清華大學深圳国际研究生院
Tsinghua Shenzhen International Graduate School

生物医药与健康工程研究院
Institute of Biopharmaceutical and Health Engineering

第二届医药健康工程杯研究生论坛

The 2nd Biopharmaceutical and Health Engineering Cup Graduate Forum

－生命链动未来、展现研学风采－

－Life Sciences Lead to Future, Showcasing the Research Spirit－

论坛指南

Forum Guidelines

2024年1月5日-6日

January 5th-6th, 2024

主办：生物医药与健康工程研究院

Host: Institute of Biopharmaceutical and Health Engineering

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主办单位 Organizer

生物医药与健康工程研究院
Institute of Biopharmaceutical and Health Engineering (iBHE)

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WU Xiaofeng	Secretary of the Communist Party, Tsinghua Shenzhen International Graduate School (SIGS)

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(音序排列 Sorted by the alphabetical order of surname)

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第二届“医药健康工程杯”研究生论坛议程

The 2nd Biopharmaceutical and Health Engineering Cup Graduate Forum Agenda

生命链动未来，展现研学风采

Life Sciences Lead to Future, Showcasing the Research Spirit

深圳·清华大学深圳国际研究生院·生物医药与健康工程研究院

2024 年 1 月 5-6 日

January 5th，2024　9:00-12:00　国际一期报告厅 C310； International Phase I，Building C310

	时间 Time	主题 Topic		发言人/报告人 Guest/Speaker	主持人 Host
上午 Morning	09:00-09:10	**开幕式致辞 Opening Remarks**		武晓峰 WU Xiaofeng	杨伊婷 YANG Yiting
	09:10-09:20	**合影留念　Group Photo**			
	09:20-09:30	口头报告 Oral Presentations	Mining methods and mechanism of action of meat-derived immunomodulatory peptides in cultured Giant Salamanders	常雲皓 CHANG Yunhao	Davit Khutsishvili
	09:30-09:40		Universal Smartphone-Assisted Label-free CRISPR/Cas12a-DNAzyme Chemiluminescence Biosensing Platform for On-site Detection of Nucleic Acid and Non-nucleic Acid Targets	陈辉 CHEN Hui	
	09:40-09:50		Targeting TFF3 to suppress survival of endocrine-therapy-induced dormancy-like ER+ mammary carcinoma models	陈淑 CHEN Shu	
	09:50-10:00		Multimodal data integration using deep learning for predicting cancer biomarker and improving risk stratification in colorectal cancer	杜知城 DU Zhicheng	
	10:00-10:10		Anti-aging effects of retinol and its impact on skin microecology	归敏燕 GUI Minyan	
	10:10-10:20		Pre-existing inflammatory cytokines overcome the probiotic Lacticaseibacillus rhamnosus GG attenuation of MAIT cell antimicrobial effector responses	何丹 HE Dan	
	10:20-10:30		High-resolution three-dimensional real-time microscopy for axonal transport visualization	胡聪 HU Cong	
	茶歇 10 分钟　Tea break 10 minutes				
	10:40-10:50	口头报告	Pre-diabetic D-glucose levels promote an oncogenic phenotype in immortalized human mammary epithelial cells via enhanced TFF3 expression	黄晶 HUANG Jing	黄瑜晴 HUANG Yuqing
	10:50-11:00		TFF3 facilitates CSC-like features with metabolism reprogramming through AKT/HSF1 axis in mammary carcinoma	黄鹏 HUANG Peng	
	11:00-11:10		Swellable microneedle patch for blood-free rapid diagnostic testing in neonatal infection	李以婷 LI Yiting	
	11:10-11:20		Single-cell Transcriptomic Analysis Reveals 3D Spheroid Culture Synchronizes Heterogeneous Mesenchymal Stem Cells into An Immunomodulatory Phenotype	卢瑞卿 LU Ruiqing	

	11:20-11:30	Oral Presentations	Circulating MAIT cells home to the gut mucosa during acute inflammation via the C-C motif chemotactic cytokine receptor 1, 2, and 4-dependent manners	伍政宇 WU Zhengyu	黄瑜晴 HUANG Yuqing
	11:30-11:40		Targeting mTOR and ULK1 in Autophagy: Exploration of Specific Drug and Virtual Screening	应华章 YING Huazhang	
	11:40-11:50		Global-Polarization Stokes Ellipsoid: A Vivid Method to Sensor Polarization Characteristics	张新贤 ZHANG Xinxian	
	11:50-12:00		Kinetics modeling of the translational regulation on the mitochondrial surface	赵景怡 ZHAO Jingyi	
January 5th，2024　14:00-17:00　国际一期 A 栋一楼大厅； International Phase I, BuildingA-1st Floor					
下午 Afternoon	14:00-17:00	**墙报展示 Poster Presentations**			杨伊婷 YANG Yiting
January 6th，2024　9:00-12:00　国际一期报告厅 C310； International Phase I, BuildingC310					
上午 Morning	09:00-09:05	**嘉宾介绍　Guest Introduction**			杨伊婷 YANG Yiting
	09:05-09:20	创新创业口头报告	猴痘病毒 CRISPR/Cas12a 化学发光检测试剂盒的研制及手持式智能手机化学发光仪的开发	陈辉 CHEN Hui	萧彤 XIAO Tong
	09:20-09:35		一款高通量、高特异性的原代肿瘤细胞药效筛选平台与癌症早筛方法设计	黄晶 HUANG Jing	
	09:35-09:50		健康之心，工程之眼- 一款辅助视力障碍者的智能感知脑机眼镜	黄逸轩 HUANG Yixuan	
	09:50-10:05		“奕心飞扬”青少年心理早筛系统	彭博远 PENG Boyuan	
	10:05-10:20		多功能面部皮肤分析仪	石雨竹 SHI Yuzhu	
	10:20-10:35		ASAP 超声颈部按摩仪	吴宇宽 WU Yukuan	
	10:35-10:50		病理切片全流程数字化平台	徐敏惠 XU Minhui	
	茶歇 30 分钟　Tea break 30 minutes				
	11:20-11:40	**颁奖典礼　Award Ceremony** (特等敢闯奖，特等创新奖，创新创业奖，最佳口头报告，最佳墙报奖，纪念奖)			杨伊婷 YANG Yiting
	11:40-12:00	**闭幕式致辞　Closing Remarks**			邢新会 XING Xinhui

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墙报展示 Poster Presentations

创新创业口头报告

Oral Presentation of Innovation and Entrepreneurship

口头报告 Oral Presentations

NO. 1

Mining methods and mechanism of action of meat-derived immunomodulatory peptides in cultured Giant Salamanders

Yunhao Chang[1]; Wei Li[1]; Xin-Hui Xing[1,2,3*]

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ABSTRACT: With the increasing improvement of people's living standards, the concept of great health has gradually taken root in people's hearts, and diet therapy has been mentioned more and more. Natural active peptides from food sources are abundant and diverse, and have a wide range of biological activities, which have potential applications as functional foods and nutraceuticals. In the modern research of food-borne bioactive peptides, the search for novel active peptides with immunomodulatory effects is obviously of great research value. Giant salamander, as a rare aquatic animal whose meat contains rich nutritional components, has received attention for its unique biological properties. The aim of this study was to explore in depth the immunomodulatory potential of giant salamander meat peptides and to screen and validate the active components using computer-assisted techniques that have been reported. On this basis, by combining experimental biology methods and computer simulation techniques, we constructed top-down and bottom-up peptide libraries of immune meat peptides from giant salamanders, aiming to provide new ideas and methods for the development of immunomodulators. The immunomodulatory efficacy of giant salamander peptides can be demonstrated by evaluating the immunomodulatory efficacy of giant salamander peptides, and the immunomodulatory mechanism of giant salamander peptides can be further revealed at the cellular level, so as to pave the way for the subsequent practical application of functional foods and nutritional nutraceuticals.

NO. 2

Universal Smartphone-Assisted Label-free CRISPR/Cas12a-DNAzyme Chemiluminescence Biosensing Platform for On-site Detection of Nucleic Acid and Non-nucleic Acid Targets

Hui Chen[1,2], Ying Feng[1], Feng Liu[1], Chunyan Tan[1,2], Naihan Xu[1,3], Yuyang Jiang[1], Ying Tan[1,2]*

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ABSTRACT: The clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein (Cas) (CRISPR/Cas) system enables sensitive and specific detection of biomolecules, thanks to its programmability, high fidelity, and powerful signal amplification capabilities. Herein, a universal smartphone-assisted label-free G-quadruplex (G4) DNAzyme-based chemiluminescence CRISPR/Cas12a biosensing platform (G4CLCas) is firstly described that achieves on-site, ultrasensitive visual detection of nucleic acid and non-nucleic acid targets. The G4CLCas-based sensing platform relies on Cas12a trans-cleavage activation that triggers the cleavage of the G4 DNAzyme, resulting in chemiluminescence signals off/on compared to that of the control. Chemiluminescence signals are captured as images that are quantitatively analyzed and visualized using a smartphone-assisted imaging cartridge. Under optimal conditions, G4CLCas achieves a low limit of detection (LOD) of 8.6 aM (~5.2 copies/μL) for monkeypox virus (MPXV) DNA within the linear concentration range of 10-300 aM and can accurately quantify viral DNA in spiked samples. G4CLCas can also detect non-nucleic acid targets, whereby it achieves a low LOD value of 84.3 nM for adenosine triphosphate (ATP) within the linear concentration range of 2-2000 μM. Here, a label-free, portable, on-site CRISPR/Cas12a chemiluminescence biosensing platform based on the G4 DNAzyme substrates is proposed with potential applications in clinical detection and bioanalytical chemistry research.

Keywords: G4 DNAzyme; CRISPR/Cas12a biosensing; Chemiluminescence; Label-free; Smartphone-assisted

NO. 3

Targeting TFF3 to suppress survival of endocrine-therapy-induced dormancy-like ER+ mammary carcinoma models

Shu Chen[1], Xi Zhang[3], Vijay Pandey[1,2] Peter E. Lobie[1,2,3]

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ABSTRACT: Tumor dormancy is one of the key clinical challenges contributing to drug resistance, metastasis and relapse of mammary carcinoma (MC), leading to nearly 90% mortality in MC. In clinic, more than 70% estrogen receptor positive (ER+) MC recur 5 to 20+ years after clinical remission majorly induced by anti-estrogen therapy, indicating long tumor dormancy period of ER+ MC patients. Herein, we aim at mimicking clinical anti-estrogen-therapy-induced dormancy in ER+ MC to explore molecular basis contributing to dormant cell survival and develop novel therapy strategies targeting dormant cells.

MCF7 (human ER+ MC cell line) orthotopic xenografts were treated with two first-line anti-estrogen agents including fulvestrant (FUL) and tamoxifen (TAM) for 4 weeks, respectively. The residual mass maintained the unchanged tumor volume during administration, exhibited repopulation property after therapy cessation in vivo and was identified as dormancy-like models. Then the constant residual tumors, relapse tumors after therapy cessation and corresponding vehicle-treated tumors were treated for primary cell culture. Subsequently, anti-estrogens-induced dormancy attributes including G0/G1 cell cycle arrest, inactive DNA replication, drug-resistance, stemness properties and dormancy molecular features were validated by cell cycle analysis, BrdU incorporation assays, cell survival assay, ALDHFLUOR assay, and qPCR and western blot analysis in generated dormancy-like cells in vitro. Then, trefoil factor 3 (TFF3) was screened out as a vital biomarker of the dormancy-like models by mRNA sequencing and its pro-survival roles were validated. Next, the inhibition of TFF3 alone and its combinatorial therapeutics were investigated. TFF3-inhibition based approaches, especially the combination of TFF3-pharmaceutic-inhibition and CDK4/6 inhibitors (CDK4/6is) exhibited therapeutic potent for treating dormancy-like models in vitro, ex vivo and in vivo. Hence, the in vivo anti-estrogens--induced models mimicking clinical scenario of the therapy-induced-dormancy in ER+ MC patients was established. The models and combination therapies herein may set the stage for better prognosis of ER+ MC patients.

NO. 4

Multimodal data integration using deep learning for predicting cancer biomarker and improving risk stratification in colorectal cancer

Zhicheng Du[1,2], Huiyan Luo[3,4], Peiwu Qin[1,2,*]

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ABSTRACT: Deep learning (DL) models can accelerate the prediction of prognostic biomarkers and improve risk stratification of colorectal cancer from computed tomography (CT), histopathological specimens and electronic health record (EHR). However, little is known about the capacity of combining features from these disparate sources to improve model's performance. Here, we construct a novel model, called **MOUNT** (**M**ultim**O**dal fusion model for m**U**lti-cli**N**ical **T**asks), to predict mortal risk and biomarkers of BRAF, Microsatellite instability (MSI), RAS and Tumor burden mutation (TMB) using a cohort of 264 CRC patients with multimodal baseline data obtained during diagnostic clinical workup. Benefiting from the effective multimodal integration of CT, pathology slide and EHR, MOUNT substantially improves the performance, generalizability, data efficiency, and interpretability as compared with current state-of-the-art algorithms. This study demonstrates a promising path toward accurate biomarkers prediction and improved risk stratification of patients with cancer through multimodal data integration.

