Resource Summary Report

Generated by NIF on Apr 17, 2025

InVEx

RRID:SCR_008734
Type: Tool

Proper Citation

InVEx (RRID:SCR_008734)

Resource Information

URL: http://www.broadinstitute.org/cancer/cga/invex/

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Description: A permutation-based method (written in Python) for ascertaining genes with a somatic mutation distribution showing evidence of positive selection for non-silent mutations.

Abbreviations: InVEx

Synonyms: Introns Vs Exons

Resource Type: software resource

Funding:

Resource Name: InVEx

Resource ID: SCR_008734

Alternate IDs: OMICS_00151

Record Creation Time: 20220129T080249+0000

Record Last Update: 20250410T065734+0000

Ratings and Alerts

No rating or validation information has been found for InVEx.

No alerts have been found for InVEx.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Yao Z, et al. (2023) Proteogenomics of different urothelial bladder cancer stages reveals distinct molecular features for papillary cancer and carcinoma in situ. Nature communications, 14(1), 5670.

Wang Y, et al. (2023) Proteogenomics of diffuse gliomas reveal molecular subtypes associated with specific therapeutic targets and immune-evasion mechanisms. Nature communications, 14(1), 505.

Riaz N, et al. (2016) Recurrent SERPINB3 and SERPINB4 mutations in patients who respond to anti-CTLA4 immunotherapy. Nature genetics, 48(11), 1327.

Guan J, et al. (2015) Cancer systems biology of TCGA SKCM: efficient detection of genomic drivers in melanoma. Scientific reports, 5, 7857.