

---

## **References**

---

**Achaz, G.**, Netter, P., *et al.* (2001). Study of intrachromosomal duplications among the eukaryote genomes. *Mol Biol Evol* **18**: 2280-8.

**Adams, M. D.**, Celtniker, S. E., *et al.* (2000). The genome sequence of *Drosophila melanogaster*. *Science* **287**: 2185-95.

**Agundez, J. A.**, Gallardo, L., *et al.* (2001). Functionally active duplications of the CYP2D6 gene are more prevalent among larynx and lung cancer patients. *Oncology* **61**: 59-63.

**Allcock, R. J.**, Atrazhev, A. M., *et al.* (2002). The MHC haplotype project: a resource for HLA-linked association studies. *Tissue Antigens* **59**: 520-1.

**Antequera, F.** and Bird, A. (1993). Number of CpG islands and genes in human and mouse. *Proc Natl Acad Sci U S A* **90**: 11995-9.

**Aparicio, S.**, Chapman, J., *et al.* (2002). Whole-genome shotgun assembly and analysis of the genome of *Fugu rubripes*. *Science* **297**: 1301-10.

**Arabidopsis Genome Initiative.** (2000). Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* **408**: 796-815.

**Averof, M.** (2002). Arthropod Hox genes: insights on the evolutionary forces that shape gene functions. *Curr Opin Genet Dev* **12**: 386-92.

**Avner, P.**, Bruls, T., *et al.* (2001). A radiation hybrid transcript map of the mouse genome. *Nat Genet* **29**: 194-200.

**Avner, P.**, Heard, E. (2001). X-chromosome inactivation: counting, choice and initiation. *Nat Rev. Genet.* **2**:59-67.

**Bailey, J. A.**, Gu, Z., *et al.* (2002). Recent segmental duplications in the human genome. *Science* **297**: 1003-7.

---

**Batzoglou, S.**, Jaffe, D. B., *et al.* (2002). ARACHNE: a whole-genome shotgun assembler. *Genome Res.* **12**: 177-89.

**Bentley, D. R.**, Todd, C., *et al.* (1992). The development and application of automated gridding for efficient screening of yeast and bacterial ordered libraries. *Genomics* **12**: 534-41.

**Bentley, D. R.**, Deloukas, P., *et al.* (2001). The physical maps for sequencing human chromosomes 1, 6, 9, 10, 13, 20 and X. *Nature* **409**: 942-3.

**Bernardi, G.**, Olofsson, B., *et al.* (1985). The mosaic genome of warm-blooded vertebrates. *Science* **228**: 953-8.

**Blacket, M. J.**, Krajewski, C., *et al.* (1999). Systematic relationships within the dasyurid marsupial tribe *Sminthopsini*--a multigene approach. *Mol Phylogenet Evol* **12**: 140-55.

**Blumenthal, T.** (1995). Trans-splicing and polycistronic transcription in *Caenorhabditis elegans*. *Trends Genet* **11**: 132-6.

**Brown, A. L.** and Kay, G. F. (1999). Bex1, a gene with increased expression in parthenogenetic embryos, is a member of a novel gene family on the mouse X chromosome. *Hum Mol Genet* **8**: 611-9.

**Brown, C. J.**, Ballabio, A., *et al.*, (1991). A gene from the region of the human X inactivation centre is expressed exclusively from the inactive X chromosome. *Nature* **349**: 38-44.

**Brown, C. J.**, Greally, J. M., (2003). A stain upon the silence: genes escaping X inactivation. *Trends Genet.* **19**: 432-438.

**Bult, C. J.**, White, O., *et al.* (1996). Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*. *Science* **273**: 1058-73.

**Burge, C.** and Karlin, S. (1997). Prediction of complete gene structures in human genomic DNA. *J Mol Biol* **268**: 78-94.

---

**Bussey, H.**, Storms, R. K., *et al.* (1997). The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI. *Nature* **387**: 103-5.

**Carninci, P.**, Shibata, Y., *et al.* (2000). Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res* **10**: 1617-30.

