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Epigenetic basis of hepatocellular carcinoma: A network-based integrative meta-analysis

Bhat V *et al.* Epigenetic basis of HCC

Venkat Bhat, Sujitha Srinathan, Elisa Pasini, Marc Angeli, Emily Chen, Cristina Baciu, Mamatha Bhat

Abstract

AIM

To identify the key epigenetically modulated genes and pathways in HCC by performing an integrative meta-analysis of all major, well-annotated and publicly available methylation datasets using tools of network analysis.

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Integrative Genomic Analysis Identifies the Core Transcriptional ...

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作者: C Allain - 2016 - 被引用次数: 2 - 相关文章

2016年9月12日 - (1)INSERM, UMR 991, Liver Metabolisms and Cancer, University of ... **Integrative** genomics helped characterize molecular heterogeneity in **hepatocellular carcinoma** ... Here, we performed a **meta-analysis** of 15 independent datasets (n ... specific hallmarks associated with protein turnover and **epigenetics**.

缺少字词: **basis network based**

Identification of Drivers from Cancer Genome Diversity in ... - NCBI - NIH

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作者: A Takai - 2014 - 被引用次数: 26 - 相关文章

2014年6月20日 - **Hepatocellular carcinoma** (HCC) is one of the most common cancers ... of breast cancers is **based** on histopathological grade and tumor type, Accordingly, a **meta-analysis** of gene expression data from eight Cancer Genome Atlas Research **Network Integrated** genomic analyses of ovarian carcinoma.

Dysregulated signaling hubs of liver lipid metabolism reveal ...

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Frontiers | Hepatocellular carcinoma: a systems biology perspective ...

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作者: LA D'Alessandro - 2013 - 被引用次数: 11 - 相关文章

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[PDF] Hepatocellular carcinoma: a systems biology perspective - Frontiers

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2013年2月25日 - Keywords: HCC, mathematical modeling, network analysis, gene expression ... systems-wide analysis based on high-throughput gene expression ... expression data and the epigenetic DNA methylation status. The integrated Clinical Omics Database (iCOD) collects all ... plex molecular basis of liver dis-

Regulation of gene expression in HBV-and HCV-related ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4276171/> - 翻译此页

作者: X Zhou - 2014 - 被引用次数: 3 - 相关文章

2014年11月15日 - HBV- and HCV-induced HCC develops in an environment of inflammation ... HBx can also regulate the epigenetic control of cDNA function in HBV ... Centralities based analysis for the co-expression network was ... Compared to most existing meta-analysis methods, this new model enables the integrative ...



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An overview of hepatocellular carcinoma study by omics-based methods

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作者: Y Pei - 2009 - 被引用次数: 57 - 相关文章

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2014年6月20日 - A **meta-analysis** of 159 **HCC** array CGHs was able to discover significant to **HCC** development through the modulation of the **epigenetic** state; ... Table 1 summarizes candidate driver genes of **HCC** based on Cancer Genome Atlas Research **Network Integrated** genomic analyses of ovarian