

List of publications

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1 Patents (5)

5. A. David, C. Hirtz, **E. Rivals**, *Method for characterising a tumour* international patent n. WO/2023/006588, published 02.02.2023.
4. L. Bauchet, A. David, C. Hirtz, S. Relier, **E. Rivals**, *Procédé d'évaluation du degré de malignité d'une tumeur gliale*, demande nationale n° 2108279 déposée à l'INPI par le CHU Montpellier le 29/07/2021.
3. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, P. Prorok, *Purification process of nascent DNA*, patent n° US 2019 / 0093149, March 28th 2019.
2. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, P. Prorok, *Purification process of nascent DNA*, patent n° US 20150267208 (2015).
1. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, *Purification process of nascent DNA*, patent n° US 61/238 315 (2011) and European patent EP2473623 (2012).

2 International journals (66 + 7)

66. **E. Rivals**, M. Sweering, P. Wang *Convergence of the Number of Period Sets in Strings*, *Algorithmica*, vol. 86(2), pp. 1-22, doi: [10.1007/s00453-025-01295-y](https://doi.org/10.1007/s00453-025-01295-y), 2025.
65. L. Dutrieux, S. Ovejero, A. Guillemin, L. Zellagui, E. De Bruyne, C. Muylaert, L. Van Hemelrijck, Y.-L. Lin, E. Loughran, A. Choquet, T. Magat, S. Bouchouika, C. Bret, G. Requirand, N. Robert, L. Vincent, G. Cartron, C. Herbaux, R. Rodriguez, M. Cogne, **E. Rivals**, J.-C. Andrau, A. David, P. Pasero, J. Moreaux, *Targeting Transcription-Replication Conflicts using G-quadruplexes stabilizers in Multiple Myeloma, Blood Neoplasia*, 100072, online, [10.1016/j.bneo.2025.100072](https://doi.org/10.1016/j.bneo.2025.100072), 2025
64. A. Amalric, A. Attina, A. Bastide, S. Mateus, C. Planque, **E. Rivals**, C. Hirtz, A. David. *Mass Spectrometry-Based Pipeline for Identifying RNA Modifications Involved in a Functional Process: Application to Cancer Cell Adaptation* *Analytical Chemistry*, 96(5):1825–1833, doi:[10.1021/acs.analchem.3c02635](https://doi.org/10.1021/acs.analchem.3c02635), 2024.
63. N. Romashchenko, B. Linard, **E. Rivals**, F. Pardi. *Computing Phylo- k-Mers*. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, in press May 19;PP. doi:[10.1109/TCBB.2023.3278049](https://doi.org/10.1109/TCBB.2023.3278049), 2023.
62. M. Mille, J. Ripoll, B. Cazaux, **E. Rivals**. *dipwmsearch: a Python package for searching di-PWM motifs*. *Bioinformatics*, 39(4):btad141, doi:[10.1093/bioinformatics/btad141](https://doi.org/10.1093/bioinformatics/btad141), 2023.
61. L. Sauer, R. Canovas, DB. Roche, H. Shams-Eldin, P. Ravel, J. Colinge, R. Schwarz, C. Ben Mamoun, **E. Rivals**, E. Cornillot. *FT-GPI, a highly sensitive and accurate predictor of GPI-anchored proteins*, *Malaria Journal*, 22(1):27. doi: [10.1186/s12936-022-04430-0](https://doi.org/10.1186/s12936-022-04430-0), 2023.

