The lethal internal face of the coronaviruses: Kidney tropism of the SARS, MERS, and COVID19 viruses
Roza Motavalli, Walid Kamal Abdelbasset, Heshu Sulaiman Rahman, Muhammad Harun Achmad, Nataliya Klunko Sergeevna, Angelina Olegovna Zekiy, Ali Adili, Farhad Motavalli Khiavi, Faroogh Marofi, Mehdi Yousefi, Shadi Ghoreishizadeh, Navid Shomali, Jalal Etemadi, Mostafa Jarahian

SARS-CoV causes proteinuria and renal impairment or failure. The SARS-CoV was identified in the distal convoluted tubules of the kidney of infected patients. Also, renal dysfunction was observed in numerous cases of MERS-CoV infection. And recently, during the 2019-nCoV pandemic, it was found that the novel coronavirus not only induces acute respiratory distress syndrome (ARDS) but also can induce damages in various organs including the liver, heart, and kidney. The kidney tissue and its cells are targeted massively by the coronaviruses due to the abundant presence of ACE2 and Dpp4 receptors on kidney cells. These receptors are characterized as the main route of coronavirus entry to the victim cells. Renal failure due to massive viral invasion can lead to undesirable complications and enhanced mortality rate, thus more attention should be paid to the pathology of coronaviruses in the kidney.

Selectively targeting cancer stem cells: Current and novel therapeutic strategies and approaches in the effective eradication of cancer
Seyed-Alireza Esmaeili, Shamim Sahranavard, Astireh Salehi, Vahid Bagheri

Cancer stem cells (CSCs) as a small subset of neoplastic cells with tumor-initiating capability, self-renewal capacity, and pluripotency due to their pivotal role in tumor initiation, growth, progression, maintenance, invasion, metastasis, and relapse, as well as resistance to anticancer drugs are very appealing targets for cancer therapies. Therefore, targeting CSCs through their metabolism and using immunotherapy and microRNAs (miRNAs) besides classical chemo- and radiotherapy may exert better therapeutic effects in the effective eradication of cancer.

Urinary proteomic analysis to identify a potential protein biomarker panel for the diagnosis of tuberculosis
Liguo Liu, Jiaheng Deng, Qianting Yang, Candong Wei, Bo Liu, Haoran Zhang, Henan Xin, Shouguo Pan, Zisen Liu, Dakuan Wang, Yu Pang, Xinchun Chen, Lei Gao, Jianhua Zheng, Rongmei Liu, Qi Jin

Rapid and accurate diagnosis of tuberculosis (TB) is one of the most direct means to reduce the incidence of TB. Here urinary proteomic profiling of TB patients was performed (Figure), and a clinically-useful disease marker panel was established and validated. A three-protein combination out of the five-protein panel (namely P22352, Q9P121, P15151, Q13291, and Q8NDA2) exhibited sensitivity rate of 82.7% in the diagnosis of TB and specificity rate of 92.3 % for the diagnosis of TB from the latent TB category. The results provided preliminary evidence that this biomarker panel could probably be a novel TB diagnostic biomarker in clinical application.

(A) non-TB control (HC) group; (B) tuberculosis (TB) patients.

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