PROCEDURA SELETTIVA, PER ESAMI, CATEGORIA D, POSIZIONE ECONOMICA D1, AREA TECNICA, TECNICO-SCIENTIFICA ED ELABORAZIONE DATI, PRESSO IL DIPARTIMENTO DI MEDICINA INTERNA E SPECIALITA' MEDICHE (DIMI), CON PROFILO DI TECNICO DI LABORATORIO – BIOLOGO, PRIORITARIAMENTE RISERVATO A FAVORE DEI VOLONTARI DELLE FORZE ARMATE AI SENSI DELL'ART. 1014, COMMI 3 E 4 E DELL'ART. 678, COMMA 9, DEL D.LGS. N. 66/2010, INDETTA CON D.D.G. N. 2062 DEL 29.05.2020, PUBBLICATO NELLA G.U. N. 48, 4^ SERIE SPECIALE, DEL 23.06.2020.

Adempimenti di cui all'art. 19 del D.lgs. n. 33/2013, come modificato dall'art. 18 del D.lgs. n. 97/2016

QUESITI PROVA ORALE

Il giorno 07.10.2020 alle ore 9.00 presso la Sala Conferenze del Dipartimento di Medicina Interna e Specialità mediche (DIMI) ha avuto luogo ha luogo la settima riunione della Commissione esaminatrice della procedura di cui al titolo per lo svolgimento della prova orale.

La Commissione, regolarmente convocata e presente al completo, dopo ampia discussione, ha stabilito, a norma dell'art. 12, comma 6 del "Regolamento di assunzione del personale tecnico amministrativo" di questo Ateneo, i seguenti gruppi di quesiti, e relativo brano d'inglese, allegati.

Genova, 07.10.2020

La Commissione:

- Firmato Prof. Alberto BALLESTRERO Presidente
- Firmato Prof.ssa Paola GHIORZO
- Firmato Dott.ssa Paola CONTINI
- Firmato Dott.ssa Clara BOERO

1) Ruolo dell'autofagia nei tumori
2) Che cos'è un sistema operativo
3) Cosa sono i DPI e quali sono i principali

Testo inglese:

The development of an oncogenic state is a complex process involving the accumulation of multiple independent mutations that lead to deregulation of cell signalling pathways central to the control of cell growth and cell fate. The ability to define cancer subtypes, recurrence of disease and response to specific therapies using DNA microarray-based gene expression signatures has been demonstrated in multiple studies.

1) Editing del genoma: applicazioni alla ricerca sul cancro
2) Quando è utile un programma di database
3) Cosa sono i DPC e quali sono i principali

Testo inglese:

Various studies have also demonstrated the potential for using gene expression profiles for the analysis of oncogenic pathways. Here we show that gene expression signatures can be identified that reflect the activation status of several oncogenic pathways. When evaluated in several large collections of human cancers, these gene expression signatures identify patterns of pathway deregulation in tumours and clinically relevant associations with disease outcomes.

1) Colture primarie di fibroblasti
2) Come si digitalizza un documento che si trova su carta
3) Pittogrammi delle sostanze chimiche

Testo inglese:

Combining signature-based predictions across several pathways identifies coordinated patterns of pathway deregulation that distinguish between specific cancers and tumour subtypes. Clustering tumours based on pathway signatures further defines prognosis in respective patient subsets, demonstrating that patterns of oncogenic pathway deregulation underlie the development of the oncogenic phenotype and reflect the biology and outcome of specific cancers.

1) Metodi di genotipizzazione murina
2) Cosa è un antivirus
3) Cosa è il Piano di Emergenza

Testo inglese:

Predictions of pathway deregulation in cancer cell lines are also shown to predict the sensitivity to therapeutic agents that target components of the pathway. Linking pathway deregulation with sensitivity to therapeutics that target components of the pathway provides an opportunity to make use of these oncogenic pathway signatures to guide the use of targeted therapeutics.

1) Xenotrapianti e allotrapianti di cellule tumorali
2) Cosa è l'hardware
3) Chi è il responsabile dalla sicurezza dell'Ateneo

Testo inglese:

We used human primary mammary epithelial cell culture (HMECs) to develop a series of pathway signatures. Recombinant adenoviruses were used to express various oncogenic activities in an otherwise quiescent cell, thereby specifically isolating the subsequent events as defined by the activation/deregulation of that single pathway. Various biochemical measures demonstrate pathway activation. RNA from multiple independent infections was collected for DNA microarray analysis using Affymetrix Human Genome U133 Plus 2.0 Array.

1) Metodi di trasduzione di una linea cellulare
2) Cosa è un software
3) Cosa sono le scuole

Testo inglese:

Gene expression signatures that reflect the activity of a given pathway are identified using supervised classification methods of analysis previously described. The analysis selects a set of genes for which the expression levels are most highly correlated with the classification of HMEC samples into oncogene-activated/deregulated versus control (green fluorescent protein, GFP). The dominant principal components from such a set of genes then defines a relevant phenotype-related metagene, and regression models assign the relative probability of pathway deregulation in tumour or cell line samples.

1) Metodi di analisi delle proteine
2) Differenza tra internet ed intranet
3) Composizione Dipartimenti

Testo inglese:

Given the potential for overlap in the pathways, we also examined the extent to which the signatures distinguish one pathway from another. Use of the first three principal components from each signature, evaluated across all experimental samples, demonstrates that the patterns of expression in each signature are specific to each pathway; the gene expression patterns accurately distinguish the individual oncogenic effects despite overlapping downstream consequences. The genes identified as comprising each signature are listed in Supplementary Table 1.

1) Metodiche di biologia molecolare per l'onco-ematologia traslazionale
2) Cosa è un foglio Excel e a cosa serve
3) Attribuzione dei dipartimenti

Testo inglese:

Further verification of the capacity of oncogenic pathway signatures to predict accurately the status of pathways made use of tumour samples derived from various mouse cancer models. Pathway signatures were regenerated from the genes common to both human and mouse data sets; the analysis was trained on the HMEC-derived signatures and then used to predict the pathway status of all tumours. These studies were carried out using three of the pathway signatures for which we had matching mouse models that could be used for validation: Myc, Ras and E2F3.

1) Metodi di analisi dell'interazione cellula-microambiente
2) Cosa è un directory
3) Organi dei dipartimenti

Testo inglese:

Across the set of mouse tumours, this analysis evaluates the relative probability of pathway deregulation of each tumour—that is, the predicted status of the pathway in each mouse tumour based only on the signatures developed in HMECs. These predictions are displayed as a colour map: red indicates a high probability of pathway deregulation and blue indicates a low probability, with predictions sorted by the relative probability of pathway deregulation. As shown in Fig. 2a, the pathway predictions exhibit close correlation with the molecular basis for tumour induction.