

## Bibliography

Abi Rached L., McDermott M. F., and Pontarotti P. (1999). The MHC big bang.

*Immunol Rev* 167: 33-44.

Abi-Rached L., Gilles A., Shiina T., Pontarotti P., and Inoko H. (2002). Evidence of en bloc duplication in vertebrate genomes. *Nat Genet* 31: 100-5.

Achermann J. C., Ito M., Hindmarsh P. C., and Jameson J. L. (1999). A mutation in the gene encoding steroidogenic factor-1 causes XY sex reversal and adrenal failure in humans. *Nat Genet* 22: 125-6.

Adams M. D., Celiker S. E., Holt R. A., Evans C. A., Gocayne J. D., Amanatides P. G., Scherer S. E., Li P. W., Hoskins R. A., Galle R. F., George R. A., Lewis S. E., Richards S., Ashburner M., Henderson S. N., Sutton G. G., Wortman J. R., Yandell M. D., Zhang Q., Chen L. X., Brandon R. C., Rogers Y. H., Blazej R. G., Champe M., Pfeiffer B. D., Wan K. H., Doyle C., Baxter E. G., Helt G., Nelson C. R., Gabor G. L., Abril J. F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D., Ballew R. M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E. M., Beeson K. Y., Benos P. V., Berman B. P., Bhandari D., Bolshakov S., Borkova D., Botchan M. R., Bouck J., Brokstein P., Brottier P., Burtis K. C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I., Cherry J. M., Cawley S., Dahlke C., Davenport L. B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A. D., Dew I., Dietz S. M., Dodson K., Douc L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P., Durbin K. J., Evangelista C. C., Ferraz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A. E., Garg N. S., Gelbart W. M., Glasser K., Glodek A., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M., Harris N. L., Harvey D., Heiman T. J., Hernandez J. R., Houck J., Hostin D., Houston K. A., Howland T. J., Wei M. H., Ibegwam C., et al. (2000). The genome sequence of *Drosophila melanogaster*. *Science* 287: 2185-95.

Altschul S. F., Gish W., Miller W., Myers E. W., and Lipman D. J. (1990). Basic local alignment search tool. *J Mol Biol* 215: 403-10.

Amores A., Force A., Yan Y. L., Joly L., Amemiya C., Fritz A., Ho R. K., Langeland J., Prince V., Wang Y. L., Westerfield M., Ekker M., and Postlethwait J. H. (1998). Zebrafish hox clusters and vertebrate genome evolution. *Science* 282: 1711-4.

Anderson S., Bankier A. T., Barrell B. G., de Brujin M. H., Coulson A. R., Drouin J., Eperon I. C., Nierlich D. P., Roe B. A., Sanger F., Schreier P. H., Smith A. J., Staden R., and Young I. G. (1981). Sequence and organization of the human mitochondrial genome. *Nature* 290: 457-65.

Aparicio S., Chapman J., Stupka E., Putnam N., Chia J. M., Dehal P., Christoffels A., Rash S., Hoon S., Smit A., Gelpke M. D., Roach J., Oh T., Ho I. Y., Wong M., Detter C., Verhoef F., Predki P., Tay A., Lucas S., Richardson P., Smith S. F., Clark M. S., Edwards Y. J., Doggett N., Zharkikh A., Tavtigian S. V., Pruss D., Barnstead M., Evans C., Baden H., Powell J., Glusman G., Rowen L., Hood L., Tan Y. H., Elgar G.,

- Hawkins T., Venkatesh B., Rokhsar D., and Brenner S. (2002). Whole-genome shotgun assembly and analysis of the genome of Fugu rubripes. *Science* 297: 1301-10.
- Autieri M. V. (1996). cDNA cloning of human allograft inflammatory factor-1: tissue distribution, cytokine induction, and mRNA expression in injured rat carotid arteries. *Biochem Biophys Res Commun* 228: 29-37.
- Bailey J. A., Gu Z., Clark R. A., Reinert K., Samonte R. V., Schwartz S., Adams M. D., Myers E. W., Li P. W., and Eichler E. E. (2002). Recent segmental duplications in the human genome. *Science* 297: 1003-7.
- Bairoch A., and Apweiler R. (1997). The SWISS-PROT protein sequence data bank and its supplement TrEMBL. *Nucleic Acids Res* 25: 31-6.
- Bankier A. T., Weston K. M., and Barrell B. G. (1987). Random cloning and sequencing by the M13/dideoxynucleotide chain termination method. *Methods Enzymol* 155: 51-93.
- Baumgartner S., Martin D., Hagios C., and Chiquet-Ehrismann R. (1994). Tenm, a Drosophila gene related to tenascin, is a new pair-rule gene. *Embo J* 13: 3728-40.
- Beck S., Kelly A., Radley E., Khurshid F., Alderton R. P., and Trowsdale J. (1992a). DNA sequence analysis of 66 kb of the human MHC class II region encoding a cluster of genes for antigen processing. *J Mol Biol* 228: 433-41.
- Beck S., Hanson I., Kelly A., Pappin D. J., and Trowsdale J. (1992b). A homologue of the Drosophila female sterile homeotic (fsh) gene in the class II region of the human MHC. *DNA Seq* 2: 203-10.
- Beck S., and Trowsdale J. (2000). The human major histocompatibility complex: lessons from the DNA sequence. *Annu Rev Genomics Hum Genet* 1: 117-37.
- Bernstein R. M., Schluter S. F., Bernstein H., and Marchalonis J. J. (1996). Primordial emergence of the recombination activating gene 1 (RAG1): sequence of the complete shark gene indicates homology to microbial integrases. *Proc Natl Acad Sci U S A* 93: 9454-9.
- Bichara M., Schumacher S., and Fuchs R. P. (1995). Genetic instability within monotonous runs of CpG sequences in Escherichia coli. *Genetics* 140: 897-907.
- Bichara M., Pinet I., Schumacher S., and Fuchs R. P. (2000). Mechanisms of dinucleotide repeat instability in Escherichia coli. *Genetics* 154: 533-42.
- Blattner F. R., Plunkett G., 3rd, Bloch C. A., Perna N. T., Burland V., Riley M., Collado-Vides J., Glasner J. D., Rode C. K., Mayhew G. F., Gregor J., Davis N. W., Kirkpatrick H. A., Goeden M. A., Rose D. J., Mau B., and Shao Y. (1997). The complete genome sequence of Escherichia coli K-12. *Science* 277: 1453-74.

