

REFERENCES

1. Darwin, C. *Origin of Species* (John Russel, London, 1859). <http://darwin-online.org.uk/Variorum/index.html>.
2. Sniegowski, P.D. & Lenski, R.E. Mutation and adaptation: The directed mutation controversy in evolutionary perspective. *Annual Review of Ecology and Systematics* **26**, 553-578 (1995).
<http://myxo.css.msu.edu/PublicationSearchResults.php?group=mr>.
3. Merlin, F. Evolutionary Chance Mutation: A Defense Of The Modern Synthesis' Consensus View. *Philos Theor Biol* **2**, e103 (2010). <http://quod.lib.umich.edu/cgi/t/text/text-idx?c=ptb;cc=ptb;q1=MERLIN;rgn=main;view=text;idno=6959004.0002.003>.
4. McClintock, B. *Discovery And Characterization of Transposable Elements: The Collected Papers of Barbara McClintock* (Garland, New York, 1987).
5. Cohen, S.N. & Shapiro, J.A. Transposable genetic elements. *Sci Am* **242**, 40-9 (1980).
<http://www.ncbi.nlm.nih.gov/pubmed/6246575>.
6. Bukhari, A.I., J.A. Shapiro, and S. L. Adhya (Eds.). *DNA insertion elements, plasmids and episomes* (Cold Spring Harbor Press, Cold Spring Harbor, New York, 1977).
7. Shapiro, J.A. *Mobile Genetic Elements*, (Academic Press, New York, 1983).
8. Craig, N., Craigie, R, Gellert, M, Lambowitz, AM. *Mobile DNA II* (American Society for Microbiology Press, Washington, 2002).
9. Holliday, R. A Different Kind of Inheritance. *Scientific American* **260**, 60-73 (1989).
<http://www.nature.com/scientificamerican/journal/v260/n6/pdf/scientificamerican0689-60.pdf>
10. Tan, S.Y. & Brown, J. Rudolph Virchow (1821-1902): "pope of pathology". *Singapore Med J* **47**, 567-8 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16810425>.
11. Wilson, P.G. Centriole inheritance. *Prion* **2**, 9-16 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/19164929>.
12. Harold, F.M. Molecules into cells: specifying spatial architecture. *Microbiol Mol Biol Rev* **69**, 544-64 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16339735>.

13. McLaren, A. & Michie, D. Factors affecting vertebral variation in mice. 4. Experimental proof of the uterine basis of a maternal effect. *J Embryol Exp Morphol* **6**, 645-59 (1958).
<http://www.ncbi.nlm.nih.gov/pubmed/13611143>.
14. McLaren, A. & Michie, D. An effect of the uterine environment upon skeletal morphology in the mouse. *Nature* **181**, 1147-8 (1958). <http://www.ncbi.nlm.nih.gov/pubmed/13541405>.
15. Grindstaff, J.L., Brodie, E.D., 3rd & Ketterson, E.D. Immune function across generations: integrating mechanism and evolutionary process in maternal antibody transmission. *Proc Biol Sci* **270**, 2309-19 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/14667346>.
16. Hasselquist, D. & Nilsson, J.A. Maternal transfer of antibodies in vertebrates: trans-generational effects on offspring immunity. *Philos Trans R Soc Lond B Biol Sci* **364**, 51-60 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/18926976>.
17. Sathananthan, A.H. Human centriole: origin, & how it impacts fertilization, embryogenesis, infertility & cloning. *Indian J Med Res* **129**, 348-50 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19535826>.
18. Barroso, G. *et al.* Developmental sperm contributions: fertilization and beyond. *Fertil Steril* **92**, 835-48 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19631936>.
19. Sonneborn, T.M. Partner of the Genes. *Scientific American* **183**, 30-39 (1950). <http://www.nature.com/scientificamerican/journal/v183/n5/pdf/scientificamerican1150-30.pdf>.
20. Sonneborn, T.M. The determination of hereditary antigenic differences in genetically identical Paramecium cells. *Proc Natl Acad Sci U S A* **34**, 413-8 (1948).
<http://www.ncbi.nlm.nih.gov/pubmed/18880985>.
21. Sonneborn, T.M. Genetics of cell-cell interactions in ciliates. *Birth Defects Orig Artic Ser* **14**, 417-27 (1978). <http://www.ncbi.nlm.nih.gov/pubmed/416861>.
22. Beisson, J. Preformed cell structure and cell heredity. *Prion* **2**, 1-8 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/19164887>.
23. Prusiner, S.B. Prions. *Scientific American* **251**, 50-59 (1984).
<http://www.ncbi.nlm.nih.gov/pubmed/6385236>.

24. Sindi, S.S. & Serio, T.R. Prion dynamics and the quest for the genetic determinant in protein-only inheritance. *Curr Opin Microbiol* **12**, 623-30 (2009).
[http://www.ncbi.nlm.nih.gov/pubmed/19864176\.](http://www.ncbi.nlm.nih.gov/pubmed/19864176)
25. Wickner, R.B. *et al.* Prion amyloid structure explains templating: how proteins can be genes. *FEMS Yeast Res* (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20726897>.
26. Halfmann, R. & Lindquist, S. Epigenetics in the Extreme: Prions and the Inheritance of Environmentally Acquired Traits. **330**, 629 - 632 (2010). PMID 21030648.
27. Benkemoun, L. & Saupe, S.J. Prion proteins as genetic material in fungi. *Fungal Genet Biol* **43**, 789-803 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16901730>.
28. Roberts, B.T. & Wickner, R.B. Heritable activity: a prion that propagates by covalent autoactivation. *Genes Dev* **17**, 2083-7 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12923060>.
29. Tuite, M.F. & Serio, T.R. The prion hypothesis: from biological anomaly to basic regulatory mechanism. *Nat Rev Mol Cell Biol* **11**, 823-33 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/21081963>.
30. Alberts, B. *et al.* *Molecular Biology of the Cell* (Garland Science, New York and London, 2002). .
31. Kuhn, T.S. *The Structure of Scientific Revolutions* (Univ. of Chicago Press, Chicago, 1962).
32. Simon, H.A. The Architecture of Complexity. *Proceedings of the American Philosophical Society* **106**, 467-482 (1962). <http://links.jstor.org/sici?&sici=0003-049X%2819621212%29106%3A6%3C467%3ATAOC%3E2.0.CO%3B2-1>.
33. Bhardwaj, N., Kim, P.M. & Gerstein, M.B. Rewiring of transcriptional regulatory networks: hierarchy, rather than connectivity, better reflects the importance of regulators. *Sci Signal* **3**, ra79 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/21045205>.
34. Welch, W.J. How Cells Respond to Stress. *Scientific American* **268**, 56-64 (1993).
<http://www.ncbi.nlm.nih.gov/pubmed/8097593>.
35. Duke, R.C., Ojcius, D.M. & Young, J.D. Cell Suicide in Health and Disease. *Scientific American* **275**, 80-87 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8923763>.

36. Horvitz, H.R., Shaham, S. & Hengartner, M.O. The genetics of programmed cell death in the nematode *Caenorhabditis elegans*. *Cold Spring Harb Symp Quant Biol* **59**, 377-85 (1994).
[http://www.ncbi.nlm.nih.gov/pubmed/7587090\.](http://www.ncbi.nlm.nih.gov/pubmed/7587090)
37. Pontier, D., Balague, C. & Roby, D. The hypersensitive response. A programmed cell death associated with plant resistance. *C R Acad Sci III* **321**, 721-34 (1998).
[http://www.ncbi.nlm.nih.gov/pubmed/9809204\.](http://www.ncbi.nlm.nih.gov/pubmed/9809204)
38. Engelberg-Kulka, H., Amitai, S., Kolodkin-Gal, I. & Hazan, R. Bacterial programmed cell death and multicellular behavior in bacteria. *PLoS Genet* **2**, e135 (2006).
[http://www.ncbi.nlm.nih.gov/pubmed/17069462.](http://www.ncbi.nlm.nih.gov/pubmed/17069462)
39. Deponte, M. Programmed cell death in protists. *Biochim Biophys Acta* **1783**, 1396-405 (2008).
[http://www.ncbi.nlm.nih.gov/pubmed/18291111.](http://www.ncbi.nlm.nih.gov/pubmed/18291111)
40. Shapiro, J.A. Bacteria are small but not stupid: cognition, natural genetic engineering and socio-bacteriology. *Stud Hist Philos Biol Biomed Sci* **38**, 807-19 (2007).
[http://www.ncbi.nlm.nih.gov/pubmed/18053935.](http://www.ncbi.nlm.nih.gov/pubmed/18053935)
41. Spiro, S., Dixon, R. & (eds.). *Sensory Mechanisms in Bacteria: Molecular Aspects of Signal Recognition* (Caister Academic Press, 2010).
42. Bray, D. *Wetware A Computer in Every Living Cell* 279 (Yale University Press, New Haven, CT, 2009).
43. Danchin, A. Bacteria as computers making computers. *FEMS Microbiol Rev* **33**, 3-26 (2009).
[http://www.ncbi.nlm.nih.gov/pubmed/19016882.](http://www.ncbi.nlm.nih.gov/pubmed/19016882)
44. Kitano, H. Systems biology: a brief overview. *Science* **295**, 1662-4 (2002).
[http://www.ncbi.nlm.nih.gov/pubmed/11872829\.](http://www.ncbi.nlm.nih.gov/pubmed/11872829)
45. Strange, K. The end of "naive reductionism": rise of systems biology or renaissance of physiology? *Am J Physiol Cell Physiol* **288**, C968-74 (2005). [http://www.ncbi.nlm.nih.gov/pubmed/15840560.](http://www.ncbi.nlm.nih.gov/pubmed/15840560)
46. Noble, D. Biophysics and systems biology. *Philos Transact A Math Phys Eng Sci* **368**, 1125-39 (2010). [http://www.ncbi.nlm.nih.gov/pubmed/20123750\.](http://www.ncbi.nlm.nih.gov/pubmed/20123750)
47. Monod, J. *Recherches sur la croissance des cultures bactériennes* (Hermann & cie, Paris, 1942).

48. Monod, J. From enzymatic adaptation to allosteric transitions. *Science* **154**, 475-83 (1966).
<http://www.ncbi.nlm.nih.gov/pubmed/5331094>.
49. Ullmann, A. Jacques Monod, 1910-1976: his life, his work and his commitments. *Res Microbiol* **161**, 68-73 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20045725>.
50. Jacob, F. & Wollman, E.L. Viruses and Genes. *Scientific American* **204**, 92-110 (1961).
<http://www.ncbi.nlm.nih.gov/pubmed/13718528>.
51. Ptashne, M. & Gilbert, W. Genetic Repressors. *Scientific American* **222**, 36-44 (1970).
<http://www.ncbi.nlm.nih.gov/pubmed/4910866>.
52. Mueller-Hill, B. *The lac operon: a short history of a genetic paradigm*, (de Gruyter, Berlin, 1996).
53. Jacob, F., Perrin, D., Sanchez, C. & Monod, J. Operon: a group of genes with the expression coordinated by an operator. *C. R. Hebd. Seances Acad. Sci* **250**, 1727–1729 (1960). PMID 15999435.
54. Nathanson, J.A. & Greengard, P. “Second Messengers” in the Brain. *Scientific American* **237**, 108-119 (1977). <http://www.ncbi.nlm.nih.gov/pubmed/18797>.
55. Rasmussen, H. The Cycling of Calcium as an Intracellular Messenger. *Scientific American* **261**, 66-73 (1989). <http://www.ncbi.nlm.nih.gov/pubmed/2551033>.
56. Scott, J.D. & Pawson, T. Cell Communication: The Inside Story. *Scientific American* **282**, 72-79 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10862426>.
57. Raju, T.N. The Nobel chronicles. 1971: Earl Wilbur Sutherland, Jr. (1915-74). *Lancet* **354**, 961 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10489991>.
58. Collado-Vides, J. A linguistic representation of the regulation of transcription initiation. II. Distinctive features of sigma 70 promoters and their regulatory binding sites. *Biosystems* **29**, 105-28 (1993). <http://www.ncbi.nlm.nih.gov/pubmed/8374063>.
59. Barbieri, M. Biosemiotics: a new understanding of life. *Naturwissenschaften* **95**, 577-99 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18365164>.
60. Jacob, F. & Monod, J. Genetic regulatory mechanisms in the synthesis of proteins. *J Mol Biol* **3**, 318-56 (1961). <http://www.ncbi.nlm.nih.gov/pubmed/13718526>.
61. Lodish, H.F. *et al. Molecular Cell Biology* (W. H. Freeman & Co, New York, 1999).
<http://www.ncbi.nlm.nih.gov/books/NBK21475/>.

62. Shapiro, J.A. & Sternberg, R.v. Why repetitive DNA is essential to genome function. *Biol. Revs. (Camb.)* **80**, 227-50 (2005). PMID 15921050.
63. Istrail, S., De-Leon, S.B. & Davidson, E.H. The regulatory genome and the computer. *Dev Biol* **310**, 187-95 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17822690>.
64. Tjian, R. Molecular Machines that Control Genes. *Scientific American* **272**, 54-61 (1995). <http://www.nature.com/scientificamerican/journal/v272/n2/pdf/scientificamerican0295-54.pdf>
65. Kuhlman, T., Zhang, Z., Saier, M.H., Jr. & Hwa, T. Combinatorial transcriptional control of the lactose operon of Escherichia coli. *Proc Natl Acad Sci U S A* **104**, 6043-8 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17376875>.
66. Muller, J., Barker, A., Oehler, S. & Muller-Hill, B. Dimeric lac repressors exhibit phase-dependent co-operativity. *J Mol Biol* **284**, 851-7 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9837708>.
67. Muller, J., Oehler, S. & Muller-Hill, B. Repression of lac promoter as a function of distance, phase and quality of an auxiliary lac operator. *J Mol Biol* **257**, 21-9 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8632456>.
68. Davidson, E.H. *The Regulatory Genome* (Academic, San Diego, 2006).
69. Changeux, J.-P. The Control of Biochemical Reactions *Scientific American* **212**, 36-45 (1965). <http://www.ncbi.nlm.nih.gov/pubmed/14261524>.
70. Koshland, D.E. Protein Shape and Biological Control. *Scientific American* **229**, 52-64 (1973). <http://www.ncbi.nlm.nih.gov/pubmed/4727696>.
71. Monod, J., Changeux, J.P. & Jacob, F. Allosteric proteins and cellular control systems. *J Mol Biol* **6**, 306-29 (1963). <http://www.ncbi.nlm.nih.gov/pubmed/13936070>.
72. Monod, J., Wyman, J. & Changeux, J.P. On the Nature of Allosteric Transitions: a Plausible Model. *J Mol Biol* **12**, 88-118 (1965). <http://www.ncbi.nlm.nih.gov/pubmed/14343300>.
73. Kimata, K., Takahashi, H., Inada, T., Postma, P. & Aiba, H. cAMP receptor protein-cAMP plays a crucial role in glucose-lactose diauxie by activating the major glucose transporter gene in Escherichia coli. *Proc Natl Acad Sci U S A* **94**, 12914-9 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9371775>.

74. Lengeler, J.W. & Jahreis, K. Bacterial PEP-dependent carbohydrate: phosphotransferase systems couple sensing and global control mechanisms. *Contrib Microbiol* **16**, 65-87 (2009). PMID 19494579.
75. Britten, R.J. & Davidson, E.H. Repetitive and non-repetitive DNA sequences and a speculation on the origins of evolutionary novelty. *Q Rev Biol* **46**, 111-38 (1971).
<http://www.ncbi.nlm.nih.gov/pubmed/5160087>.
76. Ravasz, E. Detecting hierarchical modularity in biological networks. *Methods Mol Biol* **541**, 145-60 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19381526>.
77. Cooper, S. & Helmstetter, C.E. Chromosome replication and the division cycle of Escherichia coli B/r. *J Mol Biol* **31**, 519-40 (1968). PMID 4866337.
78. Kunkel, T.A. & Bebenek, K. DNA replication fidelity. *Annu Rev Biochem* **69**, 497-529 (2000). PMID 10966467.
79. Radman, M. & Wagner, R. The high fidelity of DNA duplication. *Scientific American* **259**, 40-6 (1988). <http://www.ncbi.nlm.nih.gov/pubmed/3064293>.
80. Rennie, J. Proofreading Genes. *Scientific American* **264**, 28-32 (1991).
<http://www.nature.com/scientificamerican/journal/v264/n5/pdf/scientificamerican0591-28.pdf>.
81. Fazlieva, R. *et al.* Proofreading exonuclease activity of human DNA polymerase delta and its effects on lesion-bypass DNA synthesis. *Nucleic Acids Res* **37**, 2854-66 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19282447>.
82. Ibarra, B. *et al.* Proofreading dynamics of a processive DNA polymerase. *Embo J* **28**, 2794-802 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19661923>.
83. Modrich, P. & Lahue, R. Mismatch repair in replication fidelity, genetic recombination, and cancer biology. *Annu Rev Biochem* **65**, 101-33 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8811176>.
84. Jiricny, J. The multifaceted mismatch-repair system. *Nat Rev Mol Cell Biol* **7**, 335-46 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16612326>.
85. Iyer, R.R., Pluciennik, A., Burdett, V. & Modrich, P.L. DNA mismatch repair: functions and mechanisms. *Chem Rev* **106**, 302-23 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16464007>.

86. Kunkel, T.A. & Erie, D.A. DNA mismatch repair. *Annu Rev Biochem* **74**, 681-710 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15952900>.
87. Sancar, A. & Hearst, J.E. Molecular matchmakers. *Science* **259**, 1415-20 (1993).
<http://www.ncbi.nlm.nih.gov/pubmed/8451638>.
88. Bebenek, K. & Kunkel, T.A. Functions of DNA polymerases. *Adv Protein Chem* **69**, 137-65 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15588842>.
89. Fujii, S. & Fuchs, R.P. Interplay among replicative and specialized DNA polymerases determines failure or success of translesion synthesis pathways. *J Mol Biol* **372**, 883-93 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17707403>.
90. Garcia-Diaz, M. & Bebenek, K. Multiple functions of DNA polymerases. *CRC Crit Rev Plant Sci* **26**, 105-122 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/18496613>.
91. Nick McElhinny, S.A., Gordenin, D.A., Stith, C.M., Burgers, P.M. & Kunkel, T.A. Division of labor at the eukaryotic replication fork. *Mol Cell* **30**, 137-44 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18439893>.
92. Peltomaki, P. & de la Chapelle, A. Mutations predisposing to hereditary nonpolyposis colorectal cancer. *Adv Cancer Res* **71**, 93-119 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9111864>.
93. Kosko, B. & Isaka, S. Fuzzy Logic. *Scientific American* **269**, 76-81 (1993).
<http://www.nature.com/scientificamerican/journal/v269/n1/pdf/scientificamerican0793-76.pdf>.
94. Sadegh-Zadeh, K. Advances in fuzzy theory. *Artif Intell Med* **15**, 309-323 (1999).
95. Jamshidi, M. Tools for intelligent control: fuzzy controllers, neural networks and genetic algorithms. *Phil Trans A: Math Phys Eng Sci* **361**, 1781-1808 (2003).
96. Ganesan, A.K. & Smith, K.C. Dark recovery processes in Escherichia coli irradiated with ultraviolet light. I. Effect of rec mutations on liquid holding recovery. *J Bacteriol* **96**, 365-73 (1968).
<http://www.ncbi.nlm.nih.gov/pubmed/4877124>.
97. Das, J., Bagchi, B. & Chaudhuri, U. Liquid holding recovery of photodynamic damage in E. coli. *Photochem Photobiol* **19**, 317-9 (1974). <http://www.ncbi.nlm.nih.gov/pubmed/4595701>.
98. Howard-Flanders, P. Inducible Repair of DNA. *Scientific American* **245**, 72-80 (1981).
<http://www.ncbi.nlm.nih.gov/pubmed/7036338>.

99. Weigle, J.J. Induction of Mutations in a Bacterial Virus. *Proc Natl Acad Sci U S A* **39**, 628-36 (1953).
<http://www.ncbi.nlm.nih.gov/pubmed/16589315>.
100. Wood, R.D. & Hutchinson, F. Non-targeted mutagenesis of unirradiated lambda phage in Escherichia coli host cells irradiated with ultraviolet light. *J Mol Biol* **173**, 293-305 (1984).
<http://www.ncbi.nlm.nih.gov/pubmed/6230459>.
101. Maenhaut-Michel, G. Mechanism of SOS-induced targeted and untargeted mutagenesis in E. coli. *Biochimie* **67**, 365-9 (1985). <http://www.ncbi.nlm.nih.gov/pubmed/2931122>.
102. Calsou, P. & Defais, M. Weigle reactivation and mutagenesis of bacteriophage lambda in lexA(Def) mutants of E. coli K12. *Mol Gen Genet* **201**, 329-33 (1985).
<http://www.ncbi.nlm.nih.gov/pubmed/2935711>.
103. Hutchinson, F. & Stein, J. Mutagenesis of ultraviolet-irradiated lambda phage by host cell irradiation: induction of Weigle mutagenesis is not an all-or-none process. *Mol Gen Genet* **177**, 207-11 (1980).
<http://www.ncbi.nlm.nih.gov/pubmed/6445034>.
104. Hutchinson, F. & Stein, J. Mutagenesis of lambda phage: Weigle mutagenesis is induced by coincident lesions in the double helical DNA of the host cell genome. *Mol Gen Genet* **181**, 458-63 (1981). <http://www.ncbi.nlm.nih.gov/pubmed/6455586>.
105. Witkin, E.M. Elevated mutability of polA derivatives of Escherichia coli B/r at sublethal doses of ultraviolet light: evidence for an inducible error-prone repair system ("SOS repair") and its anomalous expression in these strains. *Genetics* **79**, Suppl:199-213 (1975). PMID 1097302.
106. Battista, J.R., Donnelly, C.E., Ohta, T. & Walker, G.C. The SOS response and induced mutagenesis. *Prog Clin Biol Res* **340A**, 169-78 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/2167481>.
107. Janion, C. Inducible SOS response system of DNA repair and mutagenesis in Escherichia coli. *Int J Biol Sci* **4**, 338-44 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18825275>.
108. Smith, K.C. Multiple pathways of DNA repair and their possible roles in mutagenesis. *Natl Cancer Inst Monogr*, 107-14 (1978). <http://www.ncbi.nlm.nih.gov/pubmed/381933>.
109. Van Houten, B. Nucleotide excision repair in Escherichia coli. *Microbiol Rev* **54**, 18-51 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/2181258>.

110. Petit, C. & Sancar, A. Nucleotide excision repair: from *E. coli* to man. *Biochimie* **81**, 15-25 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10214906>.
111. Pham, P., Rangarajan, S., Woodgate, R. & Goodman, M.F. Roles of DNA polymerases V and II in SOS-induced error-prone and error-free repair in *Escherichia coli*. *Proc Natl Acad Sci U S A* **98**, 8350-4 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11459974>.
112. Wagner, J., Etienne, H., Janel-Bintz, R. & Fuchs, R.P. Genetics of mutagenesis in *E. coli*: various combinations of translesion polymerases (Pol II, IV and V) deal with lesion/sequence context diversity. *DNA Repair (Amst)* **1**, 159-67 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12509262>.
113. Goodman, M.F. Error-prone repair DNA polymerases in prokaryotes and eukaryotes. *Annu Rev Biochem* **71**, 17-50 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12045089>.
114. Broyde, S., Wang, L., Rechkoblit, O., Geacintov, N.E. & Patel, D.J. Lesion processing: high-fidelity versus lesion-bypass DNA polymerases. *Trends Biochem Sci* **33**, 209-19 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18407502>.
115. Napolitano, R., Janel-Bintz, R., Wagner, J. & Fuchs, R.P. All three SOS-inducible DNA polymerases (Pol II, Pol IV and Pol V) are involved in induced mutagenesis. *Embo J* **19**, 6259-65 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/11080171>.
116. Walker, G.C. Understanding the complexity of an organism's responses to DNA damage. *Cold Spring Harb Symp Quant Biol* **65**, 1-10 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/12760015>.
117. Sutton, M.D., Smith, B.T., Godoy, V.G. & Walker, G.C. The SOS response: recent insights into umuDC-dependent mutagenesis and DNA damage tolerance. *Annu Rev Genet* **34**, 479-497 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/11092836>.
118. Stahl, F.W. Genetic Recombination. *Scientific American* **256**, 90-101 (1987).
<http://www.ncbi.nlm.nih.gov/pubmed/2949366>.
119. Witkin, E.M. RecA protein in the SOS response: milestones and mysteries. *Biochimie* **73**, 133-41 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1883877>.
120. Kowalczykowski, S.C., Dixon, D.A., Eggleston, A.K., Lauder, S.D. & Rehrauer, W.M. Biochemistry of homologous recombination in *Escherichia coli*. *Microbiol Rev* **58**, 401-65 (1994).
<http://www.ncbi.nlm.nih.gov/pubmed/7968921>.

121. Kowalczykowski, S.C. Initiation of genetic recombination and recombination-dependent replication. *Trends Biochem Sci* **25**, 156-65 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10754547>.
122. Lusetti, S.L. & Cox, M.M. The bacterial RecA protein and the recombinational DNA repair of stalled replication forks. *Annu Rev Biochem* **71**, 71-100 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12045091>.
123. Cox, M.M. Recombinational DNA repair of damaged replication forks in Escherichia coli: questions. *Annu Rev Genet* **35**, 53-82 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11700277>.
124. Kidane, D. & Graumann, P.L. Dynamic formation of RecA filaments at DNA double strand break repair centers in live cells. *J Cell Biol* **170**, 357-66 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16061691>.
125. Chen, Z., Yang, H. & Pavletich, N.P. Mechanism of homologous recombination from the RecA-ssDNA/dsDNA structures. *Nature* **453**, 489-4 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18497818>.
126. Stasiak, A.Z., Rosselli, W. & Stasiak, A. RecA-DNA helical filaments in genetic recombination. *Biochimie* **73**, 199-208 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1883882>.
127. Takahashi, M. & Norden, B. Structure of RecA-DNA complex and mechanism of DNA strand exchange reaction in homologous recombination. *Adv Biophys* **30**, 1-35 (1994).
<http://www.ncbi.nlm.nih.gov/pubmed/7709802>.
128. Roberts, J.W. & Roberts, C.W. Proteolytic cleavage of bacteriophage lambda repressor in induction. *Proc Natl Acad Sci U S A* **72**, 147-51 (1975). <http://www.ncbi.nlm.nih.gov/pubmed/1090931>.
129. Roberts, J.W., Roberts, C.W. & Craig, N.L. Escherichia coli recA gene product inactivates phage lambda repressor. *Proc Natl Acad Sci U S A* **75**, 4714-8 (1978).
<http://www.ncbi.nlm.nih.gov/pubmed/368796>.
130. Roberts, J.W., Phizicky, E.M., Burbee, D.G., Roberts, C.W. & Moreau, P.L. A brief consideration of the SOS inducing signal. *Biochimie* **64**, 805-7 (1982). <http://www.ncbi.nlm.nih.gov/pubmed/6814531>.
131. Phizicky, E.M. & Roberts, J.W. Induction of SOS functions: regulation of proteolytic activity of E. coli RecA protein by interaction with DNA and nucleoside triphosphate. *Cell* **25**, 259-67 (1981).
<http://www.ncbi.nlm.nih.gov/pubmed/7023697>.

