

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

iTools

RRID:SCR_009626

Type: Tool

Proper Citation

iTools (RRID:SCR_009626)

Resource Information

URL: <http://itools.loni.usc.edu/>

Proper Citation: iTools (RRID:SCR_009626)

Description: An infrastructure for managing of diverse computational biology resources - data, software tools and web-services. The iTools design, implementation and meta-data content reflect the broad NCBC needs and expertise (www.NCBCs.org).

Abbreviations: iTools

Synonyms: ITools Resourceome, NCBC iTools

Resource Type: service resource, database, web service, software resource, storage service resource, data repository, software repository, data access protocol, data or information resource

Defining Citation: [PMID:18509477](#)

Keywords: computational neuroscience, data, experiment control, hardware, imaging genomics, information specification, java, loni pipeline, model, ontology, os independent, metadata

Funding: NIH Roadmap for Medical Research ;
NCRR U54-RR021813;
NIDA U54-DA021519;
NCI U54-CA121852;
NHGRI U54-HG004028;
NIGMS U54-GM072970;
NIBIB U54-EB005149;
NLM U54-LM008748

Availability: GNU Lesser General Public License

Resource Name: iTools

Resource ID: SCR_009626

Alternate IDs: nlx_155852

Alternate URLs: <http://www.nitrc.org/projects/itools>,
<http://www.loni.usc.edu/research/software>

Old URLs: <http://itools.loni.ucla.edu/>

Record Creation Time: 20220129T080254+0000

Record Last Update: 20260728T043322+0000

Ratings and Alerts

No rating or validation information has been found for iTools.

No alerts have been found for iTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Nie J, et al. (2025) Dietary supplement of Acanthopanax senticosus decoction formula improves immune response via intestine flora of rabbits. *Frontiers in microbiology*, 16, 1508280.

Suolang Q, et al. (2025) Study on intestinal microbial communities of three different cattle populations on Qinghai-Tibet Plateau. *PloS one*, 20(2), e0312314.

Maghraby A, et al. (2025) Genome-wide identification, characterization, and functional analysis of the CHX, SOS, and RLK genes in *Solanum lycopersicum* under salt stress. *Scientific reports*, 15(1), 1142.

Li K, et al. (2025) Significant associations between high-risk sexual behaviors and enterotypes of gut microbiome in HIV-negative men who have sex with men. *mSphere*, 10(7), e0023225.

Huang J, et al. (2025) Phylogenomic relationships and species delimitation of *Cotoneaster* ser. *Pannosi*, ser. *Buxifolii*, and related taxa. *Frontiers in plant science*, 16, 1575925.

Li H, et al. (2025) Potential mechanisms underlying pathological fatigue-induced cardiac dysfunction. *FASEB journal : official publication of the Federation of American Societies*

for Experimental Biology, 39(8), e70511.

Shen Q, et al. (2025) TaxaCal: enhancing species-level profiling accuracy of 16S amplicon data. BMC bioinformatics, 26(1), 136.

Chen J, et al. (2025) Alterations in the salivary gland microbiota of *Haemaphysalis longicornis* during tick-to-host transmission of severe fever with thrombocytopenia syndrome virus. Zoological research, 46(2), 459.

Chen F, et al. (2025) Metagenomic insights into the microbial communities and functional traits of hot springs in Guizhou Province, China. Frontiers in microbiology, 16, 1615879.

Yin H, et al. (2025) Multi-dimensional annotation of porcine variants using genomic and epigenomic features in pigs. BMC biology, 23(1), 188.

Zhu D, et al. (2024) A tip of the iceberg: genome survey indicated a complex evolutionary history of *Garuga Roxb. species*. BMC genomics, 25(1), 993.

Sun Y, et al. (2024) Severe fever with thrombocytopenia syndrome virus infection shapes gut microbiome of the tick vector *Haemaphysalis longicornis*. Parasites & vectors, 17(1), 107.

Ghabban H, et al. (2024) Investigating the bacterial community of gray mangroves (*Avicennia marina*) in coastal areas of Tabuk region. PeerJ, 12, e18282.

Khan NA, et al. (2024) C/N ratio effect on oily wastewater treatment using column type SBR: machine learning prediction and metagenomics study. Scientific reports, 14(1), 22950.

Delgadillo R, et al. (2024) Increasing the efficiency of cone-beam CT based delta-radiomics using automated contours to predict radiotherapy-related toxicities in prostate cancer. Scientific reports, 14(1), 9563.

Tarique M, et al. (2024) Exopolysaccharides from *Enterococcus faecium* and *Streptococcus thermophilus*: Bioactivities, gut microbiome effects, and fermented milk rheology. Food chemistry: X, 21, 101073.

Zhang P, et al. (2024) The relationship between gastric microbiome features and responses to neoadjuvant chemotherapy in gastric cancer. Frontiers in microbiology, 15, 1357261.

Maghraby A, et al. (2024) Genome-wide identification and evolutionary analysis of the AP2/EREBP, COX and LTP genes in *Zea mays* L. under drought stress. Scientific reports, 14(1), 7610.

Wu ZY, et al. (2024) Genomic variation, environmental adaptation, and feralization in ramie, an ancient fiber crop. Plant communications, 5(8), 100942.

Ge D, et al. (2023) Genomic Consequences of and Demographic Response to Pervasive Hybridization Over Time in Climate-Sensitive Pikas. Molecular biology and evolution, 40(1).