- Bogart J. P. (1980). Evolutionary implications of polyploidy in amphibians and reptiles. In "Polyploidy: Biological Relevance" (W. H. Lewis, Ed.), Plenum, New York.
- Bonfield J. K., Smith K., and Staden R. (1995). A new DNA sequence assembly program. *Nucleic Acids Res* 23: 4992-9.
- Bouchireb N., Grutzner F., Haaf T., Stephens R. J., Elgar G., Green A. J., and Clark M. S. (2001). Comparative mapping of the human 9q34 region in Fugu rubripes. *Cytogenet Cell Genet* 94: 173-9.
- Bray S. (1998). Notch signalling in Drosophila: three ways to use a pathway. *Semin Cell Dev Biol* 9: 591-7.
- Brazma A., and Vilo J. (2001). Gene expression data analysis. *Microbes Infect* 3: 823-9.
- Brenner S. E., Chothia C., and Hubbard T. J. (1998). Assessing sequence comparison methods with reliable structurally identified distant evolutionary relationships. *Proc Natl Acad Sci U S A* 95: 6073-8.
- Bristow J., Tee M. K., Gitelman S. E., Mellon S. H., and Miller W. L. (1993). Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene overlapping P450c21B. *J Cell Biol* 122: 265-78.
- Brown N. P., Whittaker A. J., Newell W. R., Rawlings C. J., and Beck S. (1995). Identification and analysis of multigene families by comparison of exon fingerprints. *J Mol Biol* 249: 342-59.
- C. elegans* Sequencing Consortium (1998). Genome sequence of the nematode *C. elegans*: a platform for investigating biology. *Science* 282: 2012-8.
- Cebrat S., and Stauffer D. (2002). Monte Carlo simulation of genome viability with paralog replacement. *J Appl Genet* 43: 391-5.
- Chenna R., Sugawara H., Koike T., Lopez R., Gibson T. J., Higgins D. G., and Thompson J. D. (2003). Multiple sequence alignment with the Clustal series of programs. *Nucleic Acids Res* 31: 3497-500.
- Chu F. F., Esworthy R. S., Doroshow J. H., Doan K., and Liu X. F. (1992). Expression of plasma glutathione peroxidase in human liver in addition to kidney, heart, lung, and breast in humans and rodents. *Blood* 79: 3233-8.
- Colombo P., Yon J., Garson K., and Fried M. (1992). Conservation of the organization of five tightly clustered genes over 600 million years of divergent evolution. *Proc Natl Acad Sci U S A* 89: 6358-62.
- Danchin E. G., Abi-Rached L., Gilles A., and Pontarotti P. (2003). Conservation of the MHC-like region throughout evolution. *Immunogenetics*.

- Dausset J. (1958). Iso-leuco-anticorps. *Acta Haem* 20: 156-166.
- Dayhoff M. O., Schwartz R. M., and Orcutt B. C. (1978). "A model of evolutionary change in proteins," National Biomedical Research Foundation, Washington D.C.
- Deloukas P., Schuler G. D., Gyapay G., Beasley E. M., Soderlund C., Rodriguez-Tome P., Hui L., Matise T. C., McKusick K. B., Beckmann J. S., Bentolila S., Bihoreau M., Birren B. B., Browne J., Butler A., Castle A. B., Chiannilkulchai N., Clee C., Day P. J., Dehejia A., Dibling T., Drouot N., Duprat S., Fizames C., Bentley D. R., and et al. (1998). A physical map of 30,000 human genes. *Science* 282: 744-6.
- Denis G. V., and Green M. R. (1996). A novel, mitogen-activated nuclear kinase is related to a *Drosophila* developmental regulator. *Genes Dev* 10: 261-71.
- Diatchenko L., Lau Y. F., Campbell A. P., Chenchik A., Moqadam F., Huang B., Lukyanov S., Lukyanov K., Gurskaya N., Sverdlov E. D., and Siebert P. D. (1996). Suppression subtractive hybridization: a method for generating differentially regulated or tissue-specific cDNA probes and libraries. *Proc Natl Acad Sci U S A* 93: 6025-30.
- Doolittle R. F., Feng D. F., Johnson M. S., and McClure M. A. (1986). Relationships of human protein sequences to those of other organisms. *Cold Spring Harb Symp Quant Biol* 51 Pt 1: 447-55.
- Driscoll J., Brown M. G., Finley D., and Monaco J. J. (1993). MHC-linked LMP gene products specifically alter peptidase activities of the proteasome. *Nature* 365: 262-4.
- Dufaure J. P., Lareyre J. J., Schwaab V., Mattei M. G., and Drevet J. R. (1996). Structural organization, chromosomal localization, expression and phylogenetic evaluation of mouse glutathione peroxidase encoding genes. *C R Acad Sci III* 319: 559-68.
- Eichler E. E. (1998). Masquerading repeats: paralogous pitfalls of the human genome. *Genome Res* 8: 758-62.
- Eichler E. E., Archidiacono N., and Rocchi M. (1999). CAGGG repeats and the pericentromeric duplication of the hominoid genome. *Genome Res* 9: 1048-58.
- Eichler E. E., Lu F., Shen Y., Antonacci R., Jurecic V., Doggett N. A., Moyzis R. K., Baldini A., Gibbs R. A., and Nelson D. L. (1996). Duplication of a gene-rich cluster between 16p11.1 and Xq28: a novel pericentromeric-directed mechanism for paralogous genome evolution. *Hum Mol Genet* 5: 899-912.
- Ellisen L. W., Bird J., West D. C., Soreng A. L., Reynolds T. C., Smith S. D., and Sklar J. (1991). TAN-1, the human homolog of the *Drosophila* notch gene, is broken by chromosomal translocations in T lymphoblastic neoplasms. *Cell* 66: 649-61.
- Endo T., Imanishi T., Gojobori T., and Inoko H. (1997). Evolutionary significance of intra-genome duplications on human chromosomes. *Gene* 205: 19-27.

