Progress Report – Gertraud Burger
Appendix A

Publications in peer-reviewed journals
Period: Beginning of the grant to 08-31-2008

Marcantonio M, Trost M, **Courcelles M**, Desjardins M, Thibault P (2008) Combined enzymatic and data mining approaches for comprehensive phosphoproteome analyses: application to cell signaling events of interferon-gamma-stimulated macrophages. *Mol Cell Proteomics* **7**(4)**:** 645-660

Doyon FR, Zagryadskaya EI, Chen J, Steinberg SV (2004) Specific and non-specific purine trap in the T-loop of normal and suppressor tRNAs. *Journal of Molecular Biology* **343**(1)**:** 55-69

Hauth AM, Maier UG, Lang BF, Burger G (2005) The *Rhodomonas salina* mitochondrial genome: bacteria-like operons, compact gene arrangement and complex repeat region. *Nucleic Acids Res* **33**(14)**:** 4433-4442

Kannan S, Burger G (2008) Unassigned MURF1 of kinetoplastids codes for NADH dehydrogenase subunit 2. *BMC Genomics* 9(455)

Kannan S, **Hauth A**, Burger G (2008)
"Function prediction of hypothetical proteins without sequence similarity to proteins of known function." Prot Pept Let, in press (accepted April 2008)

Kotlova N, **Ishii TM**, Zagryadskaya EI, Steinberg SV (2007) Active suppressor tRNAs with a double helix between the D- and T-loops. *J Mol Biol* **373**(2)**:** 462-475

Kleinman CL, Rodrigue N, Bonnard C, Philippe H, Lartillot N (2006) A maximum likelihood framework for protein design. *BMC Bioinformatics* **7:** 326

Ladret V, Lessard S (2007) Fixation probability for a beneficial allele and a mutant strategy in a linear game under weak selection in a finite island model. *Theoretical Population Biology* **72:** 409-425

Lessard S, **Ladret V** (2007) The probability of fixation of a single mutant in an exchangeable selection model. *J Math Biol* **54**(5)**:** 721-744

Lajoie M, El-Mabrouk N (2005) Recovering haplotype structure through recombination and gene conversion. *Bioinformatics* **21 Suppl 2:** ii173-179

Lajoie M, Bertrand D, El-Mabrouk N, Gascuel O (2007) Duplication and inversion history of a tandemly repeated genes family. *J Comput Biol* **14**(4)**:** 462-478

Bertrand D, **Lajoie M**, El-Mabrouk N (2008) Inferring ancestral gene orders for a family of tandemly arrayed genes. *J Comput Biol* **15**(8)**:** 1063-1077

Brown KM, **Landry CR**, Hartl DL, Cavalieri D (2008) Cascading transcriptional effects of a naturally occurring frameshift mutation in *Saccharomyces cerevisiae*. *Mol Ecol* **17**(12)**:** 2985-2997

Lynch M, Sung W, Morris K, Coffey N, **Landry CR**, Dopman EB, Dickinson WJ, Okamoto K, Kulkarni S, Hartl DL, Thomas WK (2008) A genome-wide view of the spectrum of spontaneous mutations in yeast. *Proc Natl Acad Sci U S A* **105**(27)**:** 9272-9277

Tarassov K, Messier V, **Landry CR**, Radinovic S, Serna Molina MM, Shames I, Malitskaya Y, Vogel J, Bussey H, Michnick SW (2008) An in vivo map of the yeast protein interactome. *Science* **320**(5882)**:** 1465-1470

Landry CR, Aubin-Horth N (2007) Ecological annotation of genes and genomes through ecological genomics. *Mol Ecol* **16**(21)**:** 4419-4421

Landry CR, Castillo-Davis CI, Ogura A, Liu JS, Hartl DL (2007a) Systems-level analysis and evolution of the phototransduction network in *Drosophila*. *Proc Natl Acad Sci U S A* **104**(9)**:** 3283-3288

