *Molecular Biology and Evolution*, n. 21, p. 1800-1811, 2004.
- STUMPF, M. P. H.; THORNE, T.; SILVA, E.; STEWART, R.; AN, H. J.; LAPPE, M.; WIUF, C. Estimating the size of the human interactome. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 6959-6964, 2008.
- SUAREZ-KURTZ, G.; VARGENS, D. D.; STRUCHINER, C. J.; BASTOS-RODRIGUES, L.; PENA, S. D. J. Self-reported skin color, skin color, genomic ancestry and the distribution of GST polymorphisms. *Pharmacogenetics and Genomics*, n. 17, p. 765-771, 2007.

- SUDMANT, P. H. et al. Diversity of copy number variation and multicopy genes. *Science*, n. 330, p. 641-646, 2010.
- SUERBAUM, S. et al. The complete genome sequence of the carcinogenic bacterium *Helicobacter hepaticus*. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 7901-7906, 2003.
- SUHRE, K.; AUDIC, S.; CLAVERIE, J-M. Mimivirus gene promoters exhibit an unprecedented conservation among all eukaryotes. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 14689-14693, 2005.
- SWINGLEY, W. D. et al. Niche adaptation and genome expansion in the chlorophyll d-producing cyanobacterium *Acaryochloris marina*. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 2005-2010, 2008.
- SZABÓ, P.; SCHEURING, I.; CZÁRÁN, T.; SZATHMÁRY, E. *In silico* simulations reveal that replicators with limited dispersal evolve towards higher efficiency and fidelity. *Nature*, n. 420, p. 340-343, 2002.
- TAKAI, D.; JONES, P. A. 2002. Comprehensive analysis of CpG islands in human chromosomes 21 and 22. *Proceedings of the National Academy of Sciences*, USA, n. 99, p. 3740-3745.
- TANG, K.; THORNTON, K. R.; STONEKING, M. A new approach for using genome scans to detect recent positive selection in the human genome. *PloS Biology*, n. 5, p. e171, 2007.
- TAYLOR, W. R. A molecular model for the origin of protein translation in an RNA world. *Journal of Theoretical Biology*, 243, p. 393-406, 2006.
- TËMKIN, I.; ELDREDGE, N. Phylogenetics and material cultural evolution. *Current Anthropology*, n. 48, p. 146-153, 2007.
- TETTELIN, H.; RILEY, D.; CATTUTO, C.; MEDINI, D. Comparative genomics: the bacterial pan-genome. *Current Opinion in Microbiology*, n. 12, p. 472-477, 2008.
- Tettelin, H. et al. Genome analysis of multiple pathogenic isolates of *Streptococcus agalactiae*: implications for the microbial “pan-genome”. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 13950-13955, 2005.
- THE 1,000 GENOMES PROJECT CONSORTIUM. A map of human genome variation from population-scale sequencing. *Nature*, n. 467, p. 1061-1073, 2010.
- THOMAS, J. A.; WELCH, J. J.; WOOLFITT, M.; BROMHAM, L. There is no universal molecular clock for invertebrates, but rate variation does not scale with body size.

Proceedings of the National Academy of Sciences, USA, n. 103, p. 7366-7371, 2006.