- Erickson H. P. (1993). Tenascin-C, tenascin-R and tenascin-X: a family of talented proteins in search of functions. *Curr Opin Cell Biol* 5: 869-76.
- Escriva H., Manzon L., Youson J., and Laudet V. (2002). Analysis of lamprey and hagfish genes reveals a complex history of gene duplications during early vertebrate evolution. *Mol Biol Evol* 19: 1440-50.
- Evertsz E. M., Au-Young J., Ruvolo M. V., Lim A. C., and Reynolds M. A. (2001). Hybridization cross-reactivity within homologous gene families on glass cDNA microarrays. *Biotechniques* 31: 1182-1192.
- Felsenstein J. (1981). Evolutionary trees from DNA sequences: a maximum likelihood approach. *J Mol Evol* 17: 368-76.
- Felsenstein J. (1985). Confidence-Limits On Phylogenies - an Approach Using the Bootstrap. *Evolution* 39: 783-791.
- Felsenstein J. (1989). PHYLIP -- Phylogeny Inference Package (Version 3.2). *Cladistics* 5: 164-166.
- Feng D. F., Johnson M. S., and Doolittle R. F. (1984). Aligning amino acid sequences: comparison of commonly used methods. *J Mol Evol* 21: 112-25.
- Fiers W., Contreras R., Haegemann G., Rogiers R., Van de Voorde A., Van Heuverswyn H., Van Herreweghe J., Volckaert G., and Ysebaert M. (1978). Complete nucleotide sequence of SV40 DNA. *Nature* 273: 113-20.
- Flajnik M. F., Canel C., Kramer J., and Kasahara M. (1991). Which came first, MHC class I or class II? *Immunogenetics* 33: 295-300.
- Flajnik M. F., and Kasahara M. (2001). Comparative genomics of the MHC: glimpses into the evolution of the adaptive immune system. *Immunity* 15: 351-62.
- Flajnik M. F., Ohta Y., Namikawa-Yamada C., and Nonaka M. (1999). Insight into the primordial MHC from studies in ectothermic vertebrates. *Immunol Rev* 167: 59-67.
- Force A., Lynch M., Pickett F. B., Amores A., Yan Y. L., and Postlethwait J. (1999). Preservation of duplicate genes by complementary, degenerative mutations. *Genetics* 151: 1531-45.
- French C. A., Miyoshi I., Kubonishi I., Grier H. E., Perez-Atayde A. R., and Fletcher J. A. (2003). BRD4-NUT fusion oncogene: a novel mechanism in aggressive carcinoma. *Cancer Res* 63: 304-7.
- Friedman R., and Hughes A. L. (2001). Pattern and timing of gene duplication in animal genomes. *Genome Res* 11: 1842-7.
- Gallardo M. H., Bickham J. W., Honeycutt R. L., Ojeda R. A., and Kohler N. (1999). Discovery of tetraploidy in a mammal. *Nature* 401: 341.

- Garcia-Fernandez J., and Holland P. (1994). Archetypal organisation of the amphioxus Hox gene cluster. *Nature* 370: 563-6.
- Gaston K., and Fried M. (1994). YY1 is involved in the regulation of the bi-directional promoter of the Surf-1 and Surf-2 genes. *FEBS Lett* 347: 289-94.
- Giglio S., Broman K. W., Matsumoto N., Calvari V., Gimelli G., Neumann T., Ohashi H., Vouillaire L., Larizza D., Giorda R., Weber J. L., Ledbetter D. H., and Zuffardi O. (2001). Olfactory receptor-gene clusters, genomic-inversion polymorphisms, and common chromosome rearrangements. *Am J Hum Genet* 68: 874-83.
- Giglio S., Calvari V., Gregato G., Gimelli G., Camanini S., Giorda R., Ragusa A., Guerneri S., Selicorni A., Stumm M., Tonnies H., Ventura M., Zollino M., Neri G., Barber J., Wieczorek D., Rocchi M., and Zuffardi O. (2002). Heterozygous submicroscopic inversions involving olfactory receptor-gene clusters mediate the recurrent t(4;8)(p16;p23) translocation. *Am J Hum Genet* 71: 276-85.
- Gordon, D., Abajian, C. and Green, P. (1998) Consed: a graphical tool for sequence finishing *Genome Res* 8 (3): 195-202
- Greer J. M., Puetz J., Thomas K. R., and Capecchi M. R. (2000). Maintenance of functional equivalence during paralogous Hox gene evolution. *Nature* 403: 661-5.
- Grewal P. K., van Geel M., Frants R. R., de Jong P., and Hewitt J. E. (1999). Recent amplification of the human FRG1 gene during primate evolution. *Gene* 227: 79-88.
- Gruen J. R., and Weissman S. M. (2001). Human MHC class III and IV genes and disease associations. *Front Biosci* 6: D960-72.
- Gu X., and Huang W. (2002). Testing the parsimony test of genome duplications: a counterexample. *Genome Res* 12: 1-2.
- Habuchi T., Luscombe M., Elder P. A., and Knowles M. A. (1998). Structure and methylation-based silencing of a gene (DBCCR1) within a candidate bladder cancer tumor suppressor region at 9q32-q33. *Genomics* 48: 277-88.
- Hall L., Williams K., Perry A. C., Frayne J., and Jury J. A. (1998). The majority of human glutathione peroxidase type 5 (GPX5) transcripts are incorrectly spliced: implications for the role of GPX5 in the male reproductive tract. *Biochem J* 333 ( Pt 1): 5-9.
- Heiskanen M., Karhu R., Hellsten E., Peltonen L., Kallioniemi O. P., and Palotie A. (1994). High resolution mapping using fluorescence in situ hybridization to extended DNA fibers prepared from agarose-embedded cells. *Biotechniques* 17: 928-9, 932-3.
- Henikoff S., and Henikoff J. G. (1992). Amino acid substitution matrices from protein blocks. *Proc Natl Acad Sci U S A* 89: 10915-9.