**Chapman, M. A.**, Charchar, F. J., *et al.* (2003). Comparative and functional analyses of LYL1 loci establish marsupial sequences as a model for phylogenetic footprinting. *Genomics* **81**: 249-59.

**Chowdhary, B. P.**, Raudsepp, T., *et al.* (1998). Emerging patterns of comparative genome organization in some mammalian species as revealed by Zoo-FISH. *Genome Res* **8**: 577-89.

**Chudley, A. E.**, Tackels, D. C., *et al.* (1999). X-linked mental retardation syndrome with seizures, hypogammaglobulinemia, and progressive gait disturbance is regionally mapped between Xq21.33 and Xq23. *Am J Med Genet* **85**: 255-62.

**Cohen, D.**, Chumakov, I., *et al.* (1993). A first-generation physical map of the human genome. *Nature* **366**: 698-701.

**Collins, J.** and Bruning, H. J. (1978). Plasmids useable as gene-cloning vectors in an *in vitro* packaging by coliphage lambda: cosmids. *Gene* **4**: 85-107.

**Collins, J. E.**, Cole, C. G., *et al.* (1995). A high-density YAC contig map of human chromosome 22. *Nature* **377**: 367-79.

**Crnogorac-Jurcevic, T.** and Brown, J. R. (1997). Tetraodon fluviatilis, a new puffer fish model for genome studies. *Genomics* **41**: 177-84.

**Davuluri, R. V.**, Grosse, I., *et al.* (2001). Computational identification of promoters and first exons in the human genome. *Nat Genet* **29**: 412-7.

---

**De Leo, A. A.**, Guedelha, N., *et al.* (1999). Comparative chromosome painting between marsupial orders: relationships with a  $2n = 14$  ancestral marsupial karyotype. *Chromosome Res* **7**: 509-17.

**Dear, P. H.**, Cook, P. R. (1989). Happy mapping: a proposal for linkage mapping the human genome. *Nucleic Acids Research* **17**: 6795-6807

**Dehal, P.**, Satou, Y., *et al.* (2002). The draft genome of *Ciona intestinalis*: insights into chordate and vertebrate origins. *Science* **298**: 2157-67.

**Deloukas, P.**, Schuler, G. D., *et al.* (1998). A physical map of 30,000 human genes. *Science* **282**: 744-6.

**Dietrich, W. F.**, Miller, J., *et al.* (1996). A comprehensive genetic map of the mouse genome. *Nature* **380**: 149-52.

**Donis-Keller, H.**, Green, P., *et al.* (1987). A genetic linkage map of the human genome. *Cell* **51**: 319-37.

**Down, T. A.** and Hubbard, T. J. (2002). Computational detection and location of transcription start sites in mammalian genomic DNA. *Genome Res* **12**: 458-61.

**Dunham, I.**, Shimizu, N., *et al.* (1999). The DNA sequence of human chromosome 22. *Nature* **402**: 489-95.

**Duyk, G. M.**, Kim, S. W., *et al.* (1990). Exon trapping: a genetic screen to identify candidate transcribed sequences in cloned mammalian genomic DNA. *Proc Natl Acad Sci U S A* **87**: 8995-9.

**Emanuel, B. S.** and Shaikh, T. H. (2001). Segmental duplications: an 'expanding' role in genomic instability and disease. *Nat Rev Genet* **2**: 791-800.

---

**Faria, T. N.**, LaRosa, G. J., *et al.* (1998). Characterization of genes which exhibit reduced expression during the retinoic acid-induced differentiation of F9 teratocarcinoma cells: involvement of cyclin D3 in RA-mediated growth arrest. *Mol Cell Endocrinol* **143**: 155-66.

**Fleischmann, R. D.**, Adams, M. D., *et al.* (1995). Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd. *Science* **269**: 496-512.

**Force, A.**, Lynch, M., *et al.* (1999). Preservation of duplicate genes by complementary, degenerative mutations. *Genetics* **151**: 1531-45.

**Friedman, R.** and Hughes, A. L. (2001). Gene duplication and the structure of eukaryotic genomes. *Genome Res* **11**: 373-81.