NO. 5

Anti-aging effects of retinol and its impact on skin microecology

Minyan Gui[1], Jingmin Cheng[1], Danni Guo[1], Xiao Liu[1]*

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ABSTRACT: Retinol, as an anti-aging active ingredient, has been widely added into skincare products due to its ability to promote the proliferation of skin keratinocytes and regulate skin cell collagen expression. The skin, being the largest organ of the human body, harbors a myriad of skin commensal bacteria. However, the impact of skincare products containing retinol on the skin microbiome, as well as the role of the skin microbiome in mediating the anti-aging properties of retinol, remains poorly understood. Therefore, a cohort of 9 participants was recruited to undergo a consecutive 28-day regimen of using skincare products containing retinol. Skin epidermal swab samples were collected every 7 days for subsequent metagenomic and metabolomic analysis. Additionally, skin phenotypic data were measured using instruments such as VISIA. Multi-omics data were integrated using bioinformatics methodologies. Phenotypic data analysis revealed that skincare products containing retinol significantly improved skin conditions, including improved skin's ability to retain water, formed an acidity environment on skin, enhanced skin barrier function, and reduced wrinkle number and volume. Metagenomic and metabolomic sequencing demonstrated that the formation of a skin acidic environment was associated with a decrease in the abundance of certain opportunistic pathogens and the secretion of acid metabolites by beneficial bacterial communities, indicating the antibacterial and anti-inflammatory effects of retinol-containing products. Compared to the baseline, enrichment of the retinol metabolism pathway was significantly observed after using products containing retinol, with the abundance of a retinol metabolite, 1-O-All-Trans-Retinoyl-Beta-Glucuronic Acid, peaked on the day 7. This suggests that microorganisms may participate in retinol metabolism, utilizing glucuronic acid as a carbon source, thereby accelerating the rate of retinol metabolism and enhancing its half-life within the human body.

NO. 6

Pre-existing inflammatory cytokines overcome the probiotic Lacticaseibacillus rhamnosus GG attenuation of MAIT cell antimicrobial effector responses

Dan He[1,2], Fei Han[1, 2], Amanda Ho[1,2], Huizhong Xu[1,2], Yiting Xue[1,2], Zhengyu Wu[1], Xingchi Chen[1], Edwin Leeansyah[1, 2]

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ABSTRACT: Mucosal-associated invariant T (MAIT) cells represent the largest antimicrobial T cell population in humans. These cells play a crucial role in the defense against various bacteria at mucosal sites, including the intestines and the lungs. However, inappropriate MAIT cell antimicrobial effector responses against intestinal bacteria may contribute to the development of chronic intestinal inflammation. Further, the presence of inflammatory cytokines in such conditions may promote MAIT cell overexuberant responses, leading to more tissue damage. Lacticaseibacillus rhamnosus GG (LGG) is one of the most well-documented probiotic strains known for its potent immune regulatory function. Nevertheless, there is a limited understanding of how LGG mediates immunomodulatory activity within the human guts, particularly in the context of ongoing or pre-existing inflammation.

We previously reported that pre-treatment with LGG in the absence of initial inflammation attenuated MAIT cell antimicrobial and pro-inflammatory responses against the intestinal pathobiont Escherichia coli, including significant downmodulation of granzyme (Grz)B, interferon (IFN)γ, and tumor necrosis factor (TNF). Here, we investigated whether pre-stimulation of MAIT cells with inflammatory cytokines affects the ability of LGG to suppress MAIT cell effector functions. We found that pre-treatment of MAIT cells with inflammatory cytokines normally elevated in chronic intestinal inflammation, including IL-2, IL-7, IL-12, and IL-18, abolished LGG attenuation of MAIT cell antimicrobial effector responses. Notably, there were elevated levels of GrzB, IFNγ, and TNF when such cytokines were added to the culture prior to the LGG stimulation.

These preliminary results indicate that LGG has the capacity to dampen MAIT cell-mediated inflammatory and cytotoxic responses in the absence of initial inflammation. However, our preliminary findings also suggest that when there is already an ongoing or pre-existing inflammation, LGG may instead enhance MAIT cell effector responses that may potentially exacerbate tissue damage. Therefore, an in-depth understanding of the context and timing of lactic acid bacteria probiotic supplementation in the setting of inflammatory gut diseases is sorely needed to maximize the therapeutic benefits while minimizing the potential of further immune-mediated tissue damage.

NO. 7

High-resolution three-dimensional real-time microscopy for axonal transport visualization

Cong Hu[1], Yaoquan Su[1], Yifan pei[1], Sanyang Han[1], Yongbin Zhang[2]

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ABSTRACT: Early diagnosis and prognostic evaluation of neurodegenerative diseases, such as Alzheimer's disease and Parkinson's disease, is a hotspot and difficult research topic in China and worldwide. Axonal transport disruption is considered a common feature occurring in neurodegenerative diseases. Many fluorescence microscopes have been used to observe the axonal transport process, such as confocal microscopy, two-photon microscopy, and super-resolution microscopy. However, most of these techniques use scanning method, so the imaging time is long and it is difficult to observe the axonal transport process dynamically. The main difficulty limiting axonal transport research at present is the lack of a high spatiotemporal resolution microscopy to visualize the movement of dynein in three-dimensional space. Conventional imaging techniques are difficult to balance the inherent contradiction between temporal resolution, spatial resolution, and imaging depth. On the other hand, traditional fluorescent probes are difficult to simultaneously meet the requirements of high luminescence efficiency, low phototoxicity, and photostability. Light-field microscopy is considered a powerful technique for instant 3D imaging, but its resolution is relatively low and photobleaching occurs for long-term tracing of axonal transport. We propose light-field microscopy combining upconversion nanoparticle probes and zero-sample super-resolution networks for three-dimensional prolonged tracking of axonal transport. The use of infrared laser excitation for the upconversion probe avoids biological autofluorescence and reduces background noise, and its excellent stability enables stable tracing without photoblinking. The zero-shot super-resolution network adopts an unsupervised training method and utilizes the connection between multi-view data in the light field, which can improve the resolution of light-field microscopy and realize high-resolution tracing of axonal transport.

NO. 8

Pre-diabetic D-glucose levels promote an oncogenic phenotype in immortalized human mammary epithelial cells via enhanced TFF3 expression.

Jing Huang [1], Xi Zhang [3], Amy Yong-Chen Lau [4], Tao Zhu [3,5,6], Peter E. Lobie [1,2,3,4*], and Vijay Pandey [1,2,*]
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Background: Hyperglycemia, the defining characteristic of diabetes mellitus, has been reported to be positively associated with a higher risk of cancer development at prediabetic and diabetic levels. However, the role of hyperglycemia in oncogenic transformation is not yet fully understood.
Methods: Immortalized human mammary epithelial cells (HMEC-hTERT) were chronically exposed to monosaccharides (D-glucose/D-fructose/D-galactose) 4 or 10mM. The functional behaviour of HMEC-hTERT cells (4mM) and glucose-stimulated (GS) HMEC-hTERT cells (10mM) exposed to D-glucose was determined using various in vitro approaches such as cell viability, anchorage independent growth and colony formation in 3D Matrigel. Mechanistic analyses were performed using western blot analysis of TFF3 protein and glycolysis-associated enzymes.
Key findings: HMEC-hTERT cells chronically exposed to D-glucose at pre-diabetic levels exhibited an increased capacity for anchorage-independent growth and filled multi-acinar spheroids in 3D Matrigel culture. The oncogenic phenotype in GS-HMEC-hTERT cells was demonstrated by colony formation in soft agar and increased disorganized multi-acinar colonies with filled lumina in 3D Matrigel when exposed to D-glucose. GS-HMEC-hTERT cells exposed to D-glucose exhibited elevated protein levels of TFF3, glucose transporter 1 (GLUT1), glycolytic enzymes (PFKP), and lactate dehydrogenase (LDHA). Addition of 2-deoxy-D-glucose (2-DG), a glycolytic inhibitor, reversed the oncogenic phenotype of GS-HMEC-hTERT cells. Inhibition of glycolysis by 2-DG in GS-HMEC-hTERT cells also abrogated the protein levels of TFF3 and glycolysis-associated markers. Moreover, forced expression of TFF3 in HMEC-hTERT cells exhibited increased protein levels of glycolysis-associated protein markers. Treatment of HMEC-hTERT cells with 2-DG reversed the TFF3-stimulated levels of glycolysis-associated proteins. Chronic exposure of HMEC-hTERT cells to elevated D-fructose or D-galactose also stimulated an oncogenic phenotype, albeit less than D-glucose. siRNA-mediated depletion of TFF3 in GS-HMEC-hTERT cells resulted in significantly decreased capacity for anchorage-independent growth.
Significance: Elevated glucose concentrations, even at prediabetic levels, effectively stimulates a TFF3-dependent oncogenic phenotype in immortalized mammary epithelial cells.
Keywords: Hyperglycemia, Diabetes mellitus, Cancer, Oncogenic transformation, Trefoil factor 3 (TFF3)

NO. 9

TFF3 facilitates CSC-like features with metabolism reprogramming through AKT/HSF1 axis in mammary carcinoma

Peng Huang [1, 2], Jing Huang [1, 2], Ke Lin [2], Vipul Bhardwaj [1, 2], Xi Zhang [3], Tao Zhu [3, 4, 5], Basappa Basappa [6], Peter E. Lobie [1, 2, 3], Vijay Pandey [1, 2].

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Introduction: Trefoil factor 3 (TFF3) was oncogenic protein for mammary carcinoma (MC) involved in cancer cell growth, proliferation scattering, invasion and metastasis. TFF3 was also reported to mediate therapeutic resistance in MC, which can be attributed to enhanced cancer stemness. Besides, TFF3 was also reported to associate with multiple metabolism disorders by inhibiting gluconeogenesis and impairing fatty-acid distribution.

Aims: 1). To elucidate that TFF3 facilitates CSC-like features in MC. 2). To elucidate that TFF3 mediates metabolism reprogramming in MC. 3). To elucidate the molecular mechanism of TFF3 to facilitate CSC-like features and metabolism reprogramming. 4). To screen out a combination regimen of TFF3-inhibition and anti-metabolism to ablate MC.

Methods: To elucidate TFF3-facilating CSC-like features, function assays as well as corresponding profiles of mammosphere formation, vascular mimicry formation, acute chemotherapeutic drugs exposure, anoikis resistance assay, ALDEFLOUR assay, side population FACS, auto-fluorescence FACS on TFF3-induced or TFF3-depleted MC cell models were conducted. To elucidate TFF3-mediating metabolism reprogramming, function assays as well as corresponding profiles of real-ATP assay, glycolysis stress assay, mitochondria stress assay, LDHA reporter assay, SDH activities, mitochondrial membrane potential, mitochondrial ROS assay on TFF3-induced or TFF3-depleted MC cell models were conducted. To elucidate the molecular mechanism of TFF3-facilating CSC-like features and metabolism reprogramming, transcriptome sequencing was first conducted on TFF3-induced MC cell models. Subsequently, profile detection and functional validation of the mechanism was performed based on all above assays. To screen out a combination regimen of TFF3-inhibition and anti-metabolism to ablate MC, BLISS CI and Compusyn CI were utilized to evaluation the synergistic effect of TFF3 inhibitor AMPC with compounds from

anti-metabolism library. In vitro, ex vivo assays were subsequently performed based on the screening.

Results: 1). TFF3 facilitates CSC-like features in MC. 2). TFF3 reprograms the metabolism scheme in MC. 3). TFF3/AKT/HSF1 axis dominants the CSC-like features and metabolism reprogramming in MC. 4). AMPC synergize with Quisinostat 2HCl to ablate MC through inhibiting TFF3 and metabolism switch.

Conclusion: TFF3 facilitates CSC-like features with metabolism reprogramming through AKT/HSF1 axis in MC.

NO. 10

Swellable microneedle patch for blood-free rapid diagnostic testing in neonatal infection

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ABSTRACT: The immune system of neonatal is not yet fully developed and is highly susceptible to infection, leading to serious life-threatening complications. Therefore, detecting infections is particularly important for monitoring the health of neonatal. Rapid diagnostic testing is one of the most commonly used methods for detecting and screening infectious diseases, but it relies on the collection of blood samples. However, neonatal have thinner blood vessels and poor compliance, making traditional blood collection difficult. Here, we report a sampling and storage tool for assisting in the rapid detection of protein biomarkers in skin interstitial fluid using a swelling microneedle (MN) patch. The hydrophilic swelling microneedle array can be used for temporary storage of sample collection. When the microneedle array is mixed with a specific sample diluent, the temporarily stored protein biomarkers in the microneedle array will freely diffuse into the sample diluent along the concentration gradient. Therefore, we can use a simple colloidal gold lateral chromatography test strip to achieve the detection of protein biomarkers. For Proof of concept, the device is used to detect C-reactive protein (infectious biomarker). MN array can quickly sample within 5 minutes, and each test can be completed within 20 minutes without any auxiliary equipment. The diagnostic tool is easy to operate, minimally invasive, and painless, does not need professional medical staff to sample, and can also be easily used to detect other protein biomarkers in dermal interstitial fluid, making it a promising real-time detection strategy.