- THOMPSON, C. E.; FERNANDES, C. L.; SOUZA, O. N.; FREITAS, L. B.; SALZANO, F. M. Evaluation of the impact of functional diversification on Poaceae, Brassicaceae, Fabaceae, and Pinaceae alcohol dehydrogenase enzymes. *Journal of Molecular Modeling*, n. 16, p. 919-928, 2010.
- TIAN, F.; STEVENS, N. M.; BUCKLER, E. S. IV. Tracking footprints of maize domestication and evidence for a massive selective sweep on chromosome 10. *Proceedings of the National Academy of Sciences*, USA, n. 106 (Suppl. 1), p. 9979-9986, 2009.
- TISHKOFF, S. A.; GONDER, M. K. Human origins within and out of Africa. In: CRAWFORD, M. H. (Ed.). *Anthropological Genetics. Theory, Methods and Applications*. Cambridge: Cambridge University Press, 2007. p. 337-379.
- TOCCHINI-VALENTINI, G. D.; FRUSCOLONI, P.; TOCCHINI-VALENTINI, G. P. Structure, function, and evolution of the tRNA endonucleases of Archaea: an example of subfunctionalization. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 8933-8938, 2005.
- TODD, P. M.; PENKE, L.; FASOLO, B.; LENTON, A. P. Different cognitive processes underlie human mate choices and mate preferences. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 15011-15016, 2007.
- TOURNAMILLE, C.; BLANCHER, A.; LE VAN KIM, C.; GANE, P.; APOIL, P. A.; NAKAMOTO, W.; CARTRON, J. P.; COLIN, Y. Sequence, evolution and ligand binding properties of mammalian Duffy antigen/receptor for chemokines. *Immunogenetics*, n. 55, p. 682-694, 2004.
- TOURNAMILLE, C.; COLIN, Y.; CARTRON, J. P.; LE VAN KIM, C. Disruption of a GATA motif in the Duffy gene promoter abolishes erythroid gene expression in Duffy-negative individuals. *Nature Genetics*, n. 10, p. 224-228, 1995.
- TOVO-RODRIGUES, L.; CALLEGARI-JACQUES, S. M.; PETZL-ERLER, M. L.; TSUNETO, L. T.; SALZANO, F. M.; HUTZ, M. H. 2010. Dopamine Receptor D4 allele distribution in Amerindians: a reflection of past behavior differences? *American Journal of Physical Anthropology*, n. 143, p. 458-464.
- TRIBOLIUM GENOME SEQUENCING CONSORTIUM. The genome of the model beetle and pest *Tribolium castaneum*. *Nature*, n. 452, p. 949-955, 2008.

- TRINKAUS, E.; SHIPMAN, P. *The Neanderthals*. Of Skeletons, Scientists, and Scandal. Nova York: Vintage Books, 1994.
- TRINKS, H.; SCHRÖDER, W.; BIEBRICHER, C. K. Ice and the origin of life. *Origins of Life and Evolution of the Biosphere*, n. 35, p. 429-445, 2005.
- TUZUN, E. et al. Fine-scale structural variation of the human genome. *Nature Genetics*, n. 37, p. 727-732, 2005.
- UDDIN, M.; GOODMAN, M.; EREZ, O.; ROMERO, R.; LIU, G.; ISLAM, M.; OPAZO, J. C.; SHERWOOD, C. C.; GROSSMAN, L. I.; WILDMAN, D. E. Distinct genomic signatures of adaptation in pre- and postnatal environments during human evolution. *Proceedings of the National Academy of Sciences*, USA, n. 105, p. 3215-3220, 2008.
- UEDA, H. R.; HAYASHI, S.; MATSUYAMA, S.; YOMO, T.; HASHIMOTO, S.; KAY, S. A.; Hogenesch, J. B.; IINO, M. Universality and flexibility in gene expression from bacteria to human. *Proceedings of the National Academy of Sciences*, USA, n. 101, p. 3765-3769, 2004.
- UPTON, C.; LEFKOWITZ, E. J. Comparative genomics of viruses using bioinformatics tools. In: BROWN, J. R. (Ed.). *Comparative Genomics*. Basic and Applied Research. Boca Raton: CRC Press, 2008. p. 49-72.
- VALENTE, A. X. C. N.; ROBERTS, S. B.; BUCK, G. A.; GAO, Y. Functional organization of the yeast proteome by a yeast interactome map. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 1490-1495, 2009.
- VAN DE GUCHTE, M. et al. The complete genome sequence of *Lactobacillus bulgaricus* reveals extensive and ongoing reductive evolution. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 9274-9279, 2006.
- VAN DISHOECK, E. F. Chemistry in low-mass protostellar and protoplanetary regions. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 12249-12256, 2006.
- VARGAS, A. E.; MARRERO, A. R.; SALZANO, F. M.; BORTOLINI, M. C.; CHIES, J. A. B. Frequency of CCR5 Δ 32 in Brazilian populations. *Brazilian Journal of Medical and Biological Research*, n. 39, p. 321-325, 2006.
- VARKI, A.; GESCHWIND, D. H.; EICHLER, E. E. Explaining human uniqueness: genome interactions with environment, behaviour and culture. *Nature Reviews Genetics*, n. 9, p. 749-763, 2008.