**Frints, S. G.** *et al.* (2002). X-linked mental retardation: vanishing boundaries between non-specific (MRX) and syndromic (MRXS) forms. *Clin. Genet.* **62**: 423-432.

**Frohman, M. A.**, Dush, M. K., *et al.* (1988). Rapid production of full-length cDNAs from rare transcripts: amplification using a single gene-specific oligonucleotide primer. *Proc Natl Acad Sci U S A* **85**: 8998-9002.

**Gibbs, R. A.**, Belmont, J. W., *et al.* (2003). The international HapMap project. *Nature* **426**: 789-96.

**Glas, R.**, Marshall-Graves, J. A., *et al.* (1999). Cross-species chromosome painting between human and marsupial directly demonstrates the ancient region of the mammalian X. *Mamm Genome* **10**: 1115-6.

**Gottgens, B.**, Barton, L. M., *et al.* (2002). Transcriptional regulation of the stem cell leukemia gene (SCL) - comparative analysis of five vertebrate SCL loci. *Genome Res* **12**: 749-59.

**Gow, A.** (1997). Redefining the lipophilin family of proteolipid proteins. *J Neurosci Res* **50**: 659-64.

---

**Graves, J.** and Westerman, M. (2002). Marsupial genetics and genomics. *Trends Genet* **18**: 517.

**Gregory, S. G.**, Howell, G. R., *et al.* (1997). Genome mapping by fluorescent fingerprinting. *Genome Res* **7**: 1162-8.

**Gregory, S. G.**, Sekhon, M., *et al.* (2002). A physical map of the mouse genome. *Nature* **418**: 743-50.

**Grutzner, F.**, Crolius, H. R., *et al.* (2002). Four-hundred million years of conserved synteny of human Xp and Xq genes on three tetraodon chromosomes. *Genome Res* **12**: 1316-22.

**Gu, X.**, Wang, Y., *et al.* (2002). Age distribution of human gene families shows significant roles of both large- and small-scale duplications in vertebrate evolution. *Nat Gen* **31**: 205-9.

**Guigo, R.**, Agarwal, P., *et al.* (2000). An assessment of gene prediction accuracy in large DNA sequences. *Genome Res* **10**: 1631-42.

**Herold, A.**, Suyama, M., *et al.* (2000). TAP (NXF1) belongs to a multigene family of putative RNA export factors with a conserved modular architecture. *Mol Cell Biol* **20**: 8996-9008.

**Hescheler, J.** and Schultz, G. (1993). G-proteins involved in the calcium channel signalling system. *Curr Opin Neurobiol* **3**: 360-7.

**Holland, J.**, Coffey, A. J., *et al.* (1993). Vertical integration of cosmid and YAC resources for interval mapping on the X-chromosome. *Genomics* **15**: 297-304.

**Howell, G. R.**, (2002). Physical, transcriptional and comparative mapping on the human X chromosome. PhD thesis, The Open University.

---

**Huang, S.-H.**, Yang, A. Y., *et al.* (1993). Amplification of genes ends from gene libraries by polymerase chain reaction with single-sided specificity. In *Methods in Molecular Biology, PCR Protocols: Current Methods and Applications*. (B. A. White, ed.). Humana Press, Totowa, New Jersey. pp 357-363.

**Hudson, T. J.**, Church, D. M., *et al.* (2001). A radiation hybrid map of mouse genes. *Nat Genet* **29**: 201-5.

**Huff, T.**, Muller, C. S., *et al.* (2001). beta-Thymosins, small acidic peptides with multiple functions. *Int J Biochem Cell Biol* **33**: 205-20.

**Inoue, K.**, Osaka, H., *et al.* (1996). A duplicated PLP gene causing Pelizaeus-Merzbacher disease detected by comparative multiplex PCR. *Am J Hum Genet* **59**: 32-9.

**Jurka, J.** (2000). Repbase update: a database and an electronic journal of repetitive elements. *Trends Genet* **16**: 418-20.

**Kikuno, R.**, Nagase, T., *et al.* (2002). HUGE: a database for human large proteins identified in the Kazusa cDNA sequencing project. *Nucleic Acids Res* **30**: 166-8.

