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The Cancer Genome Atlas Program - National Cancer Institute

<https://www.cancer.gov/about-nci/organization/ccg/research/structural-genomics/tcga> ▾

The **Cancer Genome Atlas** (TCGA) is a landmark **cancer** genomics program that sequenced and molecularly characterized over 11,000 cases of primary **cancer** samples. Learn more about how the program transformed the **cancer** research community and beyond.

Annexin A8 can serve as potential prognostic biomarker and ...

<https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-019-2023-z> ▾

Sep 02, 2019 · Annexins are involved in vesicle trafficking, cell proliferation and apoptosis, but their functional mechanisms in ovarian **cancer** remain unclear. In this study, we analyzed Annexins in ovarian **cancer** using different databases and selected Annexin A8 (ANXA8), which showed the greatest **prognostic** value, for subsequent validation in immunohistochemical (IHC) assays.

Author: Rui Gou, Liancheng Zhu, Mingjun Zheng... **Publish Year:** 2019

Author: Rui Gou

Current advances in esophageal cancer proteomics | Request PDF

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Multivariate **analysis identified** miR-200c expression as the most valuable **prognostic** factor for patients with **esophageal cancer** who receive neoadjuvant chemotherapy.

(PDF) A multi-omics approach for identifying important ...

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A **multi-omics** approach for identifying important pathways and genes in human **cancer** Article (PDF Available) in BMC Bioinformatics 19(1) · December 2018 with 105 Reads How we measure 'reads'

An overview of esophageal squamous cell carcinoma ...

<https://www.researchgate.net/publication/224917266...>

Esophageal squamous cell carcinoma (ESCC), which is the most common subtype of **esophageal** cancers, is the sixth leading cause of **cancer** death worldwide with a five-year survival rate of 19%.

MUC1 | Cancer Genetics Web

www.cancer-genetics.org/MUC1.htm ▾

Sep 01, 2019 · MUC1 is sometimes involved in t(1;14) translocations in Non Hodgkin's Lymphoma, but otherwise there aren't many reports of the gene being regularly mutated in **cancer**. However, MUC1 protein is overexpressed in a diverse range of carcinomas and expression of MUC1 is a **prognostic** factor in several types of **cancer**.

Name of Journal: *World Journal of Gastroenterology*

Manuscript NO: 51543

Manuscript Type: ORIGINAL ARTICLE

Basic Study

Comprehensive multi-omics analysis identified core molecular processes in esophageal cancer and revealed GNGT2 is a potential prognostic marker

Liu GM *et al.* Core molecular processes in esophageal cancer

Guo-Min Liu, Tian-Cheng Lu, Li-Wei Duan, Wen-Yuan Jia, Yun Liu, Xuan Ji, Mao-Lei Sun, Yun-Gang Luo

Abstract

BACKGROUND

Esophageal cancer is one of the most poorly diagnosed and fatal cancers in the world. Although a series of studies on esophageal cancer have been reported, the molecular pathogenesis of the disease is still elusive.

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Current advances in esophageal cancer proteomics | Request ...

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Esophageal cancer (EC) is an aggressive malignant solid tumor with rapid progression and unfavorable prognosis. The 5-year survival rate for EC patients was estimated to be less than 10 %.

Radiomics with artificial intelligence for precision ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6373667>

Radiomics is the comprehensive analysis of massive numbers of medical images in order to extract a large number of phenotypic features (radiomic biomarkers) reflecting cancer traits, and it explores the associations between the features and patients' prognoses in order to improve decision-making in precision medicine.

RB1 | Cancer Genetics Web

www.cancer-genetics.org/RB1.htm ▾

The LinkedOmics database contains multi-omics data and clinical data for 32 cancer types and a total of 11 158 patients from The Cancer Genome Atlas (TCGA) project. It is also the first multi-omics database that integrates mass spectrometry (MS)-based global proteomics data generated by the Clinical Proteomic Tumor Analysis Consortium (CPTAC) on selected TCGA tumor samples.

Annexin A8 can serve as potential prognostic biomarker and ...

<https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-019-2023-z> ▾

Sep 02, 2019 · The genes co-expressed with ANXA8 identified using the cBioPortal database were subjected to functional and pathway enrichment analyses, and the results indicated that they are mainly involved in biological processes, such as cell migration, cell adhesion, angiogenesis, and inflammatory responses, as well as in regulating various cancer related signaling pathways, such as PI3K-Akt, focal adhesion, and proteoglycans in cancer...

Author: Rui Gou, Liancheng Zhu, Mingjun Zhe... Publish Year: 2019

Author: Rui Gou

Expression profile and clinical significance of Wnt ...