- VELLAI, T.; VIDA, G. The origin of eukaryotes: the difference between prokaryotic and eukaryotic cells. *Proceedings of the Royal Society London Series B*, n. 266, p. 1571-1577, 1999.
- VENDRUSCOLO, M.; DOBSON, C. M. A glimpse at the organization of the protein universe. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 5641-5642, 2005.
- VETSIGIAN, K.; WOESE, C.; GOLDENFELD, N. Collective evolution and the genetic code. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 10696-10701, 2006.
- VETSIGIAN, K.; GOLDENFELD. Genome rhetoric and the emergence of compositional bias. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 215-220, 2009.
- VIBRANOVSKI, M. D.; SAKABE, N. J.; OLIVEIRA, R. S.; SOUZA, S. J. Signs of ancient and modern exon-shuffling are correlated to the distribution of ancient and modern domains along proteins. *Journal of Molecular Evolution*, n. 61, p. 341-350, 2005.
- VICOSO, B.; CHARLESWORTH, B. Evolution on the X chromosome: unusual patterns and processes. *Nature Reviews Genetics*, n. 7, p. 645-653, 2006.
- VIEIRA, C. L. Computador de DNA. Entrevista com E. Shapiro. *Ciência Hoje*, n. 35, v. 206, p. 8-12, 2004.
- VIEYRA, A.; SOUZA-BARROS, F.; FERREIRA, R. Evolução molecular da vida. In: NUSSENZVEIG, H. M. *Complexidade e Caos*. Rio de Janeiro: Editora da Universidade Federal do Rio de Janeiro/COPEA, 2003. p. 258-276.
- VINOGRADOV, A. E. Evolution of genome size: multilevel selection, mutation bias or dynamical chaos? *Current Opinion in Genetics; Development*, n. 14, p. 620-626, 2004.
- VINOGRADOV, S. N.; HOOGEWIJS, D.; BAILLY, X.; ARREDONDO-PETER, R.; GUERTIN, M.; GOUGH, J.; DEWILDE, S.; MOENS, L.; VANFLETEREN, J. R. Three globin lineages belonging to two structural classes in genomes from the three kingdoms of life. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 11385-11389, 2005.
- VOIGHT, B. F.; KUDARAVALLI, S.; WEN, X.; PRITCHARD, J. K. A map of recent positive selection in the human genome. *PloS Biology*, n. 4, p. 446-458, 2006.

- VOLTAIRE (AROUET, F. M.) 1759 (tradução 1998). *Cândido ou o Otimismo*. Porto Alegre: L&PM Editores, 1998.
- WALL, J. D.; LOHMUELLER, K. E.; PLAGNOL, V. Detecting ancient admixture and estimating demographic parameters in multiple human populations. *Molecular Biology and Evolution*, n. 26, p. 1823-1827, 2009.
- WALLACE, D. C. A mitochondrial paradigm of metabolic and degenerative diseases, aging, and cancer: a dawn for evolutionary medicine. *Annual Review of Genetics*, n. 39, p. 359-407, 2005.
- WALLACE, D. C. Why do we still have a maternally inherited mitochondrial DNA? Insights from evolutionary medicine. *Annual Review of Biochemistry*, n. 76, p. 781-821, 2007.
- WANG, E. T.; KODAMA, G.; BALDI, P.; MOYZIS, R. K. Global landscape of recent inferred Darwinian selection for *Homo sapiens*. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 135-140, 2006.
- WANG, S. et al. Genetic variation and population structure in Native Americans. *PLoS Genetics*, n. 3, p. 2049-2067, 2007.
- WANG, X.; GRUS, W. E.; ZHANG, J. Gene losses during human origins. *PLoS Biology*, n. 4, p. 366-377, 2006.
- WARREN, W. C. et al. Genome analysis of the platypus reveals unique signatures of evolution. *Nature*, n. 453, p. 175-183, 2008.
- WATERS, E. et al. The genome of *Nanoarchaeum equitans*: insights into early archaeal evolution and derived parasitism. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 12984-12988, 2003.
- WATERSTON, R. H.; LANDER, E. S.; SULSTON, J. E. On the sequencing of the human genome. *Proceedings of the National Academy of Sciences*, USA, n. 99, p. 3712-3716, 2002.
- WATERSTON, R. H.; LANDER, E. S.; SULSTON, J. E. More on the sequencing of the human genome. *Proceedings of the National Academy of Sciences*, USA, n. 100, p. 3022-3024, 2003.
- WATSON, J. D.; CRICK, F. H. C. Molecular structure of nucleic acids. A structure for deoxyribose nucleic acid. *Nature*, n. 171, p. 737-738, 1953.