- Herberg J. A., Beck S., and Trowsdale J. (1998a). TAPASIN, DAXX, RGL2, HKE2 and four new genes (BING 1, 3 to 5) form a dense cluster at the centromeric end of the MHC. *J Mol Biol* 277: 839-57.
- Herberg J. A., Sgouros J., Jones T., Copeman J., Humphray S. J., Sheer D., Cresswell P., Beck S., and Trowsdale J. (1998b). Genomic analysis of the Tapasin gene, located close to the TAP loci in the MHC. *Eur J Immunol* 28: 459-67.
- Holland L. Z., Rached L. A., Tamme R., Holland N. D., Kortschak D., Inoko H., Shiina T., Burgdorf C., and Lardelli M. (2001). Characterization and developmental expression of the amphioxus homolog of Notch (AmphiNotch): evolutionary conservation of multiple expression domains in amphioxus and vertebrates. *Dev Biol* 232: 493-507.
- Holland P. W. (2003). More genes in vertebrates? *J Struct Funct Genomics* 3: 75-84.
- Holland P. W., Garcia-Fernandez J., Williams N. A., and Sidow A. (1994). Gene duplications and the origins of vertebrate development. *Dev Suppl*: 125-33.
- Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H., and Weiss E. H. (1995). Cloning and genomic characterization of LST1: a new gene in the human TNF region. *Immunogenetics* 42: 315-22.
- Houzelstein D., Bullock S. L., Lynch D. E., Grigorieva E. F., Wilson V. A., and Beddington R. S. (2002). Growth and early postimplantation defects in mice deficient for the bromodomain-containing protein Brd4. *Mol Cell Biol* 22: 3794-802.
- Hubbard T., Barker D., Birney E., Cameron G., Chen Y., Clark L., Cox T., Cuff J., Curwen V., Down T., Durbin R., Eyras E., Gilbert J., Hammond M., Huminiecki L., Kasprzyk A., Lehvaslaiho H., Lijnzaad P., Melsopp C., Mongin E., Pettett R., Pocock M., Potter S., Rust A., Schmidt E., Searle S., Slater G., Smith J., Spooner W., Stabenau A., Stalker J., Stupka E., Ureta-Vidal A., Vastrik I., and Clamp M. (2002). The Ensembl genome database project. *Nucleic Acids Res* 30: 38-41.
- Hudson T. J., Stein L. D., Gerety S. S., Ma J., Castle A. B., Silva J., Slonim D. K., Baptista R., Kruglyak L., Xu S. H., and et al. (1995). An STS-based map of the human genome. *Science* 270: 1945-54.
- Hughes A. L., and Nei M. (1993). Evolutionary relationships of the classes of major histocompatibility complex genes. *Immunogenetics* 37: 337-46.
- Hughes A. L. (1994). Phylogeny of the C3/C4/C5 complement-component gene family indicates that C5 diverged first. *Mol Biol Evol* 11: 417-25.
- Hughes A. L., and Yeager M. (1997). Molecular evolution of the vertebrate immune system. *Bioessays* 19: 777-86.
- Hughes A. L. (1998). Phylogenetic tests of the hypothesis of block duplication of homologous genes on human chromosomes 6, 9, and 1. *Mol Biol Evol* 15: 854-70.

- Hughes A. L., and Pontarotti P. (2000). Gene duplication and MHC origins. *Immunogenetics* 51: 982-3.
- Hughes A. L., and Friedman R. (2003). 2R or not 2R: testing hypotheses of genome duplication in early vertebrates. *J Struct Funct Genomics* 3: 85-93.
- Huxley C., and Fried M. (1990). The mouse surfeit locus contains a cluster of six genes associated with four CpG-rich islands in 32 kilobases of genomic DNA. *Mol Cell Biol* 10: 605-14.
- International Human Genome Sequencing Consortium (IHGSC) (2001). Initial sequencing and analysis of the human genome. *Nature* 409: 860-921.
- Ishiguro H., Kobayashi K., Suzuki M., Titani K., Tomonaga S., and Kurosawa Y. (1992). Isolation of a hagfish gene that encodes a complement component. *Embo J* 11: 829-37.
- Jackson D. A., Pombo A., and Iborra F. (2000). The balance sheet for transcription: an analysis of nuclear RNA metabolism in mammalian cells. *Faseb J* 14: 242-54.
- Jentsch T. J., Stein V., Weinreich F., and Zdebik A. A. (2002). Molecular structure and physiological function of chloride channels. *Physiol Rev* 82: 503-68.
- Jones D. T., Taylor W. R., and Thornton J. M. (1992). The rapid generation of mutation data matrices from protein sequences. *Comput Appl Biosci* 8: 275-82.
- Jones M. H., Numata M., and Shimane M. (1997). Identification and characterisation of BRDT: A testis-specific gene related to the bromodomain genes RING3 and Drosophila fsh. *Genomics* 45: 529-34.
- Jurka J. (2000). Repbase update: a database and an electronic journal of repetitive elements. *Trends Genet* 16: 418-20.
- Karlin S., and Altschul S. F. (1990). Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. *Proc Natl Acad Sci U S A* 87: 2264-8.
- Kasahara M., Hayashi M., Tanaka K., Inoko H., Sugaya K., Ikemura T., and Ishibashi T. (1996a). Chromosomal localization of the proteasome Z subunit gene reveals an ancient chromosomal duplication involving the major histocompatibility complex. *Proc Natl Acad Sci U S A* 93: 9096-101.
- Kasahara M., Kandil E., Salter-Cid L., and Flajnik M. F. (1996b). Origin and evolution of the class I gene family: why are some of the mammalian class I genes encoded outside the major histocompatibility complex? *Res Immunol* 147: 278-84; discussion 284-5.
- Kasahara M. (1997). New insights into the genomic organization and origin of the major histocompatibility complex: role of chromosomal (genome) duplication in the emergence of the adaptive immune system. *Hereditas* 127: 59-65.

