

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 platform 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

Usage and Citation Metrics

We found 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

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.

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

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.

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

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

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.

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.

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.

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

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.

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

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.

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.

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

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.

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.

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.