Landry CR, Hartl DL, Ranz JM (2007b) Genome clashes in hybrids: insights from gene expression. *Heredity* **99**(5)**:** 483-493

Landry CR, Lemos B, Rifkin SA, Dickinson WJ, Hartl DL (2007c) Genetic properties influencing the evolvability of gene expression. *Science* **317**(5834)**:** 118-121

Stefan E, Aquin S, Berger N, **Landry CR**, Nyfeler B, Bouvier M, Michnick SW (2007) Quantification of dynamic protein complexes using Renilla luciferase fragment complementation applied to protein kinase A activities in vivo. *Proc Natl Acad Sci U S A* **104**(43)**:** 16916-16921

Wang TT, Tavera-Mendoza LE, **Laperriere D**, Libby E, MacLeod NB, Nagai Y, Bourdeau V, Konstorum A, Lallemant B, Zhang R, Mader S, White JH (2005) Large-scale in silico and microarray-based identification of direct 1,25-dihydroxyvitamin D3 target genes. *Mol Endocrinol* **19**(11)**:** 2685-2695

Mongodin EF, Nelson KE, Daugherty S, Deboy RT, Wister J, Khouri H, Weidman J, Walsh DA, Papke RT, Sanchez Perez G, Sharma AK, Nesbo CL, MacLeod D, Bapteste E, Doolittle WF, Charlebois RL, **Legault BA**, Rodriguez-Valera F (2005) The genome of *Salinibacter ruber*: convergence and gene exchange among hyperhalophilic bacteria and archaea. *Proc Natl Acad Sci U S A* **102**(50)**:** 18147-18152

Legault BA, Lopez-Lopez A, Alba-Casado JC, Doolittle WF, Bolhuis H, Rodriguez-Valera F, Papke RT (2006) Environmental genomics of *Haloquadratum walsbyi* in a saltern crystallizer indicates a large pool of accessory genes in an otherwise coherent species. *BMC Genomics* **7:** 171

Zaballos M, Lopez-Lopez A, Ovreas L, Bartual SG, D'Auria G, Alba JC, **Legault BA**, Pushker R, Daae FL, Rodriguez-Valera F (2006) Comparison of prokaryotic diversity at offshore oceanic locations reveals a different microbiota in the Mediterranean Sea. *FEMS Microbiol Ecol* **56**(3)**:** 389-405

Mokdad A, Frankel AD (2008) ISFOLD: structure prediction of base pairs in non-helical RNA motifs from isostericity signatures in their sequence alignments. *J Biomol Struct Dyn* **25**(5)**:** 467-472

Sarver M, Zirbel CL, Stombaugh J, **Mokdad A**, Leontis NB (2008) FR3D: finding local and composite recurrent structural motifs in RNA 3D structures. *J Math Biol* **56**(1-2)**:** 215-252

Razga F, Koca J, **Mokdad A**, Sponer J (2007) Elastic properties of ribosomal RNA building blocks: molecular dynamics of the GTPase-associated center rRNA. *Nucleic Acids Res* **35**(12)**:** 4007-4017

Sponer JE, Reblova K, **Mokdad A**, Sychrovsky V, Leszczynski J, Sponer J (2007) Leading RNA tertiary interactions: structures, energies, and water insertion of A-minor and P-interactions. A quantum chemical view. *J Phys Chem B* **111**(30)**:** 9153-9164

Rodrigue N, Philippe H, Lartillot N (2008) Uniformization for sampling realizations of Markov processes: applications to Bayesian implementations of codon substitution models. *Bioinformatics* **24**(1)**:** 56-62

Rodrigue N, Philippe H, Lartillot N (2007) Exploring fast computational strategies for probabilistic phylogenetic analysis. *Syst Biol* **56**(5)**:** 711-726

Zhou Y, **Rodrigue N**, Lartillot N, Philippe H (2007) Evaluation of the models handling heterotachy in phylogenetic inference. *BMC Evol Biol* **7:** 206

