



Yves Van de Peer

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• Research Interests

As an evolutionary biologist and a bioinformatician, I'm interested in using bioinformatics approaches to study the evolution of organisms, genes and genomes. Regarding genome structure and evolution (which forms a major part of our research), I'm particularly interested in the study of gene and genome duplications as well as in the evolution of novel gene functions after duplication. Gene duplication events have been considered important mechanisms that facilitated the increasing complexity of organisms and also speciation because they might have permitted functional diversification of genes, created complex gene families and generally increased genomic and phenotypic complexity. However, great controversy still exists about how and how fast duplicated genes evolve new functions. Another point of discussion is whether most gene duplications are the result of local (e.g., tandem) gene duplications or of large-scale gene or even entire genome duplication events. Although the number of sequence data that can provide us with answers to the questions raised above increases at a fast rate, the interpretation of the data and mapping and interpreting (large scale) gene duplication events remains often difficult. For example, typically, developmental control genes belong to multigene families and, more often than not, the evolutionary relationships within these gene families in comparative developmental studies are unknown and potentially complex. Also the elucidation of the exact relationships between gene family members therefore forms part of our research. For a more comprehensive overview of my research interests, I'd like to point to our [research](#) section.

• Curriculum Vitae

Birthdate: 26 April 1965, Turnhout, Belgium.

October 2002: **Professor** in Bioinformatics and Genome Biology at Ghent University, Belgium

June 2001 - September 2002: **Group Leader** of Bioinformatics and **Guest Professor** at the Department of Plant Systems Biology at Ghent University (Belgium) and at the Department of Biomedical Sciences at the University of Antwerp (Belgium).

October 1995 - September 2002: **Postdoctoral Fellow** of the Fund for Scientific Research (FWO - Flanders), Department of Biochemistry, University of Antwerp (UIA), Belgium.

April 1999 - May 2001: **Assistant-Professor** in the Research group '[Evolutionary Biology](#)' of Prof. Dr. Axel Meyer at the Department of Biology, University of Konstanz, Germany.

October 1987 - February 1995: **Ph.D. studies** 'Ribosomal RNA as a tool in molecular evolution', Department of Biochemistry, University of Antwerp (UIA), Belgium.

October 1983 - September 1987: **Undergraduate studies Biology**. University of Antwerp (UIA), Belgium.

Service as reviewer: Journal of Molecular Evolution, Molecular Biology and Evolution, Bioinformatics, Genome Research, Nucleic Acid Research, Trends in Genetics, Genome Biology, BMC Bioinformatics, BMC Plant Biology, Plant Molecular Biology, Plant Cell, Plant Physiology, BioEssays, Nature, Nature Reviews Genetics, Proceedings of the National Academy of Sciences USA, PLoS Computational Biology, Science

Membership in Editorial Boards: [Journal of Molecular Evolution](#) (Associate Editor), [PLoS Computational Biology](#) (Associate Editor), [Molecular Genetics and Genomics](#) (Editor).

• Publications

- **(177)** Saeys, Y. & **Van de Peer, Y.** (2007) Enhancing coding potential prediction for short sequences using complementary sequence features and feature selection. Lect. Notes in Bioinf. (LNBI, vol. 4366) (in press) [\(Abstract\)](#)

- **(176)** Sterck, L., Rombauts, S., Vandepoele, K., Rouzé, P. & **Van de Peer, Y.** (2007) How many genes are there in plants (... and why are they there)? Curr Opin Plant Biol (in Press) [\(PMID: 17289424\)](#)

- **(175)** Robbens, S., Derelle, E., Ferraz, C., Wuyts, J., Moreau, H. & **Van de Peer, Y.** (2007) The Complete Chloroplast and Mitochondrial DNA Sequence of *Ostreococcus tauri*: Organelle Genomes of the Smallest Eukaryote are Examples of Compaction Mol. Biol. Evol. ; doi: 10.1093/molbev/msm012 (in press) [\(Abstract\)](#) [\(PMID: 17251180\)](#)

- **(174)** * Michoel, T., * Maere, S., Bonnet, E., Joshi, A., Saeys, Y., Van den Bulcke, T., Van Leemput, K., van Remortel, P., Kuiper, M., Marchal, K. & **Van de Peer, Y.** (2007) Validating module networks learning algorithms using simulated data. BMC Bioinformatics (in press) [\(Abstract\)](#) *contributed equally

