Resource Summary Report

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UW Genome Sciences

RRID:SCR_008562
Type: Tool

Proper Citation

UW Genome Sciences (RRID:SCR_008562)

Resource Information

URL: http://repeatmasker.genome.washington.edu

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Description: Welcome to the Department of Genome Sciences, which began in September 2001 by the fusion of the Departments of Genetics and Molecular Biotechnology. Our goal is to address leading edge questions in biology and medicine by developing and applying genetic, genomic and computational approaches that take advantage of genomic information now available for humans, model organisms and a host of other species. Our faculty study a broad range of topics, including the genetics of E. coli, yeast, C. elegans, Drosophila, and mouse; human and medical genetics; mathematical, statistical and computer methods for analyzing genomes, and theoretical and evolutionary genetics; and genome-wide studies by such approaches as sequencing, transcriptional and translational analysis, polymorphism detection and identification of protein interactions. Our chair, Dr. Robert Waterston, joined the department in January 2003. Our department includes both faculty with primary appointments in Genome Sciences, as well as adjuncts in other departments and Seattle institutions. Nine faculty are members of the National Academy of Sciences, including 2001 Nobel Prize winner Dr. Lee Hartwell, who conducted much of his groundbreaking work in the Department of Genetics. Five training faculty are Howard Hughes Medical Institute Investigators. Graduate research in the Department leads to a Ph.D. in Genome Sciences and students may also choose to participate in the Computational Molecular Biology or Molecular Medicine programs. Our department has around 55 - 60 graduate students at any given time and has moved into the new William H. Foege Building.

Synonyms: UW Genome Sciences

Resource Type: organization portal, portal, data or information resource

Funding:

Resource Name: UW Genome Sciences

Resource ID: SCR_008562

Alternate IDs: nif-0000-31441

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250416T063523+0000

Ratings and Alerts

No rating or validation information has been found for UW Genome Sciences.

No alerts have been found for UW Genome Sciences.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Park JY, et al. (2016) Evolutionary constraints over microsatellite abundance in larger mammals as a potential mechanism against carcinogenic burden. Scientific reports, 6, 25246.

Ekenstedt KJ, et al. (2014) An ARHGEF10 deletion is highly associated with a juvenile-onset inherited polyneuropathy in Leonberger and Saint Bernard dogs. PLoS genetics, 10(10), e1004635.

Steward CA, et al. (2013) The non-obese diabetic mouse sequence, annotation and variation resource: an aid for investigating type 1 diabetes. Database : the journal of biological databases and curation, 2013, bat032.

Micale L, et al. (2012) A fish-specific transposable element shapes the repertoire of p53 target genes in zebrafish. PloS one, 7(10), e46642.

Huh JW, et al. (2012) Large-scale transcriptome sequencing and gene analyses in the crab-eating macaque (Macaca fascicularis) for biomedical research. BMC genomics, 13, 163.

Ferguson AA, et al. (2012) Mutator-like elements with multiple long terminal inverted repeats in plants. Comparative and functional genomics, 2012, 695827.

Traherne JA, et al. (2010) Mechanisms of copy number variation and hybrid gene formation in the KIR immune gene complex. Human molecular genetics, 19(5), 737.

Drögemüller C, et al. (2009) A missense mutation in the SERPINH1 gene in Dachshunds with osteogenesis imperfecta. PLoS genetics, 5(7), e1000579.

Boles MK, et al. (2009) Discovery of candidate disease genes in ENU-induced mouse mutants by large-scale sequencing, including a splice-site mutation in nucleoredoxin. PLoS genetics, 5(12), e1000759.

Diekmann K, et al. (2009) Complete chloroplast genome sequence of a major allogamous forage species, perennial ryegrass (Lolium perenne L.). DNA research : an international journal for rapid publication of reports on genes and genomes, 16(3), 165.

Zimmermann T, et al. (2008) Cloning and characterization of the promoter of Hugl-2, the human homologue of Drosophila lethal giant larvae (lgl) polarity gene. Biochemical and biophysical research communications, 366(4), 1067.

Haase B, et al. (2007) Allelic heterogeneity at the equine KIT locus in dominant white (W) horses. PLoS genetics, 3(11), e195.

Waters PD, et al. (2007) Evolutionary history of LINE-1 in the major clades of placental mammals. PloS one, 2(1), e158.

McElwee JJ, et al. (2007) Evolutionary conservation of regulated longevity assurance mechanisms. Genome biology, 8(7), R132.

Gunji T, et al. (2007) Functional polymorphisms of the FPR1 gene and aggressive periodontitis in Japanese. Biochemical and biophysical research communications, 364(1), 7.

Leeb T, et al. (2006) A human-horse comparative map based on equine BAC end sequences. Genomics, 87(6), 772.

Paulis M, et al. (2006) A set of duplicons on human chromosome 9 is involved in the origin of a supernumerary marker chromosome. Genomics, 87(6), 747.

Weber MJ, et al. (2006) Mammalian small nucleolar RNAs are mobile genetic elements. PLoS genetics, 2(12), e205.

Barta E, et al. (2005) DoOP: Databases of Orthologous Promoters, collections of clusters of orthologous upstream sequences from chordates and plants. Nucleic acids research, 33(Database issue), D86.

Drews VL, et al. (2005) Multiple transcripts of sodium channel SCN8A (Na(V)1.6) with alternative 5'- and 3'-untranslated regions and initial characterization of the SCN8A promoter. Genomics, 85(2), 245.