Rodrigue N, Philippe H, Lartillot N (2006) Assessing site-interdependent phylogenetic models of sequence evolution. *Mol Biol Evol* **23**(9)**:** 1762-1775

Rodriguez-Ezpeleta N, Brinkmann H, **Roure B**, Lartillot N, Lang BF, Philippe H (2007) Detecting and overcoming systematic errors in genome-scale phylogenies. *Syst Biol* **56**(3)**:** 389-399

Roure B, Rodriguez-Ezpeleta N, Philippe H (2007) SCaFoS: a tool for selection, concatenation and fusion of sequences for phylogenomics. *BMC Evol Biol* **7 Suppl 1:** S2

Rodriguez-Ezpeleta N, Brinkmann H, Burey SC, **Roure B**, Burger G, Loffelhardt W, Bohnert HJ, Philippe H, Lang BF (2005) Monophyly of primary photosynthetic eukaryotes: green plants, red algae, and glaucophytes. *Current Biology* **15**(14)**:** 1325-1330

Shen YQ, Burger G (2007) "Unite and conquer": enhanced prediction of protein subcellular localization by integrating multiple specialized tools. *BMC Bioinformatics* **8**(420)

Shen YQ (2008) Plasticity of a key metabolic pathway in fungi. *Funct Integr Genomics*

Invited conferences presentations and conference contributions
Period: 09-01-2007 to 08-31-2008

Abd-Rabbo D, Abaji C, Filali-Mouhim A, Arous C, Portelance L, Escobar Espinoza DE, Cloutier S, Tonin PN, Provencher DM, Mes-Masson AM, Maugard CM (2008). Relation between transcriptome and genotype in non-tumoral ovarian surface epithelial cells from women carriers of a BRCA 1/2 mutation (poster). *Fourth Canadian Conference on Ovarian Cancer Research* May 5, 2008; Hôtel Delta, Montréal, Québec.

Abd-Rabbo D, Abaji C, Filali-Mouhim A, Arous C, Portelance L, Escobar Espinoza DE, Cloutier S, Tonin PN, Provencher DM, Mes-Masson AM, Maugard CM (2008). Identification des profils d'expression associés à une mutation de l'un des gènes BRCA1 et BRCA2 dans les cellules non-tumorales de l'épithélium de surface de l'ovaire. April 15, 2008; Institut du cancer de Montréal.

Abd-Rabbo D, Abaji C, Filali-Mouhim A, Arous C, Portelance L, Escobar Espinoza DE, Cloutier S, Tonin PN, Provencher DM, Mes-Masson AM, Maugard CM (2008). Relation entre transcriptome et génotype dans les tissus normaux des hétérozygotes pour une mutation des gènes BRCA. *Dix-huitième journée scientifique de l'Institut du Cancer de Montréal*; February 22, 2008; Montréal, Québec.

Abd-Rabbo D, Abaji C, Filali-Mouhim A, Arous C, Portelance L, Escobar Espinoza DE, Cloutier S, Tonin PN, Provencher DM, Mes-Masson AM, Maugard CM (2007). Relation entre transcriptome et génotype dans les tissus normaux des hétérozygotes pour une mutation des gènes BRCA (poster). *Dixième congrès annuel des étudiants stagiaires et résidents du Centre de recherche du CHUM*; December 8, 2007; Montréal, Québec.

Abd-Rabbo D, Abaji C, Filali-Mouhim A, Arous C, Portelance L, Escobar Espinoza DE, Cloutier S, Tonin PN, Provencher DM, Mes-Masson AM, Maugard CM (2007). Relation entre transcriptome et génotype dans les tissus normaux des hétérozygotes pour une mutation des gènes BRCA (poster). *Robert Cedergren Bioinformatics Colloquium*; November 8, 2007; Université de Montréal.

Bachand P (2005). Pour le projet SOCLe, Système intégré de validation UML/OCL. *OCTAS 2005 - Relève universitaire*; École Polytechnique de Montréal.