- **(173)** Robbens, S., Petersen, J., Brinkmann, H., Rouzé, P. & **Van de Peer, Y.** (2007) Unique regulation of the Calvin cycle in the ultrasmall green alga *Ostreococcus*. J. Mol. Evol. (in press) [\(Abstract\)](#)

- **(172)** Saeys, Y., Rouzé, P. & **Van de Peer, Y.** (2007) In search of the small ones: improved prediction of short exons in vertebrates, plants, fungi, and protists. Bioinformatics 23(4):414-420 [\(Abstract\)](#) [\(Supplementary Data\)](#) [\(PMID: 17204465\)](#)

- **(171)** Carlton, J.M., Hirt, H., Silva, E.P., Delcher, A.L., Schatz, M., Zhao, Q., Wortman, J.R., Bidwell, S.L., Alsmark, C.M., Besteiro, S., Sicheritz-Ponten, T., Noel, C.J., Dacks, J.B., Foster, P.G., Simillion, C., **Van de Peer, Y.**, Miranda-Saavedra, D., Barton, G.J., Westrop, G.D., Miller, S., Dessi, D., Fiori, L.P., Paulsen, I., Zhang, J., Bastida-Corcuera, F.D., Barbosa, A., Brown, M.T., Hayes, R.D., Mukherjee, M., Okumura, C.Y., Schneider, M., Villalvazo, M., Haase, G., Perlea, M., Feldblyum, T., Utterback, T.R., Shu, C.-L., Osoegawa, K., de Jong, P.J., Dolezal, P., Hrd, I., Malik, S.-B., Logsdon, Jr., Henze, K., Gupta, A., Wang, X., Dunne, R.L., Upcroft, J.A., Upcroft, P., White, O., Salzberg, S.L., Tanghe, K., Chiu, C.-H., Embley, T.M., Coombs, G.H., Mottram, J.C., Tachezy, J., Fraser-Liggett, C.M. & Johnson, P.J. (2007) Draft Genome Sequence of the Sexually-Transmitted Pathogen *Trichomonas vaginalis*. Science 315, 206-212 [\(Abstract\)](#) [\(PMID: 17218520\)](#)

- **(170)** Gevers, D. & **Van de Peer, Y.** (2006) Gene duplicates in vibrio genomes. Invited book chapter in The Biology of Vibrios. Editors: Thompson, F.L., Austin, B. & Swings, J. ASM press. (In Press)

- **(169)** Bonet, I., Garcia, M.M., Salazar, S., Sanchez, R., Saeys, Y., **Van de Peer, Y.** & Grau, R. (2006) Feature Extraction Using Clustering of Proteins. Lect. Notes in Comput. Sci. pp. 614-623. (in press) [\(Abstract\)](#)

- **(168)** Van Hellefont, R., Blomme, T., **Van de Peer, Y.** & Marchal, K. (2006) Divergence of regulatory sequences in duplicated fish genes. Invited book chapter in 'Genome Dynamics'. [\(Related\)](#)

- **(167)** Van den Bulcke, T., Lemmens, K., **Van de Peer, Y.** & Marchal, K. (2006) Inferring transcriptional

networks by mining 'omics' data. *Current Bioinformatics* 1, 301-313 ([Abstract](#))

