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Barcelona Bio Centers to Team on Structural Genomics Projects

April 30, 2012

Barcelona Bio Centers to Team on Structural Genomics Projects

By [a GenomeWeb staff reporter](#)

NEW YORK (GenomeWeb News) – Two Barcelona biotech research centers have struck a joint agreement to collaborate and share resources in sequencing and computational analysis-focused studies, the Centre for Genomic Regulation, or CRG, said today.

Under the partnership, CRG, which is based in the Barcelona Biomedical Research Park, and the National Center for Genomic Analysis, or CNAG, located in the Barcelona Science Park, will partner in research and share expertise and technologies. Also under the plan, CNAG's Structural Genomics Group will join the CRG's Gene Regulation, Stem Cells and Cancer program to enable the partners to share their respective computational and experimental resources.

Based at the CRG, this new joint group will have access to CRG's facilities and researchers and it will provide expertise in 3D genome analysis. The computational activities, involving sequencing and sequencing analysis, will continue to be based at CNAG's computing lab.

CNAG Director Ivo Gut said in a statement that the center already is engaged in "joint projects with the CRG but this agreement will foster an even closer collaboration which will increase the capacity of both institutions. This collaboration not only optimizes resources but also increases the capacity of Spanish institutions to retain research talent."

"Modern science is increasingly interdisciplinary, it is impossible for a single centre to have all the expertise and technology necessary to be globally competitive. That is why strategic partnerships such as that we have with the CNAG contribute to increasing the competitiveness of national centers," added CRG Director Luis Serrano.

The Structural Genomics Group focuses on studies of the molecular mechanisms that regulate the cell, and uses computational methods to predict the 3D structure of macromolecules and their complexes, with a particular focus on determining the structures of genomes and genomic domains, determination and prediction of RNA molecules, and prediction of proteins and their complexes.

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