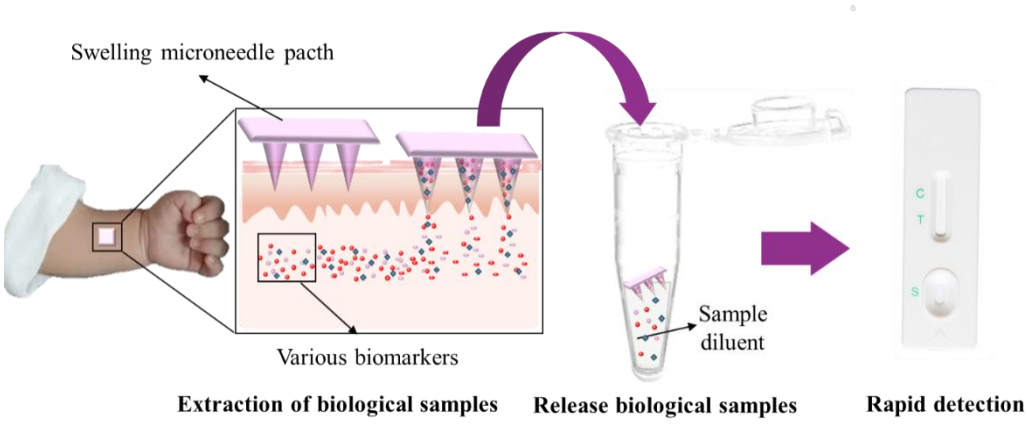

Figure 1. Schematic diagram of swelling microneedle sampling and detection.

NO. 11

Single-cell Transcriptomic Analysis Reveals 3D Spheroid Culture Synchronizes Heterogeneous Mesenchymal Stem Cells into An Immunomodulatory Phenotype

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Background: Mesenchymal stem cells (MSC) are expanded in vitro and transplanted for the treatment of ischemic stroke, arthritis, graft-versus-host disease, and a variety of other immune disorders due to their low immunogenicity and immunomodulatory functions. However, factors such as donors, tissue sources, isolation and culture methods, and passaging pose a non-negligible heterogeneity problem for MSC, which reduces the reproducibility of the effects of basic research and clinical applications.

Methods: We cultured MSC in 3D spheroid, examined MSC heterogeneity at morphology, and investigated MSC heterogeneity as well as immunoregulatory functions using bulk RNA sequencing and single-cell RNA sequencing.

Results: Our study found that 3D (three-dimension) spherical culture may be a promising approach to address MSC heterogeneity. Compared with conventional 2D (two-dimension) MSC, 3D spheroid culture resulted in reduced cell size, less morphological heterogeneity, and expression of higher levels of immunomodulatory and growth factors. Moreover, 3D MSC exhibited a more anti-aging state compared to 2D MSC. Single-cell transcriptomics analysis revealed that 3D spheroidal culture reduced the heterogeneity of 2D MSC: 2D MSC consisted of six cellular subpopulations, whereas 3D MSC mainly consisted of two cellular subpopulations, which (95%) expressed significantly higher levels of immunomodulatory factors, whereas this subpopulation only accounted for a small proportion in 2D MSC. Extracellular matrix (ECM) remodeling may be responsible for the reprogramming of 2D MSC into the strongly secreted immunosuppressive phenotype of 3D MSC.

Conclusions: Our results thus reveal that 3D spheroid culture synchronizes 2D MSC and reprograms 2D MSC with strong immunosuppressive properties, suggesting a promising prospect for clinical treatment of MSC.

Keywords: MSC; heterogeneity; single-cell sequence; immunomodulation

NO. 12

Circulating MAIT cells home to the gut mucosa during acute inflammation via the C-C motif chemotactic cytokine receptor 1, 2, and 4-dependent manners

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ABSTRACT: Mucosa-associated invariant T (MAIT) cells represent the largest population of antimicrobial T cells and are abundant in the human gut. Circulating MAIT cells home towards inflamed tissues during infections and inflammation due to the high expression of chemotactic cytokine (chemokine) receptors and homing molecules directing them to these sites. However, there is a lack of knowledge on the mechanisms underlying MAIT cell homing to gut mucosal tissues in these pathological conditions.

To model circulating MAIT cells homing to the gut, we established a human intestinal organoid co-culture with MAIT cells in the absence or presence of inflammatory stimulations. Using advanced polychromatic flow cytometry and time-lapse confocal live imaging and microscopy, we showed that MAIT cells readily migrated, closely associated with the epithelium, and penetrated the enterocyte cell junctions of the intestinal organoids. Such MAIT cell tissue-homing capacity was markedly enhanced following stimulations of MAIT cells with pro-inflammatory cytokines and treatment of the intestinal organoids with the gut pathobiont Escherichia coli.

Next, as an example of acute intestinal inflammation, we established patient-derived organoid (PDO) cultures from inflamed appendix tissues surgically resected from children with acute appendicitis. Secretomes from the PDO cultures contained high levels of gut tissue-associated and pro-inflammatory chemotactic cytokines that resembled those measured in the inflamed appendix tissue of acute appendicitis patients. Our findings indicated that circulating MAIT cells rapidly migrated in response to stimulation using original PDO secretomes through the C-C motif chemokine receptor (CCR)1-, CCR2-, and CCR4-dependent manners.

In summary, our findings indicate novel mechanisms underlying MAIT cell tissue homing into the gut tissues in such pathological conditions. Our findings further reveal the intricate relationship between MAIT cells and gut mucosal tissues in the setting of acute intestinal inflammation in humans.

Keywords: MAIT cells, tissue-homing, chemokines, intestinal inflammation, organoids.

NO. 13

Targeting mTOR and ULK1 in Autophagy: Exploration of Specific Drug and Virtual Screening

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ABSTRACT: Drug design for key proteins in the autophagy pathway, whether inhibitor or activator, is studied for diseases treatment like Alzheimer's. Mammalian target of rapamycin (mTOR) is one of the most popular drug targets. However, challenges such as modest efficacy and drug resistance persist. Unc-51-like autophagy activating kinase 1 (ULK1/Atg1), the autophagy initiating protein, is bounded and regulated by mTOR and indirectly regulated through AMPK. ULK1 has been confirmed to exert stronger regulatory effects on autophagy than mTOR, positioning it as a promising novel target to drug discovery.

This work try to explore potential drugs targeting the essential autophagy regulators mTOR and ULK. we conducted reverse target fishing on known affinity molecules for mTOR and ULK1 from the ChEMBL database. We established Ligand similarity-based AI model for mTOR and ULK1 ligand virtual screening. Then, molecular docking was performed on potential compounds and ADMET was predicted. We also used one of best target fishing tool SEA to validate the effective targeting of potential compounds. In conclusion, we have confirmed the deficiency of strong specific ligand for ULK1. A cohort of potential small molecule lead compounds with favorable pharmacological and toxicological indicators (especially those capable of crossing the blood-brain barrier) was identified. And these compounds were subsequently utilized in affinity experiments for validation. This work holds significant implications for the treatment of Alzheimer's, Parkinson's and autophagy-related cancers.

NO. 14

Global-Polarization Stokes Ellipsoid: A Vivid Method to Sensor Polarization Characteristics

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ABSTRACT: In polarization imaging, circular and linear polarization are conventionally used for incident light detection. However, relying solely on these modes may lead to a loss of crucial polarization data. This study expands the incident polarization state from a single point on the Poincaré sphere to its entire surface, yielding the Global-Polarization Stokes Ellipsoids (GPSE). GPSE offers an intuitive representation of polarization response discrepancies. It reveals distinct characteristics when birefringence and scattering effects act independently and analyzes their coupled effects in concurrent operation. In systems with both birefringence and scattering, GPSE parameters provide a robust characterization of anisotropy, overcoming issues for linear phase retardation, like phase wrapping and helicity flip associated with circular polarization. This approach provides a novel perspective and methodology for polarization imaging and information extraction.

Keywords: polarization, birefringence, scattering, Monte Carlo simulation, anisotropy

NO. 15

Kinetics modeling of the translational regulation on the mitochondrial surface

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ABSTRACT: Mitochondria are the important organelles for energy metabolism in a cell. Numerous nuclear-encoded proteins are imported into the mitochondria to maintain their functions. mRNA localization assures the precise spatiotemporal control of gene expression for the cell. In our previous research, we observed higher protein expression when we tethered mRNA to mitochondria using the MS2-MCP system. We inserted MS2-sequences in GFP mRNA, which was tethered to the MCP combined with Tom70, mitochondrial outer membrane transporter protein. We hypothesized that there may be a certain influencing factor playing a role in this process, or it may be due to an increase in local mRNA concentration leading to a higher rate of translation. To further investigate this mechanism, we perturbed the quantity of regulatory elements. We explored the weak promoter (TIM50p) and strong promoter (TDH3p) for regulating protein production. We found that for TIM50p, the GFP level is enhanced up to four-fold, whereas for TDH3p, it was only enhanced two-fold. This suggests that there are some feedback regulations to restrict the top limit of gene expression. We then simulated the translation process of GFP mRNA after its localization on the surface of mitochondria through mathematical modeling and computation. We developed dynamic equations that described the relationships between the concentration of GFP mRNA, the concentration of the MS2-MCP complex, and the synthesis rate of GFP. We tested three scenarios: 1. mRNA of GFP can be depleted. 2. Both mRNA and free TOM70-MCP can be depleted. 3. Both mRNA and ribosomes around mitochondria can be depleted. The simulation results suggested that the concentration of mRNA and TOM70-MCP might be key variables. Currently, we are conducting experiments with different TOM70-MCP copy numbers to validate the accuracy of the model. We will further improve the model and combine experimental data to explore the relationship between mitochondrial localization and protein synthesis rate, in order to better understand translational regulation on the mitochondrial surface.

Key Words: mRNA localization; mitochondria; yeast; translation; simulation

墙报展示 Poster Presentations

NO. 1

Association of CCL17 and CCL22-producing infiltrating leukocytes with MAIT cell accumulation in the inflamed appendix of children with acute appendicitis

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ABSTRACT: Appendicitis in children is a leading acute surgical condition in children worldwide. It is commonly caused by infection of the obstructed appendix by enteric gram-negative bacteria. Mucosa-associated invariant T (MAIT) cells are the largest population of antimicrobial T cells in humans and are widely distributed along the gastrointestinal tract (GIT). In our previous study, we showed that MAIT cells activation and recruitment into the appendix drives inflammation and tissue damage in acute appendicitis.

In this study, we found MAIT cell accumulation in the inflamed appendix was linked with infiltration of neutrophils as well as elevated levels of multiple pro-inflammatory chemokines, including CCL17 and CCL22. This was coupled by accumulation of MAIT cells with elevated expression of CCR4 – the chemokine receptor for CCL17 and CCL22. Moreover, we found an enrichment of CCL17- and CCL22-producing CD45+ pan-leukocytes within the inflamed appendix. Further analyses indicate that the predominant leukocyte sources of CCL17 and CCL22 within the appendix were infiltrating neutrophils and B cells. Spearman's analyses indicated that the levels of MAIT cells within the inflamed appendix were positively correlated with the levels of CCL17+ and CCL22+ infiltrating pan-leukocytes and neutrophils. Interestingly, plasma levels of the inflammatory marker C-reactive protein (CRP) were also positively correlated with the levels of CCL17+ pan-leukocytes and neutrophils within the inflamed appendix.

Taken together, our results suggest that appendix infiltration by CCL17- and CCL22-producing leukocytes, particularly neutrophils and B cells, may drive MAIT cell recruitment during acute appendicitis. Future studies will need to ascertain the significance of CCL17 and CCL22 and their cellular sources as well as the mechanisms underlying production of these chemokines in the pathogenesis of acute appendicitis in children.

Keywords: MAIT cells, neutrophils, chemokines, inflammation, gastrointestinal

NO. 2

CD34+ progeny cells act as stem cells to contribute to the epithelial restitution following injury

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ABSTRACT: It's widely recognized that CD34 is a marker of hair follicle stem cells in skin epidermis, which is crucial for epidermal homeostasis. However, the role of $CD34^+$ cells in maintaining other epithelial cell renewal and reproduction remains to be elucidated. Here, we generated *CD34- CrePGR-tdTomato* mice and crossed with *mT/mG* mice to get *CD34-Cre PGR; mT/mG* mice, which helped to tracing CD34+ cells in various epithelial tissues. It was showed that the progeny of CD34+ cells participated the renewal of epithelial cells in variant tissues, including hair follicles, airway epithelium, pulmonary epithelium and other acinous cells in kinds of glands. Further, CD34+ progeny cells have properties of stem cells, which contribute to the epithelial restitution and form stem cell like clone in the HCl-induced epithelial injury models. In addition, in view of the fact that CD34 expression across several cell types, such as embryonic fibroblasts, further explore should be made to clarify which types of CD34+ progeny cells are involved in the epithelial cells. Therefore, *Pdgfra-CreERT; mT/mG* mice were specifically used to tracing embryonic fibroblasts, which adjacent to the epithelial cells. The data showed that the contribution that fibroblast restitute the epithelial cells directly in the epithelial injury models is insignificant. Maybe acute wound induced the expression of CD34+ progeny cells in the epithelial cells rapidly. Our findings provide a basis for understanding the biological function of CD34+ cells in epithelial restitution when suffering acute injurious.