- **(166)** Faes, P., Minnaert, B., Christiaens, M., Bonnet, E., Saeys, Y., Stroobandt, D. & **Van de Peer, Y.** (2006) A Scalable Hardware Accelerator for Comparing Protein Sequences.. Proceedings of the First International Conference on Scalable Information Systems. Hong Kong, April 2006, on CD. ([Abstract](#))
- **(165)** Blomme, T., Vandepoele, K., De Bodt, S., Simillion, C., Maere, S. & **Van de Peer, Y.** (2006) The gain and loss of genes during 600 million years of vertebrate evolution. *Genome Biology* 7:R43 ([Abstract](#)) ([Supplementary Data](#)) **Highly accessed**
- **(164)** Bonet, I., Garcia, M.M., Salazar, S., Sanchez, R., Saeys, Y., **Van de Peer, Y.** & Grau, R. (2006) Predicting Human Immunodeficiency Virus (HIV) Drug Resistance using Recurrent Neural Networks. Proceedings of the 10th International Electronic Conference on Synthetic Organic Chemistry, 2006 ([Abstract](#))
- **(163)** Saeys, Y. & **Van de Peer, Y.** (2006) Enhancing coding potential prediction for short sequences using complementary sequence features and feature selection. Proceedings of the 15th Dutch Belgian Machine Learning Conference (Benelearn 2006), pp. 105-112.
- **(162)** Saeys, Y. & **Van de Peer, Y.** (2006) Combining signal processing and machine learning techniques for coding potential prediction. Proceedings of the First International Workshop on Bioinformatics Cuba-Flanders 2006, Santa Clara, Cuba
- **(161)** De Bodt, S., Theissen, G. & **Van de Peer, Y.** (2006) Promoter analysis of MADS-box genes in eudicots through phylogenetic footprinting. *Mol. Biol. Evol.* 23, 1293-1303 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 16581940](#))
- **(160)** Bonnet, E., **Van de Peer, Y.** & Rouzé, P. (2006) The small RNA world of plants. *New Phytol.* 171, 451- 468 ([PMID: 16866953](#))
- **(159)** Vandepoele, K., Casneuf, T. & **Van de Peer, Y.** (2006) Identification of novel regulatory modules in dicot plants using expression data and comparative genomics. *Genome Biology* 2006, 7:R103 ([Abstract](#)) ([Supplementary Data](#)) **Highly accessed**
- **(158)** * Derelle, E., * Ferraz, C., * Rombauts, S., * Rouzé, P., Worden, A.Z., Robbens, S., Partensky, F., Degroeve, S., Echeynie, S., Cooke, R., Saeys, Y., Wuys, J., Jabbari, K., Bowler, C., Panaud, O., Piegu, B., Ball, S., Ral, J.P., Bouget, F.-Y., Piganeau, G., De Baets, B., Picard, A., Delseny, M., Demaille, J., **Van de Peer, Y.** & Moreau, H. (2006) Genome analysis of the smallest free-living eukaryote *Ostreococcus tauri* unveils many unique features. *Proc. Natl. Acad. Sci. USA* 103, 11647-11652 ([Abstract](#)) ([Supplementary Data](#)) ([Related](#)) *contributed equally
- **(157)** Tuskan, G., * DiFazio, S., * Jansson, S., * Bohlmann, J., * Grigoriev, I., * Hellsten, U., * Putnam, N., * Ralph, S., * Rombauts, S., * Salamov, A., * Schein, J., * Sterck, L., Aerts, A., Bhalerao, R.R., Bhalerao, R.P., Blaudez, D., Boerjan, W., Brun, A., Brunner, A., Busov, V., Campbell, M., Carlson, J., Chalot, M., Chapman, J., Chen, G.-L., Cooper, D., Coutinho, P., Couturier, J., Covert, S., Cronk, Q., Cunningham, R., Davis, J., Degroeve, S., Dejardin, A., dePamphilis, C., Detter, J., Dirks, B., Dubchak, I., Duplessis, S., Ehlting, J., Ellis, B., Gendler, K., Goodstein, D., Gribskov, M., Grimwood, J., Groover, A., Gunter, L., Hamberger, B., Heinze, B., Helariutta, Y., Henrissat, B., Holligan, D., Holt, R., Huang, W., Islam-Faridi, N., Jones, S., Jones-Rhoades, M., Jorgensen, R., Joshi, C., Kangasjarvi, J., Karlsson, J., Kelleher, C., Kirkpatrick, R., Kirst, M., Kohler, A., Kalluri, U., Larimer, F., Leebens-Mack, J., Leple, J., Locascio, P., Luo, Y., Lucas, S., Martin, F., Montanini, B., Napoli, C., Nelson, D.R., Nelson, C., Nieminen, K., Nilsson, O., Peter, G., Philippe, R., Pilate, G., Poliakov, A., Razumovskaya, J., Richardson, P., Rinaldi, C., Ritland, K., Rouzé, P., Ryaboy, D., Schmutz, J., Schrader, J., Segerman, B., Shin, H., Siddiqui, A., Sterky, F., Terry, A., Tsai, C., Uberbacher, E., Unneberg, P., Vahala, J., Wall, K., Wessler, S., Yang, G., Yin, T., Douglas, C., Marra, M., Sandberg, G., **Van de Peer, Y.** & Rokhsar, D. (2006) The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray ex Brayshaw). *Science* 313, 1596 - 1604 ([Abstract](#)) ([Supplementary Data](#)) ([Related](#)) ([PMID: 16973872](#)) *contributed equally