Boulay F (2005). tRNA conformity at atomic level (poster). *Scientific Meeting Louis-Philippe Bouthillier*; June 10-11, 2005; Manoir Saint-Sauveur.

Chen JH (2006). Sliding between RNA helical elements revealed by a molecular dynamics simulation study (poster). *Robert Cedergren Bioinformatics Colloquium*; November 14-15, 2006; Université de Montréal, Montréal, Québec.

Gagnon M, Mukhopadhyay A, Butorin Y, **Chen J**, Chteinberg S (2005). A new type of Structural compensation in ribosomal RNA. *Tenth Annual Meeting of the RNA Society*; Banff, Alberta, Canada.

Chen JG, M. Chteinberg, S. (2005). A large Scale Conformational Changes in the Ribosome. *Nineteenth Vassar Workshop* June 17-19, 2005; Amberst, USA.

Chen J, Gagnon M, Chteinberg S (2005). A signal Transduction Pathway in the Ribosome. *Scientific Meeting Louis-Philippe Bouthillier*; June 10-11, 2005; Manoir Saint-Sauveur.

Chen JG, MG. Chteinberg SV (2004). Studies of Molecular Mechanisms of Internal Dynamics in the Ribosome (poster). *Robert Cedergren Bioinformatics Colloquium*; September 23-24, 2004.

Gagnon M, Mukhopadhyay A, Butorin Y, **Chen J**, Chteinberg S (2004). Sequence Perturbations of the Along-Groove Packing Motif within the Ribosome (poster). *Eleventh Annual Meeting of the RNA Society*; June 20-25, 2004; Seattle, Washington, USA.

Christin S (2005). Recherche de snoRNAs de type boîte C/D en corrélation avec le signal de reconnaissance de l'enzyme Rnt1p. *Réunion de bio-informatique comparative et intégrative* June 6-7, 2005; Mont-Orford, Québec.

Courcelles M (2008). MSdatabase: A novel proteomics and phosphoproteomics analysis platform (poster). *ISBM - ProtoeConnections: an analysis platform to accelerate proteomes and phosphoproteomes exploration*; Toronto, Ontario.

Courcelles M (2008). ProteoConnections: an analysis platform to accelerate proteomes and phosphoproteomes exploration. *Protéomique, Bio-informatique et biologie des systèmes*; Université Laval, Québec.

Fortier M, Caron E, **Courcelles M**, Perreault P, Thibeault P (2008). The mTOR signaling pathway and its influence on the MHC Class I peptide repertoire. *ASMS Denver*; Denver, Colorado, USA.

Gharib M, **Courcelles M**, Verreault A, Thibault P (2008). Silver staining-induced sulfonation: an obstacle in the identification of genuine protein phosphorylation. *ASMS Denver*; Denver Colorado, USA.

Trost M, Marcantonio M, **Courcelles M**, Desjardins M, Thibault P (2007). System-biology analysis of Interferon-ψ activated mouse macrophages: from the cytosol to the phagosome (poster). *ASMS 2007*; Denver, Colorado.

Courcelles M (2007). MSdatabase: A novel proteomics and phosphoproteomics analysis platform. *Robert Cedergren Bioinformatics Colloquium*; Université de Montréal.

Courcelles M (2007). Phosphoproteome data mining: tools and challenges. *Progress Report IRIC*; April 13, 2007; IRIC, Montréal.

Darmon D (2005). Profiles of Mutation Density in DNA: Comparison of the human and chimpanzee genomes. *Meeting of Comparative and Integrative Bioinformatics* June 6-7, 2005; Hôtel Chéribourg.

Darmon D (2005). Profiles of Mutation Density in DNA: Comparison of the human and chimpanzee genome (poster). *XXe congrès annuel de la recherche des étudiants gradués et post-gradués*; June 3, 2005; Centre de recherche, Hôpital Sainte-Justine.

Doyon F (2005). RNA: Shape and Function. *Scientific Meeting Louis-Philippe Bouthillier*; June, 2005; Saint-Sauveur-des-Monts, Québec.

