

Resource Summary Report

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CpG Island Searcher

RRID:SCR_008609

Type: Tool

Proper Citation

CpG Island Searcher (RRID:SCR_008609)

Resource Information

URL: <http://www.cpgislands.com>

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Description: The CpG island searcher screens for CpG islands which meet the criteria selected below in submitted DNA sequences. Abstract The unique variability in the 5' region of the GR gene, with 9 alternative first exons and 13 splice variants plays a critical role in transcriptional control maintaining homeostasis of the glucocorticoid receptor (GR). This 5'mRNA heterogeneity, common to all species investigated, remains untranslated since the alternative first exons are spliced to exon 2 immediately upstream of the translation initiation codon. These alternative first exons are located either immediately upstream of the coding exons in the CpG island (exons B-H and J), or further upstream (exons 1A and 1I). The mechanisms regulating the differential usage of these first exons in different tissues and individuals, and the role of the 5'UTR in the splicing of the coding exons are still poorly understood. Here we review some of the mechanisms that have so far been identified. Data from our laboratory and others have shown that the multiple first exons represent only a first layer of complexity orchestrated probably by tissue-specific transcription factors. Modulation of alternative first exon activity by epigenetic methylation of their promoters represents a second layer of complexity at least partially controlled by perinatal programming. The alternative promoter usage also appears to affect the 3' splicing generating the different GR coding variants, GRalpha, GRbeta, and GR-P. Aberrant GR levels are associated with stress-related disorders such as depression, and affect social behaviour, mood, learning and memory. Dissecting how tissue-specific GR levels are regulated, in particular in the brain, is a first step to understand the significance of aberrant GR levels in disease and behaviour. Copyright 2010. Published by Elsevier Inc.

Synonyms: CpG Island Searcher

Resource Type: database, data or information resource

Resource Name: CpG Island Searcher

Resource ID: SCR_008609

Alternate IDs: nif-0000-31955

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260803T040527+0000

Ratings and Alerts

No rating or validation information has been found for CpG Island Searcher.

No alerts have been found for CpG Island Searcher.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Zhou J, et al. (2025) Discovery and validation of Hsa-microRNA-3665 promoter methylation as a potential biomarker for the prognosis of esophageal squamous cell carcinoma. International journal of clinical oncology, 30(2), 309.

Lin Z, et al. (2020) LXR activation potentiates sorafenib sensitivity in HCC by activating microRNA-378a transcription. Theranostics, 10(19), 8834.

Ming XY, et al. (2018) RHCG Suppresses Tumorigenicity and Metastasis in Esophageal Squamous Cell Carcinoma via Inhibiting NF- κ B Signaling and MMP1 Expression. Theranostics, 8(1), 185.

Baquedano MS, et al. (2017) DNA methylation is not involved in specific down-regulation of HSD3B2, NR4A1 and RARB genes in androgen-secreting cells of human adrenal cortex. Molecular and cellular endocrinology, 441, 46.

Schmid G, et al. (2016) Expression and promotor hypermethylation of miR-34a in the various histological subtypes of ovarian cancer. BMC cancer, 16, 102.

Xu G, et al. (2014) Small nucleolar RNA 113-1 suppresses tumorigenesis in hepatocellular carcinoma. Molecular cancer, 13, 216.

Prasad SB, et al. (2014) Down Regulation of FOXO1 Promotes Cell Proliferation in Cervical Cancer. Journal of Cancer, 5(8), 655.

Yang TC, et al. (2014) Malondialdehyde mediates oxidized LDL-induced coronary toxicity through the Akt-FGF2 pathway via DNA methylation. Journal of biomedical science, 21(1),

11.

Lu S, et al. (2014) Zn²⁺ blocks annealing of complementary single-stranded DNA in a sequence-selective manner. *Scientific reports*, 4, 5464.

Soung YH, et al. (2014) Epigenetic silencing of ARRDC3 expression in basal-like breast cancer cells. *Scientific reports*, 4, 3846.

Thériault BL, et al. (2014) Transcriptional and epigenetic regulation of KIF14 overexpression in ovarian cancer. *PloS one*, 9(3), e91540.

Cai J, et al. (2013) Deregulation of let-7e in epithelial ovarian cancer promotes the development of resistance to cisplatin. *Oncogenesis*, 2(10), e75.

Liu Y, et al. (2013) Low expression of miR-196b enhances the expression of BCR-ABL1 and HOXA9 oncogenes in chronic myeloid leukemogenesis. *PloS one*, 8(7), e68442.

Babu K, et al. (2012) Epigenetic regulation of ABCG2 gene is associated with susceptibility to xenobiotic exposure. *Journal of proteomics*, 75(12), 3410.

Cebrian V, et al. (2011) KISS1 methylation and expression as tumor stratification biomarkers and clinical outcome prognosticators for bladder cancer patients. *The American journal of pathology*, 179(2), 540.

Hyldig SM, et al. (2011) Epigenetic reprogramming in the porcine germ line. *BMC developmental biology*, 11, 11.

Incoronato M, et al. (2011) Epigenetic regulation of miR-212 expression in lung cancer. *PloS one*, 6(11), e27722.

Qiu X, et al. (2010) Equitoxic doses of 5-azacytidine and 5-aza-2'deoxyctidine induce diverse immediate and overlapping heritable changes in the transcriptome. *PloS one*, 5(9).

Wang XH, et al. (2010) S100A6 overexpression is associated with poor prognosis and is epigenetically up-regulated in gastric cancer. *The American journal of pathology*, 177(2), 586.

Zhang Y, et al. (2009) DNA methylation analysis of chromosome 21 gene promoters at single base pair and single allele resolution. *PLoS genetics*, 5(3), e1000438.