132. Craig, N.L. & Roberts, J.W. E. coli recA protein-directed cleavage of phage lambda repressor requires polynucleotide. *Nature* **283**, 26-30 (1980). <http://www.ncbi.nlm.nih.gov/pubmed/6444245>.
133. McCann, J., Spingarn, N.E., Kobori, J. & Ames, B.N. Detection of carcinogens as mutagens: bacterial tester strains with R factor plasmids. *Proc Natl Acad Sci U S A* **72**, 979-83 (1975).
<http://www.ncbi.nlm.nih.gov/pubmed/165497>.
134. Inman, M.A., Butler, M.A., Connor, T.H. & Matney, T.S. The effects of excision repair and the plasmid pKM101 on the induction of his⁺ revertants by chemical agents in *Salmonella typhimurium*. *Teratog Carcinog Mutagen* **3**, 491-501 (1983). <http://www.ncbi.nlm.nih.gov/pubmed/6140768>.
135. Walker, G.C. Mutagenesis-enhancement by plasmids in mutagenesis tester strains. *Basic Life Sci* **34**, 111-20 (1985). <http://www.ncbi.nlm.nih.gov/pubmed/3904713>.
136. Devoret, R. Bacterial tests for potential carcinogens. *Sci Am* **241**, 40-9 (1979).
<http://www.ncbi.nlm.nih.gov/pubmed/386496>.
137. Huisman, O., D'Ari, R. & Gottesman, S. Cell-division control in *Escherichia coli*: specific induction of the SOS function SfiA protein is sufficient to block septation. *Proc Natl Acad Sci U S A* **81**, 4490-4 (1984). <http://www.ncbi.nlm.nih.gov/pubmed/6087326>.
138. Higashitani, A., Higashitani, N. & Horiuchi, K. A cell division inhibitor SulA of *Escherichia coli* directly interacts with FtsZ through GTP hydrolysis. *Biochem Biophys Res Commun* **209**, 198-204 (1995). <http://www.ncbi.nlm.nih.gov/pubmed/7726836>.
139. Hartwell, L., Weinert, TA. Checkpoints: controls that ensure the order of cell cycle events. *Science* **246**, 629-634 (1989). PMID 2683079.
140. Weinert, T.A. & Hartwell, L.H. The RAD9 gene controls the cell cycle response to DNA damage in *Saccharomyces cerevisiae*. *Science* **241**, 317-22 (1988).
<http://www.ncbi.nlm.nih.gov/pubmed/3291120>.
141. Watanabe, K., Morishita, J., Umezawa, K., Shirahige, K. & Maki, H. Involvement of RAD9-dependent damage checkpoint control in arrest of cell cycle, induction of cell death, and chromosome instability caused by defects in origin recognition complex in *Saccharomyces cerevisiae*. *Eukaryot Cell* **1**, 200-12 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12455955>.

142. Mazia, D. The Cell Cycle. *Scientific American* **230**, 54-64 (1974).
<http://www.ncbi.nlm.nih.gov/pubmed/4808784>.
143. Murray, A. & Kirschner, M. What controls the cell cycle. *Scientific American* **264**, 56-63 (1991).
<http://www.ncbi.nlm.nih.gov/pubmed/1828616>.
144. Weinberg, R.A. How cancer arises. *Scientific American* **275**, 62-70 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8701295>.
145. Hartwell, L. Defects in a cell cycle checkpoint may be responsible for the genomic instability of cancer cells. *Cell* **71**, 543-6 (1992). <http://www.ncbi.nlm.nih.gov/pubmed/1423612>.
146. Paulovich, A.G. & Hartwell, L.H. A checkpoint regulates the rate of progression through S phase in *S. cerevisiae* in response to DNA damage. *Cell* **82**, 841-7 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/7671311>.
147. Ishikawa, K., Ishii, H. & Saito, T. DNA damage-dependent cell cycle checkpoints and genomic stability. *DNA Cell Biol* **25**, 406-11 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16848682>.
148. McIntosh, J.R. & McDonald, K.L. The Mitotic Spindle. *Scientific American* **261**, 48-56 (1989).
<http://www.nature.com/scientificamerican/journal/v261/n4/pdf/scientificamerican1089-48.pdf>.
149. Nicklas, R.B. How cells get the right chromosomes. *Science* **275**, 632-7 (1997).
<http://www.ncbi.nlm.nih.gov/pubmed/9005842>.
150. Hoyt, M.A. A new view of the spindle checkpoint. *J Cell Biol* **154**, 909-11 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11535614>.
151. Taylor, S.S., Scott, M.I. & Holland, A.J. The spindle checkpoint: a quality control mechanism which ensures accurate chromosome segregation. *Chromosome Res* **12**, 599-616 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15289666>.
152. Glover, D.M., Gonzalez, C. & Raff, J.W. The Centrosome. *Scientific American* **268**, 62-68 (1993).
<http://www.ncbi.nlm.nih.gov/pubmed/8516675>.
153. Santaguida, S. & Musacchio, A. The life and miracles of kinetochores. *Embo J* **28**, 2511-31 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19629042>.
154. Burke, D.J. & Stukenberg, P.T. Linking kinetochore-microtubule binding to the spindle checkpoint. *Dev Cell* **14**, 474-9 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18410725>.

155. Cross, F., Hartwell, L.H., Jackson, C. & Konopka, J.B. Conjugation in *Saccharomyces cerevisiae*. *Annu Rev Cell Biol* **4**, 429-57 (1988). <http://www.ncbi.nlm.nih.gov/pubmed/2848554>.
156. Jackson, C.L. & Hartwell, L.H. Courtship in *Saccharomyces cerevisiae*: an early cell-cell interaction during mating. *Mol Cell Biol* **10**, 2202-13 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/2183023>.
157. Jackson, C.L., Konopka, J.B. & Hartwell, L.H. *S. cerevisiae* alpha pheromone receptors activate a novel signal transduction pathway for mating partner discrimination. *Cell* **67**, 389-402 (1991).
<http://www.ncbi.nlm.nih.gov/pubmed/1655282>.
158. Dorer, R., Pryciak, P., Schrick, K. & Hartwell, L.H. The induction of cell polarity by pheromone in *Saccharomyces cerevisiae*. *Harvey Lect* **90**, 95-104 (1994).
<http://www.ncbi.nlm.nih.gov/pubmed/8803321>.
159. Jackson, C.L. & Hartwell, L.H. Courtship in *S. cerevisiae*: both cell types choose mating partners by responding to the strongest pheromone signal. *Cell* **63**, 1039-51 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/2257622>.
160. Linder, M.E. & Gilman, A.G. G Proteins. *Scientific American* **267**, 56-65 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1502510>.
161. Ameisen, J.C. On the origin, evolution, and nature of programmed cell death: a timeline of four billion years. *Cell Death Differ* **9**, 367-93 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11965491>.
162. Huettenbrenner, S. *et al.* The evolution of cell death programs as prerequisites of multicellularity. *Mutat Res* **543**, 235-49 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12787815>.
163. Cheng, W.C., Leach, K.M. & Hardwick, J.M. Mitochondrial death pathways in yeast and mammalian cells. *Biochim Biophys Acta* **1783**, 1272-9 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18477482>.
164. Zuzarte-Luis, V. & Hurle, J.M. Programmed cell death in the embryonic vertebrate limb. *Semin Cell Dev Biol* **16**, 261-9 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15797836>.
165. Burhans, W.C. *et al.* Apoptosis-like yeast cell death in response to DNA damage and replication defects. *Mutat Res* **532**, 227-43 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/14643439>.
166. Fulda, S., Gorman, A.M., Hori, O. & Samali, A. Cellular stress responses: cell survival and cell death. *Int J Cell Biol* **2010**, 214074 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20182529>.

167. Heath, M.C. Hypersensitive response-related death. *Plant Mol Biol* **44**, 321-34 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/11199391>.
168. Kolodkin-Gal, I., Hazan, R., Gaathon, A., Carmeli, S. & Engelberg-Kulka, H. A linear pentapeptide is a quorum-sensing factor required for mazEF-mediated cell death in *Escherichia coli*. *Science* **318**, 652-5 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17962566>.
169. Kolodkin-Gal, I. & Engelberg-Kulka, H. The extracellular death factor: physiological and genetic factors influencing its production and response in *Escherichia coli*. *J Bacteriol* **190**, 3169-75 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18310334>.
170. Jarpe, M.B. *et al.* Anti-apoptotic versus pro-apoptotic signal transduction: checkpoints and stop signs along the road to death. *Oncogene* **17**, 1475-82 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/9779994>.
171. Marini, P. & Belka, C. Death receptor ligands: new strategies for combined treatment with ionizing radiation. *Curr Med Chem Anticancer Agents* **3**, 334-42 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12871079>.
172. Holoch, P.A. & Griffith, T.S. TNF-related apoptosis-inducing ligand (TRAIL): a new path to anti-cancer therapies. *Eur J Pharmacol* **625**, 63-72 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19836385>.
173. Linseman, D.A. *et al.* Insulin-like growth factor-I blocks Bcl-2 interacting mediator of cell death (Bim) induction and intrinsic death signaling in cerebellar granule neurons. *J Neurosci* **22**, 9287-97 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12417654>.
174. Linseman, D.A. *et al.* Suppression of death receptor signaling in cerebellar Purkinje neurons protects neighboring granule neurons from apoptosis via an insulin-like growth factor I-dependent mechanism. *J Biol Chem* **277**, 24546-53 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11964396>.
175. Slee, E.A. & Lu, X. The ASPP family: deciding between life and death after DNA damage. *Toxicol Lett* **139**, 81-7 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12628742>.
176. Loewer, A. & Lahav, G. Cellular conference call: external feedback affects cell-fate decisions. *Cell* **124**, 1128-30 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16564006>.

177. Song, J. EMT or apoptosis: a decision for TGF-beta. *Cell Res* **17**, 289-90 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17426696>.
178. Falschlehner, C., Emmerich, C.H., Gerlach, B. & Walczak, H. TRAIL signalling: decisions between life and death. *Int J Biochem Cell Biol* **39**, 1462-75 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17403612>.
179. Meredith, J.E., Jr., Fazeli, B. & Schwartz, M.A. The extracellular matrix as a cell survival factor. *Mol Biol Cell* **4**, 953-61 (1993). <http://www.ncbi.nlm.nih.gov/pubmed/8257797>.
180. Park, D.S. *et al.* Multiple pathways of neuronal death induced by DNA-damaging agents, NGF deprivation, and oxidative stress. *J Neurosci* **18**, 830-40 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/9437005>.
181. O'Rourke, D.M. *et al.* Conversion of a radioresistant phenotype to a more sensitive one by disabling erbB receptor signaling in human cancer cells. *Proc Natl Acad Sci U S A* **95**, 10842-7 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/9724792>.
182. Crick, F. On protein synthesis. *Symp Soc Exp Biol* **12**, 138-163 (1958). .
183. Temin, H.M. RNA-Directed DNA Synthesis. *Scientific American* **226**, 24-33 (1972).
<http://www.ncbi.nlm.nih.gov/pubmed/4332962>.
184. Temin, H., S Mizutani. RNA-dependent DNA polymerase in virions of Rous sarcoma virus. *Nature* **226**, 1211-1213 (1970). PMID 4316301.
185. Crick, F. Central dogma of molecular biology. *Nature* **227**, 561-563 (1970). PMID 4913914.
186. Collins, F.S. & Jegalian , K.G. Deciphering the Code of Life. *Scientific American* **281**, 86-91 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10614070>.
187. Shapiro, J.A. Genome informatics: The role of DNA in cellular computations. *Biological Theory* **1**, 288-301 (2006). <http://shapiro.bsd.uchicago.edu/publications.shtml>.
188. Shapiro, J.A. Revisiting the Central Dogma in the 21st Century. *Annals of the New York Academy of Sciences* **1178**, 6-28 (2009). PMID 19845625.
189. Judson, H. *The Eighth Day of Creation: Makers of the Revolution in Biology*, (Simon & Schuster, New York, 1979).
190. Huxley, J. *Evolution: the modern synthesis*, (Allen & Unwin, London, 1942).

191. Koonin, E.V. Darwinian evolution in the light of genomics. *Nucleic Acids Res* **37**, 1011-34 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19213802>.
192. Kutschera, U. & Niklas, K.J. The modern theory of biological evolution: an expanded synthesis. *Naturwissenschaften* **91**, 255-76 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15241603>.
193. Rose, M.R. & Oakley, T.H. The new biology: beyond the Modern Synthesis. *Biol Direct* **2**, 30 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/18036242>.
194. Ryan, F.P. Genomic creativity and natural selection: a modern synthesis. *Biological Journal of the Linnean Society* **88**, 655-672 (2006).
195. Britten, R.J. Cases of ancient mobile element DNA insertions that now affect gene regulation. *Mol Phylogenet Evol* **5**, 13-7 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8673282>.
196. Britten, R.J. DNA sequence insertion and evolutionary variation in gene regulation. *Proc Natl Acad Sci U S A* **93**, 9374-7 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8790336>.
197. Britten, R., Kohne, DE. Repeated sequences in DNA. Hundreds of thousands of copies of DNA sequences have been incorporated into the genomes of higher organisms. *Science* **161**, 529-540 (1968). PMID 4874239.
198. Shapiro, J.A. Natural genetic engineering in evolution. *Genetica* **86**, 99-111 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1334920>.
199. Shapiro, J.A. Genome system architecture and natural genetic engineering in evolution. *Ann N Y Acad Sci* **870**, 23-35 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10415470>.
200. Shapiro, J.A. Transposable elements as the key to a 21st century view of evolution. *Genetica* **107**, 171-9 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10952210>.
201. Shapiro, J.A. Retrotransposons and regulatory suites. *Bioessays* **27**, 122-5 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15666350>.
202. Shapiro, J.A. A 21st century view of evolution: genome system architecture, repetitive DNA, and natural genetic engineering. *Gene* **345**, 91-100 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15716117>.
203. Sternberg, R.v. & Shapiro, J.A. How repeated retroelements format genome function. *Cytogenet. Genome Res* **110**, 108-116 (2005). PMID 16093662.

204. Shapiro, J.A. Mobile DNA and evolution in the 21st century. *Mob DNA* **1**, 4 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20226073>.
205. Long, M. Evolution of novel genes. *Curr Opin Genet Dev* **11**, 673-80 (2001). PMID 11682312.
206. Betrán, E., Thornton, K. & Long, M. Retroposed new genes out of the X in Drosophila. *Genome Res* **12**, 1854-1859 (2002). PMID 12466289.
207. Jorgensen, R.A. Restructuring the genome in response to adaptive challenge: McClintock's bold conjecture revisited. *Cold Spring Harb Symp Quant Biol* **69**, 349-54 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/16117667>.
208. Bourque, G. Transposable elements in gene regulation and in the evolution of vertebrate genomes. *Curr Opin Genet Dev* **19**, 607-12 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19914058>.
209. Bourque, G. *et al.* Evolution of the mammalian transcription factor binding repertoire via transposable elements. *Genome Res* **18**, 1752-62 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18682548>.
210. Marino-Ramirez, L., Lewis, K.C., Landsman, D. & Jordan, I.K. Transposable elements donate lineage-specific regulatory sequences to host genomes. *Cytogenet Genome Res* **110**, 333-41 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16093685>.
211. Jordan, I.K., Rogozin, I.B., Glazko, G.V. & Koonin, E.V. Origin of a substantial fraction of human regulatory sequences from transposable elements. *Trends Genet* **19**, 68-72 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12547512>.
212. Bowen, N.J. & Jordan, I.K. Transposable elements and the evolution of eukaryotic complexity. *Curr Issues Mol Biol* **4**, 65-76 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12074196>.
213. Jiang, N., Bao, Z., Zhang, X., Eddy, S.R. & Wessler, S.R. Pack-MULE transposable elements mediate gene evolution in plants. *Nature* **431**, 569-73 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15457261>.
214. Wessler, S.R., Bureau, T.E. & White, S.E. LTR-retrotransposons and MITEs: important players in the evolution of plant genomes. *Curr Opin Genet Dev* **5**, 814-21 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/8745082>.
215. Wessler, S.R. Transposable elements and the evolution of gene expression. *Symp Soc Exp Biol* **51**, 115-22 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/10645433>.

216. Wessler, S.R. Transposable elements and the evolution of eukaryotic genomes. *Proc Natl Acad Sci U S A* **103**, 17600-1 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/17101965>.
217. Piryapongsa, J., Marino-Ramirez, L. & Jordan, I.K. Origin and evolution of human microRNAs from transposable elements. *Genetics* **176**, 1323-37 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17435244>.
218. Brandt, J. *et al.* Transposable elements as a source of genetic innovation: expression and evolution of a family of retrotransposon-derived neogenes in mammals. *Gene* **345**, 101-11 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15716091>.
219. Volff, J.N. & Brosius, J. Modern genomes with retro-look: retrotransposed elements, retroposition and the origin of new genes. *Genome Dyn* **3**, 175-90 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/18753792>.
220. Oliver, K.R. & Greene, W.K. Transposable elements: powerful facilitators of evolution. *Bioessays* **31**, 703-14 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19415638>.
221. Deininger, P.L., Moran, J.V., Batzer, M.A. & Kazazian, H.H., Jr. Mobile elements and mammalian genome evolution. *Curr Opin Genet Dev* **13**, 651-8 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14638329>.
222. Kazazian, H.H., Jr. Mobile elements: drivers of genome evolution. *Science* **303**, 1626-32 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15016989>.
223. Bohne, A., Brunet, F., Galiana-Arnoux, D., Schultheis, C. & Volff, J.N. Transposable elements as drivers of genomic and biological diversity in vertebrates. *Chromosome Res* **16**, 203-15 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18293113>.
224. Biemont, C. & Vieira, C. What transposable elements tell us about genome organization and evolution: the case of *Drosophila*. *Cytogenet Genome Res* **110**, 25-34 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16093655>.
225. Arguello, J.R., Fan, C., Wang, W. & Long, M. Origination of chimeric genes through DNA-level recombination. *Genome Dyn* **3**, 131-46 (2007). PMID 18753789.
226. Feschotte, C. & Pritham, E.J. DNA transposons and the evolution of eukaryotic genomes. *Annu Rev Genet* **41**, 331-68 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/18076328>.

227. Beadle, G.W. The genes of men and molds. *Sci Am* **179**, 30-9 (1948).
<http://www.ncbi.nlm.nih.gov/pubmed/18884635>.
228. Ast, G. The Alternative Genome. *Scientific American* **292**, 58-65 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15915813>.
229. Portin, P. The elusive concept of the gene. *Hereditas* **146**, 112-7 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19712221>.
230. Hinman, V.F., Yankura, K.A. & McCauley, B.S. Evolution of gene regulatory network architectures: examples of subcircuit conservation and plasticity between classes of echinoderms. *Biochim Biophys Acta* **1789**, 326-32 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19284985>.
231. Erwin, D.H. & Davidson, E.H. The evolution of hierarchical gene regulatory networks. *Nat Rev Genet* **10**, 141-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19139764>.
232. Ray, P.S., Arif, A. & Fox, P.L. Macromolecular complexes as depots for releasable regulatory proteins. *Trends Biochem Sci* **32**, 158-64 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17321138>.
233. McClintock, B. Intranuclear systems controlling gene action and mutation. *Brookhaven Symp Biol*, 58-74 (1956). <http://www.ncbi.nlm.nih.gov/pubmed/13293421>.
234. Wunderlich, Z. & Mirny, L.A. Different gene regulation strategies revealed by analysis of binding motifs. *Trends Genet* **25**, 434-40 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19815308>.
235. Ptashne, M. & Gann, A. *Genes and Signals* (Laboratory Press, Cold Spring Harbor, NY, 2002).
236. Waddington, C.H. How do Cells Differentiate? *Scientific American* **189**, 108-116 (1953).
<http://www.nature.com/scientificamerican/journal/v189/n3/pdf/scientificamerican0953-108.pdf>.
237. Waddington, C.H. & Robertson, E. Selection for developmental canalisation. *Genet Res* **7**, 303-12 (1966). <http://www.ncbi.nlm.nih.gov/pubmed/5940870>.
238. Waddington, C.H. Gene regulation in higher cells. *Science* **166**, 639-40 (1969).
<http://www.ncbi.nlm.nih.gov/pubmed/5823305>.
239. Van Speybroeck, L. From epigenesis to epigenetics: the case of C. H. Waddington. *Ann N Y Acad Sci* **981**, 61-81 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12547674>.
240. Jablonka, E. & Lamb, M.J. The changing concept of epigenetics. *Ann N Y Acad Sci* **981**, 82-96 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12547675>.

241. Holliday, R. Epigenetics: a historical overview. *Epigenetics* **1**, 76-80 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17998809>.
242. Reik, W., Dean, W. & Walter, J. Epigenetic reprogramming in mammalian development. *Science* **293**, 1089-93 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11498579>.
243. Reik, W. Stability and flexibility of epigenetic gene regulation in mammalian development. *Nature* **447**, 425-32 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17522676>.
244. Jaenisch, R., Hochedlinger, K. & Eggan, K. Nuclear cloning, epigenetic reprogramming and cellular differentiation. *Novartis Found Symp* **265**, 107-18; discussion 118-28 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16050253>.
245. Feng, S., Jacobsen, S.E. & Reik, W. Epigenetic Reprogramming in Plant and Animal Development. *Science* **330**, 622 - 627 (2010). PMID 21030646.
246. Sapienza, C. Parental imprinting of genes. *Sci Am* **263**, 52-60 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/2146740>.
247. Shire, J.G. Unequal parental contributions: genomic imprinting in mammals. *New Biol* **1**, 115-20 (1989). <http://www.ncbi.nlm.nih.gov/pubmed/2488703>.
248. Sapienza, C. Genome imprinting: an overview. *Dev Genet* **17**, 185-7 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/8565324>.
249. Ohlsson, R., Tycko, B. & Sapienza, C. Monoallelic expression: 'there can only be one'. *Trends Genet* **14**, 435-8 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9825668>.
250. Nur, U. Heterochromatization and euchromatization of whole genomes in scale insects (Coccoidea: Homoptera). *Dev Suppl*, 29-34 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/2090427>.
251. van Driel, R., Fransz, P.F. & Verschure, P.J. The eukaryotic genome: a system regulated at different hierarchical levels. *J Cell Sci* **116**, 4067-75 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12972500>.
252. Chandler, V.L. Paramutation: from maize to mice. *Cell* **128**, 641-5 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17320501>.
253. Cuzin, F., Grandjean, V. & Rassoulzadegan, M. Inherited variation at the epigenetic level: paramutation from the plant to the mouse. *Curr Opin Genet Dev* **18**, 193-6 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18280137>.

254. Chandler, V.L. Paramutation's Properties and Puzzles. *Science* **330**, 628 - 629 (2010). PMID 21030647.
255. Weaver, I.C. Epigenetic effects of glucocorticoids. *Semin Fetal Neonatal Med* **14**, 143-50 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19217839>.
256. Weaver, J.R., Susiarjo, M. & Bartolomei, M.S. Imprinting and epigenetic changes in the early embryo. *Mamm Genome* **20**, 532-43 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19760320>.
257. Skinner, M.K., Manikkam, M. & Guerrero-Bosagna, C. Epigenetic transgenerational actions of environmental factors in disease etiology. *Trends Endocrinol Metab* **21**, 214-22 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20074974>.
258. Anway, M.D. & Skinner, M.K. Transgenerational effects of the endocrine disruptor vinclozolin on the prostate transcriptome and adult onset disease. *Prostate* **68**, 517-29 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18220299>.
259. Boyko, A. & Kovalchuk, I. Transgenerational response to stress in *Arabidopsis thaliana*. *Plant Signal Behav* **5**(2010). <http://www.ncbi.nlm.nih.gov/pubmed/20724818>.
260. Boyko, A. *et al.* Transgenerational adaptation of *Arabidopsis* to stress requires DNA methylation and the function of Dicer-like proteins. *PLoS One* **5**, e9514 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20209086>.
261. Lang-Mladek, C. *et al.* Transgenerational inheritance and resetting of stress-induced loss of epigenetic gene silencing in *Arabidopsis*. *Mol Plant* **3**, 594-602 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20410255>.
262. Szyf, M. The early life environment and the epigenome. *Biochim Biophys Acta* **1790**, 878-85 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19364482>.
263. Lange, U.C. & Schneider, R. What an epigenome remembers. *Bioessays* **32**, 659-68 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20658704>.
264. Henikoff, S. Heterochromatin function in complex genomes. *Biochim Biophys Acta* **1470**, O1-8 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10656988>.
265. Elgin, S.C. & Grewal, S.I. Heterochromatin: silence is golden. *Curr Biol* **13**, R895-8 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14654010>.

266. Huisenga, K.L., Brower-Toland, B. & Elgin, S.C. The contradictory definitions of heterochromatin: transcription and silencing. *Chromosoma* **115**, 110-22 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16506022>.
267. Spradling, A.C. Position effect variegation and genomic instability. *Cold Spring Harb Symp Quant Biol* **58**, 585-96 (1993). <http://www.ncbi.nlm.nih.gov/pubmed/7956073>.
268. Henikoff, S. A reconsideration of the mechanism of position effect. *Genetics* **138**, 1-5 (1994).
<http://www.ncbi.nlm.nih.gov/pubmed/8001776>.
269. Karpen, G.H. Position-effect variegation and the new biology of heterochromatin. *Curr Opin Genet Dev* **4**, 281-91 (1994). <http://www.ncbi.nlm.nih.gov/pubmed/8032206>.
270. Hazelrigg, T., Levis, R. & Rubin, G.M. Transformation of white locus DNA in drosophila: dosage compensation, zeste interaction, and position effects. *Cell* **36**, 469-81 (1984).
<http://www.ncbi.nlm.nih.gov/pubmed/6319027>.
271. Kornberg, R.D. & Klug, A. The Nucleosome *Scientific American* **244**, 52-64 (1981).
<http://www.ncbi.nlm.nih.gov/pubmed/7209486>.
272. Grunstein, M. Histones as Regulators of Genes. *Scientific American* **267**, 68-74 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1411455>.
273. McBryant, S.J., Adams, V.H. & Hansen, J.C. Chromatin architectural proteins. *Chromosome Res* **14**, 39-51 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16506095>.
274. Chodaparambil, J.V., Edayathumangalam, R.S., Bao, Y., Park, Y.J. & Luger, K. Nucleosome structure and function. *Ernst Schering Res Found Workshop*, 29-46 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16568947>.
275. Segal, E. *et al.* A genomic code for nucleosome positioning. *Nature* **442**, 772-8 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16862119>.
276. Peckham, H.E. *et al.* Nucleosome positioning signals in genomic DNA. *Genome Res* **17**, 1170-7 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17620451>.
277. Kaplan, N. *et al.* The DNA-encoded nucleosome organization of a eukaryotic genome. *Nature* **458**, 362-6 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19092803>.

278. Sapienza, C., Peterson, A.C., Rossant, J. & Balling, R. Degree of methylation of transgenes is dependent on gamete of origin. *Nature* **328**, 251-4 (1987).
<http://www.ncbi.nlm.nih.gov/pubmed/3600806>.
279. Henikoff, S., Furuyama, T. & Ahmad, K. Histone variants, nucleosome assembly and epigenetic inheritance. *Trends Genet* **20**, 320-6 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15219397>.
280. Chen, Z.J. & Tian, L. Roles of dynamic and reversible histone acetylation in plant development and polyploidy. *Biochim Biophys Acta* **1769**, 295-307 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17556080>.
281. Jenuwein, T. & Allis, C.D. Translating the histone code. *Science* **293**, 1074-80 (2001). PMID 11498575.
282. Peterson, C.L. & Laniel, M.A. Histones and histone modifications. *Curr Biol* **14**, R546-51 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15268870>.
283. Sims, R.J., 3rd & Reinberg, D. Is there a code embedded in proteins that is based on post-translational modifications? *Nat Rev Mol Cell Biol* **9**, 815-20 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18784729>.
284. Campos, E.I. & Reinberg, D. Histones: Annotating Chromatin. *Annu Rev Genet* **43**, 559-599 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19886812>.
285. Margueron, R., Trojer, P. & Reinberg, D. The key to development: interpreting the histone code? *Curr Opin Genet Dev* **15**, 163-76 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15797199>.
286. Appelgren, H., Kniola, B. & Ekwall, K. Distinct centromere domain structures with separate functions demonstrated in live fission yeast cells. *J Cell Sci* **116**, 4035-42 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12928332>.
287. Pidoux, A.L. & Allshire, R.C. The role of heterochromatin in centromere function. *Philos Trans R Soc Lond B Biol Sci* **360**, 569-79 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15905142>.
288. Scott, K.C., Merrett, S.L. & Willard, H.F. A heterochromatin barrier partitions the fission yeast centromere into discrete chromatin domains. *Curr Biol* **16**, 119-29 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16431364>.

