

BARCELONA IN THE SPOTLIGHT OF BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

- **From today until Wednesday 6th April, Barcelona hosts the Next Generation Sequencing (NGS) Conference for second consecutive time.**
- **The event, which will be focused on genome annotation, is organized by the International Society for Computational Biology (ISCB) and the Centre for Genomic Regulation (CRG) and it brings together leading scientists in computational biology and bioinformatics.**
- **By hosting this event, Barcelona and the CRG consolidate their positioning as a reference and an interesting hub for research in genomics.**

It's only 15 years since the human genome was decoded but in this short period of time and thanks to enormous technological advances, the –omics sciences have become one of the pillars for research and innovation.

The International Society for Computational Biology (ISCB) and the Centre for Genomic Regulation in Barcelona, Spain, host the 2016 edition of the Next Generation Sequencing Conference. The meeting, which gathers together 185 participants from 32 countries world wide, takes place in the Centre for Genomic Regulation from today until Wednesday 6th April.

“Barcelona and the pool of scientists working in genomics based in this city, already are in a leading position in these fields. Hosting the NGS meeting for the second consecutive time demonstrates that Barcelona is in the spotlight on bioinformatics and computational biology,” says Alfonso Valencia, president of the International Society for Computational Biology, director of the Spanish node of ELIXIR and of the Structural Biology and Biocomputing Programme at the Spanish National Cancer Research Centre (CNIO).

This year's edition is focused on Genome Annotation, which are the methods in genome analysis that allows us to attach biological information to the genomic sequences. It is a dedicated meeting on cutting-edge approaches to the processing and analysis of Genome Annotation methods highlighting projects and improvements in this subject. The conference brings together researchers involved in the development of genome annotation methods, along with biologists interested in the establishment and annotation of new reference genomes. It will address a wide range of issues including RNASeq-based genome annotation, non-coding RNA analysis, proteomics data integration and data visualization. Sizeable space will also be dedicated to emerging and future trends in genomics including eco-system analysis and novel reference genomes.



“We have come a long way on bioinformatics research but there is still a long way off. Thanks to meetings like the NGS, scientists working on different aspects of genome research can share not only new tools and improvements but also success stories or challenging projects that make us progress,” says Cedric Notredame, senior group leader at the Centre for Genomic Regulation and co-chair of this conference. *“Even though they have different approaches, they all contribute to a better processing and analysis of genomic data, which is crucial for understanding evolution and biological or medical aspects of the genome,”* concludes Notredame.

MORE INFORMATION:

NGS 2016 Conference:

- Website: <http://www.iscb.org/ngs2016>
- Keynote speakers: <http://www.iscb.org/ngs2016-keynote-speakers>

Organizers:

- International Society for Computational Biology (ISCB): <http://www.iscb.org>
- Centre for Genomic Regulation (CRG): www.crg.eu

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