

Resource Summary Report

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Simrank

RRID:SCR_014614

Type: Tool

Proper Citation

Simrank (RRID:SCR_014614)

Resource Information

URL: <http://search.cpan.org/search?mode=all&query=Simrank>

Proper Citation: Simrank (RRID:SCR_014614)

Description: A rapid and sensitive general-purpose k-mer search tool.

Resource Type: software resource

Keywords: microbiome, kmer, search tool

Availability: Free, Users can modify the resource

Resource Name: Simrank

Resource ID: SCR_014614

License: GNU General Public License, Artistic License

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260829T182500+0000

Ratings and Alerts

No rating or validation information has been found for Simrank.

No alerts have been found for Simrank.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Bohar B, et al. (2025) Patient-Specific Regulatory Network Rewiring in Inflammatory Bowel Disease: How Genetic Polymorphisms Divert Incoming Signals and Contribute to Disease Pathogenesis. *Inflammatory bowel diseases*, 31(10), 2665.

Zhang Q, et al. (2025) Enhancing intercultural competence in technical higher education through AI-driven frameworks. *Scientific reports*, 15(1), 22019.

Abbas K, et al. (2021) Application of network link prediction in drug discovery. *BMC bioinformatics*, 22(1), 187.

Yan C, et al. (2020) Computational Methods and Applications for Identifying Disease-Associated lncRNAs as Potential Biomarkers and Therapeutic Targets. *Molecular therapy. Nucleic acids*, 21, 156.

Liang L, et al. (2019) Integrating data and knowledge to identify functional modules of genes: a multilayer approach. *BMC bioinformatics*, 20(1), 225.

Li X, et al. (2018) SRMDAP: SimRank and Density-Based Clustering Recommender Model for miRNA-Disease Association Prediction. *BioMed research international*, 2018, 5747489.

Qi J, et al. (2018) Micro-blog user community discovery using generalized SimRank edge weighting method. *PloS one*, 13(5), e0196447.

Shakibian H, et al. (2017) Mutual information model for link prediction in heterogeneous complex networks. *Scientific reports*, 7, 44981.

Wall K, et al. (2015) Biodiversity hot spot on a hot spot: novel extremophile diversity in Hawaiian fumaroles. *MicrobiologyOpen*, 4(2), 267.

Yoon SH, et al. (2014) Link-based similarity measures using reachability vectors. *TheScientificWorldJournal*, 2014, 741608.

Baquiran JP, et al. (2013) Culture-independent investigation of the microbiome associated with the nematode *Acroboloides maximus*. *PloS one*, 8(7), e67425.

Hermann-Bank ML, et al. (2013) The Gut Microbiotassay: a high-throughput qPCR approach combinable with next generation sequencing to study gut microbial diversity. *BMC genomics*, 14, 788.

Harrell L, et al. (2012) Standard colonic lavage alters the natural state of mucosal-associated microbiota in the human colon. *PloS one*, 7(2), e32545.

Dougherty U, et al. (2011) American ginseng suppresses Western diet-promoted tumorigenesis in model of inflammation-associated colon cancer: role of EGFR. *BMC complementary and alternative medicine*, 11, 111.

Glad T, et al. (2010) Bacterial diversity in faeces from polar bear (*Ursus maritimus*) in Arctic Svalbard. *BMC microbiology*, 10, 10.

Wang Y, et al. (2010) Regional mucosa-associated microbiota determine physiological expression of TLR2 and TLR4 in murine colon. *PloS one*, 5(10), e13607.

Wang Y, et al. (2010) Automatic symptom name normalization in clinical records of traditional Chinese medicine. *BMC bioinformatics*, 11, 40.

Wang Y, et al. (2009) 16S rRNA gene-based analysis of fecal microbiota from preterm infants with and without necrotizing enterocolitis. *The ISME journal*, 3(8), 944.