

Bibliografía

- Bayley, H. (2015). Nanopore sequencing: from imagination to reality. *Clinical Chemistry*, 61(1), 25–31. DOI:10.1373/clinchem.2014.223016
- da Fonseca R.R., Albrechtsen A., Themudo G.E., Ramos-Madrigal J., Sibbesen J.A., Maretty L., Zepeda-Mendoza M.L., Campos P.F., Heller R. & Pereira R.J. (2016). Next-generation biology: Sequencing and data analysis approaches for non-model organisms. *Marine Genomics*, pii: S1874-7787(16), 30036-30038. DOI: 10.1016/j.margen.2016.04.012. [Epub ahead of print]
- Derrington, I.M., Butler, T. Z., Collins, M. D., Manrao E., Pavlenok, M., Niederweis M. & Gundlach J.H. (2010) Nanopore DNA sequencing with MspA. *Proceedings of the National Academy of Sciences of the United States of America*, 107(37), 16060-16065.
- Dodsworth S. (2015). Genome skimming for next-generation biodiversity analysis. *Trends in Plant Science*, 20(9), 525-527. DOI: 10.1016/j.tplants.2015.06.012
- Ellegren, H. (2014). Genome sequencing and population genomics in non-model organisms. *Trends in Ecology & Evolution*, 29(1), 51- 63. Doi: 10.1016/j.tree.2013.09.008
- Feng, Y., Zhang, Y., Ying, C., Wang, D. & Du, C. (2015). Nanopore-based Fourth-generation DNA Sequencing Technology. *Genomics, Proteomics & Bioinformatics*, 13(1) 4-16. DOI: 10.1016/j.gpb.2015.01.009
- Griffiths, A., Wessler, S., Lewontin, R. & Carroll, S. (2008). *Genética*. Madrid: McGrawHill
- Gupta P.D. (2016). Nanopore Technology: A Simple, Inexpensive, Futuristic Technology for DNA Sequencing. *Indian Journal of Clinical Biochemistry*, 31(4), 359-360. DOI: 10.1007/s12291-016-0593-6
- Heather, J.M. & Chain, B. (2016). The sequence of sequencers: The history of sequencing DNA. *Genomics*, 107, 1-8. Doi: 10.1016/j.ygeno.2015.11.003
- Laver, T., Harrison J., O'Neill P.A., Moore, K., Farbos, A., Paszkiewicz K. & Studholme, D.J. (2015). Assessing the performance of the Oxford Nanopore Technologies MinION. *Biomolecular Detection and Quantification*, 3, 1-8. DOI: 10.1016/j.bdq.2015.02.001
- Li Z., Chen, Y., Mu D., Yuan, J., Shi Y., Zhang, H, Gan, J., Li, N., Hu, X., Liu, B., Yang B. & Fan, W. (2012). Comparison of the two major classes of assembly algorithms: overlap-layout-consensus and de-bruijn-graph. *Briefings in Functional Genomics*, 11(1), 25-37. DOI: 0.1093/bfpg/elr035
- Loman, N. J., Quick, J. & Simpson, J. T. (2015) A complete bacterial genome assembled de novo using only nanopore sequencing data. *Nature Methods*, 12(8), 733-735. DOI: 10.1038/nmeth.3444
- Lu, H., Giordano, F. & Ning, Z. (2016). Oxford Nanopore MinION Sequencing and Genome Assembly. *Genomics, Proteomics & Bioinformatics*. Doi: 10.1016/j.gpb.2016.05.004
- Maxam, A.M. & Gilbert W. (1977). A new method for sequencing DNA. *Proceedings of the National Academy of Sciences of the United States of America*, 74(2), 560-564.
- Miller, J.R., Koren, S. & Sutton, G. (2010). Assembly algorithms for next-generation sequencing data. *Genomics*, 95, 315-327. DOI:10.1016/j.ygeno.2010.03.001
- Pierce, B. A. (2008). *Genomics and Proteomics. Genetics: A conceptual Approach (3ra.ed)*, 548-552. W. H. Freeman & Company
- Reuter, J.A., Spacek, D. V. & Snyder, M.P. (2015) High-Throughput Sequencing Technologies. *Molecular Cell*, 58, 586-597. DOI: 10.1016/j.molcel.2015.05.004
- Sanger, F. & Coulson, A.R. (1975). A rapid method for determining sequences in DNA by primed synthesis with DNA polymerase. *Journal of Molecular Biology*, 94(3), 441-448. DOI: 10.1016/0022-2836(75)90213-2
- Vincent, A.T., Derome, N., Boyle, B., Culley, A.I. & Charette, S. J. (2016). Next-generation sequencing (NGS) in the microbiological world: How to make the most of your money. *Journal of Microbiological Methods*. DOI: 10.1016/j.mimet.2016.02.01
- Watson, J.D. & Crick, F.H.C. (1953). Molecular Structure of Deoxyribose Nucleic Acids. *Nature*, 171, 737-738