Resource Summary Report

Generated by dkNET on May 8, 2025

X:MAP

RRID:SCR_006029
Type: Tool

Proper Citation

X:MAP (RRID:SCR_006029)

Resource Information

URL: http://xmap.picr.man.ac.uk

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Description: X:Map is a project for mapping between Affymetrix Exon Arrays and their corresponding genome data. It consists of a website for general visualisation of Gene/Transcript/Exon/Probeset relationships, and an R package exonmap to support statistical analysis of Exon Array experiments. Affymetrix exon arrays aim to target every known and predicted exon in the human, mouse or rat genomes, and have reporters that extend beyond protein coding regions to other areas of the transcribed genome. This combination of increased coverage and precision is important because a substantial proportion of protein coding genes are predicted to be alternatively spliced, and because many non-coding genes are known also to be of biological significance. In order to fully exploit these arrays, it is necessary to associate each reporter on the array with the features of the genome it is targeting, and to relate these to gene and genome structure. X:Map is a genome annotation database that provides this information. Data can be browsed using a novel Google-maps based interface, and analysed and further visualized through an associated BioConductor package.

Synonyms: X:MAP

Resource Type: data or information resource, database

Funding:

Resource Name: X:MAP

Resource ID: SCR_006029

Alternate IDs: nif-0000-03645

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250507T060346+0000

Ratings and Alerts

No rating or validation information has been found for X:MAP.

No alerts have been found for X:MAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Mucaki EJ, et al. (2020) Expression Changes Confirm Genomic Variants Predicted to Result in Allele-Specific, Alternative mRNA Splicing. Frontiers in genetics, 11, 109.

Qu Z, et al. (2019) Visual Analytics of Genomic and Cancer Data: A Systematic Review. Cancer informatics, 18, 1176935119835546.

Leslie EJ, et al. (2016) A Genome-wide Association Study of Nonsyndromic Cleft Palate Identifies an Etiologic Missense Variant in GRHL3. American journal of human genetics, 98(4), 744.

Pavlopoulos GA, et al. (2015) Visualizing genome and systems biology: technologies, tools, implementation techniques and trends, past, present and future. GigaScience, 4, 38.

Rehrer CW, et al. (2012) Regional differences in subcutaneous adipose tissue gene expression. Obesity (Silver Spring, Md.), 20(11), 2168.

Vergara IA, et al. (2012) Genomic "Dark Matter" in Prostate Cancer: Exploring the Clinical Utility of ncRNA as Biomarkers. Frontiers in genetics, 3, 23.

White RE, et al. (2010) Extensive co-operation between the Epstein-Barr virus EBNA3 proteins in the manipulation of host gene expression and epigenetic chromatin modification. PloS one, 5(11), e13979.

Bradford JR, et al. (2010) A comparison of massively parallel nucleotide sequencing with

oligonucleotide microarrays for global transcription profiling. BMC genomics, 11, 282.

Bitton DA, et al. (2010) An integrated mass-spectrometry pipeline identifies novel protein coding-regions in the human genome. PloS one, 5(1), e8949.

Turro E, et al. (2010) MMBGX: a method for estimating expression at the isoform level and detecting differential splicing using whole-transcript Affymetrix arrays. Nucleic acids research, 38(1), e4.

Langer W, et al. (2010) Exon array analysis using re-defined probe sets results in reliable identification of alternatively spliced genes in non-small cell lung cancer. BMC genomics, 11, 676.

Shah SH, et al. (2009) Identifying differential exon splicing using linear models and correlation coefficients. BMC bioinformatics, 10, 26.

Phang T, et al. (2009) R and Bioconductor solutions for alternative splicing detection. Human genomics, 4(2), 131.

Jung K, et al. (2008) SNUGB: a versatile genome browser supporting comparative and functional fungal genomics. BMC genomics, 9, 586.

Barton G, et al. (2008) EMAAS: an extensible grid-based rich internet application for microarray data analysis and management. BMC bioinformatics, 9, 493.

Bitton DA, et al. (2008) Exon level integration of proteomics and microarray data. BMC bioinformatics, 9, 118.

Okoniewski MJ, et al. (2007) An annotation infrastructure for the analysis and interpretation of Affymetrix exon array data. Genome biology, 8(5), R79.