Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

ArrayOligoSelector

RRID:SCR_013494
Type: Tool

Proper Citation

ArrayOligoSelector (RRID:SCR_013494)

Resource Information

URL: http://arrayoligosel.sourceforge.net/

Proper Citation: ArrayOligoSelector (RRID:SCR_013494)

Description: Software program to systematically design gene specific long oligonucleotide probes for entire genomes, for the purpose of developing whole genome microarrays. For each open reading frame, the program optimizes the oligo selection based upon several parameters, including uniqueness in the genome, sequence complexity, lack of self-binding, GC content and proximity to the 3''end of the gene.

Abbreviations: ArrayOligoSelector

Resource Type: software resource

Defining Citation: PMID:12620119

Funding:

Availability: Free, Public, Commercial requires license, Use of the blat or gfclient options requires license

Resource Name: ArrayOligoSelector

Resource ID: SCR_013494

Alternate IDs: OMICS_00826

Record Creation Time: 20220129T080316+0000

Record Last Update: 20250410T070414+0000

Ratings and Alerts

No rating or validation information has been found for ArrayOligoSelector.

No alerts have been found for ArrayOligoSelector.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Degani G, et al. (2016) Genomic and functional analyses unveil the response to hyphal wall stress in Candida albicans cells lacking ?(1,3)-glucan remodeling. BMC genomics, 17, 482.

Ghosh S, et al. (2014) Copy number variation in the horse genome. PLoS genetics, 10(10), e1004712.

Abromaitis S, et al. (2013) Bartonella quintana deploys host and vector temperature-specific transcriptomes. PloS one, 8(3), e58773.

Dunn B, et al. (2012) Analysis of the Saccharomyces cerevisiae pan-genome reveals a pool of copy number variants distributed in diverse yeast strains from differing industrial environments. Genome research, 22(5), 908.

Schrimpe-Rutledge AC, et al. (2012) Comparative omics-driven genome annotation refinement: application across Yersiniae. PloS one, 7(3), e33903.

Papazisi L, et al. (2011) Investigating the genome diversity of B. cereus and evolutionary aspects of B. anthracis emergence. Genomics, 98(1), 26.

Papazisi L, et al. (2010) Tracing phylogenomic events leading to diversity of Haemophilus influenzae and the emergence of Brazilian Purpuric Fever (BPF)-associated clones. Genomics, 96(5), 290.

Ferrante MI, et al. (2009) Convergent extension movements and ciliary function are mediated by ofd1, a zebrafish orthologue of the human oral-facial-digital type 1 syndrome gene. Human molecular genetics, 18(2), 289.

Wardle FC, et al. (2006) Zebrafish promoter microarrays identify actively transcribed embryonic genes. Genome biology, 7(8), R71.

Goda T, et al. (2006) Genetic screens for mutations affecting development of Xenopus tropicalis. PLoS genetics, 2(6), e91.

Ralph SA, et al. (2005) Transcriptome analysis of antigenic variation in Plasmodium falciparum--var silencing is not dependent on antisense RNA. Genome biology, 6(11), R93.

Urisman A, et al. (2005) E-Predict: a computational strategy for species identification based on observed DNA microarray hybridization patterns. Genome biology, 6(9), R78.

Bozdech Z, et al. (2003) Expression profiling of the schizont and trophozoite stages of Plasmodium falciparum with a long-oligonucleotide microarray. Genome biology, 4(2), R9.