289. Bonisch, C., Nieratschker, S.M., Orfanos, N.K. & Hake, S.B. Chromatin proteomics and epigenetic regulatory circuits. *Expert Rev Proteomics* **5**, 105-19 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18282127>.
290. Holmes, R. & Soloway, P.D. Regulation of imprinted DNA methylation. *Cytogenet Genome Res* **113**, 122-9 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16575171>.
291. Zheng, Y.G., Wu, J., Chen, Z. & Goodman, M. Chemical regulation of epigenetic modifications: opportunities for new cancer therapy. *Med Res Rev* **28**, 645-87 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18271058>.
292. Choudhary, C. *et al.* Lysine acetylation targets protein complexes and co-regulates major cellular functions. *Science* **325**, 834-40 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19608861>.
293. Szyf, M. The dynamic epigenome and its implications in toxicology. *Toxicol Sci* **100**, 7-23 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17675334>.
294. Cairns, B.R. The logic of chromatin architecture and remodelling at promoters. *Nature* **461**, 193-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19741699>.
295. Ikegami, K., Ohgane, J., Tanaka, S., Yagi, S. & Shiota, K. Interplay between DNA methylation, histone modification and chromatin remodeling in stem cells and during development. *Int J Dev Biol* **53**, 203-14 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19412882>.
296. Mattick, J.S. The Hidden Genetic Program of Complex Organisms. *Scientific American* **291**, 60-67 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15487671>.
297. Kelley, R.L. & Kuroda, M.I. Noncoding RNA genes in dosage compensation and imprinting. *Cell* **103**, 9-12 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11051542>.
298. Mattick, J.S. Non-coding RNAs: the architects of eukaryotic complexity. *EMBO Rep* **2**, 986-91 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11713189>.
299. Matzke, M.A. & Birchler, J.A. RNAi-mediated pathways in the nucleus. *Nat Rev Genet* **6**, 24-35 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15630419>.
300. Amaral, P.P. & Mattick, J.S. Noncoding RNA in development. *Mamm Genome* **19**, 454-92 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18839252>.

301. Andersen, A.A. & Panning, B. Epigenetic gene regulation by noncoding RNAs. *Curr Opin Cell Biol* **15**, 281-9 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12787769>.
302. Martienssen, R.A., Zaratiegui, M. & Goto, D.B. RNA interference and heterochromatin in the fission yeast *Schizosaccharomyces pombe*. *Trends Genet* **21**, 450-6 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15979194>.
303. Verdel, A., Vavasseur, A., Le Gorrec, M. & Touat-Todeschini, L. Common themes in siRNA-mediated epigenetic silencing pathways. *Int J Dev Biol* **53**, 245-57 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19412884>.
304. Koerner, M.V., Paufer, F.M., Huang, R. & Barlow, D.P. The function of non-coding RNAs in genomic imprinting. *Development* **136**, 1771-83 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19429783>.
305. Wheeler, B.S., Blau, J.A., Willard, H.F. & Scott, K.C. The impact of local genome sequence on defining heterochromatin domains. *PLoS Genet* **5**, e1000453 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19360117>.
306. Kellum, R. & Elgin, S.C. Chromatin boundaries: punctuating the genome. *Curr Biol* **8**, R521-4 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9705921>.
307. Bushey, A.M., Dorman, E.R. & Corces, V.G. Chromatin insulators: regulatory mechanisms and epigenetic inheritance. *Mol Cell* **32**, 1-9 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18851828>.
308. Eissenberg, J.C. & Elgin, S.C. Boundary functions in the control of gene expression. *Trends Genet* **7**, 335-40 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1781031>.
309. Kellum, R. & Schedl, P. A group of scs elements function as domain boundaries in an enhancer-blocking assay. *Mol Cell Biol* **12**, 2424-31 (1992). <http://www.ncbi.nlm.nih.gov/pubmed/1569958>.
310. Gerasimova, T.I., Byrd, K. & Corces, V.G. A chromatin insulator determines the nuclear localization of DNA. *Mol Cell* **6**, 1025-35 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11106742>.
311. de Laat, W. & Grosveld, F. Spatial organization of gene expression: the active chromatin hub. *Chromosome Res* **11**, 447-59 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12971721>.
312. Osborne, C.S. *et al.* Active genes dynamically colocalize to shared sites of ongoing transcription. *Nat Genet* **36**, 1065-71 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15361872>.

313. Scott, K.C., White, C.V. & Willard, H.F. An RNA polymerase III-dependent heterochromatin barrier at fission yeast centromere 1. *PLoS One* **2**, e1099 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17971862>.
314. Sutherland, H. & Bickmore, W.A. Transcription factories: gene expression in unions? *Nat Rev Genet* **10**, 457-66 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19506577>.
315. Lippman, Z. *et al.* Role of transposable elements in heterochromatin and epigenetic control. *Nature* **430**, 471-6 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15269773>.
316. Kotnova, A.P., Salenko, V.B., Lyubomirskaya, N.V. & Ilyin, Y.V. Structural organization of heterochromatin in *Drosophila melanogaster*: inverted repeats of transposable element clusters. *Dokl Biochem Biophys* **429**, 293-5 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/20101823>.
317. Buhler, M. & Gasser, S.M. Silent chromatin at the middle and ends: lessons from yeasts. *Embo J* **28**, 2149-2161 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19629038>.
318. Guetg, C. *et al.* The NoRC complex mediates the heterochromatin formation and stability of silent rRNA genes and centromeric repeats. *Embo J* **29**, 2135-46 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20168299>.
319. Thomas, C.M. Paradigms of plasmid organization. *Mol Microbiol* **37**, 485-91 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/10931342>.
320. Contursi, P. *et al.* Identification and autonomous replication capability of a chromosomal replication origin from the archaeon *Sulfolobus solfataricus*. *Extremophiles* **8**, 385-91 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15480865>.
321. O'Donnell, M. Replisome architecture and dynamics in *Escherichia coli*. *J Biol Chem* **281**, 10653-6 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16421093>.
322. Toro, E. & Shapiro, L. Bacterial chromosome organization and segregation. *Cold Spring Harb Perspect Biol* **2**, a000349 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20182613>.
323. Berbenetz, N.M., Nislow, C. & Brown, G.W. Diversity of Eukaryotic DNA Replication Origins Revealed by Genome-Wide Analysis of Chromatin Structure. *PLoS Genet* **6**, e1001092 (2010). PMID 20824081.

324. Sclafani, R.A. & Holzen, T.M. Cell cycle regulation of DNA replication. *Annu Rev Genet* **41**, 237-80 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17630848>.
325. Muck, J. & Zink, D. Nuclear organization and dynamics of DNA replication in eukaryotes. *Front Biosci* **14**, 5361-71 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19482618>.
326. Hazan, R. & Ben-Yehuda, S. Resolving chromosome segregation in bacteria. *J Mol Microbiol Biotechnol* **11**, 126-39 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16983190>.
327. Ebersbach, G. & Gerdes, K. Plasmid segregation mechanisms. *Annu Rev Genet* **39**, 453-79 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16285868>.
328. Tourand, Y., Lee, L. & Chaconas, G. Telomere resolution by Borrelia burgdorferi ResT through the collaborative efforts of tethered DNA binding domains. *Mol Microbiol* **64**, 580-90 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17462009>.
329. Kobryn, K. & Chaconas, G. The circle is broken: telomere resolution in linear replicons. *Curr Opin Microbiol* **4**, 558-64 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11587933>.
330. Greider, C.W. & Blackburn, E.H. Telomeres, Telomerase and Cancer. *Scientific American* **274**, 92-97 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8560215>.
331. Pardue, M.L. & DeBaryshe, P.G. Drosophila telomeres: two transposable elements with important roles in chromosomes. *Genetica* **107**, 189-96 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10952212>.
332. Hug, N. & Lingner, J. Telomere length homeostasis. *Chromosoma* **115**, 413-25 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16741708>.
333. Grandin, N. & Charbonneau, M. Protection against chromosome degradation at the telomeres. *Biochimie* **90**, 41-59 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/17764802>.
334. Villasante, A., de Pablos, B., Mendez-Lago, M. & Abad, J.P. Telomere maintenance in Drosophila: rapid transposon evolution at chromosome ends. *Cell Cycle* **7**, 2134-8 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18635962>.
335. Misri, S., Pandita, S., Kumar, R. & Pandita, T.K. Telomeres, histone code, and DNA damage response. *Cytogenet Genome Res* **122**, 297-307 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/19188699>.

336. Schoeftner, S. & Blasco, M.A. A 'higher order' of telomere regulation: telomere heterochromatin and telomeric RNAs. *Embo J* **28**, 2323-36 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19629032>.
337. Moser, B.A. & Nakamura, T.M. Protection and replication of telomeres in fission yeast. *Biochem Cell Biol* **87**, 747-58 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19898524>.
338. Lowe, J. & Amos, L.A. Evolution of cytomotive filaments: the cytoskeleton from prokaryotes to eukaryotes. *Int J Biochem Cell Biol* **41**, 323-9 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/18768164>.
339. Thanbichler, M. Synchronization of chromosome dynamics and cell division in bacteria. *Cold Spring Harb Perspect Biol* **2**, a000331 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20182599>.
340. Schumacher, M.A. Structural biology of plasmid partition: uncovering the molecular mechanisms of DNA segregation. *Biochem J* **412**, 1-18 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18426389>.
341. Sharp, J.A. & Kaufman, P.D. Chromatin proteins are determinants of centromere function. *Curr Top Microbiol Immunol* **274**, 23-52 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12596903>.
342. Vos, L.J., Famulski, J.K. & Chan, G.K. How to build a centromere: from centromeric and pericentromeric chromatin to kinetochore assembly. *Biochem Cell Biol* **84**, 619-39 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16936833>.
343. Heit, R., Underhill, D.A., Chan, G. & Hendzel, M.J. Epigenetic regulation of centromere formation and kinetochore function. *Biochem Cell Biol* **84**, 605-18 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16936832>.
344. Wenner, M. Nuclear Architecture. *Scientific American* **301**, 20-22 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19780440>.
345. Hozak, P. The nucleoskeleton and attached activities. *Exp Cell Res* **229**, 267-71 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8986608>.
346. Dechat, T. *et al.* Nuclear lamins: major factors in the structural organization and function of the nucleus and chromatin. *Genes Dev* **22**, 832-53 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18381888>.
347. Fedorova, E. & Zink, D. Nuclear genome organization: common themes and individual patterns. *Curr Opin Genet Dev* **19**, 166-71 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19321336>.

348. Zhao, R., Bodnar, M.S. & Spector, D.L. Nuclear neighborhoods and gene expression. *Curr Opin Genet Dev* **19**, 172-9 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19339170>.
349. O'Sullivan, J.M., Sontam, D.M., Grierson, R. & Jones, B. Repeated elements coordinate the spatial organization of the yeast genome. *Yeast* **26**, 125-38 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19235779>.
350. Pombo, A. *et al.* Specialized transcription factories within mammalian nuclei. *Crit Rev Eukaryot Gene Expr* **10**, 21-9 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10813391>.
351. Bartlett, J. *et al.* Specialized transcription factories. *Biochem Soc Symp*, 67-75 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16626288>.
352. Xu, M. & Cook, P.R. The role of specialized transcription factories in chromosome pairing. *Biochim Biophys Acta* **1783**, 2155-60 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18706455>.
353. Faro-Trindade, I. & Cook, P.R. Transcription factories: structures conserved during differentiation and evolution. *Biochem Soc Trans* **34**, 1133-7 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17073768>.
354. Xu, M. & Cook, P.R. Similar active genes cluster in specialized transcription factories. *J Cell Biol* **181**, 615-23 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18490511>.
355. Mitchell, J.A. & Fraser, P. Transcription factories are nuclear subcompartments that remain in the absence of transcription. *Genes Dev* **22**, 20-5 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18172162>.
356. Sandqvist, A. & Sistonen, L. Nuclear stress granules: the awakening of a sleeping beauty? *J Cell Biol* **164**, 15-7 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/14709538>.
357. Chiodi, I. *et al.* RNA recognition motif 2 directs the recruitment of SF2/ASF to nuclear stress bodies. *Nucleic Acids Res* **32**, 4127-36 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15302913>.
358. Brown, J.M. *et al.* Association between active genes occurs at nuclear speckles and is modulated by chromatin environment. *J Cell Biol* **182**, 1083-97 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18809724>.

359. Schneider, R. & Grosschedl, R. Dynamics and interplay of nuclear architecture, genome organization, and gene expression. *Genes Dev* **21**, 3027-43 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/18056419>.
360. Martin, W. & Koonin, E.V. Introns and the origin of nucleus-cytosol compartmentalization. *Nature* **440**, 41-5 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16511485>.
361. Haaf, T., Golub, E.I., Reddy, G., Radding, C.M. & Ward, D.C. Nuclear foci of mammalian Rad51 recombination protein in somatic cells after DNA damage and its localization in synaptonemal complexes. *Proc Natl Acad Sci U S A* **92**, 2298-302 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/7892263>.
362. Raderschall, E., Golub, E.I. & Haaf, T. Nuclear foci of mammalian recombination proteins are located at single-stranded DNA regions formed after DNA damage. *Proc Natl Acad Sci U S A* **96**, 1921-6 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10051570>.
363. Lisby, M. & Rothstein, R. Localization of checkpoint and repair proteins in eukaryotes. *Biochimie* **87**, 579-89 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15989975>.
364. Hediger, F., Neumann, F.R., Van Houwe, G., Dubrana, K. & Gasser, S.M. Live imaging of telomeres: yKu and Sir proteins define redundant telomere-anchoring pathways in yeast. *Curr Biol* **12**, 2076-89 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12498682>.
365. Corredor, E., Lukaszewski, A.J., Pachon, P., Allen, D.C. & Naranjo, T. Terminal regions of wheat chromosomes select their pairing partners in meiosis. *Genetics* **177**, 699-706 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17720899>.
366. Moralli, D., Chan, D.Y., Jefferson, A., Volpi, E.V. & Monaco, Z.L. HAC stability in murine cells is influenced by nuclear localization and chromatin organization. *BMC Cell Biol* **10**, 18 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19267891>.
367. Taddei, A. *et al.* The functional importance of telomere clustering: global changes in gene expression result from SIR factor dispersion. *Genome Res* **19**, 611-25 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19179643>.

368. Sakuno, T. & Watanabe, Y. Studies of meiosis disclose distinct roles of cohesion in the core centromere and pericentromeric regions. *Chromosome Res* **17**, 239-49 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19308704>.
369. Verschure, P.J. Positioning the genome within the nucleus. *Biol Cell* **96**, 569-77 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15519692>.
370. Mora, L., Sanchez, I., Garcia, M. & Ponsa, M. Chromosome territory positioning of conserved homologous chromosomes in different primate species. *Chromosoma* **115**, 367-75 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16607509>.
371. Kumaran, R.I., Thakar, R. & Spector, D.L. Chromatin dynamics and gene positioning. *Cell* **132**, 929-34 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18358806>.
372. Simonis, M. & de Laat, W. FISH-eyed and genome-wide views on the spatial organisation of gene expression. *Biochim Biophys Acta* **1783**, 2052-60 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18721832>.
373. Sengupta, K. *et al.* Position of human chromosomes is conserved in mouse nuclei indicating a species-independent mechanism for maintaining genome organization. *Chromosoma* **117**, 499-509 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18563425>.
374. Ferrai, C., de Castro, I.J., Lavitas, L., Chotalia, M. & Pombo, A. Gene positioning. *Cold Spring Harb Perspect Biol* **2**, a000588 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20484389>.
375. Parada, L.A., McQueen, P.G. & Misteli, T. Tissue-specific spatial organization of genomes. *Genome Biol* **5**, R44 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15239829>.
376. Rosa, A. & Everaers, R. Structure and dynamics of interphase chromosomes. *PLoS Comput Biol* **4**, e1000153 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18725929>.
377. Britten, R.J. & Kohne, D.E. Repeated Segments of DNA. *Scientific American* **222**, 24-31 (1970).
<http://www.ncbi.nlm.nih.gov/pubmed/5417826>.
378. Schmidt, T. LINEs, SINEs and repetitive DNA: non-LTR retrotransposons in plant genomes. *Plant Mol Biol* **40**, 903-10 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10527415>.

379. Sharma, S. & Raina, S.N. Organization and evolution of highly repeated satellite DNA sequences in plant chromosomes. *Cytogenet Genome Res* **109**, 15-26 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15753554>.
380. Richard, G.F., Kerrest, A. & Dujon, B. Comparative genomics and molecular dynamics of DNA repeats in eukaryotes. *Microbiol Mol Biol Rev* **72**, 686-727 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/19052325>.
381. Feschotte, C., Keswani, U., Ranganathan, N., Guibotsy, M.L. & Levine, D. Exploring repetitive DNA landscapes using REPCLASS, a tool that automates the classification of transposable elements in eukaryotic genomes. *Genome Biol Evol* **2009**, 205-20 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/20333191>.
382. Lander, E.S. *et al.* Initial sequencing and analysis of the human genome. *Nature* **409**, 860-921 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11237011>.
383. Saunders, N.J. *et al.* Repeat-associated phase variable genes in the complete genome sequence of *Neisseria meningitidis* strain MC58. *Mol Microbiol* **37**, 207-15 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/10931317>.
384. Ugarkovic, D. Functional elements residing within satellite DNAs. *EMBO Rep* **6**, 1035-9 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16264428>.
385. von Sternberg, R. & Shapiro, J.A. How repeated retroelements format genome function. *Cytogenet Genome Res* **110**, 108-16 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16093662>.
386. Nishihara, H. & Okada, N. Retroposons: genetic footprints on the evolutionary paths of life. *Methods Mol Biol* **422**, 201-25 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18629669>.
387. Bosco, G., Campbell, P., Leiva-Neto, J.T. & Markow, T.A. Analysis of *Drosophila* species genome size and satellite DNA content reveals significant differences among strains as well as between species. *Genetics* **177**, 1277-90 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/18039867>.
388. Kuhn, G.C., Sene, F.M., Moreira-Filho, O., Schwarzacher, T. & Heslop-Harrison, J.S. Sequence analysis, chromosomal distribution and long-range organization show that rapid turnover of new and old pBuM satellite DNA repeats leads to different patterns of variation in seven species of the

- Drosophila buzzatii cluster. *Chromosome Res* **16**, 307-24 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18266060>.
389. Ferree, P.M. & Barbash, D.A. Species-Specific Heterochromatin Prevents Mitotic Chromosome Segregation to Cause Hybrid Lethality in *Drosophila*. *PLoS Biol* **7**, e1000234 (2009). PMID 19859525.
390. Moller-Krull, M. *et al.* Retroposed elements and their flanking regions resolve the evolutionary history of xenarthran mammals (armadillos, anteaters, and sloths). *Mol Biol Evol* **24**, 2573-82 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17884827>.
391. Churakov, G. *et al.* Rodent evolution: back to the root. *Mol Biol Evol* **27**, 1315-26 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20100942>.
392. Berg, J.M., Tymoczko, J.L. & Stryer, L. *Biochemistry*, (W. H. Freeman and Co, New York, 2002). .
393. Griffith, F. The Significance of Pneumococcal Types. *J Hyg (Lond)* **27**, 113-59 (1928).
<http://www.ncbi.nlm.nih.gov/pubmed/20474956>.
394. Avery, O.T., C.M. MacLeod, M. McCarty. Studies on the chemical nature of the substance inducing transformation of Pneumococcal types: Induction of transformation by a desoxyribonucleic acid fraction isolated from Pneumococcus Type III. *J. Exp. Med.* **79**, 137-158 (1944). PMID 19871359.
395. Dubnau, D. DNA uptake in bacteria. *Annu Rev Microbiol* **53**, 217-44 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10547691>.
396. Chen, I., Dubnau, D. DNA uptake during bacterial transformation. *Nat Rev Microbiol* **2**, 241-249 (2004). PMID 15083159.
397. Hayes, W. *The Genetics of Bacteria and their Viruses* (2nd ed.), (Blackwell, London, 1968).
398. Prangishvili, D. *et al.* Conjugation in archaea: frequent occurrence of conjugative plasmids in Sulfolobus. *Plasmid* **40**, 190-202 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9806856>.
399. Juhas, M., Crook, D.W. & Hood, D.W. Type IV secretion systems: tools of bacterial horizontal gene transfer and virulence. *Cell Microbiol* **10**, 2377-86 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18549454>.

400. Frank, A.C., Alsmark, C.M., Thollesson, M. & Andersson, S.G. Functional divergence and horizontal transfer of type IV secretion systems. *Mol Biol Evol* **22**, 1325-36 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15746011>.
401. Averhoff, B. & Friedrich, A. Type IV pili-related natural transformation systems: DNA transport in mesophilic and thermophilic bacteria. *Arch Microbiol* **180**, 385-93 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14593449>.
402. Cascales, E. & Christie, P.J. The versatile bacterial type IV secretion systems. *Nat Rev Microbiol* **1**, 137-49 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/15035043>.
403. Alvarez-Martinez, C.E. & Christie, P.J. Biological diversity of prokaryotic type IV secretion systems. *Microbiol Mol Biol Rev* **73**, 775-808 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19946141>.
404. Heinemann, J.A. & Sprague, G.F., Jr. Bacterial conjugative plasmids mobilize DNA transfer between bacteria and yeast. *Nature* **340**, 205-9 (1989). <http://www.ncbi.nlm.nih.gov/pubmed/2666856>.
405. Zupan, J., Muth, T.R., Draper, O. & Zambryski, P. The transfer of DNA from agrobacterium tumefaciens into plants: a feast of fundamental insights. *Plant J* **23**, 11-28 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/10929098>.
406. Yoon, Y.G. & Koob, M.D. Transformation of isolated mammalian mitochondria by bacterial conjugation. *Nucleic Acids Res* **33**, e139 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16157861>.
407. Waters, V.L. Conjugation between bacterial and mammalian cells. *Nat Genet* **29**, 375-6 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11726922>.
408. Zupan, J.R. & Zambryski, P. Transfer of T-DNA from Agrobacterium to the plant cell. *Plant Physiol* **107**, 1041-7 (1995). <http://www.ncbi.nlm.nih.gov/pubmed/7770515>.
409. Gelvin, S.B. Agrobacterium-mediated plant transformation: the biology behind the "gene-jockeying" tool. *Microbiol Mol Biol Rev* **67**, 16-37, table of contents (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12626681>.
410. Broothaerts, W. *et al.* Gene transfer to plants by diverse species of bacteria. *Nature* **433**, 629-33 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15703747>.

411. Tzfira, T. & Citovsky, V. Agrobacterium-mediated genetic transformation of plants: biology and biotechnology. *Curr Opin Biotechnol* **17**, 147-54 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16459071>.
412. Haber, J.E., Ira, G., Malkova, A. & Sugawara, N. Repairing a double-strand chromosome break by homologous recombination: revisiting Robin Holliday's model. *Philos Trans R Soc Lond B Biol Sci* **359**, 79-86 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15065659>.
413. Cavalier-Smith, T. Origins of the machinery of recombination and sex. *Heredity* **88**, 125-41 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/11932771>.
414. Page, S.L. & Hawley, R.S. The genetics and molecular biology of the synaptonemal complex. *Annu Rev Cell Dev Biol* **20**, 525-58 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15473851>.
415. Zetka, M. Homologue pairing, recombination and segregation in *Caenorhabditis elegans*. *Genome Dyn* **5**, 43-55 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/18948706>.
416. Lao, J.P. & Hunter, N. Trying to Avoid Your Sister. *PLoS Biol* **8**, e1000519 (2010). PMID 20976046.
417. Udall, J.A., Quijada, P.A. & Osborn, T.C. Detection of chromosomal rearrangements derived from homologous recombination in four mapping populations of *Brassica napus* L. *Genetics* **169**, 967-79 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15520255>.
418. Lupski, J.R. & Stankiewicz, P. Genomic disorders: molecular mechanisms for rearrangements and conveyed phenotypes. *PLoS Genet* **1**, e49 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16444292>.
419. Mieczkowski, P.A., Lemoine, F.J. & Petes, T.D. Recombination between retrotransposons as a source of chromosome rearrangements in the yeast *Saccharomyces cerevisiae*. *DNA Repair (Amst)* **5**, 1010-20 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16798113>.
420. Gu, W., Zhang, F. & Lupski, J.R. Mechanisms for human genomic rearrangements. *Pathogenetics* **1**, 4 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/19014668>.
421. Argueso, J.L. *et al.* Double-strand breaks associated with repetitive DNA can reshape the genome. *Proc Natl Acad Sci U S A* **105**, 11845-50 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18701715>.
422. Lewis, L.K. & Resnick, M.A. Tying up loose ends: nonhomologous end-joining in *Saccharomyces cerevisiae*. *Mutat Res* **451**, 71-89 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10915866>.

423. Pastwa, E. & Blasiak, J. Non-homologous DNA end joining. *Acta Biochim Pol* **50**, 891-908 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14739985>.
424. Weterings, E. & Chen, D.J. The endless tale of non-homologous end-joining. *Cell Res* **18**, 114-24 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18166980>.
425. Stephanou, N.C. *et al.* Mycobacterial nonhomologous end joining mediates mutagenic repair of chromosomal double-strand DNA breaks. *J Bacteriol* **189**, 5237-46 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17496093>.
426. Zhuang, J., Jiang, G., Willers, H. & Xia, F. Exonuclease function of human Mre11 promotes deletional nonhomologous end joining. *J Biol Chem* **284**, 30565-73 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19744924>.
427. Yu, X. & Gabriel, A. Reciprocal translocations in *Saccharomyces cerevisiae* formed by nonhomologous end joining. *Genetics* **166**, 741-51 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15020464>.
428. Haber, J.E. Transpositions and translocations induced by site-specific double-strand breaks in budding yeast. *DNA Repair (Amst)* **5**, 998-1009 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16807137>.
429. Lisby, M. & Rothstein, R. Choreography of recombination proteins during the DNA damage response. *DNA Repair (Amst)* **8**, 1068-76 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19473884>.
430. Gopaul, D.N. & Duyne, G.D. Structure and mechanism in site-specific recombination. *Curr Opin Struct Biol* **9**, 14-20 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10047575>.
431. Grindley, N.D., Whiteson, K.L. & Rice, P.A. Mechanisms of site-specific recombination. *Annu Rev Biochem* **75**, 567-605 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16756503>.
432. Van Duyne, G.D. A structural view of cre-loxp site-specific recombination. *Annu Rev Biophys Biomol Struct* **30**, 87-104 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11340053>.
433. Ghosh, K. & Van Duyne, G.D. Cre-loxP biochemistry. *Methods Cell Biol* **28**, 374-83 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12431441>.

434. Chen, Y. & Rice, P.A. New insight into site-specific recombination from Flp recombinase-DNA structures. *Annu Rev Biophys Biomol Struct* **32**, 135-59 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12598365>.
435. Segall, A.M. & Craig, N.L. New wrinkles and folds in site-specific recombination. *Mol Cell* **19**, 433-5 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16109368>.
436. Smith, M.C. & Thorpe, H.M. Diversity in the serine recombinases. *Mol Microbiol* **44**, 299-307 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11972771>.
437. Weinacht, K.G. *et al.* Tyrosine site-specific recombinases mediate DNA inversions affecting the expression of outer surface proteins of *Bacteroides fragilis*. *Mol Microbiol* **53**, 1319-30 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15387812>.
438. Manson, J.M. & Gilmore, M.S. Pathogenicity island integrase cross-talk: a potential new tool for virulence modulation. *Mol Microbiol* **61**, 555-9 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16879637>.
439. Juhas, M. *et al.* Genomic islands: tools of bacterial horizontal gene transfer and evolution. *FEMS Microbiol Rev* **33**, 376-93 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19178566>.
440. Rolland, T., Neuveglise, C., Sacerdot, C. & Dujon, B. Insertion of horizontally transferred genes within conserved syntenic regions of yeast genomes. *PLoS One* **4**, e6515 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19654869>.
441. McClintock, B. The origin and behavior of mutable loci in maize. *Proc Natl Acad Sci U S A* **36**, 344-55 (1950). <http://www.ncbi.nlm.nih.gov/pubmed/15430309>.
442. McClintock, B. Induction of Instability at Selected Loci in Maize. *Genetics* **38**, 579-99 (1953).
<http://www.ncbi.nlm.nih.gov/pubmed/17247459>.
443. Shapiro, J.A. Letting *Escherichia coli* teach me about genome engineering. *Genetics* **183**, 1205-14 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19996374>.
444. Siguier, P., Filee, J. & Chandler, M. Insertion sequences in prokaryotic genomes. *Curr Opin Microbiol* **9**, 526-31 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16935554>.
445. Bessereau, J.L. Transposons in *C. elegans*. *WormBook*, 1-13 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/18023126>.