Key words: CD34+ progeny cells; Epithelial restitution; lineage tracing; stem cells; acute wound;

NO. 3

Preparation and immunogenicity of a therapeutic TEM8-mRNA vaccine for triple-negative breast cancer

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ABSTRACT: Triple-negative breast cancer (TNBC) is associated with aggressive progression, high metastasis rate and poor prognosis, and the treatment of TNBC patients remains a great clinical challenge. mRNA vaccines have great potential for application in the field of tumour therapy. Relying on the rapid development of mRNA vaccine technology, it is promising to prepare clinically effective therapeutic mRNA vaccine for triple-negative breast cancer, and the results of the study will provide scientific basis for the immunotherapy targeting TEM8 as a strategy for the treatment of TNBC, and provide a basis for the research of the TEM8- mRNA vaccine.

NO. 4

RCA-CRISPR-Cas12a-G4 based bimodal detection of circular RNA

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ABSTRACT: Primary liver cancer is a common malignant tumor in China and one of the diseases that seriously threatens public health. The onset of primary liver cancer is insidious, early diagnosis is difficult, most patients have reached the advanced stage after clinical symptoms, and the degree of malignancy of primary liver cancer is high, with high metastasis rate and high recurrence rate, the 5-year survival rate of patients is very low, and the prognosis is extremely poor. Genome sequencing of bacteria and archaea revealed the presence of clusters of regularly spaced short palindromic repeats (CRISPR). The CRISPR locus is transcribed and processed into mature crRNA, and after binding to CRISPR-related proteins (Cas), it can capture and recognize exogenous nucleic acid sequences and break them, exerting immune defense roles against viruses, plasmids, and exogenous nucleic acid invasion CRISPR/Cas system. The CRISPR/Cas system is a heritable adaptive immune system of bacteria and archaea. The electrochemical method is a low-cost, highly sensitive, and accurate rapid analytical detection technique. The electrochemical sensor detects measurable changes in electrode interface potential, current, and impedance caused by the target analyte in the solution, and is easy to miniaturize, and can analyze optically opaque samples such as blood, urine, and other matrices, and has the unique advantage of anti-interference rapid analysis and detection technology. Electrochemical sensors detect measurable changes in electrode interface potential, current, and impedance caused by the target analyte in the solution, are easy to miniaturize, and can analyze optically opaque samples such as blood, urine, and other matrices, with the unique advantage of being resistant to interference. The clinical stage of liver cancer is complex and the recurrence is very high, which makes clinical treatment difficult. Therefore, there is an urgent need for a method to identify the occurrence and development stages of liver cancer, which is helpful for clinical staging treatment and improves the overall survival rate of patients. Due to its high sensitivity and specificity, the CRISPR/Cas system has played a unique advantage in the field of disease diagnosis, greatly shortened the detection time, and is easy to operate, making it a promising method for home detection of diseases. The method proposed in this study is simple and sensitive, which is helpful for the diagnosis and treatment of liver cancer.

NO. 5

Specific peptide PROTAC regulated by CB[8] targets the degradation of DHHC3

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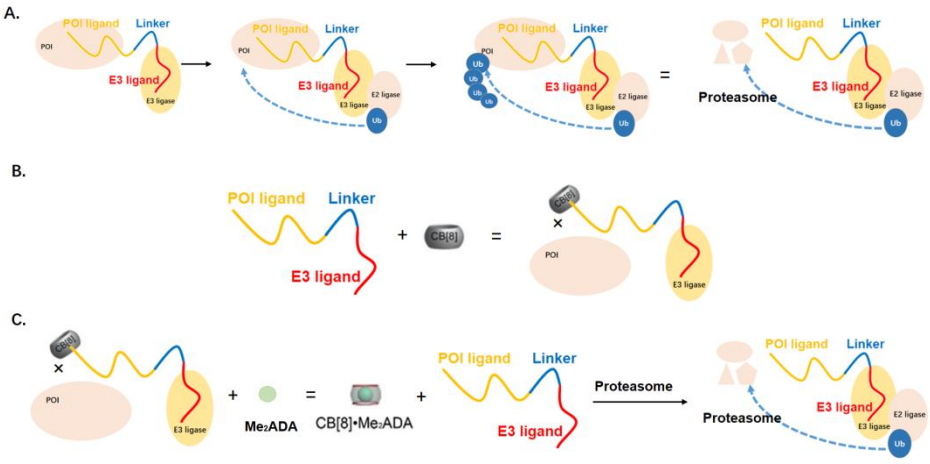
ABSTRACT: Proteolysis Targeting Chimera(PROTAC) technology utilizes the ubiquitin-proteasome system to degrade targeted proteins, thereby converting an initially "undruggable" target into a "druggable" one. However, current developments in PROTAC still encounter several challenges, Of particular concern is the non-cancer-specific toxicity of PROTAC, which compromises its safety. Due to the indiscriminate attack on cancer protein targets expressed in both normal and cancerous tissues, drug resistance and other issues. In our study, we designed a polypeptide PROTAC that can be regulated by supramolecular cucurbituril[8](CB[8]). Based on the property that CB[8] can bind to phenylalanine as a host-guest without complex chemical modification, PROTAC can be regulated through the self-assembly and guest competition effect between CB[8] and polypeptide PROTAC. This method innovatively proposed a study on the use of supramolecules to construct steric hindrant regulation of PROTAC, which enriched the application of supramolecular CB[8] in the biomedical field and realized the regulation of PROTAC.



NO. 6

Therapeutic effect of 3D-MSCs on dermatofibrosis and its mechanism study

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ABSTRACT: Fibrosis has long been of great concern as one of the most prevalent features affecting populations with millions of associated diseases, in which excessive ECM deposition can lead to irreversible tissue damage and organ failure or dysfunction. Scar formation is usually due to collagen reorganization during the wound healing process and is a fibrotic disease of the skin caused by an abnormal wound healing response. Stem cells, with their ability to self-renew and differentiate into specific functional cell types, are extremely valuable cells in tissue regeneration. In scar treatment, stem cells may have a role in promoting tissue repair and regeneration. Current research has focused on skin regeneration and scar treatment. Several experimental studies have shown that stem cell therapy may help reduce scar formation, improve scar texture, and promote regeneration of normal skin tissue. It has been shown that MMPs are highly expressed in 3D-MSCs, which act as important protein hydrolases to degrade various protein substrates in the ECM, including collagen and elastin.MMPs activity is critical for extracellular matrix conversion associated with physiological and pathological tissue remodeling.

NO. 7

Conserved mRNA regulatory mechanism on mitochondrial surface from yeast to human cell

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ABSTRACT: Post-transcriptional regulation plays a pivotal role in gene expression, particularly in eukaryotic cells where the coordination of translation and mRNA decay processes is essential. P-body is a cytoplasmic focus found in eukaryotic cells, which is particularly associated with mRNA degradation and storage. Non-translating mRNAs have the potential to accumulate in the P-body, where mRNA decay machinery is concentrated. In addition, the size of cells changes during the cell cycle and in response to external stimuli. This requires the tight coordination of mRNA and protein quantities with the cell volume to maintain biomolecule concentrations and cell density. It can be seen that the size of the cell significantly affects the formation or interaction of various molecules in the cell. While several mRNA degradation regulatory mechanisms have been proposed, a notable gap exists in understanding how cell size influences these processes. Yeast cell size is much smaller than human cell size, so we tested how cell size is important in the mRNA regulatory mechanism and if the mechanism is conserved from yeast to human cells. we build yeast cell size separation microfluidic chips to explore the relationships between yeast cell size and P-body formation. We screened the microfluidic chip size that best suits our yeast strain W303 (Saccharomyces cerevisiae), which ranges from 5.1 to 7.5μm. We have trapped different yeast cell sizes and investigated the formation of P-bodies. Preliminary findings showed that smaller yeast cells exhibit relatively smaller and larger numbers of P-bodies, whereas larger cells have larger P-bodies with decreased numbers. We are currently incorporating mathematical modeling to analyze the relation between yeast cell size and P-body formation. By analyzing the relationship between yeast cell size and P-body formation, we will help propose new insights and mechanisms in translational regulation and mRNA degradation, which can provide a more comprehensive understanding of gene expression regulation.

Key Words: mitochondrial, mRNA, P-bodies, microfluidics, mRNA degradation and translation

NO. 8

Inhibitor of TFF3 Synergies with c-MET Inhibitors to Decrease CSC-like Phenotypes in ER+ HER2+ Mammary Carcinoma

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ABSTRACT: Mammary carcinoma (MC) is the most common malignant neoplasm and the second leading cause of cancer death in women worldwide. In Asia Pacific regions, breast cancer is enriched in younger patients and rapidly rising in incidence with a higher proportion of estrogen receptor positive (ER^+) and human epidermal growth factor receptor 2 (HER2+) subtype. AMPC ((2-amino-4-(4-(6-fluoro-5-methylpyridin-3-yl) phenyl)-5-oxo-4H,5H-pyrano [3,2-c] chromene-3-carbonitrile) is a small molecule inhibitor of the pro-survival protein trefoil factor 3 (TFF3) that has an established oncogenic function and a highly significant association with clinical progression of MC. To gain additional insights into the rational combination of AMPC-based therapies, we performed a high-throughput drug screening for identification of potential regimens that have both mechanistic complementarity and active clinical programs in ER^+ $HER2^+$ MC models. Our screening findings identified the molecular underpinnings of AMPC potency and established pharmaceutically dual targeting TFF3 and c-MET as a promising therapeutic strategy in ER^+ $HER2^+$ MC. The combination of AMPC and c-MET inhibitors synergically suppressed CSC-like phenotypes, which may function as potential biomarkers and therapeutic targets in ER^+ $HER2^+$ breast cancer.

NO. 9

Development of a novel assay to examine the cross-talk between regulatory T cells and MAIT cells

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ABSTRACT: The gut is one of the largest immune organs in the body. Mucosa-associated invariant T (MAIT) cells are a population of antimicrobial T cells that are highly abundant in the gut, acting as one of the first lines of defense against invading pathogens. However, these cells may excessively respond to inappropriate changes in the gut microbiota composition, leading to damaging inflammatory responses. Regulatory T cells (Treg) can suppress immune responses, excessive inflammation and proliferation of effector T cell populations through various mechanisms, including releasing immunosuppressive cytokines, such as IL-10. Interactions between Tregs and other gut immune cells are key in maintaining homeostasis and self-tolerance. However, there is no study to date which explores the interactions between MAIT cells and Treg cells.

Here, we report the development of a novel assay to examine the cross-talk between Treg and MAIT cells and the effects on MAIT cell effector function. To this end, $CD25^{hi}$ $CD4^{+}$ Treg cells and/or $CD25^{neg}$ $CD4^{+}$ control T cell populations were depleted or isolated and expanded from peripheral blood mononuclear cells (PBMCs) as appropriate. Following activation with *Escherichia coli,* the MAIT cell population in Treg cell-depleted PBMCs had increased TNF production compared to those in total PBMCs. MAIT cells cocultured with supernatants from anti-CD3/CD28 bead-activated Treg cell cultures exhibited a decreased functional response with lower expression of GrzB, CD107a, and TNF, compared to MAIT cells cocultured with $CD25^{neg}$ control T cell supernatants. Compared to $CD25^{neg}$ control T cells, Treg cell culture supernatants had increased levels of IL-10, IL-4, and IL-13 cytokines that were sustained up to 72 hours after activation.

These data are the first steps in uncovering the interplays between these two specialized T cell subsets and identifying novel approaches to modulate excessive MAIT cell function in the setting of intestinal chronic inflammatory diseases such as IBD.

Keywords: MAIT cell; regulatory T cell; pro-inflammatory cytokine; suppression; immune regulation

NO. 10

Generation of Hair Follicle Organoids Utilizing 3D Printing for Drug Test

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ABSTRACT: In skin repair and regenerative medicine, fabricating hair follicle-like structures remains challenging, especially in mimicking skin cell dynamics and tissue architecture. Traditional methods fall short in replicating complex skin cell interactions and structures, impeding effective hair follicle regeneration and skin repair strategies. Our study leverages 3D printing to innovate a method involving Matrigel microspheres with integrated epidermal and dermal cells. The results show that these microspheres facilitate spontaneous cell migration and aggregation, offering a novel approach for emulating the cellular dynamics of hair follicle-like organ precursors. Overall, this research, utilizing 3D printing to produce microspheres with bud-sprouting features, provides a novel tool for simulating cellular dynamics in hair follicle-like organs, potentially enhancing the understanding of cell behaviors in hair follicle development.

NO. 11

Exploring the Neural Organoid in High Definition: Physics-Inspired High-Throughout Super-Resolution 3D Image Reconstruction

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ABSTRACT: Organoids serve as a versatile platform for biomedical research, including drug screening, disease progression, cancer, developmental, and mechanobiology studies. However, precise 3D modeling of organoids remains a formidable challenge due to the complexity of tissue architecture, resolution limitations of confocal microscopy, and the time and labor-intensive process of acquiring data to achieve peak results. In this paper, we propose a novel strategy named LayerLink to enhance the 3D structure of Neural Organoids' TUJ1 fluorescently labeled nerve fibers using neighboring layers of stacked 3D image. By leveraging the Beer-Lambert law, we link each vertical layer to its neighboring layers through a blending process where the weights of each layer are from a generalized normal distribution, forming the input for a super-resolution diffusion model to reconstruct the entire volume. When data is limited, our reconstructed layers achieve an 11.02% improvement over the conventional deep learning method with a peak signal-to-noise ratio of 22.46. Notably, the reconstructed nerve fibers and fascicles in the vertical sections exhibit remarkable continuity. This precise modeling algorithm shows great promise for high-resolution monitoring of organoids and tissues exhibiting continuous fine structures. Furthermore, it holds the potential for advancing our understanding of cell-to-tissue-to-organ interactions and advancing 3D tissue bioprinting techniques in the future.