Doyon F (2004). How tRNA keeps Its L-shape? (oral and poster). *Ninth Annual meeting of the RNA society*; June, 2004; Madison, WI, USA.

Doyon F (2004). Structural interactions between the D and the T-loops in tRNA: How does it keep its L-shape? *Vassar RNA Meeting*; June, 2004; Boston, MA, USA.

Doyon F (2003). Structural Diversity in Normal and Suppressor tRNAs. *Ribo-club Meeting* November, 2003; Sherbrooke, Québec.

Doyon F (2003). Specific and Non-specific Purine Trap in the T-loop of Normal and Suppressor tRNAs (oral and poster). *Twentieth International tRNA Workshop* October, 2003; Banz, Germany.

Duchesne J (2004). Approximate matching of RNA secondary structure. *Robert Cedergren Bioinformatics Colloquium*; September 23-24, 2004.

Duchesne J (2004). Recherche approchée de motifs de la structure secondaire de l'ARN. *ACFAS 2004*; May 10-14, 2004; Université du Québec à Trois-Rivières, Trois-Rivières, Québec.

Dupuis L, Mousseau N (2008). A holographic multi-scale approach for simulation of protein flexibility (poster). *Symposium annuel 2008: Les bases moléculaires et génétiques des arythmies cardiaques*; Université de Montréal, Montréal, Québec.

Dupuis L (2007). Multiscale simulations of protein flexibility (oral and poster). *Robert Cedergren Bioinformatics Colloquium*; November 17, 2007; Université de Montréal, Montréal, Québec.

Dupuis L, Mousseau N, Derreumaux P (2007). Finding pathways at different reality levels in simulations of Protein Flexibility (poster). *Réunion annuelle du Réseau québécois des matériaux de pointe*; Centre Mont-Royal, Montréal, Québec.

Dupuis L, Mousseau N, Derreumaux P (2007). Finding pathways at different reality levels in simulations of Protein Flexibility (poster). *Annual meeting of Réseau québécois des matériaux de pointe*; May 14, 2007; Centre Mont-Royal, Montréal, Québec.

Dupuis L (2007). Pivots and flexibility in proteins. *Flexweb - Analysis of Flexibility in Biomolecules and Networks*; April 12, 2007; From Université de Montréal to Arizona State University.

Dupuis L (2007). Multiscale simulations of protein flexibility (oral and poster). *Workshop on Dynamics under constraint II*; February 15, 2007; Bellairs Research Institute of McGill University, Holetown, Barbados.

Dupuis L (2006). Simulations multi-échelle de la flexibilité des protéines. *Robert Cedergren Bioinformatics Colloquium*; November 14-15, 2006; Université de Montréal, Montréal, Québec.

Dupuis L, Mousseau N, Derreumaux P (2006). Simulations of protein flexibility (poster). *Colloque provincial du Réseau québécois des matériaux de pointe* August 3, 2006; Hôtel Chéribourg, Magog, Québec.

Dupuis L, Mousseau N, Derreumaux P (2006). Simulations of protein flexibility (poster). *Ecole d'été du Réseau québécois des matériaux de pointe*; Hôtel Chéribourg, Magog, Québec.

Dupuis L, Mousseau N, Derreumaux P (2006). Simulations of protein flexibility (poster). *Rigidity, Flexibility, and Motion in Biomolecules workshop*; May 15, 2006; Fiesta Inn Resort, Tempe, Arizona, USA.

Hauth AM (2005). Automating contiguous and non-contiguous repetition in genomic sequences (poster). *Fourth European Conference on Computational Biology*; September 28-October 1, 2005; Madrid, Spain.

Hauth AM (2005). Complex repetition in mitochondrial genomes (poster). *Annual Meeting of the CIAR Evolutionary Biology Program*; September 15-19, 2005; Parksville, British Columbia, Canada.

Hauth AM (2005). Analysis of complex repetition in genomes. *Conference of Department of Biochemistry and Microbiology*; September 13, 2005; University of Victoria, British Columbia, Canada.