446. Filee, J., Siguier, P. & Chandler, M. Insertion sequence diversity in archaea. *Microbiol Mol Biol Rev* **71**, 121-57 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17347521>.
447. Parks, A.R. & Peters, J.E. Tn7 elements: engendering diversity from chromosomes to episomes. *Plasmid* **61**, 1-14 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/18951916>.
448. Peters, J.E. & Craig, N.L. Tn7 recognizes transposition target structures associated with DNA replication using the DNA-binding protein TnsE. *Genes Dev* **15**, 737-47 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11274058>.
449. Posey, J.E., Pytlos, M.J., Sinden, R.R. & Roth, D.B. Target DNA structure plays a critical role in RAG transposition. *PLoS Biol* **4**, e350 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/17105341>.
450. Tobes, R. & Pareja, E. Bacterial repetitive extragenic palindromic sequences are DNA targets for Insertion Sequence elements. *BMC Genomics* **7**, 62 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16563168>.
451. Mizuuchi, K. Mechanism of transposition of bacteriophage Mu: polarity of the strand transfer reaction at the initiation of transposition. *Cell* **39**, 395-404 (1984).
<http://www.ncbi.nlm.nih.gov/pubmed/6094017>.
452. Haniford, D.B. & Chaconas, G. Mechanistic aspects of DNA transposition. *Curr Opin Genet Dev* **2**, 698-704 (1992). <http://www.ncbi.nlm.nih.gov/pubmed/1333854>.
453. Chaconas, G. Studies on a "jumping gene machine": higher-order nucleoprotein complexes in Mu DNA transposition. *Biochem Cell Biol* **77**, 487-91 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10668626>.
454. Hickman, A.B., Chandler, M. & Dyda, F. Integrating prokaryotes and eukaryotes: DNA transposases in light of structure. *Crit Rev Biochem Mol Biol* **45**, 50-69 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20067338>.
455. Duval-Valentin, G., Marty-Cointin, B. & Chandler, M. Requirement of IS911 replication before integration defines a new bacterial transposition pathway. *Embo J* **23**, 3897-906 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15359283>.

456. Shapiro, J.A. Molecular model for the transposition and replication of bacteriophage Mu and other transposable elements. *Proc Natl Acad Sci U S A* **76**, 1933-7 (1979).
<http://www.ncbi.nlm.nih.gov/pubmed/287033>.
457. Roberts, A.P. *et al.* Revised nomenclature for transposable genetic elements. *Plasmid* **60**, 167-73 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18778731>.
458. Chandler, M., Roulet, E., Silver, L., Boy de la Tour, E. & Caro, L. Tn10 mediated integration of the plasmid R100.1 into the bacterial chromosome: inverse transposition. *Mol Gen Genet* **173**, 23-30 (1979). <http://www.ncbi.nlm.nih.gov/pubmed/381840>.
459. Muster, C.J., MacHattie, L.A. & Shapiro, J.A. p lambda CM system: observations on the roles of transposable elements in formation and breakdown of plasmids derived from bacteriophage lambda replicons. *J Bacteriol* **153**, 976-90 (1983). <http://www.ncbi.nlm.nih.gov/pubmed/6296061>.
460. Nag, D.K. *et al.* IS50-mediated inverse transposition: specificity and precision. *Gene* **34**, 17-26 (1985). <http://www.ncbi.nlm.nih.gov/pubmed/2989101>.
461. Engels, W.R. Gene Duplication. *Science* **214**, 786-787 (1981).
<http://www.ncbi.nlm.nih.gov/pubmed/17744398>.
462. Engels, W.R. & Preston, C.R. Formation of chromosome rearrangements by P factors in Drosophila. *Genetics* **107**, 657-78 (1984). <http://www.ncbi.nlm.nih.gov/pubmed/6086453>.
463. Preston, C.R., Sved, J.A. & Engels, W.R. Flanking duplications and deletions associated with P-induced male recombination in Drosophila. *Genetics* **144**, 1623-38 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8978050>.
464. Gray, Y.H. It takes two transposons to tango: transposable-element-mediated chromosomal rearrangements. *Trends Genet* **16**, 461-8 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11050333>.
465. Laski, F.A., Rio, D.C. & Rubin, G.M. Tissue specificity of Drosophila P element transposition is regulated at the level of mRNA splicing. *Cell* **44**, 7-19 (1986).
<http://www.ncbi.nlm.nih.gov/pubmed/3000622>.
466. Siebel, C.W. & Rio, D.C. Regulated splicing of the Drosophila P transposable element third intron in vitro: somatic repression. *Science* **248**, 1200-8 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/2161558>.

467. Rho, M., Choi, J.H., Kim, S., Lynch, M. & Tang, H. De novo identification of LTR retrotransposons in eukaryotic genomes. *BMC Genomics* **8**, 90 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17407597>.
468. Llorens, C., Munoz-Pomer, A., Bernad, L., Botella, H. & Moya, A. Network dynamics of eukaryotic LTR retroelements beyond phylogenetic trees. *Biol Direct* **4**, 41 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19883502>.
469. Coffin, J.M., Hughes, S.H. & Varmus, H.E. *Retroviruses* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1997).
470. Varmus, H. Reverse Transcription. *Scientific American* **257**, 56-64 (1987).
<http://www.ncbi.nlm.nih.gov/pubmed/2443971>.
471. Temin, H. The participation of DNA in rous sarcoma virus production. *Virology* **23**, 486-494 (1964). PMID 14204701.
472. Lwoff, A. Lysogeny. *Bacteriol Rev* **17**, 269-337 (1953).
<http://www.ncbi.nlm.nih.gov/pubmed/13105613>.
473. Lwoff, A. The Life Cycle of a Virus. *Scientific American* **190**, 34-37 (1954).
<http://www.nature.com/scientificamerican/journal/v190/n3/pdf/scientificamerican0354-34.pdf>.
474. Lwoff, A. Interaction among virus, cell, and organism. *Science* **152**, 1216-20 (1966).
<http://www.ncbi.nlm.nih.gov/pubmed/5937114>.
475. Cheng, Z. & Menees, T.M. RNA Branching and Debranching in the Yeast Retrovirus-like Element Ty1. *Science* **303**, 240-243 (2004). PMID 14716018.
476. Eickbush, T.H. & Jamburuthugoda, V.K. The diversity of retrotransposons and the properties of their reverse transcriptases. *Virus Res* **134**, 221-34 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18261821>.
477. Basu, V.P. *et al.* Strand transfer events during HIV-1 reverse transcription. *Virus Res* **134**, 19-38 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18279992>.
478. Engelman, A., Mizuuchi, K. & Craigie, R. HIV-1 DNA integration: mechanism of viral DNA cleavage and DNA strand transfer. *Cell* **67**, 1211-21 (1991).
<http://www.ncbi.nlm.nih.gov/pubmed/1760846>.

479. Polard, P. & Chandler, M. Bacterial transposases and retroviral integrases. *Mol Microbiol* **15**, 13-23 (1995). <http://www.ncbi.nlm.nih.gov/pubmed/7752887>.
480. Li, M., Mizuuchi, M., Burke, T.R., Jr. & Craigie, R. Retroviral DNA integration: reaction pathway and critical intermediates. *Embo J* **25**, 1295-304 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16482214>.
481. Goodwin, T.J. & Poulter, R.T. The DIRS1 group of retrotransposons. *Mol Biol Evol* **18**, 2067-82 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11606703>.
482. Poulter, R.T. & Goodwin, T.J. DIRS-1 and the other tyrosine recombinase retrotransposons. *Cytogenet Genome Res* **110**, 575-88 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16093711>.
483. Rous, P. A transmissible avian neoplasm. *J Exp Med* **12**, 696-705 (1910). .
484. Van Epps, H.L. Peyton Rous, father of the tumor virus. *Journal of Experimental Medicine* **201**, 320 (2005). PMID 15756727.
485. Maeda, N., Fan, H. & Yoshikai, Y. Oncogenesis by retroviruses: old and new paradigms. *Rev Med Virol* **18**, 387-405 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18729235>.
486. Swain, A. & Coffin, J.M. Mechanism of transduction by retroviruses. *Science* **255**, 841-5 (1992). PMID 1371365.
487. Tsichlis, P.N., Strauss, P.G. & Hu, L.F. A common region for proviral DNA integration in MoMuLV-induced rat thymic lymphomas. *Nature* **302**, 445-9 (1983).
<http://www.ncbi.nlm.nih.gov/pubmed/6300684>.
488. Tsichlis, P.N. Oncogenesis by Moloney murine leukemia virus. *Anticancer Res* **7**, 171-80 (1987).
<http://www.ncbi.nlm.nih.gov/pubmed/3592629>.
489. Uren, A.G., Kool, J., Berns, A. & van Lohuizen, M. Retroviral insertional mutagenesis: past, present and future. *Oncogene* **24**, 7656-72 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16299527>.
490. Mellentin-Michelotti, J., John, S., Pennie, W.D., Williams, T. & Hager, G.L. The 5' enhancer of the mouse mammary tumor virus long terminal repeat contains a functional AP-2 element. *J Biol Chem* **269**, 31983-90 (1994). <http://www.ncbi.nlm.nih.gov/pubmed/7989375>.

491. Errede, B. *et al.* Mating signals control expression of mutations resulting from insertion of a transposable repetitive element adjacent to diverse yeast genes. *Cell* **22**, 427-36 (1980).
<http://www.ncbi.nlm.nih.gov/pubmed/6256080>.
492. Errede, B. *et al.* Studies on transposable elements in yeast. I. ROAM mutations causing increased expression of yeast genes: their activation by signals directed toward conjugation functions and their formation by insertion of Ty1 repetitive elements. II. deletions, duplications, and transpositions of the COR segment that encompasses the structural gene of yeast iso-1-cytochrome c. *Cold Spring Harb Symp Quant Biol* **45 Pt 2**, 593-607 (1981). <http://www.ncbi.nlm.nih.gov/pubmed/6266753>.
493. Modolell, J., Bender, W. & Meselson, M. Drosophila melanogaster mutations suppressible by the suppressor of Hairy-wing are insertions of a 7.3-kilobase mobile element. *Proc Natl Acad Sci U S A* **80**, 1678-82 (1983). <http://www.ncbi.nlm.nih.gov/pubmed/6300868>.
494. Peifer, M. & Bender, W. Sequences of the gypsy transposon of Drosophila necessary for its effects on adjacent genes. *Proc Natl Acad Sci U S A* **85**, 9650-4 (1988).
<http://www.ncbi.nlm.nih.gov/pubmed/2849113>.
495. Harrison, D.A., Geyer, P.K., Spana, C. & Corces, V.G. The gypsy retrotransposon of Drosophila melanogaster: mechanisms of mutagenesis and interaction with the suppressor of Hairy-wing locus. *Dev Genet* **10**, 239-48 (1989). <http://www.ncbi.nlm.nih.gov/pubmed/2472241>.
496. Corces, V.G. & Geyer, P.K. Interactions of retrotransposons with the host genome: the case of the gypsy element of Drosophila. *Trends Genet* **7**, 86-90 (1991).
<http://www.ncbi.nlm.nih.gov/pubmed/1851585>.
497. Ilyin, Y.V., Lyubomirskaya, N.V. & Kim, A.I. Retrotransposon Gypsy and genetic instability in Drosophila (review). *Genetica* **85**, 13-22 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1723391>.
498. Pelisson, A., Mejlumian, L., Robert, V., Terzian, C. & Bucheton, A. Drosophila germline invasion by the endogenous retrovirus gypsy: involvement of the viral env gene. *Insect Biochem Mol Biol* **32**, 1249-56 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12225916>.
499. Gdula, D.A., Gerasimova, T.I. & Corces, V.G. Genetic and molecular analysis of the gypsy chromatin insulator of Drosophila. *Proc Natl Acad Sci U S A* **93**, 9378-83 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8790337>.

500. Cai, H.N. & Levine, M. The gypsy insulator can function as a promoter-specific silencer in the Drosophila embryo. *Embo J* **16**, 1732-41 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9130717>.
501. Chen, S. & Corces, V.G. The gypsy insulator of Drosophila affects chromatin structure in a directional manner. *Genetics* **159**, 1649-58 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11779804>.
502. Byrd, K. & Corces, V.G. Visualization of chromatin domains created by the gypsy insulator of Drosophila. *J Cell Biol* **162**, 565-74 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12925706>.
503. Fawcett, D.H., Lister, C.K., Kellett, E. & Finnegan, D.J. Transposable elements controlling I-R hybrid dysgenesis in *D. melanogaster* are similar to mammalian LINEs. *Cell* **47**, 1007-15 (1986). <http://www.ncbi.nlm.nih.gov/pubmed/2430722>.
504. Bucheton, A. I transposable elements and I-R hybrid dysgenesis in Drosophila. *Trends Genet* **6**, 16-21 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/2158161>.
505. Busseau, I., Chaboissier, M.C., Pelisson, A. & Bucheton, A. I factors in *Drosophila melanogaster*: transposition under control. *Genetica* **93**, 101-16 (1994). <http://www.ncbi.nlm.nih.gov/pubmed/7813907>.
506. Lyozin, G.T. *et al.* The structure and evolution of Penelope in the virilis species group of Drosophila: an ancient lineage of retroelements. *J Mol Evol* **52**, 445-56 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11443348>.
507. Yang, H.P. & Barbash, D.A. Abundant and species-specific DINE-1 transposable elements in 12 Drosophila genomes. *Genome Biol* **9**, R39 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18291035>.
508. Sezutsu, H., Nitasaka, E. & Yamazaki, T. Evolution of the LINE-like I element in the *Drosophila melanogaster* species subgroup. *Mol Gen Genet* **249**, 168-78 (1995). <http://www.ncbi.nlm.nih.gov/pubmed/7500938>.
509. Brosius, J. RNAs from all categories generate retrosequences that may be exapted as novel genes or regulatory elements. *Gene* **238**, 115–134 (1999). PMID 10570990.
510. Pavlicek, A., Gentles, A.J., Paces, J., Paces, V. & Jurka, J. Retroposition of processed pseudogenes: the impact of RNA stability and translational control. *Trends Genet* **22**, 69-73 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16356584>.

511. Druker, R. & Whitelaw, E. Retrotransposon-derived elements in the mammalian genome: a potential source of disease. *J Inher Metab Dis* **27**, 319-30 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15190191>.
512. Gogvadze, E. & Buzdin, A. Retroelements and their impact on genome evolution and functioning. *Cell Mol Life Sci* **66**, 3727-42 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19649766>.
513. Goodier, J.L., Ostertag, E.M. & Kazazian, H.H., Jr. Transduction of 3'-flanking sequences is common in L1 retrotransposition. *Hum Mol Genet* **9**, 653-7 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/10699189>.
514. Moran, J.V., DeBerardinis, R.J. & Kazazian, H.H., Jr. Exon shuffling by L1 retrotransposition. *Science* **283**, 1530-4 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10066175>.
515. Szak, S.T., Pickeral, O.K., Landsman, D. & Boeke, J.D. Identifying related L1 retrotransposons by analyzing 3' transduced sequences. *Genome Biol* **4**, R30 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12734010>.
516. Ejima, Y. & Yang, L. Trans mobilization of genomic DNA as a mechanism for retrotransposon-mediated exon shuffling. *Hum Mol Genet* **12**, 1321-8 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12761047>.
517. Lovering, R., Harden, N. & Ashburner, M. The molecular structure of TE146 and its derivatives in *Drosophila melanogaster*. *Genetics* **128**, 357-72 (1991).
<http://www.ncbi.nlm.nih.gov/pubmed/1649070>.
518. Mills, R.E. *et al.* Recently mobilized transposons in the human and chimpanzee genomes. *Am J Hum Genet* **78**, 671-9 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16532396>.
519. Bantysh, O.B. & Buzdin, A.A. Novel Family of Human Transposable Elements Formed Due to Fusion of the First Exon of Gene MAST2 with Retrotransposon SVA. *Biochemistry (Mosc)* **74**, 1393-9 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19961423>.
520. Wang, H. *et al.* SVA elements: a hominid-specific retroposon family. *J Mol Biol* **354**, 994-1007 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16288912>.

521. Ostertag, E.M., Goodier, J.L., Zhang, Y. & Kazazian, H.H., Jr. SVA elements are nonautonomous retrotransposons that cause disease in humans. *Am J Hum Genet* **73**, 1444-51 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14628287>.
522. Hancks, D.C., Ewing, A.D., Chen, J.E., Tokunaga, K. & Kazazian, H.H., Jr. Exon-trapping mediated by the human retrotransposon SVA. *Genome Res* **19**, 1983-91 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19635844>.
523. Damert, A. *et al.* 5'-Transducing SVA retrotransposon groups spread efficiently throughout the human genome. *Genome Res* **19**, 1992-2008 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19652014>.
524. Xing, J. *et al.* Mobile elements create structural variation: analysis of a complete human genome. *Genome Res* **19**, 1516-26 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19439515>.
525. Mills, R.E., Bennett, E.A., Iskow, R.C. & Devine, S.E. Which transposable elements are active in the human genome? *Trends Genet* **23**, 183-91 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17331616>.
526. Ferat, J.L. & Michel, F. Group II self splicing introns in bacteria. *Nature* **364**, 358-361 (1993). PMID 7687328.
527. Dunny, G.M. & McKay, L.L. Group II introns and expression of conjugative transfer functions in lactic acid bacteria. *Antonie Van Leeuwenhoek* **76**, 77-88 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10532373>.
528. Lambowitz, A.M. & Zimmerly, S. Mobile group II introns. *Annu. Rev. Genet.* **38**, 1-35 (2004). PMID 15568970.
529. Valles, Y., Halanych, K.M. & Boore, J.L. Group II introns break new boundaries: presence in a bilaterian's genome. *PLoS One* **3**, e1488 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18213396>.
530. Mohr, G. & Lambowitz, A.M. Putative proteins related to group II intron reverse transcriptase/maturases are encoded by nuclear genes in higher plants. *Nucleic Acids Res* **31**, 647-52 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12527773>.
531. Cech, T.R. RNA as an Enzyme. *Scientific American* **255**, 64-75 (1986).
<http://www.ncbi.nlm.nih.gov/pubmed/2430331>.

532. Roitzsch, M. & Pyle, A.M. The linear form of a group II intron catalyzes efficient autocatalytic reverse splicing, establishing a potential for mobility. *RNA* **15**, 473-82 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19168748>.
533. Fedorova, O. & Zingler, N. Group II introns: structure, folding and splicing mechanism. *Biol Chem* **388**, 665-78 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17570818>.
534. Lehmann, K. & Schmidt, U. Group II introns: structure and catalytic versatility of large natural ribozymes. *Crit Rev Biochem Mol Biol* **38**, 249-303 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12870716>.
535. Morl, M. & Schmelzer, C. Integration of group II intron bII into a foreign RNA by reversal of the self-splicing reaction in vitro. *Cell* **60**, 629-36 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/2406027>.
536. Eickbush, T.H. Mobile introns: retrohoming by complete reverse splicing. *Curr Biol* **9**, R11-4 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/9889113>.
537. Eskes, R. *et al.* Multiple homing pathways used by yeast mitochondrial group II introns. *Mol Cell Biol* **20**, 8432-46 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11046140>.
538. Zimmerly, S., Guo, H., Perlman, P.S. & Lambowitz, A.M. Group II intron mobility occurs by target DNA-primed reverse transcription. *Cell* **82**, 545-54 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/7664334>.
539. Mohr, S., Matsuura, M., Perlman, P.S. & Lambowitz, A.M. A DEAD-box protein alone promotes group II intron splicing and reverse splicing by acting as an RNA chaperone. *Proc Natl Acad Sci U S A* **103**, 3569-74 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16505350>.
540. Smith, D., Zhong, J., Matsuura, M., Lambowitz, A.M. & Belfort, M. Recruitment of host functions suggests a repair pathway for late steps in group II intron retrohoming. *Genes Dev* **19**, 2477-87 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16230535>.
541. Watanabe, K. & Lambowitz, A.M. High-affinity binding site for a group II intron-encoded reverse transcriptase/maturase within a stem-loop structure in the intron RNA. *RNA* **10**, 1433-43 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15273321>.

542. Cui, X., Matsuura, M., Wang, Q., Ma, H. & Lambowitz, A.M. A group II intron-encoded maturase functions preferentially in cis and requires both the reverse transcriptase and X domains to promote RNA splicing. *J Mol Biol* **340**, 211-31 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15201048>.
543. Toor, N., Rajashankar, K., Keating, K.S. & Pyle, A.M. Structural basis for exon recognition by a group II intron. *Nat Struct Mol Biol* **15**, 1221-2 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18953333>.
544. Dickson, L. *et al.* Retrotransposition of a yeast group II intron occurs by reverse splicing directly into ectopic DNA sites. *Proc Natl Acad Sci U S A* **98**, 13207-12 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11687644>.
545. Costa, M., Michel, F. & Toro, N. Potential for alternative intron-exon pairings in group II intron RmInt1 from Sinorhizobium meliloti and its relatives. *RNA* **12**, 338-41 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16431983>.
546. Zhong, J. & Lambowitz, A.M. Group II intron mobility using nascent strands at DNA replication forks to prime reverse transcription. *Embo J* **22**, 4555-65 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12941706>.
547. Robart, A.R., Seo, W. & Zimmerly, S. Insertion of group II intron retroelements after intrinsic transcriptional terminators. *Proc Natl Acad Sci U S A* **104**, 6620-5 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17420455>.
548. Karberg, M. *et al.* Group II introns as controllable gene targeting vectors for genetic manipulation of bacteria. *Nat Biotechnol* **19**, 1162-7 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11731786>.
549. Zhong, J., Karberg, M. & Lambowitz, A.M. Targeted and random bacterial gene disruption using a group II intron (targetron) vector containing a retrotransposition-activated selectable marker. *Nucleic Acids Res* **31**, 1656-64 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12626707>.
550. Jones, J.P., 3rd *et al.* Retargeting mobile group II introns to repair mutant genes. *Mol Ther* **11**, 687-94 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15851007>.
551. Guo, H. *et al.* Group II introns designed to insert into therapeutically relevant DNA target sites in human cells. *Science* **289**, 452-7 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10903206>.

552. Rawsthorne, H., Turner, K.N. & Mills, D.A. Multicopy integration of heterologous genes, using the lactococcal group II intron targeted to bacterial insertion sequences. *Appl Environ Microbiol* **72**, 6088-93 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16957233>.
553. Mohr, G., Ghanem, E. & Lambowitz, A.M. Mechanisms used for genomic proliferation by thermophilic group II introns. *PLoS Biol* **8**, e1000391 (2010). PMID 20543989.
554. Liu, X.Q. Protein-splicing intein: Genetic mobility, origin, and evolution. *Annu Rev Genet* **34**, 61-76 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11092822>.
555. Gogarten, J.P., Senejani, A.G., Zhaxybayeva, O., Olendzenski, L. & Hilario, E. Inteins: structure, function, and evolution. *Annu Rev Microbiol* **56**, 263-87 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12142479>.
556. Elleuche, S. & Poggeler, S. Inteins, valuable genetic elements in molecular biology and biotechnology. *Appl Microbiol Biotechnol* **87**, 479-89 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20449740>.
557. Gimble, F.S. Invasion of a multitude of genetic niches by mobile endonuclease genes. *FEMS Microbiol Lett* **185**, 99-107 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10754232>.
558. Gogarten, J.P. & Hilario, E. Inteins, introns, and homing endonucleases: recent revelations about the life cycle of parasitic genetic elements. *BMC Evol Biol* **6**, 94 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17101053>.
559. Raghavan, R. & Minnick, M.F. Group I introns and inteins: disparate origins but convergent parasitic strategies. *J Bacteriol* **191**, 6193-202 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19666710>.
560. Perler, F.B. InBase: the Intein Database. *Nucleic Acids Res* **30**, 383-4 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/11752343>.
561. Goodwin, T.J., Butler, M.I. & Poulter, R.T. Multiple, non-allelic, intein-coding sequences in eukaryotic RNA polymerase genes. *BMC Biol* **4**, 38 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17069655>.
562. Liu, M. *et al.* Reverse transcriptase-mediated tropism switching in *Bordetella* bacteriophage. *Science* **295**, 2091-4 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11896279>.

563. Doulatov, S. *et al.* Tropism switching in *Bordetella* bacteriophage defines a family of diversity-generating retroelements. *Nature* **431**, 476-81 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15386016>.
564. Guo, H. *et al.* Diversity-generating retroelement homing regenerates target sequences for repeated rounds of codon rewriting and protein diversification. *Mol Cell* **31**, 813-23 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18922465>.
565. Medhekar, B. & Miller, J.F. Diversity-generating retroelements. *Curr Opin Microbiol* **10**, 388-95 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17703991>.
566. Wisniewski-Dye, F. & Vial, L. Phase and antigenic variation mediated by genome modifications. *Antonie Van Leeuwenhoek* **94**, 493-515 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18663597>.
567. Silverman, M., Zieg, J., Hilmen, M. & Simon, M. Phase variation in *Salmonella*: genetic analysis of a recombinational switch. *Proc Natl Acad Sci U S A* **76**, 391-5 (1979).
<http://www.ncbi.nlm.nih.gov/pubmed/370828>.
568. Lysnyansky, I., Ron, Y. & Yogev, D. Juxtaposition of an active promoter to vsp genes via site-specific DNA inversions generates antigenic variation in *Mycoplasma bovis*. *J Bacteriol* **183**, 5698-708 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11544233>.
569. Blomfield, I.C. The regulation of pap and type 1 fimbriation in *Escherichia coli*. *Adv Microb Physiol* **45**, 1-49 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11450107>.
570. Emerson, J.E. *et al.* A novel genetic switch controls phase variable expression of CwpV, a *Clostridium difficile* cell wall protein. *Mol Microbiol* **74**, 541-56 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19656296>.
571. Kutsukake, K., Nakashima, H., Tominaga, A. & Abo, T. Two DNA invertases contribute to flagellar phase variation in *Salmonella enterica* serovar *Typhimurium* strain LT2. *J Bacteriol* **188**, 950-7 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16428399>.
572. Plasterk, R.H., Simon, M.I. & Barbour, A.G. Transposition of structural genes to an expression sequence on a linear plasmid causes antigenic variation in the bacterium *Borrelia hermsii*. *Nature* **318**, 257-63 (1985). <http://www.ncbi.nlm.nih.gov/pubmed/4069202>.

573. Stern, A., Brown, M., Nickel, P. & Meyer, T.F. Opacity genes in *Neisseria gonorrhoeae*: control of phase and antigenic variation. *Cell* **47**, 61-71 (1986). <http://www.ncbi.nlm.nih.gov/pubmed/3093085>.
574. Stern, A. & Meyer, T.F. Common mechanism controlling phase and antigenic variation in pathogenic neisseriae. *Mol Microbiol* **1**, 5-12 (1987). <http://www.ncbi.nlm.nih.gov/pubmed/2455211>.
575. Borst, P. & Greaves, D.R. Programmed gene rearrangements altering gene expression. *Science* **235**, 658-67 (1987). <http://www.ncbi.nlm.nih.gov/pubmed/3544215>.
576. Barbour, A.G., Dai, Q., Restrepo, B.I., Stoermer, H.G. & Frank, S.A. Pathogen escape from host immunity by a genome program for antigenic variation. *Proc Natl Acad Sci U S A* **103**, 18290-5 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/17101971>.
577. Komano, T. Shufflons: multiple inversion systems and integrons. *Annu Rev Genet* **33**, 171-91 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10690407>.
578. Gyohda, A., Furuya, N., Ishiwa, A., Zhu, S. & Komano, T. Structure and function of the shufflon in plasmid R64. *Adv Biophys* **38**, 183-213 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15493334>.
579. Tam, C.K., Hackett, J. & Morris, C. Rate of inversion of the *Salmonella enterica* shufflon regulates expression of invertible DNA. *Infect Immun* **73**, 5568-77 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16113273>.
580. Cerdeno-Tarraga, A.M. *et al.* Extensive DNA inversions in the *B. fragilis* genome control variable gene expression. *Science* **307**, 1463-5 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15746427>.
581. Campbell, A.M. How Viruses Insert their DNA into the DNA of the Host Cell. *Scientific American* **235**, 102-113 (1976). <http://www.ncbi.nlm.nih.gov/pubmed/1006304>.
582. Nash, H.A. Integration and excision of bacteriophage lambda: the mechanism of conservation site specific recombination. *Annu Rev Genet* **15**, 143-67 (1981). <http://www.ncbi.nlm.nih.gov/pubmed/6461289>.
583. Landy, A. Dynamic, structural, and regulatory aspects of lambda site-specific recombination. *Annu Rev Biochem* **58**, 913-49 (1989). <http://www.ncbi.nlm.nih.gov/pubmed/2528323>.
584. Van Duyne, G.D. Lambda integrase: armed for recombination. *Curr Biol* **15**, R658-60 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16139195>.

