



A four-methylated mRNA signature-based risk score system ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6339794>

Jan 15, 2019 · Here, Risk Score (patient) is a MDEG signature risk score for a HCC patient. In addition, mRNA_i represents the *i*th prognostic mRNA, while expression (mRNA_i) is the expression value of mRNA_i for the patient. Coefficient (mRNA_i) is the regression coefficient of mRNA_i, which represents the contribution of mRNA_i to the prognostic risk score. Based on the risk score, patients can be ...

Cited by: 1 Author: Yu Wang, Zhiping Ruan, Sizhe Yu, Tao Ti...
Publish Year: 2019

Connectivity-based risk score for hepatocellular carcinoma ...

<https://aasidpubs.onlinelibrary.wiley.com/doi/10.1002/hep.26348>

Kim et al. 1 proposed a 65-gene-based risk score classifier of overall survival in hepatocellular carcinoma (HCC). The risk score, derived by multiplying the expression level of a gene by its Cox coefficient, could robustly predict overall survival of HCC patients. Its clinical usefulness was further confirmed in a second test cohort.

Cited by: 1 Author: Hua Ye, Wei Liu
Publish Year: 2013

The Radiogenomic Risk Score: Construction of a Prognostic ...

<https://pubs.rsna.org/doi/10.1148/radiol.2015150800>

A SOMA for a clear-cell renal cell carcinoma prognostic multigene signature, termed a radiogenomic risk score, was trained (n = 70) and validated (n = 77) in independent data sets and shown to predict disease-specific survival, independent of disease stage, disease grade, and performance status (multivariate Cox model, P < .05 and log-rank P < .001).

Cited by: 25 Author: Neema Jamshidi, Eric Jonasch, Matthew ...
Publish Year: 2015

Sixty-five gene-based risk score classifier predicts ...

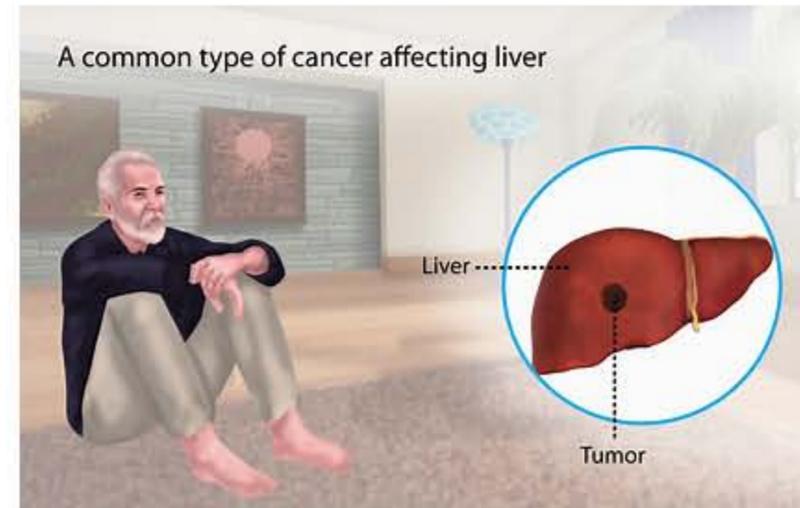
<https://aasidpubs.onlinelibrary.wiley.com/doi/full/10.1002/hep.24813>

Nov 22, 2011 · In the current study we aimed to develop an easy-to-use risk score with a limited number of genes that can robustly predict prognosis of patients with hepatocellular carcinoma (HCC). The risk score was developed using Cox coefficient values of 65 genes in the training set (n = 139) and its robustness was validated in test sets (n = 292).

Cited by: 73 Author: Soo Mi Kim, Soo Mi Kim, Sun Hee Leem...
Publish Year: 2012

Hepatocellular Carcinoma

Medical Condition



The most common form of liver cancer often seen in people with chronic liver diseases like cirrhosis.

- Rare (Fewer than 200,000 cases per year in US)
- May be preventable by vaccine
- Often requires lab test or imaging
- Treatment from medical professional advised
- Can last several months or years

Caused mainly due to the chronic infection of the liver or DNA mutation of the liver cells. Characterized by unexplained weight loss, upper abdominal pain and yellowing of the skin. Treatment options include hepatectomy, target drug delivery and the use of radiation to kill the cancerous cells.

Symptoms

The early stages of the disease do not present any symptoms but in the later stages the symptoms which are noted are as follows:

- Upper abdominal pain



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Name of Journal: *World Journal of Gastroenterology*

Manuscript NO: 51680

Manuscript Type: ORIGINAL ARTICLE

Basic Study

Construction of a risk score prognosis model based on hepatocellular carcinoma microenvironment

Zhang FP *et al.* Risk score prognosis model for HCC

Abstract

BACKGROUND

Hepatocellular carcinoma (HCC) is a common cancer with a poor prognosis.