Hauth AM (2004). *Rhodomonas salina*: Analysis of structure and history of complex repetitive genome regions (poster). *Annual Meeting of the CIAR Evolutionary Biology Program*; October 13-17, 2004; Pine Hill, Québec.

Hauth AM, Burger G, Lang BF (2004). Towards automated analysis of complex repetition in genomes (oral and poster). *Robert Cedergren Bioinformatics Colloquium*; September 23-24, 2004; Université de Montréal, Montréal, Québec.

Hauth AM, Burger G, Lang BF (2004). Analysis of structure and history of complex repetitive genome regions. *Twelfth International Conference on Intelligent Systems for Molecular Biology (poster)*; July 31-August 4, 2004; Glasgow, Scotland, United Kingdom.

Hussin J, Lefebvre JF, **Nadeau P**, Labuda D (2008). Haplotype allelic classes in the lactase persistence locus. *Retraite du centre de recherche de Ste-Justine*; Sainte-Adèle, Québec.

Hussin J, Lefebvre JF, **Nadeau P**, Labuda D (2008). Haplotype allelic classes in the lactase persistence locus (poster). *Biology of genomes - CSHL*; New York, USA.

Hussin J, Lefebvre JF, **Nadeau P**, Labuda D (2008). Haplotype allelic classes in the lactase persistence locus (poster). *Journées génétiques 2008*; Québec.

Hussin J, Labuda D (2007). Recombinaison méiotique et structure du génome humain (poster). *Robert Cedergren Bioinformatics Colloquium*; November 8-9, 2007; Université de Montréal, Montréal, Québec.

Hussin J, Lefebvre JF, Labuda D (2007). Signatures génomiques de sélection (oral presentation). *Robert Cedergren Bioinformatics Colloquium*; November 8-9, 2007; Université de Montréal, Montréal, Québec.

Ishii T (2006). Selenocysteine tRNA (tRNAsec) delivers a rare amino acid selenocysteine in response to a UGA stop codon and a certain downstream stem loop signal in mRNA (poster). *Robert Cedergren Bioinformatics Colloquium*; November 14-15, 2006; Université de Montréal, Montréal, Québec.

Ishii T, Chteinberg S (2006). General Constraints imposed of the Structure of the Bacterial elenocysteine tRNA as deduced from in vivo selection from Combinatorial Gene Libraries (poster). *The RNA Society 2006 Annual Meeting*; June 20-25, 2006; University of Washington, Seattle, Washington.

Ishii T, Chteinberg S (2005). General constraints imposed on the structure of the *E.coli* selenocysteine tRNA in vivo. *Scientific Meeting Louis-Philippe Bouthillier*; June 2005; Saint-Sauveur-des-Monts, Québec.

Ishii T, Chteinberg S (2004). Determining the necessary and sufficient nucleotide requirements for *E. coli* Selenocysteine tRNA for structure and function (poster). *Robert Cedergren Bioinformatics Colloquium*; September 23-24, 2004; Université de Montréal, Montréal, Québec.

Kannan S (2006). Protein Function Annotation using Data Mining Algorithms. *Robert Cedergren Bioinformatics Colloquium*; November 2-4, 2006; Université de Montréal, Montréal, Québec.

Kannan S, Burger G (2006). Evaluating ORF Function Predictions Using Domain-specific Knowledge (poster). *Eleventh International Conference on Intelligent Systems for Molecular Biology (ISMB 2006)*; August 6-11, 2006; Fortaleza, Brazil.

Kannan S (2006). Protein Function Annotation using Data Mining Algorithms (poster). *First Robert Cedergren Centre Retreat*; June 17-18, 2006; Station de biologie des Laurentides de l'Université de Montréal, St-Hypolyte, Québec.

Kannan S (2005). Proteins Function Annotation using Data Mining Algorithms. *Robert Cedergren Bioinformatics Colloquium*; November 2-4, 2005; Université de Montréal, Montréal, Québec.