- Kasahara M. (1999a). The chromosomal duplication model of the major histocompatibility complex. *Immunol Rev* 167: 17-32.
- Kasahara M. (1999b). Genome dynamics of the major histocompatibility complex: insights from genome paralogy. *Immunogenetics* 50: 134-45.
- Kasahara M., Yawata M., and Suzuki T. (2000). "The MHC paralogous group: Listing of members and a brief overview," Springer-Verlag,, Tokyo-Berlin-Heidelberg-New York.
- Katsanis N., Fitzgibbon J., and Fisher E. M. (1996). Paralogy mapping: identification of a region in the human MHC triplicated onto human chromosomes 1 and 9 allows the prediction and isolation of novel PBX and NOTCH loci. *Genomics* 35: 101-8.
- Kent W. J., and Haussler D. (2001). Assembly of the working draft of the human genome with GigAssembler. *Genome Res* 11: 1541-8.
- Klein J., and Sato A. (1998). Birth of the major histocompatibility complex. *Scand J Immunol* 47: 199-209.
- Kobayashi K., Nakahori Y., Miyake M., Matsumura K., Kondo-Iida E., Nomura Y., Segawa M., Yoshioka M., Saito K., Osawa M., Hamano K., Sakakihara Y., Nonaka I., Nakagome Y., Kanazawa I., Nakamura Y., Tokunaga K., and Toda T. (1998). An ancient retrotransposal insertion causes Fukuyama-type congenital muscular dystrophy. *Nature* 394: 388-92.
- Kumar S., Tamura K., and Nei M. (1994). MEGA: Molecular Evolutionary Genetics Analysis software for microcomputers. *Comput Appl Biosci* 10: 189-91.
- Kumar S., Tamura K., Jakobsen I. B., and Nei M. (2001). MEGA2: molecular evolutionary genetics analysis software. *Bioinformatics* 17: 1244-5.
- Lacazette E., Gachon A. M., and Pitiot G. (2000). A novel human odorant-binding protein gene family resulting from genomic duplicates at 9q34: differential expression in the oral and genital spheres. *Hum Mol Genet* 9: 289-301.
- Lardelli M., Dahlstrand J., and Lendahl U. (1994). The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-repeats and is expressed in proliferating neuroepithelium. *Mech Dev* 46: 123-36.
- Larhammar D., Lundin L. G., and Hallbook F. (2002). The Human Hox-bearing Chromosome Regions Did Arise by Block or Chromosome (or Even Genome) Duplications. *Genome Res* 12: 1910-20.
- Lennard A., Gaston K., and Fried M. (1994). The Surf-1 and Surf-2 genes and their essential bidirectional promoter elements are conserved between mouse and human. *DNA Cell Biol* 13: 1117-26.
- Lesk A. (2002). "Introduction to bioinformatics," Oxford University Press, Oxford.

- Lewis J. (1998). Notch signalling and the control of cell fate choices in vertebrates. *Semin Cell Dev Biol* 9: 583-9.
- Lewis S. A., and Cowan N. J. (1990). Tubulin genes: structure, expression, and regulation. In "Microtubule proteins" (J. Avila, Ed.), pp. 37-66, CRC Press, Inc, Boca Raton.
- Li W.-H. (1997). "Molecular Evolution," Sunderland Sinauer.
- Li W. H., Gu Z., Wang H., and Nekrutenko A. (2001). Evolutionary analyses of the human genome. *Nature* 409: 847-9.
- Lundin L. G. (1993). Evolution of the vertebrate genome as reflected in paralogous chromosomal regions in man and the house mouse. *Genomics* 16: 1-19.
- Lundin L. G., and Larhammar D. (1998). "Paralogous genes and nervous systems," Oxford, UK.
- Lundin L. G., Larhammar D., and Hallbook F. (2003). Numerous groups of chromosomal regional paralogies strongly indicate two genome doublings at the root of the vertebrates. *J Struct Funct Genomics* 3: 53-63.
- Lynch M., and Conery J. S. (2000). The evolutionary fate and consequences of duplicate genes. *Science* 290: 1151-5.
- Lynch M., and Force A. (2000). The probability of duplicate gene preservation by subfunctionalization. *Genetics* 154: 459-73.
- Mackiewicz P., Kowalcuk M., Gierlik A., Dudek M. R., and Cebrat S. (1999). Origin and properties of non-coding ORFs in the yeast genome. *Nucleic Acids Res* 27: 3503-9.
- Mackiewicz P., Kowalcuk M., Mackiewicz D., Nowicka A., Dudkiewicz M., Laszkiewicz A., Dudek M. R., and Cebrat S. (2002). How many protein-coding genes are there in the *Saccharomyces cerevisiae* genome? *Yeast* 19: 619-29.
- Makalowski W. (2001). Are we polyploids? A brief history of one hypothesis. *Genome Res* 11: 667-70.
- Mangelsdorf D. J., Borgmeyer U., Heyman R. A., Zhou J. Y., Ong E. S., Oro A. E., Kakizuka A., and Evans R. M. (1992). Characterisation of three RXR genes that mediate the action of 9-cis retinoic acid. *Genes Dev* 6: 329-44.
- Maresco D. L., Chang E., Theil K. S., Francke U., and Anderson C. L. (1996). The three genes of the human FCGR1 gene family encoding Fc gamma RI flank the centromere of chromosome 1 at 1p12 and 1q21. *Cytogenet Cell Genet* 73: 157-63.
- Marshall E. (2001). Genome sequencing. Celera assembles mouse genome; public labs plan new strategy. *Science* 292: 822.

- Marzluff W. F., Gongidi P., Woods K. R., Jin J., and Maltais L. J. (2002). The human and mouse replication-dependent histone genes. *Genomics* 80: 487-98.
- Mazet F., and Shimeld S. M. (2002). Gene duplication and divergence in the early evolution of vertebrates. *Curr Opin Genet Dev* 12: 393-6.
- McKean P. G., Vaughan S., and Gull K. (2001). The extended tubulin superfamily. *J Cell Sci* 114: 2723-33.
- McLysaght A., Hokamp K., and Wolfe K. H. (2002). Extensive genomic duplication during early chordate evolution. *Nat Genet* 31: 200-4.
- Mewes H. W., Albermann K., Bahr M., Frishman D., Gleissner A., Hani J., Heumann K., Kleine K., Maierl A., Oliver S. G., Pfeiffer F., and Zollner A. (1997). Overview of the yeast genome. *Nature* 387: 7-65.
- Miyata T., and Suga H. (2001). Divergence pattern of animal gene families and relationship with the Cambrian explosion. *Bioessays* 23: 1018-27.
- Modrek B., and Lee C. (2002). A genomic view of alternative splicing. *Nat Genet* 30: 13-9.
- Monaco J. J. (1992). A molecular model of MHC class-I-restricted antigen processing. *Immunol Today* 13: 173-9.
- Monica K., Galili N., Nourse J., Saltman D., and Cleary M. L. (1991). PBX2 and PBX3, new homeobox genes with extensive homology to the human proto-oncogene PBX1. *Mol Cell Biol* 11: 6149-57.
- Muller H. J. (1925). Why polyploidy is rarer in animals than in plants. *American Naturalist* 59: 346-353.
- Nadeau J. H., and Sankoff D. (1997). Comparable rates of gene loss and functional divergence after genome duplications early in vertebrate evolution. *Genetics* 147: 1259-66.
- Nagata T., Weiss E. H., Abe K., Kitagawa K., Ando A., Yara-Kikuti Y., Seldin M. F., Ozato K., Inoko H., and Taketo M. (1995). Physical mapping of the retinoid X receptor B gene in mouse and human. *Immunogenetics* 41: 83-90.
- Neefjes J. J., and Ploegh H. L. (1992). Intracellular transport of MHC class II molecules. *Immunol Today* 13: 179-84.
- Nei M., and Kumar S. (2000). "Molecular Evolution and Phylogenetics," Oxford University Press, New York.
- Nicholls A. C., McCarron S., Narcisi P., and Pope F. M. (1994). Molecular abnormalities of type V collagen in Ehlers Danlos syndrome. *Am. J. Hum. Genet* 55: A233.