60. S. Relier, A. Amalric, A. Attina, IB. Koumare, V. Rigau, F. Burel Vandebos, D. Fontaine, M. Baroncini, JP. Hugnot, H. Duffau, L. Bauchet, C. Hirtz, **E. Rivals**, A. David. *Multivariate Analysis of RNA Chemistry Marks Uncovers Epitranscriptomics-Based Biomarker Signature for Adult Diffuse Glioma Diagnostics* *Analytical Chemistry*, 94(35):11967-11972, doi: [10.1021/acs.analchem.2c01526](https://doi.org/10.1021/acs.analchem.2c01526), 2022.
59. G. Therizols, Z. Bash-Imam, B. Panthu, C. Machon, A. Vincent, J. Ripoll, S. Nait-Slimane, M. Chalabi-Dchar, A. Gaucherot, M. Garcia, F. LaforÃats, V. Marcel, J. Boubaker-Vitre, MA. Monet, C. Bouclier, C. Vanbelle, G. Souahlia, E. Berthel, MA. Albaret, HC. Mertani, M. Prudhomme, M. Bertrand, A. David, JC. Saurin, P. Bouvet, **E. Rivals**, T. Ohlmann, J. Guitton, N. Dalla Venezia, J. Pannequin, F. Catez, JJ. Diaz. *Alteration of ribosome function upon 5-fluorouracil treatment favors cancer cell drug-tolerance* *Nature Communications* 13(1), p. 173 doi: [10.1038/s41467-021-27847-8](https://doi.org/10.1038/s41467-021-27847-8), 2022.
58. S. Relier, **E. Rivals**, A. David. *The multifaceted functions of the Fat mass and Obesity-associated protein (FTO) in normal and cancer cells* *submitted RNA Biology* 19(1), p. 132-142, doi: [10.1080/15476286.2021.2016203](https://doi.org/10.1080/15476286.2021.2016203), 2022.
57. S. Relier, J. Ripoll, H. Guillorit, A. Amalric, F. BoissiÃre, J. Vialaret, A. Attina, F. Debart, A. Choquet, F. Macari, V. Marchand, Y. Motorin, E. Samalin, J.-J. Vasseur, J. Pannequin, F. Aguilo, E. Crapez, C. Hirtz, **E. Rivals**, A. Bastide, A. David *FTO-mediated cytoplasmic m6Am demethylation adjusts stem-like properties in colorectal cancer cell* *Nature Communications* 12, p. 1716 doi: [10.1038/s41467-021-21758-4](https://doi.org/10.1038/s41467-021-21758-4), 2021.
56. G.E. Scholz, B. Linard, N. Romashchenko, **E. Rivals**, F. Pardi. *Rapid screening and detection of inter-type viral recombinants using phylo-k-mers* *Bioinformatics*, btaa1020; doi: [10.1093/bioinformatics/btaa1020](https://doi.org/10.1093/bioinformatics/btaa1020), 2020.
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54. B. Cazaux, **E. Rivals**, *Hierarchical Overlap Graph*, *Information Processing Letters* 155, doi: [10.1016/j.ipl.2019.105862](https://doi.org/10.1016/j.ipl.2019.105862), 2020.
53. Oldfield AJ, Henriques T, Kumar D, Burkholder AB, Cinghu S, Paulet D, Bennett BD, Yang P, Scruggs BS, Laverder CA, **Rivals E**, Adelman K, Jothi R. *NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region*. *Nature Communications* Jul 11;10(1):3072. doi: [10.1038/s41467-019-10905-7](https://doi.org/10.1038/s41467-019-10905-7), 2019.
52. B. Cazaux, G. Castel, **E. Rivals**, *AquaPony: visualization and interpretation of phylogeographic information on phylogenetic trees*, *Bioinformatics* 35 (17), 3163-3165, btz011, doi: [10.1093/bioinformatics/btz011](https://doi.org/10.1093/bioinformatics/btz011), 2019.
51. B. Cazaux, T. Lecroq, **E. Rivals**, *Linking indexing data structures to de Bruijn Graphs: construction and update*, *J. of Computer and System Sciences* 104: 165-183, doi: [10.1016/j.jcss.2016.06.008](https://doi.org/10.1016/j.jcss.2016.06.008), 2019.
50. T. Marschall, M. Marz, . . . , **E. Rivals**, . . . et al., *Computational Pan-Genomics: Status, Promises and Challenges*, *Briefings in Bioinformatics*, doi: [10.1093/bib/bbw089](https://doi.org/10.1093/bib/bbw089), (online 2016), Vol 19(1), p. 118-135, 2018.
49. B. Cazaux, **E. Rivals**, *Relationship between superstring and compression measures: new insights on the greedy conjecture*, *Discrete Applied Mathematics* doi: [10.1016/j.dam.2017.04.017](https://doi.org/10.1016/j.dam.2017.04.017), Vol. 245, p. 59-64, 2018.
48. A. Diwedi, C. Reynes, A. Kuehn, DB. Roche, N. Khim, M. Hebrard, S. Milanese, **E. Rivals**, R. Frutos, D. Menard, CB. Mamoun, J. Colinge, E. Cornillot, *Functional analysis of Plasmodium falciparum subpopulations associated with artemisinin resistance in Cambodia*, *Malaria Journal* 16:493, DOI: [10.1186/s12936-017-2140-1](https://doi.org/10.1186/s12936-017-2140-1) 2017.
47. X. Argout, G. Martin, G. Droc, O. Fouet, K. Labadie, **E. Rivals**, J.M. Aury, C. Lanaud, *The cacao Criollo genome v2.0: an improved version of the genome for genetic and functional genomic studies*, *BMC Genomics* 18:730, DOI: [10.1186/s12864-017-4120-9](https://doi.org/10.1186/s12864-017-4120-9) 2017.
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44. D. Paulet, A. David, **E. Rivals**, *Ribo-seq enlightens Codon Usage Bias*, *DNA Research* dsw062. doi: 10.1093/dnares/dsw062, 2017.
43. A. Limasset, B. Cazaux, **E. Rivals**, P. Peterlongo, *Read mapping on de Bruijn Graphs*, *BMC Bioinformatics* doi:10.1186/s12859-016-1103-9, 17:237, 2016.
42. L. Salmela, R. Walve, **E. Rivals**, E. Ukkonen, *Accurate selfcorrection of errors in long reads using de Bruijn graphs*, *Bioinformatics*, (online 2016) doi: 10.1093/bioinformatics/btw321, 33 (6): 799-806, 2017.
41. B. Cazaux, **E. Rivals**, *A linear time algorithm for shortest cyclic cover of strings* doi: 10.1016/j.jda.2016.05.001, *Journal of Discrete Algorithms*, vol. 37, p. 56–67, 2016.
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39. B. Cazaux, **E. Rivals**, *The power of greedy algorithms for approximating Max-ATSP, Cyclic Cover, and superstrings* doi:10.1016/j.dam.2015.06.003, PSC 2014 Special Issue, online in 2015 *Discrete Applied Mathematics*, Vol. 212, p. 48–60, 2016.
38. R. Uricaru, C. Michotey, H. Chiapello, **E. Rivals**, *YOC, a new strategy for pairwise alignment of collinear genomes*, *BMC Bioinformatics*, doi:10.1186/s12859-015-0530-3, 16:111, 2015.
37. C. Keyser, C. Hollard, A. Gonzalez, L. Fausser, **E. Rivals**, A. Alexeev, A. Riberon, E. CrubÃ©zy, B. Ludes, *The ancient Yakuts: a population genetic enigma*, in press *Philosophical Transactions of the Royal Society series B*, doi: 10.1098/rstb.2013.0385, Jan 19;370(1660), 2015.
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33. J. Buard, **E. Rivals**, D. Dunoyer de Segonzac, C. Garres, P. Caminade, B. de Massy, P. Boursot, *Diversity of Prdm9 ZnF array in wild mice unravels new facets of the evolutionary turnover of this coding minisatellite*, *PLOS One* doi: 10.1371/journal.pone.0085021, 2014.
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30. **E. Rivals**, N. Philippe, M. Salson, M. LÃ©onard, T. Commes, T. Lecroq, *A Scalable Indexing Solution to Mine Huge Genomic Sequence Collections*, *ERCIM News*, 89, p. 20-21, 2012.
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26. A. Mancheron, R. Uricaru, **E. Rivals**, *An Alternative Approach to Multiple Genome Comparison*, *Nucleic Acids Research*, Vol. 39, No. 15, p. e101, 2011.
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23. S. Leclercq, **E. Rivals**, P. Jarne, *DNA slippage occurs at microsatellite loci without minimal threshold length in humans : a comparative genomic approach*, *Genome Biology & Evolution*, vol. 2, p. 325-335, 2010.
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12. F. Nicolas, **E. Rivals**, *Hardness Results for the Center and Median String Problems under the Weighted and Unweighted Edit Distances*, *J. of Discrete Algorithms*, 3(2-4), p. 390-415, 2005.
11. O. Delgrange, **E. Rivals**, *STAR: an algorithm to Search for Tandem Approximate Repeats*, *Bioinformatics*, Vol. 20, No. 16, p. 2812-2820, 2004.
10. **E. Rivals**, *A Survey on Algorithmic Aspects of Tandem Repeat Evolution*, *International Journal on Foundations of Computer Science*, Vol. 15, No. 2, p. 225-257, 2004.
9. **E. Rivals**, S. Rahmann, *Combinatorics of Periods in Strings*, *J. of Combinatorial Theory series A*, 104(1), p. 95-113, 2003.
8. S. Rahmann, **E. Rivals**, *On the Distribution of the Number of Missing Words in Random Texts*, *Combinatorics, Probability and Computing*, p. 73-87, vol. 12, 2003.