- **(156)** * Cannon, S.B., * Sterck, L., * Rombauts, S., Sato, S., Wang, X., Mudge, J., Vasdewani, J., Cheung, F., Gouzy, J.P., Schiex, T., Spanngl, M., Schoof, H., Nicholson, C., Humphrays, S., Mayer, K., Rogers, J., Quetier, F., Oldroyd, G.E., Debelle, F., Cook, D.R., Town, C.D., Roe, B.A., Tabata, S., **Van de Peer, Y.** & Young, N.D. (2006) Legume genome evolution viewed through the *Medicago truncatula* and *Lotus japonicus* genomes. *Proc. Natl. Acad. Sci. USA* 103, 14959-14964 ([Abstract](#)) ([PMID: 17003129](#)) *contributed equally

- **(155)** Baele, G., Raes, J., **Van de Peer, Y.** & Vansteelandt, S. (2006) An improved statistical method for detecting heterotachy in nucleotide sequences. *Mol. Biol. Evol.* 23, 1397-1405 ([Abstract](#)) ([PMID: 16672284](#))

- **(154)** Casneuf, T., De Bodt, S., Raes, J., Maere, S. & **Van de Peer, Y.** (2006) Nonrandom divergence of gene expression following gene and genome duplications in the flowering plant *Arabidopsis thaliana*. *Genome Biology* 7, R13 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 16507168](#)) **Highly accessed**

- **(153)** Michoel, T. & **Van de Peer, Y.** (2006) A helicoidal transfer matrix model for inhomogeneous DNA melting. *Physical Review E*. 73, 011908 ([Abstract](#))

- **(152)** **Van de Peer, Y.** (2006) When duplicated genes don't stick to the rules. *Heredity* 96, 204-205 ([Abstract](#)) ([PMID: 16288315](#))

- **(151)** Gevers, D., Cohan, F.M., Lawrence, J.G., Spratt, B.G., Coenye, T., Feil, E.J., Stackebrandt, E., **Van de Peer, Y.**, Vandamme, P., Thompson, F.L. & Swings, J. (2005) Re-evaluating prokaryotic species. *Nature Rev. Microbiol.* 3, 733-739 ([Abstract](#)) ([discussion](#)) ([PMID: 16138101](#))

- **(150)** * De Bodt, S., * Maere, S. & **Van de Peer, Y.** (2005) Genome duplication and the origin of angiosperms. *Trends Ecol. Evol.* 20, 591-597 *contributed equally

- **(149)** Van Hellefont, R., Monsieurs, P., Thijs, G., De Moor, B., **Van de Peer, Y.** & Marchal, K. (2005) A novel approach to identifying regulatory motifs in distantly related genomes. *Genome Biology* 6, R:113 ([Abstract](#)) ([PMID: 16420672](#)) **Highly accessed**

- **(148)** Paterson, A.H., Bowers, J. E., **Van de Peer, Y.** & Vandepoele, K. (2005) Ancient duplication of cereal genomes. *New Phytol.* 165, 658 - 661 ([Abstract](#)) ([PMID: 15720677](#))

- **(147)** **Van de Peer, Y.** (2005) Horizontal plant biology on the rise. *Genome Biology* 6, 302 ([Abstract](#)) ([PMID: 15642110](#))

- **(146)** * Coenye, T., * Gevers, D., **Van de Peer, Y.**, Vandamme, P. & Swings, J. (2005) Review: Towards a prokaryotic genomic taxonomy. *FEMS Microbiol. Rev.* 29: 147-167 ([Abstract](#)) ([PMID: 15808739](#)) *contributed equally

- **(145)** * Maere, S., * De Bodt, S., Raes, J., Casneuf, T., Van Montagu, M., Kuiper, M. & **Van de Peer, Y.** (2005) Modeling gene and genome duplications in eukaryotes. *Proc. Natl. Acad. Sci. USA* 102, 5454-5459 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 15800040](#)) ([faculty-of-1000](#)) *contributed equally