- WATTS, J. M.; DANG, K. K.; GORELICK, R. J.; LEONARD, C. W.; BESS JR., J. W.; SWANSTROM, R.; BURCH, C. L.; WEEKS, K. M. Architecture and secondary structure of an entire HIV-1 RNA genome. *Nature*, n. 460, p. 711-716, 2009.
- WEAVER, T. D.; ROSEMAN, C. C. Ancient DNA, late Neanderthal survival, and modern-human-Neandertal genetic admixture. *Current Anthropology*, n. 46, p. 677-683, 2005.
- WEAVER, T. D.; STEUDEL-NUMBERS. Does climate or mobility explain the differences in body proportions between Neanderthals and their Upper Paleolithic successors? *Evolutionary Anthropology*, n. 14, p. 218-223, 2005.
- WEBSTER, M. A.; KAPING, D.; MIZOKAMI, Y.; DUHAMEL, P. Adaptation to natural facial categories. *Nature*, n. 428, p. 557-561, 2004.
- WEIGMANN, K. The code, the text and the language of God. *EMBO Reports*, n. 5, p. 116-118, 2004.
- WEIR, B. S.; CARDON, R. L.; ANDERSON, A. D.; NIELSEN, D. M.; HILL, W. G. Measures of human population structure show heterogeneity among genomic regions. *Genome Research*, n. 15, p. 1468-1476, 2005.
- WEISS, K. M.; KURLAND, J. A. Going on an antedate. A strange history of imperfect perfect proportions. *Evolutionary Anthropology*, n. 16, p. 204-209, 2007.
- WHITE JR., L. The historical roots of our ecological crisis. *Science*, n. 155, p. 1203-1207, 1967.
- WHITE, T. Early hominids – diversity or distortion? *Science*, n. 299, p. 1994-1997, 2003.
- WILKINS, M. H. F.; STOKES, A. R.; WILSON, H. R. Molecular structure of deoxypentose nucleic acids. *Nature*, n. 171, p. 738-740, 1953.
- WILLIAMS, B. A. P.; SLAMOVITS, C. H.; PATRON, N. J.; FAST, N. M.; KEELING, P. J. A high frequency of overlapping gene expression in compacted eukaryotic genomes. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 10936-10941, 2005.
- WILLIAMSON, S. H.; HUBISZ, M. J.; CLARK, A. G.; PAYSEUR, B. A.; BUSTAMANTE, C. D.; NIELSEN, R. Localizing recent adaptive evolution in the human genome. *PloS Genetics*, n. 3, p. e90, 2007.
- WILSON, E. O. *On Human Nature*. Cambridge (MA): Harvard University Press, 1978.

- WILSON, E. O. *Da Natureza Humana*. São Paulo: T.A. Queiroz e Editora da Universidade de São Paulo, 1981.
- WILSON, W. H. et al. Complete genome sequence and lytic phase transcription profile of a *Coccolithovirus*. *Science*, n. 309, p. 1090-1092, 2005.
- WOESE, C. The universal ancestor. *Proceedings of the National Academy of Sciences*, USA, n. 95, p. 6854-6859, 1998.
- WOLF, Y. I.; NOVICKHOV, P. S.; KAREV, G. P.; KOONIN, E. V.; LIPMAN, D. J. The universal distribution of evolutionary rates of genes and distinct characteristics of eukaryotic genes of different apparent ages. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 7273-7280, 2009.
- WONG, K. K. et al. A comprehensive analysis of common copy-number variations in the human genome. *American Journal of Human Genetics*, n. 80, p. 91-104, 2007.
- WOO, P. C. Y. et al. The complete genome and proteome of *Laribacter hongkongensis* reveal potential mechanisms for adaptations to different temperatures and habitats. *PLoS Genetics*, n. 5, p. e1000416, 2009.
- WOOD, V. et al. The genome sequence of *Schizosaccharomyces pombe*. *Nature*, n. 415, p. 871-880, 2002.
- WRANGHAM, R.; CARMODY, R. Human adaptation to the control of fire. *Evolutionary Anthropology*, n. 19, p. 187-199, 2010.
- WU, G. A.; JUN, S-R.; SIMS, G. E.; KIM, S-H. Whole- proteome phylogeny of large dsDNA virus families by an alignment-free method. *Proceedings of the National Academy of Sciences*, USA, n. 106, p. 12826-12831, 2009.
- XIA, Q. et al. A draft sequence of the genome of the domesticated silkworm (*Bombyx mori*). *Science*, n. 306, p. 1937-1940, 2004.
- XIE, X.; MIKKELSEN, T. S.; GNIRKE, A.; LINDBLAD-TOH, K.; KELLIS, M.; LANDER, E. S. Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 7145-7150, 2007.
- XU, J.; BJURSELL, M. K.; HIMROD, J.; DENG, S.; CARMICHAEL, L. K.; CHIANG, H. C.; HOOPER, L. V. A genomic view of the human-*Bacteroides thetaiotaomicron* symbiosis. *Science*, n. 299, p. 2074-2076, 2003.
- XU, J. et al. Dandruff-associated *Malassezia* genomes reveal convergent and divergent virulence traits shared with plant and human fungal pathogens. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 18730-18735, 2007.