NO. 12

Evaluating accessibility and usability of *Kluyveromyces marxianus* yeast through genome-scale modeling using proteome constraints

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ABSTRACT: The advances of synthetic biology and systems biology have highlighted the importance of genome-scale metabolic models (GEMs) as tools in comprehensively studying cellular metabolism. GEMs also have significant application values in guiding the metabolic engineering of microbial cell factories for bioproduction of proteins and value-added compounds. Yeasts are popular eukaryotic hosts for recombinant protein production because of their posttranslational modification machinery when comparing to bacteria. Among them, the thermotolerant yeast *Kluyveromyces marxianus* has gained special attention because of its fast growth, high stability and protein secretion capability under high temperature. Here, we first summarize the current research status of yeast genome-scale metabolic models, including their construction and curation process, their applications in synthetic biology, and introduce new technologies to integrate omic data for better simulation. We also propose a plan of research to study the construction of a proteome-constrained genome-scale protein secretory model of yeast *K. marxianus*, which can be used to study its genotype-phenotype correlations in the protein secretory pathway, and guide metabolic engineering to address bottlenecks in the secretory pathway for high-level protein production.

NO. 13

Imbalanced Multi-Lesion Classification in Myopia using Ultra-widefield Images

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ABSTRACT: The benefits of deep learning in computer vision have led to a leap forward in the efficiency and accuracy of retinal disease screening. As one of the most known retinal diseases, myopia is a leading cause of visual impairment and blindness. Regular screening with fundus photography has become prevalent in the clinical diagnosis and treatment of myopia. Existing studies using fundus photography intrinsically ignore characterized lesions in the peripheries of the eye due to the limited view. Meanwhile, they focus on either multi-disease classification containing myopia or multi-grade classification of myopia, which discards lesion dependencies of myopia. Ultra-widefield imaging (UWFI) as a promising modality, captures a larger retinal field of view potentially involving both central and peripheral lesions. Therefore, we collect a large UWFI myopia dataset from several hospitals with expertise in lesion-wise labeling. We cast this challenge in a multi-label fashion to naturally consider the complications between lesions and investigate their underlying dependencies. Besides, multiple cost-sensitive approaches are developed to mitigate the imbalance issue. Extensive experiments in both internal and external datasets have demonstrated that our implementation is effective and efficient for lesion-wise myopia classification and generalizes well to other retinal diseases.

NO. 14

Volumetric compression by hydrogel embedding promotes cerebral organoid maturation

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ABSTRACT: While biochemical regulation has been extensively studied in cerebral organoid modeling protocols, the role of mechano-regulation in directing stem cell fate and organoid development has been relatively unexplored. Although the influences of environmental machinal properties on 2D-cultured cells, including neurons, have been reported and suggests that mechanical signals may also have an important role in organoid development, there has been a lack of methods to provide continuous mild forces on small 3D tissues like brain organoids. In our study, we cultured cerebral organoids in various mechanical environments and observed that they showed different morphology and cell proportions. We have developed a novel method of heterogeneous embedding using an alginate-shell-Matrigel-core system. This approach allows for cell-Matrigel remodeling by the inner layer and provides moderate normal compression through the soft alginate outer layer. Our results show significant improvements in cell proliferation and maturation of cerebral organoids, as evidenced by increased expression of neuronal markers such as neurofilament (NF) and microtubule-associated protein 2 (MAP2). Our findings demonstrate the successful mechanical regulation of cerebral organoids, which not only mimics the mechanical environment of brain development but also exhibits a regular growth profile with enhanced maturation. These results highlight the importance and potential practical applications of mechano-regulation in the establishment of brain organoids.

NO. 15

Analysis of Heterogeneous Distribution of ATP Synthase Components in the Mitochondrial Network Structure

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ABSTRACT: ATP synthases are inner-membrane-anchored rotating enzymes in mitochondria and are composed of an F1 motor driven by ATP-hydrolysis and an F0 motor driven by proton translocation. While the structural identification of ATP synthase is well described, the expression, localization, and assembly process of ATP synthase proteins have not been fully explored yet. F1F0 ATP synthase could participate in mitochondrial permeability transition pore (mPTP) formation, which mediates mitochondrial permeability transition. Graph theory became an important tool in biological and medical research. We utilized network theory to analyze the distribution of ATP synthase protein in mitochondria and its relationship to mitochondrial morphology and function. First, we used quantitative microscopy to observe mitochondrial dynamic changes and protein distribution. We found that ATP3p, ATP4p, and ATP5p were localized to specific regions of mitochondria, while ATP1p, ATP2p, and ATP7p were evenly distributed throughout the mitochondrial network. Second, we analyzed the relationship between the mitochondrial network structure and the protein expression of ATP synthase components by network theory. We computationally reconstructed the mitochondrial network structure and quantified the protein expression level of each protein using the previously developed software Mitograph. We found ATP2p distributed in 97% of mitochondria regions, while ATP4p and ATP3p were localized to 44% and 75% of mitochondria regions separately. ATP4p showed larger missing probabilities than ATP3p in SC, YPAD, and YPAGE media. ATP4p's missing probability decreased from nodes with lower branch numbers to ones with higher branch numbers. These suggest that ATP4p has a distinctive regulatory mechanism compared to the other ATP synthetase proteins. Now, we are exploring if ATP4p function and the regulatory mechanism are related to cristae morphology and ATP synthase dimerization. This research will accelerate the study of the mechanisms of mitochondrial ATP synthase protein distribution and promote understanding of ATP synthase structure and assembly process.

NO. 16

Evaluation of MAIT cell killing of cancer cell lines treated with sub-lethal doses of chemotherapeutic drugs

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ABSTRACT: Mucosal-associated-invariant T (MAIT) cells are an unconventional T cell population with innate and adaptive immunity characteristics. Although MAIT cells are predominantly antimicrobial, they are able to mediate cytotoxicity and kill cancerous cells through both T cell receptor (TCR)-dependent and -independent manners. Here, we explore the ability of MAIT cells to kill cancerous cell lines treated with sub-lethal doses of chemotherapeutical drugs to assess the potential benefit of combining chemotherapy- and MAIT cells for future MAIT cell-based cancer immunotherapy development.

To this end, we initially treated the cervical cancer HeLa cell line with sub-lethal doses of 5-fluorouracil (5-FU), cisplatin, paclitaxel, and cytarabine. All these chemotherapeutic agents promoted the expression of the cellular stress ligands major histocompatibility complex class I-related chains A/B (MICA/B) and UL16-binding protein 1 (ULBP1). These proteins are ligands to the natural killer group 2D (NKG2D) cytotoxic receptor expressed on MAIT cells shown by flow cytometry. Next, we performed coculture of chemotherapeutic agents-treated HeLa cells with MAIT cells. We found that MAIT cells readily killed HeLa cells that were pre-treated with these drugs but not untreated HeLa cells. Moreover, such MAIT cell killing mechanism was not through a TCR-dependent pathway.

In summary, our preliminary findings suggest that MAIT cells could kill cancer cell lines that were stressed by sub-lethal concentrations of chemotherapeutic drugs. Further work on other cancer cell lines and to determine the mechanisms of MAIT cell killing of stressed cancer cells are currently ongoing.

NO. 17

IL-15 fine-tunes the MAIT cell antimicrobial effector function through the regulation of cytolytic protein expression

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ABSTRACT: Mucosa-associated invariant T (MAIT) cells are innate-like T cells known for their rapid and potent antimicrobial activity. Upon recognizing bacteria-derived riboflavin metabolites presented by MHC class Ib protein (MR1), MAIT cells rapidly respond by secreting pro-inflammatory cytokines and cytolytic proteins. The antimicrobial activity of MAIT cells is partly dependent on the activity of the cytolytic proteins Perforin (Prf), Granzyme B (GrzB), and Granulysin (Gnly). Various cytokines regulate MAIT cell activation during bacterial infection. Given that the levels of cytolytic proteins secreted by MAIT cells correlate with MAIT cell antimicrobial activity, we investigated the effect of various cytokines on regulating these cytolytic proteins in MAIT cells.

Here, we investigated the effect on cytolytic protein regulation by a set of cytokines known to have strong effects on MAIT cells, including IL-1β, IL-2, IL-7, IL-12, IL-15, IL-18, and IL-23. Considering the potential synergistic effects performed by these cytokines, we further extended our findings by using distinct combinations of these cytokines for MAIT cell stimulation, including IL-12+IL-18, IL-1β+IL-23, IL-2+IL-7, and IL-2+IL-7+IL-15. In the presence of MAIT cell-activating MR1 ligands, these cytokine treatments induced substantial proliferation of MAIT cells while upregulating Prf, GrzB, and Gnly expression by MAIT cells at different rates and magnitudes. We further demonstrated that various cytokine stimuli resulted in varying levels of MAIT cell-mediated cytotoxicity, with IL-15 having the most potent effect on MAIT cells, killing of target cells pulsed with MR1 ligands. The administration of multiple cytokines diminished the TCR-dependency in MAIT cell-mediated cytotoxicity compared to MAIT cells treated with individual cytokines.

These results indicate temporal and differential effects by various cytokines on MAIT cell expression of cytolytic protein expression and MAIT cell-mediated antimicrobial activity. Going forward, further optimization of MAIT cell cytolytic and antimicrobial responses is necessary, which will be important for developing a safe and effective MAIT cell-based antimicrobial therapy.

Keywords: MAIT cell, cytolytic proteins, cytokines, cytotoxicity, immune regulation

NO. 18

BSSDNet: A Novel Solution for Segmenting Medical Imaging in Deficient Datasets Guided by Super-Resolution related Features

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ABSTRACT: In the field of medical image segmentation, the datasets used for model training often face problems such as small dataset and insufficient labeling with missing masks, which severely limit the generalizability of various image segmentation models. We introduce an innovative two-branch semi-supervised breast cancer tumor segmentation network model, BSSRNet, which introduces image texture information and morphological information as a priori information to enhance the semi-supervised model's identification of tumor regions and the overall generalizability of the model. The model adopts an improved semi-supervised super-segmentation network based on enhanced morphological information as the sub-branch, and uses its unsupervised feature map combined with the pyramid model in the decoder part to enhance the supervised data of the main network at each pyramid layer, so as to realize the introduction of the a priori information of morphology and texture. Our model is a solution provided for the problem of small, dirty data and lack of labeling in medical images.

NO. 19

Synergistic Targeting of pBAD Ser99 and pERK: A Promising Approach for EGFR-TKI Resistant LUAD

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ABSTRACT: Targeting EGFR mutation, a frequent oncogenic alteration in LUAD, is crucial for effective treatment. However, the development of resistance to EGFR tyrosine kinase inhibitors (EGFR-TKIs) remains a major obstacle. In our study, high throughput drug screening identifies combined pBAD inhibitor and EKR inhibitor have a potential synergistic effect in EGFR-TKI resistant LUAD cell lines. RNA-seq analysis highlights the significant differential expression of MAPK pathway between resistant LUAD cell and its parental cell. Therefore, to address EGFR-TKIs resistance in LUAD treatment, we propose a synergistic approach by inhibiting pBAD Ser99 and ERK in TKI resistant LUAD. *In vitro* and *ex-vivo* assays validated the efficacy of this combinatorial strategy in suppressing LUAD growth. Hence, these promising results highlight the potential of our approach as a future clinical treatment for EGFR-TKI resistant LUAD, warranting further in vivo exploration and mechanistic elucidation.

NO. 20

PROTAC Targeting RAD51 for the Treatment of Triple Negative Breast Cancer

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ABSTRACT: Proteolysis-Targeting Chimeras (PROTACs) are important bifunctional molecules capable of targeting target proteins for degradation by ubiquitination mechanisms, including traditional non-druggable proteins, and are a promising technology. RAD51 proteins are important proteins in DNA double-stranded repair processes and are highly expressed in the TNBC cell lines are highly expressed. In this study, we were inspired to propose peptide PROTACs for degradation of RAD51. The idea was to design a plasmid molecule (RAD51-PROTAC) based on peptide PROTACs (p-PROTACs) capable of targeted degradation of the target proteins to be expressed upon entry into the cell and then to perform its ubiquitin-proteasome system (UPS)-based targeting function to degrade the target proteins. The strategy was validated. In order to verify the feasibility of this strategy, green fluorescent protein was introduced into the design process of this study to verify the expression of the corresponding sequences. In this paper, the expression of fluorescent proteins was firstly characterised by cellular imaging to verify the translational ability of the sequence, and then m-PROTAC-1 was treated with RAD51 overexpressing breast cancer cells (MDA-MB-231 cells), and the degradation function was verified by using immunoblotting experiments and immunofluorescence staining; different experimental groups were set up to study the effects of transfection conditions, time and concentration on the degradation of RAD-PROTAC-1, which is the most effective way to prevent the degradation of the target protein. PROTAC-1 degradation function.
In summary, this paper proposes a strategy for the design of RAD51-PROTACs to expand the molecular form of PROTACs technology, while this strategy is expected to provide new ideas for the clinical application of encoded peptide PROTACs.