- **(144)** Meyer, A. & **Van de Peer, Y.** (2005) From 2R to 3R: evidence for a fish-specific genome duplication (FSGD). *BioEssays* 27, 937-945 ([Abstract](#)) ([PMID: 16108068](#))

- **(143)** Raes, J. & **Van de Peer, Y.** (2005) Functional divergence of proteins through frameshift mutations. *Trends Genet.* 21, 428-431 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 15951050](#))

- **(142)** Beysen, D., Raes, J., Leroy, B.P., Lucassen, A., Yates, J.R., Clayton-Smith, J., Ilyina, H., Sklower Brooks, S., Christin-Maitre, S., Fellous, M., Fryns, J.P., Kim, J.R., Lapunzina, P., Lemyre, E., Meire, F., Messiaen, L.M., Oley, C., Splitt, M., Thomson, J., **Van de Peer, Y.**, Veitia, R.A., De Paepe, A. & De Baere, E. (2005) Deletions involving long-range conserved non-genic sequences (CNGs) upstream and downstream of FOXL2 as novel disease-causing mechanism in bpes. *Am. J. Hum. Genet.* 77, 205-218

[\(Abstract\)](#) [\(PMID: 15962237\)](#)

- **(141)** Vandepoele, K., Vlieghe, K., Florquin, K., Hennig, L., Beemster, G.T.S., Gruissem, W., **Van de Peer, Y.**, Inzé, D. & De Veylder, L. (2005) Genome-wide identification of potential plant E2F target genes. *Plant Physiol.* 139, 316-328 [\(Abstract\)](#) [\(PMID: 16126853\)](#)
- **(140)** Robbins, S., Khadaroo, B., Camasses, A., Derelle, E., Ferraz, C., Inzé, D., **Van de Peer, Y.** & Moreau, H. (2005) Genome-wide analysis of core cell cycle genes in the unicellular green alga *Ostreococcus tauri*. *Mol. Biol. Evol.* 22, 589-597 [\(Abstract\)](#) [\(PMID: 15537805\)](#) [\(faculty-of-1000\)](#)
- **(139)** Florquin, K., Degroeve, S., Saeys, Y. & **Van de Peer, Y.** (2005) Large-scale structural analysis of the core promoter in Mammalian and plant genomes. *Nucleic Acids Res.* 33, 4255-4264 [\(Abstract\)](#) [\(Supplementary Data\)](#) [\(PMID: 16049029\)](#)
- **(138)** Sterck, L., Rombauts, S., Jansson, S., Sterky, F., Rouzé, P. & **Van de Peer, Y.** (2005) EST data suggest that poplar is an ancient polyploid. *New Phytol.* 167, 165-70 [\(Abstract\)](#) [\(PMID: 15948839\)](#)
- **(137)** Saeys, Y., Degroeve, S. & **Van de Peer, Y.** (2005) Feature ranking using an EDA-based wrapper approach. Invited book chapter in 'Towards a new evolutionary computation : advances in Estimation of Distribution algorithms.' Editors: Jose A. Lozano, Pedro Larranaga, Inaki Inza and Endika Bengoetxea
- **(136)** Degroeve, S., Saeys, Y., De Baets, B., **Van de Peer, Y.** & Rouzé, P. (2005) Splice Site Prediction in Eukaryote Genome Sequences. Book chapter in 'The New Avenues in Bioinformatics'. Editors: Seckbach, J., Rubin, E. [\(Link\)](#)
- **(135)** Vandepoele, K. & **Van de Peer, Y.** (2005) Exploring the plant transcriptome through phylogenetic profiling *Plant Physiol.* 137, 31 - 42 [\(Abstract\)](#) [\(Supplementary Data\)](#) [\(PMID: 15644465\)](#)
- **(134)** **Van de Peer, Y.** & Meyer, A. (2005) Large-scale gene and ancient genome duplications. Book chapter in: *The Evolution of the Genome*, edited by T.R. Gregory. Elsevier, San Diego. [\(Link\)](#)
- **(133)** Saeys, Y., Degroeve, S. & **Van de Peer, Y.** (2004) Digging into acceptor splice site prediction: an iterative feature selection approach. *Proceedings of ECML/PKDD 2004*, Lecture Notes in Artificial Intelligence 3202, 386-397 [\(Abstract\)](#)
- **(132)** Bonnet, E., Wuyts, J., Rouzé, P. & **Van de Peer, Y.** (2004) Detection of 91 potential conserved plant microRNAs in *Arabidopsis thaliana* and *Oryza sativa* identifies important new target genes. *Proc. Natl. Acad. Sci. USA* 101, 11511-11516 [\(Abstract\)](#) [\(Supplementary Data\)](#) [\(PMID: 15272084\)](#) [\(faculty-of-1000\)](#)
- **(131)** Degroeve, S., Saeys, Y., De Baets, B., Rouzé, P. & **Van de Peer, Y.** (2004) Predicting splice sites from high-dimensional local context representations. *Bioinformatics* 20, 1332-1338 [\(Abstract\)](#) [\(Supplementary Data\)](#) [\(PMID: 15564294\)](#)
- **(130)** **Van de Peer, Y.** (2004) Computational approaches to unveiling ancient genome duplications. *Nat. Rev. Genet.* 5, 752-763 [\(Abstract\)](#) [\(PMID: 15510166\)](#)
- **(129)** **Van de Peer, Y.** (2004) Tetraodon genome confirms Takifugu findings: most fish are ancient polyploids. *Genome Biology* 2004, 5:250 [\(Abstract\)](#) [\(PMID: 15575976\)](#)
- **(128)** * Bonnet, E., * Wuyts, J., Rouzé, P. & **Van de Peer, Y.** (2004) Evidence that microRNA precursors, unlike other non-coding RNAs, have lower folding free energies than random sequences. *Bioinformatics* 20, 2911-2917 [\(Abstract\)](#) [\(Supplementary Data\)](#) [\(Link\)](#) [\(PMID: 15217813\)](#) *contributed equally
- **(127)** Simillion, C., Vandepoele, K. & **Van de Peer, Y.** (2004) Recent developments in computational approaches for uncovering genomic homology. *BioEssays* 26, 1225-1235 [\(Abstract\)](#) [\(PMID: 15499578\)](#)