- Nonaka M., and Takahashi M. (1992). Complete complementary DNA sequence of the third component of complement of lamprey. Implication for the evolution of thioester containing proteins. *J Immunol* 148: 3290-5.
- Ohno S. (1970). "Evolution by Gene Duplication," Springer-Verlag, New York.
- Ohno S. (1973). Ancient linkage groups and frozen accidents. *Nature* 244: 259-62.
- Oliver S. G., van der Aart Q. J., Agostoni-Carbone M. L., Aigle M., Alberghina L., Alexandraki D., Antoine G., Anwar R., Ballesta J. P., Benit P., and et al. (1992). The complete DNA sequence of yeast chromosome III. *Nature* 357: 38-46.
- Olson M. V., Dutchik J. E., Graham M. Y., Brodeur G. M., Helms C., Frank M., MacCollin M., Scheinman R., and Frank T. (1986). Random-clone strategy for genomic restriction mapping in yeast. *Proc Natl Acad Sci U S A* 83: 7826-30.
- Ortmann B., Androlewicz M. J., and Cresswell P. (1994). MHC class I/beta 2-microglobulin complexes associate with TAP transporters before peptide binding. *Nature* 368: 864-7.
- Padgett R. A., Grabowski P. J., Konarska M. M., Seiler S., and Sharp P. A. (1986). Splicing of messenger RNA precursors. *Annu Rev Biochem* 55: 1119-50.
- Panopoulou G., Hennig S., Groth D., Krause A., Poustka A. J., Herwig R., Vingron M., and Lehrach H. (2003). New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes. *Genome Res* 13: 1056-66.
- Pébusque M. J., Coulier F., Birnbaum D., and Pontarotti P. (1998). Ancient large-scale genome duplications: phylogenetic and linkage analyses shed light on chordate genome evolution. *Mol Biol Evol* 15: 1145-59.
- Perry A. C., Jones R., Niang L. S., Jackson R. M., and Hall L. (1992). Genetic evidence for an androgen-regulated epididymal secretory glutathione peroxidase whose transcript does not contain a selenocysteine codon. *Biochem J* 285 (Pt 3): 863-70.
- Pieters J. (1997). MHC class II restricted antigen presentation. *Curr Opin Immunol* 9: 89-96.
- Pinkel D., Gray J. W., Trask B., van den Engh G., Fuscoe J., and van Dekken H. (1986). Cytogenetic analysis by *in situ* hybridization with fluorescently labeled nucleic acid probes. *Cold Spring Harb Symp Quant Biol* 51 Pt 1: 151-7.
- Pollard S. L., and Holland P. W. (2000). Evidence for 14 homeobox gene clusters in human genome ancestry. *Curr Biol* 10: 1059-62.
- Postlethwait J. H., Yan Y. L., Gates M. A., Horne S., Amores A., Brownlie A., Donovan A., Egan E. S., Force A., Gong Z., Goutel C., Fritz A., Kelsh R., Knapik E.,

