

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

## COLT-Cancer

RRID:SCR\_006485

Type: Tool

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### Proper Citation

COLT-Cancer (RRID:SCR\_006485)

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### Resource Information

**URL:** <http://colt.ccbbr.utoronto.ca/cancer/>

**Proper Citation:** COLT-Cancer (RRID:SCR\_006485)

**Description:** The COLT-Cancer database is a collection of shRNA dropout signatures profiles, covering ~16000 human genes, and derived from more than 70 Pancreatic, Ovarian and Breast human cancer cell-lines using the microarray detection platform developed in the COLT (CCBR-OICR Lentiviral Technology) facility at the Moffat Lab. All shRNA dropout profiles are freely available through download or queries via this website.

**Abbreviations:** COLT-Cancer

**Synonyms:** CCBR-OICR Lentiviral Technology Cancer, COLT-Cancer database

**Resource Type:** production service resource, data or information resource, database, service resource, data analysis service, analysis service resource

**Defining Citation:** [PMID:22102578](#)

**Keywords:** gene, shrna profile, shrna, functional genetics, cancer, cell line, bio.tools

**Related Condition:** Pancreatic cancer, Ovarian cancer, Breast cancer

**Funding:** Ontario Institute for Cancer Research ;  
Terry Fox Research Institute ;  
Canadian Institutes of Health Research ;  
Canada Foundation for Innovation ;  
Ontario Research Fund

**Availability:** Free

**Resource Name:** COLT-Cancer

**Resource ID:** SCR\_006485

**Alternate IDs:** biotools:colt-cancer, nlx\_149426

**Alternate URLs:** <https://bio.tools/colt-cancer>

**Record Creation Time:** 20220129T080236+0000

**Record Last Update:** 20260803T040455+0000

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## Ratings and Alerts

No rating or validation information has been found for COLT-Cancer.

No alerts have been found for COLT-Cancer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

McGee SR, et al. (2017) Network Analysis Reveals A Signaling Regulatory Loop in the PIK3CA-mutated Breast Cancer Predicting Survival Outcome. Genomics, proteomics & bioinformatics, 15(2), 121.

Jaiswal A, et al. (2017) Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. Genome medicine, 9(1), 51.

Bridgett S, et al. (2017) CancerGD: A Resource for Identifying and Interpreting Genetic Dependencies in Cancer. Cell systems, 5(1), 82.

Kanhaiya K, et al. (2017) Controlling Directed Protein Interaction Networks in Cancer. Scientific reports, 7(1), 10327.

Davoli T, et al. (2016) Functional genomics reveals that tumors with activating phosphoinositide 3-kinase mutations are dependent on accelerated protein turnover. Genes & development, 30(24), 2684.

Pritykin Y, et al. (2015) Genome-Wide Detection and Analysis of Multifunctional Genes. PLoS computational biology, 11(10), e1004467.

Vu V, et al. (2015) Natural Variation in Gene Expression Modulates the Severity of Mutant Phenotypes. Cell, 162(2), 391.

Chen CY, et al. (2014) Dissecting the human protein-protein interaction network via phylogenetic decomposition. Scientific reports, 4, 7153.

Zaman N, et al. (2013) Signaling network assessment of mutations and copy number variations predict breast cancer subtype-specific drug targets. *Cell reports*, 5(1), 216.

Shao DD, et al. (2013) ATARiS: computational quantification of gene suppression phenotypes from multisample RNAi screens. *Genome research*, 23(4), 665.

Galperin MY, et al. (2012) The 2012 Nucleic Acids Research Database Issue and the online Molecular Biology Database Collection. *Nucleic acids research*, 40(Database issue), D1.