

Resource Summary Report

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ABNER

RRID:SCR_011868

Type: Tool

Proper Citation

ABNER (RRID:SCR_011868)

Resource Information

URL: <http://pages.cs.wisc.edu/~bsettles/abner/>

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Description: A software tool for molecular biology text analysis. At ABNER's core is a statistical machine learning system using linear-chain conditional random fields (CRFs) with a variety of orthographic and contextual features.

Abbreviations: ABNER

Resource Type: software resource

Keywords: bio.tools

Resource Name: ABNER

Resource ID: SCR_011868

Alternate IDs: biotools:abner, OMICS_01168

Alternate URLs: <https://bio.tools/abner>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190722+0000

Ratings and Alerts

No rating or validation information has been found for ABNER.

No alerts have been found for ABNER.

Data and Source Information

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Pérez-Pérez M, et al. (2024) Tracking the Spread of Pollen on Social Media Using Pollen-Related Messages From Twitter: Retrospective Analysis. *Journal of medical Internet research*, 26, e58309.

Li H, et al. (2020) Systematic analysis of ovarian cancer platinum-resistance mechanisms via text mining. *Journal of ovarian research*, 13(1), 27.

He RQ, et al. (2018) MicroRNA-124-3p expression and its prospective functional pathways in hepatocellular carcinoma: A quantitative polymerase chain reaction, gene expression omnibus and bioinformatics study. *Oncology letters*, 15(4), 5517.

Zhang R, et al. (2018) Potential role of microRNA-223-3p in the tumorigenesis of hepatocellular carcinoma: A comprehensive study based on data mining and bioinformatics. *Molecular medicine reports*, 17(2), 2211.

Ren FH, et al. (2018) Analysis of microarrays of miR-34a and its identification of prospective target gene signature in hepatocellular carcinoma. *BMC cancer*, 18(1), 12.

Zhang X, et al. (2017) Down-regulation of miR-146a-5p and its potential targets in hepatocellular carcinoma validated by a TCGA- and GEO-based study. *FEBS open bio*, 7(4), 504.

Yang H, et al. (2017) From big data to diagnosis and prognosis: gene expression signatures in liver hepatocellular carcinoma. *PeerJ*, 5, e3089.

Liu CZ, et al. (2017) A qRT-PCR and Gene Functional Enrichment Study Focused on Downregulation of miR-141-3p in Hepatocellular Carcinoma and Its Clinicopathological Significance. *Technology in cancer research & treatment*, 16(6), 835.

Zhen C, et al. (2017) Systematic analysis of molecular mechanisms for HCC metastasis via text mining approach. *Oncotarget*, 8(8), 13909.

Lv H, et al. (2017) An integrated bioinformatical analysis of miR-19a target genes in multiple myeloma. *Experimental and therapeutic medicine*, 14(5), 4711.

Chen L, et al. (2017) Data mining and pathway analysis of glucose-6-phosphate dehydrogenase with natural language processing. *Molecular medicine reports*, 16(2), 1900.

Ding H, et al. (2017) Downregulation of miR-136-5p in hepatocellular carcinoma and its clinicopathological significance. *Molecular medicine reports*, 16(4), 5393.

Liang HW, et al. (2017) A comprehensive insight into the clinicopathologic significance of miR-144-3p in hepatocellular carcinoma. *OncoTargets and therapy*, 10, 3405.

Iqbal H, et al. (2017) Children's friendships in super-diverse localities: Encounters with social and ethnic difference. *Childhood (Copenhagen, Denmark)*, 24(1), 128.

Larsson K, et al. (2017) Text mining for improved exposure assessment. *PloS one*, 12(3), e0173132.

Kim J, et al. (2017) An analysis of disease-gene relationship from Medline abstracts by DigSee. *Scientific reports*, 7, 40154.

Zhang X, et al. (2016) An Encapsulation of Gene Signatures for Hepatocellular Carcinoma, MicroRNA-132 Predicted Target Genes and the Corresponding Overlaps. *PloS one*, 11(7), e0159498.

Huang WT, et al. (2016) Lower expressed miR-198 and its potential targets in hepatocellular carcinoma: a clinicopathological and in silico study. *OncoTargets and therapy*, 9, 5163.

Jorge P, et al. (2016) Construction of antimicrobial peptide-drug combination networks from scientific literature based on a semi-automated curation workflow. *Database : the journal of biological databases and curation*, 2016.

Taha K, et al. (2016) Predicting the functions of a protein from its ability to associate with other molecules. *BMC bioinformatics*, 17, 34.