

gene therapy

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36087416	Circular RNAs in neuroblastoma: Pathogenesis, potential biomarker, and therapeutic target	Mohsen Karami Fath Sasan Pourbagher Benam Kiana Salmani Sina Naderi Zahra Fahham Shamim Ghiabi Seyed Armin Houshmand Kia Malihe Naderi Maryam Darvish Ghasem Barati	Neuroblastoma (NB) is a common cancer in childhood responsible for 15 % of fatalities by pediatric cancers. Epigenetic factors play an important role in the pathogenesis of NB. Recently, it has been demonstrated that circular RNAs (circRNAs, ciRNAs), a newly identified class of non-coding RNAs, are also dysregulated in NB. CircRNAs mediate their functions by regulating gene expression mainly through microRNA (miRNA) sponging. The dysregulation (abnormal upregulation or downregulation) of...	pmid:36087416 doi:10.1016/j.prp.2022.154094	Sat, 10 Sep 2022 06:00:00 -0400
2	pubmed:36087505	Agalsidase- should be proposed as first line therapy in classic male Fabry patients with undetectable -galactosidase A activity	Albina Nowak Olivier Dormond Véronique Monzambani Uyen Huynh-Do Frédéric Barbey	CONCLUSION: Agalsidase- at licensed dose is significantly more effective than agalsidase- to reduce Lyso-Gb3 levels in classic Fabry patients, and should be used as first line therapy in classic males with no residual enzyme activity.	pmid:36087505 doi:10.1016/j.ymgme.2022.08.003	Sat, 10 Sep 2022 06:00:00 -0400
3	pubmed:36087682	DNMT and EZH2 inhibitors synergize to activate therapeutic targets in hepatocellular carcinoma	Lian Zhang Hong-Tao Li Rachel Shereda Qianjin Lu Daniel J Weisenberger Casey O'Connell Keigo Machida Woojin An Heinz-Josef Lenz Anthony El-Khoueiry Peter A Jones Minmin Liu Gangning Liang	The development of more effective targeted therapies for hepatocellular carcinoma (HCC) patients due to its aggressiveness is urgently needed. DNA methyltransferase inhibitors (DNMTis) represented the first clinical breakthrough to target aberrant cancer epigenomes. However, their clinical efficacies are still limited, in part due to an "epigenetic switch" in which a large group of genes that are demethylated by DNMTi treatment remain silenced by polycomb repressive complex 2 (PRC2) occupancy....	pmid:36087682 doi:10.1016/j.canlet.2022.215899	Sat, 10 Sep 2022 06:00:00 -0400
4	pubmed:36088044	LncRNA TUG1 promotes the migration and invasion in type I endometrial carcinoma cells by regulating E-N cadherin switch	Qin Chen Christoph Schatz Yixuan Cen Xiaojing Chen Johannes Haybaeck Baohua Li	CONCLUSION: Collectively, our data reveal that TUG1 might be regarded as an oncogenic molecule that promotes type I EC cells metastasis leading to tumor progression, at least partially, by regulating E-N cadherin switch and the AKT pathway.	pmid:36088044 doi:10.1016/j.tjog.2022.03.045	Sat, 10 Sep 2022 06:00:00 -0400
5	pubmed:36088072	Translation termination codons in protein synthesis and disease	Silvia Lombardi Maria Francesca Testa Mirko Pinotti Alessio Branchini	Fidelity of protein synthesis, a process shaped by several mechanisms involving specialized ribosome regions and external factors, ensures the precise reading of sense as well as stop codons (UGA, UAG, UAA), which are usually localized at the 3' of mRNA and drive the release of the polypeptide chain. However, either natural (NTCs) or premature (PTCs) termination codons, the latter arising from nucleotide changes, can undergo a recoding process named ribosome or translational readthrough, which...	pmid:36088072 doi:10.1016/bs.apcsb.2022.06.001	Sat, 10 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
6	pubmed:36088413	Prevalence of Antibiotic-Resistant Lactobacilli in Sepsis Patients with Long-Term Antibiotic Therapy	Negin Yarahmadi Shahnaz Halimi Parnia Moradi Mohammad Hossein Zamanian Akram Rezaei Siavash Vaziri Alisha Akya Amirhooshang Alvandi Shaghayegh Yazdani Darab Ghadimi Jale Moradi	Lactobacilli are the most common probiotic bacteria found in the human gut microbiota, and the presence of acquired antibiotic resistance determinants carried on mobile genetic elements must be screened due to safety concerns. Unnecessary and inappropriate antibiotic therapy, as well as ingested antibiotic resistance bacteria (originating from food or food products), influence the abundance of antibiotic resistance genes in human guts, with serious clinical consequences. The current study looked...	pmid:36088413 doi:10.1007/s00284-022-03010-4	Sat, 10 Sep 2022 06:00:00 -0400
7	pubmed:36088543	The genetic algorithm-aided three-stage ensemble learning method identified a robust survival risk score in patients with glioma	Sujie Zhu Weikaixin Kong Jie Zhu Liting Huang Shixin Wang Suzhen Bi Zhengwei Xie	Ensemble learning is a kind of machine learning method which can integrate multiple basic learners together and achieve higher accuracy. Recently, single machine learning methods have been established to predict survival for patients with cancer. However, it still lacked a robust ensemble learning model with high accuracy to pick out patients with high risks. To achieve this, we proposed a novel genetic algorithm-aided three-stage ensemble learning method (3S score) for survival prediction....	pmid:36088543 doi:10.1093/bib/bbac344	Sun, 11 Sep 2022 06:00:00 -0400