7. S. Bérard, **E. Rivals**, *Comparison of Minisatellites*, *J. of Computational Biology*, p. 357-372, vol. 10(3-4), 2003.
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5. J.-S. Varrault, J.-P. Delahaye, **E. Rivals**, *The Transformation Distance: a Dissimilarity Measure Based on Movements of Segments*, *Bioinformatics*, p. 194-202, vol. 15(3), 1999.
4. E. Bornberg-Bauer, **E. Rivals**, M. Vingron, *Strategies for Identifying Leucine Zippers*, *Nucleic Acids Research*, p. 2740-2746, vol. 26(11), 1998.
3. **Eric Rivals**, Jean-Paul Delahaye, *Optimal Representation in Average using Kolmogorov Complexity*, *Theoretical Computer Science*, p. 261-287, vol. 200(1-2), 1998.
2. **E. Rivals**, O. Delgrange, J-P. Delahaye, M. Dauchet, M-O. Delorme, H. Naut A., Ollivier E., *Detection of significant patterns by compression algorithms: the case of Approximate Tandem Repeats in DNA sequences*, *CABIOS (Computer Applications in BIOSciences)*, p. 131-136, vol. 13(2), 1997.
1. **E. Rivals**, M. Dauchet, J-P. Delahaye, O. Delgrange, *Compression and genetic sequences analysis*, *Biochimie*, p. 315-322, vol. 78(4), 1996.

