

Resource Summary Report

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SEEK

RRID:SCR_002651

Type: Tool

Proper Citation

SEEK (RRID:SCR_002651)

Resource Information

URL: <http://www.seek4science.org/>

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Description: An open-source, web-based platform and suite of software tools for for sharing heterogeneous scientific research datasets, models or simulations, processes and research outcomes - and collaborations between scientists. It preserves associations between them, along with information about the people and organizations involved. Underpinning SEEK is the ISA infrastructure, a standard format for describing how individual experiments are aggregated into wider studies and investigations. Within SEEK, ISA has been extended and is configurable to allow the structure to be used outside of Biology. SEEK is incorporating semantic technology allowing sophisticated queries over the data, yet without getting in the way of your users. Access to the RESTful API to access the data within SEEK is available.

Abbreviations: SEEK

Synonyms: SEEK Platform, SEEK for Science

Resource Type: data access protocol, data management software, data processing software, data repository, data storage software, service resource, software application, software resource, source code, storage service resource, web service

Defining Citation: [PMID:21943917](#)

Keywords: data sharing, data set, systems biology, standard exchange format, metadata standard, data management, data citation, publishing software, bio.tools

Funding: BBSRC ;
BMBF

Availability: Free, Available for download, Freely available

Resource Name: SEEK

Resource ID: SCR_002651

Alternate IDs: nlx_156079, OMICS_01012, biotools:seek

Alternate URLs: <http://www.force11.org/node/4806>, <https://bio.tools/seek>

License: BSD License

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260821T193648+0000

Ratings and Alerts

No rating or validation information has been found for SEEK.

No alerts have been found for SEEK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Tang X, et al. (2026) Single-cell transcriptomics identifies fibroblast associated immune heterogeneity and prognostic signatures in bladder cancer. Scientific reports, 16(1), 7151.

Müller D, et al. (2026) Structural Aspects of Lithium-Ion Conduction in the Phosphidotitanate Li₈TiP₄ and Its Comparison With Li₇₊₅ xTa₁₋ xP₄ and Li₈₋ xTi₁₋ xTaxP₄. Chemistry (Weinheim an der Bergstrasse, Germany), 32(13), e03124.

McGrouther CC, et al. (2025) Heterogeneity analysis provides evidence for a genetically homogeneous subtype of bipolar-disorder. PloS one, 20(1), e0314288.

McGrouther CC, et al. (2024) Heterogeneity analysis provides evidence for a genetically homogeneous subtype of bipolar-disorder. ArXiv.

Qiu X, et al. (2024) Integrative transcriptome analysis identifies MYBL2 as a poor prognosis marker for osteosarcoma and a pan-cancer marker of immune infiltration. Genes & diseases, 11(3), 101004.

Brandes-Leibovitz R, et al. (2024) Sepsis pathogenesis and outcome are shaped by the balance between the transcriptional states of systemic inflammation and antimicrobial response. Cell reports. Medicine, 5(11), 101829.

Badia-Aguarón T, et al. (2024) Combining mindfulness and cognitive training in children with attention deficit hyperactivity disorder: study protocol of a pilot randomized controlled trial (the NeuroMind study). *Frontiers in psychology*, 15, 1291198.

Engström M, et al. (2023) Validation of the Swedish version of the safe environment for every kid (SEEK) parent screening questionnaire. *BMC public health*, 23(1), 1989.

Campbell N, et al. (2023) A repeatable scoring system for assessing Smartphone applications ability to identify herbaceous plants. *PloS one*, 18(4), e0283386.

Kjølle S, et al. (2023) Hypoxia induced responses are reflected in the stromal proteome of breast cancer. *Nature communications*, 14(1), 3724.

Moller AB, et al. (2023) Midwifery care providers' childbirth and immediate newborn care competencies: A cross-sectional study in Benin, Malawi, Tanzania and Uganda. *PLOS global public health*, 3(6), e0001399.

Silva L, et al. (2022) Introducing genetic testing with case finding for familial hypercholesterolaemia in primary care: qualitative study of patient and health professional experience. *The British journal of general practice : the journal of the Royal College of General Practitioners*, 72(720), e519.

Mohammadi Z, et al. (2021) Risk Assessment of Nano-Flame Retardants Coating in the Selected Construction Industry of Iran by Control Banding Approach. *International journal of preventive medicine*, 12, 96.

Steele Gray C, et al. (2021) Assessing the Implementation and Effectiveness of the Electronic Patient-Reported Outcome Tool for Older Adults With Complex Care Needs: Mixed Methods Study. *Journal of medical Internet research*, 23(12), e29071.

Huna A, et al. (2021) PLA2R1 promotes DNA damage and inhibits spontaneous tumor formation during aging. *Cell death & disease*, 12(2), 190.

Pomey MP, et al. (2021) The patient advisor, an organizational resource as a lever for an enhanced oncology patient experience (PAROLE-onco): a longitudinal multiple case study protocol. *BMC health services research*, 21(1), 10.

Hume S, et al. (2021) The NUCKS1-SKP2-p21/p27 axis controls S phase entry. *Nature communications*, 12(1), 6959.

Mancuso CA, et al. (2020) A flexible, interpretable, and accurate approach for imputing the expression of unmeasured genes. *Nucleic acids research*, 48(21), e125.

Dubowitz H, et al. (2020) Protocol for comparing two training approaches for primary care professionals implementing the Safe Environment for Every Kid (SEEK) model. *Implementation science communications*, 1, 78.

Yang WR, et al. (2019) SQuIRE reveals locus-specific regulation of interspersed repeat expression. *Nucleic acids research*, 47(5), e27.