**Kimura, M.** (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol* **16**: 111-20.

**Kitagawa, K.**, Sinoway, M. P., *et al.* (1993). A proteolipid protein gene family: expression in sharks and rays and possible evolution from an ancestral gene encoding a pore-forming polypeptide. *Neuron* **11**: 433-48.

**Kong, A.**, Gudbjartsson, D. F., *et al.* (2002). A high-resolution recombination map of the human genome. *Nat Genet* **31**: 241-7.

**Konietzko, U.** and Kuhl, D. (1998). A subtractive hybridisation method for the enrichment of moderately induced sequences. *Nucleic Acids Res* **26**: 1359-61.

---

**Korf, I.**, Flieck, P., *et al.* (2001). Integrating genomic homology into gene structure prediction. *Bioinformatics* **17**: S140-8.

**Kumar, S.** and Hedges, S. B. (1998). A molecular timescale for vertebrate evolution. *Nature* **392**: 917-20.

**Kumar, S.**, Tamura, K., *et al.* (2001). MEGA2: molecular evolutionary genetics analysis software. *Bioinformatics* **17**: 1244-5.

**Kurochkin, I. V.**, Yonemitsu, N., *et al.* (2001). ALEX1, a novel human armadillo repeat protein that is expressed differentially in normal tissues and carcinomas. *Biochem Biophys Res Commun* **280**: 340-7.

**Lander, E. S.**, Linton, L. M., *et al.* (2001). Initial sequencing and analysis of the human genome. *Nature* **409**: 860-921.

**Li, X.**, Zimmerman, A., *et al.* (1996). The mouse thymosin beta 4 gene: structure, promoter identification, and chromosome localization. *Genomics* **32**: 388-94.

**Lovett, M.**, Kere, J., *et al.* (1991). Direct selection: a method for the isolation of cDNAs encoded by large genomic regions. *Proc Natl Acad Sci U S A* **88**: 9628-32.

**Lyon, M. F.** (1998). X-chromosome inactivation: a repeat hypothesis. *Cytogenet Cell Genet* **80**: 133-7.

**Lyon, M. F.** (1999). X-chromosome inactivation. *Curr. Biol.* **9**: R235-R237

**Ma, Y.**, Zhang, S., *et al.* (2002). Molecular characterization of the TCP11 gene which is the human homologue of the mouse gene encoding the receptor of fertilization promoting peptide. *Mol Hum Reprod* **8**: 24-31.

**Makalowski, W.** (2001). Are we polyploids? A brief history of one hypothesis. *Genome Res.* **11**: 667-70.

---

**Marra, M. A.**, Kucaba, T. A., *et al.* (1997). High throughput fingerprint analysis of large-insert clones. *Genome Res* **7**: 1072-84.

**Mayor, C.**, Brudno, M., *et al.* (2000). VISTA : visualizing global DNA sequence alignments of arbitrary length. *Bioinformatics* **16**: 1046-7.

**Mazarakis, N. D.**, Nelki, D., *et al.* (1991). Isolation and characterisation of a testis-expressed developmentally regulated gene from the distal inversion of the mouse t-complex. *Development* **111**: 561-71.

**Mazzarella, R.** and Schlessinger, D. (1998). Pathological consequences of sequence duplications in the human genome. *Genome Res* **8**: 1007-21.

**McLysaght, A.**, Hokamp, K., *et al.* (2002). Extensive genomic duplication during early chordate evolution. *Nat Genet* **31**: 200-4.

**Mukai, J.**, Suvant, P., *et al.* (2003). Nerve growth factor-dependent regulation of NADE-induced apoptosis. *Vitam Horm* **66**: 385-402.

**Mukai, J.**, Shoji, S., *et al.* (2002). Structure-function analysis of NADE: identification of regions that mediate nerve growth factor-induced apoptosis. *J Biol Chem* **277**: 13973-82.

