

Resource Summary Report

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xCell

RRID:SCR_026446

Type: Tool

Proper Citation

xCell (RRID:SCR_026446)

Resource Information

URL: <https://github.com/dviraran/xCell>

Proper Citation: xCell (RRID:SCR_026446)

Description: Software R package for generating cell type scores and R scripts for development of xCell. Web tool that performs cell type enrichment analysis from gene expression data for immune and stroma cell types. Used for Cell types enrichment analysis.

Resource Type: web application, software toolkit, source code, software resource

Defining Citation: [PMID:29141660](#)

Keywords: Cell types enrichment analysis, cell type, enrichment analysis, generating cell type scores and R scripts, development of xCell,

Funding: Gruss Lipper Postdoctoral Fellowship ;
NCI U24 CA195858;
NIAID

Availability: Free, Available for download, Freely available

Resource Name: xCell

Resource ID: SCR_026446

Alternate URLs: <http://xCell.ucsf.edu/>

Record Creation Time: 20250221T060325+0000

Record Last Update: 20260817T040725+0000

Ratings and Alerts

No rating or validation information has been found for xCell .

No alerts have been found for xCell .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 170 mentions in open access literature.

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

Lisá Z, et al. (2026) Global RNA expression analysis of patient samples identified potential diagnostic biomarkers specific for peritoneal, ovarian and deep endometriosis. Scientific reports, 16(1), 5070.

Wang Y, et al. (2026) Stromal NNMT overexpression as an independent prognostic biomarker in lung adenocarcinoma and breast carcinoma. Carcinogenesis, 47(2).

Yu J, et al. (2026) High SOX17 expression is correlated with favorable prognosis and CD8(+) TILs expression in patients with pancreatic cancer after curative resection. Translational oncology, 70, 102859.

Guskov AV, et al. (2026) A Comparative Bioinformatics Analysis of the Transcriptomic Profiles of Peri-Implantitis and Periodontitis and Their Common Signaling Pathways with Atherosclerosis. Current issues in molecular biology, 48(4).

Chi Z, et al. (2026) Comprehensive single-cell analysis reveals cellular heterogeneity and immune interactions in colorectal cancer. Translational oncology, 68, 102761.

Wang C, et al. (2026) Tumor-intrinsic KLRC1 exerts tumor-suppressive functions in colorectal cancer. Discover oncology, 17(1).

Stemmer E, et al. (2026) Sex-Specific Transcriptomic Profiles in Psoriatic Lesions: A Large-Scale Integrative Study. International journal of molecular sciences, 27(10).

Cai Y, et al. (2026) Identification of STMN1 as a lactylation-related driver of lung cancer progression using Mendelian randomization. Molecular medicine reports, 33(5).

Huang K, et al. (2026) Extrachromosomal DNA drives molecular and clinical heterogeneity in hepatocellular carcinoma: a multi-omics analysis and prognostic model development. Human genomics, 20(1).

Xie Z, et al. (2026) Digital spatial profiling uncovers transcriptomic features of distinct plasma cell-like phenotypes in diffuse large B-cell lymphoma. Blood advances, 10(11), 3966.

Xu Y, et al. (2026) GPC2 provides prognostic value in pan-pediatric cancers and is associated with MYCN amplification in neuroblastoma: bioinformatics analysis and validation. *BMC cancer*, 26(1).

Zhao T, et al. (2026) Human umbilical cord mesenchymal stem cells alleviate colon epithelial apoptosis in ulcerative colitis by activating inositol-requiring enzyme 1/X-box binding protein 1 signaling. *Stem cells translational medicine*, 15(1).

Wang X, et al. (2026) CHS-114: An Afucosylated Anti-CCR8 Monoclonal Antibody that Selectively Depletes Intratumoral Treg Cells and Induces Antitumor Immune Responses. *Molecular cancer therapeutics*, 25(5), 685.

Wang FX, et al. (2026) Whole-transcriptome analysis of Aortic Stenosis reveals dysregulated RNA networks, immune cell infiltration, and NADK2 as a candidate regulator. *Hereditas*, 163(1).

Yin Y, et al. (2026) Anti-oncogenic and immunological functions of ATP23 in CMS4 colon adenocarcinoma based on a machine learning computational framework. *PeerJ*, 14, e20838.

Wu C, et al. (2026) Diagnostic and prognostic signatures of glomerular membrane dysregulation in immune nephropathies. *Frontiers in immunology*, 17, 1800258.

Spampinato S, et al. (2026) Immune checkpoint landscape in CD4⁺ T cells stratifies HIV-infected individuals by clinical progression. *Immunologic research*, 74(1).

Yang C, et al. (2026) Prognostic model of immune -related immune models of ANLN single gene based on TCGA lung adenocarcinoma database. *Discover oncology*, 17(1).

Padelli M, et al. (2026) The epigenetic regulator SETDB1 as a key component of cancer stem cells and drug resistance in primary liver cancer. *Cellular oncology (Dordrecht, Netherlands)*, 49(1), 18.

Zhou H, et al. (2026) Migrasomes in Ischemic Stroke: Molecular Landscape and Pathophysiological Impact. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(6), e20608.