Kannan S, Burger G (2005). Data Rich But information Poor: Applying Data Mining for Protein Function Annotation (poster). *Thirteenth Annual International Conference on Intelligent Systems for Molecular Biology (ISBM 2005)*; June 25-29, 2005; Michigan, USA.

Kannan S (2005). Protein Function Annotation / What is Astrobioinformatics? *Astrobiology and the Origins of Life Conference and Workshop*; May 24-June 4, 2005; McMaster University, Hamilton, Ontario.

Kannan S, Burger G (2004). Gene Function Annotation: A Predictive Data Mining Approach (poster). *Annual Meeting of the Canadian Institute for Advanced Research (CIAR) Evolutionary Biology Program*; October 13-17, 2004; Hôtel du Lac Carling, Québec, Québec.

Kannan S, Burger G (2004). Gene Function Annotation: A Predictive Data Mining Approach (poster). *Robert Cedergren Bioinformatics Colloquium*; September 23-24, 2004; Université de Montréal, Montréal, Québec.

Kannan S (2003). Gene Function Annotation: A predictive Data Mining Approach. *Sixth Annual Chemistry and Biochemistry Graduate Research Conference (CBGRC 2003)*; November 14-15, 2003; Concordia University, Montréal, Québec.

Kannan S, Burger G (2003). Gene Function Annotation: A predictive Data Mining Approach (poster). *MITACS Quebec Interchange*; November 13-14, 2003; Centre Mont-Royal and McGill University, Montréal, Québec.

Kannan S, Burger G (2003). Gene Function Annotation: A Predictive Data Mining Approach (poster). *HUPO Second annual and IUBMB XIX Joint World Congress*; October 8-11, 2003; Montréal, Québec.

Kleinman CL, Rodrigue N, Philippe H, Lartillot N (2007). Protein structure and sequence evolution: statistical potentials for phylogeny. *Society for Molecular Biology and Evolution*; December 6-8, 2007; Halifax, Nova-Scotia.

Kleinman CL, Bonnard C, **Rodrigue N**, Philippe H, Lartillot N (2006). Statistical potentials for phylogeny and protein design (oral and poster). *Robert Cedergren Bioinformatics Colloquium*; November 14-15, 2006; Université de Montréal, Montréal, Québec.

Kleinman CL (2006). Statistical potentials for computational protein design. *Seminaires de Cience et Technologie*; August, 2006; Universidad Nacional de Quilmes, Argentina.

Kleinman CL (2006). Statistical potentials for computational protein design. August, 2006; Instituto Leloir, Buenos Aires, Argentina.

Kleinman CL, Bonnard C, **Rodrigue N**, Burger G, Philippe H, Lartillot N (2006). Protein structure and sequence evolution: devising statistical potentials for phylogenetic analysis (poster). *First Robert Cedergren Centre Retreat*; 2006; Station de biologie des Laurentides, Saint-Hypolyte, Québec.

Kleinman CL, Bonnard C, **Rodrigue N**, Burger G, Philippe H, Lartillot N (2006). Statistical potentials for phylogeny and protein design. *Conference Simon-Pierre Noel 2006*; Department of Biochemistry, Université de Montréal, Montréal, Québec.

Kleinman CL, Bonnard C, **Rodrigue N**, Philippe H, Lartillot N (2006). Potentiels statistiques pour le design de protéines. *Soixante-quatorzième congrès annuel de l'ACFAS*; 2006; Montréal, Québec.

Kleinman CL, **Rodrigue N**, Bonnard C, Burger G, Philippe H, Lartillot N (2006). Protein structure and sequence evolution: devising statistical potentials for phylogenetics (poster). *Phylogenomics Conference*; March 15-19, 2006; Sainte-Adèle, Québec.

Kleinman CL (2006). Statistical potentials for phylogeny and protein design. January, 2006; Instituto de Quimica y Fisicoquimica Biologicas (IQUIFIB), Universidad de Buenos Aires, Argentina.