NO. 21

The Multimodal, Cross-scale Canine Brain Atlas and Cortical Cytoarchitectonic Fine-grained Parcellation

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ABSTRACT: Brain atlas represents a cornerstone in neuroscience. Modern digital brain atlases with precise partitioning have become essential tools in exploring the relationship between brain structure and function. Cytoarchitectonics, the fundamental principle of microstructural brain parcellation, has facilitated the creation of numerous brain partition atlases. However, the explosion of data and conservative approaches in cytoarchitectural research impede further refinement in microstructural division. In addition, there is an inter-species imbalance in the development of modern brain atlases. In this work, we introduce a novel cortical partitioning method based on hypergraph analysis of cytoarchitectonics, offering finer and more accurate cerebral cortex divisions. We verify the method's applicability and efficacy for cross-species research using data from human and canine brains. Additionally, we present a new multimodal canine brain atlas, which integrates connections between mesoscopic and macroscopic scales and beyond the limitations of existing canine brain maps. This atlas, to be shared publicly, and our novel partitioning method, together help to optimize the understanding of brain structure and function, showcasing both innovation and extensive scientific value.

NO. 22

Optogenetic engineered cells controlled by ultrasound enable GLP-1 secretion in vivo

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ABSTRACT: For a long time, diabetes has been one of the chronic diseases that endanger human health. About 90%-95% of diabetics have type 2 diabetes. Type 2 diabetes can be controlled by injecting GLP-1 agonist. GLP-1 is an incretin hormone which can effectively promote insulin secretion and then lower blood sugar. At present, most drugs with GLP-1 agonist are based on injection. In order to reduce the trauma and achieve controllable treatment, we transformed the cells into engineering cells that are sensitive to far red light and can secrete GLP-1 under far red light illumination. Besides, by encapsulating the cells that can secrete GLP-1 with LED in hydrogel, at the same time, making LED work through ultrasonic electricity generation. Finally, the purpose of further effectively controlling the secretion of GLP-1 by controlling LED by ultrasound is realized.

Key words: engineered cells; far red light; GLP-1; ultrasound.

NO.23

Simple and Point-of-Care Detection of Cobalt Pollution Based on CRISPR-Cas12a and Terminal Deoxynucleotidyl Transferase

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ABSTRACT: The widespread utilization of cobalt in various chemical applications, including battery materials, alloys, pigments, and dyes, has exacerbated the contamination of cobalt in the food supply and the environment, necessitating an urgent need for on-site monitoring. In this study, a terminal deoxynucleotidyl transferase (TdT) was developed as a recognition element utilizing enzyme dependence on metal cofactors. Subsequently, TdT was combined with CRISPR-Cas12a to establish a dual amplification sensing strategy for the highly selective and sensitive detection of cobalt concentrations in diverse water samples. The biosensor demonstrated exceptional sensitivity (0.83 nM) and specificity for cobalt over other ions. Furthermore, the method was successfully employed for the detection of cobalt in tap water and river samples. To enable sensitive on-site detection, Cas12a-based immunoassay strip was also evaluated in this study, revealing the capability to detect concentrations as low as 10 nM in tap water and river samples through strip analysis. These findings suggest that analytical biosensors utilizing TdT and Cas12a hold significant promise for the monitoring and management of cobalt pollution.

Keywords: Cobalt detection; Terminal deoxynucleotidyl Transferase; CRISPR-Cas12a assay; Cas12a-based immunoassay strip

NO.24

A novel dissolving bubble microneedle patch used for drug transdermal delivery of cosmetics

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ABSTRACT: With the gradual popularisation of skincare knowledge, it has been discovered that microneedles can overcome the barrier of the stratum corneum in a minimally invasive and painless manner, effectively promoting the transdermal penetration of efficacy molecules, and is particularly effective in the transdermal delivery of large molecules of drugs.However, existing microneedle patches have a number of limitations, such as water-soluble matrix materials cannot load oil-soluble efficacy substances, or comfort and convenience can be reduced with a prolonged action on the skin surface. Therefore, this project introduces a bubble structure in soluble microneedles and proposes to prepare a soluble bubble microneedle loaded with both oil-soluble and water-soluble components. At the same time, the presence of the bubble structure hinders the diffusion of efficacy molecules from the tip of the microneedle to the body, which increases the efficiency of subcutaneous drug delivery. In addition, the weak mechanical strength at the bubble structure makes the microneedle easy to break and remove at the bubble after piercing subcutaneously, and the user does not need to press it for a long time. The idea and preparation process of dissolvable bubble microneedles have been fully proved through pre-experiments, with controllable bubble size and distribution, and excellent uniformity of microneedles on the same patch. The soluble bubble microneedles have good mechanical properties, which are verified by the dynamometer and puncture experiments.

NO. 25

Structural design and biological evaluation of potent fourth generation EGFR kinase inhibitors

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ABSTRACT: Targeted therapy against mutated cell surface epidermal growth factor receptor, which is an important therapeutic target for NSCLC, exhibits good clinical response, whilst drug-resistant mutations occurred in cancer cells will eventually lead to the treatment failure. Currently there are three generations of EGFR-TKIs, and the concurrent occurrence of T790M and C797S acquired drug-resistant mutation can cause cell insensitivity to drugs of all three generations, leading to the emerging requirement for new generations of inhibitor. This project investigates the design innovation and principle of fourth-generation inhibitors published recently, and is planning to obtain a new wild-type sparing compound with great targeting ability, as well as high tolerance to wide spectrum of existing drug-resistance mechanisms, through well-formed structure design, chemical synthesis and screen of compounds. Structural analysis of brigatinib possessing fourth generation EGFR-TKI activity is the start point of our idea. Commercial lung cancer cell lines will first be utilized for screening and characterization, followed by the generation of a wider range of lung cancer cell models displaying varied drug-resistance mechanisms, using methods such as gene editing. These innovative models will further be utilized as in vitro and in vivo cell evaluation system, offering in-depth characterization of anti-cancer activity and drug-resistant mutation tolerance for newly synthesized compounds. Similar procedures will be performed to evaluate the ALK-TKI activity discovered in our compounds. Our structural design will definitely benefit the investigation of new-generation EGFR-TKI design, and the experimental results will hopefully fill the gap of NSCLC clinical treatment.

Keywords: EGFR, EGFR-TKI, NSCLC, C797S, drug resistance

NO. 26

Analysis of a feedback loop mechanism by Puf3 RNA binding protein in yeast

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ABSTRACT: Puf family RNA binding proteins play important roles in post-transcriptional regulation of specific gene expression. Puf3p, which is present on the surface of mitochondria, is known among the PUF-family proteins for binding to the mRNAs of nuclear-encoded mitochondrial genes in yeast. It has been shown to have a strong influence on mRNA stability and translational regulation of mitochondrial proteins. However, the regulatory mechanism of Puf3p itself has not been well described. We investigated a previous RNA-seq data set and found that Puf3p binds Puf3 mRNA. We also found that target mRNAs of Puf3p have a consensus motif within 3'-UTR sequences, which is also present in PUF3 mRNA 3'-UTR. These findings raise questions about whether this binding introduces a feedback loop regulation in gene expression and if this has a significant role in cellular activity. In this study, we visualized the mRNAs that Puf3p targets by the MS2-MCP system and analyzed the relationship with mitochondria under different carbon sources. We found that the expression of Puf3p had a positive impact on the number and localization ratio of target mRNAs, especially in glycerol compared with glucose media. We are currently analyzing the mechanism and physiological factors of this feedback regulation by altering the growth conditions. This research will help us better understand the important role of PUF3 in nuclear-encoded mitochondrial genes and the specific mechanism of cellular feedback regulation under environmental stress. By focusing on the feedback loop mechanism of the Puf3 RNA binding protein, we hope to gain a deeper understanding of mitochondria biogenesis regulatory networks.

NO. 27

Mathematical modeling for mRNA length and conformation: Three-dimensional RNA Illustration Program (TRIP)

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ABSTRACT: The compression and folding of RNA affects the stability of its functions such as transcription, translation, and catalysis. Therefore, structure determination of RNA is very important to reveal the regulation of biological reactions. The current techniques for determining RNA structure involve complex and inefficient methods such as X-ray crystallography, NMR, and cryo-electron microscopy. Therefore, various computer simulation methods and models have been developed to predict RNA conformation, from the earliest thermodynamic and molecular dynamic-based RNA structure predictions to deep learning-based conformation predictions in the past decade. In recent years, deep learning-based methods such as DMfold, CDPfold, UFOLD, and ARES have been developed for predicting structure. However, these conformation prediction model and method can only be achieved for short-stranded RNAs. Here we show that computer simulation model called the Three-dimensional RNA Illustration Program (TRIP). TRIP is based on single-chain models and angle restriction of each bead component from previously reported single-molecule fluorescence *in situ* hybridization (smFISH) experiments. The results of our model show that the distance from the 5' to the 3' of the mRNAs is increased when the ribosome is attached to the mRNA, correlating with previous findings. Furthermore, based on previous studies on the distance between mRNA and the mitochondrial surface, a plane was introduced in the simulation to explore the relationship between mRNA structure and the mitochondrial surface. TRIP is a fast and efficient application that only requires up to three inputs, RNA nucleotides, ribosome number, and trial number to acquire outputs, end to end distance. It can also provide a rough visualization of the 3D conformation of RNA, making it a valuable tool for predicting RNA end to end distance. In the future, we will develop more accurate, efficient, and lower-cost computational models and tools related to RNA structure.

Key Words: (mRNA conformation, bead-chain models, translation, RNA end to end distance)

NO. 28

Mitochondria-dependent Mechanisms of Nanoplastic Toxicity Revealed by Proximity Labeling Proteomics

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ABSTRACT: Nanoplastics, an emerging environmental pollutant of the 21st century, are increasingly accumulating in the human body, presenting potential health risks. The cytotoxicity of nanoplastics is intricately connected to the 'protein corona,' and nanoplastics disrupt normal mitochondrial dynamics via oxidative stress and induction of mitochondrial apoptosis, despite both the elusive mechanisms involved. In this research, our primary objective is to employ proximity labelling proteomics techniques to identify proteins and their networks that interact with nanoplastics during the cytotoxicity and mitochondria damage process. Following this, we will apply image processing and mitochondrial morphology analysis to decipher key genes and associated molecular mechanisms implicated in mitochondrial damage induced by nanoplastics. This study strives to contribute to the comprehensive understanding of the intricate interplay between nanoplastics and mitochondria, enhancing our knowledge of the potential health implications posed by these environmental pollutants.

NO. 29

Conjugated Polyelectrolyte/Single Strand DNA Hybrid Polyplexes for Efficient Nucleic Acid Delivery and Targeted Protein Degradation

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ABSTRACT: Nucleic acid-based therapeutics have gained increasing attention due to their ability to regulate various genetic disorders. However, the safe and effective delivery of nucleic acids to their intended cellular sites remains a challenge, primarily due to poor cell membrane permeation and low in vivo stability. Limitations associated with the commonly used nucleic acid delivering agent viral vectors such as carcinogenesis and immunogenicity have driven scientists to develop various non-viral vectors. In this study, we present a highly efficient nucleic acid-delivery system based on cationic conjugated polyelectrolytes (CPE) and single strand DNA (ssDNA) polyplexes with further application in the efficient ubiquitin-regulated targeting protein degradation. These polyplexes, formed by 9TC, an aptamer sequence for estrogen receptor (ERα), and cationic $PPET_3N_2$ through electrostatic and hydrophobic interactions, demonstrate improved cellular uptake efficiency as well as enhanced stability against nuclease degradation. Furthermore, by incorporating 9TC into a proteolysis targeting chimera (PROTAC) molecule (P9TC), $PPET_3N_2$/P9TC polyplexes significantly enhance the target protein ERα degradation efficiency. Collectively, our findings suggest that $PPET_3N_2$ provides a versatile, low cytotoxicity platform for safe, efficient, and simplified delivery of nucleic acids.

NO. 30

Multimodal-AIR-BERT: A Multimodal Pre-trained Model for Antigen Specificity Prediction in Adaptive Immune Receptors

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ABSTRACT: The in silico prediction of antigen binding in adaptive immune receptors (AIRs), which include T-cell receptors (TCRs) and B-cell receptors (BCRs), encompassing both antigen-binding specificity and affinity, remains at the forefront of understanding immunological processes and formulating targeted therapies. The V(D)J gene rearrangement is crucial in diversifying amino acid (AA) sequences in antigen-binding regions, equipping AIRs to discern a plethora of antigens from varied pathogens and the "altered self cells" manifest in cancers. The profound diversity of AIRs brings significant challenges to modern computational techniques aiming for AIR antigen-binding characteristics analysis. While the latest single-cell technologies can concurrently capture AIR sequences and their corresponding V(D)J gene data, there exists a gap in sophisticated multimodal computational strategies to holistically integrate these datasets for enhanced representations. Addressing these challenges, we introduce Multimodal-AIR-BERT, a cutting-edge multimodal pre-trained model tailored to enhance both specificity and affinity predictions in AIRs. This model incorporates a pre-trained sequence encoder, a gene encoder, and a pioneering multimodal fusion module using gating-based attention and tensor fusion. This design ensures a fluid integration of the V(D)J gene and AA sequence traits of AIRs, leading to more enriched representations. By incorporating V(D)J gene insights, which often go unnoticed in sequence-only analyses, Multimodal-AIR-BERT notably outperforms its sequence-only counterparts. In summary, our contribution represents a monumental stride in the realm of AIR antigen-binding characteristics analysis. As the accuracy of these predictions heightens, it promises to usher in precise immune therapies and a profound understanding of immune system intricacies.