**Mukai, J.**, Hachiya, T., *et al.* (2000). NADE, a p75NTR-associated cell death executor, is involved in signal transduction mediated by the common neurotrophin receptor p75NTR. *J Biol Chem* **275**: 17566-70.

**Mullikin, J. C.** and Ning, Z. (2003). The phusion assembler. *Genome Res.* **13**: 81-90.

**Murphy, W. J.**, Stanyon, R., *et al.* (2001). Evolution of mammalian genome organization inferred from comparative gene mapping. *Genome Biol* **2**: REVIEWS0005.

---

**Neitz, M.** and Neitz, J. (1995). Numbers and ratios of visual pigment genes for normal red-green color vision. *Science* **267**: 1013-6.

**Neuman, S.**, A. Kaban, A., *et al.* (2001). The dystrophin / utrophin homologues in Drosophila and in sea urchin. *Gene* **263**: 17-29.

**Nicholas, K.B.**, Nicholas, H.B. Jr., and Deerfield, D.W. II. (1997). GeneDoc: Analysis and Visualization of Genetic Variation, *EMBNEW.NEWS* **4**:14

**Nowell, P.**, Hungerford, D. (1960). A minute chromosome in human chronic granulocytic leukaemia. *Science* **132**: 1497.

**O'Brien, S. J.**, Menotti-Raymond, M., *et al.* (1999). The promise of comparative genomics in mammals. *Science* **286**: 458-62, 479-81.

**Ohno, S.** (1999). Gene duplication and the uniqueness of vertebrate genomes circa 1970-1999. *Semin Cell Dev Biol* **10**: 517-22.

**Parra, G.**, Agarwal, P., *et al.* (2003). Comparative gene prediction in human and mouse. *Genome Res* **13**: 108-17.

**Peifer, M.**, Berg, S., *et al.* (1994). A repeating amino acid motif shared by proteins with diverse cellular roles. *Cell* **76**: 789-91.

**Pennisi, E.** (2003). Drafting a tree. *Science* **300**: 1694.

**Perry, J.**, Short, K. M., *et al.* (1999). FXY2/MID2, a gene related to the X-linked Opitz syndrome gene FXY/MID1, maps to Xq22 and encodes a FNIII domain-containing protein that associates with microtubules. *Genomics* **62**: 385-94.

**Pillutla, R. C.**, Shimamoto, A., *et al.* (1999). Genomic structure and chromosomal localization of TCEAL1, a human gene encoding the nuclear phosphoprotein p21/SIIR. *Genomics* **56**: 217-20.

---

**Rapp, G.**, Freudenstein, J., *et al.* (1990). Characterization of three abundant mRNAs from human ovarian granulosa cells. *DNA Cell Biol* **9**: 479-85.

**Rappold, G. A.**, (1993). The pseudoautosomal regions of the human sex chromosomes. *Hum. Genet.* **92**: 315-324.

**Reboul, J.**, Vaglio, P., *et al.* (2003). *C. elegans* ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression. *Nat Genet* **34**: 35-41.

**Roberts, R. G.** (2001). Dystrophins and dystrobrevins. *Genome Biol* **2**: REVIEWS3006.

**Roberts, R. G.**, Freeman, T. C., *et al.* (1996). Characterization of DRP2, a novel human dystrophin homologue. *Nat Genet* **13**: 223-6.

**Rosenfeld, M. R.**, Eichen, J. G., *et al.* (2001). Molecular and clinical diversity in paraneoplastic immunity to Ma proteins. *Ann Neurol* **50**: 339-48.

**Rozen, S.** and Skaletsky, H. (2000). Primer3 on the WWW for general users and for biologist programmers. *Methods Mol Biol* **132**: 365-86.

**Rozen, S.**, Skaletsky, H., *et al.* (2003). Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. *Nature* **423**: 873-6.

**Saito-Ohara, F.**, Fukuda, Y., *et al.* (2002). The Xq22 inversion breakpoint interrupted a novel ras-like GTPase gene in a patient with Duchenne Muscular Dystrophy and profound mental retardation. *Am J Hum Genet* **71**: 637-45.

