

## 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.*

Lecompte O.

relationships. 3rd World DNA and Genome Day (Xi'an, China, 2012). (Invited conference)

*The protein barcode: capturing evolutionary histories in vertebrates.*

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

Quest for Orthologs 2 (Cambridge, UK, 2011)

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

Luu TD., Nguyen NH., Friedrich A., Muller J., Moulinier L., Poch O.

International Conference on Bioscience, Biochemistry and Bioinformatics; Singapore 2011.  
IEEE Catalog Number: CFP1134M-PRT. ISBN: 978-1-4244-9388-3.

*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.*

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

Journée Ouvertes en Biologie, Informatique et Mathématiques (Montpellier, France, 2010)

*Genome wide study of STAF transcription factor binding sites in the human genome.*

Anno YN, Myslinski E, Poch O, Carbon P, Lecompte O.

Journée Ouvertes en Biologie, Informatique et Mathématiques (Nantes, France, 2009)

*Comparative genomic analysis of the core-TFIID.*

Bedez F, Ripp R, Lecompte O, Moras D, Poch O.

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.

4th International Symposium on Chemosynthesis-Based Ecosystems (Okinawa, Japan, 2009)

*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.

*Study of the molecular response to thermal challenge of the hydrothermal annelid *Paralvinella grasslei**

Tanguy A, Jollivet D, Shillito B, Lecompte O

Comparative biochemistry and physiology A-molecular & integrative physiology 2008  
151(1):S42-S43

*A Geometric Representation of Protein Sequences.*

Shengyin Gu S., Poch O., Hamann B., Koehl P. (2007)

In: Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine, BIBM  
2007, 135-142



*Structure cristallographique d'une jonction de Holliday, intermédiaire principal de la recombinaison.*

Piton J, Lecompte O, Mauffret O, Poch O, Mayer C.

GTBIO 2007 (Lille, France, 2007)

*Premières signatures moléculaires de l'adaptation thermique chez le polychète Alvinella pompejana par analyse du transcriptome.*

Jollivet D, Boutet-Tanguy I, Tanguy A, Mary J, Lecompte O, Segurens B, Weissenbach J, Poch O.

Kick off Meeting GIS Europôle Mer (Roscoff, 2007)

*Alvinella pompejana cDNA collection.*

Gagnière N, Bigot Y, Brelivet Y, Busso D, Chénais B, Gaill F, Higuët D, Jollivet D, Leize E, Rees JF, Thierry JC, Weissenbach J, Zal F, Moras D, Poch O, Lecompte O.

SPINE2 First Annual Congress (Prague, Czech Republic, 2007)

*From cDNA to integrative protein annotation and beyond: application to Alvinella pompejana cDNA collection.*

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)

*Tandem mass spectrometry data searches in uninterpreted and complete genome sequences.*

Carapito C, Gallien S, Heymann M, Bertin PN, Lecompte O, Poch O, Schaeffer C, Van Dorsselaer A.

Congrès 2006 de la Société Française d'Electrophorèse et d'Analyse Protéomique (Saint-Malo, France, 2006)

*Proteome Annotation with MACSIMS (Multiple Alignment of Complete Sequences Information*

*Management System).*

Thompson JD, Lecompte O, Muller A, Perrodou E, Waterhouse A, Procter J, Barton GJ, Plewniak F, Koehl P, Poch O.

The Second Automated Function Prediction Meeting (San Diego, California, 2006)

*PtdIns5P regulation through evolution.*

Lecompte O, Poch O, Laporte J.

Biochemical Society Annual Symposium (Birmingham, UK, 2006)

*Alvinella Consortium : a large scale sequencing project at the french Genoscope.*

Lecompte, O., Poch, O., Bigot, Y., Cormier, P., Conti, E., Dietrich, J., Duchiron, F., Gaill, F., Higuete, D., Hourdez, S., Jollivet, D., Knoop, B., Lallier, F., Laullier, M., Leize-Wagner, E., Moras, D., Rees, J.-F., Vandorsselaer, A., Shillito, B., Thierry, J.-C. & Zal, F..

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.*

Lecompte O, Argentini M, Reyrat JM, Poch O, Van Dorsselaer A.

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.*

Lecompte O, Ripp R, Thierry JC, Moras M, Poch O.

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

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

Lecompte O.

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.*

Raffin JP, Henneke G, De Falco M, Lecompte O, Cambon M.A, Querellou J, Zieger M, Dupret D, Dietrich J.

Third Meeting on Extremophiles as Cell Factories (Graz, Austria, 1999)

*Cloning and expression of the PCNA from two hyperthermophilic archaea.*

Henneke G, Raffin JP, Lecompte O, Dietrich J.