NO. 31

Whole-Bacterium SELEX Aptamer Selection of *Porphyromonas gingivalis* and Application to Colorectal Cancer Noninvasive Screening in Human Feces

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ABSTRACT: In terms of cancer diagnoses and cancer-related deaths worldwide, colorectal cancer (CRC) is now the third most common malignancy. The drawbacks of current screening methods are their exorbitant costs, difficult procedures, and lengthy implementation timelines. The benefits of fecal screening for CRC are ease of operation, noninvasiveness, cost-effectiveness, and superior sensitivity. As a result of its enrichment in the malignant tissues and feces of CRC patients, Porphyromonas gingivalis has emerged as a crucial biomarker for the incipient detection, identification, and prognostic prediction of CRC. Here, the whole-bacterium SELEX method was used to screen the highly specific and affinity aptamers against Porphyromonas gingivalis by 15 cycles of selection. Hybrid chain reactions have attracted much attention because of their mild reaction conditions and their constant temperature and absence of enzymes. Therefore, HCR was used to amplify the signal and to detect Porphyromonas gingivalis rapidly and sensitively. The results of the experiment using fecal samples revealed a substantial disparity between the microorganisms in the CRC patients' feces and those in the feces of healthy individuals and were consistent with those of qPCR. The aptamers may therefore offer a crucial approach to identifying Porphyromonas gingivalis and hold tremendous promise for CRC diagnosis and prognostic prediction.

NO. 32

Dual-Stream Multi-Instance Learning with Shortcut Suppression for Whole Slide Image Classification

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ABSTRACT: MIL is a typical method for WSI analysis, as it allows the model to learn from weakly labeled data, where only the slide-level labels are available. However, MIL also faces some challenges, such as the large number of patches generated from the WSI, which have billions of pixels. Existing methods mostly use an attention module to identify salient instances from the patches. However, the attention module does not always help deep models capture essential features, as they may suffer from shortcut learning, which is a phenomenon where the model learns spurious correlations from the data instead of the true underlying patterns. The incorporation of MIL amplifies this issue, making the model more likely to rely on erroneous and easy-to-learn features, while ignoring reliable features. This leads to incorrect attention allocation of the model, affecting its final performance and generalization. To tackle this, we propose a new dual-stream shortcut suppression MIL (DSSMIL). Specifically, DSSMIL consists of a bag-level branch, an instance-level branch, and a shortcut suppression module. The attention module in the bag-level branch generates the corresponding attention score for each instance and aggregates them to form bag-level features. The instance-level branch trains an instance-level scorer, which assesses the difficulty of each instance. The shortcut suppression module contains two steps: the mix-step and the drop-step, which effectively solve the two shortcut learning ways of the model in MIL. In addition, we designed a gate filtering strategy to control the quality of the operations in the shortcut suppression module for better classification. The results on three large public benchmark datasets (Camelyon16, TCGA-NSCLC, and TCGA-RCC) demonstrate that our proposed DSSMIL outperforms other state-of-the-art methods in classification.

NO. 33

Generating Bright-Field Images of Stained Tissue Slices from Mueller Matrix Polarimetric Images with CycleGAN Using Unpaired Dataset

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ABSTRACT: Recently, Mueller matrix polarimetric imaging assisted pathology detection methods are showing great potential in clinical diagnosis. However, since our human eyes cannot observe polarized light directly, it raises a notable challenge for interpreting the measurement results by pathologists who have limited familiarity with polarization images. One feasible approach is to combine Mueller matrix polarimetric imaging with virtual staining techniques to generate standardized stained images, inheriting the advantages of information-abundant Mueller matrix polarimetric imaging. In this study, we develop a model using unpaired Mueller matrix polarimetric images and bright-field images for generating standard hematoxylin and eosin (H&E) stained tissue images. Compared with the existing polarization virtual staining techniques primarily based on the model training with paired images, the proposed Cycle-Consistent Generative Adversarial Networks (CycleGAN) based model simplifies data acquisition and data preprocessing to a great extent. The outcomes demonstrate the feasibility of training CycleGAN with unpaired polarization images and their corresponding bright-field images as a viable approach, which provides an intuitive manner for pathologists for future polarization assisted digital pathology.

NO. 34

Polarization feature fusion and calculation of birefringence dynamics in complex anisotropic media

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ABSTRACT: As a complex anisotropic medium, the variation in birefringence within biological tissues is closely associated with a myriad of physiological behaviors and phenomena. In this Letter, to explore and present an optimized solution from a methodological perspective, we propose a polarization feature fusion method and corresponding polarimetric parameters based on backscattering Mueller matrix (MM) polarimetry, which exhibit exceptional characterization performance for capturing the birefringence dynamic variation process in complex anisotropic media. To begin with, employing the information extraction method of feature fusion, we combine and transform the polarization basis parameters (PBPs) from the Mueller matrix polar decomposition (MMPD) and Mueller matrix transformation (MMT) methods. This enables us to derive fused polarization feature parameters (PFPs), which are characterized by explicit expressions. Subsequently, for the PBPs and the fused PFPs, Monte Carlo simulation is conducted from the birefringence direction and modulus variations in two dimensions. Leveraging mathematical modeling and linear transformations, we investigate and abstract the corresponding response patterns. Finally, experimental validation demonstrates that the proposed polarization feature fusion method and corresponding polarimetric parameters exhibit superior adaptability and interpretability in characterizing the complexity of the dynamic process. The findings presented in this Letter not only provide new methodological insights for information extraction and characterization calculation in the field of computational polarized optical imaging, but also highlight great application potential in the field of biomedical research.

NO. 35

Features and strategies of complex spatial illuminations on backscattering Mueller matrix

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ABSTRACT: Non-collinear backscatter Mueller matrix (MM) measurement is promising for disease diagnosis, while the MM imaging aberrations induced by uneven biological tissue surfaces should not be ignored. In this study, we quantitatively analyzed the aberrations on MM elements at different spatial illumination angles based on the DoFP camera backward MM measurement. We found that the obliquely incident and normal detection measurement scheme caused a significant increase in M12, M13, while in the normal incident and oblique detection measurement scheme, increasing angle caused a significant increase in M21, M31. Furtherly, we found that in the scheme of oblique incidence and oblique detection angle, there is a recovery effect on the aberration of polarization parameters caused by large spatial illumination angles, such as linear retardance and anisotropy. Based on methods such as regression fitting, we found a linear relationship between the cosine value of the oblique detection angle and the degree of imaging deformation. The results presented in this study suggest that backscatter polarization imaging needs to pay attention to the effect of polarization aberration and imaging deformation caused by the spatial illumination angles, to promote the development of backward polarization diagnosis.

NO. 36

Comparative learning based mitochondrial morphology analysis for drug screening

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ABSTRACT: Mitochondria are the core of cellular metabolism, and highly dynamic mitochondrial morphology is closely related to cellular energy metabolism. The changes of mitochondrial morphology are associated with numerous pathological states, including aging, neurodegenerative diseases, and metabolic diseases. By utilizing the implicit information of mitochondrial morphology, it is possible to monitor the physiological and pathological status of cells, making low-cost and high-throughput drug screening based on mitochondrial images possible. However, in order to comprehensively analyze mitochondrial morphology, using 3D images is necessary, which are time-consuming and also occupy more storage space. Mitochondrial morphology analysis mostly uses pixel-based methods, which are suitable for regular spatial structures. Graph-based methods are better at analyzing irregular and complex network structures, like mitochondria. To improve these inadequacies, a new comparative learning based mitochondrial morphology analysis model with graph neural networks is proposed for drug screening. This model combines convolutional neural networks and graph neural networks, extracts latent features from 3D mitochondrial microscopy images, and uses contrastive learning for training. Down-sampling original 3D images is applied to construct positive samples for contrastive learning. The model can learn consistent feature representations between original images and down-sampled images. As shorter scanning time cost and smaller storage occupation, low resolution image-based mitochondrial morphology analysis for drug screening is available and useful.

Key Words: Comparative learning, Mitochondrial morphology, Drug screening, Graph neural network, 3D Image processing

NO.37

Analysis of the influence on polarization characteristics of fibrous structures caused by staining using multispectral Mueller matrix microscopy

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ABSTRACT: Stained sections of biological tissue are standard samples archived in hospital for clinical pathological diagnosis, while the potential impact of dyes on polarization characteristics should not be overlooked. Hematoxylin and eosin are the most common dyes clinically. In this study, we quantitatively analyze the influence of the staining mechanism and absorption spectrums of hematoxylin and eosin dyes on diattenuation and linear retardation of fibrous structures based on the multispectral Mueller matrix microscopy. Furtherly, we obtain wavelength-dependent curves of MMPD_D and MMPD_δ for visualizing the variation trend. We find significant enhancement in the diattenuation of fibrous structures under the high absorption coefficient of dyes corresponding to the wavelength range. In addition, it is proven that varying dyes enhance the linear retardation of fibrous structures to different extent. Based on the statistical analysis results, fibrous tissue stained by eosin can provide more abundant structural information on diattenuation and linear retardation at appropriate wavelengths. The findings presented in this study suggest absorption spectrums of influence of dyes and incident wavelength should be considered on polarization microscopy imaging, promoting the development of polarization pathological diagnosis.

NO. 38

An ice-inhibiting and photothermal composite cryoprotectant for monolayer cell cryopreservation

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ABSTRACT: Cryopreservation technology is the most widely used way to preserve biological samples for a long time, which plays an irreplaceable role in the fields of food security, biodiversity, reproduction and health. As the most common pollinator in the natural environment, bees play a key role in maintaining the balance and stability of ecosystems and protecting biodiversity. It is estimated that more than 70% of the crops and wild plants depend on the pollination services of bees in the world. Bee larvae are a critical period of bee development, during which bee epigenetic modification changes are intensified and bees become more sensitive to changes in the external environment. In this paper, a petri dish was used as a cryopreservation container. From the perspectives of ice suppression and photothermal, a composite material of polyvinyl alcohol (PVA) and polypyrrole (PPy), PPy@PVA, was designed as a cryopreservation agent for honeybee larvae. The real-time, non-destructive and high-throughput monitoring and analysis of honeybee larvae during cryopreservation were realized by photoacoustic and photothermal imaging techniques. A cryopreservation method combining low biotoxicity, rapid heating rate and strong ice suppression performance was proposed and a corresponding cryopreservation effect evaluation system was established.

NO.39

Integrated Simulation of RNA Motion Systems for Realistic Imaging

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ABSTRACT: RNA localization within cells is fundamental to understanding gene expression and cellular processes. Precise tracking of RNA dynamics is crucial for unraveling the intricate mechanisms that govern cellular functions. Traditional microscopy techniques face challenges in accurately capturing RNA dynamics due to motion artifacts induced by exposure time and rolling shutter modes, hindering the precise localization of RNA molecules within live cells. This study aims to address challenges posed by motion artifacts in the context of intracellular RNA imaging, focusing on developing a foundation for accurate RNA localization in microscopy images. Here, we utilized Python to generate particles undergoing random motion in three-dimensional space, adhering to a Gaussian diffusion pattern. Concurrently, a plane moving along the Z-axis was generated to emulate the scanning plane of a camera. Leveraging Gaussian functions, the vertical distance from particles to the scanning plane was calculated, determining the intensity percentage of the particle's projection onto the scanning plane. This intensity percentage correlates with the opacity of the particle's projected intensities, with higher percentages resulting in stronger intensities. Particles beyond a predefined threshold distance were considered uncaptured by the camera, resulting in a percentage of 0 and a blank particle projection. Building upon this foundational setup, we introduced a simulated scanning line moving along the x-axis to traverse the scanning plane, mimicking the rolling shutter of a CMOS camera. By configuring parameters such as exposure time and particle velocity, we dynamically observed the simulated particles' actual positions and their projections on the scanning plane, encompassing motion artifacts. This comprehensive simulation provides insights into the challenges faced in realistically capturing the motion of RNA systems, aiding in the understanding and mitigating artifacts that may occur during experimental imaging of RNA dynamics. In the broader context of cell biology and molecular imaging, addressing motion artifacts in live-cell microscopy through deep learning methodologies holds promise for advancing our understanding of various cellular processes.

Key Words: RNA localization, Intracellular RNA dynamics, Live-cell imaging, Motion artifacts

NO.40

Ionic, compliant, dry and self-healing electrodes adhesive to skin for epidermal electrophysiology and human-machine-interaction

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ABSTRACT: Flexible ionic conductive electrodes play a crucial role in skin-surface electronic devices, serving as a fundamental component for the transmission of electrical signals in applications such as continuous health monitoring and efficient human-machine interactions. In this work, we introduce an innovative ionic, compliant, dry, and self-healing electrode (CEAB) that leverages deep eutectic solvents (DESs) and zwitterionic ionic conductors. Comprising Choline Chloride (ChCl) and Ethylene Glycol (EG) as the DES, betaine as the zwitterionic network, and crosslinked acrylic acid (AA) as the conductive framework, the CEAB electrode demonstrates remarkable attributes, including high conductivity, reduced noise levels, and the capability to consistently collect epidermal biopotential signals (e.g., ECG, sEMG, EEG) during dynamic detection. Notably, the CEAB electrode exhibits promising potential in clinical applications by effectively distinguishing aberrant EEG signals associated with depressive patients. Through the integration of this electrode with digital processing and advanced algorithms, real-time control of artificial limbs based on sEMG signals is achieved, highlighting its capacity to significantly enhance human-machine interaction.

