Resource Summary Report

Generated by dkNET on May 11, 2025

TransFIC

RRID:SCR_010788
Type: Tool

Proper Citation

TransFIC (RRID:SCR_010788)

Resource Information

URL: http://bg.upf.edu/transfic/home

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Description: A method to transform Functional Impact scores taking into account the differences in basal tolerance to germline SNVs of genes that belong to different functional classes.

Abbreviations: TransFIC

Synonyms: TRANSformed Functional Impact for Cancer

Resource Type: data analysis software, software application, data processing software, analysis service resource, service resource, production service resource, data analysis service, software resource

Related Condition: Cancer

Funding:

Resource Name: TransFIC

Resource ID: SCR_010788

Alternate IDs: OMICS_00164

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250509T055934+0000

Ratings and Alerts

No rating or validation information has been found for TransFIC.

No alerts have been found for TransFIC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Koh HYK, et al. (2024) Machine learning optimized DriverDetect software for high precision prediction of deleterious mutations in human cancers. Scientific reports, 14(1), 22618.

Ozturk K, et al. (2022) Predicting functional consequences of mutations using molecular interaction network features. Human genetics, 141(6), 1195.

Raimondi D, et al. (2021) Current cancer driver variant predictors learn to recognize driver genes instead of functional variants. BMC biology, 19(1), 3.

Donato L, et al. (2020) Possible A2E Mutagenic Effects on RPE Mitochondrial DNA from Innovative RNA-Seq Bioinformatics Pipeline. Antioxidants (Basel, Switzerland), 9(11).

Chen H, et al. (2020) Comprehensive assessment of computational algorithms in predicting cancer driver mutations. Genome biology, 21(1), 43.

Zhao X, et al. (2019) Integrative analysis of cancer driver genes in prostate adenocarcinoma. Molecular medicine reports, 19(4), 2707.

Namgoong S, et al. (2018) Association analysis of RTEL1 variants with risk of adult gliomas in a Korean population. PloS one, 13(11), e0207660.

Wooller SK, et al. (2017) Bioinformatics in translational drug discovery. Bioscience reports, 37(4).

Qiao L, et al. (2017) Mitochondrial DNA depletion, mitochondrial mutations and high TFAM expression in hepatocellular carcinoma. Oncotarget, 8(48), 84373.

Jaratlerdsiri W, et al. (2017) Next generation mapping reveals novel large genomic rearrangements in prostate cancer. Oncotarget, 8(14), 23588.

Fancello L, et al. (2017) The ribosomal protein gene RPL5 is a haploinsufficient tumor

suppressor in multiple cancer types. Oncotarget, 8(9), 14462.

Castellana S, et al. (2017) High-confidence assessment of functional impact of human mitochondrial non-synonymous genome variations by APOGEE. PLoS computational biology, 13(6), e1005628.

Mao R, et al. (2017) Whole genome sequencing of matched tumor, adjacent non-tumor tissues and corresponding normal blood samples of hepatocellular carcinoma patients revealed dynamic changes of the mutations profiles during hepatocarcinogenesis. Oncotarget, 8(16), 26185.

Tian R, et al. (2015) Computational methods and resources for the interpretation of genomic variants in cancer. BMC genomics, 16 Suppl 8(Suppl 8), S7.