2.1 Conference Abstracts in Journals (7)

7. N. Philippe, M. Salson, T. Commes, **E. Rivals**, *A combinatorial and integrated method to analyse RNA-seq reads*, *EMBnet Journal*, 17(Supp. B):11, mar 2012.
6. N. Philippe, M. Salson, F. Rufflé, E. Bou Samara, A. Boureux, T. Commes, **E. Rivals**, *Digital gene expression data, cross-species conservation and noncoding RNA*, *EMBnet Journal*, 17(Supp. B):32, mar 2012.
5. N. Philippe, M. Salson, T. Lecroq, M. L. Onard, T. Commes, **E. Rivals**, *Read Indexing*, *EMBnet Journal*, 17(Supp. B):45, mar 2012.
4. N. Philippe, M. Salson, F. Rufflé, E. Bou Samara, A. Boureux, T. Commes, **E. Rivals**, *Prediction of chimeric RNA from RNA sequencing*, *Bulletin du cancer*, 98(Sp. Iss. 5):S45, oct 2011.
3. N. Philippe, F. Rufflé, E. Bou Samara, A. Boureux, T. Commes, **E. Rivals**, *ARN sequencing, conservation and non-coding ARN*, *Bulletin du cancer*, 97(Sp. Iss. 4):S44, oct 2010.
2. N. Philippe, A. Boureux, L. Br. hlin, J. Tarhio, T. Commes, **E. Rivals**, *Estimation of sequence errors and capacity of genomic annotation in transcriptomic and DNA-protein interaction assays based on next generation sequencers*, *Cellular Oncology*, 31(2):145-6, 2009.
1. A. Boureux, L. Br. hlin, **E. Rivals**, T. Commes, *New approaches based on high throughput sequencing and bioinformatics to study the transcriptomes of leukemic stem cells*, *Bulletin du cancer*, 96(Sp. Iss. 3):S33, oct 2009.