585. Radman-Livaja, M., Biswas, T., Ellenberger, T., Landy, A. & Aihara, H. DNA arms do the legwork to ensure the directionality of lambda site-specific recombination. *Curr Opin Struct Biol* **16**, 42-50 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16368232>.
586. Barre, F.X. *et al.* Circles: the replication-recombination-chromosome segregation connection. *Proc Natl Acad Sci U S A* **98**, 8189-95 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11459952>.
587. Piggot, P.J. & Hilbert, D.W. Sporulation of *Bacillus subtilis*. *Curr Opin Microbiol* **7**, 579-86 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15556029>.
588. Zhang, C.C., Laurent, S., Sakr, S., Peng, L. & Bedu, S. Heterocyst differentiation and pattern formation in cyanobacteria: a chorus of signals. *Mol Microbiol* **59**, 367-75 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16390435>.
589. Stragier, P., Kunkel, B., Kroos, L. & Losick, R. Chromosomal rearrangement generating a composite gene for a developmental transcription factor. *Science* **243**, 507-12 (1989). <http://www.ncbi.nlm.nih.gov/pubmed/2536191>.
590. Carrasco, C.D. & Golden, J.W. Two heterocyst-specific DNA rearrangements of nif operons in *Anabaena cylindrica* and *Nostoc* sp. strain Mac. *Microbiology* **141** (Pt 10), 2479-87 (1995). <http://www.ncbi.nlm.nih.gov/pubmed/7582007>.
591. Hallet, B. & Sherratt, D.J. Transposition and site-specific recombination: adapting DNA cut-and-paste mechanisms to a variety of genetic rearrangements. *FEMS Microbiol Rev* **21**, 157-78 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9348666>.
592. Haber, J.E. Mating-type gene switching in *Saccharomyces cerevisiae*. *Annu Rev Genet* **32**, 561-99 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9928492>.
593. Egel, R. Fission yeast mating-type switching: programmed damage and repair. *DNA Repair (Amst)* **4**, 525-36 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15811625>.
594. Klar, A.J. Lessons learned from studies of fission yeast mating-type switching and silencing. *Annu Rev Genet* **41**, 213-36 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17614787>.
595. Nasmyth, K. Regulating the HO endonuclease in yeast. *Curr Opin Genet Dev* **3**, 286-94 (1993).
596. Haber, J.E. In vivo biochemistry: physical monitoring of recombination induced by site-specific endonucleases. *Bioessays* **17**, 609-20 (1995). PMID 7646483.

597. Barsoum, E., Martinez, P. & Åström, S.U. α 3, a transposable element that promotes host sexual reproduction. *Genes Dev* **24**, 33-44 (2010). PMID 20008928.
598. Rusche, L.N. & Rine, J. Switching the mechanism of mating type switching: a domesticated transposase supplants a domesticated homing endonuclease. *Genes Dev* **24**, 10-4 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20047997>.
599. Prescott, D.M. Genome gymnastics: unique modes of DNA evolution and processing in ciliates. *Nat Rev Genet* **1**, 191-8 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11252748>.
600. Juranek, S.A. & Lipps, H.J. New insights into the macronuclear development in ciliates. *Int Rev Cytol* **262**, 219-51 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17631190>.
601. Betermier, M. Large-scale genome remodelling by the developmentally programmed elimination of germ line sequences in the ciliate Paramecium. *Res Microbiol* **155**, 399-408 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15207872>.
602. Chalker, D.L. Dynamic nuclear reorganization during genome remodeling of Tetrahymena. *Biochim Biophys Acta* **1783**, 2130-6 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18706458>.
603. Jonsson, F., Postberg, J. & Lipps, H.J. The unusual way to make a genetically active nucleus. *DNA Cell Biol* **28**, 71-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19196049>.
604. Mochizuki, K. & Gorovsky, M.A. Small RNAs in genome rearrangement in Tetrahymena. *Curr Opin Genet Dev* **14**, 181-7 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15196465>.
605. Nowacki, M. *et al.* RNA-mediated epigenetic programming of a genome-rearrangement pathway. *Nature* **451**, 153-8 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18046331>.
606. Meyer, E. & Duharcourt, S. Epigenetic regulation of programmed genomic rearrangements in Paramecium aurelia. *J Eukaryot Microbiol* **43**, 453-61 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8976603>.
607. Garnier, O., Serrano, V., Duharcourt, S. & Meyer, E. RNA-mediated programming of developmental genome rearrangements in Paramecium tetraurelia. *Mol Cell Biol* **24**, 7370-9 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15314149>.
608. Wong, L.C. & Landweber, L.F. Evolution of programmed DNA rearrangements in a scrambled gene. *Mol Biol Evol* **23**, 756-63 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16431850>.

609. Mollenbeck, M. *et al.* The pathway to detangle a scrambled gene. *PLoS One* **3**, e2330 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18523559>.
610. Duharcourt, S., Lepere, G. & Meyer, E. Developmental genome rearrangements in ciliates: a natural genomic subtraction mediated by non-coding transcripts. *Trends Genet* **25**, 344-50 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19596481>.
611. Greider, C.W. & Blackburn, E.H. Identification of a specific telomere terminal transferase activity in Tetrahymena extracts. *Cell* **43**, 405-13 (1985). PMID 3907856.
612. Greider, C.W. & Blackburn, E.H. A telomeric sequence in the RNA of Tetrahymena telomerase required for telomere repeat synthesis. *Nature* **337**, 331-7 (1989). PMID 2463488.
613. Kano, H. *et al.* L1 retrotransposition occurs mainly in embryogenesis and creates somatic mosaicism. *Genes Dev* **23**, 1303-12 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19487571>.
614. Muotri, A.R. & Gage, F.H. Generation of neuronal variability and complexity. *Nature* **441**, 1087-93 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16810244>.
615. Muotri, A.R. *et al.* Somatic mosaicism in neuronal precursor cells mediated by L1 retrotransposition. *Nature* **435**, 903-10 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15959507>.
616. Kuwabara, T. *et al.* Wnt-mediated activation of NeuroD1 and retro-elements during adult neurogenesis. *Nat Neurosci* **12**, 1097-105 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19701198>.
617. Muotri, A.R., Zhao, C., Marchetto, M.C. & Gage, F.H. Environmental influence on L1 retrotransposons in the adult hippocampus. *Hippocampus* **19**, 1002-7 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19771587>.
618. Muotri, A.R., Marchetto, M.C., Coufal, N.G. & Gage, F.H. The necessary junk: new functions for transposable elements. *Hum Mol Genet* **16 Spec No. 2**, R159-67 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17911158>.
619. Muotri, A.R. *et al.* L1 retrotransposition in neurons is modulated by MeCP2. *Nature* **468**, 443–446 (2010). PMID 21085180.
620. Coufal, N.G. *et al.* L1 retrotransposition in human neural progenitor cells. *Nature* **460**, 1127-31 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19657334>.

621. Singer, T., McConnell, M.J., Marchetto, M.C., Coufal, N.G. & Gage, F.H. LINE-1 retrotransposons: mediators of somatic variation in neuronal genomes? *Trends Neurosci* **33**, 345-54 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20471112>.
622. Samaco, R.C., Nagarajan, R.P., Braunschweig, D. & LaSalle, J.M. Multiple pathways regulate MeCP2 expression in normal brain development and exhibit defects in autism-spectrum disorders. *Hum Mol Genet* **13**, 629-39 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/14734626>.
623. Peddada, S., Yasui, D.H. & LaSalle, J.M. Inhibitors of differentiation (ID1, ID2, ID3 and ID4) genes are neuronal targets of MeCP2 that are elevated in Rett syndrome. *Hum Mol Genet* **15**, 2003-14 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16682435>.
624. Vanderhaeghen, P. Wnts blow on NeuroD1 to promote adult neuron production and diversity. *Nat Neurosci* **12**, 1079-81 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19710645>.
625. Sarachana, T., Zhou, R., Chen, G., Manji, H.K. & Hu, V.W. Investigation of post-transcriptional gene regulatory networks associated with autism spectrum disorders by microRNA expression profiling of lymphoblastoid cell lines. *Genome Med* **2**, 23 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20374639>.
626. St Laurent, G., 3rd, Hammell, N. & McCaffrey, T.A. A LINE-1 component to human aging: do LINE elements exact a longevity cost for evolutionary advantage? *Mech Ageing Dev* **131**, 299-305 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20346965>.
627. Iskow, R.C. *et al.* Natural mutagenesis of human genomes by endogenous retrotransposons. *Cell* **141**, 1253-61 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20603005>.
628. Burnet, M. How Antibodies are Made. *Scientific American* **191**, 74-78 (1954).
<http://www.nature.com/scientificamerican/journal/v191/n5/pdf/scientificamerican1154-74.pdf>.
629. Burnet, M. The Mechanism of Immunity. *Scientific American* **204**, 58-67 (1961).
<http://www.ncbi.nlm.nih.gov/pubmed/13689162>.
630. Ada, G.L. & Nossal, G. The clonal-selection theory. *Sci Am* **257**, 62-9 (1987).
<http://www.ncbi.nlm.nih.gov/pubmed/3303323>.
631. Tonegawa, S. The molecules of the immune system. *Sci Am* **253**, 122-31 (1985).
<http://www.ncbi.nlm.nih.gov/pubmed/3934752>.

632. Edelman, G.M. The structure and function of antibodies. *Sci Am* **223**, 34-42 (1970).
<http://www.ncbi.nlm.nih.gov/pubmed/5447968>.
633. Leder, P. The genetics of antibody diversity. *Sci Am* **246**, 102-15 (1982).
<http://www.ncbi.nlm.nih.gov/pubmed/6177035>.
634. Nossal, G.J.V. Life, Death and the Immune System. *Scientific American* **269**, 52-62 (1993).
<http://www.ncbi.nlm.nih.gov/pubmed/8211091>.
635. Clatworthy, A.E., Valencia, M.A., Haber, J.E. & Oettinger, M.A. V(D)J recombination and RAG-mediated transposition in yeast. *Mol Cell* **12**, 489-99 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14536087>.
636. Lamrani, S. *et al.* Starvation-induced Mucts62-mediated coding sequence fusion: a role for ClpXP, Lon, RpoS and Crp. *Mol Microbiol* **32**, 327-43 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10231489>.
637. Ilves, H., Horak, R., Teras, R. & Kivisaar, M. IHF is the limiting host factor in transposition of *Pseudomonas putida* transposon Tn4652 in stationary phase. *Mol Microbiol* **51**, 1773-85 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15009901>.
638. Horak, R., Ilves, H., Pruunsild, P., Kuljus, M. & Kivisaar, M. The ColR-ColS two-component signal transduction system is involved in regulation of Tn4652 transposition in *Pseudomonas putida* under starvation conditions. *Mol Microbiol* **54**, 795-807 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15491368>.
639. Kinsey, P.T. & Sandmeyer, S.B. Ty3 transposes in mating populations of yeast: a novel transposition assay for Ty3. *Genetics* **139**, 81-94 (1995). <http://www.ncbi.nlm.nih.gov/pubmed/7705653>.
640. Ke, N., Irwin, P.A. & Voytas, D.F. The pheromone response pathway activates transcription of Ty5 retrotransposons located within silent chromatin of *Saccharomyces cerevisiae*. *Embo J* **16**, 6272-80 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9321406>.
641. Sehgal, A., Lee, C.Y. & Espenshade, P.J. SREBP controls oxygen-dependent mobilization of retrotransposons in fission yeast. *PLoS Genet* **3**, e131 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17696611>.

642. Shapiro, J.A. Observations on the formation of clones containing araB-lacZ cistron fusions. *Mol Gen Genet* **194**, 79-90 (1984). <http://www.ncbi.nlm.nih.gov/pubmed/6233472>.
643. Stebbins, J., G.L. Cataclysmic Evolution. *Scientific American* **184**, 54 –59 (1951).
<http://www.nature.com/scientificamerican/journal/v184/n4/pdf/scientificamerican0451-54.pdf>.
644. McClintock, B. The significance of responses of the genome to challenge. *Science* **226**, 792-801 (1984). <http://www.ncbi.nlm.nih.gov/pubmed/15739260>.
645. Feldman, M. & Levy, A.A. Allopolyploidy--a shaping force in the evolution of wheat genomes. *Cytogenet Genome Res* **109**, 250-8 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15753584>.
646. Kidwell, M.G. Hybrid dysgenesis in *Drosophila melanogaster*: nature and inheritance of P element regulation. *Genetics* **111**, 337-50 (1985). <http://www.ncbi.nlm.nih.gov/pubmed/2996978>.
647. Kidwell, M.G., Kimura, K. & Black, D.M. Evolution of hybrid dysgenesis potential following P element contamination in *Drosophila melanogaster*. *Genetics* **119**, 815-28 (1988).
<http://www.ncbi.nlm.nih.gov/pubmed/2842225>.
648. Bregliano, J., Kidwell, M. Hybrid dysgenesis. in *Mobile Genetic Elements* (ed. Shapiro, J.) 363–410. (Academic Press,, New York, 1983).
649. Woodruff, R.C. & Thomson, J.N. The fundamental theorem of neutral evolution: rates of substitution and mutation should factor in premeiotic clusters. *Genetica* **125**, 333-9 (2005). PMID 16247704.
650. Kocur, G.J., Drier, E.A. & Simmons, M.J. Sterility and hypermutability in the P-M system of hybrid dysgenesis in *Drosophila melanogaster*. *Genetics* **114**, 1147-63 (1986).
<http://www.ncbi.nlm.nih.gov/pubmed/3100389>.
651. Thorp, M.W., Chapman, E.J. & Simmons, M.J. Cytotype regulation by telomeric P elements in *Drosophila melanogaster*: variation in regulatory strength and maternal effects. *Genet Res* **91**, 327-36 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19922696>.
652. Jensen, P.A., Stuart, J.R., Goodpaster, M.P., Goodman, J.W. & Simmons, M.J. Cytotype regulation of P transposable elements in *Drosophila melanogaster*: repressor polypeptides or piRNAs? *Genetics* **179**, 1785-93 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18579507>.

653. Simmons, M.J. *et al.* Cytotype regulation by telomeric P elements in *Drosophila melanogaster*: interactions with P elements from M' strains. *Genetics* **176**, 1957-66 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17565961>.
654. Belinco, C. *et al.* Cytotype regulation in *Drosophila melanogaster*: synergism between telomeric and non-telomeric P elements. *Genet Res* **91**, 383-94 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/20122295>.
655. Brennecke, J. *et al.* Discrete small RNA-generating loci as master regulators of transposon activity in *Drosophila*. *Cell* **128**, 1089-103 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17346786>.
656. Brennecke, J. *et al.* An epigenetic role for maternally inherited piRNAs in transposon silencing. *Science* **322**, 1387-92 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/19039138>.
657. Kunin, V., Sorek, R. & Hugenholtz, P. Evolutionary conservation of sequence and secondary structures in CRISPR repeats. *Genome Biol* **8**, R61 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17442114>.
658. Bolotin, A., Quinquis, B., Sorokin, A. & Ehrlich, S.D. Clustered regularly interspaced short palindrome repeats (CRISPRs) have spacers of extrachromosomal origin. *Microbiology* **151**, 2551-61 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16079334>.
659. Marraffini, L.A. & Sontheimer, E.J. Invasive DNA, chopped and in the CRISPR. *Structure* **17**, 786-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19523896>.
660. Mojica, F.J., Diez-Villasenor, C., Garcia-Martinez, J. & Almendros, C. Short motif sequences determine the targets of the prokaryotic CRISPR defence system. *Microbiology* **155**, 733-40 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19246744>.
661. Hale, C., Kleppe, K., Terns, R.M. & Terns, M.P. Prokaryotic silencing (psi)RNAs in *Pyrococcus furiosus*. *RNA* **14**, 2572-9 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18971321>.
662. Hale, C.R. *et al.* RNA-guided RNA cleavage by a CRISPR RNA-Cas protein complex. *Cell* **139**, 945-56 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19945378>.
663. Hale, C.J., Erhard, K.F., Jr., Lisch, D. & Hollick, J.B. Production and processing of siRNA precursor transcripts from the highly repetitive maize genome. *PLoS Genet* **5**, e1000598 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19680464>.

664. Marraffini, L.A. & Sontheimer, E.J. CRISPR interference: RNA-directed adaptive immunity in bacteria and archaea. *Nat Rev Genet* **11**, 181-190 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20125085>.
665. Horvath, P. *et al.* Diversity, activity, and evolution of CRISPR loci in *Streptococcus thermophilus*. *J Bacteriol* **190**, 1401-12 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18065539>.
666. Luria, S.E. & Delbrück, M. Mutations of Bacteria from Virus Sensitivity to Virus Resistance. *Genetics* **28**, 491–51 (1943). PMID 17247100.
667. Horvath, P. & Barrangou, R. CRISPR/Cas, the immune system of bacteria and archaea. *Science* **327**, 167-70 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20056882>.
668. Jaskiewicz, M., Conrath, U. & Peterhansel, C. Chromatin modification acts as a memory for systemic acquired resistance in the plant stress response. *EMBO Rep* **12**, 50-5 (2011).
<http://www.ncbi.nlm.nih.gov/pubmed/21132017>.
669. Cairns, J., Overbaugh, J. & Miller, S. The origin of mutants. *Nature* **335**, 142-5 (1988).
<http://www.ncbi.nlm.nih.gov/pubmed/3045565>.
670. Maenhaut-Michel, G. & Shapiro, J.A. The roles of starvation and selective substrates in the emergence of araB-lacZ fusion clones. *Embo J* **13**, 5229-39 (1994).
<http://www.ncbi.nlm.nih.gov/pubmed/7957088>.
671. Weismann, A. *The Germ-Plasm: A Theory of Heredity*, (Charles Scribner's Sons, New York, 1893).
<http://www.esp.org/books/weismann/germ-plasm/facsimile/>.
672. Bushman, F.D. Targeting survival: integration site selection by retroviruses and LTR-retrotransposons. *Cell* **115**, 135-8 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/14567911>.
673. Devine, S.E. & Boeke, J.D. Integration of the yeast retrotransposon Ty1 is targeted to regions upstream of genes transcribed by RNA polymerase III. *Genes Dev* **10**, 620-33 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8598291>.
674. Bolton, E.C. & Boeke, J.D. Transcriptional interactions between yeast tRNA genes, flanking genes and Ty elements: a genomic point of view. *Genome Res* **13**, 254-63 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12566403>.

675. Fauvarque, M.O. & Dura, J.M. polyhomeotic regulatory sequences induce developmental regulator-dependent variegation and targeted P-element insertions in *Drosophila*. *Genes Dev* **7**, 1508-20 (1983).
<http://www.ncbi.nlm.nih.gov/pubmed/8101825>.
676. Hama, C., Ali, Z. & Kornberg, T.B. Region-specific recombination and expression are directed by portions of the *Drosophila engrailed* promoter. *Genes Dev* **4**, 1079-93 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/1976568>.
677. Kassis, J.A., Noll, E., VanSickle, E.P., Odenwald, W.F. & Perrimon, N. Altering the insertional specificity of a *Drosophila* transposable element. *Proc Natl Acad Sci U S A* **89**, 1919-23 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1311855>.
678. Taillebourg, E. & Dura, J.M. A novel mechanism for P element homing in *Drosophila*. *Proc Natl Acad Sci U S A* **96**, 6856-61 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10359803>.
679. Bender, W. & Hudson, A. P element homing to the *Drosophila* bithorax complex. *Development* **127**, 3981-92 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10952896>.
680. Kassis, J.A. Pairing-sensitive silencing, polycomb group response elements, and transposon homing in *Drosophila*. *Adv Genet* **46**, 421-38 (2002). PMID 11931233.
681. Rubin, G.M. & Spradling, A.C. Genetic transformation of *Drosophila* with transposable element vectors. *Science* **218**, 348-53 (1982). <http://www.ncbi.nlm.nih.gov/pubmed/6289436>.
682. Spradling, A.C. & Rubin, G.M. Transposition of cloned P elements into *Drosophila* germ line chromosomes. *Science* **218**, 341-7 (1982). <http://www.ncbi.nlm.nih.gov/pubmed/6289435>.
683. Spradling, A.C. *et al.* Gene disruptions using P transposable elements: an integral component of the *Drosophila* genome project. *Proc Natl Acad Sci U S A* **92**, 10824-30 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/7479892>.
684. Rubin, G.M. & Spradling, A.C. Vectors for P element-mediated gene transfer in *Drosophila*. *Nucleic Acids Res* **11**, 6341-51 (1983). <http://www.ncbi.nlm.nih.gov/pubmed/6312420>.
685. Bateson, W. *Materials for the Study of Variation Treated With Especial Regard to Discontinuity in the Origin of Species.*, (Macmillan, London, 1894). <http://chla.library.cornell.edu/cgi/t/text/textidx?c=chla;idno=3111077>.

686. de Vries, H. *Species and varieties, their origin by mutation; lectures delivered at the University of California*, (Open Court Publishing Co., Chicago, 1905). <http://www.gutenberg.org/ebooks/7234>.
687. Goldschmidt, R. Some aspects of evolution. *Science* **78**, 539-47 (1933). PMID 17811930.
688. Margulis, L. Symbiosis and evolution. *Sci Am* **225**, 48-57 (1971).
<http://www.ncbi.nlm.nih.gov/pubmed/5089455>.
689. Levy, S.B. The challenge of antibiotic resistance. *Sci Am* **278**, 46-53 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/9487702>.
690. Gorini, L. Antibiotics and the Genetic Code. *Scientific American* **214**, 102-109 (1966).
<http://www.nature/scientificamerican/journal/v214/n4/pdf/scientificamerican0466-102.pdf>.
691. Ryan, F.J. Evolution observed. *Scientific American* **189**, 78 – 82 (1953).
<http://www.nature.com/scientificamerican/journal/v189/n4/pdf/scientificamerican1053-78.pdf>.
692. Fauci, A.S. Infectious diseases: considerations for the 21st century. *Clin Infect Dis* **32**, 675-85 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11229834>.
693. Watanabe, T. & Fukasawa, T. Episome-mediated transfer of drug resistance in Enterobacteriaceae. III. Transduction of resistance factors. *J Bacteriol* **82**, 202-9 (1961).
<http://www.ncbi.nlm.nih.gov/pubmed/13783346>.
694. Watanabe, T. Episome-Mediated Transfer of Drug Resistance in Enterobacteriaceae. Vi. High-Frequency Resistance Transfer System in Escherichia Coli. *J Bacteriol* **85**, 788-94 (1963).
<http://www.ncbi.nlm.nih.gov/pubmed/14044944>.
695. Watanabe, T. Infectious drug resistance. *Sci Am* **217**, 19-28 (1967).
<http://www.ncbi.nlm.nih.gov/pubmed/6061177>.
696. Benveniste, R. & Davies, J. Mechanisms of antibiotic resistance in bacteria. *Annu Rev Biochem* **42**, 471-506 (1973). <http://www.ncbi.nlm.nih.gov/pubmed/4581231>.
697. Foster, T.J. Plasmid-determined resistance to antimicrobial drugs and toxic metal ions in bacteria. *Microbiol Rev* **47**, 361-409 (1983). <http://www.ncbi.nlm.nih.gov/pubmed/6355806>.
698. Mazel, D. & Davies, J. Antibiotic resistance in microbes. *Cell Mol Life Sci* **56**, 742-54 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/11212334>.

699. Iyer, L.M., Balaji, S., Koonin, E.V. & Aravind, L. Evolutionary genomics of nucleo-cytoplasmic large DNA viruses. *Virus Res* **117**, 156-84 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16494962>.
700. Filee, J., Pouget, N. & Chandler, M. Phylogenetic evidence for extensive lateral acquisition of cellular genes by Nucleocytoplasmic large DNA viruses. *BMC Evol Biol* **8**, 320 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/19036122>.
701. Yutin, N., Wolf, Y.I., Raoult, D. & Koonin, E.V. Eukaryotic large nucleo-cytoplasmic DNA viruses: clusters of orthologous genes and reconstruction of viral genome evolution. *Virol J* **6**, 223 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/20017929>.
702. Yutin, N. & Koonin, E.V. Evolution of DNA ligases of Nucleo-Cytoplasmic Large DNA viruses of eukaryotes: a case of hidden complexity. *Biol Direct* **4**, 51 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/20021668>.
703. Hall, R.M. & Collis, C.M. Mobile gene cassettes and integrons: capture and spread of genes by site-specific recombination. *Mol Microbiol* **15**, 593-600 (1995).
<http://www.ncbi.nlm.nih.gov/pubmed/7783631>.
704. Rowe-Magnus, D.A. & Mazel, D. The role of integrons in antibiotic resistance gene capture. *Int J Med Microbiol* **292**, 115-25 (2002). PMID 12195734.
705. Labbate, M., Case, R.J. & Stokes, H.W. The integron/gene cassette system: an active player in bacterial adaptation. *Methods Mol Biol* **532**, 103-25 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19271181>.
706. Bouvier, M., Ducos-Galand, M., Loot, C., Bikard, D. & Mazel, D. Structural features of single-stranded integron cassette attC sites and their role in strand selection. *PLoS Genet* **5**, e1000632 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19730680>.
707. Fluit, A.C. & Schmitz, F.J. Resistance integrons and super-integrons. *Clin Microbiol Infect* **10**, 272-88 (2004). PMID 15059115.
708. Vaisvila, R., Morgan, R.D., Posfai, J. & Raleigh, E.A. Discovery and distribution of super-integrons among pseudomonads. *Mol Microbiol* **42**, 587-601 (2001). PMID 11722728.
709. Rowe-Magnus, D.A., Guérout, A.M. & Mazel, D. Super-integrons. *Res Microbiol* **150**, 641-51 (1999). PMID 10673003.

710. Lee, C.A., Babic, A. & Grossman, A.D. Autonomous plasmid-like replication of a conjugative transposon. *Mol Microbiol* **75**, 268-79 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/19943900>.
711. Burrus, V., Pavlovic, G., Decaris, B. & Guedon, G. Conjugative transposons: the tip of the iceberg. *Mol Microbiol* **46**, 601-10 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12410819>.
712. Sonea, S. & Panisset, M. *A New Bacteriology*, (Jones and Batlett, Boston, 1983).
713. Sonea, S. Bacterial plasmids instrumental in the origin of eukaryotes? *Rev Can Biol* **31**, 61-3 (1972). <http://www.ncbi.nlm.nih.gov/pubmed/4336057>.
714. Sonea, S. A bacterial way of life. *Nature* **331**, 216 (1988). <http://www.ncbi.nlm.nih.gov/pubmed/3336435>.
715. van der Meer, J.R. & Sentchilo, V. Genomic islands and the evolution of catabolic pathways in bacteria. *Curr Opin Biotechnol* **14**, 248-54 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12849776>.
716. Tallent, S.M., Langston, T.B., Moran, R.G. & Christie, G.E. Transducing particles of *Staphylococcus aureus* pathogenicity island SaPI1 are comprised of helper phage-encoded proteins. *J Bacteriol* **189**, 7520-4 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17693489>.
717. Tormo, M.A. *et al.* *Staphylococcus aureus* pathogenicity island DNA is packaged in particles composed of phage proteins. *J Bacteriol* **190**, 2434-40 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18223072>.
718. Tormo-Mas, M.A. *et al.* Moonlighting bacteriophage proteins derepress staphylococcal pathogenicity islands. *Nature* **465**, 779-82 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20473284>.
719. Reed, C. Sequencing Sea World. *Scientific American* **295**, 23-24 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16866278>.
720. Tyson, G.W. *et al.* Community structure and metabolism through reconstruction of microbial genomes from the environment. *Nature* **428**, 37-43 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/14961025>.
721. Venter, J.C. *et al.* Environmental genome shotgun sequencing of the Sargasso Sea. *Science* **304**, 66-74 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15001713>.
722. Ventura, M. *et al.* Microbial diversity in the human intestine and novel insights from metagenomics. *Front Biosci* **14**, 3214-21 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19273267>.