- Liao E., Paw B., Ransom D., Singer A., Thomson M., Abduljabbar T. S., Yelick P., Beier D., Joly J. S., Larhammar D., Rosa F., and et al. (1998). Vertebrate genome evolution and the zebrafish gene map. *Nat Genet* 18: 345-9.
- Price P., Witt C., Allcock R., Sayer D., Garlepp M., Kok C. C., French M., Mallal S., and Christiansen F. (1999). The genetic basis for the association of the 8.1 ancestral haplotype (A1, B8, DR3) with multiple immunopathological diseases. *Immunol Rev* 167: 257-74.
- Prince V. E., and Pickett F. B. (2002). Splitting pairs: the diverging fates of duplicated genes. *Nat Rev Genet* 3: 827-37.
- Pryde F. E., Gorham H. C., and Louis E. J. (1997). Chromosome ends: all the same under their caps. *Curr Opin Genet Dev* 7: 822-8.
- Radley E., Alderton R. P., Kelly A., Trowsdale J., and Beck S. (1994). Genomic organization of HLA-DMA and HLA-DMB. Comparison of the gene organization of all six class II families in the human major histocompatibility complex. *J Biol Chem* 269: 18834-8.
- Radosavljevic M., Cuillerier B., Wilson M. J., Clement O., Wicker S., Gilfillan S., Beck S., Trowsdale J., and Bahram S. (2002). A cluster of ten novel MHC class I related genes on human chromosome 6q24.2-q25.3. *Genomics* 79: 114-23.
- Reid K. B., and Porter R. R. (1981). The proteolytic activation systems of complement. *Annu Rev Biochem* 50: 433-64.
- Reiter L. T., Murakami T., Koeuth T., Pentao L., Muzny D. M., Gibbs R. A., and Lupski J. R. (1996). A recombination hotspot responsible for two inherited peripheral neuropathies is located near a mariner transposon-like element. *Nat Genet* 12: 288-97.
- Rice P., Longden I., and Bleasby A. (2000). EMBOSS: the European Molecular Biology Open Software Suite. *Trends Genet* 16: 276-7.
- Rouquier S., Taviaux S., Trask B. J., Brand-Arpon V., van den Engh G., Demaille J., and Giorgi D. (1998). Distribution of olfactory receptor genes in the human genome. *Nat Genet* 18: 243-50.
- Rozen S., and Skaletsky H. (2000). Primer3 on the WWW for general users and for biologist programmers. *Methods Mol Biol* 132: 365-86.
- Saglio G., Storlazzi C. T., Giugliano E., Surace C., Anelli L., Rege-Cambrin G., Zagaria A., Jimenez Velasco A., Heiniger A., Scaravaglio P., Torres Gomez A., Roman Gomez J., Archidiacono N., Banfi S., and Rocchi M. (2002). A 76-kb dupilon maps close to the BCR gene on chromosome 22 and the ABL gene on chromosome 9: possible involvement in the genesis of the Philadelphia chromosome translocation. *Proc Natl Acad Sci U S A* 99: 9882-7.
- 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., Air G. M., Barrell B. G., Brown N. L., Coulson A. R., Fiddes C. A., Hutchison C. A., Slocombe P. M., and Smith M. (1977a). Nucleotide sequence of bacteriophage phi X174 DNA. *Nature* 265: 687-95.
- Sanger F., Nicklen S., and Coulson A. R. (1977b). DNA sequencing with chain-terminating inhibitors. *Proc Natl Acad Sci U S A* 74: 5463-7.
- Sanger F., Coulson A. R., Friedmann T., Air G. M., Barrell B. G., Brown N. L., Fiddes J. C., Hutchison C. A., 3rd, Slocombe P. M., and Smith M. (1978). The nucleotide sequence of bacteriophage phiX174. *J Mol Biol* 125: 225-46.
- Sanger F., Coulson A. R., Hong G. F., Hill D. F., and Petersen G. B. (1982). Nucleotide sequence of bacteriophage lambda DNA. *J Mol Biol* 162: 729-73.
- Schmidt H. A., Strimmer K., Vingron M., and von Haeseler A. (2002). TREEPUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. *Bioinformatics* 18: 502-4.
- Schughart K., Kappen C., and Ruddle F. H. (1988). Mammalian homeobox-containing genes: genome organization, structure, expression and evolution. *Br J Cancer Suppl* 9: 9-13.
- Schultz R. J. (1980). Role of polyploidy in the evolution of fishes. In "Polyploidy: Biological Relevance" (W. H. Lewis, Ed.), Plenum, New York.
- Sharman A. C. (1999). Some new terms for duplicated genes. *Semin Cell Dev Biol* 10: 561-3.
- Shiina T., Tamiya G., Oka A., Takishima N., Yamagata T., Kikkawa E., Iwata K., Tomizawa M., Okuaki N., Kuwano Y., Watanabe K., Fukuzumi Y., Itakura S., Sugawara C., Ono A., Yamazaki M., Tashiro H., Ando A., Ikemura T., Soeda E., Kimura M., Bahram S., and Inoko H. (1999). Molecular dynamics of MHC genesis unraveled by sequence analysis of the 1,796,938-bp HLA class I region. *Proc Natl Acad Sci U S A* 96: 13282-7.
- Shiina T., Ando A., Suto Y., Kasai F., Shigenari A., Takishima N., Kikkawa E., Iwata K., Kuwano Y., Kitamura Y., Matsuzawa Y., Sano K., Nogami M., Kawata H., Li S., Fukuzumi Y., Yamazaki M., Tashiro H., Tamiya G., Kohda A., Okumura K., Ikemura T., Soeda E., Mizuki N., Kimura M., Bahram S., and Inoko H. (2001). Genomic anatomy of a premier major histocompatibility complex paralogous region on chromosome 1q21-q22. *Genome Res* 11: 789-802.
- Sidow A. (1996). Gen(om)e duplications in the evolution of early vertebrates. *Curr Opin Genet Dev* 6: 715-22.
- Skrabanek L., and Wolfe K. H. (1998). Eukaryote genome duplication - where's the evidence? *Curr Opin Genet Dev* 8: 694-700.

- Smit A. F. (1999). Interspersed repeats and other mementos of transposable elements in mammalian genomes. *Curr Opin Genet Dev* 9: 657-63.
- Smith L. C., Azumi K., and Nonaka M. (1999). Complement systems in invertebrates. The ancient alternative and lectin pathways. *Immunopharmacology* 42: 107-20.
- Soderlund C., Longden I., and Mott R. (1997). FPC: a system for building contigs from restriction fingerprinted clones. *Comput Appl Biosci* 13: 523-35.
- Spring J., Goldberger O. A., Jenkins N. A., Gilbert D. J., Copeland N. G., and Bernfield M. (1994). Mapping of the syndecan genes in the mouse: linkage with members of the myc gene family. *Genomics* 21: 597-601.
- Spring J. (1997). Vertebrate evolution by interspecific hybridisation--are we polyploid? *FEBS Lett* 400: 2-8.
- Staden R. (1980). A new computer method for the storage and manipulation of DNA gel reading data. *Nucleic Acids Res* 8: 3673-94.
- Staden R., Beal K. F., and Bonfield J. K. (2000). The Staden package, 1998. *Methods Mol Biol* 132: 115-30.
- Stephens R., Horton R., Humphray S., Rowen L., Trowsdale J., and Beck S. (1999). Gene organisation, sequence variation and isochore structure at the centromeric boundary of the human MHC. *J Mol Biol* 291: 789-99.
- Strippoli P., D'Addabbo P., Lenzi L., Giannone S., Canaider S., Casadei R., Vitale L., Carinci P., and Zannotti M. (2002). Segmental paralogy in the human genome: a large-scale triplication on 1p, 6p, and 21q. *Mamm Genome* 13: 456-62.
- Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A., Inoko H., and Ikemura T. (1994). Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBX2 homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3. *Genomics* 23: 408-19.
- Sugaya K., Sasanuma S., Nohata J., Kimura T., Fukagawa T., Nakamura Y., Ando A., Inoko H., Ikemura T., and Mita K. (1997). Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3. *Gene* 189: 235-44.
- Tamkun J. W. (1995). The role of brahma and related proteins in transcription and development. *Curr Opin Genet Dev* 5: 473-7.
- Tee M. K., Thomson A. A., Bristow J., and Miller W. L. (1995). Sequences promoting the transcription of the human XA gene overlapping P450c21A correctly predict the presence of a novel, adrenal-specific, truncated form of tenascin-X. *Genomics* 28: 171-8.

The MHC Sequencing Consortium (1999). Complete sequence and gene map of a human major histocompatibility complex. The MHC sequencing consortium. *Nature* 401 (6756): 921-3.

Thompson J. D., Higgins D. G., and Gibson T. J. (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.

Thomson G. (1995). HLA disease associations: models for the study of complex human genetic disorders. *Crit Rev Clin Lab Sci* 32: 183-219.

Thorpe K. L., Gorman P., Thomas C., Sheer D., Trowsdale J., and Beck S. (1997). Chromosomal localization, gene structure and transcription pattern of the ORFX gene, a homologue of the MHC-linked RING3 gene. *Gene* 200: 177-83.