- **(126)** Trindade, G.S., Da Fonseca, F.G., Marques, J.T., Diniz, S., Leite, J.A., De Bodt, S., **Van de Peer, Y.**, Bonjardim, C.A., Ferreira, P.C.P. & Kroon, E.G. (2004) The Belo Horizonte virus: a vaccinia-like virus lacking the A-type inclusion body gene isolated from infected mice. *J. Gen. Virol.* 85, 2015-2021 ([Abstract](#)) ([PMID: 15218187](#))
- **(125)** Alvares, L.E., Wuyts, J., **Van de Peer, Y.**, Silva, E.P., Coutinho, L.L., Brison, O. & Ruiz, I.R.G. (2004) The 18S rRNA from *Odontophrynus americanus* 2n and 4n (Amphibia, Anura) reveals unusual extra sequences in the variable region V2. *Genome* 47,421-428 ([Abstract](#)) ([PMID: 15190359](#))
- **(124)** Gevers, D., Vandepoele, K., Simillion, C. & **Van de Peer, Y.** (2004) Gene duplication and biased functional retention of paralogs in bacterial genomes. *Trends Microbiol.* 12,148-154 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 15116722](#))
- **(123)** Vandepoele, K., Simillion, C. & **Van de Peer, Y.** (2004) The quest for genomic homology. *Curr. Genomics* 5, 299-308 ([Abstract](#))
- **(122)** Simillion, C., Vandepoele, K., Saeys, Y. & **Van de Peer, Y.** (2004) Building genomic profiles for uncovering segmental homology in the twilight zone. *Genome Res.* 14, 1095-1106 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 15173115](#))
- **(121)** Saeys, Y., Degroeve, S., Aeyels, D., Rouz , P. & **Van de Peer, Y.** (2004) Feature selection for splice site prediction: A new method using EDA-based feature ranking. *BMC Bioinformatics* 5, 64 ([Abstract](#)) ([PMID: 15154966](#))
- **(120)** Saeys, Y., Degroeve, S., Aeyels, D., Rouz , P. & **Van de Peer, Y.** (2004) Selecting relevant features for gene structure prediction. *Proceedings of Benelearn* 13, 103-109 ([Abstract](#))
- **(119)** Khadaroo, B., Robbens, S., Ferraz, C., Derelle, E., Eychenie, S., Cooke, R., Peaucellier, G., Delseny, M., Demaille, J., **Van de Peer, Y.**, Picard, A. & Moreau, H. (2004) The First Green Lineage *cdc25* Dual-Specificity Phosphatase. *Cell Cycle* 3, 513-518 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 15004533](#))
- **(118)** Vandepoele, K., De Vos, W., Taylor, J.S., Meyer, A. & **Van de Peer, Y.** (2004) Major events in the genome evolution of vertebrates: paranome age and size differs considerably between fishes and land vertebrates. *Proc. Natl. Acad. Sci. USA* 101, 1638 - 1643 ([Abstract](#)) ([Supplementary Data](#)) ([Review](#)) ([PMID: 14757817](#))
- **(117)** Degroeve, S., Saeys, Y., De Baets, B., **Van de Peer, Y.** & Rouz , P. (2004) Splice site prediction in eukaryote genome sequences: the algorithmic issues. (in press) J. Seckbach (ed.) another book of the Cellular Origin and Life in Extreme Habitats Book Series. Kluwer Academic Publishers, Dordrecht, The Netherlands. (2004)
- **(116)** Wuyts, J., Perriere, G. & **Van de Peer, Y.** (2004) The European ribosomal RNA database. *Nucleic Acids Res.* 32, D101-D103 ([Abstract](#)) ([PMID: 14681368](#))
- **(115)** Raes, J., Rohde, A., Holst-Christensen, J., **Van de Peer, Y.** & Boerjan, W. (2003) Genome-wide characterization of the lignification toolbox in *Arabidopsis*. *Plant Physiol.* 133, 1051-1071 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 14612585](#))
- **(114)** De Bodt, S., Raes, J., Florquin, K., Rombauts, S., Rouz , P., Theissen, G. & **Van de Peer, Y.** (2003) Genomewide structural annotation and evolutionary analysis of the type I MADS-box genes in plants. *J. Mol. Evol.* 56, 573-586. ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 12698294](#))
- **(113)** Raes, J., Vandepoele, K., Saeys, Y., Simillion, C. & **Van de Peer, Y.** (2003) Investigating ancient duplication events in the *Arabidopsis* genome. *J. Struct. Func. Genomics.* 3, 117-129. ([Abstract](#)) ([PMID: 12836691](#))
- **(112)** **Van de Peer, Y.**, Taylor, J.S. & Meyer, A. (2003) Are all fishes ancient polyploids? *J. Struct. Func.*