723. Wooley, J.C., Godzik, A. & Friedberg, I. A primer on metagenomics. *PLoS Comput Biol* **6**, e1000667 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20195499>.
724. Ellrott, K., Jaroszewski, L., Li, W., Wooley, J.C. & Godzik, A. Expansion of the protein repertoire in newly explored environments: human gut microbiome specific protein families. *PLoS Comput Biol* **6**, e1000798 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20532204>.
725. Jones, B.V., Sun, F. & Marchesi, J.R. Comparative metagenomic analysis of plasmid encoded functions in the human gut microbiome. *BMC Genomics* **11**, 46 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20085629>.
726. Qin, J. *et al.* A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* **464**, 59-65 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20203603>.
727. Nelson, K.E. *et al.* A catalog of reference genomes from the human microbiome. *Science* **328**, 994-9 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20489017>.
728. Achtman, M. & Wagner, M. Microbial diversity and the genetic nature of microbial species. *Nat Rev Microbiol* **6**, 431-40 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18461076>.
729. Schloss, P.D. & Handelsman, J. Metagenomics for studying unculturable microorganisms: cutting the Gordian knot. *Genome Biol* **6**, 229 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16086859>.
730. Handelsman, J. Metagenomics: application of genomics to uncultured microorganisms. *Microbiol Mol Biol Rev* **68**, 669-85 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15590779>.
731. Edwards, R.A. & Rohwer, F. Viral metagenomics. *Nat Rev Microbiol* **3**, 504-10 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15886693>.
732. Bench, S.R. *et al.* Metagenomic characterization of Chesapeake Bay virioplankton. *Appl Environ Microbiol* **73**, 7629-41 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17921274>.
733. Sandaa, R.A., Clokie, M. & Mann, N.H. Photosynthetic genes in viral populations with a large genomic size range from Norwegian coastal waters. *FEMS Microbiol Ecol* **63**, 2-11 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/17999684>.
734. Yanofsky, C. Gene Structure and Protein Structure. *Scientific American* **216**, 80-94 (1967).
<http://www.ncbi.nlm.nih.gov/pubmed/6042535>.

735. Wilson, A.C. The Molecular Basis of Evolution. *Scientific American* **253**, 164-173 (1985).
<http://www.ncbi.nlm.nih.gov/pubmed/4071031>.
736. Doolittle, R.F. & Bork, P. Evolutionarily mobile modules in proteins. *Sci Am* **269**, 50-6 (1993).
<http://www.ncbi.nlm.nih.gov/pubmed/8235550>.
737. Bjorklund, A.K., Ekman, D. & Elofsson, A. Expansion of protein domain repeats. *PLoS Comput Biol* **2**, e114 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16933986>.
738. Bjorklund, A.K., Ekman, D., Light, S., Frey-Skott, J. & Elofsson, A. Domain rearrangements in protein evolution. *J Mol Biol* **353**, 911-23 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16198373>.
739. Schmidt, E.E. & Davies, C.J. The origins of polypeptide domains. *Bioessays* **29**, 262-70 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17295290>.
740. Doolittle, R.F. The Roots of Bioinformatics in Protein Evolution. *PLoS Comput Biol* **6**, e1000875 (2010). PMID 20686682.
741. Pabo, C.O., Sauer, R.T., Sturtevant, J.M. & Ptashne, M. The lambda repressor contains two domains. *Proc Natl Acad Sci U S A* **76**, 1608-12 (1979). <http://www.ncbi.nlm.nih.gov/pubmed/287002>.
742. McKnight, S.L. Molecular Zippers in Gene Regulation. *Scientific American* **264**, 54-64 (1991).
<http://www.ncbi.nlm.nih.gov/pubmed/1876825>.
743. Lewis, M. The lac repressor. *C R Biol* **328**, 521-48 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15950160>.
744. Marsden, R.L. *et al.* Exploiting protein structure data to explore the evolution of protein function and biological complexity. *Philos Trans R Soc Lond B Biol Sci* **361**, 425-40 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16524831>.
745. Gonzalez, M.W. & Pearson, W.R. RefProtDom: A Protein Database with Improved Domain Boundaries and Homology Relationships. *Bioinformatics* (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20693322>.
746. Kolkman, J.A. & Stemmer, W.P. Directed evolution of proteins by exon shuffling. *Nat Biotechnol* **19**, 423-8 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11329010>.
747. Miller, J.H. *et al.* Fusions of the lac and trp Regions of the Escherichia coli Chromosome. *J Bacteriol* **104**, 1273-9 (1970). <http://www.ncbi.nlm.nih.gov/pubmed/16559103>.

748. Casadaban, M.J. Transposition and fusion of the lac genes to selected promoters in Escherichia coli using bacteriophage lambda and Mu. *J Mol Biol* **104**, 541-55 (1976).
<http://www.ncbi.nlm.nih.gov/pubmed/781293>.
749. Moran, J.V. Human L1 retrotransposition: insights and peculiarities learned from a cultured cell retrotransposition assay. *Genetica* **107**, 39-51 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10952196>.
750. Xing, J. *et al.* Emergence of primate genes by retrotransposon-mediated sequence transduction. *Proc Natl Acad Sci U S A* **103**, 17608-13 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/17101974>.
751. Lisch, D. Pack-MULEs: theft on a massive scale. *Bioessays* **27**, 353-5 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15770680>.
752. Lai, J., Li, Y., Messing, J. & Dooner, H.K. Gene movement by Helitron transposons contributes to the haplotype variability of maize. *Proc Natl Acad Sci U S A* **102**, 9068-73 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15951422>.
753. Lal, S.K. & Hannah, L.C. Helitrons contribute to the lack of gene colinearity observed in modern maize inbreds. *Proc Natl Acad Sci U S A* **102**, 9993-4 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16009929>.
754. Lal, S.K. & Hannah, L.C. Plant genomes: massive changes of the maize genome are caused by Helitrons. *Heredity* **95**, 421-2 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16222326>.
755. Young, J.M. & Trask, B.J. The sense of smell: genomics of vertebrate odorant receptors. *Hum Mol Genet* **11**, 1153-60 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12015274>.
756. Tatusov, R.L., Koonin, E.V. & Lipman, D.J. A genomic perspective on protein families. *Science* **278**, 631-7 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9381173>.
757. Harrison, P.M. & Gerstein, M. Studying genomes through the aeons: protein families, pseudogenes and proteome evolution. *J Mol Biol* **318**, 1155-74 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12083509>.
758. Lespinet, O., Wolf, Y.I., Koonin, E.V. & Aravind, L. The role of lineage-specific gene family expansion in the evolution of eukaryotes. *Genome Res* **12**, 1048-59 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12097341>.

759. Jordan, I.K., Makarova, K.S., Spouge, J.L., Wolf, Y.I. & Koonin, E.V. Lineage-specific gene expansions in bacterial and archaeal genomes. *Genome Res* **11**, 555-65 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11282971>.
760. Pushker, R., Mira, A. & Rodriguez-Valera, F. Comparative genomics of gene-family size in closely related bacteria. *Genome Biol* **5**, R27 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15059260>.
761. Gordon, S.V. *et al.* Genomics of *Mycobacterium bovis*. *Tuberculosis (Edinb)* **81**, 157-63 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11463237>.
762. Brennan, M.J. & Delogu, G. The PE multigene family: a 'molecular mantra' for mycobacteria. *Trends Microbiol* **10**, 246-9 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11973159>.
763. Axel, R. The Molecular Logic Of Smell. *Scientific American* **295**, 68-75 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/7481719>.
764. Crasto, C., Singer, M.S. & Shepherd, G.M. The olfactory receptor family album. *Genome Biol* **2**, REVIEWS1027 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11597337>.
765. Niimura, Y. & Nei, M. Evolutionary dynamics of olfactory and other chemosensory receptor genes in vertebrates. *J Hum Genet* **51**, 505-17 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16607462>.
766. Young, J.M. *et al.* Different evolutionary processes shaped the mouse and human olfactory receptor gene families. *Hum Mol Genet* **11**, 535-46 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11875048>.
767. Sogin, S.J., Sogin, M.L. & Woese, C.R. Phylogenetic measurement in prokaryotes by primary structural characterization. *J Mol Evol* **1**, 173-84 (1971).
<http://www.ncbi.nlm.nih.gov/pubmed/5006250>.
768. Lake, J.A. The Ribosome. *Scientific American* **245**, 84-97 (1981).
<http://www.ncbi.nlm.nih.gov/pubmed/6168018>.
769. Woese, C.R. Archaebacteria. *Scientific American* **244**, 98 – 122 (1981).
<http://www.nature.com/scientificamerican/journal/v244/n6/pdf/scientificamerican0681-98.pdf>.
770. Balch, W.E., Magrum, L.J., Fox, G.E., Wolfe, R.S. & Woese, C.R. An ancient divergence among the bacteria. *J Mol Evol* **9**, 305-11 (1977). <http://www.ncbi.nlm.nih.gov/pubmed/408502>.
771. Woese, C.R. & Fox, G.E. Phylogenetic structure of the prokaryotic domain: the primary kingdoms. *Proc Natl Acad Sci U S A* **74**, 5088-90 (1977). <http://www.ncbi.nlm.nih.gov/pubmed/270744>.

772. Woese, C.R., Magrum, L.J. & Fox, G.E. Archaebacteria. *J Mol Evol* **11**, 245-51 (1978).
<http://www.ncbi.nlm.nih.gov/pubmed/691075>.
773. Balch, W.E., Fox, G.E., Magrum, L.J., Woese, C.R. & Wolfe, R.S. Methanogens: reevaluation of a unique biological group. *Microbiol Rev* **43**, 260-96 (1979).
<http://www.ncbi.nlm.nih.gov/pubmed/390357>.
774. Woese, C.R. A proposal concerning the origin of life on the planet earth. *J Mol Evol* **13**, 95-101 (1979). <http://www.ncbi.nlm.nih.gov/pubmed/480373>.
775. DeLong, E.F. Everything in moderation: archaea as 'non-extremophiles'. *Curr Opin Genet Dev* **8**, 649-54 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9914204>.
776. Woese, C.R., Kandler, O. & Wheelis, M.L. Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya. *Proc Natl Acad Sci U S A* **87**, 4576-9 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/2112744>.
777. Raymond, J. The role of horizontal gene transfer in photosynthesis, oxygen production, and oxygen tolerance. *Methods Mol Biol* **532**, 323-38 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19271194>.
778. Aravind, L., Tatusov, R.L., Wolf, Y.I., Walker, D.R. & Koonin, E.V. Evidence for massive gene exchange between archaeal and bacterial hyperthermophiles. *Trends Genet* **14**, 442-4 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/9825671>.
779. Kyrpides, N.C. & Olsen, G.J. Archaeal and bacterial hyperthermophiles: horizontal gene exchange or common ancestry? *Trends Genet* **15**, 298-9 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10431189>.
780. Pereira, S.L. & Reeve, J.N. Histones and nucleosomes in Archaea and Eukarya: a comparative analysis. *Extremophiles* **2**, 141-8 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9783158>.
781. Robinson, N.P. & Bell, S.D. Origins of DNA replication in the three domains of life. *FEBS J* **272**, 3757-66 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16045748>.
782. Hickey, A.J., Conway de Macario, E. & Macario, A.J. Transcription in the archaea: basal factors, regulation, and stress-gene expression. *Crit Rev Biochem Mol Biol* **37**, 537-99 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12540196>.

783. Horiike, T., Hamada, K. & Shinozawa, T. Origin of eukaryotic cell nuclei by symbiosis of Archaea in Bacteria supported by the newly clarified origin of functional genes. *Genes Genet Syst* **77**, 369-76 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12441648>.
784. Horiike, T., Hamada, K., Kanaya, S. & Shinozawa, T. Origin of eukaryotic cell nuclei by symbiosis of Archaea in Bacteria is revealed by homology-hit analysis. *Nat Cell Biol* **3**, 210-4 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11175755>.
785. Martin, W. Archaebacteria (Archaea) and the origin of the eukaryotic nucleus. *Curr Opin Microbiol* **8**, 630-7 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16242992>.
786. Yutin, N., Makarova, K.S., Mekhedov, S.L., Wolf, Y.I. & Koonin, E.V. The deep archaeal roots of eukaryotes. *Mol Biol Evol* **25**, 1619-30 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18463089>.
787. Cox, C.J., Foster, P.G., Hirt, R.P., Harris, S.R. & Embley, T.M. The archaeabacterial origin of eukaryotes. *Proc Natl Acad Sci U S A* **105**, 20356-61 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/19073919>.
788. Fournier, G.P., Huang, J. & Gogarten, J.P. Horizontal gene transfer from extinct and extant lineages: biological innovation and the coral of life. *Philos Trans R Soc Lond B Biol Sci* **364**, 2229-39 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19571243>.
789. Huang, J. & Gogarten, J.P. Ancient gene transfer as a tool in phylogenetic reconstruction. *Methods Mol Biol* **532**, 127-39 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19271182>.
790. Honegger, R. Simon Schwendener (1829–1919) and the dual hypothesis in lichens. *Bryologist* **103**, 307–13 (2000).
791. Sapp, J. *Evolution by Association: A History of Symbiosis*, (Oxford University Press, Oxford, 1994).
792. Sapp, J., Carrapico, F. & Zolotonosov, M. Symbiogenesis: the hidden face of Constantin Merezhkowsky. *Hist Philos Life Sci* **24**, 413-40 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/15045832>.
793. Kozo-Polyansky, B.M. *Symbiogenesis: A New Principle of Evolution* (1924), (Harvard University Press, Cambridge, MA, 2010).
794. Walin, I.E. *Symbiontism and the origin of species*, (Williams & Wilkins, Baltimore, 1927).
<http://www.archive.org/details/symbionticismor00wall>.

795. Dippell, R.V. Mutations of the killer plasmagene, kappa, in variety 4 of *Paramecium aurelia*. *Am Nat* **82**, 43-50 (1948). PMID 18873203.
796. Sonneborn, T.M. Gene and Cytoplasm: I. The Determination and Inheritance of the Killer Character in Variety 4 of *Paramecium Aurelia*. *Proc Natl Acad Sci U S A* **29**, 329-38 (1943).
<http://www.ncbi.nlm.nih.gov/pubmed/16588622>.
797. Sonneborn, T.M. Cellular development and heredity. *J Indiana State Med Assoc* **60**, 1036-8 (1967).
<http://www.ncbi.nlm.nih.gov/pubmed/6065483>.
798. Gibson, I. The endosymbionts of *Paramecium*. *CRC Crit Rev Microbiol* **3**, 243-73 (1974).
<http://www.ncbi.nlm.nih.gov/pubmed/4605256>.
799. Preer, J.R., Jr., Preer, L.B. & Jurand, A. Kappa and other endosymbionts in *Paramecium aurelia*. *Bacteriol Rev* **38**, 113-63 (1974). <http://www.ncbi.nlm.nih.gov/pubmed/4599970>.
800. Engelstadter, J. & Telschow, A. Cytoplasmic incompatibility and host population structure. *Heredity* **103**, 196-207 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19436325>.
801. Sharon, G. *et al.* Commensal bacteria play a role in mating preference of *Drosophila melanogaster*. *Proceedings of the National Academy of Sciences* **107**, 20051-6 (2010). PMID 21041648.
802. Stams, A.J. Metabolic interactions between anaerobic bacteria in methanogenic environments. *Antonie Van Leeuwenhoek* **66**, 271-94 (1994). <http://www.ncbi.nlm.nih.gov/pubmed/7747937>.
803. Stams, A.J., Oude Elferink, S.J. & Westermann, P. Metabolic interactions between methanogenic consortia and anaerobic respiring bacteria. *Adv Biochem Eng Biotechnol* **81**, 31-56 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/12747560>.
804. Stams, A.J. & Plugge, C.M. Electron transfer in syntrophic communities of anaerobic bacteria and archaea. *Nat Rev Microbiol* **7**, 568-77 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19609258>.
805. Paerl, H.W. & Pinckney, J.L. A Mini-review of Microbial Consortia: Their Roles in Aquatic Production and Biogeochemical Cycling. *Microb Ecol* **31**, 225-47 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8661534>.
806. Froestl, J.O., J. Overmann. Phylogenetic affiliation of the bacteria that constitute phototrophic consortia. *Arch Microbiol* **174**, 50–58 (2000). PMID 10985742.

807. Wanner, G., Vogl, K. & Overmann, J. Ultrastructural characterization of the prokaryotic symbiosis in "Chlorochromatium aggregatum". *J Bacteriol* **190**, 3721-30 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18344357>.
808. Kanzler, B.E., Pfannes, K.R., Vogl, K. & Overmann, J. Molecular characterization of the nonphotosynthetic partner bacterium in the consortium "Chlorochromatium aggregatum". *Appl Environ Microbiol* **71**, 7434-41 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16269785>.
809. Martin, F., Kohler, A. & Duplessis, S. Living in harmony in the wood underground: ectomycorrhizal genomics. *Curr Opin Plant Biol* **10**, 204-10 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17291823>.
810. Martin, F. & Nehls, U. Harnessing ectomycorrhizal genomics for ecological insights. *Curr Opin Plant Biol* **12**, 508-15 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19540154>.
811. Delano-Frier, J.P. & Tejeda-Sartorius, M. Unraveling the network: Novel developments in the understanding of signaling and nutrient exchange mechanisms in the arbuscular mycorrhizal symbiosis. *Plant Signal Behav* **3**, 936-44 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/19513196>.
812. Teixeira, L., Ferreira, A. & Ashburner, M. The bacterial symbiont Wolbachia induces resistance to RNA viral infections in *Drosophila melanogaster*. *PLoS Biol* **6**, e2 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/19222304>.
813. Zientz, E., Feldhaar, H., Stoll, S. & Gross, R. Insights into the microbial world associated with ants. *Arch Microbiol* **184**, 199-206 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16205909>.
814. Zientz, E., Dandekar, T. & Gross, R. Metabolic interdependence of obligate intracellular bacteria and their insect hosts. *Microbiol Mol Biol Rev* **68**, 745-70 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15590782>.
815. de Souza, D.J., Bezier, A., Depoix, D., Drezen, J.M. & Lenoir, A. Blochmannia endosymbionts improve colony growth and immune defence in the ant *Camponotus fellah*. *BMC Microbiol* **9**, 29 (2009). PMID 19200360.
816. Sun, S. & Cline, T.W. Effects of Wolbachia infection and ovarian tumor mutations on Sex-lethal germline functioning in *Drosophila*. *Genetics* **181**, 1291-301 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19171941>.

817. Sacchi, L. *et al.* Bacteriocyte-like cells harbour Wolbachia in the ovary of *Drosophila melanogaster* (Insecta, Diptera) and *Zyginidia pullula* (Insecta, Hemiptera). *Tissue Cell* **42**, 328-33 (2010). PMID 20817243.
818. Buchner, P. *Endosymbiosis of animals with plant microorganisms*, (John Wiley and Sons, Chichester, 1965).
819. Heddi, A. *et al.* Molecular and cellular profiles of insect bacteriocytes: mutualism and harm at the initial evolutionary step of symbiogenesis. *Cell Microbiol* **7**, 293-305 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15659072>.
820. Feldhaar, H. & Gross, R. Insects as hosts for mutualistic bacteria. *Int J Med Microbiol* **299**, 1-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/18640072>.
821. McFall-Ngai, M. Host-microbe symbiosis: the squid-Vibrio association--a naturally occurring, experimental model of animal/bacterial partnerships. *Adv Exp Med Biol* **635**, 102-12 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18841707>.
822. McFall-Ngai, M.J. Negotiations between animals and bacteria: the 'diplomacy' of the squid-vibrio symbiosis. *Comp Biochem Physiol A Mol Integr Physiol* **126**, 471-80 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/10989339>.
823. Baumann, P. Biology bacteriocyte-associated endosymbionts of plant sap-sucking insects. *Annu Rev Microbiol* **59**, 155-89 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16153167>.
824. Douglas, A.E. Nutritional interactions in insect-microbial symbioses: aphids and their symbiotic bacteria Buchnera. *Annu Rev Entomol* **43**, 17-37 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/15012383>.
825. Narita, S., Kageyama, D., Nomura, M. & Fukatsu, T. Unexpected mechanism of symbiont-induced reversal of insect sex: feminizing Wolbachia continuously acts on the butterfly *Eurema hecabe* during larval development. *Appl Environ Microbiol* **73**, 4332-41 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17496135>.
826. Gehrig, H., Schüssler, A. & Kluge, M. *Geosiphon pyriforme*, a fungus forming endocytobiosis with *Nostoc* (cyanobacteria), is an ancestral member of the Glomales: evidence by SSU rRNA analysis. *J Mol Evol* **43**, 71-81 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8660431>.

827. Queller, D.C. & Strassmann, J.E. Beyond society: the evolution of organismality. *Philos Trans R Soc Lond B Biol Sci* **364**, 3143-55 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19805423>.
828. Goodenough, U.W. & Levine, R.P. The Genetic Activity of Mitochondria and Chloroplasts *Scientific American* **223**, 22-29 (1970). <http://www.ncbi.nlm.nih.gov/pubmed/5482575>.
829. Bonen, L. & Doolittle, W.F. On the prokaryotic nature of red algal chloroplasts. *Proc Natl Acad Sci U S A* **72**, 2310-4 (1975). <http://www.ncbi.nlm.nih.gov/pubmed/1056032>.
830. Zablen, L.B., Kissil, M.S., Woese, C.R. & Buetow, D.E. Phylogenetic origin of the chloroplast and prokaryotic nature of its ribosomal RNA. *Proc Natl Acad Sci U S A* **72**, 2418-22 (1975). <http://www.ncbi.nlm.nih.gov/pubmed/806081>.
831. Woese, C.R. Endosymbionts and mitochondrial origins. *J Mol Evol* **10**, 93-6 (1977). <http://www.ncbi.nlm.nih.gov/pubmed/592424>.
832. Gray, M.W., Burger, G. & Lang, B.F. Mitochondrial evolution. *Science* **283**, 1476-81 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10066161>.
833. Nozaki, H. A new scenario of plastid evolution: plastid primary endosymbiosis before the divergence of the "Plantae," emended. *J Plant Res* **118**, 247-55 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16032387>.
834. Archibald, J.M.K., P. J. Keeling. Recycled plastids: a 'green movement' in eukaryotic evolution. *Trends Genet* **18**, 577-584 (2002). PMID 12414188.
835. Lane, C.E. & Archibald, J.M. The eukaryotic tree of life: endosymbiosis takes its TOL. *Trends Ecol Evol* **23**, 268-75 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18378040>.
836. Bhattacharya, D., Yoon, H.S. & Hackett, J.D. Photosynthetic eukaryotes unite: endosymbiosis connects the dots. *Bioessays* **26**, 50-60 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/14696040>.
837. Reyes-Prieto, A., Weber, A.P. & Bhattacharya, D. The origin and establishment of the plastid in algae and plants. *Annu Rev Genet* **41**, 147-68 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17600460>.
838. Martin, W. *et al.* Early cell evolution, eukaryotes, anoxia, sulfide, oxygen, fungi first (?), and a tree of genomes revisited. *IUBMB Life* **55**, 193-204 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12880199>.

839. 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. *Proc Natl Acad Sci U S A* **103**, 13080-5 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16938841>.
840. Embley, T.M. Multiple secondary origins of the anaerobic lifestyle in eukaryotes. *Philos Trans R Soc Lond B Biol Sci* **361**, 1055-67 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16754614>.
841. Embley, T.M. & Martin, W. Eukaryotic evolution, changes and challenges. *Nature* **440**, 623-30 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16572163>.
842. Grivell, L.A. Mitochondrial DNA. *Scientific American* **248**, 78-89 (1983).
<http://www.ncbi.nlm.nih.gov/pubmed/6188212>.
843. Gray, M.W., Burger, G. & Lang, B.F. The origin and early evolution of mitochondria. *Genome Biol* **2**, REVIEWS1018 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11423013>.
844. Lang, B.F., Gray, M.W. & Burger, G. Mitochondrial genome evolution and the origin of eukaryotes. *Annu Rev Genet* **33**, 351-97 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/10690412>.
845. Burger, G., Gray, M.W. & Lang, B.F. Mitochondrial genomes: anything goes. *Trends Genet* **19**, 709-16 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/14642752>.
846. Archibald, J.M., Rogers, M.B., Toop, M., Ishida, K. & Keeling, P.J. Lateral gene transfer and the evolution of plastid-targeted proteins in the secondary plastid-containing alga *Bigelowiella natans*. *Proc Natl Acad Sci U S A* **100**, 7678-83 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12777624>.
847. Huang, J. *et al.* Phylogenomic evidence supports past endosymbiosis, intracellular and horizontal gene transfer in *Cryptosporidium parvum*. *Genome Biol* **5**, R88 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15535864>.
848. Bock, R. & Timmis, J.N. Reconstructing evolution: gene transfer from plastids to the nucleus. *Bioessays* **30**, 556-66 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18478535>.
849. Gray, M.W., Lang, B.F. & Burger, G. Mitochondria of protists. *Annu Rev Genet* **38**, 477-524 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15568984>.
850. Westenberger, S.J. *et al.* Trypanosoma cruzi mitochondrial maxicircles display species- and strain-specific variation and a conserved element in the non-coding region. *BMC Genomics* **7**, 60 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16553959>.

851. Lukes, J., Hashimi, H. & Zikova, A. Unexplained complexity of the mitochondrial genome and transcriptome in kinetoplastid flagellates. *Curr Genet* **48**, 277-99 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16215758>.
852. Stuart, K., Allen, T.E., Heidmann, S. & Seiwert, S.D. RNA editing in kinetoplastid protozoa. *Microbiol Mol Biol Rev* **61**, 105-20 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/9106367>.
853. Byrne, E.M., Connell, G.J. & Simpson, L. Guide RNA-directed uridine insertion RNA editing in vitro. *Embo J* **15**, 6758-65 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/8978701>.
854. Landweber, L.F. & Gilbert, W. Phylogenetic analysis of RNA editing: a primitive genetic phenomenon. *Proc Natl Acad Sci U S A* **91**, 918-21 (1994).
<http://www.ncbi.nlm.nih.gov/pubmed/8302867>.
855. Thomas, S., Martinez, L.L., Westenberger, S.J. & Sturm, N.R. A population study of the minicircles in *Trypanosoma cruzi*: predicting guide RNAs in the absence of empirical RNA editing. *BMC Genomics* **8**, 133 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17524149>.
856. Keeling, P.J. Chromalveolates and the evolution of plastids by secondary endosymbiosis. *J Eukaryot Microbiol* **56**, 1-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19335769>.
857. Gould, S.B., Waller, R.F. & McFadden, G.I. Plastid evolution. *Annu Rev Plant Biol* **59**, 491-517 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18315522>.
858. Deschamps, P. et al. Metabolic symbiosis and the birth of the plant kingdom. *Mol Biol Evol* **25**, 536-48 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18093994>.
859. Mittag, M. Circadian rhythms in microalgae. *Int Rev Cytol* **206**, 213-47 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11407761>.
860. Hader, D.P. Gravitaxis in unicellular microorganisms. *Adv Space Res* **24**, 843-50 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/11542630>.
861. Ginger, M.L. Trypanosomatid biology and euglenozoan evolution: new insights and shifting paradigms revealed through genome sequencing. *Protist* **156**, 377-92 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16310743>.
862. Hader, D.P. & Lebert, M. Photoorientation in photosynthetic flagellates. *Methods Mol Biol* **571**, 51-65 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19763958>.

863. Goto, K. & Beneragama, C.K. Circadian clocks and antiaging: do non-aging microalgae like Euglena reveal anything? *Ageing Res Rev* **9**, 91-100 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/19800033>.
864. Leander, B.S., Esson, H.J. & Breglia, S.A. Macroevolution of complex cytoskeletal systems in euglenids. *Bioessays* **29**, 987-1000 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17876783>.
865. Cavalier-Smith, T. The phagotrophic origin of eukaryotes and phylogenetic classification of Protozoa. *Int J Syst Evol Microbiol* **52**, 297-354 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11931142>.
866. Archibald, J.M. Nucleomorph genomes: structure, function, origin and evolution. *Bioessays* **29**, 392-402 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17373660>.
867. Silver, T.D. *et al.* Phylogeny and nucleomorph karyotype diversity of chlorarachniophyte algae. *J Eukaryot Microbiol* **54**, 403-10 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17910684>.
868. Cavalier-Smith, T. Kingdom protozoa and its 18 phyla. *Microbiol Rev* **57**, 953-94 (1993). <http://www.ncbi.nlm.nih.gov/pubmed/8302218>.
869. Roberts, K., Granum, E., Leegood, R.C. & Raven, J.A. Carbon acquisition by diatoms. *Photosynth Res* **93**, 79-88 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17497225>.
870. Nisbet, R.E., Kilian, O. & McFadden, G.I. Diatom genomics: genetic acquisitions and mergers. *Curr Biol* **14**, R1048-50 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15620637>.
871. Armbrust, E.V. *et al.* The genome of the diatom *Thalassiosira pseudonana*: ecology, evolution, and metabolism. *Science* **306**, 79-86 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15459382>.
872. Gould, S.B. *et al.* Nucleus-to-nucleus gene transfer and protein retargeting into a remnant cytoplasm of cryptophytes and diatoms. *Mol Biol Evol* **23**, 2413-22 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16971693>.
873. Venn, A.A., Loram, J.E. & Douglas, A.E. Photosynthetic symbioses in animals. *J Exp Bot* **59**, 1069-80 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18267943>.
874. Martin, W. & Muller, M. The hydrogen hypothesis for the first eukaryote. *Nature* **392**, 37-41 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/9510246>.
875. Gross, J. & Bhattacharya, D. Uniting sex and eukaryote origins in an emerging oxygenic world. *Biol Direct* **5**, 53 (2010). PMID 20731852.