Utans U., Arceci R. J., Yamashita Y., and Russell M. E. (1995). Cloning and characterization of allograft inflammatory factor-1: a novel macrophage factor identified in rat cardiac allografts with chronic rejection. *J Clin Invest* 95: 2954-62.

Utans U., Quist W. C., McManus B. M., Wilson J. E., Arceci R. J., Wallace A. F., and Russell M. E. (1996). Allograft inflammatory factory-1. A cytokine-responsive macrophage molecule expressed in transplanted human hearts. *Transplantation* 61: 1387-92.

van Geel M., Heather L. J., Lyle R., Hewitt J. E., Frants R. R., and de Jong P. J. (1999). The FSHD region on human chromosome 4q35 contains potential coding regions among pseudogenes and a high density of repeat elements. *Genomics* 61: 55-65.

van Geel M., Eichler E. E., Beck A. F., Shan Z., Haaf T., van der Maarel S. M., Frants R. R., and de Jong P. J. (2002). A cascade of complex subtelomeric duplications during the evolution of the hominoid and Old World monkey genomes. *Am J Hum Genet* 70: 269-78.

van Slegtenhorst M., de Hoogt R., Hermans C., Nellist M., Janssen B., Verhoef S., Lindhout D., van den Ouwehand A., Halley D., Young J., Burley M., Jeremiah S., Woodward K., Nahmias J., Fox M., Ekong R., Osborne J., Wolfe J., Povey S., Snell R. G., Cheadle J. P., Jones A. C., Tachataki M., Ravine D., Kwiatkowski D. J., and et al. (1997). Identification of the tuberous sclerosis gene TSC1 on chromosome 9q34. *Science* 277: 805-8.

Venter J. C., Adams M. D., Myers E. W., Li P. W., Mural R. J., Sutton G. G., Smith H. O., Yandell M., Evans C. A., Holt R. A., Gocayne J. D., Amanatides P., Ballew R. M., Huson D. H., Wortman J. R., Zhang Q., Kodira C. D., Zheng X. H., Chen L., Skupski M., Subramanian G., Thomas P. D., Zhang J., Gabor Miklos G. L., Nelson C., Broder S., Clark A. G., Nadeau J., McKusick V. A., Zinder N., Levine A. J., Roberts R. J., Simon M., Slayman C., Hunkapiller M., Bolanos R., Delcher A., Dew I., Fasulo D., Flanigan M., Florea L., Halpern A., Hannenhalli S., Kravitz S., Levy S., Mobarry C., Reinert K., Remington K., Abu-Threideh J., Beasley E., Biddick K.,

Bonazzi V., Brandon R., Cargill M., Chandramouliwaran I., Charlab R., Chaturvedi K., Deng Z., Di Francesco V., Dunn P., Eilbeck K., Evangelista C., Gabrielian A. E., Gan W., Ge W., Gong F., Gu Z., Guan P., Heiman T. J., Higgins M. E., Ji R. R., Ke Z., Ketchum K. A., Lai Z., Lei Y., Li Z., Li J., Liang Y., Lin X., Lu F., Merkulov G. V., Milshina N., Moore H. M., Naik A. K., Narayan V. A., Neelam B., Nusskern D., Rusch D. B., Salzberg S., Shao W., Shue B., Sun J., Wang Z., Wang A., Wang X., Wang J., Wei M., Wides R., Xiao C., Yan C., et al. (2001). The sequence of the human genome. *Science* 291: 1304-51.

Vernier P., Mastrippolito R., Helin C., Bendali M., Mallet J., and Tricoire H. (1996). Radioimager quantification of oligonucleotide hybridization with DNA immobilized on transfer membrane: application to the identification of related sequences. *Anal Biochem* 235: 11-9.

von Lindern M., van Baal S., Wiegant J., Raap A., Hagemeijer A., and Grosveld G. (1992). Can, a putative oncogene associated with myeloid leukemogenesis, may be activated by fusion of its 3-prime half to different genes: characterization of the 'set' gene. *Mol. Cell. Biol.* 12: 3346-3355.

Wagner A. (2001). Birth and death of duplicated genes in completely sequenced eukaryotes. *Trends Genet* 17: 237-9.

Walter M. A., Spillett D. J., Thomas P., Weissenbach J., and Goodfellow P. N. (1994). A method for constructing radiation hybrid maps of whole genomes. *Nat Genet* 7: 22-8.

Wang Y., and Gu X. (2000). Evolutionary patterns of gene families generated in the early stage of vertebrates. *J Mol Evol* 51: 88-96.

Wendel J. F. (2000). Genome evolution in polyploids. *Plant Mol Biol* 42: 225-49.

Wilke C. M., Guo S. W., Hall B. K., Boldog F., Gemmill R. M., Chandrasekharappa S. C., Barcroft C. L., Drabkin H. A., and Glover T. W. (1994). Multicolor FISH mapping of YAC clones in 3p14 and identification of a YAC spanning both FRA3B and the t(3;8) associated with hereditary renal cell carcinoma. *Genomics* 22: 319-26.

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., and et al. (1994). 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*. *Nature* 368: 32-8.

Wittbrodt J., Meyer A., and Schartl M. (1998). More genes in fish? *Bioessays* 20: 511-515.

Wolfe K. H. (2001). Yesterday's polyploids and the mystery of diploidization. *Nat Rev Genet* 2: 333-41.

Xia Y., Brown L., Yang C. Y., Tsan J. T., Siciliano M. J., Espinosa R., III, Le Beau M. M., and Baer R. J. (1991). TAL2, a helix-loop-helix gene activated by the (7;9)(q34;q32) translocation in human T-cell leukemia. *Proc Natl Acad Sci U S A* 88: 11416-20.

Yon J., Jones T., Garson K., Sheer D., and Fried M. (1993). The organization and conservation of the human Surfeit gene cluster and its localization telomeric to the c-abl and can proto-oncogenes at chromosome band 9q34.1. *Hum Mol Genet* 2: 237-40.

Zhu Z., Yao J., Johns T., Fu K., De Bie I., Macmillan C., Cuthbert A. P., Newbold R. F., Wang J., Chevrette M., Brown G. K., Brown R. M., and Shoubridge E. A. (1998). SURF1, encoding a factor involved in the biogenesis of cytochrome c oxidase, is mutated in Leigh syndrome. *Nat Genet* 20: 337-43.