Previous studies revealed that the tumor microenvironment (TME) plays an important role in HCC progression, recurrence, and metastasis, leading to poor prognosis. However, the influence of genes involved in TME on the prognosis

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Development and validation of a TP53-associated immune ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6491941>

Mar 16, 2019 · The expression of CTLA-4, PD-1 and TIM-3 in the high-risk HCC group was significantly higher than that in the low-risk HCC group ($P < 0.05$), indicating that the poor prognosis of high-risk HCC patients is partly due to the immunosuppressive microenvironment (Fig. 5 B).

The Radiogenomic Risk Score: Construction of a Prognostic ...

<https://pubs.rsna.org/doi/10.1148/radiol.2015150800>

A SOMA for a clear-cell renal cell carcinoma prognostic multigene signature, termed a radiogenomic risk score, was trained ($n = 70$) and validated ($n = 77$) in independent data sets and shown to predict disease-specific survival, independent of disease stage, disease grade, and performance status (multivariate Cox model, $P < .05$ and log-rank $P < .001$).

Cited by: 26 Author: Neema Jamshidi, Eric Jonasch, Matthew ...

Publish Year: 2015

Risk Prediction of Hepatocellular Carcinoma in Patients ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4553222>

Nov 15, 2014 · Based on the final model, heretofore named the ADRESS-HCC (reflecting the 6 identified predictors-age, diabetes, race, etiology of cirrhosis, sex, and severity of liver dysfunction), a risk score was developed to calculate the 1-year risk of HCC as shown in Table 3.

Cited by: 79 Author: Jennifer A. Flemming, Ju Dong Yang, Eric...

Publish Year: 2014

Sixty-five gene-based risk score classifier predicts ...

<https://aasldpubs.onlinelibrary.wiley.com/doi/full/10.1002/hep.24813>

Nov 22, 2011 · In the current study we aimed to develop an easy-to-use risk score with a limited number of genes that can robustly predict prognosis of patients with hepatocellular carcinoma (HCC). The risk score was developed using Cox coefficient values of 65 genes in the training set ($n = 139$) and its robustness was validated in test sets ($n = 292$).

Cited by: 74 Author: Soo Mi Kim, Soo Mi Kim, Sun Hee Leem...

Publish Year: 2012

Mining TCGA Database for Tumor Microenvironment ...

<https://www.hindawi.com/journals/bmri/2019/2408348>



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Development and validation of a TP53-associated immune ...

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Mar 16, 2019 - Therefore, in our model, the risk score was compatible with the ability of **tumour-infiltrating** immune cells to determine the expression of immune checkpoints, suggesting that the poor prognosis of the high-risk group may be due to the stronger immunosuppressive environment and immune checkpoint expression in this group than in the **low-risk** group, and these differences promoted HCC growth, progression, invasion, and angiogenesis and resulted in poor **prognosis**.

The Radiogenomic Risk Score: Construction of a Prognostic ...

<https://pubs.rsna.org/doi/10.1148/radiol.2015150800>

A **SOMA** for a clear-cell renal cell carcinoma prognostic multigene signature, termed a radiogenomic risk score, was trained ($n = 70$) and validated ($n = 77$) in independent data sets and shown to predict disease-specific survival, independent of disease stage, disease grade, and performance status (multivariate Cox model, $P < .05$ and log-rank $P < .001$).

Cited by: 26

Author: Neema Jamshidi, Eric Jonasch, Matthew ...

Publish Year: 2015

Development and validation of a CIMP-associated ...

<https://www.sciencedirect.com/science/article/pii/S2352396419305869>

In addition, we identify the CIMP-associated prognostic model (CPM) in HCC, which was trained and validated using four independent datasets. This model is on the basis of **four genes that could screen out the HCC patients with high risk of poor prognosis in both the training and validation cohorts.**

Author: Ganxun Li, Weiqi Xu, Lu Zhang, Tongt... Publish Year: 2019

Risk score and prognosis modeling based on mRNA ...

https://ascopubs.org/doi/abs/10.1200/JCO.2019.37.4_suppl.608

Jan 29, 2019 - The expressivity of **191 genes** enriched in cellular and structural components of the TME and clinical data were analyzed using machine learning, **multivariable COX model**, and **Kaplan-Meier (KM)** analysis to model risk score (RS) to predict prognosis.

Author: Sunyoung S. Lee, Jessica Jerez, Ah... Publish Year: 2019