Genomics. 3, 65-73. ([Abstract](#)) ([PMID: 12836686](#))

- **(111)** Meyer, A. & **Van de Peer, Y.** (2003) Natural selection merely modified while redundancy created - Susumu Ohno's idea of the evolutionary importance of gene and genome duplications. J. Struct. Func. Genomics. 3, 7-9. ([Abstract](#)) ([PMID: 12836679](#))
- **(110)** Rombauts, S., **Van de Peer, Y.** & Rouzé, P. (2003) AFLPinsilico, simulating AFLP fingerprints. Bioinformatics 19, 776-777. ([Abstract](#)) ([PMID: 12691992](#))
- **(109)** Taylor, J.S., Braasch, I., Frickey, T., Meyer, A. & **Van de Peer, Y.** (2003) Genome duplication, a trait shared by 22,000 species of ray-finned fish. Genome Res. 13, 382-390. ([Abstract](#)) ([PMID: 12618368](#)) ([faculty-of-1000](#))
- **(108)** * Rombauts, S., * Florquin, K., Lescot, M., Marchal, K., Rouzé, P. & **Van de Peer, Y.** (2003) Computational approaches to identify promoters and cis-regulatory elements in plant genomes. Plant Physiol. 132, 1162-1176 ([Abstract](#)) ([Supplementary Data](#)) ([PMID: 12857799](#)) ([faculty-of-1000](#))
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- **(107)** Raes, J. & **Van de Peer, Y.** (2003) Gene duplications, the evolution of novel gene functions, and detecting functional divergence of duplicates in silico. Applied Bioinformatics 2, 92-101 ([Abstract](#)) ([PMID: 15130825](#))
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