# Resource Summary Report

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## Instituto Nacional de Bioinformtica

RRID:SCR_008586
Type: Tool

### Proper Citation

Instituto Nacional de Bioinformtica (RRID:SCR_008586)

### Resource Information

**URL:** http://www.inab.org

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**Description:** INB is a technological plattform of Genoma Espaa. A National Network for coordination, integration and development of Spanish Bioinformatics Resources in genomics and proteomics projects. The INB (Instituto Nacional de Bioinformtica) is a community-driven technology platform of Genoma Espana founded in 2003 with the mission to consolidate Bioinformatics as a scientific discipline and to generate and apply solutions for the development and execution of projects related to genomics and proteomics, providing technical support in Bioinformatics to laboratories, institutions and companies throughout the Spanish territory.

**Synonyms:** INB

**Resource Type:** data or information resource, organization portal, portal

**Resource Name:** Instituto Nacional de Bioinformtica

**Resource ID:** SCR_008586

**Alternate IDs:** nif-0000-31887

**Record Creation Time:** 20220129T080248+0000

**Record Last Update:** 20260905T133044+0000

### Ratings and Alerts

No rating or validation information has been found for Instituto Nacional de Bioinformtica.

No alerts have been found for Instituto Nacional de Bioinformtica.

### Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 74 mentions in open access literature.

**Listed below are recent publications.** The full list is available at Kravitz .


Mayer G, et al. (2019) A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. Briefings in bioinformatics, 20(4), 1215.

Piñeiro-Yáñez E, et al. (2018) PanDrugs: a novel method to prioritize anticancer drug treatments according to individual genomic data. Genome medicine, 10(1), 41.

Rodriguez JM, et al. (2018) APPRIS 2017: principal isoforms for multiple gene sets. Nucleic acids research, 46(D1), D213.

Gallego A, et al. (2016) Functional Implications of Human-Specific Changes in Great Ape microRNAs. PloS one, 11(4), e0154194.

Santpere G, et al. (2016) Differences in molecular evolutionary rates among microRNAs in the human and chimpanzee genomes. BMC genomics, 17, 528.

Luisi P, et al. (2015) Recent positive selection has acted on genes encoding proteins with more interactions within the whole human interactome. Genome biology and evolution, 7(4), 1141.

Rodriguez JM, et al. (2015) APPRIS WebServer and WebServices. Nucleic acids research, 43(W1), W455.

Amadoz A, et al. (2015) Using activation status of signaling pathways as mechanism-based biomarkers to predict drug sensitivity. Scientific reports, 5, 18494.

Carbonell-Caballero J, et al. (2015) A Phylogenetic Analysis of 34 Chloroplast Genomes Elucidates the Relationships between Wild and Domestic Species within the Genus Citrus. Molecular biology and evolution, 32(8), 2015.

Abascal F, et al. (2015) Alternatively Spliced Homologous Exons Have Ancient Origins and Are Highly Expressed at the Protein Level. PLoS computational biology, 11(6), e1004325.

Dobon B, et al. (2015) The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. Scientific reports, 5, 9996.

Sebastian-Leon P, et al. (2014) Understanding disease mechanisms with models of signaling pathway activities. BMC systems biology, 8, 121.

Engelken J, et al. (2014) Extreme population differences in the human zinc transporter ZIP4 (SLC39A4) are explained by positive selection in Sub-Saharan Africa. PLoS genetics, 10(2), e1004128.

Pybus M, et al. (2014) 1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. Nucleic acids research, 42(Database issue), D903.

Alemán A, et al. (2014) A web-based interactive framework to assist in the prioritization of disease candidate genes in whole-exome sequencing studies. Nucleic acids research, 42(Web Server issue), W88.

, et al. (2014) The common marmoset genome provides insight into primate biology and evolution. Nature genetics, 46(8), 850.

Garcia-Alonso L, et al. (2014) The role of the interactome in the maintenance of deleterious variability in human populations. Molecular systems biology, 10(9), 752.

Alemán A, et al. (2014) A web tool for the design and management of panels of genes for targeted enrichment and massive sequencing for clinical applications. Nucleic acids research, 42(Web Server issue), W83.

Ezkurdia I, et al. (2014) Multiple evidence strands suggest that there may be as few as 19,000 human protein-coding genes. Human molecular genetics, 23(22), 5866.

Muñoz-Mérida A, et al. (2014) Sma3s: a three-step modular annotator for large sequence datasets. DNA research : an international journal for rapid publication of reports on genes and genomes, 21(4), 341.