- XU, P. et al. The genome of *Cryptosporidium hominis*. *Nature*, n. 431, p. 1107-1112, 2004.
- XUE, Y. et al. Population differentiation as an indicator of recent positive selection in humans: an empirical evaluation. *Genetics*, n. 183, p. 1065-1077, 2009.
- YANG, J.; LUSK, R.; LI, W-H. Organismal complexity, protein complexity, and gene duplicability. *Proceedings of the National Academy of Sciences*, USA, n. 100, p'. 15661-15665, 2003.
- YANG, S.; DOOLITTLE, R. F.; BOURNE, P. E. Phylogeny determined by protein domain content. *Proceedings of the National Academy of Sciences*, USA, n. 102, p. 373-378, 2005.
- YARUS, M.; CAPORASO, G.; KNIGHT, R. Origins of the genetic code: the escaped triplet theory. *Annual Review of Biochemistry*, n. 74, p. 179-198, 2005.
- YNGVADOTTIR, B.; XUE, Y.; SEARLE, S.; HUNT, S.; DELGADO, M.; MORRISON, J.; WHITTAKER, P.; DELOUKAS, P.; TYLER-SMITH, C. A genome-wide survey of the prevalence and evolutionary forces acting on human nonsense SNPs. *American Journal of Human Genetics*, n. 84, p. 224-234, 2009.
- YOUNG, L.; CAMPRODON, J. A.; HAUSER, M.; PASCUAL-LEONE, A.; SAXE, R. Disruption of the right temporoparietal junction with transcranial magnetic stimulation reduces the role of beliefs in moral judgements. *Proceedings of the National Academy of Sciences*, USA, n. 107, p. 6753-6758, 2011.
- YU, P.; MA, D.; XU, M. Nested genes in the human genome. *Genomics*, n. 86, p. 414-422, 2005.
- YUNES, J. J.; PRAKASH, O. The origin of man: a chromosomal pictorial legacy. *Science*, n. 215, p. 1525-1530, 1982.
- ZAIA, D. A. M.; ZAIA, C. T. B. V. Os cristais e a origem da vida. A seleção quiral de aminoácidos na terra primitiva. *Ciência Hoje*, n. 37, v. 222, p. 38-43, 2011.
- ZEMBRZUSKI, V. M.; BASTA, P. C.; CALLEGARI-JACQUES, S. M.; SANTOS, R. V.; COIMBRA JR., C. E. A.; SALZANO, F. M.; HUTZ, M. H. Cytokine genes are associated with tuberculin skin test response in a native Brazilian population. *Tuberculosis*, n. 90, p. 44-49, 2010.
- ZHANG, X. H-F.; CHASIN, L. A. Comparison of multiple vertebrate genomes reveals the birth and evolution of human exons. *Proceedings of the National Academy of Sciences*, USA, n. 103, p. 13427-13432, 2006.

- ZHOU, S. et al. Shotgun optical mapping of the entire *Leishmania major* Friedlin genome. *Molecular; Biochemical Parasitology*, n. 138, p. 97-106, 2004.
- ZHUO, D.; MADDEN, R.; ELELA, S. A.; CHABOT, B. Modern origin of numerous alternatively spliced human introns from tandem arrays. *Proceedings of the National Academy of Sciences*, USA, n. 104, p. 882-886, 2007.
- ZIMMER, C. Pistas evolutivas do câncer. *Scientific American Brazil*, n. 5, v. 57, p. 54-61, 2007.