

Conference proceedings

PARSEC: a new web platform for the localization and characterization of genomic sites in complete eukaryotic genomes.

Allot A, Poidevin, P, Ripp R, Poch O, Lecompte O.

ISMB/ECCB 2013 (Berlin, Germany, 2013)

PARSEC: a new web platform for the localization and characterization of genomic sites in complete eukaryotic genomes.

Allot A, Poidevin, P, Ripp R, Poch O, Lecompte O.

Journée Ouvertes en Biologie, Informatique et Mathématiques (Toulouse, France, 2013)

Classification multi-étiquettes pour l'alignement multiple de séquences protéiques.

Fahed L, Frey G, Thompson JD, Lachiche N.

13th conférence : Extraction et Gestion des Connaissances (Toulouse, France) (2013)

OrthoInspector, an intuitive way to investigate orthology and paralogy.

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The protein barcode: capturing evolutionary histories in vertebrates.

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Extracting Knowledge from a Mutation Database Related to Human Monogenic Disease Using Inductive Logic Programming.

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OrthoInspector: comprehensive orthology analysis and visual exploration.

Linard B, Thompson JD, Poch O, Lecompte O.

Computational Biology and Innovation PhD Symposium (Dublin, Ireland, 2010)

OrthoInspector: comprehensive orthology analysis and visual exploration.

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Comparative genomic analysis of the core-TFIID.

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14th Evolutionary Biology Meeting at Marseilles (Marseille, France, 2009)

Molecular adaptation to high temperatures in the deep-sea vent polychaete Alvinella pompejana.

Jollivet D, Gagnière N, Mary J, Tanguy A., Boutet, I, Hourdez S, Lallier F, Segurens B, Poch O, Lecompte, O.

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Molecular adaptation to high temperatures in the deep-sea vent polychaete Alvinella pompejana: search for adaptive signatures from an EST collection.

Jollivet D, Gagnière N, Mary J, Tanguy A., Boutet, I, Hourdez S, Lallier F, Segurens B, Poch O, Lecompte, O.

ASLO Aquatic Sciences Meeting (Nice, France, 2009)

Sequencing and biodiversity in the post-genomic era: cDNA analysis of the thermotolerant annelid Alvinella pompejana.

Gagnière N, Lecompte O, Poch O.

ULP-JSPS Joint Forum on “Frontiers in Biology/Chemistry/Physics” (Strasbourg, France, 2008)

Introduction to the new Biomedical Decryphon Data Center.

Nguyen H, Friedrich A. Berthommier G. Poidevin L. Moulinier L. Ripp R. Poch O.

CORIA 2008, Hermès Edition.

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Gagnière N, Bigot Y, Gaill F, Higuët D, Jollivet D, Leize E, Rees JF, Weissenbach J, Zal F, Poch O, Lecompte O.

AFP/Biosapiens (Vienna, Austria, 2007)

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Third International Symposium on Hydrothermal Vent and Seep Biology (La Jolla, California 2005)

Prédiction et validation des codons d'initiation : approches croisées bioinformatique et protéomique.

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Journée du Réseau National Genopole : Quelle informatique et bioinformatique pour la protéomique ? (Grenoble, France, 2004)

Comparative analysis of ribosomal proteins in complete genomes: ribosome "striptease" in Archaea.

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Second JSPS Forum in France: « Postgenome » (Strasbourg, France, 2003)

Analyse de Séquences – Du gène à la famille de protéines.

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XXVIII Forum des Jeunes Chercheurs (Strasbourg, France, 2001)

Replication in archaea : DNA polymerases I and II, Proliferating Cell Nuclear Antigen and Replication Factor C from Pyrococcus abyssi.

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Book Chapters

Intelligent Integrative knowledge bases: bridging genomics, integrative biology and translational medicine

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Andreas Holzinger and Igor Jurisca. Interactive Knowledge Discovery and Data Mining: State-of-the-Art and Future Challenges in Biomedical Informatics. Springer LNCS, Volume 8401 (2014).

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Posters and Oral communications

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