876. Lake, J.A. Evidence for an early prokaryotic endosymbiosis. *Nature* **460**, 967-71 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19693078>.
877. Rivera, M.C.L., J. A. Lake. The ring of life: evidence for a genome fusion origin of eukaryotes. *Nature* **431**, 152–155 (2004). PMID 15356622.
878. Dagan, T., Roettger, M., Bryant, D. & Martin, W. Genome networks root the tree of life between prokaryotic domains. *Genome Biol Evol* **2**, 379-92 (2010). PMID 20624742.
879. Margulis, L. *Symbiosis in Cell Evolution.*, (W.H. Freeman Co, London, 1981).
880. Dolan, M.F., Melnitsky, H., Margulis, L. & Kolnicki, R. Motility proteins and the origin of the nucleus. *Anat Rec* **268**, 290-301 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12382325>.
881. Chapman, M.J., Dolan, M.F. & Margulis, L. Centrioles and kinetosomes: form, function, and evolution. *Q Rev Biol* **75**, 409-29 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11125699>.
882. Margulis, L., Dolan, M.F. & Guerrero, R. The chimeric eukaryote: origin of the nucleus from the karyomastigont in amitochondriate protists. *Proc Natl Acad Sci U S A* **97**, 6954-9 (2000).
<http://www.ncbi.nlm.nih.gov/pubmed/10860956>.
883. Wier, A.M. *et al.* Spirochete attachment ultrastructure: Implications for the origin and evolution of cilia. *Biol Bull* **218**, 25-35 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20203251>.
884. Carvalho-Santos, Z. *et al.* Stepwise evolution of the centriole-assembly pathway. *J Cell Sci* **123**, 1414-26 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20392737>.
885. Williamson, D. *Larvae and evolution: toward a new zoology*, (Chapman and Hall, New York, 1992).
886. Williamson, D.I. *The Origins of Larvae*, (Kluwer, Dordrecht, 2003).
887. Williamson, D.I. Caterpillars evolved from onychophorans by hybridogenesis. *Proc Natl Acad Sci U S A* **106**, 19901-5 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19717430>.
888. Epel, D. The Program of Fertilization. *Scientific American* **237**, 128-138 (1977).
<http://www.ncbi.nlm.nih.gov/pubmed/562535>.
889. Wassarman, P.M. Fertilization in Mammals. *Scientific American* **259**, 78-84 (1988).
<http://www.ncbi.nlm.nih.gov/pubmed/2849808>.
890. Schatten, H. & Sun, Q.Y. The role of centrosomes in mammalian fertilization and its significance for ICSI. *Mol Hum Reprod* **15**, 531-8 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19549764>.

891. Oldroyd, G.E., Harrison, M.J. & Paszkowski, U. Reprogramming plant cells for endosymbiosis. *Science* **324**, 753-4 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19423817>.
892. Jones, K.M., Kobayashi, H., Davies, B.W., Taga, M.E. & Walker, G.C. How rhizobial symbionts invade plants: the Sinorhizobium-Medicago model. *Nat Rev Microbiol* **5**, 619-33 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17632573>.
893. Wang, D. *et al.* A nodule-specific protein secretory pathway required for nitrogen-fixing symbiosis. *Science* **327**, 1126-9 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20185723>.
894. Van de Velde, W. *et al.* Plant peptides govern terminal differentiation of bacteria in symbiosis. *Science* **327**, 1122-6 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20185722>.
895. Cao, H. *et al.* Complex quorum-sensing regulatory systems regulate bacterial growth and symbiotic nodulation in Mesorhizobium tianshanense. *Arch Microbiol* **191**, 283-9 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19115053>.
896. Deakin, W.J. & Broughton, W.J. Symbiotic use of pathogenic strategies: rhizobial protein secretion systems. *Nat Rev Microbiol* **7**, 312-20 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19270720>.
897. Chesnick, J.M. & Cox, E.R. Synchronized sexuality of an algal symbiont and its dinoflagellate host, Peridinium balticum (Levander) Lemmermann. *Biosystems* **21**, 69-78 (1987). <http://www.ncbi.nlm.nih.gov/pubmed/3689888>.
898. O'Donnell, A.J., Schneider, P., McWatters, H.G. & Reece, S.E. Fitness costs of disrupting circadian rhythms in malaria parasites. *Proceedings of the Royal Society B: Biological Sciences* (2011). PMID 21208950.
899. Gramzow, L., Ritz, M.S. & Theissen, G. On the origin of MADS-domain transcription factors. *Trends Genet* **26**, 149-53 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20219261>.
900. Larroux, C. *et al.* Genesis and expansion of metazoan transcription factor gene classes. *Mol Biol Evol* **25**, 980-96 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18296413>.
901. Derelle, R., Lopez, P., Le Guyader, H. & Manuel, M. Homeodomain proteins belong to the ancestral molecular toolkit of eukaryotes. *Evol Dev* **9**, 212-9 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17501745>.

902. Piriayapongsa, J., Rutledge, M.T., Patel, S., Borodovsky, M. & Jordan, I.K. Evaluating the protein coding potential of exonized transposable element sequences. *Biol Direct* **2**, 31 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/18036258>.
903. Piriayapongsa, J., Polavarapu, N., Borodovsky, M. & McDonald, J. Exonization of the LTR transposable elements in human genome. *BMC Genomics* **8**, 291 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17725822>.
904. Corvelo, A. & Eyras, E. Exon creation and establishment in human genes. *Genome Biol* **9**, R141 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18811936>.
905. Sorek, R. The birth of new exons: mechanisms and evolutionary consequences. *RNA* **13**, 1603-8 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17709368>.
906. Schwartz, S. *et al.* Alu exonization events reveal features required for precise recognition of exons by the splicing machinery. *PLoS Comput Biol* **5**, e1000300 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19266014>.
907. Nekrutenko, A. & Li, W.H. Transposable elements are found in a large number of human protein-coding genes. *Trends Genet* **17**, 619-21 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11672845>.
908. Sela, N. *et al.* Comparative analysis of transposed element insertion within human and mouse genomes reveals Alu's unique role in shaping the human transcriptome. *Genome Biol* **8**, R127 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17594509>.
909. Sela, N., Mersch, B., Hotz-Wagenblatt, A. & Ast, G. Characteristics of transposable element exonization within human and mouse. *PLoS One* **5**, e10907 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20532223>.
910. Knerr, I. *et al.* Endogenous retroviral syncytin: compilation of experimental research on syncytin and its possible role in normal and disturbed human placentogenesis. *Mol Hum Reprod* **10**, 581-8 (2004). PMID 15181178.
911. Ono, R. *et al.* Deletion of Peg10, an imprinted gene acquired from a retrotransposon, causes early embryonic lethality. *Nat Genet* **38**, 101-6 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16341224>.
912. Sekita, Y. *et al.* Role of retrotransposon-derived imprinted gene, Rtl1, in the feto-maternal interface of mouse placenta. *Nat Genet* **40**, 243-8 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18176565>.

913. Esnault, C. *et al.* A placenta-specific receptor for the fusogenic, endogenous retrovirus-derived, human syncytin-2. *Proc Natl Acad Sci U S A* **105**, 17532-7 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18988732>.
914. Heidmann, O., Vernochet, C., Dupressoir, A. & Heidmann, T. Identification of an endogenous retroviral envelope gene with fusogenic activity and placenta-specific expression in the rabbit: a new "syncytin" in a third order of mammals. *Retrovirology* **6**, 107 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19943933>.
915. Noorali, S. *et al.* Role of HERV-W syncytin-1 in placentation and maintenance of human pregnancy. *Appl Immunohistochem Mol Morphol* **17**, 319-28 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19407656>.
916. Blackburn, D.G. Saltationist and punctuated equilibrium models for the evolution of viviparity and placentation. *Journal of Theoretical Biology* **174**, 199-216 (1995). PMID 7643614.
917. Beraldi, R., Pittoggi, C., Sciamanna, I., Mattei, E. & Spadafora, C. Expression of LINE-1 retroposons is essential for murine preimplantation development. *Mol Reprod Dev* **73**, 279-87 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16365895>.
918. Perrin, D. *et al.* Specific hypermethylation of LINE-1 elements during abnormal overgrowth and differentiation of human placenta. *Oncogene* **26**, 2518-24 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17043645>.
919. Kaneko-Ishino, T. & Ishino, F. Retrotransposon silencing by DNA methylation contributed to the evolution of placentation and genomic imprinting in mammals. *Dev Growth Differ* **52**, 533-43 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20646026>.
920. Wessler, S.R., Baran, G. & Varagona, M. The maize transposable element Ds is spliced from RNA. *Science* **237**, 916-8 (1987). <http://www.ncbi.nlm.nih.gov/pubmed/3039661>.
921. Wessler, S.R. The maize transposable Ds1 element is alternatively spliced from exon sequences. *Mol Cell Biol* **11**, 6192-6 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1658627>.
922. Zabala, G. & Vodkin, L. Novel exon combinations generated by alternative splicing of gene fragments mobilized by a CACTA transposon in Glycine max. *BMC Plant Biol* **7**, 38 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17629935>.

923. Varagona, M.J., Purugganan, M. & Wessler, S.R. Alternative splicing induced by insertion of retrotransposons into the maize waxy gene. *Plant Cell* **4**, 811-20 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1327340>.
924. Gal-Mark, N., Schwartz, S. & Ast, G. Alternative splicing of Alu exons--two arms are better than one. *Nucleic Acids Res* **36**, 2012-23 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18276646>.
925. Kreahling, J. & Graveley, B.R. The origins and implications of Alu alternative splicing. *Trends Genet* **20**, 1-4 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/14698612>.
926. Han, J.S., Szak, S.T. & Boeke, J.D. Transcriptional disruption by the L1 retrotransposon and implications for mammalian transcriptomes. *Nature* **429**, 268-74 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15152245>.
927. Han, J.S. & Boeke, J.D. LINE-1 retrotransposons: modulators of quantity and quality of mammalian gene expression? *Bioessays* **27**, 775-84 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16015595>.
928. Ustyugova, S.V., Lebedev, Y.B. & Sverdlov, E.D. Long L1 insertions in human gene introns specifically reduce the content of corresponding primary transcripts. *Genetica* **128**, 261-72 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17028956>.
929. Comfort, N.C. "The real point is control": The reception of Barbara McClintock's controlling elements. *Journal of the History of Biology* **32**, 133–6 (1999). PMID 11623812.
930. Shapiro, J.A. Mutations caused by the insertion of genetic material into the galactose operon of *Escherichia coli*. *J Mol Biol* **40**, 93-105 (1969). PMID 4903362.
931. De Crombrugghe B, A.S., Gottesman M, Pastan I. Effect of Rho on transcription of bacterial operons. *Nature New Biology* **241**, 260-4 (1973). PMID 4348358.
932. Pilacinski, W. *et al.* Insertion sequence IS2 associated with int-constitutive mutants of bacteriophage lambda. *Gene* **2**, 61-74 (1977). <http://www.ncbi.nlm.nih.gov/pubmed/344135>.
933. Nusse, R. & Varmus, H.E. Many tumors induced by the mouse mammary tumor virus contain a provirus integrated in the same region of the host genome. *Cell* **31**, 99-109 (1982).
<http://www.ncbi.nlm.nih.gov/pubmed/6297757>.
934. Nusse, R. Insertional mutagenesis in mouse mammary tumorigenesis. *Curr Top Microbiol Immunol* **171**, 43-65 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1667629>.

935. Tsichlis, P.N. *et al.* Activation of multiple genes by provirus integration in the Mlvi-4 locus in T-cell lymphomas induced by Moloney murine leukemia virus. *J Virol* **64**, 2236-44 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/1691313>.
936. Marino-Ramirez, L. & Jordan, I.K. Transposable element derived DNaseI-hypersensitive sites in the human genome. *Biol Direct* **1**, 20 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16857058>.
937. Romanish, M.T., Lock, W.M., van de Lagemaat, L.N., Dunn, C.A. & Mager, D.L. Repeated recruitment of LTR retrotransposons as promoters by the anti-apoptotic locus NAIP during mammalian evolution. *PLoS Genet* **3**, e10 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17222062>.
938. Qureshi, I.A. & Mehler, M.F. Regulation of non-coding RNA networks in the nervous system--what's the REST of the story? *Neurosci Lett* **466**, 73-80 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19679163>.
939. Johnson, R. *et al.* Evolution of the vertebrate gene regulatory network controlled by the transcriptional repressor REST. *Mol Biol Evol* **26**, 1491-507 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19318521>.
940. Johnson, R. *et al.* Identification of the REST regulon reveals extensive transposable element-mediated binding site duplication. *Nucleic Acids Res* **34**, 3862-77 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16899447>.
941. Peaston, A.E. *et al.* Retrotransposons regulate host genes in mouse oocytes and preimplantation embryos. *Dev Cell* **7**, 597-606 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15469847>.
942. Wang, J., Bowen, N.J., Marino-Ramirez, L. & Jordan, I.K. A c-Myc regulatory subnetwork from human transposable element sequences. *Mol Biosyst* **5**, 1831-9 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19763338>.
943. Slotkin, R.K. & Martienssen, R. Transposable elements and the epigenetic regulation of the genome. *Nat Rev Genet* **8**, 272-85 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17363976>.
944. Fontanillas, P., Hartl, D.L. & Reuter, M. Genome organization and gene expression shape the transposable element distribution in the *Drosophila melanogaster* euchromatin. *PLoS Genet* **3**, e210 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/18081425>.

945. Huda, A. & Jordan, I.K. Epigenetic regulation of Mammalian genomes by transposable elements. *Ann NY Acad Sci* **1178**, 276-84 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19845643>.
946. Gao, X., Hou, Y., Ebina, H., Levin, H.L. & Voytas, D.F. Chromodomains direct integration of retrotransposons to heterochromatin. *Genome Res* **18**, 359-69 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18256242>.
947. Bennetzen, J.L. The structure and evolution of angiosperm nuclear genomes. *Curr Opin Plant Biol* **1**, 103-8 (1998). <http://www.ncbi.nlm.nih.gov/pubmed/10066579>.
948. Nagaki, K. *et al.* Structure, divergence, and distribution of the CRR centromeric retrotransposon family in rice. *Mol Biol Evol* **22**, 845-55 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15616142>.
949. Kanizay, L. & Dawe, R.K. Centromeres: long intergenic spaces with adaptive features. *Funct Integr Genomics* **9**, 287-92 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19434433>.
950. Wolfgruber, T.K. *et al.* Maize Centromere Structure and Evolution: Sequence Analysis of Centromeres 2 and 5 Reveals Dynamic Loci Shaped Primarily by Retrotransposons. *PLoS Genet* **5**, e1000743 (2009). PMID 19956743.
951. Walter, J., Hutter, B., Khare, T. & Paulsen, M. Repetitive elements in imprinted genes. *Cytogenet Genome Res* **113**, 109-15 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16575169>.
952. Suzuki, S. *et al.* Retrotransposon silencing by DNA methylation can drive mammalian genomic imprinting. *PLoS Genet* **3**, e55 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17432937>.
953. Fujimoto, R. *et al.* Evolution and control of imprinted FWA genes in the genus Arabidopsis. *PLoS Genet* **4**, e1000048 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18389059>.
954. Pask, A.J. *et al.* Analysis of the platypus genome suggests a transposon origin for mammalian imprinting. *Genome Biol* **10**, R1 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19121219>.
955. Gehring, M., Bubb, K.L. & Henikoff, S. Extensive demethylation of repetitive elements during seed development underlies gene imprinting. *Science* **324**, 1447-51 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19520961>.
956. Amaral, P.P., Dinger, M.E., Mercer, T.R. & Mattick, J.S. The eukaryotic genome as an RNA machine. *Science* **319**, 1787-9 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18369136>.

957. Glinsky, G.V. Phenotype-defining functions of multiple non-coding RNA pathways. *Cell Cycle* **7**, 1630-9 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18469518>.
958. Zuckerkandl, E. & Cavalli, G. Combinatorial epigenetics, "junk DNA", and the evolution of complex organisms. *Gene* **390**, 232-42 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17223284>.
959. Mattick, J.S. The genetic signatures of noncoding RNAs. *PLoS Genet* **5**, e1000459 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19390609>.
960. Piriayapongsa, J. & Jordan, I.K. Dual coding of siRNAs and miRNAs by plant transposable elements. *RNA* **14**, 814-21 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18367716>.
961. Kuang, H. *et al.* Identification of miniature inverted-repeat transposable elements (MITEs) and biogenesis of their siRNAs in the Solanaceae: new functional implications for MITEs. *Genome Res* **19**, 42-56 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19037014>.
962. Hanada, K. *et al.* The functional role of pack-MULEs in rice inferred from purifying selection and expression profile. *Plant Cell* **21**, 25-38 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19136648>.
963. Obbard, D.J., Gordon, K.H., Buck, A.H. & Jiggins, F.M. The evolution of RNAi as a defence against viruses and transposable elements. *Philos Trans R Soc Lond B Biol Sci* **364**, 99-115 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/18926973>.
964. Smalheiser, N.R. & Torvik, V.I. Mammalian microRNAs derived from genomic repeats. *Trends Genet* **21**, 322-6 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/15922829>.
965. Mariner, P.D. *et al.* Human Alu RNA is a modular transacting repressor of mRNA transcription during heat shock. *Mol Cell* **29**, 499-509 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18313387>.
966. Yakovchuk, P., Goodrich, J.A. & Kugel, J.F. B2 RNA and Alu RNA repress transcription by disrupting contacts between RNA polymerase II and promoter DNA within assembled complexes. *Proc Natl Acad Sci U S A* **106**, 5569-74 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19307572>.
967. Lehnert, S. *et al.* Evidence for co-evolution between human microRNAs and Alu-repeats. *PLoS One* **4**, e4456 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19209240>.
968. Devor, E.J., Peek, A.S., Lanier, W. & Samollow, P.B. Marsupial-specific microRNAs evolved from marsupial-specific transposable elements. *Gene* **448**, 187-91 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19577616>.

969. White, M.J. Chromosomes of the vertebrates. *Evolution* **3**, 379-81 (1949).
<http://www.ncbi.nlm.nih.gov/pubmed/15396755>.
970. Carson, H.L., Clayton, F.E. & Stalker, H.D. Karyotypic stability and speciation in Hawaiian Drosophila. *Proc Natl Acad Sci U S A* **57**, 1280-5 (1967). PMID 5231734.
971. Stalker, H.D. Intergroup phylogenies in Drosophila as determined by comparisons of salivary banding patterns. *Genetics* **70**, 457-74 (1972). <http://www.ncbi.nlm.nih.gov/pubmed/5024716>.
972. Nakatani, Y., Takeda, H., Kohara, Y. & Morishita, S. Reconstruction of the vertebrate ancestral genome reveals dynamic genome reorganization in early vertebrates. *Genome Res* **17**, 1254-65 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17652425>.
973. Schubert, I. Chromosome evolution. *Curr Opin Plant Biol* **10**, 109-15 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17289425>.
974. Kemkemer, C. *et al.* Gene synteny comparisons between different vertebrates provide new insights into breakage and fusion events during mammalian karyotype evolution. *BMC Evol Biol* **9**, 84 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19393055>.
975. Kikuta, H. *et al.* Genomic regulatory blocks encompass multiple neighboring genes and maintain conserved synteny in vertebrates. *Genome Res* **17**, 545-55 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17387144>.
976. Olinski, R.P., Lundin, L.G. & Hallbook, F. Conserved synteny between the Ciona genome and human paralogs identifies large duplication events in the molecular evolution of the insulin-relaxin gene family. *Mol Biol Evol* **23**, 10-22 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16135778>.
977. Tang, H. Synteny and collinearity in plant genomes. *Science* **320**, 486-488 (2008)..
978. Waterston, R.H. *et al.* Initial sequencing and comparative analysis of the mouse genome. *Nature* **420**, 520-62 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12466850>.
979. Samonte, R.V. & Eichler, E.E. Segmental duplications and the evolution of the primate genome. *Nat Rev Genet* **3**, 65-72 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/11823792>.
980. Koszul, R. & Fischer, G. A prominent role for segmental duplications in modeling eukaryotic genomes. *C R Biol* **332**, 254-66 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19281956>.

981. Coulibaly, M.B. *et al.* Segmental duplication implicated in the genesis of inversion 2Rj of *Anopheles gambiae*. *PLoS One* **2**, e849 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17786220>.
982. Stankiewicz, P., Shaw, C.J., Withers, M., Inoue, K. & Lupski, J.R. Serial segmental duplications during primate evolution result in complex human genome architecture. *Genome Res* **14**, 2209-20 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15520286>.
983. Wolfe, K.H. Yesterday's polyploids and the mystery of diploidization. *Nat Rev Genet* **2**, 333-41 (2001). <http://www.ncbi.nlm.nih.gov/pubmed/11331899>.
984. Ma, X.F. & Gustafson, J.P. Genome evolution of allopolyploids: a process of cytological and genetic diploidization. *Cytogenet Genome Res* **109**, 236-49 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15753583>.
985. Tate, J.A., Joshi, P., Soltis, K.A., Soltis, P.S. & Soltis, D.E. On the road to diploidization? Homoeolog loss in independently formed populations of the allopolyploid *Tragopogon miscellus* (Asteraceae). *BMC Plant Biol* **9**, 80 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19558696>.
986. Carbone, L. *et al.* Evolutionary breakpoints in the gibbon suggest association between cytosine methylation and karyotype evolution. *PLoS Genet* **5**, e1000538 (2009). PMID 19557196.
987. Lemaitre, C. *et al.* Analysis of fine-scale mammalian evolutionary breakpoints provides new insight into their relation to genome organisation. *BMC Genomics* **10**, 335 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19630943>.
988. Sankoff, D. The where and wherefore of evolutionary breakpoints. *J Biol Chem* **8**, 66 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19664183>.
989. Larkin, D.M. *et al.* Breakpoint regions and homologous synteny blocks in chromosomes have different evolutionary histories. *Genome Res* **19**, 770-7 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19342477>.
990. Glover, T.W. Common fragile sites. *Cancer Lett* **232**, 4-12 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16229941>.
991. Arlt, M.F., Durkin, S.G., Ragland, R.L. & Glover, T.W. Common fragile sites as targets for chromosome rearrangements. *DNA Repair (Amst)* **5**, 1126-35 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16807141>.

992. Ruiz-Herrera, A. & Robinson, T.J. Chromosomal instability in Afrotheria: fragile sites, evolutionary breakpoints and phylogenetic inference from genome sequence assemblies. *BMC Evol Biol* **7**, 199 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17958882>.
993. Durkin, S.G. & Glover, T.W. Chromosome fragile sites. *Annu Rev Genet* **41**, 169-92 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17608616>.
994. von Grothuss, M., Ashburner, M. & Ranz, J.M. Fragile regions and not functional constraints predominate in shaping gene organization in the genus *Drosophila*. *Genome Res* **20**, 1084-96 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20601587>.
995. Rachidi, N., Barre, P. & Blondin, B. Multiple Ty-mediated chromosomal translocations lead to karyotype changes in a wine strain of *Saccharomyces cerevisiae*. *Mol Gen Genet* **261**, 841-50 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10394922>.
996. Longo, M.S., Carone, D.M., Green, E.D., O'Neill, M.J. & O'Neill, R.J. Distinct retroelement classes define evolutionary breakpoints demarcating sites of evolutionary novelty. *BMC Genomics* **10**, 334 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19630942>.
997. Kehrer-Sawatzki, H. & Cooper, D.N. Molecular mechanisms of chromosomal rearrangement during primate evolution. *Chromosome Res* **16**, 41-56 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18293104>.
998. Caceres, M., Ranz, J.M., Barbadilla, A., Long, M. & Ruiz, A. Generation of a widespread *Drosophila* inversion by a transposable element. *Science* **285**, 415-8 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10411506>.
999. Evgen'ev, M.B. *et al.* Mobile elements and chromosomal evolution in the virilis group of *Drosophila*. *Proc Natl Acad Sci U S A* **97**, 11337-42 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11016976>.
1000. Caceres, M., Puig, M. & Ruiz, A. Molecular characterization of two natural hotspots in the *Drosophila buzzatii* genome induced by transposon insertions. *Genome Res* **11**, 1353-64 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11483576>.
1001. Lyttle, T.W. & Haymer, D.S. The role of the transposable element hobo in the origin of endemic inversions in wild populations of *Drosophila melanogaster*. *Genetica* **86**, 113-26 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1334904>.

1002. Delprat, A., Negre, B., Puig, M. & Ruiz, A. The transposon Galileo generates natural chromosomal inversions in Drosophila by ectopic recombination. *PLoS One* **4**, e7883 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19936241>.
1003. Girirajan, S. *et al.* Sequencing human-gibbon breakpoints of synteny reveals mosaic new insertions at rearrangement sites. *Genome Res* **19**, 178-90 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19029537>.
1004. Yunis, J.J. Multiple recurrent genomic rearrangements and fragile sites in human cancer. *Somat Cell Mol Genet* **13**, 397-403 (1987). <http://www.ncbi.nlm.nih.gov/pubmed/3331831>.
1005. Le Beau, M.M. Chromosomal fragile sites and cancer-specific rearrangements. *Blood* **67**, 849-58 (1986). <http://www.ncbi.nlm.nih.gov/pubmed/3513870>.
1006. Pichiorri, F. *et al.* Molecular parameters of genome instability: roles of fragile genes at common fragile sites. *J Cell Biochem* **104**, 1525-33 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18393361>.
1007. Zhang, J. *et al.* Alternative Ac/Ds transposition induces major chromosomal rearrangements in maize. *Genes Dev* **23**, 755-65 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19299561>.
1008. Cuvier, G. *Le règne animal distribué d'après son organisation, pour servir de base à l'histoire naturelle des animaux et d'introduction à l'anatomie comparée*, (Deterville, Paris, 1817).
1009. Cuvier, G., M'Murtrie, H. (transl.). *The animal kingdom, arranged in conformity with its organization*, (G. & C. & H. Carvill, New York, 1832).
<http://www.archive.org/details/animalkingdomarr00cuv>.
1010. Darwin, E. *The Botanic Garden, Part II, The Loves of the Plants*, (J. Johnson, London, 1789).
<http://www.gutenberg.org/ebooks/10671>.
1011. Darwin, E. *Zoonomia; or, The Laws of Organic Life. Part I* (J. Johnson, London, 1794).
<http://www.gutenberg.org/ebooks/15707>.
1012. Darwin, E. *Zoonomia; or, The Laws of Organic Life. Part II* (London, 1796).
<http://www.gutenberg.org/ebooks/27600>.
1013. Darwin, E. *The Temple of Nature; or, The Origin of Society* (J. Johnson, 1806–1807, 1806–1807).
<http://www.gutenberg.org/ebooks/26861>.

1014. Carroll, S.B., Prud'homme, B. & Gompel, N. Regulating Evolution. *Scientific American* **298**, 60-67 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18444326>.
1015. Muller, G.B. & Newman, S.A. The innovation triad: an EvoDevo agenda. *J Exp Zool B Mol Dev Evol* **304**, 487-503 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16299770>.
1016. De Robertis, E.M. Evo-devo: variations on ancestral themes. *Cell* **132**, 185-95 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18243095>.
1017. Carroll, S.B. Evo-devo and an expanding evolutionary synthesis: a genetic theory of morphological evolution. *Cell* **134**, 25-36 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18614008>.
1018. Kuratani, S. Modularity, comparative embryology and evo-devo: developmental dissection of evolving body plans. *Dev Biol* **332**, 61-9 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19467227>.
1019. Gehring, W.J. The Molecular Basis of Development. *Scientific American* **253**, 152-162 (1985).
<http://www.ncbi.nlm.nih.gov/pubmed/3934753>.
1020. De Robertis, E.M., Oliver, G. & Wright, C.V. Homeobox genes and the vertebrate body plan. *Sci Am* **263**, 46-52 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/1973846>.
1021. McGinnis, W. & Kuziora, M. The Molecular Architects of Body Design. *Scientific American* **270**, 58-66 (1994). <http://www.ncbi.nlm.nih.gov/pubmed/7906436>.
1022. Holland, P.W. & Garcia-Fernandez, J. Hox genes and chordate evolution. *Dev. Biol.* **173**, 382-395 (1996). PMID 8605999.
1023. Lemons, D. & McGinnis, W. Genomic evolution of Hox gene clusters. *Science* **313**, 1918-22 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17008523>.
1024. Ryan, J.F. & Baxevanis, A.D. Hox, Wnt, and the evolution of the primary body axis: insights from the early-divergent phyla. *Biol Direct* **2**, 37 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/18078518>.
1025. Kuraku, S. & Meyer, A. The evolution and maintenance of Hox gene clusters in vertebrates and the teleost-specific genome duplication. *Int J Dev Biol* **53**, 765-73 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19557682>.
1026. Maeda, R.K. & Karch, F. The bithorax complex of Drosophila an exceptional Hox cluster. *Curr Top Dev Biol* **88**, 1-33 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19651300>.