**Saitou, N.** and Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* **4**: 406-25.

---

**Sanger, F.**, Coulson, A. R., *et al.* (1978). The nucleotide sequence of bacteriophage phiX174. *J Mol Biol* **125**: 225-46.

**Sargent, C. A.**, Boucher, C. A., *et al.* (2001). Characterization of the human Xq21.3/Yp11 homology block and conservation of organization in primates. *Genomics* **73**: 77-85.

**Scherf, M.**, Klingenhoff, A., *et al.* (2000). Highly specific localization of promoter regions in large genomic sequences by PromoterInspector: a novel context analysis approach. *J Mol Biol* **297**: 599-606.

**Schmucker, D.**, Clemens, J. C., *et al.* (2000). Drosophila Dscam is an axon guidance receptor exhibiting extraordinary molecular diversity. *Cell* **101**: 671-84.

**Schwartz, S.**, Zhang, Z., *et al.* (2000). PipMaker - a web server for aligning two genomic DNA sequences. *Genome Res* **10**: 577-86.

**Segalat, L.** (2002). Dystrophin and functionally related proteins in the nematode *Caenorhabditis elegans*. *Neuromuscul Disord* **12**: S105-9.

**Serluca, F. C.**, Sidow, A., *et al.* (2001). Partitioning of tissue expression accompanies multiple duplications of the Na<sup>+</sup>/K<sup>+</sup> ATPase alpha subunit gene. *Genome Res* **11**: 1625-31.

**Shibata, K.**, Itoh, M., *et al.* (2000). RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res* **10**: 1757-71.

**Shizuya, H.**, Birren, B., *et al.* (1992). Cloning and stable maintenance of 300-kilobase-pair fragments of human DNA in *Escherichia coli* using an F-factor-based vector. *Proc Natl Acad Sci U S A* **89**: 8794-7.

**Sidman, R. L.**, Dickie, M. M., *et al.* (1964). Mutant mice (Quaking and Jimpy) with deficient myelination in the central nervous system. *Science* **144**: 309-11.

---

**Simmons, D. L.** (1993). Cloning cell surface molecules by transient expression in mammalian cells. In *Cellular Interactions and Development*. (D. Hartley, ed.). IRL Press at Oxford Universiyu Pres, Oxford. pp 93-127.

**Soderlund, C.**, Longden, I., *et al.* (1997). FPC: a system for building contigs from restriction fingerprinted clones. *Comput Appl Biosci* **13**: 523-35.

**Solovyev, V.** and Salamov, A. (1997). The Gene-Finder computer tools for analysis of human and model organisms genome sequences. *Proc Int Conf Intell Syst Mol Biol* **5**: 294-302.

**Sonnhammer, E. L.** and Durbin, R. (1995). A dot-matrix program with dynamic threshold control suited for genomic DNA and protein sequence analysis. *Gene* **167**: GC1-10.

**Spencer, J. A.**, Sinclair, A. H., *et al.* (1991). Genes on the short arm of the human X chromosome are not shared with the marsupial X. *Genomics* **11**: 339-45.

**Srivastava, A. K.**, McMillan, S., *et al.* (1999). Integrated STS/YAC physical, genetic, and transcript map of human Xq21.3 to q23/q24 (DXS1203-DXS1059). *Genomics* **58**: 188-201.

**Stankiewicz, P.** and Lupski, J. R. (2002). Genome architecture, rearrangements and genomic disorders. *Trends Genet* **18**: 74-82.

**Sternberg, N. L.** (1992). Cloning high molecular weight DNA fragments by the bacteriophage P1 system. *Trends Genet* **8**: 11-6.

**Strausberg, R. L.**, Feingold, E. A., *et al.* (1999). The mammalian gene collection. *Science* **286**: 455-7.

**Sun, M.**, Zhou, G., *et al.* (2004). SAGE is far more sensitive than EST for detecting low-abundance transcripts. *BMC Genomics* **5**: 1.

**Takai, Y.**, Sasaki, T., *et al.* (2001). Small GTP-binding proteins. *Physiol Rev* **81**: 153-208.

---

**Tennyson, C. N.**, Klamut, H. J., *et al.* (1995). The human dystrophin gene requires 16 hours to be transcribed and is cotranscriptionally spliced. *Nat Genet* **9**: 184-90.

