

Resource Summary Report

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Assembly/Alignment/Annotation of 12 Related Drosophila Species

RRID:SCR_002921

Type: Tool

Proper Citation

Assembly/Alignment/Annotation of 12 Related Drosophila Species (RRID:SCR_002921)

Resource Information

URL: <http://rana.lbl.gov/drosophila>

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Description: A single source for sequences, assemblies, annotations and analyses of the genomes of members of the fruitfly genus *Drosophila*. It is meant as resource for Drosophilists and other researchers interested in comparative analysis of these species and their genomes. There are pages for each species, as well as pages for different types of multi-species resources (e.g. alignments). If you have a public resource that will help this project, please consider making it available through this page by emailing multiple_at_fruitfly.org.

Synonyms: AAA: 12 Drosophila Genomes

Resource Type: data set, data or information resource, organism-related portal, topical portal, portal

Keywords: sequence, annotation, analysis, genome, fruitfly, drosophila, research, comparative, alignment, assembly

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Assembly/Alignment/Annotation of 12 Related Drosophila Species

Resource ID: SCR_002921

Alternate IDs: nif-0000-30021

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260729T044034+0000

Ratings and Alerts

No rating or validation information has been found for Assembly/Alignment/Annotation of 12 Related Drosophila Species.

No alerts have been found for Assembly/Alignment/Annotation of 12 Related Drosophila Species.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Leung W, et al. (2015) Drosophila muller f elements maintain a distinct set of genomic properties over 40 million years of evolution. G3 (Bethesda, Md.), 5(5), 719.

Gu W, et al. (2014) The impact of RNA structure on coding sequence evolution in both bacteria and eukaryotes. BMC evolutionary biology, 14, 87.

Lyu Y, et al. (2014) New microRNAs in Drosophila--birth, death and cycles of adaptive evolution. PLoS genetics, 10(1), e1004096.

Gao G, et al. (2014) A long-term demasculinization of X-linked intergenic noncoding RNAs in Drosophila melanogaster. Genome research, 24(4), 629.

Will S, et al. (2013) Structure-based whole-genome realignment reveals many novel noncoding RNAs. Genome research, 23(6), 1018.

Baggio F, et al. (2013) 2mit, an intronic gene of Drosophila melanogaster timeless2, is involved in behavioral plasticity. PloS one, 8(9), e76351.

Seetharam A, et al. (2012) Whole genome phylogenies for multiple Drosophila species. BMC research notes, 5, 670.

Miura S, et al. (2011) Evolutionary changes of the target sites of two microRNAs encoded in the Hox gene cluster of Drosophila and other insect species. Genome biology and evolution, 3, 129.

Callahan B, et al. (2011) Correlated evolution of nearby residues in Drosophilid proteins. PLoS genetics, 7(2), e1001315.

Nozawa M, et al. (2010) Origins and evolution of microRNA genes in Drosophila species. Genome biology and evolution, 2, 180.

Conceição IC, et al. (2010) Odorant receptor (Or) genes: polymorphism and divergence in the D. melanogaster and D. pseudoobscura lineages. PloS one, 5(10), e13389.

Farlow A, et al. (2010) Nonsense-mediated decay enables intron gain in *Drosophila*. *PLoS genetics*, 6(1), e1000819.

Sánchez-Gracia A, et al. (2010) Two frequenins in *Drosophila*: unveiling the evolutionary history of an unusual neuronal calcium sensor (NCS) duplication. *BMC evolutionary biology*, 10, 54.

Granzotto A, et al. (2009) The evolutionary dynamics of the Helena retrotransposon revealed by sequenced *Drosophila* genomes. *BMC evolutionary biology*, 9, 174.

Yang L, et al. (2009) A comparative analysis of divergently-paired genes (DPGs) among *Drosophila* and vertebrate genomes. *BMC evolutionary biology*, 9, 55.

Zhu B, et al. (2008) *Drosophila* neurotrophins reveal a common mechanism for nervous system formation. *PLoS biology*, 6(11), e284.

Paquet ER, et al. (2008) Modeling an evolutionary conserved circadian cis-element. *PLoS computational biology*, 4(2), e38.

Zhou T, et al. (2008) Detecting clusters of mutations. *PloS one*, 3(11), e3765.

Yang HP, et al. (2008) Abundant and species-specific DINE-1 transposable elements in 12 *Drosophila* genomes. *Genome biology*, 9(2), R39.

Hahn MW, et al. (2007) Bias in phylogenetic tree reconciliation methods: implications for vertebrate genome evolution. *Genome biology*, 8(7), R141.