Resource Summary Report

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MoKCa- Mutations of Kinases in Cancer

RRID:SCR_007805
Type: Tool

Proper Citation

MoKCa- Mutations of Kinases in Cancer (RRID:SCR_007805)

Resource Information

URL: http://strubiol.icr.ac.uk/extra/mokca/

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Description: The database has been developed to structurally and functionally annotate, and where possible predict, the phenotypic consequences of mutations in protein kinases implicated in cancer. The 518 human protein kinases identified in KinBase, are listed alphabetically to facilitate browsing, and each gene is labelled with tumour type(s) in which mutations have been found. The list can also be sorted by selective pressure - the ratio of non-synonymous:synonymous mutations compared to that expected by chance, and by "rank" - the probability of the mutated gene containing at least 1 driver mutation. Both these measures can be used to predict which kinases contain driver mutations, i.e. those that are causal of the cancer, rather than passenger mutations that have arisen by chance but do not contribute to disease. Entries can be searched directly by gene name. Mutational data from the Cancer Genome Project have been mapped onto the crystal structures of the affected human protein domains where known, or onto the most closely related homologous structure if not known. Proteins are linked to functional annotation resources and are annotated with structural and functional features such as domains and phosphorylation sites, and protein interaction partners. This annotation is being expanded to include PROSITE patterns, which identify short peptide segments of functional consequence and sites of post-translation modifications, and Driver/Passenger assessment of the mutations.

Abbreviations: MokCa

Synonyms: Mutations of Kinases in Cancer

Resource Type: database, data or information resource

Resource Name: MoKCa- Mutations of Kinases in Cancer

Resource ID: SCR_007805

Alternate IDs: nif-0000-03155

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260807T042701+0000

Ratings and Alerts

No rating or validation information has been found for MoKCa- Mutations of Kinases in Cancer.

No alerts have been found for MoKCa- Mutations of Kinases in Cancer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Mirza Z, et al. (2024) Landscape of FLT3 Variations Associated with Structural and Functional Impact on Acute Myeloid Leukemia: A Computational Study. International journal of molecular sciences, 25(6).

Sudhakar P, et al. (2022) Tailoring Multi-omics to Inflammatory Bowel Diseases: All for One and One for All. Journal of Crohn's & colitis, 16(8), 1306.

Huang KK, et al. (2018) Genomic and Epigenomic Profiling of High-Risk Intestinal Metaplasia Reveals Molecular Determinants of Progression to Gastric Cancer. Cancer cell, 33(1), 137.

Baeissa H, et al. (2017) Identification and analysis of mutational hotspots in oncogenes and tumour suppressors. Oncotarget, 8(13), 21290.

Pavlopoulou A, et al. (2015) Human cancer databases (review). Oncology reports, 33(1), 3.

Izarzugaza JM, et al. (2012) Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. Frontiers in physiology, 3, 323.

Bulk E, et al. (2012) Mutations of the EPHB6 receptor tyrosine kinase induce a pro-metastatic phenotype in non-small cell lung cancer. PloS one, 7(12), e44591.