1027. Duboule, D. & Dolle, P. The structural and functional organization of the murine HOX gene family resembles that of Drosophila homeotic genes. *Embo J* **8**, 1497-505 (1989).
<http://www.ncbi.nlm.nih.gov/pubmed/2569969>.
1028. Izpisua-Belmonte, J.C., Falkenstein, H., Dolle, P., Renucci, A. & Duboule, D. Murine genes related to the Drosophila AbdB homeotic genes are sequentially expressed during development of the posterior part of the body. *Embo J* **10**, 2279-89 (1991). <http://www.ncbi.nlm.nih.gov/pubmed/1676674>.
1029. McGinnis, N., Kuziora, M.A. & McGinnis, W. Human Hox-4.2 and Drosophila deformed encode similar regulatory specificities in Drosophila embryos and larvae. *Cell* **63**, 969-76 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/1979526>.
1030. Malicki, J., Schughart, K. & McGinnis, W. Mouse Hox-2.2 specifies thoracic segmental identity in Drosophila embryos and larvae. *Cell* **63**, 961-7 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/1979525>.
1031. Li, E. & Davidson, E.H. Building developmental gene regulatory networks. *Birth Defects Res C Embryo Today* **87**, 123-30 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19530131>.
1032. Ho, M.C. *et al.* Functional evolution of cis-regulatory modules at a homeotic gene in Drosophila. *PLoS Genet* **5**, e1000709 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19893611>.
1033. Garcia-Fernandez, J. The genesis and evolution of homeobox gene clusters. *Nat Rev Genet* **6**, 881-92 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16341069>.
1034. Valentine, J.W., Jablonski, D. & Erwin, D.H. Fossils, molecules and embryos: new perspectives on the Cambrian explosion. *Development* **126**, 851-9 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/9927587>.
1035. Valentine, J.W. & Jablonski, D. Morphological and developmental macroevolution: a paleontological perspective. *Int J Dev Biol* **47**, 517-22 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/14756327>.
1036. Finnerty, J.R. The origins of axial patterning in the metazoa: how old is bilateral symmetry? *Int J Dev Biol* **47**, 523-9 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/14756328>.
1037. Finnerty, J.R., Pang, K., Burton, P., Paulson, D. & Martindale, M.Q. Origins of bilateral symmetry: Hox and dpp expression in a sea anemone. *Science* **304**, 1335-7 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15131263>.

1038. Garcia-Fernandez, J. Hox, ParaHox, ProtoHox: facts and guesses. *Heredity* **94**, 145-52 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15578045>.
1039. Manuel, M. Early evolution of symmetry and polarity in metazoan body plans. *C R Biol* **332**, 184-209 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19281951>.
1040. Thomas-Chollier, M., Ledent, V., Leyns, L. & Vervoort, M. A non-tree-based comprehensive study of metazoan Hox and ParaHox genes prompts new insights into their origin and evolution. *BMC Evol Biol* **10**, 73 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20222951>.
1041. Chiori, R. *et al.* Are Hox genes ancestrally involved in axial patterning? Evidence from the hydrozoan *Clytia hemisphaerica* (Cnidaria). *PLoS One* **4**, e4231 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19156208>.
1042. Knoll, A.H., Javaux, E.J., Hewitt, D. & Cohen, P. Eukaryotic organisms in Proterozoic oceans. *Philos Trans R Soc Lond B Biol Sci* **361**, 1023-38 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16754612>.
1043. Xiao, S. & Laflamme, M. On the eve of animal radiation: phylogeny, ecology and evolution of the Ediacara biota. *Trends Ecol Evol* **24**, 31-40 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/18952316>.
1044. Peterson, K.J., Cotton, J.A., Gehling, J.G. & Pisani, D. The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. *Philos Trans R Soc Lond B Biol Sci* **363**, 1435-43 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18192191>.
1045. Conway Morris, S. & Whittington, H.B. The Animals of the Burgess Shale. *Scientific American* **241**, 122-135 (1979).
<http://www.nature.com/scientificamerican/journal/v241/n1/pdf/scientificamerican0779-122.pdf>.
1046. Levinton, J.S. The Big Bang of Animal Evolution. *Scientific American* **267**, 84-91 (1992).
<http://www.ncbi.nlm.nih.gov/pubmed/1411464>.
1047. Freeman, G. A developmental basis for the Cambrian radiation. *Zoolog Sci* **24**, 113-22 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17409724>.
1048. Budd, G.E. & Jensen, S. A critical reappraisal of the fossil record of the bilaterian phyla. *Biol Rev Camb Philos Soc* **75**, 253-95 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10881389>.
1049. Conway Morris, S. Darwin's dilemma: the realities of the Cambrian 'explosion'. *Philos Trans R Soc Lond B Biol Sci* **361**, 1069-83 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16754615>.

1050. Brysse, K. From weird wonders to stem lineages: the second reclassification of the Burgess Shale fauna. *Stud Hist Philos Biol Biomed Sci* **39**, 298-313 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18761282>.
1051. Chen, J.Y. *et al.* Complex embryos displaying bilaterian characters from Precambrian Doushantuo phosphate deposits, Weng'an, Guizhou, China. *Proc Natl Acad Sci U S A* **106**, 19056-60 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19858483>.
1052. Wigglesworth, V.B. Metamorphosis, Polymorphism, Differentiation. *Scientific American* **200**, 100-110 (1959). <http://www.nature.com/scientificamerican/journal/v200/n2/pdf/scientificamerican0259-100.pdf>.
1053. Hadorn, E. Transdetermination in Cells. *Scientific American* **219**, 110-120 (1968).
<http://www.ncbi.nlm.nih.gov/pubmed/5684924>.
1054. García-Bellido, A., Lawrence, P.A. & Morata, G. Compartments in Animal Development. *Scientific American* **241**, 102-111 (1979).
<http://www.nature.com/scientificamerican/journal/v241/n1/pdf/scientificamerican0779-102.pdf>.
1055. Nusslein-Volhard, C. Gradients that organize embryo development. *Sci Am* **275**, 54-5; 58-61 (1996).
<http://www.ncbi.nlm.nih.gov/pubmed/8693324>.
1056. Nusslein-Volhard, C. & Wieschaus, E. Mutations affecting segment number and polarity in *Drosophila*. *Nature* **287**, 795-801 (1980). <http://www.ncbi.nlm.nih.gov/pubmed/6776413>.
1057. Gordon, R. & Jacobson, A.G. The Shaping of Tissues in Embryos. *Scientific American* **238**, 106-113 (1978). <http://www.ncbi.nlm.nih.gov/pubmed/684401>.
1058. Riddle, R.D. & Tabin, C.J. How Limbs Develop. *Scientific American* **280**, 74-79 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/9924814>.
1059. Duboule, D. & Wilkins, A.S. The evolution of 'bricolage'. *Trends Genet* **14**, 54-9 (1998).
<http://www.ncbi.nlm.nih.gov/pubmed/9520598>.
1060. Wilkins, A.S. *The Evolution of Developmental Pathways*, (Sinauer, 2002).
1061. Wilkins, A.S. Recasting developmental evolution in terms of genetic pathway and network evolution ... and the implications for comparative biology. *Brain Res Bull* **66**, 495-509 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16144639>.

1062. Wilkins, A.S. Between "design" and "bricolage": genetic networks, levels of selection, and adaptive evolution. *Proc Natl Acad Sci U S A* **104 Suppl 1**, 8590-6 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17494754>.
1063. Albert, M. & Peters, A.H. Genetic and epigenetic control of early mouse development. *Curr Opin Genet Dev* **19**, 113-21 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19359161>.
1064. Mattick, J.S. A new paradigm for developmental biology. *J Exp Biol* **210**, 1526-47 (2007). PMID 17449818.
1065. Vasanthi, D. & Mishra, R.K. Epigenetic regulation of genes during development: a conserved theme from flies to mammals. *J Genet Genomics* **35**, 413-29 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18640621>.
1066. Vavouri, T., Walter, K., Gilks, W.R., Lehner, B. & Elgar, G. Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. *Genome Biol* **8**, R15 (2007). <http://www.ncbi.nlm.nih.gov/pubmed/17274809>.
1067. Borok, M.J., Tran, D.A., Ho, M.C. & Drewell, R.A. Dissecting the regulatory switches of development: lessons from enhancer evolution in Drosophila. *Development* **137**, 5-13 (2010).
<http://www.ncbi.nlm.nih.gov/pubmed/20023155>.
1068. Gehring, W.J., Kloter, U. & Suga, H. Evolution of the Hox gene complex from an evolutionary ground state. *Curr Top Dev Biol* **88**, 35-61 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19651301>.
1069. Mungpakdee, S. *et al.* Differential evolution of the 13 Atlantic salmon Hox clusters. *Mol Biol Evol* **25**, 1333-43 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18424774>.
1070. Spring, J. Genome duplication strikes back. *Nat Genet* **31**, 128-9 (2002).
<http://www.ncbi.nlm.nih.gov/pubmed/12040374>.
1071. Ohno, S. *Evolution by Gene Duplication* (George Allen and Unwin, London, 1970).
1072. Volff, J.N. & Schartl, M. Evolution of signal transduction by gene and genome duplication in fish. *J Struct Funct Genomics* **3**, 139-50 (2003). <http://www.ncbi.nlm.nih.gov/pubmed/12836693>.
1073. Dehal, P. & Boore, J.L. Two rounds of whole genome duplication in the ancestral vertebrate. *PLoS Biol* **3**, e314 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16128622>.

1074. Kawasaki, K., Buchanan, A.V. & Weiss, K.M. Gene duplication and the evolution of vertebrate skeletal mineralization. *Cells Tissues Organs* **186**, 7-24 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17627116>.
1075. Hulse, J.H. & Spurgeon, D. Tricale. *Scientific American* **231**, 72-80 (1974).
<http://www.nature.com/scientificamerican/journal/v231/n2/pdf/scientificamerican0874-72.pdf>.
1076. Wilson, A. Wheat and rye hybrids. *Edinburgh Botanical Society Transactions* **12**, 286–288 (1876).
1077. Meister, G. Natural hybridization of wheat and rye in Russia. *Journal of Heredity* **12**, 467–470 (1921).
1078. Ma, X.F. & Gustafson, J.P. Allopolyploidization-accommodated genomic sequence changes in tricale. *Ann Bot (Lond)* **101**, 825-32 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18252766>.
1079. Anderson, E., Stebbins, G.L., Jr. . Hybridization as an evolutionary stimulus. *Evolution* **8**, 378–388 (1954). .
1080. Arnold, M.L. Transfer and origin of adaptations through natural hybridization: were Anderson and Stebbins right? *Plant Cell* **16**, 562-70 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/15004269>.
1081. Crow, J.F. Plant breeding giants. Burbank, the artist; Vavilov, the scientist. *Genetics* **158**, 1391-5 (2001). PMID 11514434.
1082. Eakin, G.S. & Behringer, R.R. Tetraploid development in the mouse. *Dev Dyn* **228**, 751-66 (2003).
<http://www.ncbi.nlm.nih.gov/pubmed/14648853>.
1083. Beaulieu, J., Jean, M. & Belzile, F. The allotetraploid *Arabidopsis thaliana*-*Arabidopsis lyrata* subsp. *petraea* as an alternative model system for the study of polyploidy in plants. *Mol Genet Genomics* **281**, 421-35 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19148683>.
1084. Mallet, J., Beltran, M., Neukirchen, W. & Linares, M. Natural hybridization in heliconiine butterflies: the species boundary as a continuum. *BMC Evol Biol* **7**, 28 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17319954>.
1085. Mallet, J. Hybrid speciation. *Nature* **446**, 279-83 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17361174>.

1086. Dasmahapatra, K.K., Silva-Vasquez, A., Chung, J.W. & Mallet, J. Genetic analysis of a wild-caught hybrid between non-sister *Heliconius* butterfly species. *Biol Lett* **3**, 660-3 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17804337>.
1087. Salazar, C. *et al.* Genetic evidence for hybrid trait speciation in *heliconius* butterflies. *PLoS Genet* **6**, e1000930 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20442862>.
1088. Darwin, F., Seward, AC, eds. *More Letters of Charles Darwin* (John Murray, London, 1903).
<http://www.gutenberg.org/ebooks/2739> (vol. 1) & <http://www.gutenberg.org/ebooks/2740> (vol. 2).
1089. Cui, L. Widespread genome duplications throughout the history of flowering plants. *Genome Res.* **16**, 738-749 (2006). .
1090. Doyle, J.J. *et al.* Evolutionary genetics of genome merger and doubling in plants. *Annu Rev Genet* **42**, 443-61 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18983261>.
1091. Lim, K.Y. *et al.* Rapid chromosome evolution in recently formed polyploids in *Tragopogon* (Asteraceae). *PLoS One* **3**, e3353 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18843372>.
1092. Soltis, D.E. Polyploidy and angiosperm diversification. *Am. J. Bot.* **96**, 336-348 (2009). .
1093. Wolfe, K.H. & Shields, D.C. Molecular evidence for an ancient duplication of the entire yeast genome. *Nature* **387**, 708-713 (1997). PMID 9192896.
1094. Musso, G., Zhang, Z. & Emili, A. Retention of protein complex membership by ancient duplicated gene products in budding yeast. *Trends Genet* **23**, 266-9 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17428571>.
1095. Conant, G.C. & Wolfe, K.H. Increased glycolytic flux as an outcome of whole-genome duplication in yeast. *Mol. Syst. Biol.* **3**, 129 (2007). .
1096. Aury, J.M. Global trends of whole-genome duplications revealed by the ciliate *Paramecium tetraurelia*. *Nature* **444**, 171-178 (2006). .
1097. Veron, A.S., Kaufmann, K. & Bornberg-Bauer, E. Evidence of interaction network evolution by whole-genome duplications: a case study in MADS-box proteins. *Mol Biol Evol* **24**, 670-8 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17175526>.

1098. Gillis, W.Q., John, J.S., Bowerman, B. & Schneider, S.Q. Whole genome duplications and expansion of the vertebrate GATA transcription factor gene family. *BMC Evol Biol* **9**, 207 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19695090>.
1099. Wilkins, A.S. Genetic networks as transmitting and amplifying devices for natural genetic tinkering. *Novartis Found Symp* **284**, 71-86; discussion 86-9, 110-5 (2007).
<http://www.ncbi.nlm.nih.gov/pubmed/17710848>.
1100. Kassahn, K.S., Dang, V.T., Wilkins, S.J., Perkins, A.C. & Ragan, M.A. Evolution of gene function and regulatory control after whole-genome duplication: comparative analyses in vertebrates. *Genome Res* **19**, 1404-18 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19439512>.
1101. Bray, D. Intracellular signalling as a parallel distributed process. *J Theor Biol* **143**, 215-31 (1990).
<http://www.ncbi.nlm.nih.gov/pubmed/2385105>.
1102. Morelli, M.J., Ten Wolde, P.R. & Allen, R.J. DNA looping provides stability and robustness to the bacteriophage lambda switch. *Proc Natl Acad Sci U S A* **106**, 8101-6 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19416825>.
1103. Jacob, F. Evolution and tinkering. *Science* **196**, 1161-6 (1977).
<http://www.ncbi.nlm.nih.gov/pubmed/860134>.
1104. Bubanovic, I., Najman, S. & Andjelkovic, Z. Origin and evolution of viruses: escaped DNA/RNA sequences as evolutionary accelerators and natural biological weapons. *Med Hypotheses* **65**, 868-72 (2005). <http://www.ncbi.nlm.nih.gov/pubmed/16084025>.
1105. Claverie, J.M. Viruses take center stage in cellular evolution. *Genome Biol* **7**, 110 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/16787527>.
1106. Forterre, P. The origin of viruses and their possible roles in major evolutionary transitions. *Virus Res* **117**, 5-16 (2006). PMID 16476498.
1107. Forterre, P. & Gadelle, D. Phylogenomics of DNA topoisomerases: their origin and putative roles in the emergence of modern organisms. *Nucleic Acids Res* **37**, 679-92 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19208647>.
1108. Koonin, E.V., Senkevich, T.G. & Dolja, V.V. The ancient Virus World and evolution of cells. *Biol Direct* **1**, 29 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16984643>.

1109. Koonin, E.V. Temporal order of evolution of DNA replication systems inferred by comparison of cellular and viral DNA polymerases. *Biol Direct* **1**, 39 (2006).
<http://www.ncbi.nlm.nih.gov/pubmed/17176463>.
1110. Delaroche, N. & Boland, W. The genome of the brown alga *Ectocarpus siliculosus* contains a series of viral DNA pieces, suggesting an ancient association with large dsDNA viruses. *BMC Evol Biol* **8**, 110 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18405387>.
1111. Bell, P.J. The viral eukaryogenesis hypothesis: a key role for viruses in the emergence of eukaryotes from a prokaryotic world environment. *Ann N Y Acad Sci* **1178**, 91-105 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19845630>.
1112. Keller, J. *et al.* A protein encoded by a new family of mobile elements from Euryarchaea exhibits three domains with novel folds. *Protein Sci* **18**, 850-5 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19319959>.
1113. Groves, D.I., Dunlop, J.S.R. & Buick, R. An Early Habitat of Life. *Scientific American* **245**, 64-73 (1981). <http://www.nature.com/scientificamerican/journal/v245/n4/pdf/scientificamerican1081-64.pdf>.
1114. Allwood, A.C., Walter, M.R., Kamber, B.S., Marshall, C.P. & Burch, I.W. Stromatolite reef from the Early Archaean era of Australia. *Nature* **441**, 714-8. (2006). PMID 16760969.
1115. Trewavas, A. Plant intelligence. *Naturwissenschaften* **92**, 401-13 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/16142448>.
1116. Brenner, E.D. *et al.* Plant neurobiology: an integrated view of plant signaling. *Trends Plant Sci* **11**, 413-9 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16843034>.
1117. Barlow, P.W. Reflections on 'plant neurobiology'. *Biosystems* **92**, 132-47 (2008).
<http://www.ncbi.nlm.nih.gov/pubmed/18336993>.
1118. Cvrckova, F., Lipavska, H. & Zarsky, V. Plant intelligence: why, why not or where? *Plant Signal Behav* **4**, 394-9 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19816094>.
1119. Perkins, T.J. & Swain, P.S. Strategies for cellular decision-making. *Mol Syst Biol* **5**, 326 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19920811>.

1120. Darwin, C.R. *The Power of Movements in Plants* (John Murray, London, 1880). http://darwin-online.org.uk/EditorialIntroductions/Freeman_ThePowerofMovementinPlants.html.
1121. Baluska, F., Mancuso, S., Volkmann, D. & Barlow, P.W. The 'root-brain' hypothesis of Charles and Francis Darwin: Revival after more than 125 years. *Plant Signal Behav* **4**, 1121-7 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/20514226>.
1122. Campbell, J.H., Lengyel, J.A. & Langridge, J. Evolution of a second gene for beta-galactosidase in *Escherichia coli*. *Proc Natl Acad Sci U S A* **70**, 1841-5 (1973).
<http://www.ncbi.nlm.nih.gov/pubmed/4124306>.
1123. Hall, B.G. & Hauer, B. Acquisition of new metabolic activities by microbial populations. *Methods Enzymol* **224**, 603-13 (1993). <http://www.ncbi.nlm.nih.gov/pubmed/8264414>.
1124. Hunt, P. *et al.* Experimental evolution, genetic analysis and genome re-sequencing reveal the mutation conferring artemisinin resistance in an isogenic lineage of malaria parasites. *BMC Genomics* **11**, 499 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20846421>.
1125. Comai, L. *et al.* Phenotypic instability and rapid gene silencing in newly formed arabidopsis allotetraploids. *Plant Cell* **12**, 1551-68 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/11006331>.
1126. Pontes, O. *et al.* Chromosomal locus rearrangements are a rapid response to formation of the allotetraploid *Arabidopsis suecica* genome. *Proc Natl Acad Sci U S A* **101**, 18240-5 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/15604143>.
1127. Madlung, A. *et al.* Genomic changes in synthetic *Arabidopsis* polyploids. *Plant J* **41**, 221-30 (2005).
<http://www.ncbi.nlm.nih.gov/pubmed/15634199>.
1128. Wang, J. *et al.* Genomewide nonadditive gene regulation in *Arabidopsis* allotetraploids. *Genetics* **172**, 507-17 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/16172500>.
1129. Driesch, H. *The science and philosophy of the organism : Gifford lectures delivered at Aberdeen university, 1907-1908 by Hans Driesch*, (Printed for the University, Aberdeen :, 1908).
<http://www.archive.org/details/cu31924010498040>.
1130. Melzer, S.J. Vitalism and mechanism in biology and medicine. *Science* **19**, 18-22 (1904). PMID 17782338.

1131. Lillie, R.S. The philosophy of biology: vitalism versus mechanism. *Science* **40**, 840-846 (1914). PMID 17796813.
1132. Holliday, R. Physics and the origins of molecular biology. *J Genet Genomics* **85**, 93-7 (2006). <http://www.ncbi.nlm.nih.gov/pubmed/17072076>.
1133. Wiener, N. *Cybernetics or Control and Communication in the Animal and the Machine*, (MIT Press, Cambridge, 1965).
1134. Hopfield, J.J. Neural networks and physical systems with emergent collective computational abilities. *Proc. Natl Acad. Sci. USA* **79**, 2554-2558 (1982). PMID 6953413.
1135. Alvarez, W. & Asaro, F. An Extraterrestrial Impact. *Scientific American* **263**, 78-84 (1990). <http://www.ncbi.nlm.nih.gov/pubmed/11536473>.
1136. Alvarez, L.W., Alvarez, W., Asaro, F. & Michel, H.V. Extraterrestrial cause for the cretaceous-tertiary extinction. *Science* **208**, 1095-108 (1980). <http://www.ncbi.nlm.nih.gov/pubmed/17783054>.
1137. Schulte, P. *et al.* The Chicxulub asteroid impact and mass extinction at the Cretaceous-Paleogene boundary. *Science* **327**, 1214-8 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20203042>.
1138. Raup, D.M. & Sepkoski, J.J., Jr. Mass extinctions in the marine fossil record. *Science* **215**, 1501-3 (1982). <http://www.ncbi.nlm.nih.gov/pubmed/17788674>.
1139. Raup, D.M. & Sepkoski, J.J., Jr. Periodic extinction of families and genera. *Science* **231**, 833-6 (1986). <http://www.ncbi.nlm.nih.gov/pubmed/11542060>.
1140. Raup, D.M. & Boyajian, G.E. Patterns of generic extinction in the fossil record. *Paleobiology* **14**, 109-25 (1988). <http://www.ncbi.nlm.nih.gov/pubmed/11542145>.
1141. Rampino, M.R., Haggerty, B.M. & Pagano, T.C. A unified theory of impact crises and mass extinctions: quantitative tests. *Ann N Y Acad Sci* **822**, 403-31 (1997). <http://www.ncbi.nlm.nih.gov/pubmed/11543121>.
1142. Sengor, A.M., Atayman, S. & Ozeren, S. A scale of greatness and causal classification of mass extinctions: implications for mechanisms. *Proc Natl Acad Sci U S A* **105**, 13736-40 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18779562>.
1143. Kirchner, J.W. & Weil, A. Correlations in fossil extinction and origination rates through geological time. *Proc Biol Sci* **267**, 1301-9 (2000). <http://www.ncbi.nlm.nih.gov/pubmed/10972124>.

1144. Pave, A., Herve, J.C. & Schmidt-Laine, C. Mass extinctions, biodiversity explosions and ecological niches. *C R Biol* **325**, 755-65 (2002). <http://www.ncbi.nlm.nih.gov/pubmed/12360843>.
1145. Alroy, J. Colloquium paper: dynamics of origination and extinction in the marine fossil record. *Proc Natl Acad Sci U S A* **105 Suppl 1**, 11536-42 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/18695240>.
1146. Foote, M. & Raup, D.M. Fossil preservation and the stratigraphic ranges of taxa. *Paleobiology* **22**, 121-40 (1996). <http://www.ncbi.nlm.nih.gov/pubmed/11539203>.
1147. Foote, M. & Sepkoski, J.J., Jr. Absolute measures of the completeness of the fossil record. *Nature* **398**, 415-7 (1999). <http://www.ncbi.nlm.nih.gov/pubmed/11536900>.
1148. Payne, J.L. *et al.* Two-phase increase in the maximum size of life over 3.5 billion years reflects biological innovation and environmental opportunity. *Proc Natl Acad Sci U S A* **106**, 24-7 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19106296>.
1149. Mayhew, P.J., Jenkins, G.B. & Benton, T.G. A long-term association between global temperature and biodiversity, origination and extinction in the fossil record. *Proc Biol Sci* **275**, 47-53 (2008). <http://www.ncbi.nlm.nih.gov/pubmed/17956842>.
1150. Cloud, P. The Biosphere. *Scientific American* **249**, 176-189 (1983).
<http://www.nature.com/scientificamerican/journal/v249/n3/pdf/scientificamerican0983-176.pdf>.
1151. Gould, S.J. The Evolution of Life on Earth. *Scientific American* **290**, 92-100 (2004).
<http://www.ncbi.nlm.nih.gov/pubmed/7939569>.
1152. Gould, S.J. Punctuated Equilibrium and the Fossil Record. *Science* **219**, 439-440 (1983).
<http://www.ncbi.nlm.nih.gov/pubmed/17742803>.
1153. Gould, S.J. & Eldredge, N. Punctuated equilibrium comes of age. *Nature* **366**, 223-7 (1993).
<http://www.ncbi.nlm.nih.gov/pubmed/8232582>.
1154. Zeh, D.W., Zeh, J.A. & Ishida, Y. Transposable elements and an epigenetic basis for punctuated equilibria. *Bioessays* **31**, 715-26 (2009). <http://www.ncbi.nlm.nih.gov/pubmed/19472370>.
1155. David, L.A. & Alm, E.J. Rapid evolutionary innovation during an Archaean genetic expansion. *Nature* **469**, 93-96 (2011). <http://www.ncbi.nlm.nih.gov/pubmed/21170026>.
1156. Holland, J.H. Genetic Algorithms. *Scientific American* **267**, 66-72 (1992).
<http://www.nature.com/scientificamerican/journal/v267/n1/pdf/scientificamerican0792-66.pdf>.

1157. Foster, J.A. Evolutionary computation. *Nat Rev Genet* **2**, 428-36 (2001).
<http://www.ncbi.nlm.nih.gov/pubmed/11389459>.
1158. Francois, P. & Hakim, V. Design of genetic networks with specified functions by evolution in silico. *Proc Natl Acad Sci U S A* **101**, 580-5 (2004). <http://www.ncbi.nlm.nih.gov/pubmed/14704282>.
1159. Rodrigo, G., Carrera, J. & Elena, S.F. Network design meets in silico evolutionary biology. *Biochimie* **92**, 746-52 (2010). <http://www.ncbi.nlm.nih.gov/pubmed/20399826>.
1160. Muller-Hill, B. Towards a linguistics of DNA and protein. *Hist Philos Life Sci* **21**, 53-63 (1999).
<http://www.ncbi.nlm.nih.gov/pubmed/10865878>.
1161. Newman, S.A. & Bhat, R. Dynamical patterning modules: a "pattern language" for development and evolution of multicellular form. *Int J Dev Biol* **53**, 693-705 (2009).
<http://www.ncbi.nlm.nih.gov/pubmed/19378259>.
1162. Pinker, S. *The Language Instinct: The New Science of Language and Mind*, (Penguin, 1994).