

Resource Summary Report

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Hydra

RRID:SCR_005260

Type: Tool

Proper Citation

Hydra (RRID:SCR_005260)

Resource Information

URL: <http://code.google.com/p/hydra-sv/>

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Description: Software that detects structural variation (SV) breakpoints by clustering discordant paired-end alignments whose signatures corroborate the same putative breakpoint. Hydra can detect breakpoints caused by all classes of structural variation. Moreover, it was designed to detect variation in both unique and duplicated genomic regions; therefore, it will examine paired-end reads having multiple discordant alignments. Hydra does not attempt to classify SV breakpoints based on the mapping distances and orientations of each breakpoint cluster, it merely detects and reports breakpoints. This is an intentional decision, as it was observed that in loci affected by complex rearrangements, the type of variant suggested by the breakpoint signature is not always correct. Hydra does report the orientations, distances, number of supporting read-pairs, etc., for each breakpoint. It is suggested that downstream methods be used to classify variants based on the genomic features that they overlap and the co-occurrence of other breakpoints. For example, they developed BEDTools for exactly this purpose and the breakpoints reported by Hydra are in the BEDPE format used by BEDTools. Future releases of Hydra will include scripts that assist in the classification process.

Abbreviations: Hydra

Synonyms: hydra-sv

Resource Type: software resource

Keywords: structural variation, genome, genomic, breakpoint, c++, cnv, pem, paired-end, segmental duplication, rearrangement

Resource Name: Hydra

Resource ID: SCR_005260

Alternate IDs: OMICS_00318

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260815T182302+0000

Ratings and Alerts

No rating or validation information has been found for Hydra.

No alerts have been found for Hydra.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 119 mentions in open access literature.

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

Groh R, et al. (2026) EdgeVolution: democratizing multi-objective neural architecture search and end-to-end deployment on microcontrollers. Communications engineering, 5(1).

Han C, et al. (2026) A Controlled Study of Physics-Informed Auxiliary Supervision and Scalar Triplet Attention in Equivariant Molecular Force Fields. Molecules (Basel, Switzerland), 31(12).

Martínez-Buitrago E, et al. (2026) National representative survey of pretreatment HIV drug resistance in Colombia: analysis of antiretroviral resistance-associated mutations using next-generation sequencing. The Journal of antimicrobial chemotherapy, 81(1).

Zhang H, et al. (2025) Subtypes of Insomnia Disorder Identified by Cortical Morphometric Similarity Network. Human brain mapping, 46(1), e70119.

Han S, et al. (2025) Common neuroanatomical differential factors underlying heterogeneous gray matter volume variations in five common psychiatric disorders. Communications biology, 8(1), 238.

Gimferrer M, et al. (2025) Accurate vibrational hydrogen-bond shift predictions with multicomponent DFT. Chemical science, 16(24), 11002.

Turner LD, et al. (2025) Inhibiting inositol transport disrupts metabolite profiles and mimics heat stress in a model cnidarian-Symbiodiniaceae symbiosis. Communications biology, 8(1), 755.

Alzugaray ME, et al. (2025) Piezo proteins, mechano reception and behaviour in Hydra. Scientific reports, 15(1), 6440.

Ruambo FA, et al. (2025) Brute-force attack mitigation on remote access services via software-defined perimeter. *Scientific reports*, 15(1), 18599.

Stoilova MI, et al. (2025) Shedding Light on Patterns of Unconventional Expression of Opsin Genes in *Hydra vulgaris*. *Integrative and comparative biology*, 65(3), 648.

Mittmann G, et al. (2025) Pathologist-like explainable AI for interpretable Gleason grading in prostate cancer. *Nature communications*, 16(1), 8959.

van der Weg K, et al. (2025) TopEC: prediction of Enzyme Commission classes by 3D graph neural networks and localized 3D protein descriptor. *Nature communications*, 16(1), 2737.

Dotrang T, et al. (2025) HIVGenoPipe: a nextflow pipeline for the detection of HIV-1 drug resistance using a real-time sample-specific reference sequence. *BMC bioinformatics*, 26(1), 168.

Klein D, et al. (2025) Mapping cells through time and space with moscot. *Nature*, 638(8052), 1065.

Logrippo S, et al. (2025) Toward the Optimal Choice of Gelled Vehicles for Oral Drug Administration in Dysphagic Patients. *Pharmaceutics*, 17(2).

Weevers SL, et al. (2025) Mechanochemical patterning localizes the organizer of a luminal epithelium. *Science advances*, 11(26), eadu2286.

Agam O, et al. (2025) Stochastic morphological swings in *Hydra* regeneration: A manifestation of noisy canalized morphogenesis. *Proceedings of the National Academy of Sciences of the United States of America*, 122(1), e2415736121.

Liu L, et al. (2024) Elucidating Multimodal Imaging Patterns in Accelerated Brain Aging: Heterogeneity through a Discriminant Analysis Approach Using the UK Biobank Dataset. *Bioengineering (Basel, Switzerland)*, 11(2).

Gosztyla ML, et al. (2024) Integrated multi-omics analysis of zinc-finger proteins uncovers roles in RNA regulation. *Molecular cell*, 84(19), 3826.

Sahm A, et al. (2024) *Hydra* has mammal-like mutation rates facilitating fast adaptation despite its nonaging phenotype. *Genome research*, 34(12), 2217.