**The *C. elegans* Sequencing Consortium** (1998). Genome sequence of the nematode *C. elegans*: a platform for investigating biology. *Science* **282**: 2012-8.

**Thomas, J. W.**, Prasad, A. B., *et al.* (2002). Parallel construction of orthologous sequence-ready clone contig maps in multiple species. *Genome Res* **12**: 1277-85.

**Thomas, J. W.**, Touchman, J. W., *et al.* (2003). Comparative analyses of multi-species sequences from targeted genomic regions. *Nature* **424**: 788-93.

**Thompson, J. D.**, Higgins, D. G., *et al.* (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* **22**: 4673-80.

**Thompson, J. D.**, Gibson, T. J., *et al.* (1997). The CLUSTAL\_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* **25**: 4876-82.

**Toder, R.**, Wakefield, M. J., *et al.* (2000). The minimal mammalian Y chromosome - the marsupial Y as a model system. *Cytogenet Cell Genet* **91**: 285-92.

**Tourmen, Y.**, Baris, O., *et al.* (2002). Structure and chromosomal distribution of human mitochondrial pseudogenes. *Genomics* **80**: 71-7.

**Ureta-Vidal, A.**, Ettwiller, L., *et al.* (2003). Comparative genomics: genome-wide analysis in metazoan eukaryotes. *Nat Rev Genet* **4**: 251-62.

**Venter, J. C.**, Adams, M. D., *et al.* (2001). The sequence of the human genome. *Science* **291**: 1304-51.

- 
- Veyrunes, J. L.**, Campbell, G. P., *et al.* (1996). A localisation signal in the 3' untranslated region of c-myc mRNA targets c-myc mRNA and beta-globin reporter sequences to the perinuclear cytoplasm and cytoskeletal-bound polysomes. *J Cell Sci* **109**: 1185-94.
- Wall, J. D.** and Pritchard, J. K., (2003). Haplotype blocks and linkage disequilibrium in the human genome. *Nat Rev Genet* **4**: 587-97.
- Wang, P. J.**, McCarrey, J. R., *et al.* (2001). An abundance of X-linked genes expressed in spermatogonia. *Nat Genet* **27**: 422-6.
- Waterston, R. H.**, Lindblad-Toh, K., *et al.* (2002). Initial sequencing and comparative analysis of the mouse genome. *Nature* **420**: 520-62.
- Weissenbach, J.**, Gyapay, G., *et al.* (1992). A second-generation linkage map of the human genome. *Nature* **359**: 794-801.
- Whistler, J. L.**, Enquist, J., *et al.* (2002). Modulation of postendocytic sorting of G protein-coupled receptors. *Science* **297**: 615-20.
- Williams, J. G.** and Firtel, R. A., (2000). HAPPY days for the Dictyostelium genome project. *Genome Res* **10**: 1658-9.
- Wingender, E.**, Chen, X., *et al.* (2001). The TRANSFAC system on gene expression regulation. *Nucleic Acids Res* **29**: 281-3.
- Wolfe, K. H.** and Shields, D. C., (1997). Molecular evidence for an ancient duplication of the entire yeast genome. *Nature* **387**: 708-13.
- Xu, Y.**, Einstein, J. R., *et al.* (1994). An improved system for exon recognition and gene modeling in human DNA sequences. *Proc Int Conf Intell Syst Mol Biol* **2**: 376-84.

---

**Yoshida, M.**, Shan, W. S., *et al.* (1999). Conserved and divergent expression patterns of the proteolipid protein gene family in the amphibian central nervous system. *J Neurosci Res* **57**: 13-22.

**Yudate, H. T.**, Suwa, M., *et al.* (2001). HUNT: launch of a full-length cDNA database from the Helix Research Institute. *Nucleic Acids Res* **29**: 185-8.

**Zhang, M. Q.** (1998). Statistical features of human exons and their flanking regions. *Hum Mol Genet* **7**: 919-32.