3 Keynote speaker (22)

22. **E. Rivals**, *Superchaînes: des chevauchements entre mots aux graphes d'assemblage aux Leçons de Mathématiques et d'Informatique d'Aujourd'hui*, 14 April 2022, Université de Bordeaux.
21. **E. Rivals**, *Searching for probabilistic motifs in a pan-genome graph* Workshop Computational Pan-Genomics, 30 September – 2 October 2019, Bielefeld University, Germany.
20. **E. Rivals**, *Enjeux computationnels de la pan-génomique* Computational Pan-Genomics Journée Pangénomique végétale GIS Biotechnologies Vertes 1 July 2019, INRA Paris.
19. **E. Rivals**, *High performance text indexing and applications in life sciences*, UK-France Bilateral International Meeting on High Performance Computing and Biomathematics Chicheley, UK, on the 20-21 Feb. 2019

18. **E. Rivals**, *Indexing data structures*, 7th Workshop on Monte-Carlo Methods and Big Data, Heidelberg, Allemagne, 10-11 feb. 2017.
17. **E. Rivals**, *LoRDEC: a tool for correcting errors in long sequencing reads*, Montpellier Omics Days 2016, Montpellier, 8-9 feb. 2016.
16. **E. Rivals**, *La fouille des données (data mining)*, 16ème *Rencontre E. Markiewicz*, CHU J. Bordet, Bruxelles, Belgique, 14 nov. 2015.
15. **E. Rivals**, *LoRDEC: a tool for correcting errors in long sequencing reads*, German Conference in Bioinformatics 2015, Dortmund, Allemagne, 27-30th sep. 2015.
14. **E. Rivals**, *Correction of long sequencing reads: a novel approach*, Annual Symposium From Nucleotides to Networks 2015, Gand, Belgique, 21 may 2015.
13. **E. Rivals**, *Défis computationnels des séquençage et phénotypage haut-débit en science de la vie*, Journée Big Data, Strasbourg, 7 nov. 2014.
12. **E. Rivals**, *Building the Assembly De Bruijn Graph from an Implicit Suffix Tree*, *Workshop on the Storage, Search and Annotation of Multiple Similar Genomes*, Univ. Bielefeld, Bielefeld, Allemagne, 9-10 décembre, 2013.
11. **E. Rivals**, *CRAC: A multi-purpose program to analyse large read collections*, *Analyse bio-informatique des données NGS*, Institut Pasteur, Lille, 7 décembre 2011.
10. **E. Rivals**, *An integrated approach to read analysis*, *LIX Bioinformatics Symposium 2010*, Ecole Polytechnique, Paris, 8-10 Novembre 2010.
9. **E. Rivals**, *Investigating the transcriptomic repertoire based on High Throughput Sequencing data*, *Colloque 2009 du GDR de Bioinformatique Moléculaire*, Institut Henri Poincaré, Paris, 12-13 Novembre 2009.
8. **E. Rivals**, *La comparaison de séquences de génomes complets et l'amélioration de la sensibilité dans les approches par ancres*, *Groupe de Travail en Génomique Comparative*, Nantes, 8 juin 2009.
7. **E. Rivals**, *Estimation of sequence errors and prediction capacity in transcriptomic and DNA-protein interaction assays*, *Journée thématique : nouveaux séquenceurs (NGS)*, Rennes, 2 avril 2009.
6. **E. Rivals**, *L'analyse de marqueurs minisatellites variables suggèrent de fréquents échanges génétiques entre sous-espèces de la souris commune*, *Bioinformatique, modélisation des systèmes biologiques*, Institut Henri Poincaré, Paris, 4-5 octobre 2007.
5. **E. Rivals**, *Combinatorics of Periods in Strings*, *Workshop on Algorithms on Words*, Turku, Finlande, 28-30 mars 2007.
4. **E. Rivals**, *Tandem Repeats Analysis*, *South African Bioinformatics Workshop*, Johannesburg, Afrique du Sud, 28-30 janvier 2007.
3. **E. Rivals**, *Analyse des génomes: quels enjeux algorithmiques ?*, *Rencontres des ASTI : Sciences et Technologies de l'Information*, Clermont-Ferrand, 24 au 26 octobre 2005.
2. **E. Rivals**, *Histoire de duplications et répétitions en tandem*, *Journées Montoises d'Informatique Théorique*, Montpellier, septembre 2002.
1. **E. Rivals**, *Apports futurs de la bioinformatique*, *Colloque AUF-AUPELF "Des modèles biologiques à l'amélioration des plantes"*, Montpellier, 3-5 juillet 2000.

3.1 Invited speaker in training schools (5)

5. **E. Rivals**, *Indexing data structures*, Summer School Open access, Open data, Université de Strasbourg, June 19-21, 2018.
4. **E. Rivals**, *Data mining*, *Rencontres de Venise: Peut-on Mathématiser le vivant ?* Venise, Italie, 8-9 jan. 2016.
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