Kleinman CL, Bonnard C, **Rodrigue N**, Burger G, Philippe H, Lartillot N (2005). Protein structure and sequence evolution: devising statistical potentials for phylogenetic analysis (poster). *Robert Cedergren Bioinformatics Colloquium*; November 2-4, 2005; Université de Montréal, Montréal, Québec.

Kleinman CL, Bonnard C, **Rodrigue N**, Burger G, Philippe H, Lartillot N (2005). Protein structure and sequence evolution: devising statistical potentials for phylogenetic analysis. *Scientific Meeting Louis-Philippe Bouthillier*; 2005; Saint-Sauveur, Québec.

Kleinman CL, Burger G (2004). *In silico* approaches to RNA editing. *International Conference on Intelligent Systems for Molecular Biology / Third European Conference in Computational Biology (ISMB/EEEC)*; 2004; Scotland, United Kingdom.

Kleinman CL, Burger G (2004). *In silico* approaches to RNA editing in plant mitochondria (poster). *Robert Cedergren Bioinformatics Colloquium*; September 23-24, 2004; Université de Montréal, Montréal, Québec.

Ladret V (2008). Jeux évolutionnaires et évolution de la coopération en population finie subdivisée. *Journée Modélisation Aléatoire et Statistique (MAS) - Session gènes, individus, populations*; August 27, 2008; Rennes, France.

Ladret V (2008). Jeux évolutionnaires dans le modèle de l'île à nombre fini de colonies et évolution de la coopération. *Seminar of Mathematics and Statistics Department*; April 29, 2008; Département de Mathématiques et de statistiques, Université Montpellier 2.

Ladret V (2007). Probabilité de fixation pour un allèle bénéfique et une stratégie mutante dans un jeu linéaire pour le modèle de l'île à nombre fini de colonies sous sélection fiable. *Department of Mathematics & Statistics Seminar*; November 29, 2007; Université de Sherbrooke, Sherbrooke, Québec.

Ladret V (2007). Statistical properties of allelic haplotype classes and statistical tests of natural selection. *Robert Cedergren Bioinformatics Colloquium*; November 8-9, 2007; Université de Montréal, Montréal, Québec.

Ladret V (2007). Une approche par coalescence pour le calcul de la probabilité de fixation d'un allèle mutant en population finie subdivisée avec schéma de sélection de type jeu linéaire (poster). *Symposium on game theory in an ecological context*; August 21, 2007; Uppsala, Sweden.

Lajoie M (2007). Evolution of tandemly arrayed genes in multiple species. *Robert Cedergren Bioinformatics Colloquium*; November 8-9, 2007; Université de Montréal, Montréal, Québec.

Lajoie M (2007). Evolution of tandemly arrayed genes in multiple species. *Fifth Annual RECOMB Satellite Workshop on Comparative Genomics (2007)*; September 16-18, 2007; University of California, San Diego, USA.

Lajoie M (2006). Repeated Tandem. *Robert Cedergren Bioinformatics Colloquium*; November 14-15, 2006; Université de Montréal, Montréal, Québec.

Lajoie M (2006). Evolution of Tandemly Repeated Sequences through Duplication and Inversion. *Fourth RECOMB Comparative Genomics Satellite Workshop* September 24-26, 2006; Montréal, Québec.

Bertrand DL, **Lajoie M.** El-Mabrouk N, Gascuel O. (2006). Evolution of Tandemly Repeated Sequences through Duplication and Inversion. *Fourth RECOMB Comparative Genomics Satellite Workshop LNCS/LNBI*.

Lajoie M (2005). Estimation des taux de conversion génique à partir des haplotypes (poster). *Robert Cedergren Bioinformatics Colloquium*; November 2-4, 2005; Université de Montréal, Montréal, Québec.

Lajoie M (2005). Recovering haplotype structure through recombination and gene conversion. *Fourth European Conference on Computational Biology*; September 28-October 1, 2005; Madrid, Spain.

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