26th FEBS Meeting (Nice, France, 1999)

*Complete genome sequencing of the hyperthermophilic Archaeon Pyrococcus abyssi.*

Heilig R, Barbe V, Duprat S, Robert C, Vico V, Petit JL, Wincker P, Brottier P, Lecompte O, Querellou J, Erauso G, Prieur D, Poch O, Thierry JC, Forterre P, Weissenbach J, Zivanovich Y, Saurin W.

THERMOPHILES '98 Conference (Brest, France, 1998)

*Génétique moléculaire du virus de la rage, un siècle après Pasteur.*

Tordo N., Poch O., Ermine A., Keith G. and Rougeon F. (1988)

in : *Molecular Biology and Infectious Diseases* (M. Scharz, ed.) Colloque International du Centenaire de l'Institut Pasteur. Elsevier. Paris: 31-40.

## Reviews

*SPINE bioinformatics and data-management aspects of high-throughput structural biology.*

Albeck S, Alzari P, Andreini C, Banci L, Berry IM, Bertini I, Cambillau C, Canard B, Carter L, Cohen SX, Diprose JM, Dym O, Esnouf RM, Felder C, Ferron F, Guillemot F, Hamer R, Ben Jelloul M, Laskowski RA, Laurent T, Longhi S, Lopez R, Luchinat C, Malet H, Mochel T, Morris RJ, Moulinier L, Oinn T, Pajon A, Peleg Y, Perrakis A, Poch O, Prilusky J, Rachedi A, Ripp R, Rosato A, Silman I, Stuart DI, Sussman JL, Thierry JC, Thompson JD, Thornton JM, Unger T, Vaughan B, Vranken W, Watson JD, Whamond G, Henrick K.

Acta Crystallogr D Biol Crystallogr. (2006) 62(Pt 10):1184-95.

*Multiple sequence alignment as a workbench for molecular systems biology.*

Thompson J.D. and Poch O.



Current Bioinformatics, (2005) 1: 95-104.

*Multiple alignment of complete sequences (MACS) in the post-genomic era.*

Lecompte O, Thompson J.D, Plewniak F, Thierry J.C, Poch O.

Gene. (2001) 270(1-2):17-30

*Functional and structural analysis of the subunits of human transcription factor TFIID.*

Davidson I., Romier C., Lavigne A.C., Birck C., Mengus G., Poch O. and Moras D. (1998)

Cold Spring Harbor Symposia on Quantitative Biology LXIII: 233-241.

*Evolution of negative-stranded RNA genomes.*

Tordo N., De Haan P., Goldbach R. and Poch O.

Seminars in Virology, (1992) 3(1): 341-357.

*Converting sequence block alignments into structural insights.*

Poch O. and Delarue M.

Methods Enzymol., (1996) 266: 662-680.

*One century latter...the rabies virus.*

Poch O., Tordo N., Ermine A., Keith G. and Rougeon F.

Bull. Acad. Natl. Med., (1987) 171(8): 1087-1094.

## **Book Chapters**

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

Hoan Nguyen, Julie D.Thompson, Patrick Schutz and Olivier Poch.

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).

*Strategies for efficient exploitation of the informational content of protein multiple alignments. in Sequence Alignment,*

Friedrich A., Poch O. and Moulinier L.

éd. M.S. Rosenberg (2009).

*New Challenges and Strategies for Multiple Sequence Alignment in the Proteomics Era.*

Thompson J.D. and Poch O.

The Proteomics Protocols Handbook, Humana Press, (2005) pp. 475-492.

*Sequence Alignment.*

Thompson J.D. and Poch O.

Nature Encyclopedia of the human genome, Nature Publishing Group, (2003)

*Multiple Alignment.*

Thompson J.D. and Poch O. (2003)

Nature Encyclopedia of the human genome, Nature Publishing Group, (2003)

*Structure of the rabies virus.*

Tordo N. and Poch O.

in : *Rabies* (Campbell J.B. and Charlton K.M., eds) Kluwer Academic Publishers: 25-45. (1988)



## Posters and Oral communications

*Type II DNA polymerase from Pyrococcus abyssi*

Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O, Querellou J, Weissenbach J, Saurin W, Heilig R, Flament D, Raffin JP, Henneke G, Gueguen Y, Rolland JL. (2002)

EP 1196583

*Genome Sequence and Polypeptides of Pyrococcus abyssi, fragment and uses thereof.*

Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O, Querellou J, Weissenbach J, Saurin W, Heilig R, Flament D, Raffin JP, Henneke G, Gueguen Y, Rolland JL. (2000)

WO 2000/0065062

## Other

*Bioinformatics: Targets and developments within the Strasbourg, Alsace and Lorraine Genopôle project.*

Poch O. and Thierry J.C. (2000)

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