创新创业口头报告
Oral Presentation of Innovation and Entrepreneurship

NO.1

项目名称 猴痘病毒 CRISPR/Cas12a 化学发光检测试剂盒的研制及手持式智能手机化学发光仪的开发

项目简介 现行检测猴痘病毒（Mpox virus，MPXV）的方法主要有实时荧光聚合酶链式反应（qPCR），酶联免疫吸附测定（ELISA），病毒分离培养等。这些基于实验室的方法具有灵敏准确的优势，但是因其存在耗时长，技术要求高，需要专业仪器设备等原因，难以满足现场快速检测的要求。因此，本研究拟基于 CRISPR/Cas12a 化学发光生物传感体系，研制猴痘病毒简单、灵敏、特异、价格低廉的检测试剂盒，以实现对猴痘病毒的快速准确鉴别，适合家庭、小型医院和社区诊所等地区使用，为病毒快速检测提供新的思路。同时，结合移动智能手机，开发配套的手持式智能手机化学发光仪，进行成像和分析，实现进样出结果检测，方便现场使用。

团队介绍 陈辉 清华大学深圳国际研究生院化学 2021 级博士 研究方向为分子诊断方法的开发及临床应用，在本领域发表 SCI 文章 6 篇，其中 JCR 一区文章 3 篇，申报发明专利 1 项。其长期从事现场检测技术相关研究，有着丰富的产品研发经验，本团队中主要负责产品理论设计和实验研究以及团队的统筹工作。

冯颖 清华大学深圳国际研究生院 OPEN FIESTA 精准医学与公共健康 2022 级硕士 研究方向为蛋白质工程方法和分子工具的开发。近年来发表 SCI 文章 2 篇。在本团队中负责产品的临床研究、产业转化以及生产线的搭建。

李沅恒 清华大学深圳国际研究生院深生硕制药工程 2023 级硕士研究方向为化学生物学新技术的开发，在本团队中负责产品工艺优化和后续产品研发。

滕卉景 清华大学深圳国际研究生院深生硕制药工程 2023 级硕士研究方向为体外诊断试剂和仪器设备的应用，在本团队中负责产品市场推广、销售对接、产品的市场调查以及网络平台搭建。同时协助产品的生产和质量控制保障，以及产品包装设计注册事务材料整理。

本团队由在读博士 1 名，硕士 3 名组成。团队成员的研究领域包括分析化学、分子生物学、生物信息学、临床应用等，在前期已完成的相关的项目中积累了一定的经验，并在在国际学术期刊上发表了多篇相关的学术论文。

NO.2

项目名称 一款高通量、高特异性的原代肿瘤细胞药效筛选平台与癌症早筛方法设计

项目简介 现行检测猴痘病毒（Mpox virus，MPXV）的方法主要有实时荧光聚合酶链式反应（qPCR），酶联免疫吸附测定（ELISA），病毒分离培养等。这些基于实验室的方法具有灵敏准确的优势，但是因其存在耗时长，技术要求高，需要专业仪器设备等原因，难以满足现场快速检测的要求。因此，本研究拟基于 CRISPR/Cas12a 化学发光生物传感体系，研制猴痘病毒简单、灵敏、特异、价格低廉的检测试剂盒，以实现对猴痘病毒的快速准确鉴别，适合家庭、小型医院和社区诊所等地区使用，为病毒快速检测提供新的思路。同时，结合移动智能手机，开发配套的手持式智能手机化学发光仪，进行成像和分析，实现进样出结果检测，方便现场使用。

传统的药物研发和治疗策略在面对不同患者的差异性时面临着一系列的挑战。传统的动物模型和细胞模型往往无法真实反映患者的生物学特征，导致药物研发效率低下，临床治疗效果不尽如人意。

随着个性化医疗理念的兴起，寻找更具特异性的药物治疗方案成为亟待解决的问题。而原代肿瘤细胞作为患者个体化信息的携带者，具有更接近患者真实生物学特征的优势。因此，我们着手建立高通量、高特异性的原代肿瘤细胞药效筛选平台，以满足个体化治疗的需求，加速新药研发与临床精准用药的过程。

我们的项目致力于建立一种高通量、高特异性的原代肿瘤细胞药效筛选平台。通过对不同患者的药物药效进行预判，在短时间内获取具有临床意义的药效学实验数据，将为医学领域的研究和实践带来创新的可能性，促进个性化医疗的推广和发展。

团队介绍 项目申请人一直专注于肿瘤研究，擅长恶性肿瘤的精准治疗，对分子靶向治疗药物研究、肿瘤代谢等方面的研究工作。申请人在恶性肿瘤的分子生物学和临床转化研究等领域积累了良好的研究基础与丰富的研究经验。

本课题组的核心科学家新西兰皇家科学院院士 Peter E. Lobie 教授与 Vijay Pandey 副教授在肿瘤学以及开发新颖的疗法和生物标记物方面拥有丰富的经验。致力于研究癌症靶向治疗，特别是在肿瘤相关生长因子的致癌机制中做出了开创性研究。

本课题组研究人员还包括在癌症研究领域拥有丰富的经验 3 名助理研究员。此外，我们还有合作的本地三甲医院的临床医生协助我们管理在所需的各种基于临床患者的数据及来自疾病模型诊断方面的顾问专家协助利用辅助诊断方法来完成本课题的研究目标。同样，本课题组还有生物信息学专家教授及免疫学专家为此课题提供所需的支持。

NO.3

项目名称 健康之心，工程之眼-一款辅助视力障碍者的智能感知脑机眼镜

项目简介 在现代社会中，虽然科技不断进展，但视障人群的比例却不断上升，这可能与不当的生活习惯、延长的人类寿命、青少年时期的过度用眼等因素有关。在本项目中，我们将介绍一类概念产品，该产品通过利用多模态、电信号-视觉信号转换、大语言模型、图像识别算法等关键技术，实现了盲人从看不见，到“看”见世界的转换。

除了技术上的优势，我们在成本方面也具有优势，采用国产平替级芯片以及自有的算法，有效降低硬件和软件成本；此外，由于直接在大脑视觉皮层给信号，有效解决视网膜、视神经通路、视觉皮层这三类问题导致的视障。

团队介绍 **黄逸轩** 深生化硕 23 级硕士，负责产品的统筹工作。

张瑞豪 深生化硕 23 级硕士，负责市场调研和行业发展分析。

丁　晗 深生化硕 23 级硕士，负责产品功能及结构的宣传介绍。

邱　蔚 深生化硕 23 级硕士，负责残障人士各类辅助产品的调研。

邹长宏 深生化硕 22 级硕士，负责技术调研及产品核心竞争力。

吕柄学 深生医硕 23 级硕士，负责产品的原理分析及可行性研究。

刘佳乐 深生化硕 23 级硕士，负责产品的销售、宣传及商业运作。

团队成员来自清华大学国际研究生院 IBHE 的不同专业，包含生医以及生化的不同专业人才，从事的研究背景包括计算机视觉、湿实验、生物算法等不同研究方向，提出的“健康之心，工程之眼”产品，将通过融合多项关键技术，实现残障人士“看世界“的目标，符合联合国可持续发展目标 8：”体面工作与经济增长“，助力中国大健康行业发展。

NO.4

项目名称 “奕心飞扬”青少年心理早筛系统

项目简介 该青少年心理健康机器人集成自研的多模态心理分析模型，通过提供的游戏环节和问答环节，在测试者无防备的情况下，产品通过传感器结合各类检测组件，实现人脸、视频、音频以及其他生理指标的采集，例如心率、心率变异性、血氧指标、眼球转动、微表情、血压变化等。通过一台机器实现对被试者四个模态数据的同时检出并融合分析出结果。采集真实的生理指标、语音、文本及视频信息，并通过人工智能算法实现对测试者心理健康状况的评估。

团队介绍 本项目在秦培武老师的指导下开展，项目已于去年参与医药健康工程杯，并取得特等奖，由同实验室的杜知城同学负责前期模型开发，由陈正林博士后与李方博士后提供技术与数据支持，取得了较好的实验成果，目前交由同实验室具备深度学习学术成果背景以及创业经验意愿的商业研发运营团队进行落地，目前项目核心成员为：

彭博远同学（队长）接手模型开发，进行更多模态模型融合研究以及总体运营推广

陈嘉驹同学（队员），对接医院进行数据采集以及使用反馈，并负责整体机器人后端开发

彭翠仪同学（队员），负责产品包装，对接产品前端开发，以及宣传推广工作。

NO.5

项目名称 多功能面部皮肤分析仪

项目简介 皮肤是人体最大的器官，是抵御病原生物和外来物质入侵的物理屏障，也是一个生态系统，拥有微生物环境，皮肤组织的结构形式、生理特征以及疾病控制与人体的正常活动与健康生存关系重大。因此，研究皮肤的组织结构，并发展出合适的手段以对皮肤相关生理参数进行测量，表达出皮肤的状态，辅助后续的诊疗工作是十分必要的。我们团队提出的产品为多功能面部皮肤分析仪，利用白光、偏振光、紫外光等实现对受试者进行多角度面部皮肤无创测量，生成一系列高分辨率图像，并定量地判断患者的整体皮肤状况，如色斑、皱纹、纹理、毛孔、紫外线斑、褐斑、红区和卟啉，提供了新的测量方法以指导护肤品和治疗方案的选择。

团队介绍

石雨竹 清华大学深圳国际研究生院深生医硕 22 级硕士（队长）
樊嘉豪 清华大学深圳国际研究生院深生医硕 22 级硕士（队员）
郝　睿 清华大学深圳国际研究生院深生医硕 22 级硕士（队员）
张钰新 清华大学深圳国际研究生院深生医硕 21 级硕士（队员）
邓凯莎 清华大学深圳国际研究生院深生医硕 23 级硕士（队员）
焦　炜 清华大学深圳国际研究生院深生医硕 23 级硕士（队员）

团队成员来自于清华大学生物医学工程专业，从事偏振光学在临床应用领域的研究。秉持推动偏振光学在皮肤诊断领域的应用，为用户提供一款高质量高性价比的皮肤检测设备，同时让中国的偏光技术获得世界认可的使命。我们希望通过不懈努力，能够在未来成为一家优秀的民族，全球先进的偏光医疗器械团队。

NO.6

项目名称 ASAP 超声颈部按摩仪

项目简介 ASAP 颈部按摩仪是一款带有个性化健康监测功能的颈部按摩仪。它可以在按摩颈部的同时，通过内部的超声装置实时监测血液流速和血管壁厚度、质地变化，尽早检出可能形成的粥样斑块，从而预警和规避脑梗、心梗等风险，守护用户的健康安全。此外还能通过与手机连接，将这些数据同步到手机上进行统计和分析，从而起到及时发现身体健康问题的作用。

团队介绍 **吴宇宽**（队长）：制药工程专业硕士二年级，研究方向为可穿戴生物标志物传感器，负责项目的整体规划及传感器开发。

于泽（队员）：制药工程专业硕士二年级，研究方向为生物活性物质应用于心脑血管疾病的防治，负责市场调研、竞争分析和产品营销策略的制定。

邓玉菡（队员）：制药工程专业硕士二年级，北京大学临床医学专业本科毕业，负责项目的医学基础理论支撑（病理学基础）。

凌天祎（队员）：生物医学工程专业硕士二年级，研究方向为基于柔性可拉伸应变传感器的穿戴式人机交互系统，负责项目的信号处理、传输及 APP 界面开发。

NO.7

项目名称 病理切片全流程数字化平台

项目简介 病理切片全流程数字化平台致力于解决病理科医生培训不足、染色切片信息浪费及数字化标准化的问题。

我们提供一个云端平台，医生可将染色切片上传，标注像素级别的可疑致病区域，注明患者的病症的信息。平台设立实时同行评审论坛，医生可将有疑问或疑难的病理切片分享至社区，不同科室的医生可在专业模块中进行深入讨论，促进互动与解答。将高质量病理切片及其解释移至学习库，医生可据此学习参考。引入评价标准，如打分，确保入库的切片质量。借助学习库积累的大量高质量病理切片，我们计划训练大模型，提高医生标注效率，为医学 AI 的发展提供更丰富的数据集。

通过平台，我们目标促进医学知识共享，提升病理学培训质量。

团队介绍 **徐敏惠**（队长）清华大学深圳国际研究生院（生物组织信息提取方向，负责 ROI 标注开发）；

吕炯颖（队员）清华大学深圳国际研究生院（偏振图像处理方向，负责图像评价算法）；

傅雨秋（队员）清华大学深圳国际研究生院（AI 病理图像处理方向，负责大模型开发）；

张新贤（队员）清华大学深圳国际研究生院（病理表征方法研究，负责平台开发）